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Microfungi associated with *Camellia sinensis*: A case study of leaf and shoot necrosis on Tea in Fujian, China

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Abstract

Camellia sinensis, commonly known as tea, is one of the most economically important crops in China. Shoot and leaf necrosis in tea is of considerable concern as it directly affects the quality and quantity of tea leaf harvest. In the present study, diseased leaves and shoots were collected from Fujian Province to identify the fungal species associated with the disease. In total 110 strains were isolated and they were identified by morphological characteristics and multi-locus phylogenetic approaches. Thirty–two species belonging to 13 genera and 11 families associated with shoot and leaf necrosis of tea were identified. Five new species; *Chaetomium camelliae*, *Diaporthe fujianensis*, *D. fusiformis*, *D. sinensis* and *Trichoderma camelliae* are introduced. In addition, nine novel host records are reported. These results indicate high species richness on tea leaves and shoots. In addition, a checklist for fungi associated with *C. sinensis* worldwide is provided. Information presented in this study provides new insights into fungi associated with leaf necrosis and shoot blight of *C. sinensis* in China. However, further studies are necessary to understand the pathogenic potential and biocontrol ability of the species identified in this study.

Keywords – Checklist – Five new species – Nine new host records – Tea pathogens

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Introduction

Tea is one of the oldest beverages in the world. The leaves and buds of *Camellia sinensis* (L.) Kuntze, either as black tea or green tea, play an important role in traditional cultures especially in Asia and Europe (Lu et al. 2016). Tea is popular due to its medicinal properties and as a stimulant (Namita et al. 2012). *Camellia* comprises over 200 species (Sealy 1958) but *C. sinensis* is the most cultivated species of tea. *Camellia sinensis* is grown in tropical and subtropical climatic regions (Jayasinghe & Kumar 2019). *Camellia sinensis* is a perennial plant, belonging to *Theaceae* (Meegahakumbura et al. 2016). It requires specific agro–climatic conditions with temperature of 10ºC–30ºC, annual precipitation of >1250 mm, acidic soil, 0.50–10–degree slopes and elevations up to 2000m (Jayasinghe & Kumar 2019). These factors limit the world's tea production to certain countries and regions such as Far East Asia, Africa, Latin America and the Caribbean islands (Meegahakumbura et al. 2016). Tea is grown as mostly a monocrop in over 52 countries in the

world (Lu et al. 2016). China is the largest tea exporting country in the world and has been for centuries (FAOSTAT 2019). According to the FAOSTAT data, annual tea production in the world is nearly 2.9 million tons. The world's black tea production increased by 2.2% annually and green tea production increased by 7.5% annually during the last decade. China is the world's largest tea producer followed by India. In 2016, China accounted for 42.6% of world tea production, with an output of 2.44 million tonnes (FAOSTAT 2019). The main tea growing regions in China are Shandong, Jiangsu, Zhejiang, Fujian, Guangdong, Guangxi, Yunnan, Guizhou, Sichuan, Chongqiong, Shaanxi, Taiwan, Hainan, Tibet, Hubei, Hunan, Henan, Jiangxi, Anhui and Gansu (Boehm et al. 2016).

Camellia sinensis is affected by a number of diseases caused by bacteria, fungi, insects, nematodes and viruses. To increase the productivity and quality of tea, it is important to identify the pathogens associated with different parts of the plant. The most devastating diseases of tea are caused by fungi (Sarmah et al. 2016, Liu et al. 2019). Microfungi widely and commonly associated with tea diseases are *Colletotrichum* spp., *Exobasidium vexans* (blister blight), *Macrophoma theicola* (stem canker and twig dieback), *Pellicularia koleroga* (black blight, thread blight), *Pestalotiopsis* (brown blight), *Pseudopestalotiopsis theae* (grey blight) and *Tunstallia aculeate* (thorny stem blight) (Liu et al. 2017, Yang et al. 2018a, b). In China, over 100 fungal species have been identified as causal organisms of diseases on buds, leaves and shoots, which are the most economically important parts of the plant (Jayawardena et al. 2016b, Gao et al. 2016, Liu et al. 2016a, b, Li et al. 2019).

During the last few years there has been a significant improvement in the identification of new diseases and fungal species from tea plantations in China (Jayawardena et al. 2016b, Li et al. 2019). To develop effective control measures, early detection and correct species identification are essential. In the present study, we isolated fungi associated diseased leaves and shoots of *Camellia sinensis*. The objectives of this study were to (i) identify and characterise the isolates, (ii) provide detailed descriptions of fungi and (iii) provide a worldwide checklist of fungi associated with *Camellia* species. These results will provide new insights into knowledge on microfungi associated with tea in China.

Materials & Methods

Sampling and isolation

Field surveys were conducted during June 2015 in ten tea plantations in Zhangzhou County, Fujian Province, China. Samples were collected from diseased leaves and shoots of Purple Rose cultivar (Fig. 1). Symptomatic tissue samples were taken to the laboratory in zip–lock plastic bags containing wet sterilised tissues. Samples were photographed and relevant data were documented. Fungi were isolated by a tissue isolation method. Infected leaves or shoots were cut into small pieces comprising both disease and healthy tissues. Tissue samples were surface sterilised by dipping into 70% ethanol for 30 sec and then transferring to 10% NaOCl for 30 sec followed by three washes with sterilised distilled water. Once the samples were dried on sterilised filter paper, they were placed on potato dextrose agar (PDA) plates supplemented with ampicillin (100 µg/mL) and incubated at 25°C. Pure cultures were obtained following 3–4 times of hypal tip isolation. Cultures were deposited in the Culture Collection of Institute of Plant and Environmental Protection, Beijing Academy of Agriculture and Forestry Sciences (JZB).

DNA extraction, PCR amplification and sequence assembly

Approximately 10 mg of aerial mycelium was scraped from five to seven days old cultures grown on PDA. Total genomic DNA was extracted using the DNeasy Plant Mini Kit (QIAGEN GmbH, QIAGEN Strasse 1, 40742 Hilden, Germany). The PCR mixtures for all gene regions were as follows: 25 µl total volumes consisted of 0.3 µl of TaKaRa *Ex–Taq* DNA polymerase, 2.5 µl of 10 × *Ex–Taq* DNA polymerase buffer, 3.0 µl of dNTPs, 2 µl of genomic DNA, 1 µl of each primer and 15.2 ddH_2O. Polymerase Chain Reactions (PCR) were conducted in a Bio–Rad C1000 thermal

cycler (Germany). The thermal cycler conditions for each locus are given in Table 1. The PCR products were visualised on a 1% agarose gel stained with ethidium bromide under UV light using a Gel Doc^{TM} XR Molecular Imager (Bio–Rad, USA). Positive amplicons were sequenced by Beijing Biomed Gene Technology Co LTD. Resulting sequence chromatograms were checked with BioEdit v.5 (Hall 1999) to confirm sequence quality. At first, the internal transcribed spacer (ITS) region was sequenced and the resulting sequences were compared with those in GenBank using the MegaBLAST tool (https://blast.ncbi.nlm.nih.gov/Blast.cgi). Depending on BLAST identification and morphological characteristics for each isolate, other relevant gene regions were sequenced (Table 2). Consensus sequences were obtained using DNAStar v. 5.1 (DNASTAR, Inc.).

Figure 1 – *Camellia sinensis* plantation and field symptoms on Purple Rose cultivar bushes at different ages. a, b Collection site of the study Zhangzhou, Fujian Province, China. c, d Healthy young tea buds. e Healthy shrub. f–h Diseased shrubs (sample collected).

Table 1 Gene regions and primer pairs used in the present study

Locus	Primers (Forward and Reverse)	PCR amplification	Reference
ACT	ACT–512F & ACT–783R	95°C: 5 min, (95°C: 30 s, 55°C: 50 s,72°C: 1 min) ×39 cycles 72°C: 10 min	Carbone & Kohn (1999)
GAPDH	GDF & GDR	95°C 3 min (95°C 1 min 60°C 30 s 72°C 45 s) ×34 cycles 72°C: 10 min	Templeton et al. (1992)
ITS	ITS4 & ITS5	94°C: 3 min, (94°C: 30 s, 58°C: 30 s, 72°C: 1 min) × 32 cycles; 72°C: 10 min	White et al. (1990)
LSU	LR0R & LR5	94°C: 5 min, (94°C: 1 min, 53°C: 50 s, 72°C: 1 min) × 37 cycles, 72°C: 10 min	Vilgalys & Hester (1990)
rpb2	fRPB2–5F & fRPB2–7cR	95°C: 5 min, (95°C: 15 s, 56°C: 50 s, 72°C: 2 min) × 37 cycles, 72°C: 10 min	Liu et al. (1999)
SSU	NS1 & NS4	94°C: 4 min, (94°C: 50 s, 56°C: 1 min, 72°C: 1 min,72°C: 10 min) × 37 cycles	White et al. (1990)
tef1	EF1728F & EF1986R,	(95°C: 5 min, 95°C: 30 s, 58°C: 50 s, 72°C: 1 min) × 40 cycles, 72°C: 10 min	Carbone & Kohn (1999)
tub2	Bt2a & Bt2b	95°C: 5 min, (95°C: 30 s, 58°C: 50 s, 72°C: 1 min) × 40 cycles; 72°C: 10 min	Glass & Donaldson (1995)
	BT2Fw & BT4Rd	95°C: 5 min, (94°C: 30 s, 55°C: 50 s, 72°C: 1 min) × 40 cycles; 72°C: 7 min	Woudenberg et al. (2009)

Phylogenetic analyses

Reference sequences were obtained from GenBank for each genus. The sequences obtained in this study were aligned with sequences downloaded from GenBank using MAFFT (Katoh & Toh 2010) and manually adjusted using BioEdit v.5 (Hall 1999) wherever necessary. Ambiguous regions in the alignment were excluded from further analyses, and gaps were treated as missing data. Phylogenetic relationships were inferred using maximum parsimony (MP) implemented in PAUP (v4.0) (Swofford & Sullivan 2003), maximum likelihood (ML) in RAxML (Silvestro & Michalak 2016) and Bayesian posterior probability analysis (BYPP) in MrBayes (v3.0b4*)* (Ronquist & Huelsenbeck 2003).

In PAUP, the stability of the trees was evaluated by 1000 bootstrap replications. Branches of zero length were collapsed and all multiple most parsimonious trees were saved. Parameters, including tree–length (TL), consistency index (CI), retention index (RI), relative consistency index (RC) and homoplasy index (HI) were calculated. Differences between the trees inferred under different optimality criteria were evaluated using Kishino–Hasegawa tests (KHT) (Kishino & Hasegawa 1989).

The evolutionary models for Bayesian and ML analyses were selected using MrModeltest v. 2.3 (Nylander 2004). The GTR + I + G model of evolution with 1000 non–parametric bootstrapping iterations was used for the ML analyses. For the BYPP, different evolutionary models were used in response to the gene regions and gene combinations. The ML analyses were done with RAxML–HPC2 on XSEDE (8.2.8) (Stamatakis et al. 2008, Stamatakis 2014) in the CIPRES Science Gateway platform (Miller et al. 2010). For each phytogenetic tree, 1000 nonparametric bootstrapping iterations were used.

In Bayesian posterior probability analysis, posterior probabilities (PPs) were determined by Markov chain Monte Carlo sampling (BMCMC). Six simultaneous Markov chains were run for 10^6 generations, sampling the trees at every 100th generation. From the 10,000 trees obtained, the first 2,000 representing the burn–in phase were discarded. The remaining 8000 trees were used to calculate PPs in a majority rule consensus tree (Ronquist & Huelsenbeck 2003).

Taxonomic novelties were submitted to the Faces of Fungi database (Jayasiri et al. 2015) and Index Fungorum (2020). Sequences generated in this study were deposited in GenBank (Table 2). Species descriptions, phylogenetic results and notes for these identified taxa are presented under the

relevant family and genus. Classes, orders, families and genera were treated according to Wijayawardene et al. (2020).

Table 2 Genbank accession numbers of taxa isolated in the present study

No.	Species	ID	ITS	LSU	*tub2*	*tef1*	*rpb2*	SSU	ACT	CAL	CHS	GAPDH
1	*B. dothidea*	JZB310190	MT497875	–	MT513138	MT513143	–	–	–	–	–	–
		JZB310191	MT497876	–	MT513139	MT513144	–	–	–	–	–	–
		JZB310192	MT497877	–	MT513140	MT513145	–	–	–	–	–	–
		JZB310193	MT497878	–	MT513141	MT513146	–	–	–	–	–	–
		JZB310194	MT497879	–	MT513142	MT513147	–	–	–	–	–	–
2	*E. layuense*	JZB380035	MT497880	MT497881	–	–	MT513137	–	–	–	–	–
3	*S. yingyisheniae*	JZB3270001	MT523022	MT523028	–	–	–	–	–	–	–	–
		JZB3270002	MT523023	MT523029	–	–	–	–	–	–	–	–
		JZB3270003	MT523024	MT523030	–	–	–	–	–	–	–	–
		JZB3270004	MT523025	MT523031	–	–	–	–	–	–	–	–
4	*D. biguttulata*	JZB320166	MW010210	–	MW055998	–	–	–	–	MW205204	–	–
5	*D. eucalyptorum*	JZB320153	MW010211	–	MW055999	MW205223	–	–	–	MW205205	–	–
6	*D. fuijianensis*	**JZB320149**	**MW010212**	**–**	**MW056008**	**MW205231**	**–**	**–**	**–**	**MW205212**	–	–
		JZB320150	MW010213	–	MW056009	MW205232	–	–	–	MW205213	–	–
		JZB320151	MW010214	–	MW056010	–	–	–	–	MW205214	–	–
		JZB320152	MW010215	–	MW056011	MW205233	–	–	–	MW205215	–	–
7	*D. fusiformis*	JZB320154	MW010216	–	MW056012	–	–	–	–	MW205216	–	–
		JZB320155	MW010217	–	MW056013	–	–	–	–	MW205217	–	–
		JZB320156	**MW010218**	**–**	**MW056014**	**MW205234**	**–**	**–**	**–**	**MW205218**	–	–
		JZB320157	MW010219	–	MW056015	–	–	–	–	MW205219	–	–
8		JZB320158	MW010220	–	–	–	–	–	–	–	–	–
		JZB320159	MW010221	–	MW056000	MW205224	–	–	–	–	–	–
9	*D. sackstonii*	JZB320165	MW010222	–	–	–	–	–	–	–	–	–
10	*D. sennae*	JZB320147	MW010223	–	MW056001	MW205225	–	–	–	MW205206	–	–
11	*D. sinensis*	JZB320167	MW010224	–	MW056016	MW205235	–	–	–	MW205220	–	–
		JZB320168	MW010225	–	MW056017	MW205236	–	–	–	MW205221	–	–
		JZB320169	MW010226	–	MW056018	MW205237	–	–	–	MW205222	–	–
12	*D. unshiuensis*	JZB320160	MW010227	–	MW056002	MW205226	–	–	–	–	–	–
		JZB320161	MW010228	–	MW056003	–	–	–	–	MW205207	–	–
		JZB320162	MW010229	–	MW056004	MW205227	–	–	–	MW205208	–	–
		JZB320163	MW010230	–	MW056005	MW205228	–	–	–	MW205209	–	–
		JZB320164	MW010231	–	MW056006	MW205229	–	–	–	MW205210	–	–
13	*D. viniferae*	JZB320148	MW010232	–	MW056007	MW205230	–	–	–	MW205211	–	–

Table 2 Continued.

No.	Species	ID	ITS	LSU	*tub2*	*tef1*	*rpb2*	SSU	ACT	CAL	CHS	GAPDH
14	*C. camelliae*	JZB330153	MW007830	–	MW013330		–	–	MW013328	–	–	–
15	*C. fructicola*	JZB330154	MW007831	–	MW013331	–	–	–	MW013329	–	–	–
16	*T. atroviride*	JZB3360001	MW008450	–	–	–	–	–	–	–	–	–
17	*T. camelliae*	**JZB3360002**	**MW008451**	–	–	–	–	–	–	–	–	–
		JZB3360003	MW008452	–	–	–	–	–	–	–	–	–
		JZB3360004	MW008453	–	–	–	–	–	–	–	–	–
		JZB3360005	MW008454	–	–	–	–	–	–	–	–	–
		JZB3360006	MW008455	–	–	–	–	–	–	–	–	–
18	*T. lixii*	JZB3360007	MW008456	–	–	–	–	–	–	–	–	–
		JZB3360008	MW008457				–	–	–	–	–	–
19	*F. asiaticum*	JZB3110018	–	–	–	MW056027	MW055992	–	–	–	–	–
		JZB3110019	–	–	–	MW056028	MW055993	–	–	–	–	–
		JZB3110020	–	–	–	MW056029	MW055994	–	–	–	–	–
		JZB3110021	–	–	–	MW056030	MW055995	–	–	–	–	–
		JZB3110022	–	–	–	MW056031	MW055996	–	–	–	–	–
20	*F. concentricum*	JZB3110010	–	–	–	MW056019	MW055984	–	–	–	–	–
		JZB3110011	–	–	–	MW056020	MW055985	–	–	–	–	–
		JZB3110012	–	–	–	MW056021	MW055986	–	–	–	–	–
		JZB3110013	–	–	–	MW056022	MW055987	–	–	–	–	–
		JZB3110014	–	–	–	MW056023	MW055988	–	–	–	–	–
21	*F. fijikuroi*	JZB3110016	–	–	–	MW056025	MW055990	–	–	–	–	–
		JZB3110017	–	–	–	MW056026	MW055991	–	–	–	–	–
22	*F. proliferatum*	JZB3110015	–	–	–	MW056024	MW055989	–	–	–	–	–
23	*Ch. camelliae*	**JZB3340001**	**MT535751**	**MT535749**	**MT535533**	**MT535535**	**MT535537**	–	–	–	–	–
		JZB3340002	MT535752	MT535750	MT535534	MT535536	MT535538	–	–	–	–	–
24	*A. jiangxiense*	JZB3260001	MT525316	–	MW034378	MW026028	–	–	–	–	–	–
25	*Ni. camelliae–sinensis*	JZB3230016	MT525317	–	MW034379	MW026029	–	–	–	–	–	–
26	*P. camelliae*	JZB340064	MT509821	–	MT535513	MW205238	–	–	–	–	–	–
		JZB340063	MT509822	–	MT535514	MW205239	–	–	–	–	–	–
27	*P. kenyana*	JZB340062	MT509823	–	MT535515	MW205240	–	–	–	–	–	–
		JZB340061	MT509824	–	MT535516	MW205241	–	–	–	–	–	–
28	*P. lushanensis*	JZB340059	MT509825	–	MT535517	MW205242	–	–	–	–	–	–
29	*P. rhodomyrtus*	JZBH340060	MT509826	–	MT535518	MW205243	–	–	–	–	–	–

Table 2 Continued.

No.	Species	ID	ITS	LSU	*tub2*	*tef1*	*rpb2*	SSU	ACT	CAL	CHS	GAPDH
30	*Ps. camelliae–sinensis*	JZB340040	MT509827	–	MT535519	MW034366	–	–	–	–	–	–
		JZB340041	MT509828	–	MT535520	MW034367	–	–	–	–	–	–
		JZB340042	MT509829	–	–	MW034368	–	–	–	–	–	–
		JZB340043	MT509830	–	–	–	–	–	–	–	–	–
		JZB340044	MT509831	–	MT535521	–	–	–	–	–	–	–
		JZB340045	MT509832	–	MT535522	–	–	–	–	–	–	–
		JZB340046	MT509833	–	MT535523	–	–	–	–	–	–	–
		JZB340047	MT509834	–	MT535524	MW034369	–	–	–	–	–	–
		JZB340048	MT509835	–	–	–	–	–	–	–	–	–
		JZB340049	MT509836	–	MT535525	MW034370	–	–	–	–	–	–
		JZB340050	MT509837	–	MT535526	MW034371	–	–	–	–	–	–
		JZB340051	MT509838	–	MT535527	MW034372	–	–	–	–	–	–
		JZB340052	MT509839	–	MT535528	–	–	–	–	–	–	–
		JZB340053	MT509840	–	–	–	–	–	–	–	–	–
		JZB340054	MT509841	–	MT535529	MW034373	–	–	–	–	–	–
31	*Ps. chinensis*	JZB340055	MT509842	–	MT535530	MW034374	–	–	–	–	–	–
		JZB340056	MT509843	–	MT535531	MW034375	–	–	–	–	–	–
		JZB340057	MT509844	–	–	MW034376	–	–	–	–	–	–
		JZB340058	MT509845	–	MT535532	MW034377	–	–	–	–	–	–
32	*Nemania diffusa*	JZB3370001	MT509575	–	–	–	MT512899	–	–	–	–	–
		JZB3370002	MT509576	–	–	–	MT512900	–	–	–	–	–
		JZB3370003	MT509577	–	–	–	MT512901	–	–	–	–	–

Ex–type cultures are bold. ITS: internal transcribed spacer regions 1 & 2 including 5.8S nrDNA gene; LSU: Large subunit nrDNA gene; *tef1*: Partial translation elongation factor 1–α; *tub2*: partial sequences of beta–tubulin; rpb2: RNA polymerase II gene; SSU: small subunit nrDNA gene; ACT: Partial actine; CAL: calmodulin; CHS: Chalcone synthase; GAPDH: Glyceraldehyde 3–phosphate dehydrogenase. (JZB: Culture Collection of Institute of Plant and Environmental Protection, Beijing Academy of Agriculture and Forestry Sciences. Type sequnces of newly generated taxa are **bold**.

Morphology and culture characteristics

Colony morphology and conidial characteristics were examined for each species isolated. Colony colours were recorded according to the colour charts of Rayner (1970) after five to seven days of growth on PDA at 25°C. Digital images of morphological structures mounted in water were taken using an Axio Imager Z2 photographic microscope (Carl Zeiss Microscopy, Oberkochen, Germany). Measurements were taken using ZEN PRO 2012 (Carl Zeiss Microscopy). For each isolate, conidial length and width were measured for 40 conidia and the mean values were calculated. In addition, conidial shape, colour and guttulation were recorded.

Checklist

The checklist was based on articles in refereed journals, Index to Saccardo's Sylloge Fungorum, Petrak's Lists, Index of Fungi, graduate student theses, books and web–based resources such as annual reports on tea and the USDA fungal database Fungus–Host Distributions database (https://nt.ars–grin.gov/fungaldatabases/fungushost/fungushost.cfm) (Accessed 10th June 2020). The mode of life, i.e. pathogen, endophyte or saprotroph, is listed. The checklist includes species names, family, life modes, disease name (if any), locality and references. The current name used is according to Index Fungorum (2020) and the classification follows Wijayawardene et al. (2020). Genera and species are listed in alphabetical order. In some cases, the host names given in the original citation were changed to be consistent with current taxonomy. In a few cases, neither the species cited nor a proper synonym was identified and the species name was used as originally cited.

Results

In this study, we identified 32 species belong to 11 fungal families. Species descriptions, phylogenetic results and notes for these identified taxa are presented under the relevant family and genus. Classes, orders, families and genera were treated according to Wijayawardene et al. (2020).

Dothideomycetes P.M. Kirk, P.F. Cannon, J.C. David & Stalpers ex C.L. Schoch, Spatafora, Crous & Shoemaker, Mycologia 98 (6): 1045 (2007)

For taxonomic treatments, we follow Hongsanan et al. (2020a, b).

Botryosphaeriales C.L. Schoch, Crous & Shoemaker, Mycologia 98 (6): 1050 (2007)

Notes – Six families; *Aplosporellaceae*, *Botryosphaeriaceae*, *Melanopsaceae*, *Phyllostictaceae*, *Planistromellaceae* and *Saccharataceae* are accepted in Botryosphaeriales. Taxonomic treatments follow Phillips et al. (2019) and Hongsanan et al. (2020b).

Botryosphaeriaceae Theiss. & Syd [as 'Botryosphaeriacae'], Annls mycol. 16(1/2): 16 (1918)

Notes – *Botryosphaeriaceae* species are endophytes, pathogens and saprobes on a wide range of hosts (Manawasinghe et al. 2016, Rashmi et al. 2019). They are well–known opportunists on many economically important crops (Chethana et al. 2016). Currently, more than 279 species and 22 genera are included with this family (Dissanayake et al. 2016, Phillips et al. 2013, 2019, Hongsanan et al. 2020b).

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

Botryosphaeria comprises 13 species based on both morphology and molecular data (Dissanayake et al. 2016, Jayawardena et al. 2019). In the present study, five isolates clustered in the main clade with *B. dothidea* type sequence. (ML and BYPP) (Fig. 2). Depending on morphology and sequence similarites we confirmed these five strains as *B. dothidea.*

Botryosphaeria dothidea (Moug.: Fr.) Ces. & De Not., Comm. Soc. crittog. Ital. 1 (fasc. 4): 212 (1863) Fig. 3

Index Fungorum: IF 183247; Facesoffungi number: FoF03512

Pathogenic or saprobic on *Camellia sinensis* leaves and shoots. Sexual morph: Not observed. Asexual morph: *Conidiomata* stromatic, *Conidiophores* hyaline, cylindrical, smooth. *Conidiogenous cells* 11.5–14 × 4–6.5 μm (x = 13 × 6 μm, n = 20), hyaline, sub–cylindrical. *Conidia* 18–40 × 5–10 μm ($\overline{x}$ = 24 × 7 μm, n = 20), hyaline, unicellular, narrowly fusiform, with a sub–truncate to bluntly rounded base, forming a septum before germination, smooth–walled with granular contents.

Culture characteristics – Colonies on PDA reaching 50 mm diam., after four days at 28°C. Initially, white becoming grey, moderately dense, margin smooth, olivaceous.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead leaves and shoots of *Camellia sinensis*, June 2015, H.L. Li (dried cultures JZBH310190–JZBH310194), and living cultures JZB310190–JZB31094.

Notes – The colony morphology of taxa isolated in this study are similar to typical strains of *B. dothidea* (Phillips et al. 2013). In the multilocus phylogenetic analysis, the five isolates from the present study clustered together with 56% ML bootstrap and less than 0.90 BYPP. Morphologically these taxa are similar to the type description of *B. dothidea* (Phillips et al. 2013). *Botryosphaeria dothidea* has a wide range of hosts and it is a well–known woody host–pathogen (Phillips et al. 2005, 2013, Dissanayake et al. 2016, Hyde et al. 2020a). *Botryosphaeria dothidea* had been reported to cause diseases on many different hosts in China (Manawasinghe et al. 2018). This species was first reported as shoot blight pathogen in Chinese tea plants in 2016 (Jayawardena et al. 2016b).

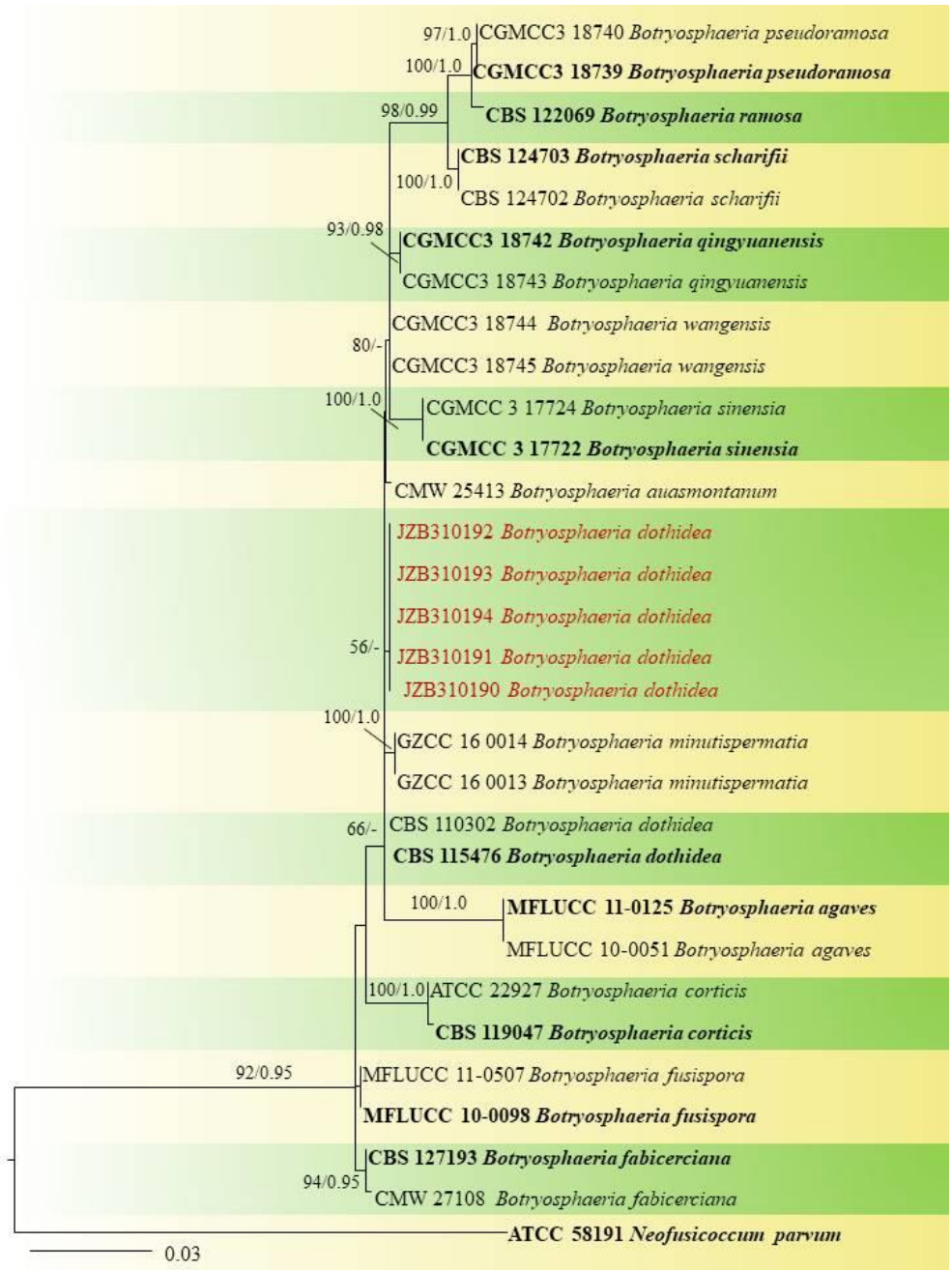

Figure 2 – The phylogenetic tree generated by ML analysis of combined ITS and translation elongation factor 1–alpha (*tef1*) sequence data of *Botryosphaeria* species. The phylogenetic tree is rooted with *Neofusicoccum parvum* (ATCC 58191). Tree topology of the ML analysis was similar

to the BYPP. The best scoring RAxML tree with a final likelihood value of –24349.980578 is presented. The matrix had 1172 distinct alignment patterns, with 9.91% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.251668, C = 0.245757, G = 0.259668, T = 0.242908; substitution rates AC = 1.353890, AG = 4.605576, AT = 1.059439, CG = 0.801610, CT = 9.121730, GT = 1.000000; gamma distribution shape parameter α = 0.944898. RAxML bootstrap support values ≥50% and Bayesian posterior probabilities ≥0.95 (BYPP) are given near the nodes. The scale bar indicates 0.02 changes per site. Ex–type/ex–epitype strains are in **bold** and isolates belong to this study are given in red.

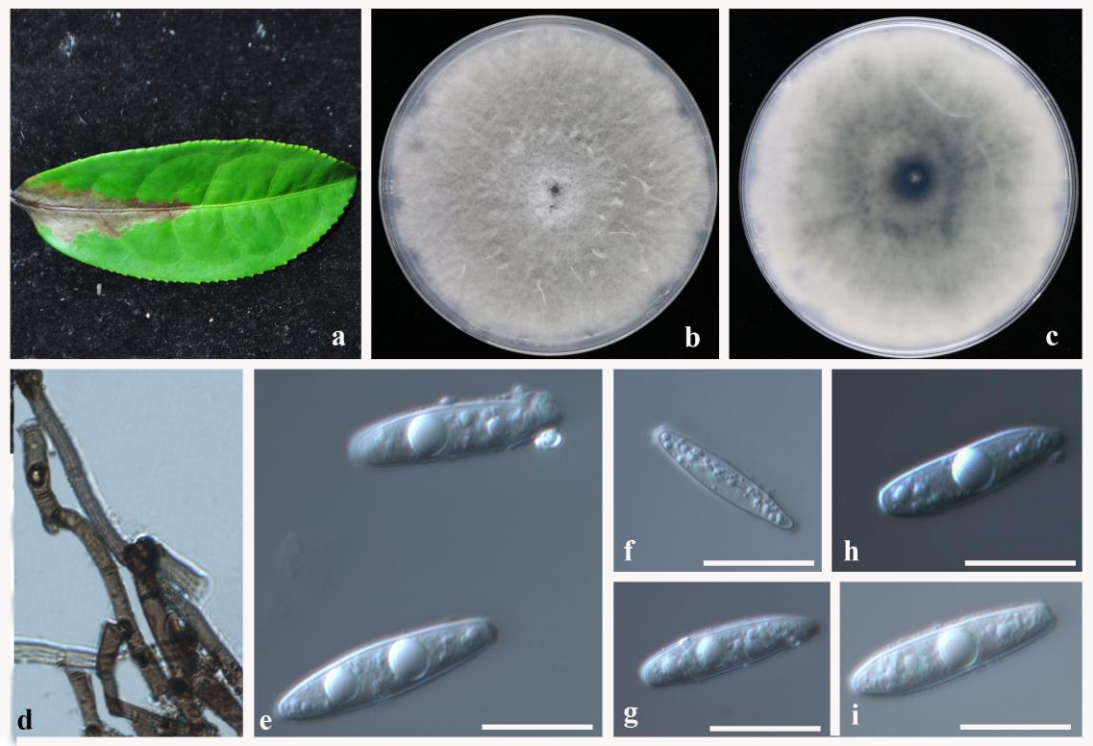

Figure 3 – *Botryosphaeria dothidea* (JZB310193) a Material examined. b Upper view of the colony on PDA after four days. c Reverse view of the colony on PDA after four days. d Mycelia. e–i Conidia. Scale bars: e–i = 20 µm.

Pleosporales Luttr. ex M.E. Barr, Prodromus to class Loculoascomycetes: 67 (1987)

Notes – Pleosporales is the largest order of Dothideomycetes (Liu et al. 2017). It comprises highly diverse taxa that are endophytes, epiphytes, parasites, lichenicolous, or saprobes in terrestrial or aquatic environments or even occur on animal dung (Zhang et al. 2009). For the taxonomic treatment of Pleosporales, we follow Kirk et al. (2008), Zhang et al. (2009) and Hongsanan et al. (2020a).

Didymellaceae Gruyter, Aveskamp & Verkley, Mycol. Res. 113(4): 516 (2009)

Notes – Zhang et al. (2009) included *Didymellaceae* in Pleosporales within the suborder Pleosporineae. The family *Didymellaceae* was established by de Gruyter et al. (2009). *Didymellaceae* includes economically important plant pathogens (Salam et al. 2011, de Gruyter et al. 2013) endophytes, as well as fungicolous and lichenicolous taxa (Aveskamp et al. 2010, Chen et al. 2015, Valenzuela-Lopez et al. 2018). Recent taxonomic treatments are given in Wanasinghe et al. (2018), Marin-Felix et al. (2019) and Hongsanan et al. (2020a).

Epicoccum Link., Mag. Gesell. naturf. Freunde, Berlin 7: 32 (1816) [1815]

Notes – *Epicoccum* is characterized by epicoccoid and sub–cylindrical conidia (Chen et al. 2015). Species belonging to this genus are ubiquitous (Chen et al. 2015). They have been reported

as common causal agents of leaf spot diseases in various hosts (Chen et al. 2015, Liu et al. 2019). The taxon isolated in the present study formed a clade together with *Epicoccum layuense* with 64% ML and 77% MP bootstrap values in the phylogenetic tree (Fig. 4).

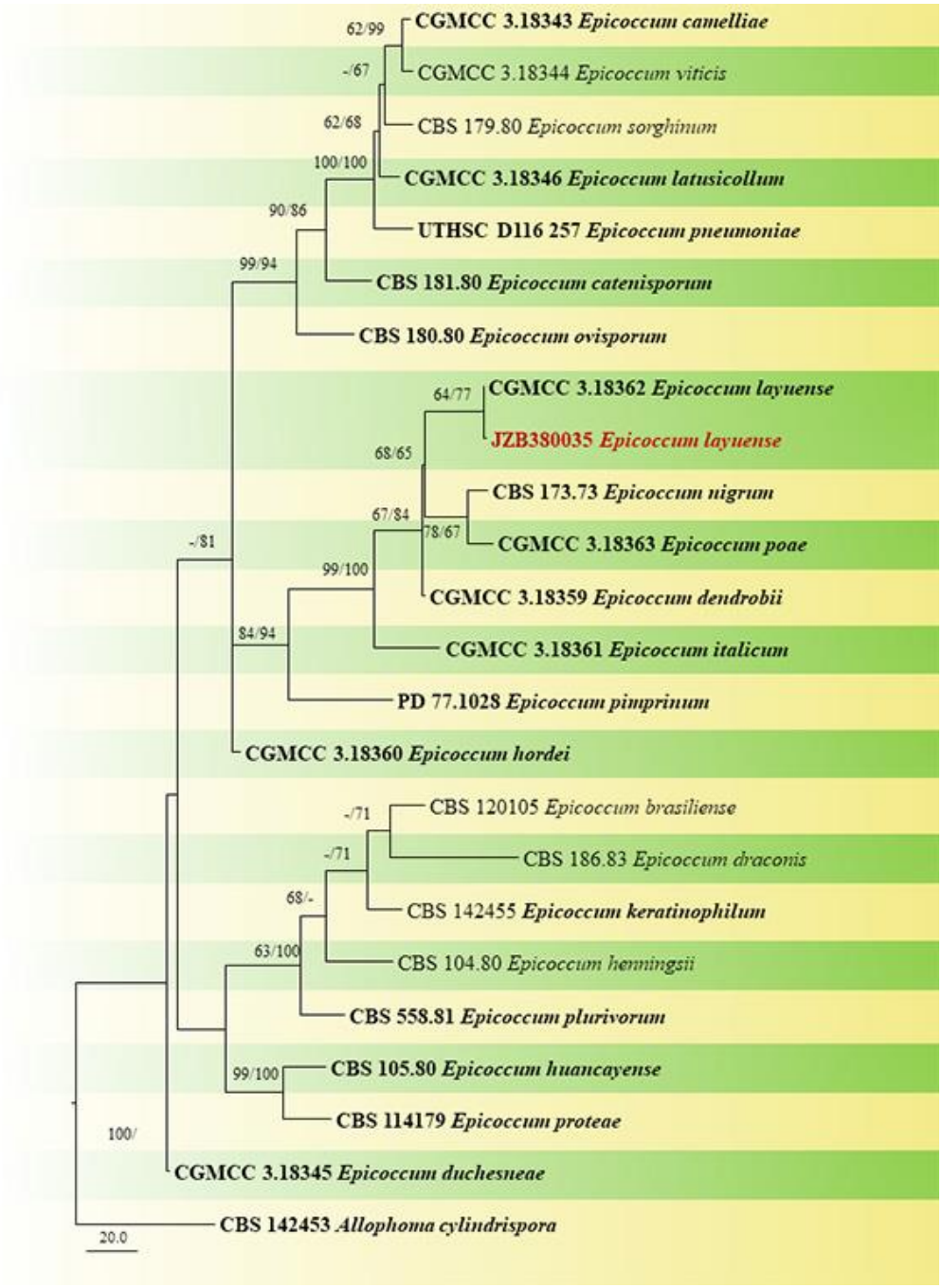

Figure 4 – Phylogenetic tree generated by ML analysis of combined LSU, ITS, and *rpb2* sequence data of *Epicoccum* species. The tree is rooted with *Allophoma cylindrispora* (CBS 142453). Tree topology of the ML analysis was similar to the MP. The best scoring RAxML tree with a final likelihood value of –4626.221244 is presented. The matrix had 298 distinct alignment patterns, with 1.09% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.252747, C = 0.210997, G = 0.301466, T = 0.234790; substitution rates AC = 1.405315, AG = 3.684928, AT = 2.423691, CG = 1.931133, CT = 14.809240, GT = 1.000000; gamma distribution shape parameter α = 0.269921. Maximum parsimony analysis of 1737 constant characters and 221 informative characters resulted in 738 equally most parsimonious tree of 462 steps (CI = 0.564, RI = 0.672, RC = 0.379, HI = 0.436). RAxML bootstrap support values ≥50% and MP bootstrap

support values ≥50% are shown near the nodes. The scale bar indicates 20.0 changes per site. Ex–type/ ex–epitype strains are in **bold** and taxon isolated in this study is in red.

Epicoccum layuense Qian Chen, Crous & L. Cai, in Chen et al., Stud. Mycol. 87: 145 (2017) Fig. 5

Index Fungorum: IF818963; Facesoffungi number: FoF09381

Pathogenic or saprobic on *Camellia sinensis* leaves. Sexual morph: Not observed. Asexual morph: *Hyphae* about 2.5 µm, septate, branched, conidiomata on PDA, aggregated, superficial, clavate, *Conidiomatal wall* pseudoparenchymatous, multi–layered, outer wall brown olivaceous. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells*, light brown, simple. *Conidia* 12–13 × 20–18 µm ($\bar{x}$ = 12 × 20 µm n = 30) µm diam, globose to subglobose, one basal cell, terminal, solitary, smooth, dark brown.

Culture characteristics – Colonies on PDA, 60 mm diam., after seven days, margin irregular, aerial mycelia floccose, bright yellow; reverse yellow to pale brown, with a brown concentric ring near the centre.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead leaves of *Camellia sinensis*, June 2015, H.L. Li (dried culture JZBH380035), and living cultures JZB380035.

Notes – The phylogenetic analysis of combined LSU, ITS and *rpb2* DNA data set placed this taxon with the *Epicoccum layuense* with 67% and 77% bootstrap support values. *Epicoccum layuense* (JZB380035) shares similar colony morphology and spore characters with the type description of *Epicoccum layuense* (Chen et al. 2015). A recent study conducted by Del Frari et al. (2019) has shown the potential of *Epicoccum layuense* as a biocontrol agent against grapevine trunk disease caused by *Phaeomoniella chlamydospora*, *Fomitiporia mediterranea*, and *Phaeoacremonium minimum*. This is the first report of *E. layuense* on *C. sinensis* (Farr & Rossman 2020).

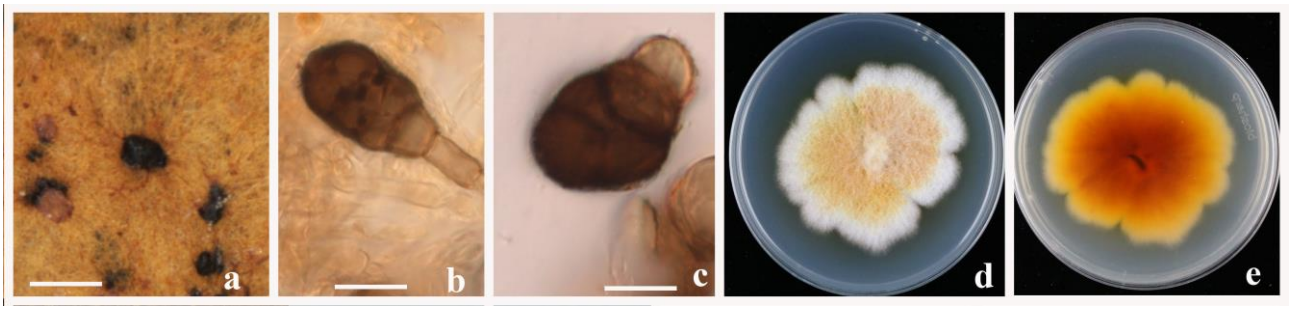

Figure 5 – *Epicoccum layuense* (JZB380035). a conidiomata on PDA. b Developing spore. c Conidium. d Upper view of a colony on PDA after seven days. e Reverse view of the colony on PDA after seven days. Scale bars: a = 100 µm, b–c = 10 µm.

Phaeosphaeriaceae M.E. Barr, Mycologia 71(5): 948 (1979)

Notes – *Phaeosphaeriaceae* consists of economically important plant pathogens (Phookamsak et al. 2014), endophytes or saprobes on plants. *Phaeosphaeriaceae* has undergone several revisions and species additions during the last years (Phookamsak et al. 2014). For the taxonomic treatment of *Phaeosphaeriaceae*, we follow Hongsanan et al. (2020a).

Setophoma Gruyter, Aveskamp & Verkley, in de Gruyter, Woudenberg, Aveskamp, Verkley, Groenewald & Crous, Mycologia 102(5): 1077 (2010)

Notes – *Setophoma* was introduced by de Gruyter et al. (2010) and is typified by *S. terrestris* (= *Phoma terrestris*). *Setophoma* species are characterised by setose pycnidia, phialidic conidiogenous cells and hyaline, ellipsoidal to subcylindrical, aseptate conidia (de Gruyter et al. 2010, Quaedvlieg et al. 2013). Species belonging to this genus are well–known pathogens on

economically important crops including tea (Liu et al. 2019). Four isolates belonging to *Setophoma* were isolated and identified here (Fig. 6).

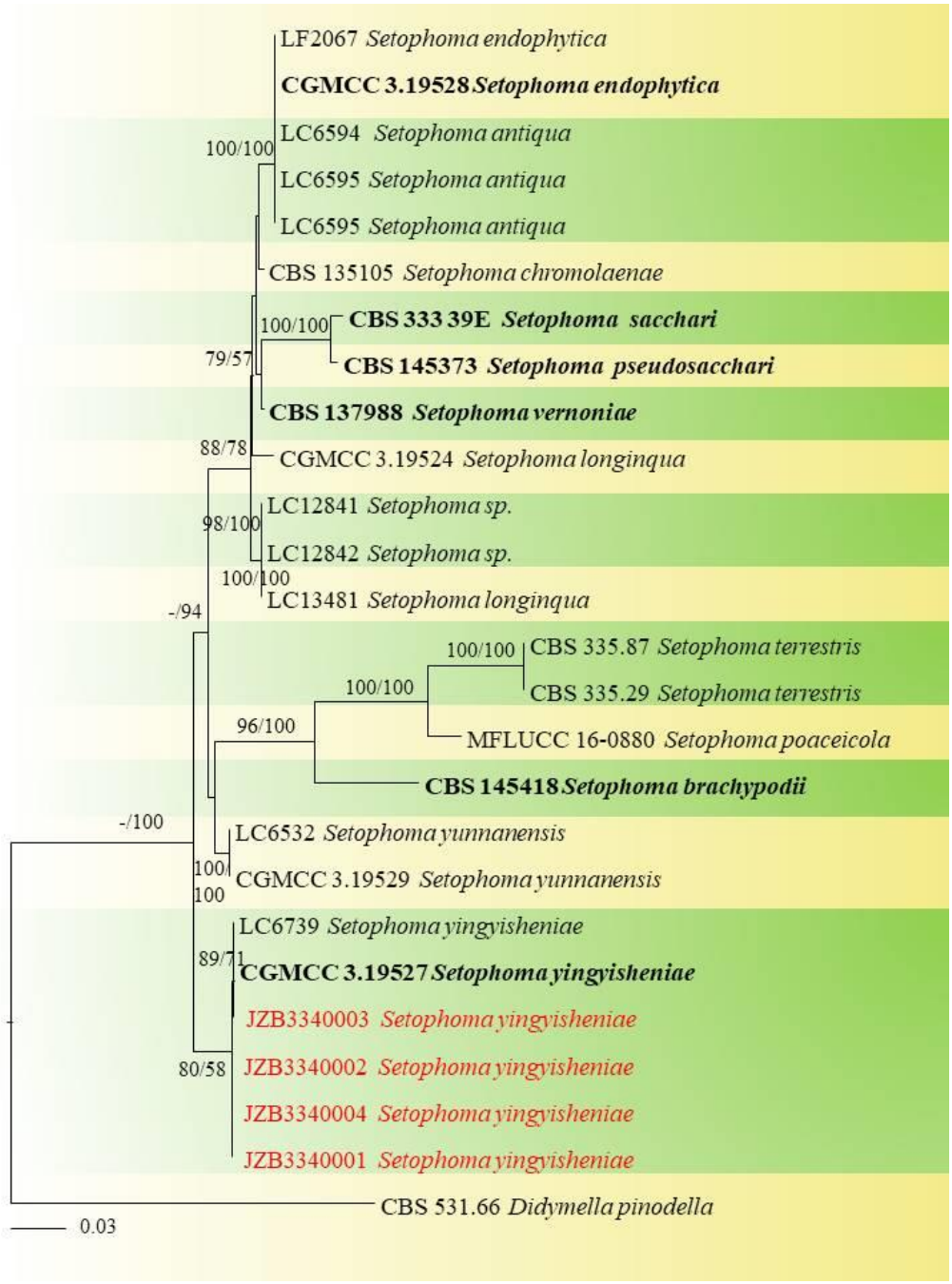

Figure 6 – Phylogenetic tree generated by ML analysis of combined LSU and ITS sequence data of *Setophoma* species. The tree is rooted with *Didymella pinodella* (CBS 531.66). Tree topology of the ML analysis was similar to the MP. The best scoring RAxML tree with a final likelihood value of – 4077.859174 is presented. The matrix had 232 distinct alignment patterns, with 8.92% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.242298, C = 0.217889, G = 0.274550, T = 0.265263; substitution rates AC = 1.307115, AG = 3.702431, AT = 3.436097, CG = 0.690224, CT = 8.860042, GT = 1.000000; gamma distribution shape parameter α = 0 0.692111. Maximum parsimony analysis of 1111 constant characters and 173 informative characters resulted in 62 equally most parsimonious tree of 462 steps (CI = 0.727, RI = 0.836, RC = 0.608, HI = 0.273). RAxML bootstrap support values ≥50% and MP bootstrap support values ≥50% are shown near the nodes. The scale bar indicates 0.03 changes per site. Ex–type/ex–epitype strains are in **bold**. Isolates from this study are in red.

Setophoma yingyisheniae F. Liu & L. Cai, in Liu, Wang, Li, Wang & Cai, Fungal Systematics and Evolution 4: 54 (2019) Fig. 7

Index Fungorum: IF829903; Facesoffungi number: FoF09382

Pathogenic or saprobic on *Camellia sinensis* leaves. Sexual morph: not observed. Asexual morph: *Conidiomata* 100–200 µm, pycnidial, black, globose or subglobose. *Pycnidial wall* brown, with 3–5 layers, walls pseudoparenchymatous. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, smooth, ampulliform, aseptate. *Conidia* 3.5–4.5 × 2–3 µm ($\bar{x}$ = 4 × 2.5 µm, n = 40) hyaline, aseptate, ellipsoid.

Culture characteristics – Grows up to 50 mm diam., after five days on PDA, irregular, filamentous margins, flat, superficial, grey and wrinkled with a white margin. Reverse black with a white margin.

Material examined – CHINA, Fujian Province, Zhangzhou County, on deseased leaves of *Camellia sinensis*, June 2015, H.L. Li (dried cultures JZBH3270001–4), and living cultures JZB3270001–4.

Notes – In the BLAST results, four isolates obtained in the present study showed similarities to the species in *Phaeosphaeriaceae*. A phylogenetic analysis was conducted using combined LSU and ITS gene regions for *Phaeosphaeriaceae*. In the phylogenetic tree of *Setophoma*, isolates from this study grouped with the ex–type strain of *Setophoma yingyisheniae* (CGMCC 3.195.27). Morphologically, isolates in this study were similar to the original description of *S. yunnanensis* (Liu et al. 2019) and all the sequences generated in this study were similar to the *Setophoma yingyisheniae* (CGMCC 3.195.27). *Setophoma yingyisheniae* was introduced by Liu et al. (2019) as a species associated with leaf spots of tea plants in Yunnan province. This is a new geographical report for *S. yunnanensis*.

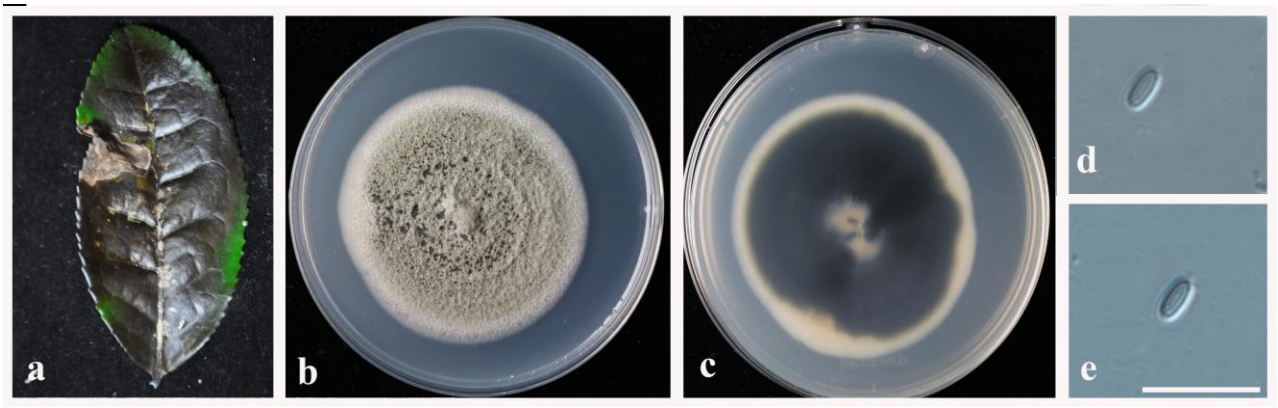

Figure 7 – *Setophoma yunnanensis* **(**JZB3270002). a Diseased leaf. b Upper view of a colony on PDA after five days. c Reverse view of the colony on PDA after five days. d, e Conidia. Scale bar: d, e = 10 µm.

Sordariomycetes

Notes – For the taxonomic treatments of Sordariomycetes we follow Hyde et al. (2020b).

Subclass Diaporthomycetidae Senan., Maharachch. & K.D. Hyde, in Maharachchikumbura et al., Fungal Diversity 72: 208 (2015)

Notes – Maharachchikumbura et al. (2016) introduced Diaporthomycetidae based on combined analysis of LSU, small subunit ribosomal RNA gene (SSU), *tef1* and *rpb2* sequence data. For the taxonomic treatment of Diaporthomycetidae we follow Hyde et al. (2020b).

Diaporthales Nannf., Nova Acta Regiae Societatis Scientiarum Upsaliensis 8 (2): 53 (1932)

Notes – Based on morphology and molecular data, currently 27 families and 138 genera are accepted within Diaporthales (Senanayake et al. 2017, Hyde et al. 2020b).

Diaporthe Nitschke Pyrenomyc. Germ. 2: 240 (1870)

Notes – Species in this genus are well known pathogens on many hosts including economically important plants (Hyde et al. 2014, Udayanga et al. 2014a, b, 2015, Dissanayake et al. 2017a). *Diaporthe* species are cryptic species, therefore the modern taxonomic classification and identification are based on molecular phylogeny. Hence in this study, latest classification as proposed by Marin-Felix et al. (2019), Manawasinghe et al. (2019), Hyde et al. (2019) was followed.

In the present study, 45 isolates were obtained from tea leaves and shoots. However, only 23 isolates were used in the phylogenetic analysis due to sequencing errors and to obtain better resolved phylogenies. A preliminary analysis was conducted using ITS, *tef1*, β–tubulin (*tub2*), calmodulin (*cal*) and partial histone (*his*) gene regions with 250 *Diaporthe* species (including ex–type strains) and tree was rooted with *Diaportherella corylina*. Once the placements of the species were confirmed, the final phylogenetic tree was arranged including only the taxa from respective species complex. (Fig. 8).

In the phylogenetic analysis, nine *Diaporthe* isolates clustered together with the *Diaporthe eucalyptoum* (CBS132525), *D. lithocarpus* (CGMCC 3.15175) and *D. hongkongensis* (CBS115448). In this clade, branch lengths and divergence times were indistinguishable. Therefore, we conducted a recombination test for delimitation of species. In this analysis, we included four strains comprising ex–type strains of *D. lithocarpus* (CGMCC3.15175), *D. eucalyptorum* (CBS132525), *D. fujianensis* (JZBH3340150) and *D. fusiformis* (JZBH3340154). The pairwise homoplasy index (PHI) test results using both LogDet transformation and splits decomposition revealed that the PHI test did not find statistically significant evidence for recombination (p = 1.0) (Fig. 9). Therefore, the two species identified in this study were treated as novel taxa.

Diaporthe biguttulata F. Huang, K.D. Hyde & Hong Y. Li, in Huang et al., Fungal Biology (2015) Fig. 10

Index Fungorum: IF810579; Facesoffungi number: FoF09383

Pathogenic or *saprobic* on *Camellia sinensis* leaves. Sexual morph: Not observed. Asexual morph: *Pycnidia* in culture, black, erumpent; walls 3–6 layers, light brown textura angularis. *Paraphyses* not observed. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 10–30 × 2–3 µm, phialidic, cylindrical, terminal and lateral. *Alpha conidia* 5.5–8 × 2–3.5 µm ($\overline{x}$ = 6 × 2.5 µm, n = 30), aseptate, hyaline, smooth, guttulate, fusoid, tapering towards both ends, apex subobtuse, base subtruncate. *Beta conidia* and *gamma conidia* not seen.

Culture characteristics – Colonies on PDA covers entire petri dish after10 days at 25ºC. Abundant tufted white aerial mycelia, buff, numerous black pycnidia 0.5 mm in diam., typically in the direction of the edge of the colony. Reverse buff with concentric lines.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* leaves, June 2015, H.L. Li (dried culture JZBH320166), and living culture JZB320166

Notes – A toxon isolated in the present study formed a well–supported cluster with the *Diaporthe biguttulata* (ZJUD47) with 100% ML, 99%, MP and 1.00 BYPP values. The morphological characteristics of the isolated taxa are similar to the ex–type description (Huang et al. 2015). *Diaporthe biguttulata* was introduced from *Citrus limon* in China (Huang et al. 2015). This species has also been reported on *Juglans regia* in China. This is the first report of *D. biguttulata* on *Camellia sinensis* (Farr & Rossman 2020).

Diaporthe eucalyptorum Crous & R.G. Shivas., in Crous et al. Persoonia 28: 153 (2012) Fig. 11

Index Fungorum: IF 800374; Facesoffungi number: FoF09077

Pathogenic or saprobic on *Camellia sinensis* leaves. Sexual morph: Not observed. Asexual morph: *Pycnidia* black, erumpent, cream conidial droplets exuding from central ostioles. *Pycnidial wall* consisting of 3–6 layers of hyaline outer layers and light brown inner layers, textura angularis. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* phialidic, cylindrical, terminal and lateral, with a slight taper towards the apex. *Paraphyses* hyaline, smooth, cylindrical, 1–3

septa. *Alpha conidia* 5.5–7 × 2–3 µm ($\bar{x}$ = 6 × 2.5 µm, n = 30), aseptate, hyaline, smooth, guttulate, fusoid, tapering towards both ends, straight, apex subobtuse, base subtruncate, *Beta* and *gamma* conidia not seen.

Culture characteristics – Colonies on PDA reach 90 mm diam., after 10 days at 25ºC (covers the total surface), abundant tufted white aerial mycelia, buff, numerous black pycnidia 0.5 mm in diam. occur in the mycelium, typically in the direction of the edge of the colony; reverse buff with concentric lines.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* leaves, June 2015, H.L. Li (dried culture JZBH320153), and living culture JZB320153.

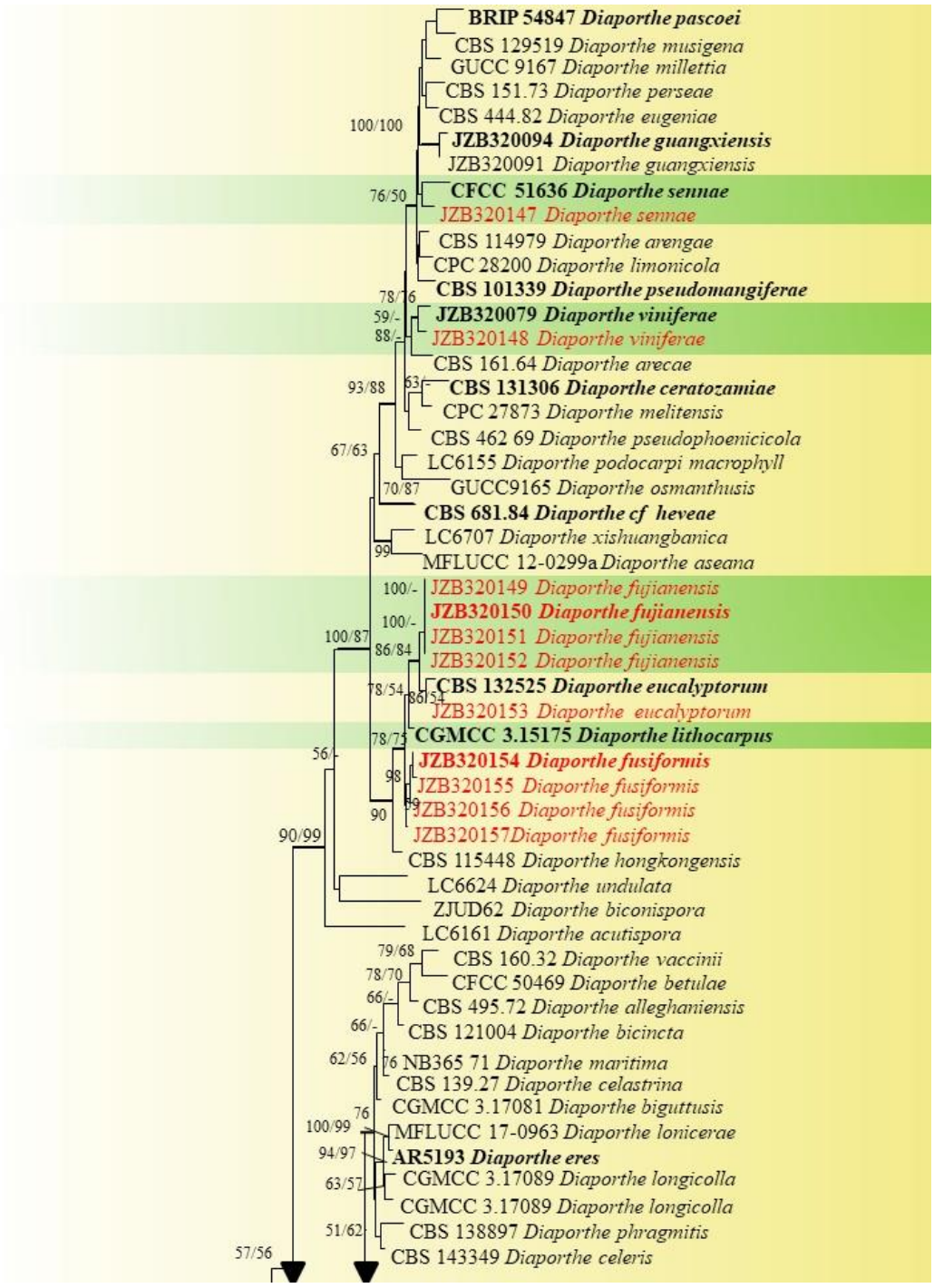

Figure 8 – Phylogenetic tree generated by ML analysis of combined ITS, *tef1*, *tub2*, Cal and HIS sequence data of *Diaporthe* species. The analyses included 166 strains and the tree was rooted with *Diaporthella corylina* (CBS 121124). Tree topology of the ML analysis was similar to the MP and

BYPP. The best scoring RAxML tree with a final likelihood value of – 24349.980578 is presented. The matrix had 1172 distinct alignment patterns, with 9.91% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.251668, C = 0.245757, G = 0.259668, T = 0.242908; substitution rates AC = 1.353890, AG = 4.605576, AT = 1.059439, CG = 0.801610, CT = 9.121730, GT = 1.000000; gamma distribution shape parameter α = 0.944898. Maximum parsimony analysis of 1145 constant characters and 1168 informative characters resulted in 100 equally most parsimonious tree of 1000 steps (CI = 0.325, RI = 0.757, RC = 0.246, HI = 0.675). RAxML bootstrap support values ≥50% and maximum parsimony bootstrap support values ≥50% are shown near the nodes. Nodes with ≥0.95 (BYPP) Bayesian posterior probabilities are indicated with thickened lines. The scale bar indicates 0.1 changes per site. Ex–type/ ex–epitype strains are in **bold**. New isolates recovered in this are in red.

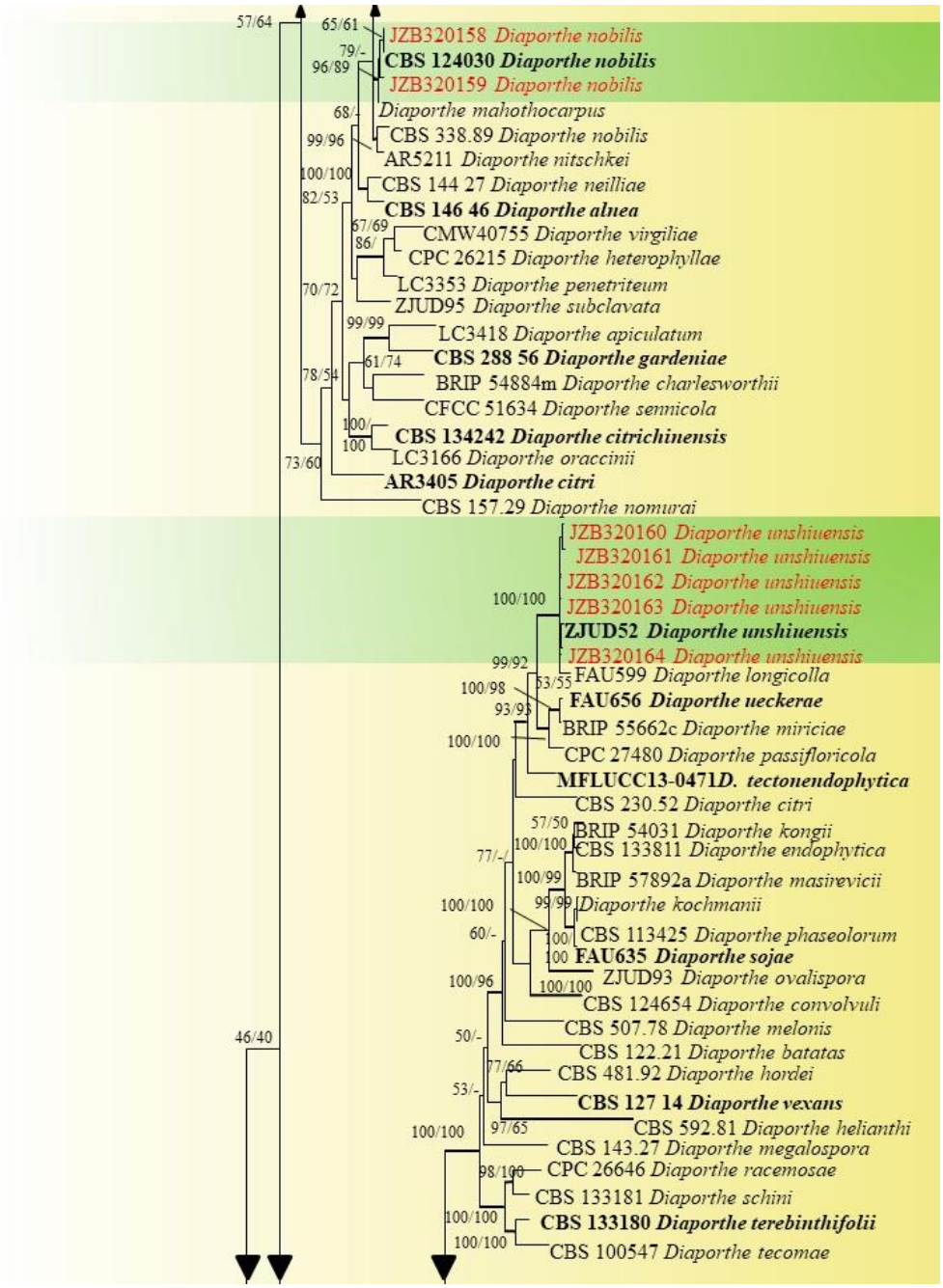

Figure 8 – Continued.

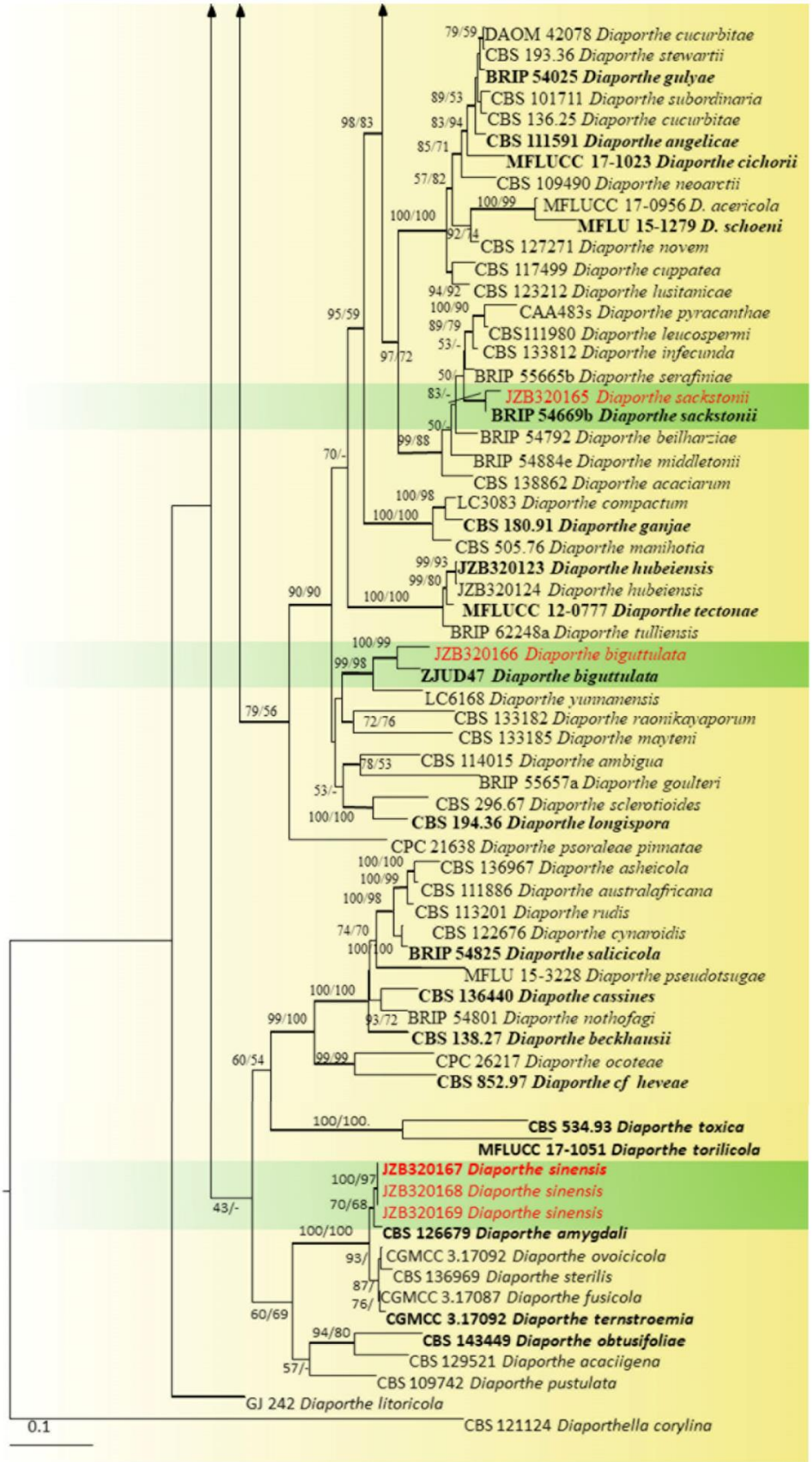

Figure 8 – Continued.

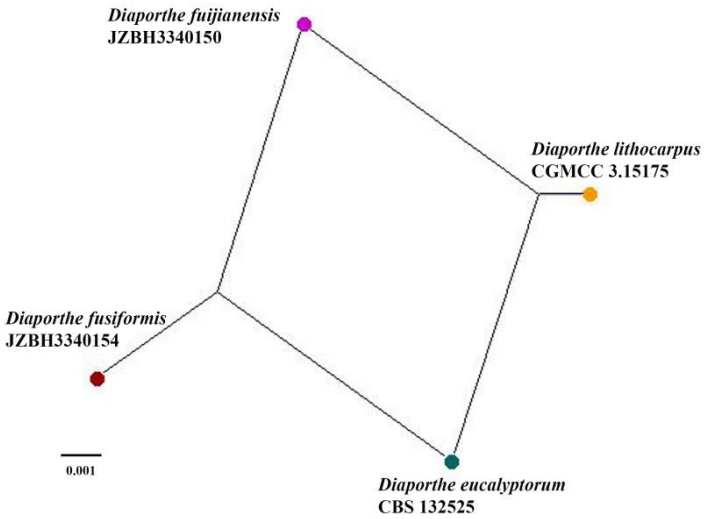

Figure 9 – Results of the pairwise homoplasy index (PHI) test of closely related species using both LogDet transformation and splits decomposition. The phi test did not find statistically significant evidence for recombination (p = 1.0).

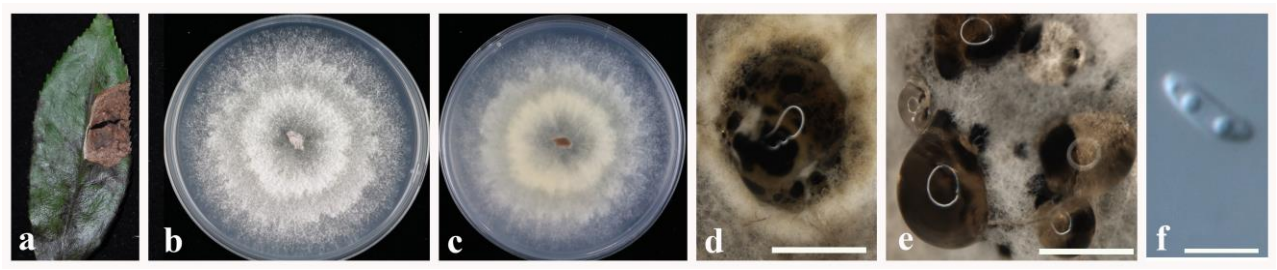

Figure 10 – *Diaporthe biguttulata* (JZBH3340160). a Diseased leaf. b Upper view of colony on PDA after 10 days. c Reverse view of colony on PDA after 10 days. d, e Pycnidia on PDA. f Conidium. Scale bars: d, e = 100, f = 10 µm. µm.

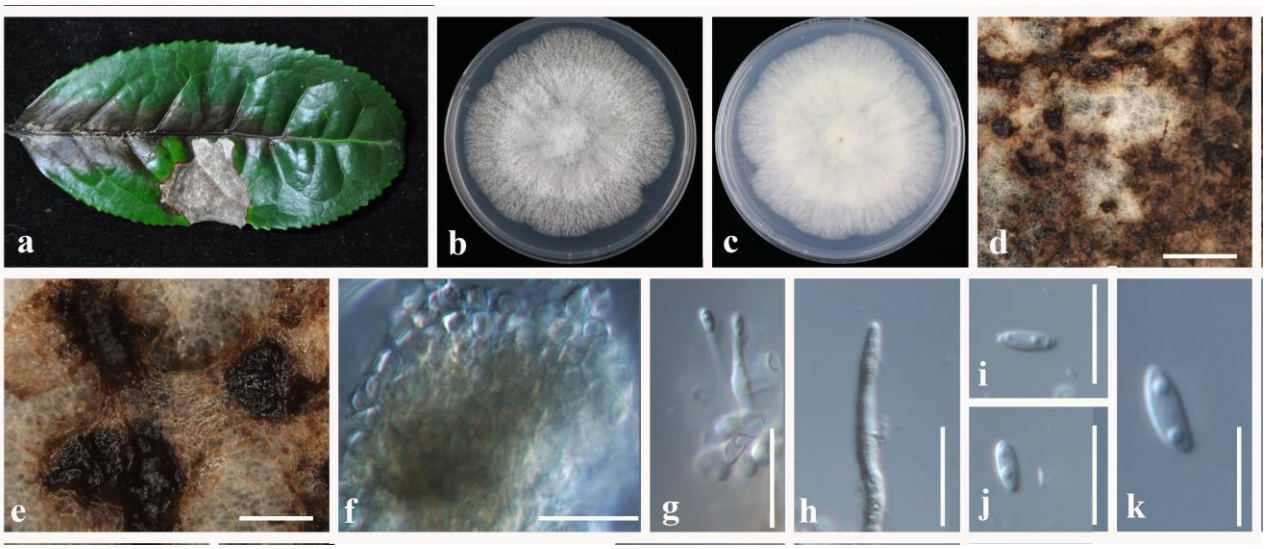

Figure 11 – *Diaporthe eucalyptorum* (JZBH3340153). a Diseased leaf. b Upper view on of colony PDA after 10 days. c Reverse view of colony on PDA after 10 days. d, e Pycnidia on PDA. f Pycnidial wall. g conidiogenous cell. f hypal end. i–k alpha conidia. Scale bars: d, e = 100 µm, f–h = 20 µm, h–k = 10 µm.

Notes – The taxon isolated in the present study formed a well–supported cluster with *Diaporthe eucalyptorum* (CBS 132525) with 88% ML, 54% MP and 0.98 BYPP values. The morphological characteristics of the isolated taxon are similar to the ex–type isolate of this species (Crous et al. 2012). *Diaporthe eucalyptorum* was introduced by Crous et al. (2012) as a leaf spot causing fungus on *Eucalyptus* L. This is the first report of *D. eucalyptorum* on *Camellia sinensis* (Farr & Rossman 2020).

Diaporthe fujianensis Jayaward., Manawas., X.H. Li, J.Y. Yan, & K. D. Hyde, sp. nov.

Fig. 12

Index Fungorum: IF557997; Facesoffungi number: FoF09384

Etymology – Epithet refers to the Fujian province from where the type was collected.

Holotype – JZBH3340150

Pathogenic or saprobic on *Camellia sinensis* shoots. Sexual morph: not observed; Asexual morph: *Pycnidia* on PDA superficial, scattered, black, globose, solitary in most. *Conidiophores* not observed. *Conidiogenous cells* terminal, hyaline and smooth. *Alpha conidia* 4–6 × 2–3 µm ($\overline{x}$ = 5 × 2.5 µm n = 40), biguttulate, hyaline, oval and or ellipsoidal, both ends obtuse. *Beta conidia* and *gamma conidia* were not observed.

Culture characteristics – Colonies on PDA reach 90 mm diam. after five days at 25°C, producing abundant white aerial mycelia and reverse fuscous white.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* shoots, June 2015, H.L. Li (dried cultures JZBH320150 holotype; JZBH320149, JZBH320151 and JZBH320152 paratype), and living cultures JZBH320150 ex–holotype; JZBH320149, JZBH320151 and JZBH320152 ex–Paratype.

Notes – In the phylogenetic analysis four isolates obtained in this study clustered in a well–supported clade with 100% ML and 84% MP bootstrap values and 0.98 BYPP. In the recombination analysis, PHI test indicated that the current isolates belong to a species separated from all other *Diaporthe* species included in the phylogenetic tree. *Diaporthe fujianensis* resides in a sister clade to *Diaporthe eucalyptorum*. Morphologically the alpha conidia produced by this species are smaller than those in *Diaporthe eucalyptorum* (6 × 2.5 µm). A pairwise nucleotide comparison between *Diaporthe eucalyptorum* ex type strain (CBS 132525) and *Diaporthe fujianensis* ex type strain (JZBH320150) in ITS region showed 1.75% base pair differences along 519 bp. Based on the molecular evidences we consider that these isolates belong to a novel species.

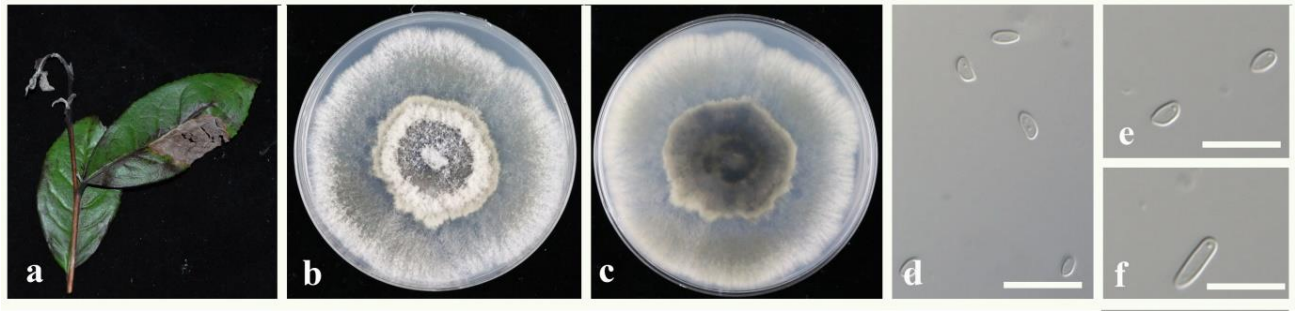

Figure 12 – *Diaporthe fujianensis* (JZBH3340150 holotype) a Diseased shoot. b Upper view on of colony PDA after five days. c Reverse view of colony on PDA after five days. d–f alpha conidia. Scale bars: d–f = 10 µm.

Diaporthe fusiformis Jayaward., Manawas., X.H. Li, J.Y. Yan, & K. D. Hyde, sp. nov.

Fig. 13

Index fungorum: IF557998; Facesoffungi number: FoF09385

Etymology – refers to the fusiform conidia

Holotype – JZBH3340154

Pathogenic or saprobic on *Camellia sinensis* leaves. Sexual morph*:* not observed; Asexual morph*: Pycnidia* on PDA superficial, scattered, black, globose, solitary and clustered. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, smooth–walled clustered. *Alpha conidia* 8–5 × 2–3 µm ($\overline{x}$ = 7 × 2 µm, n = 40), eguttulate, hyaline, fusiform, both ends angular. *Beta conidia* 23–32 ×1.2–1.6 µm ($\overline{x}$ = 27× 1.5 µm, n = 40), aseptate, hyaline, hamate, filiform, tapering towards both ends. *Gamma conidia* not observed.

Culture characteristics – Colonies on PDA reach 90 mm diam. after five days at 25°C, producing abundant white aerial mycelia and reverse fuscous white becoming gray.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* leaves, June 2015, H.L. Li (dried cultures JZBH320154–JZBH320157), and living cultures JZB320154–7, dried cultures JZBH320154 holotype; JZBH320155–JZBH320157 paratype), and living cultures JZBH320154 ex–holotype; JZBH320155–7 ex–paratype.

Notes – In the phylogenetic analysis four isolates obtained in this study formed a well–supported clade with 100% ML and 0.98 PP values. In the recombination analysis, PHI test indicated that these isolates belong to a species separate from all other species in *Diaporthe* (Fig. 9). *Diaporthe fusiformis* is phylogenetically close to *Diaporthe eucalyptorum* (CBS132525) and *Diaporthe fujianensis* (This study). *Diaporthe eucalyptorum* (CBS132525) has larger conidia and *Diaporthe fujianensis* has smaller conidia (4–6 × 2–3 µm) than *Diaporthe fusiformis* (8–5 × 2–3 µm). In addition, the conidia of *Diaporthe fusiformis* are fusiform whereas *Diaporthe eucalyptorum* has biguttulate fusoid conidia and *Diaporthe fujianensis* has oval to ellipsoidal conidia. In comparison with *Diaporthe lithocarpus*; *Diaporthe fujianensis* has smaller conidia (4–6 × 2–3 µm) than *Diaporthe lithocarpus* (6–8 × 2–3 µm). *Diaporthe lithocarpus* develop both alpha conidia and beta conidia whereas *Diaporthe fujianensis* is prominent with alpha conidia. Based on morphological and phylogenetic characters we identified this taxon as a novel species.

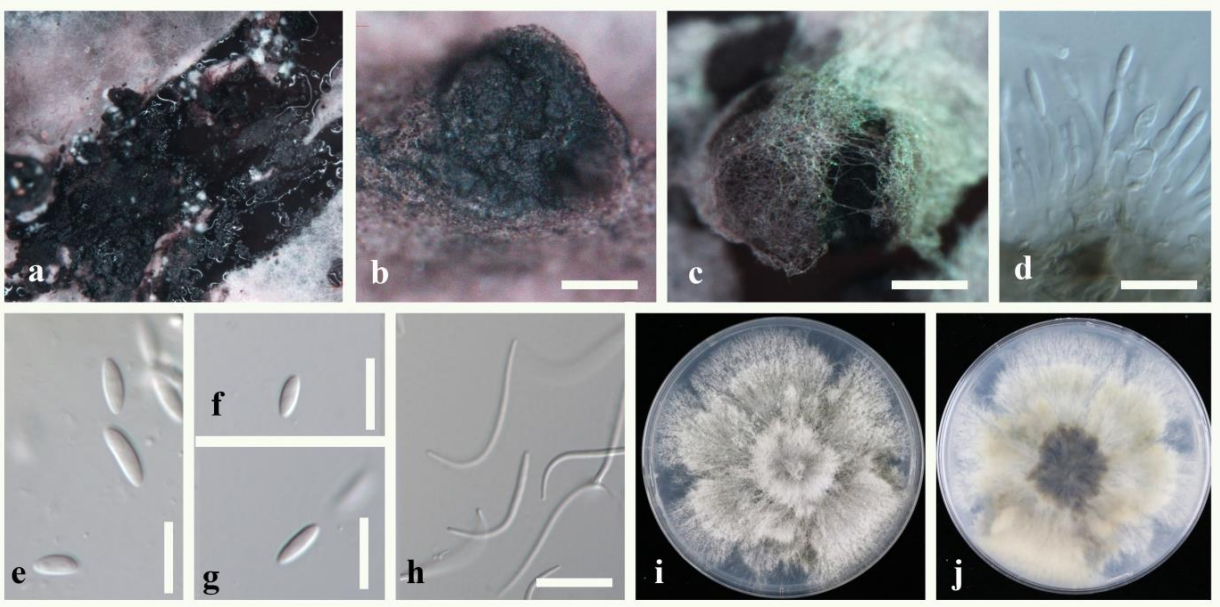

Figure 13 – *Diaporthe fusiformis* (JZBH3340154 Holotype). a–c Pycnidia on PDA. d Conidiogenus cells. e–g Alpha conidia. h Beta conidia. i Upper view of colony on PDA after five days. j Reverse view of colony on PDA after five days. Scale bars: b–c = 100 µm, d = 20 µm, e–h = 10 µm.

Diaporthe nobilis Sacc. & Speg., Michelia 1(no. 4): 386 (1878) Fig. 14

Index fungorum: IF 153616; Facesoffungi number: FoF02717

Pathogenic or saprobic on *Camellia sinensis* leaves and shoots. Sexual morph: Not observed. Asexual morph: *Conidiomata* 200–350 µm in widest diam, globose, ostiolate, embedded in the PDA, scattered. *Conidiophores* 15–22 × 1.5–2 µm, cylindrical, hyaline, rough, branched, septate,

straight or slightly curved. Alpha conidia 5.5–8 × 2–3 µm ($\bar{x}$ = 6 × 2.5 µm, n = 30), unicellular, hyaline, aseptate, oval, rounded at both ends. *Beta* and *gamma conidia* not seen.

Culture characteristics – Cultures incubated on PDA at 25°C in darkness, reach 70 mm diam., after seven days. Upper view white, cottony, regular margin. Reverse becoming brownish with age.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* leaves and shoots, June 2015, H.L. Li (dried cultures JZBH320158 and JZBH320159), and living cultures JZB320158 and JZB320159.

Notes – In combined multigene phylogenetic analysis of ITS, *tef1*, *tub2*, Cal and HIS, two strains clustered together with the *Diaporthe nobilis* (CBS 124030) with 65% ML 61%, MP and 0.99 BYPP values. Colony morphology, spore shape and dimensions are similar to those of *Diaporthe nobilis* (Li et al. 2017). So far, this species has been reported on several woody hosts including tea (Farr & Rossman 2020). In China, *Diaporthe nobilis* associated with tea was first reported by Li et al. (2017). However, the pathogenicity of this species has not yet been confirmed.

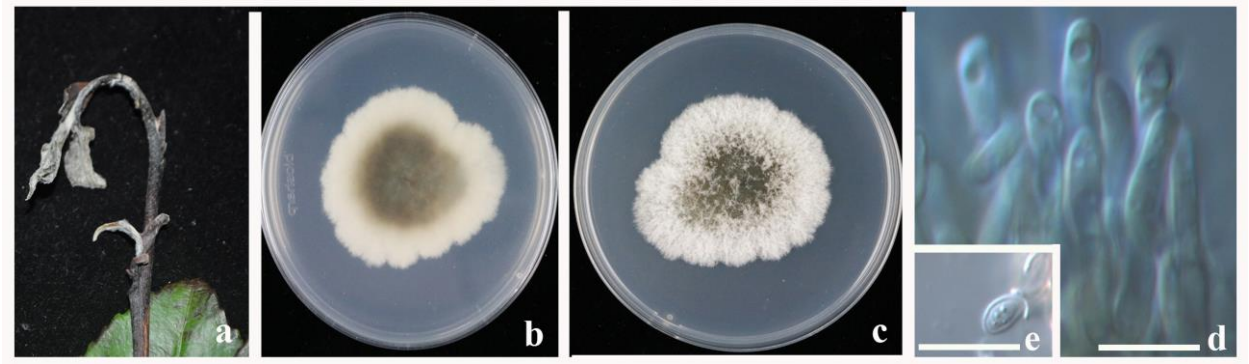

Figure 14 – *Diaporthe nobilis* (JZBH3340158). a Diseased shoot. b Upper view of the colony on PDA after seven days. c Reverse view of the colony on PDA after seven days. d Conidiogenous cell. e An alpha conidium. Scale bars: d–e = 10 µm.

Diaporthe sackstonii R.G. Shivas, S.M. Thomps. & Y.P. Tan, Persoonia 35: 46 (2015) Fig. 15

Index Fungorum: IF 808674; Facesoffungi number: FoF09386

Pathogenic or saprobic on *Camellia sinensis* shoots. Sexual morph: Not observed. Asexual morph: *Pycnidia* on PDA solitary, scattered, ostiolate, cream conidial droplets exuded from some ostioles. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* filiform, hyaline to pale yellowish–brown. *Alpha conidia* 6–8 × 2–2.5 µm ($\bar{x}$ = 6.5 × 2 µm, n = 30), abundant, fusiform, rounded at the apex, obconically truncate at base, hyaline. *Beta conidia* not observed.

Culture characteristics – Colonies on PDA covering entire plate after 10 days. White areal myclilum, entire margine, with age a few scattered dark stromata up to 1 mm diam., buff. Reverse white and become black with age.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* shoots, June 2015, H.L. Li (dried culture JZBH320165), and living culture JZB320165.

Notes – The single isolate obtained from the present study formed a well–supported clade with the ex–type strain of *Diaporthe sackstonii* (BRIP54669b) with 83% ML, 83% MP and 0.98 BYPP values. Morphologically these two isolates are similar and they share sequences difference of less than 1% at each gene region (at three genes ITS, *tub2* and *tef1*). *Diaporthe sackstonii* was introduced by Thompson et al. (2015) on *Helianthus annuus* in Australia. This is the first report of *Diaporthe sackstonii* on *Camellia sinensis* (Farr & Rossman 2020).

Diaporthe sennae C.M. Tian & Qin Yang, in Yang et al., Phytotaxa 302(2): 149 (2017)

Fig. 16

Index Fungorum: IF820452; Facesoffungi number: FoF08696

Pathogenic or saprobic on *Camellia sinensis* shoots. Sexual morph: Not observed. Asexual morph: *Conidiomata* pycnidial, circular to ovoid, immersed, scattered on PDA, *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, phialidic, straight or slightly curved. *Alpha conidia* 5–7 × 1.5–2 µm ($\overline{x}$ = 6.0 × 2 µm, n = 30), hyaline, aseptate, smooth, ellipsoidal to oval, usually one guttulate at each end, rarely 3 small guttulate. *Beta conidia* not observed.

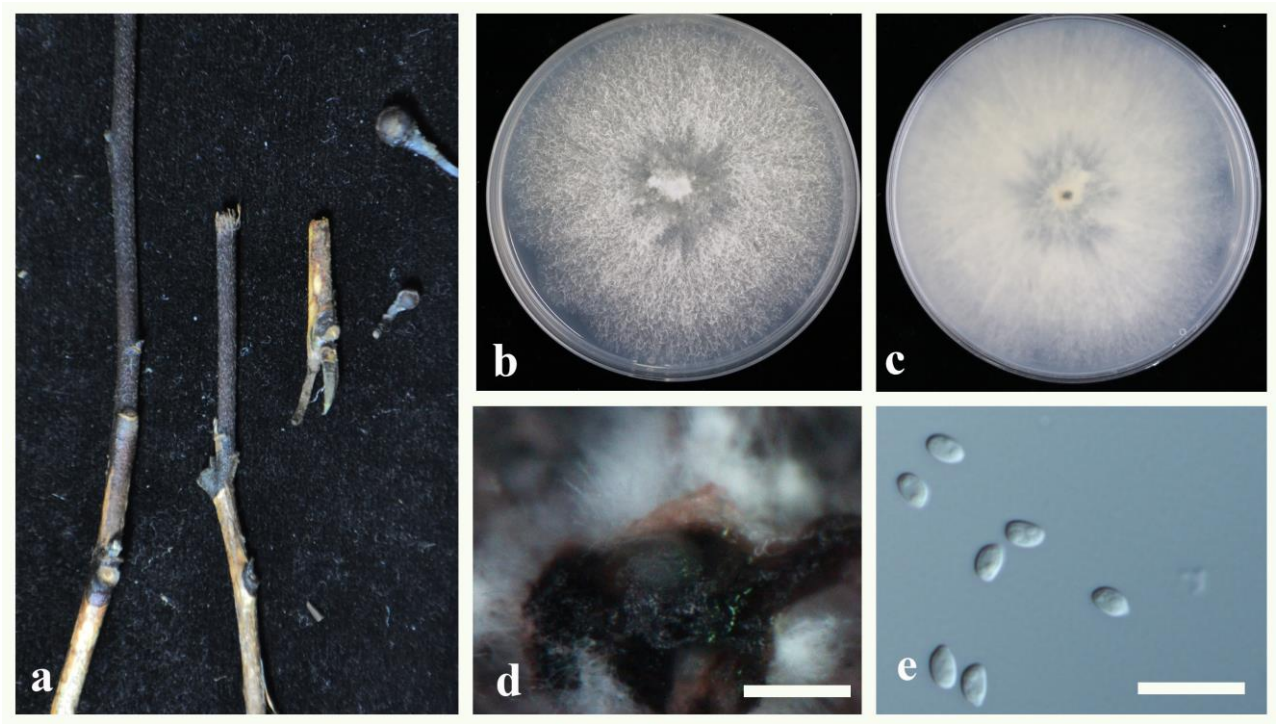

Figure 15 – *Diaporthe sackstonii* (JZBH3340165) a Diseased shoot. b Upper view of mycelium on PDA after 10 days. c Reverse view of mycelium on PDA after 10 days. d Pycnidia on PDA. e Alpha conidia. Scale bars: d = 100 µm, e = 10 µm.

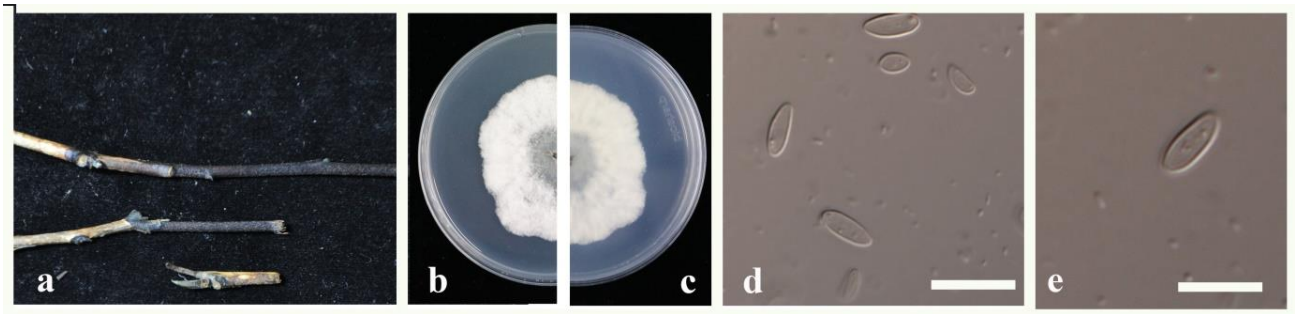

Figure 16 – *Diaporthe sennae* (JZBH3340147). a Diseased shoot. b Upper view of mycelium on PDA after 10 days. c Reverse view of mycelium on PDA after 10 days. d–e Alpha conidia. Scale bars: d–e = 10 µm.

Culture characteristics – Colonies on PDA covering the entire plate after 10 days. Colony flat with white flat aerial mycelium, becoming pale brown mycelium due to pigment formation, conidiomata absent

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* shoots, June 2015, H.L. Li (dried culture JZBH320147), and living culture JZB320147.

Notes – One isolate from the present study clustered together with the ex–type of *Diaporthe sennae* (CFCC 51636) with 76% ML, 50% MP and 1.00 BYPP. Morphologically the strain isolated in this study shares similar characters with the type description (Yang et al. 2017). *Diaporthe*

sennae was introduced from infected branches/twigs of *Senna bicapsularis* in China (Yang et al. 2017). However, pathogenicity of this species has not been confirmed. To our knowledge, this is the first report of *Diaporthe sennae* on *Camellia sinensis* (Farr & Rossman 2020).

Diaporthe sinensis Jayaward., Manawas., X.H. Li, J.Y. Yan, & K. D. Hyde, sp. nov. Fig. 17

Index Fungorum: IF557999; Facesoffungi number: FoF09387

Etymology – Name derived from the epithet of the host

Holotype – JZBH320167

Pathogenic or saprobic on *Camellia sinensis* leaves. Sexual morph: not observed: Asexual morph: *Pycnidia* on PDA 360–900 µm ($\bar{x}$ = 500 µm, n = 20) in diam., superficial, scattered, dark brown to black, globose, solitary in most. *Conidiophores* reduced to Conidiogenous cells. *Conidiogenous cells* hyaline, simple, smooth terminal. *Alpha conidia* 7–4 ×2–3 µm ($\overline{x}$ = 5 × 3 µm, n = 40) hyaline, oval, both ends obtuse. *Beta conidia* and *gamma conidia* not observed.

Culture characteristics – Colonies on PDA reach 90 mm diam., after five days at 25°C, producing abundant white aerial mycelia and reverse fuscous white.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* leaves, June 2015, H.L. Li (dried cultures JZBH320167 holotype, JZBH320168–9 paratype), and living cultures ZBH320167 ex–holotype; JZBH320168–9 ex–paratype.

Notes – In the phylogenetic analysis, four isolates obtained in this study formed a well–supported clade with 70% ML and 68% MP bootstrap values and 0.97 BYPP. These taxa show particular neighbour relation to *Diaporthe amygdali* (CBS 126679). Compared to the sister species, *Diaporthe sinensis* develops oval and shorter alpha conidia whereas conidia of *Diaporthe amygdali* are fusiform, and biguttulate (Gomes et al. 2013). A comparison of the ITS (497bp), *tef1* (492bp), and Cal (300bp) between our species (JZBH3340167) and closely associated *Diaporthe amygdali* (CBS 126679) revealed 2%, 2.4% and 14% base pair differences respectively. Therefore, based on both morphological and phylogenetic evidence we identified these isolates as a novel *Diaporthe* species associated with tea.

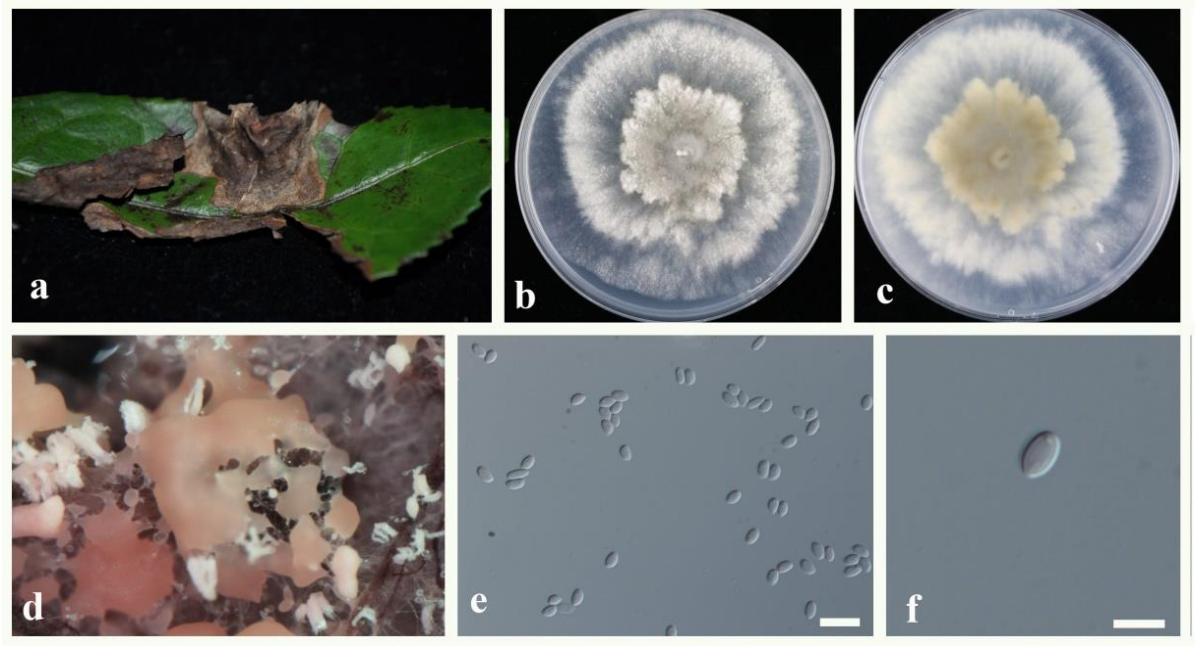

Figure 17 – *Diaporthe sinensis* (JZBH3340167 Holotype) a Diseased leaf. b Upper view of mycelium on PDA five days. c Reverse view of mycelium on PDA five days. d Pycnidia on PDA. e–f Alpha conidia. Scale bars: e = 10 µm, f = 5 µm.

Diaporthe unshiuensis F. Huang, K.D. Hyde & Hong Y. Li, in Huang et al., Fungal Biology 119(5): 344 (2015) Fig. 18

Index Fungorum: IF 810845; Facesoffungi number: FoF 09422

Pathogenic or saprobic on *Camellia sinensis* leaves and shoots. Sexual morph: Not observed. Asexual morph: *Conidiomata* 100–300 µm in diam., globose to subglobose, dark brown to black, cream conidial drops exuded from the ostioles. *Conidiophores* not observed. *Conidiogenous cells* cylindrical, hyaline. *Alpha conidia* 6–8 × 2–3 µm ($\bar{x}$ = 6 × 3 µm, n = 30), unicellular, aseptate, fusiform, hyaline, biguttulate and tapering towards both ends. *Beta conidia* not observed.

Culture characteristics – Cultures incubated on PDA at 25°C reach 90 mm., after seven days. Colony at first white, becoming pale brownish, reverse pale yellowish at the centre with age. Aerial mycelium white, cottony, with slightly fringed margin and conidiomata visible at maturity.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* leaves and shoots, June 2015, H.L. Li (dried cultures JZBH320160– JZBH320164), and living cultures JZB320160– JZB320164.

Notes – Five isolates obtained in the present study clustered together with the ex–type of *Diaporthe unshiuensis* (ZJUD52) with 100% ML, 100% MP and 1.00 BYPP values. Morphologically isolates from this study are similar to the type description of *Diaporthe unhuensis* (Huang et al. 2015). This species was reported on *Citrus unshiu* in China (Huang et al. 2015) and this is the first report of *D. unshiuensis* on *Camellia sinensis* (Farr & Rossman 2020).

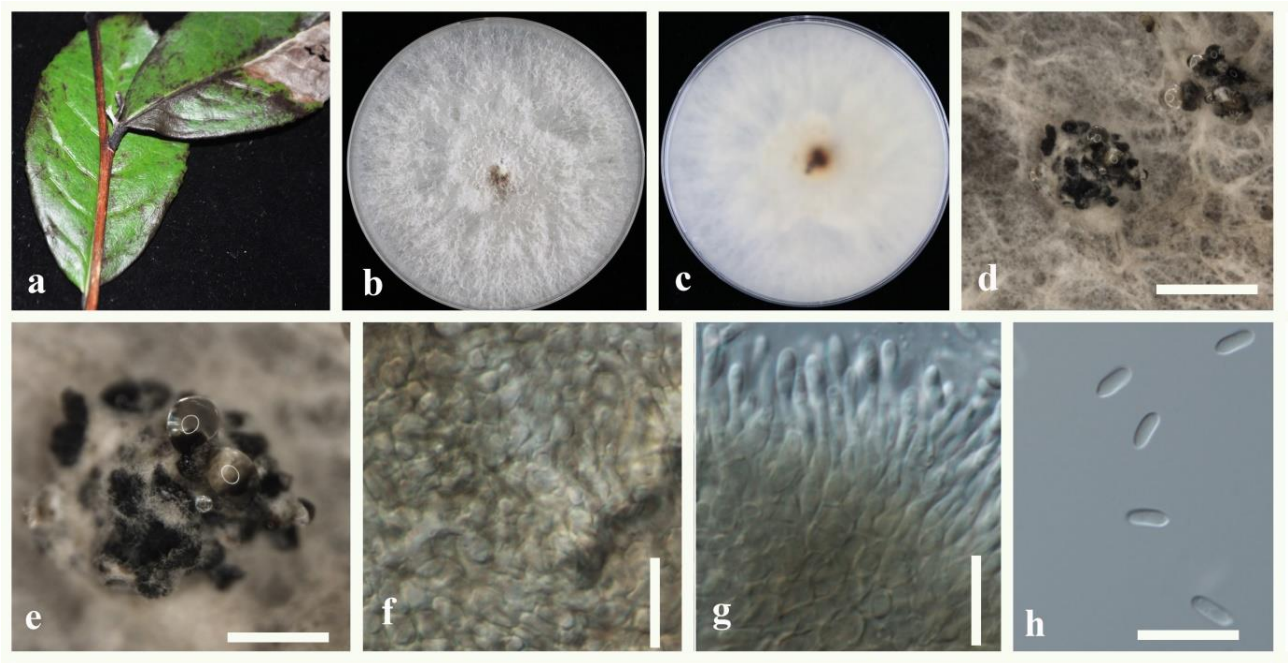

Figure 18 – *Diaporthe unhuensis* (JZBH3340163) a Diseased leaves and shoot. b Upper view of mycelium on PDA after seven days. c Reverse view of mycelium on PDA after seven days. d–e Pycnidia on PDA. f Pycnidial wall. g Conidiogenus cells attached to the pycnidial wall. h Alpha conidia. Scale bars: d, e = 100 µm, f–g = 20 µm, h= 10 µm.

Diaporthe viniferae Dissanayake, X.H. Li & K.D. Hyde, in Manawasinghe et al., Frontiers in Microbiology 10: 21 (2019) Fig. 19

Index Fungorum: IF552002; Facesoffungi number: FoF05981

Pathogenic or saprobic on *Camellia sinensis* shoots. Sexual morph*:* not observed; Asexual morph*: Pycnidia* on PDA 400–900 µm ($\bar{x}$ = 500 µm, n = 20) superficial, scattered, dark brown to black, globose, solitary in most. *Conidiophores* not observed. *Conidiogenous cells* not observed. *Alpha conidia* 5–8 × 1–2.5 µm ($\bar{x}$ = 6 × 2 µm, n = 40), biguttulate, hyaline, fusiform or oval, both ends obtuse, *Beta conidia* 20–30 ×1–1.5 µm ($\bar{x}$ = 27 × 1 µm, n = 40), aseptate, hyaline, filiform.

Culture characteristics – Colonies on PDA reach 90 mm diam., after five days at 25°C, producing abundant white aerial mycelia and reverse fuscous white.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* shoots, June 2015, H.L. Li (dried culture JZBH320148), and living culture JZB320148.

Notes – In the phylogenetic analysis, the single isolate clustered together with *Diaporthe viniferae* (JZBH3340148), 85% ML and 76% MP bootstrap values and 1.00 BYPP. Morphologically these two isolates are similar with no differences in sequence data. This species was first introduced by Manawasinghe et al. (2019) as a pathogen associated with grapevine dieback in China. This is the first report of *Diaporthe viniferae* on *Camellia sinensis* (Farr & Rossman 2020).

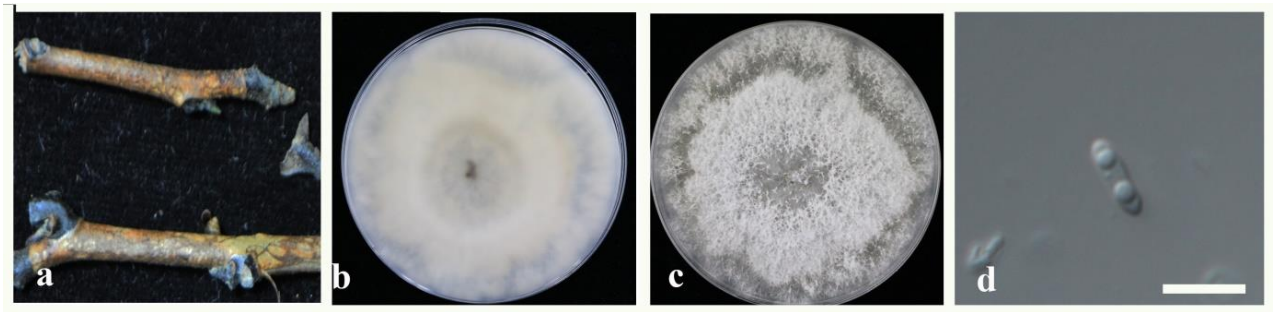

Figure 19 – *Diaporthe viniferae* (JZBH3340148). a Diseased shoot. b Upper view on PDA after five days. c Reverse view on PDA after five days. d An alpha conidium. Scale bar: d = 10 µm.

Subclass Hypocreomycetidae O.E. Erikss. & Winka, Myconet 1: 6 (1997)

Notes – Currently there are seven orders; Coronophorales, Falcocladiales, Glomerellales, Hypocreales, Microascales, Parasympodiellales and Torpedosporales associated with Hypocreomycetidae with 37 families (Hyde et al. 2020b).

Glomerellales Chadef. ex Réblová, W. Gams & Seifert, Studies in Mycology 68: 170

Notes – Chadefaud (1960) introduced Glomerellales. This order is composed of endophytic fungi and phytopathogens with ascomata varying from endostromatal to apostromatal and ascospores that are often unicellular and hyaline. Currently, five families are accepted in the Glomerellales: *Glomerellaceae*, *Australiascaceae*, *Malaysiascaceae*, *Plectosphaerellaceae* and *Reticulascacea* (Hyde et al. 2020b).

Glomerellaceae Locq., Mycol. gén. struct. (Paris): 175 (1984).

Notes – Almost all species identified in this family are well–known plant pathogens on a wide range of hosts (Jayawardena et al. 2016a). Type genus of this family is *Colletotrichum* (Hyde et al. 2014, Maharachchikumbura et al. 2016).

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

Notes – Species in this genus are known as pathogens on a wide range of crops and some species are endophytes or saprotrophs (Hyde et al. 2014, Jayawardena et al. 2016a, 2020). Species delimitation based on morphology alone is difficult in *Colletotrichum* due to overlapping morphological characters in the asexual morphs (Hyde et al. 2009, Cannon et al. 2012). Therefore, polyphasic approaches including multi–locus sequence analyses are essential (Jayawardena et al. 2016a). Currently, 14 species complexes (Jayawardena et al. 2016a, Damm et al. 2019, Bhunjun et al. 2021) are accepted in this genus. In the present study, we obtained two isolates belonging to two known species of *Colletotrichum* (Fig. 20).

Colletotrichum camelliae Massee, Bull. Misc. Inf., Kew: 91 (1899) Fig. 21

Index Fungorum: IF176099; Facesoffungi number: FoF09388

Pathogenic or saprobic on *Camellia sinensis* leaves, Sexual morph: *Ascomata* on PDA perithecia, globose, ovoid, obpyriform, aggregated or scattered, immersed, single ostiole. *Ascomata*

wall thick, the outer wall of ascomata composed of flattened angular cells, Asci clavate, 60–80 × 10–14 µm ($\bar{x}$ = 60 × 12 µm, n = 40) long, 8 spored, apex truncated and a small apical point. Asci covered with a thick sheath. *Ascospores* hyaline 13–18 × 4–5 µm ($\bar{x}$ = 16 × 4.5 n = 20), one–celled, allantoid or fusiform. Asexual morph: not observed.

Culture characteristics – Colonies reach <90 mm diam., in 10 days, flat with an entire edge, aerial mycelium white, cottony, sparse; reverse white at first, then grey to black at the centre.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* leaves, June 2015, H.L. Li (dried culture JZBH330153), and living culture JZB330153.

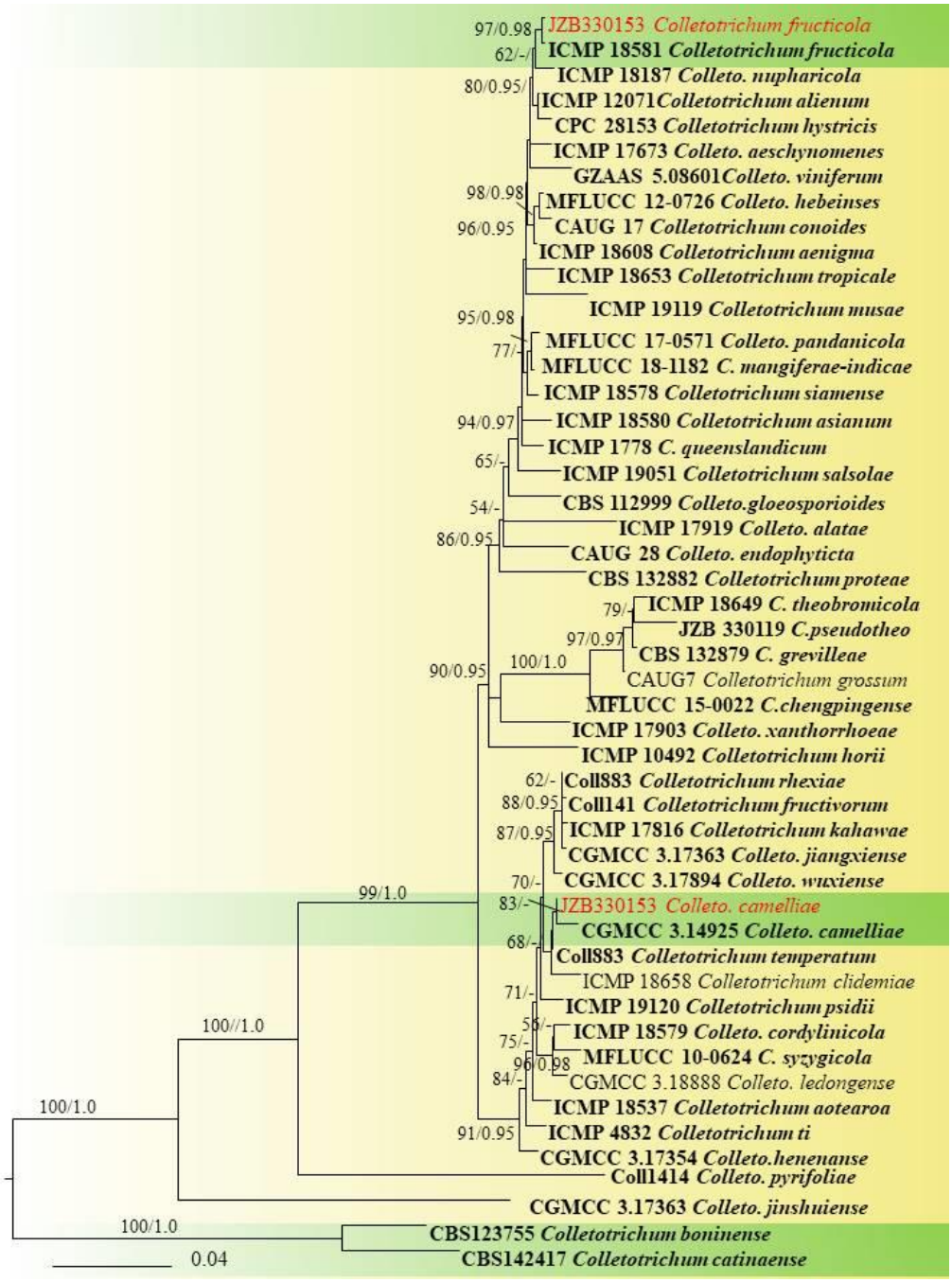

Figure 20 – Phylogenetic tree generated by ML analysis of combined ITS, glyceraldehyde–3–phosphate dehydrogenase (GAPDH), chitin synthase (CHS–1), actin ACT and *tub2* sequence data of *Colletotrichum* species. In the phylogenetic tree, *Colletotrichum boninense* (CBS123755) and *Colletotrichum catinaense* (CBS 142417) used as outgroup. Tree topology of the ML analysis was similar to the BI. The best scoring RAxML tree with a final likelihood value of –10102.441238 is presented. The matrix had 812 distinct alignment patterns, with 15.39% of undetermined characters

or gaps. Estimated base frequencies were as follows: A 0.229139, C = 0.296735, G = 0.244809, T = 0.229316; substitution rates AC = 1.065846, AG = 2.974226, AT = 0.978030, CG = 0.858886, CT = 4.711667, GT = 1.000000; gamma distribution shape parameter α = 1.663370. RAxML bootstrap support values ≥50% and Bayesian posterior probabilities ≥0.95 (BYPP) are shown near the nodes. The scale bar indicates 0.04 changes per site. Ex–type/ex–epitype) strains are in **bold** and new isolates recovered in the the present study are in red.

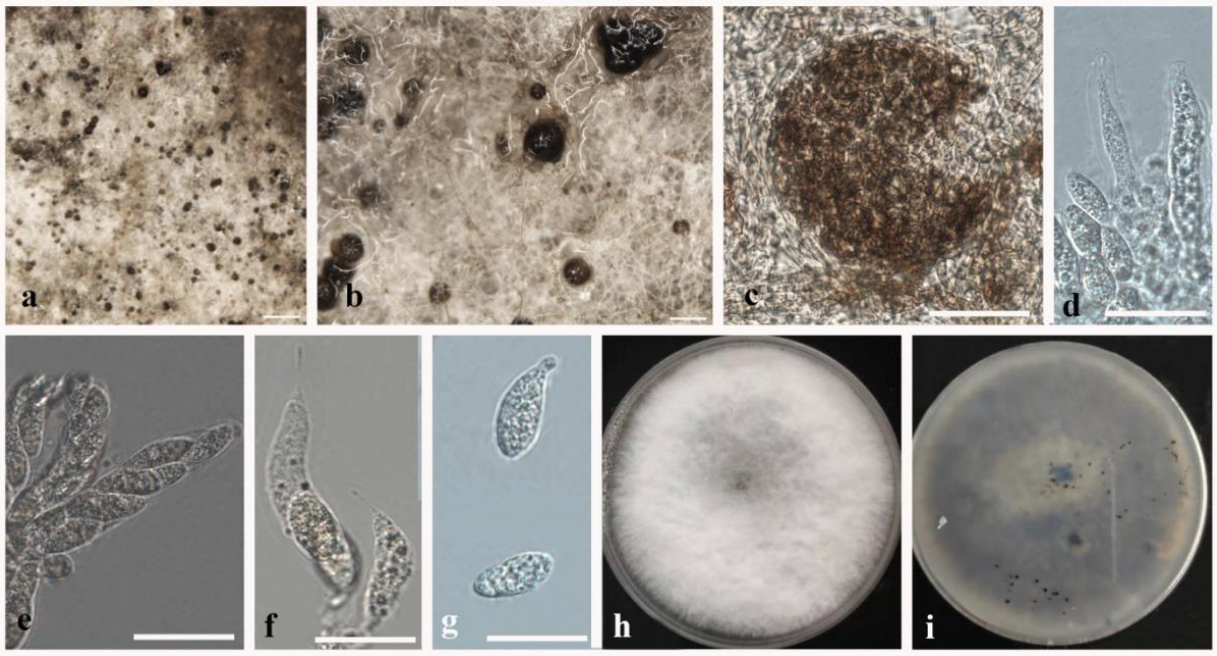

Figure 21 – *Colletotrichum camelliae* (JZB330153). a–b Ascomata on PDA. c Ascomatal wall (surface view). d–f Developing and mature asci. g Ascospores. h Upper view of the colony on PDA after 10 days. i Reverse view of the colony on PDA after 10 days. Scale bars: a–c = 100 µm. d–f = 20 µm, g = 10 µm.

Notes – A strain isolated in the present study clustered together with the *C. camelliae* (CGMCC 3.14925) within the gloeosporioides complex with 83% ML bootstrap value and 0.90 BYPP. The species isolated in this study was confirmed as *C. camelliae* based on both morphological characters and phylogenetic placement. *Colletotrichum camelliae* was introduced as *Glomerella cingulata* 'f. sp. *camelliae*' Dickens & R.T.A. Cook., which has been reported as causing twig blight and brown blight of *Camellia*. This species can be observed in many tea growing regions (Liu et al. 2015, Wang et al. 2016b).

Colletotrichum fructicola Prihast., L. Cai & K.D. Hyde, in Prihastuti et al., Fungal Diversity 39: 96 (2009) Fig. 22

Index Fungorum: IF515409; Facesoffungi number: FoF06767

Pathogenic or saprobic on *Camellia sinensis* leaves. Sexual morph: not observed. Asexual morph: *Conidiophore* reduced to a conidiogenous cell. *Conidiogenous cell* hyaline, thick ampliform, *Conidia* 10–14 × 3–4 µm ($\bar{x}$ = 10 × 3 µm, n = 40), common in mycelium, one–celled, smooth–walled with a large guttule at the centre and surrounded by smaller guttules, hyaline, cylindrical with obtuse to slightly rounded ends, sometimes oblong.

Culture characteristics – colonies on PDA reaches 90 mm at mm diam., in seven days at 25°C. Colonies are white initially then become grey to dark grey with age. Reverse greyish to black. Aerial mycelium pale grey, dense, cottony, without visible conidial masses.

Material(s) examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* leaves, June 2015, H.L. Li (dried culture JZBH330154), and living culture JZB330154.

Notes – In the present study an isolate obtained from tea leaves (out of two *Colletotrichum* isolates) clustered together with *Colletotrichum fructicola* (ICMP 18581) with 97% ML bootstrap and 0.97 PP. Colony characters and morphology (conidial shape and sizes) are similar to the ex–type isolate (Prihastuti et al. 2009). Based on morphology and phylogeny we confirmed our isolate as *Colletotrichum fructicola*. This species was introduced by Prihastuti et al. (2009) as a taxon associated with *Coffea arabica*. However, this species has been reported on *C. sinensis* from China and Indonesia (Liu et al. 2015).

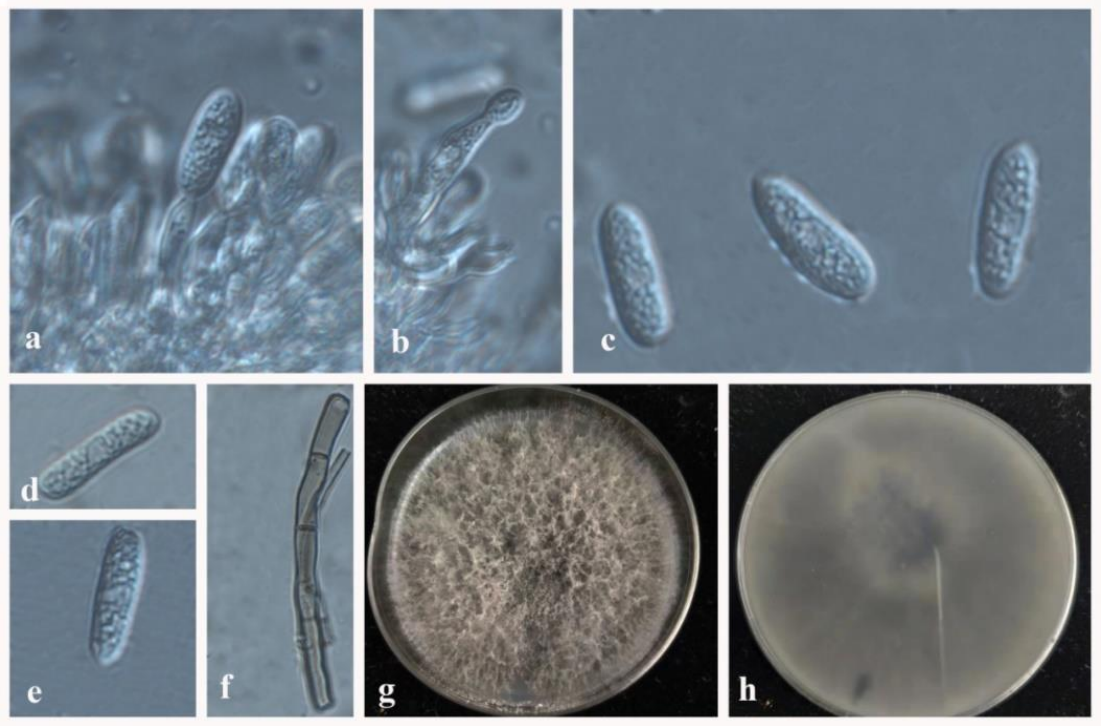

Figure 22 – *Colletotrichum fructicola* (JZB330154). a–b Conidiogenus cells with developing conidia. c–e Conidia. f Hyphae. g Upper view of the colony on PDA after 10 days. h Reverse view of the colony on PDA after 10 days. Scale bars: a–b = 20 µm, c–f = 10 µm.

Hypocreales Lindau, Natürl. Pflanzenfam.: 343 (1897)

Notes – Species belonging to Hypocreales are highly diverse in the tropics, subtropics and temperature regions (Põldmaa 2011). Hypocreales accepted with family *Bionectriaceae, Calcarisporiaceae, Clavicipitaceae, Cocoonihabitaceae, Cordycipitaceae, Flammocladiellaceae, Hypocreaceae, Myrotheciomycetaceae, Nectriaceae, Niessliaceae, Ophiocordycipitaceae, Sarocladiaceae, Stachybotryaceae,* and *Tilachlidiaceae* (Maharachchikumbura et al. 2016, Hyde et al. 2020b).

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

Notes – Species belonging to this family are diverse are biotrophic, hemibiotrophic, saprobic or hypersaprobic on a wide range of hosts. For recent taxonomic treatments, we follow Hyde et al. (2020b).

Trichoderma Pers., Neues Magazin für die Botanik 1: 92 (1794)

Notes – Species belonging to *Trichoderma* have a wide range of life modes that includes hypersaprobic on Basidiomycetes (Schuster & Schmoll 2001, Chen & Zhuang 2017). Some of the taxa are important as they produce industrially important enzymes (cellulases and hemicellulases), antibiotics, and some are used in biocontrol agents (Sivasithamparam & Ghisalberti 1998). In this study, we isolated eight strains belonging to three species including one novel species (Fig. 23).

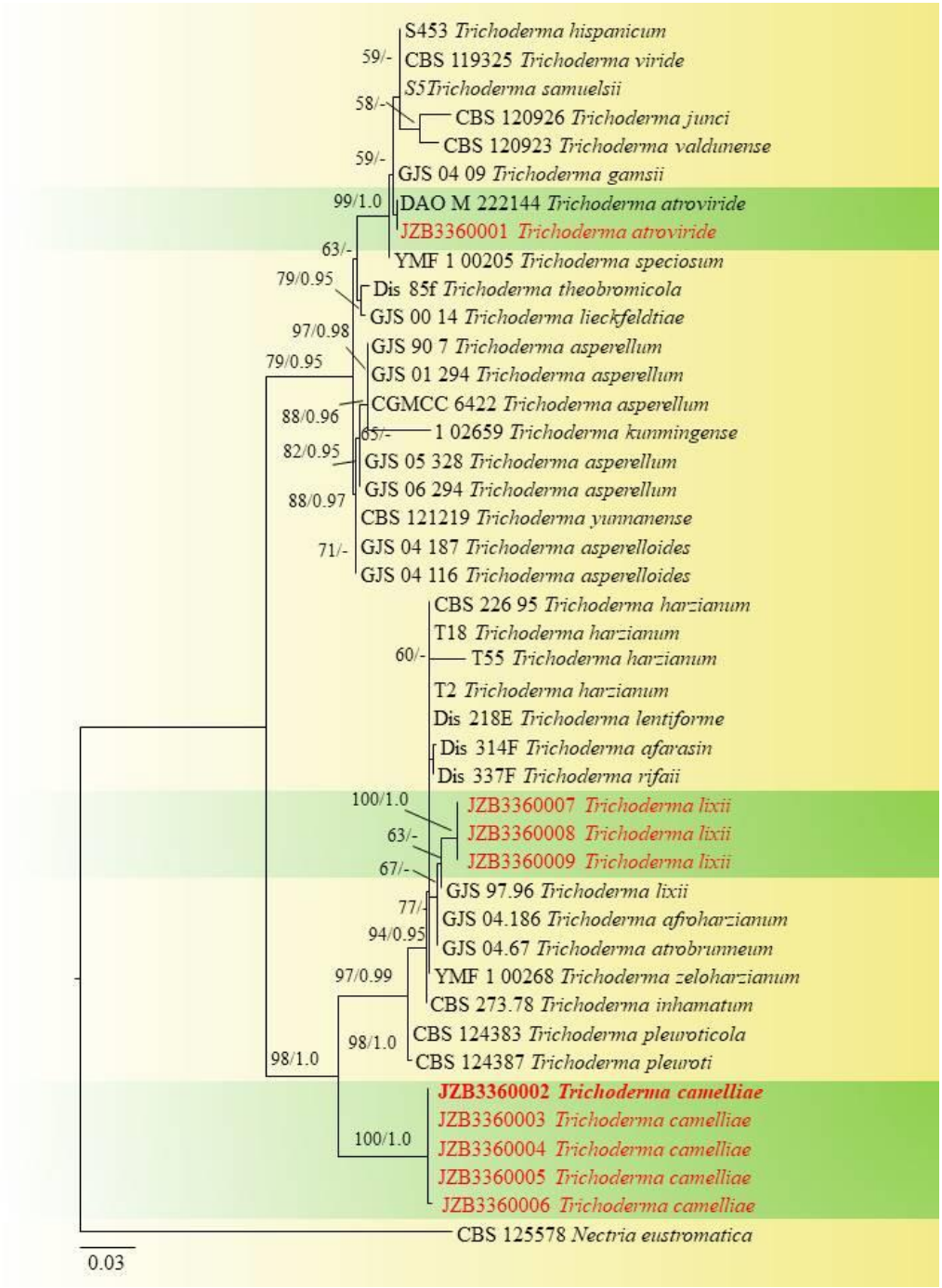

Figure 23 – Phylogenetic tree generated by ML analysis of combined ITS, *rpb2* sequence data *Trichoderma* species. 65 strains are included in the analyses. The tree is rooted with *Nectria eustromatica* (CBS 125578). Tree topology of the ML analysis was similar to BI. The best scoring RAxML tree with a final likelihood value of – 24349.980578 is presented. The matrix had 1172 distinct alignment patterns, with 9.91% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.251668, C = 0.245757, G = 0.259668, T = 0.242908; substitution rates AC = 1.353890, AG = 4.605576, AT = 1.059439, CG = 0.801610, CT = 9.121730, GT = 1.000000; gamma distribution shape parameter α = 0.944898. RAxML bootstrap support values ≥50% and Bayesian posterior probabilities ≥0.95 (BYPP) are shown near the nodes. The scale bar indicates 0.02 changes per site. Ex–type/ex–epitype strains are in **bold**. New isolates recovered in this study are in red.

Trichoderma atroviride P. Karst. 1892 Fig. 24

Index Fungorum: IF451289; Facesoffungi number: FoF09389

Pathogenic or saprobic on *Camellia sinensis* shoots. Sexual morph: Undetermined. Asexual morph *Conidiophores* tree–like, comprising a main axis with second branches, second branches paired, sometimes second branches branched again, main axis and branches terminating in whorls of up to five phialides. *Conidiogenous cells* phialidic, lageniform or ampulliform, arising singly, non–equilateral when curved. *Conidia* 4–5 × 3–3.5 µm ($\overline{x}$ = 4 ×3 µm, n = 30), ovoid, verrucose.

Culture characteristics – On PDA mycelium covers plate after three days at 25°C. Margin conspicuous and radial. Aerial hyphae, hairy to floccose, dense internal zone, but relative sparse on margin, abundantly and flat in a large green disc around the inoculum, turning green after 24 h of conidiation.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* shoots, June 2015, H.L. Li (dried culture JZBH3360001), and living cultures JZB3360001.

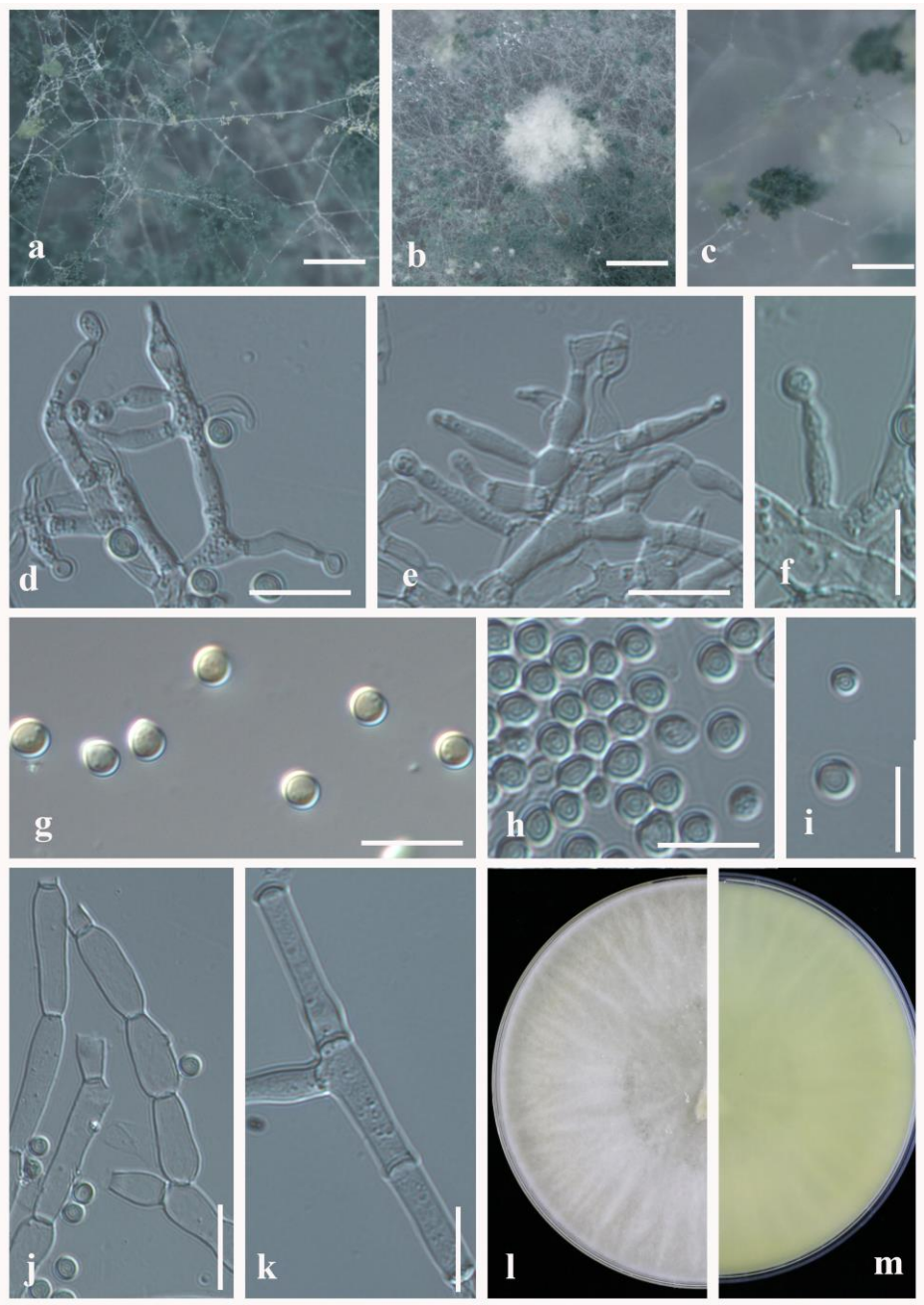

Figure 24 – *Trichoderma atroviride* (JZB3360001). a–c Conidiomata on PDA. d–f Branched conidiogenous cells. g–i Conidia. j, k Septate mycelia. l Upper view of the colony on PDA after three days. m Reverse view of the colony on PDA after three days. Scale bars: a–c, j, k = 100 µm, d–j = 10 µm.

Notes – The single isolate obtained in the present study clustered together with the *Trichoderma atroviride* (GAOM 222144) with 99% ML and 1.0 BYPP. Morphologically the strain isolated in the present study is similar to the species description of the type specimen (Brunner et al. 2005). *Trichoderma atroviride* is commonly isolated from soil and it is a well–known biocontrol agent (Brunner et al. 2005). This species has been reported on *Betula papyrifera, Morus* sp., *Triticosecale* sp., *Vitis vinifera,* and *Zea mays* (Farr & Rossman 2020). This is the first report of *T. atroviride* on *Camellia* species (Farr & Rossman 2020).

Trichoderma camelliae Jayaward., Manawas., X.H. Li, J.Y. Yan, & K. D. Hyde, sp. nov.

Fig. 25

Index Fungorum: IF558000, Facesoffungi Number: FoF09390

Etymology – refers the host genus

Holotype – JZBH3360002

Pathogenic or saprobic on *Camellia sinensis* leaves and shoots. Sexual morph: Not observed. Asexual morph Mycelia aseptate, branched, effused *Conidiophores* scattered, dark green to greyish–green, tree–like, comprising a main axis. *Conidiogenous cells* ampulliform, arising singly as clusters. *Conidia* developed at the hyphal end also observed. *Conidia* 1.5 –2× 1–2 µm ($\overline{x}$ = 2×2 µm, n = 40) ovoid to short ellipsoidal, verrucose.

Culture characteristics – On PDA mycelium covers plate after three days at 25°C. Aerial hyphae, hairy dense internal zone, initially white mycelium with time become pale yellow. Develop abundant, and flat large green disc around the inoculum, turning green.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* leaves and shoots, June 2015, H.L. Li (dried cultures JZBH3360002 holotype; JZBH3360003 – JZBH3360006 paratypes), and living JZB3360002 ex–holotype; JZB3360003 – JZB3360006 ex–paratypes.

Notes – The isolates obtained in the present study fit well morphologically within the *Trichoderma*. The present species, *Trichoderma camelliae*, developed a strongly supported monophyletic clade with 100% ML and 1.0 BYPP values. Morphologically this species differs from the type species of *Trichoderma viride*, by developing ellipsoidal and larger conidia, whereas conidia of the type species are mostly ovoid and smaller than the species identified in this study (0.7 µm long and 1 µm diam.) (Lieckfeldt et al. 1999).

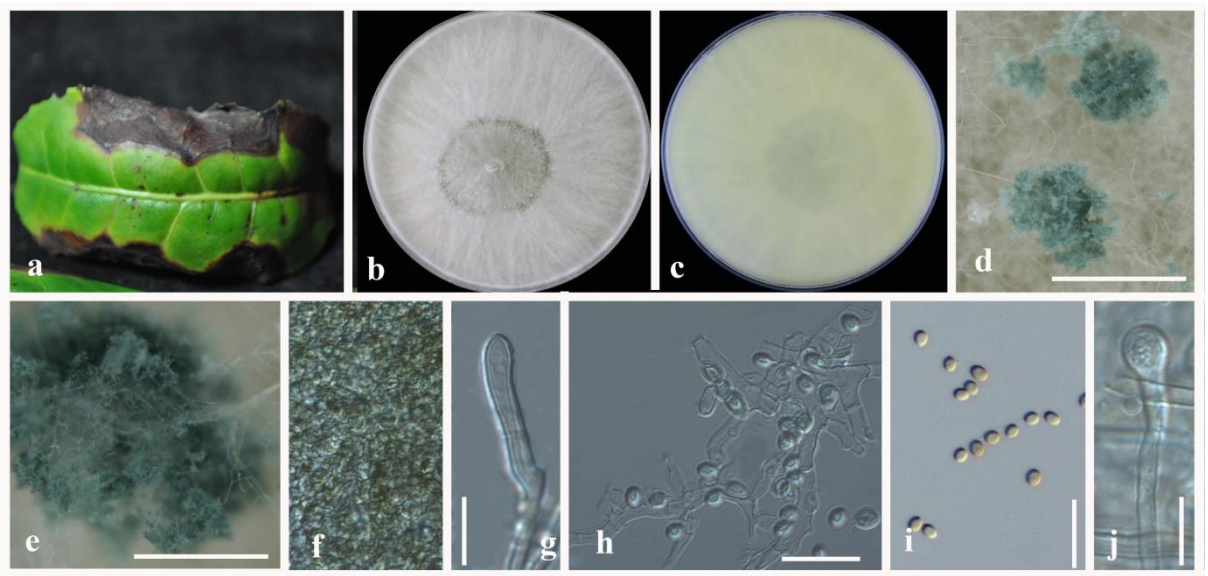

Figure 25 – *Trichoderma camelliae* (JZB3360002 ex–holotype). a Diseased leaf. b Upper view of the colony on PDA after three days. c Reverse view of the colony on PDA after three days. d–e Conidiomata on PDA. f Pycnidal wall. g Conidiogenous cell. h–i Conidia. j Germinating conidium. Scale bars: d, e = 100 µm, f, g = 100 µm, h–j = 10 µm.

Trichoderma lixii (Pat.) P. Chaverri, in Chaverri et al., Mycologia 107(3): 578 (2015) Fig. 26

Index Fungorum: IF 809999; Facesoffungi number: FoF09391

Pathogenic or saprobic on *Camellia sinensis* leaves. Sexual morph: Undetermined. Asexual morph: *Mycelium* aseptate, less branched, developed effused. *Conidiomata* pycnidial, black, superficial. *Conidiophores* less branched, branches arise horizontally from the main axis initially yellow later turning grey. *Conidiogenous cells* phialidic ampulliform, arising solitary, haline thin–walled, smooth, Conidia 2–4 × 1–2 µm ($\bar{x}$ = 3–1.5 µm, n = 30), ovoid, verrucose *Clamydospres* developed at the terminals of the hyphal tips, ovoid, various in size, develop single germination tube.

Culture characteristics – On PDA mycelium covers the plate after three days at 25°C. Colony layered distinctly, margin conspicuous and radial. Arial hyphae, hairy to the floccose, dense internal zone. Pycnidia appear as concentric rings, dense near the edge of the plate. Initially white and become olivaceous yellow. Reverse olivaceous brown.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* leaves, June 2015, H.L. Li (dried cultures JZBH3360007 and JZBH3360008), living cultures JZB3360007 and JZB3360008.

Notes – The species identified in the present study clusters together with *Trichoderma lixii* (GJS 97.96) with 44% ML, and 1.0 BYPP values. This isolate is morphologically similar to the type species description of *T. lixii* (Chaverri et al. 2015). In pairwise nucleotide comparison of ITS region (534bp) between our species (JZB3360008) and closely associated *Trichoderma lixii* (GJS 97.96) revealed 0.37% base pair differences. However, *rpb2* sequence is available for only one strain isolated in this study. This might be the reason the three isolates obtained in this study develop a distinct cluster. Based on these we identified the strains in this study as *T. lixii*. This is the first report of *T. lixii* on *Camellia* species (Farr & Rossman 2020).

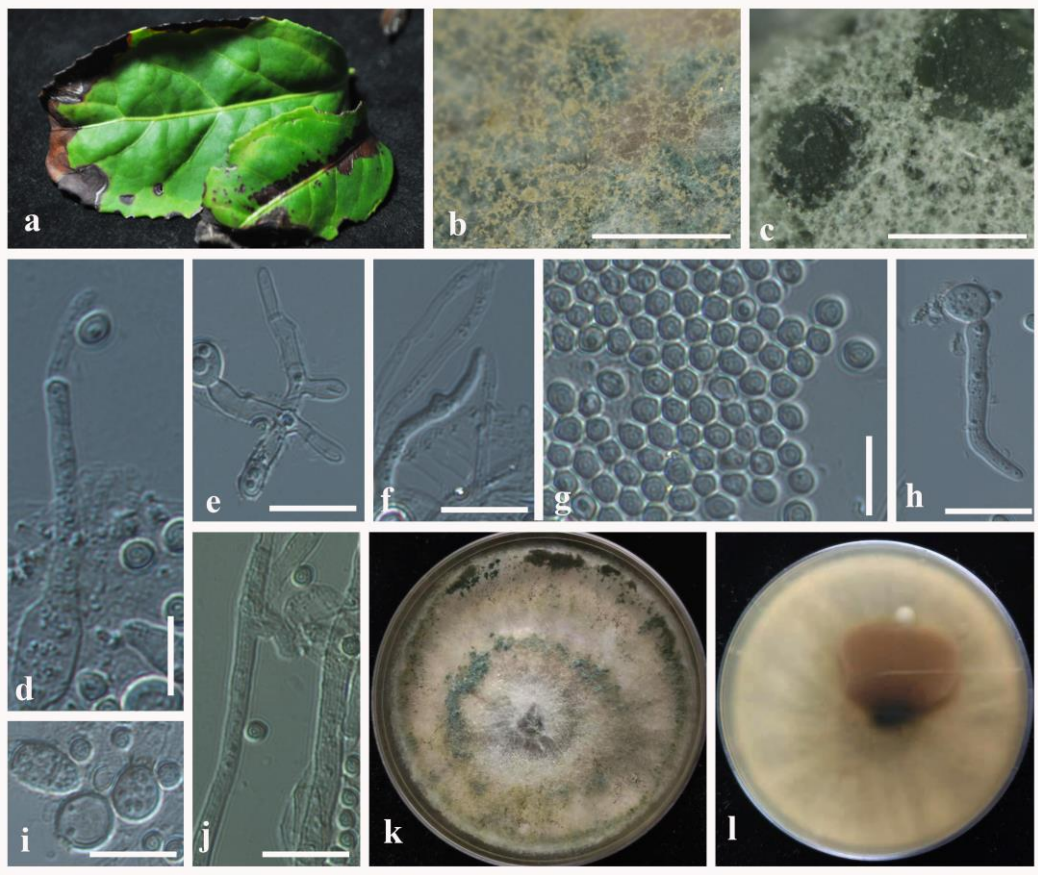

Figure 26 – *Trichoderma lixii* (ZB3360007). a–c Conidiomata on PDA. d–f Conidiogenous cells e–f Branched conidiogenous cells. g–i Conidia. j Septate mycelia. j Upper view of the colony on

PDA after three days. k Reverse view of the colony on PDA after three days. Scale bars: a–c = 100 µm. d–f, j = 20 µm. g–i = 10 µm.

Nectriaceae Tul. & C. Tul., Selecta Fungorum Carpologia: Nectriei–Phacidiei– Pezizei 3: 3 (1865)

Notes – *Nectriaceae* species are commonly found as saprobes, plant endophytes or pathogens, mycopathogen or pathogens on insects (Hyde et al. 2020b). For taxonomic treatments, we follow Hyde et al. (2020b).

Fusarium Link, Magazin der Gesellschaft Naturforschenden Freunde Berlin 3 (1): 10 (1809

Notes – *Fusarium* species are well–known plant pathogens, saprobes and some species produce mycotoxins that can contaminate food (Perincherry et al. 2019). For the species level characterisation of *Fusarium* morphological characters together with molecular data are required. In this study, we isolated nine strains that belong to three species representing three new host records (Fig. 27).

Fusarium asiaticum O'Donnell, T. Aoki, Kistler & Geiser, in O'Donnell, Ward, Geiser, Kistler & Aoki, Fungal Genetics Biol. 41(6): 619 (2004) Fig. 28

Index Fungorum: IF809999; Facesoffungi number: FoF09392

Pathogenic or saprobic on *Camellia sinensis* shoots. Sexual morph: not observed. Asexual morph: Conidia develop in the aerial mycelium. *Conidiophores* not observed. *Conidia* conidia 30–40 × 2–4 µm ($\overline{x}$ = 30 × 3 µm, n = 30), sporodochial conidia gradually curved and frequently widest above the mid–region, septate, smooth and thin–walled. *Chlamydospores* not seen.

Culture characteristics – Colonies on PDA covers the entire plate within five days. Entire margin, aerial mycelium reddish–white velvety to lanose. Pigmentation in reverse, sclerotia absent later becomes dark purple.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* shoots, June 2015, H.L. Li dried cultures JZBH110019–23), and living cultures JZB110019–23.

Notes – Five isolates from in this study cluster together with the *Fusarium asiaticum* (CBS110257) with 99% ML and 87% MP bootstrap values. These isolates share similar morphology to the type description of *F. asiaticum* (Leslie & Summerell 2008). *Fusarium asiaticum* is a well–known pathogen causing Fusarium head blight (Qiu et al. 2019). This species has been reported on *Bletilla striata*, *Glycine max*, *Hordeum vulgare*, *Lolium multiflorum*, *Oryza sativa*, *Triticum aestivum* and *Zea mays*, which are all monocot plants (Farr & Rossman 2020). This is the first report of *Fusarium asiaticum* associated with *Camellia sinensis* (Farr & Rossman 2020).

Fusarium concentricum Nirenberg & O'Donnell Mycologia 90(3): 442 (1998) Fig. 29

Index Fungorum: IF 809999; Facesoffungi number: FoF 09423

Pathogenic or saprobic on *Camellia sinensis* leaves and shoots. Sexual morph: Not observed. Asexual morph: Sporulation is starting early in the aerial mycelium. *Conidia* develop in false heads, the aerial conidiophores. *Conidiogenous cells* monophialides and polyphialides cylindrical flask–shaped. *Conidia* 8–12 × 3–4 µm ($\overline{x}$ = 10 × 3 µm, n = 30), develop in the aerial mycelium, oval, obovoid to allantoid, aseptate, smooth– and thin–walled, *Chlamydospores* not observed. Sporodochial conidia not observed.

Culture characteristics – Colonies on PDA grow 45mm diam., after five days. Entire margin, aerial mycelium white velvety. Pigmentation in reverse initiates after 10–14 days, pale orange and reddish grey concentric rings, later becoming dark purple.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* leaves and shoots, June 2015, H.L. Li dried cultures JZBH3110010– JZBH3110014), and living cultures JZB3110010– JZB3110014.

Notes – Six isolates obtained in the present study cluster together with the *Fusarium concentricum* in the phylogenetic analysis forming strongly supported clade with 100% ML and

100% MP bootstrap values. Morphologically species identified in the present study share similar characters to those of the *Fusarium concentricum* type species (Leslie & Summerell 2008). However, we did not observe sporodochial conidia after 10 days of incubation. This species has been reported on several different hosts including *Capsicum annum* (Wang et al. 2013), *Musa* sp. (Sandoval–Denis et al. 2018), *Nilaparvata lugens* (Nirenberg & O'Donnell 1998), *Oryza sativa* (Aoki et al. 2002, Choi et al. 2019), *Paris polyphylla* var. *chinensis* (Xiao et al. 2019), *Triticum aestivum* (Aoki et al. 2002) and *Vanilla* sp. (Koyyappurath et al. 2016). This is the first report of *Fusarium concentricum* on *Camellia sinensis* (Farr & Rossman 2020).

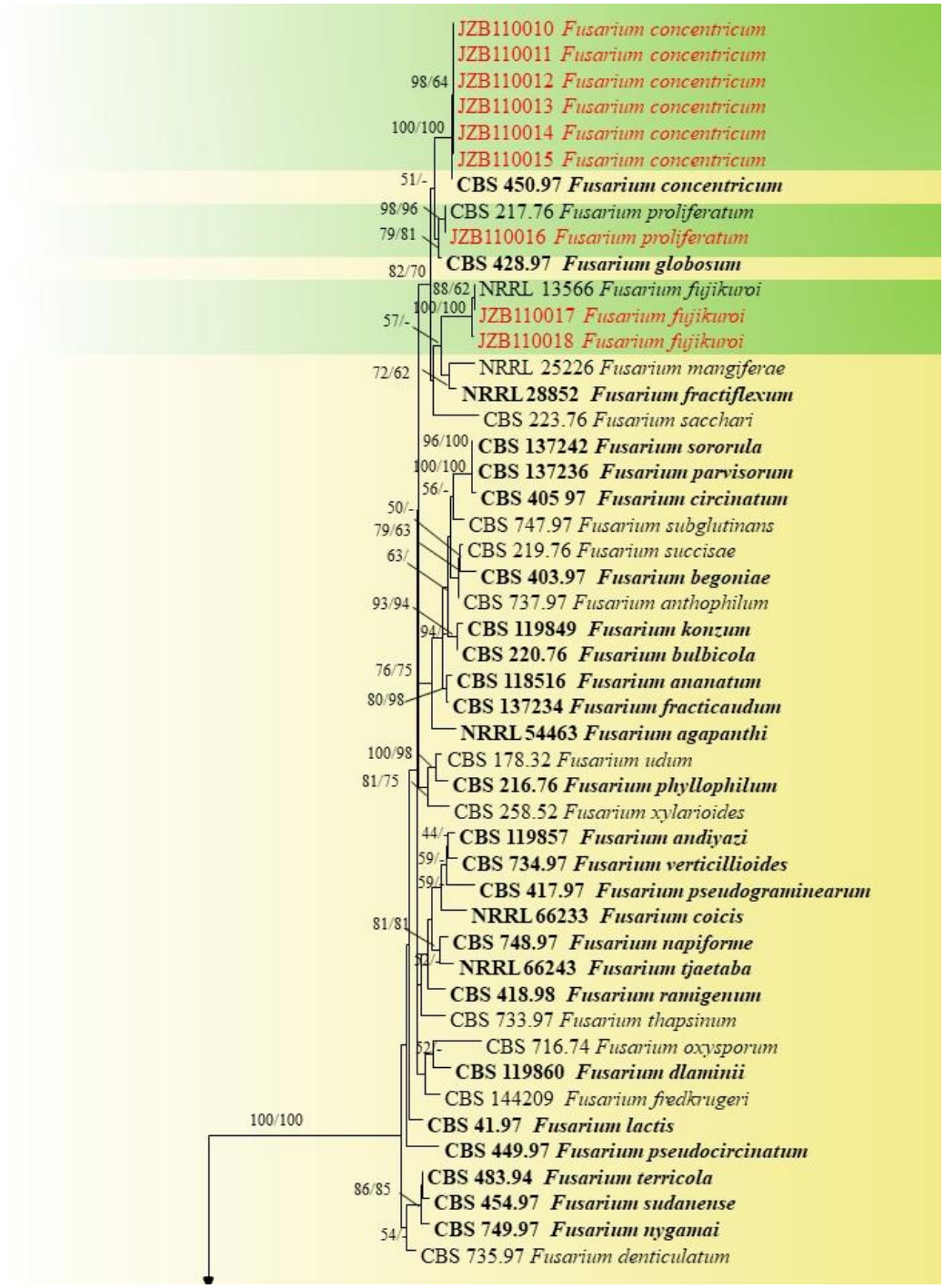

Figure 27 – Phylogenetic tree generated by MP analysis of combined *tef1* and *rpb2* sequence data of *Fusarium* species. Eighty strains are included in the analyses. *Fusarium buharicum* (CBS 796.70) and *Fusarium* sp. NRRL 66182 were used to root the tree. Tree topology of the ML analysis was similar to the MP and BI. The best scoring RAxML tree was with a final likelihood

value of –7573.307178 is presented. The matrix had 358 distinct alignment patterns, with 2.33% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.280950, C = 0.235343, G = 0.263312, T = 0.220394; substitution rates AC = 2.323636, AG = 8.480494, AT = 2.016299, CG = 1.445800, CT = 22.415448, GT = 1.000000; gamma distribution shape parameter α = 1.499621**.** Maximum parsimony analysis of 864 constant characters and 302 informative characters resulted in 62 equally most parsimonious tree of 462 steps (CI = 0.381, RI = 0.836, RC = 0.318, HI = 0.619). RAxML bootstrap support and maximum parsimony bootstrap support values ≥50% are shown near the nodes. The scale bar indicates 0.05 changes per site. Ex–type (ex–epitype) strains are in **bold**. New isolates recovered in this study are given in red.

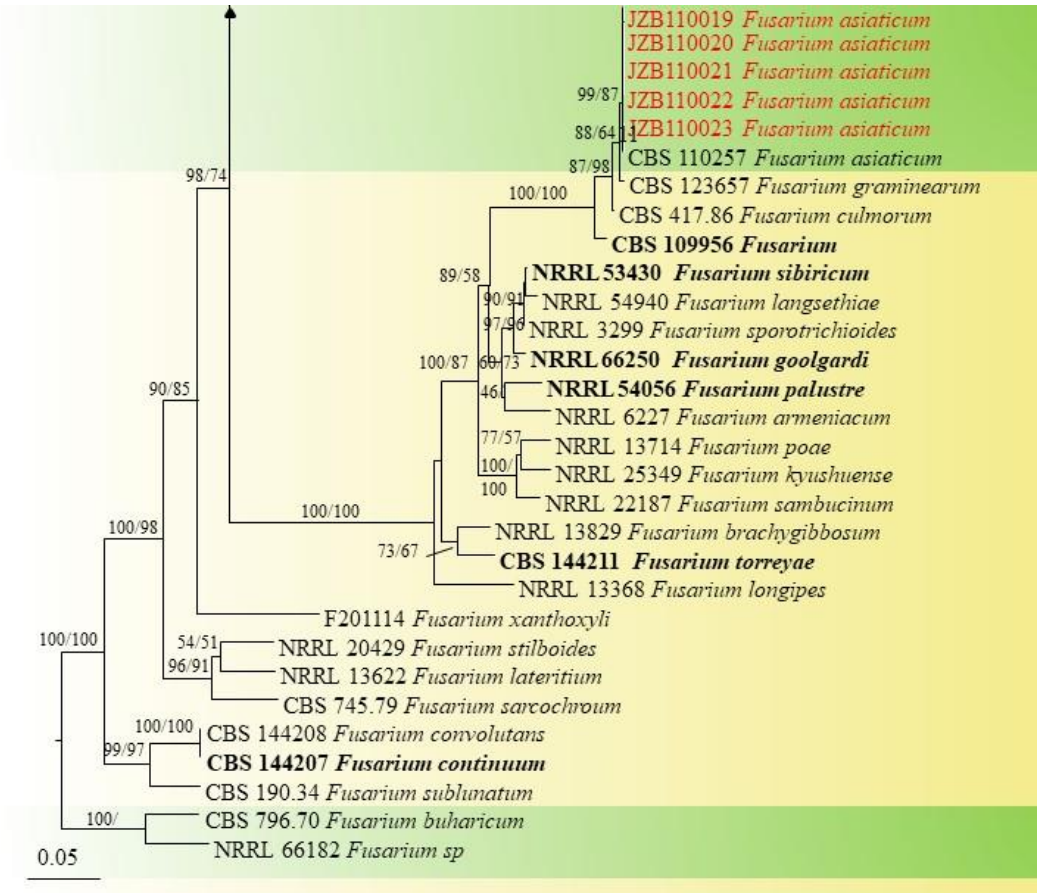

Figure 27 – Continued.

Fusarium fujikuroi Nirenberg, Mitt. biol. BundAnst. Ld– u. Forstw. 169: 32 (1976) Fig. 30

Index Fungorum: IF 809999; Facesoffungi number: FoF09393

Pathogenic or saprobic on *Camellia sinensis* leaves and shoots. Sexual morph: not observed. Asexual morph: Sporulation is starting early in the aerial mycelium. Aerial conidiophores cynlindrical mono and polyphialidic. *Conidia* 8–26 × 2–5 µm ($\bar{x}$ = 16 × 3 µm, n = 40), develop in the aerial mycelium obovoid and oval to allanoid, asepatae, smooth– and thin–walled, chlamydospores absent.

Culture characteristics – Colonies on PDA grows covers the entire plate within five days. Colony margin entire, aerial mycelium reddish–white velvety to lanose. Pigmentation in reverse consisting of the concentric pink ring the middle and pale orange ring at the margin. Later becoming dark purple.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* leaves and shoots, June 2015, H.L. Li dried cultures JZBH110017 and JZBH110018), and living cultures JZB110017 and JZB110018.

Notes – Two isolates obtained in this study cluster with *Fusarium fujikuroi* (NRRL13566) representative strain by forming a strongly supported clade with 100% ML, and 100% MP bootstrap values. In a comparison of morphology and sequence data, these two strains did not show any significant differences. Therefore, we confirmed these two strains as *Fusarium fujikuroi*. This species has been reported causing Fusarium wilt of soybean, rice and barnyard grass in Korea (Choi et al. 2019). This the first report of this species associated with *Camellia sinensis* in China (Farr & Rossman 2020).

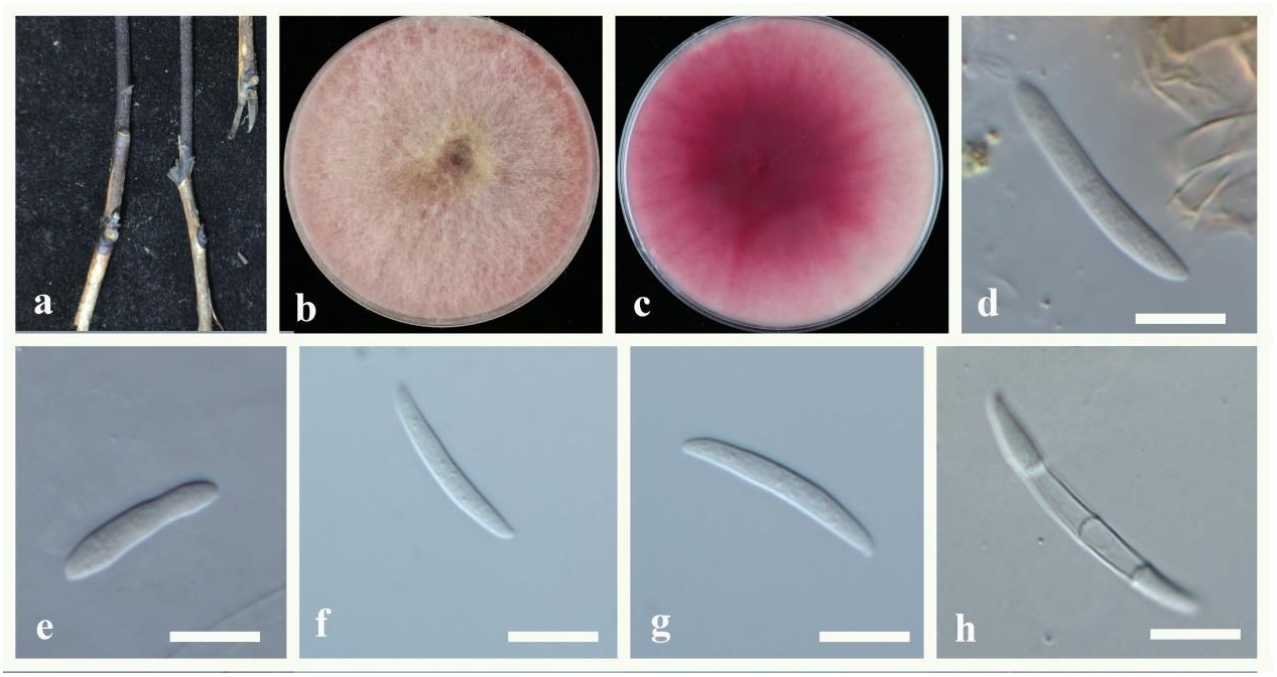

Figure 28 – *Fusarium asiaticum* (JZB110020). a Diseased shoot. b Upper view of the colony on PDA after five days. c Reverse view of the colony on PDA after five days. d Conidiophores of aerial mycelium. e Conidia. Scale bars: d 20 μm. e = 10 μm.

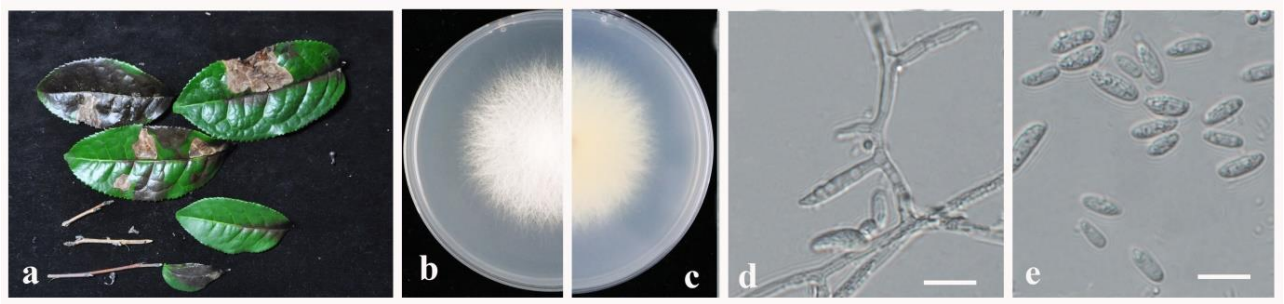

Figure 29 – *Fusarium concentricum* (JZB110013). a Diseased leaves and shoots. b Upper view of the colony on PDA after five days. c Reverse view of the colony on PDA after five days. d Conidiophores of aerial mycelium. e Conidia. Scale bars: d = 20 μm, e = 10 μm.

Fusarium proliferatum (Matsush.) Nirenberg ex Gerlach & Nirenberg, Mitt. biol. BundAnst. Ld– u. Forstw. 169: 38 (1982) Fig. 31

Index Fungorum: IF 809999; Facesoffungi number: FoF09394

Pathogenic or *saprobic* on *Camellia sinensis* shoots. Sexual morph: not observed. Asexual morph: Sporulation is starting early in the aerial mycelium. *Conidia* develop in false heads of mycelia, the aerial conidiophores cynlindrical mono and pluphyialidic, phialides flask–shaped. *Conidia* 12–21 × 2–5 μm ($\overline{x}$ = 16 × 3 μm, n = 30), develop in the aerial mycelium obovoid and oval

to allanoid, mostly asepatae occasionally one septate, smooth and thin–walled, *Sporodochial conidia* rare, septate, smooth and thin–walled. Chlamydospores not observed.

Culture characteristics – Colonies on PDA grows 45mm diam., after five days. Colony margin is entire aerial mycelium white velvety to lanose. Pigmentation not observed. Colony surface dry, white becoming livid pink towards the margin, turning completely light pink with age.

Material examined – CHINA, Fujian Province, Zhangzhou County, pathogenic on dead *Camellia sinensis* shoot, June 2015, H.L. Li dried cultures JZBH110016, and living cultures JZB110016.

Notes – The single isolate obtained in this study clustered together with *Fusarium proliferatum* (CBS 217.76) representative strain by developing a strong clade with 98% ML and 96% MP bootstrap values. In a comparison of morphology and sequence data, these two strains share the same characters. This species is a well–known pathogenic species causing diseases in Maize (Visentin et al. 2009). There are 199 records under this species in Farr & Rossman (2020) database. This the first report of this species associated with *Camellia sinensis* in China (Farr & Rossman 2020).

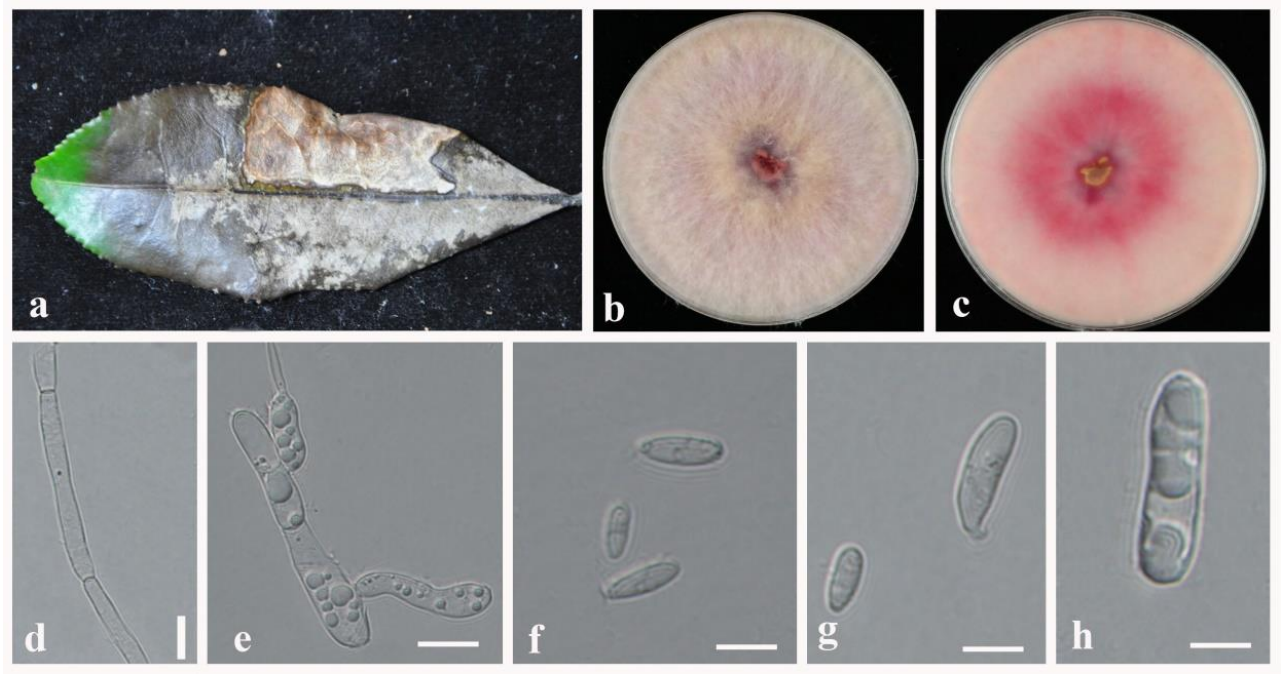

Figure 30 – *Fusarium fujikuroi* (JZB110018). a Diseased leaf. b Upper view of the colony on PDA after five days. c Reverse view of the colony on PDA after five days. d Hyphae. e conidiophores. f–h conidia**.** Scale bars: d–h = 10 µm.

Figure 31 – *Fusarium proliferatum* (JZB110016). a Sporocadial conidia. b–d conidia. e Septate mycelia. f Upper view of the colony on PDA after five days. g Reverse view of the colony on PDA after five days. Scale bars: a–e = 10 µm.

Subclass Sordariomycetidae O.E. Erikss. & Winka, Myconet 1: 10 (1997)

Sordariales Chadef. ex D. Hawksw. & O.E. Erikss., Systema Ascomycetum 5: 182 (1986)

Notes – Sordariales was introduced by Hawksworth & Eriksson (1986) and consists of three families *Chaetomiaceae*, *Sordariaceae* and *Lasiosphaeriaceae*. The Sordariales species are characterized by membranous or coriaceous ascomata, and hyaline or brown ascospores often with appendages or sheaths (Zhang et al. 2006). The taxonomic treatment follows Maharachchikumbura et al. (2016) and Hyde et al. (2020b).

Chaetomiaceae G. Winter]as 'Chaetomieae'[, Rabenh. Krypt.–Fl., Edn 2 (Leipzig) 1.2: 153 (1885)

Notes – *Chaetomiaceae* belongs to *Sordariales* (Wijayawardene et al. 2020). The species in this family are mostly opportunistic fungi in both animals and plants (Plumlee et al. 2017). Some species are commonly found in plant debris and they play a significant role in degradation of plant debris (Plumlee et al. 2017).

Chaetomium Kunze, Mykologische Hefte (Leipzig) 1: 15 (1817)

Notes – *Chaetomium* was established by Kunze (Kunze & Schmidt 1817). Since then, this genus has undergone several taxonomic reassignments (Wang et al. 2016a). For taxonomic treatments we refer to Wang et al. (2016a). In the present study, we identified two strains that belong to a novel species based on both morphology and phylogeny (Fig. 32).

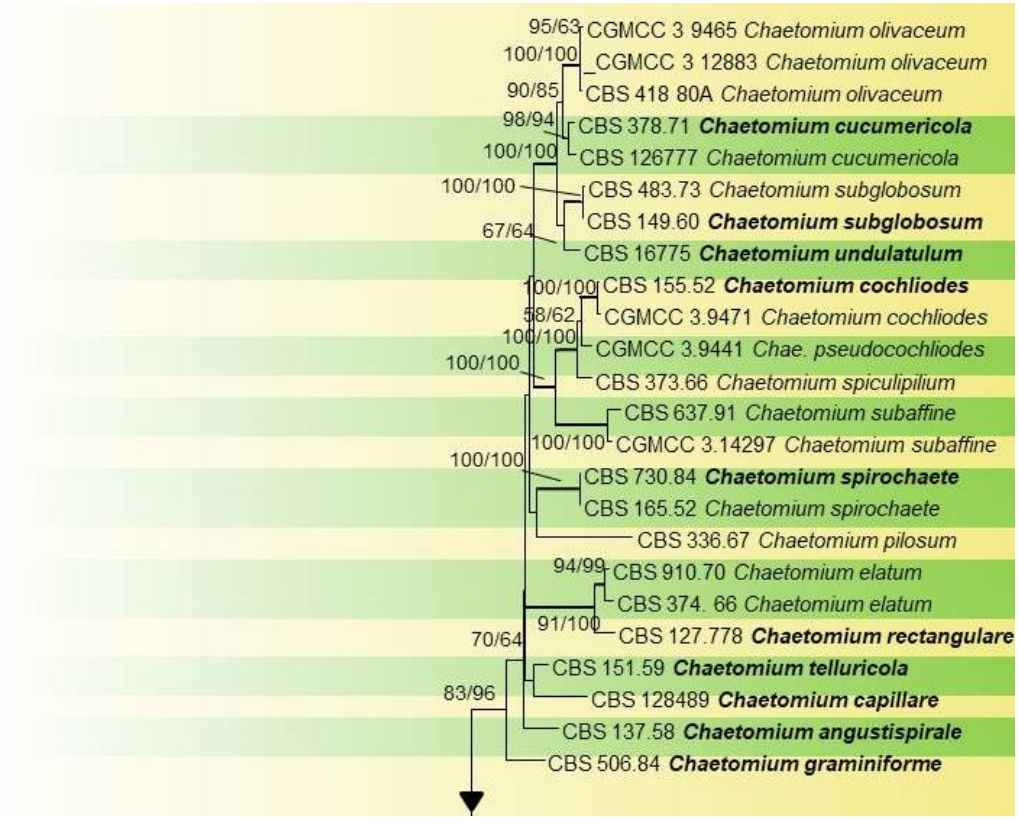

Figure 32 – Phylogenetic trees generated by MP analysis of combined LSU, ITS, *tub2*, *tef1* and *rpb2* sequence data of *Chaetomium* species. The tree is rooted with *Achaetomium strumarium* **(**CBS 333.67**)**. Tree topology of the ML analysis was similar to the MP and BI. The best scoring RAxML tree was with a final likelihood value of –16838.646969. The matrix had 853 distinct alignment patterns, with 4.88% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.229473, C = 0.292519, G = 0.272427, T = 0.205580; substitution rates AC = 0.805009, AG = 3.277592, AT = 0.803238, CG = 1.189987, CT = 5.975471, GT = 1.000000; gamma distribution shape parameter α = 0.564760. Maximum parsimony analysis of 3388 constant

characters and 639 informative characters resulted in five equally most parsimonious tree (TL = 2253, CI = 0.525, RI = 0.828, RC = 0.435, HI = 0.475). RAxML bootstrap support values ≥75% and MP bootstrap support values ≥50% are shown near the nodes. Nodes with BYPP ≥0.95 are thicked. The scale bar indicates 0.02 changes per site. Ex–type/ ex–epitype strains are in **bold** and new isolates recovered in the present study are in red.

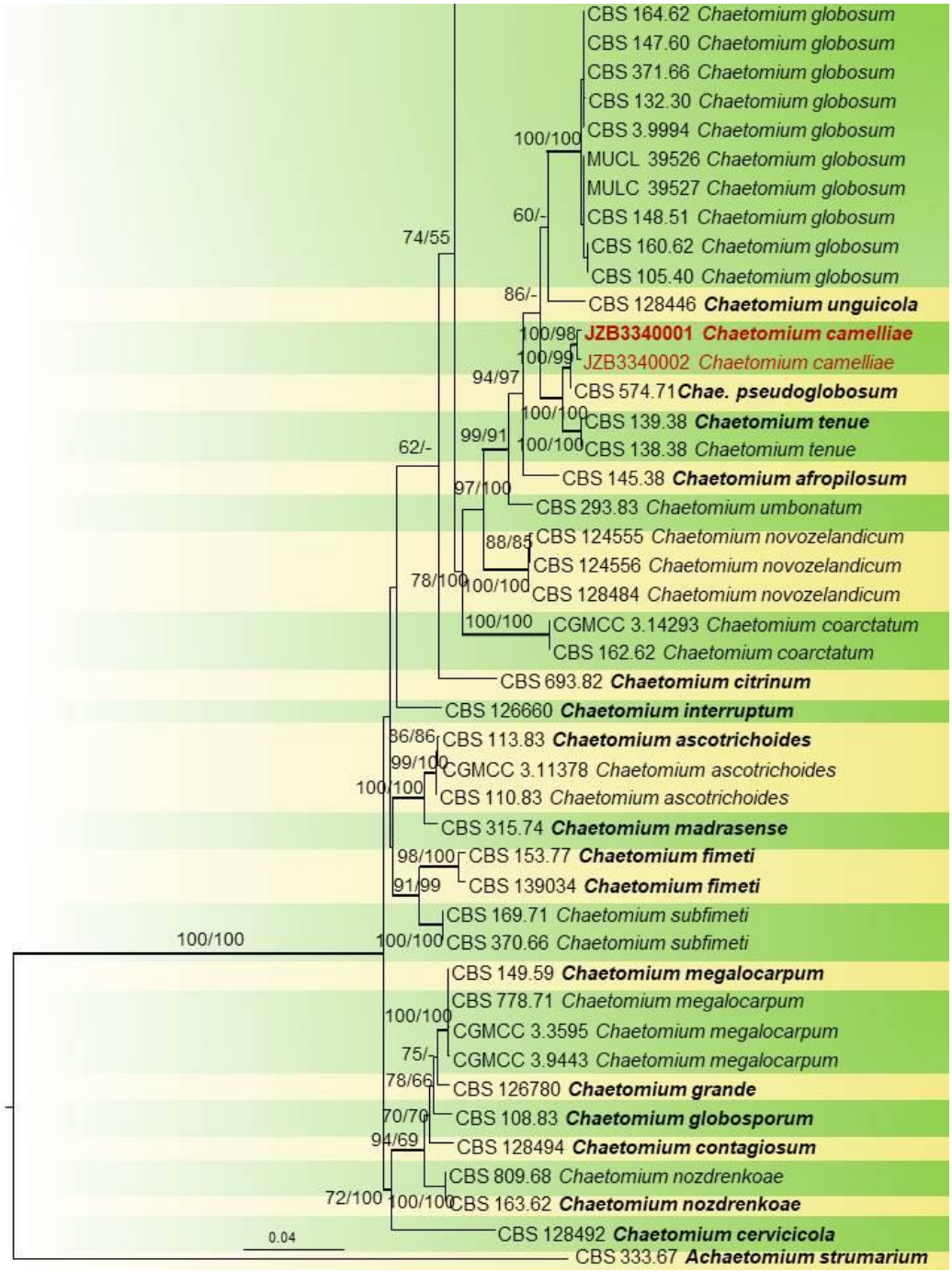

Figure 32 – Continued.

Chaetomium camelliae Jayaward., Manawas., X.H. Li, J.Y.Yan, & K. D. Hyde, sp. nov. Fig. 33

Index fungorum: IF558001; Facesoffungi number: FoF03512

Etymology – The specific epithet is derived from that of the host plant

Holotype – JZBH3340001

Pathogenic or saprobic on *Camellia sinensis* leaves. Sexual morph: *Ascomata* superficial, ostiolate, yellowish to greenish olivaceous subglobose, 165–315 µm diam. *Ascomatal wall* brown,

composed of hypha–like cells, *textura intricata* in surface view. *Asci* fasciculate, clavate, 20–30 × 10–15 µm ($\overline{x}$ = 20 × 10 µm, n = 20), stalks 20–40 µm long, with 6–7 ascospores, *Ascospores* 10–12 × 6–8 µm ($\overline{x}$ = 10 × 7 µm, n = 40), hyaline at the begin become olivaceous brown when mature, limoniform, bilaterally flattened slightly with age, with an apical germ pore. Asexual morph: not observed.

Culture characteristics – Colonies on PDA grow 95 mm diam., within five days, yellowish floccose aerial hyphae, and greenish exudates; reverse light brown.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* leaves, June 2015, H.L. Li (dried cultures; JZBH3340001 holotype; JZBH3340002 isotype–2) and living cultures JZB3340001 ex–holotype; JZB3340002 ex–isotype.

Notes – Preliminary data analysis of ITS region revealed the taxon isolated in the present study belongs to *Chaetomium*. According to the phylogenetic analysis based on LSU, ITS, *tef1* and *tub2*, the isolates obtained from the current study developed a clade sister to *Chaetomium pseudoglobosum* (CBS 574.71) with 100% ML bootstrap, 99% MP bootstrap and 1.0 BYPP. In a pairwise sequence comparison between the sequences of the type of the present study and *Chaetomium pseudoglobosum* (CBS 574.71), there was 8% nucleotide difference in LSU along with the 584 nucleotides and 4% nucleotide difference in ITS along the 521 nucleotides. In comparisons of protein-coding regions; there were 3% differences in *tef1* (out of 926 nucleotides), 1% differences in *tub2* (465 nucleotides) and 7% differences in *rpb2* (565 nucleotides). Based on both morphological and molecular data the strains isolated in the present study were identified as a new species. There is only one record of species of *Chaetomium* associated with *Camellia* flowers (Watson 1950).

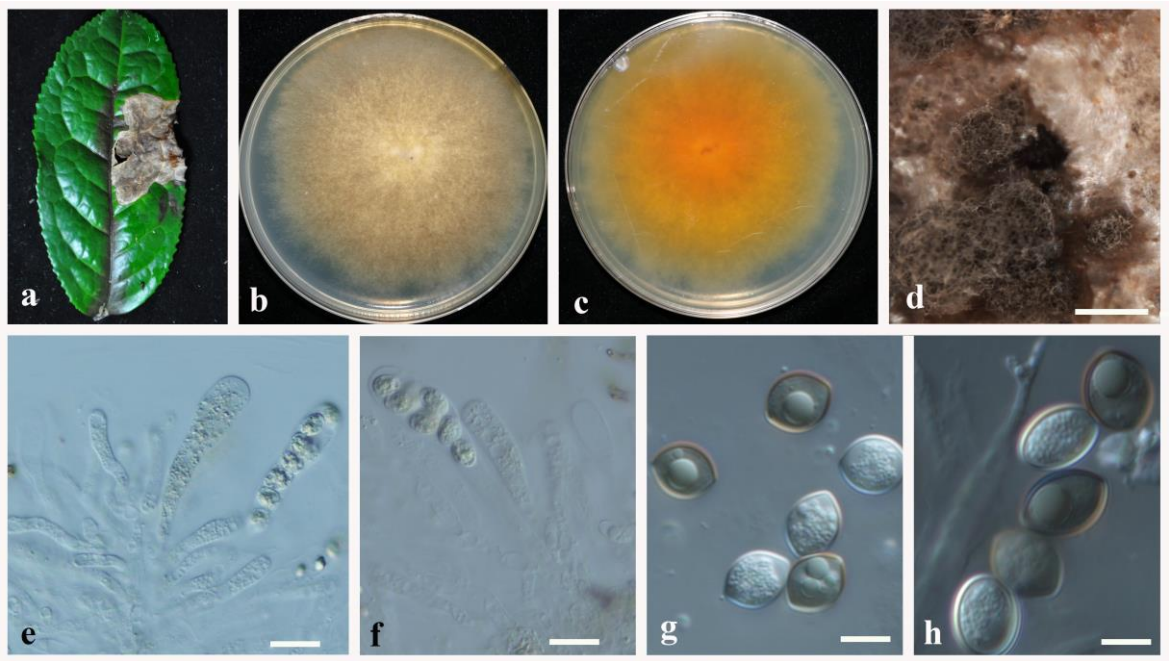

Figure 33 – *Chaetomium camelliae* (JZB340001 Ex-holotype). a Diseased leaf. b Upper view of the colony on PDA after five days. c Reverse view of the colony on PDA after five days. d ascomata on PDA. e–f Asci. g–h Ascospores. Scale bars: d = 1000 µm, e–f = 20 µm, g, h = 10 µm.

Subclass Xylariomycetidae O.E. Erikss & Winka, Myconet 1: 12 (1997)

Amphisphaeriales D. Hawksw. & O.E. Erikss., Systema Ascomycetum 5: 177 (1986)

Notes – Currently there are 17 families and 88 genera in this order (Hyde et al. 2020b). For recent taxonomic treatment we follow Hyde et al. (2020b).

Apiosporaceae K.D. Hyde, J. Fröhl., Joanne E. Taylor & M.E. Barr., in Hyde, Fröhlich & Taylor, Sydowia 50(1): 23 (1998)

Notes – *Apiosporaceae* was introduced by Hyde et al. (1998). After several years of taxonomic conflicts, it is now accepted under *Xylariales* (Smith et al. 2003, Daranagama et al. 2018). The type genus of this family is *Apiospora* Sacc. *Apiosporaceae* species are endophytes pathogens and saprobes on a wide range of hosts (Hyde et al. 1998).

Arthrinium Kunze., in Kunze & Schmidt, Mykologische Hefte (Leipzig) 1: 9 (1817)

Notes – Species in *Arthrinium* are found in a wide range of hosts as plant pathogens (Chen et al. 2014), lichens (He & Zhang 2012) marine algae (Suryanarayanan 2012), soil (Singh et al. 2012) and human pathogens (de Hoog et al. 2000). The current study identified one strain of *Arthrinium jiangxiense* (Fig. 34).

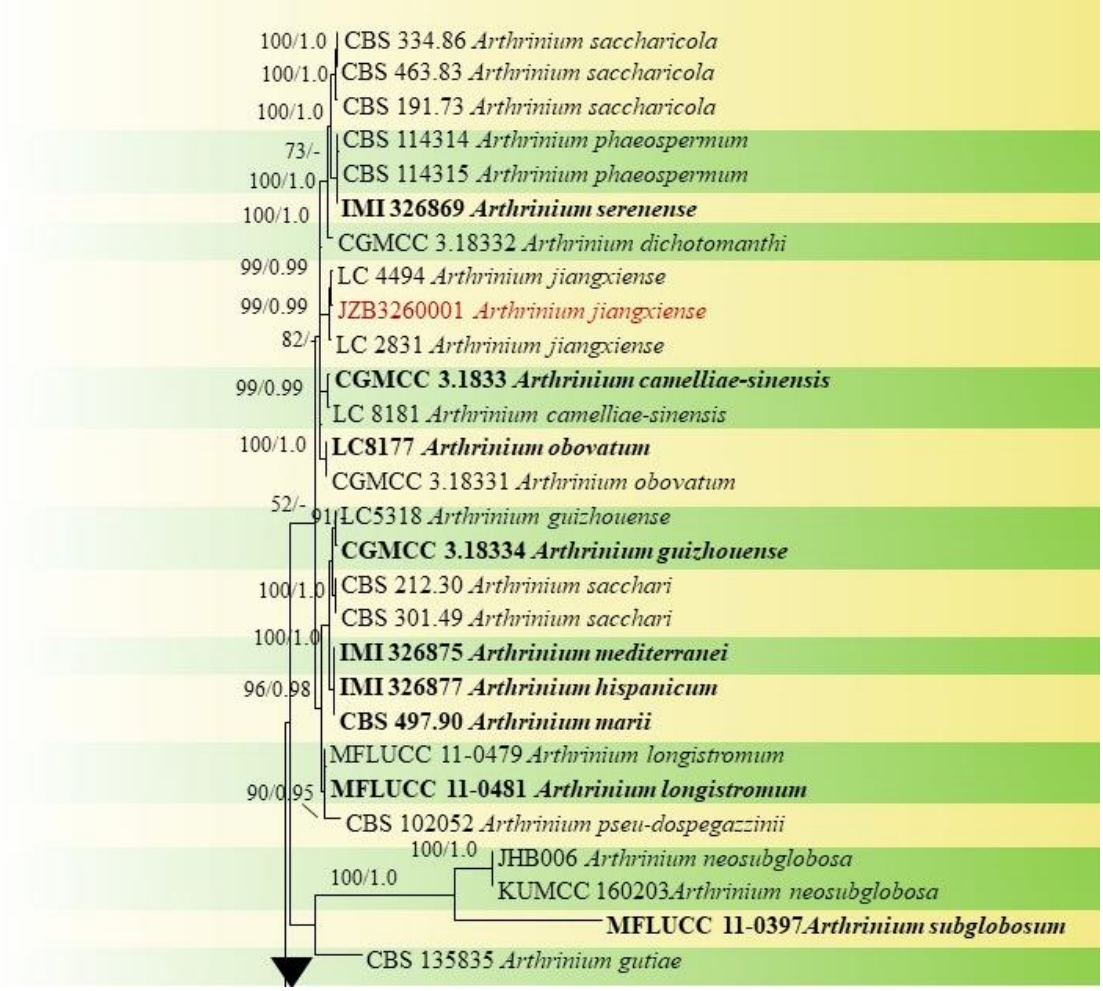

Figure 34 – Phylogenetic tree generated by ML analysis of combined ITS, *tub2* and *tef1* sequence data of *Arthrinium* species. Eighty strains are included in the analyses. The tree is rooted with *Nigrospora gorlenkoana* (CBS 480.73). Tree topology of the ML analysis was similar to the BI. The best scoring RAxML tree with a final likelihood value of –17931.476388 is presented. The matrix had 1327 distinct alignment patterns, with 35.59% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 1.219297, C = 3.435344, G = 1.309116, T = 1.132730; substitution rates AC = 1.219297, AG = 3.435344, AT = 1.309116, CG = 1.132730, CT = 4.469358, GT = 1.000000; gamma distribution shape parameter α = 1.241093. RAxML bootstrap support values ≥50% and Bayesian posterior probabilities ≥0.95 (BYPP) are shown near the nodes. The scale bar indicates 0.02 changes per site. Ex–type/ex–epitype strains are in **bold** and new isolates recovered in this study are in red.

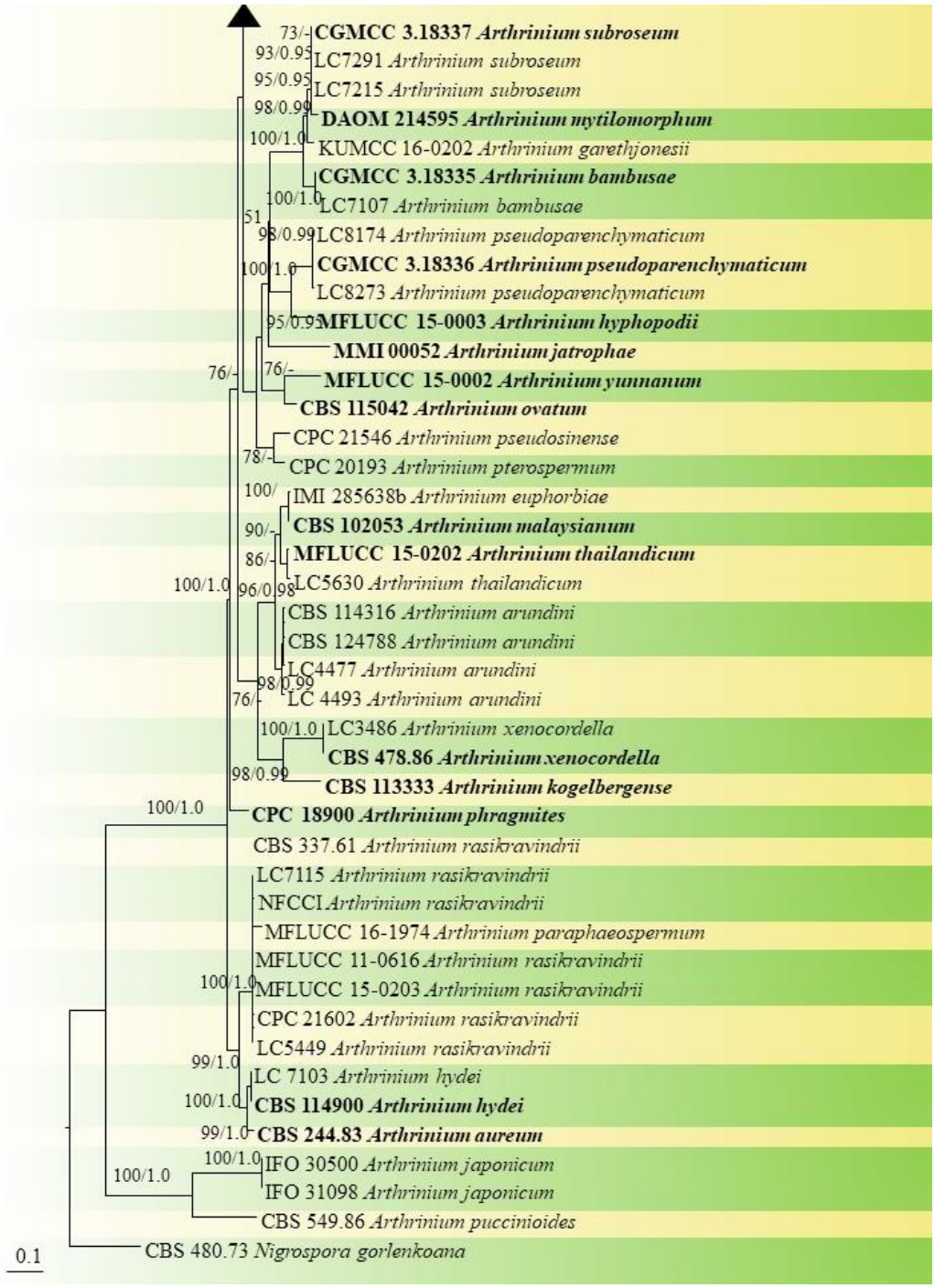

Figure 34 – Continued.

Arthrinium jiangxiense M. Wang & L. Cai., in Wang, Tan, Liu & Cai, MycoKeys 34(1): 14 (2018) Fig. 35

Index Fungorum: IF824910; Facesoffungi number: FoF09395

Pathogenic or saprobic on dead *Camellia sinensis* leaves. Sexual morph: not observed. Asexual morph: *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* erect, scattered or aggregated in clusters on hyphae, hyaline to pale brown, smooth, ampulliform. *Conidia* 6–10 µm ($\bar{x}$ = 8 µm, n = 40) diam., brown, smooth to finely roughened, granular, globose to ellipsoid in surface view.

Culture characteristics – Colonies on PDA reaching 85 mm diam., in five days at 25°C. Initially white and later become greyish–yellow, woolly, circular margin, with sparse aerial mycelia reaching, hyphae hyaline, branched, septate.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* leaves, June 2015, H.L. Li (dried culture JZBH3260001), and living culture JZB3260001.

Notes – In phylogenetic tree constructed using ITS, *tub2* and *tef1* sequences, two isolates from the present study clustered together with the *Arthrinium jiangxiense* (LC4494) with 99% ML bootstrap and 0.99 BYPP supports. *Arthrinium jiangxiense* was introduced in 2018 by Wang et al. (2018). This species has been isolated from several different hosts including *C. sinensis*, *Imperata cylindrica*, *Machilus* sp., *Maesa* sp., *Phyllostachy*s sp. However, the status of the pathogenicity of *Arthrinium jiangxiense* is understudied. In addition to the taxa identified in this study, there are three *Arthrinium* species *A. arundinis*, *A. camelliae–sinensis*, and *A. xenocordella* associated with *C. sinensis* (Farr & Rossman 2020).

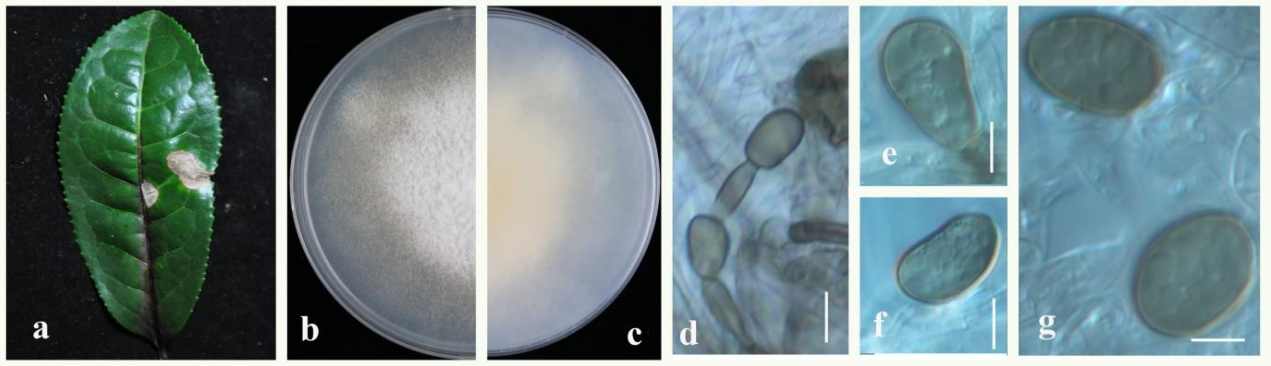

Figure 35 – *Arthrinium jiangxiense* (JZB3260001). a Diseased leaf. d Upper view of the colony on PDA after five days. e Reverse view of the colony on PDA after five days. d Conidiogenus cells with conidia. e–g Conidia. Scale bars: d–f = 10 µm.

Nigrospora Zimm., in Centbl. Bakt. ParasitKde, Abt. I 8: 220 (1902)

Notes – This genus is a cosmopolitan fungal group that comprises endophytes, saprobes, plant pathogens and opportunistic fungal pathogens in human (Wang et al. 2017a). *Nigrospora* spores are one of the more dominant groups in the atmosphere (Wu et al. 2004). The present study isolated and identified one strain that belongs to *Nigrospora camellia–sinensis* (Fig. 36).

Nigrospora camelliae–sinensis Mei Wang & L. Cai, in Wang, Liu, Crous & Cai, Persoonia 39: 127 (2017) Fig. 37

Index Fungorum: IF820731; Facesoffungi number: FoF09396

Pathogenic or saprobic on *Camellia sinensis* leaves. Sexual morph: not observed. Asexual morph: *Conidiophores*, reduced to conidiogenous cells and aggregated in clusters on hyphae. *Conidiogenous cells* hyaline to pale brown, globose to ampulliform, sometimes appearing as a bulge directly from the mycelia without septa, *Conidia* 3–20 µm ($\bar{x}$ = 16 µm, n = 40) diam., solitary spherical, black, shiny, smooth, aseptate.

Culture characteristics – Colonies on PDA reach 80 mm diam. within five days at 25°C. Initially white, later becoming grey, reverse black.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* leaves, June 2015, H.L. Li (dried culture JZBH3230016), and living culture JZB3230016.

Notes – Multi–locus phylogenetic analysis of ITS, *tef1* and *tub2* placed the isolate in the present study together with *Nigrospora camellia–sinensis* supported by 86% ML bootstrap values and 0.95 BYPP. The colony characters and morphology of the current species are similar to *N. camellia–sinensis* (Wang et al. 2017a). So far eight species of *Nigrospora* have been reported on *Camellia sinensis* and all those records are from Chinese tea plants (Farr & Rossman 2020).

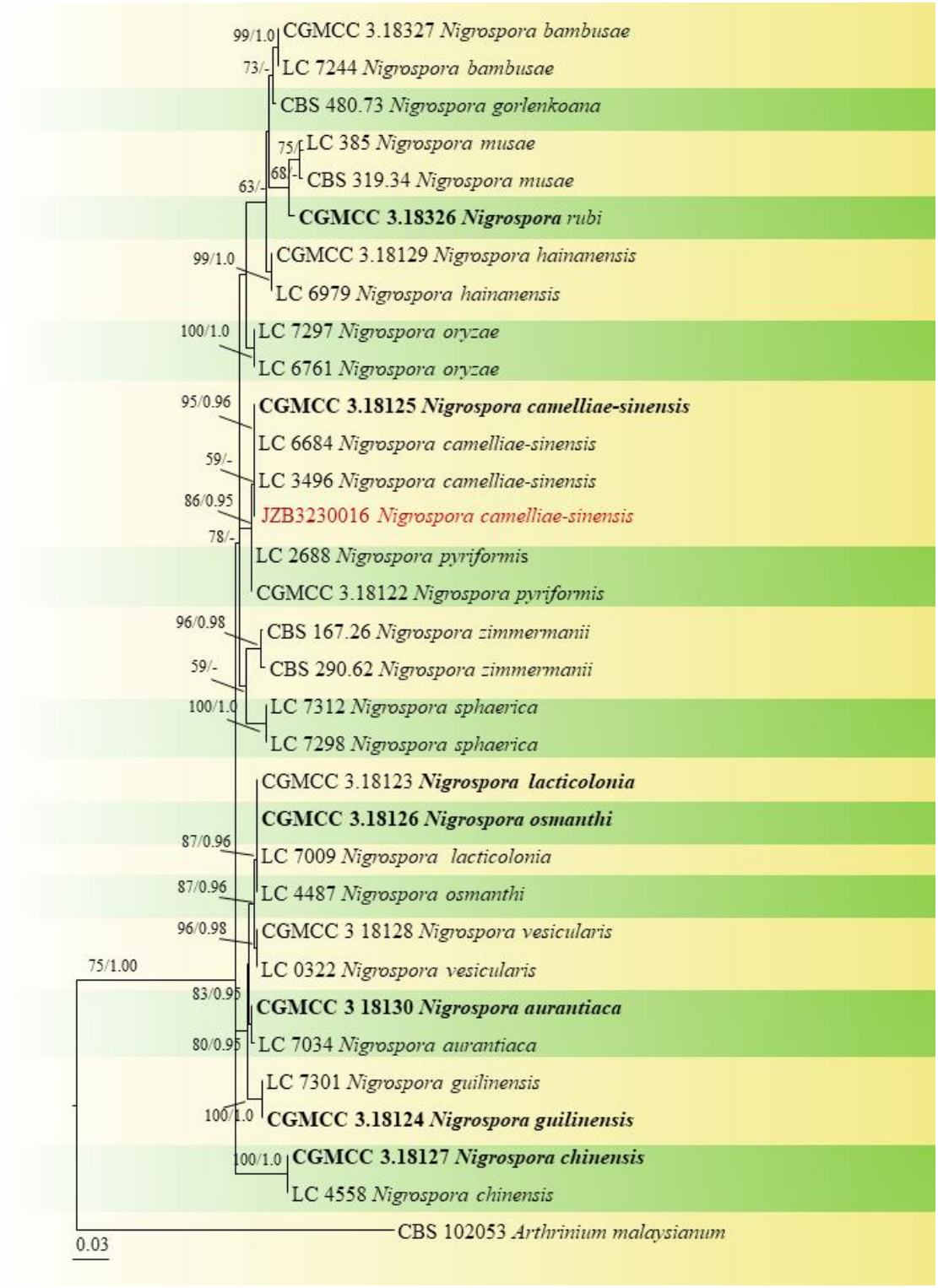

Figure 36 – Phylogenetic tree generated by ML analysis of combined ITS, *tub2* and *tef1*sequence data of *Nigrospora* species. The tree is rooted with *Arthrinium malaysianum* (CBS 102053). Tree topology of the ML analysis was similar to the BI. The best scoring RAxML tree with a final likelihood value of –1480.382026 is presented. The matrix had 107 distinct alignment patterns, with 2.77% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.232659, C = 0.262146, G = 0.226065, T = 0.279129; substitution rates AC = 1.499597, AG = 0.544505, AT = 0.620143, CG = 0.815512, CT = 4.394781, GT = 1.000000; gamma distribution shape parameter α = 0.641856. RAxML bootstrap support values ≥50% and Bayesian posterior probabilities ≥0.95 (BYPP) are shown near the nodes. The scale bar indicates 0.02 changes per site. Ex–type/ex–epitype strains are in **bold** and isolates recovered in the present study are in red.

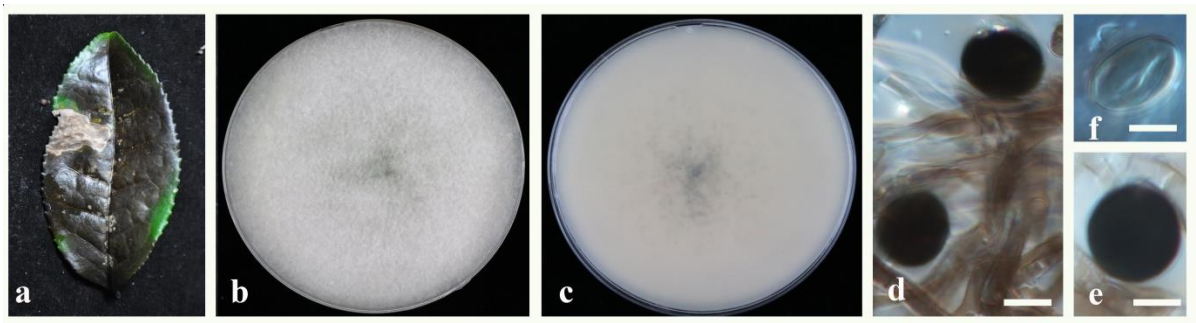

Figure 37 – *Nigrospora camellia–sinensis* (JZB3230016) a Diseased leaf. d Upper view of the colony on PDA after five days. e Reverse view of the colony on PDA after five days. d–f conidia. Scale bars: d–f = 10 µm.

Sporocadaceae Corda, Icones fungorum hucusque cognitorum 5: 34 (1842)

Notes – *Sporocadaceae* consists of the pestalotioid fungi, which are typically appendaged coelomycetes (Nag Raj 1993). They are characterised by multiseptate conidia with more or less fusiform appendages at one or both ends. Many species belonging to this family are well–known pathogens, but they can also be found as endophytes and saprobes (Maharachchikumbura et al. 2014).

Pestalotiopsis Steyaert, Bulletin du Jardin Botanique de l'État à Bruxelles 19 (3): 300 (1949)

Notes – *Pestalotiopsis* is a species–rich asexual genus with appendage bearing conidia (Maharachchikumbura et al. 2013) that is widely distributed throughout tropical and temperate regions. The species belong to this genus are well–known phytopathogens causing various diseases in economically important crops (Maharachchikumbura et al. 2013, 2014). In the present study, four *Pestalotiopsis* species were identified associated with leaf and shoot blights on *Camellia sinensis.* (Fig. 38).

Pestalotiopsis camelliae Yan M. Zhang, Maharachch. & K.D. Hyde, in Zhang et al., Sydowia 64(2): 337 (2012) Fig. 39

Index Fungorum: IF800980; Facesoffungi number: FoF09351

Pathogenic or saprobic on *Camellia sinensis* leaves. Sexual morph: Not observed. Asexual morph: *Conidiomata* pycnidial on PDA, globose, scattered, semi–immersed, black, conidial masses globose, black conidial masses. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* subcylindrical, hyaline, smooth, proliferating, *Conidia* 27–30 × 7–10 µm ($\overline{x}$ = 30 × 9 µm, n = 40), fusoid, straight to slightly curved, 4 septate. *Basal cell* 4–7 µm ($\overline{x}$ = 5 µm, n = 40), obconic, hyaline, smooth, thin–walled, *Median cells* 20–22 µm ($\overline{x}$ = 20.5 µm, n = 40), three, doliiform to subcylindrical, walls thick verruculose, slightly constricted at the septa, concolourous, olivaceous, septa and periclinal walls darker than the rest of the cell, *Apical appendages* three, tubular, arising from the upper portion of the apical cell, various in length. *Basal appendages* not observed.

Culture characteristics – Colonies on PDA attaining up to 40 mm diam., after seven days at 25°C, with an undulate edge, whitish, with medium dense aerial mycelium on the surface with black, gregarious conidiomata; reverse similar in colour.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* leaves, June 2015, H.L. Li (dried cultures JZBH340062–3), and living cultures JZB340062–3.

Notes – In the present study two *Pestalotiopsis* isolates obtained from tea leaves clustered together with the *Pestalotiopsis camelliae* (MFLUCC 12–0277) type species with 58% ML bootstrap and less than 0.90 BYPP. These isolates are similar to the ex–type isolate. Hence, we identified two isolates from our study as *Pestalotiopsis camelliae.* This species was introduced by Liu et al. (2017) from *Camellia sinensis* leaves in China. Pathogenicity of this species was proven by (Wang et al. 2019b).

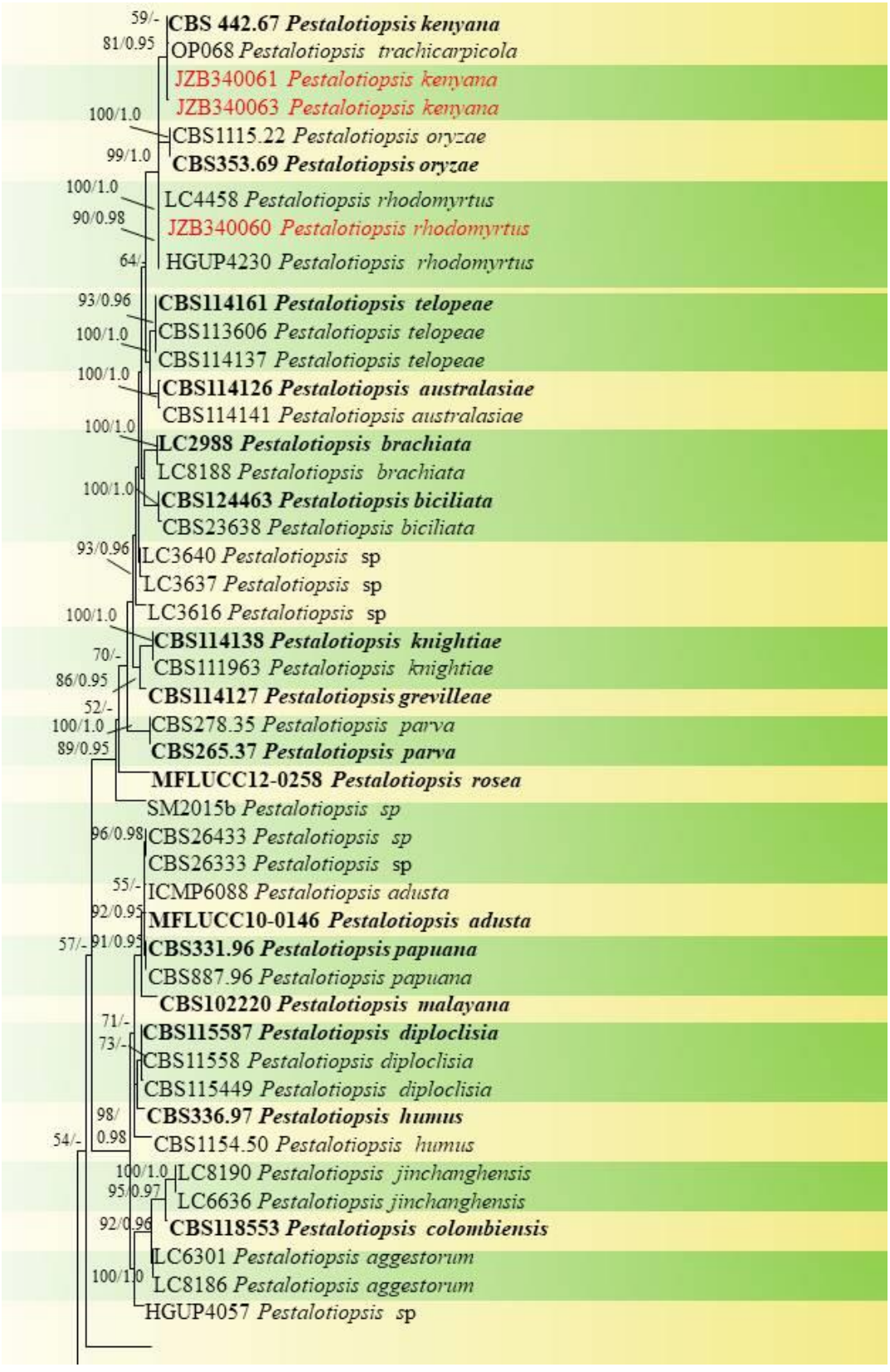

Figure 38 – Phylogenetic tree generated by ML analysis of combined ITS, *tub2* and *tef1* sequence data of *Pestalotiopsis* species. Eighty strains are included in the analyses. *Pseudopestalotiopsis longiappendiculata* (LC3013) and *Pseudopestalotiopsis cocos* (CBS27229) used as the out–group. Tree topology of the ML analysis was similar to the BI. The best scoring RAxML tree with a final likelihood value of – 24349.980578 is presented. The matrix had 1172 distinct alignment patterns, with 9.91% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.251668, C = 0.245757, G = 0.259668, T = 0.242908; substitution rates AC = 1.353890, AG =

4.605576, AT = 1.059439, CG = 0.801610, CT = 9.121730, GT = 1.000000; gamma distribution shape parameter α = 0.944898. RAxML bootstrap support values ≥50% and Bayesian posterior probabilities ≥0.95 (BYPP) are shown near the nodes. The scale bar indicates 0.05 changes per site. Ex–type/ex–epitype strains are in **bold** and isolates recovered in this this study are in red.

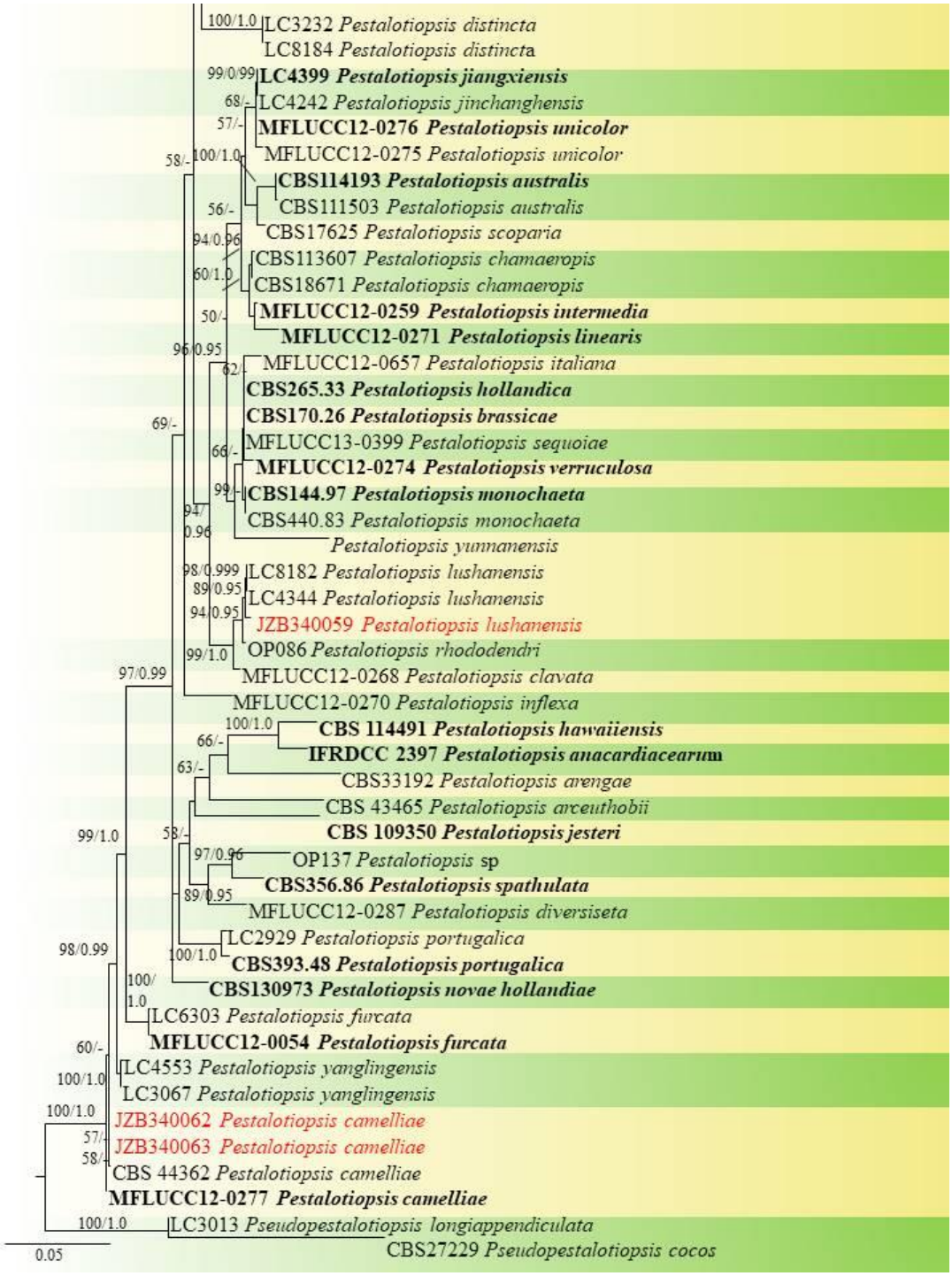

Figure 38 – Continued.

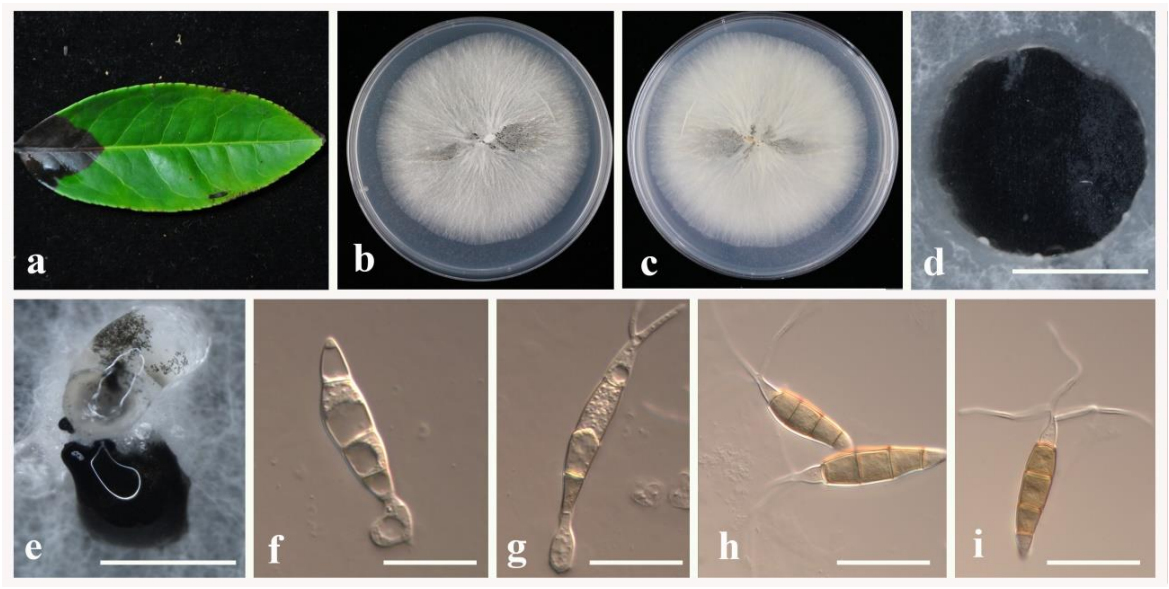

Figure 39 – *Pestalotiopsis camelliae* (JZB340062). a Diseased leaf. b Upper view of the colony on PDA after seven days. c Reverse view of the colony on PDA after seven days. d–e Pycnida on PDA. f–g Conidiogenus cells with conidia. h–i Conidia. Scale bars: d, e = 100 µm. f–i = 10 µm.

Pestalotiopsis kenyana K.D. Hyde & Crous, in Maharachchikumbura et al., Studies in Mycology 79: 166 (2014) Fig. 40

Index fungorum: IF809741; Facesoffungi number: FoF06981

Pathogenic or saprobic on *Camellia sinensis* leaves. Sexual morph: Not observed. Asexual morph: *Conidiomata* pycnidial in culture on PDA, pycnidial globose, scattered, semi–immersed, black, conidial masses black, globose, Conidiophores, reduced to conidiogenous cells. *Conidiogenous cells* discrete, lageniform to subcylindrical, hyaline, smooth, proliferating 1–3 times percurrently. *Conidia* 20 – 40 × 7–10 µm ($\overline{x}$ = 25 × 8 µm, n = 40), fusoid, subcylindrical, straight to slightly curved, 4–septate *Basal cell* conic to obconic, truncate base, hyaline, and thin–walled. *Median cells* 15–20 µm ($\overline{x}$ = 16 µm, n = 40), three, doliform, concolourous, brown, septa darker than the rest of the cell. *Apical appendages* mostly 3 arising from the apical crest, unbranched, filiform.

Culture characteristics – Colonies on PDA attaining 30–40 mm diam., after seven days at 25°C, with an undulate edge, whitish, medium dense aerial mycelium on the surface with black, gregarious conidiomata. Reverse white.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* leaves, June 2015, H.L. Li (dried culture JZBH340062 and JZBH340063), and living culture JZB340062– JZB340063.

Notes – In the present study, two species isolated from tea leaves developed a sister clade with *Pestalotiopsis kenyana* (CBS 442.67 and OP068) with 81% ML bootstrap and 0.95 BYPP. Based on phylogeny and morphology these isolates were identified as *Pestalotiopsis kenyana.* This species was introduced by Maharachchikumbura et al. (2014) from a branch of *Coffea* sp. in Kenya. Liu et al. (2016a) first reported this species from tea plants in China. There are no other hosts reported for this species (Farr & Rossman 2020).

Pestalotiopsis lushanensis F. Liu & L. Cai, in Liu et al., Scientific Reports (2017) Fig. 41

Index Fungorum: IF818919; Facesoffungi number: FoF09397

Pathogenic or saprobic on *Camellia sinensis* shoots. Sexual morph: Not observed. Asexual morph: *Conidiomata* pycnidial in culture on PDA, globose, aggregated or scattered, semi–immersed, black, exuding conidial masses. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* discrete or integrated, ampulliform, clavate or subcylindrical, hyaline,

smooth–walled. *Conidia* 20–30 × 7–10 µm ($\bar{x}$ = 20 × 8 µm, n = 40), fusoid, ellipsoid, straight to slightly curved, 4 septate *Basal cell* obconic truncate base, hyaline, verruculose, thin–walled, 3.5–6 µm long. *Median cells* 10–20 µm ($\bar{x}$ = 15 µm, n = 40) three, doliiform, long, pale brown to brown, septa darker than the rest of cell. *Apical appendages* 20–25 µm ($\bar{x}$ = 20 µm, n = 40), 2–3 tubular, unbranched, filiform, *Basal appendage* single, tubular, unbranched, filiform. *Basal appendage* single, tubular, and unbranched.

Culture characteristics – Colonies on PDA attaining 30–40 mm diam., after seven days at 25°C, with undulate edge, whitish, with medium dense aerial mycelium on the surface with black, gregarious conidiomata; reverse similar in colour.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* shoot, June 2015, H.L. Li (dried culture JZBH340059), and living culture JZB340059.

Notes – In the present study, a single isolate clustered together with the *Pestalotiopsis lushanensis* with 94% ML and 0.99 BYPP values. According to the type species description given by Liu et al. (2017), the current isolate is morphologically similar to *P. lushanensis* species. This species was introduced by Liu et al. (2017) as a pestaloid species associated with *Camellia sinensis* China.

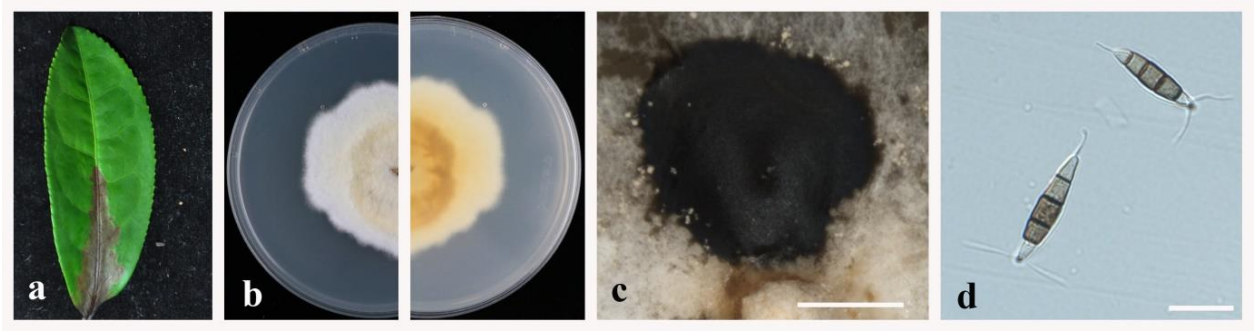

Figure 40 – *Pestalotiopsis kenyana* (JZB340062) a Diseased leaf. b Upper view of the colony on PDA after seven days. c Reverse view of the colony on PDA after seven days. c Pycnida on PDA. d Conidia. Scale bars: c = 100 µm, c = 10 µm.

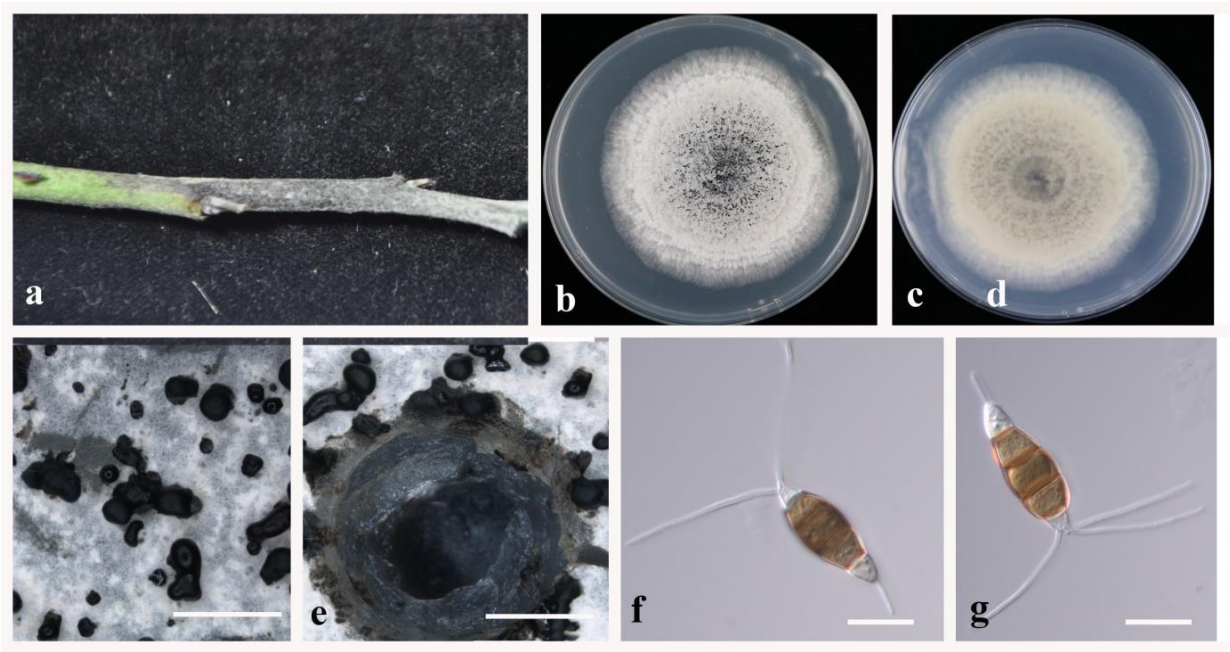

Figure 41 – *Pestalotiopsis lushanensis* (JZB340059). a Diseased shoot. b Upper view of the colony on PDA after seven days. c Reverse view of the colony on PDA after seven days. d–e Pycnida on PDA. f–g Conidia. Scale bars: d–e = 100 µm. f–g = 10 µm.

Pestalotiopsis rhodomyrtus Song, K. Geng, K.D. Hyde & Yong Wang bis, in Song et al. Phytotaxa 126(1): 27 (2013) Fig. 42

Index Fungorum: IF804968; Facesoffungi number: FoF09398

Pathogenic or saprobic on *Camellia sinensis* shoots. Sexual morph: not observed. Asexual morph: *Conidiomata* pycnidial in culture on PDA, globose, scattered, semi–immersed, conidial mass black, *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* discrete, hyaline, filiform. *Conidia* 20–25 × 5–6 µm ($\overline{x}$ = 24 × 5 µm, n = 40), fusoid, straight to slightly curved, 4–septate. *Basal cell* 3–6 µm ($\overline{x}$ = 5 µm, n = 40), conic, pale brown, smooth, thin–walled. *Median cells* 12–20 µm ($\overline{x}$ = 16 µm, n = 30) three, brown, thin septa, septa darker than cells, milled cell dark brown than the other cells. *Apical appendages* 7.5–15 µm ($\overline{x}$ = 11 µm, n = 30), three, tubular unequal. *Basal appendage* one and filiform.

Culture characteristics – Colonies on PDA reaching 90 mm diam., after seven days at 28°C. White mycelium, crenate edge, whitish, surface aerial mycelium, fruiting bodies start to appear after 7 days, black, reverse of pinkish–white become black when old.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* shoots, June 2015, H.L. Li (dried culture JZBH340060), and living culture JZB340060.

Notes – *Pestalotiopsis rhodomyrtus* was previously isolated from *Rhodomyrtus tomentosa* in China (Song et al. 2013). In the present study, a single strain obtained from a diseased tea shoot clustered together with the *P. rhodomyrtus* (LC4458 type species) with 90% ML and 0.98 BYPP values. The taxon identified in the present study is similar to the type specimen. This is the first report of *P. rhodomyrtus* on *Camellia sinensis* (Farr & Rossman 2020).

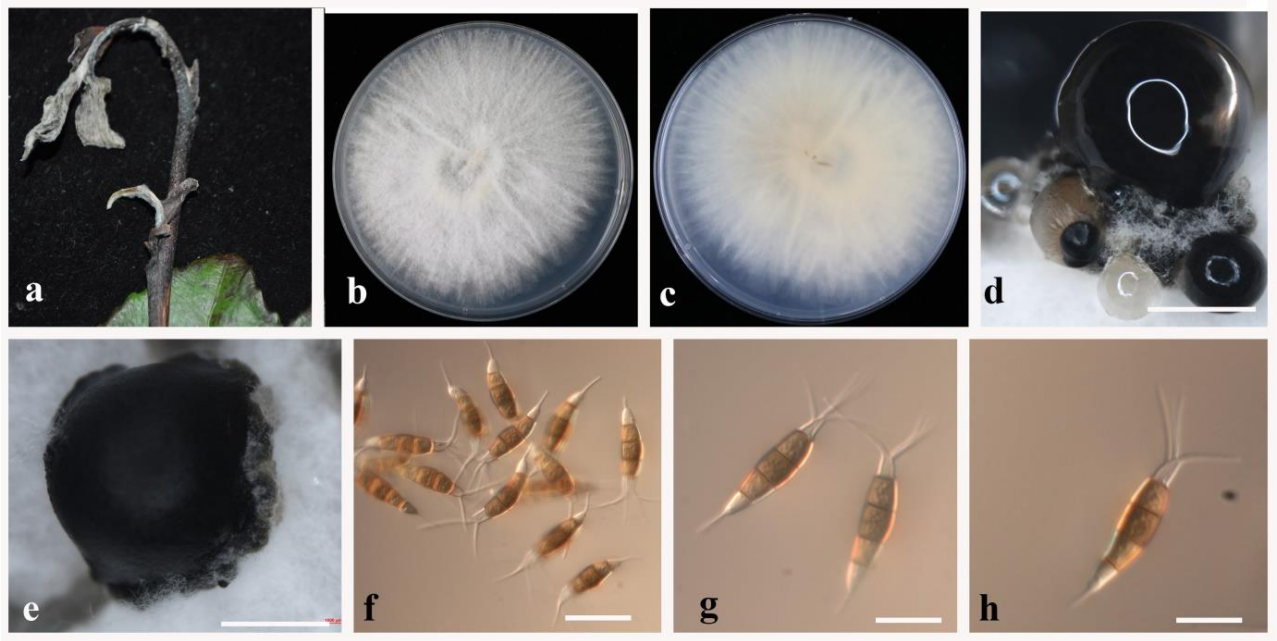

Figure 42 – *Pestalotiopsis rhodomyrtus* (JZB340060). a Diseased shoot. b Upper view of the colony on PDA after seven days. c Reverse view of the colony on PDA after seven days. d–e Pycnida on PDA. f–h Conidia. Scale bars: d, e = 100 µm, f–h = 10 µm.

Pseudopestalotiopsis Maharachch., K.D. Hyde & Crous, in Maharachchikumbura et al., Studies in Mycology 79: 180 (2014)

Notes – This genus was introduced by Maharachchikumbura et al. (2014) to accommodate pestaloid species with dark concolourous median cells and knobbed apical appendages. Combined gene phylogenetic analysis of ITS, *tub2* and *tef1*, showed that taxa from current study belong to two species. The phylogenetic placements of those taxa are given in Fig. 43.

Pseudopestalotiopsis camelliae–sinensis F. Liu & L. Cai in Liu et al., Scientific Reports 7(no. 866): 12 (2017) Fig. 44

Index Fungorum: IF818924; Facesoffungi number: FoF09351

Pathogenic or saprobic on *Camellia sinensis* leaves and shoots. Sexual morph: not observed. Asexual morph: *Conidiomata* pycnidial in culture on PDA, globose, scattered, semi–immersed, black, exuding globose, dark brown to black conidial masses. *Conidiophores* not observed. *Conidiogenous cells* 10–20 × 2–5 μm ($\overline{x}$ 20 × 4 μm, n = 30), discrete, subcylindrical, hyaline, smooth, proliferating 1–3 times percurrently. *Conidia* 20–30 × 7–10 μm ($\overline{x}$ = 25 × 8 μm, n = 40), fusoid, ellipsoid, straight, 4–septate, *Basal cell* conic, truncate base, hyaline, minutely verruculose and thin. *Median cells* 15–20 μm ($\overline{x}$ 16 μm, n = 40), three, doliiform, middle cell darker than the other two. *Apical appendages* 8–20 ($\overline{x}$ 15 μm, n = 40), three, arising from the apical crest, unbranched, filiform. *Basal appendages* two, centric, tubular and flexuous.

Culture characteristics – Colonies on PDA attaining 30–40 mm diam., after seven days at 25°C, with an undulate edge, whitish, with medium dense aerial mycelium on the surface with black, gregarious conidiomata; reverse similar in colour.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* leaves and shoots, June 2015, H.L. Li (dried cultures JZBH340040–JZBH340054), and living cultures JZB340040–JZB340054.

Notes – In the present study 14 strains isolated from diseased leaf and shoots samples clustered with *Pseudopestalotiopsis camelliae–sinensis*. Morphologically both cultural and structural characters such as conidial shape and dimensions of the isolated taxa were similar to the type description of *Pseudopestalotiopsis camelliae–sinensis* (Liu et al. 2017). All isolates in the present study share 98–100% nucleotide similarities at three gene regions. This species was introduced by Liu et al. (2017) associated with *Camellia sinensis* in China. In addition, the only other host reported so far is *Vitis vinifera* (Farr & Rossman 2020). *Pseudopestalotiopsis camelliae–sinensis* was the most isolated species in the present study.

Pseudopestalotiopsis chinensis F. Liu & L. Cai Liu et al., Scientific Reports 7(no. 866): 12 (2017) Fig. 45

Index Fungorum: IF818923; Facesoffungi number: FoF09399

Pathogenic or saprobic on *Camellia sinensis*. Sexual morph: not observed. Asexual morph: *Conidiomata* pycnidial in culture on PDA, globose, scattered, semi–immersed, black, exuding globose, dark brown to black conidial masses. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* discrete, lageniform to subcylindrical, hyaline, smooth, proliferating. *Conidia* 20–30 × 7–10 μm ($\overline{x}$ = 25 × 8 μm, n = 40), fusoid, ellipsoid to subcylindrical, straight to slightly curved, 4–septate, Pigmentation occurs while attached to the conidiogenous cell. *Basal cell* 15–20 μm ($\overline{x}$ = 16 μm, n = 40). *Median cells* three, doliiform, wall verruculose concolourous, brown, septa darker than the cells. *Apical cell* 4–6 μm long, hyaline, subcylindrical, rugose and thin–walled. *Apical appendages* 2–3 tubular, initiate from the apical crest, unbranched, filiform. *Basal appendages* two, centric, tubular, flexuous.

Culture characteristics – Colonies on PDA attaining 80–90 mm diam., after seven days at 25°C. Medium dense aerial mycelium, undulate, whitish, surface with black, gregarious conidiomata. Reverse white and become darker with age.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* leaves, June 2015, H.L. Li (dried cultures JZBH340055–JZBH340058), and living cultures JZB340055–JZB340058.

Notes – In the present study, the four isolates clustered with the ex–type isolate of *Ps. chinensis* (LC3011) with 81% ML and 0.95 BYPP values. These strains are similar to the type species description of *Pseudopestalotiopsis chinensis* (Chen et al. 2018a). This species was introduced by Chen et al. (2018a) from *Camellia sinensis* leaves. Other than *Camellia sinensis* there are no other host records for this species (Farr & Roseman 2020).

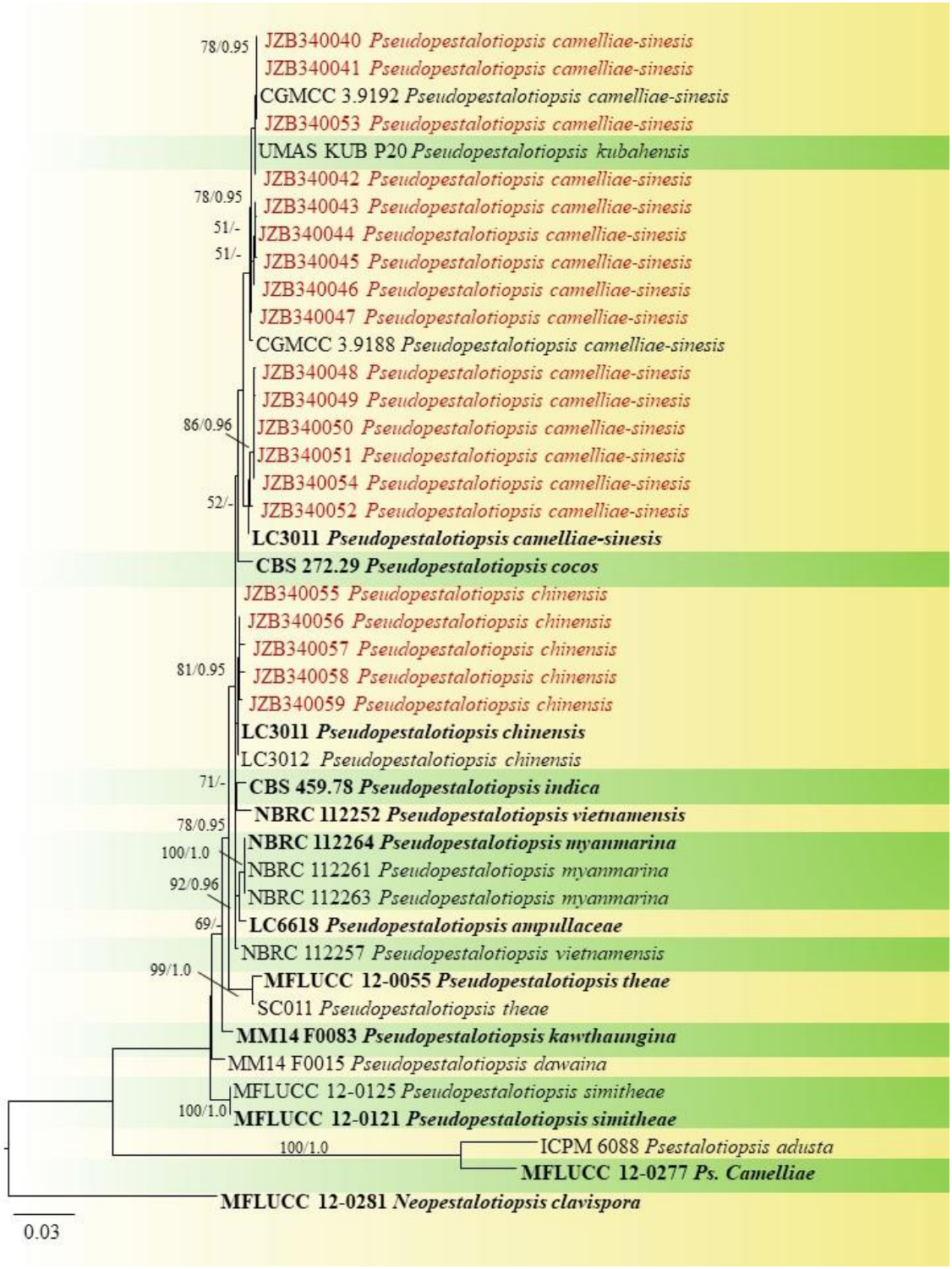

Figure 43 – Phylogenetic tree generated by ML analysis of combined ITS, *tub2* and *tef1* sequence data of *Pseudopestalotiopsis* species. The tree is rooted with *Neopetalotiopsis clavispora* (MFLUCC 12–0277). Tree topology of the ML analysis was similar to the MP and BI. The best scoring RAxML tree with a final likelihood value of – 24349.980578 is presented. The matrix had 354 distinct alignment patterns, with 12.95% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.251912, C = 0.252891, G = 0.233751, T = 0.261446; substitution rates AC = 1.202821, AG = 5.554634, AT = 2.143706, CG = 1.053081, CT = 6.705276, GT = 1.000000; gamma distribution shape parameter α = 0.440726. RAxML bootstrap support values ≥50% and Bayesian posterior probabilities ≥0.95 (BYPP) are shown near the nodes. The scale bar indicates 0.03 changes per site. Ex–type/ex–epitype strains are in **bold**. New isolates recovered in the present study are in red.

Figure 44 – *Pseudopestalotiopsis camelliae–sinensis* (JZBH340040). a Pycnidial wall with developing conidiogenous cells and developing conidia. b–c Conidia. d–e Pycnidia on PDA. f Upper view of culture on PDA after seven days. g Reverse view of culture on PDA after seven days. Scale bars: a = 20 µm, b–c = 10 µm, d–e = 100 µm.

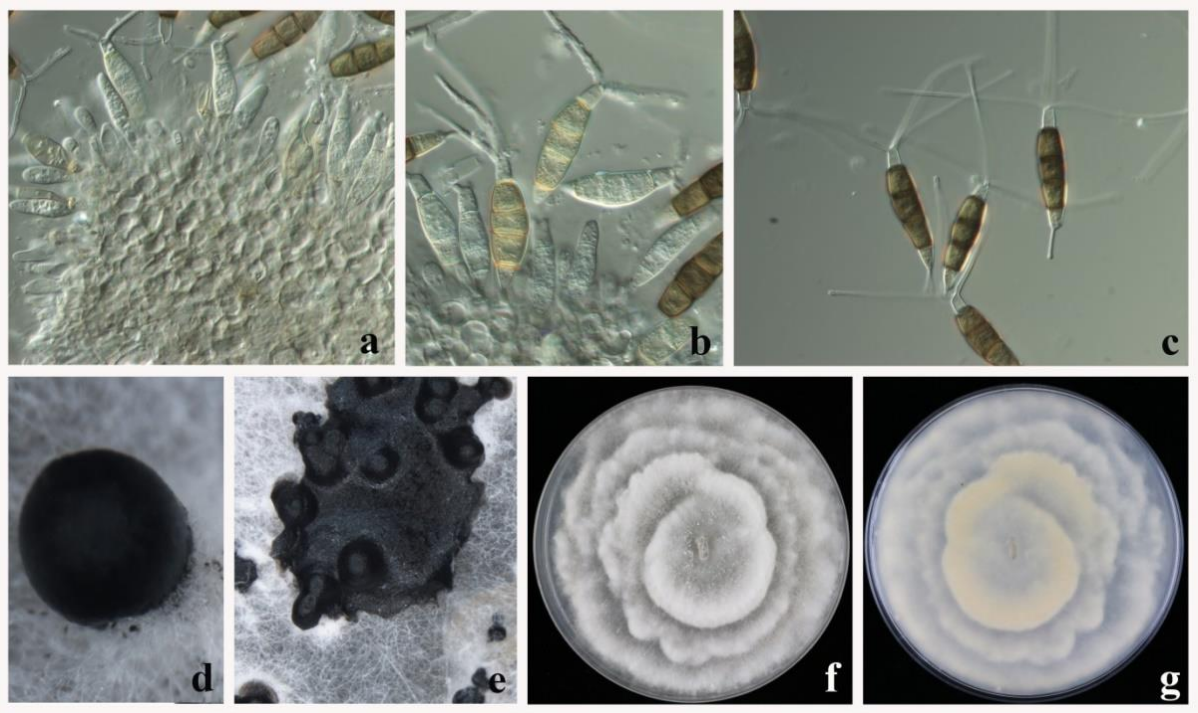

Figure 45 – *Pseudopestalotiopsis chinensis* (JZB340058). a Pycnidial wall with developing conidiogenous cells and developing conidia. b Conidiogenous cells and developing conidia. c Conidia. d–e Different shapes of pycnidia. f Front view of culture on PDA after seven days. g Reverse view of culture on PDA after seven days. Scale bars: a = 20 µm, b–c = 10 µm, d–e = 100 µm.

Xylariales Nannf., Nova Acta Regiae Societatis Scientiarum Upsaliensis 8 (2): 66 (1932)

Notes – In recent taxonomic treatments by Hyde et al. (2020b) 15 families are accepted in Xylariales; *Barrmaeliaceae*, *Cainiaceae*, *Clypeosphaeriaceae*, *Coniocessiaceae*, *Diatrypaceae*, *Graphostromataceae*, *Hansfordiaceae*, *Hypoxylaceae*, *Induratiaceae*, *Lopadostomataceae*, *Microdochiaceae*, *Polystigmataceae*, *Requienellaceae*, *Xylariaceae* and *Zygosporiaceae* with 160 genera (Hyde et al. 2020b).

Xylariaceae Tul. & C. Tul., Selecta Fungorum Carpologia, Tomus Secundus. Xylariei – Valsei – Sphaeriei 2: 3 (1863)

Notes – Up to now 32 genera are accepted in Xylariaceae (Hyde et al. 2020b). *Xylariaceae* species are saprobic, pathogenic, or endophytic on a wide range of hosts, some are important producers of bioactive compounds and secondary metabolites (Stadler & Hellwig 2005, Helaly et al. 2018).

Nemania Gray, A natural arrangement of British plants 1: 516 (1821)

Notes – *Nemania* consists of xylariaceous species that are more or less carbonaceous, dark brown to black stromata that do not release coloured pigments in 10% potassium hydroxide (KOH) (Ju & Rogers 2002). They are mostly reported as endophytes on different hosts. In the present study, we isolated three strains belonging to *Nemania diffiusa* (Fig. 46).

Nemania diffusa (Sowerby) Gray, Nat. Arr. Brit. Pl. (London) 1: 517 (1821) Fig. 47

Index Fungorum: IF477312; Facesoffungi number: FoF09400

Pathogenic or Saprobic on *Camellia sinensis* leaves. Sexual morph: not observed. Asexual morph: *Conidiomata* pycnidial in culture on PDA, scattered or aggregated, irregular black. *Conidiophores* not observed. *Conidiogenus cells* not observed. *Conidia* 8–10 × 3–4 µm ($\overline{x}$ = 8 × 3 µm, n = 40), hyaline, ellipsoidal, guttulate, single germination tube.

Culture characteristics – Colonies on PDA, reaching 50 mm diam., after seven days at 28°C. White fluffy mycelium, entire, smooth margin, reverse become dark brown with age.

Material examined – CHINA, Fujian Province, Zhangzhou County, on dead *Camellia sinensis* leaves, June 2015, H.L. Li (dried cultures JZBH3370001– JZBH3370003), and living cultures JZB3370001– JZB3370003.

Notes – In the present study we obtained three isolates belonging to *Nemania*. In the phylogenetic analysis, these isolates clustered together with the *Nemania diffusa* (type strain NC0608 and other representative strains) with 100% ML and 1.0 BYPP values. Based on morphological and phylogenetic analyses we confirmed the isolates obtained in this study as *Nemania diffusa*. This species has been reported in tea plantations causing soft rot in shoots in Sri Lanka (Balasuriya & Adikaram 2008). This species has also been reported on *Alnus glutinosa*, *Betula* sp., *Fagus* sp., *Fraxinus* sp., *Metrosideros polymorpha*, *Nothofagus menziesii*, *Nothofagus solandri*, *Nothofagus* sp., *Quercus robur* and *Ulmus suberosa* (Farr & Rossman 2020). However, this is the first report of *Nemania diffusa* in Chinese tea cultivations.

Discussion

This study revealed the diversity of fungi associated with diseased leaves and shoots of tea in a plantation in China. The 110 isolates obtained comprised 32 species in 13 genera in 11 families. Of these 32 species, five were determined to represent hitherto unknown species and thus were introduced as new. In addition, nine new host records were reported. These taxa were associated with typical symptoms of leaf necrosis and shoots blights on *C. sinensis*. Moreover, some of these taxa belong to genera well–established as pathogenic on tea, namely *Arthrinium*, *Botryosphaeria* (Jayawardena et al. 2016b) *Colletotrichum* (Liu et al. 2015), *Diaporthe* (Gao et al. 2016), *Pestalotiopsis*, *Pseudopestalotiopsis* (Maharachchikumbura et al. 2013), *Nigrospora* and *Trichoderma* (Dutta et al. 2015). However, this study reported several genera, *Chaetomium* *Epicoccum* and *Setophoma* for which pathogenicity has not been confirmed on tea.

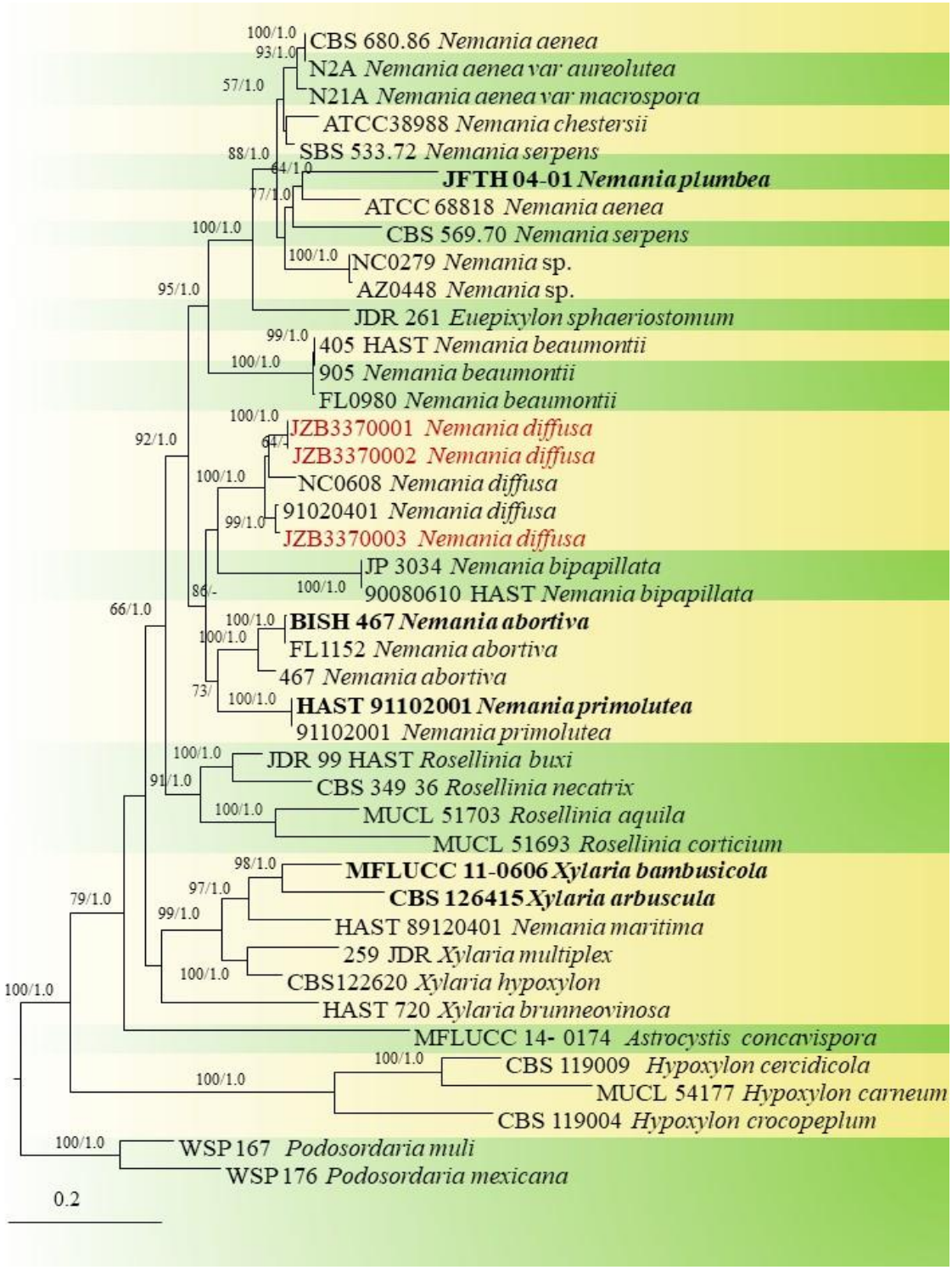

Figure 46 – Phylogenetic tree generated by ML analysis of combined ITS and *rpb2* sequence data of *Nemania* species. *Podosordaria muli* (WSP 167) and *P. mexicana* (WSP 176) were used as the outgroup taxa. Tree topology of the ML analysis was similar to the MP. The best scoring RAxML tree with a final likelihood value of – 24349.980578 is presented. The matrix had 1172 distinct alignment patterns, with 9.91% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.251668, C = 0.245757, G = 0.259668, T = 0.242908; substitution rates AC = 1.353890, AG = 4.605576, AT = 1.059439, CG = 0.801610, CT = 9.121730, GT = 1.000000; gamma distribution shape parameter α = 0.944898. RAxML bootstrap support values ≥50% and Bayesian posterior probabilities ≥0.95 (BYPP) are shown near the nodes. The scale bar indicates 0.02 changes per site. Ex–type/ex–epitype strains are in **bold** and isolates recovered in the present study are in red.

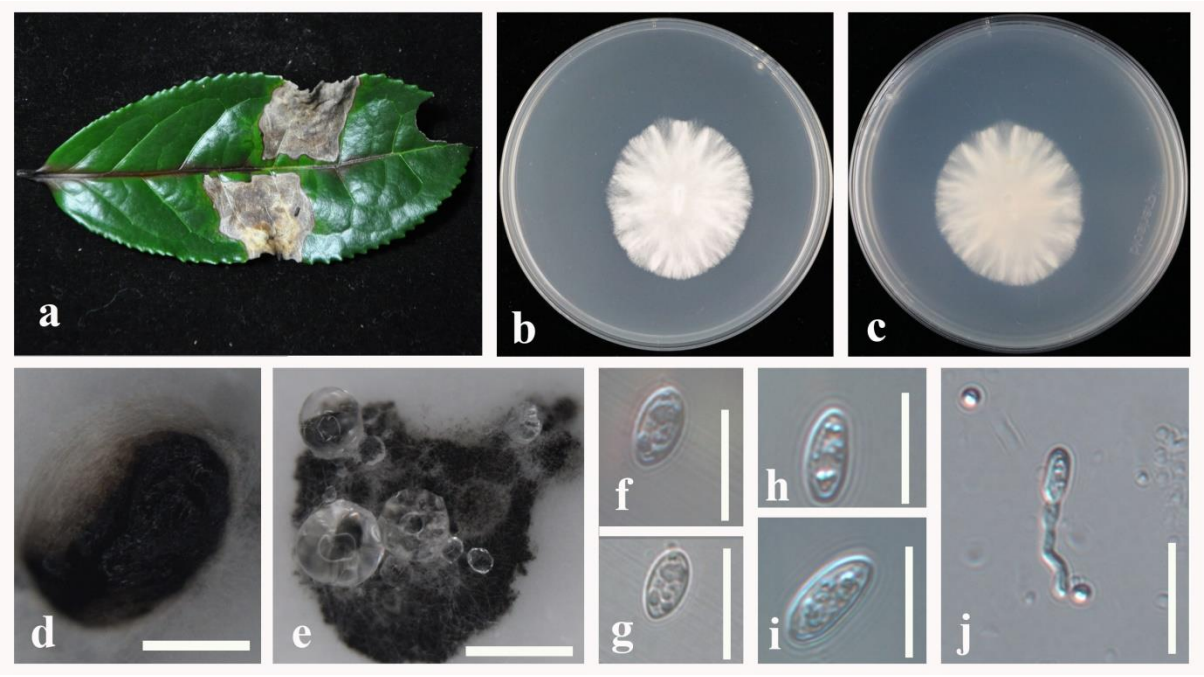

Figure 47 – *Nemania diffus*a (JZBH3370001). a Diseased leaf. b Upper view of the colony on PDA after seven days. c Reverse view of the colony on PDA after seven days. d–e Pycnidia on PDA. f–i Conidia. j Germinating conidia. Scale bars: d, e = 100 μm, f–i = 10 μm.

In the present study we isolated five *Botryosphaeria dothidea* strains associated with shoot blights on tea. *Botryosphaeriaceae* species are normally regarded as opportunistic pathogens. Even though the exact underlying mechanism is unknown, it is thought that these fungi become pathogenic when the environmental conditions are unfavourable for the host (Chethana et al. 2016, Manawasinghe et al. 2016). In addition to *Botryosphaeria dothidea, Lasiodiplodia theobromae* and *L. pseudotheobromae* have been reported causing leaf necrosis on *Camellia sinensis* in China (Li et al. 2019). In comparison of disease symptoms caused by these *Botryosphaeriaceae* taxa, all species induce brown lesions on young and mature leaves that become necrotic with age. However, in this study we also isolated *Botryosphaeria dothidea* from dead shoots. Twig die–back caused by *Macrophoma theicola* Petch, (*Botryosphaeriaceae*) is considered to be one of the major stem diseases of *C. sinensis* (Mareeswaran et al. 2015). The disease symptoms associated with this species are identical to the dieback caused by *Botryosphaeria dothidea* observed in the present study (Mareeswaran et al. 2015). Furthermore, colony morphology and conidial characters of these two species are quite similar (Phillips et al. 2013). Therefore, it is important to identify these species using molecular data to avoid misidentifications. Furthermore, considering the confused nature of *Macrophoma* (Sutton 1980) there is a need to re-collect and epitypify *M. theicola* to establish its phylogenetic position. Other than opportunistic pathogens, in this study, we also identified species belonging to well established phytopathogenic genera in *Camellia sinensis.*

Two *Colletotrichum* species were isolated from tea leaves with leaf necrosis symptoms. Up until now, 24 *Colletotrichum* species have been associated with tea worldwide (Farr & Rossman 2020). From these, 17 species have been observed in China, namely: *C. alienum, C. boninense, C. camelliae, C. cliviae, C. fioriniae, C. fructicola, C. gloeosporioides, C. karstii, C. Siamense, C. henanense* and *C. jiangxiense* (Farr & Rossman 2020), *C. acutatum* (Chen et al. 2017b), *C. aenigma* (Chen et al. 2019), *C. endophyticum* (Wang et al. 2016b), *C. plurivorum* (Damm et al. 2019), *C. truncatum, C. wuxiense* (Wang et al. 2016b). The study conducted by Chen et al. (2017b) showed that *C. camelliae* is the most dominant taxon occurring on *Camellia*. In this study, we isolated *C. fructicola* and *C. camelliae* associated with tea leaf necrosis. However, the isolation rate of *C. Camelliae* was lower in this study compared to the other phytopathogenic genera such as *Diaporthe*. This might be due to selective sampling. Our sampling area was limited to Fujian

province and the only cultivar was cv purple rose. In addition, within a small range our sampling rate was high and the present study focused on different symptoms rather looking at particular symptoms or specific genera or species.

The greatest numbers of species isolated in this study were in *Diaporthe* (ten of the 32 species). These includes three novel species and four new host records. So far 21 *Diaporthe* species have been reported as associated with *C. sinensis* (Farr & Rossman, 2020). Among them, *D. amygdali*, *D. apiculata*, *D. compacta*, *D. discoidispora*, *D. eres*, *D. hongkongensis*, *D. oraccinii*, *D. penetriteum*, *D. tectonigena* (Gao et al. 2016), *D. incompleta*, *D. masirevicii*, *D. ueckerae*, *D. velutina*, *D. xishuangbanica* (Gao et al. 2017) and *Diaporthe nobilis* (Li et al. 2017) have been reported in China. Among this pathogenicity has been proven only for *Diaporthe penetriteum* (Table 3). All species isolated in this study were associated with either shoot blight or leaf necrosis on tea. Therefore, further studies are necessary to understand the pathogenicity of each species on *Camellia sinensis.*

Grey blight of tea is one of the most destructive foliar diseases in tea worldwide including China (Chen et al. 2017c, Wang et al. 2019c) and southern India (Joshi et al. 2009). The symptoms associated with this disease are pale yellow–green leaf spots that initially are small, oval and surrounded by a narrow yellow zone. With age the spots become brown or grey with concentric rings and scattered, tiny black dots can be observed. When the disease becomes severe it can result in defoliation (Chen et al. 2017c). This disease is caused by Pestalotiopsis–like species in many tea cultivation regions including China (Chen et al. 2017c). There are 220 records of *Pestalotiopsis* species associated with *C. sinensis* (Farr & Rossman 2020). In this study we observed symptoms on leaves similar to grey blight. However, most of the taxa isolated in this study associated with shoot blight appeared in necrotic regions on young leaves. These isolates belong to two species; *Pseudopestalotiopsis camelliae–sinensis* and *Pseudopestalotiopsis chinensis*. *Pseudopestalotiopsis camelliae–sinensis* is one of the main causal organisms associated with grey blight in China (Chen et al. 2018a). Since *Pseudopestalotiopsis camelliae–sinensis* was the most isolated species from diseased samples, it might be the prominent phytopathogenic species in Fujian tea plantations. In addition to that, *Ps. ampullacea* and *Ps. theae* also have been reported on tea (Chen et al. 2018a).

Nigrospora camelliae-sinensis is the only *Nigrospora* species isolated in this study. The pathogenicity of this species has not been confirmed on tea. *Nigrospora* includes well–known plant pathogens on economically important crops, fruits and ornamentals (Wang et al. 2019b). *Nigrospora sphaerica* has been reported causing leaf blight on *C. sinensis* in China (Liu et al. 2015). Apart from being plant pathogens, the species in this genus are important allergenic fungi and some also produce useful natural by–products (Saha & Bhattacharya 2015, Chen et al. 2016). In addition to this species, we isolated a single *Arthrinium* species associated with leaf necrosis. *Arthrinium* species are widely distributed on a range of hosts as endophytes, pathogens or saprobes (Hong et al. 2015). Moreover, they have been reported as the causal organisms of cutaneous infections of humans (Crous et al. 2012). They are known to produce bioactive compounds as well (Hong et al. 2015). Wang et al. (2018) identified *Arthrinium camelliae–sinensis* from tea plants. However, the pathogenicity of *Arthrinium camelliae–sinensis* has not been confirmed.

Setophoma yingyisheniae is one of the Pleosporaceae species identified in this study. A recent study conducted by Liu et al. (2019) introduced four new species belonging to *Setophoma*, namely *S. antiqua*, *S. longinqua*, *S. yingyisheniae* and *S. yunnanensis* associated with leaf spots on tea from seven provinces in China. Until now, *S. yingyisheniae* has been isolated from five provinces in China (Liu et al. 2019). However, pathogenicity of this species is unknown. In the present study, several genera were identified for the first time associated with *Camellia sinensis.* In addition, we isolated one species belonging to *Didymellaceae, Epicoccum layuense*. So far three species belonging to this genus (*E. camelliae E. latusicollum* and *E. sorghinum*) have been reported on tea plants (Chen et al. 2017a). This is the first report of *Epicoccum layuense* associated with tea.

A novel species belonging to *Chaetomium* based on morphological characters and molecular data was identified. Species in *Chaetomium* are not common on *Camellia sinensis*. The only record

of this host–fungus relationship is reported by Watson (1950) who did not mention the species name. In the present study, our isolates of this genus represent a novel taxon *Chaetomium camelliae.* Therefore, this is the first report of *Chaetomium camelliae* on tea pants in China. In addition, three *Fusarium* species were identified and these are novel host records on *Camellia sinensis*. Seven other *Fusarium* species have been reported on *C. sinensis* (Farr & Rossman 2020).

By comparing the results of this study and the checklist, it is clear that *Camellia sinensis* supports a high diversity of fungal species. These fungal communities might have different effects on the plants, most importantly to increase host fitness to tolerate biotic and abiotic stresses. In addition, these taxa play different roles as endophytes, saprobes and pathogens, possibly interacting. Thus, it it is possible that a small ecosystem exists within a single host in nature. In the present study we found that fungal species with potential biocontrol ability co–exist with pathogenetic taxa on tea bushes. Some species belonging to *Trichoderma* have potential to attack or inhibit the growth of other fungi through their production of inhibitory secondary metabolites (Degenkolb et al. 2008, Lopes et al. 2012). A recent study conducted by Del Frari et al. (2019) has shown the potential of *Epicoccum* species to act against Esca disease on grapevines.. In this way they may be acting as natural biocontrol agents keeping the diseases under natural control when the conditions are favourable for plant and fungus (De Silva et al. 2019). In almost all the tea–growing regions, blister blight, horse–hair blight, and twig dieback/stem canker have become the most destructive diseases (Keith et al. 2006). Therefore, many plantation practices focus of the control these pathogens often via addition of excessive amounts of fungicides. This might provide a chance for other species to develop into more aggressive or pathogenic strains unnoticed. Human–mediated factors, such as application of the excessive amounts of fungicides together with environmental changes, provide both challenging and opportunistic environments for pathogenic species. Since fungi have potential for rapid adaptation, they might either switch their host or emerge as novel taxa (Manawasinghe et al. 2018). Therefore, it is important to understand the diversity of fungi, the roles they play in this small ecosystem and their interactions with one another. This will provide new insights into the development of new management strategies by enhancing the antagonists and thus suppress severity of the diseases.

Table 3 Checklist of fungi associated with Tea. The checklist includes species names, family, life modes, disease name (if any), locality and references. The current name is used according to Index Fungorum (2020) and the classification follows Wijayawardene et al. (2020). Genera and species are listed in alphabetical order.

Species	**Family**	**Life mode**	***Disease caused***	**locality**	**References**
Acremoniella atra (Corda) Sacc.,	*Incertae sedis* Ascomycota			Japan	Kobayashi (2007)
Alternaria alternata (Fr.) Keissl*	*Pleosporaceae*	S, P**	Leaf spots	China, India, Japan	Tai (1979), Chakraborty et al. (2006), Kobayashi (2007), Zhou et al. (2014), Chen et al. (2018b), Farr & Rossman (2020)
Alternaria sp.				Greece	Pantidou (1973)
Annulohypoxylon michelianum (Ces. & De Not.) Y.M. Ju, J.D. Rogers & H.M. Hsieh	*Hypoxylaceae*			Kenya	Nattrass (1961)
Athelia rolfsii (Curzi) C.C. Tu & Kimbr	*Atheliaceae*			Japan, Malawi Taiwan (China)	Kobayashi (2007) Farr & Rossman (2020)

Table 3 Continued.

Species	Family	Life mode	*Disease caused*	locality	References
Armillaria mellea (Vahl) P. Kumm	*Physalacriaceae*			Japan, Kenya, Malawi Malay, Peninsula, Papua New Guinea, Tanzania, Zimbabwe	Thompson & Johnston (1953), Wiehe (1953), Riley (1960), Nattrass (1961), Whiteside (1966), Shaw (1984), Kobayashi (2007)
Armillaria sp.	*Physalacriaceae*	OP, S		Brazil, Kenya, Zimbabwe	Mendes et al. (1998), Perez Sierra et al. (2003), Jimu et al. (2015)
Arthrinium arundinis (Corda) Dyko & B. Sutton*	*Apiosporaceae*	P**	N/A	China	Thangaraj et al. (2019)
Arthrinium camelliae–sinensis M. Wang, F. Liu & L. Cai*	*Apiosporaceae*	S	N/A	China	Wang et al. (2019b), Yan et al. (2019), This study
Arthrinium jiangxiense M. Wang & L. Cai*	*Apiosporaceae*	S	N/A	China	Wang et al. (2019b), Yan et al. (2019)
Arthrinium xenocordella Crous*	*Apiosporaceae*	S	N/A	China	Wang et al. (2019b)
Aschersonia eugeniae Koord.	*Clavicipitaceae*			India	Mathur (1979)
Ascochyta sp.	*Didymellaceae*			Papua New Guinea	Farr & Rossman (2020)
Ascochyta theae Hara	*Didymellaceae*			Japan	Kobayashi (2007)
Asterina theae W. Yamam.	*Asterinaceae*			China	Tai (1979), Farr & Rossman (2020)
Athelia rolfsii (Curzi) C.C. Tu & Kimbr	*Atheliaceae*			Papua New Guinea	Thompson & Johnston (1953)
Beltrania rhombica Penz.,	*Beltraniaceae*			Malaysia	Johnston (1960), Heredia–Abarca (1994)
Beltraniella japonica Matsush.	*Amphisphaeriaceae*			Japan	Matsushima (1975), Kobayashi (2007)
Bifusella camelliae C.L. Hou*	*Rhytismataceae*	P, S	Branch rot	China	Hou (2000), Chen et al. (2011)
Botryosphaeria dothidea (Moug.: Fr.) Ces. & De Not*	*Botryosphaeriaceae*	P	Dieback**	Australia, China, Japan	Cunnington et al. (2007), Kobayashi (2007), Dissanayake et al. (2016), Jayawardena et al. (2016b), Burgess et al. (2019), This study
Botryosphaeria microspora Petch	*Botryosphaeriaceae*			Sri Lanka	Farr & Rossman (2020)
*Botryosphaeri*a sp.	*Botryosphaeriaceae*			China	Tai (1979)
Botrytis cinerea Pers	*Sclerotiniaceae*			Japan, USA	Watson (1950), Kobayashi (2007)
Botryotinia sp.	*Sclerotiniaceae*			India	Richardson (1990)
Byssosphaeria rhodomphala (Berk.) Cooke	*Melanommataceae*			Japan	Kobayashi (2007)
Calonectria colhounii Peerally*	*Nectriaceae*	S		Indonesia, Mauritius, USA	Crous (2002), Lombard et al. (2014, 2016), Liu & Chen (2017), Wang et al. (2019a)
Calonectria indusiata (Seaver) Crous	*Nectriaceae*			China Germany, Sri Lanka, Thailand	Thompson & Johnston (1953), Tai (1979), Crous (2002), Lombard et al. (2016)
Calonectria kyotensis Terash	*Nectriaceae*			Mauritius, Sri Lanka	Crous (2002)

Table 3 Continued.

Species	Family	Life mode	*Disease caused*	locality	References
Calonectria reteaudii (Bugnic.) C. Booth	*Nectriaceae*			Mauritius	Crous (2002)
Calonectria spathiphylli El–Gholl, J.Y. Uchida, Alfenas, T.S. Schub., Alfieri & A.R. Chase*	*Nectriaceae*	S		Mauritius	Risede & Simoneau (2001), Crous (2002)
Calonectria brassicae (Panwar & Bohra) L. Lombard, M.J. Wingf. & Crous	*Nectriaceae*			Mauritius	Crous (2002)
Calycellina camelliae Dennis	*Pezizellaceae*			Papua New Guinea	Shaw (1984)
Capnodium sp.	*Capnodiaceae*			Fiji	Firman (1972), Dingley et al. (1981)
Cephaleuros sp.	*Trentepohliaceae*			Thailand	Giatgong (1980)
Ceratobasidium sp.	*Ceratobasidiaceae*			Japan	Kobayashi (2007)
Ceratocystis fimbriata Ellis & Halst*	*Ceratocystidaceae*	P**	Wilt and Canker	China	Xu et al. (2019)
Cercospora chaae Hara	*Mycosphaerellaceae*			Japan	Kobayashi (2007)
Ceriporiopsis hypolateritia (Berk. ex Cooke) Ryvarden	*Phanerochaetaceae*			Thailand	Thompson & Johnston (1953)
Chaetomium camelliae Jayaward., Manawas., X.H. Li, J.Y.Yan, & K. D. Hyde	*Chaetomiaceae*	S or P		China	This study
Chaetothyrium javanicum (Zimm.) Boedijn	*Chaetothyriaceae*	S		China, Taiwan	Tai (1979)
Chaetothyrium spinigerum (Höhn.) W. Yamam	*Chaetothyriaceae*			China	Tai (1979), Farr & Rossman (2020)
Chaetothyrium setosum (Zimm.) Hansf	*Chaetothyriaceae*			China	Tai (1979), Farr & Rossman (2020)
Cladosporium herbarum (Pers.) Link*	*Cladosporiaceae*	P		Japan, Korea	Cho & Shin (2004), Kobayashi (2007)
Cladosporium sp.	*Cladosporiaceae*			Thailand	Thompson & Johnston (1953)
Clonostachys rosea (Link) Schroers, Samuels, Seifert & W. Gams	*Bionectriaceae*			Japan	Kobayashi (2007)
Clypeolella camelliae (Syd., P. Syd. & E.J. Butler) Hansf	*Englerulaceae*			Thailand	Thompson & Johnston (1953)
Colletotrichum acutatum J.H. Simmonds*	*Glomerellaceae*	P**	Brown blight	China	Arzanlou & Torbati (2013), Chen et al. (2016, 2017b)
Colletotrichum aenigma B.S. Weir & P.R. Johnst*	*Glomerellaceae*	P**	Anthracnose	China	Jayawardena et al. (2016a), Wang et al. (2016b), Chen et al. (2019)
Colletotrichum alienum B.S. Weir & P.R. Johnst.	*Glomerellaceae*	OP**, S		China	Liu et al. (2015)
Colletotrichum boninense Moriwaki, Toy. Sato & Tsukib	*Glomerellaceae*	OP**, S	Anthracnose	New Zealand	Vieira et al. (2014), Hou et al. (2016), Liu et al. (2016a), Chen et al. (2017b), Diao et al. (2017), Douanla–Meli et al. (2018)

Table 3 Continued.

Species	Family	Life mode	*Disease caused*	locality	References
Colletotrichum camelliae Massee*	*Glomerellaceae*	E, P**	Leaf spots	China Jamaica, Korea, Thailand, USA	Larter & Martyn (1943), Thompson & Johnston (1953), Tai (1979), Alfieri et al. (1984), Cho & Shin (2004), Alizadeh et al. (2015), Liu et al. (2015), Jayawardena, et al. (2016a), Wang et al. (2016b), De Silva et al. (2017), Chen et al. (2017b), This study
Colletotrichum cliviicola Damm & Crous*	*Glomerellaceae*	S, P	Anthracnose	Brazil, China	Liu et al. (2015), Jayawardena et al. (2016a), Wang et al. (2016b)
Colletotrichum endophyticum Manamgoda, Udayanga, L. Cai & K.D. Hyde*	*Glomerellaceae*	OP, P**		China	Wang et al. (2016b)
Colletotrichum fioriniae R.G. Shivas & Y.P. Tan*	*Glomerellaceae*	OP**, S		China	Liu et al. (2015)
Colletotrichum fructicola Prihast., L. Cai & K.D. Hyde*	*Glomerellaceae*	E, P**	Leaf spots	China, Indonesia	Weir et al. (2012), Liu et al. (2015), Jayawardena et al. (2016a), Wang et al. (2016b), This study
Colletotrichum gigasporum Rakotonir. & Munaut*	*Glomerellaceae*	E, P		Iran	Alizadeh et al. (2015)
Colletotrichum gloeosporioides (Penz.) Penz. & Sacc*	*Glomerellaceae*	E, P**	Leaf spots	Brazil, China, Fiji, Japan, Kenya, Korea, Malaysia, Papua New Guinea, Taiwan, Tanzania, USA, Zimbabwe	Riley (1960), Nattrass (1961), Whiteside (1966), Turner (1971), Firman (1972), Williams & Liu (1976), Tai (1979), Dingley et al. (1981), Alfieri et al. (1984), Shaw (1984), Mendes et al. (1998), Cho & Shin (2004), Kobayashi (2007), Liu et al. (2015), Chen et al. (2017b)
Colletotrichum henanense Liu & L. Cai*	*Glomerellaceae*	P**	Leaf spots	China	Alizadeh et al. (2015), Liu et al. (2015), Jayawardena et al. (2016a), Wang et al. (2016b), De Silva et al. (2017)
Colletotrichum jiangxiense F. Liu & L. Cai*	*Glomerellaceae*	E, P**	Leaf spots	China	Liu et al. (2015), Jayawardena et al. (2016a)
Colletotrichum karsti You L. Yang, Zuo Y. Liu, K.D. Hyde & L. Cai*	*Glomerellaceae*	OP**, S		China	Wang et al. (2016b)
Colletotrichum plurivorum Damm, Alizadeh & Toy. Sato*	*Glomerellaceae*	S, P		China	Damm et al. (2019)

Table 3 Continued.

Species	Family	Life mode	*Disease caused*	locality	References
Colletotrichum pseudomajus F. Liu, L. Cai, Crous & Damm*	*Glomerellaceae*	S, P		Taiwan	Liu et al. (2014), Alizadeh et al. (2015), Jayawardena et al. (2016a), Costa et al. (2019)
Colletotrichum siamense Prihast., L. Cai & K.D. Hyde*	*Glomerellaceae*	E, P**	Leaf spots	China	Jayawardena et al. (2016a), Wang et al. (2016b).
Colletotrichum sp.*	*Glomerellaceae*	E, P, S		China, India, Fiji, Thailand	Giatgong (1980), Dingley et al. (1981), Sharma et al. (2015), Chen et al. (2017b), Liu et al. (2015).
Colletotrichum truncatum (Schwein.) Andrus & W.D. Moore*	*Glomerellaceae*	P**	Anthracnose	China	Wang et al. (2016b)
Colletotrichum wuxiense Yu Chun Wang, X.C. Wang & Y.J. Yang*	*Glomerellaceae*	OP**, S		China	Jayawardena et al. (2016a), Wang et al. (2016b)
Coniothyrium sp.	*Coniothyriaceae*			Malawi	Corbett (1964)
Corticium sp.	*Corticiaceae*			Papua New Guinea	Shaw (1984)
Corynespora polyphragmia (Syd. & P. Syd.) M.B. Ellis	*Corynesporascaceae*			Japan	Kobayashi (2007)
Corallomycetella repens (Berk. & Broome) Rossman & Samuels	*Nectriaceae*			Thailand	Thompson & Johnston (1953)
Cryptomyces theae Sawada	*Rhytismataceae*			Taiwan	Farr & Rossman (2020)
Cylindrocladiella novae–zelandiae (Boesew.) Boesew	*Nectriaceae*			New Zealand	Crous et al. (2006)
Cylindrocladium peruvianum Bat., J.L. Bezerra & M.P. Herrera	*Nectriaceae*			USA	Alfieri et al. (1984), Crous (2002)
Cylindrocladiella parva (P.J. Anderson) Boesew	*Nectriaceae*			Malawi	Wiehe (1953)
Cylindrocarpon lichenicola (Massal.) D. Hawksw	*Nectriaceae*			Papua New Guinea	Shaw (1984)
Cylindrocladium sp.	*Nectriaceae*			Brazil, Japan	Mendes et al. (1998), Kobayashi (2007).
Clypeolella camelliae (Syd., P. Syd. & E.J. Butler) Hansf *	*Englerulaceae*			India, Java	Hosagoudar (2003)
Cytospora ceratosperma (Tode) G.C. Adams & Rossman	*Valsaceae*			Japan	Kobayashi (2007)
Dematophora necatrix R. Hartig*	*Xylariaceae*	P**	White rot	China, Japan	Tai (1979), Kobayashi (2007), Sun et al. (2008)
Diaporthe amygdali (Delacr.) Udayanga, Crous & K.D. Hyde*	*Diaporthaceae*	E, S		China	Gao et al. (2016)

Table 3 Continued.

Species	Family	Life mode	*Disease caused*	locality	References
Diaporthe apiculata Y.H. Gao & L. Cai*	*Diaporthaceae*	E, S		China	Du et al. (2016), Gao et al. (2016), Yang et al. (2017), Gao et al. (2017), Yang et al. (2018), Dissanayake et al. (2017a), Yang et al. (2017), Fan et al. (2018)
Diaporthe biguttulata F. Huang, K.D. Hyde & Hong Y. Li	*Diaporthaceae*	S or P		China	This study
Diaporthe compacta Y.H. Gao & L. Cai*	*Diaporthaceae*	E		China	Yang et al. (2015), Dissanayake et al. (2017a, b), Gao et al. (2017), Yang et al. (2018)
Diaporthe discoidispora F. Huang, K.D. Hyde & Hong Y. Li*	*Diaporthaceae*	E		China	Gao et al. (2016), Dissanayake et al. (2017a), Gao et al. (2017)
Diaporthe eres Nitschke*	*Diaporthaceae*	E, P		China, Japan	Kobayashi (2007), Gao et al. (2016), Dissanayake et al. (2017a), Gao et al. (2017)
Diaporthe eucalyptorum Crous & R.G. Shivas.	*Diaporthaceae*	S or P		China	This study
Diaporthe foeniculacea Niessl*	*Diaporthaceae*			Italy	Udayanga et al. (2012), Gomes et al. (2013), Chen et al. (2014), Lombard et al. (2014)
Diaporthe fujianensis Jayaward., Manawas., X.H. Li, J.Y.Yan, & K. D. Hyde	*Diaporthaceae*	S or P		China	This study
Diaporthe fusiformis Jayaward., Manawas., X.H. Li, J.Y.Yan, & K. D. Hyde	*Diaporthaceae*	S or P		China	This study
Diaporthe hongkongensis R.R. Gomes, Glienke & Crous*	*Diaporthaceae*			China	Gao et al. (2016), Dissanayake et al. (2017a)
Diaporthe incompleta Y.H. Gao & L. Cai*	*Diaporthaceae*	S		China	Gao et al. (2017), Yang et al. (2018b).
Diaporthe masirevicii R.G. Shivas, L. Morin, S.M. Thomps. & Y.P. Tan*	*Diaporthaceae*	S			Gao et al. (2017)
Diaporthe nobilis Sacc. & Speg*	*Diaporthaceae*	P, S		China	Li et al. (2017)
Diaporthe oraccinii Y.H. Gao, F. Liu & L. Cai*	*Diaporthaceae*	P, S		China	Du et al. (2016), Gao et al. (2016, 2017), Yang et al. (2017), Dissanayake et al. (2017a, b), Yang et al. (2017, 2018a, b)
Diaporthe penetriteum Y.H. Gao & L. Cai*	*Diaporthaceae*	E, P**		China	Du et al. (2016), Dissanayake et al. (2017 a, b), Gao et al. (2017), Yang et al. (2017, 2018)

Table 3 Continued.

Species	Family	Life mode	*Disease caused*	locality	References
Diaporthe sackstonii R.G. Shivas, S.M. Thomps. & Y.P. Tan	*Diaporthaceae*	S or P		China	This study
Diaporthe sennae C.M. Tian & Qin Yang	*Diaporthaceae*	S or P		China	This study
Diaporthe sinensis Jayaward., Manawas., X.H. Li, J.Y.Yan, & K. D. Hyde	*Diaporthaceae*	S or P		China	This study
Diaporthe sp*	*Diaporthaceae*	E, S, P		China, India, Papua New Guinea	Gao et al. (2017), Mathur (1979), Farr & Rossman (2020)
Diaporthe tectonigena Doilom, Dissan. & K.D. Hyde*	*Diaporthaceae*	S		China	Gao et al. (2017)
Diaporthe ueckeri Udayanga & Castl. *	*Diaporthaceae*	S		China	Gao et al. (2016), Dissanayake et al. (2017a), Gao et al. (2017)
Diaporthe unshiuensis F. Huang, K.D. Hyde & Hong Y. Li	*Diaporthaceae*	S or P		China	This study
Diaporthe velutina Y.H. Gao & L. Cai*	*Diaporthaceae*	S		China	Gao et al. (2017)
Diaporthe viniferae Dissanayake, X.H. Li & K.D. Hyde	*Diaporthaceae*	S or P		China	This study
Diaporthe xishuangbanica Y.H. Gao & L. Cai*	*Diaporthaceae*	S		China	Dissanayake et al. (2017a), Gao et al. (2017), Yang et al. (2018a)
Diaporthe theae (Petch) Rossman & Udayanga	*Diaporthaceae*	S		Japan, Papua New Guinea, Tanzania	Ebbels & Allen (1979), Kobayashi (2007)
Diatrype conferta Petch	*Diatrypaceae*			Sri Lanka	Rappaz (1987)
Diatrype falcata (Syd. & P. Syd.) Sacc	*Diatrypaceae*			Japan	Kobayashi (2007)
Diatrype stigma (Hoffm.) Fr	*Diatrypaceae*			Japan	Kobayashi (2007)
Diatrype theae Hara	*Diatrypaceae*			Japan	Kobayashi (2007)
Dictyochaeta assamica (Agnihothr.) Aramb., Cabello & Mengasc	*Chaetosphaeriaceae*			New Zealand	Hughes & Kendrick (1968)
Dimeriellopsis theicola Sawada & W. Yamam	*Pseudoperisporiaceae*			China	Tai (1979)
Dimerina nantoensis (Sawada) W. Yamam	*Valsariaceae*			China	Farr & Rossman (2020)
Dinemasporium neottiosporoides (Agnihothr.) W.P. Wu	*Xylariomycetidae*			India	Duan et al. (2007)
Discosia artocreas (Tode) Fr.	*Discosiaceae*			Southeastern states	Watson (1950)
Discosia strobilina Lib	*Discosiaceae*			Japan	Kobayashi (2007)
Discula theae–sinensis (I. Miyake) Moriwaki & Toy*	*Gnomoniaceae*	P** S	Anthracnose	Japan, China	Tai (1979), Kobayashi (2007), Moriwaki & Sato (2009)
Discosiella longiciliata Agnihothr	*Ascomycota*			India	Mathur (1979), Nag Raj (1993)

Table 3 Continued.

Species	Family	Life mode	*Disease caused*	locality	References
Dyfrolomyces sinensis Samarak., Tennakoon & K.D. Hyde*	*Dyfrolomycetaceae*	P, S		Thailand	Hyde et al. (2018)
Elsinoe theae Bitanc. & Jenkins*	*Elsinoaceae*	P, S		Brazil, Japan, Korea Tanzania	Riley (1960), Mendes et al. (1998), Cho & Shin (2004), Kobayashi (2007), Fan et al. (2018)
Epicoccum camelliae Qian Chen, Crous & L. Cai*	*Didymellaceae*	P, S		China	Chen et al. (2017a), Valenzuela-Lopez et al. (2018)
Epicoccum latusicollum Qian Chen, Crous & L. Cai*	*Didymellaceae*	P, S		China	Chen et al. (2017a), Valenzuela-Lopez et al. (2018)
Epicoccum layuense	*Didymellaceae*	S or P		China	This study
Epicoccum sorghinum (Sacc.) Aveskamp, Gruyter & Verkley*	*Didymellaceae*	P, S		China	Chen et al. (2017a), Bao et al. (2019)
Erythricium salmonicolor (Berk. & Broome) Burds	*Corticiaceae*			Japan, Papua New Guinea, Thailand	Thompson & Johnston (1953), Kobayashi (2007)
Exobasidium camelliae Shirai*	*Exobasidiaceae*	P		China, USA	Alfieri et al. (1984)
Exobasidium reticulatum S. Ito & Sawada*	*Exobasidiaceae*	P		China, Japan	Tai (1979), Chen (2002), Kobayashi (2007)
Exobasidium vexans Massee*	*Exobasidiaceae*	P**	Blister blight	China, India, Japan, Korea, Myanmar, Korea, Thailand	Thompson & Johnston (1953), Tai (1979), Giatgong (1980), Richardson (1990), Chen (2002), Cho & Shin (2004), Kobayashi (2007), Thaung (2007), Silva et al. (2015).
Exobasidium yunnanense Zhen Ying Li & L. Guo	*Exobasidiaceae*	P, S		China	Li & Guo (2009)
Fusarium asiaticum O'Donnell, T. Aoki, Kistler & Geiser	Nectriaceae	S or P		China	This study
Fusarium concentricum Nirenberg & O'Donnell	Nectriaceae	S or P		China	This study
Fusarium fujikuroi Nirenberg	Nectriaceae	S or P		China	This study
Fusarium oxysporum Schltdl	*Nectriaceae*	S		India, Kenya, Southeast Asia	Nattrass (1961), Sarbhoy & Agarwal (1990), Lombard et al. (2019)
Fusarium proliferatum (Matsush.) Nirenberg ex Gerlach & Nirenberg	Nectriaceae	S or P		China	This study
Fusarium sp.	*Nectriaceae*			Malaysia, Papua New Guine, Sri Lanka	Liu (1977), Sinniah et al. (2017), Aoki et al. (2018), Na et al. (2018)
Fusicladium theae Hara	*Venturiaceae*			China, Japan	Tai (1979), Kobayashi (2007).

Table 3 Continued.

Species	Family	Life mode	*Disease caused*	locality	References
Gliocladiopsis tenuis (Bugnic.) Crous & M.J. Wingf.	*Nectriaceae*			Mauritius	Crous (2002)
Gliocladiopsis tenuis (Bugnic.) Crous & M.J. Wingf.	*Nectriaceae*			Japan	Kobayashi (2007)
Globisporangium debaryanum (R. Hesse) Uzuhashi, Tojo & Kakish	*Pythiaceae*			Philippines	Teodoro (1937)
Globisporangium mamillatum (Meurs) Uzuhashi, Tojo & Kakish	*Pythiaceae*			Greece	Pantidou (1973)
Globisporangium spinosum (Sawada) Uzuhashi, Tojo & Kakish	*Pythiaceae*			Japan	Kobayashi (2007)
Gnomoniopsis fructicola (G. Arnaud) Sogonov	*Gnomoniaceae*			Malaysia	Liu (1977)
Graphium rigidum (Pers.) Sacc	*Microascaceae*			Japan	Matsushima (1975), Kobayashi (2007)
Guignardia abeana W. Yamam. & K. Konno	*Phyllostictaceae*			Japan	Kobayashi (2007)
Guignardia theae (Racib.) C. Bernard	*Phyllostictaceae*			China	Tai (1979)
Helicobasidium longisporum Wakef	*Helicobasidiaceae*			Indonesia, China	Whiteside (1966)
Helicobasidium purpureum (Tul.) Pat	*Helicobasidiaceae*			Japan	Kobayashi (2007)
Helicobasidium sp.	*Helicobasidiaceae*			Malawi	Wiehe (1953)
Hendersonia theae Hara	*Phaeosphaeriaceae*			China, Japan, India	Mathur (1979), Tai (1979), Kobayashi (2007)
Hypohelion durum Y.R. Lin, C.L. Hou & S.J. Wang	*Rhytismataceae*	P, S	Branch rot	China	Lin et al. (2004), Chen et al. (2011)
Hypoxylon howeanum Peck	*Hypoxylaceae*			Japan	Kobayashi (2007) as *Hypoxylon coccinellu* Sacc.
Hypoxylon fuscopurpureum (Schwein.) M.A. Curtis	*Hypoxylaceae*			Japan	Kobayashi (2007)
Ilyonectria destructans (Zinssm.) Rossman, L. Lombard & Crous	*Hypocreales*			Japan	Kobayashi (2007)
Julella vitrispora (Cooke & Harkn.) M.E. Barr	*Thelenellaceae*			Japan	Kobayashi (2007)
Lasiodiplodia gonubiensis Pavlic, Slippers & M.J. Wingf*	*Botryosphaeriaceae*	E, P		Australia	Tan et al. (2019), Burgess et al. (2019)
Lasiodiplodia pseudotheobromae A.J.L. Phillips, A. Alves & Crous*	*Botryosphaeriaceae*	P**	Leaf necrosis	China	Li et al. (2019)
Lasiodiplodia theobromae (Pat.) Griffon & Maubl*	*Botryosphaeriaceae*	P**	Leaf necrosis	China, Malawi, Malaysia, Papua New	Wiehe (1953), Turner (1971), Liu (1977), Shaw (1984), Whiteside (1966),

Table 3 Continued.

Species	Family	Life mode	*Disease caused*	locality	References
				Guinea, Tanzania. Zimbabwe	Li et al. (2019)
Leptosphaerulina sp.	*Didymellaceae*			Malawi	Corbett (1964)
Lophodermium sinens Y.R. Lin, C.L. Hou & Jiang L. Chen	*Rhytismataceae*	P		China	Chen et al. (2011)
Macrophoma sp.	*Botryosphaeriaceae*			Thailand	Thompson & Johnston (1953)
Macrophoma theicola Petch	*Botryosphaeriaceae*			Malawi	Wiehe (1953)
Macrophomina phaseolina (Tassi) Goid	*Botryosphaeriaceae*			India, Malawi, Malaysia, Tanzania	Wiehe (1953), Johnston (1960), Riley (1960), Mathur (1979)
Marasmiellus scandens (Massee) Dennis & D.A. Reid	*Omphalotaceae*			Malaysia	Turner (1971)
Marasmius crinis–equi F. Muell. ex Kalchbr	*Marasmiaceae*			Fiji, Japan	Firman (1972), Dingley et al. (1981), Kobayashi (2007)
Marasmius sp.	*Marasmiaceae*			Thailand	Thompson & Johnston (1953)
Marasmius tenuissimus (Sacc.) Singer	*Marasmiaceae*			Japan	Kobayashi (2007).
Marssonina sp.	*Dermateaceae*			Thailand	Giatgong (1980)
Meliola camelliae (Catt.) Sacc	*Meliolaceae*			China	Tai (1979)
Microcera coccophila Desm	*Nectriaceae*			Papua New Guinea	Shaw (1984)
Monilochaetes camelliae (Alcorn & Sivan.) Réblová, W. Gams & Seifert	*Australiascaceae*			Australia	Réblová et al. (2011)
Mycosphaerella ikedae Hara	*Mycosphaerellaceae*			China, Japan, Malaysia	Johnston (1960), Tai (1979), Kobayashi (2007)
Mycosphaerella sp.	*Mycosphaerellaceae*			Mauritius, Tanzania	Riley (1960), Orieux & Felix (1968)
Mycosphaerella theae Hara				China, Japan, Samoa, Zimbabwe	Whiteside (1966), Tai (1979), Dingley et al. (1981), Kobayashi (2007)
Myriangium duriaei Mont. & Berk	*Myriangiaceae*			Japan	Kobayashi (2007)
Nectria bolbophylli Henn	*Nectriaceae*			Japan	Kobayashi (2007)
Nectria cinnabarina (Tode) Fr	*Nectriaceae*			Japan	Kobayashi (2007)
Nectria diversispora Petch	*Nectriaceae*			Taiwan	Farr & Rossman (2020)
Nectria sp.	*Nectriaceae*			Malawi, Papua New Guinea	Wiehe (1953), Shaw (1984)
Nectria pseudotrichia Berk. & M.A. Curtis	*Nectriaceae*			Papua New Guinea, Tanzania, Thailand	Thompson & Johnston (1953), Riley (1960), Shaw (1984)
Nectricladiella viticola (Berk. & M.A. Curtis) Hirooka, Rossman & P. Chaverri	*Nectriaceae*			India	Crous (2002)

Table 3 Continued.

Species	Family	Life mode	*Disease caused*	locality	References
Neocosmospora ambrosia Gadd & Loos) L. Lombard & Crous*	*Nectriaceae*	P, S		India, Sri Lanka	Lombard et al. (2014), Guarnaccia & Crous (2018), Sandoval–Denis et al. (2018, 2019)
Neocosmospora sp.*	*Nectriaceae*			Sri Lanka	Sandoval–Denis et al. (2019)
Neocosmospora haematococca (Berk. & Broome) Samuels, Nalim & Geiser	*Nectriaceae*			Japan	Kobayashi (2007)
Neocosmospora ipomoeae (Halst.) L. Lombard & Crous	*Nectriaceae*			China	Tai (1979)
Neocosmospora solani (Mart.) L. Lombard & Crous	*Nectriaceae*			India, Japan	Sarbhoy & Agarwal (1990), Kobayashi (2007), Aoki et al. (2018)
Neocapnodium tanakae (Shirai & Hara) W. Yamam	*Trichomeriaceae*			China	Tai (1979)
Neofusicoccum ribis (Slippers, Crous & M.J. Wingf.) Crous, Slippers & A.J.L. Phillips	*Botryosphaeriaceae*			Malawi	Wiehe (1953)
Pyrrhoderma noxium (Corner) L.W. Zhou & Y.C. Dai				China, Thailand	Thompson & Johnston (1953), Riley (1960)
Neocosmospora ambrosia (Gadd & Loos) L. Lombard & Crous*	*Nectriaceae*	P, S		India, Sri Lanka	Freeman et al. (2013), Aoki et al. (2018), Na et al. (2018)
Neonectria ditissima (Tul. & C. Tul.) Samuels & Rossman	*Nectriaceae*			Japan	Kobayashi (2007)
Neopestalotiopsis clavispora (G.F. Atk.) Maharachch., K.D. Hyde & Crous*	*Sporocadaceae*	P**	Grey blight	China	Wei et al. (2005, 2007), Ge et al. (2009), Wang et al. (2017b), Chen et al. (2018a)
Neopestalotiopsis clavispora as *Pestalotiopsis clavispora* (G.F. Atk.) Steyaert*	*Sporocadaceae*	E, P**	Brown–black spot		Wei et al. (2005, 2007), Ge et al. (2009), Wang et al. (2017b), Chen et al. (2018a)
Neopestalotiopsis ellipsospora (Maharachch. & K.D. Hyde) Maharachch., K.D. Hyde & Crous*	*Sporocadaceae*	P**	Grey blight	China	Wang et al. (2019b)
Neopestalotiopsis sp.*	*Sporocadaceae*	P**, S	Grey blight	China, France	Maharachchikumbura et al. (2014), Chen et al. (2018a)
Nemania diffusa (Sowerby) Gray	*Xylariaceae*	S or P		China	This study
Nigrospora camelliae–sinensis Mei Wang & L. Cai*	*Apiosporaceae*	P, S		China	Wang et al. (2017b), This study
Nigrospora chinensis Mei Wang & L. Cai*	*Apiosporaceae*	P, S		China	Wang et al. (2017b)
Nigrospora guilinensis Mei Wang & L. Cai*	*Apiosporaceae*	P, S		China	Wang et al. (2017b)

Table 3 Continued.

Species	Family	Life mode	*Disease caused*	locality	References
Nigrospora lacticolonia Mei Wang & L. Cai*	*Apiosporaceae*	P, S		China	Wang et al. (2017b)
Nigrospora musae McLennan & Hoëtte*	*Apiosporaceae*	P, S		China	Wang et al. (2017b)
Nigrospora oryzae (Berk. & Broome) Petch*	*Apiosporaceae*	P, S		China	Wang et al. (2017b)
Nigrospora sphaerica (Sacc.) E.W. Mason*	*Apiosporaceae*	P**, S	leaf blight	China, India	Dutta et al. (2015), Liu et al. (2016b). Wang et al. (2017b)
Nigrospora pyriformis Mei Wang & L. Cai*	*Apiosporaceae*	P, S		China	Wang et al. (2017b)
Nigrospora sp.*	*Apiosporaceae*	P, S		China	Wang et al. (2017b)
Ophioirenina theae Sawada & W. Yamam*	*Meliolaceae*	P, S		China, Taiwan	Tai (1979), Hongsanan et al. (2015)
*Ophiognomonia setacea (*Pers.) Sogonov	*Gnomoniaceae*			Japan	Kobayashi (2007)
Ophiovalsa theae (Hara) Tak. Kobay	*Gnomoniaceae*			Japan	Kobayashi (2007)
Paraconiothyrium fuckelii (Sacc.) Verkley & Gruyter	*Didymosphaeriaceae*			Japan	Kobayashi (2007)
Paraconiothyrium fuckelii (Sacc.) Verkley & Gruyter*	*Didymosphaeriaceae*			Japan	Kobayashi (2007)
Penicillium corylophilum Dierckx	*Aspergillaceae*			Kenya	Nattrass (1961)
Pestalotiopsis acaciae (Thüm.) K. Yokoy. & S. Kaneko*	*Sporocadaceae*	S		China	Ge et al. (2009)
Pestalotiopsis aggestorum F. Liu & L. Cai*	*Sporocadaceae*	S		China	Liu et al. (2017)
Pestalotiopsis algeriensis (Sacc. & Berl.) W.P. Wu*	*Sporocadaceae*	S		China	Zhang et al. (2012)
Pestalotiopsis camelliae Yan M. Zhang, Maharachch. & K.D. Hyde*	*Sporocadaceae*	P**, S	Grey blight	China, Turkey	Maharachchikumbura et al. (2014), Moslemi & Taylor (2015), Chen et al. (2017c), Liu et al. (2017), Wang et al. (2017b), Solarte et al. (2017), This study
Pestalotiopsis chamaeropis Maharachch., K.D. Hyde & Crous*	*Sporocadaceae*	P, S	Grey blight	China	Liu et al. (2017), Wang et al. (2019b)
Pestalotiopsis dilucida F. Liu & L. Cai*	*Sporocadaceae*	E, P, S		China	Liu et al. (2017)
Pestalotiopsis disseminata (Thüm.) Steyaert*	*Sporocadaceae*	P, S		China	Zhang et al. (2012)
Pestalotiopsis funerea (Desm.) Steyaert*	*Sporocadaceae*	S		China	Ge et al. (2009)
Pestalotiopsis furcata Maharachch. & K.D. Hyde*	*Sporocadaceae*	S		China, Thailand	Zhang et al. (2012), Maharachchikumbura et al. (2013), 2014), Liu et al. (2017), Chen et al. (2018a), Solarte et al. (2017)

Table 3 Continued.

Species	Family	Life mode	*Disease caused*	locality	References
Pestalotiopsis gigas Steyaert	*Sporocadaceae*			Kenya	Nattrass (1961)
Pestalotiopsis jinchanghensis F. Liu & L. Cai*	*Sporocadaceae*	E, P, S		China	Liu et al. (2017)
Pestalotiopsis kenyana Maharachch., K.D. Hyde & Crous*	*Sporocadaceae*	E, P, S		China	Liu et al. (2017), This study
Pestalotiopsis longiappendiculata F. Liu & L. Cai*	*Sporocadaceae*	E, P, S		China	Liu et al. (2017)
Pestalotiopsis longiseta (Speg.) K. Dai & Tak. Kobay*	*Sporocadaceae*	P, S		Japan, Korea	Kobayashi (2007)
Pestalotiopsis lushanensis F. Liu & L. Cai *	*Sporocadaceae*	P**	Grey blight	China	Chen et al. (2018c), This study
Pestalotiopsis maculans (Corda) Nag Raj*	*Sporocadaceae*	P, S		China Czechoslovakia, France, Germany, Japan, USA	Nag Raj (1993), Jeewon et al. (2002, 2003), Kobayashi (2007), Ge et al. (2009), Maharachchikumbura et al. (2011)
Pestalotiopsis menezesiana (Bres. & Torrend) Bissett*	*Sporocadaceae*	P, S		China	Zhang et al. (2012)
Pestalotiopsis microspora (Speg.) Bat. & Peres*	*Sporocadaceae*	E, P		China	Wei et al. (2005, 2007), Ge et al. (2009), Zhang et al. (2012)
Pestalotiopsis nattrassii Steyaert*	*Sporocadaceae*			China, Kenya	Nattrass (1961), Lu et al. (2000), Zhuang (2001)
Pestalotiopsis neglecta (Thüm.) Steyaert*	*Sporocadaceae*	E, S		China	Wei et al. (2005, 2007), Ge et al. (2009)
Pestalotiopsis palmarum (Cooke) Steyaert	*Sporocadaceae*			Japan, Taiwan (China)	Kobayashi (2007)
Pestalotiopsis photiniae (Thüm.) Y.X. Chen*	*Sporocadaceae*	E		China	Tejesvi et al. (2009)
Pestalotiopsis rhodomyrtus Yu Song, K. Geng, K.D. Hyde & Yong Wang bis*	*Sporocadaceae*	P, S		China	Liu et al. (2017), Wang et al. (2019b), This study
Pestalotiopsis sp.*	*Sporocadaceae*	E, P, S		China, Fiji, Papua New Guinea, Samoa, Thailand	Firman (1972), Giatgong (1980), Dingley et al. (1981), Zhang et al. (2012)
Pestalotiopsis sydowiana (Bres.) B. Sutton*	*Sporocadaceae*			China	Zhuang (2001), Ge et al. (2009)
*Pestalotiopsis trachycarpicola*Yan M. Zhang & K.D. Hyde*	*Sporocadaceae*	P, S		China	Liu et al. (2017)
Pestalotiopsis versicolor (Speg.) Steyaert*	*Sporocadaceae*	P, S		China	Zhang et al. (2012)
Pestalotiopsis virgatula (Kleb.) Steyaert*	*Sporocadaceae*	P, S		China	Zhang et al. (2012)
Pestalotiopsis yanglingensis F. Liu & L. Cai*	*Sporocadaceae*	P**, S	Grey blight	China	Liu et al. (2017)
Phacidium lauri (Sowerby) Crous & D. Hawksw	*Phacidiaceae*			Japan	Ando et al. (1989), Kobayashi (2007)

Table 3 Continued.

Species	Family	Life mode	*Disease caused*	locality	References
Phaeodothis winteri (Niessl) Aptroot	*Didymosphaeriaceae*			Tanzania	Aptroot (1995)
Phaeoisaria clematidis (Fuckel) S. Hughes	*Diatrypaceae*			Indonesia	Seifert (1990)
Phaeosphaerella theae Petch	*Venturiaceae*			Thailand	Thompson & Johnston (1953)
Phoma herbarum Westend*	*Didymellaceae*	P**	Leaf spot	China	Thangaraj et al. (2019)
Phoma sp.	*Didymellaceae*			Florida	Alfieri et al. (1984)
Phyllosticta camelliae Westend*	*Phyllostictaceae*	P, S		China, Japan	Bai (2000), Kobayashi (2007)
Phyllosticta capitalensis Henn*	*Phyllostictaceae*	P**	Leaf spot	China	Cheng et al. (2019)
Phyllosticta citricarpa (McAlpine)				Papua New Guinea	Shaw (1984)
Phyllosticta erratica Ellis & Everh	*Phyllostictaceae*			Florida, Japan	Alfieri et al. (1984), Kobayashi (2007)
Phyllosticta sp*	*Phyllostictaceae*	P, S		Fiji, Hong Kong	Firman (1972), Dingley et al. (1981), Lu et al. (2000), Zhuang (2001)
Phyllosticta theae Speschnew*	*Phyllostictaceae*			China, Fiji, Japan, Tanzania, Thailand	Thompson & Johnston (1953), Riley (1960), Firman (1972), Tai (1979), Dingley et al. (1981), Kobayashi (2007)
Phyllosticta theicola Curzi	*Phyllostictaceae*			China, Japan	Tai (1979), Kobayashi (2007)
Pleospora theae Speschnew	*Pleosporaceae*			Japan	Kobayashi (2007)
Pseudocercospora camelliae (Deighton) U. Braun*	*Mycosphaerellaceae*	P, S		Georgia, New Zealand	Pennycook (1989), Gadgil (2005), Braun et al. (2012)
Pseudocercospora camelliicola U. Braun & C.F. Hill*	*Mycosphaerellaceae*	P, S	Leaf spot	Mauritius, New Zealand, Taiwan	Braun & Hill (2002), Gadgil (2005), Kirschner et al. (2009)
Pseudocercospora javanica Deighton	*Mycosphaerellaceae*	P, S		Java, India, Indonesia, Japan, Nigeria, Sri Lanka, Tanzania	Kobayashi (2007), Kamal (2010), Braun et al. (2012)
Pseudocercospora ocellata (Deighton) Deighton	*Mycosphaerellaceae*	P, S		Brazil, China, Ethiopia, Japan, Kenya, Mauritius, Nigeria, Taiwan, Tanzania	Riley (1960), Tai (1979), Ragazzi & Marino (1990), Mendes et al. (1998), Crous & Braun (2003)
Pseudocercospora theae (Cavara) Deighton	*Mycosphaerellaceae*	P**, S		Argentina, China, Hong Kong, Taiwan, USA	Deighton (1976), Alfieri et al. (1984), Hsieh, & Goh (1990), Zhuang (2001), Braun et al. (2012), Lu et al. (2000)
Pseudolachnea hispidula (Schrad.) B. Sutton				India	Mathur (1979)
Pseudopestalotiopsis ampullacea F. Liu & L. Cai*	*Pestalotiopsidaceae*	E, P, S		China	Chen et al. (2018a), Liu et al. (2017), Nozawa et al. (2018)
Pseudopestalotiopsis camelliae Maharachch., L.D. Guo & K.D. Hyde*	*Pestalotiopsidaceae*	S, E		China	Maharachchikumbura et al. (2014), Nozawa et al. (2018), Chen et al.

Table 3 Continued.

Species	Family	Life mode	*Disease caused*	locality	References
					(2018a), This study
Pseudopestalotiopsis camelliae–sinensis F. Liu & L. Cai*	*Pestalotiopsidaceae*	S, E		China	Chen et al. (2018a), Nozawa et al. (2018), This study
Pseudopestalotiopsis chinensis F. Liu & L. Cai	*Pestalotiopsidaceae*	P*	Grey blight	China	Liu et al. (2017), Chen et al. (2018a), Nozawa et al. (2018)
Pseudopestalotiopsis sp.	*Pestalotiopsidaceae*	S, P		China, Thailand	Liu et al. (2017), Wang et al. (2019b)
Pseudopestalotiopsis theae (Sawada) Maharachch., K.D. Hyde & Crous*	*Pestalotiopsidaceae*	E, P**, S	Grey blight	Brazil, China (Thaiwan), India, Japan, Kenya, Korea, Malawi, Malaysia, Papua New Guinea, Taiwan, Tanzania, Thailand, Zimbabwe	Zhuang (2001), Cho & Shin (2004), Kobayashi (2007), Maharachchikumbura et al. (2011), Watanabe et al. (2012), Zhang et al. (2012), Maharachchikumbura et al. (2013, 2014), Nozawa et al. (2018)
Pyrenochaetopsis decipiens (Marchal) Gruyter, Aveskamp & Verkley	*Cucurbitariaceae*			India	Mathur (1979)
Pyrrhoderma noxium (Corner) L.W. Zhou & Y.C. Dai	*Hymenochaetaceae*			Sri Lanka	Adikaram & Yakandawal (2020)
Pythium sp.	*Pythiaceae*			Japan	Kobayashi (2007)
Ramularia theicola Curzi	*Mycosphaerellaceae*			Georgia, Italy, Kazakhstan	Farr & Rossman (2020)
Rigidoporus microporus (Sw.) Overeem	*Meripilaceae*			Papua New Guinea, Thailand	Thompson & Johnston (1953), Shaw (1984)
Rigidoporus vinctus (Berk.) Ryvarden *Rigidop*	*Meripilaceae*			Thailand	Thompson & Johnston (1953)
Rhizoctonia noxia (Donk) Oberw., R. Bauer, Garnica & R. Kirschner	*Ceratobasidiaceae*			Brazil	Mendes et al. (1998)
Rhizoctonia solani J.G. Kühn	*Ceratobasidiaceae*			Japan, Malaysia, Thailand	Thompson & Johnston (1953), Turner (1971), Kobayashi (2007)
Rossmania aculeata (Petch) Lar.N. Vassiljeva	*Xylariaceae*			India, Sri Lanka	Agnihothrudu (1961), Adikaram & Yakandawala (2020)
Rossmania aculeata (Petch) Lar.N. Vassiljeva	*Xylariaceae*			China	Tai (1979)
Rosellinia sp.	*Xylariaceae*			Brazil, Japan, Tanzania, Thailand	Thompson & Johnston (1953), Riley (1960), Alvarez (1976), Kobayashi (2007)

Table 3 Continued.

Species	Family	Life mode	*Disease caused*	locality	References
Sadasivanella indica Agnihothr	*Ascomycota*			India	Mathur (1979)
Sarocladium sp.	*Hypocreales*			Fiji	Dingley et al. (1981)
Scorias capitata Sawada	*Capnodiaceae*			Taiwan (China)	Tai (1979)
Scytalidium terminale G.V. Rao & de Hoog	*Hyaloscyphaceae*			Netherlands	Rao & De Hoog (1975)
Septobasidium acaciae Sawada	*Septobasidiaceae*			Taiwan (China)	Kobayashi (2007)
Septobasidium *bogoriense* Pat	*Septobasidiaceae*			Japan	Kobayashi (2007)
Septobasidium pilosum Boedijn & B.A. Steinm	*Septobasidiaceae*			Japan	Kobayashi (2007)
Septobasidium sp.	*Septobasidiaceae*			Thailand	Thompson & Johnston (1953)
Septobasidium tanakae (Miyabe) Boedijn & B.A. Steinm	*Septobasidiaceae*			Japan	Kobayashi (2007)
Setophoma antiqua F. Liu & L. Cai*	*Phaeosphaeriaceae*	P	Leaf spot	China	Liu et al. (2019)
Setophoma endophytica F. Liu & L. Cai*	*Phaeosphaeriaceae*	P	Leaf spot	China	Liu et al. (2019)
Setophoma longinqua F. Liu & L. Cai*	*Phaeosphaeriaceae*	P	Leaf spot	China	Liu et al. (2019)
Setophoma yingyisheniae F. Liu & L. Cai*	*Phaeosphaeriaceae*	P	Leaf spot	China	Liu et al. (2019), This study
Setophoma yunnanensis F. Liu & L. Cai*	*Phaeosphaeriaceae*	P	Leaf spot	China	Liu et al. (2019)
Sillia theae Hara	*Sydowiellaceae*	S		Japan	Senanayake et al. (2017)
Sporidesmium tropicale M.B. Ellis	*Pleosporomycetidae*			Malaysia	Johnston (1960)
Stagonospora theae Hara	*Phaeosphaeriaceae*			Japan	Kobayashi (2007)
Stilbum sp.	*Chionosphaeraceae*			Malawi	Wiehe (1953)
Taeniolella sp.	*Mytilinidiaceae*			Papua New Guinea	Shaw (1984)
Terriera camelliicola (Minter) Y.R. Lin & C.L. Hou*	*Rhytismataceae*	P, S		China, India	Zhang et al. (2015)
Thozetellopsis tocklaiensis Agnihothr	*Chaetosphaeriaceae*			India	Agnihothrudu (1961)
Thelonectria lucida (Höhn.) P. Chaverri & Salgado as *Nectria lucida* Höhn	*Nectriaceae*			Malaysia	Thompson & Johnston (1953), Turner (1971)
Thelonectria mammoidea (W. Phillips & Plowr.) C. Salgado & R.M. Sánchez	*Nectriaceae*			Japan	Kobayashi (2007)
Tinctoporellus epimiltinus (Berk. & Broome) Ryvarden	*Polyporaceae*			Papua New Guinea	Shaw (1984)
Trichoderma atroviride P. Karst	*Hypocreaceae*	S or P		China	This study
richoderma camelliae Jayaward., Manawas., X.H. Li, J.Y.Yan, & K. D. Hyde	*Hypocreaceae*	S or P		China	This study
Trichoderma lixii (Pat.) P. Chaverri	*Hypocreaceae*	S or P		China	This study
Trichoderma longibrachiatum Rifai	*Hypocreaceae*	E		China	Wu et al. (2009)
Trichoderma viride Pers	*Hypocreaceae*			Kenya	Nattrass (1961)

Table 3 Continued.

Species	Family	Life mode	*Disease caused*	locality	References
Trichosphaeria corynephora (Cooke) Sacc	*Trichosphaeriaceae*			Japan	Kobayashi (2007)
Tripospermum sp.	*Capnodiaceae*			Malaysia	Turner (1971)
Valsaria insitiva (Tode) Ces. & De Not	*Valsariaceae*			Japan	Kobayashi (2007)

Identification confirmed by molecular data is marked with an asterisk (*). For the species, those with confirmed pathogenicity data are marked with a double asterisk (**). The mode of life is given as (E) endophyte, (P) pathogen and (S) saprotroph.

Declarations

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Conflicts of interest/Competing interests

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Availability of data and material

The sequence data generated in this study are deposited in NCBI GenBank (https://www.ncbi.nlm.nih.gov/genbank). All accession numbers are given in Table 1. All isolates obtained in this study are deposited in culture collection and herbarium of Institute of Plant and Environmental Protection, Beijing Academy of Agriculture and Forestry Sciences (JZB).

Authors' contributions

JYY conceived the research. ISM and RSJ planned the basic research. HYL provided materials. ISM RSJ and YYZ conducted the experiments and prepared the manuscript. WZ, AJLP, DNW, AJD, XHL, HLL, SB, RSJ, YHL, JYY and KH revised the manuscript. All authors read and approved the final manuscript.

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