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

Manawasinghe IS\textsuperscript{1,2,4}, Jayawardena RS\textsuperscript{2}, Li HL\textsuperscript{3}, Zhou YY\textsuperscript{1}, Zhang W\textsuperscript{1}, Phillips AJL\textsuperscript{5}, Wanasinghe DN\textsuperscript{6}, Dissanayake AJ\textsuperscript{7}, Li XH\textsuperscript{1}, Li YH\textsuperscript{1}, Hyde KD\textsuperscript{2,4} and Yan JY\textsuperscript{1*}

\textsuperscript{1}Institute of Plant and Environment Protection, Beijing Academy of Agriculture and Forestry Sciences, Beijing 100097, People’s Republic of China
\textsuperscript{2}Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand
\textsuperscript{3}Tea Research Institute, Fujian Academy of Agricultural Sciences, Fu’an 355015, People’s Republic of China
\textsuperscript{4}Innovative Institute for Plant Health, Zhongkai University of Agriculture and Engineering, Guangzhou 510225, People’s Republic of China
\textsuperscript{5}Universidade de Lisboa, Faculdade de Ciências, Biosystems and Integrative Sciences Institute (BioISI), Campo Grande, 1749–016 Lisbon, Portugal
\textsuperscript{6}CAS, Key Laboratory for Plant Biodiversity and Biogeography of East Asia (KLPB), Kunming Institute of Botany, Chinese Academy of Science, Kunming 650201, Yunnan, People’s Republic of China
\textsuperscript{7}School of Life Science and Technology, University of Electronic Science and Technology of China, Chengdu 611731, People’s Republic of China

Manawasinghe IS, Jayawardena RS, Li HL, Zhou YY, Zhang W, Phillips AJL, Wanasinghe DN, Dissanayake AJ, Li XH, Li YH, Hyde KD, Yan JY 2021 – Microfungi associated with *Camellia sinensis*: A case study of leaf and shoot necrosis on Tea in Fujian, China. Mycosphere 12(1), 430–518, Doi 10.5943/mycosphere/12/1/6

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

Table of contents

Ascomycota R.H. Whittaker
Dothideomycetes O.E. Erikss. & Winka
Dothideomycetidae P.M. Kirk, P.F. Cannon, J.C. David & Stalpers ex C.L. Schoch, Spatafora, Crous & Shoemaker
Botryosphaeriales C.L. Schoch
Botryosphaeriaceae Theiss
1. Botryosphaeria dothidea (Moug.) Ces. & De Not., in Comm. Soc. crittog. Ital. 1(fasc. 4): 212 (1863)

Pleosporomycetidae C.L. Schoch, Spatafora, Crous & Shoemaker
Pleosporales Luttr. ex M.E. Barr
Didymellaceae Gruyter
2. Epicoccum layuense Qian Chen, Crous & L. Cai, in Chen et al., Stud. Mycol. 87: 145 (2017): New host record

Phaeosphaeriaceae M.E. Barr
3. Setophoma yingyisheniae F. Liu & L. Cai, in Liu et al., Fungal Systematics and Evolution 4: 54 (2019)

Sordariomycetes O.E. Erikss. & Winka
Subclass Diaporthomycetidae Senan., Maharachch. & K.D. Hyde
Diaporthales Nannf
Diaporthaceae Höhn
4. Diaporthe biguttulata F. Huang, K.D. Hyde & Hong Y. Li, in Huang et al., Fungal Biology (2015): New host record
5. Diaporthe eucalyptorum Crous & R.G. Shivas., in Crous et al. Persoonia 28: 153 (2012): New host record
6. Diaporthe fujianensis Jayaward., Manawas., X.H. Li, J.Y.Yan, & K. D. Hyde, sp. nov.
7. Diaporthe fusiformis Jayaward., Manawas., X.H. Li, J.Y.Yan, & K. D. Hyde, sp. nov.
8. Diaporthe nobilis Sacc. & Speg., Michelia 1(no. 4): 386 (1878)
9. Diaporthe sackstonii R.G. Shivas, S.M. Thomps. & Y.P. Tan, in Thompson et al., Persoonia 35: 46 (2015)
10. Diaporthe sennea C.M. Tian & Qin Yang, in Yang et al., Phytotaxa 302(2): 149 (2017)
11. Diaporthe sinensis Jayaward., Manawas., X.H. Li, J.Y.Yan, & K. D. Hyde, sp. nov.
12. Diaporthe unshiuensis F. Huang, K.D. Hyde & Hong Y. Li, in Huang et al., Fungal Biology 119(5): 344 (2015): New host record
13. Diaporthe viniferae Dissanayake, X.H. Li & K.D. Hyde, in Manawasinghe et al., Frontiers in Microbiology 10: 21 (2019): New host record

Subclass Hypocreomycetidae O.E. Erikss. & Winka
Glomerellales Chade. ex Réblová, W. Gams & Seifert
Glomerellaceae Locq. ex Seifert & W. Gams
14. Colletotrichum camelliae Massee, in Bull. Misc. Inf., Kew: 91 (1899)
15. Colletotrichum fruticola Prihast., L. Cai & K.D. Hyde, in Prihastuti et al., Fungal Diversity 39: 96 (2009)

Hypocreales Lindau, Natürl. Pflanzenfam
Hypocreaceae De Not
16. Trichoderma atroviride P. Karst., in Bidr. Känn. Finl. Nat. Folk 51: 363 (1892): New host record
17. Trichoderma camelliae Jayaward., Manawas., X.H. Li, J.Y.Yan, & K. D. Hyde, sp. nov.
18. Trichoderma lixii (Pat.) P. Chaverri, in Chaverri et al., Mycologia 107(3): 578 (2015): New host record
Nectriaceae Tul. & C. Tul

19. *Fusarium asiaticum* O’Donnell, T. Aoki, Kistler & Geiser in O’Donnell et al., Fungal Genetics Biol. 41(6): 619 (2004): New host record

20. *Fusarium concentricum* Nirenberg & O’Donnell in Nirenberg & O’Donnell Mycologia 90(3): 442 (1998): New host record

21. *Fusarium fujikuroi* Nirenberg, in Nirenberg Mitt. biol. BundAnst. Ld–u. Forstw. 169: 32 (1976): New host record

22. *Fusarium proliferatum* (Matsush.) Nirenberg ex Gerlach & Nirenberg, in Nirenberg Mitt. biol. BundAnst. Ld–u. Forstw. 169: 38 (1982): New host record

Subclass Sordariomycetidae O.E. Erikss., & Winka

Sordariales Chad., ex D. Hawksw. & O.E. Erikss

Chaetomiaceae G. Winter [as ‘Chaetomieae’], Rabenh

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

Xylariomycetidae O.E. Erikss. & Winka

Amphisphaeriales D. Hawksw. & O.E. Erikss

Apiosporaceae K.D. Hyde, J. Fröhhl., Joanne E. Taylor & M.E. Barr

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

25. *Nigrospora camelliae–sinensis* M. Wang & L. Cai, in Wang, Liu, Crous & Cai, Persoonia 39: 127 (2017)

Sporocadaceae Corda

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

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

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

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

30. *Pseudopestalotiopsis camelliae–sinensis* F. Liu & L. Cai, in Liu et al., Scientific Reports 7 (No. 866): 12 (2017)

31. *Pseudopestalotiopsis chinensis* F. Liu & L. Cai, in Liu et al., Scientific Reports 7 (No. 866): 12 (2017)

Xylariales Nannf

Xylariaceae Tul. & C. Tul

32. *Nemania diffusa* (Sowerby) Gray: New host record

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 10°C–30°C, 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
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 (blist blight), Macrophoma theicola (stem canker and twig dieback), Pellicularia koleroa (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–Tag DNA polymerase, 2.5 µl of 10 × Ex–Tag DNA polymerase buffer, 3.0 µl of dNTPs, 2 µl of genomic DNA, 1 µl of each primer and 15.2 ddH2O. 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™ 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 phylogenetic tree, 1000 nonparametric bootstrapping iterations were used.

In Bayesian posterior probability analysis, posterior probabilities (PPs) were determined by Markov chain Monte Carlo sampling (BMC2MC). 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. yingyisheniana    | JZB327001 | MT523022   | MT523028   | –          | –          | –          | –          | –          | –          | –          | –      |
|     |                      | JZB327002 | MT523023   | MT523029   | –          | –          | –          | –          | –          | –          | –          | –      |
|     |                      | JZB327003 | MT523024   | MT523030   | –          | –          | –          | –          | –          | –          | –          | –      |
|     |                      | JZB327004 | MT523025   | MT523031   | –          | –          | –          | –          | –          | –          | –          | –      |
| 4   | D. bigutulata        | 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   | MW205232   | –          | –          | –          | –          | –          | MW205214  | –      |
|     |                      | JZB320152 | MW010215   | MW056011   | MW205233   | –          | –          | –          | –          | –          | MW205215  | –      |
| 7   | D. fusiformis        | JZB320154 | MW010216   | MW056012   | –          | –          | –          | –          | –          | –          | MW205216  | –      |
|     |                      | JZB320155 | MW010217   | MW056013   | –          | –          | –          | –          | –          | –          | MW205217  | –      |
|     |                      | JZB320156 | MW010218   | MW056014   | MW205234   | –          | –          | –          | –          | –          | MW205218  | –      |
| 8   |                      | JZB320157 | MW010219   | MW056015   | –          | –          | –          | –          | –          | –          | MW205219  | –      |
| 9   | D. sackstonii        | JZB320165 | MW010222   | –          | –          | –          | –          | –          | –          | –          | –         | –      |
| 10  | D. sennaee           | 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  | –         | –      |
| 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 | –   | –    | –    | –    | –   | –    | –   | –    | –     |
| 18  | T. lixii             | JZB3360007    | MW008456 | –   | –    | –    | –    | –   | –    | –   | –    | –     |
| 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. fijikiuroi        | 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         | JZB3400064    | MT509821 | –    | MT535513 | MW205238 | –    | –   | –    | –   | –    | –     |
|     |                     | JZB3400063    | MT509822 | –    | MT535514 | MW205239 | –    | –   | –    | –   | –    | –     |
| 27  | P. kenyana           | JZB340062     | MT509823 | –    | MT535515 | MW205240 | –    | –   | –    | –   | –    | –     |
|     |                     | JZB340061     | MT509824 | –    | MT535516 | MW205241 | –    | –   | –    | –   | –    | –     |
| 28  | P. lushanensis       | JZB340059     | MT509825 | –    | MT535517 | MW205242 | –    | –   | –    | –   | –    | –     |
| 29  | P. rhodomyrtus       | JZB3400060    | 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       | –              | –         | MT53551  | –        | 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       | –              | –         | MT535526 | 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 sequences 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 Syllogle 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 ‘Botryosphaeriaceae’], 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 similarities we confirmed these five strains as B. dothidea.

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

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 (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 JZBH310190–JZBH31094.

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 \(\alpha = 0.944898\). RAxML bootstrap support values \(\geq 50\%\) and Bayesian posterior probabilities \(\geq 0.95\) (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 $\alpha = 0.269921$. 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 \( \geq 50\% \) 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)

Index Fungorum: IF818963; Facesoffungi number: FoF09381

Pathogenic or saprobic on *Camellia sinensis* leaves. Sexual morph: Not observed. Asexual morph: *Hyphae* about 2.5 \( \mu m \), 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 \( \times \) 20–18 \( \mu m \) (\( \bar{x} = 12 \times 20 \mu m \) \( n = 30 \)) \( \mu m \) 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).

---

**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 $\alpha = 0.092111$. 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 $\geq 50\%$ and MP bootstrap support values $\geq 50\%$ 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)

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. Pycnidal 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 (x̄ = 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 diseased 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).
**Diaporthë** 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). **Diaporthë** 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 **Diaporthë** species (including ex-type strains) and tree was rooted with **Diaporthërella corylinæ**. 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 **Diaporthë** isolates clustered together with the **Diaporthë eucalyptorum** (CBS132525), **D.olithocarpus** (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.

**Diaporthë 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 (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 25°C. 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 **Diaporthë 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). **Diaporthë 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).

**Diaporthë 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 (\( \bar{x} = 6 \times 2.5 \) 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.

![Phylogenetic tree](image)

**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 $\alpha = 0.944898$. 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 $\geq 50\%$ and maximum parsimony bootstrap support values $\geq 50\%$ are shown near the nodes. Nodes with $\geq 0.95$ (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 of colony PDA after 10 days. c Reverse view of colony on PDA after 10 days. d, e Pycnidia on PDA. f Pycnidal 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.

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 (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.

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 (μ = 7 × 2 μm, n = 40), eguttulate, hyaline, fusiform, both ends angular. Beta *conidia* 23–32 × 1.2–1.6 μm (μ = 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 JZBH320154–7, 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 Conidiogenous 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. & Spege., *Michelia* 1(no. 4): 386 (1878)  
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 (\(\bar{x} = 6 \times 2.5 \mu m, n = 30\)), 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.

Diaporthe nobilis R.G. Shiv, 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 (\(\bar{x} = 6.5 \times 2 \mu m, n = 30\)), 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 mycelium, 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 sackstonii R.G. Shiv, S.M. Thomps. & Y.P. Tan, Persoonia 35: 46 (2015) Fig. 15

Index Fungorum: IF 808674; Facesoffungi number: FoF09386

Diaporthe sackstonii R.G. Shiv, 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 (\(\bar{x} = 6.5 \times 2 \mu m, n = 30\)), 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 mycelium, 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 sacconi 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 (\( \bar{x} = 6.0 \times 2 \mu m, n = 30 \)), 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 sennae** Jayaward., Manawas., X.H. Li, J.Y. Yan, & K. D. Hyde, sp. nov.  
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 (x̄ = 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 (x̄ = 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 sennae* 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 sennae* (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
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 (x̅ = 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 Conidiogenous 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)

Pathogenic or saprobic on *Camellia sinensis* shoots. Sexual morph: not observed; Asexual morph: *Pycnidia* on PDA 400–900 μm (x̅ = 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 (x̅ = 6 × 2 μm, n = 40), biguttulate, hyaline, fusiform or oval, both ends obtuse, *Beta conidia* 20–30 ×1–1.5 μm (x̅ = 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 *Reticulasceaceae* (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, Damn 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)  
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 (x̄ = 60 × 12 µm, n = 40) long, 8 spored, apex truncated and a small apical point. Ascii covered with a thick sheath. Ascospores hyaline 13–18 × 4–5 µm (x̄ = 16 × 4.5 µm, 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 (CBS 123755) 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 \( \alpha \) = 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 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 \( \mu \)m. d–f = 20 \( \mu \)m, g = 10 \( \mu \)m.

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)

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 \( \mu \)m (\( \bar{x} = 10 \times 3 \mu \)m, 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 temperate regions (Põldmaa 2011). Hypocreales accepted with family Bionectriaceae, Calcarisporiaceae, Clavicipitaceae, Cocoonihabitaceae, Cordycipitaceae, Flammocladiiellaceae, 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 $\alpha = 0.944898$. 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

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 (\( \bar{x} = 4 \times 3 \) 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.

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 (x̄ = 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)  

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 (x̅ = 3–1.5 μm, n = 30), ovoid, verrucose *Clamydospores* 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. Aerial 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
Fusarium asiaticum O’Donnell, T. Aoki, Kistler & Geiser, in O’Donnell, Ward, Geiser, Kistler & Aoki, Fungal Genetics Biol. 41(6): 619 (2004)  
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 (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)  
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 (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
The 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 cylindrical mono and polyphialidic. Conidia 8–26 × 2–5 μm (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).

![Images](image-url)

**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.

![Images](image-url)

**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. Bund.Anst. Ld.–u. Forstw. 169: 38 (1982)

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 cylindrical mono and pluphyalidic, phialides flask–shaped. **Conidia** 12–21 × 2–5 µm (̅ = 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. Chlamydoospores 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 ['Chaetomieae’], Rabenh. Krypt.–Fl., Edn 2 (Leipzig) 1: 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](image-url) – 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 (x̄ = 20 × 10 μm, n = 20), stalks 20–40 μm long, with 6–7 ascospores, *Ascospores* 10–12 × 6–8 μm (x̄ = 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 Ascii. 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. Fröhlich, 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 golenkoana* (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)

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 (x̄ = 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., *Phyllostachys* 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 Conidiogenous 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 (̄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 JZBH32300016), and living culture JZB32300016.

Notes – Multi-locus phylogenetic analysis of ITS, *tef1* and *tub2* placed the isolate in the present study together with *Nigrospora camelliae–sinensis* supported by 86% ML bootstrap values and 0.95 BYPP. The colony characters and morphology of the current species are similar to *N. camelliae–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 -1480.32026 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**.
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 multisepate 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)

Index Fungorum: IF800980; Facesoffungi number: FoF09351

Pathogenic or saprobie 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 (x̅ = 30 × 9 µm, n = 40), fusoid, straight to slightly curved, 4 septate. Basal cell 4–7 µm (x̅ = 5 µm, n = 40), obconic, hyaline, smooth, thin–walled, Median cells 20–22 µm (x̅ = 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 \( \alpha = 0.944898 \). RAxML bootstrap support values \( \geq 50\% \) and Bayesian posterior probabilities \( \geq 0.95 \) (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 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 Pycnidia on PDA. f–g Conidiogenous 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)

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 (μ = 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 (μ = 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)

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 (x̅ = 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 (x̅ = 15 μm, n = 40) three, doliform, long, pale brown to brown, septa darker than the rest of cell. Apical appendages 20–25 μm (x̅ = 20 μm, n = 40), 2–3 tubular, unbranched, filiform, Basal appendage single, tubular, unbranched, 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)

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 (x̅ = 24 × 5 μm, n = 40), fusoid, straight to slightly curved, 4–septate. *Basal cell* 3–6 μm (x̅ = 5 μm, n = 40), conic, pale brown, smooth, thin-walled. *Median cells* 12–20 μm (x̅ = 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 (x̅ = 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)  

**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 (x̄ 20 × 4 μm, n = 30), discrete, subcylindrical, hyaline, smooth, proliferating 1–3 times percurrently. *Conidia* 20–30 × 7–10 μm (x̄ = 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 (x̄ 16 μm, n = 40), three, doliform, middle cell darker than the other two. **Apical appendages** 8–20 (x̄ 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)  

**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 (x̄ = 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 (x̄ = 16 μm, n = 40). **Median cells** three, doliform, 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 $\alpha = 0.440726$. RAxML bootstrap support values $\geq 50\%$ and Bayesian posterior probabilities $\geq 0.95$ (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 Pycnidal 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 Pycnidal 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, Conioceciaceae, Diatrypaceae, Graphostromataceae, Hansfordiaceae, Hypoxylaceae, Induratiaceae, Lopadostomataceae, Microdochiaeae, Polystigmatea, Requienellaceae, Xylariaceae and Zygosporiaceae with 160 genera (Hyde et al. 2020b).

Xylariaceae Tul. & C. Tul., Selecta Fungorum Carpologia, Tomus Secundus. Xylariei – Valsei – Sphaerii 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 diffusa (Fig. 46).

Nemania diffusa (Sowerby) Gray, Nat. Arr. Brit. Pl. (London) 1: 517 (1821)  
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. Conidiogenous cells not observed. Conidia 8–10 × 3–4 µm (x̅ = 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, Pseudopezicula, Setosphaeria (Mitarachi & Kikumura 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 \textit{rpb2} sequence data of \textit{Nemania} species. \textit{Podosordaria muli} (WSP 167) and \textit{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 $\alpha = 0.944898$. RAxML bootstrap support values $\geq 50$\% and Bayesian posterior probabilities $\geq 0.95$ (BYPP) are shown near the nodes. The scale bar indicates 0.02 changes per site. Ex--type/ex--epitype strains are in \textbf{bold} and isolates recovered in the present study are in \textcolor{red}{red}. 

\hspace{1cm}
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. amygduali, D. apiculata, D. compacta, D. discoidispora, D. eres, D. hongkongensis, D. oraccinii, D. penetriteum, D. tectonigena* (Gao et al. 2016), *D. incompleta, D. mastrevicii, D. uckeriae, D. velatina, 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 (Yang 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 yingyishieniae* 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. longiquia, S. yingyishieniae* and *S. yunnanensis* associated with leaf spots on tea from seven provinces in China. Until now, *S. yingyishieniae* 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 layience*. 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 layience* 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 plants 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 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 | S, P** | Leaf spots | Japan | Kobayashi (2007) |
| Alternaria alternata (Fr.) Keissl* | Pleosporaceae | | | China, India, Japan | Tai (1979), Chakraborty et al. (2006), Kobayashi (2007), Zhou et al. (2014), Chen et al. (2018b), Farr & Rossman (2020) |
| Alternaria sp. | | | | | Pantidou (1973) |
| Annulohypoxylon michelianum (Ces. & De Not.) Y.M. Ju, J.D. Rogers & H.M. Hsieh | Hypoxylaceae | | | Greece | Nattrass (1961) |
| Athelia rolfsii (Curzi) C.C. Tu & Kimbr | Atheliaceae | | | Japan, Malawi Taiwan | Kobayashi (2007) Farr & Rossman (2020) |
| Species | Family | Life mode | Disease caused | locality | References |
|---------|--------|-----------|----------------|----------|------------|
| Armillaria mellea (Vahl) P. Kumm | Physalaciaceae | | | 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. | Physalaciaceae | 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 |
| Aschersonia eugeniae | Clavicipitaceae | | | India | Mathur (1979) |
| Ascochyta sp. | Didymellaceae | P | N/A | Papua New Guinea | Farr & Rossman (2020) |
| Ascochyta theae | Didymellaceae | P | N/A | 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), Johnston (1960), Heredia–Abarca (1994) |
| Beltrania rhombica Penz., Beltraniaceae | | | | Malaysia | Matsushima (1975), Kobayashi (2007) |
| Beltrantella japonica Matsush. | Clavicipitaceae | | | Japan | Hou (2000), Chen et al. (2011) |
| Bifusella camelliae C.L. Hou* | Rhytismataceae | P, S | Branch rot | Australia, China, Japan | Cunnington et al. (2007), Kobayashi (2007), Dissanayake et al. (2016), Jayawardena et al. (2016b), Burgess et al. (2019), This study |
| Botryosphaeria dothidea (Moug.: Fr.) Ces. & De Not* | Botryosphaeriaceae | P | Dieback** | Sri Lanka | Farr & Rossman (2020) |
| Botryosphaeria microspora Petch | Botryosphaeriaceae | | | China | Tai (1979) |
| Botryosphaeria sp. | Botryosphaeriaceae | | | Japan, USA | Watson (1950), Kobayashi (2007) |
| Botrytis cinerea Pers | Sclerotiniaceae | | | India | Richardson (1990) |
| Botryotinia sp. | Sclerotiniaceae | | | Japan | Kobayashi (2007) |
| Byssosphaeria rhodomphala (Berk.) Cooke | Melanommataceae | | | Indonesia, Mauritius, USA | Crous (2002), Lombard et al. (2014, 2016), Liu & Chen (2017), Wang et al. (2019a) |
| 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) |
| 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., Alferi & 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) |
| *Cephalurus* 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) |
| 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                      |                                                                           |
| 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)                                                        |
| 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), Giatgong (1980), Dingley et al. (1981), Sharma et al. (2015), Chen et al. (2017b), Liu et al. (2015) |
| Colletotrichum sp.* | Glomerellaceae | E, P, S |  | China, India, Fiji, Thailand | |
| 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 |  |  |  | Corbett (1964) |
| Corticium sp. | Corticiaceae |  |  |  | Shaw (1984) |
| Corynespora polyphragmia (Syd. & P. Syd.) M.B. Ellis | Corynesporascaceae |  |  |  | Kobayashi (2007) |
| Corallomyctella repens (Berk. & Broome) Rossman & Samuels | Nectriaceae |  |  |  | Thompson & Johnston (1953) |
| Cryptomyces theae Sawada | Rhytismataceae |  |  |  | Farr & Rossman (2020) |
| Cylindrocladiella novae–zelandiae (Boesew.) Boesew | Nectriaceae |  |  |  | Crous et al. (2006) |
| Cylindrocladium peruvianum Bat., J.L. Bezerra & M.P. Herrera | Nectriaceae |  |  |  | Alfieri et al. (1984), Crous (2002) |
| Cylindrocladiella parva (P.J. Anderson) Boesew | Nectriaceae |  |  |  | Wiehe (1953) |
| Cylindrocarpon lichenicola (Massal.) D. Hawksw | Nectriaceae |  |  |  | Shaw (1984) |
| Cylindrocladium sp. | Nectriaceae |  |  |  | |
| Clypeolella camelliae (Syd., P. Syd. & E.J. Butler) Hansf * | Englerulaceae |  |  | Brazil, Japan | Mendes et al. (1998), Kobayashi (2007), Hosagoudar (2003) |
| Cytopsora 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    | Yang et al. (2015), Dissanayake et al. (2017a, b), Gao et al. (2017), Yang et al. (2018) |
| 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    | Yang et al. (2015), Dissanayake et al. (2017a, b), Gao et al. (2017), Yang et al. (2018) |
| Diaporthe eucalyptorum Crous & R.G. Shivas. | Diaporthaceae | E         |                | China    | This study                                                                 |
| Diaporthe eucalyptorum Crous & R.G. Shivas. | Diaporthaceae | S or P     |                | Italy    | Udayanga et al. (2012), Gomes et al. (2013), Chen et al. (2014), Lombard et al. (2014) |
| Diaporthe eucalyptorum Crous & R.G. Shivas. | Diaporthaceae | S or P     |                | China    | This study                                                                 |
| Diaporthe fuseiformis 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, Glenke & Crous* | Diaporthaceae | E         |                | 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), Gao et al. (2017)                     |
| Diaporthe masirevicii R.G. Shivas, L. Morin, S.M. Thomps., & Y.P. Tan* | Diaporthaceae    | S         |                | China    | Li et al. (2017)                                                           |
| Diaporthe nobilis Sacc. & Speg* | 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 oraccinti Y.H. Gao, F. Liu & L. Cai* | Diaporthaceae    | P, S      |                | China    | Du et al. (2016), Dissanayake et al. (2017a, b), Yang et al. (2017, 2018a, b) |
| Diaporthe penetrifera Y.H. Gao & L. Cai* | Diaporthaceae    | E, P**    |                | China    | Du et al. (2016), Dissanayake et al. (2017a, b), Yang et al. (2017, 2018a, b) |

**Notes:**
- P: Pathogen
- E: Epiphyte
- S: Saprotroph
| Species                                      | Family             | Life mode | Disease caused | locality              | References                                      |
|---------------------------------------------|--------------------|-----------|----------------|----------------------|------------------------------------------------|
| *Diaporthe sackstonii* R.G. Shivas, S.M.    | Diaporthaceae      | S or P    |                | China                | This study                                      |
| Thoms. & Y.P. Tan                           |                    |           |                |                      |                                                 |
| *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 viniferæ* 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 assimica* (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.             | Discosiacae        |           |                | Southeastern states  | Watson (1950)                                   |
| *Discosia strobilina* Lib                   | Discosiacae        |           |                | Japan                | Kobayashi (2007)                                |
| *Discula theæ–sinensis* (I. Miyake) Moriwaki & Toy* | Gnomoniaceae       | P** S     | Anthracnose    | Japan, China         | Tai (1979), Kobayashi (2007), Moriwaki & Sato (2009) |
| *Discosilla 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* | Dyfrolomyctaceae      | 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, China, USA | Thompson & Johnston (1953), Kobayashi (2007), Alfieri et al. (1984)         |
| **Exobasidium camelliae** Shirai*     | Exobasidiaceae        | P         |                | China, Japan                    | Tai (1979), Chen (2002), Kobayashi (2007)                                 |
| **Exobasidium reticulatum** S. Ito & Sawada* | Exobasidiaceae       | P         |                | China                           | This study                                                                |
| **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         |                | China                           | This study                                                                |
| **Fusarium oxysporum** Schldl        | 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 Guinea, 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).                                             |
| 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      | Teodor (1937)                                                              |
| *Globisporangium manillatum* (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.* Hara                               | 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 coccinella* 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), | 498
| Species | Family | Life mode | Disease caused | locality | References |
|---------|--------|-----------|----------------|----------|------------|
| *Leptosphaerulina sp.* | Didymellaceae | | Guinea, Tanzania, Zimbabwe | Li et al. (2019) |
| *Lophodermium sinens Y.R. Lin, C.L. Hou & Jiang L. Chen* | Rhytismataceae | P | Malawi | Corbett (1964) |
| *Macrophoma sp.* | Botryosphaeriaceae | | China | Chen et al. (2011) |
| *Macrophoma theicola Petch* | Botryosphaeriaceae | | India, Malawi, Malaysia, Tanzania | Wiehe (1953), Johnston (1960), Mathur (1979) |
| *Macrophomina phaseolina (Tassi) Goid* | Botryosphaeriaceae | | Thailand | Thompson & Johnston (1953) |
| *Marasmiellus scandens (Massee) Dennis & D.A. Reid* | Omphalotaceae | | Thailand | Thompson & Johnston (1953) |
| *Marasmius crinis–equi F. Muell. ex Kalchbr* | Marasmiaceae | | Malawi | Chen et al. (2011) |
| *Marasmius sp.* | Marasmiaceae | | Malawi | Chen et al. (2011) |
| *Meliola camelliae (Catt.) Sacc* | Meliaceae | | China | Tai (1979) |
| *Microcera coccophila Desm* | Nectriaceae | | Papua New Guinea | Shaw (1984) |
| *Monilochaetes camelliae (Alcorn & Sivan.) Réblová, W. Gams & Seifert* | Australiasaceae | | Tibet | 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* | Mycosphaerellaceae | | China, Japan, Samoa, Zimbabwe | Whiteside (1966), Tai (1979), Dingley et al. (1981), Kobayashi (2007) |
| *Myriangium duriaeii Mont. & Berk* | Myriangiaceae | | Japan | Kobayashi (2007) |
| *Nectria bolophylli 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) |
| *Nectriocladiella 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 ipomoaeae (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                     | Sporocadaceae    | E, P**    | Brown–black spot |               | Wei et al. (2005, 2007), Ge et al. (2009), Wang et al. (2017b), Chen et al. (2018a) |
| Pestalotiopsis ellipsoidalis (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)                                                        |
| 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)                                                       |
| *Ophiurenina 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 &  | Didymosphaeriaceae |           |                | Japan          | Kobayashi (2007)                                                         |
| Gruyter*                                        |                    |           |                |                |                                                                           |
| *Paraconiothyrium fuckelii* (Sacc.) Verkley &  | Didymosphaeriaceae |           |                | Japan          | Kobayashi (2007)                                                         |
| Gruyter*                                        |                    |           |                |                |                                                                           |
| *Penicillium corylophilum* Dierckx             | Aspergillaceae     |           |                | Kenya          | Nattrass (1961)                                                          |
| *Pestalotiopsis acaciae* (Thüm.) K. Yokoy. &   | Sporocadaceae      | S         |                | China          | Ge et al. (2009)                                                          |
| S. Kaneko*                                      |                    |           |                |                |                                                                           |
| *Pestalotiopsis aggestorum* F. Liu & L. Cai*   | Sporocadaceae      | S         |                | China          | Liu et al. (2017)                                                         |
| *Pestalotiopsis algeriensis* (Sacc. & Berl.)   | Sporocadaceae      | S         |                | China          | Zhang et al. (2012)                                                       |
| W.P. Wu*                                        |                    |           |                |                |                                                                           |
| *Pestalotiopsis camelliae* Yan M. Zhang,       | Sporocadaceae      | P**, S    | Grey blight    | China, Turkey   | Maharachchikumbura et al. (2014), Moslemi & Taylor (2015), Chen et al.   |
| Maharachch. & K.D. Hyde*                        |                    |           |                |                | (2017c), Liu et al. (2017), Wang et al. (2017b), Solarte et al. (2017),  |
|                                                |                    |           |                |                | This study Liu et al. (2017), Wang et al. (2019b)                         |
| *Pestalotiopsis chamaeropis* Maharachch.,      | Sporocadaceae      | P, S      | Grey blight    | China          |                                                                           |
| K.D. Hyde & Crous*                              |                    |           |                |                |                                                                           |
| *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.    | 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) |
| Species | Family | Life mode | Disease caused | locality | References |
|---------|--------|-----------|----------------|----------|------------|
| *Pestalotiopsis gigas* Steyaert | Sporocadaceae | | | | Nattrass (1961) |
| *Pestalotiopsis jinchangensis* F. Liu & L. Cai* | Sporocadaceae | E, P, S | | Kenya | 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 | | | Zhang et al. (2012) |
| *Pestalotiopsis microsperma* (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* (Thüml.) 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* (Thüml.) Y.X. Chen* | Sporocadaceae | E | | China | Tejevisi 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* & K.D. Hyde* | Sporocadaceae | P, S | | China, Thailand | Zhuang (2001), Ge et al. (2009), Liu et al. (2017) |
| *Pestalotiopsis trachycarpicola* Yan M. Zhang & K.D. Hyde* | Sporocadaceae | P, S | | China | Zhang et al. (2012) |
| *Pestalotiopsis versicolor* (Speg.) Steyaert* | Sporocadaceae | P, S | | China | Zhang et al. (2012), Zhang et al. (2012) |
| *Pestalotiopsis virgatula* (Kleh.) Steyaert* | Sporocadaceae | P, S | | China | Liu et al. (2017) |
| *Pestalotiopsis yanglingensis* F. Liu & L. Cai* | Sporocadaceae | P**, S | Grey blight | China | Ando et al. (1989), Kobayashi (2007) |

**Table 3 Continued.**
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                   | Venturaceae               |           |                | Thailand                  | Thompson & Johnston (1953)                       |
| *Phoma herbarum* Westend*                       | Didymellaceae             | P**       | Leaf spot      | China                     | Thangaraj et al. (2019)                         |
| *Phoma sp.*                                     | Didymellaceae             |           |                | Florida                   | Alfieri et al. (1984)                           |
| *Phylllosticta camelliae* Westend*              | Phylllostictaceae         | P, S      |                | China, Japan              | Bai (2000), Kobayashi (2007)                    |
| *Phylllosticta capitalensis* Henn*              | Phylllostictaceae         | P**       | Leaf spot      | China                     | Cheng et al. (2019)                             |
| *Phylllosticta citricarpa* (McAlpine)           | Phylllostictaceae         |           |                | Papua New Guinea          | Alfieri et al. (1984), Kobayashi (2007)         |
| *Phylllosticta erratica* Ellis & Everh          | Phylllostictaceae         | P, S      |                | Fiji, Hong Kong           | Firman (1972), Dingley et al. (1981), Lu et al. (2000), Zhuang (2001) |
| *Phylllosticta theae* Speschnew*                | Phylllostictaceae         |           |                | China, Fiji, Japan, Tanzania, Thailand | Thompson & Johnston (1953), Riley (1960), Firman (1972), Tai (1979), Dingley et al. (1981), Kobayashi (2007) Tai (1979), Kobayashi (2007) |
| *Phylllosticta theicola* Curzi                  | Phylllostictaceae         |           |                | Japan                     | Kobayashi (2007)                                |
| *Pleospora theae* Speschnew                     | Pleosporaceae             |           |                | Japan                     | Pennycook (1989), Gadgil (2005), Braun et al. (2012) |
| *Pseudocercospora camelliae* (Deighton) U. Braun* | Mycosphaerellaceae       | P, S      |                | Georgia, New Zealand      | Braun & Hill (2002), Gadgil (2005), Kirschner et al. (2009) |
| *Pseudocercospora camellicola* U. Braun & C.F. Hill* | Mycosphaerellaceae | P, S      | Leaf spot      | Mauritius, New Zealand, Taiwan | Kobayashi (2007), Kamal (2010), Braun et al. (2012) |
| *Pseudocercospora javanica* Deighton            | Mycosphaerellaceae        | P, S      |                | Java, India, Indonesia, Japan, Nigeria, Sri Lanka, Tanzania | Riley (1960), Tai (1979), Ragazzi & Marino (1990), Mendes et al. (1998), Crous & Braun (2003) |
| *Pseudocercospora ocellata* (Deighton) Deighton | Mycosphaerellaceae        | P, S      |                | Brazil, China, Ethiopia, Japan, Kenya, Mauritius, Nigeria, Taiwan, Tanzania | Deighton (1976), Alfieri et al. (1984), Hsieh, & Goh (1990), Zhuang (2001), Braun et al. (2012), Lu et al. (2000) Mathur (1979) |
| *Pseudocercospora theae* (Cavara) Deighton       | Mycosphaerellaceae        | P**, S    |                | Argentina, China, Hong Kong, Taiwan, USA | Chen et al. (2018a), Liu et al. (2017), Nozawa et al. (2018) |
| *Pseudolachnea hispidula* (Schrad.) B. Sutton    | Mycosphaerellaceae        |           |                | India                     | Chenachikumbura et al. (2014), Nozawa et al. (2018), Chen et al. |
Table 3 Continued.

| Species                                             | Family             | Life mode | Disease caused | locality                                                                 | References                                                                 |
|-----------------------------------------------------|--------------------|-----------|----------------|---------------------------------------------------------------------------|----------------------------------------------------------------------------|
| *Pseudopestalotiopsis camelliae*-sinensis F. Liu & L. Cai* | Pestalotiopsidaceae | S, E      |                | China                                                                     | (2018a), This study Chen et al. (2018a), Nozawa et al. (2018), This study |
| *Pseudopestalotiopsis chinensis* F. Liu & L. Cai     | Pestalotiopsidaceae | P*        | Grey blight    | China, Thailand                                                           | Liu et al. (2017), Chen et al. (2018a), Nozawa et al. (2018)               |
| *Pseudopestalotiopsis sp.*                          | Pestalotiopsidaceae | S, P      |                | Brazil, 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 (Taiwan), 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)              |
| *Rosellinia sp.*                                     | Xylariaceae         |           |                | Japan                                                                     | Agnihothrudu (1961), Adikaram & Yakandawala (2020)                         |
| *Rosellinia aculeata* (Petch) Lar.N. Vassiljeva      | Xylariaceae         |           |                | India, Sri Lanka                                                          | Tai (1979)                                                                |
| *Rosellinia aculeata* (Petch) Lar.N. Vassiljeva      | Xylariaceae         |           |                | China                                                                     |                                                                 |
| *Rossmania aculeata* (Petch) Lar.N. Vassiljeva       | Xylariaceae         |           |                | Brazil, Japan, Tanzania, Thailand                                         | Thompson & Johnston (1953), Riley (1960), Alvarez (1976), Kobayashi (2007) |
| 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 | | | Thailand | Thompson & Johnston (1953) |
| | | | | 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 yunnanensis F. Liu & L. Cai* | Phaeosphaeriaceae | P | Leaf spot | China | Liu et al. (2019), This study |
| 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. | Chiosphaeraceae | | | Malawi | Wiehe (1953) |
| Taeniolella sp. | Mytilinidiaceae | | | Papua New Guinea | Shaw (1984) |
| Terriera camelllicola (Minter) Y.R. Lin & C.L. Hou* | Rhytismataceae | P, S | | China, India | Zhang et al. (2015) |
| Thozetelopsis 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 |
| Trichoderma camelliae Jayaward., Manawas., X.H. Li, J.Y.Yan, & K. D. Hyde | 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)    |
| Valvarsia 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

#### Funding

The research was funded by Beijing Talent Program for Dr Jiye Yan.

#### 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.

#### Acknowledgements

We would like to thank Dr Shaun Pennycook for the guidance with naming new species. Alan JL Phillips acknowledges the support from UIDB/04046/2020 and UIDP/04046/2020 Centre grants from FCT, Portugal (to BioISI). Dhanushka Wanasinghe thanks CAS President’s International Fellowship Initiative (PIFI) for funding his postdoctoral research (number 2021FYB0005) and the Postdoctoral Fund from Human Resources and Social Security Bureau of Yunnan Province.
References

Adikaram NKB, Yakandawala DMD. 2020 – A checklist of plant pathogenic fungi and Oomycota in Sri Lanka. Ceylon Jernol of Science 49, 93–123.

Agnihothrudu V. 1961 – Notes on fungi from North–East India VII. Tunstallia gen. nov. causing the “Thorny Stem Blight” of tea (Camellia sinensis (L.) O. Kuntze). Phytopathology 40, 277–282.

Alfieri Jr SA, Langdon KR, Wehlburg C, Kinbrrough JW. 1984 – Index of plant diseases in Florida (Revised). Florida Department of Agriculture and Consumer Services, Division of Plant Industry Bulletin 11, 1–389.

Alizadeh A, Javani–Nikkhah M, Zare R, Fotouhifar KB et al. 2015 – New records of Colletotrichum species for the mycobiota of Iran. Mycologia Iranica 2, 95–109.

Aptroot A. 1995 – Redisposition of some species excluded from Didymosphaeria (Ascomycotina). Nova Hedwigia 60, 325–379.

Arzanlou M, Torbati M. 2013 – Phenotypic and molecular characterisation of Colletotrichum acutatum, the causal agent of anthracnose disease on Cornus mas in Iran. Archives of Phytopathology and Plant Protection 46, 518–525.

Aveskamp MM, de Gruyter J, Woudenberg JHC, Verkley GJM, Crous PW. 2010 – Highlights of the Didymellaceae: A polyphasic approach to characterise Phoma and related pleosporalean genera. Studies in Mycology 65, 1–60.

Aptroot A. 1995 – Redisposition of some species excluded from Didymosphaeria (Ascomycotina). Nova Hedwigia 60, 325–379.

Bai JK. 2000 – Flora Fungorum Sinicorum. Vol. 15. Sphaeropsidales, Phoma, Phyllosticta. Science Press, Beijing.

Balasuriya A, Adikaram NKB. 2009 – Some spatial, temporal and spatio-temporal considerations of wood decay of tea (Camellia sinensis), caused by Nemania diffusa (Syn. Hypoxylon vestitum). Crop Protection 28, 273–279.

Bao XT, Dharmasena DSP, Li DX, Wang X et al. 2019 – First report of Epicoccum sorghinum causing leaf spot on tea in China. Plant Disease 103, 3282.

Bhunjun CS, Phukhamsakda C, Jayawardena RS, Jeewon R et al. 2021 – Investigating species boundaries in Colletotrichum. Fungal Diversity 107, 107–127.

Boehm R, Cash SB, Anderson BT, Ahmed S et al. 2016 – Association between empirically estimated monsoon dynamics and other weather factors and historical tea yields in China: results from a yield response model. Climate 4, 1–20.

Braun U, Hill CF. 2002 – Some new micromycetes from New Zealand. Mycological Progress 1, 19–30.

Braun U, Rybak M, Rybak R, Cabrera MG. 2012 – Foliar diseases on tea and maté in Argentina caused by Pseudocercospora species. Plant Pathology & Quarantine 2, 103–110.

Brunner K, Zeilinger S, Cilento R, Woo SL et al. 2005 – Improvement of the fungal biocontrol agent Trichoderma atroviride to enhance both antagonism and induction of plant systemic disease resistance. Applied Environmental Microbiology 71, 3959–3965.

Burgess TI, Tan YP, Garnas J, Edwards J et al. 2019 – Current status of the Botryosphaeriaceae in Australia. Australasian Plant Pathology 48, 35–44.

Cannon PF, Damm U, Johnston PR, Weir BS. 2012 – Colletotrichum current status and future directions. Studies in Mycology 73, 181–213.
Crous PW. 2002 – Taxonomy and pathology of *Cylindrocladium* (*Calonectria*) and allied genera. American Phytopathological Society, St. Paul, Minnesota.

Crous PW, Braun U. 2003 – *Mycosphaerella* and its anamorphs: 1. Names published in *Cercospora* and *Passalora*. Centraalbureau voor Schimmelcultures (CBS).

Crous PW, Groenewald JZ, Risse–J–M, Simoneau P, Hyde KD. 2006 – *Calonectria* species and their *Cylindrocladium* anamorphs: species with clavate vesicles. Studies in Mycology 55, 213–226.

Crous PW, Summerell BA, Shivas RG, Burgess TI et al. 2012 – Fungal planet description sheets: 107–127. Persoonia 28, 138–182.

Cunnington JH, Priest MJ, Powney RA, Cother NJ. 2007 – Diversity of *Botryosphaeria* species on horticultural plants in Victoria and New South Wales. Australasian Plant Pathology 36, 157–159.

Damm U, Sato T, Alizadeh A, Groenewald JZ, Crous PW. 2019 – The *Colletotrichum dracaenophilum*, *C. magnum* and *C. orchidearum* species complexes. Studies in Mycology 92, 1–46.

Daranagama DA, Hyde KD, Sir EB, Thambugala KM et al. 2018 – Towards a natural classification and backbone tree for *Graphostromataceae*, *Hypoxylaceae*, *Lopadostomataceae* and *Xylariaceae*. Fungal Diversity 88, 1–165.

de Gruyter J, Woudenberg JHC, Aveskamp MM, Verkley GJ et al. 2010 – Systematic reappraisal of species in *Phoma* section *Paraphoma*, *Pyrenochaeta* and *Pleurophoma*. Mycologia 102, 1066–1081.

de Gruyter J, Aveskamp MM, Woudenberg JHC, Verkley GJM et al. 2009 – Molecular phylogeny of *Phoma* and allied anamorph genera: Towards a reclassification of the *Phoma* complex. Mycological Research 113, 508–519.

de Gruyter J, Woudenberg JHC, Aveskamp MM, Verkley GJM et al. 2013 – Redisposition of *Phoma*–like anamorphs in *Pleosporales*. Studies in Mycology 75, 1–36.

de Hoog GS, Guarro J, Gene J, Figueras MJ et al. 2000 – Atlas of Clinical Fungi (2nd edn). Centraalbureau voor Schimmelcultures, Utrecht, the Netherlands, 1–1160.

De Silva DD, Ades PK, Crous PW, Taylor PWJ. 2017 – *Colletotrichum* species associated with chili anthracnose in Australia. Plant Pathology 66, 254–267.

De Silva NI, Brooks S, Lumyong S, Hyde KD. 2019 – Use of endophytes as biocontrol agents. Fungal Biology Reviews 33, 133–148.

Degenkolb T, Dieckmann R, Nielsen KF, Gräfenhan T et al. 2008 – The *Trichoderma brevicompactum* clade: a separate lineage with new species, new peptaibiotics, and mycotoxins. Mycological Progress 7, 177–219.

Deighton FC. 1976 – Studies on *Cercospora* and allied genera. VI. *Pseudocercospora* Spec., *Pantospora* Cif. And *Cercoseptoria* Petr. Mycological Papers 140, 1–168.

Del Frari G, Cabral A, Nascimento T, Ferreira RB, Oliveira H. 2019 – *Epicoccum layuense* a potential biological control agent of esca–associated fungi in grapevine. PloS One 14, e0213273.

Diao YZ, Zhang C, Liu F, Wang WZ et al. 2017 – *Colletotrichum* species causing anthracnose disease of chili in China. Persoonia 38, 20–37.

Dingley JM, Fullerton RA, McKenzie EHC. 1981 – Survey of Agricultural Pests and Diseases. Technical Report, Volume 2. Records of Fungi, Bacteria, Algae, and Angiosperms Pathogenic on Plants in Cook Islands, Fiji, Kiribati, Niue, Tonga, Tuvalu, and Western Samoa. F.A.O.

Dissanayake AJ, Phillips AJL, Hyde KD, Yan JY, Li XH. 2017a – The current status of species in *Diaporthe*. Mycosphere 8, 1106–1156.

Dissanayake AJ, Phillips AJL, Li XH, Hyde KD. 2016 – *Botryosphaeriaeae*: current status of genera and species. Mycosphere 7, 1001–1073.

Dissanayake AJ, Zhang W, Liu M, Hyde KD et al. 2017b – *Diaporthe* species associated with peach tree dieback in Hubei, China. Mycosphere 8, 533–549.
Douanla–Meli C, Unger JG, Langer E. 2018 – Multi–approach analysis of the diversity in *Colletotrichum cliviae* sensu lato. Antonie Van Leeuwenhoek 111, 423–435.

Duan JX, Wu WP, Liu XZ. 2007 – *Dinemasporium* (coelomycetes). Fungal Diversity 26, 205–218.

Dutta J, Gupta S, Thakur D, Handique PJ. 2015 – First report of *Nigrospora* leaf blight on tea caused by *Nigrospora sphaerica* in India. Plant Disease 99, 417.

Ebbels DL, Allen DJ. 1979 – A supplementary and annotated list of plant diseases, pathogens and associated fungi in Tanzania. Commonwealth Mycological Institute, 1–89.

Fan XL, Yang Q, Bezerra JDP, Alvarez LV, Tian CM. 2018 – *Diaporthe* from walnut tree (*Juglans regia*) in China, with insight of the *Diaporthe eres* complex. Mycological Progress 17, 841–853.

FAOSTAT. 2019 – Tea: crop production from http://www.fao.org/faostat/en/ (Retrieved on December 30, 2019).

Farr DF, Rossman AY. 2020 – Fungal databases, US National fungus collections from http://nt.ars–grin.gov/fungaldatabases (Retrieved on March 11, 2019).

Firman ID. 1972 – A list of fungi and plant parasitic bacteria, viruses and nematodes in Fiji. A list of fungi and plant parasitic bacteria, viruses and nematodes in Fiji, 1–36.

Freeman S, Sharon M, Maymon M, Mendel Z et al. 2013 – *Fusarium euwallaceae* sp. nov. a symbiotic fungus of *Euwallacea* sp., an invasive ambrosia beetle in Israel and California. Mycologia 105, 1595–1606.

Gadgil PD. 2005 – Fungi on trees and shrubs in New Zealand. The fungi of New Zealand Volume 4. Fungal Divers Press, Hong Kong.

Gao Y, Liu F, Cai L. 2016 – Unravelling *Diaporthe* species associated with *Camellia*. Systematics and Biodiversity 14, 102–117.

Gao Y, Liu F, Duan W, Crous PW, Cai L. 2017 – *Diaporthe* is paraphyletic. IMA Fungus 8, 153–187.

Ge Q, Chen Y, Xu T. 2009 – *Flora Fungorum Sinicum*. Volume 38. Pestalotiopsis. Science Press, Beijing.

Giatgong P. 1980 – Host Index of Plant Diseases in Thailand. Second Edition. Mycology Branch, Plant Pathology and Microbiology Division, Department of Agriculture and Cooperatives, Bangkok, Thailand.

Glass NL, Donaldson GC. 1995 – Development of primer sets designed for use with the PCR to amplify conserved genes from filamentous ascomycetes. Applied Environmental Microbiology 61, 1323–1330.

Gomes RR, Glienke C, Videira SIR, Lombard L et al. 2013 – *Diaporthe*: a genus of endophytic, saprobic and plant pathogenic fungi. Persoonia 31, 1–41.

Guarnaccia V, Crous PW. 2018 – Species of *Diaporthe* on *Camellia* and *Citrus* in the Azores Islands. Phytopathologia Mediterranea 57, 307–319.

Hall TA. 1999 – BioEdit: A user–friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symposium Series 41, 95–98. London, England: Information Retrieval.

Hawksworth DL, Eriksson OE. 1986 – The names of accepted orders of ascomycetes. Systema Ascomycetum 5, 175–184.

He Y, Zhang Z. 2012 – Diversity of organism in the Usnea longissima lichen. African Journal of Microbiology Research 6, 4797–4804.

Helaly SE, Thongbai B, Stadler M. 2018 – Diversity of biologically active secondary metabolites from endophytic and saprotrophic fungi of the ascomycete order Xylariales. Natural product reports 35, 992–1014.

Heredia–Abarca G. 1994 – Hifomicetes dematiáceos en bosque mesófilo de montaña. Registros nuevos para México. Acta Botanica Mexica 27, 15–32.

Hong JH, Jang S, Heo YM, Min M et al. 2015 – Investigation of marine–derived fungal diversity and their exploitable biological activities. Marine drugs 13, 4137–4155.
Hongsanan S, Hyde KD, Phookamsak R, Wanasinghe DN et al. 2020a – Refined families of Dothideomycetes: Dothideomycetidae and Pleosporomycetidae. Mycosphere 11, 1553–2107.
Hongsanan S, Hyde KD, Phookamsak R, Wanasinghe DN et al. 2020b – Refined families of Dothideomycetes: Orders and families incertae sedis in Dothideomycetes. Fungal Diversity 24, 1–302.
Hongsanan S, Tian Q, PerSoh D, Zeng XY et al. 2015 – Meliolales. Fungal Diversity 74, 91–141.
Hosagoudar VB. 2003 – The genus Schiffnerula and its synanamorphs. Zoos Print Journal 18, 1071–1078.
Hou CL. 2000 – A new species of Bifusella on Camellia sinensis. Mycosystema 19, 7–9.
Hou LW, Liu F, Duan WJ, Cai L et al. 2016 – Colletotrichum aracearum and C. camelliae–japonicae, two holomorphic new species from China and Japan. Mycosphere 7, 1111–1123.
Huang F, Udayanga D, Wang X, Hou X et al. 2015 – Endophytic Diaportha associated with Citrus: A phylogenetic reassessment with seven new species from China. Fungal Biology 119, 331–347.
Hughes SJ, Kendrick WB. 1968 – New Zealand Fungi 12. Menispora, Codinaea, Menisporopsis. New Zealand Journal of Botany 6, 323–375.
Hyde KD, Cai L, McKenzie EHC, Yang YL et al. 2009 – Colletotrichum: a catalogue of confusion. Fungal Diversity 39, 1–17.
Hyde KD, Danushka S, Tennakoon DS, Jeewon R et al. 2019 – Fungal Divers notes 1036–1150: taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity 96, 1–242
Hyde KD, de Silva N, Jeewon R, Bhat DJ et al. 2020a – AJOM new records and collections of fungi: 1–100. Asian Journal of Mycology 3, 22–294.
Hyde KD, Fröhlich J, Taylor JE. 1998 – Fungi from palms. XXXVI. Reflections on unitunicate ascomycetes with apiospores. Sydowia 50, 21–80.
Hyde KD, Nilsson RH, Alias SA, Ariyawansa HA et al. 2014 – One stop shop: backbones tree for important phytopathogenic genera: I. Fungal Diversity 67, 21–125.
Hyde KD, Norphanphoun C, Maharachkumbura SSN, Bhat DJ et al. 2020b – Refined families of Sordariomycetes 11, 305–1059.
Index Fungorum. 2020 – http://www.indexfungorum.org/names/Names.asp (Retrieved on December 20, 2020).
Jayasinghe SL, Kumar L. 2019 – Modeling the climate suitability of tea [Camellia sinensis (L.) O. Kuntze] in Sri Lanka in response to current and future climate change scenarios. Agricultural and Forest Meteorology 272, 102–117.
Jayasiri SC, Hyde KD, Ariyawansa HA, Bhat J et al. 2015 – The Faces of Fungi database: fungal names linked with morphology, phylogeny and human impacts. Fungal Diversity 74, 3–18.
Jayawardena RS, Hyde KD, Danum U, Cai L et al. 2016a – Notes on currently accepted species of Colletotrichum. Mycosphere 7, 1192–1260.
Jayawardena RS, Hyde KD, Jeewon R, Ghobad–Nejhad M et al. 2019 – One stop shop II: taxonomic update with molecularphylogeny for important phytopathogenic genera: 26–50. Fungal Divers 94, 41–129.
Jayawardena RS, Li XH, Xu W, Yan JY et al. 2016b – First report of Botryosphaeria dothidea causing leaf necrosis of Camellia sinensis in Fujian Province, China. Plant Disease 100, 854.
Jeewon R, Liew ECY, Hyde KD. 2002 – Phylogenetic relationships of Pestalotiopsis and allied genera inferred from ribosomal DNA sequences and morphological characters. Molecular phylogenetics and evolution 25, 378–392.
Jeewon R, Liew ECY, Hyde KD. 2003 – Molecular systematics of the Amphisphaeriaceae based on cladistic analyses of partial LSU rDNA gene sequences. Mycological Research 107, 1392–1402.
Jimu L, Wingfield MJ, Mwenje E, Roux J. 2015 – Diseases on Eucalyptus species in Zimbabwean plantations and woodlots. Southern Forests: a Journal of Forest Science 77, 221–230.

511
Joshi SD, Sanjay R, Baby UI, Mandal AKA. 2009 – Molecular characterization of Pestalotiopsis spp. associated with tea (Camellia sinensis) in southern India using RAPD and ISSR markers. Indian Journal of Biotechnology 8, 377–383.

Johnston A. 1960 – A supplement to a host list of plant diseases in Malaya. Mycological Papers 77, 1–30.

Ju YM, Rogers JD. 2002 – The genus Nemania (Xylariaceae). Nova Hedwigia 74, 75–120.

Kamal 2010 – Cercosporoid fungi of India. Bishen Singh Mahendra Pal Singh, Dehra Dun, India N/A, 351.

Katoh K, Toh H. 2010 – Recent developments in the MAFFT multiple sequence alignment program. Brief Bioinform 9, 286–298.

Keith L, Ko WH. Sato DM. 2006 – Identification guide for diseases of tea (Camellia sinensis).

Kirschner R, Hou CL, Chen CJ. 2009 – Co-occurrence of Pseudocercospora species and rhytismatalean ascomycetes on maple and Camellia in Taiwan. Mycological Progress 8, 1–8.

Kirk PM, Cannon PF, Minter DW, Staplers JA. 2008 – Dictionary of the Fungi 10th edn. CABI Bioscience, UK.

Kishino H, Hasegawa M. 1989 – Evaluation of the maximum likelihood estimate of the evolutionary tree topologies from DNA sequence data, and the branching order in Hominoidea. Journal of molecular evolution 29, 170–179.

Kobayashi T. 2007 – Index of fungi inhabiting woody plants in Japan. Host, Distribution and Literature. Zenkoku-Noson-Kyoiku Kyouiku Kyokai Publishing Co., Ltd., Japan.

Koyyappurath S, Atuahiva T, Le GR, Batina H et al. 2016 – Fusarium oxysporum f. sp. radicis-vanillae is the causal agent of the root and stem rot of vanilla. Plant Pathology 65, 612–625.

Kunze G, Schmidt JK. 1817 – Mykologische Hefte 1. Leipzig, Germany.

Larter LNH, Martyn EB. 1943 – A preliminary list of plant diseases in Jamaica. Mycological Papers 8, 1–16.

Liu PSW. 1977 – A supplement to a host list of plant diseases in Sabah, Malaysia. Phytopathol. Pap. 21, 1–49.

Liu F, Hou L, Raza M, Cai L. 2017 – Pestalotiopsis and allied genera from Camellia, with description of 11 new species from China. Scientific Reports 7, 1–19.

Liu F, Tang G, Zheng X, Li Y et al. 2016a – Molecular and phenotypic characterization of Colletotrichum species associated with anthracnose disease in peppers from Sichuan Province, China. Scientific Reports 6, 32761.

Liu F, Wang J, Li H, Wang W, Cai L. 2019 – Sclerotinia spp. on Camellia sinensis. Fungal systematics and evolution 4, 43–57.
Liu F, Weir BS, Damm U, Crous PW et al. 2015 – Unravelling Colletotrichum species associated with Camellia: employing ApMat and GS loci to resolve species in the C. gloeosporioides complex. Persoonia 35, 63–86.

Liu YJ, Tang Q, Fang L. 2016b – First report of Nigrospora sphaerica causing leaf blight on Camellia sinensis in China. Plant Disease 100, 221.

Liu YJ, Whelen S, Hall BD. 1999 – Phylogenetic relationships among ascomycetes: evidence from an RNA polymerase II subunit. Molecular biology and evolution 16, 1799–1808.

Lombard L, van Leeuwen GCM, Guarnaccia V, Polizzi G et al. 2014 – Diaporthe species associated with Vaccinium, with specific reference to Europe. Phytopathologia Mediterranea 53, 287–299.

Lombard L, Wingfield MJ, Alfenas AC, Crous PW. 2016 – The forgotten Calonectria collection: Pouring old wine into new bags. Studies in Mycology 85, 159–198.

Lopes FAC, Steindorff AS, Geraldine AM, Brandão RS et al. 2012 – Biochemical and metabolic profiles of Trichoderma strains isolated from common bean crops in the Brazilian Cerrado, and potential antagonism against Sclerotinia sclerotiorum. Fungal Biology 116, 815–824.

Lu B, Hyde KD, Ho WH, Tsui KM et al. 2000 – Checklist of Hong Kong Fungi. Fungal Divers Press, Hong Kong.

Lu H, Zhang J, Yang Y, Yang X et al. 2016 – Earliest tea as evidence for one branch of the Silk Road across the Tibetan Plateau. Scientific Reports 6, 18955.

Maharachchikumbura SSN, Chukeatirote E, Guo LD, Crous PW et al. 2013 – Pestalotiopsis species associated with Camellia sinensis (tea). Mycotaxon, 123, 47–61.

Maharachchikumbura SSN, Guo LD, Chukeatirote E, Bahkali AH, Hyde KD. 2011 – Pestalotiopsis–morphology, phylogeny, biochemistry and diversity. Fungal Diversity 50: 167–187.

Maharachchikumbura SSN, Hyde KD, Groenewald JZ, Xu J, Crous PW. 2014 – Pestalotiopsis revisited. Studies in Mycology 79, 121–186.

Manawasinghe IS, Dissanayake A, Liu M, Wanasinghe D et al. 2019 – High genetic diversity and species complexity of Diaporthe associated with grapevine dieback in China. Frontiers in Microbiology 10, 1936.

Manawasinghe IS, Phillips AJL, Hyde KD, Chethana KWT et al. 2016 – Mycosphere Essays 14: Assessing the aggressiveness of plant pathogenic Botryosphaeriaceae. Mycosphere 7, 883–892.

Manawasinghe IS, Zhang W, Li X, Zhao W et al. 2018 – Novel microsatellite markers reveal multiple origins of Botryosphaeria dothidea causing the Chinese grapevine trunk disease. Fungal Ecology 33, 134–142.

Marin-Felix Y, Hernández–Restrepo M, Wingfield MJ, Akulov A et al. 2019 – Genera of phytopathogenic fungi: GOPHY 2. Studies in Mycology 92, 47–133.

Mareeswaran J, Nepokan P, Jayanthi R, Premkumar Samuel Asir R, Radhakrishnan B. 2015 – In vitro studies on branch canker pathogen (Macrophoma sp) infecting tea. Journal of plant pathology and Microbiology 6, 284.

Mathur RS. 1979 – The Coelomycetes of India. Bishen Singh Mahendra Pal Singh, Delhi, India, 460.

Matsushima T. 1975 – Icones Microfungorum a Matsushima Lectorum. Nippon Printing Publishing Co., Osaka, 209–415.

Meegahakumbura MK, Wambulwa MC, Thapa KK, Li MM et al. 2016 – Indications for three independent domestication events for the tea plant (Camellia sinensis (L.) O. Kuntze) and new insights into the origin of tea germplasm in China and India revealed by nuclear microsatellites. PloS one 11, e0155369.
Ragazzi A, Marino M. 1990 – II genere *Cercospora* in Africa, con particolare riferimento alla *Cercospora angolensis*. Riv Agric Subtrop Trop 84, 171–184.

Rao V, De Hoog GS. 1975 – Some notes on *Torula*. Persoonia 8: 199–206.

Rappaz F. 1987 – Taxonomy and nomenclature of the octosporous *Diatrypaceae*. Mycol Helv 2, 285–648.

Rashmi M, Kushveer JS, Sarma VV. 2019 – A worldwide list of endophytic fungi with notes on ecology and diversity. Mycosphere 10, 798–1079.

Rayner RW. 1970 – A mycological colour chart. London, UK: British Mycological Society.

Réblová M, Gams W, Seifert KA. 2011 – Monilochaetes and allied genera of the Glomerellales, and a reconsideration of families in the Microascales. Studies in Mycology 68, 163–191.

Richardson MJ. 1990 – An Annotated List of Seed–Borne Diseases. Fourth Edition. International Seed Testing Association, Zurich.

Riley EA. 1960 – A revised list of plant diseases in Tanganyika Territory. Mycological Papers 75: 1–42.

Risede JM, Simoneau P. 2001 – Typing *Cylindrocladium* species by analysis of ribosomal DNA spacers polymorphism: application to field isolates from the banana rhizosphere. Mycologia 93, 494–504.

Ronquist F, Huelsenbeck JP. 2003 – MrBayes 3: Bayesian phylogenetic inference under mixed models. Bioinformatics 19, 1572–1574.

Saha M, Bhattacharya K. 2015 – Aeromycoflora over rice field and their allergenic effect on farmers of N24 Perganas, West Bengal, India.

Salam MU, MacLeod WJ, Maling T, Prichard I et al. 2011 – A meta–analysis of severity and yield loss from ascochyta blight on field pea in Western Australia. Australasian Plant Pathology 40, 591–600.

Sandoval–Denis M, Guarinaccia V, Polizzi G, Crous PW. 2018 – Symptomatic *Citrus* trees reveal a new pathogenic lineage in *Fusarium* and two new *Neocosmospora* species. Persoonia 40, 1–25.

Sandoval–Denis M, Lombard L, Crous PW. 2019 – Back to the roots: a reappraisal of *Neocosmospora*. Persoonia 43, 90–185

Sarbhoy AK, Agarwal DK. 1990 – Descriptions of Tropical Plant Pathogenic Fungi. Set 1. Malhotra Publ. House, New Delhi.

Sarmah SR, Dutta P, Bhattacharyya PN, Payeng B, Tanti AJ. 2016 – Growth habit of tea pathogens and evaluation of relative susceptibility of selected tea cultivars. Int Res J Biol Sci 5, 1–9.

Schuster A, Schmoll M. 2010 – Biology and biotechnology of *Trichoderma*. Applied microbiology and biotechnology 87, 787–799.

Sealy JR. 1958 – A Revision of the Genus Camellia. The Royal Horticultural Society, London.

Seifert KA. 1990 – Synnematous hyphomycetes. Pages 109–154 in Samuels, G.J., and al. et. Contributions toward a mycobiota of Indonesia: Hypocreales, synnematous Hyphomycetes, Aphyllophorales, Phragmobasidiomycetes, and Myxomycetes. Mem. New York Botanical Garden, 1–180.

Senanayake IC, Crous PW, Groenewald JZ, Maharachchikumbura SS, Jeewon R, Phillips AJ, Bhat JD, Perera RH, Li QR, Li, WJ, Tangthirasunun N. 2017 – Families of Diaporthales based on morphological and phylogenetic evidence. Studies in Mycology 86, 217–296.

Sharma G, Tanti AJ, Kumar Pinnaka A, Shenoy BD. 2015 – Resolving the *Colletotrichum siamense* species complex using *ApMat* marker. Fungal Diversity 71, 247–264.

Shaw DE. 1984 – Microorganisms in Papua New Guinea. Dept. Primary Ind., Res. Bull. 33, 1–344.

Silva MRC, Diogo E, Bragança H, Machado H, Phillips AJL. 2015 – *Teratosphaeria gauchensis* associated with trunk, stem and foliar lesions of *Eucalyptus globulus* in Portugal. Forest Pathology 45, 224–234.

Silvestro D, Michalak I. 2016 – RaxmlGUI: A graphical front–end for RAxML. Organisms Diversity & Evolution 12, 335–337.
Singh SM, Yadav LS, Singh PN, Hepat R et al. 2012 – *Arthrinium rasikravindrii* sp. nov. from Svalbard, Norway. Mycotaxon 122, 449–460.

Sinniah GD, Munasinghe CE, Mahadevan N, Jayasinghe SK, Kulanthaigalingam DCM. 2017 – Recent incidence of collar canker and dieback of tea (*Camellia sinensis*) caused by *Fusarium solani* species complex in Sri Lanka. Australasian Plant Disease Notes 12, 41.

Sivasithamparam K, Ghisalberti EL. 1998 – Secondary metabolism in *Trichoderma* and *Gliocladium*. In: Harman GE, Kubicek CP (eds) *Trichoderma* and *Gliocladium*. Taylor and Francis, London, 139–192.

Smith GJD, Liew ECY, Hyde KD. 2003 – The Xylariales: a monophyletic order containing 7 families.

Solarte F, Muñoz CG, Maharachchikumbura SSN, Álvarez E. 2017 – Diversity of *Neopestalotiopsis* and *Pestalotiopsis* spp., causal agents of guava scab in Colombia. Plant Disease 102, 49–59.

Song Y, Geng K, Hyde KD, Zhao WS et al. 2013 – Two new species of *Pestalotiopsis* from Southern China. Phytotaxa 126: 22–32.

Stadler M, Hellwig V. 2005 – Chemotaxonomy of the Xylariaceae and remarkable bioactive compounds from Xylariales and their associated asexual stages. Recent Research Developments in Phytochemistry 9, 41–93.

Stamatakis A. 2014 – RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics 30, 1312–1313.

Stamatakis A, Hoover P, Rougemont J. 2008 – A rapid bootstrap algorithm for the RAxML web servers. Systematic biology 57, 758–771.

Sun EL, Lin HS, Hsieh HJ. 2008 – Study of *Rosellinia necatrix* isolates causing white root rot disease in Taiwan. Journal of Phytopathology 156, 104–111.

Suryanarayanan TS. 2012 – Fungal endosymbionts of seaweeds. In: *Biology of Marine Fungi* (Raghukumar C, ed.): 53–70. Dordrecht: Springer.

Sutton BC. 1980 – The Coelomycetes: Fungi imperfecti with pycnidia, acervuli and stromata. Commonwealth Mycological Institute, Kew, Surrey, England.

Tai FL. 1979 – *Sylloge Fungorum Sinicorum*. Sci. Press, Acad. Sin., Peking, 1527.

Teodoro NG. 1937 – An enumeration of Philippine fungi. Techn Bull Dept Agric Comm Manila 4, 1–585.

Tejeshvi MV, Tamhanka SA, Kini KR, Rao VS, Prakash HS. 2009 – Phylogenetic analysis of endophytic *Pestalotiopsis* species from ethnopharmacologically important medicinal trees. Fungal Diversity 38, 167–183.

Thaung MM. 2007 – A preliminary survey of macromycetes in Burma. Australasian Mycological Institute, Kew, Surrey, England.

Thompson SM, Tan YP, Shivas RG, Neate SM et al. 2015 – ‘Green’ and ‘brown bridges’ between weed and crop hosts reveal novel *Diaporthe* spp. in Australia. Persoonia 35, 39–49.

Turner GJ. 1971 – Fungi and plant disease in Sarawak. Phytopathol Paper 13, 1–55.
Udayanga D, Castlebury LA, Rossman AY, Chukeatirote E, Hyde KD. 2014a – Insights into the genus *Diaporthe*: Phylogenetic species delimitation in the *D. eres* species complex. Fungal Diversity 67, 203–229.

Udayanga D, Castlebury LA, Rossman AY, Hyde KD. 2014b – Species limits in *Diaporthe*: molecular re-assessment of *D. citri, D. cytopsorella, D. foeniculina* and *D. rudis*. Persoonia 32, 83–101.

Udayanga D, Castlebury LA, Rossman AY, Chukeatirote E, Hyde KD. 2015 – The *Diaporthe sojae* species complex: Phylogenetic re-assessment of pathogens associated with soybean, cucurbits and other field crops. Fungal Biology 119, 383–407.

Udayanga D, Liu X, Crous PW, McKenzie EHC et al. 2012 – A multi-locus phylogenetic evaluation of *Diaporthe* (*Phomopsis*). Fungal Diversity 56, 157–171.

Vilgalys R, Hester M. 1990 – Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. Journal of bacteriology, 172, 4238–4246.

Visentin I, Tamiotti G, Valentino D, Portis E et al. 2009 – The ITS region as a taxonomic discriminator between *Fusarium verticillioides* and *Fusarium proliferatum*. Mycological Research 113, 1137–1145.

Wanasinghe DN, Jeewon R, Peršoh D, Jones EBG et al. 2018 – Taxonomic circumscription and phylogenetics of novel didymellaceous taxa with brown muriform spores. Studies in Fungi 3, 152–175.

Wang JH, Feng ZH, Han Z, Song SQ et al. 2013 – First report of pepper fruit rot caused by *Fusarium concentricum* in China. Plant Disease 97, 1657.

Wang M, Liu F, Crous PW, Cai L. 2017a – Phylogenetic reassessment of *Nigrospora*: ubiquitous endophytes, plant and human pathogens. Persoonia 39, 118–142.

Wang M, Tan XM, Liu F, Cai L. 2018 – Eight new *Arthrinium* species from China. MycoKeys 3, 1–24.

Wang Q, Liu Q, Chen S. 2019a – Novel species of *Calonectria* isolated from soil near *Eucalyptus* plantations in southern China. Mycologia 111, 1028–1040.

Wang S, Mi X, Wu Z, Zhang L, Wei C. 2019b – Characterization and pathogenicity of *Pestalotiopsis*-like species associated with gray blight disease on *Camellia sinensis* in Anhui Province, China. Plant Disease 103, 2786–2797.

Wang Y, Xiong F, Fu Q, Hao X et al. 2019c – Diversity of *Pestalotiopsis*-like species causing gray blight disease of tea plants (*Camellia sinensis*) in China, including two novel *Pestalotiopsis* species, and analysis of their pathogenicity. Plant Disease 103, 2548–2558.

Wang YC, Hao XY, Wang L, Xiao B et al. 2016b – Diverse *Colletotrichum* species cause anthracnose of tea plants (*Camellia sinensis* (L.) O. Kuntze) in China. Scientific Reports 6, 35287.

Wang ZH, Zhao ZX, Hong N, Ni DJ et al. 2017b – Characterization of causal agents of a novel disease inducing brown–black spots on tender tea leaves in China. Plant Disease 101, 1802–1811.

Watanabe K, Nakazono T, Ono Y. 2012 – Morphology evolution and molecular phylogeny of *Pestalotiopsis* (*Coelomycetes*) based on ITS2 secondary structure. Mycoscience 53, 227–237.

Watson AJ. 1950 – Fungi associated with *Camellia* flowers. Plant Disease Reports 34, 186–187.
Wei JG, Xu T, Guo LD, Pan XH. 2005 – Endophytic Pestalotiopsis species from southern China. Mycosystema 24, 481–493.

Wei JG, Xu T, Guo LD, Liu AR et al. 2007 – Endophytic Pestalotiopsis species associated with plants of Podocarpaceae, Theaceae and Taxaceae in southern China. Fungal Diversity 24, 55–74.

Weir BS, Johnston PR, Damm U. 2012 – The Colletotrichum gloeosporioides species complex. Studies in Mycology 73, 115–180.

White TJ, Bruns TD, Lee SB, Taylor JW. 1990 – Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In Innis MA, Gelfand DH, Sninsky JJ, White TJ (eds), PCR protocols: a guide to methods and applications New York: Academic Press.

Whiteside JO. 1966 – A revised list of plant diseases in Rhodesia. Kirkia 5, 87–196

Wiehe PO. 1953 – The plant diseases of Nyasaland. Phytopathology Papers 53, 1–39.

Wijayawardene NN, Hyde KD, Al-Ani LKT, Tedersoo L et al. 2020 – Outline of Fungi and fungus–like taxa. Mycosphere 11, 1060–1456.

Wilлиams TH, Liu PSW. 1976 – A host list of plant diseases in Sabah, Malaysia. Phytopathology Papers 19, 1–67.

Woudenberg JHC, Aveskamp MM, De Gruyter J, Spiers AG, Crous PW. 2009 – Multiple Didymella teleomorphs are linked to the Phoma clematidina morphotype. Persoonia 22, 56.

Wu HQ, Su JQ, Xu MY, Yang MH. 2009 – An endophytic Trichoderma species from Camellia sinensis: its characterization and endophytism. Mycosystema 28, 342–348.

Xu KC, Zhang RQ, Li J, Bai YH et al. 2019 – Camellia sinensis, a new host plant of Ceratocystis fimбриata from China. Plant Diseases 103, 2670–2671.

Xiao RF, Wang JP, Zheng MX, Su HL et al. 2019 – First Report of Fusarium concentricum causing stem rot disease on the medicinal plant Paris polyphylla var. chinensis in China. Plant Diseases 103, 1418–1418.

Yang Q, Fan XL, Guarnaccia V, Tian CM. 2018a – Phylogeny and morphology reveal two new species of Diaporthe from traditional Chinese medicine in Northeast China. Phytotaxa 336, 159–170.

Yang Q, Du Z, Tian CM. 2018b – High diversity of Diaporthe species associated with dieback diseases in China, with twelve new species described. MycoKeys 39, 97–149.

Zhang N, Castelbury LA, Miller AN, Huhndorf SM et al. 2006 – An overview of the systematics of the Sordariomycetes based on a four–gene phylogeny. Mycologia 98, 1076–1087.

Zhang TT, Tong X, Lin YR, Hou CL. 2015 – A new species and a new combination of Terriera based on morphological and molecular data. Mycological Progress 14, 1–6.

Zhang Y, Schoch CL, Fournier J, Crous PW. 2009 – Multi–locus phylogeny of Pleosporales: a taxonomic, ecological and evolutionary re–evaluation. Studies in Mycology 64, 85–102.

Zhang YM, Maharachchikumbura SSN, Wei JG, McKenzie EHC, Hyde KD. 2012 – Pestalotiopsis camelliae, a new species associated with grey blight of Camellia japonica in China. Sydowia 64, 335–344.

Zhou LX, Xu WX. 2014 – First report of Alternaria alternata causing leaf spots of tea Camellia sinensis in China. Plant Disease 98, 697.

Zhuang WY. 2001 – Higher Fungi of Tropical China. Mycotaxon, Ltd., Ithaca, NY.