Mycosphere 14(2): 1–106 (2023) www.mycosphere.org ISSN 2077 7019

Article

Doi 10.5943/mycosphere/14/si2/1

Genome-scale and multi-gene phylogenetic analyses of *Colletotrichum* spp. host preference and associated with medicinal plants

Zhang Q[1], Nizamani MM[1], Feng Y[2,5], Yang YQ[1], Jayawardena RS[3,4], Hyde KD[3,4], Wang Y[1*] and Li C[1*]

[1]*College of Agriculture, Key Laboratory of Agricultural Microbiology of Guizhou Province, Guizhou University, Guiyang, Guizhou 550025, China*
[2]*College of Ethnic-Minority Medicine, Guizhou Minzu University, Guiyang, Guizhou 550025, China*
[3]*Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai, 57100, Thailand*
[4]*School of Science, Mae Fah Luang University, Chiang Rai, 57100, Thailand*
[5]*Guizhou Key Laboratory of Agricultural Biotechnology, Guizhou Academy of Agricultural Sciences, Guiyang, Guizhou 550006, China*

Zhang Q, Nizamani MM, Feng Y, Yang YQ, Jayawardena RS, Hyde KD, Wang Y, Li C 2023 – Genome-scale and multi-gene phylogenetic analyses of *Colletotrichum* spp. host preference and associated with medicinal plants. Mycosphere 14(2), 1–106, Doi 10.5943/mycosphere/14/si2/1

Abstract

Colletotrichum is one of the most common phytopathogens worldwide, causing diseases in various commercially valuable hosts. Several *Colletotrichum* species have been reported to infect medicinal plants. Although China is a large-scale producer of medicinal plant resources, the species of *Colletotrichum* that have been locally linked to medicinal plants are poorly understood. Therefore, samples were collected from four provinces of China to determine the *Colletotrichum* species associated with local medicinal plants, resulting in a total of 141 *Colletotrichum* isolates. In conjunction with morphology, multi-locus phylogenetic analyses (ITS, *gapdh*, *chs-1*, *his3*, *act*, and *tub2*), and PHI test revealed that these strains belong to 23 species in eight species complexes, including seven new species (*C. castaneae*, *C. cypericola*, *C. gardeniae*, *C. kunmingense*, *C. ligustri*, *C. radermacherae*, and *C. schefflerae*) and three new host records (*C. celtidis*, *C. iris*, and *C. vittalense*). In addition, we synonymise *C. wuxuhaiense* to *C. karsti*, and *C. menglaense*, *C. pandanicola*, and *C. parvisporum* to *C. siamense*. Furthermore, to understand mechanisms responsible for host range and preference we also sequenced and assembled whole-genome sequences of four species in the *C. gloeosporioides* complex and constructed whole-genome phylogenies of *Colletotrichum* species covering ten species complexes and three singleton species. The comparative genome of *Colletotrichum* species from different lineages revealed that expanded gene families encoding CAZymes are thought to be one of the likely explanations for the widespread and polyphagous nature of species in the *C. acutatum*, *C. boninense*, and *C. gloeosporioides* species complexes. A possible explanation for the host preference of the *C. graminicola* species complex may be the less pectinase-encoding gene families. The current study improves the understanding of *Colletotrichum* species diversity found on medicinal plants and suggests that the members of CAZymes might serve as an important mechanism for host range and preference.

Keywords – Comparative genomics – Genome prediction – Multi-locus phylogeny – Phylogenomics – Seven new species

Submitted 18 November 2022, Accepted 22 February 2023, Published 23 March 2023
Corresponding Author: Yong Wang – e-mail – yongwangbis@aliyun.com,
Cheng Li – e-mail – licheng20070242@126.com

Introduction

Colletotrichum is one of the most common phytopathogens, causing diseases in various herbaceous and woody plants (Cannon et al. 2012, Jayawardena et al. 2021b), especially grain crops (Crouch et al. 2009), fruits (Jayawardena et al. 2016, Damm et al. 2020, Liu et al. 2020a, Liu et al. 2020b), vegetables (Damm et al. 2013, Damm et al. 2014, de Silva et al. 2019), and ornamental plants (Yang et al. 2011, Hou et al. 2016, Wang et al. 2021), leading to yield or economic loss. Besides being plant pathogens, members of *Colletotrichum* are also endophytes, such as *C. fioriniae*, *C. gigasporum*, *C. godetiae*, *C. iris* and *C. karsti* (Liu et al. 2022), saprobes in the soil, water, and air, like *C. aenigma* and *C. siamense* (Liu et al. 2014, Liu et al. 2022), entomopathogens, like *C. nymphaeae* (Wynns et al. 2020) and human pathogens, like *C. dematium* and *C. truncatum*, which can lead to subcutaneous infections and keratitis (Howard et al. 2016, Buchta et al. 2019). Due to their ubiquity, substantial capacity for destruction, and scientific importance, taxa in this genus have been ranked as the eighth most important fungi by plant pathologists in terms of economic/scientific importance (Dean et al. 2012).

Accurate species delineation is crucial, especially among pathogenic plant genera and in studies focusing on biodiversity, pathogenicity-related characteristics, conservation and evolution, and establishing quarantine measures (Cai et al. 2009, Bhunjun et al. 2021). However, the diversity of *Colletotrichum* species on medicinal plants has been relatively understudied. China is one of the international trading centers of medicinal plants and has abundant medicinal plant resources (Khan & Rauf 2014). The value of traditional Chinese medicine amounted to RMB 786.6 billion, and the gross export value reached $3.72 billion in China in 2015 according to The State Council Information Office of the People's Republic of China (2016). Guangxi, Guizhou, Sichuan, and Yunnan provinces are rich in medicinal plant resources. An estimated 92.65% of all listed medicinal plants in China are distributed from these four provinces, according to the Plant Data Center of Chinese Academy of Sciences (https://www.plantplus.cn/cn/dataset/C5479810BBA68B09). However, most counties of these four provinces are rich in threatened medicinal plants, especially in the border areas of Yunnan and Guangxi Provinces (Chi et al. 2017). The main threats are climate change, habitat loss, and over-collection to meet the rising demand for medicines (Khanum et al. 2013, Chi et al. 2017). Fungal pathogens are also a key threat to medicinal plants (Guan et al. 2020, Li et al. 2022). However, previous studies on medicinal plants mainly focused on the endophytic *Colletotrichum*, and it was discovered that *Colletotrichum* is primarily associated with dicotyledon medicinal plants (Lima et al. 2012, Rai et al. 2014). Only six of the 87 samples of medicinal plants related to the endophytic *Colletotrichum* are monocotyledon plants (Rai et al. 2014). Our knowledge of the reason for host preference of *Colletotrichum* on monocot/dicot plants and *Colletotrichum* spp. associated with symptomatic medicinal plants in these four provinces is extremely limited.

In the previous investigations, many *Colletotrichum* species have key traits which correlate with their host preference and host range (Jayawardena et al. 2021a, Talhinhas & Baroncelli 2021). The vast majority of members in the *C. acutatum*, *C. dematium*, *C. destructivum*, *C. gloeosporioides*, *C. orbiculare*, and *C. truncatum* species complexes have been associated with dicotyledonous hosts (Jayawardena et al. 2021a, Talhinhas & Baroncelli 2021). Some of these are rather polyphagous, and a very small number are host-specific in these complexes. In particular, most species within *C. acutatum*, *C. boninense*, and *C. gloeosporioides* species complexes are polyphagous (Jayawardena et al. 2021a, Talhinhas & Baroncelli 2021). By contrast, members of the *C. bambusicola*, *C. caudatum* and *C. graminicola* species complexes appear to be restricted to monocotyledons, mostly Poaceae (commelinoid monocotyledons) (Crouch et al. 2014, Jayawardena et al. 2021a, Liu et al. 2022).

Plant cell walls (PCW) of commelinoid monocotyledons (e.g. Poaceae and Cyperaceae), in comparison with those of gymnosperms, dicots, and non-commelinoid monocotyledons (e.g. Acoraceae, Araceae, and Orchidaceae), mainly differ in the relative abundances of non-cellulosic polysaccharides and their associations/linkages in the primary wall (Carpita & Gibeaut 1993, Cosgrove 1997, Vogel 2008). For instance, relative to dicotyledons, grasses have very low levels of pectin, xyloglucan, and structural proteins and high levels of xylans and mixed linkage glucans (Cosgrove 1997, Vogel 2008). Plant cell walls (PCW) are considered the first line of defense against pathogens, providing effective physical barrier protection for plants (Engelsdorf et al. 2016). Plant cell wall degrading enzymes (PCWDEs), such as pectinases and xylanases, act as a microorganisms strategy for plant invasion or plant degradation which is demonstrated to be related to pathogenicity or virulence (Douaiher et al. 2007, Kikot et al. 2009).

O'Connell et al. (2012) first reported that *Colletotrichum* species might tailor their families of genes encoding pectin-degrading enzymes according to their lifestyle by comparative analyses of the genome and transcriptome of *C. graminicola* and *C. higginsianum*. Gan et al. (2016) showed that *C. incanum* (in the *spaethianum* complex) infects both monocotyledons and dicotyledons and has more hemicellulose in GH10 and pectin-degrading enzyme-encoding genes in PL1, PL3, PL4, PL9 and GH28 relative to *C. graminicola* and *C. sublineola* (in *C. graminicola* complex). However, their results only concerned a few strains within limited species complexes. Genome analyses of as many *Colletotrichum* strains as possible with contrasting host preference could help us to identify commonalities, understand host-fungus interactions and provide a way to resolve species delimitation problems. As of 10 February 2023, 237 *Colletotrichum* genomes including 61 species covering 13 species complexes and three singleton species, were publicly available in National Center for Biotechnology Information (NCBI: https://www.ncbi.nlm.nih.gov/), DOE Joint Genome Institute - JGI MycoCosm (Nordberg et al. 2014, https://mycocosm.jgi.doe.gov/mycocosm/home) and EnsemblFungi (http://fungi.ensembl.org/), which provides an impetus to research the host preference of *Colletotrichum* (Supplementary Table 2).

In this study, we aimed to investigate the *Colletotrichum* species associated with medicinal plants in four provinces of China (Guangxi, Guizhou, Sichuan, and Yunnan), which are rich in threatened medicinal plants, and determine whether the PCW degrading enzymes are correlated to the host preference of *Colletotrichum* by whole-genome sequences analyses.

Materials & Methods

Collection, isolation, and conservation

From 2017 to 2019, samples of different medicinal plants were collected from different locations in Guangxi, Guizhou, Sichuan, and Yunnan Provinces in China. Pure cultures were obtained by single-spore and single hyphal tip culture methods (Senanayake et al. 2020). Single spores or single hyphal tips were cultured on potato dextrose agar (PDA) after an incubation period of 1−2 days at 25 °C. The holotype specimens have been deposited in the Herbarium of the Department of Plant Pathology, Agricultural College, Guizhou University (HGUP) and herbarium of Guizhou Academy of Agricultural Sciences (GZAAS), Guiyang, China. The living cultures have been deposited at the Culture Collection at the Department of Plant Pathology, Agriculture College, Guizhou University, China (GUCC) and Guizhou Culture Collection (GZCC) in Guiyang, China. The records in our study are deposited in the Greater Mekong Subregion fungal database (Chaiwan et al. 2021). According to Jayasiri et al. (2015) and Index Fungorum (2022), the Index Fungorum Registration Identifier and Facesoffungi number of the new species were obtained, respectively.

Morphological Studies

For conidia or ascospores absent on plant tissue, mycelial plugs (5 mm) harvested from the margin of actively growing cultures were placed in the centre of culture dishes (90 mm) which contain PDA and synthetic nutrient-poor agar (SNA) (Fu et al. 2019) and incubated at 25 ℃ under UV light with 12 h day/night regime for 10 d. Plant tissues with conidia and ascospores were directly observed. Morphological and cultural features were characterized following the method, according to Damm et al. (2019). By using a slide culture technique, appressoria were observed and measured (Yang et al. 2011). Microscopic preparations were made in distilled H_2O. Characteristic structures were observed and photographed using either a compound microscope (Olympus BX53, Japan) or a stereoscopic zoom microscope (Motic SMZ168 series, China) with a camera (Nikon E80i, Japan). Thirty measurements were made for each structure using the Tarosoft (R) Image Frame Work (Tarosoft, Nontha Buri, Thailand). Colony diameter was measured after 7 d.

DNA extraction and PCR amplification

In accordance with the manufacturer's instructions, genomic DNA was extracted from the mycelium of *Colletotrichum* strains using a BIOMIGA Fungus Genomic DNA Extraction Kit (Biomiga GD2416, USA). The internal transcribed spacer regions (ITS), the glyceraldehyde-3-phosphate dehydrogenase (*gapdh*), partial sequences of the chitin synthase 1 (*chs-1*), histone H3 (*his3*), actin (*act*), and *β*-Tubulin 2(*tub2*) gene regions were employed for identification on the species level using the primers ITS-4 + ITS-5 (White et al. 1990), GDF + GDR (Templeton et al. 1992), CHS-79F + CHS-354R (Carbone & Kohn 1999), CYLH3F + CYLH3R (Crous et al. 2004), ACT-512F + ACT-783R (Carbone & Kohn 1999) and T1 (O'Donnell & Cigelnik 1997) + Bt2b (Glass & Donaldson 1995). The DNA fragments were amplified in a 20 μL reaction volume containing 10 μL 2 × Master Mix (2 × Bench Top^{TM} Taq Master Mix), 1 μL template DNA, 1 μL of each primer (10 μM), and 7 μL dd H_2O followed the thermal cycle programme outlined by Weir et al. (2012). The Biometra Thermal Cycler (Biometra TRIO) was used for the PCR reactions. Successful PCR products were sequenced in SinoGenoMax (Beijing, China). Raw sequences were obtained and submitted to GenBank (Supplementary Table 1).

Whole-genome sequencing and Assembly

The mycelia of each isolate (GUCC 12049, GUCC 12055, GUCC 12108, and GUCC 12174) were put in 300 mL of potato dextrose broth (PDB) culture medium using a 500 mL conical flask at 25 °C for 3–6 days while being shaken at 150 rpm by a Laboratory Shaking Incubator (ZHICHENG ZWYR-D2401, China). Fresh mycelia were filtered through a sterile Buchner funnel with sterile filter paper and stored at -80 °C. For Illumina and PacBio, sequencing were performed using an Illumine Nova PE150 system and Pacbio Sequel ll by the Beijing Novogene Bioinformatics Technology Co., Ltd, respectively. In order to obtain high-quality Illumina sequencing, the raw Illumina reads were filtered by removing bases with a quality score of 40 or lower, contaminated reads, adapter sequences, and reads with “N” bases longer than ten bp. For PacBio sequences, the subreads were filtered using SMRTlink v 5.0 (-minLength = 50, -minReadScore = 0.8).

High quality PacBio subreads were assembled using Canu v1.8 (Koren et al. 2017), flye v2.4.2 (Kolmogorov et al. 2019), HGAP4 v4.0.0 (Chin et al. 2013, Chin et al. 2016), MECAT v1.3 (Xiao et al. 2017), NextDenovo v2.1-beta.0 (https://github.com/Nextomics/NextDenovo/) and Wtdbg2 v2.4 (Ruan & Li 2020). Using Pilon v1.23 (Walker et al. 2014) with Illumina paired-end reads, the assembled PacBio genome contigs were corrected. Assembly completeness was evaluated by checking for telomeric repeats (TTAGGG/CCCTAA) (Sankaranarayanan et al. 2020).

Gene Prediction and Annotations

GeneMark+ES v4.0 (Ter-Hovhannisyan et al. 2008) and Augustus v3.3.2 (Stanke et al. 2006) were used to predict the protein-coding regions of *Colletotrichum*. EvidenceModeler (EVM) v2012-06-25 (Haas et al. 2008) was used to combine the final protein-coding regions. EggNOG-mapper v2 (Cantalapiedra et al. 2021, https://eggnog-mapper.embl.de/) was used to search for functional annotations of the predicted genes. The dbCAN meta server (Zhang et al. 2018) was used to annotate carbohydrate active enzymes which were classified by the Carbohydrate-Active Enzymes (CAZy) database (Drula et al. 2021, http://www.cazy.org/), and ambiguous enzymes were examined using Pfam (Mistry et al. 2020). The pathogen-host interactions database was used to search for genes similar to known pathogenic genes (Urban et al. 2020).

Phylogenomic tree construction

Sequencing using and multi-locus phylogeny

Sequences included in this investigation were retrieved from GenBank in accordance with previous publications (Bhunjun et al. 2021, Jayawardena et al. 2021a, Liu et al. 2022) (Supplementary Table 1). All the strains were assigned to different species complexes after searching in the NCBI database utilizing the ITS gene. MAFFT (Katoh et al. 2019, https://mafft.cbrc.jp/alignment/server/) was used to align individual genes. Using BioEdit version 7.0.5 the alignments were inspected and manually improved wherever deemed necessary (Hall et al. 2011). The maximum likelihood (ML) method and Bayesian Inference (BI) method were performed on the concatenated sequencing of ITS, *gapdh*, *chs-1*, *his3*, *act*, and *tub2* for *C. acutatum*, *C. boninense*, *C. destructivum*, *C. dracaenophilum*, *C. orchidearum*, *C. spaethianum*, *C. truncatum* species complexes. However, the *his3* sequences are unavailable for several taxa in the *C. gloeosporioides* species complex. Therefore, a concatenated dataset of the *C. gloeosporioides* species complex and 16 species complexes of *Colletotrichum* comprising ITS, *gapdh*, *chs-1*, *act*, and *tub2* were employed.

The ML analysis was performed through the IQ-TREE web server (Trifinopoulos et al. 2016) using a model selected by auto with rapid bootstrap analysis followed by 1000 bootstrap replicates. The BI analyses were constructed using MrBayes (Huelsenbeck & Ronquist 2001) with the best fitting substitution models using ModelFinder (Kalyaanamoorthy et al. 2017) for every single gene, and the two software were integrated into the PhyloSuite v1.2.1 (Zhang et al. 2020). Four Markov Chain Monte Carlo (MCMC) chains were conducted from random trees with five million (M) generations for the *C. acutatum*, *C. destructivum*, *C. spaethianum*, and *C. truncatum* species complexes, three M generations for the *C. boninense* species complex, one M generation for *C. dracaenophilum* and *C. orchidearum* species complexes, 22 M generations for *C. gloeosporioides* species complex and 20 M generations for the tree containing 16 species complexes. Trees were sampled every 1000th generation. Bootstrap support values for ML greater than or equal to 70% and Bayesian posterior probabilities (BYPP) for BI greater than or equal to 0.90 are given near nodes of each phylogenetic tree, respectively.

Whole-genome phylogeny

Whole-genome protein-coding genes of *Colletotrichum* (Supplementary Table 3) were orthogrouped with Orthofinder v. 2.3.8 (Emms & Kelly 2015), using *Verticillium dahliae* (GCF_000150675.1) as the outgroup. MAFFT v. 7.505 (Katoh et al. 2002) with default settings was used to align the amino acid sequences of 1,362 single-copy orthologs. Single-copy orthologs in the alignment were concatenated using paste v. 8.22. Then the resulting alignment was trimmed using trimAl v1.4 (Capella-Gutiérrez et al. 2009) set to automated1. We structured the maximum likelihood (ML) algorithm IQ-TREE v. 2.2.0.3 (Nguyen et al. 2015) using 1,362 single-copy orthologs with 1000 rapid bootstrap iterations. Using the ModelFinder feature in IQ-TREE, we found that Q. plant + F + R7 is the best-fit model.

Pairwise Homoplasy Index (PHI)

The Genealogical Concordance Phylogenetic Species Recognition (GCPSR) is a pragmatic approach for determining the bounds of species (Quaedvlieg et al. 2014, Chethana et al. 2021). Pairwise homoplasy index (PHI) (Bruen et al. 2006) test conducted in SplitsTree4 (Huson & Bryant 2006, Quaedvlieg et al. 2014) was used to evaluate the level of recombination within phylogenetically related species using combined datasets for a new species and its closely related species. If the PHI is more than the 0.05 threshold ($P > 0.05$), it suggests that there is no significant recombination in the dataset.

Results

Whole-genome analysis

Phylogenomic analysis

The *Colletotrichum* genomes ranged from 35.03 Mbp (*C. godetiae* GCA_001663355.1) to 109.66 Mbp (*C. trifolii* GCA_004367215.1) and encoded gene varies between 10,419 (*C. chlorophyti* GCA_001937105.1) and 18,694 (*C. lupini* GCA_023278565.1) what in number (Fig. 1, Supplementary Tables 2–3). We assigned all genes in this study to orthogroups using protein homology. Approximately 97.34% (807,569 of all 829,605 genes) were assigned to 26,905 orthogroups. The number of orthogroups of *Colletotrichum* genomes varied from 9,130 (*C. falcatum* GCA_019425465.1) to 14,255 (*C. filicis* GCA_023376865.1) (Supplementary Table 3). A total of 1,362 orthogroups are single-copy orthogroups. A total of 3,676 genes were assigned to 726 species-specific orthogroups. A total of 429 orthogroups had no homologs in any other species complexes except *C. graminicola* species complex, which represented the species-specific orthogroups unique in *C. graminicola* species complex. 49, 46, 44, 35, 31, 18, 7, 2, and 1 orthogroups are species-specific to *C. gloeosporioides*, *C. truncatum*, *C. acutatum*, *C. spaethianum*, *C. destructivum*, *C. orchidearum*, *C. orbiculare*, *C. magnum*, and *C. boninense* species complexes, respectively. However, *C. agaves* do not have species-specific orthogroups.

The phylogenetic tree was constructed using a concatenated alignment of 1,362 single-copy orthologs with 744,156 characters including alignment gaps, 244,895 parsimony-informative, 117,793 singleton sites, and 381,468 constant sites. The combined data sets consist of 59 *Colletotrichum* strains covering ten species complexes, with *Verticillium dahlia* (GCF_000150675.1) as outgroup. The inferred phylogeny tree indicated the presence of 11 main clades. The *C. spaethianum* species complex is not monophyletic in the phylogenomic tree (Fig. 1).

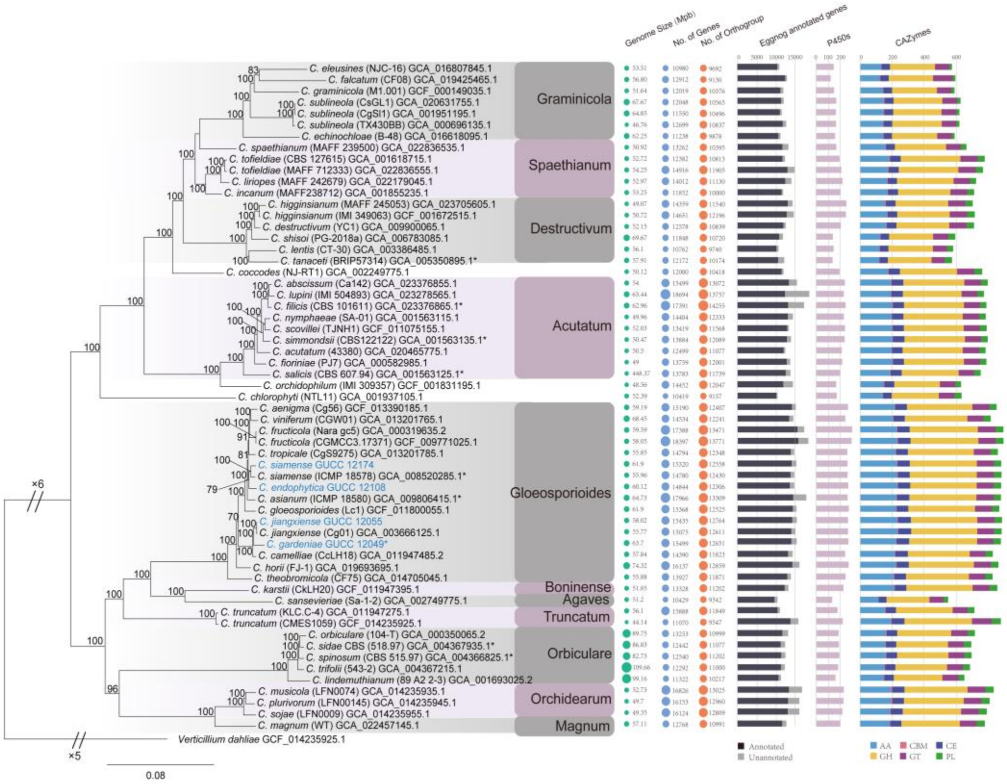


Figure 1 – Maximum likelihood phylogenomic tree using 1,362 single-copy orthologs protein sequences and genome features. Ex-type strains are denoted with "*". From left to right: Phylogenomic tree, Genome size in Mb; Number of predicted genes; Number of predicted genes with and without functional annotation annotated by eggNOG-mapper; CAZymes: hierarchical clustering of CAZyme classes, the auxiliary activities (AA), carbohydrate-binding modules (CBM), carbohydrate esterases (CE), glycoside hydrolases (GH), glycosyltransferases (GT) and polysaccharide lyases (PL).

CAZymes

Carbohydrate-active enzymes (CAZymes) are enzymes involved in the synthesis, metabolism, and recognition of complex carbohydrates, for example, cellulase, hemicellulose and pectase.

The analysis of the carbohydrate-active enzymes with dbCAN reveals that CAZymes are more in *C. acutatum*, *C. gloeosporioides*, *C. magnum*, *C. orbiculare*, *C. spaethianum* and *C. truncatum* complexes (Fig. 1, Supplementary Table 4). Several CAZymes involved in cellulase, hemicellulase, pectinase and cutinase were differentially abundant between lines, including GH3, GH5, GH28, GH43, GH78, CE5, PL1 and PL3 (Fig. 2, Supplementary Table 4). The expansions in members of *C. acutatum*, *C. boninense*, *C. destructivum*, *C. gloeosporioides*, *C. magnum*, *C. orbiculare*, *C. spaethianum* and *C. truncatum* complexes, which infect both monocots and dicots or majority associated with eudicot hosts were noted in GH43 (hemicellulose/pectin-degrading enzyme), CE5 (hemicellulose/cutin-degrading enzyme), GH3 and GH5 (cellulose/hemicelulose-degrading enzyme) and PL1, PL3, GH28 and GH78 (pectin-degrading enzyme) relative to members in *C. graminicola* complex (Figs 2–3, Supplementary Table 4). However, the graminaceous monocot-specific *Colletotrichum* members (*C. graminicola* species complex) showed the cell wall degrading enzymes that were clustering away from the rest of the *Colletotrichum* species analyzed (Fig. 2). Comparison of gene families encoding pectinase, it was found that the gene families encoding pectinase of *C. graminicola* species complex was significantly less than that of other species complexes in this study (Fig. 3). This indicates that pectinase gene loss from members of the *C. graminicola* clade may have been a consequence of their monocot-specific lifestyle.

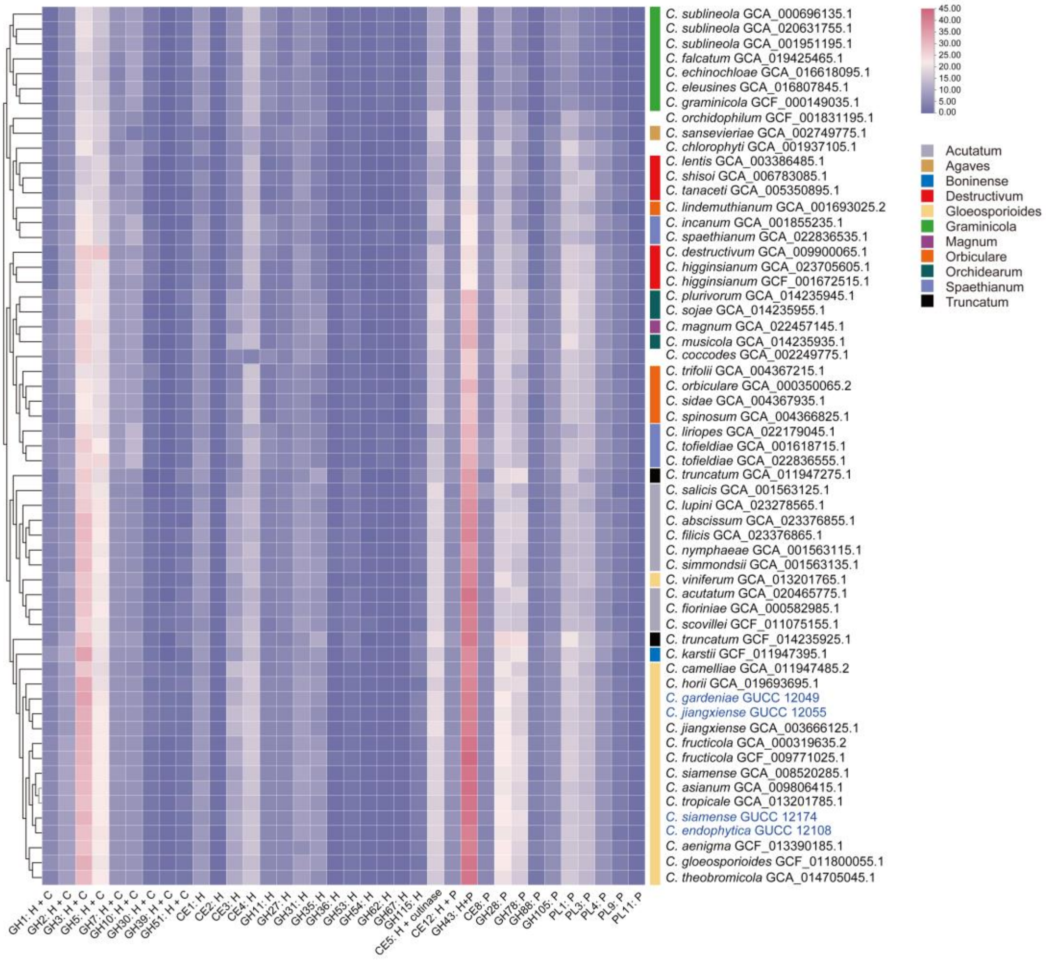


Figure 2 – Comparison of gene families encoding PCWDEs in *Colletotrichum*. C: Cellulase, H: Hemicellulase, P: Pectase.

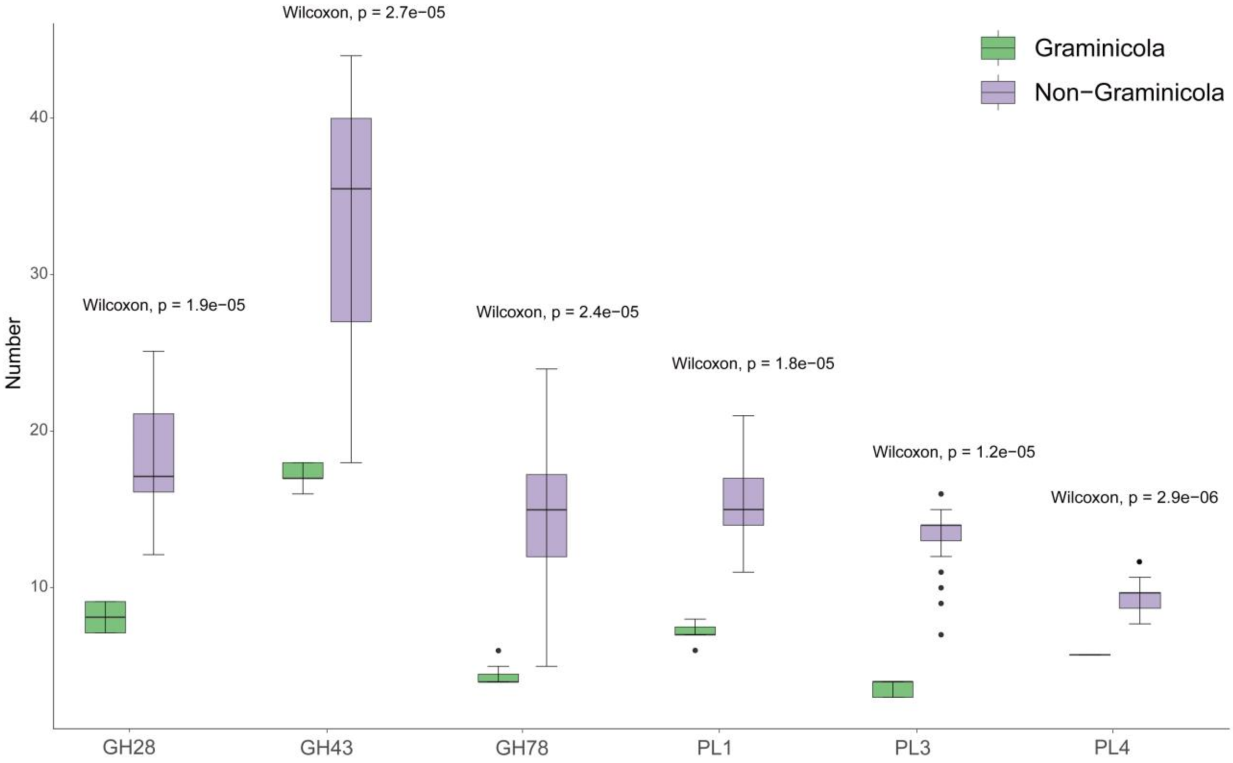


Figure 3 – Comparison of gene families encoding pectinase which showed obvious differentiation among the *C. graminicola* species complex and other species complexes.

Pathogen-host interactions genes

The number of genes with homologs in the database of pathogen-host interactions ranges from 429 to 550 for each strain, the majority of which belong to the category that exhibits reduced virulence and unaffected pathogenicity (Supplementary Table 3). In contrast, others belong to different functional categories relevant to pathogenicity.

Cytochrome P450 monoxygenases (P450s) and transporters

Cytochrome P450 enzymes are usually related to fungal developmental processes and pathogenesis. In the *Colletotrichum* genome, the range of 119–294 putative genes had homologs with cytochrome P450 (Fig. 1, Supplementary Table 3). The largest number of P450 homologous sequences were found in the *C. gloeosporioides* complex (Fig. 1, Supplementary Table 3).

The *Colletotrichum acutatum* species complex

Phylogenetic analyses

In the *C. acutatum* species complex (Fig. 4), the analyzed alignment consisted of combined ITS (1–544 bp), *gapdh* (545–811 bp), *chs-1* (812–1,093 bp), *his3* (1,094–1,482 bp), *act* (1,483–1,731 bp) and *tub2* (1,732–2,228 bp) sequence data including gaps. *Colletotrichum orchidophilum* (strains CBS 631.80, CBS 632.80 and IMI 309357) were selected as the outgroup taxa. The ML search revealed the best score of -9800.412. The best nucleotide substitution models were recommended by ModelFinder and used in the Bayesian analysis: K2P+I+G4 for ITS and *chs-1*, K2P+G4 for *gapdh*, GTR+F+I+G4 for *his3*, *act*, and *tub2*. The phylogenetic tree including our eight *Colletotrichum* isolates, indicated one novel species and one known species (Fig. 4).

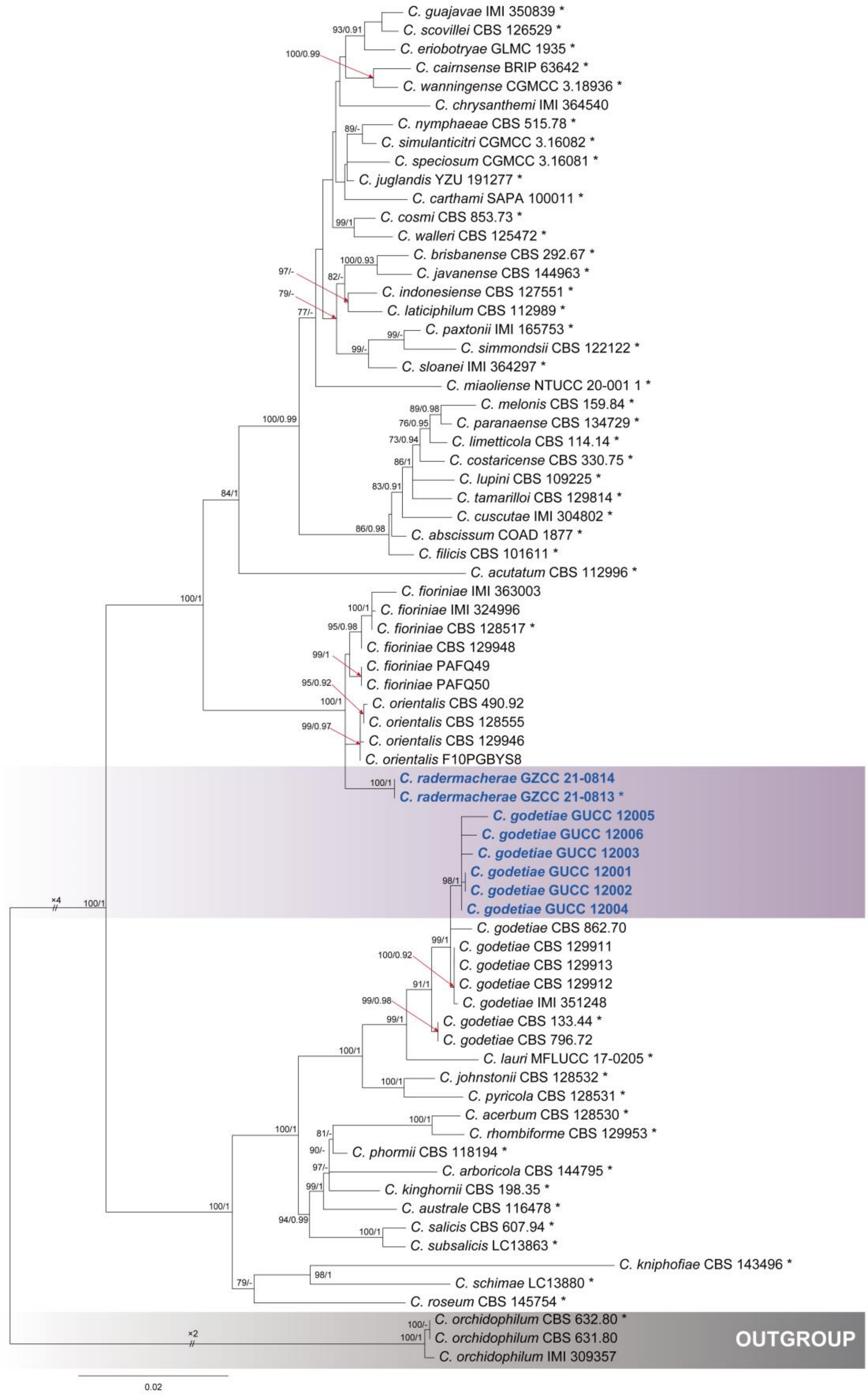


Figure 4 – Maximum likelihood tree of the *C. acutatum* species complex. *Colletotrichum orchidophilum* (CBS 631.80, CBS 632.80, and IMI 309357) were selected as an outgroup. At the nodes, bootstrap support values for ML (≥ 70%) and BYPP (≥ 0.90) are displayed (ML/PP). Type species strains are denoted by "*". Newly generated sequences are in blue bold.

Genealogical concordance phylogenetic species recognition analysis

The PHI test revealed that there is no significant recombination (P = 0.1365), between *C. radermacherae* and its closely related taxa *C. fioriniae* (CBS 128517, CBS 129948, IMI 324996, IMI 363003, PAFQ49 and PAFQ50) and *C. orientalis* (CBS 490.92, CBS128555, CBS 129946 and F10PGBYS8) (Fig. 5).

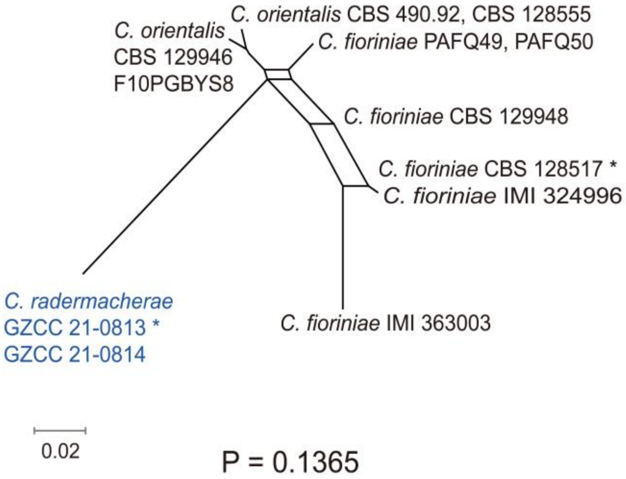


Figure 5 – The pairwise homoplasy index (PHI) tests results of *C. radermacherae* and it phylogenetically related species, respectively.

Taxonomy

Colletotrichum godetiae Neerg., Friesia 4(1-2): 72 (1950) Fig. 6

Index Fungorum number: IF440867

Associated with spots on leaves of *Eriobotrya japonica*, *Hedera nepalensis*, and *Mahonia fortune*. Sexual morph not observed. Asexual state on PDA (GUCC 12006). *Vegetative hyphae* 1.5−5.5 µm diam, hyaline to pale brown, smooth-walled, septate, branched. *Conidiomata*, globose to irregular, milk orange. *Setae* not observed. *Conidiophores* hyaline, smooth-walled, simple, 10.5−37 × 2.5−5 µm. *Conidia* hyaline, smooth-walled, aseptate, straight, cylindrical to fusiform with both ends acute or one end round and one end slightly acute, 14.5−19 × 5−7 µm, mean ± SD = 16.4 ± 1.0 × 5.5 ± 0.4 µm, L/W ratio = 3.0. *Appressoria* solitary, pale to medium brown, smooth-walled, clavate to irregular, undulate to lobate margin, 7.5−15 × 5−11.5 µm, mean ± SD = 11.8 ± 2.3 × 7.8 ± 1.8 µm, L/W ratio = 1.5.

Culture characteristics – Colonies on PDA flat with entire margin, surface partly covered with woolly white to pale grey aerial mycelium in rings, reverse same colour, growth 82 mm in 7 d.

Material examined – China, Yunan Province, Kunming City, Kunming Botanical Garden, on leaf spot of *Eriobotrya japonica* (Rosaceae), 15 January 2018, Q. Zhang, (HGUP 22001), living culture GUCC 12001, GUCC 12002; *ibid*., on leaf spot of *Mahonia fortunei* (Berberidaceae), (HGUP 22002), living culture GUCC 12003, GUCC 12004; *ibid*., on leaf spot of *Hedera nepalensis* (Araliaceae), (HGUP 22004), living culture GUCC 12005, GUCC 12006.

Notes – *Colletotrichum godetiae* was introduced from the seed of *Clarkia hybrida* cv. Kelvedon Glory by Neergaard (1943). The effective descriptions and illustrations for the asexual morph of this taxon were provided by Damm et al. (2012a). The morphology from our collection (GUCC 12006) is similar to the asexual morph of strain CBS 862.70, which has longer conidia (14.5−19 × 5−7 *vs.* 8–24 × 4–5.5). The phylogenetic analysis shows that six strains grouped with *C. godetiae* (Fig. 4). We, therefore, propose our collections as *C. godetiae.*

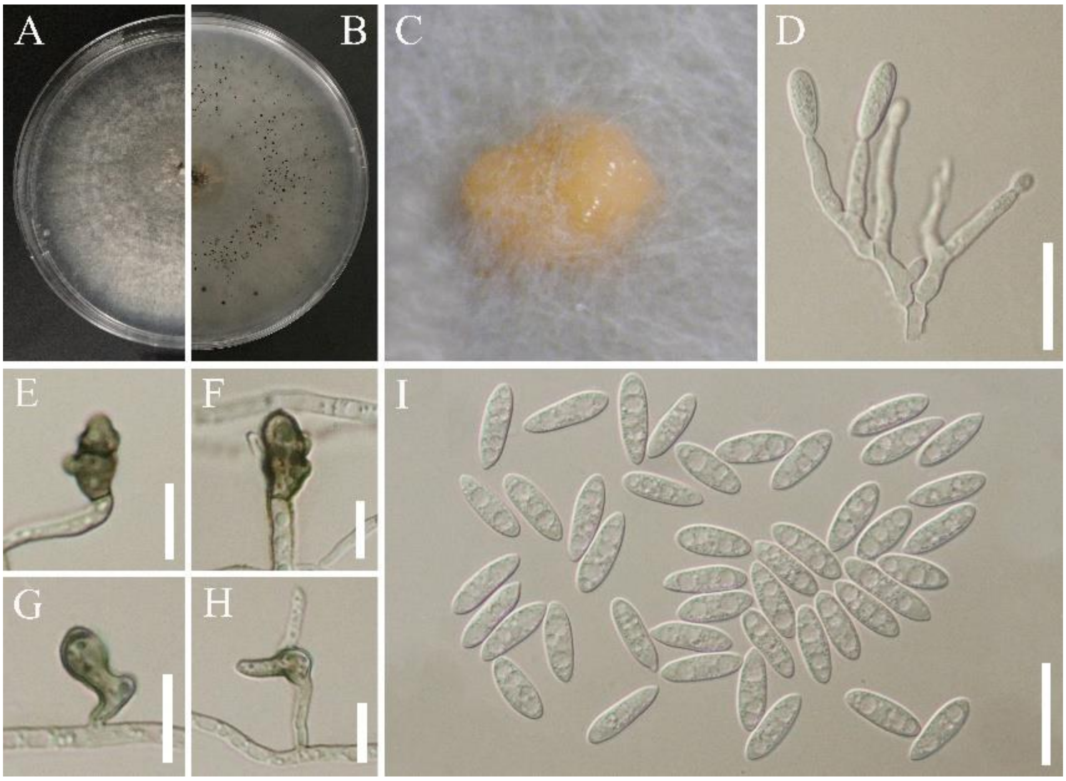


Figure 6 – *Colletotrichum godetiae* (GUCC 12006). A, B Upper and Reverse view of the colony. C Conidiomata. D Conidiophores. E−H Appressoria. I conidia. Scale bars: D, I = 20 µm, E−H = 10 µm.

Colletotrichum radermacherae Y. Feng, Q. Zhang, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 7

Index Fungorum number: IF900004; Facesoffungi numbers: FoF 13369

Etymology – Named after the host on which it occurs, *Radermachera sinica*.

Holotype – GZAAS 21-0300

Saprobic on dried branches of *Radermachera sinica* and associated with spots on leaves of *Cinnamomum camphora*. Sexual morph unknown. Asexual morph on host. *Conidiomata* forming a cushion of pale brown, orange. *Setae* not observed. *Conidiophores* hyaline to pale brown, smooth-walled, septate, branched. *Conidiogenous cells* hyaline to pale brown, smooth-walled, cylindrical, 18−29 × 3−4 µm. *Conidia* hyaline, smooth-walled, aseptate, straight, fusiform to cylindrical with both ends acute, 14−21 × 4.5−6 µm, mean ± SD = 17.4 ± 1.5 × 5.3 ± 0.3 µm, L/W ratio = 3.3.

Culture characteristics – Colonies on PDA flat with entire margin; surface white, the centre of colonies rosy buff, covered with salmon acervuli, aerial mycelium, reverse salmon, growth 50 mm in 7 d.

Material examined – China, Guizhou Province, Guiyang City, Huaxi Road, on branches of *Radermachera sinica* (Bignoniaceae), 28 December 2017, Y. Feng, 65 (GZAAS 21-0300, holotype); ex-type living culture GZCC 21-0814; *ibid.*, Qianxinan Buyi and Miao Autonomous Prefecture, Ceheng County, on the leaves of *Cinnamomum camphora* (Lauraceae), 13 May 2018, GZAAS 21-0299, living culture GZCC 21-0813.

Notes – *Colletotrichum radermacherae* was isolated from dead and dying branches of *Radermachera sinic* and leaves of *Cinnamomum camphora* in Guizhou, China. The characters of conidia match the species concept in *C. acutatum* species complex (Damm et al. 2012a). Phylogenetic analyses show that *C. radermacherae* forms a distinct lineage closely related to *C. fioriniae* (Fig. 4). *Colletotrichum radermacherae* showing 99.60% (504/506 bp), 97.25% (212/218 bp including 2 bp of gaps), 98.35% (239/243 bp including 1 bp of gap), 97.72% (214/219 bp including 2 bp of gaps) and 98.98% (486/491 bp) sequence similarity with *C. fioriniae* of ITS, *gapdh*, *chs-1*, *act* and *tub2* sequences, respectively. *C. radermacherae* differs from *C. fioriniae* in having longer conidiogenous cells (18−29 µm *vs.* 10–22 µm) and slightly larger *Conidia* (14−21 × 4.5−6, mean = 17.4 × 5.3 *vs.* 10–19.5 × 4–5.5, mean = 15.0 × 4.5) (Damm et al. 2012a). The PHI test on *C. radermacherae* revealed that there is no significant recombination (P = 0.1365 > 0.05) between *C. radermacherae* and its closely related taxa (Fig. 5). Therefore, *Colletotrichum radermacherae* is introduced as a new species based on morphological characters and phylogenetic evidence.

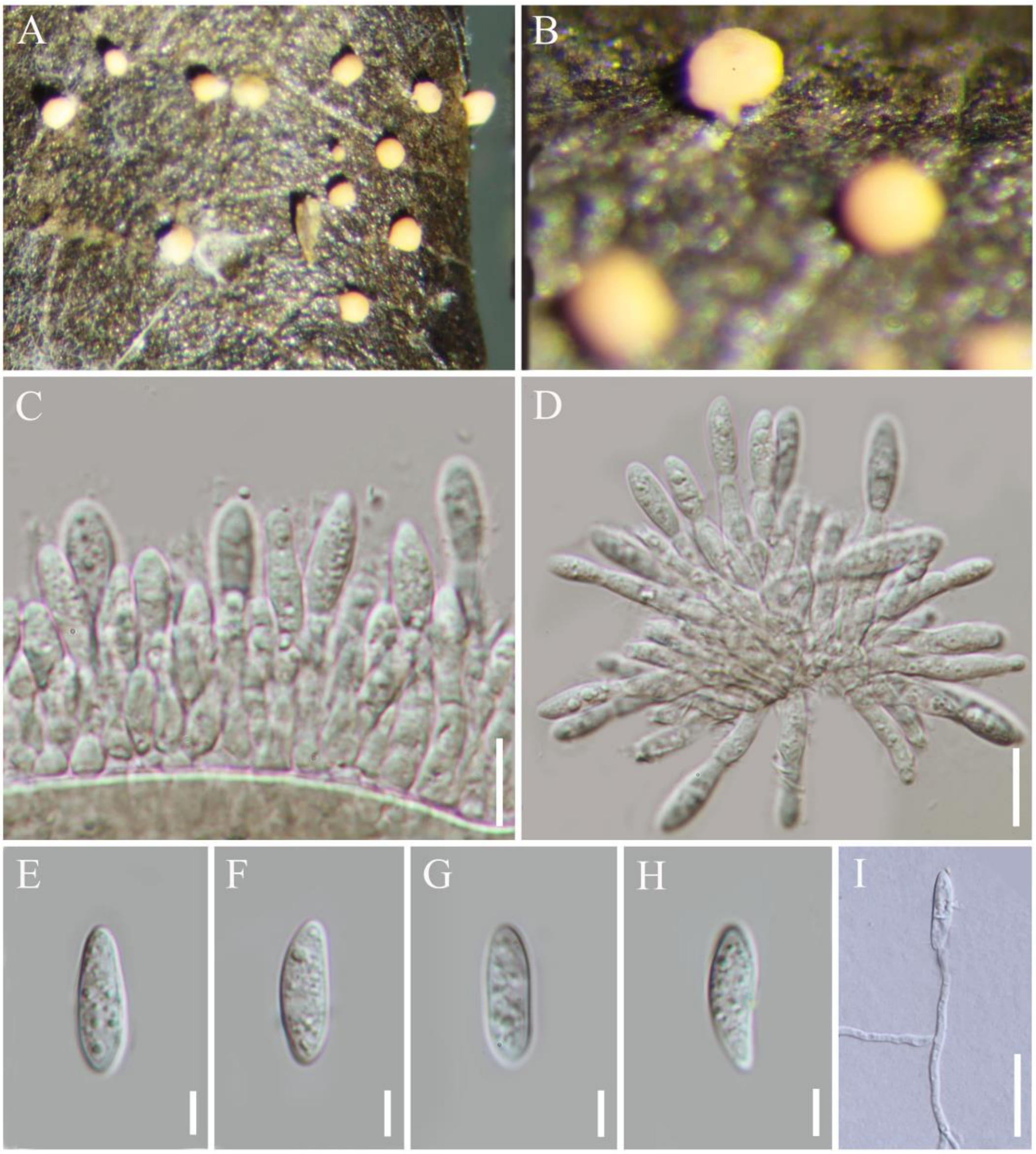


Figure 7 – *Colletotrichum radermacherae* (GZAAS 21-0300). A–B Conidiomata. C−D Conidiophores. E–H Conidia. I Germinating conidia. Scale bars: C = 20 µm, D = 25 µm, E–H = 5 µm, I = 10 µm.

The *Colletotrichum boninense* species complex

Phylogenetic analyses

In the *C. boninense* species complex, the aligned sequence matrix comprises ITS (1–559), *gapdh* (560–830), *chs-1* (831–1,076), *his3* (1,077–1,440), *act* (1,441–1,701), and *tub2* region (1,702–2,365) sequence data for a total of 2,365 characters, including coded alignment gaps. *Colletotrichum agaves* (CBS 118190), *C. euphorbiae* (CBS 134725), and *C. ledebouriae* (CBS

141284) were selected as the outgroup taxa. The ML search revealed the best score of -11670.134. The best nucleotide substitution models were recommended by ModelFinder and used in the Bayesian analysis: K2P+I+G4 for ITS and *chs*, K2P+G4 for *gapdh*, HKY+F+G4 for *his*, *act* and *tub2*. Our 35 isolates clustered into three subclades in this species complex, which indicates one novel record and two known species (Fig. 8).

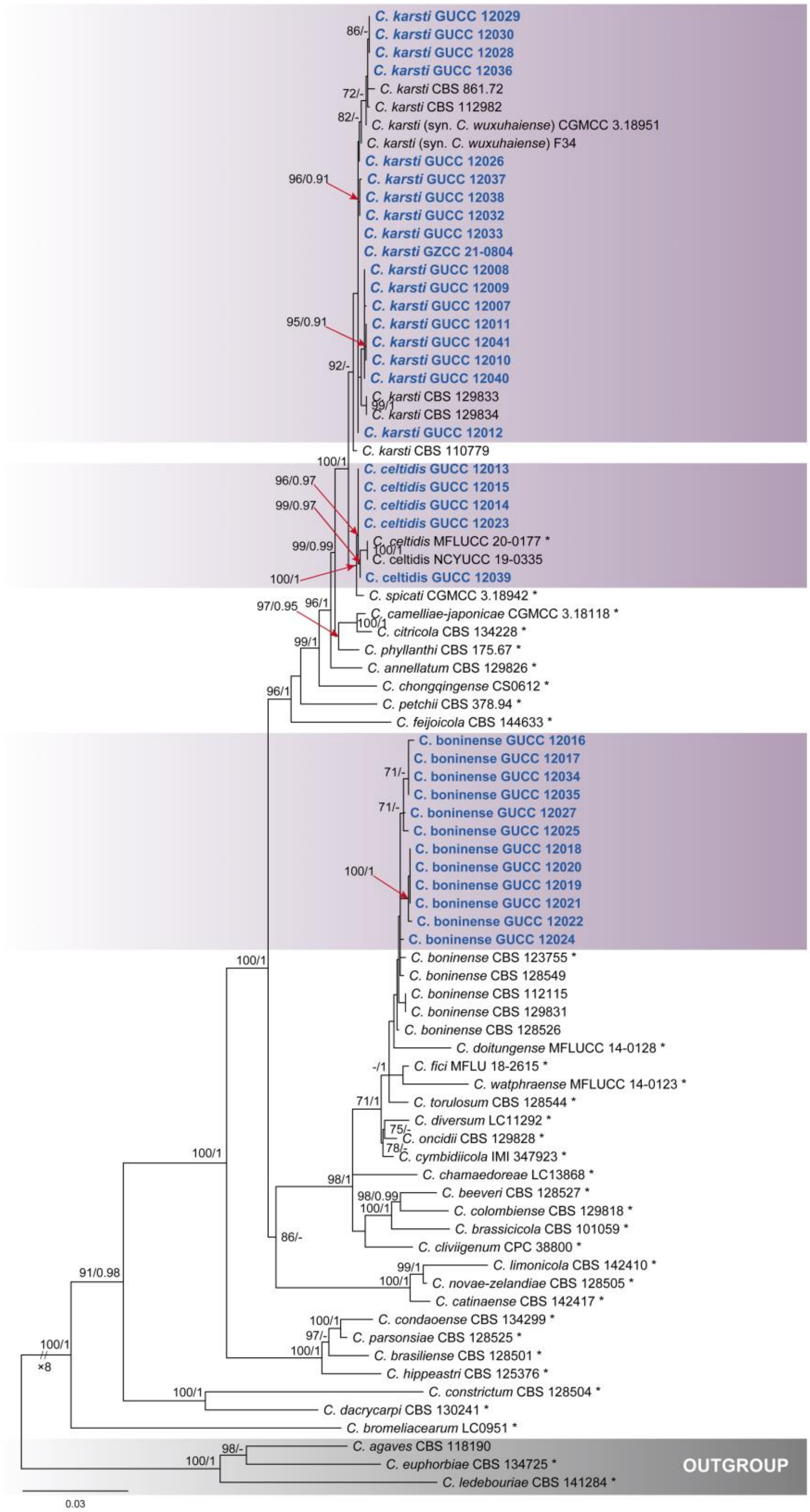


Figure 8 – Maximum likelihood tree of the *C. boninense* species complex. *Colletotrichum agaves* (CBS118190), *C. euphorbiae* (CBS 134725), and *C. ledebouriae* (CBS 141284) were selected as

outgroups. At the nodes, bootstrap support values for ML (≥ 70%) and BYPP (≥ 0.90) are displayed (ML/PP). Type species strains are denoted by "*". Newly generated sequences are in blue bold.

Taxonomy

Colletotrichum boninense Moriwaki, Toy. Sato & Tsukib., Mycoscience 44(1): 48 (2003) Fig. 9

Index Fungorum number: IF372362

Associated with spots on leaves of *Aucuba japonica*, *Fatsia japonica*, *Ilex chinensis*, and *Yulania denudate*. Asexual morph not observed. Sexual morph on PDA (GUCC 12017), *Vegetative hyphae* 2–4 µm diam, *Ascomata* perithecia, clustered, superficial on the agar medium, globose, glabrous, medium to dark brown, outer wall composed of flattened angular cells. *Ascogenous* hyphae hyaline, smooth. *Asci* unitunicate, 8–spored, cylindrical to clavate, tapering to apex and base, smoothwalled, 34.5–80 × 7.5–15 µm. *Ascospores* bis- or multiseriately arranged, aseptate, hyaline, smooth-walled, variable in shape, ovoid to fusiform, slightly curved, both sides rounded, 6.5–21 × 4–8.5 µm, mean ± SD = 15.9 ± 2.6 × 6.3 ± 0.9 µm, L/W ratio = 2.5.

Culture characteristics – Colonies on PDA flat with entire margin, surface partly covered with woolly white to pale grey aerial mycelium, reverse pale yellow, growth 54 mm in 7 d.

Material examined – China, Guizhou Province, Guiyang City, Huaxi Road, on leaf spot of *Fatsia japonica* (Araliaceae), 6 September 2017, Q. Zhang, (HGUP 22007), living culture GUCC 12016, GUCC 12017; *ibid*., on leaf spot of *Aucuba japonica* (Cornaceae), 17 July 2018, (HGUP 22008), living culture GUCC 12018; *ibid*., on leaf spot of *Aucuba japonica* (Cornaceae), 24 July 2018, (HGUP 22009), living culture GUCC 12019, GUCC 12020, GUCC 12021, GUCC 12022; *ibid*., on leaf spot of *Yulania denudata* (Desrousseaux), 8 September 2017, Q. Zhang, (HGUP 22010), living culture GUCC 12024, GUCC 12025; *ibid*., on leaf spot of *Ilex chinensis* (Aquifoliaceae), 18 September 2017, (HGUP 22011), living culture GUCC 12027; *ibid*., on leaf spot of *Ilex chinensis* (Aquifoliaceae), 25 October 2017, (HGUP 22005), living culture GUCC 12034, GUCC 12035.

Notes – In the phylogenetic analysis, our strains (GUCC 12016, GUCC 12017, GUCC 12018, GUCC 12019, GUCC 12020, GUCC 12021, GUCC 12022, GUCC 12024, GUCC 12025, GUCC 12027, GUCC 12034, GUCC 12035) clustered with *C. boninense* (Fig. 8). *Colletotrichum boninense* was introduced by Moriwaki et al. (2003) which has a very diverse plants host family *Amaryllidaceae*, *Annonaceae*, *Bignoniaceae*, *Lauracea*, *Olivaceae*, *Orchidaceae*, *Piperaceae*, *Podocarpaceae*, *Protaceae*, *Rubiaceae*, *Rutaceae*, *Solanaceaea* and *Theaceae* (Damm et al. 2012b, Jayawardena et al. 2021a). In comparison with the description of Damm et al. (2012b), our strain (GUCC 12017) is similar to the sexual morph of *C. boninense* (CBS 123756) which collection from *Crinum asiaticum* var. *sinicum* (Damm et al. 2012b). Therefore, we name the collection *C. boninense*.

Colletotrichum celtidis Tennakoon, C.H. Kuo & K.D. Hyde, Fungal Diversity 108: 158 (2021) Fig. 10

Index Fungorum number: IF555477

Associated with spots on leaves of *Rhododendron simsii* and *Yulania denudate*. Sexual morph on PDA (GUCC 12013). *Ascomata* perithecia, clustered, superficial on PDA, globose, glabrous, pale to medium brown, outer wall composed of flattened angular cells. *Ascogenous* hyphae hyaline, smooth. *Asci* 8-spored, smooth-walled, cylindrical to clavate, tapering to apex and base, 40.5–78 × 8.2–20 µm. *Ascospores* hyaline, bis- or multiseriate arranged, aseptate, smooth-walled, variable in shape, ovoid to fusiform, slightly curved, both sides rounded, 16.5–25 × 4.5–8 µm, mean ± SD = 19.4 ± 1.4 × 6.3 ± 1 µm, L/W ratio = 3.1. Asexual morph on PDA. *Vegetative hyphae* 1.5–3.5 µm diam, smooth-walled, hyaline to pale brown, branched, septate. *Conidiomata*, subglobose, orange. *Setae* not observed. *Conidiophores* hyaline to pale brown, septate, branched, smooth-walled. *Conidiogenous cells* hyaline, cylindrical, smooth-walled, 5.5–39.5 × 3.5–6 µm, collarette 0.5–1.5 µm long, periclinal thickening observed. *Conidia* hyaline, straight, cylindrical, aseptate, the apex and base rounded, smooth-walled, with a prominent hilum, 12.5–17 × 5–7.5 µm, mean ± SD = 15.1 ± 1 × 6.5 ± 0.5 µm, L/W ratio = 2.3. *Appressoria* solitary, medium to dark brown, smooth-walled, subglobose to elliptical in outline, with an entire, crenate to undulate margin, 7–13.5 × 6.5–9 µm, mean ± SD = 10.4 ± 1.4 × 8 ± 0.7 µm, L/W ratio = 1.3.

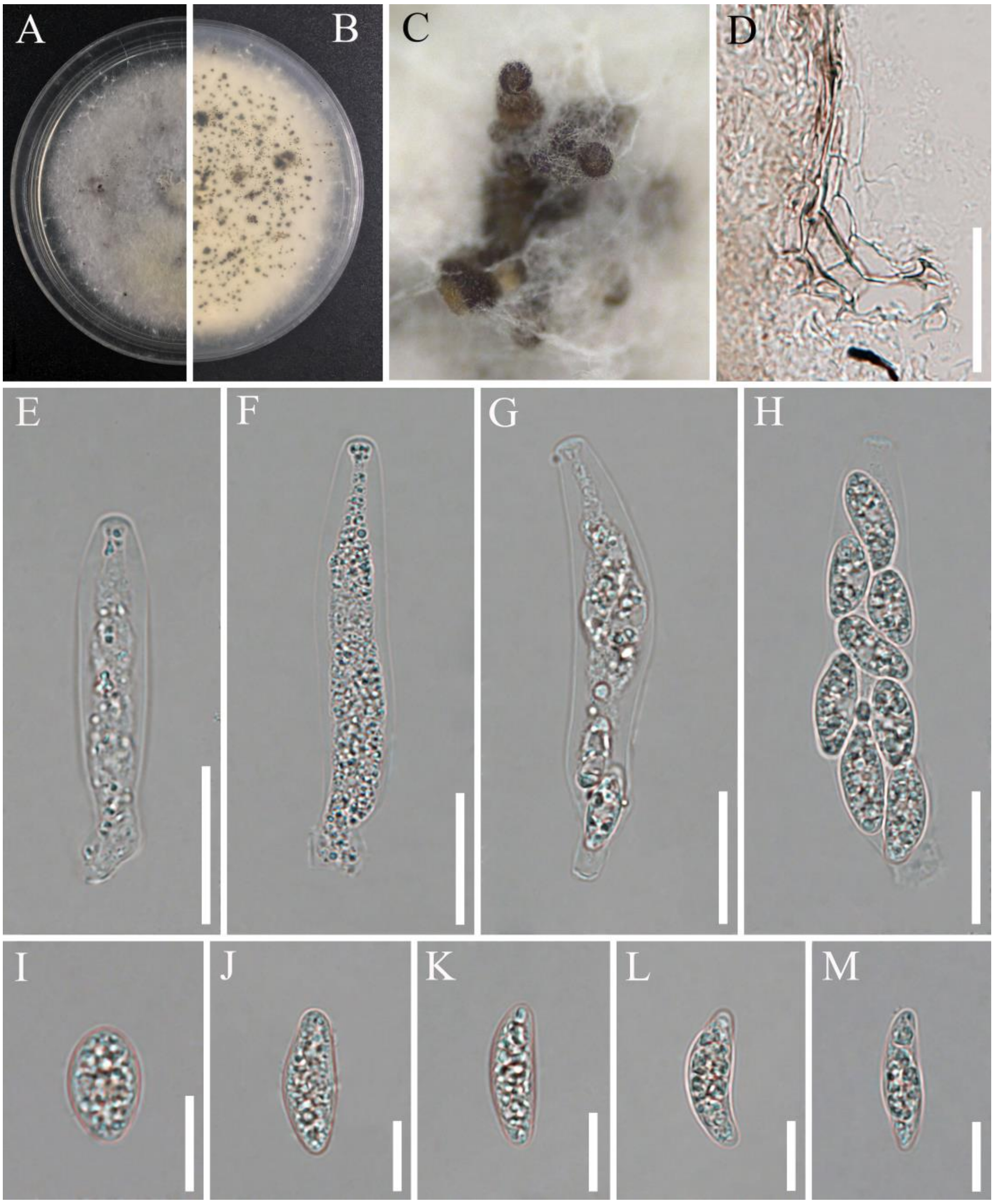


Figure 9 – *Colletotrichum boninense* (GUCC 12017). A Upper view of the colony. B Reverse view of the colony. C Ascomata. D Peridium in cross section. E–H Asci. I–M Ascospore. Scale bars: D–H = 20 µm, I–M = 10 µm.

Culture characteristics – Colonies on PDA flat with entire margin, surface partly covered with white to grey aerial mycelium, reverse same colour, growth 76 mm in 7 d.

Material examined – China, Yunan Province, Kunming City, Kunming Botanical Garden, on leaf spot of *Rhododendron simsii* (Ericaceae), 15 January 2018, Q. Zhang, (HGUP 22014), living culture GUCC 12013, GUCC 12014, GUCC 12015; *ibid*., Guizhou Province, Guiyang City, Huaxi Road, on leaf spot of *Yulania denudata* (Desrousseaux), 8 September 2017, (HGUP 22012), living culture GUCC 12023; *ibid*., China, Yunan Province, Kunming City, Kunming Botanical Garden, on leaf spot of undetermined host species, 15 January 2018, (HGUP 22013), living culture GUCC 12039 (new host record and sexual morph record).

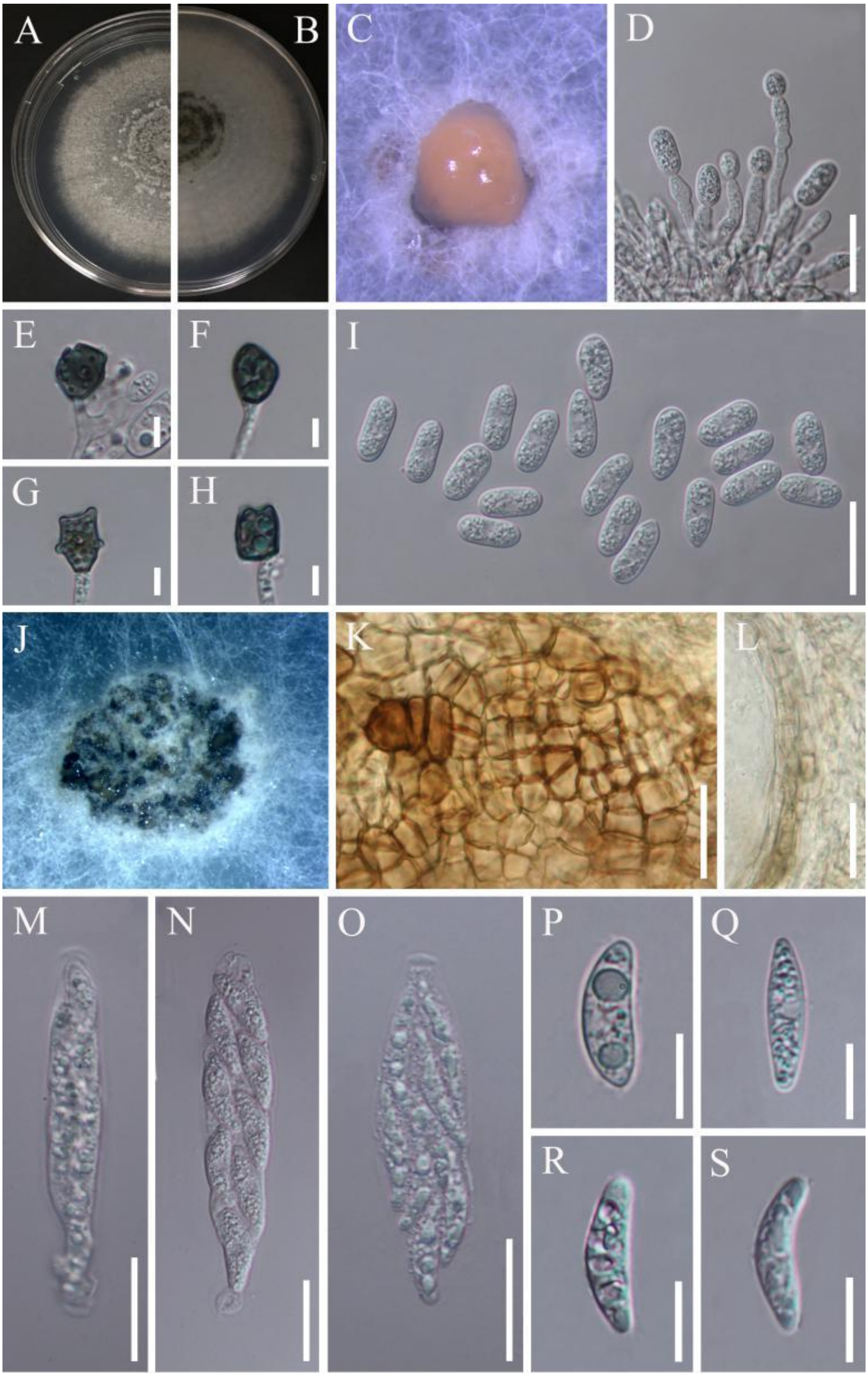


Figure 10 – *Colletotrichum celtidis* (GUCC 12013). A, B Upper and Reverse view of the colony. C Conidiomata. D Conidiophores. E–H Appressoria. I Conidia. J. Ascomata. K Outer surface of

Peridium. L Peridium in cross section. M–O Asci. P–S Appressoria. Scale bars: D, I, K−O = 20 µm, E−H = 5 µm, P−S = 10 µm.

Notes – Phylogenetic analyses show that our strains (GUCC 12013, GUCC 12014, GUCC 12015, GUCC 12023, GUCC 12039) grouped with the type strain of *C. celtidis* (MFLUCC 20-0177) with high bootstrap support (ML/BI: 96%/0.97, Fig. 8). Our collection (GUCC 12013, Fig. 10) has similar asexual morphology to *C. celtidis* from *Celtis formosana* (Tennakoon et al. 2021). *Colletotrichum celtidis*, however, is only observed as an asexual morph (Tennakoon et al. 2021), so we were unable to compare the sexual morph characteristics of our strains to those of *C. celtidis*. We identify our collection as *C. celtidis*, and our strains represent a new host record and sexual morph record for *C. celtidis*.

Colletotrichum karsti You L. Yang, Zuo Y. Liu, K.D. Hyde & L. Cai, Cryptogamie Mycologie 32 (3): 241 (2011) Fig. 11

≡ *Colletotrichum wuxuhaiense* Z.F. Yu & H. Zheng, in Zheng, Yu, Jiang, Fang & Qiao, Journal of Fungi 8(1, no. 87): 20 (2022)

Index Fungorum number: IF581687

Associated with spots on leaves of *Camellia japonica*, *Capsicum annuum*, *Chimonanthus praecox*, *Cinnamomum camphora*, *Ilex chinensis*, Liliaceae sp., *Mahonia fortune* and *Photinia serratifolia*. Asexual morph on PDA (GUCC 12009). *Vegetative hyphae* 1–5 µm diam, hyaline to pale brown, smooth-walled, septate, branched. *Conidiomata*, subglobose, orange. *Setae* not observed. *Conidiophores* hyaline to pale brown, smooth-walled, septate, branched, 9.5–21.5 × 3–6 µm. *Conidia* hyaline, smooth-walled, aseptate, straight, cylindrical, the apex and base rounded, with a prominent hilum, 15–21 × 5.5–8 µm, mean ± SD = 17.7 ± 1.4 × 6.5 ± 0.5 µm, L/W ratio = 2.7. *Appressoria* solitary, medium to dark brown, smooth-walled, subglobose, to elliptical in outline, with an entire, crenate to undulate margin, 5.5–15 × 5.5–11 µm, mean ± SD = 8.8 ± 2 × 7.8 ± 1.2 µm, L/W ratio = 1.1. Asexual morph undetermined.

Culture characteristics – Colonies on PDA flat with entire margin, surface partly covered with white to grey aerial mycelium, reverse same colour, growth 67 mm in 7 d.

Material examined – China, Yunan Province, Kunming City, Kunming Botanical Garden, on leaf spot of *Mahonia fortunei* (Berberidaceae), 15 January 2018, Q. Zhang, (HGUP 22021), living culture GUCC 12007, GUCC 12008, GUCC 12009, GUCC 12010, GUCC 12011; *ibid*., (HGUP 22006), living culture GUCC 12012 ; *ibid*., Guizhou Province, Guiyang City, Huaxi Road, on leaf spot of *Cinnamomum camphora* (Lauraceae), 8 September 2017, (HGUP 22015), living culture GUCC 12026; *ibid*., Guizhou Province, Guiyang City, Huaxi Road, on leaf spot of Liliaceae sp., 8 Nov 2018, Y. Wang, (HGUP 22016), living culture GUCC 12028, GUCC 12029, GUCC 12030; *ibid*., Guizhou Province, Duyun City, Dongshan Park, on leaf spot of *Capsicum annuum* (Solanaceae), 19 April 2019, C. R. Meng, (HGUP 22017), living culture GUCC 12032; *ibid*., Guizhou Province, Guiyang City, Huaxi Road, on leaf spot of *Ilex chinensis* (Aquifoliaceae), 25 October 2017, Y. Wang, (HGUP 22018), living culture GUCC 12033; *ibid*., Guizhou Province, Guiyang City, Xifeng County, on leaf spot of *Chimonanthus praecox* (Calycanthaceae), 26 Jun 2019, C. R. Meng, (HGUP 22023), living culture GUCC 12036; *ibid*., on leaf spot of *Photinia serratifolia* (Rosaceae), (HGUP 22019), living culture GUCC 12037, GUCC 12038; *ibid*., on leaf spot of undetermined host species, (HGUP 22020), living culture GUCC 12040, GUCC 12041; *ibid*, Guizhou Province, Guiyang City, Qianling Mountain Park, *Camellia japonica* (Theaceae), 3 May 2018, Y. Feng, GZAAS 21-0290, living culture GZCC 21-0804.

Notes – *Colletotrichum karsti* occurs on many host plants and is the most common and geographically diverse species in the *C. boninense* complex. In this study, our strains and *C. wuxuhaiense* grouped with *C. karsti* (ML/BI: 92%/-, Fig. 8). Morphological and genetic variation of *C. karsti* are very high (Jayawardena et al. 2021a). When comparing our strains and *C. wuxuhaiense* with the description of Yang et al. (2011), they are similar in morphology. We, therefore, name our collection as *C. karsti* and synonymize *C. wuxuhaiense* as *C. karsti* based on phylogenetic analyses.

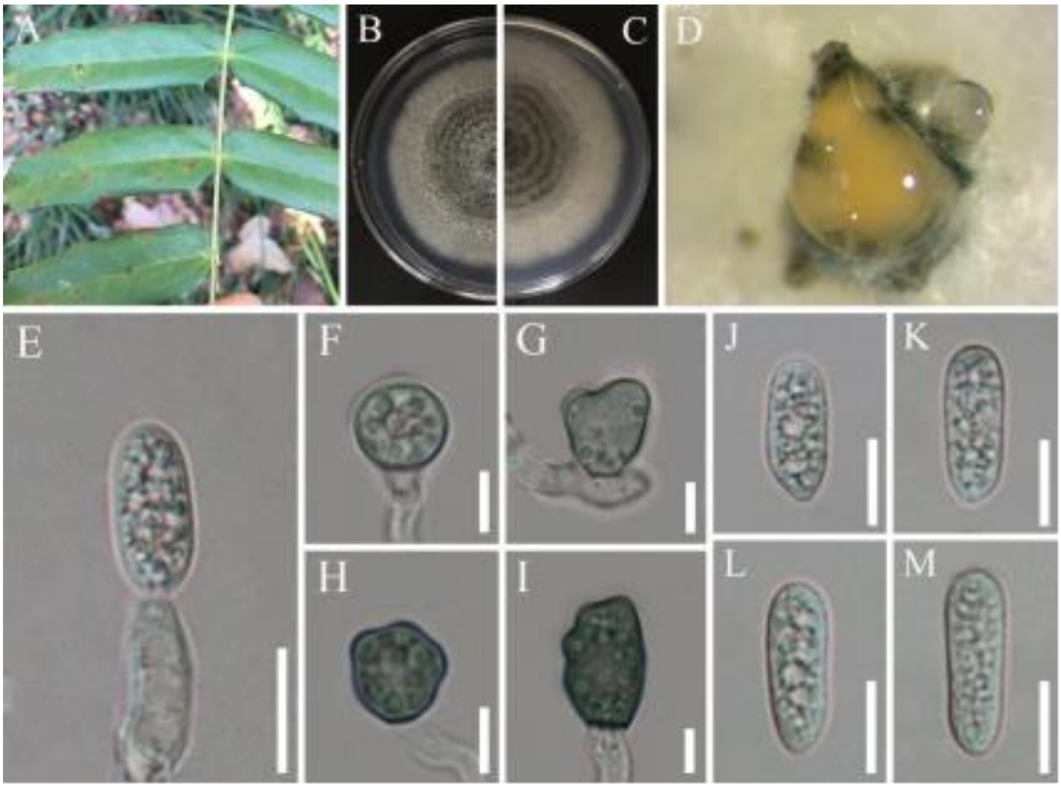


Figure 11 – *Colletotrichum karstii* (GUCC 12009). A Host. B, C Upper and Reverse view of the colony. D Conidiomata. E Conidiophores. F–I Appressoria. J–M Conidia. Scale bars: E, J–M = 10 µm, F–I = 5 µm.

The *Colletotrichum destructivum* species complex

Phylogenetic analyses

In the *C. destructivum* species complex, a total of 2,334 characters of nucleotides and gaps (ITS: 1–559, *gapdh*: 560–873, *chs-1*: 874–1,153, *his3*: 1,154–1,544, act: 1,545–1,811, *tub2*: 1,1812–2334) were included in the phylogenetic analysis. *Colletotrichum dematium* (CBS 125.25) and *C. fructi* (CBS 346.37) were selected as the outgroup taxa. The ML search revealed the best score of -7737.655. The best nucleotide substitution models were recommended by ModelFinder and used in the Bayesian analysis: K2P+I+G4 for ITS, K2P+I for *gapdh*, SYM+G4 for *chs-1*, *act* and *tub2* and HKY+F+G4 for *his*. Only one of our strains was grouped with the ex-type of *C. tabacum* (CPC 18945) in this species complex (Fig. 12).

Taxonomy

Colletotrichum tabacum Böning, Prakt. Bl. Pflanzenbau Pflanzen-schutz 10: 89 (1932) Fig. 13

Index Fungorum number: IF119597

Associated with spots on leaves of *Piper sarmentosum*. Sexual morph undetermined. Asexual morph on PDA (GUCC 12042). *Conidiomata* and *conidiophores* formed on a small cushion of hyaline to pale brown, angular cells. *Conidiophores* hyaline to pale brown, smooth-walled and septate, branched, to 81 µm long. *Conidiogenous cells* hyaline to pale brown, smooth-walled, cylindrical, 14.5–38.5 × 2.5–5.5 µm, collarette 0.5–1 µm long, periclinal thickening distinct. *Conidia* hyaline, mostly straight, narrowly cylindrical, smooth-walled, aseptate, with round ends, one of the ends sometimes very slightly bent to one side, 16–21 × 3.5–4.5 µm, mean ± SD = 18.3 ±

1.2 × 4.0 ± 0.3 µm, L/W ratio = 4.6. *Appressoria* solitary, pale to medium brown, smooth-walled, subglobose, to elliptical in outline, with an entire, crenate to undulate margin, 7–14 × 6–10 µm, mean ± SD = 9.2 ± 1.8 × 8.3 ± 1.2 µm, L/W ratio = 1.1.

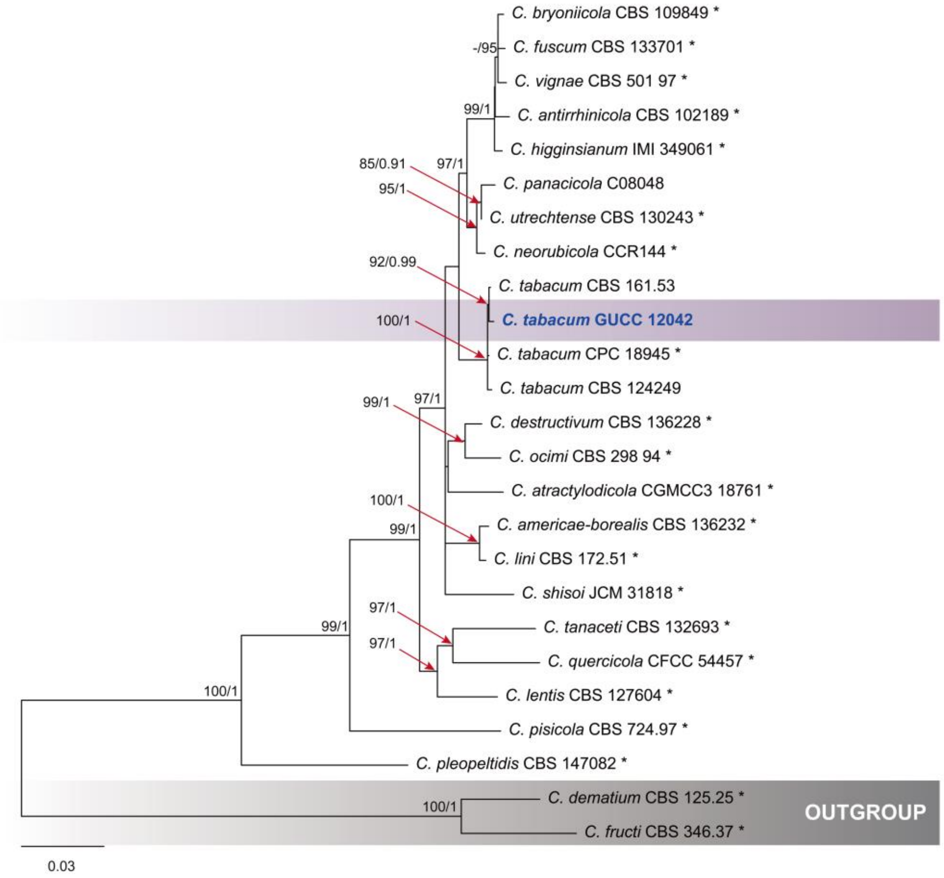


Figure 12 – Maximum likelihood tree of the *C. destructivum* species complex. *Colletotrichum dematium* (CBS 125.25) and *C. fructi* (CBS 346.37) were selected as outgroups. At the nodes, bootstrap support values for ML (≥ 70%) and BYPP (≥ 0.90) are displayed (ML/PP). Type species strains are denoted by "*". Newly generated sequences are in blue bold.

Culture characteristics – Colonies on PDA flat with entire margin; isabelline, buff to rosy buff, aerial mycelium lacking, reverse buff, vinaceous buff, hazel to pale olivaceous-grey, growth 70 mm in 7 d.

Material examined – China, Guangxi Province, Nanning City, Guangxi Medicinal Botanical Garden, on leaf spot of *Piper sarmentosum* (Piperaceae), 1 October 2017, Q. Zhang, (HGUP 22024), living culture GUCC 12042.

Notes – The phylogenetic analysis shows that the strain GUCC 12042 clusters with the ex-neotype strain of *Colletotrichum tabacum* (Fig. 12). Morphological characters of conidial dimensions from our collection (GUCC 12042) are similar to the neotype of *C. tabacum* which was designated by Damm et al. (2014). Hence, based on both morphology and phylogeny, we identify our collection as *C. tabacum*.

The *Colletotrichum dracaenophilum* species complex

Phylogenetic analyses

In the *C. dracaenophilum* species complex, a total of 2,251 characters of nucleotides and gaps (ITS: 1–542, *gapdh*: 543–831, *chs-1*: 832–1,106, *his3*: 1,107–1,501, act: 1,502–1,755, *tub2*: 1,756–

2,251) were included in the phylogenetic analysis. *Colletotrichum magnum* (CBS 519.97) and *C. merremiae* (CBS 124955) were selected as the outgroup taxa. The ML search revealed the best score of -7889.859. The best nucleotide substitution models were recommended by ModelFinder and used in the Bayesian analysis: K2P+I for ITS and *chs*, K2P+G4 for *gapdh*, HKY+F+G4 for *his*, *act*, and *tub2*. Our three isolates within the C. dracaenophilum species complex represent two novel taxa (Fig. 14).

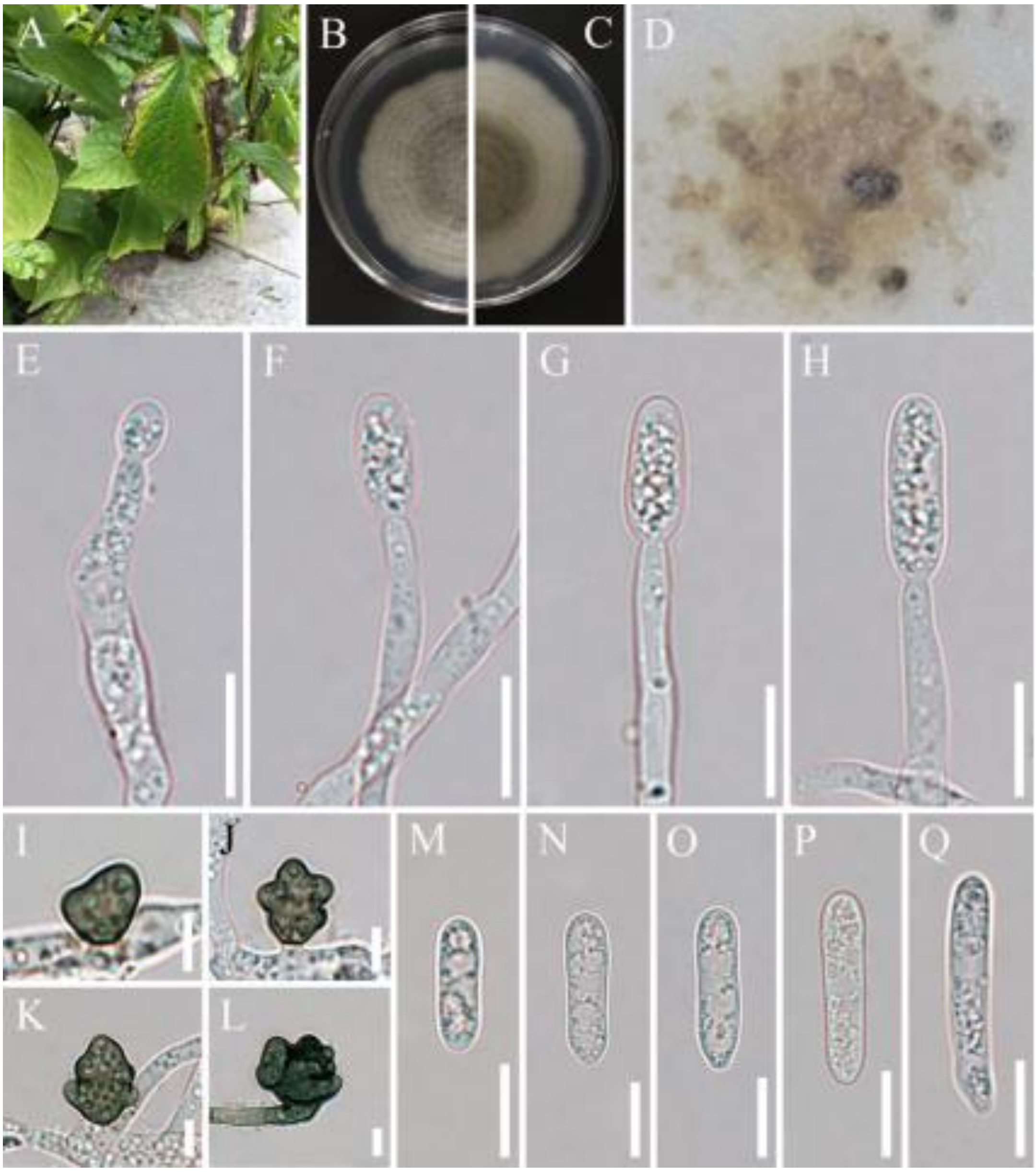


Figure 13 – *Colletotrichum tabacum* (GUCC 12042). A Host. B, C Upper and Reverse view of the colony. D Conidiomata. E–H Conidiophores. I–L Appressoria. M–Q Conidia. Scale bars: E–H, M–Q = 10 µm, I–L =5 µm.

Genealogical concordance phylogenetic species recognition analysis

The PHI test revealed that there is no significant recombination (P = 0.9137) between *C. cypericola* and its closely related taxa *C. buxi* (LC13873), *C. dracaenophilum* (CBS 118199), *C. yunnanense* (CBS 132135), and *C. sinuatum* (LC13874) (Fig. 15A). The *C. schefflerae* based on PHI test confirmed that there is no significant recombination (P = 1.0) between *C. schefflerae* and its closely related taxa *C. robustum* (CGMCC 3.16077), *C. tongrenense* (GMBC 0209), *C. excelsum-altitudinum* (CGMCC 3.15130), and *C. tropicicola* (BCC 38877) (Fig. 15B).

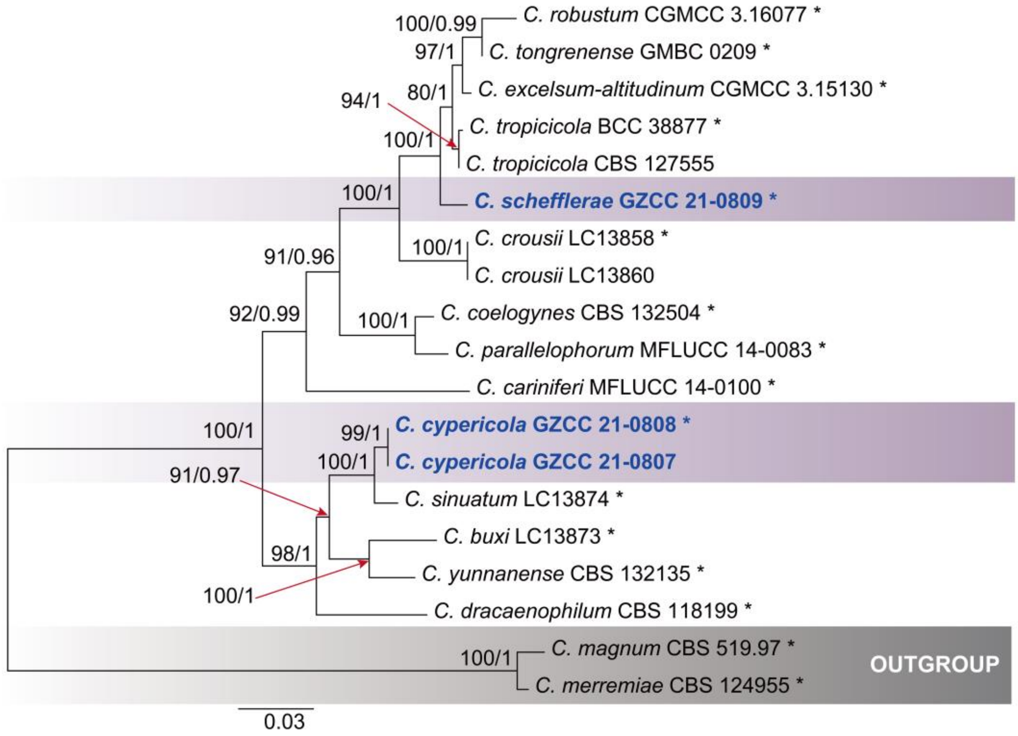


Figure 14 – Maximum likelihood tree of the *C. dracaenophilum* species complex. *Colletotrichum magnum* (CBS 519.97) and *C. merremiae* (CBS 124955) were selected as outgroups. At the nodes, bootstrap support values for ML (≥ 70%) and BYPP (≥ 0.90) are displayed (ML/PP). Type species strains are denoted by "*". Newly generated sequences are in blue bold.

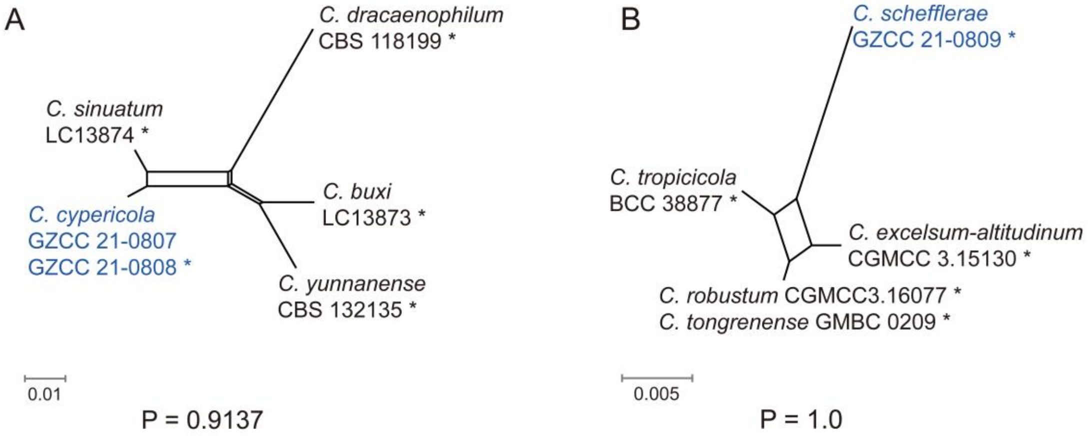


Figure 15 – The pairwise homoplasy index (PHI) tests of *C. dracaenophilum* species complex. A The PHI of *C. cypericola*. B *C. schefflerae*, and their phylogenetically related species, respectively.

Taxonomy

Colletotrichum cypericola Y. Feng, Q. Zhang, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 16

Index Fungorum number: IF559999; Facesoffungi numbers: FoF 13365

Etymology – Named after the host on which it occurs, *Cyperus rotundus*.

Holotype – GZAAS 21-0293

Saprobic on dried leaves of *Cyperus rotundus*. Sexual morph not observed. Asexual morph on the host. *Conidiomata* superficial or semi-immersed, solitary or scattered, subglobose, blackened. *Setae* and Conidiophores formed on pale brown, angular cells. *Setae* covering the Conidiomata, dark brown, unbranched, smooth-walled, septate. *Conidiophores* hyaline, smooth-walled, and simple. *Conidiogenous cells* hyaline, smooth-walled, cylindrical, 12−19 × 2−4 µm. *Conidia* hyaline, aseptate, smooth-walled, straight, cylindrical, both ends rounded, 11−18 × 3.5−6 µm, mean ± SD = 15.7 ± 1.6 × 4.6 ± 0.6 µm, L/W ratio = 3.4.

Culture characteristics – Flat with entire margin on PDA, surface white, aerial hyphae in centre and margin; reverse same colour; 40 mm in 7 d.

Material examined – China, Guizhou Province, Guiyang City, Daozhen autonomous County, on leaves of *Cyperus rotundus* (Cyperaceae), 15 August 2018, Y. Feng, DZ14 (GZAAS 21-0293, holotype); ex-type living culture GZCC 21-0807; *ibid.*, Zunyi City, Chishui County, 2 July 2018, GZAAS21-0294, living culture, GZCC21-0808.

Notes – In the phylogenetic tree, there is strong evidence that *Colletotrichum cypericola* forms a distinct clade (ML/BI = 100/1 in Fig. 14), and our strains are closely related to *C. sinuatum* in *C. dracaenophilum* species complex (Fig. 14). *Colletotrichum cypericola* can be distinguished from *C. sinuatum* based on ITS, *gapdh, chs-1, act,* and *tub2* loci (5/326 in ITS, 5/219 in gapdh, 2/205 in *chs-1*, 8/193 in *act* and 14/697 in *tub2*), and differs in producing shorter conidia (11−18 µm *vs.* 14.5−21 µm) (Liu et al. 2022). According to the PHI test of *Colletotrichum cypericola*, there was no significant recombination (P = 0.9137 > 0.05) within *C. cypericola* and its closely related species (Fig. 15A). We, therefore, introduce *C. cypericola* as a new species.

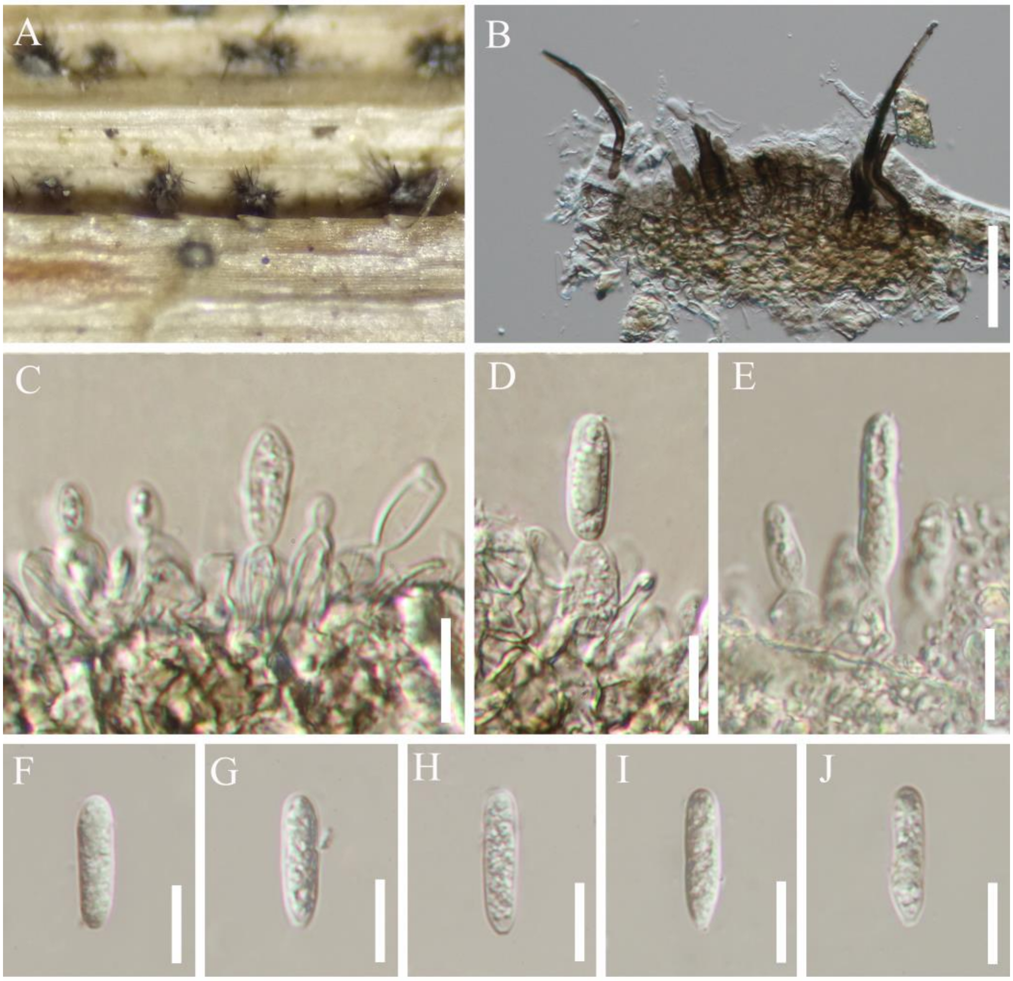


Figure 16 – *Colletotrichum cypericola* (GZAAS 21-0293). A Conidiomata. B Vertical section of acervulus. C−E Conidiophores. F–J Conidia. Scale bars: B = 20 µm, C–J = 10 µm.

Colletotrichum schefflerae Y. Feng, Q. Zhang, Yong Wang bis & K.D. Hyde, sp. nov.

Fig. 17

Index Fungorum number: IF900005; Facesoffungi numbers: FoF 13370

Etymology – Named after the host on which it occurs, *Schefflera heptaphylla*.

Holotype – GZAAS 21-0295

Saprobic on dried branches of *Schefflera heptaphylla*. Sexual morph not observed. Asexual morph on host. *Conidiomata* oval, semi-immersed. *Setae* not observed. *Conidiophores* hyaline, smooth-walled, septate, branched. *Conidiogenous cells* hyaline, smooth-walled, cylindrical, 18−28 × 3−6 µm. *Conidia* hyaline, smooth-walled, aseptate, straight, cylindrical, both ends rounded, 13−19(−22) × 5−7 µm, mean ± SD = 15.6 ± 1.6 × 6 ± 0.4 µm, L/W ratio = 2.6.

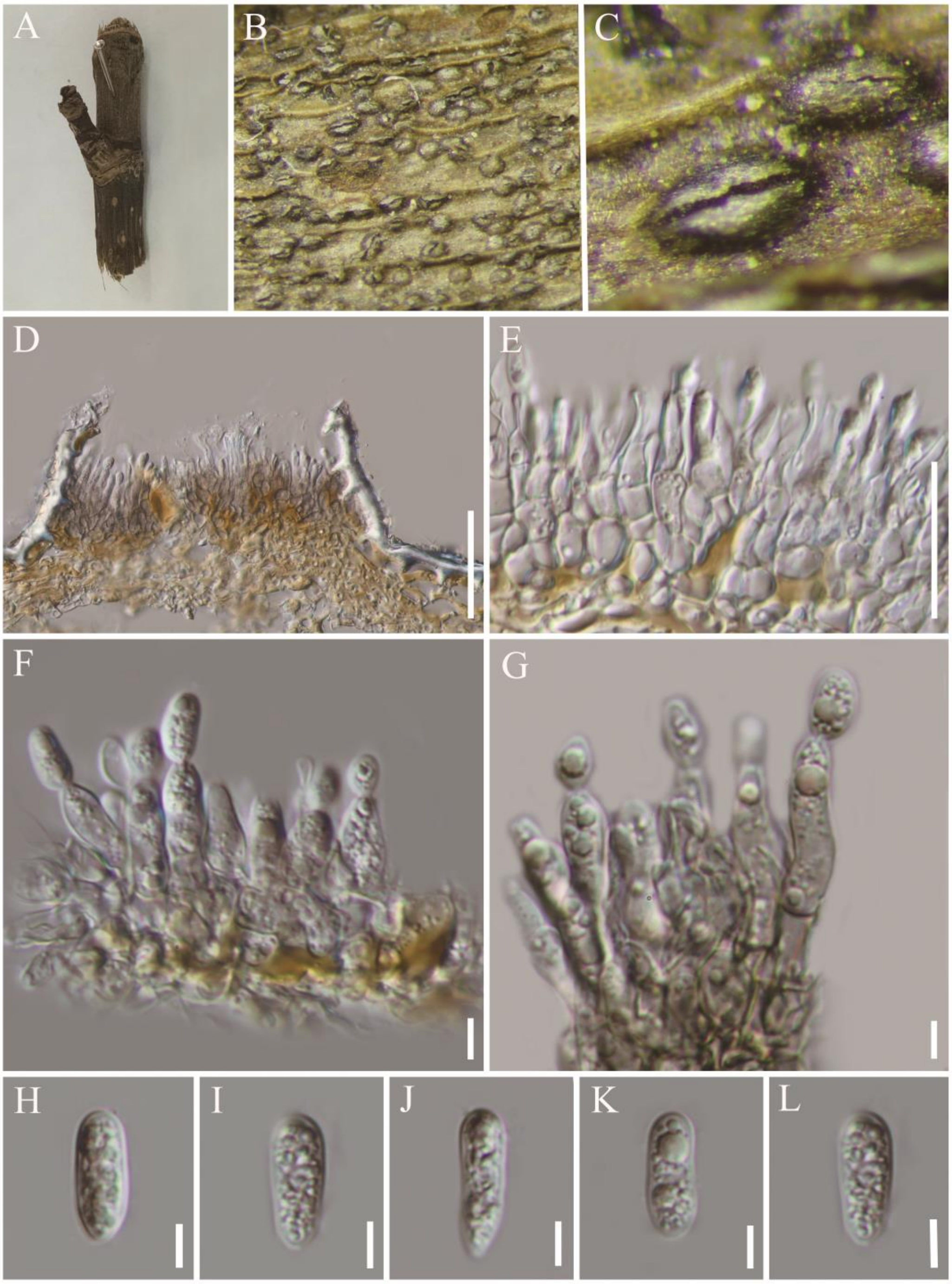


Figure 17 – *Colletotrichum schefflerae* (GZAAS 21-0295). A Host. B–C Conidiomata. D Vertical section of pycnidium. E Peridium. F−G Conidiophores. H–L Conidia. Scale bars: D = 50 µm, E= 25 µm, F–L = 5 µm.

Culture characteristics – Colonies on PDA flat with entire margin, surface white, aerial hyphae lack in centre and margin; reverse same colour; 50 mm in 7 d.

Material examined – China, Guizhou Province, Guiyang City, Huaxi Industrial Park, on branches of *Schefflera heptaphylla* (Araliaceae), 28 December 2017, Y. Feng, H100-1 (GZAAS 21-0295, holotype); ex-type living culture GZCC 21-0809.

Notes – In a BLASTn search, the closest match of the ITS sequences with 99.14% similarity was *C. tongrenense* (GZU_TRJ1_37). The closest match of the *chs* sequences with 100% similarity was *C. tropicicola* (BCC 38877). The closest match of the *act* sequences with 97.01% similarity was *C. tongrenense* (GZU_TRJ1_37). The closest match of the *gapdh* sequences with 95.09% similarity was *C. tongrenense* (GZU_TRJ1_37). In the phylogenetic analysis, *C. schefflerae* (GZCC 21-0809) is closely related to *C. tropicicola*, *C. excelsum-altitudinum*, *C. tongrenense* and *C. robustum* in *C. dracaenophilum* species complex with 100% ML and 1 BYPP bootstrap support (Fig. 14). *Colletotrichum schefflerae* appears to be most closely related to *C. tropicicola*. *Colletotrichum schefflerae* be distinguished from *C. tropicicola* (3/347 bp in ITS, 14/283 bp in gapdh, and 9/234 bp in act). Morphologically, *C. schefflerae* differs from *C. tropicicola* in longer conidia (13−22 *vs.* 15−19 µm) (Noireung et al. 2012), differs from *C. excelsum-altitudinum* in longer conidia (13−22 *vs.* 13–16.5 µm) (Tao et al. 2013), differs from *C. tongrenense* in longer conidia (13−22 *vs.* 11–14 µm) (Zhou et al. 2019) and differs from *C. robustum* in longer conidia (13−22 *vs.* 12.5–16 µm) (Yu et al. 2022). The PHI test on *C. schefflerae* revealed that there is no significant recombination (P = 1.0 > 0.05) between *C. schefflerae* and its closely related taxa (Fig. 15B). We, therefore, introduce *C. schefflerae* as a new species based on phylogenetic evidence.

The *Colletotrichum gloeosporioides* species complex

Phylogenetic analyses

In the *C. gloeosporioides* species complex, the alignment is comprised of 2024 characters (ITS: 1–540, *gapdh*: 541–835, *chs-1*: 836–1,080, act: 1,081–1,343, *tub2*: 1,344–2,023, including alignment gaps). *Colletotrichum arecacearum* (LC13850 and LC13851), *C. pyrifoliae* (CGMCC 3.18902 and PAFQ22a) were served as outgroup taxa. The ML search revealed the best score of -13176.513. The best nucleotide substitution models were recommended by ModelFinder and used in the Bayesian analysis: SYM+I+G4 for ITS, K2P+I+G4 for *chs-1*, and HKY+F+G4 for *gapdh*, *act* and *tub2*. In this phylogenetic tree (Fig. 18), our 75 *Colletotrichum* isolates include four new species and seven known species.

Genealogical concordance phylogenetic species recognition analysis

The pairwise homoplasy index (PHI) test revealed that there is no significant recombination (P = 0.1636), between *C. castaneae* and its closely related taxa *C. yulongense* (CFCC 50818), *C. subhenanense* (CGMCC3.16073), *C. henanense* (CGMCC 3.17354) and *C. chiangmaiense* (MFLUCC 18-0945) (Fig. 19A). Additionally, there is no significant recombination (P = 0.2042) between *C. gardeniae* and its closely related taxa *C. wuxiense* (CGMCC 3.17894), *C. temperatum* (CBS 133122), *C. camelliae* (ICMP 10646 and CGMCC 3.14925), and *C. analogum* (GMCC 3.16079 and YMF1_07327) (Fig. 19B). Similar result also occurred in *C. kunmingense* (P = 0.2974) (Fig. 19C) and *C. ligustri* (P = 0.6342) (Fig. 19D), indicating there is no significant recombination between them and their closely related species.

Taxonomy

Colletotrichum castaneae Y.Q. Yang, Q. Zhang, K.D. Hyde & Yong Wang bis, sp. nov.

Fig. 20

Index Fungorum number: IF559998; Facesoffungi numbers: FoF 05681

Etymology – castaneae, in reference to the host *Castanea mollissima* Bl., from which the fungus was isolated.

Holotype – HGUP 22097

Associated with spots on leaves of *Castanea mollissima*. Sexual morph not observed. Asexual morph on SNA (GUCC 12178). *Vegetative hyphae* 1.5−6.5 µm diam, hyaline to medium brown, branched, septate. *Conidiomata*, irregular, orange. *Setae* not observed. *Conidiophores* hyaline, simple. *Conidiogenous cells* hyaline, ampulliform to obclavate, 5.5–26 × 2−4.5 µm. *Conidia* hyaline, aseptate, smooth-walled, straight, cylindrical, the apex and base rounded, 14−19 × 4−5.5 µm, mean ± SD = 17.2 ± 1.1 × 5 ± 0.3 µm, L/W ratio = 3.4. *Appressoria* solitary, smooth-walled, pale brown, elliptical to clavate in outline, with an entire, undulate margin, 9−20 × 5.5−9 µm, mean ± SD = 13.6 ± 3.2 × 7.1 ± 0.8 µm, L/W ratio = 1.9.

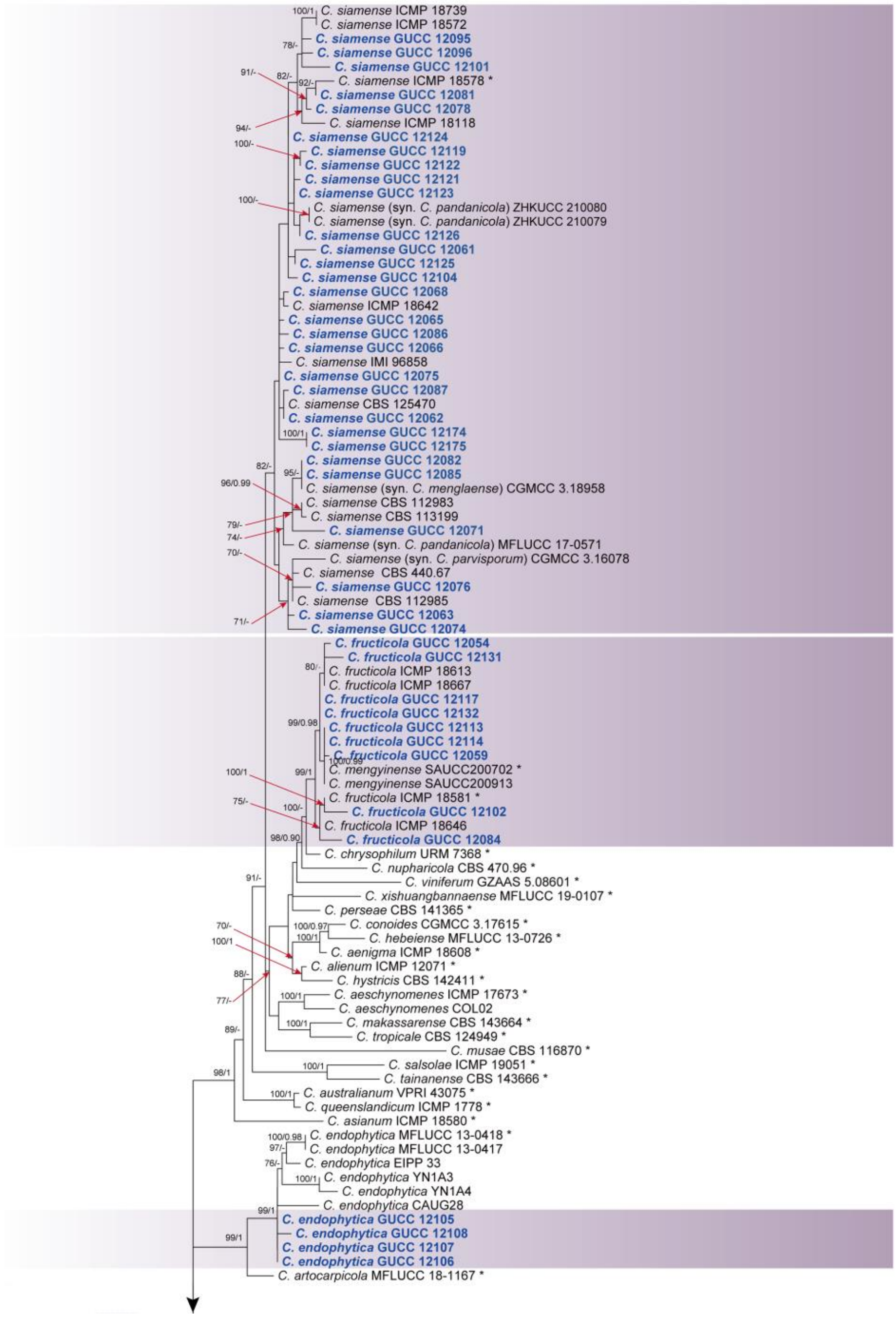


Figure 18 – Maximum likelihood tree of the *C. gloeosporioides* species complex. *Colletotrichum arecacearum* (LC 13850 and LC13851) and *C. pyrifoliae* (CGMCC 3.18902 and PAFQ22a) were selected as the outgroup. At the nodes, bootstrap support values for ML (≥ 70%) and BYPP (≥ 0.90) are displayed (ML/PP). Type species strains are denoted by "*". Newly generated sequences are in blue bold.

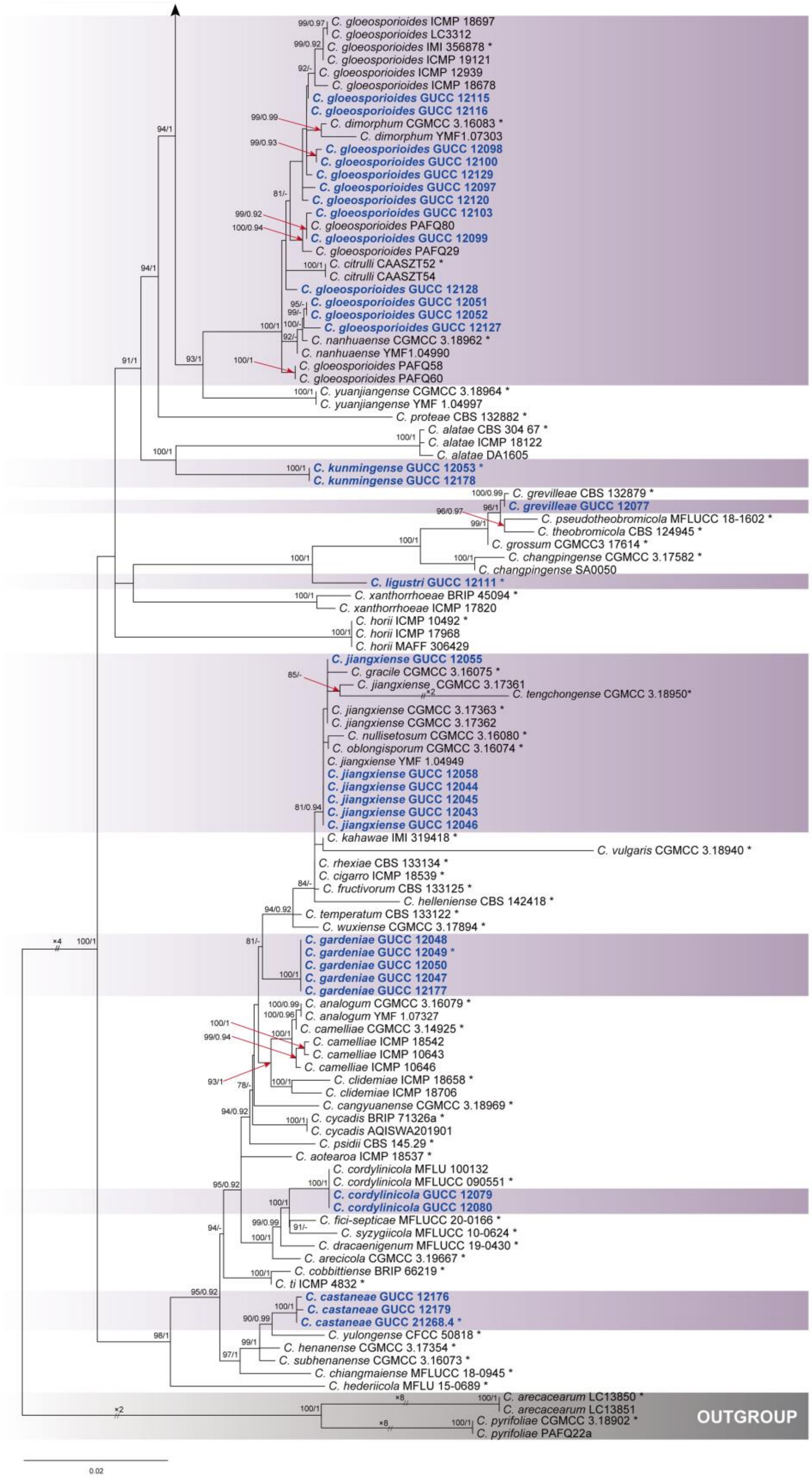


Figure 18 – Continued.

Culture characteristics – Undulate edge and flat, white to pale luteous, aerial mycelium sparse, in reverse pale luteous towards the margin and pale orange towards the centre. Colonies on PDA 65 mm diam in 7 d.

Material examined – China, Guizhou Province, Qiannan Autonomous Prefecture, Wengan County, on leaf spot of *Castanea mollissima* (Fagaceae), 15 May 2021, Y. Q. Yang, (HGUP 21268, holotype); ex-type living culture GUCC 21268.4; *ibid*., (HGUP 22099), living culture GUCC 12176, GUCC 12179.

Note – *Colletotrichum castaneae* resides within the *C. gloeosporioides* species complex and is closely related to *C. yulongense* with good support (ML/BI: 90/0.99, Fig. 18). It be distinguished from *C. yulongense* (6/212 in *gapdh*, 2/235 in act and 5/400 in tub), and produces longer conidia (14−19 µm *vs.* 11−13 µm) and larger appressoria (9−20 × 5.5−9 µm *vs.* 10−16 × 5−7 µm) (Wang et al. 2019). As determined by the PHI test, *C. castaneae* and its closely related taxa have no significant recombination (P = 0.1636 > 0.05, Fig. 19A). Therefore, we introduce *C. castaneae* as a new species.

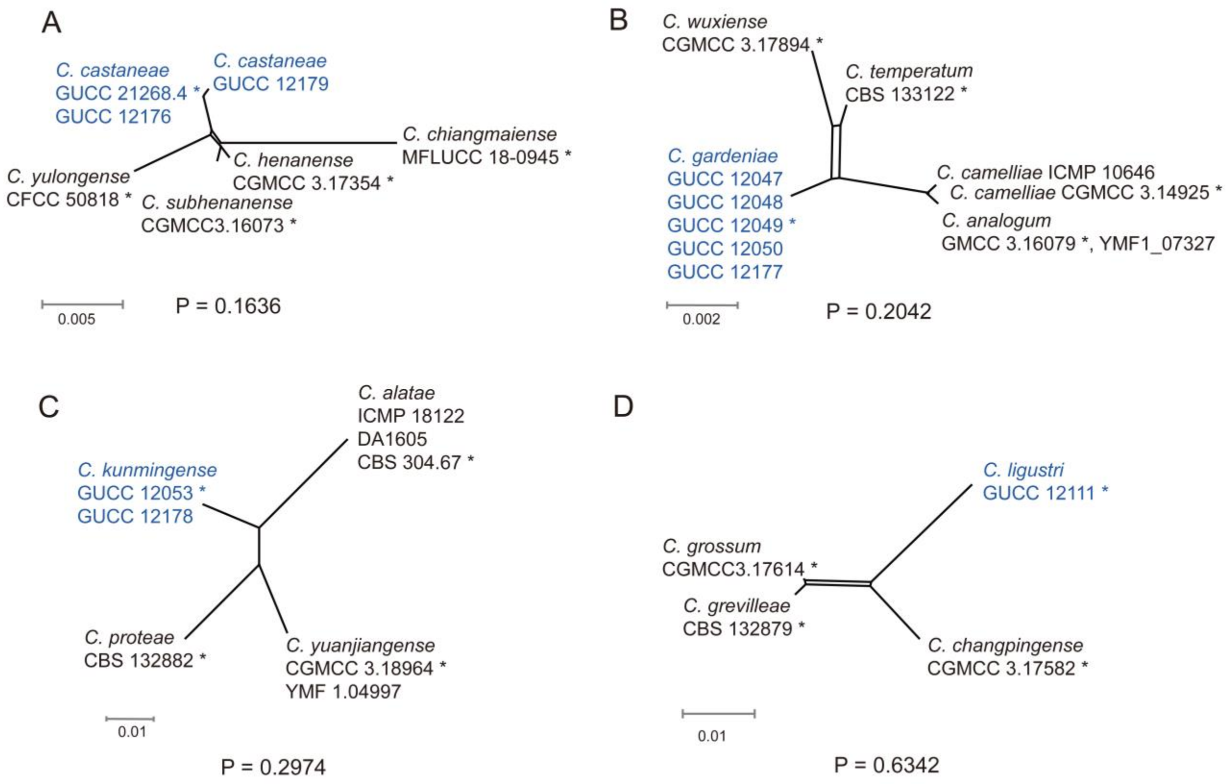


Figure 19 – The pairwise homoplasy index (PHI) tests of *C. gloeosporioides* species complex. A The PHI of *C. castaneae*. B *C. gardenia*. C *C. kunmingense*. D *C. ligustri*, and their phylogenetically related species, respectively.

Colletotrichum cordylinicola Phouliv., L. Cai & K.D. Hyde, Mycotaxon 114: 251 (2011)

Fig. 21

Index Fungorum number: IF518577

Associated with spots on leaves of *Cordyline fruticose*. Sexual morph not observed. Asexual state on PDA (GUCC 12079). *Vegetative hyphae* 2.5−4 µm diam, hyaline, smooth-walled, septate, branched. *Conidiomata*, irregular, orange. *Setae* not observed. *Conidiophores* hyaline, smooth-walled, septate, branched, to 34 µm long. *Conidiogenous cells* hyaline to pale brown, smooth-walled, cylindrical, sometimes 10−27 × 2.5−5.5 µm, opening 1.5−3 µm diam, collarette 0.5−1 µm long, periclinal thickening distinct. *Conidia* hyaline, smooth-walled, aseptate, straight, cylindrical, the apex and base rounded, with a prominent hilum, 13−18.5 × 5−7 µm, mean ± SD = 15.6 ± 1.2 × 6 ± 0.6 µm, L/W ratio = 2.6. *Appressoria* solitary, pale to medium brown, smooth-walled, aseptate, 6−11 × 5−9.5 µm, mean ± SD = 8 ± 1.9 × 6.3 ± 1.1 µm, L/W ratio = 1.27.

Culture characteristics – Colonies on PDA flat with entire margin, white, in the centre vinaceous buff due to sporulation and partly covert with short white aerial mycelium; reverse vinaceous buff, growth 51 mm in 7 d.

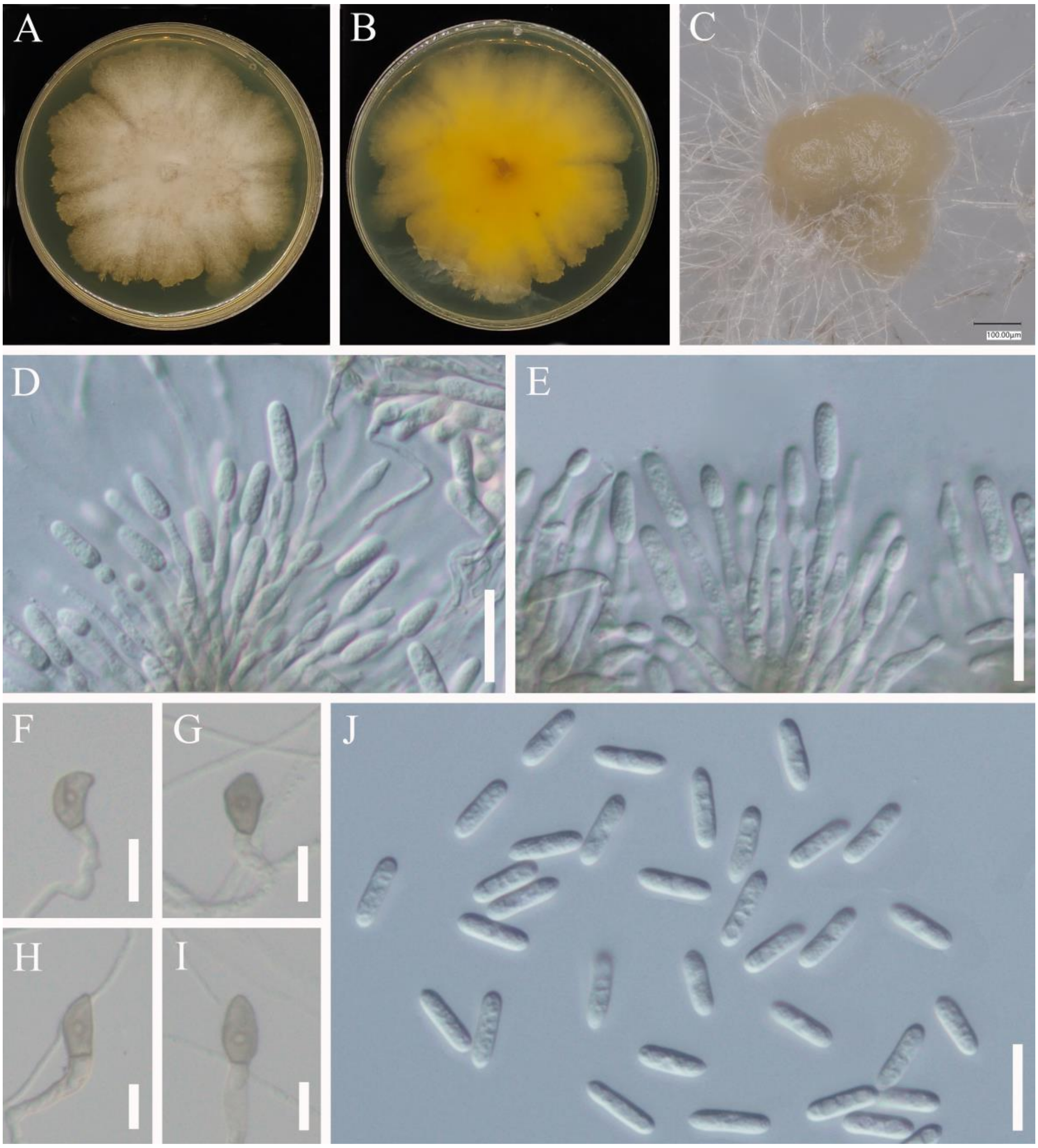


Figure 20 – *Colletotrichum castaneae* (GUCC 12178). A, B Upper and Reverse view of the colony. C Conidiomata. D−E Conidiophores. F−I Appressoria. J Conidia. Scale bars: D−E, J = 20 µm, F−I = 10 µm.

Material examined – China, Yunnan Province, Jinghong City, Mengyang Town, Xishuangbanna National Nature Reserve, on leaf spot of *Cordyline fruticose* (Liliaceae), 10 October 2018, Y. Wang, (HGUP 22025), living culture GUCC 12079, GUCC 12080.

Notes – Two isolates (GUCC 12079 and GUCC 12080) clustered with *C. cordylinicola* (MFLUCC 090551, MFLU 100132) in the multiple loci phylogenetic analysis (Fig. 18). The morphologies of our collection (GUCC 12079) have similar asexual morph to the holotype except the conidia of GUCC 12079 are wider than *C. cordylinicola* (5−7 *vs.* 4−5) (Phoulivong et al. 2010). On the basis of both morphology and phylogenetic analyses, we propose our collections as *C. cordylinicola*.

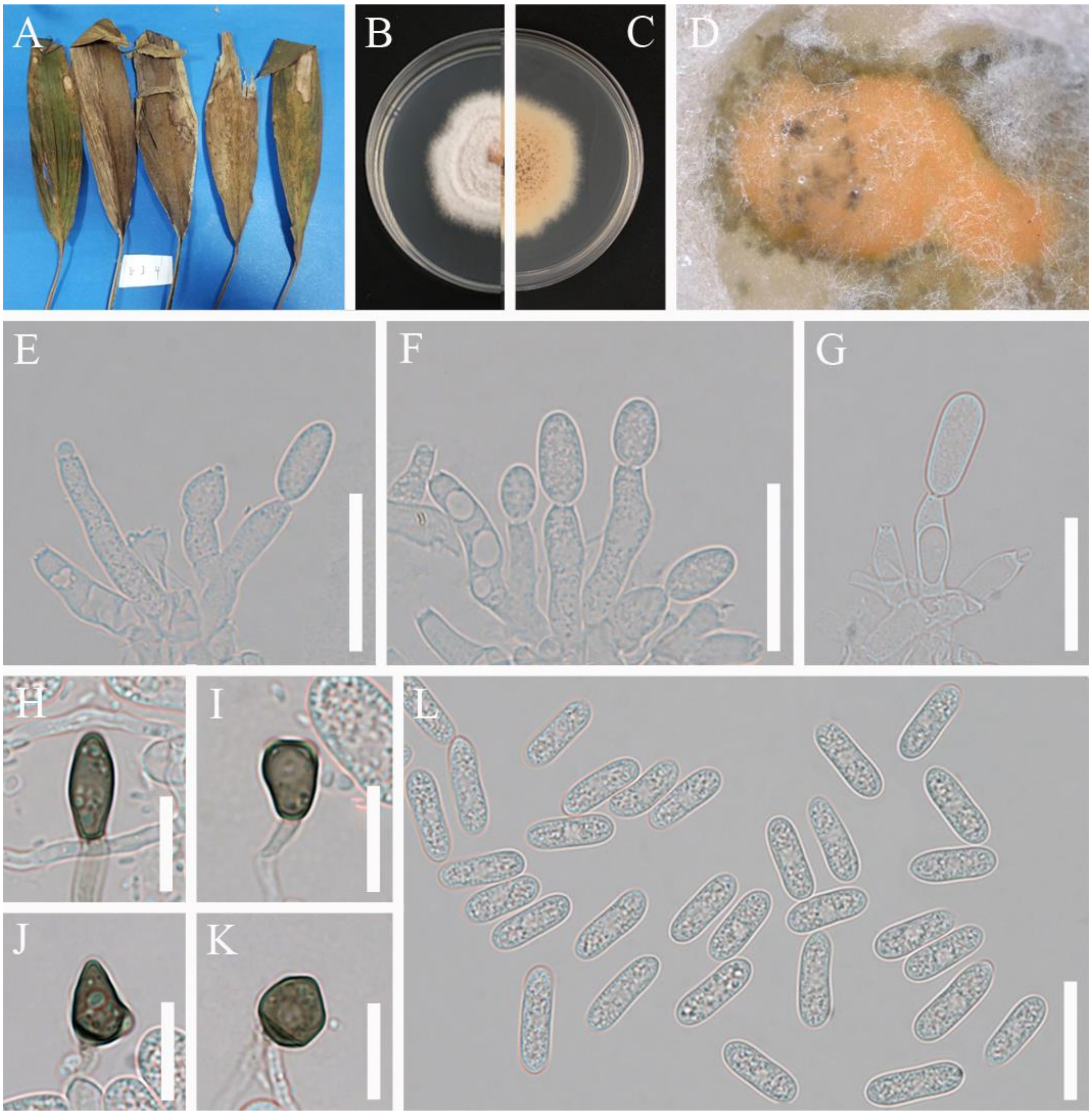


Figure 21 – *Colletotrichum cordylinicola* (GUCC 12079). A Host. B, C Upper and Reverse view of the colony. D Conidiomata. E−G Conidiophores. H−K Appressoria. L Conidia. Scale bars: E−G, L = 20 µm, H−K = 10 µm.

Colletotrichum endopyhtica Manamgoda, Udayanga, L. Cai & K.D. Hyde, Fungal Diversity 61 (1): 110 (2013) Fig. 22

Index Fungorum number: IF565248

Associated with spots on leaves of undetermined host. Sexual morph not observed. Asexual morph on SNA (GUCC 12108). *Vegetative hyphae* 3−7 µm diam, hyaline to medium brown, smooth-walled, septate, branched. *Conidiomata*, irregular, milk orange. *Setae* not observed. *Conidiophores* formed on a cushion of pale brown, hyaline, smooth-walled, branched. *Conidiogenous cells are* hyaline, smooth–walled, cylindrical, 8−21.5 × 3−4.5 µm, collarette 0.5−1.5 µm long, periclinal thickening observed. *Conidia* hyaline, smooth-walled, aseptate, straight, cylindrical, the apex and base rounded, 14−18 × 5.5−7.5 µm, mean ± SD = 16 ± 0.7× 6.7 ± 0.5 µm, L/W ratio = 2.4. *Appressoria* solitary, pale to medium brown, smooth-walled, subglobose to ellipsoidal in outline, with an entire margin, 6−9 × 5.5−7 µm, mean ± SD = 7.7 ± 0.9 × 6.4 ± 0.4 µm, L/W ratio = 1.3.

Culture characteristics – Colonies on PDA flat with entire margin, white to vinaceous buff; reverse rosy buff, growth 64 mm in 7 d.

Material examined – China, Guizhou Province, Guiyang City, Huaxi Road, on leaf spot of the unidentified host, 17 October 2019, Y. Wang, (HGUP 22086), GUCC 12105, GUCC 12106, GUCC 12107, GUCC 12108.

Notes – As a result of the multi-locus phylogenetic analyses, our strains (GUCC 12108, GUCC 12105, GUCC 12106, GUCC 12107) grouped with the ex-type strain of *C. endopyhtica* MFLUCC 13-0418 (Fig. 18), which was described as an endophyte from grass (Manamgoda et al. 2013). The morphology of GUCC 12108 is similar to the type of *C. endopyhtica*, except our collection has wider conidia (5.5−7.5 *vs.* 3.6−5.5) (Manamgoda et al. 2013). Hence, we propose our collections as *C. endopyhtica*.

Figure 22 − *Colletotrichum endopyhtica* (GUCC 12108). A, B Upper and Reverse view of the colony. C Conidiomata. D−F Conidiophores. G−J Appressoria. K Conidia. Scale bars: D−F, K = 10 µm, G−J = 5 µm.

Colletotrichum fructicola Prihast., L. Cai & K.D. Hyde, in Prihastuti, Cai, Chen, McKenzie & Hyde, Fungal Diversity 39: 96 (2009) Fig. 23

Index Fungorum number: IF515409

Associated with spots on leaves of *Camellia sinensis*, *Curcuma phaeocaulis*, *Ilex chinensis*, *Ligustrum lucidum*, and *Zingiber officinale*. Sexual morph on PDA (GUCC 12117). *Vegetative hyphae* 1.4–8.6 µm diam, hyaline to pale brown, smooth-walled, septate, branched. *Ascomata* perithecia, clustered, superficial, globose to obpyriform, covered by sparse white or grey aerial mycelium, medium to dark brown, surrounded by pale brown, smooth-walled hyphae. *Ascogenous* hyphae are hyaline, smooth, and delicate. *Asci* unitunicate, 8–spored, cylindrical, somewhat acute ape, smooth-walled, 49–87.5 × 9–16 µm. *Ascospores* uni– or biseriately arranged, aseptate, hyaline, smooth-walled, elliptical, allantoid to fusiform, slightly curved, with both end rounded, 12.5–22.5 × 4–6 µm, mean ± SD = 16.2 ± 2 × 4.8 ± 0.5 µm, L/W ratio = 3.4. Asexual morph not observed.

Culture characteristics – Colonies on PDA flat pale olivaceous-grey to olivaceous-grey, merging to olivaceous black in the centre, with copious floccose to woolly aerial mycelium, reverse same colour, growth 68 mm in 5 d.

Material examined – China, Guizhou Province, Guiyang City, Huaxi Road, on leaf spot of *Zingiber officinale* (Zingiberaceae), 6 September 2017, Q. Zhang, (HGUP 22079), living culture GUCC 12054; *ibid*., on leaf spot of *Ligustrum lucidum* (Oleaceae), 18 September 2017, (HGUP 22026), living culture GUCC 12059; *ibid*., Yunnan Province, Jinghong City, Mengyang Town, Xishuangbanna National Nature Reserve, on leaf spot of the unidentified host, 10 October 2018, Y.

Wang, (HGUP 22027), living culture GUCC 12084; *ibid*., Guangxi Province, Nanning City, Guangxi Medicinal Botanical Garden, on leaf spot of *Curcuma phaeocaulis* (Zingiberaceae), 1 October 2017, (HGUP 22028), living culture GUCC 12102; *ibid*., on leaf spot of *Ilex chinensis* (Aquifoliaceae), 25 October 2017, (HGUP 22029), living culture GUCC 12113, GUCC 12114, GUCC 12117; *ibid*, Duyun City, on leaf spot of *Camellia sinensis* (Theaceae), 5 July 2017, Y. Wang, (HGUP 22031), living culture GUCC 12131, GUCC 12132.

Notes – The phylogenetic analysis shows that our strains (GUCC 12059, GUCC 12083, GUCC 12102, GUCC 12113, GUCC 12114, GUCC 12117, GUCC 12131, GUCC 12132) clustered with *C. fructicola* (Fig. 18). The morphology of asci and ascospores dimensions from of our collection (GUCC 12117) are larger than the holotype of *C. fructicola* (asci: 49–87.5 × 8.9–15.8 *vs.* 30–55 × 6.5–8.5, ascospores: 12.5–22.5 × 3.8–6 *vs.* 9–14 × 3–4) which was collected from the berry of *Coffea arabica* in Thailand (Prihastuti et al. 2009). We suggest our collection as *C. fructicola* based on phylogenetic analysis.

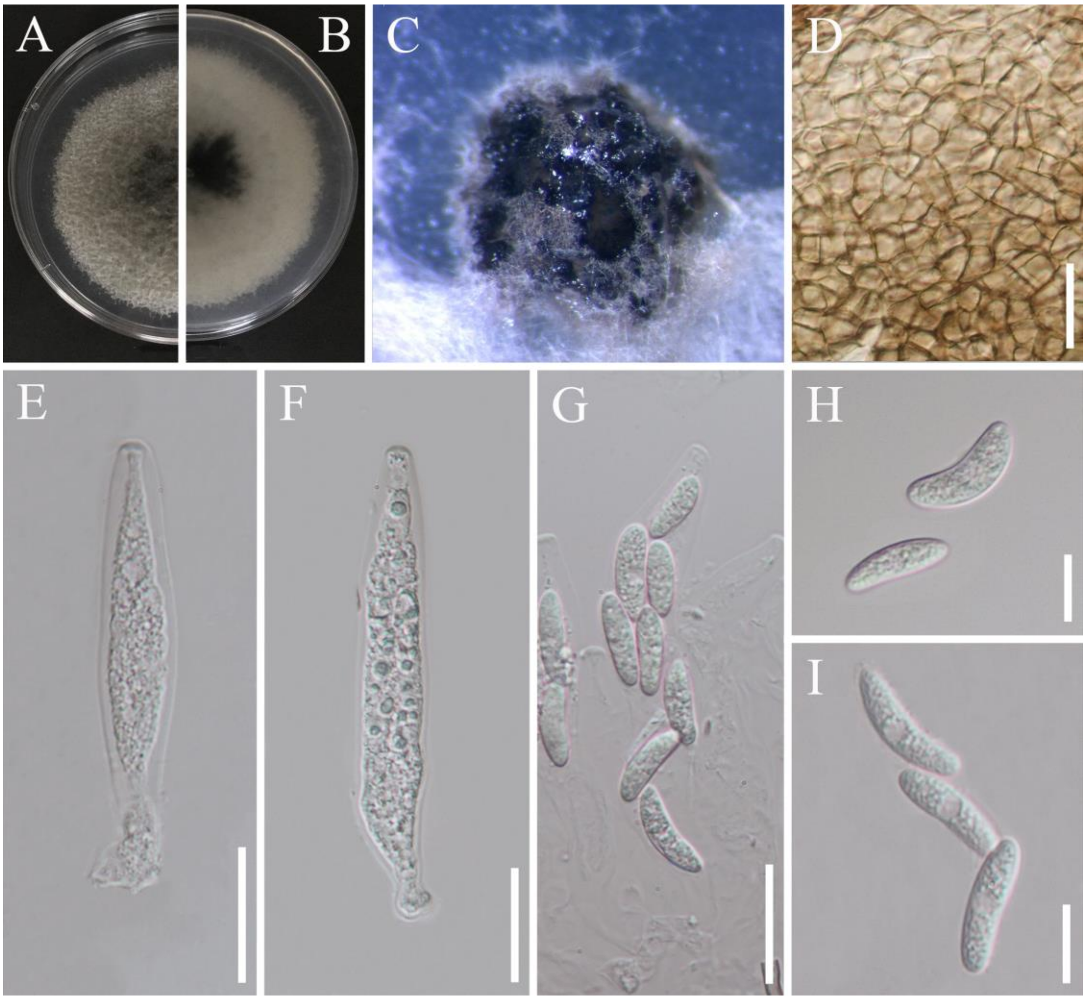


Figure 23 – *Colletotrichum fructicola* (GUCC 12117). A, B Upper and Reverse view of the colony. C Ascomata. D Outer surface of Peridium. E–G Asci. H–J. Ascospore. Scale bars: D–G = 20 µm, H–I = 10 µm.

Colletotrichum gardeniae Q. Zhang, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 24

Index Fungorum number: IF900001; Facesoffungi numbers: FoF 13366

Etymology – Named after the host on which it occurs, *Gardenia jasminoides* Ellis.

Holotype – HGUP 22032

Associated with spots on leaves of *Gardenia jasminoides*. Sexual morph not observed. Asexual morph on PDA (GUCC 12049). *Vegetative hyphae* hyaline to medium brown, 2−5.5 µm diam, septate, branched, smooth-walled. *Conidiomata*, irregular, milk orange. *Setae* not observed. *Conidiophores* hyaline, smooth-walled, and simple. *Conidiogenous cells* hyaline, cylindrical, smooth-walled, 14−25 × 3−4.5 µm. *Conidia* hyaline, aseptate, straight, smooth-walled, cylindrical, the apex and base rounded, with a prominent hilum, 14−19 × 5−7 µm, mean ± SD = 16.2 ± 0.8 × 6.1 ± 0.4 µm, L/W ratio = 2.7. *Appressoria* solitary, pale to medium brown, elliptical to clavate in outline, with an entire, undulate margin, smooth-walled, 9−13.5 × 6−11 µm, mean ± SD = 11.1 ± 1.4 × 7.8 ± 1.3 µm, L/W ratio = 1.4.

Culture characteristics –Flat with entire margin on PDA, white to vinaceous buff, orange due to sporulation in the centre and with short white aerial mycelium partly covert; rosy buff in reverse, growth 72 mm in 7 d.

Material examined – China, Yunnan Province, Kunming City, Kunming Botanical Garden, on leaf spot of *Gardenia jasminoides* (Rubiaceae), 15 January 2018, Q. Zhang, (HGUP 22032, holotype); ex-type living culture GUCC 12049; *ibid.*, (HGUP 22098), living culture GUCC 12047, GUCC 12048, GUCC 12050, GUCC 12177.

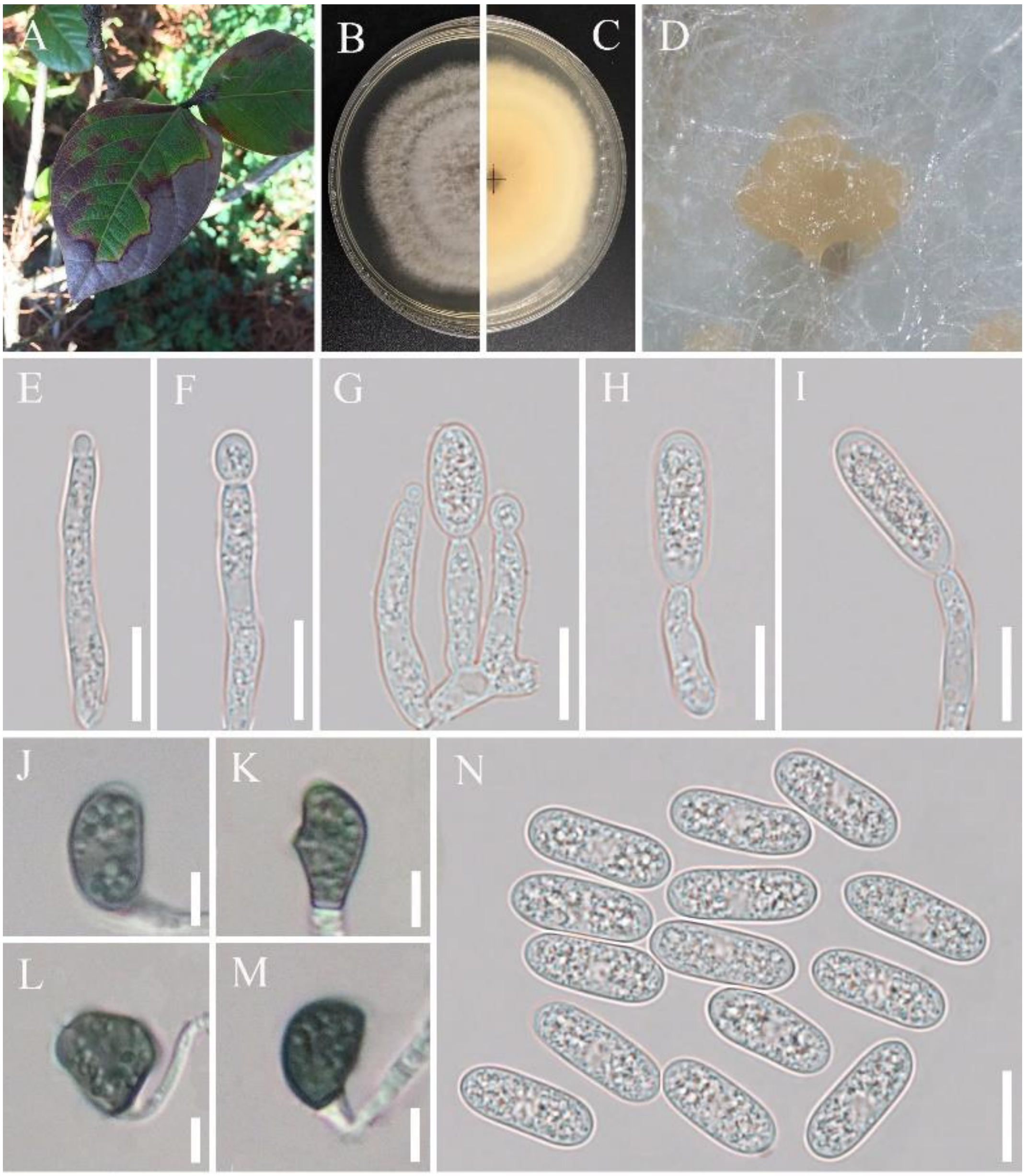


Figure 24 – *Colletotrichum gardeniae* (GUCC 12049). A Host. B, C Upper and Reverse view of the colony. D Conidiomata. E−I Conidiophores. J−M Appressoria. N Conidia. Scale bars: E−I, N = 10 µm, J−M = 5 µm.

Note – *Colletotrichum gardeniae* is phylogenetically closely related to *C. camelliae* in the *C. gloeosporioides* species complex (Fig. 18). The morphological features of conidia of *C. gardeniae* on PDA are generally similar to those of *C. camelliae* which was reported to be associated with tea (*Camellia sinensis*) from Sri Lanka (Liu et al. 2015, Wang et al. 2016). However, *C. gardeniae* differs from the ex-type strain of *C. camelliae* by 7 bp in *gapdh*, 5 bp in ITS, 4 bp in *tub2*, 2 bp in *act*. *Colletotrichum gardeniae* formed a distinct clade in the phylogenomic tree (ML/BI = 81/-, Fig. 18). There is no significant recombination in the PHI test (P = 0.2042 > 0.05) between C. *gardeniae* and its closely related taxa (Fig. 19B). We, therefore, introduce *C. gardeniae* as a new taxon.

Colletotrichum gloeosporioides (Penz.) Penz. & Sacc., Atti Inst. Veneto Sci. lett., ed Arti, Sér. 6 2(5): 670 (1884) Fig. 25

Index Fungorum number: IF158410

Associated with spots on leaves of *Achyranthes bidentata*, *Cycas bifida*, *Fatsia japonica*, *Ilex chinensis*, *Rhododendron simsii*, *Spatholobus suberectus* and *Viburnum dilatatum*. Sexual morph not observed. Asexual morph on PDA (GUCC 12127). *Vegetative hyphae* 1.5–2.5 µm diam, hyaline to medium brown, smooth-walled, septate, branched. *Conidiomata*, sub-globose, dark orange. *Setae* not observed. *Conidiophores* formed on a cushion of pale brown, hyaline, smooth-walled, branched. *Conidiogenous cells* hyaline, smooth-walled, cylindrical, 11–26.5 × 3–6.5 µm, collarette 0.5–1.5 µm long, periclinal thickening observed. *Conidia* hyaline, smooth-walled, aseptate, straight, clavate to narrowly cylindrical, the apex rounded, the base rounded or truncate, 14.5–20 × 5–7 µm, mean ± SD = 17.2 ± 1.4 × 5.9 ± 0.5 µm, L/W ratio = 2.9. *Appressoria* single, medium to dark brown, smooth-walled, subcircular, elliptical or irregular in outline, with an undulate to lobate margin, 7–16 × 6.5–9 µm, mean ± SD = 10 ± 2.1 × 7.6 ± 0.7 µm, L/W ratio = 1.3.

Culture characteristics – Colonies on PDA with undulate margin, in the centre white to pale grey aerial mycelium, medium grey aerial mycelium in the margin; reverse same colour, growth 83 mm in 7 d.

Material examined – China, Yunan Province, Kunming City, Kunming Botanical Garden, on leaf spot of *Rhododendron simsii* (Ericaceae), 15 January 2018, Q. Zhang, (HGUP 22033), living culture GUCC 12051, GUCC 12052; *ibid*., Guangxi Province, Nanning City, Guangxi Medicinal Botanical Garden, on leaf spot of *Cycas bifida* (Cycadaceae), 1 October 2017, (HGUP 22036), living culture GUCC 12097; *ibid*., Jinghong City, Mengyang Town, Xishuangbanna National Nature Reserve, on leaf spot of undetermined host species, 10 October 2018, Y. Wang, (HGUP 22037) living culture GUCC 12098, GUCC 12099, GUCC 12100, GUCC 12103; *ibid*., Guizhou Province, Guiyang City, Huaxi Road, on leaf spot of *Ilex chinensis* (Aquifoliaceae), 25 October 2017, Y. Wang, (HGUP 22041), living culture GUCC 12115, GUCC 12116; *ibid*., Sichuan Province, Chengdu City, Chengdu Botanical Garden, on leaf spot of *Viburnum dilatatum* (Caprifoliaceae), 22 July 2019, C. R. Meng, (HGUP 22042), living culture GUCC 12120; *ibid*., on leaf spot of *Fatsia japonica* (Araliaceae), (HGUP 22043), living culture GUCC 12127; *ibid*., Guizhou Province, Guiyang City, Guiyang Medicinal Botanical Garden, on leaf spot of *Spatholobus suberectus* (Fabaceae), 30 September 2019, C. R. Meng, (HGUP 22044), living culture GUCC 12128; *ibid*., Guizhou Province, Guiyang City, Guiyang Medicinal Botanical Garden, on leaf spot of *Achyranthes bidentata* (Amaranthaceae), 30 September 2019, C. R. Meng, (HGUP 22045), living culture GUCC 12129.

Notes – A comprehensive study on *C. gloeosporioides* and related species was conducted by Weir et al. (2012), which resolved most of the species under the name of *C. gloeosporioides*. It is mostly associated with *Citrus* sp. (Weir et al. 2012). Fourteen strains from our study were included in our phylogeny and grouped in the *C. gloeosporioides* clade (ML/BI: 100/1, Fig. 18). The morphology of our collection (GUCC 12127) is similar to the type of *C. gloeosporioides* except with larger appressoria (7–16 × 6.5–9 µm *vs.* 7.2–12 × 4.7–6 µm) (Cannon et al. 2008). Hence, we suggest our collection as *C. gloeosporioides* based on morphology and phylogenetic analysis.

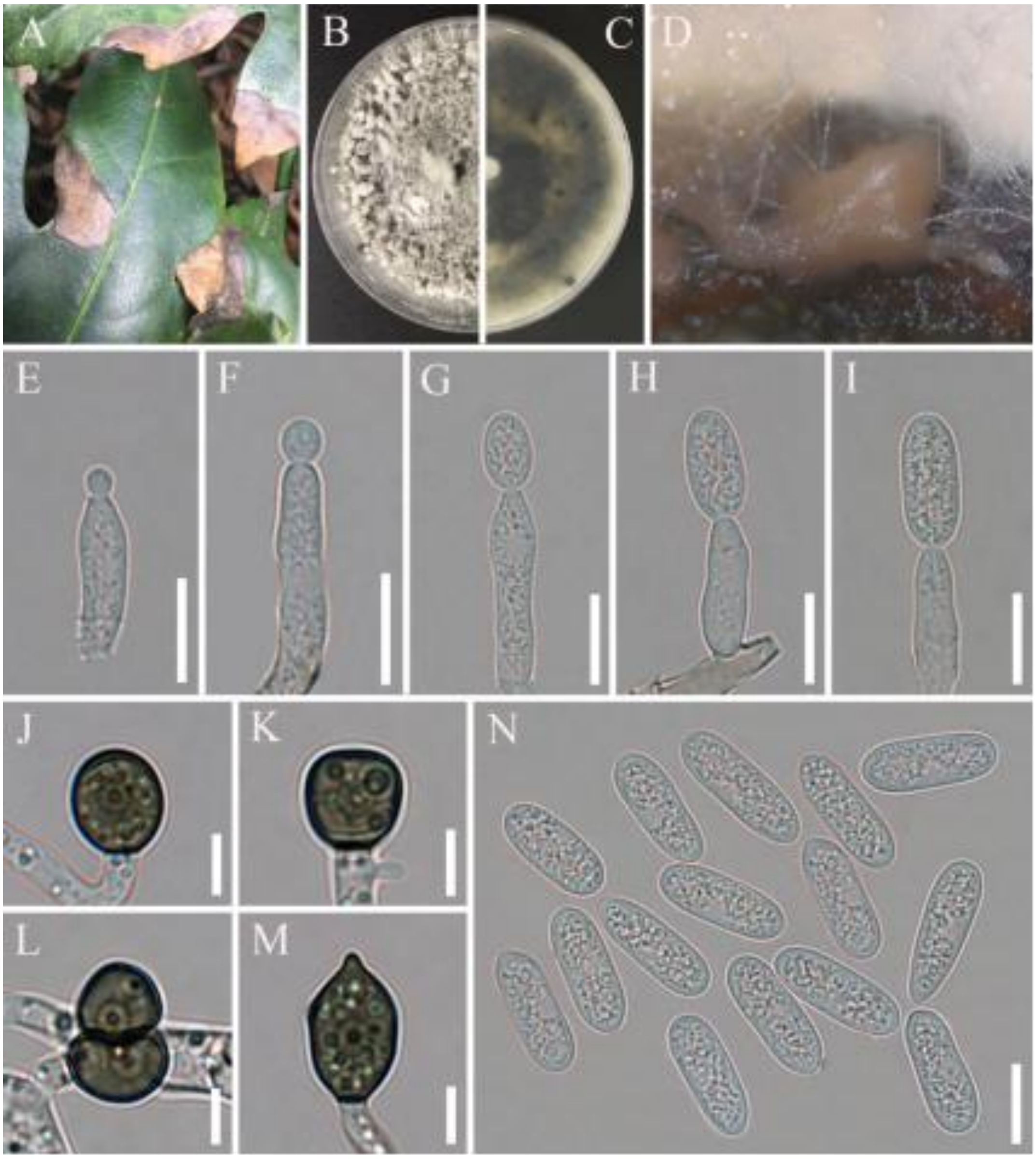


Figure 25 – *Colletotrichum gloeosporioides* (GUCC 12127). A Host. B, C Upper and Reverse view of the colony. D Conidiomata. E–I Conidiophores. J–M Appressoria. N Conidia. Scale bars: E–I, N = 10 µm, J–M = 5 µm.

Colletotrichum grevilleae F. Liu, U. Damm, L. Cai & P.W. Crous, Fungal Diversity 61: 98 (2013) Fig. 26

Index Fungorum number: IF802496

Associated with spots on leaves of undetermined host. Sexual morph not observed. Asexual state on SNA (GUCC 12077). *Vegetative hyphae* 1.5−5.5 µm diam, hyaline to medium brown, usually smooth-walled, septate, branched. *Conidiomata*, irregular, orange. *Setae* not observed. *Conidiophores* formed directly on a cushion of pale brown, hyaline to pale brown, simple or septate, sometimes branched, 18.5–51 × 2.2–4 µm. *Conidiogenous cells* hyaline to pale brown, cylindrical, straight to flexuous, collarette rarely observed, 0.5–1.5 µm long. *Conidia* hyaline, smooth-walled, aseptate, straight, clavate to narrowly cylindrical, the apex rounded, the base rounded or truncate, 15.5–22 × 4–6.5 µm, mean ± SD = 17.5 ± 1.5 × 4.6 ± 0.5 µm, L/W ratio = 3.8. *Appressoria* single, medium to dark brown, smooth-walled, subcircular, elliptical, with an entire margin, 5.5–12 × 4.5–10.5 µm, mean ± SD = 9.1 ± 1.7 × 6.3 ± 0.7 µm, L/W ratio = 1.3.

Culture characteristics – Colonies on PDA low convex with entire margin, surface olivaceous black to dark slate blue with a white margin, reverse dark slate blue; colony diam 57 mm in 7 d.

Colonies on SNA flat with entire margin, short sparse white aerial mycelium and buff pigment around transplant location, conidial mass salmon; colony diam 74 mm in 7 d.

Material examined – China, Yunnan Province, Jinghong City, Mengyang Town, Xishuangbanna National Nature Reserve, on leaf spot of undetermined host species, 10 October 2018, Y. Wang, (HGUP 22048), living culture GUCC 12077.

Notes – Phylogenetic analyses show that GUCC 12077 grouped with *Colletotrichum grevilleae* with support ML/BI: 100/0.99 (Fig. 18). The morphology of our collection (GUCC 12077) is similar to *C. grevilleae* described by Liu et al. (2013). We report appressoria for this species from our collection. Thus, we conclude our collection as *C. grevilleae*.

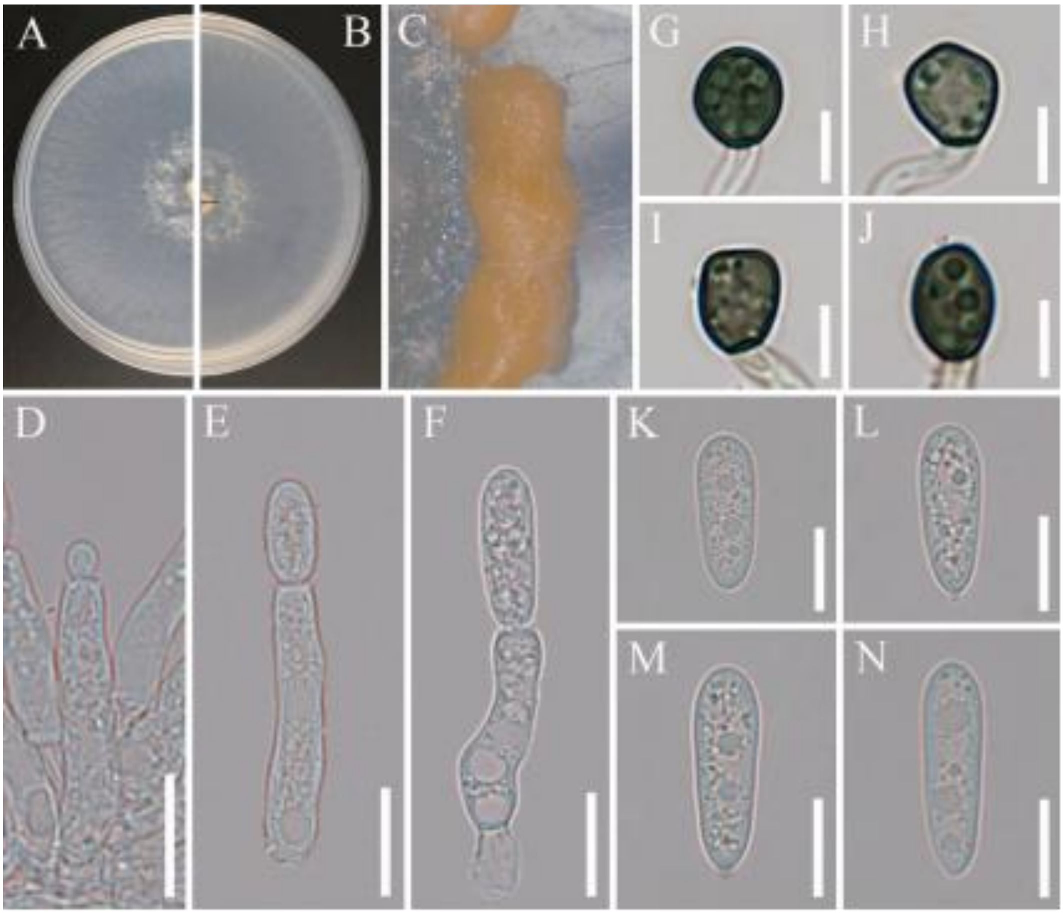


Figure 26 – *Colletotrichum grevilleae* (GUCC 12077). A, B Upper and Reverse view of the colony. C Conidiomata. D–F Conidiophores. G–J Appressoria. K–N Conidia. Scale bars: D–F, K–N = 10 µm, G–J = 5 µm.

Colletotrichum jiangxiense F. Liu & L. Cai, in Liu, Weir, Damm, Crous, Wang, Liu, Zhang & Cai, Persoonia 35: 82 (2015) Fig. 27

Index Fungorum number: IF809161

Associated with spots on leaves of *Cinnamomum camphora*, *Fatsia japonica* and *Illicium simonsii*. Sexual morph not observed. Asexual morph on PDA (GUCC 12055). *Vegetative hyphae* 2.5–5.5 µm diam, hyaline to medium brown, smooth-walled, septate, branched. *Conidiomata* subglobose, orange. *Setae* not observed. *Conidiophores,* hyaline, smooth-walled, branched, 5–35 × 3.5–5.5 µm. *Conidiogenous cells* hyaline, smooth–walled, cylindrical, sometimes extending to form new conidiogenous loci, collarette 0.5−2 µm long, periclinal thickening observed. *Conidia* hyaline, smooth-walled, aseptate, straight, cylindrical, the apex and base rounded, 10.5–17.5 × 7–9.5 µm, mean ± SD = 14 ± 1.3 × 8.2 ± 0.5 µm, L/W ratio= 1.7. *Appressoria* solitary, pale to medium brown, smooth-walled, subglobose to ellipsoidal in outline, with an entire margin, 7.5–12.5 × 6–13 µm, mean ± SD = 9.9 ± 1.1 × 8.1 ± 1.2 µm, L/W ratio = 1.2.

Culture characteristics – Colonies on PDA flat with entire margin, white to vinaceous buff; reverse rosy buff, growth 62 mm in 7 d.

Material examined – China, Yunan Province, Kunming City, Kunming Botanical Garden, on leaf spot of *Illicium simonsii* (Magnoliaceae), 15 January 2018, Q. Zhang, (HGUP 22083), living culture GUCC 12043, GUCC 12044, GUCC 12045, GUCC 12046; *ibid*., Guizhou Province, Guiyang City, Huaxi Road, on leaf spot of *Fatsia japonica* (Araliaceae), 6 September 2017, (HGUP 22050), living culture GUCC 12055; *ibid*., Guizhou Province, Guiyang City, Huaxi Road, on leaf spot of *Cinnamomum camphora* (Lauraceae), 8 September 2017, (HGUP 22084), living culture GUCC 12058.

Notes – Strains GUCC 12043–12046, GUCC 12055 and GUCC 12058 are phylogenetically related to *Colletotrichum jiangxiense* (Fig. 18). When comparing our strain with the type specimen of *C. jiangxiense* (CGMCC 3.17363), they are similar in morphology in length of conidia. However, our strain has wider conidia (7–9.5 µm *vs.* 4–6 µm) compared to the type strain (Liu et al. 2015). *Colletotrichum nullisetosum* and *C. oblongisporum* also grouped in *C. jiangxiense*.

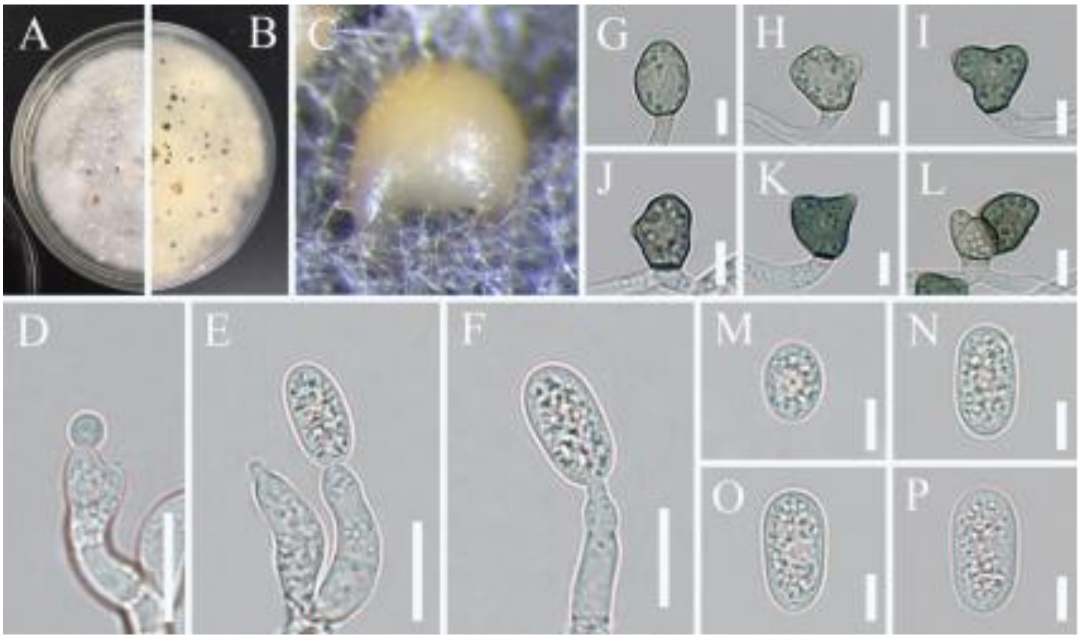


Figure 27 – *Colletotrichum jiangxiense* (GUCC 12055). A, B Upper and Reverse view of the colony. C Conidiomata. D–F Conidiophores. G–L Appressoria. M–P Conidia. Scale bars: D–F = 10 µm, G–P = 5 µm.

Colletotrichum kunmingense Q. Zhang, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 28

Index Fungorum number: IF900002; Facesoffungi numbers: FoF 13367

Etymology – The epithet "*kunmingense*" refers to Kunming City, Yunnan Province in China where the fungus was found.

Holotype – HGUP 22049

Associated with spots on leaves of *Ophiopogon japonicus*. Sexual morph not observed. Asexual morph on PDA (GUCC 12053). *Vegetative hyphae* 2−7 µm diam, hyaline to medium brown, smooth-walled, septate, branched. *Conidiomata*, sub-globose, milk orange. *Setae* not observed. *Conidiophores* formed on a cushion of pale brown, hyaline, smooth-walled, branched. *Conidiogenous cells* hyaline, smooth-walled, cylindrical, 12−32.5 × 2.5−6.5 µm, collarette 0.5−1 µm long, periclinal thickening observed. *Conidia* hyaline, smooth-walled, aseptate, straight, clavate to narrowly cylindrical, the apex rounded, the base rounded or truncate, 17.5−23.5 × 5−7.5 µm, mean ± SD = 20.6 ± 1.3 × 5.7 ± 0.6 µm, L/W ratio = 3.6. *Appressoria* single, medium to dark brown, smooth-walled, subcircular, elliptical or irregular in outline, with an undulate to lobate margin, 8.5−17 × 5.5−13 µm, mean ± SD = 11.3 ± 1.5 × 8.5 ± 1.9 µm, L/W ratio = 1.3.

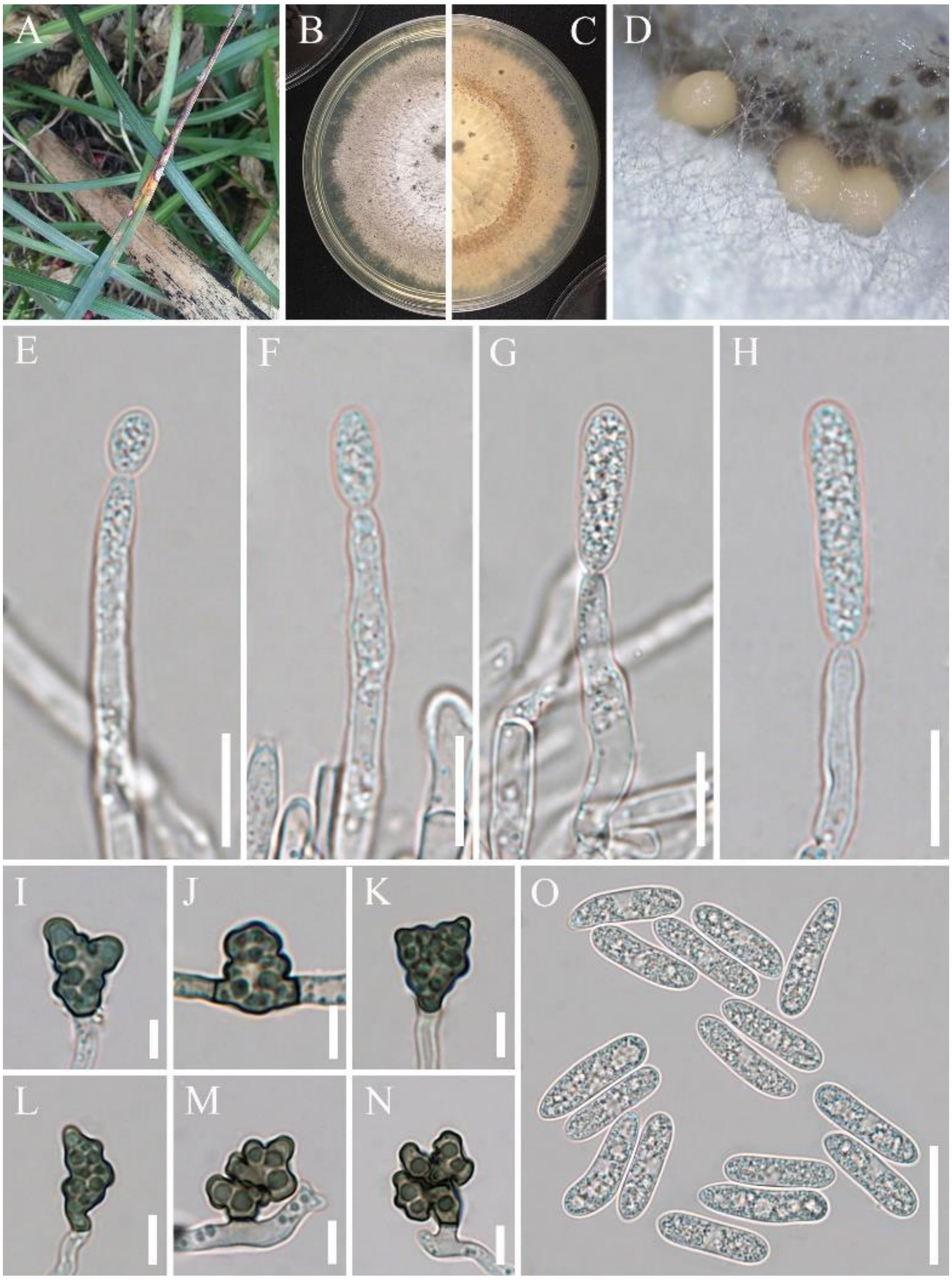


Figure 28 − *Colletotrichum kunmingense* (GUCC 12053). A Host. B, C Upper and Reverse view of the colony. D Conidiomata. E−H Conidiophores. I−N Appressoria. O Conidia. Scale bars: O = 20 µm, E−H = 10 µm, I−N = 5 µm.

Culture characteristics – Colonies on PDA with undulate margin, in the centre white to pale grey aerial mycelium, medium grey aerial mycelium in margin; reverse same colour, growth 36 mm in 7 d.

Material examined – China, Yunan Province, Kunming City, Kunming Botanical Garden, on leaf spot of *Ophiopogon japonicus* (Liliaceae), 15 January 2018, Q. Zhang, (HGUP 22049, holotype); ex-type living culture GUCC 12053, GUCC 12178.

Note – In the phylogenetic analyses, *Colletotrichum kunmingense*, belonging *C. gloeosporioides* species complex, was sister to *C. alatae* with good support (ML/BI: 100/1, Fig. 18). The ITS, *gapdh*, *chs-1*, *act* and *tub2* sequences similarity of the type strain of *C. kunmingense* and *C. alatae* was 98.45% (508/516 bp), 88.21% (217/246 bp), 96.27% (258/268 bp), 91.53% (216/236 bp) and 93.94% (651/693 bp), respectively. Moreover, *C. kunmingense* have wider conidia than *C. alatae* (5−7.5 *vs.* 4.5−6.5), and larger appressoria (8.5−17 × 5.5−13 *vs.* 7−13.5 × 5−10.5) (Weir et al. 2012). The PHI test resulted that there is no significant recombination (P = 0.2974 > 0.05) between C. *kunmingense* and its closely related taxa (Fig. 19C). Therefore, we consider the new collections as a new species.

Colletotrichum ligustri Q. Zhang, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 29

Index Fungorum number: IF900003; Facesoffungi numbers: FoF 13368

Etymology – ligustri, in reference to the host *Ligustrum* Linn., from which the fungus was isolated.

Holotype – HGUP 22051

Associated with spots on leaves of *Ilex chinensis*. Sexual morph not observed. Asexual morph on PDA (GUCC 12111). *Vegetative hyphae* 1.5−3 µm diam, hyaline to pale brown, smooth-walled, septate, branched. *Conidiomata*, subglobose, pale orange. *Setae* not observed. *Conidiophores* hyaline, smooth-walled, branched. *Conidiogenous cells* hyaline, obclavate to cylindrical, 13.5−27.5 × 2−4 µm, collarette 0.5−1.5 µm long, periclinal thickening observed. *Conidia* hyaline, smooth-walled, aseptate, straight, few conidia slightly curved, cylindrical, the apex and base rounded, 14−19 × 4−6.5 µm, mean ± SD = 16.7 ± 0.9 × 5.5 ± 0.4 µm, L/W ratio = 3. *Appressoria* solitary, pale to medium brown, smooth-walled, subglobose to ellipsoidal in outline, with an entire margin, 6.5−9 × 5−7.5 µm, mean ± SD = 7.9 ± 0.7 × 6.4 ± 7 µm, L/W ratio = 1.2.

Culture characteristics – Colonies on PDA flat with entire margin, surface partly covered with woolly hazel to pale olivaceous-grey aerial mycelium, pale grey in the margin; reverse same colour, growth 74 mm in 7 d.

Material examined – China, Guizhou Province, Guiyang City, Huaxi Road, on leaf spot of *Ilex chinensis* (Aquifoliaceae), 25 October 2017, Q. Zhang, (HGUP 22051, holotype); ex-type living culture GUCC 12111.

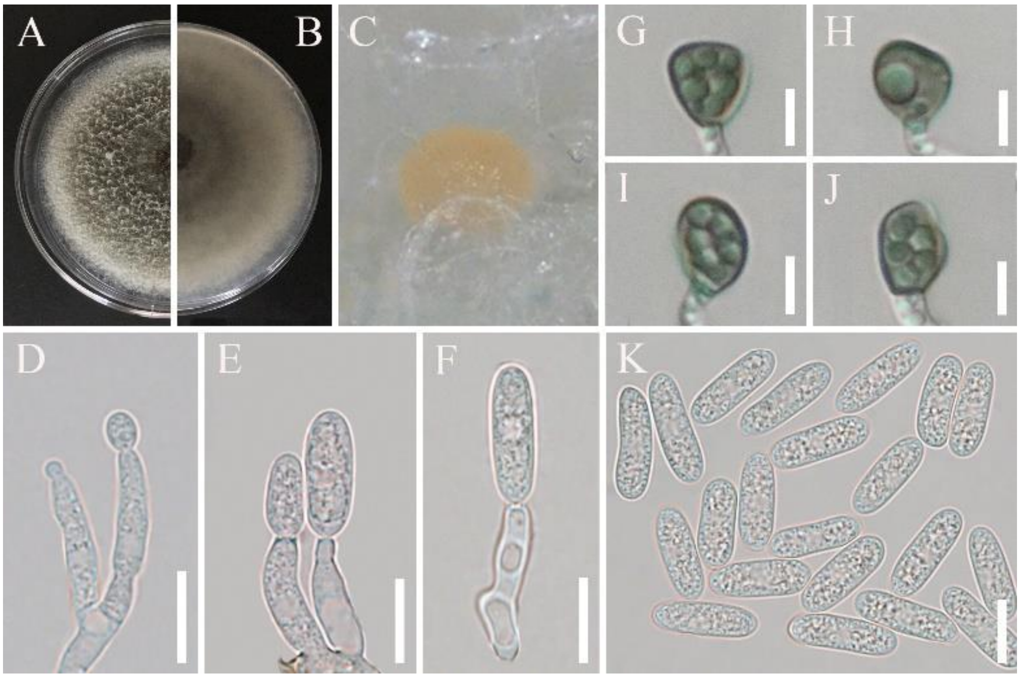


Figure 29 − *Colletotrichum ligustri* (GUCC 12111). A, B Upper and Reverse view of the colony. C Conidiomata. D−F Conidiophores. G−J Appressoria. K Conidia. Scale bars: D−F, K = 10 µm, G−J = 5 µm.

Note – *Colletotrichum ligustri* belongs to the *C. gloeosporioides* species complex. The multi-locus phylogenetic analyses showed that the ex-type strain of *C. ligustri*, GUCC 12111, is sister to the ex-type strain of *C. changpingense* MFLUCC 15-0022 with good support (ML/BI: 100/1, Fig.

18), which was described from rhizome of *Fragaria* × *ananassa* (Jayawardena et al. 2016), whereas *C. ligustri* showing 98.98% (497/492 bp including 5 bp of gaps), 96.93% (221/228 bp including 3 bp of gaps), 97.34% (222/228 bp), 98.94% (186/188 bp including 1 bp of gap) and 91.43% (661/723 bp including 17 bp of gaps) sequence similarity with *C. changpingense* of ITS, *gapdh*, *chs-1*, *act* and *tub2* sequences, respectively. Moreover, *C. ligustri* have longer conidia than *C. changpingense* (14−19 *vs.* 9−15) (Jayawardena et al. 2016). The PHI test on *C. ligustri* revealed that there is no significant recombination (P = 0.6342 > 0.05) between *C. ligustri* and its closely related taxa (Fig. 19D). We, therefore, introduce *C. ligustri* as a new species.

Colletotrichum siamense Prihast., L. Cai & K.D. Hyde, in Prihastuti, Cai, Chen, McKenzie & Hyde, Fungal Diversity 39: 98 (2009) Fig. 30

≡ *Colletotrichum menglaense* M. Qiao & Z.F. Yu, in Qiao, Li, Fang, Li & Yu, Pathogens 10(10, no. 1243): 6 (2021)

≡ *Colletotrichum pandanicola* Tibpromma & K.D. Hyde, in Tibpromma, Hyde, Bhat, Mortimer, Xu, Promputtha, Doilom, Yang, Tang & Karunarathna, MycoKeys 33: 47 (2018)

≡ *Colletotrichum parvisporum* Z.F. Yu, in Yu, Jiang, Zheng, Zhang & Qiao, Journal of Fungi 8(2, no. 185): 21 (2022)

Index Fungorum number: IF515410

Associated with spots on leaves of *Alocasia macrorrhiza*, *Ardisia japonica*, *Aucuba japonica*, *Bauhinia championii*, *Camellia japonica*, *Chamaedorea elegans*, *Curcuma phaeocaulis*, *Eriobotrya japonica*, *Fatsia japonica*, *Heteropanax fragrans*, *Houttuynia cordata*, *Hymenocallis littoralis*, *Ilex chinensis*, *Osmanthus fragrans,* and *Piper sarmentosum*. Sexual morph not observed. Asexual morph on PDA (GUCC 12086). *Vegetative hyphae* 2−3.5 µm diam, hyaline, smooth-walled, septate, branched. *Conidiomata*, subglobose, pale orange. *Setae* not observed. *Conidiophores* hyaline to pale brown, smooth-walled, branched, to 45 µm long. *Conidiogenous cells* hyalin, smooth-walled, 5−26 µm, opening 1−2.5 µm diam. *Conidia* hyaline, smooth-walled, aseptate, straight, cylindrical, the apex and base rounded, 13−18 × 4−6 µm, mean ± SD = 15.3 ±1 × 5.5 ± 0.4 µm, L/W ratio = 2.8. *Appressoria* solitary, pale to medium brown, smooth-walled, subcircular, elliptical or irregular in outline, with an undulate to lobate margin, 6.5−11 × 6−10 µm, mean ± SD = 9 ± 1.3 × 7.4 ± 1.1 µm, L/W ratio = 1.2.

Culture characteristics – Colonies on PDA flat with entire margin, surface partly covered with woolly hazel to pale olivaceous-grey aerial mycelium, pale grey in margin; reverse same colour, growth 83 mm in 7 d.

Material examined – China, Guangxi Province, Nanning City, Guangxi Medicinal Botanical Garden, on leaf spot of *Hymenocallis littoralis* (Amaryllidaceae), 1 October 2017, Q. Zhang, (HGUP 22054), living culture GUCC 12061; *ibid*., on leaf spot of *Alocasia macrorrhiza* (Araceae), (HGUP 22055), living culture GUCC 12062; *ibid*., on leaf spot of *Bauhinia championii* (Fabaceae), (HGUP 22056), living culture GUCC 12063; *ibid*., on leaf spot of *Osmanthus fragrans* (Oleaceae), (HGUP 22057), living culture GUCC 12065, GUCC 12066, GUCC 12068; *ibid*., on leaf spot of *Houttuynia cordata* (Saururaceae), (HGUP 22058), living culture GUCC 12071; *ibid*., Yunnan Province, Jinghong City, Mengyang Town, Xishuangbanna National Nature Reserve, on leaf spot of undetermined host species, 10 October 2018, Y. Wang, (HGUP 22060), living culture GUCC 12074; *ibid*., on leaf spot of *Ardisia japonica* (Myrsinaceae), (HGUP 22061), living culture GUCC 12075; *ibid*., Yunnan Province, Jinghong City, Mengyang Town, Xishuangbanna National Nature Reserve, on leaf spot of undetermined host species, 10 October 2018, Y. Wang, (HGUP 22062), living culture GUCC 12076, GUCC 12078, GUCC 12081, GUCC 12082, GUCC 12085, GUCC 12095, GUCC 12096; *ibid*., on leaf spot of *Camellia japonica* (Theaceae), (HGUP 22053), living culture GUCC 12086, GUCC 12087; *ibid*., on leaf spot of *Curcuma phaeocaulis* (Zingiberaceae), (HGUP 22069), living culture GUCC 12101; *ibid*., on leaf spot of *Piper sarmentosum* (Piperaceae), (HGUP 22070), living culture GUCC 12104; *ibid*., Sichuan Province, Chengdu City, Chengdu Botanical Garden, on leaf spot of undetermined host species, 22 July 2019, (HGUP 22071), living culture GUCC 12119; *ibid*., Sichuan Province, Chengdu City, Chengdu Botanical Garden, on leaf spot of *Eriobotrya japonica* (Rosaceae), 22 July 2019, (HGUP 22072), living culture GUCC 12121; *ibid*., Sichuan Province, Chengdu City, Chengdu Botanical Garden, on leaf spot of *Aucuba japonica* (Cornaceae), 22 July 2019, (HGUP 22073), living culture GUCC 12122; *ibid*., Sichuan Province, Chengdu City, Chengdu Botanical Garden, on leaf spot of *Camellia japonica* (Theaceae), 22 July 2019, (HGUP 22074), living culture GUCC 12123; *ibid*., Sichuan Province, Chengdu City, Chengdu Botanical Garden, on leaf spot of *Chamaedorea elegans* (Arecaceae), 22 July 2019, (HGUP 22075), living culture GUCC 12124; *ibid*., Sichuan Province, Chengdu City, Chengdu Botanical Garden, on leaf spot of *Heteropanax fragrans* (Araliaceae), 22 July 2019, (HGUP 22076), living culture GUCC 12125; *ibid*., Sichuan Province, Chengdu City, Chengdu Botanical Garden, on leaf spot of *Fatsia japonica* (Araliaceae), 22 Jul 2019, (HGUP 22077), living culture GUCC 12126; *ibid*., Guizhou Province, Guiyang City, Huaxi Road, on leaf spot of *Ilex chinensis* (Aquifoliaceae), 30 Oct 2017, (HGUP 22095), living culture GUCC 12174, GUCC 12175.

Notes – Phylogenetic analyses show that our strains grouped within the *Colletotrichum siamense* clade (Fig. 18), which is biologically and geographically diverse, found on many hosts across several tropical and subtropical regions (Weir et al. 2012). Our collection (GUCC 12086) is similar to the holotype of *C. siamense* (ICMP 18578). While the appressoria of our collection (GUCC 12086) is larger than strain ICMP 18578 (6.5−11 × 6−10 *vs*. a 4.7−8.3 × 3.5−5 μm) (Prihastuti et al. 2009). We, therefore, identify our isolate as *C. siamense*. *Colletotrichum menglaense*, *C. pandanicola*, and *C. parvisporum* also grouped in *C. siamense*, we could not reproduce the phylogenetically inferred by using the data deposited in those previously published (Tibpromma et al. 2018; Yu et al. 2022). *Colletotrichum menglaense* is introduced by the dimensions of conidia differences with phylogenetically closely related *C. aeschynomenes* and *C. dianesei* (Qiao et al. 2021). When comparing *C. menglaense* and the type of *C. siamense* with the description of Prihastuti et al. (2009), they are similar in conidia. *Colletotrichum pandanicola* is introduced by the molecular differences with close phylogenetic relative species *C. tropicale* (Tibpromma et al. 2018). *Colletotrichum tropicale* is closely related with *C. siamense* in our phylogenetic tree (Fig. 18). Comparing the nucleotides found on *C. siamense* showed fewer different site with *C. pandanicola* (ITS: 4 bp, *gapdh*: 6 bp, *chs-1*: 4 bp, *act*: 2 bp, *tub2*: 1 bp) than *C. tropicale* (ITS: 0 bp, *gapdh*: 11 bp, *chs-1*: 7 bp, *act*: 3 bp, *tub2*: 7 bp). *Colletotrichum parvisporum* is introduced based on having appressoria compared with *C. pandanicola* (Yu et al. 2022). The presence of appressoria should not be individual basis for classification criteria (Jayawardena et al. 2021b). Accordingly, C. *menglaense*, *C. pandanicola* and *C. parvisporum* are synonymized to *C. siamense* based on phylogenetic evidence.

The *Colletotrichum orchidearum* species complex

Phylogenetic analyses

In the multi-locus sequence analyses (ITS: 1–540, *gapdh*: 541–774, *chs-1*: 775–1,043, *his3*: 1,044–1,431, act: 1,432–1,680, *tub2*: 1,681–2,211) of our nine isolates from medicinal plants and 16 reference strains of *C. orchidearum* species complex, 2,211 characters including alignment gaps were processed. *Colletotrichum magnum* (CBS 519.97) and *C. merremiae* (CBS 124955) were selected as the outgroup taxa. The ML search revealed the best score of -5745.331. The best nucleotide substitution models were recommended by ModelFinder and used in the Bayesian analysis: K2P+I for ITS, HKY+F+G4 for *gapdh, chs-1, his, act,* and *tub2*. Our nine isolates correspond to *C. plurivorum* and *C. vittalense* (Fig. 31).

Taxonomy

Colletotrichum plurivorum Damm, Alizadeh & Toy. Sato, Studies in Mycology 92: 31 (2018)
Fig. 32

Index Fungorum number: IF824228

Associated with spots on leaves of *Piper sarmentosum* and *Syngonium podophyllum*. Sexual morph on PDA (GUCC 12140). *Vegetative hyphae* 1.5−5 µm diam, hyaline to pale brown, smooth-walled, septate, branched. *Ascomata* perithecia, solitary or clustered, superficial or immersed, globose to obpyriform, glabrous or covered by sparse white or grey aerial mycelium, medium to dark brown, surrounded by pale brown, smooth-walled hyphae. *Ascogenous* hyphae hyaline, smooth, delicate. *Asci* unitunicate, 8-spored, cylindrical to clavate, smoothwalled, 65–106 × 8.5–12 µm, the base broadly truncate. *Ascospores* uni- or biseriately arranged, aseptate, initially hyaline, turning pale brown with age, smooth-walled, allantoid to fusiform, with both ends rounded, 13.5–21 × 5–8 µm, mean ± SD = 17 ± 1.8 × 6.1 ± 0.5 µm, L/W ratio = 2.8. Asexual morph undetermined.

Culture characteristics – Colonies on PDA flat with entire margin, surface partly covered with woolly hazel to rosy buff aerial mycelium, reverse dark vinaceous buff, growth 72 mm in 7 d.

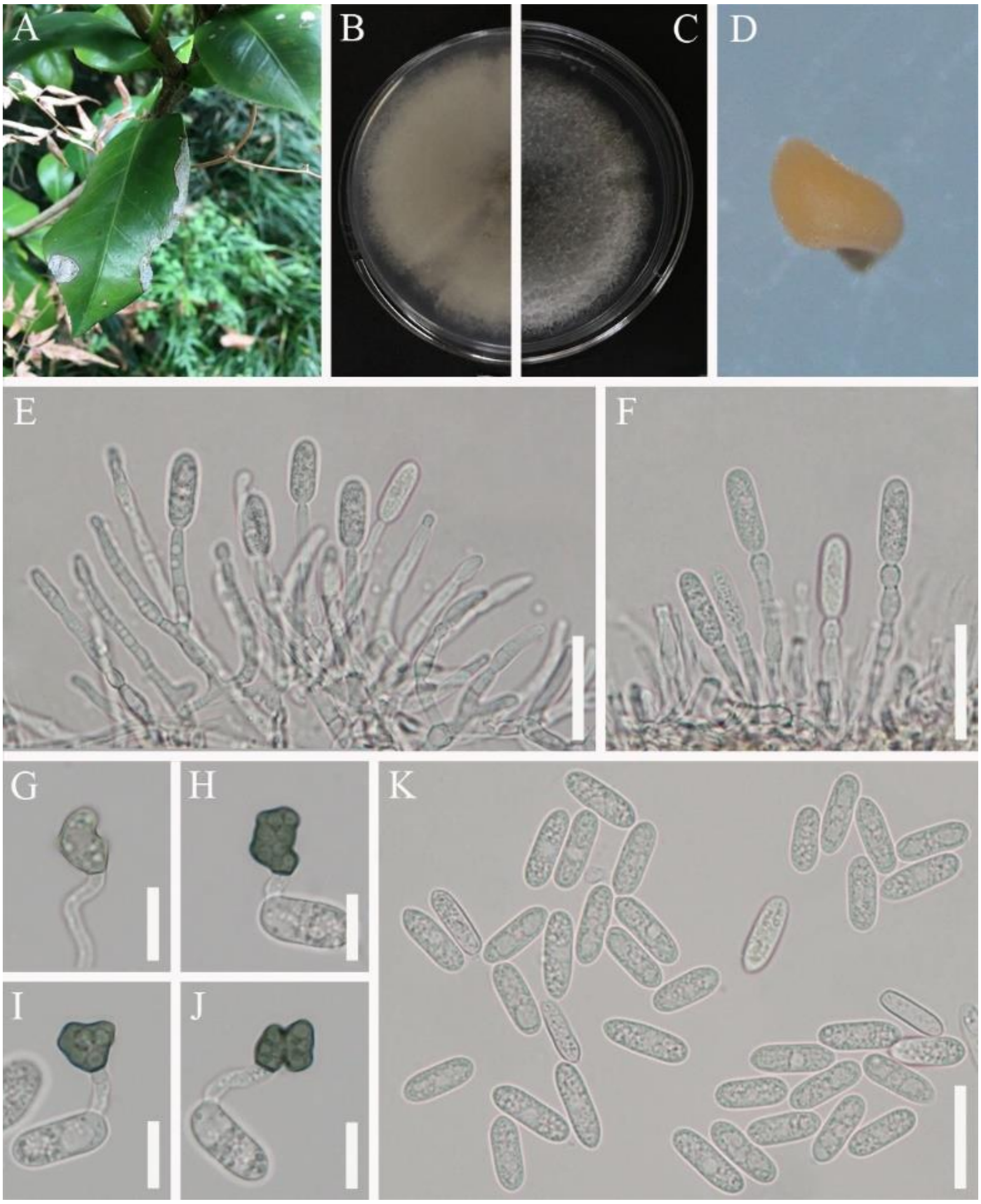


Figure 30 – *Colletotrichum siamense* (GUCC 12086). A Host. B, C Upper and Reverse view of the colony. D Conidiomata. E−F. Conidiophores. G−J Appressoria. K Conidia. Scale bars: E−F, K = 20 µm, G−J = 10 µm.

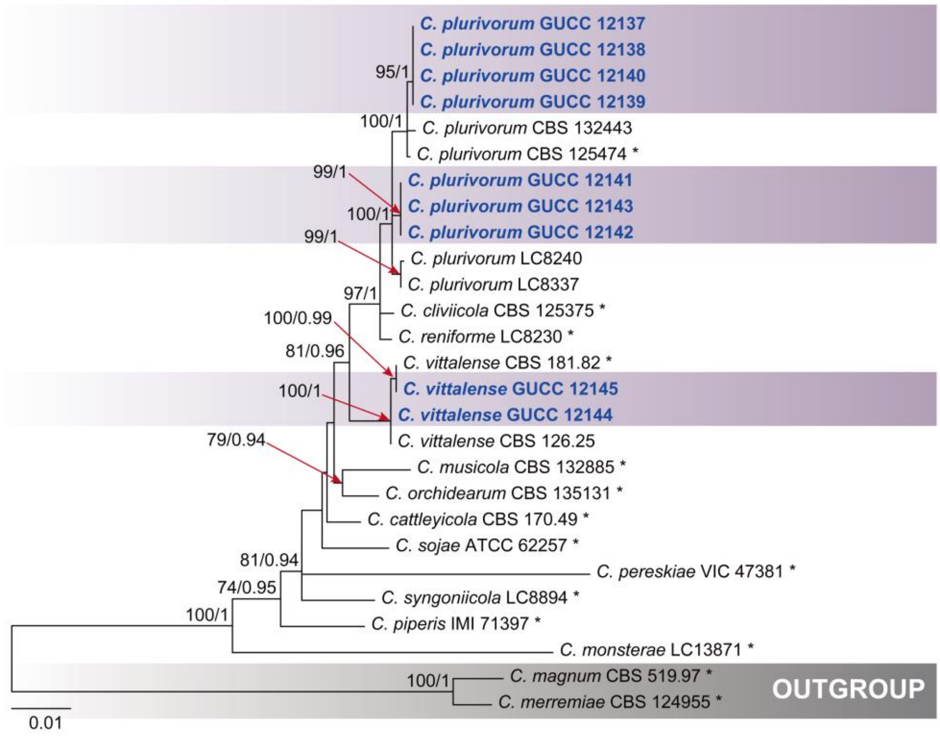


Figure 31 – Maximum likelihood tree of the *C. orchidearum* species complex. *Colletotrichum magnum* (CBS 519.97) and *C. merremiae* (CBS 124955) were selected as outgroups. At the nodes, bootstrap support values for ML (≥ 70%) and BYPP (≥ 0.90) are displayed (ML/PP). Type species strains are denoted by "*". Newly generated sequences are in blue bold.

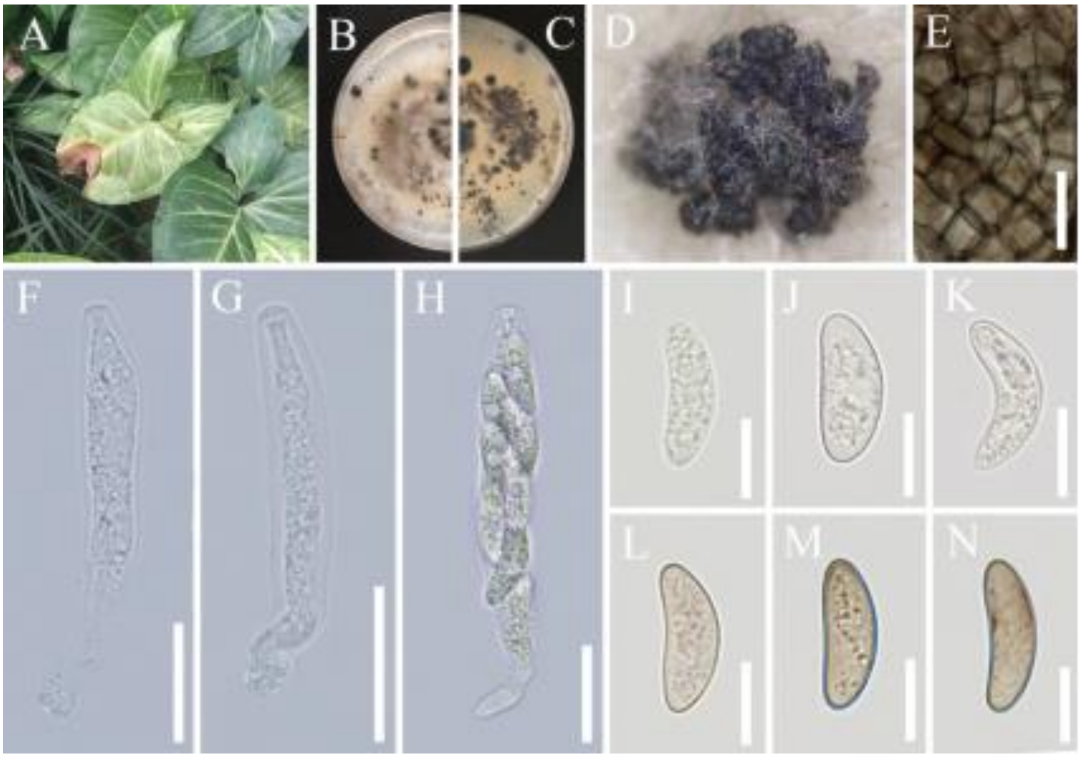


Figure 32 – *Colletotrichum plurivorum* (GUCC 12140). A Host. B, C Upper and Reverse view of the colony. D Ascomata. E Outer surface of Peridium. F–H Asci. I–N Ascospore. Scale bars: E–H = 20 μm, I–N = 10 μm.

Material examined – China, Guangxi Province, Nanning City, Guangxi Medicinal Botanical Garden, on leaf spot of *Syngonium podophyllum* (Araceae), 1 October 2017, Q. Zhang, (HGUP 22089), living culture GUCC 12137, GUCC 12138, GUCC 12139, GUCC 12140; *ibid*., on leaf spot of *Piper sarmentosum* (Piperaceae), (HGUP 22088), living culture GUCC 12141, GUCC 12142, GUCC 12143.

Notes – *Colletotrichum plurivorum* belongs to the *C. orchidearum* species complex, species of which are very common and occur on many host species and a number of less common species that seem to be either host-specific (Damm et al. 2019). Some species in the *C. orchidearum* complex were only/predominantly producing the sexual or the asexual morph (Damm et al. 2019). We only observed the sexual morph from our collections, and the morphology of our strain (GUCC 12140) is similar to the *C. plurivorum* described by Damm et al. (2019). Phylogenetic analyses show that our strains (GUCC 12137, GUCC 12138, GUCC 12139, GUCC 12140, GUCC 12141, GUCC 12142, GUCC 12143) grouped with the type strain of *C. plurivorum* (CBS 125474) with high bootstrap support (ML/BI: 100/1, Fig. 31). Thus we, identify our collections as *C. plurivorum*.

Colletotrichum vittalense Damm, Studies in Mycology 92: 38 (2018) Fig. 33

Index Fungorum number: IF824230

Associated with spots on leaves of *Piper sarmentosum*. Sexual morph undetermined. Asexual morph on PDA (GUCC 12144). *Vegetative hyphae* 1.5–3.5 µm diam, hyaline to pale brown, smooth-walled, branched, septate. *Conidiomata irregular*, orange. *Setae* medium to dark brown, smooth-walled to verruculose, 58–122 µm long, 2–3-septate, base cylindrical to conical, 3–7 µm diam, tip ± acute. *Conidiophores* hyaline to pale brown, smooth-walled, septate, branched, to 35 µm long. *Conidiogenous cells* pale brown, smooth-walled, cylindrical to clavate, 10–30 × 3–7 µm, collarette 0.5–1.5 µm long, periclinal thickening distinct. *Conidia* hyaline, smooth-walled, aseptate, straight, cylindrical, 13–20 × 5.5–7.5 µm, mean ± SD = 16.4 ± 1.2 × 6.4 ± 0.4 µm, L/W ratio = 2.6. *Appressoria* single, pale to medium brown, smooth-walled, navicular, bullet-shaped, elliptical or irregular in outline, with a lobate or undulate margin, 5.5–15.5 × 4–10 µm, mean ± SD = 9.4 ± 2.3 × 6 ± 1.3 µm, L/W ratio = 1.6.

Culture characteristics – Colonies on PDA flat with entire margin; grey olivaceous to olivaceous, partly covered with short felty whitish aerial mycelium, reverse olivaceous to olivaceous grey, growth 73 mm in 7 d.

Material examined – China, Guangxi Province, Nanning City, Guangxi Medicinal Botanical Garden, on leaf spot of *Piper sarmentosum* (Piperaceae), 1 October 2017, Q. Zhang, (HGUP 22090), living culture GUCC 12144, GUCC 12145. (new host record)

Notes – Our collection (GUCC 12144 and GUCC 12145) groups with ex-holotype strain of *Colletotrichum vittalense* (CBS 181.82), which was isolated from *Theobroma cacao* in India (Damm et al. 2019), with high statistical support (ML/BI: 100/1, Fig. 31). Our collection is morphologically similar to *C. vittalense*. Strains of *C. vittalense* were distributed in India on *Calamus thwaitesii*, *Orchid* sp., and *Theobroma cacao* (Damm et al. 2019). Hence, it is reported here as a new host record of *C. vittalense*.

The *Colletotrichum spaethianum* species complex

Phylogenetic analyses

In the *C. spaethianum* species complex (Fig. 34), a total of 2,190 characters of nucleotides and gaps (ITS: 1–534, *gapdh*: 535–805, *chs-1*: 806–1,056, *his3*: 1,057–1,434 act: 1,435–1,682, *tub2*: 1,683–2,190) were included in the phylogenetic analysis. *Colletotrichum destructivum* (CBS 136228) and *C. higginsianum* (IMI 349061) were selected as the outgroup taxa. The ML search revealed the best score of -6961.485. The best nucleotide substitution models were recommended by ModelFinder and used in the Bayesian analysis: K2P+I for ITS, *chs*, and *gapdh*, HKY+F+G4 for *his*, *act*, and *tub2*. In the phylogenetic tree (Fig. 34), our two strains were grouped with *C. iris* (LC36697).

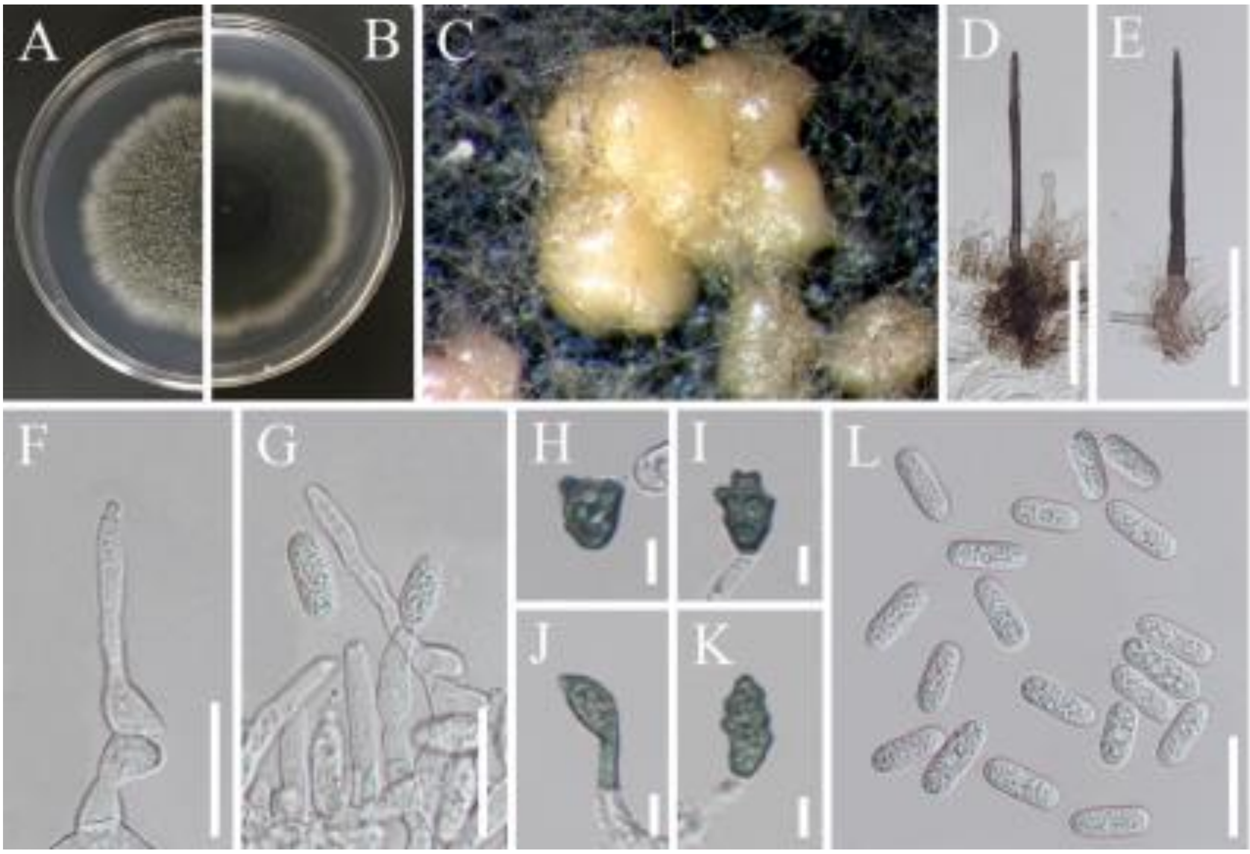


Figure 33 – *Colletotrichum vittalense* (GUCC 12144). A, B Upper and Reverse view of the colony. C Conidiomata. D–E Seta. F–G Conidiophores. H–K Appressoria. L Conidia. Scale bars: D–E = 50 µm, F–G, L = 20 µm, H–K = 5 µm.

Taxonomy

Colletotrichum iris F. Liu & L. Cai, in Liu, Ma, Hou, Diao, Wu, Damm, Song & Cai, Stud. Mycol. 101: 26 (2022) Fig. 35

Index Fungorum number: IF841383

Associated with spots on leaves of *Aspidistra elatior*. Sexual morph not observed. Asexual morph on PDA (GUCC 12172). *Vegetative hyphae* 2.5–5 µm diam, hyaline to pale brown, smooth-walled, septate, branched. *Conidiomata* and *Setae* not observed. *Conidiophores*, hyaline, smooth-walled, branched. *Conidiogenous cells* hyaline, smooth–walled, cylindrical, sometimes extending to form new conidiogenous loci. *Conidia* hyaline, smooth-walled, aseptate, curved, apex ± acute, base usually broader and truncate, 14–25 × 3–4.5 µm, mean ± SD = 21 ± 2.8 × 3.7 ± 0.5 µm, L/W ratio = 5.5. *Appressoria* solitary, pale to medium brown, smooth-walled, mostly irregular shaped, 6.5–19.5 × 3.5–11 µm, mean ± SD = 12.1 ± 3.5 × 7.7 ± 2 µm, L/W ratio = 1.5.

Culture characteristics – Colonies on PDA flat, glaucous grey to smoke grey in the centre, pale grey at the margin, reverse pale grey with margin, a dark greenish grey ring more towards the centre of the colony, growth 46 mm diam in 7 d.

Material examined – China, Guangxi Province, Nanning City, Guangxi Medicinal Botanical Garden, on leaf spot of *Aspidistra elatior* (Liliaceae), 1 October 2019, Q. Zhang, (HGUP 22096), living culture GUCC 12172, GUCC 12173. (new host record)

Notes – Phylogenetic analyses show that our strains grouped within the *Colletotrichum iris* clade (ML/BI: 98/1, Fig. 34) which isolated from the monocotyledon plant, *Iris japonica* in China. Our collection (GUCC 12172) is similar to the holotype of *C. iris* (Liu et al. 2022) and isolated from another monocotyledon plant, *Aspidistra elatior*. We, therefore, identify our isolate as a new host record of *C. iris*.

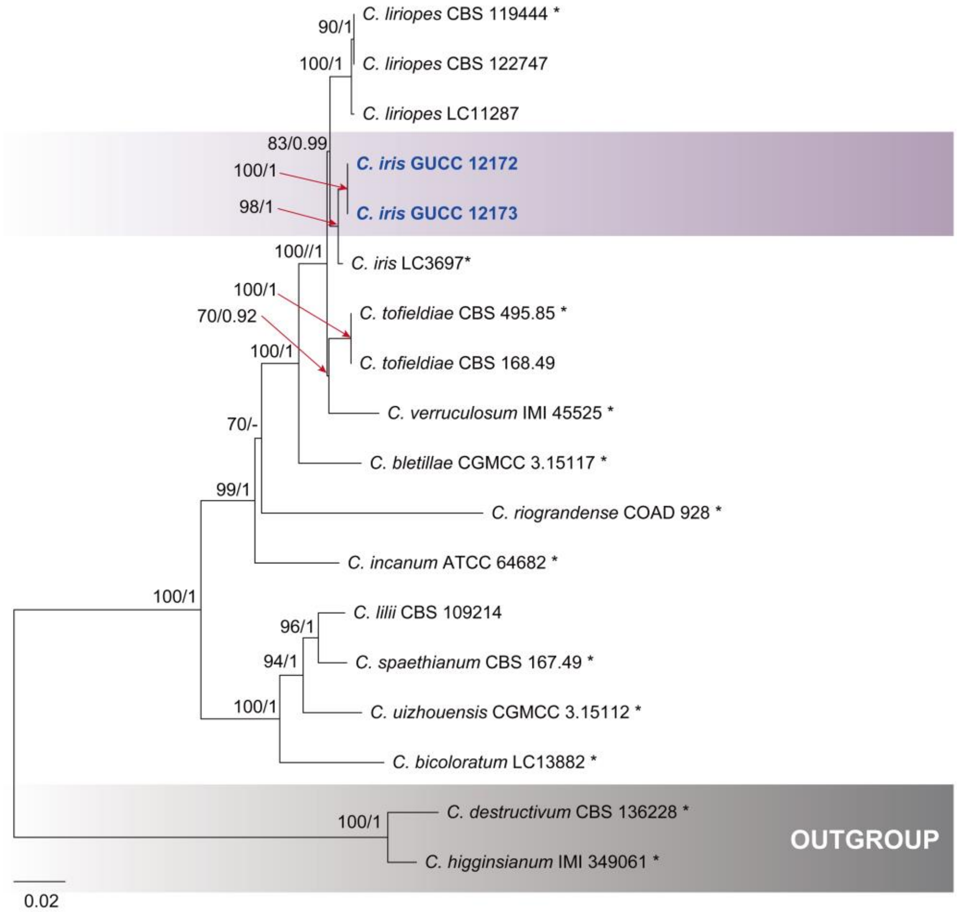


Figure 34 – Maximum likelihood tree of the *C. spaethianum* species complex. *Colletotrichum destructivum* (CBS 136228) and *C. higginsianum* (IMI 349061) were selected as outgroups. At the nodes, bootstrap support values for ML (≥ 70%) and BYPP (≥ 0.90) are displayed (ML/PP). Type species strains are denoted by "*". Newly generated sequences are in blue bold.

The *Colletotrichum truncatum* species complex

Phylogenetic analyses

In the *C. truncatum* species complex, a total of 2,234 characters of nucleotides and gaps (ITS: 1–559, *gapdh*: 536–838, *chs-1*: 839–1,101, *his3*: 1,102–1,465, act: 1,466–1,733, *tub2*: 1,734–2,234) were included in the phylogenetic analysis. *Colletotrichum boninense* (CBS 123755) and *C. chamaedoreae* (LC13868) were selected as the outgroup taxa. The ML search revealed the best score of -6162.967. The best nucleotide substitution models were recommended by ModelFinder and used in the Bayesian analysis: K2P+I for ITS and *chs*, K2P+F+I for *gapdh*, HKY+F+G4 for *his*, *act*, and *tub2*. In the phylogenetic tree (Fig. 36), our eight *Colletotrichum* isolates nearly without phylogenetic distance cluster together with two strains of *C. truncatum* (CBS 151.35 and CBS 120709).

Taxonomy

Colletotrichum truncatum (Schwein.) Andrus & W.D. Moore, Phytopathology 25: 121 (1935)

Fig. 37

Index Fungorum number: IF280780

Associated with spots on leaves of *Cissus hexangularis*, *Houttuynia cordata*, *Hymenocallis littoralis*, and *Piper sarmentosum*. Sexual morph undetermined. Asexual morph on SNA (GUCC

12167), *Vegetative hyphae* 2–5.5 µm diam, hyaline to pale brown, smooth-walled, septate, branched. *Conidiomata* irregular, dark orange. *Setae* pale brown to medium brown up to the tip, smooth, 42–92 µm long, 2- to 5-septate, tapering only slightly towards the slightly acute to roundish tip, base cylindrical to conical, 3.5–8.5 µm diam. *Conidiophores* pale brown, septate, branched, densely clustered. *Conidiogenous cells* hyaline to pale brown, cylindrical, 6–11.5 × 2.5–5 µm, collarette 0.5–1 µm long, periclinal thickening visible. *Conidia* hyaline, smooth-walled, aseptate, long central part of conidia usually slightly curved with parallel walls, ending abruptly at the round and truncate base, while tapering towards the acute and more strongly curved apex, with granular content, 20–30 × 4–6 µm, mean ± SD = 25.8 ± 2.1 × 5.1 ± 0.5 µm, L/W ratio = 5.1. *Appressoria* solitary, in groups or dense clusters, light to medium brown, entire edge to lobed, outline roundish to ellipsoidal or clavate, base truncate, 8–52.5 × 6.5–17 µm, mean ± SD = 15.8 ± 12 × 9.6 ± 2.2 µm, L/W ratio = 1.6.

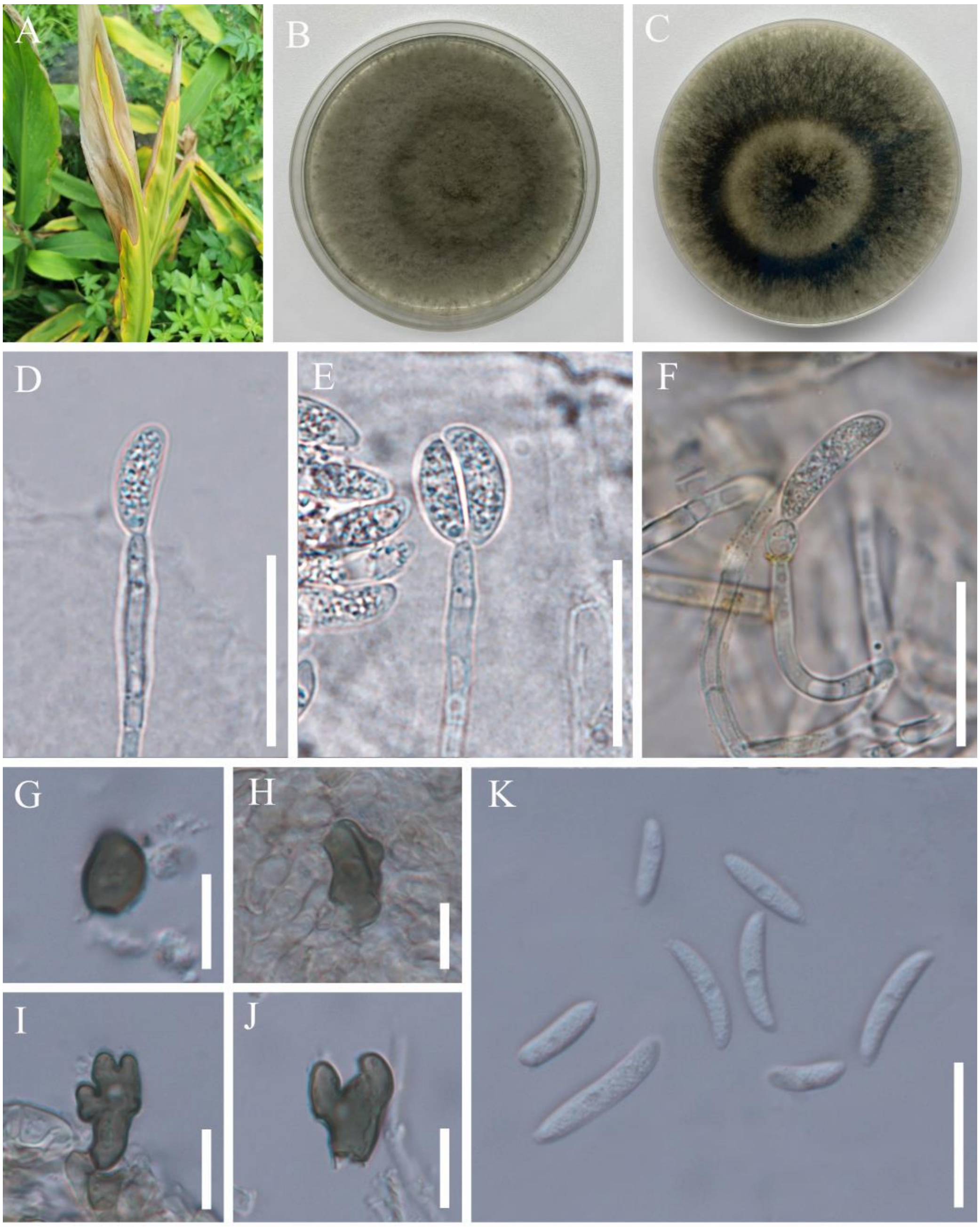


Figure 35 – *Colletotrichum iris* (GUCC 12172). A Host. B, C Upper and Reverse view of the colony. D–F Conidiophores. G–J Appressoria. K Conidia. Scale bars: D–F, K = 20 µm, G–J = 10 µm.

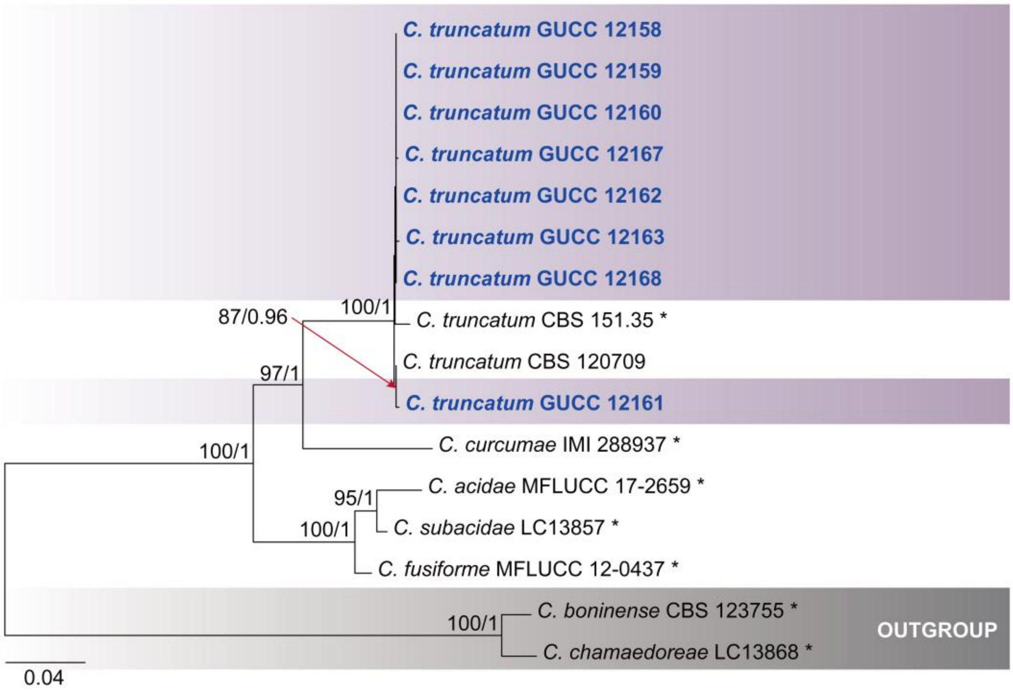


Figure 36 – Maximum likelihood tree of the *C. truncatum* species complex. *Colletotrichum boninense* (CBS 123755) and *C. chamaedoreae* (LC13868) were selected as outgroups. At the nodes, bootstrap support values for ML (≥ 70%) and BYPP (≥ 0.90) are displayed (ML/PP). Type species strains are denoted by "*". Newly generated sequences are in blue bold.

Culture characteristics – Colonies on PDA flat with entire margin, no aerial mycelium, surface buff, covered with olivaceous-grey to iron-grey acervuli, reverse buff to pale olivaceous-grey, growth 67 mm in 7 d.

Material examined – China, Guangxi Province, Nanning City, Guangxi Medicinal Botanical Garden, on leaf spot of *Hymenocallis littoralis* (Amaryllidaceae), 1 October 2017, Q. Zhang, (HGUP 22091), living culture GUCC 12158, GUCC 12159; *ibid*., on leaf spot of *Houttuynia cordata* (Saururaceae), (HGUP 22092), living culture GUCC 12160, GUCC 12161; *ibid*., on leaf spot of *Piper sarmentosum* (Piperaceae), (HGUP 22093), living culture GUCC 12162, GUCC 12163; *ibid*., on leaf spot of *Cissus hexangularis* (Vitaceae), (HGUP 22094), living culture GUCC 12167, GUCC 12168.

Notes – The strains (GUCC 12158, GUCC 12159, GUCC 12160, GUCC 12161, GUCC 12162, GUCC 12163, GUCC 12167 and GUCC 12168) are phylogenetically grouped with *Colletotrichum truncatum* with high bootstrap support (ML/BI: 100/1, Fig. 36). The conidiogenous and conidia of strain GUCC 12167 are quite similar to *C. truncatum* illustrated and described by Damm et al. (2009). However, the strain (GUCC 12167) in this study has larger appressoria (8–52.5 × 6.5–17 µm *vs.* 4–19 × 4–10 µm). Based on the phylogenetic tree and the morphology of conidiogenous and conidia, we identified our collections as *C. truncatum*.

Discussion

With the inclusion of four genomes (*C. gardenia* GUCC 12049, *C. jiangxiense* GUCC 12055, *C. endopyhtica* GUCC 12108, and *C. siamense* GUCC 12174) presented in this study, more genomes within this genus are now available, enabling analysis of evolution between different members of *Colletotrichum* at a genus-wide level. The comparative analyses show that they vary significantly in the number of CAZymes. For example, twenty of them have more than 800 CAZymes, and eight have fewer than 600 CAZymes. In general, the *C. gloeosporioides* species complex contains the largest average number (866) of CAZymes, which might be one of the feasible explanations for why the species of *C. gloeosporioides* species complex can infect 283 eudicots, monocots, and gymnosperms plants (Talhinhas & Baroncelli 2021). In contrast, *Colletotrichum sansevieriae* in the *C. agaves* species complex contains a minimum amount (549) of CAZymes, which might explain why *C. sansevieriae* only appears *Sansevieria* sp. plants. Furthermore, the number of CAZymes within the genus differed based on host range rather than phylogenetic relationship. In keeping with the hypothesis that the numbers of CAZyme proteins are influenced by their host ranges. It was observed that the larger members of the *C. acutatum* species complex showed more similarities in their CAZymes to that of the *C. gloeosporioides* and *C. boninense* species complexes rather than to more closely related species such as *C. orchidophilum* IMI 309357 (Fig. 1). Coincidentally, the species in the *C. acutatum*, *C. boninense*, and *C. gloeosporioides* complexes are especially common and polyphagous (Jayawardena et al. 2021a, Talhinhas & Baroncelli 2021). It has previously also been shown that the larger number of fungi CAZymes may be partly responsible for the wide host range (Blanco-Ulate et al. 2014, Chen et al. 2022, Liu et al. 2022).

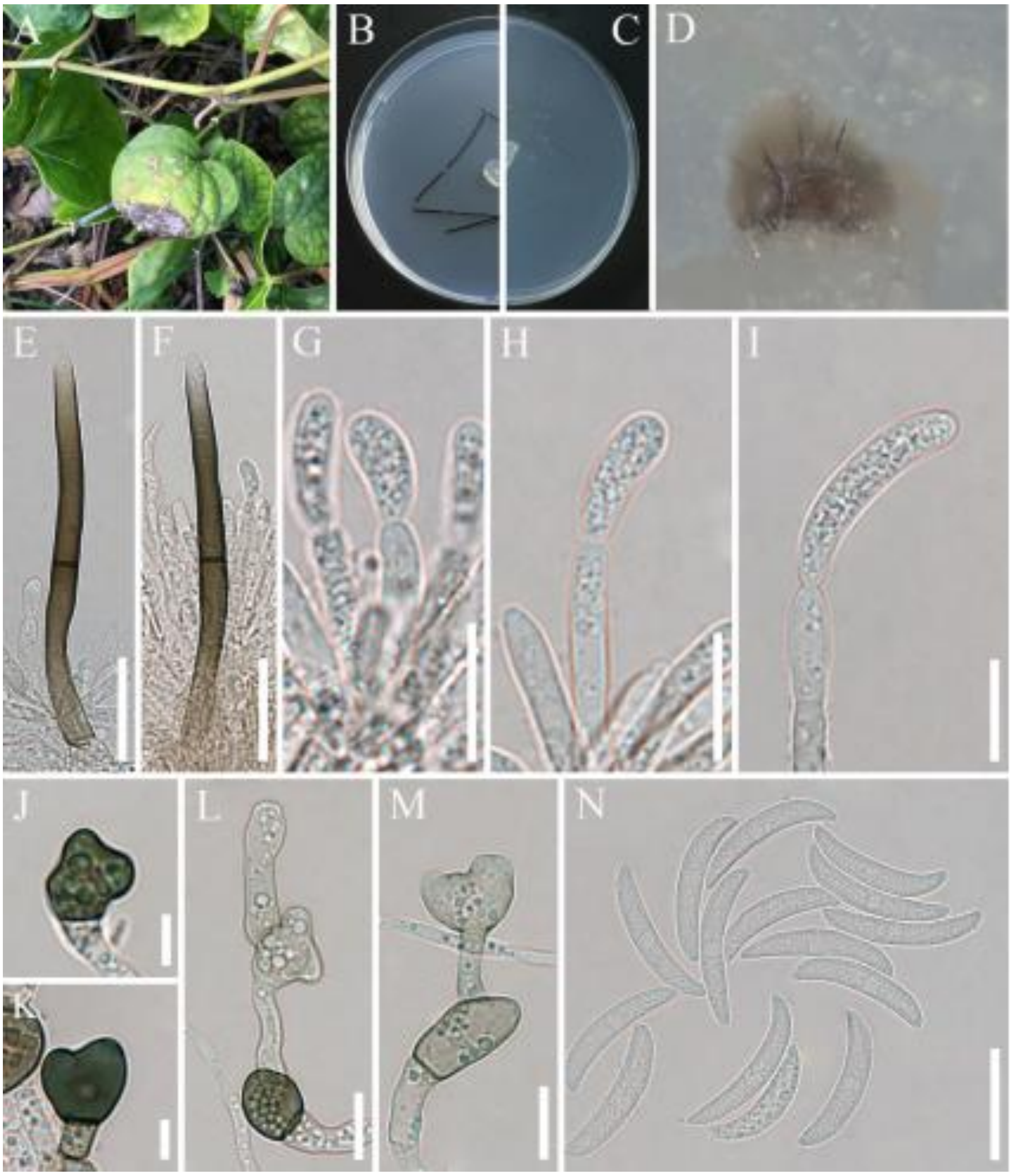


Figure 37 – *Colletotrichum truncatum* (GUCC 12167). A Host. B, C Upper and Reverse view of the colony. D Conidiomata. E–F Seta. G–I Conidiophores. J–M Appressoria. N. Conidia. Scale bars: E–F, N = 20 µm, G–I, L–M = 10 µm, J–K = 5 µm.

Species in *C. acutatum*, *C. boninense*, *C. dracaenophilum*, and *C. gloeosporioides* species complexes have been associated with both dicots and monocots, such as *C. fioriniae* and *C. siamense* (Jayawardena et al. 2021a). However, members of *C. bambusicola*, *C. caudatum*, and *C. graminicola* species complexes are mostly restricted to Poaceae (Crouch et al. 2009, Crouch 2014, Talhinhas & Baroncelli 2021, Liu et al. 2022). Relative to dicotyledons, grasses have very low levels of pectin, xyloglucan in plant cell walls (Cosgrove 1997, Vogel 2008). The activities of PCW degrading enzymes in grasses or dicot plants are also known to have a preference (King et al. 2011). To detect whether the PCW degrading enzymes diversity is correlated to the specificity of their hosts, we compared the number of PCW degrading enzymes coding genes of species restricted to Poaceae with other. In general, species in *C. graminicola* species complex have lesser pectinases belonging to families PL1, PL3, PL4, GH28, GH43, and GH78 than fungi not restricted in commelinoid monocotyledons plants (e.g. Poaceae and Cyperaceae) (Fig. 3), which agrees with the fact that plant cell walls of grasses are composed of lower levels of pectin than dicots and non-commelinoid monocotyledons plants (Cosgrove 1997, Vogel 2008). This is consistent with that monocot pathogens typically contain fewer pectinases than fungal pathogens that infect dicots (Zhao et al. 2014). This hypothesis was also confirmed by *C. higginsianum* encoding more than twice as many pectin-degrading enzymes as *C. graminicola* (86 *vs.* 42), and most of the pectin-degrading enzymes (62%) in *C. higginsianum* are activated during necrotrophy (O'Connell et al. 2012), which explained the importance of pectinase for *Colletotrichum* infected plants. Excepting GH3, there are no significant differences in the diversity of number of hemicellulose degrading enzymes between *C. graminicola* species complex and other fungi in this study. It should be noted that dicots and grasses have different levels of xylans and xyloglucan in the primary cell wall but approximately the same level in the secondary cell wall (Cosgrove 1997, Vogel 2008). Consequently, we hypothesize that the host preference of *Colletotrichum* may be linked to the type and quantity of gene families encoding pectinase.

Morphological and multi-locus phylogenetic analyses were employed to identify *Colletotrichum* species associated with medicinal plants from Guangxi, Guizhou, Sichuan, and Yunnan provinces in China. Our 141 isolates were allocated to eight different *Colletotrichum* species complexes, including the *C. acutatum* (*C. godetiae* and *C. radermacherae*), *C. boninense* (*C. boninense*, *C. celtidis*, and *C. karstii*), *C. destructivum* (*C. tabacum*), *C. dracaenophilum* (*C. cypericola* and *C. schefflerae*), *C. gloeosporioides* (*C. castaneae*, *C. cordylinicola*, *C. endopyhtica*, *C. fructicola*, *C. gardeniae*, *C. gloeosporioides*, *C. grevilleae*, *C. jiangxiense*, *C. kunmingense*, *C. ligustri*, and *C. siamense*), *C. orchidearum* (*C. plurivorum* and *C. vittalense*), *C. spaethianum* (*C. iris*) and *C. truncatum* (*C. truncatum*) complexes. Particularly, this study differentiated seven novel species, viz. *C. castaneae*, *C. cypericola*, *C. gardeniae*, *C. kunmingense*, *C. ligustri*, *C. radermacherae* and *C. schefflerae*. Among our 141 strains, only 24 were isolated from monocot medicinal plants. Among them, *C. fructicola* (*C. gloeosporioides* species complex), *C. karsti* (*C. boninense* species complex), *C. siamense* (*C. gloeosporioides* species complex), and *C. truncatum* (*C. truncatum* species complex) appeared on both monocot/dicot medicinal plants. This proves that these complexes have a broad host range.

There are 16 species complexes accepted in *Colletotrichum* (Chen et al. 2022, Liu et al. 2022). The *C. gloeosporioides* complex has the largest number of members, followed by the *C. acutatum* and *C. boninense* complexes (Bhunjun et al. 2021, Jayawardena et al. 2021a, Liu et al. 2022). Coincidentally, most strains (110/141) analayzed in this study belong to the *C. boninense* and *C. gloeosporioides* complexes, with more than half of the strains (75/141) assigned to the *C. gloeosporioides* species complex (Fig. 18). Yet, only eight strains in this study were assigned to the *C. acutatum* complex. One possibility is the result of insufficient sampling, whereas only 7.1% of strains (68/952) belong to the *C. acutatum* complex from examined 952 *Colletotrichum* strains in China (Liu et al. 2022). Alternatively, the *C. acutatum* complex probably occurs in medicinal plants or the subtropical regions of southwest China at a low frequency. Yang et al (2011) and Zheng et al (2022) confirmed this hypothesis, showing that no members of the *C. acutatum* complex were found on Orchidaceae and aquatic plants in southwest China. Although species in the *C. acutatum* complex are known to inhabit a wide variety of hosts, the range of known hosts appears to be lower than previously assumed (Damm et al. 2012a, Talhinhas & Baroncelli 2021).

Colletotrichum siamense, in the *C. gloeosporioides* complex, was the most prevalent isolate in this study (20% of total isolates). Strains of *C. siamense* are also associated with medicinal plants *Capsicum annuum* and *Morus alba* in Southwest China (Liu et al. 2016b, Xue et al. 2019). Talhinhas & Baroncelli (2021) found that *C. siamense* and *C. gloeosporioides* were associated with the greatest number of host species by recording 1358 different species host of *Colletotrichum*. These findings are consistent with the fact that *C. siamense* populations often appear in tropical and subtropical regions. This species is a common pathogen of a wide range of plants (Weir et al. 2012, de Silva et al. 2019). Small subclades within the *C siamense* clade are consistent with the phylogenomic tree (Figs 1,18). Based on our phylogenetic data, this taxon has a high intra-specific diversity. *Colletotrichum siamense sensu lato*, as a distinct species within the *C. gloeosporioides* complex, has been the subject of much controversy in the past (Weir et al. 2012, Sharma et al. 2015). There are seven species previously described closely related to *C. siamense*, i.e., *C. communis* (Sharma et al. 2015), *C. dianesei* (Lima et al. 2013), *C. endomangiferae* (Vieira et al. 2014), *C. hymenocallidis* (Yang et al. 2009), *C. jasmini-sambac* (Wikee et al. 2011), *C. melanocaulon* (Doyle et al. 2013) and *C. murrayae* (Peng et al. 2012). Due to the lack of independent evolutionary lineages within *C. siamense sensu lato*, Liu et al. (2016a) concluded that it was a single species rather than a species complex. However, some species in this clade remain ambiguous. Using previously published data (Tibpromma et al. 2018, Qiao et al. 2021, Yu et al. 2022), we could not reproduce the phylogenetic separation of these four species (*C. menglaense*, *C. pandanicola*, *C. parvisporum*, and *C. siamense*). *Colletotrichum menglaense*, *C. pandanicola* and *C. parvisporum* are close to *C. siamense* in our phylogenetic tree (Fig. 18). Based on evidence from phylogeny, we synonymise *C. menglaense*, *C. pandanicola* and *C. parvisporum* to *C. siamense*.

To provide a better understanding when defining the species complex boundaries of *Colletotrichum*, we generated a whole-genome phylogenetic tree. The phylogenomic tree (Fig. 1) exhibited a roughly similar topology to the five-locus gene tree (Supplementary Fig. 1). Additionally, most species complexes formed well-supported clades, except the *C. spaethianum* species complex, which did not form a monophyletic clade. The same phenomenon was also introduced by Liu et al. (2022). Moreover, we found that the bootstrap value of the *C. spaethianum* species complex was not high (ML/BI = 78/-, Supplementary Fig. 1), which represents the instability of this branch. Whether the species within this group could form one species complex should be further studied. All of the species complexes, except for the *C. truncatum* species complex, were found to occupy the same placement in the phylogenomic tree (Fig. 1) and the five-locus gene tree (Supplementary Fig. 1). The addition of more strains in the five-locus gene tree (Supplementary Fig. 1) may be responsible for the different placement of the *C. truncatum* species complex in the two data sets. This phenomenon is also observed in Liu et al. (2022). The branch lengths of the *C. gloeosporioides* species complex were much shorter than other species complexes (Fig. 1, Supplementary Fig. 1) due to the small number of phylogenetically informative characters. This phenomenon was also mentioned by Weir et al. (2012). Some clades of the *C. gloeosporioides* species complex in the five-locus gene tree (Supplementary Fig. 1) had low bootstrap values and had different placements compared to the whole-genome tree (Fig. 1). the species boundaries are still not well defined for several species in this species complex, e.g., in the case of the sequences of the five loci (Fig. 18) of *C. citrulli*, *C. dimorphum*, *C. jiangxiense*, *C. kahawae* and its closest relatives. A follow-up study is thus necessary to clarify these species.

In conclusion, our study obtained 141 isolates representing 23 taxa, including seven novel species, by investigating *Colletotrichum* species associated with medicinal plants in southwest China. We also systemically identified gene families encoding CAZymes from the predicted proteomes of 59 genomes belonging to different species complexes of *Colletotrichum*. Comparative analysis revealed that *Colletotrichum* spp. exhibit tremendous diversity in the number and variety of CAZymes. In addition, *Colletotrichum* species which are common and polyphagous, contain more CAZymes. Furthermore, species in the *C. graminicola* species complex that only infect Poaceae plants, contain less pectinase-encoding genes than the rest of fungi. Results from this study provide insights into the variety and expansion of *Colletotrichum* CAZyme families and reveal the relationships of gene families encoding pectinase of *Colletotrichum* with their host preference. In the future, we can utilize host preference to understand and minimize disease prevalence and focus on pectinase-coding genes to understand the mechanism of host preference of *Colletotrichum*.

Acknowledgements

Acknowledgement for the data support from Plant Data Center of Chinese Academy of Sciences (https://www.plantplus.cn). This research is supported by the following projects: Guizhou Science & Technology Department of International Cooperation Base project ([2018]5806), National Natural Science Foundation of China (No. 31972222, 31660011), Program of Introducing Talents of Discipline to Universities of China (111 Program, D20023), Talent project of Guizhou Science and Technology Cooperation Platform ([2019]5641, [2019]13), the project of Guizhou Provincial Education Department ([2021]001), and Guizhou Science and Technology Innovation Talent Team Project ([2020]5001). RS Jayawardena would like to thank the National Research Council of Thailand, Grant for new researcher NRCT5-TRG630010-01, entitled "Biodiversity, taxonomy, phylogeny and evolution of *Colletotrichum* in northern Thailand". We would like to thank Elizabeth Mary Anderson for language editing. K.D. Hyde thanks the NRCT for the grant "Total fungal diversity in a given forest area with implications towards species numbers, chemical diversity and biotechnology" (grant no. N42A650547). Li Cheng would like to thank the National Natural Science Foundation of China: Grant No. 32260653, Top Technology Talent Project from Guizhou Education Department of China: Grant No. Qian jiao ji [2022]074; Guizhou Provincial Science and Technology Projects of China: Grant No. ZK [2021]142. Feng Yao would like to thank the Science Research Youth Program in Colleges and Universities entitled "lsolation and Diversity studies of Endophytic Fungi from Bamboo" (Qiankeji [2022]153).

References

Bhunjun CS, Phukhamsakda C, Jayawardena RS, Jeewon R et al. 2021 – Investigating species boundaries in *Colletotrichum*. Fungal Diversity 107(1), 107−127. Doi 10.1007/s13225-021-00471-z

Blanco-Ulate B, Morales-Cruz A, Amrine KCH, Labavitch JM et al. 2014 – Genome-wide transcriptional profiling of *Botrytis cinerea* genes targeting plant cell walls during infections of different hosts. Frontiers in plant science 5, 435. Doi 10.3389/fpls.2014.00435

Bruen TC, Philippe H, Bryant D. 2006 – A simple and robust statistical test for detecting the presence of recombination. Genetics 172(4), 2665−2681. Doi 10.1534/genetics.105.048975

Buchta V, Nekolová J, Jirásková N, Bolehovská R et al. 2019 – Fungal Keratitis Caused by *Colletotrichum dematium*: Case Study and Review. Mycopathologia 184(3), 441–453. Doi 10.1007/s11046-019-00335-w

Cai L, Hyde KD, Taylor PWJ, Weir BS et al. 2009 – A polyphasic approach for studying *Colletotrichum*. Fungal Diversity 39(1), 183–204.

Cannon PF, Buddie AG, Bridge PD. 2008 – The typification of *Colletotrichum gloeosporioides*. Mycotaxon 104, 189–204.

Cannon PF, Damm U, Johnston PR, Weir BS. 2012 – *Colletotrichum*: current status and future directions. Studies in mycology 73(1), 181–213. Doi 10.3114/sim0014

Cantalapiedra CP, Hernández-Plaza A, Letunic I, Bork P et al. 2021 – eggNOG-mapper v2: Functional Annotation, Orthology Assignments, and Domain Prediction at the Metagenomic Scale, Molecular Biology and Evolution 38(12), 5825–5829. Doi 10.1093/molbev/msab293

Capella-Gutiérrez S, Silla-Martínez JM, Gabaldón T. 2009 – trimAl: a tool for automated alignment trimming in large-scale phylogenetic analyses. Bioinformatics 25(15), 1972–1973. Doi 10.1093/bioinformatics/btp348

Carbone I, Kohn LM. 1999 – A method for designing primer sets for speciation studies in filamentous ascomycetes. Mycologia 91(3), 553–556. Doi 10.1080/00275514.1999.12061051

Carpita NC, Gibeaut DM. 1993 – Structural models of primary cell walls in flowering plants: consistency of molecular structure with the physical properties of the walls during growth. The Plant Journal 3(1), 1–30. Doi 10.1111/j.1365-313X.1993.tb00007.x

Chaiwan N, Gomdola D, Wang S, Monkai J et al. 2021 – https://gmsmicrofungi.org: an online database providing updated information of microfungi in the Greater Mekong Subregion. Mycosphere 12(1), 1409–1422. Doi 10.5943/mycosphere/12/1/19

Chen Y, Wu T, Tian W, Ilyukhin E et al. Maharachchikumbura S. 2022 – Comparative genomics provides new insights into the evolution of *Colletotrichum*. Mycosphere 13(2), 134–187. Doi 10.5943/mycosphere/si/1f/5

Chethana KWT, Manawasinghe IS, Hurdeal VG, Bhunjun CS et al. 2021 – What are fungal species and how to delineate them? Fungal Diversity 109(1), 1–25. Doi 10.1007/s13225-021-00483-9

Chi XL, Zhang ZJ, Xu XT, Zhang XB et al. 2017 – Threatened medicinal plants in China: Distributions and conservation priorities. Biological Conservation 210, 89–95. Doi 10.1016/j.biocon.2017.04.015

Chin C-S, Alexander DH, Marks P, Klammer AA et al. 2013 – Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. Nature methods 10(6), 563−569. Doi 10.1038/nmeth.2474

Chin C-S, Peluso P, Sedlazeck FJ, Nattestad M et al. 2016 – Phased diploid genome assembly with single-molecule real-time sequencing. Nature Methods 13(12), 1050−1054. Doi 10.1038/nmeth.4035

Cosgrove DJ. 1997 – Assembly and enlargement of the primary cell wall in plants. Annual Review of Cell and Developmental Biology 13, 171–201. Doi 10.1146/annurev.cellbio.13.1.171

Crouch J, O'Connell R, Gan P, Buiate E et al. 2014 – The genomics of *Colletotrichum*. In: Genomics of plant-associated fungi: monocot pathogens. Springer, pp. 69–102. Doi 10.1007/978-3-662-44053-7_3

Crouch JA. 2014 – *Colletotrichum caudatum s. l.* is a species complex. IMA fungus 5(1), 17−30. Doi 10.5598/imafungus.2014.05.01.03

Crouch JA, Clarke BB, White Jr JF, Hillman BI. 2009 – Systematic analysis of the falcate-spored graminicolous *Colletotrichum* and a description of six new species from warm-season grasses. Mycologia 101(5), 717−732. Doi 10.3852/08-230

Crous PW, Groenewald JZ, Risède J-M, Simoneau P et al. 2004 – Calonectria species and their *Cylindrocladium anamorphs*: species with sphaeropedunculate vesicles. Studies in Mycology 50, 415–430.

Damm U, Cannon PF, Liu F, Barreto RW et al. 2013 – The *Colletotrichum orbiculare* species complex: Important pathogens of field crops and weeds. Fungal Diversity 61(1), 29−59. Doi 10.1007/s13225-013-0255-4

Damm U, Cannon PF, Woudenberg JHC, Crous PW. 2012a – The *Colletotrichum acutatum* species complex. Studies in mycology 73, 37−113. Doi 10.3114/sim0010

Damm U, Cannon PF, Woudenberg JHC, Johnston PR et al. 2012b – The *Colletotrichum boninense* species complex. Studies in mycology 73, 1−36. Doi 10.3114/sim0002

Damm U, O'Connell RJ, Groenewald JZ, Crous PW. 2014 – The *Colletotrichum destructivum* species complex – hemibiotrophic pathogens of forage and field crops. Studies in mycology 79, 49−84. Doi 10.1016/j.simyco.2014.09.003

Damm U, Sato T, Alizadeh A, Groenewald JZ et al. 2019 – The *Colletotrichum dracaenophilum*, *C. magnum* and *C. orchidearum* species complexes. Studies in Mycology 92, 1−46. Doi 10.1016/j.simyco.2018.04.001

Damm U, Sun YC, Huang CJ. 2020 – *Colletotrichum eriobotryae* sp. nov. and *C. nymphaeae*, the anthracnose pathogens of loquat fruit in central Taiwan, and their sensitivity to azoxystrobin. Mycological Progress 19(4), 367−380. Doi 10.1007/s11557-020-01565-9

Damm U, Woudenberg JHC, Cannon PF, Crous PW. 2009 – *Colletotrichum* species with curved conidia from herbaceous hosts. Fungal Diversity 39, 45–87.

de Silva DD, Groenewald JZ, Crous PW, Ades PK et al. 2019 – Identification, prevalence and pathogenicity of *Colletotrichum* species causing anthracnose of *Capsicum annuum* in Asia. IMA fungus 10(1), 1−32. Doi 10.1186/s43008-019-0001-y

Dean R, Van Kan JA, Pretorius ZA, Hammond-Kosack KE et al. 2012 – The Top 10 fungal pathogens in molecular plant pathology. Molecular Plant Pathology 13(4), 414−430. Doi 10.1111/j.1364-3703.2011.00783.x

Douaiher MN, Nowak E, Durand R, Halama P et al. 2007 – Correlative analysis of *Mycosphaerella graminicola* pathogenicity and cell wall-degrading enzymes produced in vitro: the importance of xylanase and polygalacturonase. Plant pathology 56(1), 79–86. Doi 10.1111/j.1365-3059.2006.01460.x

Doyle VP, Oudemans PV, Rehner SA, Litt A. 2013 – Habitat and host indicate lineage identity in *Colletotrichum gloeosporioides s.l.* from wild and agricultural landscapes in North America. PLoS One 8(5), e62394. Doi 10.1371/journal.pone.0062394

Drula E, Garron M-L, Dogan S, Lombard V et al. 2021 – The carbohydrate-active enzyme database: functions and literature. Nucleic Acids Research 50(D1), D571−D577. http://www.cazy.org/ Doi 10.1093/nar/gkab1045

Emms DM, Kelly S. 2015 – OrthoFinder: solving fundamental biases in whole genome comparisons dramatically improves orthogroup inference accuracy. Genome Biology 16(1), 157. Doi 10.1186/s13059-015-0721-2

Engelsdorf T, Will C, Hofmann J, Schmitt C et al. 2016 – Cell wall composition and penetration resistance against the fungal pathogen *Colletotrichum higginsianum* are affected by impaired starch turnover in Arabidopsis mutants. Journal of Experimental Botany 68(3), 701–713. Doi 10.1093/jxb/erw434

Ensembl Fungi. 2023 – http://fungi.ensembl.org/ (Accessed on February 10, 2023).

Fu M, Crous PW, Bai Q, Zhang PF et al. 2019 – *Colletotrichum* species associated with anthracnose of Pyrus spp. in China. Persoonia: Molecular Phylogeny and Evolution of Fungi 42, 1–35. Doi 10.3767/persoonia.2019.42.01

Gan P, Narusaka M, Kumakura N, Tsushima A et al. 2016 – Genus-wide comparative genome analyses of *Colletotrichum* species reveal specific gene family losses and gains during adaptation to specific infection lifestyles. Genome biology and evolution 8(5), 1467–1481. Doi 10.1093/gbe/evw089

Glass NL, Donaldson GC 1995 – Development of primer sets designed for use with the PCR to amplify conserved genes from filamentous ascomycetes. Applied and Environmental Microbiology 61, 1323–1330. Doi 10.1128/aem.61.4.1323-1330.1995

Guan YM, Ma YY, Jin Q, Wang QX et al. 2020 – Multi-locus phylogeny and taxonomy of the fungal complex associated with rusty root rot of *Panax ginseng* in China. Frontiers in Microbiology 11, 618942. Doi 10.3389/fmicb.2020.618942

Haas BJ, Salzberg SL, Zhu W, Pertea M et al. 2008 – Automated eukaryotic gene structure annotation using EVidenceModeler and the Program to Assemble Spliced Alignments. Genome Biology 9, R7. Doi 10.1186/gb-2008-9-1-r7

Hall T, Biosciences I, Carlsbad C. 2011 – BioEdit: an important software for molecular biology. GERF Bull Biosci 2(1), 60−61.

Hou LW, Liu F, Duan WJ, Cai L. 2016 – *Colletotrichum aracearum* and *C. camelliae-japonicae*, two holomorphic new species from China and Japan. Mycosphere 7(8), 1111–1123. Doi 10.5943/mycosphere/si/2c/4

Howard LM, Gilbert L, Zwerner JP, Snyder KM et al. 2016 – Subcutaneous *Colletotrichum truncatum* infection in a child. The Pediatric infectious disease journal 35(4), 455–457. Doi 10.1097/inf.0000000000001038

Huelsenbeck JP, Ronquist F. 2001 – MRBAYES: Bayesian inference of phylogenetic trees. Bioinformatics 17(8), 754–755. Doi 10.1093/bioinformatics/17.8.754

Huson DH, Bryant D. 2006 – Application of phylogenetic networks in evolutionary studies. Molecular biology and evolution 23(2),254–267. Doi 10.1093/molbev/msj030

Index fungorum. 2022 – http://www.indexfungorum.org/Names/Names.asp

Trifinopoulos J, Nguyen LT, von Haeseler A, Minh BQ. 2016 – W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. Nucleic Acids Research 44 (W1), W232–W235. Doi 10.1093/nar/gkw256

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(1), 3–18. Doi 10.1007/s13225-015-0351-8

Jayawardena RS, Bhunjun CS, Hyde KD, Gentekaki E et al. 2021a – *Colletotrichum*: lifestyles, biology, morpho-species, species complexes and accepted species. Mycosphere 12(1), 519–669. Doi 10.5943/mycosphere/12/1/7

Jayawardena RS, Huang JK, Jin BC, Yan JY et al. 2016 – An account of *Colletotrichum* species associated with strawberry anthracnose in China based on morphology and molecular data. Mycosphere 7(8), 1147−1191. Doi 10.5943/mycosphere/si/2c/6

Jayawardena RS, Hyde KD, de Farias ARG, Bhunjun CS et al. 2021b – What is a species in fungal plant pathogens? Fungal Diversity 109(1), 239–266. Doi 10.1007/s13225-021-00484-8

Kalyaanamoorthy S, Minh BQ, Wong TKF, von Haeseler A et al. 2017 – ModelFinder: fast model selection for accurate phylogenetic estimates. Nature Methods 14, 587–589. Doi 10.1038/nmeth.4285

Katoh K, Misawa K, Kuma KI, Miyata T. 2002 – MAFFT: A novel method for rapid multiple sequence alignment based on fast Fourier transform. Nucleic Acids Research 30(14), 3059−3066. Doi 10.1093/nar/gkf436

Katoh K, Rozewicki J, Yamada KD. 2019 – MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. Briefings in bioinformatics 20(4), 1160−1166. Doi 10.1093/bib/bbx108

Khan H, Rauf A. 2014 – Medicinal plants: economic perspective and recent developments. World Applied Sciences Journal 31(11), 1925–1929.

Khanum R, Mumtaz AS, Kumar S. 2013 – Predicting impacts of climate change on medicinal asclepiads of Pakistan using Maxent modeling. Acta Oecologica 49, 23–31. Doi 10.1016/j.actao.2013.02.007

Kikot GE, Hours RA, Alconada TM. 2009 – Contribution of cell wall degrading enzymes to pathogenesis of *Fusarium graminearum*: a review. Journal of basic microbiology 49(3), 231–241. Doi 10.1002/jobm.200800231

King B C, Waxman K D, Nenni N V, Walker L P et al. 2011 – Arsenal of plant cell wall degrading enzymes reflects host preference among plant pathogenic fungi. Biotechnology for Biofuels 4, 4. Doi 10.1186/1754-6834-4-4

Kolmogorov M, Yuan J, Lin Y, Pevzner PA. 2019 – Assembly of long, error-prone reads using repeat graphs. Nature biotechnology 37, 540−546. Doi 10.1038/s41587-019-0072-8

Koren S, Walenz BP, Berlin K, Miller JR et al. 2017 – Canu: scalable and accurate long-read assembly via adaptive k-mer weighting and repeat separation. Genome research 27(5), 722−736. Doi 10.1101/gr.215087.116

Li JB, Bao YL, Wang ZR, Yang Q et al. 2022 – Research progress in diseases of *Panax notoginseng*. Physiological and Molecular Plant Pathology 121, 101878. Doi 10.1016/j.pmpp.2022.101878

Lima JS, Figueiredo JG, Gomes RG, Stringari D et al. 2012 – Genetic diversity of *Colletotrichum* spp. an endophytic fungi in a medicinal plant, Brazilian pepper tree. International Scholarly Research Notices, 2012, 7. Doi 10.5402/2012/215716

Lima NB, de A. Batista MV, De Morais MA, Barbosa MAG et al. 2013 – Five *Colletotrichum* species are responsible for mango anthracnose in northeastern Brazil. Fungal Diversity 61(1), 75–88. Doi 10.1007/s13225-013-0237-6

Liu F, Cai L, Crous PW, Damm U. 2014 – The *Colletotrichum gigasporum* species complex. Persoonia: Molecular Phylogeny and Evolution of Fungi 33, 83–97. Doi 10.3767/003158514x684447

Liu F, Damm U, Cai L, Crous PW. 2013 – Species of the *Colletotrichum gloeosporioides* complex associated with anthracnose diseases of Proteaceae. Fungal Diversity 61(1), 89–105. Doi 10.1007/s13225-013-0249-2

Liu F, Ma Z, Hou L, Diao Y et al. 2022 – Updating species diversity of *Colletotrichum*, with a phylogenomic overview. Studies in Mycology 101, 1–56. Doi 10.3114/sim.2022.101.01

Liu F, Wang M, Damm U, Crous PW et al. 2016a – Species boundaries in plant pathogenic fungi: a *Colletotrichum* case study. BMC evolutionary biology 16, 81. Doi 10.1186/s12862-016-0649-5

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: Molecular Phylogeny and Evolution of Fungi 35, 63−86. Doi 10.3767/003158515x687597

Liu FL, Tang GT, Zheng XJ, Li Y et al. 2016b – Molecular and phenotypic characterization of *Colletotrichum* species associated with anthracnose disease in peppers from Sichuan Province, China. Scientific Reports 6, 32761. Doi 10.1038/srep32761

Liu LP, Wang Y, Qiu PL, Zhang B et al. 2020a – *Colletotrichum neorubicola* sp. nov., a new leaf anthracnose pathogen of raspberry from northeast China. Mycological Progress 19, 947−955. Doi 10.1007/s11557-020-01614-3

Liu X, Zheng XJ, Khaskheli MI, Sun Xf et al. 2020b – Identification of *Colletotrichum* Species Associated with Blueberry Anthracnose in Sichuan, China. Pathogens 9(9), 718. Doi 10.3390/pathogens9090718

Manamgoda DS, Udayanga D, Cai L, Chukeatirote E et al. 2013 – Endophytic *Colletotrichum* from tropical grasses with a new species *C. endophytica*. Fungal Diversity 61, 107−115. Doi 10.1007/s13225-013-0256-3

Mistry J, Chuguransky S, Williams L, Qureshi M et al. 2020 – Pfam: The protein families database in 2021. Nucleic Acids Research 49(D1), D412–D419. Doi 10.1093/nar/gkaa913

Moriwaki J, Sato T, Tsukiboshi T. 2003 – Morphological and molecular characterization of *Colletotrichum boninense* sp. nov. from Japan. Mycoscience 44(1), 47–53. Doi 10.1007/s10267-002-0079-7

National Center for Biotechnology Information. 2023 – https://www.ncbi.nlm.nih.gov/ (Accessed on February 10, 2023).

Neergaard P. 1943 – Aarsberetning fra J. E. Ohlens Enkes Plantepatologiske Laboratorium 1 April 1942–31 Marts 8.

Nguyen LT, Schmidt HA, Von Haeseler A, Minh BQ. 2015 – IQ-TREE: A fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Molecular Biology and Evolution 32(1), 268−274. Doi 10.1093/molbev/msu300

Noireung P, Phoulivong S, Liu F, Cai L et al. 2012 – Novel species of *Colletotrichum* revealed by morphology and molecular analysis. Cryptogamie, Mycologie 33(3), 347−362. Doi 10.7872/crym.v33.iss3.2012.347

Nordberg H, Cantor M, Dusheyko S, Hua S et al. 2014 – The genome portal of the Department of Energy Joint Genome Institute: 2014 updates. Nucleic Acids Research 42(D1), D26–D31. https://mycocosm.jgi.doe.gov/mycocosm/home (Accessed on February 10, 2023). Doi 10.1093/nar/gkt1069

O’Connell RJ, Thon MR, Hacquard S, Amyotte SG et al. 2012 – Lifestyle transitions in plant pathogenic *Colletotrichum* fungi deciphered by genome and transcriptome analyses. Nature genetics 44(9), 1060–1065. Doi 10.1038/ng.2372

O’Donnell K, Cigelnik E. 1997 – Two divergent intragenomic rDNA ITS2 types within a monophyletic lineage of the fungus *Fusarium* are nonorthologous. MoIecular Phylogenetics and Evolution 7, 103–116. Doi 10.1006/mpev.1996.0376

Peng LJ, Yang YL, Hyde KD, Bahkali AH et al. 2012 – *Colletotrichum* species on Citrus leaves in Guizhou and Yunnan provinces, China. Cryptogamie, Mycologie 33(3), 267–283. Doi 10.7872/crym.v33.iss3.2012.267

Phoulivong S, Cai L, Parinn N, Chen H et al. 2010 – A new species of *Colletotrichum* from *Cordyline fruticosa* and *Eugenia javanica* causing anthracnose disease. Mycotaxon 114(1), 247−257. Doi 10.5248/114.247

Prihastuti H, Cai L, Chen H, McKenzie E et al. 2009 – Characterization of *Colletotrichum* species associated with coffee berries in northern Thailand. Fungal Diversity 39(1), 89−109.

Qiao M, Li J, Fang LL, Li JY et al. 2021 – Morphology, Phylogeny and Pathogenicity of *Colletotrichum menglaense* sp. nov., Isolated from Air in China. Pathogens 10(10), 1243. Doi 10.3390/pathogens10101243

Quaedvlieg W, Binder M, Groenewald JZ, Summerell BA et al. 2014 – Introducing the consolidated species concept to resolve species in the Teratosphaeriaceae. Persoonia - Molecular Phylogeny and Evolution of Fungi 33(1), 1–40. Doi 10.3767/003158514x681981

Rai M, Agarkar G, Rathod D. 2014 – Multiple applications of endophytic *Colletotrichum* species occurring in medicinal plants. Novel plant bioresources: applications in food, medicine and Cosmetics 227–236. Doi 10.1002/9781118460566.ch18

Ruan J, Li H. 2020 – Fast and accurate long-read assembly with wtdbg2. Nature Methods 17(2), 155−158. Doi 10.1038/s41592-019-0669-3

Sankaranarayanan SR, Ianiri G, Coelho MA, Reza MH et al. 2020 – Loss of centromere function drives karyotype evolution in closely related *Malassezia* species. eLife 9. Doi 10.7554/elife.53944

Senanayake IC, Rathnayaka AR, Marasinghe DS, Calabon MS et al. 2020 – Morphological approaches in studying fungi: collection, examination, isolation, sporulation and preservation. Mycosphere 11(1), 2678−2754. Doi 10.5943/mycosphere/11/1/20

Sharma G, Pinnaka AK, Shenoy BD. 2015 – Resolving the *Colletotrichum siamense* species complex using ApMat marker. Fungal Diversity 71(1), 247–264. Doi 10.1007/s13225-014-0312-7

Stanke M, Keller O, Gunduz I, Hayes A et al. 2006 – AUGUSTUS: *ab initio* prediction of alternative transcripts. Nucleic Acids Research 34, W435−W439. Doi 10.1093/nar/gkl200

Templeton MD, Rikkerink EHA, Solon SL, Crowhurst RN. 1992 – Cloning and molecular characterization of the glyceraldehyde-3-phosphate dehydrogenase-encoding gene and cDNA from the plant pathogenic fungus *Glomerella cingulata*. Gene 122(1), 225–230. Doi 10.1016/0378-1119(92)90055-t

The State Council Information Office of the People's Republic of China, 2016 − The China white paper for traditional Chinese medicine.
http://wwwsciogovcn/zfbps/32832/Document/1534713/1534713html
(Accessed on September 5, 2022).

Talhinhas P, Baroncelli R. 2021 – *Colletotrichum* species and complexes: geographic distribution, host range and conservation status. Fungal Diversity 110(1), 109–198. Doi 10.1007/s13225-021-00491-9

Tao G, Liu ZY, Liu F, Gao YH et al. 2013 – Endophytic *Colletotrichum* species from *Bletilla ochracea* (Orchidaceae), with descriptions of seven new speices. Fungal Diversity 61(1), 139−164. Doi 10.1007/s13225-013-0254-5

Tennakoon DS, Kuo CH, Maharachchikumbura SSN, Thambugala KM et al. 2021 – Taxonomic and phylogenetic contributions to *Celtis formosana*, *Ficus ampelas*, *F. septica*, *Macaranga* *tanarius* and *Morus australis* leaf litter inhabiting microfungi. Fungal Diversity 108(1), 1–215. Doi 10.1007/s13225-021-00474-w

Ter-Hovhannisyan V, Lomsadze A, Chernoff YO, Borodovsky M. 2008 – Gene prediction in novel fungal genomes using an ab initio algorithm with unsupervised training. Genome Research 18(12), 1979−1990. Doi 10.1101/gr.081612.108

Tibpromma S, Hyde KD, Bhat JD, Mortimer PE et al. 2018 – Identification of endophytic fungi from leaves of Pandanaceae based on their morphotypes and DNA sequence data from southern Thailand. MycoKeys 33, 25−67. Doi 10.3897/mycokeys.33.23670

Urban M, Cuzick A, Seager J, Wood V et al. 2020 – PHI-base: the pathogen–host interactions database. Nucleic Acids Research 48(D1), D613−D620. Doi 10.1093/nar/gkz904

Vieira WAS, Michereff SJ, de Morais MA, Hyde KD et al. 2014 – Endophytic species of *Colletotrichum* associated with mango in northeastern Brazil. Fungal Diversity 67(1), 181–202. Doi 10.1007/s13225-014-0293-6

Vogel J. 2008 – Unique aspects of the grass cell wall. Current Opinion in Plant Biology 11(3), 301–307. Doi 10.1016/j.pbi.2008.03.002

Walker BJ, Abeel T, Shea T, Priest M et al. 2014 – Pilon: An integrated tool for comprehensive microbial variant detection and genome assembly improvement. PLoS ONE 9(11): e112963. Doi 10.1371/journal.pone.0112963

Wang QT, Liu F, Hou CL, Cai L. 2021 – Species of *Colletotrichum* on bamboos from China. Mycologia 113(2), 450−458. Doi 10.1080/00275514.2020.1837567

Wang QT, Liu XT, Ma HY, Shen XY et al. 2019 – *Colletotrichum yulongense* sp. nov. and *C. rhombiforme* isolated as endophytes from *Vaccinium dunalianum* var. *urophyllum* in China. Phytotaxa 394(4), 285−298. Doi 10.11646/phytotaxa.394.4.6

Wang YC, Hao XY, Wang L, Xiao B et al. 2016 – Diverse *Colletotrichum* species cause anthracnose of tea plants(*Camellia sinensis* (L.) O. Kuntze). Scientific Reports 6, 35287. Doi 10.1038/srep35287

Weir B, Johnston P, Damm U. 2012 – The *Colletotrichum gloeosporioides* species complex. Studies in Mycology 73, 115−180. Doi 10.3114/sim0011

White TJ, Bruns T, Lee S, Taylor JL. 1990 – Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. PCR protocols: a guide to methods and applications 18, 315–322. Doi 10.1016/b978-0-12-372180-8.50042-1

Wikee S, Cai L, Pairin N, McKenzie EHC et al. 2011 – *Colletotrichum* species from Jasmine (*Jasminum sambac*). Fungal Diversity 46(1), 171–182. Doi 10.1007/s13225-010-0049-x

Wynns AA, Jensen AB, Eilenberg J, Delalibera Júnior I. 2020 – *Colletotrichum nymphaeae* var. *entomophilum* var. nov. a natural enemy of the citrus scale insect, *Praelongorthezia praelonga* (Hemiptera: Ortheziidae). Scientia Agricola 77(5). Doi 10.1590/1678-992x-2018-0269

Xiao CL, Chen Y, Xie SQ, Chen KN et al. 2017 – MECAT: fast mapping, error correction, and de novo assembly for single-molecule sequencing reads. Nature Methods 14(11), 1072−1074. Doi 10.1038/nmeth.4432

Xue LH, Zhang L, Yang XX, Huang XQ et al. 2019 – Characterization, Phylogenetic Analyses, and Pathogenicity of *Colletotrichum* Species on *Morus alba* in Sichuan Province, China. Plant Disease 103(10), 2624−2633. Doi 10.1094/pdis-06-18-0938-re

Yang Y, Liu Z, Cai L, Hyde K et al. 2009 – *Colletotrichum* anthracnose of Amaryllidaceae. Fungal Diversity 39(2), 123–146.

Yang YL, Cai L, Yu ZN, Liu ZY et al. 2011 – *Colletotrichum* species on Orchidaceae in southwest China. Cryptogamie, Mycologie 32(3), 229−253. Doi 10.7872/crym.v32.iss3.2011.229

Yu Z, Jiang X, Zheng H, Zhang H et al. 2022 – Fourteen new species of foliar *Colletotrichum* associated with the invasive plant *Ageratina adenophora* and surrounding crops. Journal of Fungi 8(2), 185. Doi 10.3390/jof8020185

Zhang D, Gao F, Jakovlić I, Zou H et al. 2020 – PhyloSuite: an integrated and scalable desktop platform for streamlined molecular sequence data management and evolutionary phylogenetics studies. Molecular ecology resources 20(1), 348–355. Doi 10.1111/1755-0998.13096

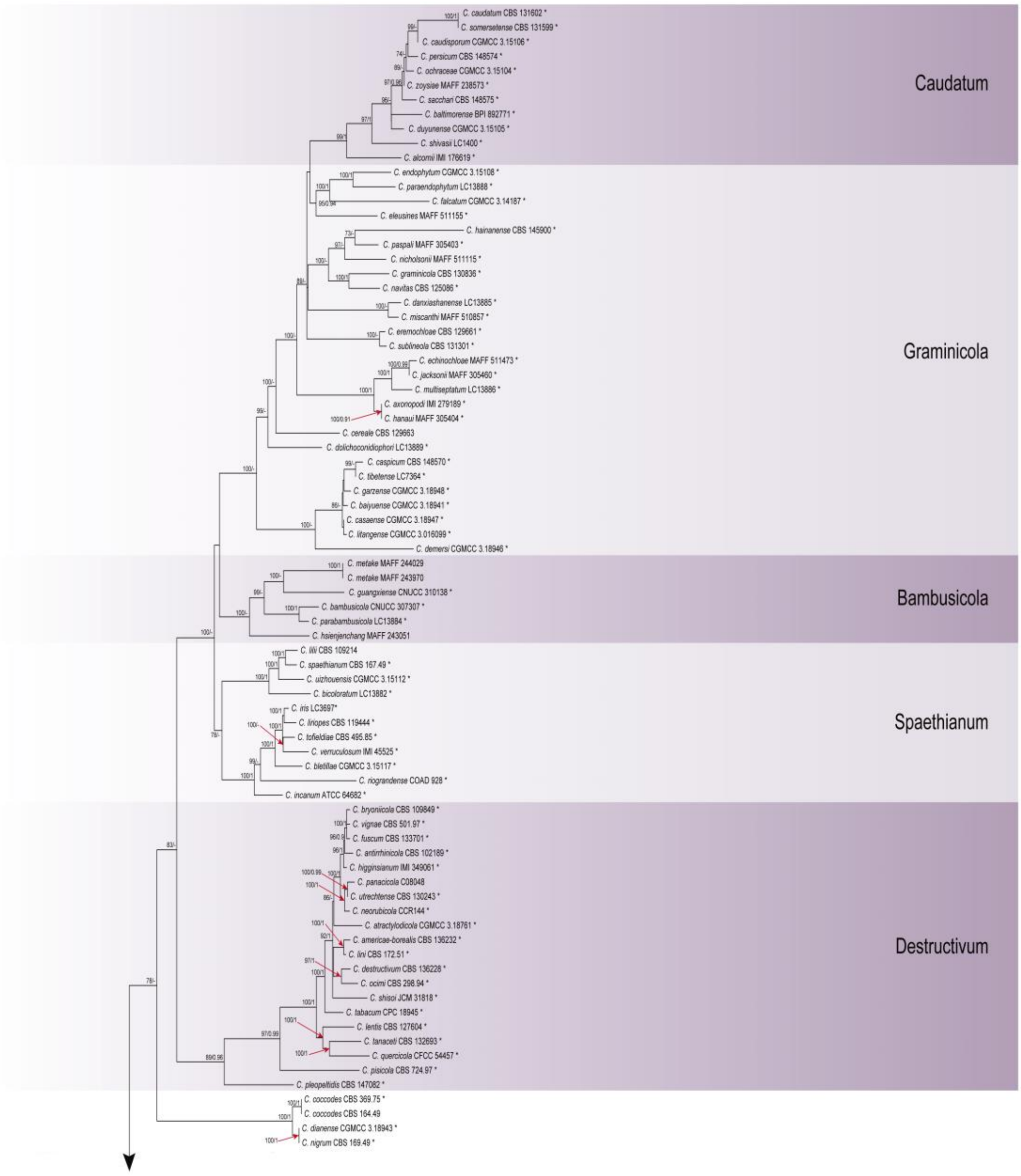
Zhang H, Yohe T, Huang L, Entwistle S et al. 2018 – dbCAN2: a meta server for automated carbohydrate-active enzyme annotation. Nucleic Acids Research 46(W1), W95–W101. Doi 10.1093/nar/gky418

Zhao ZT, Liu HQ, Wang CF, Xu JR. 2014 – Erratum to: comparative analysis of fungal genomes reveals different plant cell wall degrading capacity in fungi. BMC genomics 15, 6. Doi 10.1186/1471-2164-15-6

Zheng H, Yu ZF, Jiang XW, Fang LL et al. 2022 – Endophytic *Colletotrichum* Species from Aquatic Plants in Southwest China. Journal of Fungi 8(1), 87. Doi 10.3390/jof8010087

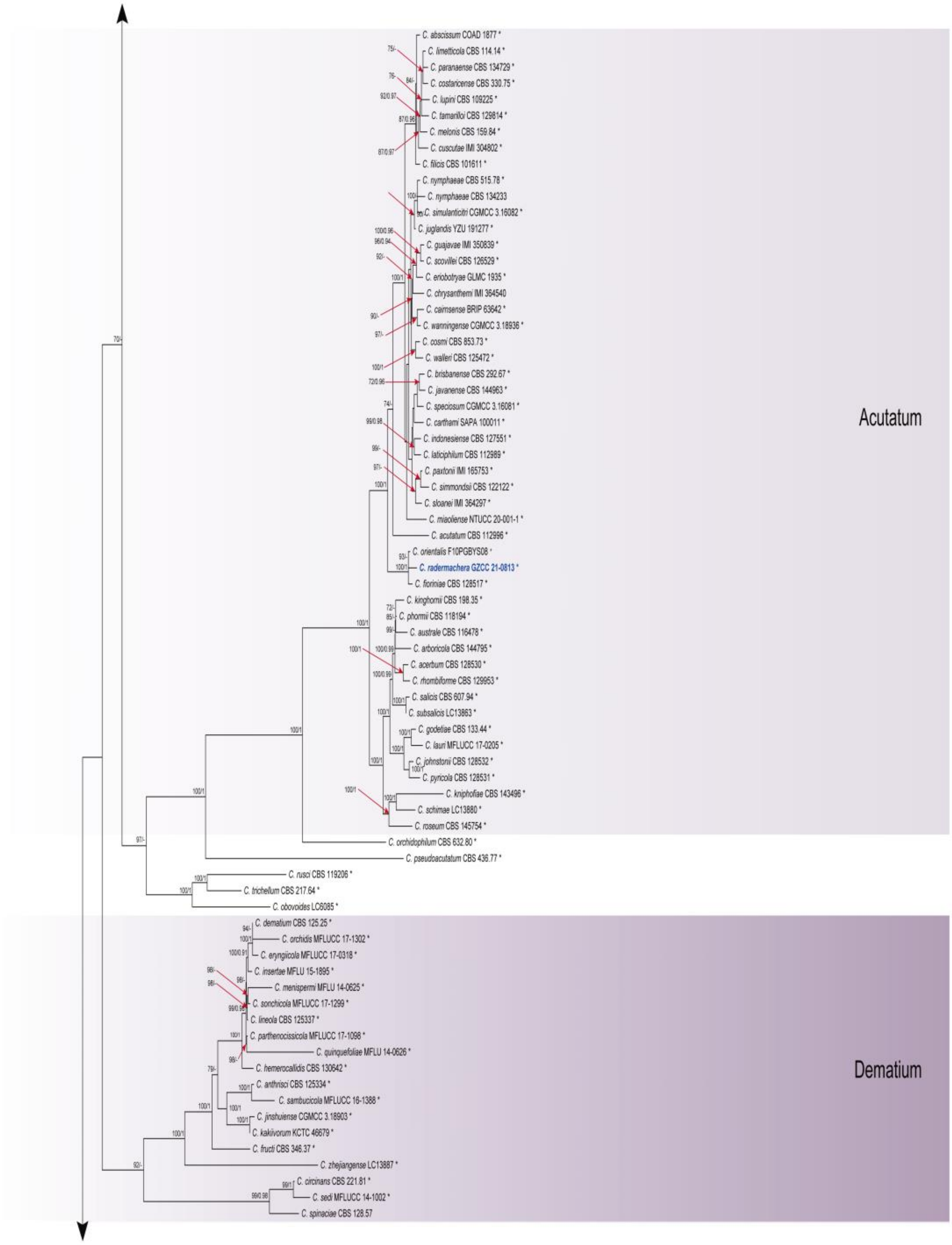
Zhou SX, Qiao LJ, Jayawardena RS, Hyde KD et al. 2019 – Two new endophytic *Colletotrichum* species from *Nothapodytes pittosporoides* in China. MycoKeys 49, 1−49. Doi 10.3897/mycokeys.49.31904

Supplementary Materials

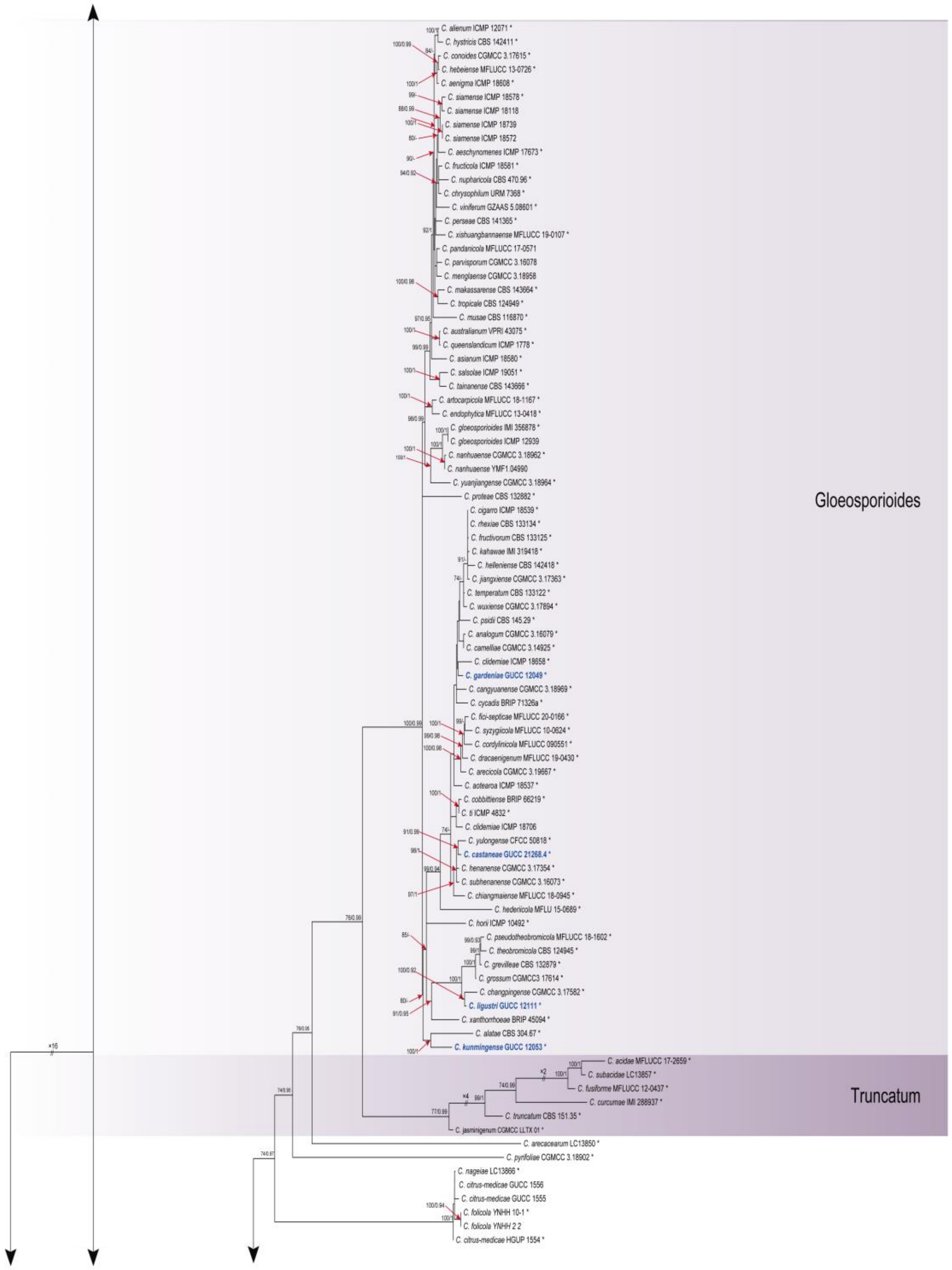


Supplementary Figure 1 – Maximum likelihood tree of *Colletotrichum*. *Verticillium dahliae* (CBS 130341) were selected as an outgroup. At the nodes, bootstrap support values for ML (≥ 70%) and

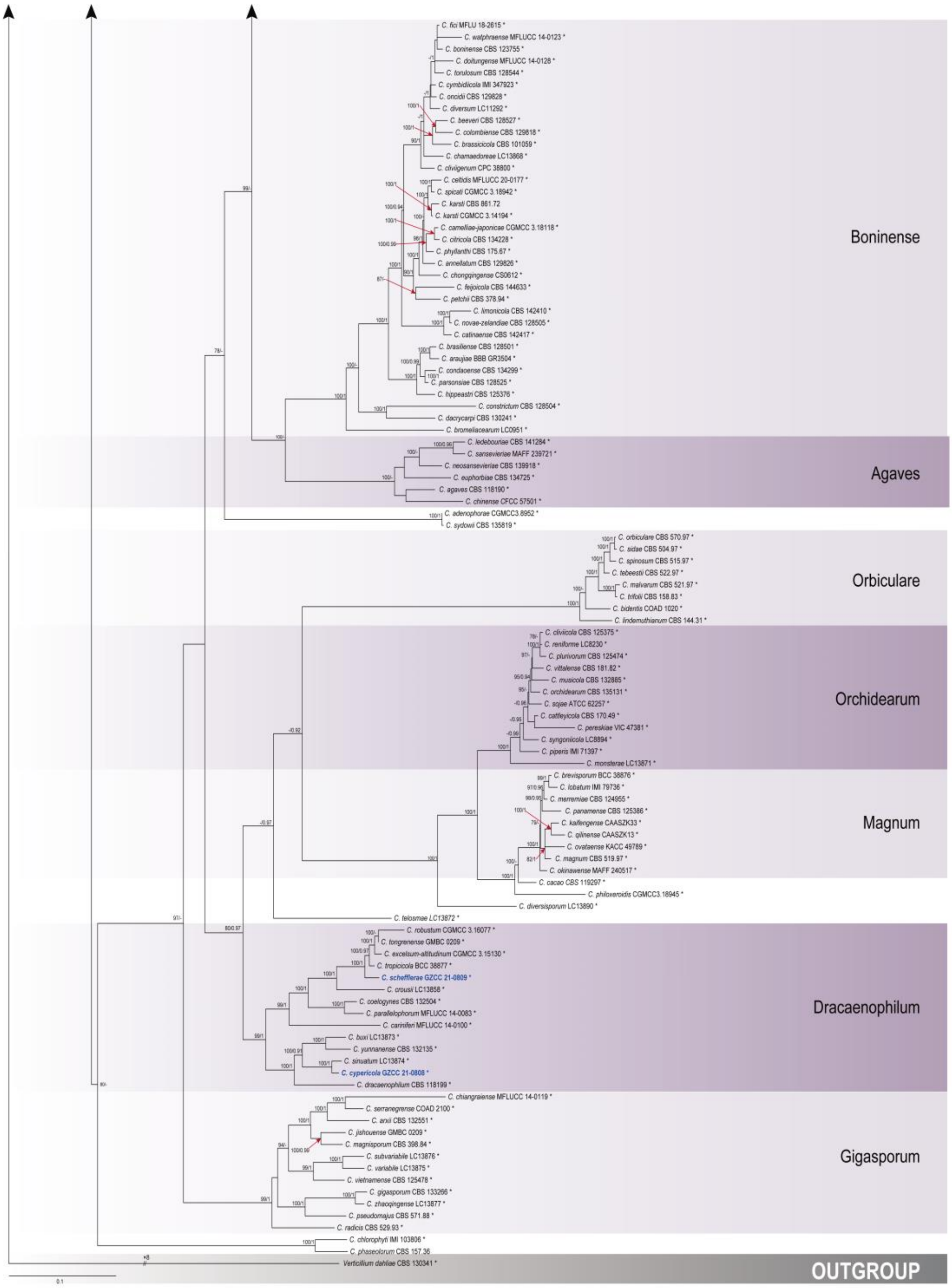
BYPP (≥ 0.90) are displayed (ML/PP). Type species strains are denoted by "*". Newly generated sequences are in blue bold.



Supplementary Figure 1 – Continued.



Supplementary Figure 1 – Continued.



Supplementary Figure 1 – Continued.

Supplementary Table 1 GenBank accession numbers used in this study.

Species	**Culture**	**Group**	**Host**	**Country**	**ITS**	***gapdh***	***chs-1***	***his3***	***act***	***tub2***
C. abscissum	COAD 1877*	Acutatum	*Citrus sinensis* cv. Pera	Brazil	KP843126	KP843129	KP843132	KP843138	KP843141	KP843135
C. acerbum	CBS 128530, ICMP 12921, PRJ 1199.3*	Acutatum	*Malus domestica*	New Zealand	JQ948459	JQ948790	JQ949120	JQ949450	JQ949780	JQ950110
C. acidae	MFLUCC 17-2659*	Truncatum	*Phyllanthus acidus*	Thailand	MG996505	MH003691	MH003694		MH003697	MH003700
C. acutatum	CBS 112996, ATCC 56816, STE-U 5292*	Acutatum	*Carica papaya*	Australia	JQ005776	JQ948677	JQ005797	JQ005818	JQ005839	JQ005860
C. adenophorae	CGMCC3.18952, YMF 1.04952*	singleton	*Ageratina adenophora*	China	OK030859	OK513662	OK513558			
C. aenigma	ICMP 18608*	Gloeosporioides	*Persea americana*	Israel	JX010244	JX010044	JX009774		JX009443	JX010389
C. aeschynomenes	ICMP 17673, ATCC 201874*	Gloeosporioides	*Aeschynomene virginica*	USA	JX010176	JX009930	JX009799		JX009483	JX010392
C. aeschynomenes	COL02	Gloeosporioides	*Myrciaria dubia*	Brazil		MK792457				MK792460
C. agaves	CBS 118190*	Agaves	*Agave striate*	Mexico	DQ286221					
C. alatae	CBS 304.67, ICMP 17919*	Gloeosporioides	*Dioscorea alata*	India	JX010190	JX009990	JX009837		JX009471	JX010383
C. alatae	ICMP 18122	Gloeosporioides	*Dioscorea*	Nigeria	JX010191	JX010011	JX009846		JX009470	JX010449
C. alatae	DA1605	Gloeosporioides	*Dioscorea alata*	China	KY689723	KY689726	KY689725		KY689724	
C. alcornii	IMI 176619*	Caudatum	*Imperata cylindrica* var. *major*	Australia	JX076858					
C. alienum	ICMP 12071*	Gloeosporioides	*Malus domestica*	New Zealand	JX010251	JX010028	JX009882		JX009572	JX010411
C. americae-borealis	CBS 136232*	Destructivum	*Medicago sativa*	USA	KM105224	KM105579	KM105294	KM105364	KM105434	KM105504
C. analogum	CGMCC3.16079, YMF 1.06943*	Gloeosporioides	*Ageratina adenophora*	China	OK030860	OK513663	OK513559		OK513599	OK513629
C. analogum	YMF1.07327	Gloeosporioides	*Ageratina adenophora*	China	OK030861	OK513664	OK513560		OK513600	OK513630
C. annellatum	CBS 129826, CH1*	Boninense	*Hevea indica*	Colombia	JQ005222	JQ005309	JQ005396	JQ005483	JQ005570	JQ005656
C. anthrisci	CBS 125334*	Dematium	*Anthriscus sylvestris*	Netherlands	GU227845	GU228237	GU228335	GU228041	GU227943	GU228139
C. antirrhinicola	CBS 102189*	Destructivum	*Antirrhinum majus*	New Zealand	KM105180	KM105531	KM105250	KM105320	KM105390	KM105460

Supplementary Table 1 Continued.

Species	Culture	Group	Host	Country	ITS	*gapdh*	*chs-1*	*his3*	*act*	*tub2*
C. aotearoa	ICMP 18537*	Gloeosporioides	*Coprosma* sp.	New Zealand	JX010205	JX010005	JX009853		JX009564	JX010420
C. araujiae	BBB:GR3504*	Boninense	*Araujia hortorum*	Argentina	OP035058	OP067659				OP067660
C. arboricola	CBS 144795, SAG 53350-12*	Acutatum	*Fuchsia magellanica*	Chile	MH817944	MH817950			MH817956	MH817962
C. arecacearum	LC13850, MH0003*	singleton	*Arecaceae*	China	MZ595867	MZ664049	MZ799262	MZ673887	MZ664165	MZ673986
C. arecacearum	LC13851, MH0003-1	singleton	*Arecaceae*	China	MZ595868	MZ664050	MZ799263	MZ673888	MZ664166	MZ673987
C. arecicola	CGMCC 3.19667*	Gloeosporioides	*Areca catechu*	China	MK914635	MK935455	MK935541		MK935374	MK935498
C. artocarpicola	MFLUCC 18-1167*	Gloeosporioides	*Artocarpus heterophyllus*	Thailand	MN415991	MN435568	MN435569		MN435570	MN435567
C. arxii	CBS 132551, Paphi 2-1*	Gigasporum	*Paphiopedilum* sp.	Germany	KF687716	KF687843	KF687780	KF687858	KF687802	KF687881
C. asianum	ICMP 18580, CBS 130418*	Gloeosporioides	*Coffea arabica*	Thailand	FJ972612	JX010053	JX009867		JX009584	JX010406
C. atractylodicola	CGMCC3.18761, SAUCC 1307*	Destructivum	*Atractylodes chinensis*	China	KR149280	KR259334	KR259333		KR132243	KU058178
C. australe	CBS 116478, HKUCC 2616*	Acutatum	*Trachycarpus fortunei*	South Africa	JQ948455	JQ948786	JQ949116	JQ949446	JQ949776	JQ950106
C. australianum	VPRI 43075*	Gloeosporioides	*Citrus sinensis*	Australia	MG572138	MG572127	MW091987		MN442109	MG572149
C. axonopodi	IMI 279189*	Graminicola	*Axonopus affinis*	Australia	MN521699					
C. baiyuense	CGMCC3.18941, YMF 1.04941*	Graminicola	*Hippuris vulgaris*	China	OL842184	OL981279	OL981305		OL981253	
C. baltimorense	BPI 892771, SD-11*	Caudatum	*Sorghastrum nutans*	USA	JX076866					
C. bambusicola	CNUCC 307307*	Bambusicola	*Phyllostachys edulis*	China	MT199632	MT192844	MT192871		MT188638	MT192817
C. beeveri	CBS 128527, ICMP 18594*	Boninense	*Brachyglottis repanda*	New Zealand	JQ005171	JQ005258	JQ005345	JQ005432	JQ005519	JQ005605
C. bicoloratum	LC13882, NN055229*	Spaethianum	*Ophiopogon japonicus*	China	MZ595899	MZ664100	MZ799332	MZ673919	MZ664197	MZ674017
C. bidentis	COAD 1020, CPC 21930*	Orbiculare	*Bidens subalternans*	Brazil	KF178481	KF178506	KF178530	KF178554	KF178578	KF178602
C. bletillae	CGMCC 3.15117, LC2340*	Spaethianum	*Bletilla ochracea*	China	JX625178	KC843506	MZ799322	MZ673854	KC843542	JX625207

Supplementary Table 1 Continued.

Species	Culture	Group	Host	Country	ITS	*gapdh*	*chs-1*	*his3*	*act*	*tub2*
C. boninense	CBS 123755, MAFF 305972*	Boninense	*Crinum asiaticum* var. *sinicum*	Japan	JQ005153	JQ005240	JQ005327	JQ005414	JQ005501	JQ005588
C. boninense	CBS 128549, ICMP 15444	Boninense	*Solanum betaceum*	New Zealand	JQ005156	JQ005243	JQ005330	JQ005417	JQ005504	JQ005590
C. boninense	CBS 112115, STE-U2966	Boninense	*Leucospermum* sp.	Australia	JQ005160	JQ005247	JQ005334	JQ005421	JQ005508	JQ005594
C. boninense	CBS 129831, STE-U 2965	Boninense	*Leucospermum* sp.	Australia	JQ005161	JQ005248	JQ005335	JQ005422	JQ005509	JQ005595
C. boninense	CBS 128526, ICMP 18591	Boninense	*Dacrycarpus dacrydioides*	New Zealand	JQ005162	JQ005249	JQ005336	JQ005423	JQ005510	JQ005596
C. boninense	**GUCC 12027**	**Boninense**	***Ilex chinensis***	**China**	**OP723102**	**OP784074**	**OP730627**	**OP784192**	**OP740171**	**OP761940**
C. boninense	**GUCC 12016**	**Boninense**	***Fatsia japonica***	**China**	**OP723094**	**OP784068**		**OP784187**	**OP740164**	**OP761934**
C. boninense	**GUCC 12017**	**Boninense**	***Fatsia japonica***	**China**	**OP723095**	**OP784069**		**OP784188**	**OP740165**	**OP761935**
C. boninense	**GUCC 12018**	**Boninense**	***Aucuba japonica***	**China**	**OP723099**	**OP784062**	**OP730616**	**OP784182**	**OP740158**	**OP761929**
C. boninense	**GUCC 12019**	**Boninense**	***Aucuba japonica***	**China**	**OP723097**	**OP784063**	**OP730617**	**OP784183**	**OP740159**	
C. boninense	**GUCC 12020**	**Boninense**	***Aucuba japonica***	**China**	**OP723100**	**OP784064**	**OP730618**	**OP784184**	**OP740160**	**OP761930**
C. boninense	**GUCC 12021**	**Boninense**	***Aucuba japonica***	**China**	**OP723098**	**OP784065**	**OP730619**	**OP784185**	**OP740161**	**OP761931**
C. boninense	**GUCC 12022**	**Boninense**	***Aucuba japonica***	**China**	**OP723101**	**OP784066**	**OP730620**	**OP784186**	**OP740162**	**OP761932**
C. boninense	**GUCC 12024**	**Boninense**	***Yulania denudata***	**China**	**OP723096**	**OP784071**	**OP730623**	**OP784190**	**OP740167**	**OP761937**
C. boninense	**GUCC 12025**	**Boninense**	***Yulania denudata***	**China**	**OP723105**	**OP784072**	**OP730624**	**OP784191**	**OP740168**	**OP761938**
C. boninense	**GUCC 12034**	**Boninense**	***Ilex chinensis***	**China**	**OP723093**	**OP784136**		**OP784213**		
C. boninense	**GUCC 12035**	**Boninense**	***Ilex chinensis***	**China**	**OP723103**	**OP784137**		**OP784214**		
C. brasiliense	CBS 128501, ICMP 18607, PAS12*	Boninense	*Passiflora edulis*	Brazil	JQ005235	JQ005322	JQ005409	JQ005496	JQ005583	JQ005669
C. brassicicola	CBS 101059, LYN 16331*	Boninense	*Brassica oleracea* var. *gemmifera*	New Zealand	JQ005172	JQ005259	JQ005346	JQ005433	JQ005520	JQ005606

Supplementary Table 1 Continued.

Species	Culture	Group	Host	Country	ITS	*gapdh*	*chs-1*	*his3*	*act*	*tub2*
C. brevisporum	BCC 38876, LC0600*	Magnum	*Neoregalia* sp.	Thailand	JN050238	JN050227	MZ799287	MZ673841	JN050216	JN050244
C. brisbanense	CBS 292.67, DPI 11711*	Acutatum	*Capsicum annuum*	Australia	JQ948291	JQ948621	JQ948952	JQ949282	JQ949612	JQ949942
C. bromeliacearum	LC0951*	Boninense	*Bromeliad*	China	MZ595832	MZ664077	MZ799267	MZ673843	MZ664130	MZ673956
C. bryoniicola	CBS 109849*	Destructivum	*Bryonia dioica*	Netherlands	KM105181	KM105532	KM105251	KM105321	KM105391	KM105461
C. buxi	LC13873, NN047139*	Dracaenophilum	*Buxus* sp.	China	MZ595886	MZ664056	MZ799285	MZ673906	MZ664184	MZ674004
C. cacao	CBS 119297*	Magnum	*Theobroma cacao*	Costa Rica	MG600772	MG600832	MG600878	MG600916	MG600976	MG601039
C. cairnsense	BRIP 63642*	Acutatum	*Capsicum annuum*	Australia	KU923672	KU923704	KU923710	KU923722	KU923716	KU923688
C. camelliae	ICMP 18542	Gloeosporioides	*Camellia sasanqua*	USA	JX010223	JX009994	JX009857		JX009488	JX010429
C. camelliae	ICMP 10643	Gloeosporioides	*Camellia* × *williamsii*	UK	JX010224	JX009908	JX009891		JX009540	JX010436
C. camelliae	ICMP 10646	Gloeosporioides	*Camellia sasanqua*	USA	JX010225	JX009993	JX009892		JX009563	JX010437
C. camelliae	CGMCC 3.14925, LC1364*	Gloeosporioides	*Camellia sinensis*	China	KJ955081	KJ954782	MZ799255	MZ673847	KJ954363	KJ955230
C. camelliae-japonicae	CGMCC 3.18118, LC6416*	Boninense	*Camellia japonica*	China	KX853165	KX893584	MZ799271	MZ673859	KX893576	KX893580
C. cangyuanense	CGMCC3.18969, YMF 1.05001*	Gloeosporioides	*Ageratina adenophora*	China	OK030864	OK513667	OK513563		OK513603	OK513633
C. cariniferi	MFLUCC 14-0100*	Dracaenophilum	*Dendrobium cariniferum*	Thailand	MF448521					MH351274
C. carthami	SAPA 100011*	Acutatum	*Carthamus tinctorium*	Japan	AB696998					AB696992
C. casaense	CGMCC 3.18947, YMF 1.04947*	Graminicola	*Hippuris vulgaris*	China	OL842180	OL981275	OL981301		OL981249	
C. caspicum	CBS 148570, UTFC 365, DSM 113396, GLMC 2641*	Graminicola	*Cyperus* sp.	IRAN	MW741443					MW740344
C. castaneae	**GUCC 12176**	**Gloeosporioides**	***Castanea mollissima***	**China**	**OP722990**	**OP737972**	**OP715777**		**OP715811**	**OP720867**
C. castaneae	**GUCC 21268.4***	**Gloeosporioides**	***Castanea mollissima***	**China**	**OP722991**	**OP737973**	**OP715778**		**OP715812**	**OP720868**

Supplementary Table 1 Continued.

Species	Culture	Group	Host	Country	ITS	*gapdh*	*chs-1*	*his3*	*act*	*tub2*
C. castaneae	**GUCC 12179**	**Gloeosporioides**	***Castanea mollissima***	**China**	**OP722992**	**OP737974**	**OP715779**		**OP715813**	
C. catinaense	CBS 142417, CPC 27978*	Boninense	*Citrus reticulata*	Italy	KY856400	KY856224	KY856136	KY856307	KY855971	KY856482
C. cattleyicola	CBS 170.49*	Orchidearum	*Cattleya* sp.	Belgium	MG600758	MG600819	MG600866	MG600905	MG600963	MG601025
C. caudatum	CBS 131602, BPI 892767, NY07-CC04*	Caudatum	*Sorghastrum nutans* cv. Rumsey	USA	JX076860					
C. caudisporum	CGMCC 3.15106, LC2311*	Caudatum	*Bletilla ochracea*	China	JX625162	KC843512	MZ799318	MZ673852	KC843526	JX625190
C. celtidis	MFLUCC 20-0177*	Boninense	*Celtis formosana*	China, Taiwan	MW114362		MW177696		MW151580	MW148274
C. celtidis	NCYUCC 19-0335	Boninense	*Celtis formosana*	China, Taiwan	MW114363		MW177697		MW151581	MW148275
C. celtidis	**GUCC 12013**	**Boninense**	***Rhododendron simsii***	**China**	**OP723038**	**OP784059**	**OP730612**	**OP784179**	**OP740154**	**OP761925**
C. celtidis	**GUCC 12014**	**Boninense**	***Rhododendron simsii***	**China**	**OP723045**	**OP784060**	**OP730613**	**OP784180**	**OP740155**	**OP761926**
C. celtidis	**GUCC 12015**	**Boninense**	***Rhododendron simsii***	**China**	**OP723037**	**OP784061**	**OP730614**	**OP784181**	**OP740156**	**OP761927**
C. celtidis	**GUCC 12023**	**Boninense**	***Yulania denudata***	**China**	**OP723046**	**OP784070**	**OP730622**	**OP784189**	**OP740166**	**OP761936**
C. celtidis	**GUCC 12039**	**Boninense**	**unidentified host**	**China**	**OP723047**	**OP784148**	**OP730689**		**OP740226**	**OP762013**
C. cereale	CBS 129663, KS20BIG	Graminicola	*Bromus inermis*	USA	JQ005774		JQ005795	JQ005816	JQ005837	JQ005858
C. chamaedoreae	LC13868, NN052885*	Boninense	*Chamaedorea erumpens*	China	MZ595890	MZ664084	MZ799274	MZ673910	MZ664188	MZ674008
C. changpingense	CGMCC 3.17582, SA0016, MFLUCC 15-0022*	Gloeosporioides	*Fragaria × ananass*	China	KP683152	KP852469	KP852449		KP683093	KP852490
C. changpingense	SA0050	Gloeosporioides	*Fragaria × ananass*	China	KY214473	KY214472	KY214471		KY214470	KY214474
C. chiangmaiense	MFLUCC 18-0945*	Gloeosporioides	*Magnolia garrettii*	Thailand	MW346499	MW548592	MW623653		MW655578	
C. chiangraiense	MFLUCC 14-0119*	Gigasporum	*Dendrobium* sp.	Thailand	MF448522				MH376383	MH351275

Supplementary Table 1 Continued.

Species	Culture	Group	Host	Country	ITS	*gapdh*	*chs-1*	*his3*	*act*	*tub2*
C. chinense	CFCC 57501*	Agaves	*Yucca gloriosa*	China	ON692808	ON755050	ON755046		ON755042	ON755054
C. chlorophyti	IMI 103806*	singleton	*Chlorophytum* sp.	India	GU227894	GU228286	GU228384	GU228090	GU227992	GU228188
C. chongqingense	CS0612*	Boninense	*Camellia sinensis*	China	MG602060	MG602022	MT976117		MT976107	MG602044
C. chrysanthemi	IMI 364540, CPC 18930	Acutatum	*Chrysanthemum coronarium*	China	JQ948273	JQ948603	JQ948934	JQ949264	JQ949594	JQ949924
C. chrysophilum	URM 7368, CMM 4268*	Gloeosporioides	*Musa* sp.	Brazil	KX094252	KX094183	KX094083		KX093982	KX094285
C. cigarro	ICMP 18539*	Gloeosporioides	*Olea europaea*	Australia	JX010230	JX009966	JX009800	MZ673837	JX009523	JX010434
C. circinans	CBS 221.81*	Dematium	*Allium cepa*	Serbia	GU227855	GU228247	GU228345	GU228051	GU227953	GU228149
C. citricola	CBS 134228, ZJUC34, CGMCC 3.15227*	Boninense	*Citrus unshiu*	China	KC293576	KC293736			KC293616	KC293656
C. citrulli	CAASZT52*	Gloeosporioides	*Citrullus lanatus*	China	MZ475133	OL456685	OL901153	ON479082	OL449283	OL456644
C. citrulli	CAASZT54	Gloeosporioides	*Citrullus lanatus*	China	MZ475134	OL456686	OL901154	ON479083	OL449284	OL456645
C. citrus-medicae	HGUP 1554*	singleton	*Citrus medica*	China	MN959910	MT006331	MT006328	MT006334	MT006325	
C. citrus-medicae	GUCC 1555	singleton	*Citrus medica*	China	MN959911	MT006332	MT006329	MT006335	MT006326	
C. citrus-medicae	GUCC 1556	singleton	*Citrus medica*	China	MN959912	MT006333	MT006330	MT006336	MT006327	
C. clidemiae	ICMP 18658*	Gloeosporioides	*Clidemia hirta*	USA	JX010265	JX009989	JX009877		JX009537	JX010438
C. clidemiae	ICMP 18706	Gloeosporioides	*Vitis* sp.	USA	JX010274	JX009909	JX009777		JX009476	JX010439
C. cliviicola	CBS 125375*	Orchidearum	*Clivia miniata*	China	MG600733	MG600795	MG600850	MG600892	MG600939	MG601000
C. cliviigenum	CPC 38800, CBS 146825*	Boninense	*Clivia* sp.	South Africa	MZ064415	MZ078178	MZ078161	MZ078180	MZ078143	MZ078260
C. cobbittiense	BRIP 66219*	Gloeosporioides	*Cordyline stricta × C. australis*	Australia	MH087016	MH094133	MH094135	MH094136	MH094134	MH094137
C. coccodes	CBS 164.49	singleton	*Solanum tuberosum*	Netherlands	JQ005775	HM171672	JQ005796	JQ005817	JQ005838	JQ005859
C. coccodes	CBS 369.75*	singleton	*Solanum tuberosum*	Netherlands	HM171679	HM171673	JX546681	JX546779	HM171667	JX546873
C. coelogynes	CBS 132504*	Dracaenophilum	*Coelogyne* sp.	Germany	MG600713	MG600776	MG600836	MG600882	MG600920	MG600980
C. colombiense	CBS 129818*	Boninense	*Passiflora edulis*	Colombia	JQ005174	JQ005261	JQ005348	JQ005435	JQ005522	JQ005608

Supplementary Table 1 Continued.

Species	**Culture**	**Group**	**Host**	**Country**	**ITS**	***gapdh***	***chs-1***	***his3***	***act***	***tub2***
C. condaoense	CBS 134299*	Boninense	*Ipomoea pes-caprae*	Vietnam	MH229914	MH229920	MH229926	MH229927		MH229923
C. conoides	CGMCC 3.17615, CAUG17, LC6226*	Gloeosporioides	*Chili pepper*	China	KP890168	KP890162	KP890156		KP890144	KP890174
C. constrictum	CBS 128504, ICMP 12941*	Boninense	*Citrus limon*	New Zealand	JQ005238	JQ005325	JQ005412	JQ005499	JQ005586	JQ005672
C. cordylinicola	MFLUCC 090551, BCC38872, LC0856*	Gloeosporioides	*Cordyline fruticosa*	Thailand	HM470246	HM470240			HM470234	HM470249
C. cordylinicola	MFLU 100132, LC0955	Gloeosporioides	*Cordyline fruticosa*	Thailand	HM470247	HM470241			HM470235	HM470250
C. cordylinicola	**GUCC 12079**	**Gloeosporioides**	***Cordyline fruticose***	**China**	**OP722972**	**OP784099**	**OP730652**		**OP740194**	**OP761965**
C. cordylinicola	**GUCC 12080**	**Gloeosporioides**	***Cordyline fruticose***	**China**	**OP722973**	**OP784100**	**OP730653**		**OP740195**	**OP761966**
C. cosmi	CBS 853.73, PD 73/856*	Acutatum	*Cosmos* sp.	Netherlands	JQ948274	JQ948604	JQ948935	JQ949265	JQ949595	JQ949925
C. costaricense	CBS 330.75*	Acutatum	*Coffea arabica* cv. Typica	Costa Rica	JQ948180	JQ948510	JQ948841	JQ949171	JQ949501	JQ949831
C. crousii	LC13858, MH0588*	Dracaenophilum	*Rhaphidophora* sp.	China	MZ595876	MZ664059	MZ799281	MZ673896	MZ664174	MZ673995
C. crousii	LC13860, MH0592	Dracaenophilum	*Rhaphidophora* sp.	China	MZ595878	MZ664061	MZ799282	MZ673898	MZ664176	MZ673997
C. curcumae	IMI 288937*	Truncatum	*Curcuma longa*	India	GU227893	GU228285	GU228383	GU228089	GU227991	GU228187
C. cuscutae	IMI 304802, CPC 18873*	Acutatum	*Cuscuta* sp.	Dominica	JQ948195	JQ948525	JQ948856	JQ949186	JQ949516	JQ949846
C. cycadis	BRIP 71326a*	Gloeosporioides	*Cycas revoluta*	China	MT439915	MT439919	MT439917			MT439921
C. cycadis	AQISWA201901	Gloeosporioides	*Cycas revoluta*	China	MT439916	MT439920	MT439918			MT439922
C. cymbidiicola	IMI 347923*	Boninense	*Cymbidium* sp.	Australia	JQ005166	JQ005253	JQ005340	JQ005427	JQ005514	JQ005600
C. cypericola	**GZCC 21-0808***	**Dracaenophilum**	***Cyperus rotundus***	**China**	**OP723074**	**OP737969**	**OP715774**		**OP715808**	**OP720865**
C. cypericola	**GZCC 21-0807**	**Dracaenophilum**	***Cyperus rotundus***	**China**	**OP723073**	**OP737970**	**OP715775**		**OP715809**	**OP720866**
C. dacrycarpi	CBS 130241, ICMP 19107*	Boninense	*Dacrycarpus dacrydioides*	New Zealand	JQ005236	JQ005323	JQ005410	JQ005497	JQ005584	JQ005670

Supplementary Table 1 Continued.

Species	Culture	Group	Host	Country	ITS	*gapdh*	*chs-1*	*his3*	*act*	*tub2*
C. danxiashanense	LC13885, NN055218*	Graminicola	Probably dead leaves of *Miscanthus* sp.	China	MZ595898	MZ664101	MZ799330	MZ673918	MZ664196	MZ674016
C. dematium	CBS 125.25*	Dematium	*Eryngium campestre*	France	GU227819	GU228211	GU228309	GU228015	GU227917	GU228113
C. demersi	CGMCC3.18946, YMF 1.04946*	Graminicola	*Ceratophyllum demersum*	China	OL842177	OL981272	OL981298		OL981246	OL981232
C. destructivum	CBS 136228*	Destructivum	*Trifolium hybridum*	USA	KM105207	KM105561	KM105277	KM105347	KM105417	KM105487
C. dianense	CGMCC3.18943, YMF 1.04943*	singleton	*Alternanthera philoxeroides*	China	OL842189	OL981284	OL981310		OL981258	
C. dimorphum	YMF1.07303	Gloeosporioides	*Ageratina adenophora*	China	OK030866	OK513669	OK513565		OK513605	OK513635
C. dimorphum	CGMCC3.16083, YMF 1.07309*	Gloeosporioides	*Ageratina adenophora*	China	OK030867	OK513670	OK513566		OK513606	OK513636
C. diversisporum	LC13890, NN072578*	singleton	*Dracaena angustifolia*	China	MZ595911	MZ664122	MZ799302	MZ673931	MZ664209	MZ674029
C. diversum	LC11292, CQ775*	Boninense	*Philodendron selloum*	China	MZ595844	MZ664081	MZ799272	MZ673864	MZ664142	MZ673965
C. doitungense	MFLUCC 14-0128*	Boninense	*Dendrobium* sp.	Thailand	MF448524	MH049480			MH376385	MH351277
C. dolichoconidiophori	LC13889, NN054966*	Graminicola	*Poaceae*	China	MZ595896	MZ664094	MZ799329	MZ673916	MZ664194	MZ674014
C. dracaenigenum	MFLUCC 19-0430*	Gloeosporioides	*Dracaena* sp.	Thailand	MN921250	MT215577	MT215575		MT313686	
C. dracaenophilum	CBS 118199*	Dracaenophilum	*Dracaena sanderana*	China	JX519222	JX546707	JX519230	JX546756	JX519238	JX519247
C. duyunense	CGMCC 3.15105, LC2307*	Caudatum	*Bletilla ochracea*	China	JX625160	KC843515	MZ799320	MZ673851	KC843530	JX625187
C. echinochloae	MAFF 511473*	Graminicola	*Echinochloa esculenta*	Japan	AB439811					
C. eleusines	MAFF 511155*	Graminicola	*Eleusine indica*	Japan	JX519218		JX519226		JX519234	JX519243
C. endophytica	MFLUCC 13-0417, LC1216	Gloeosporioides	*Pennisetum purpureum*	Thailand	KC633853	KC832853			KC692467	
C. endophytica	MFLUCC 13-0418, LC0324*	Gloeosporioides	*Pennisetum purpureum*	Thailand	KC633854	KC832854	MZ799261	MZ673839	KF306258	MZ673954
C. endophytica	CAUG28	Gloeosporioides	*chilli pepper*	China	KP145441	KP145413	KP145385		KP145329	KP145469

Supplementary Table 1 Continued.

Species	**Culture**	**Group**	**Host**	**Country**	**ITS**	***gapdh***	***chs-1***	***his3***	***act***	***tub2***
C. endophytica	YN1A3	Gloeosporioides	*Camellia sinensis*	China	KU251559	KU252013	KU251907		KU251640	KU252167
C. endophytica	YN1A4	Gloeosporioides	*Camellia sinensis*	China	KU251561	KU252015	KU251909		KU251642	KU252169
C. endophytica	EIPP 33	Gloeosporioides	*Coffea arabica*	China	MK330020	MK344238	MK344261		MK344284	MK344215
C. endophytica	**GUCC 12105**	**Gloeosporioides**	**unidentified host**	**China**	**OP722960**	**OP784125**				**OP761991**
C. endophytica	**GUCC 12106**	**Gloeosporioides**	**unidentified host**	**China**	**OP722961**					**OP761992**
C. endophytica	**GUCC 12107**	**Gloeosporioides**	**unidentified host**	**China**	**OP722962**	**OP784126**				**OP761993**
C. endophytica	**GUCC 12108**	**Gloeosporioides**	**unidentified host**	**China**	**OP722963**	**OP784127**	**OP730676**		**OP740213**	**OP761994**
C. endophytum	CGMCC 3.15108, LC2338*	Graminicola	*Bletilla ochracea*	China	JX625177	KC843521	MZ799327	MZ673853	KC843533	JX625206
C. eremochloae	CBS 129661*	Graminicola	*Eremochloa ophiuroides*	USA	JX519220		JX519228		JX519236	JX519245
C. eriobotryae	GLMC 1935*	Acutatum	*Eriobotrya japonica*	China, Taiwan	MF772487	MF795423	MN191653	MN191658	MN191648	MF795428
C. eryngiicola	MFLUCC 17-0318*	Dematium	*Eryngium*	Russia	KY792726	KY792723	KY792720		KY792717	KY792729
C. euphorbiae	CBS 134725*	Agaves	*Euphorbia* sp.	South Africa	KF777146	KF777131	KF777128	KF777134	KF777125	KF777247
C. excelsum-altitudinum	CGMCC 3.15130, LC2344*	Dracaenophilum	*Bletilla ochracea*	China	HM751815	KC843502	MZ799280	MZ673855	KC843548	JX625211
C. falcatum	CGMCC 3.14187, CBS 147945*	Graminicola	*Saccharum officinarum*	Indonesia	HM171677		JQ005793	JQ005814	JQ005835	JQ005856
C. feijoicola	CBS 144633*	Boninense	*Acca sellowiana*	Portugal	MK876413	MK876475			MK876466	MK876507
C. fici	MFLU 18-2615*	Boninense	*Ficus ampelas*	China, Taiwan	MW114364		MW177698		MW151582	
C. fici-septicae	MFLUCC 20-0166*	*Gloeosporioides*	*Ficus septica*	China, Taiwan	MW114367	MW183774	MW177701		MW151585	
C. filicis	CBS 101611*	Acutatum	an unidentified fern (*Pteridophyta*)	Costa Rica	JQ948196	JQ948526	JQ948857	JQ949187	JQ949517	JQ949847
C. fioriniae	CBS 128517, ARSEF 10222, ERL 1257, EHS 58*	Acutatum	*Fiorinia externa* (elongate hemlock scale, insect)	USA	JQ948292	JQ948622	JQ948953	JQ949283	JQ949613	JQ949943

Supplementary Table 1 Continued.

Species	Culture	Group	Host	Country	ITS	*gapdh*	*chs-1*	*his3*	*act*	*tub2*
C. fioriniae	IMI 324996, CPC 18880	Acutatum	*Malus pumila*	USA	JQ948301	JQ948631	JQ948962	JQ949292	JQ949622	JQ949952
C. fioriniae	CBS 490.92	Acutatum	*Solanum lycopersicum*	New Zealand	JQ948326	JQ948656	JQ948987	JQ949317	JQ949647	JQ949977
C. fioriniae	IMI 363003, CPC 18928	Acutatum	*Camellia reticulata*	China	JQ948339	JQ948669	JQ949000	JQ949330	JQ949660	JQ949990
C. fioriniae	CBS 129946	Acutatum	*Olea europaea*	Portuga	JQ948342	JQ948672	JQ949003	JQ949333	JQ949663	JQ949993
C. fioriniae	CBS 129948, RB128	Acutatum	*Tulipa* sp.	UK	JQ948344	JQ948674	JQ949005	JQ949335	JQ949665	JQ949995
C. fioriniae	PAFQ49	Acutatum	*Pyrus pyrifolia*	China	MG748060	MG747978	MG747896		MG747750	MG748140
C. fioriniae	PAFQ50	Acutatum	*Pyrus pyrifolia*	China	MG748061	MG747979	MG747897		MG747751	MG748141
C. folicola	YNHH 2-2	singleton	*Prunus persica* cv.	China	MN807724	MN829585	MN829704	MN829754	MN829635	MN829785
C. folicola	YNHH 10-1*	singleton	*Prunus persica* cv.	China	MN807725	MN829586	MN829705	MN829755	MN829636	MN829786
C. fructi	CBS 346.37*	Dematium	*Malus sylvestris*	USA	GU227844	GU228236	GU228334	GU228040	GU227942	GU228138
C. fructicola	ICMP 18581, CBS 130416*	Gloeosporioides	*Coffea arabica*	Thailand	JX010165	JX010033	JX009866		FJ907426	JX010405
C. fructicola	ICMP 18613	Gloeosporioides	*Limonium sinuatum*	Israel	JX010167	JX009998	JX009772		JX009491	JX010388
C. fructicola	ICMP 18667	Gloeosporioides	*Limonium* sp.	Israel	JX010169	JX009951	JX009775		JX009464	
C. fructicola	ICMP 18646, CBS125397	Gloeosporioides	*Tetragastris panamensis*	Panama	JX010173	JX010032	JX009874		JX009581	JX010409
C. fructicola	**GUCC 12059**	**Gloeosporioides**	***Ligustrum lucidum***	**China**	**OP723017**	**OP784075**	**OP730628**		**OP740172**	**OP761941**
C. fructicola	**GUCC 12054**	**Gloeosporioides**	***Zingiber officinale***	**China**	**OP722955**		**OP730615**		**OP740157**	**OP761928**
C. fructicola	**GUCC 12084**	**Gloeosporioides**	**unidentified host**	**China**	**OP723004**	**OP784103**	**OP730656**		**OP740196**	**OP761969**
C. fructicola	**GUCC 12102**	**Gloeosporioides**	***Curcuma phaeocaulis***	**China**	**OP723019**	**OP784115**	**OP730667**		**OP740203**	**OP761981**
C. fructicola	**GUCC 12113**	**Gloeosporioides**	***Ilex chinensis***	**China**	**OP723025**	**OP784133**	**OP730681**		**OP740219**	**OP761999**
C. fructicola	**GUCC 12114**	**Gloeosporioides**	***Ilex chinensis***	**China**	**OP723003**	**OP784135**	**OP730683**		**OP740221**	**OP762001**
C. fructicola	**GUCC 12117**	**Gloeosporioides**	***Ilex chinensis***	**China**	**OP723005**	**OP784139**	**OP730686**			**OP762003**
C. fructicola	**GUCC 12131**	**Gloeosporioides**	***Camellia sinensis***	**China**	**OP723000**	**OP784159**	**OP730695**		**OP740232**	**OP762022**

Supplementary Table 1 Continued.

Species	**Culture**	**Group**	**Host**	**Country**	**ITS**	***gapdh***	***chs-1***	***his3***	***act***	***tub2***
C. fructicola	**GUCC 12132**	**Gloeosporioides**	***Camellia sinensis***	**China**	**OP723006**	**OP784160**	**OP730696**		**OP740233**	**OP762023**
C. fructivorum	CBS 133125, Coll1414, BPI 884103*	Gloeosporioides	*Vaccinium macrocarpon*	Burlington	JX145145	MZ664047	MZ799259		MZ664126	JX145196
C. fuscum	CBS 133701*	Destructivum	*Digitalis lanata*	Germany	KM105174	KM105524	KM105244	KM105314	KM105384	KM105454
C. fusiforme	MFLUCC 12-0437*	Truncatum	*Dead leaves*	Thailand	KT290266	KT290255	KT290253		KT290251	KT290256
C. gardeniae	**GUCC 12047**	**Gloeosporioides**	***Gardenia jasminoides***	**China**	**OP722964**	**OP737961**	**OP715764**		**OP715799**	**OP720856**
C. gardeniae	**GUCC 12048**	**Gloeosporioides**	***Gardenia jasminoides***	**China**	**OP722989**	**OP737962**	**OP715765**		**OP715800**	**OP720857**
C. gardeniae	**GUCC 12049***	**Gloeosporioides**	***Gardenia jasminoides***	**China**	**OP722995**	**OP737963**	**OP715766**		**OP715801**	**OP720858**
C. gardeniae	**GUCC 12177**	**Gloeosporioides**	***Gardenia jasminoides***	**China**	**OP722966**		**OP715767**		**OP715802**	**OP720859**
C. gardeniae	**GUCC 12050**	**Gloeosporioides**	***Gardenia jasminoides***	**China**	**OP722956**	**OP737964**	**OP715768**		**OP715803**	**OP720860**
C. garzense	CGMCC 3.18948, YMF 1.04948*	Graminicola	*Hippuris vulgaris*	China	OL842185	OL981280	OL981306		OL981254	
C. gigasporum	CBS 133266, MUCL 44947*	Gigasporum	*Centella asiatica*	Madagascar	KF687715	KF687822	KF687761	KF687844		KF687866
C. gloeosporioides	ICMP 19121, CBS 273.51	Gloeosporioides	*Citrus limon*	Italy	JX010148	JX010054	JX009903		JX009558	
C. gloeosporioides	ICMP 12939	Gloeosporioides	*Citrus* sp.	New Zealand	JX010149	JX009931	JX009747		JX009462	
C. gloeosporioides	ICMP 18678, CBS 119204	Gloeosporioides	*Pueraria labata*	USA	JX010150	JX010013	JX009790		JX009502	
C. gloeosporioides	IMI 356878, ICMP 17821, CBS 112999*	Gloeosporioides	*Citrus sinensis*	Italy	JX010152	JX010056	JX009818	JQ005413	JX009531	JX010445
C. gloeosporioides	ICMP 18697	Gloeosporioides	*Vitis vinifera*	USA	JX010154	JX009987	JX009780		JX009557	
C. gloeosporioides	LC3312, LF534	Gloeosporioides	*Camellia sinensis*	*China*	KJ955158	KJ954859			KJ954434	KJ955305
C. gloeosporioides	PAFQ29	Gloeosporioides	*Pyrus pyrifolia* cv. Hohsui	China	MG748027	MG747945	MG747863		MG747717	MG748109
C. gloeosporioides	PAFQ58	Gloeosporioides	*Pyrus pyrifolia* cv. Cuiguan	China	MG748030	MG747948	MG747866		MG747720	MG748112

Supplementary Table 1 Continued.

Species	**Culture**	**Group**	**Host**	**Country**	**ITS**	***gapdh***	***chs-1***	***his3***	***act***	***tub2***
C. gloeosporioides	PAFQ60	Gloeosporioides	*Pyrus pyrifolia* cv. Cuiguan	China	MG748032	MG747950	MG747868		MG747722	MG748114
C. gloeosporioides	PAFQ80	Gloeosporioides	*Pyrus pyrifolia* cv. Guangyangxueli	China	MG748035	MG747953	MG747871		MG747725	MG748117
C. gloeosporioides	**GUCC 12051**	**Gloeosporioides**	***Rhododendron simsii***	**China**	**OP723007**	**OP784052**	**OP730606**		**OP740148**	**OP761919**
C. gloeosporioides	**GUCC 12052**	**Gloeosporioides**	***Rhododendron simsii***	**China**	**OP723009**	**OP784053**	**OP730607**		**OP740149**	**OP761920**
C. gloeosporioides	**GUCC 12097**	**Gloeosporioides**	***Cycas bifida***	**China**	**OP722994**	**OP784109**	**OP730662**		**OP740200**	**OP761975**
C. gloeosporioides	**GUCC 12098**	**Gloeosporioides**	**unidentified host**	**China**	**OP723010**	**OP784110**	**OP730663**			**OP761976**
C. gloeosporioides	**GUCC 12099**	**Gloeosporioides**	**unidentified host**	**China**	**OP723011**	**OP784111**	**OP730664**		**OP740201**	**OP761977**
C. gloeosporioides	**GUCC 12100**	**Gloeosporioides**	**unidentified host**	**China**	**OP723028**	**OP784112**				**OP761978**
C. gloeosporioides	**GUCC 12103**	**Gloeosporioides**	**unidentified host**	**China**	**OP723015**	**OP784113**	**OP730665**			**OP761979**
C. gloeosporioides	**GUCC 12115**	**Gloeosporioides**	***Ilex chinensis***	**China**	**OP723008**		**OP730684**		**OP740222**	
C. gloeosporioides	**GUCC 12116**	**Gloeosporioides**	***Ilex chinensis***	**China**	**OP723021**	**OP784138**	**OP730685**		**OP740223**	**OP762002**
C. gloeosporioides	**GUCC 12120**	**Gloeosporioides**	***Viburnum dilatatum***	**China**	**OP723014**	**OP784141**				**OP762006**
C. gloeosporioides	**GUCC 12127**	**Gloeosporioides**	***Fatsia japonica***	**China**	**OP723022**	**OP784153**				**OP762018**
C. gloeosporioides	**GUCC 12128**	**Gloeosporioides**	***Spatholobus suberectus***	**China**	**OP723013**	**OP784154**				**OP762019**
C. gloeosporioides	**GUCC 12129**	**Gloeosporioides**	***Achyranthes bidentata***	**China**	**OP723016**	**OP784155**				**OP762020**
C. godetiae	CBS 133.44*	Acutatum	*Clarkia hybrida* cv. Kelvon Glory	Denmark	JQ948402	JQ948733	JQ949063	JQ949393	JQ949723	JQ950053
C. godetiae	CBS 796.72	Acutatum	*Aeschynomene virginica*	USA	JQ948407	JQ948738	JQ949068	JQ949398	JQ949728	JQ950058
C. godetiae	IMI 351248	Acutatum	*Ceanothus* sp.	UK	JQ948433	JQ948764	JQ949094	JQ949424	JQ949754	JQ950084
C. godetiae	CBS 129911	Acutatum	*Podocarpus* sp.	South Africa	JQ948434	JQ948765	JQ949095	JQ949425	JQ949755	JQ950085
C. godetiae	CBS 129912	Acutatum	*Podocarpus* sp.	South Africa	JQ948435	JQ948766	JQ949096	JQ949426	JQ949756	JQ950086
C. godetiae	CBS 129913	Acutatum	*Podocarpus* sp.	South Africa	JQ948436	JQ948767	JQ949097	JQ949427	JQ949757	JQ950087
C. godetiae	CBS 862.70	Acutatum	*Sambucus nigra*	Netherlands	JQ948437	JQ948768	JQ949098	JQ949428	JQ949758	JQ950088

Supplementary Table 1 Continued.

Species	Culture	Group	Host	Country	ITS	*gapdh*	*chs-1*	*his3*	*act*	*tub2*
C. godetiae	**GUCC 12001**	**Acutatum**	***Eriobotrya japonica***	**China**	**OP723055**	**OP784028**	**OP730586**	**OP784161**	**OP740126**	**OP761897**
C. godetiae	**GUCC 12002**	**Acutatum**	***Eriobotrya japonica***	**China**	**OP723057**	**OP784029**	**OP730587**	**OP784162**	**OP740127**	**OP761898**
C. godetiae	**GUCC 12003**	**Acutatum**	***Mahonia fortunei***	**China**	**OP723054**	**OP784036**	**OP730593**	**OP784167**	**OP740133**	**OP761904**
C. godetiae	**GUCC 12004**	**Acutatum**	***Mahonia fortunei***	**China**	**OP723056**	**OP784041**	**OP730598**	**OP784168**	**OP740138**	**OP761909**
C. godetiae	**GUCC 12005**	**Acutatum**	***Hedera nepalensis***	**China**	**OP723058**	**OP784048**	**OP730604**	**OP784173**	**OP740144**	**OP761915**
C. godetiae	**GUCC 12006**	**Acutatum**	***Hedera nepalensis***	**China**	**OP723059**	**OP784049**	**OP730605**	**OP784174**	**OP740145**	**OP761916**
C. gracile	CGMCC 3.16075, YMF 1.06939*	Gloeosporioides	*Ageratina adenophora*	China	OK030868	OK513671	OK513567		OK513607	OK513637
C. graminicola	CBS 130836, M 1.001*	Graminicola	*Zea mays*	USA	JQ005767		JQ005788		JQ005830	JQ005851
C. grevilleae	CBS 132879, CPC 15481*	Gloeosporioides	*Grevillea* sp.	Italy	KC297078	KC297010	KC296987	KC297056	KC296941	KC297102
C. grevilleae	**GUCC 12077**	**Gloeosporioides**	**unidentified host**	**China**	**OP723026**	**OP784097**	**OP730650**		**OP740192**	**OP761963**
C. grossum	CGMCC3.17614, CAUG7, LC6227*	Gloeosporioides	*Chili pepper*	China	KP890165	KP890159	KP890153	JQ949261	KP890141	KP890171
C. guajavae	IMI 350839, CPC 18893*	Acutatum	*Psidium guajava*	India	JQ948270	JQ948600	JQ948931		JQ949591	JQ949921
C. guangxiense	CNUCC 310138*	Bambusicola	*Phyllostachys edulis*	China	MT199633	MT192834	MT192861		MT188628	MT192805
C. guizhouensis	CGMCC 3.15112, LC2305*	Spaethianum	*Bletilla ochracea*	China	JX625158	KC843507	MZ799321	MZ673850	KC843536	JX625185
C. hainanense	CBS 145900*	Graminicola	*Axonopus compressus*	China	KY242705					
C. hanaui	MAFF 305404*	Graminicola	*Digitaria ciliaris*	Japan	JX519217		JX519225			JX519242
C. hebeiense	MFLUCC13–0726*	Gloeosporioides	*Vitis vinifera*	China	KF156863	KF377495	KF289008		KF377532	KF288975
C. hederiicola	MFLU 15-0689*	Gloeosporioides	*Hedera helix*	Italy	MN631384		MN635794		MN635795	
C. helleniense	CBS 142418, CPC 26844*	Gloeosporioides	*Poncirus trifoliata*	Greece	KY856446	KY856270	KY856186	KY856361	KY856019	KY856528

Supplementary Table 1 Continued.

Species	Culture	Group	Host	Country	ITS	*gapdh*	*chs-1*	*his3*	*act*	*tub2*
C. hemerocallidis	CBS 130642, CDLG5, CGMCC 3.14971*	Dematium	*Hemerocallis fulva* var. *kwanso*	China	JQ400005	JQ400012	JQ399998		JQ399991	JQ400019
C. henanense	CGMCC 3.17354, LC3030, LF238 *	Gloeosporioides	*Camellia sinensis*	China	KJ955109	KJ954810	MZ799256	MZ673835	KM023257	KJ955257
C. higginsianum	IMI 349061, CPC 19379*	Destructivum	*Brassica chinensis*	Trinidad and Tobago	KM105184	KM105535	KM105254	KM105324	KM105394	KM105464
C. hippeastri	CBS 125376, CSSG1*	Boninense	*Hippeastrum vittatum*	China	JQ005231	JQ005318	JQ005405	JQ005492	JQ005579	JQ005665
C. horii	ICMP 10492, NBRC 7478, MTCC 10841*	Gloeosporioides	*Diospyros kaki*	Japan	GQ329690	GQ329681	JX009752		JX009438	JX010450
C. horii	ICMP 17968	Gloeosporioides	*Diospyros kaki*	China	JX010212	GQ329682	JX009811		JX009547	JX010378
C. horii	MAFF 306429, ICMP 17970	Gloeosporioides	*Diospyros kaki*	Japan	JX010213	GQ329686	JX009824		JX009467	
C. hsienjenchang	MAFF 243051	Bambusicola	*Phyllostachys bambusoides*	Japan	AB738855		AB738846	AB738847	AB738845	
C. hystricis	CBS 142411, CPC 28153*	Gloeosporioides	*Citrus hystrix*	Italy	KY856450	KY856274	KY856190	KY856365	KY856023	KY856532
C. incanum	ATCC 64682*	Spaethianum	*Phaseolus vulgaris*	Canada	KC110789	KC110807		KC110798	KC110825	KC110816
C. indonesiense	CBS 127551, CPC 14986*	Acutatum	*Eucalyptus* sp.	Indonesia	JQ948288	JQ948618	JQ948949	JQ949279	JQ949609	JQ949939
C. insertae	MFLU 15-1895*	Dematium	*Parthenocissus inserta*	Russia	KX618686	KX618684	KX618683		KX618682	KX618685
C. iris	LC3697, ZN169*	Spaethianum	*Iris japonica*	China	MZ595837	MZ664090	MZ799323	MZ673856	MZ664135	MZ673958
C. iris	**GUCC 12172**	**Spaethianum**	***Aspidistra elatior***	**China**	**OP723062**	**OP784156**	**OP730692**	**OP784217**	**OP740229**	
C. iris	**GUCC 12173**	**Spaethianum**	***Aspidistra elatior***	**China**	**OP723063**	**OP784157**	**OP730693**	**OP784218**	**OP740230**	
C. jacksonii	MAFF 305460*	Graminicola	*Echinochloa esculenta*	Japan	JX519216		JX519224		JX519233	JX519241
C. jasminigenum	CGMCC LLTX–01, MFLU 10–0273*	Truncatum	*Jasminum sambac*	Vietnam	HM131513	HM131499			HM131508	HM153770
C. javanense	CBS 144963*	Acutatum	*Capsicum annuum*	Indonesia	MH846576	MH846572	MH846573	MH846571	MH846575	MH846574

Supplementary Table 1 Continued.

Species	Culture	Group	Host	Country	ITS	*gapdh*	*chs-1*	*his3*	*act*	*tub2*
C. jiangxiense	CGMCC 3.17361, LC3266, LF488	Gloeosporioides	*Camellia sinensis*	China	KJ955149	KJ954850	MZ799257		KJ954427	OK236389
C. jiangxiense	CGMCC 3.17362, LC3260, LF684	Gloeosporioides	*Camellia sinensis*	China	KJ955198	KJ954899			KJ954469	KJ955345
C. jiangxiense	CGMCC 3.17363, LC3263, LF678*	Gloeosporioides	*Camellia sinensis*	China	KJ955201	KJ954902			KJ954471	KJ955348
C. jiangxiense	YMF 1.04949	Gloeosporioides	*Aquatic Plants*	China	OL842166	OL981261	OL981287		OL981235	
C. jiangxiense	**GUCC 12043**	**Gloeosporioides**	***Illicium simonsii***	**China**	**OP722998**	**OP784037**	**OP730594**		**OP740134**	**OP761905**
C. jiangxiense	**GUCC 12044**	**Gloeosporioides**	***Illicium simonsii***	**China**	**OP722970**	**OP784038**	**OP730595**		**OP740135**	**OP761906**
C. jiangxiense	**GUCC 12045**	**Gloeosporioides**	***Illicium simonsii***	**China**	**OP723001**	**OP784039**	**OP730596**		**OP740136**	**OP761907**
C. jiangxiense	**GUCC 12046**	**Gloeosporioides**	***Illicium simonsii***	**China**	**OP722999**	**OP784040**	**OP730597**		**OP740137**	**OP761908**
C. jiangxiense	**GUCC 12055**	**Gloeosporioides**	***Fatsia japonica***	**China**	**OP722969**	**OP784067**	**OP730621**		**OP740163**	**OP761933**
C. jiangxiense	**GUCC 12058**	**Gloeosporioides**	***Cinnamomum camphora***	**China**	**OP722971**	**OP784073**	**OP730626**		**OP740170**	**OP761939**
C. jinshuiense	CGMCC 3.18903, PAFQ26*	Dematium	*Pyrus pyrifolia* cv. Jinshui	China	MG748077	MG747995	MG747913		MG747767	MG748157
C. jishouense	GMBC 0209*	Gigasporum	*Nothapodytes pittosporoides*	China	MH482929	MH681658			MH708135	MH727473
C. johnstonii	CBS 128532, ICMP 12926, PRJ 1139.3*	Acutatum	*Solanum lycopersicum*	Zealand	JQ948444	JQ948774	JQ949105	JQ949435	JQ949765	JQ950095
C. juglandis	YZU 191277*	Acutatum	*Juglans regia*	China	OM755762	OM913576	OM913546		OM913553	
C. kahawae	IMI 319418, ICMP 17816*	Gloeosporioides	*Coffea arabica*	Kenya	JX010231	JX010012	JX009813	MZ673838	JX009452	JX010444
C. kaifengense	CAASZK33*	Magnum	*Citrullus lanatus*	China	MZ475244	OL456714	OL901182	OM057723	OL449312	OL456673
C. kakiivorum	KCTC 46679*	Dematium	*Diospyros kaki*	Korea	LC324781	LC324787	LC324783	LC324789	LC324785	LC324791
C. karsti	CGMCC 3.14194*	Boninense	*Vanda* sp.	China	HM585409	HM585391	HM582023		HM581995	HM585428
C. karsti	CBS 129833	Boninense	*Musa* sp.	Mexico	JQ005175	JQ005262	JQ005349	JQ005436	JQ005523	JQ005609
C. karsti	CBS 129834	Boninense	*Musa* sp.	Mexico	JQ005176	JQ005263	JQ005350	JQ005437	JQ005524	JQ005610
C. karsti	CBS 112982	Boninense	*Protea cynaroides*	Zimbabwe	JQ005183	JQ005270	JQ005357	JQ005444	JQ005531	JQ005617

Supplementary Table 1 Continued.

Species	**Culture**	**Group**	**Host**	**Country**	**ITS**	***gapdh***	***chs-1***	***his3***	***act***	***tub2***
C. karsti	CBS 861.72	Boninense	*Bombax aquaticum*	Brazil	JQ005184	JQ005271	JQ005358	JQ005445	JQ005532	JQ005618
C. karsti	CBS 110779	Boninense	*Eucalyptus grandis*	South Africa	JQ005198	JQ005285	JQ005372	JQ005459	JQ005546	JQ005632
C. karsti	**GUCC 12007**	**Boninense**	***Mahonia fortunei***	**China**	**OP723041**	**OP784030**	**OP730588**	**OP784163**	**OP740128**	**OP761899**
C. karsti	**GUCC 12008**	**Boninense**	***Mahonia fortunei***	**China**	**OP723030**	**OP784031**	**OP730589**	**OP784164**	**OP740129**	**OP761900**
C. karsti	**GUCC 12009**	**Boninense**	***Mahonia fortunei***	**China**	**OP723031**	**OP784032**	**OP730590**	**OP784165**	**OP740130**	**OP761901**
C. karsti	**GUCC 12010**	**Boninense**	***Mahonia fortunei***	**China**	**OP723032**	**OP784033**	**OP730591**	**OP784166**	**OP740131**	**OP761902**
C. karsti	**GUCC 12011**	**Boninense**	***Mahonia fortunei***	**China**	**OP723042**	**OP784034**	**OP730592**		**OP740132**	**OP761903**
C. karsti	**GUCC 12012**	**Boninense**	***Mahonia fortunei***	**China**	**OP723040**	**OP784035**				
C. karsti	**GUCC 12026**	**Boninense**	***Cinnamomum camphora***	**China**	**OP723039**		**OP730625**		**OP740169**	
C. karsti	**GUCC 12028**	**Boninense**	***Liliaceae* sp.**	**China**	**OP723048**	**OP784080**	**OP730633**	**OP784197**	**OP740177**	**OP761946**
C. karsti	**GUCC 12029**	**Boninense**	***Liliaceae* sp.**	**China**	**OP723033**	**OP784081**	**OP730634**	**OP784198**		**OP761947**
C. karsti	**GUCC 12030**	**Boninense**	***Liliaceae* sp.**	**China**	**OP723049**	**OP784082**	**OP730635**	**OP784199**		**OP761948**
C. karsti	**GUCC 12032**	**Boninense**	***Capsicum annuum***	**China**	**OP723050**	**OP784130**				**OP761996**
C. karsti	**GUCC 12033**	**Boninense**	***Ilex chinensis***	**China**	**OP723034**	**OP784134**	**OP730682**	**OP784212**	**OP740220**	**OP762000**
C. karsti	**GUCC 12036**	**Boninense**	***Chimonanthus praecox***	**China**	**OP723051**					**OP762004**
C. karsti	**GUCC 12037**	**Boninense**	***Photinia serratifolia***	**China**	**OP723043**	**OP784144**	**OP730687**	**OP784215**	**OP740224**	**OP762009**
C. karsti	**GUCC 12038**	**Boninense**	***Photinia serratifolia***	**China**	**OP723044**	**OP784145**	**OP730688**	**OP784216**	**OP740225**	**OP762010**
C. karsti	**GUCC 12040**	**Boninense**	**unidentified host**	**China**	**OP723035**	**OP784149**	**OP730690**		**OP740227**	**OP762014**
C. karsti	**GUCC 12041**	**Boninense**	**unidentified host**	**China**	**OP723036**	**OP784150**	**OP730691**		**OP740228**	**OP762015**
C. karsti	**GZCC 21-0804**	**Boninense**	***Camellia japonica***	**China**	**OP723029**	**OP784158**	**OP730694**		**OP740231**	**OP762021**
C. karsti (syn. *C. wuxuhaiense*)	CGMCC3.18951, YMF 1.04951(*)	Boninense	*Potamogeton crispus*	China	OL842173	OL981268	OL981294		OL981242	OL981228

Supplementary Table 1 Continued.

Species	Culture	Group	Host	Country	ITS	*gapdh*	*chs-1*	*his3*	*act*	*tub2*
C. karsti (syn. *C. wuxuhaiense*)	F34	Boninense	*Potamogeton pectinatus*	*China*	OL842175	OL981270	OL981296		OL981244	OL981230
C. kinghornii	CBS 198.35*	Acutatum	*Phormium* sp.	UK	JQ948454	JQ948784	JQ949115	JQ949445	JQ949775	JQ950105
C. kniphofiae	CBS 143496*	Acutatum	*Kniphofia uvaria*	UK	MH107884	MH107998	MH107990		MH107975	MH108037
C. kunmingense	**GUCC 12053***	**Gloeosporioides**	***Ophiopogon japonicus***	**China**	**OP722975**	**OP737965**	**OP715769**		**OP715804**	**OP720861**
C. kunmingense	**GUCC 12178**	**Gloeosporioides**	***Ophiopogon japonicus***	**China**	**OP722974**	**OP784058**	**OP715770**		**OP715805**	
C. laticiphilum	CBS 112989, IMI 383015, STE-U 5303*	Acutatum	*Hevea brasiliensis*	India	JQ948289	JQ948619	JQ948950	JQ949280	JQ949610	JQ949940
C. lauri	MFLUCC 17-0205, IT2505_1a*	Acutatum	*Laurus nobilis*	Italy	KY514347	KY514344	KY514341		KY514338	KY514350
C. ledebouriae	CBS 141284*	Agaves	*Ledebouria floridunda*	South Africa	KX228254			KX228365	KX228357	
C. lentis	CBS 127604, DAOM 235316, CT21*	Destructivum	*Lens culinaris*	Canada	JQ005766	KM105597	JQ005787	JQ005808	JQ005829	JQ005850
C. ligustri	**GUCC 12111***	**Gloeosporioides**	***Ilex chinensis***	**China**	**OP722988**	**OP737968**	**OP715773**		**OP740216**	**OP720864**
C. lilii	CBS 109214	Spaethianum	*Lilium* sp.	Japan	GU227810	GU228202	GU228300	GU228006	GU227908	GU228104
C. limetticola	CBS 114.14*	Acutatum	*Citrus aurantifolia*	Florida	JQ948193	JQ948523	JQ948854	JQ949184	JQ949514	JQ949844
C. limonicola	CBS 142410, CPC 31141*	Boninense	*Citrus limon*	Malta	KY856472	KY856296	KY856213	KY856388	KY856045	KY856554
C. lindemuthianum	CBS 144.31*	Orbiculare	*Phaseolus vulgaris*	Germany	JQ005779	JX546712	JQ005800	JQ005821	JQ005842	JQ005863
C. lineola	CBS 125337*	Dematium	*Apiaceae* sp.	Czech Republic	GU227829	GU228221	GU228319	GU228025	GU227927	GU228123
C. lini	CBS 172.51*	Destructivum	*Linum usitatissimum*	Netherlands	JQ005765	KM105581	JQ005786	JQ005807	JQ005828	JQ005849
C. liriopes	CBS 119444*	Spaethianum	*Liriope muscari*	Mexico	GU227804	GU228196	GU228294	GU228000	GU227902	GU228098
C. liriopes	CBS 122747	Spaethianum	*Liriope muscari*	Mexico	GU227805	GU228197	GU228295	GU228001	GU227903	GU228099
C. liriopes	LC11287, MZ06	Spaethianum	*Liriope spicata*	China	MZ595843	MZ664092	MZ799325	MZ673863	MZ664141	MZ673964
C. litangense	CGMCC 3.016099*, YMF 1.06700	*Graminicola*	*Hippuris vulgaris*	China	MW722955					MW776748

Supplementary Table 1 Continued.

Species	**Culture**	**Group**	**Host**	**Country**	**ITS**	***gapdh***	***chs-1***	***his3***	***act***	***tub2***
C. lobatum	IMI 79736*	Magnum	*Piper catalpaefolium*	Trinidad and Tobago	MG600768	MG600828	MG600874	MG600912	MG600972	MG601035
C. lupini	CBS 109225, BBA 70884*	Acutatum	*Lupinus albus*	Ukraine	JQ948155	JQ948485	JQ948816	JQ949146	JQ949476	JQ949806
C. magnisporum	CBS 398.84*	Gigasporum	Unknown	unknown	KF687718	KF687842	KF687782	KF687865	KF687803	KF687882
C. magnum	CBS 519.97*	Magnum	*Citrullus lanatus*	USA	MG600769	MG600829	MG600875	MG600913	MG600973	MG601036
C. makassarense	CBS 143664*	Gloeosporioides	*Capsicum annuum*	Indonesia	MH728812	MH728820	MH805850		MH781480	MH846563
C. malvarum	CBS 521.97, LARS 720, Lav-4*	Orbiculare	*Lavatera trimestris*	UK	KF178480	KF178504	KF178529	KF178553	KF178577	KF178601
C. melonis	CBS 159.84*	Acutatum	*Cucumis melo*	Brazil	JQ948194	JQ948524	JQ948855	JQ949185	JQ949515	JQ949845
C. mengyinense	SAUCC200913	Gloeosporioides	*Juglansregia*	*China*	MW786690	MW876473	MW883688		MW883697	MW888972
C. mengyinense	SAUCC200702*	*Gloeosporioides*	*Rosachinensis* sp.	China	MW786742	MW846240	MW883686		MW883695	MW888970
C. menispermi	MFLU 14-0625*	Dematium	*Menispermum dauricum*	Russia	KU242357	KU242356	KU242355		KU242353	KU242354
C. merremiae	CBS 124955*	Magnum	*Merremia umbellata*	Panama	MG600765	MG600825	MG600872	MG600910	MG600969	MG601032
C. metake	MAFF 244029	Bambusicola	*Pleioblastus simonii*	Japan	OK090429					OK236390
C. metake	MAFF 243970	Bambusicola	*Pleioblastus simonii*	Japan	OK090430					OK236391
C. miaoliense	NTUCC 20-001-1*	Acutatum	*Fragaria* × *ananassa*	China, Taiwan	MK908419	MK908470	MK908522		MK908573	MK908624
C. miscanthi	MAFF 510857*	Graminicola	*Miscanthus sinensis*	Japan	JX519221		JX519229		JX519237	JX519246
C. monsterae	LC13871, NN055214*	Orchidearum	*Monstera deliciosa*	China	MZ595897	MZ664121	MZ799351	MZ673917	MZ664195	MZ674015
C. multiseptatum	LC13886, NN055357*	Graminicola	Dead culm of grass	China	MZ595901	MZ664099	MZ799331	MZ673921	MZ664199	MZ674019
C. musae	CBS 116870, ICMP 19119, MTCC 11349*	Gloeosporioides	*Musa* sp.	USA	JX010146	JX010050	JX009896		JX009433	HQ596280
C. musicola	CBS 132885*	Orchidearum	*Musa* sp.	Mexico	MG600736	MG600798	MG600853	MG600895	MG600942	MG601003
C. nageiae	LC13866, NN004492*	singleton	*Nageia nagi*	China	MZ595882	MZ664087	MZ799278	MZ673902	MZ664180	MZ674000

Supplementary Table 1 Continued.

Species	Culture	Group	Host	Country	ITS	*gapdh*	*chs-1*	*his3*	*act*	*tub2*
C. nanhuaense	CGMCC3.18962, YMF1.04993*	Gloeosporioides	*Ageratina adenophora*	China	OK030870	OK513673	OK513569		OK513609	OK513639
C. nanhuaense	YMF1.04990	Gloeosporioides	*Ageratina adenophora*	China	OK030871	OK513674	OK513570		OK513610	OK513640
C. navitas	CBS 125086*	Graminicola	*Panicum virgatum*	USA	JQ005769		JQ005790	JQ005811	JQ005832	JQ005853
C. neorubicola	CCR144*	Destructivum	*Rubus idaeus*	China	MK529906	MK547520	MK547526		MK547523	MN186400
C. neosansevieriae	CBS 139918*	Agaves	*Sansevieria trifasciata*	South Africa	KR476747	KR476791		KR476792	KR476790	KR476797
C. nicholsonii	MAFF 511115*	Graminicola	*Paspalum dilatatum*	Japan	JQ005770		JQ005791	JQ005812	JQ005833	JQ005854
C. nigrum	CBS 169.49*	singleton	*Capsicum* sp.	Argentina	JX546838	JX546742	JX546693	JX546791	JX546646	JX546885
C. novae-zelandiae	CBS 128505, ICMP 12944*	Boninense	*Capsicum annuum*	Zealand	JQ005228	JQ005315	JQ005402	JQ005489	JQ005576	JQ005662
C. nullisetosum	CGMCC3.16080, YMF1.06946*	Gloeosporioides	*Mangifera indica*	China	OK030872	OK513675	OK513571		OK513611	OK513641
C. nupharicola	CBS 470.96, ICMP 18187*	Gloeosporioides	*Nuphar lutea* subsp. *polysepala*	USA	JX010187	JX009972	JX009835		JX009437	JX010398
C. nymphaeae	CBS 515.78*	Acutatum	*Nymphaea alba*	Netherlands	JQ948197	JQ948527	JQ948858	JQ949188	JQ949518	JQ949848
C. nymphaeae	CBS 134233, CGMCC 3.15228, ZJUC41*	Acutatum	*Citrus aurantifolia*	China	KC293581	KC293741	KY856138	KY856309	KY855973	KC293661
C. oblongisporum	CGMCC3.16074, YMF1.06938*	Gloeosporioides	*Ageratina adenophora*	China	OK030874	OK513677	OK513573			OK513643
C. obovoides	LC6085, JJR053*	singleton	Unknown	China	MZ595838		MZ799345	MZ673857	MZ664136	MZ673959
C. ochraceae	CGMCC 3.15104, LC2303*	Caudatum	*Bletilla ochracea*	China	JX625156	KC843513	MZ799317	MZ673849	KC843527	JX625183
C. ocimi	CBS 298.94*	Destructivum	*Ocimum basilicum*	Italy	KM105222	KM105577	KM105292	KM105362	KM105432	KM105502
C. okinawense	MAFF 240517*	Magnum	*Carica papaya*	Japan	MG600767	MG600827			MG600971	MG601034
C. oncidii	CBS 129828*	Boninense	*Oncidium* sp.	Germany	JQ005169	JQ005256	JQ005343	JQ005430	JQ005517	JQ005603
C. orbiculare	CBS 570.97, LARS 73*	Orbiculare	*Cucumis sativus*	Europe, probably UK	KF178466	KF178490	KF178515	KF178539	KF178563	KF178587
C. orchidearum	CBS 135131*	Orchidearum	*Dendrobium nobile*	Netherlands	MG600738	MG600800	MG600855	MG600897	MG600944	MG601005
C. orchidis	MFLUCC 17-1302*	Dematium	*Orchis* sp.	Italy	MK502144	MK496857	MK496855		MK496853	MK496859

Supplementary Table 1 Continued.

Species	**Culture**	**Group**	**Host**	**Country**	**ITS**	***gapdh***	***chs-1***	***his3***	***act***	***tub2***
C. orchidophilum	CBS 632.80*	singleton	*Dendrobium* sp.	USA	JQ948151	JQ948481	JQ948812	JQ949142	JQ949472	JQ949802
C. orchidophilum	CBS 631.80	singleton	*Ascocenda* sp.	USA	JQ948152	JQ948482	JQ948813	JQ949143	JQ949473	JQ949803
C. orchidophilum	IMI 309357, CPC 16815	singleton	*Phalaenopsis* sp.	UK	JQ948153	JQ948483	JQ948814	JQ949144	JQ949474	JQ949804
C. orientalis	CBS 128555*	Acutatum	*Malus domestica*	New Zealand	JQ948305	JQ948635	JQ948966	JQ949296	JQ949626	JQ949956
C. orientalis	F10PGBYS8	Acutatum	*Malus domestica*	China	KF772139	KF772109	KF772079		KF772049	KF772169
C. ovataense	KACC 49789, T72*	Magnum	*Atractylodes ovata*	South Korea	LC604492	LC604553	LC604605		LC604579	LC604524
C. panacicola	C08048	Destructivum	*Pana × ginseng*	Korea	GU935867	GU935847			GU944757	
C. panamense	CBS 125386*	Magnum	*Merremia umbellata*	Panama	MG600766	MG600826	MG600873	MG600911	MG600970	MG601033
C. parabambusicola	LC13884, NN058956*	Bambusicola	bamboo	China	MZ595904	MZ664098	MZ799338	MZ673924	MZ664202	MZ674022
C. paraendophytum	LC13888, NN054963*	Graminicola	Grass	China	MZ595895	MZ664057	MZ799328	MZ673915	MZ664193	MZ674013
C. parallelophorum	MFLUCC 14-0083*	Dracaenophilum	*Dendrobium* sp.	Thailand	MF448525	MK165695				MH351280
C. paranaense	CBS 134729*	Acutatum	*Malus domestica*	Paraná	KC204992	KC205026	KC205043	KC205004	KC205077	KC205060
C. parsonsiae	CBS 128525, ICMP 18590*	Boninense	*Parsonsia capsularis*	Zealand	JQ005233	JQ005320	JQ005407	JQ005494	JQ005581	JQ005667
C. parthenocissicola	MFLUCC 17-1098*	Dematium	*Parthenocissus quinquefolia*	Russia	MK629452	MK639362	MK639356		MK639358	MK639360
C. paspali	MAFF 305403*	Graminicola	*Paspalum notatum*	Japan	JX519219		JX519227		JX519235	JX519244
C. paxtonii	IMI 165753, CPC 18868*	Acutatum	*Musa* sp.	Saint Lucia	JQ948285	JQ948615	JQ948946	JQ949276	JQ949606	JQ949936
C. pereskiae	VIC 47381*	Orchidearum	*Pereskia aculeata*	Brazil	MZ262421	MZ265337				
C. perseae	CBS 141365, GA100*	Gloeosporioides	*Avocado*	Israel	KX620308	KX620242	MZ799260		KX620145	KX620341
C. persicum	CBS 148574, IRAN 3712C, UTFC 370, DSM 113400, GLMC 2645*	Caudatum	*Phragmites australis*	IRAN	MW741433	MW740228			MW822655	MW740367

Supplementary Table 1 Continued.

Species	**Culture**	**Group**	**Host**	**Country**	**ITS**	***gapdh***	***chs-1***	***his3***	***act***	***tub2***
C. petchii	CBS 378.94*	Boninense	*Dracaena marginata*	Italy	JQ005223	JQ005310	JQ005397	JQ005484	JQ005571	JQ005657
C. phaseolorum	CBS 157.36	singleton	*Phaseolus radiatus* var. *aureus*	Japan	GU227896	GU228288	GU228386	GU228092	GU227994	GU228190
C. philoxeroidis	CGMCC3.18945, YMF 1.04945*	Magnum	*Alternanthera philoxeroides*	China	OL842188	OL981283	OL981309		OL981257	
C. phormii	CBS 118194, AR 3546*	Acutatum	*Phormium* sp.	Germany	JQ948446	JQ948777	JQ949107	JQ949437	JQ949767	JQ950097
C. phyllanthi	CBS 175.67, MACS 271*	Boninense	*Phyllanthus acidus*	India	JQ005221	JQ005308	JQ005395	JQ005482	JQ005569	JQ005655
C. piperis	IMI 71397, CPC 21195*	Orchidearum	*Piper nigrum*	Malaysia	MG600760	MG600820	MG600867	MG600906	MG600964	MG601027
C. pisicola	CBS 724.97, LARS 60*	Destructivum	*Pisum sativum*	USA	KM105172	KM105522	KM105242	KM105312	KM105382	KM105452
C. pleopeltidis	CBS 147082*	Destructivum	*Pleopeltis* sp.	South Africa	MW883412		MW890035		MW890024	
C. plurivorum	CBS 125474*	Orchidearum	*Coffea* sp.	Vietnam	MG600718	MG600781	MG600841	MG600887	MG600925	MG600985
C. plurivorum	CBS 132443	Orchidearum	*Gossypium* sp.	Brazil	MG600719	MG600782	MG600842	MG600888	MG600926	MG600986
C. plurivorum	LC8240, M51	Orchidearum	*Paederia foetida*	China	MZ595848	MZ664113	MZ799291	MZ673868	MZ664146	MZ673969
C. plurivorum	LC8337, M151	Orchidearum	*Vigna unguiculata*	China	MZ595855	MZ664115	MZ799294	MZ673875	MZ664153	MZ673976
C. plurivorum	**GUCC 12137**	**Orchidearum**	***Syngonium podophyllum***	**China**	**OP723087**	**OP784076**	**OP730629**	**OP784193**	**OP740173**	**OP761942**
C. plurivorum	**GUCC 12138**	**Orchidearum**	***Syngonium podophyllum***	**China**	**OP723086**	**OP784077**	**OP730630**	**OP784194**	**OP740174**	**OP761943**
C. plurivorum	**GUCC 12139**	**Orchidearum**	***Syngonium podophyllum***	**China**	**OP723088**	**OP784078**	**OP730631**	**OP784195**	**OP740175**	**OP761944**
C. plurivorum	**GUCC 12140**	**Orchidearum**	***Syngonium podophyllum***	**China**	**OP723085**	**OP784079**	**OP730632**	**OP784196**	**OP740176**	**OP761945**
C. plurivorum	**GUCC 12141**	**Orchidearum**	***Piper sarmentosum***	**China**	**OP723084**	**OP784117**	**OP730669**	**OP784204**	**OP740205**	**OP761983**
C. plurivorum	**GUCC 12142**	**Orchidearum**	***Piper sarmentosum***	**China**	**OP723089**	**OP784118**	**OP730670**	**OP784205**	**OP740206**	**OP761984**
C. plurivorum	**GUCC 12143**	**Orchidearum**	***Piper sarmentosum***	**China**	**OP723090**	**OP784119**	**OP730671**	**OP784206**	**OP740207**	**OP761985**
C. proteae	CBS 132882, CPC 14859*	Gloeosporioides	*Protea* sp.	South Africa	KC297079	KC297009	KC296986	KC297045	KC296940	KC297101
C. pseudoacutatum	CBS 436.77*	singleton	*Pinus radiata*	Chile	JQ948480	JQ948811	JQ949141	JQ949471	JQ949801	JQ950131

Supplementary Table 1 Continued.

Species	**Culture**	**Group**	**Host**	**Country**	**ITS**	***gapdh***	***chs-1***	***his3***	***act***	***tub2***
C. pseudomajus	CBS 571.88*	Gigasporum	*Camellia sinensis*	China, Taiwan	KF687722	KF687826	KF687779	KF687864	KF687801	KF687883
C. pseudotheobromicola	MFLUCC 18–1602*	Gloeosporioides	*Prunus avium*	China	MH817395	MH853675	MH853678		MH853681	MH853684
C. psidii	CBS 145.29, ICMP 19120*	Gloeosporioides	*Psidium* sp.	Italy	JX010219	JX009967	JX009901		JX009515	JX010443
C. pyricola	CBS 128531, ICMP 12924, PRJ 977.1*	Acutatum	*Pyrus communis*	New Zealand	JQ948445	JQ948776	JQ949106	JQ949436	JQ949766	JQ950096
C. pyrifoliae	CGMCC 3.18902, PAFQ22*	singleton	*Pyrus pyrifolia* cv. Jinshui	China	MG748078	MG747996	MG747914		MG747768	MG748158
C. pyrifoliae	PAFQ22a	singleton	*Pyrus pyrifolia* cv. Jinshui	China	MG874834	MG874826	MG874818		MG874810	MG874842
C. qilinense	CAASZK13*	Magnum	*Citrullus lanatus*	China	MZ475217	OL456694	OL901162	OM057703	OL449292	OL456653
C. queenslandicum	ICMP 1778*	Gloeosporioides	*Carica papaya*	Australia	JX010276	JX009934	JX009899		JX009447	JX010414
C. quercicola	CFCC 54457*	Destructivum	*Quercus variabilis*	China	ON692810	ON755052	ON755048		ON755044	ON755056
C. quinquefoliae	MFLU 14-0626*	Dematium	*Parthenocissus quinquefolia*	Russia	KU236391	KU236390			KU236389	KU236392
C. radermacherae	**GZCC 21-0813***	**Acutatum**	***Cinnamomum camphora***	**China**	**OP723052**	**OP737966**	**OP715771**		**OP715806**	**OP720862**
C. radermacherae	**GZCC 21-0814**	**Acutatum**	***Radermachera sinica***	**China**	**OP723053**	**OP737967**	**OP715772**		**OP715807**	**OP720863**
C. radicis	CBS 529.93*	Gigasporum	Unknown	Costa Rica	KF687719	KF687825	KF687762	KF687847	KF687785	KF687869
C. reniforme	LC8230, M41*	Orchidearum	*Smilax cocculoides*	China	MZ595847	MZ664110	MZ799290	MZ673867	MZ664145	MZ673968
C. rhexiae	CBS 133134, Coll1026, BPI 884112*	Gloeosporioides	*Rhexia virginica*	Sussex	JX145128	MZ664046	MZ799258	MZ673834	MZ664127	JX145179
C. rhombiforme	CBS 129953, PT250, RB011*	Acutatum	*Olea europaea*	Portugal	JQ948457	JQ948788	JQ949118	JQ949448	JQ949778	JQ950108
C. riograndense	COAD 928*	Spaethianum	*Tradescantia fluminensis*	Brazil	KM655299	KM655298	KM655297		KM655295	KM655300
C. robustum	CGMCC3.16077, YMF 1.06941*	Dracaenophilum	*Ageratina adenophora*	China	OK030877		OK513576		OK513614	OK513646
C. roseum	CBS 145754*	Acutatum	*Lapageria rosea*	Chile	MK903611	MK903603			MK903604	MK903607
C. rusci	CBS 119206*	singleton	*Ruscus* sp.	Italy	GU227818	GU228210	GU228308	GU228014	GU227916	GU228112

Supplementary Table 1 Continued.

Species	Culture	Group	Host	Country	ITS	*gapdh*	*chs-1*	*his3*	*act*	*tub2*
C. sacchari	CBS 148575, IRAN 3707C, UTFC 363, DSM 113401, GLMC 2647*	Caudatum	*Saccharum spontaneum*	IRAN	MW741431	MW740229			MW822656	MW740368
C. salicis	CBS 607.94*	Acutatum	*Salix* sp.	Netherlands	JQ948460	JQ948791	JQ949121	JQ949451	JQ949781	JQ950111
C. salsolae	ICMP 19051*	Gloeosporioides	*Salsola tragus*	Hungary	JX010242	JX009916	JX009863		JX009562	JX010403
C. sambucicola	MFLUCC 16-1388*	Dematium	*Sambucus ebulus*	Italy	KY098781	KY098780	KY098779		KY098778	KY098782
C. sansevieriae	MAFF 239721*	Agaves	*Sansevieria trifasciata*	Japan	AB212991	LC180130	LC180129	LC180126	LC180127	LC180128
C. schefflerae	**GZCC 21-0809***	**Dracaenophilum**	***Cyperus rotundus***	**China**	**OP723075**	**OP737971**	**OP715776**		**OP715810**	
C. schimae	LC13880, NN046984*	Acutatum	*Schima* sp.	China	MZ595885	MZ664105	MZ799347	MZ673905	MZ664183	MZ674003
C. scovillei	CBS 126529, PD 94/921-3, BBA 70349*	Acutatum	*Capsicum* sp.	Indonesia	JQ948267	JQ948597	JQ948928	JQ949258	JQ949588	JQ949918
C. sedi	MFLUCC 14-1002*	Dematium	*Sedum* sp.	Russia	KM974758	KM974755	KM974754		KM974756	KM974757
C. serranegrense	COAD 2100*	Gigasporum	*Cattleya jongheana*	Brazil	KY400111		KY407894		KY407892	KY407896
C. shisoi	JCM 31818*	Destructivum	*Perilla frutescens* var. *crispa*	Japan	MH660930	MH660931	MH660929		MH660928	MH660932
C. shivasii	LC1400, BRIP15842a*	Caudatum	*Themeda thriandra*	Australia	MZ595836	MZ664088	MZ799316	MZ673848	MZ664134	MZ673957
C. siamense	ICMP 18572	Gloeosporioides	*Vitis vinifera*	USA	JX010160	JX010061	JX009783		JX009487	
C. siamense	ICMP 18739	Gloeosporioides	*Carica papaya*	South Africa	JX010161	JX009921	JX009794		JX009484	
C. siamense	ICMP 18118	Gloeosporioides	*Commelina* sp.	Nigeria	JX010163	JX009941	JX009843		JX009505	JX010402
C. siamense	ICMP 18578, CBS 130417*	Gloeosporioides	*Coffea arabica*	Thailand	JX010171	JX009924	JX009865		FJ907423	JX010404
C. siamense	ICMP 18642, CBS 125378	Gloeosporioides	*Hymenocallis americana*	China	JX010278	JX010019	GQ856730		JX009441	JX010410
C. siamense	CBS 112983, CPC 2291	Gloeosporioides	*Protea cynaroides*	Zimbabwe	KC297065	KC297007	KC296984		KC296929	KC297100
C. siamense	CBS 113199. CPC 2290	Gloeosporioides	*Protea cynaroides*	Zimbabwe	KC297066	KC297008	KC296985		KC296930	KC297090

Supplementary Table 1 Continued.

Species	Culture	Group	Host	Country	ITS	*gapdh*	*chs-1*	*his3*	*act*	*tub2*
C. siamense	CBS 440.67	Gloeosporioides	*Coffea* sp.	Kenya; Ruiru	KP703356	KP703276				KP703433
C. siamense	IMI 96858, CPC 16807	Gloeosporioides	*Annona squamosa*	India	KP703361	KP703288				KP703445
C. siamense	CBS 112985, IMI 319424, CPC 5295	Gloeosporioides	*Coffea arabica*	Kenya	KP703411	KP703271				KP703428
C. siamense	CBS 125470	Gloeosporioides	*Coffea* sp.	Vietnam; Yen Bai	KP703419	KP703272				
C. siamense	**GUCC 12061**	**Gloeosporioides**	***Hymenocallis littoralis***	**China**	**OP722977**	**OP784083**	**OP730636**		**OP740178**	**OP761949**
C. siamense	**GUCC 12062**	**Gloeosporioides**	***Alocasia macrorrhiza***	**China**	**OP722957**	**OP784086**	**OP730639**		**OP740181**	**OP761952**
C. siamense	**GUCC 12063**	**Gloeosporioides**	***Bauhinia championii***	**China**	**OP723020**	**OP784087**	**OP730640**		**OP740182**	**OP761953**
C. siamense	**GUCC 12065**	**Gloeosporioides**	***Osmanthus fragrans***	**China**	**OP722993**	**OP784088**	**OP730641**		**OP740183**	**OP761954**
C. siamense	**GUCC 12066**	**Gloeosporioides**	***Osmanthus fragrans***	**China**	**OP723018**	**OP784089**	**OP730642**		**OP740184**	**OP761955**
C. siamense	**GUCC 12068**	**Gloeosporioides**	***Osmanthus fragrans***	**China**	**OP723024**	**OP784090**	**OP730643**		**OP740185**	**OP761956**
C. siamense	**GUCC 12071**	**Gloeosporioides**	***Houttuynia cordata***	**China**	**OP723027**	**OP784092**	**OP730645**		**OP740187**	**OP761958**
C. siamense	**GUCC 12075**	**Gloeosporioides**	***Ardisia japonica***	**China**	**OP722958**	**OP784095**	**OP730648**		**OP740189**	**OP761961**
C. siamense	**GUCC 12074**	**Gloeosporioides**	**unidentified host**	**China**	**OP723002**	**OP784094**	**OP730647**		**OP740190**	**OP761960**
C. siamense	**GUCC 12076**	**Gloeosporioides**	**unidentified host**	**China**	**OP722976**	**OP784096**	**OP730649**		**OP740191**	**OP761962**
C. siamense	**GUCC 12078**	**Gloeosporioides**	**unidentified host**	**China**	**OP723104**	**OP784098**	**OP730651**		**OP740193**	**OP761964**
C. siamense	**GUCC 12081**	**Gloeosporioides**	**unidentified host**	**China**	**OP722978**	**OP784101**	**OP730654**			**OP761967**
C. siamense	**GUCC 12082**	**Gloeosporioides**	**unidentified host**	**China**	**OP722959**	**OP784102**	**OP730655**			**OP761968**
C. siamense	**GUCC 12085**	**Gloeosporioides**	**unidentified host**	**China**	**OP722996**	**OP784104**	**OP730657**			**OP761970**

Supplementary Table 1 Continued.

Species	**Culture**	**Group**	**Host**	**Country**	**ITS**	***gapdh***	***chs-1***	***his3***	***act***	***tub2***
C. siamense	**GUCC 12086**	**Gloeosporioides**	***Camellia japonica***	**China**	**OP722997**	**OP784107**	**OP730660**		**OP740198**	**OP761973**
C. siamense	**GUCC 12087**	**Gloeosporioides**	***Camellia japonica***	**China**	**OP722965**	**OP784108**	**OP730661**		**OP740199**	**OP761974**
C. siamense	**GUCC 12095**	**Gloeosporioides**	**unidentified host**	**China**	**OP722979**	**OP784105**	**OP730658**		**OP740197**	**OP761971**
C. siamense	**GUCC 12096**	**Gloeosporioides**	**unidentified host**	**China**	**OP722980**	**OP784106**	**OP730659**			**OP761972**
C. siamense	**GUCC 12101**	**Gloeosporioides**	***Curcuma phaeocaulis***	**China**	**OP723012**	**OP784114**	**OP730666**		**OP740202**	**OP761980**
C. siamense	**GUCC 12104**	**Gloeosporioides**	***Piper sarmentosum***	**China**	**OP723023**	**OP784116**	**OP730668**		**OP740204**	**OP761982**
C. siamense	**GUCC 12174**	**Gloeosporioides**	***Ilex chinensis***	**China**	**OP722967**	**OP784131**	**OP730679**		**OP740217**	**OP761997**
C. siamense	**GUCC 12175**	**Gloeosporioides**	***Ilex chinensis***	**China**	**OP722968**	**OP784132**	**OP730680**		**OP740218**	**OP761998**
C. siamense	**GUCC 12119**	**Gloeosporioides**	**unidentified host**	**China**	**OP722986**	**OP784140**				**OP762005**
C. siamense	**GUCC 12121**	**Gloeosporioides**	***Eriobotrya japonica***	**China**	**OP722987**	**OP784142**				**OP762007**
C. siamense	**GUCC 12122**	**Gloeosporioides**	***Aucuba japonica***	**China**	**OP722983**	**OP784143**				**OP762008**
C. siamense	**GUCC 12123**	**Gloeosporioides**	***Camellia japonica***	**China**	**OP722984**	**OP784146**				**OP762011**
C. siamense	**GUCC 12124**	**Gloeosporioides**	***Chamaedorea elegans***	**China**	**OP722982**	**OP784147**				**OP762012**
C. siamense	**GUCC 12125**	**Gloeosporioides**	***Heteropanax fragrans***	**China**	**OP722981**	**OP784151**				**OP762016**
C. siamense	**GUCC 12126**	**Gloeosporioides**	***Fatsia japonica***	**China**	**OP722985**	**OP784152**				**OP762017**
C. menglaense	CGMCC 3.18958*	*Gloeosporioides*	air	China	MH023505	MH023507	MH023508		MH023506	
C. pandanicola	MFLUCC 17-0571*	Gloeosporioides	*Pandanaceae*	Thailand	MG646967	MG646934	MG646931		MG646938	MG646926
C. pandanicola	ZHKUCC 210080	Gloeosporioides	*Reineckea carnea*	China		OL672738	OL672728		OL672718	OL739542
C. pandanicola	ZHKUCC 210079	Gloeosporioides	*Reineckea carnea*	China		OL672737	OL672727		OL672717	OL739541
C. parvisporum	CGMCC3.16078, YMF 1.06942*	Gloeosporioides	*Ageratina adenophora*	China	OK030876	OK513679	OK513575		OK513613	OK513645

Supplementary Table 1 Continued.

Species	**Culture**	**Group**	**Host**	**Country**	**ITS**	***gapdh***	***chs-1***	***his3***	***act***	***tub2***
C. sidae	CBS 504.97, LARS 76, ATCC 58399, NRRL 8096*	Orbiculare	*Sida spinosa*	USA	KF178472	KF178497	KF178521	KF178545	KF178569	KF178593
C. simmondsii	CBS 122122, BRIP 28519*	Acutatum	*Carica papaya*	Australia	JQ948276	JQ948606	JQ948937	JQ949267	JQ949597	JQ949927
C. simulanticitri	CGMCC3.16082, YMF 1.07302*	Acutatum	*Betula* sp.	China	OK030878	OK513680	OK513577		OK513615	
C. sinuatum	LC13874, NN055266*	Dracaenophilum	*Ophiopogon japonicus*	China	MZ595900	MZ664064	MZ799286	MZ673920	MZ664198	MZ674018
C. sloanei	IMI 364297, CPC 18929*	Acutatum	*Theobroma cacao*	Malaysia	JQ948287	JQ948617	JQ948948	JQ949278	JQ949608	JQ949938
C. sojae	ATCC 62257*	Orchidearum	*Glycine max*	USA	MG600749	MG600810	MG600860	MG600899	MG600954	MG601016
C. somersetense	CBS 131599, JAC 11-11*	Caudatum	*Sorghastrum nutans*	USA	JX076862					
C. sonchicola	MFLUCC 17-1299, IT3115a*	Dematium	*Sonchus* sp.	Italy	KY962757	KY962754	KY962751		KY962748	
C. spaethianum	CBS 167.49*	Spaethianum	*Funkia sieboldiana*	Germany	GU227807	GU228199	GU228297	GU228003	GU227905	GU228101
C. speciosum	CGMCC3.16081, YMF 1.07301*	Acutatum	*Ageratina adenophora*	China	OK030881					
C. spicati	CGMCC3.18942, YMF 1.04942*	Boninense	*Myriophyllum spicatum*	China	OL842171	OL981266	OL981292		OL981240	OL981226
C. spinaciae	CBS 128.57	Dematium	*Spinacia oleracea*	Netherlands	GU227847	GU228239	GU228337	GU228043	GU227945	GU228141
C. spinosum	CBS 515.97, LARS 465, DAR 48942*	Orbiculare	*Xanthium spinosum*	Australia	KF178474	KF178498	KF178523	KF178547	KF178571	KF178595
C. subacidae	LC13857, LH01*	Truncatum	*Tetrastigma obovatum*	China	MZ595846	MZ664068	MZ799307	MZ673866	MZ664144	MZ673967
C. subhenanense	CGMCC3.16073, YMF 1.06865*	Gloeosporioides	*Ageratina adenophora*	China	OK030883	OK513684	OK513581		OK513618	OK513647
C. sublineola	CBS 131301, S3.001*	Graminicola	*Sorghum vulgare*	Togo, Burkina Fasso	JQ005771		JQ005792	JQ005813	JQ005834	JQ005855
C. subsalicis	LC13863, CQ1168*	Acutatum	*Populus alba*	China	MZ852849		MZ799346	MZ673836	MZ664128	MZ673953

Supplementary Table 1 Continued.

Species	Culture	Group	Host	Country	ITS	*gapdh*	*chs-1*	*his3*	*act*	*tub2*
C. subvariabile	LC13876, NN040649*	Gigasporum	Unknown plant	China	MZ595883	MZ664054	MZ799343	MZ673903	MZ664181	MZ674001
C. sydowii	CBS 135819, CPC 20071*	singleton	*Sambucus*	China, Taiwan	KY263783	KY263785	KY263787	KY263789	KY263791	KY263793
C. syngoniicola	LC8894, M745*	Orchidearum	*Syngonium* sp.	China	MZ595863	MZ664117	MZ799296	MZ673883	MZ664161	MZ673982
C. syzygiicola	MFLUCC 10-0624, DNCL021*	Gloeosporioides	*Syzygium samarangense*	Thailand	KF242094	KF242156			KF157801	KF254880
C. tabacum	CBS 161.53	Destructivum	*Nicotiana tabacum*	Zambia	JQ005763	KM105559	JQ005784	JQ005805	JQ005826	JQ005847
C. tabacum	N150, CPC 18945*	Destructivum	*Nicotiana tabacum*	Canada	KM105204	KM105557	KM105274	KM105344	KM105414	KM105484
C. tabacum	CBS 124249, MUCL44942	Destructivum	*Centella asiatica*	Madagascar	KM105206	KM105560	KM105276	KM105346	KM105416	KM105486
C. tabacum	**GUCC 12042**	**Destructivum**	***Piper sarmentosum***	**China**	**OP723072**	**OP784124**		**OP784210**	**OP740212**	**OP761990**
C. tainanense	CBS 143666*	Gloeosporioides	*Capsicum annuum*	China, Taiwan	MH728818	MH728823	MH805845		MH781475	MH846558
C. tamarilloi	CBS 129814, T.A.6*	Acutatum	*Solanum betaceum*	Colombia	JQ948184	JQ948514	JQ948845	JQ949175	JQ949505	JQ949835
C. tanaceti	CBS 132693, BRIP 57314, UM01*	Destructivum	*Tanacetum cinerariifolium*	Australia	JX218228	JX218243			JX218238	JX218233
C. tebeestii	CBS 522.97, LARS 733, 83-43*	Orbiculare	*Malva pusilla*	Canada	KF178473	KF178505	KF178522	KF178546	KF178570	KF178594
C. telosmae	LC13872, NN052858*	singleton	*Telosma cordarum*	China	MZ595888	MZ664058	MZ799303	MZ673908	MZ664186	MZ674006
C. temperatum	CBS 133122, Coll883, BPI 884100*	Gloeosporioides	*Vaccinium macrocarpon*	Bronx	JX145159	MZ664045	MZ799254	MZ673833	MZ664125	JX145211
C. tengchongense	CGMCC3.18950, YMF 1.04950*	Gloeosporioides	*Isoetes sinensis*	China	OL842169	OL981264	OL981290		OL981238	
C. theobromicola	CBS 124945, ICMP 18649*	Gloeosporioides	*Theobroma cacao*	Panama	JX010294	JX010006	JX009869		JX009444	JX010447
C. ti	ICMP 4832*	Gloeosporioides	*Cordyline* sp.	New Zealand	JX010269	JX009952	JX009898		JX009520	JX010442
C. tibetense	LC7364*	Graminicola	*Poaceae*	China	MZ595840	MZ772866	MZ799339	MZ673860	MZ664138	MZ673961

Supplementary Table 1 Continued.

Species	Culture	Group	Host	Country	ITS	*gapdh*	*chs-1*	*his3*	*act*	*tub2*
C. tofieldiae	CBS 495.85*	Spaethianum	*Tofieldia calyculata*	Switzerland	GU227801	GU228193	GU228291	GU227997	GU227899	GU228095
C. tofieldiae	CBS 168.49	Spaethianum	*Lupinus polyphyllus*	Germany	GU227802	GU228194	GU228292	GU227998	GU227900	GU228096
C. tongrenense	GZU_TRJ1-37, GMBC 0209*	Dracaenophilum	*Nothapodytes pittosporoides*	China	MH482933	MH705332			MH717074	MH729805
C. torulosum	CBS 128544, ICMP 18586*	Boninense	*Solanum melongena*	New Zealand	JQ005164	JQ005251	JQ005338	JQ005425	JQ005512	JQ005598
C. trichellum	CBS 217.64*	singleton	*Hedera helix*	Germany	GU227812	GU228204	GU228302	GU228008	GU227910	GU228106
C. trifolii	CBS 158.83, BBA 70709*	Orbiculare	*Trifolium*	USA	KF178478	KF178502	KF178527	KF178551	KF178575	KF178599
C. tropicale	CBS 124949, ICMP 18653, MTCC 11371*	Gloeosporioides	*Theobroma cacao*	Panama	JX010264	JX010007	JX009870	MZ673832	JX009489	JX010407
C. tropicicola	BCC 38877, LC0598*	Dracaenophilum	*Citrus maxima*	Thailand	JN050240	JN050229	MZ799279	MZ673840	JN050218	JN050246
C. tropicicola	CBS 127555	Dracaenophilum	*Citrus* sp.	Mexico	MG600715	MG600778	MG600838	MG600884	MG600922	MG600982
C. truncatum	CBS 151.35*	Truncatum	*Phaseolus lunatus*	USA	GU227862	GU228254	GU228352	GU228058	GU227960	GU228156
C. truncatum	CBS 120709	Truncatum	*Capsicum frutescens*	India	GU227877	GU228269	GU228367	GU228073	GU227975	GU228171
C. truncatum	**GUCC 12158**	**Truncatum**	***Hymenocallis littoralis***	**China**	**OP723078**	**OP784084**	**OP730637**	**OP784200**	**OP740179**	**OP761950**
C. truncatum	**GUCC 12159**	**Truncatum**	***Hymenocallis littoralis***	**China**	**OP723079**	**OP784085**	**OP730638**	**OP784201**	**OP740180**	**OP761951**
C. truncatum	**GUCC 12160**	**Truncatum**	***Houttuynia cordata***	**China**	**OP723076**	**OP784091**	**OP730644**	**OP784202**	**OP740186**	**OP761957**
C. truncatum	**GUCC 12161**	**Truncatum**	***Houttuynia cordata***	**China**	**OP723077**	**OP784093**	**OP730646**	**OP784203**	**OP740188**	**OP761959**
C. truncatum	**GUCC 12162**	**Truncatum**	***Piper sarmentosum***	**China**	**OP723082**	**OP784122**	**OP730674**		**OP740210**	**OP761988**
C. truncatum	**GUCC 12163**	**Truncatum**	***Piper sarmentosum***	**China**	**OP723083**	**OP784123**	**OP730675**	**OP784209**	**OP740211**	**OP761989**
C. truncatum	**GUCC 12167**	**Truncatum**	***Cissus hexangularis***	**China**	**OP723080**	**OP784128**	**OP730677**	**OP784211**	**OP740214**	**OP761995**
C. truncatum	**GUCC 12168**	**Truncatum**	***Cissus hexangularis***	**China**	**OP723081**	**OP784129**	**OP730678**		**OP740215**	

Supplementary Table 1 Continued.

Species	Culture	Group	Host	Country	ITS	*gapdh*	*chs-1*	*his3*	*act*	*tub2*
C. utrechtense	CBS 130243*	Destructivum	*Trifolium pratense*	Netherlands	KM105201	KM105554	KM105271	KM105341	KM105411	KM105481
C. variabile	LC13875, NN040656*	Gigasporum	Unknown plant	China	MZ595884	MZ664055	MZ799344	MZ673904	MZ664182	MZ674002
C. verruculosum	IMI 45525*	Spaethianum	*Crotalaria juncea*	Zimbabwe	GU227806	GU228198	GU228296	GU228002	GU227904	GU228100
C. vietnamense	CBS 125478, LD16(L2)*	Gigasporum	*Coffea* sp.	Vietnam	KF687721	KF687832	KF687769	KF687855	KF687792	KF687877
C. vignae	CBS 501.97, LARS 56*	Destructivum	*Vigna unguiculata*	Nigeria	KM105183	KM105534	KM105253	KM105323	KM105393	KM105463
C. viniferum	GZAAS 5.08601, yg1*	Gloeosporioides	*Vitis vinifera* cv. Shuijing	China	JN412804	JN412798			JN412795	
C. vittalense	CBS 181.82*	Orchidearum	*Theobroma cacao*	India	MG600734	MG600796	MG600851	MG600893	MG600940	MG601001
C. vittalense	CBS 126.25	Orchidearum	*Orchid*	unknown	MG600735	MG600797	MG600852	MG600894	MG600941	MG601002
C. vittalense	**GUCC 12144**	**Orchidearum**	***Piper sarmentosum***	**China**	**OP723092**	**OP784120**	**OP730672**	**OP784207**	**OP740208**	**OP761986**
C. vittalense	**GUCC 12145**	**Orchidearum**	***Piper sarmentosum***	**China**	**OP723091**	**OP784121**	**OP730673**	**OP784208**	**OP740209**	**OP761987**
C. vulgaris	CGMCC3.18940, YMF 1.04940*	Gloeosporioides	*Hippuris vulgaris*	China	OL842170	OL981265	OL981291		OL981239	
C. walleri	CBS 125472, BMT(HL)19*	Acutatum	*Coffea* sp.	Vietnam	JQ948275	JQ948605	JQ948936	JQ949266	JQ949596	JQ949926
C. wanningense	CGMCC 3.18936*	Acutatum	*Hevea brasiliensis*	China	MG830462	MG830318	MG830302		MG830270	MG830286
C. watphraense	MFLUCC 14-0123*	Boninense	*Dendrobium* sp.	Thailand	MF448523	MH049479			MH376384	MH351276
C. wuxiense	CGMCC 3.17894*	Gloeosporioides	*Camellia sinensis*	China	KU251591	KU252045	KU251939		KU251672	KU252200
C. xanthorrhoeae	ICMP 17820	Gloeosporioides	*Xanthorrhoea* sp.	Australia	JX010260	JX010008	JX009814		JX009479	
C. xanthorrhoeae	BRIP 45094, ICMP 17903, CBS 127831*	Gloeosporioides	*Xanthorrhoea preissii*	Australia	JX010261	JX009927	JX009823		JX009478	JX010448
C. xishuangbannaense	MFLUCC 19-0107*	Gloeosporioides	*Magnolia liliifera*	China	MW346469	MW537586	MW660832		MW652294	
C. yuanjiangense	CGMCC3.18964, YMF 1.04996*	Gloeosporioides	*Ageratina adenophora*	China	OK030885	OK513686	OK513583		OK513620	OK513649

Supplementary Table 1 Continued.

Species	Culture	Group	Host	Country	ITS	*gapdh*	*chs-1*	*his3*	*act*	*tub2*
C. yuanjiangense	YMF1.04997	Gloeosporioides	*Ageratina adenophora*	*China*	OK030886	OK513687	OK513584		OK513621	OK513650
C. yulongense	CFCC 50818*	Gloeosporioides	*Vaccinium dunalianum* var. *urophyllum*	China	MH751507	MK108986	MH793605		MH777394	MK108987
C. yunnanense	CBS 132135, LC1526, AS 3.9167*	Dracaenophilum	*Buxus* sp.	China	JX546804	JX546706	JX519231	JX546755	JX519239	JX519248
C. zhaoqingense	LC13877, NN058985*	Gigasporum	*Palm*	China	MZ595905	MZ664065	MZ799304	MZ673925	MZ664203	MZ674023
C. zhejiangense	LC13887, NN076215*	Dematium	Unidentified tree	China	MZ595912	MZ664124	MZ799342	MZ673932	MZ664210	MZ674030
C. zoysiae	MAFF 238573*	Caudatum	*Zoysia tenuifolia*	Japan	JX076871					
Verticillium dahliae	CBS 130341*, NRRL 54785, PD322	Outgroup	*Lactuca sativa*	USA	LR026889	HQ414719			HQ206921	

a A sterisk (*) refers to ex-type strains;

b Bold indicated the sequences generated in this study.

Supplementary Table 2 The Published whole-genome sequences of *Colletotrichum* species, retrieved from NCBI, JGI and EnsemblFungi.

Species	Strain number	Species complex	Used in phylogenomic analysis	Accessable in NCBI	Accessable in JGI	Accessable in Ensembl Fungi	Assembly accession	BioSample	BioProject	Date	Assembly level	Total sequence length (bp)
C. abscissum	Ca142	Acutatum	Yes	Yes			GCA_023376855.1	SAMN10780915	PRJNA516018	2022/5/16	Scaffold	54,001,896
C. acutatum	1	Acutatum		Yes			GCA_001593745.1	SAMN04530072	PRJNA314171	2016/3/18	Contig	52,129,059
C. acutatum	83	Acutatum		Yes			GCA_021124905.1	SAMN23012514	PRJNA779114	2021/12/8	Contig	49,749,514
C. acutatum	42866	Acutatum		Yes			GCA_020458395.1	SAMN15854395	PRJNA657976	2021/10/13	Contig	48,391,918
C. acutatum	42867	Acutatum		Yes			GCA_020465915.1	SAMN16327813	PRJNA657976	2021/10/13	Contig	49,045,639
C. acutatum	42868	Acutatum		Yes			GCA_020465715.1	SAMN16093709	PRJNA657976	2021/10/13	Contig	49,422,277

Supplementary Table 2 Continued.

Species	Strain number	Species complex	Used in phylogenomic analysis	Accessable in NCBI	Accessable in JGI	Accessable in Ensembl Fungi	Assembly accession	BioSample	BioProject	Date	Assembly level	Total sequence length (bp)
C. acutatum	42869	Acutatum		Yes			GCA_020464295.1	SAMN16093710	PRJNA657976	2021/10/13	Contig	48,502,718
C. acutatum	42870	Acutatum		Yes			GCA_020464275.1	SAMN16093711	PRJNA657976	2021/10/13	Contig	48,361,109
C. acutatum	42871	Acutatum		Yes			GCA_020464265.1	SAMN16093712	PRJNA657976	2021/10/13	Contig	49,331,692
C. acutatum	42875	Acutatum		Yes			GCA_020465945.1	SAMN16327575	PRJNA657976	2021/10/13	Contig	49,335,525
C. acutatum	42876	Acutatum		Yes			GCA_020458295.1	SAMN16327576	PRJNA657976	2021/10/13	Contig	49,423,995
C. acutatum	42877	Acutatum		Yes			GCA_020458275.1	SAMN16327577	PRJNA657976	2021/10/13	Contig	48,338,876
C. acutatum	42878	Acutatum		Yes			GCA_020457915.1	SAMN16327578	PRJNA657976	2021/10/13	Contig	49,531,067
C. acutatum	42879	Acutatum		Yes			GCA_020457925.1	SAMN16327579	PRJNA657976	2021/10/13	Contig	49,885,583
C. acutatum	42883	Acutatum		Yes			GCA_020457905.1	SAMN16327580	PRJNA657976	2021/10/13	Contig	49,697,799
C. acutatum	43165	Acutatum		Yes			GCA_020465735.1	SAMN16178579	PRJNA657976	2021/10/13	Contig	51,203,636
C. acutatum	43166	Acutatum		Yes			GCA_020465745.1	SAMN16178580	PRJNA657976	2021/10/13	Contig	50,225,064
C. acutatum	43374	Acutatum		Yes			GCA_020465895.1	SAMN16288388	PRJNA657976	2021/10/13	Contig	50,870,935
C. acutatum	43375	Acutatum		Yes			GCA_020465855.1	SAMN16288389	PRJNA657976	2021/10/13	Contig	51,057,129
C. acutatum	43376	Acutatum		Yes			GCA_020465875.1	SAMN16288390	PRJNA657976	2021/10/13	Contig	51,025,733
C. acutatum	43377	Acutatum		Yes			GCA_020465835.1	SAMN16288391	PRJNA657976	2021/10/13	Contig	50,496,057
C. acutatum	43378	Acutatum		Yes			GCA_020465815.1	SAMN16178576	PRJNA657976	2021/10/13	Contig	51,018,208
C. acutatum	43379	Acutatum		Yes			GCA_020465795.1	SAMN16178577	PRJNA657976	2021/10/13	Contig	50,469,302
C. acutatum	43380	Acutatum	Yes	Yes			GCA_020465775.1	SAMN16178578	PRJNA657976	2021/10/13	Contig	50,496,501
C. acutatum	C71	Acutatum		Yes			GCA_001662755.1	SAMN04530278	PRJNA314187	2016/6/14	Scaffold	44,919,977

Supplementary Table 2 Continued.

Species	Strain number	Species complex	Used in phylogenomic analysis	Accessable in NCBI	Accessable in JGI	Accessable in Ensembl Fungi	Assembly accession	BioSample	BioProject	Date	Assembly level	Total sequence length (bp)
C. acutatum	hn1205-2	Acutatum		Yes			GCA_019022555.1	SAMN17266944	PRJNA690880	2021/6/24	Scaffold	51,608,713
C. aenigma	Cg56	Gloeosporioides	Yes	Yes			GCF_013390185.1	SAMN09531619	PRJNA670752	2020/7/6	Contig	59,189,926
C. aenigma	JS-0419	Gloeosporioides		Yes			GCA_022496045.1	SAMN23524325	PRJNA785002	2022/3/7	Contig	65,222,000
C. asianum	ICMP 18580*	Gloeosporioides	Yes	Yes		Yes	GCA_009806415.1	SAMN13475008	PRJNA504379	2019/12/27	Scaffold	64,731,264
C. asianum	FJ11	Gloeosporioides		Yes			GCA_027406305.1	SAMN30451175	PRJNA872318	2022/12/27	Contig	66,118,652
C. asianum	YN55	Gloeosporioides		Yes			GCA_027406345.1	SAMN30451174	PRJNA872318	2022/12/27	Contig	62,693,972
C. australisinense (nom. inval.)	GX1655	Acutatum		Yes			GCA_014706365.1	SAMN13693772	PRJNA597926	2020/9/23	Contig	55,304,262
C. camelliae	CcLH18	Gloeosporioides	Yes	Yes			GCA_011947485.2	SAMN14421087	PRJNA691333	2021/9/10	Scaffold	57,836,951
C. camelliae	LS-19	Gloeosporioides		Yes			GCA_018853505.1	SAMN17126018	PRJNA686827	2021/6/11	Contig	67,471,331
C. camelliae	LT-3-1	Gloeosporioides		Yes			GCA_026740055.1	SAMN31952954	PRJNA907149	2022/12/8	Contig	67,743,009
C. chlorophyti	NTL11	singleton	Yes	Yes	Yes	Yes	GCA_001937105.1	SAMN05945917	PRJNA350752	2017/1/5	Scaffold	52,387,045
C. chrysophilum	AFK154	Gloeosporioides		Yes			GCA_026319245.1	SAMN29758415	PRJNA858866	2022/11/23	Scaffold	57,854,444
C. chrysophilum	PMKnsl-1	Gloeosporioides		Yes			GCA_026319215.1	SAMN29758416	PRJNA858866	2022/11/23	Contig	56,056,391
C. cliviicola	YN31	Orchidearum		Yes			GCA_026119605.1	SAMN30451184	PRJNA872318	2022/11/10	Contig	52,051,982
C. coccodes	CcND04	singleton		Yes			GCA_020466075.1	SAMN20811665	PRJNA755315	2021/10/13	Contig	50,243,842
C. coccodes	NJ-RT1	singleton	Yes	Yes			GCA_002249775.1	SAMN03761679	PRJNA285890	2017/8/11	Scaffold	50,121,991
C. coccodes	RP180a	singleton		Yes			GCA_002249805.1	SAMN03761686	PRJNA285895	2017/8/11	Scaffold	51,499,764
C. cordylinicola	HN23	Gloeosporioides		Yes			GCA_027406065.1	SAMN30451188	PRJNA872318	2022/12/27	Contig	61,624,325

Supplementary Table 2 Continued.

Species	**Strain number**	**Species complex**	**Used in phylogenomic analysis**	**Accessable in NCBI**	**Accessable in JGI**	**Accessable in Ensembl Fungi**	**Assembly accession**	**BioSample**	**BioProject**	**Date**	**Assembly level**	**Total sequence length(bp)**
C. destructivum	YC1	Destructivum	Yes	Yes			GCA_009900065.1	SAMN13703342	PRJNA598348	2020/1/17	Contig	52,145,981
C. echinochloae	B-48	Graminicola	Yes	Yes			GCA_016618095.1	SAMN16551125	PRJNA672254	2021/1/12	Contig	62,246,358
C. eleusines	NJC-16	Graminicola	Yes	Yes			GCA_016807845.1	SAMN16552423	PRJNA671855	2021/2/4	Contig	53,507,824
C. endophytica	**GUCC 12108**	**Gloeosporioides**	**Yes**	**Yes**			**JAPHMV000000000**	**SAMN31620405**	**PRJNA898668**		**Scaffold**	**57,430,559**
C. endophytica	YN32	Gloeosporioides		Yes			GCA_027406105.1	SAMN30451185	PRJNA872318	2022/12/27	Contig	61,437,041
C. falcatum	CF08	Graminicola	Yes	Yes			GCA_019425465.1	SAMN10584380	PRJNA509540	2021/7/30	Contig	56,082,967
C. falcatum	Cf671	Graminicola		Yes			GCA_001484525.1	SAMN03287978	PRJNA272959	2016/1/4	Scaffold	48,186,431
C. filicis	CBS 101611*	Acutatum	Yes	Yes			GCA_023376865.1	SAMN05938703	PRJNA350378	2022/5/16	Scaffold	62,965,231
C. fioriniae	42949	Acutatum		Yes			GCA_020466255.1	SAMN16059226	PRJNA657976	2021/10/13	Contig	51,195,654
C. fioriniae	42872 A	Acutatum		Yes			GCA_020464245.1	SAMN15904855	PRJNA657976	2021/10/13	Contig	49,290,758
C. fioriniae	HC296	Acutatum		Yes			GCA_014705545.1	SAMN14604510	PRJNA625663	2020/9/22	Scaffold	49,753,773
C. fioriniae	HC89	Acutatum		Yes			GCA_002930455.1	SAMN08289069	PRJNA270309	2018/2/16	Scaffold	50,150,864
C. fioriniae	HC91	Acutatum		Yes			GCA_002930425.1	SAMN08289092	PRJNA270309	2018/2/16	Scaffold	49,792,461
C. fioriniae	KY116	Acutatum		Yes			GCA_014705285.1	SAMN14604520	PRJNA625663	2020/9/22	Scaffold	50,237,383
C. fioriniae	KY119	Acutatum		Yes			GCA_014705275.1	SAMN14604521	PRJNA625663	2020/9/22	Scaffold	49,840,158
C. fioriniae	KY323	Acutatum		Yes			GCA_014705335.1	SAMN14604519	PRJNA625663	2020/9/22	Scaffold	49,661,969
C. fioriniae	KY6	Acutatum		Yes			GCA_014705365.1	SAMN14604517	PRJNA625663	2020/9/22	Scaffold	49,740,091
C. fioriniae	KY615	Acutatum		Yes			GCA_014705115.1	SAMN14604530	PRJNA625663	2020/9/22	Scaffold	49,988,189
C. fioriniae	KY640	Acutatum		Yes			GCA_014705265.1	SAMN14604522	PRJNA625663	2020/9/22	Scaffold	49,691,380

Supplementary Table 2 Continued.

Species	**Strain number**	**Species complex**	**Used in phylogenomic analysis**	**Accessable in NCBI**	**Accessable in JGI**	**Accessable in Ensembl Fungi**	**Assembly accession**	**BioSample**	**BioProject**	**Date**	**Assembly level**	**Total sequence length (bp)**
C. fioriniae	KY646	Acutatum		Yes			GCA_014705245.1	SAMN14604523	PRJNA625663	2020/9/22	Scaffold	50,064,071
C. fioriniae	KY648	Acutatum		Yes			GCA_014705205.1	SAMN14604524	PRJNA625663	2020/9/22	Scaffold	50,396,376
C. fioriniae	PJ7	Acutatum	Yes	Yes	Yes	Yes	GCA_000582985.1	SAMN02580179	PRJNA244481	2014/2/27	Scaffold	49,002,765
C. fioriniae	ACFK16	Acutatum		Yes			GCA_026319165.1	SAMN29758418	PRJNA858866	2022/11/23	Contig	49,331,805
C. fioriniae	ACFK5	Acutatum		Yes			GCA_026319145.1	SAMN29758417	PRJNA858866	2022/11/23	Contig	49,445,863
C. fioriniae	IMI 355084	Acutatum		Yes			GCA_027942845.1	SAMN30184415	PRJNA786750	2023/1/23	Scaffold	49,445,812
C. fructicola	15060	Gloeosporioides		Yes			GCA_002887685.1	SAMN08031206	PRJNA418608	2018/1/17	Contig	55,915,688
C. fructicola	1104-6	Gloeosporioides		Yes			GCA_017589655.1	SAMN18080036	PRJNA705288	2021/3/26	Scaffold	56,580,086
C. fructicola	Cf245	Gloeosporioides		Yes			GCA_013201925.1	SAMN09531623	PRJNA670752	2020/6/1	Scaffold	56,060,367
C. fructicola	Cf413	Gloeosporioides		Yes			GCA_013390205.1	SAMN09531621	PRJNA670752	2020/7/6	Contig	56,528,462
C. fructicola	Cf415	Gloeosporioides		Yes			GCA_013201905.1	SAMN09531622	PRJNA670752	2020/6/1	Scaffold	56,012,246
C. fructicola	CfS4	Gloeosporioides		Yes			GCA_013201875.1	SAMN09531624	PRJNA670752	2020/6/1	Scaffold	57,426,314
C. fructicola	Cg38 S1	Gloeosporioides		Yes			GCA_012932255.1	SAMN09448926	PRJNA670752	2020/4/29	Scaffold	58,952,871
C. fructicola	CGMCC 3.17371	Gloeosporioides	Yes	Yes		Yes	GCF_009771025.1	SAMN11398962	PRJNA602459	2019/12/18	Contig	58,056,435
C. fructicola	HC540	Gloeosporioides		Yes			GCA_014705485.1	SAMN14604511	PRJNA625663	2020/9/22	Scaffold	57,126,425
C. fructicola	N425	Gloeosporioides		Yes			GCA_024000835.1	SAMN21544801	PRJNA765139	2022/6/28	Contig	56,288,449
C. fructicola	Nara gc5	Gloeosporioides	Yes	Yes		Yes	GCA_000319635.2	SAMN02981487	PRJNA225509	2020/5/12	Contig	59,598,044
C. fructicola	GZ14	Gloeosporioides		Yes			GCA_027406145.1	SAMN30451181	PRJNA872318	2022/12/27	Contig	57,249,276
C. fructicola	HN47	Gloeosporioides		Yes			GCA_027406285.1	SAMN30451176	PRJNA872318	2022/12/27	Contig	57,535,124

Supplementary Table 2 Continued.

Species	**Strain number**	**Species complex**	**Used in phylogenomic analysis**	**Accessable in NCBI**	**Accessable in JGI**	**Accessable in Ensembl Fungi**	**Assembly accession**	**BioSample**	**BioProject**	**Date**	**Assembly level**	**Total sequence length (bp)**
C. fructicola	QZ-3	Gloeosporioides		Yes			GCA_027406265.1	SAMN30451177	PRJNA872318	2022/12/27	Contig	57,493,921
C. fructicola	SX-6	Gloeosporioides		Yes			GCA_025558505.1	SAMN29020604	PRJNA848944	2022/9/27	Scaffold	56,807,082
C. gardeniae	**GUCC 12049***	**Gloeosporioides**	**Yes**	**Yes**			**JAPHMU000000000**	**SAMN31620404**	**PRJNA898668**		**Scaffold**	**63,335,798**
C. gigasporum	JS-0367	Gigasporum		Yes			GCA_024584535.1	SAMN19929846	PRJNA742180	2022/8/8	Complete Genome	87,056,302
C. gigasporum	HN42	Gigasporum		Yes			GCA_027406085.1	SAMN30451183	PRJNA872318	2022/12/27	Contig	57,891,463
C. gloeosporioides	23	Gloeosporioides		Yes			GCA_021432615.1	SAMN02673273	PRJNA196038	2021/12/27	Scaffold	58,838,139
C. gloeosporioides (New identification *C. jiangxiense*)	Cg01	Gloeosporioides	Yes	Yes			GCA_003666125.1	SAMN09759449	PRJNA484086	2018/10/17	Scaffold	55,772,594
C. gloeosporioides	Cg-14	Gloeosporioides		Yes	Yes	Yes	GCA_000446055.1	SAMN02981466	PRJNA176412	2013/8/13	Contig	53,209,944
C. gloeosporioides	CgDa01	Gloeosporioides		Yes			GCA_021650765.1	SAMN24460951	PRJNA792738	2022/1/27	Contig	62,777,491
C. gloeosporioides	CgLH19	Gloeosporioides		Yes			GCA_011947415.1	SAMN14421088	PRJNA691333	2020/4/3	2020/4/3	55,563,689
C. gloeosporioides	COLG-95	Gloeosporioides		Yes			GCA_011428055.1	SAMN12924925	PRJNA554995	2020/3/18	Scaffold	53,724,932
C. gloeosporioides	ES026	Gloeosporioides		Yes			GCA_003568745.1	SAMN09946147	PRJNA488958	2018/9/13	Scaffold	58,519,738
C. gloeosporioides	hn1205-1	Gloeosporioides		Yes			GCA_019022565.1	SAMN17266943	PRJNA690880	2021/6/24	Scaffold	57,146,622
C. gloeosporioides	KY332	Gloeosporioides		Yes			GCA_014705165.1	SAMN14604526	PRJNA625663	2020/9/22	Scaffold	58,002,434
C. gloeosporioides	Lc1	Gloeosporioides	Yes	Yes			GCF_011800055.1	SAMN13038012	PRJNA786947	2020/3/31	Scaffold	61,904,035
C. gloeosporioides	SMCG1#C	Gloeosporioides		Yes			GCA_003243855.1	SAMN09205517	PRJNA471237	2018/6/18	Scaffold	61,916,549
C. gloeosporioides	TYU	Gloeosporioides		Yes			GCA_002901105.1	SAMN07411592	PRJNA395616	2018/1/26	Contig	53,008,665
C. godetiae	C184	Acutatum	NO, receive none result in gene prediction	Yes			GCA_001663355.1	SAMN04566614	PRJNA315612	2016/6/15	Scaffold	35,034,269

Supplementary Table 2 Continued.

Species	Strain number	Species complex	Used in phylogenomic analysis	Accessable in NCBI	Accessable in JGI	Accessable in Ensembl Fungi	Assembly accession	BioSample	BioProject	Date	Assembly level	Total sequence length (bp)
C. graminicola	M1.001	Graminicola	Yes	Yes	Yes	Yes	GCF_000149035.1	SAMN02953757	PRJNA37879	2010/10/12	Scaffold	51,644,307
C. graminicola	M5.001	Graminicola		Yes			GCA_001951205.1	SAMN06043298	PRJNA354205	2017/1/13	Contig	59,914,086
C. graminicola	ARG2700-2	Graminicola		Yes			GCA_026652225.1	SAMN26589426	PRJNA815473	2022/12/5	Scaffold	53,778,362
C. graminicola	CA-CHAT-1	Graminicola		Yes			GCA_026652275.1	SAMN26631096	PRJNA815632	2022/12/5	Scaffold	59,226,624
C. graminicola	CA-N8H	Graminicola		Yes			GCA_026652265.1	SAMN26631098	PRJNA815636	2022/12/5	Scaffold	57,829,245
C. graminicola	CBS 113173	Graminicola		Yes			GCA_026652305.1	SAMN26631143	PRJNA815639	2022/12/5	Scaffold	51,539,737
C. graminicola	CBS 252.59	Graminicola		Yes			GCA_026652245.1	SAMN26631109	PRJNA815638	2022/12/5	Scaffold	44,929,710
C. graminicola	CR10370-50	Graminicola		Yes			GCA_026652285.1	SAMN26631158	PRJNA815644	2022/12/5	Scaffold	58,978,423
C. graminicola	CRO-I-35	Graminicola		Yes			GCA_026653275.1	SAMN26643332	PRJNA815829	2022/12/5	Scaffold	51,324,951
C. graminicola	CRO-I-41	Graminicola		Yes			GCA_026652315.1	SAMN26644950	PRJNA815831	2022/12/5	Scaffold	59,309,189
C. graminicola	DMSZ63127	Graminicola		Yes			GCA_026652355.1	SAMN26645038	PRJNA815832	2022/12/5	Scaffold	43,145,614
C. graminicola	F40300-1	Graminicola		Yes			GCA_026653375.1	SAMN26645044	PRJNA815838	2022/12/5	Scaffold	49,480,776
C. graminicola	F64330-2	Graminicola		Yes			GCA_026653475.1	SAMN26645053	PRJNA815839	2022/12/5	Scaffold	52,363,910
C. graminicola	F64330-7	Graminicola		Yes			GCA_026653595.1	SAMN26645112	PRJNA815847	2022/12/5	Scaffold	43,764,066
C. graminicola	NRRL13649	Graminicola		Yes			GCA_026654635.1	SAMN26646114	PRJNA815856	2022/12/5	Scaffold	49,923,410
C. graminicola	NRRL47511	Graminicola		Yes			GCA_026652695.1	SAMN26646115	PRJNA815857	2022/12/5	Scaffold	50,305,269
C. graminicola	P7565-072-1	Graminicola		Yes			GCA_026652705.1	SAMN26646122	PRJNA815858	2022/12/5	Scaffold	60,257,832
C. graminicola	SW8046-1	Graminicola		Yes			GCA_026652995.1	SAMN26646203	PRJNA815862	2022/12/5	Scaffold	60,620,047
C. graminicola	SW8046-2	Graminicola		Yes			GCA_026656465.1	SAMN26646204	PRJNA815863	2022/12/5	Scaffold	48,885,120

Supplementary Table 2 Continued.

Species	Strain number	Species complex	Used in phylogenomic analysis	Accessable in NCBI	Accessable in JGI	Accessable in Ensembl Fungi	Assembly accession	BioSample	BioProject	Date	Assembly level	Total sequence length (bp)
C. higginsianum	IMI 349063	Destructivum		Yes		Yes	GCA_000313795.2	SAMEA3138427	PRJNA47061	2012/3/15	Scaffold	49,084,868
C. higginsianum	IMI 349063	Destructivum	Yes	Yes	Yes	Yes	GCF_001672515.1	SAMN04420120	PRJNA47061	2016/6/21	Chromosome	50,716,103
C. higginsianum	MAFF 245053	Destructivum	Yes	Yes			GCA_023705605.1	SAMD00334622	PRJDB11870	2022/5/23	Contig	49,069,799
C. higginsianum	MAFF305635-RFP	Destructivum		Yes		Yes	GCA_004920355.1	SAMN06008763	PRJNA352900	2019/4/29	Contig	49,786,461
C. horii	FJ-1	Gloeosporioides	Yes	Yes			GCA_019693695.1	SAMN20339690	PRJNA748574	2021/8/13	Contig	74,324,508
C. horii	PLG3	Gloeosporioides		Yes			GCA_027406005.1	SAMN30451190	PRJNA872318	2022/12/27	Contig	68,458,539
C. incanum	MAFF 238704	Spaethianum		Yes		Yes	GCA_001625285.1	SAMN03769590	PRJNA286717	2016/4/19	Scaffold	53,597,417
C. incanum	MAFF 238712	Spaethianum	Yes	Yes	Yes	Yes	GCA_001855235.1	SAMN03199084	PRJNA267650	2016/10/27	Scaffold	53,254,579
C. jiangxiense	**GUCC 12055**	**Gloeosporioides**	**Yes**	**Yes**			**JAPHMS000000000**	**SAMN31620402**	**PRJNA898668**		**Scaffold**	**57,568,999**
C. karstii	CkLH20	Boninense	Yes	Yes			GCF_011947395.1	SAMN14421089	PRJNA613862	2020/12/8	Scaffold	51,850,041
C. liaoningense	YN33	Magnum		Yes			GCA_027406045.1	SAMN30451186	PRJNA872318	2022/12/27	Contig	51,853,301
C. lindemuthianum	83.501	Orbiculare		Yes			GCA_001693015.2	SAMN05235603	PRJNA325493	2017/2/4	Scaffold	97,411,422
C. lindemuthianum	89 A2 2-3	Orbiculare	Yes	Yes			GCA_001693025.2	SAMN05235602	PRJNA325493	2017/2/4	Scaffold	99,166,722
C. liriopes	A2	Spaethianum		Yes			GCA_015832465.1	SAMN16434550	PRJNA669110	2020/12/8	Contig	53,087,791
C. liriopes	MAFF 242679	Spaethianum	Yes	Yes			GCA_022179045.1	SAMD00334500	PRJDB11870	2022/1/6	Contig	52,972,150
C. lupini	IMI 504893	Acutatum	Yes	Yes			GCA_023278565.1	SAMN06211573	PRJNA360503	2022/5/9	Complete Genome	63,443,975
C. magnum	WT	Magnum	Yes	Yes			GCA_022457145.1	SAMN22864663	PRJNA777582	2022/3/3	Scaffold	57,112,935
C. musae	GM20	Gloeosporioides	NO, receive none result in gene prediction	Yes			GCA_002814275.1	SAMN07638925	PRJNA407219	2017/12/8	Contig	49,118,800

Supplementary Table 2 Continued.

Species	**Strain number**	**Species complex**	**Used in phylogenomic analysis**	**Accessable in NCBI**	**Accessable in JGI**	**Accessable in Ensembl Fungi**	**Assembly accession**	**BioSample**	**BioProject**	**Date**	**Assembly level**	**Total sequence length (bp)**
C. musae	GZ23	Gloeosporioides		Yes			GCA_027406025.1	SAMN30451189	PRJNA872318	2022/12/27	Contig	60,479,243
C. musicola	LFN0074	Orchidearum	Yes	Yes			GCA_014235935.1	SAMN13025166	PRJNA577394	2020/8/18	Scaffold	52,725,698
C. noveboracense	PMBrms-1	Gloeosporioides		Yes			GCA_026319125.1	SAMN29758419	PRJNA858866	2022/11/23	Contig	59,086,795
C. noveboracense	Coll940	Gloeosporioides		Yes			GCA_026319155.1	SAMN29758420	PRJNA858866	2022/11/23	Scaffold	58,178,553
C. nupharicola	CBS470	Gloeosporioides		Yes			GCA_026319135.1	SAMN29758421	PRJNA858866	2022/11/23	Contig	58,756,863
C. nupharicola	Coll922	Gloeosporioides		Yes			GCA_026319225.1	SAMN29758422	PRJNA858866	2022/11/23	Contig	72,741,875
C. nymphaeae	HC646	Acutatum		Yes			GCA_014705455.1	SAMN14604512	PRJNA625663	2020/9/22	Scaffold	51,255,053
C. nymphaeae	KY563	Acutatum		Yes			GCA_014705155.1	SAMN14604527	PRJNA625663	2020/9/22	Scaffold	50,391,861
C. nymphaeae	KY567	Acutatum		Yes			GCA_014705095.1	SAMN14604528	PRJNA625663	2020/9/22	Scaffold	51,509,711
C. nymphaeae	KY613	Acutatum		Yes			GCA_014705085.1	SAMN14604529	PRJNA625663	2020/9/22	Scaffold	50,577,973
C. nymphaeae	KY745	Acutatum		Yes			GCA_014705125.1	SAMN14604532	PRJNA625663	2020/9/22	Scaffold	50,509,097
C. nymphaeae	SA-01	Acutatum	Yes	Yes	Yes	Yes	GCA_001563115.1	SAMN02639527	PRJNA237763	2016/2/17	Scaffold	49,956,273
C. orbiculare	104-T	Orbiculare	Yes	Yes	Yes	Yes	GCA_000350065.2	SAMN02981452	PRJNA171217	2019/3/22	Scaffold	89,748,316
C. orchidophilum	IMI 309357	singleton	Yes	Yes	Yes	Yes	GCF_001831195.1	SAMN05771038	PRJNA342923	2016/10/21	Scaffold	48,556,462
C. plurivorum	LFN00145	Orchidearum	Yes	Yes			GCA_014235945.1	SAMN13025176	PRJNA577396	2020/8/18	Scaffold	49,703,650
C. salicis	CBS 607.94*	Acutatum	Yes	Yes	Yes	Yes	GCA_001563125.1	SAMN02644731	PRJNA238477	2016/2/17	Scaffold	48,373,413
C. sansevieriae	Sa-1-2	Agaves	Yes	Yes			GCA_002749775.1	SAMN07267235	PRJNA391063	2017/11/3	Contig	51,201,343
C. sansevieriae	FPH2021-6	Agaves		Yes			GCA_026260285.1	SAMN30712214	PRJNA877595	2022/11/21	Scaffold	98,568,926
C. scovillei	TJNH1	Acutatum	Yes	Yes			GCF_011075155.1	SAMN14073982	PRJNA645151	2020/3/9	Contig	52,032,179

Supplementary Table 2 Continued.

Species	Strain number	Species complex	Used in phylogenomic analysis	Accessable in NCBI	Accessable in JGI	Accessable in Ensembl Fungi	Assembly accession	BioSample	BioProject	Date	Assembly level	Total sequence length (bp)
C. scovillei	Coll-153	Acutatum		Yes			GCA_018906765.1	SAMN17370811	PRJNA692809	2021/6/16	Scaffold	50,113,654
C. scovillei	Coll-365	Acutatum		Yes			GCA_018906675.1	SAMN17370812	PRJNA692809	2021/6/16	Scaffold	49,921,975
C. scovillei	YN51	Acutatum		Yes			GCA_026540245.1	SAMN30451187	PRJNA872318	2022/11/30	Scaffold	52,197,969
C. shisoi	PG-2018a	Destructivum	Yes	Yes		Yes	GCA_006783085.1	SAMN08389744	PRJNA431477	2019/7/9	Scaffold	69,667,657
C. siamense	CAD1	Gloeosporioides		Yes			GCA_013201865.1	SAMN09531625	PRJNA670752	2020/6/1	Scaffold	58,399,603
C. siamense	CAD2	Gloeosporioides		Yes			GCA_013201745.1	SAMN09531626	PRJNA670752	2020/6/1	Scaffold	58,148,672
C. siamense	CAD4	Gloeosporioides		Yes			GCA_013201795.1	SAMN09531627	PRJNA670752	2020/6/1	Scaffold	58,153,656
C. siamense	CAD5	Gloeosporioides		Yes			GCA_013201755.1	SAMN09531628	PRJNA670752	2020/6/1	Scaffold	57,642,425
C. siamense	Cg363	Gloeosporioides	Yes	Yes			GCF_013390195.1	SAMN09531620	PRJNA476648	2020/7/6	Contig	62,936,415
C. siamense	COLG-34	Gloeosporioides		Yes			GCA_011426385.1	SAMN12924919	PRJNA554995	2020/3/18	Scaffold	50,611,973
C. siamense	COLG-38	Gloeosporioides		Yes			GCA_011426375.1	SAMN12924920	PRJNA554995	2020/3/18	Scaffold	55,426,472
C. siamense	COLG-44	Gloeosporioides		Yes			GCA_011428115.1	SAMN12924921	PRJNA554995	2020/3/18	Scaffold	55,623,133
C. siamense	COLG-50	Gloeosporioides		Yes			GCA_011428095.1	SAMN12924922	PRJNA554995	2020/3/18	Scaffold	54,084,473
C. siamense	COLG-90	Gloeosporioides		Yes			GCA_011445115.1	SAMN12924924	PRJNA554995	2020/3/19	Scaffold	55,892,736
C. siamense	CsLH17	Gloeosporioides		Yes			GCA_011947465.1	SAMN14421086	PRJNA691333	2020/4/3	Contig	60,116,880
C. siamense	**GUCC 12174**	**Gloeosporioides**	**Yes**	**Yes**			**JAPHMT000000000**	**SAMN31620403**	**PRJNA898668**		**Scaffold**	**59,282,255**
C. siamense	HBCG01	Gloeosporioides		Yes			GCA_014706345.1	SAMN13679468	PRJNA597657	2020/9/23	Contig	58,357,740
C. siamense	ICMP 18578*	Gloeosporioides	Yes	Yes			GCA_008520285.1	SAMN10390762	PRJNA504379	2019/9/18	Scaffold	55,961,623
C. siamense	KY146	Gloeosporioides		Yes			GCA_014705435.1	SAMN14604513	PRJNA625663	2020/9/22	Scaffold	58,125,311

Supplementary Table 2 Continued.

Species	**Strain number**	**Species complex**	**Used in phylogenomic analysis**	**Accessable in NCBI**	**Accessable in JGI**	**Accessable in Ensembl Fungi**	**Assembly accession**	**BioSample**	**BioProject**	**Date**	**Assembly level**	**Total sequence length (bp)**
C. siamense	KY540	Gloeosporioides		Yes			GCA_014705385.1	SAMN14604516	PRJNA625663	2020/9/22	Scaffold	58,415,579
C. siamense	KY687	Gloeosporioides		Yes			GCA_014705105.1	SAMN14604531	PRJNA625663	2020/9/22	Scaffold	57,441,683
C. siamense	KY748	Gloeosporioides		Yes			GCA_014705055.1	SAMN14604533	PRJNA625663	2020/9/22	Scaffold	57,077,230
C. siamense	KY777	Gloeosporioides		Yes			GCA_014705195.1	SAMN14604525	PRJNA625663	2020/9/22	Scaffold	57,710,956
C. siamense	KY8	Gloeosporioides		Yes			GCA_014705345.1	SAMN14604518	PRJNA625663	2020/9/22	Scaffold	57,566,763
C. siamense	GD10	Gloeosporioides		Yes			GCA_027406245.1	SAMN30451178	PRJNA872318	2022/12/27	Contig	56,189,955
C. siamense	YN56	Gloeosporioides		Yes			GCA_027406165.1	SAMN30451179	PRJNA872318	2022/12/27	Contig	60,424,442
C. sidae	CBS 518.97*	Orbiculare	Yes	Yes		Yes	GCA_004367935.1	SAMN08770262	PRJNA445190	2019/3/22	Scaffold	86,827,816
C. simmondsii	42936	Acutatum		Yes			GCA_020457885.1	SAMN16327581	PRJNA657976	2021/10/13	Contig	49,176,323
C. simmondsii	CBS122122*	Acutatum	Yes	Yes	Yes	Yes	GCA_001563135.1	SAMN02650484	PRJNA239224	2016/2/17	Scaffold	50,474,234
C. sojae	LFN0009	Orchidearum	Yes	Yes			GCA_014235955.1	SAMN13025178	PRJNA577398	2020/8/18	Scaffold	49,351,125
C. spaethianum	MAFF 239500	Spaethianum	Yes	Yes			GCA_022836535.1	SAMD00334500	PRJDB11870	2022/3/29	Contig	50,915,707
C. spinosum	CBS 515.97*	Orbiculare	Yes	Yes		Yes	GCA_004366825.1	SAMN08770268	PRJNA445190	2019/3/22	Scaffold	82,734,851
C. sublineola	CgSl1	Graminicola	Yes	Yes			GCA_001951195.1	SAMN06102611	PRJNA356071	2017/1/13	Scaffold	64,848,627
C. sublineola	CsGL1	Graminicola	Yes	Yes			GCA_020631755.1	SAMN15923890	PRJNA659716	2021/10/26	Contig	67,666,679
C. sublineola	TX430BB	Graminicola	Yes	Yes	Yes	Yes	GCA_000696135.1	SAMN02769489	PRJNA246670	2014/5/27	Scaffold	46,755,813
C. tanaceti	BRIP57314*	Destructivum	Yes	Yes		Yes	GCA_005350895.1	SAMN08130444	PRJNA421029	2019/5/14	Scaffold	57,912,474
C. theobromicola	CF75	Gloeosporioides	Yes	Yes			GCA_014705045.1	SAMN14604534	PRJNA625663	2020/9/22	Scaffold	55,881,512
C. theobromicola	KY152	Gloeosporioides		Yes			GCA_014705415.1	SAMN14604514	PRJNA625663	2020/9/22	Scaffold	56,531,194

Supplementary Table 2 Continued.

Species	**Strain number**	**Species complex**	**Used in phylogenomic analysis**	**Accessable in NCBI**	**Accessable in JGI**	**Accessable in Ensembl Fungi**	**Assembly accession**	**BioSample**	**BioProject**	**Date**	**Assembly level**	**Total sequence length (bp)**
C. tofieldiae	0861	Spaethianum		Yes	Yes	Yes	GCA_001625265.1	SAMN03769761	PRJNA286731	2016/4/19	Scaffold	52,836,184
C. tofieldiae	0861	Spaethianum		Yes			GCA_022836595.1	SAMD00443495	PRJNA858243	2022/3/29	Contig	52,991,954
C. tofieldiae	CBS 127615	Spaethianum	Yes	Yes			GCA_001618715.1	SAMN03769593	PRJNA286721	2016/4/12	Scaffold	52,719,552
C. tofieldiae	CBS 130851	Spaethianum		Yes			GCA_001618735.1	SAMN03769592	PRJNA286720	2016/4/12	Scaffold	53,216,229
C. tofieldiae	CBS 168.49	Spaethianum		Yes			GCA_001618705.1	SAMN03769595	PRJNA286723	2016/4/12	Scaffold	52,962,735
C. tofieldiae	CBS 495.85	Spaethianum		Yes			GCA_001618725.1	SAMN03769835	PRJNA286757	2016/4/12	Scaffold	53,491,261
C. tofieldiae	MAFF 712333	Spaethianum	Yes	Yes			GCA_022836555.1	SAMD00407043	PRJDB11870	2022/3/29	Contig	54,252,643
C. tofieldiae	MAFF 712334	Spaethianum		Yes			GCA_022836575.1	SAMD00407044	PRJNA858243	2022/3/29	Contig	53,983,402
C. trifolii	543-2	Orbiculare	Yes	Yes		Yes	GCA_004367215.1	SAMN10475057	PRJNA506861	2019/3/22	Scaffold	109,659,959
C. tropicale	CgS9275	Gloeosporioides	Yes	Yes			GCA_013201785.1	SAMN09531630	PRJNA476648	2020/6/1	Scaffold	55,848,179
C. tropicale	HN32	Gloeosporioides		Yes			GCA_027406125.1	SAMN30451182	PRJNA872318	2022/12/27	Contig	56,942,285
C. tropicale	IMI 366226	Gloeosporioides		Yes			GCA_027942835.1	SAMN30184424	PRJNA786750	2023/1/23	Contig	54,633,813
C. tropicicola	FJ4	Dracaenophilum		Yes			GCA_025962755.1	SAMN31250444	PRJNA889704	2022/11/2	Scaffold	55,108,579
C. truncatum	CMES1059	Truncatum	Yes	Yes			GCF_014235925.1	SAMN12683944	PRJNA670759	2020/8/18	Contig	56,102,516
C. truncatum	KLC.C5	Truncatum		Yes			GCA_008131165.1	SAMN11371088	PRJNA531610	2019/8/30	Scaffold	59,632,073
C. truncatum	MTCC 3414	Truncatum		Yes			GCA_002632455.2	SAMN06629161	PRJNA380187	2018/3/9	Scaffold	57,912,832
C. viniferum	CGW01	Gloeosporioides	Yes	Yes			GCA_013201765.1	SAMN09531629	PRJNA670752	2020/6/1	Scaffold	68,452,207
C. viniferum	CvYL2a	Gloeosporioides		Yes			GCA_020226115.1	SAMN18316538	PRJNA714705	2021/10/4	Contig	73,406,341
Colletotrichum sp.	COLG25			Yes			GCA_009801095.1	SAMN12288445	PRJNA554995	2019/12/27	Scaffold	56,915,549

Supplementary Table 2 Continued.

Species	**Strain number**	**Species complex**	**Used in phylogenomic analysis**	**Accessable in NCBI**	**Accessable in JGI**	**Accessable in Ensembl Fungi**	**Assembly accession**	**BioSample**	**BioProject**	**Date**	**Assembly level**	**Total sequence length (bp)**
Colletotrichum sp.	COLG31			Yes			GCA_009800995.1	SAMN12288446	PRJNA554995	2019/12/27	Scaffold	53,760,195
Colletotrichum sp.	JS-367			Yes			GCA_003122705.1	SAMN06272963	PRJNA368787	2018/5/14	Scaffold	87,196,530
Colletotrichum sp.	HC292			Yes			GCA_014705525.1	SAMN14604509	PRJNA625663	2020/9/22	Scaffold	54,637,437
Colletotrichum sp.	HC278			Yes			GCA_014705495.1	SAMN14604508	PRJNA625663	2020/9/22	Scaffold	53,185,075
Colletotrichum sp.	SAR 10_70			Yes			GCA_025327165.1	SAMN19298815	PRJNA728692	2022/9/20	Scaffold	59,535,609
Colletotrichum sp.	SAR 10_71			Yes			GCA_025327135.1	SAMN19298816	PRJNA728692	2022/9/20	Scaffold	59,858,058
Colletotrichum sp.	SAR 10_75			Yes			GCA_025327155.1	SAMN19298817	PRJNA728692	2022/9/20	Scaffold	60,807,691
Colletotrichum sp.	SAR 10_76			Yes			GCA_025327145.1	SAMN19298818	PRJNA728692	2022/9/20	Contig	60,132,265
Colletotrichum sp.	SAR 10_77			Yes			GCA_025330015.1	SAMN19298819	PRJNA728692	2022/9/20	2022/9/20	60,541,510
Colletotrichum sp.	SAR11_240			Yes			GCA_025328625.1	SAMN19298830	PRJNA728692	2022/9/20	Scaffold	60,035,199
Colletotrichum sp.	SAR11_57			Yes			GCA_025328355.1	SAMN19298831	PRJNA728692	2022/9/20	Scaffold	55,451,972
Colletotrichum sp.	SAR11_59			Yes			GCA_025328345.1	SAMN19298832	PRJNA728692	2022/9/20	Scaffold	65,090,038
Colletotrichum sp.	SAR 10_65			Yes			GCA_025328335.1	SAMN19298813	PRJNA728692	2022/9/20	Contig	59,664,880
Colletotrichum sp.	SAR 10_86			Yes			GCA_025327125.1	SAMN19298820	PRJNA728692	2022/9/20	Scaffold	60,722,520
Colletotrichum sp.	SAR 10_96			Yes			GCA_025329375.1	SAMN19298821	PRJNA728692	2022/9/20	Contig	56,155,263
Colletotrichum sp.	SAR11_239			Yes			GCA_025328985.1	SAMN19298829	PRJNA728692	2022/9/20	Scaffold	58,100,508

a Bold indicated the sequences generated in this study

Supplementary Table 3 Genome annotation of *Colletotrichum* used in phylogenomic analysis.

Species	**Assembly accession**	**Species complex**	**Gene Count**	**No. of annotated gene in eggNOV-mapper**	**PHI**										**P450**	**No. of Ortho group**
					Total	**Loss of pathogenicity**	**Reduced virulence**	**Unaffected pathogenicity**	**Hyper virulence**	**plant avirulence determinant**	**Enhanced antagonism**	**Lethal**	**chemistry target resistance to chemical**	**chemistry target sensitivity to chemical**		
C. eleusines	GCA_016807845.1	Graminicola	10,980	10,442	485	53	258	130	4	3	2	33	4	0	145	9692
C. falcatum	GCA_019425465.1	Graminicola	12,912	12,441	518	58	266	146	7	2	1	34	5	1	119	9130
C. echinochloae	GCA_016618095.1	Graminicola	11,238	10,677	504	54	264	144	5	4	1	29	4	0	155	9878
C. graminicola	GCF_000149035.1	Graminicola	12,019	11,257	516	58	273	142	6	3	2	30	4	1	148	10376
C. sublineola	GCA_000696135.1	Graminicola	12,699	11,783	509	58	270	137	5	4	1	31	4	1	161	10837
C. sublineola	GCA_001951195.1	Graminicola	11,550	11,035	505	58	266	139	4	3	1	32	4	1	160	10496
C. sublineola	GCA_020631755.1	Graminicola	12,048	11,364	514	61	267	140	5	3	1	33	5	1	164	10565
C. sansevieriae	GCA_002749775.1	Agaves	10,429	9,645	482	57	264	116	4	2	2	34	4	1	130	9342
C. spaethianum	GCA_022836535.1	Spaethianum	13,262	11,669	485	53	254	137	5	2	1	33	1	1	163	10395
C. orchidophilum	GCF_001831195.1	singleton	14,452	11,970	507	56	271	137	5	2	2	32	3	1	164	12047
C. lindemuthianum	GCA_001693025.2	Orbiculare	11,322	10,691	484	58	262	124	3	1	2	32	3	1	157	10217
C. lentis	GCA_003386485.1	Destructivum	10,762	10,217	501	55	265	138	4	2	1	33	4	1	144	9740
C. liriopes	GCA_022179045.1	Spaethianum	14,012	12,424	501	57	258	146	4	3	2	30	1	1	214	11130
C. acutatum	GCA_020465775.1	Acutatum	12,499	12,048	520	57	272	149	5	2	1	33	3	1	210	11077
C. fioriniae	GCA_000582985.1	Acutatum	13,759	12,859	529	57	278	149	5	2	2	34	3	1	214	12001
C. filicis	GCA_023376865.1	Acutatum	17,391	13,209	521	56	281	142	5	2	2	32	3	1	242	14255
C. lupini	GCA_023278565.1	Acutatum	18,694	12,358	502	56	267	134	5	3	2	32	4	1	224	13757
C. nymphaeae	GCA_001563115.1	Acutatum	14,404	13,085	525	56	280	145	5	2	2	33	3	1	225	12333
C. salicis	GCA_001563125.1	Acutatum	13,783	12,561	513	59	277	134	5	2	2	31	3	1	197	11739
C. simmondsii	GCA_001563135.1	Acutatum	13,884	12,825	535	58	283	149	5	2	2	34	3	1	231	12089
C. truncatum	GCA_011947275.1	Truncatum	11,070	10,453	429	50	233	111	4	2	2	26	3	0	175	9547

Supplementary Table 3 Continued.

Species	Assembly accession	Species complex	Gene Count	No. of annotated gene in eggNOV-mapper	PHI										P450	No. of Ortho group
					Total	**Loss of patho genicity**	**Reduced virulence**	**Unaffected patho genicity**	**Hyper virulence**	**plant avirulence determinant**	**Enhanced antagonism**	**Lethal**	**chemistry target resistance to chemical**	**chemistry target sensitivity to chemical**		
					495	54	255	143	7	2	2	32	1	1		
C. incanum	GCA_001855235.1	Spaethianum	11,852	11,458	525	61	272	148	5	3	1	32	4	1	199	10000
C. scovillei	GCF_011075155.1	Acutatum	13,419	12,981	529	58	284	142	5	2	1	35	3	1	233	11568
C. abscissum	GCA_023376855.1	Acutatum	15,499	13,433	520	57	283	140	5	2	2	32	1	1	235	13072
C. trifolii	GCA_004367215.1	Orbiculare	12,292	11,287	496	59	267	128	5	3	2	32	1	1	178	11000
C. viniferum	GCA_013201765.1	Gloeosporioides	14,534	13,455	503	55	278	131	4	2	1	33	1	1	237	12241
C. tofieldiae	GCA_001618715.1	Spaethianum	12,382	11,702	523	55	275	154	5	2	1	30	3	1	190	10813
C. tofieldiae	GCA_022836555.1	Spaethianum	14,916	13,02	535	60	278	157	4	2	2	31	1	1	205	11905
C. tanaceti	GCA_005350895.1	Destructivum	12,172	10,577	472	51	254	129	2	1	1	31	3	1	133	10174
C. chlorophyti	GCA_001937105.1	singleton	10,419	10,129	503	58	273	129	5	2	1	32	3	1	167	9157
C. gloeosporioides	GCF_011800055.1	Gloeosporioides	15,368	14,403	490	54	262	132	5	2	1	32	3	1	266	12525
C. spinosum	GCA_004366825.1	Orbiculare	12,540	11,440	482	57	257	129	4	3	2	30	1	1	187	11202
C. aenigma	GCF_013390185.1	Gloeosporioides	15,190	14,177	517	59	284	135	4	2	1	33	1	1	260	12407
C. asianum	GCA_009806415.1	Gloeosporioides	17,966	14,566	510	54	278	132	4	3	2	35	3	1	258	13309
C. theobromicola	GCA_014705045.1	Gloeosporioides	13,927	12,989	505	56	273	131	4	2	2	35	3	1	240	11871
C. camelliae	GCA_011947485.2	Gloeosporioides	14,390	13,195	453	54	240	121	4	2	1	29	3	1	237	11823
C. tropicale	GCA_013201785.1	Gloeosporioides	14,794	13,881	514	62	280	132	4	2	1	34	1	1	254	12348
C. siamense	**GUCC 12174**	Gloeosporioides	15,320	14,091	494	58	270	124	4	2	1	33	3	1	255	12558
C. higginsianum	GCA_023705605.1	Destructivum	14,359	13,095	550	59	289	154	6	2	1	39	1	1	247	11540
C. orbiculare	GCA_001563125.1	Orbiculare	13,253	11,739	511	59	284	128	5	2	2	30	3	1	180	10999
C. destructivum	GCA_009900065.1	Destructivum	12,578	11,958	505	55	259	145	6	3	0	34	3	1	201	10839

Supplementary Table 3 Continued.

Species	**Assembly accession**	**Species complex**	**Gene Count**	**No. of annotated gene in eggNOV-mapper**	**PHI**										**P450**	**No. of Orthogroup**
					Total	**Loss of pathogenicity**	**Reduced virulence**	**Unaffected pathogenicity**	**Hyper virulence**	**plant avirulence determinant**	**Enhanced antagonism**	**Lethal**	**chemistry target resistance to chemical**	**chemistry target sensitivity to chemical**		
C. endophytica	**GUCC 12108**	Gloeosporioides	14,844	13,695	491	55	269	123	4	2	1	35	3	1	260	12306
C. sidae	GCA_004367935.1	Orbiculare	12,442	11,282	479	57	255	128	5	3	2	29	1	1	187	11077
C. horii	GCA_019693695.1	Gloeosporioides	16,137	14,269	511	57	280	131	4	2	1	35	3	1	265	12859
C. gloeosporioides	GCA_003666125.1	Gloeosporioides	15,075	14,018	507	56	277	132	4	2	1	34	3	1	260	12611
C. jiangxiense	**GUCC 12055**	Gloeosporioides	15,435	14,234	508	59	275	131	4	2	1	34	3	1	260	12764
C. higginsianum	GCF_001672515.1	Destructivum	14,651	12,810	518	57	278	139	6	2	1	33	3	1	242	12196
C. gardeniae	**GUCC 12049**	Gloeosporioides	15,499	14,105	486	59	262	122	4	2	1	35	3	1	262	12651
C. coccodes	GCA_002249775.1	singleton	12,000	11,488	532	60	279	147	7	3	1	34	3	1	190	10418
C. siamense	GCA_008520285.1	Gloeosporioides	14,780	13,797	508	58	277	130	4	3	1	34	2	1	256	12430
C. fructicola	GCA_000319635.2	Gloeosporioides	17,388	15,632	516	57	278	138	4	2	2	33	3	1	294	13471
C. karstii	GCF_011947395.1	Boninense	13,328	12,369	527	57	290	136	5	2	2	33	3	1	221	11202
C. fructicola	GCF_009771025.1	Gloeosporioides	18,397	15,821	532	56	289	144	4	2	2	33	3	1	288	13771
C. magnum	GCA_022457145.1	Magnum	12,768	11,665	513	58	285	129	3	3	1	32	3	1	197	10991
C. sojae	GCA_014235955.1	Orchidearum	16,124	13,107	517	56	282	139	4	2	2	32	1	1	214	12809
C. plurivorum	GCA_014235945.1	Orchidearum	16,153	13,219	517	59	282	137	4	2	1	33	1	1	224	12960
C. musicola	GCA_014235935.1	Orchidearum	16,826	13,423	516	59	282	138	3	2	1	32	1	1	226	13025
C. truncatum	GCF_014235925.1	Truncatum	15,888	13,819	539	62	290	144	4	3	2	35	1	0	217	11849

a Bold indicated the sequences generated in this study

Supplementary Table 4 CAZymes annotation of *Colletotrichum* used in phylogenomic analysis.

Supplementary Table 4