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ARTICLE

Taxonomy and phylogeny of *Colletotrichum* on important forest plants in China

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Abstract

Colletotrichum spp. are well-known and highly significant plant pathogenic fungi worldwide. It is widely distributed across tropical, subtropical and temperate regions, where it causes the anthracnose disease in various forest plants. This devastating fungal infection results in detrimental consequences such as defoliation, fruit drop, branch dieback and in severe cases, even plant mortality. In this study, morphological characteristics combined with multi-gene phylogenetic (ITS, *act*, *gapdh*, *chs-1*, *his3*, *tub2*, *sod2*, *cal*, *apmat*, and *gs*) analyses were used to study 169 *Colletotrichum* strains isolated from 972 forest plants specimens collected in 12 provinces of China. The results revealed the presence of 23 distinct species, which include eight new species, i.e. *C. cunninghamiae*, *C. guiyangense*, *C. hubeiense*, *C. jixiense*, *C. lunanense*, *C. parthenocissigenum*, *C. subplurivorum*, and *C. wenzhouense*, one new record from China, and 14 known species, among them, 11 host species were reported for the first time. Furthermore, there are seven species reduced to synomymies in this study, i.e *C. spicati* and *C. celtidis* are reduced to synomymies under *C. karsti*, *C. citrulli* is reduced under *C. gloeosporioides*, *C. analogum* under *C. camelliae*, *C. mengyinense* under *C. fructicola*, *C. yulongense* under *C. henanense*, and *C. simulanticitri* under *C. nymphaeae*. Pathogenicity tests were conducted, revealing that the newly discovered species *C. luanense*, along with *C. aenigma*, *C. gloeosporioides*, and *C. siamense*, there are recorded on the new host plants, exhibited high rates of infestation and infectivity across various hosts. Contrarily, *C. pseudomajus* was exclusively isolated from branches of *Camellia sinensis*, demonstrating a remarkable host-specificity. The comparative genomics analysis revealed that *C. pseudomajus* possesses two specific carbohydrases, GT61 and AA14, which may explain its organ-specificity towards *Camellia sinensis* branches. This study provides valuable insights into the diversity of *Colletotrichum* species affecting forest plants, laying the foundation for effective control strategies against forest anthracnose.

Keywords – Anthracnose – Carbohydrate-enzyme analysis – Morphology – Multi-locus phylogeny

INTRODUCTION

Colletotrichum is recognized as one of the most significant plant pathogens globally, ranking among the top 10 (Dean et al. 2012). It exhibits a wide distribution across tropical, subtropical, and temperate regions. Anthracnose, caused by *Colletotrichum* spp., poses a significant threat to various plants and induces substantial economic losses (Hyde et al. 2009, Cannon et al. 2012). It commonly affects forest plants, including both coniferous, broad-leaved species and some vine plants, such as *Camellia oleifera* Abel., *Cinnamomum camphora*, *Cunninghamia lanceolata* (Lamb.) Hook.,

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Cocculus orbiculatus (L.) DC. and *Juglans regia* L., and with a higher prevalence observed on broad-leaved trees (Liu et al. 2016a, Wang et al. 2019a, Huang 2020, Wang et al. 2023). The leaves and fruits of trees are predominantly targeted by this disease (Xu et al. 2004). *Camellia oleifera* is susceptible to anthracnose, which leads to fruit, flower, and bud drops, as well as branch dieback, and even the death of the tree in severe cases. In China, anthracnose on *Camellia oleifera* has been reported to cause a 10% to 30% reduction in production, with heavy losses exceeding 50% in some areas (Ye et al. 2011). The *Colletotrichum* anthracnose is also a pervasive issue in the cultivation of *Cunninghamia lanceolata*, which affects all fir-growing regions in China. This disease caused wilting of the most tender tips of the fir, significantly impeding its growth (Yuan et al. 1997). *Cinnamomum camphora* (L.) Presl is also widely affected by anthracnose in its main distribution areas in China. The disease primarily targets the host seedlings, resulting in shoot and even plant death (Yuan et al. 1997). Anthracnose on *Juglans regia* predominantly impacts on the fruit, with disease index ranging from 50% to 80%. Infected fruits tend to drop prematurely or become shriveled, rendering them inedible (Yuan et al. 1997).

Previously, the pathogens responsible for anthracnose of forest plants were typically identified as *Colletotrichum gloeosporioides* (Penz.) Penz. & Sacc. *sensu lato* (Phoulivong et al. 2010). However, with the application of molecular techniques in the taxonomy and systematics of *Colletotrichum*, significant advancements have been made in the identification of *Colletotrichum* species associated with forest plants. Zhang et al. (2009) first used morphological characteristics combined with ITS sequences to identify 58 *Colletotrichum* strains obtained from forest trees in Shanxi Province, which belonged to four distinct genetic taxa.

Subsequently, a combination of morphological characteristics and multi-locus phylogenetic analysis was employed to investigate anthracnose from forest plants in China, some new species are described, such as, *Colletotrichum quercicola* Ning Jiang & C.B. Wang on *Quercus variabilis* Blume, *C. populi* C.M. Tian & Zheng Li on poplar, some known species are also described, such as, *C. siamense* Prihast., L. Cai & K.D. Hyde, *C. fructicola* Prihast., L. Cai & K.D. Hyde, *C. cangyuanense* Z.F. Yu, *C. gloeosporioides* and *C. karsti* You L. Yang, Zuo Y. Liu, K.D. Hyde & L. Cai (Li et al. 2012, Wu 2016, He et al. 2022, Wang et al. 2022). The *Colletotrichum* species on *Camellia* have attracted extensive attention in studies of anthracnose from forest trees. Morphological analysis combined with multi-locus phylogenetic analysis methods were used to identify *Colletotrichum* species on *Camellia* spp. in major tea-producing provinces in China. Three new species (*Colletotrichum henanense* F. Liu & L. Cai, *C. jiangxiense* F. Liu & L. Cai, *C. wuxiense* Yu Chun Wang, X.C. Wang & Y.J. Yang) and ten known species were described (Li et al. 2014, Liu et al. 2015, Wang et al. 2016, Li et al. 2017).

Carbohydrate-active enzymes (CAZYs) are a group of enzymes involved in the catalysis of carbohydrate degradation, modification, and biosynthesis (Cantarel et al. 2009). CAZYs play a significant role in fungal invasion of plant hosts (Ilyukhin et al. 2022). Plant pathogenic fungi can produce various enzymes, such as Glycoside Hydrolases, to deconstruct cell wall polysaccharide families involved in cellulose and hemicellulose hydrolysis (Zhao et al. 2013). Baroncelli et al. (2016) demonstrated a strong correlation between the types and quantities of carbohydrate-active enzymes and the host range. Therefore, comparative genomic analysis of carbohydrate-active enzymes can provide a deeper understanding of the relationship between plant pathogenic fungi and their hosts.

The aims of the present study were as follows:

i. To study the taxonomy of *Colletotrichum* and clarify the diversity of *Colletotrichum* species of main forest plants in China, such as the *Camellia oleifera*, *Parthenocissus tricuspidata* (Siebold & Zucc.) Planch., *Cunninghamia lanceolata*, *Cinnamomum camphora* (L.) Presl, using a polyphasic approach including comparison of morphological characteristics, single- and multi-locus phylogenetic analyses, pairwise homoplasy index test, mating compatibility test, and coalescent-based species delimitation methods such as GMYC, PTP, and PHI.

ii. To identify the highly invasive and widely hosted species of *Colletotrichum* that cause anthracnose in the forest plants by conducting pathogenicity test. This information will provide a theoretical basis for the development of effective control strategies against this disease.

iii. To understand the relationship between host specificity and carbohydrases in *Colletotrichum* species impacting forest plants by performing a comparative genomic analysis.

MATERIALS AND METHODS

Fungal isolation

A total of 2343 strains were obtained from diseased and healthy leaves, as well as diseased branches of forest plants from forests or plantations in 12 provinces in China, including Anhui, Fujian, Guangdong, Guangxi, Guizhou, Henan, Hubei, Hunan, Jiangxi, Sichuan, Yunnan, and Zhejiang (Supplementary Tables 1, 2, 3, 4, 5, 6, 7, 8, 9). Fungal cultures were obtained using the tissue isolation method (Choi et al. 1999). Fragments measuring 5 mm × 5 mm were taken from the margins of leaf and branch lesions, as well as healthy parts of leaves. These fragments underwent a disinfection process, including treatment with 75% ethanol for 30 s, followed by 10% sodium hypochlorite for 3 min, then rinsing in sterile water three times. The fragments were dried on sterilized paper towels and then placed on potato dextrose agar (PDA) at room temperature (25 ± 3 ℃). The type specimens of the newly identified species from this study were deposited in the Chinese Academy of Forestry (CAF; http://museum.caf.ac.cn), with the ex-type living cultures deposited in the Capital Normal University Culture Collection Center (CNUCC).

Morphology

Mycelial blocks measuring 5 mm in diameter were placed at the center of the culture medium and incubated in the dark at 25 °C. After 7 days of incubation, the colony characteristics were observed and recorded. If the growth was sterile on potato dextrose agar (PDA), morphological characteristics were described using synthetic low-nutrient agar (SNA; Nirenberg 1976) or agar media containing oatmeal (OA; Crous et al. 2009) or corn meal (CMA; Liu 2018) with pine needles. To observe appressoria, slide cultures were prepared following the method outlined by Su et al. (2012). Morphological observations of reproductive structures were conducted using a dissecting microscope (Nikon SMZ-1000) and an upright microscope (Olympus BX51). For each structure, 30 measurements were made. Colors were determined using ColorHexa (https://www.colorhexa.com/).

DNA extraction, amplification and sequencing

Genomic DNA extraction was carried out using the M5 Plant Genomic DNA Kit (Mei5 Biotechnology Co., Ltd., China) following the manufacturer's instructions. Ten loci, including *act*, *apmat*, *cal*, *chs-1*, *gapdh*, *gs*, *his3*, ITS, *sod2*, and *tub2*, were amplified and sequenced in this study. The primers pairs used for amplification were as follows: ACT-512F + ACT-783R (Carbone & Kohn 1999), AM-F + AM-R (Silva et al. 2012), CL1C + CL2C (Weir et al. 2012), CHS-79F + CHS-354R (Carbone & Kohn 1999), GDF + GDR (Guerber et al. 2003), GSLF2 + GSLR1 (Liu et al. 2016b), CYLH3F + CYLH3R (Crous et al. 2004), ITS-1F (White et al. 1990) + ITS-4 (White et al. 1990), SWF1 + SWR1 (This study), and T1 (O'Donnell & Cigelnik 1997) + Bt2b (Glass & Donaldson 1995) (Table 1). The 25 μL reaction volume consisted of 12.5 μL 2 × M5 HiPer Taq HiFi PCR Mix (Mei5 Biotechnology, Co., Ltd., Beijing, China), 1 μL of each forward and reverse primer (concentration around 10 μM), 1 μL template genomic DNA (concentration around 10 μM around 10 ng/μL), and 8.5 μL of distilled deionized water. PCR amplification followed the protocol described by Crouch et al. (2009a), Liu et al. (2016a) and Sui et al. (2023). The PCR products were visually examined using agarose electrophoresis gels and compared with the band intensities of a 200 bp DNA ladder. Purification and sequencing of the PCR products were conducted by Sangon Biotech Company (Shanghai, China).

Table 1 Primers used in this study, with originating loci, sequences and references.

Genes	Primers	Sequence (5'–3')	References
act (Actin)	ACT-512F	ATGTGCAAGGCCGGTTTCGC	Carbone & Kohn (1999)
	ACT-783R	TACGAGTCCTTCTGGCCCAT	
Apmat (Apn2-Mat1-2 intergenic spacer and partial mating type (Mat1-2) gene)	AM-F	TCATTCTACGTATGTGCCCG	Silva et al. (2012)
	AM-R	CCAGAAATACACCGAACTTGC	
cal (Calmodulin)	CL1C	GAATTCAAGGAGGCCTTCTC	Weir et al. (2012)
	CL2C	CTTCTGCATCATGAGCTGGAC	
chs-1 (Chitin synthase)	CHS-79F	TGGGGCAAGGATGCTTGGAAGAAG	Carbone & Kohn (1999)
	CHS-354R	TGGAAGAACCATCTGTGAGAGTTG	
gapdh (Glyceraldehyde-3-phosphate dehydrogenase)	GDF	GCCGTCAACGACCCCTTCATTGA	Guerber et al. (2003)
	GDR	GGGTGGAGTCGTACTTGAGCATGT	
gs (Glutamine synthetase)	GSLF2	TACACGAGSAAAAGGATACGC	Liu et al. (2016b)
	GSLR1	GATACGCCTCTTCCAGCGTT	
his3 (histone 3)	CYLH3F	AGGTCCACTGGTGGCAAG	Crous et al. (2004)
	CYLH3R	AGCTGGATGTCCTTGGACTG	
ITS rDNA (Internal transcribed spacer)	ITS-1F	CTTGGTCATTTAGAGGAAGTAA	White et al. (1990)
	ITS-4	TCCTCCGCTTATTGATATGC	
sod2 (manganese superoxide dismutase)	SWF1	GCACCACAGCAAACAGTAAGTC	This study
	SWR1	CGGGATGTTGTCAGCACCT	
tub2 (β-tublin 2)	T1	AACATGCGTGAGATTGTAAGT	O'Donnell & Cigelnik (1997)
	Bt2b	ACCCTCAGTGTAGTGACCCTTGGC	Glass & Donaldson (1995)

Phylogenetic analysis

The DNA sequences generated by forward and reverese sequences were used to obtain consensus sequences using SeqMan v.7.1.0 in the DNASTAR Lasergene Core Suite software (DNASTAR Inc., Madison, WI, USA). The new sequences generated in this study were submitted to the NCBI-GenBank database (https://www.ncbi.nlm.nih.gov/) (Supplementary Tables 1–9). Other reference sequences were downloaded from GenBank (Supplementary Tables 1–9). To ensure the consistency of gene segments, a segmentation homogeneity test was performed following the methods of Farris et al. (1994) and Huelsenbeck et al. (1996). All sequences were aligned using the online MAFFT (https://www.ebi.ac.uk/Tools/msa/mafft/) and edited using Gblocks (http://www.phylogeny.fr/one_task.cgi?task_type=gblocks) by selecting DNA and all options for less stringent criteria. Phylogenetic analyses were conducted using both Maximum Parsimony (MP) and the Bayesian Inference (BI) methods. For different species complexes, we used various multi-locus alignments, as detailed in Table 2. Phylogenetic analyses were conducted using PAUP v.4.0b10 for maximum parsimony (MP) analysis (Swofford 2000), and MrBayes v.3.1.2 for Bayesian Inference (BI) analysis (Ronquist & Huelsenbeck 2003).

For the Maximum Parsimony (MP) analysis, a heuristic search option was employed, including 1000 random-addition sequences with a tree bisection and reconnection (TBR) algorithm. Branches of zero length were collapsed, and all equally most parsimonious trees were saved. Bootstrap support values were calculated based on 1000 bootstrap replicates. The calculated parsimony scores included tree length (TL), consistency index (CI), retention index (RI), and rescaled consistency index (RC).

Bayesian inference (BI) analysis was conducted using a Markov chain Monte Carlo (MCMC) algorithm following the approach by Rannala & Yang (1996). The best model for each gene was estimated using MrModeltest v. 2.3 (Table 3). The MCMC chains were run for 10,000,000

generations starting from random trees. The analysis stopped when the average standard deviation of split frequencies fell below 0.01. Trees were saved every 1000 generations. During the burn-in phase, the first 25% of trees were discarded, and the remaining trees were used to calculate the posterior probabilities (PPs) (Posada & Crandall 1998). The final alignments and the retrieved topologies were deposited in TreeBASE (http://www.treebase.org), under accession ID: 31136.

Table 2 Genes of different *Colletotrichum* species complexes for multi-loci phylogenetic analysis analysis.

Species complexes	**The genes used and their order**
C. acutatum species complex	ITS-*gapdh-chs-1-act-his3-tub2*
C. boninense species complex	ITS-*gapdh-chs-1-act-his3-tub2-cal*
C. caudatum-graminicola species complex	*act-chs-1*-ITS-*sod2-tub2*
C. dematium species complex	*act-chs-1-gapdh-his3*-ITS-*tub2*
C. destructivum species complex	*act-chs-1-gapdh-his3*-ITS-*tub2*
C. gigasporum species complex	ITS-*gapdh-chs-1-act-tub2*
C. gloeosporioides species complex	*act-tub2-cal-chs-1-gapdh*-ITS *apmat-gs*
C. orchidearum species complex	*act-chs-1-gapdh-his3*-ITS-*tub2*
C. truncatum species complex	*act-chs-1-gapdh-his3*-ITS-*tub2*

Table 3 Nucleotide substitution models used in the phylogenetic analyses.

Species complex	***act***	***apmat***	***cal***	***chs-1***	***gapdh***	***gs***	***his3***	**ITS**	***sod2***	***tub2***
C. acutatum species complex	GTR + G	–	–	GTR + I + G	SYM + G	–	GTR + I + G	K80 + I + G	–	GTR + I
C. boninense species complex	HKY + G	–	HKY + G	GTR + G	HKY + G	–	GTR + G	SYM + I +G	–	HKY + I
C. caudatum-graminicola species complex	HKY + G	–	–	GTR + G	–	–	–	GTR + I + G	HKY + G	–
C. dematium species complex	GTR + I	–	–	GTR + G	HKY + G	–	–	K80 + I + G	–	GTR + G
C. destructivum species complex	HKY + G	–	–	SYM + I	HKY + I	–	HKY + I	HKY + I + G	–	GTR + G
C. gigasporum species complex	HKY + G	–	–	K80 + G	HKY + I	–	–	SYM + I +G	–	HKY + I + G
C. gloeosporioides species complex	HKY + I	HKY + G	GTR + G	K80 +I +G	HKY + G	GTR + I + G	–	GTR + I + G	–	HKY + G
C. orchidearum species complex	HKY + G	–	–	GTR + I + G	HKY + G	–	HKY + I	GTR + I	–	HKY + G
C. truncatum species complex	HKY + G	–	–	K80 + I	HKY + I	–	HKY + I	SYM	–	SYM + G

Note: "–" represents that this gene is not used in this species complex.

Pairwise homoplasy index (PHI) test

For species that are phylogenetically close but not clearly delimited, we analysed sequences using the GCPSR model. This involved conducting a pairwise homoplasy index (PHI) test as described by Quaedvlieg et al. (2014). The PHI test, performed using SplitsTree v.4.14.6 (Huson 1998, Huson & Kloepper 2005, Huson & Bryant 2006), assessed the level of recombination within closely related species. This assessment was based on a concatenated gene dataset, organized according to species complexes. A pairwise homoplasy index below the 0.05 threshold ($\Phi w < 0.05$) indicated significant recombination within the dataset. The relationship between closely related species was visualized by constructing a split graph.

General Mixed Yule Coalescent (GMYC)

The General Mixed Yule Coalescent (GMYC) method combines neutral coalescence theory (Fujisawa & Barraclough 2013) with the Yule species model (Parnmen et al. 2012) to detect changes in branching rates within intra- and interspecific relationships. The GMYC algorithm requires a supersymmetric phylogenetic tree, which was constructed using BEAST v.1.8.1 (R Core Team 2017). The following parameters and unique haplotypes were used in the BEAST analysis: the GTR substitution model, the loci heterogeneity model for Gamma, a random start tree, and 5×10^7 Markov chain Monte Carlo (MCMC) iterations sampled every 10,000 generations. Convergence was evaluated using effective sample size (ESS) values (≥200). A 10% conservative burn-in was performed after examining the log-likelihood curves in Tracer v.1.6. The generated trees were summarized into a maximum clade credibility tree using TreeAnnotator v.2.6.7. To fit the tree to both single-transition and multiple-transition GMYC models, the GMYC website (The Exelixis Lab: http://species.hits.org/gmyc/) was utilized.

Poisson Tree Processes (PTP)

The species boundaries on a rooted phylogenetic tree were defined using the Poisson Tree Processes (PTP) model (Kapli et al. 2017). The PTP method uses the branch length data from a phylogeny to estimate the mean expected number of substitutions per site between two branching events. It then applies two separate classes of poisson processes (intra and inter-specific branching events) before clustering the phylogenetic tree in accordance with the results. As advocated for this approach (Kapli et al. 2017), the analysis was carried out on the PTP the website server (http://species.hits.org/ptp/) using the RAxML tree.

Pathogenicity assay

Healthy mature leaves from *Camellia oleifera*, *C. sinensis*, *Cinnamomum camphora*, and *Cunninghamia lanceolata*, as well as healthy mature branches from *Camellia sinensis*, were collected for the experiment. The collected plant materials were disinfected by immersing it in 75% ethanol for 1 min, followed by rinsing in sterile water for three times and drying in the air. To create wounds for inoculation, each disinfected leaf was punctured five times on both sides using sterile needles with a diameter of 0.5 mm. Initially, conidia suspensions with concentrations of 10^2, 10^4, 10^6, and 10^8 /mL were used for inoculation, but these attempts were unsuccessful. Subsequently, the method described by Wang et al. (2019b) was followed, and mycelial plugs were used for inoculation instead. For inoculation, the 5-mm PDA medium plugs with mycelia from a 5-day-old culture were placed on the left side of wounded and unwounded leaves, and sterile PDA plugs with no mycelia were placed in parallel on the right side of wounded and unwounded leaves as control, with three repetitions. The inoculated leaves were placed in a sterile dish, placed on sterilized filter paper saturated with sterilized water to maintain high humidity, and incubated in a growth cabinet at 28 °C with a 12/12 h light/dark photoperiod for 7 days. The experiment was repeated twice. The entire leaves were photographed using a cell-phone (Huawei P30 Pro), while the lesion was captured using a dissecting microscope (Nikon SMZ-1000). Pathogens causing lesions were reisolated from the infected leaves, and their identification was carried out based on morphological characteristics and molecular data.

Genome sequencing, assembly, annotation, and comparative genomics analysis of carbohydrate enzymes

The strains exhibiting host-specificity and organ-specificity were subjected to comprehensive analysis using comparative genomics analysis to elucidate their relationship with the host or organ. The genomic data of 5 strains (CNUCC 307307, CNUCC 310138, CNUCC 3041, CFCC 59258, and CFCC 59180) were obtained for this study. Mycelia of each strain (CNUCC 307307, CNUCC 310138, CNUCC 3041, CFCC 59258, and CFCC 59180) grown on PDA for 4–5 days were transferred to PDB, placed on a shaker set at 25 °C and 180 rpm, and incubated for 4 days. The sediment was washed with sterile water and stored at –80 °C. The samples were sent to Novogene (Beijing, China) for Illumina sequencing. Additional genomic data were obtained through NCBI (https://www.ncbi.nlm.nih.gov/) and JGI Genome Portal (https://genome.jgi.doe.gov/portal/) (Supplementary Tables 10, 11).

The assembly was performed using SPAdes assembly software, starting with Clean Data from the Novogene, the resulting assembly was then integrated using the minimus2 module in Amos v.3.1.0. GapCloser was employed to optimize and fill gaps in the preliminary assembly, resulting in the final assembly. Fragments below 200 bp were filtered out, and the assembly results were evaluated using quast v. 5.2.0. Genome assemblies were deposited in National Center for Biotechnology Information (NCBI, https://www.ncbi.nlm.nih.gov/).

For gene prediction, GeneMaker-ES and Liftoff software were used. Additionally, Gffread-Master was used to extract protein sequences from the gene prediction results. The predicted genes were compared against functional databases using BLAST with specific criteria (blastp, e-value ≤ 1e-5). The annotation process selected the BLAST result with the highest score, considering default identity (>40%) and coverage (>40%). Annotation was performed online using the dbCAN database (https://bcb.unl.edu/dbCAN2/blast.php). Three databases were chosen for protein sequence annotation: HMMER: dbCAN (e-value < 1e-15, coverage > 0.35), DIAMOND: CAZy (e-value < 1e-102), and HMMER: dbCAN-sub (e-value < 1e-15, coverage > 0.35). To ensure data validity and correctness, the CUPP database was also used for annotation. The final annotation results were obtained by comparing and filtering the above annotation outcomes. The annotation results were imported into TBtools, and a Venn diagram was constructed using the UpSet plot to visualize the shared and unique annotations.

RESULTS

Phylogenetic analyses and analysis based on coalescent-based species delimitation methods

One hundred and sixty-nine isolates were selected for multi-locus phylogenetic analyses based on their ITS phylogenetic positions and the hosts. The consensus trees obtained from maximum parsimony analyses were confirmed by the tree topologies obtained with Bayesian inference. The phylogenetic trees of single loci in different species complexs show topologies similar to those of the multi-locus phylogenetic trees (Supplementary Figs 1–54).

In the phylogenetic tree of *Colletotrichum acutatum* complex (Fig. 1), seven strains (CNUCC 766B-1-3, CNUCC 815-1-1, CNUCC 234-3-4, CNUCC 469-3-1, CNUCC 819B-2-2, CNUCC 820A-2-2, and CNUCC 163-2-2-1) grouped together with *C. nymphaeae* (Pass.) Aa, (MBP = 78, PP = -), while *C. simulanticitri* Z.F. Yu also clustered into this clade. Two strains (CNUCC 528-2-2 and CNUCC 324C-1-5-2) formed one clade (MPB = 100, PP = 1.00) with *Colletotrichum schimae* F. Liu, W.P. Wu & L. Cai. Four strains (CNUCC 354-4-2, CNUCC 456-2-1, CNUCC 363A-1-1, and CNUCC 354-2-1) clustered with *C. godetiae* Neerg. with high support values (MBP = 82, PP = 1.00). Twenty-six strains clustered with *Colletotrichum fioriniae* (Marcelino & Gouli) Pennycook, forming a clade with a high support value (MBP = 98, PP = 1.00). Pairwise homoplasy index (PHI) tests showed no significant reorganization between these two subclades, but the support value was low (Φw = 0.1927) (Fig. 2). The two subclades were the same species based on ML-bPTP analysis (Fig. 3), but they were different species based on Bayes-bPTP analysis (Fig. 4). The Generalized Mixed Yule Coalescent (GMYC) single-threshold analysis indicates that these two subclades are

the same entity (Fig. 5); however, the multi-threshold analysis indicates that each of these two subclades contains several different entities (Fig. 6).

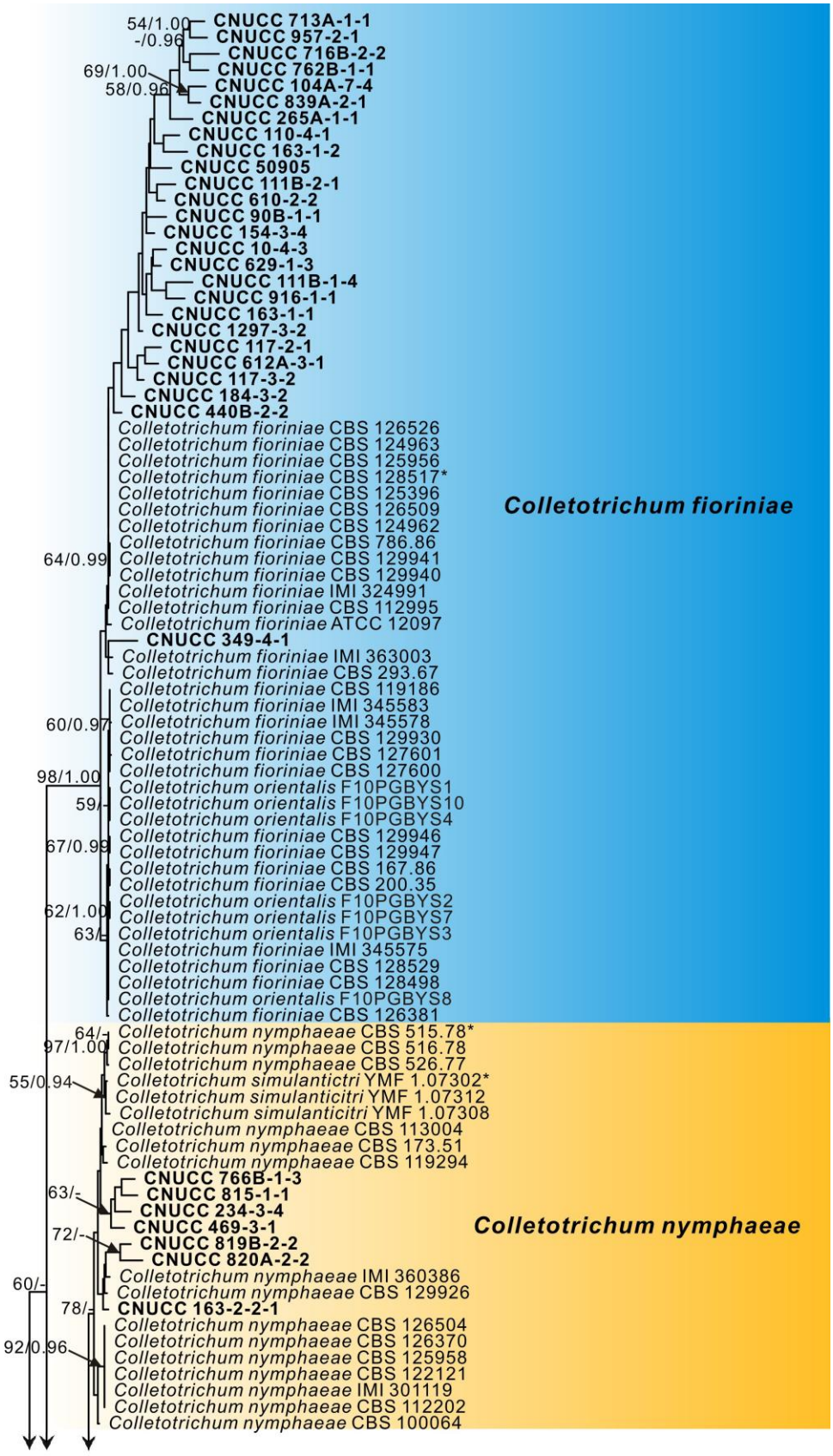


Figure 1 – Phylogenetic tree of *Colletotrichum acutatum* species complex derived from maximum parsimony analysis of the combined ITS–*gapdh*–*chs-1*–*act*–*his3*–*tub* sequences, using

C. orchidophilum (CBS 632.80) as the outgroup. Maximum parsimony bootstrap values (BP > 50%) and bayesian posterior probabilities (PP > 0.95) are shown above the branches. Type species strains are marked with an " * ". Newly generated sequences are represented in **bold**.

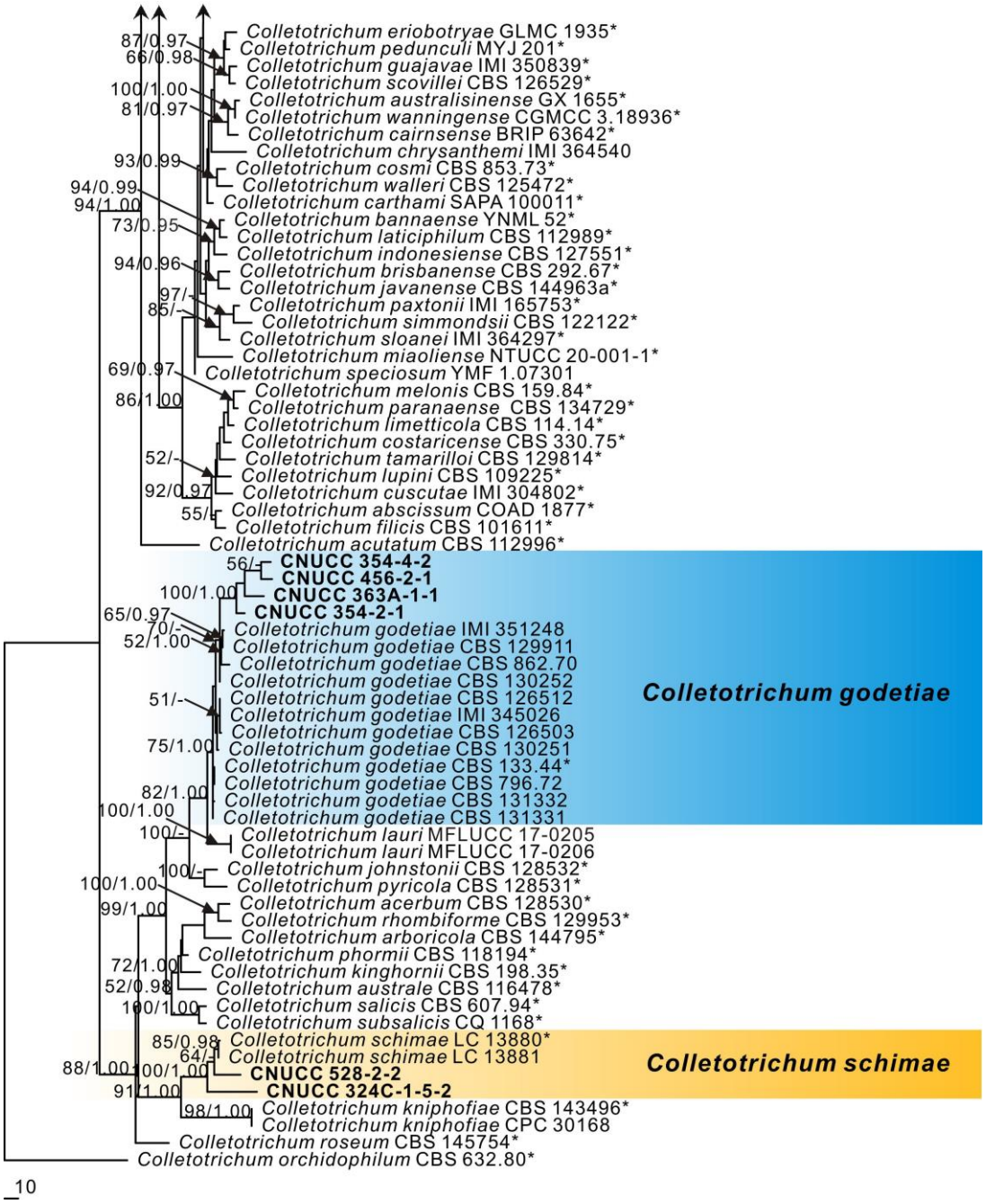


Figure 1 – Continued.

In the *Colletotrichum boninense* species complex (Fig. 7), 11 strains clustered in one clade with *C. karsti* and had high support values (MBP = 99, PP = 1.00). *Colletotrichum spicati* Z.F. Yu & H. Zheng and *C. celtidis* Tennakoon, C.H. Kuo & K.D. Hyde also cluster within this clade (Fig. 7).

Among the *Colletotrichum caudatum-graminicola* species complex (Fig. 8), CNUCC 253B-3-2 formed an independent clade and was more closely related to *C. multiseptatum* F. Liu, W.P. Wu & L. Cai, *C. echinochloae* Moriwaki & Tsukib., and *C. jacksonii* J.A. Crouch, B.B. Clarke, J.F. White & B.I. Hillman.

In the *Colletotrichum dematium* species complex (Fig. 9), three strains (CNUCC P7-4-5-3-3, CNUCC P7-4-5, CNUCC P7-4-5-2-3) formed a sister clade with *C. jinshuiense* M. Fu & G.P. Wang (MBP = 100, PP = 1.00) (Fig. 9). However, the PHI test showed no significant reorganization between these two clades and had a high support value (Φw = 0.8966) (Fig. 10).

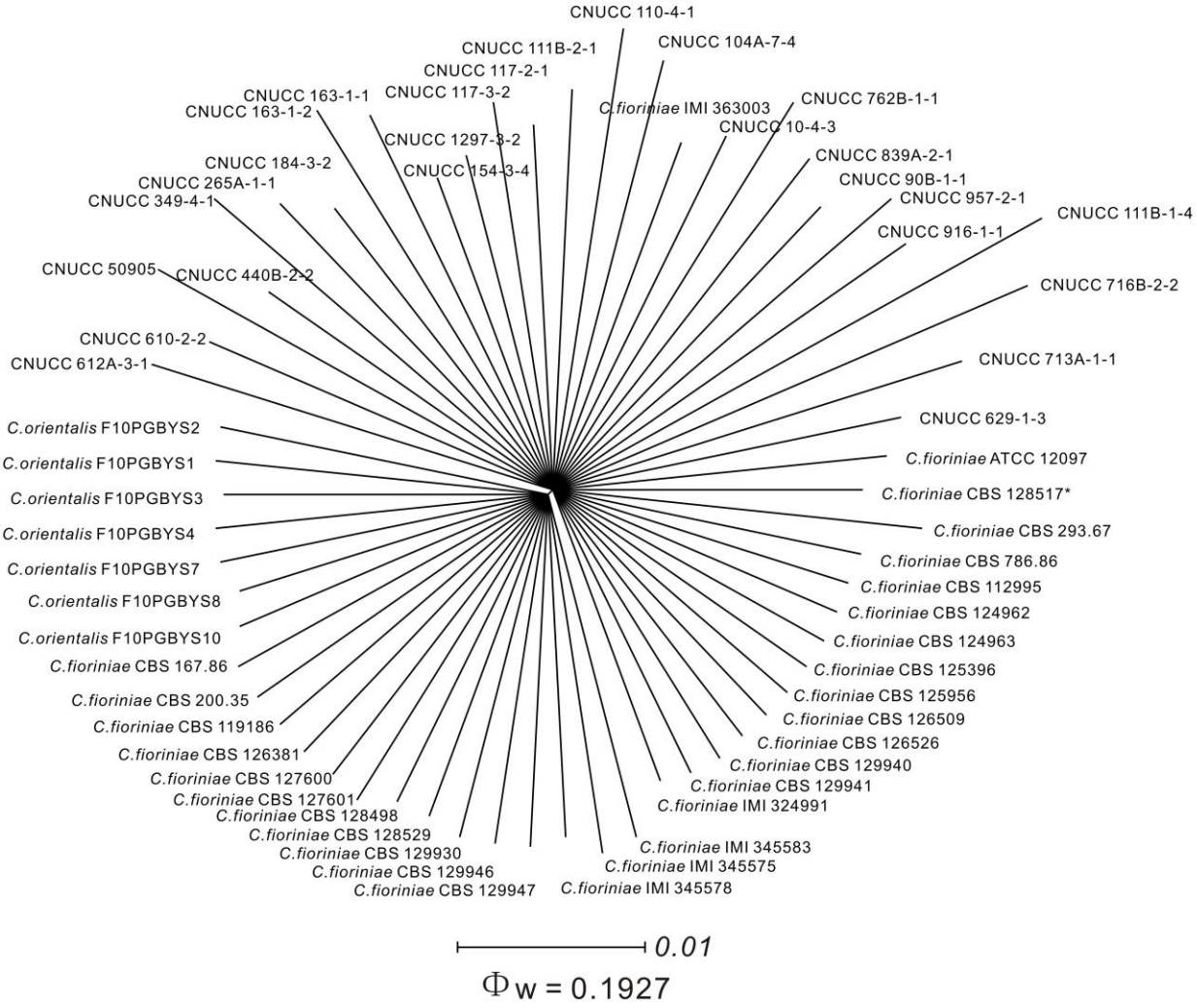


Figure 2 – The result of the pairwise homoplasy index (PHI) tests for closely related species and *Colletotrichum fioriniae* using both LogDet transformation and splits decomposition.

In the *Colletotrichum destructivum* species complex (Fig. 11), two strains (CNUCC 157A-4-4, CNUCC 157A-4-4-2) formed a highly supported clade (MBP = 100, PP = 1.00), and clustered together with *Colletotrichum utrechtense* Damm. (MBP = –, PP = –), and closely related to *Colletotrichum neorubicola* Yu Li, J. Gao & L.P. Liu, *Colletotrichum panacicola* Uyeda & S. Takim. The strains CNUCC 58-61-2 and CNUCC 58-57-2 have formed an independent clade with high support values (MBP = 100, PP = 1.00). Strains of CNUCC 408-1-1 and CNUCC 408-1-1-2 formed a highly supported clade (MBP = 100, PP = 1.00), and clustered together with *Colletotrichum pleopeltidis* Crous & Jol. Roux as sister taxa (MBP = 98, PP = 1.00). (Fig. 11).

In the *Colletotrichum gigasporum* species complex (Fig. 12), two strains (CNUCC 1311-1-3 and CNUCC 1391-1-1) and *C. pseudomajus* F. Liu, L. Cai, Crous & Damm clustered in one clade with high support values (MBP = 100, PP = 1.00). Three strains (CNUCC 714-1-1, CNUCC 747-1-3, and CNUCC 110A-4-4) clustered within the sequences of *Colletotrichum zhaoqingense* F. Liu & L. Cai clade and had high support values (MBP = 99, PP = 1.00) (Fig. 12).

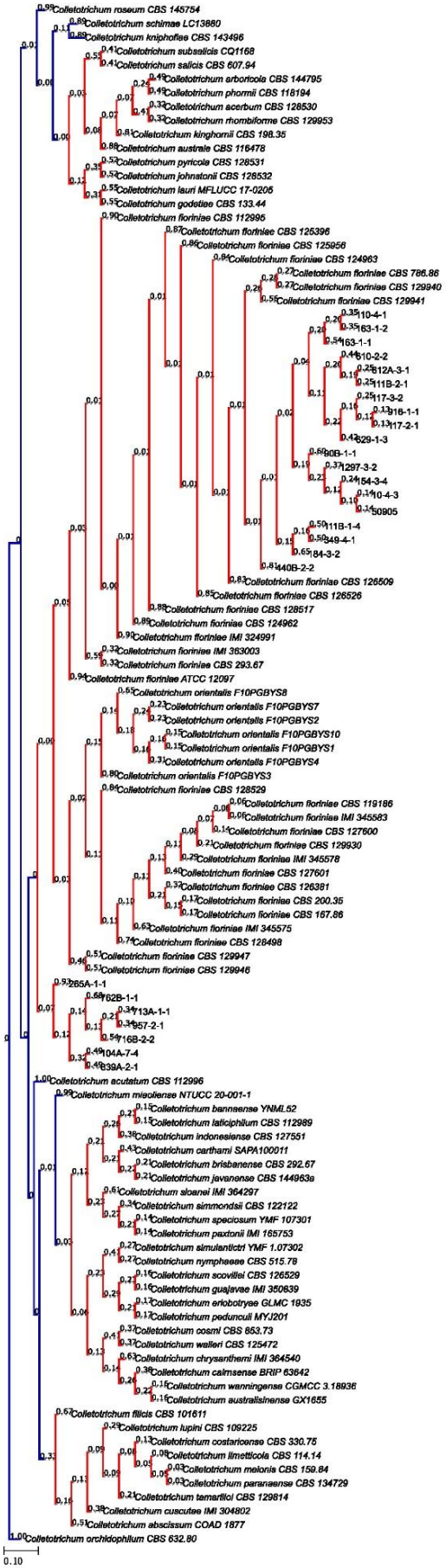


Figure 3 – Results of the bPTP analysis based on the ML topologies. Putative species clusters are indicated using transitions between blue-colored to red-colored branches.

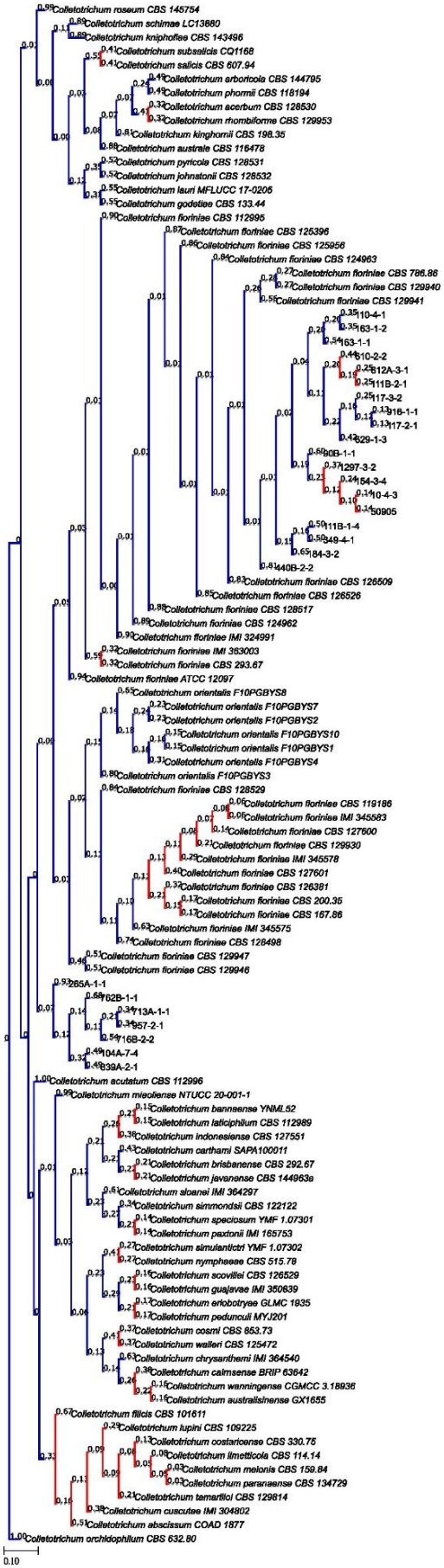


Figure 4 – Results of the bPTP analysis based on the BI. Putative species clusters are indicated using transitions between blue-colored to red-colored branches.

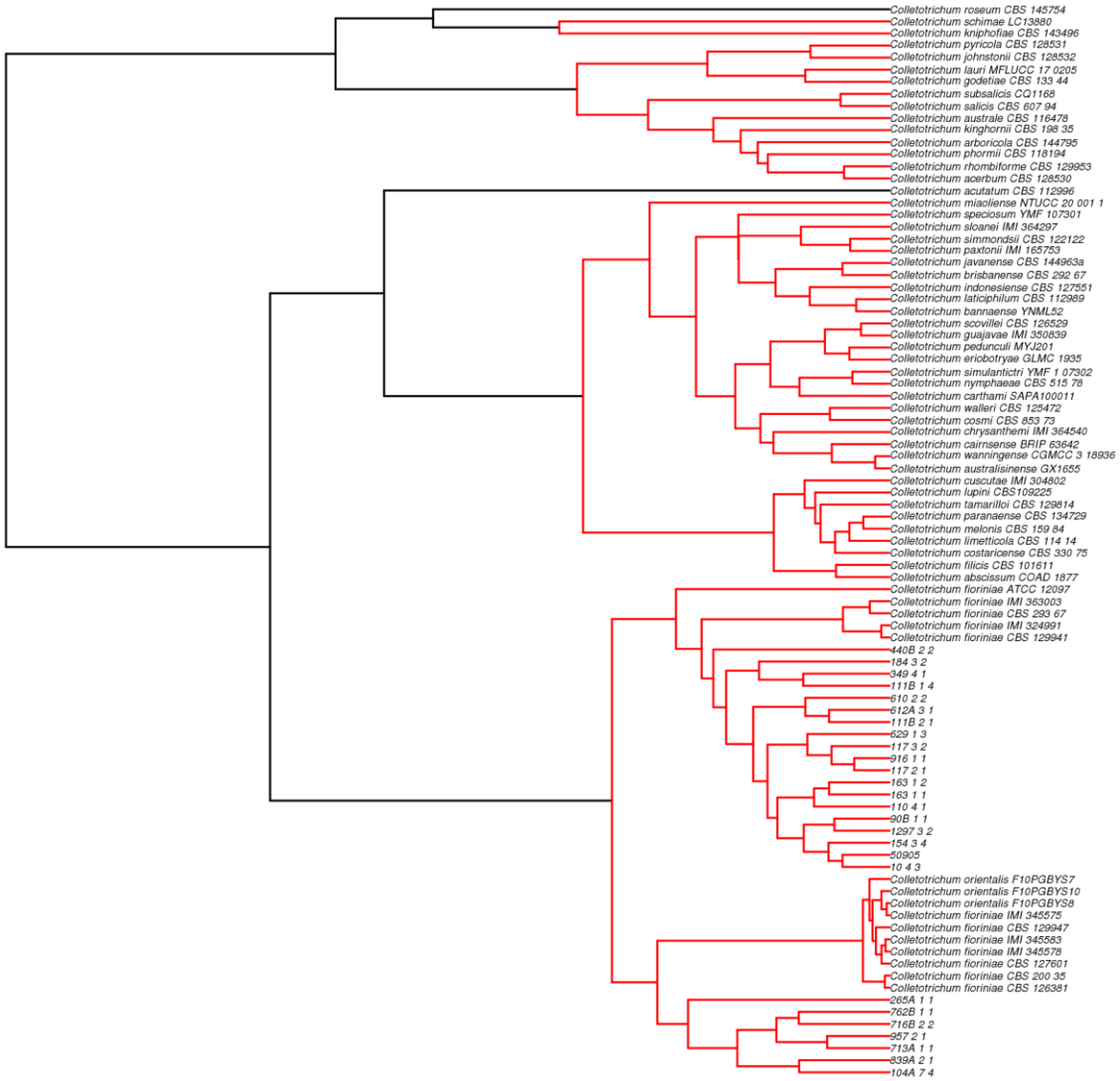


Figure 5 – The clustering result based on the single-threshold method of GMYC. Putative species clusters are indicated using transitions between black-colored to red-colored branches. The inter- and intraspecific portions of the tree are divided with a vertical line.

In the *Colletotrichum gloeosporioides* species complex (Figs 18, 19), 22 strains clustered with *C. gloeosporioides* showing high support values (MBP = 97, PP = 1.00) in the six-locus phylogenetic tree, *C. citrulli* Z. Guo, H. J. Wu, B. Peng, C. X. Luo, Q. S. Gu also clustered into this clade (Fig. 18). The strains CNUCC 5-21-2-1 and CNUCC 5-21-2-2 formed an independent clade with high support values (six-locus MBP = 79, PP = 1.00; two-locus MBP = 100, PP = 1.00). Twenty-nine strains clustered with *Colletotrichum fructicola* and *C. mengyinense* T.C. Mu, J.W. Xia, X.G. Zhang & Z. Li in one clade (six-locus MBP = 74, PP = 1.00; two-locus MBP = 59, PP = 1.00). Five strains (CNUCC 221A-1-1, CNUCC 1297-3-3, CNUCC 257-2-4, CNUCC 781-1-2, and CNUCC 742A-1-1), and *C. camelliae* Massee clustered in the same clade with high support values (MBP = 89, PP = 1.00) in six-locus phylogenetic tree, and *C. analogum* Z.F. Yu also clustered in this clade. Two strains (CNUCC 823-1-1-1 and CNUCC 823-1-1-2) formed a high support clade (six-locus MBP = 100, PP = 1.00; two-locus MBP = 99, PP = 1.00). Thirteen strains clustered with *Colletotrichum cangyuanense* Z.F. Yu and had high support values (six-locus MBP = 100, PP = 1.00; two-locus MBP = 96, PP = 1.00). Five strains (CNUCC 163-2-1, CNUCC 409B-3-2, CNUCC 898-1-1, CNUCC 71C-2-2, and CNUCC 90C-4-2) clustered with the *C. henanense* clade, which

was not well-supported in the six-locus phylogenetic tree (MBP = 64, PP = 0.97) but had high support in the two-locus phylogenetic tree (MBP = 100, PP = 1.00) (Fig. 19), and the sequences of *C. yulongense* C.L. Hou & X.T. Liu also clustered in this clade.

In the *Colletotrichum orchidearum* species complex (Fig. 20), the strain CNUCC 942-2-4-1 and *C. sojae* Damm & Alizadeh clustered with a clade with high support values (MBP = 100, PP = 1.00). Five strains (CNUCC 811A-1-1, CNUCC 833B-1-1, CNUCC 175C-1-3, CNUCC 184-5-5, and CNUCC 824-1-2) formed a highly supported clade (MBP = 98, PP = 1.00), sister to *Colletotrichum plurivorum* Damm, Alizadeh & Toy. Sato (MBP = 98, PP = 1.00), and based on the result of PHI testing no significant recombination events could be detected between these two clades (Φw = 0.7341) (Fig. 21).

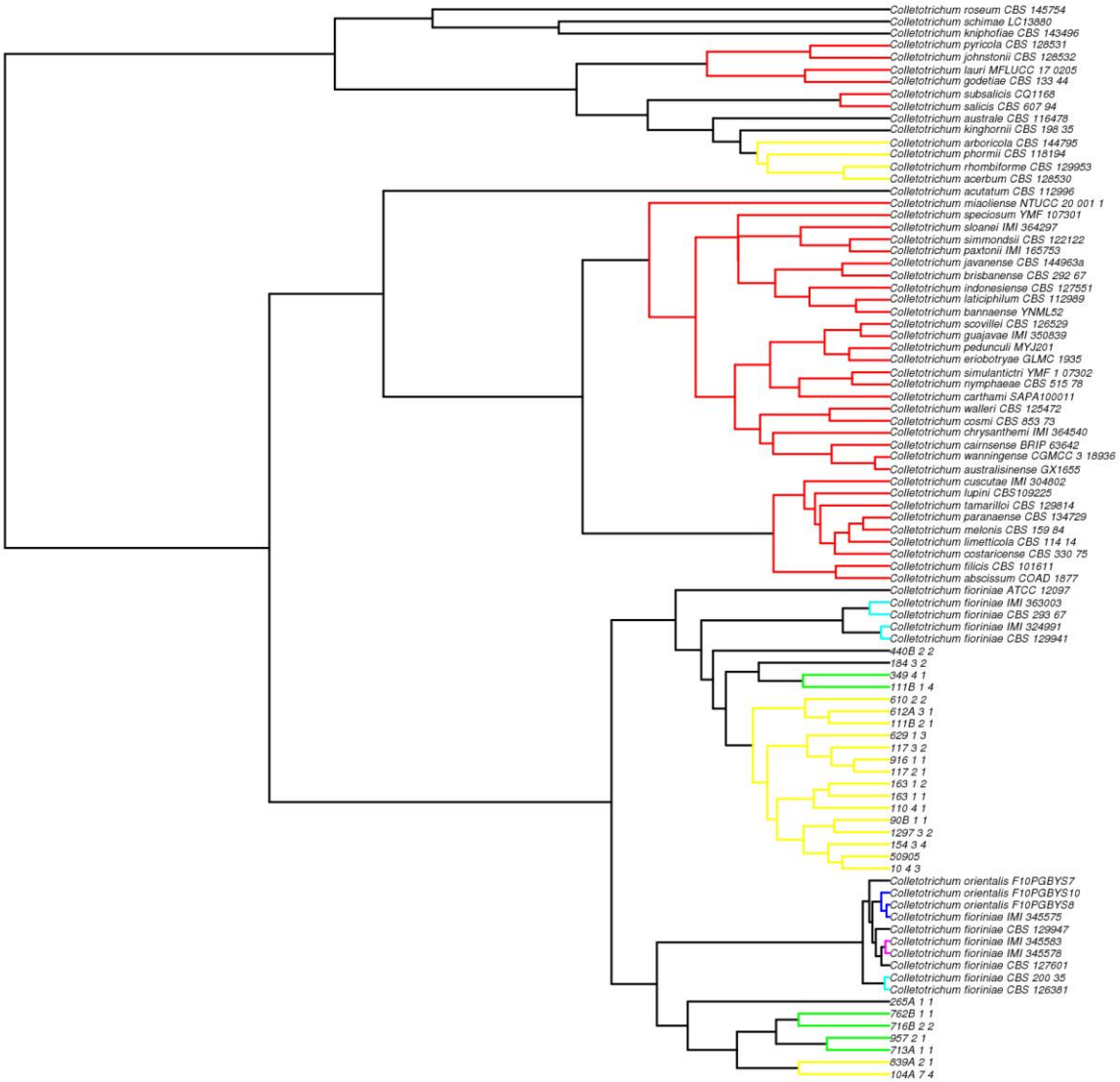


Figure 6 – The clustering result based on the multi-threshold method of GMYC. Putative species clusters are indicated using transitions between black-colored to red-colored branches. The inter- and intraspecific portions of the tree are divided with a vertical line.

In the *Colletotrichum truncatum* species complex (Fig. 22), the strain CNUCC 764B-2 clustered with *Colletotrichum subacidae* F. Liu, Z.Y. Ma & L. Cai, but did not have high support (Fig. 22). PHI test results Φw < 0.05 (Φw = 0.0297) (Fig. 23) indicate significant recombination within the dataset.

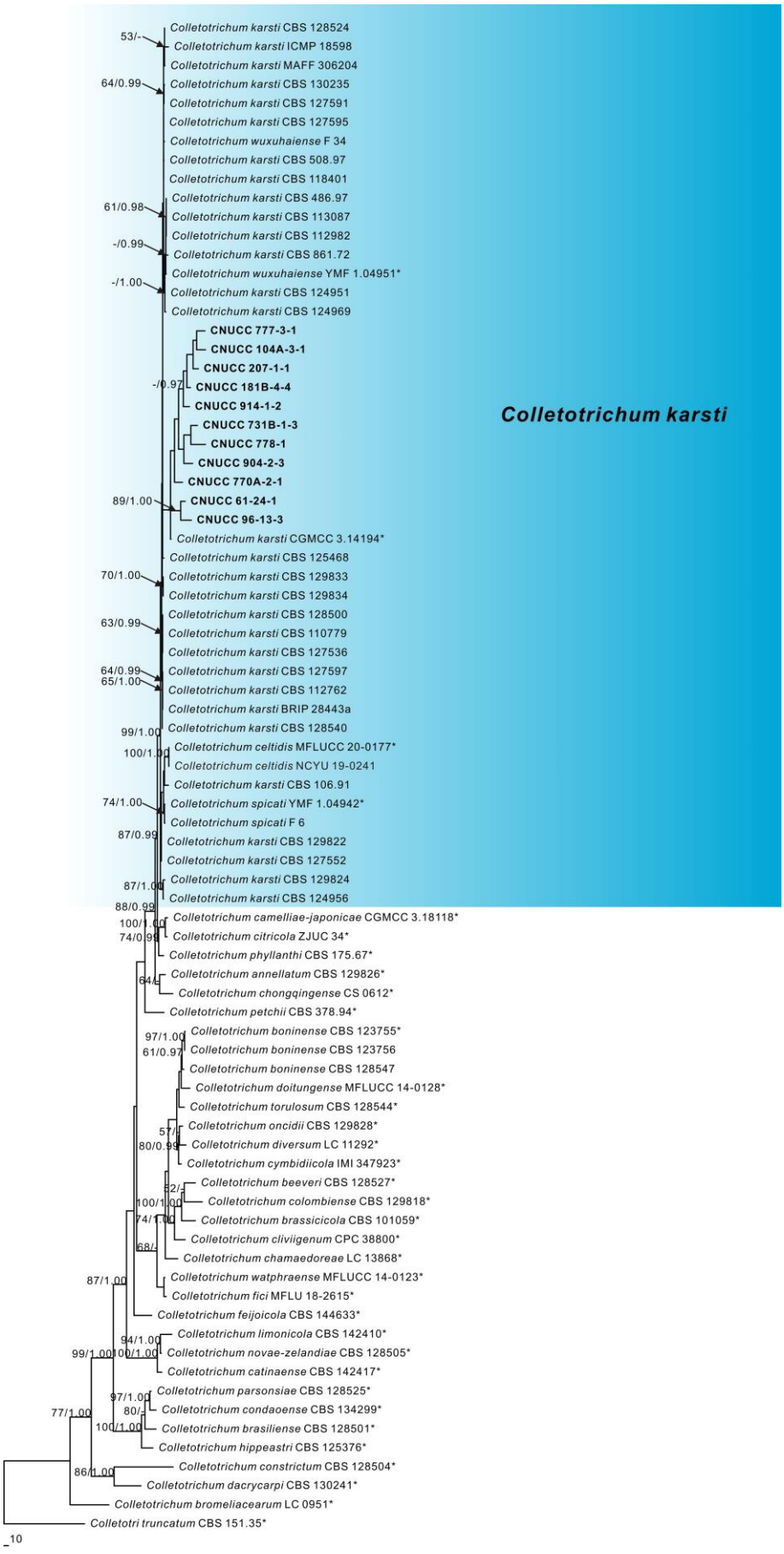


Figure 7 – Phylogenetic tree of *Colletotrichum boninense* species complex derived from maximum parsimony analysis of the combined ITS–*gapdh*–*chs-1*–*act*–*his3*–*tub*–*cal* sequences, using

C. truncatum (CBS 151.35) as the outgroup. Maximum parsimony bootstrap values (BP > 50%) and bayesian posterior probabilities (PP > 0.95) are shown above or below the branches. Type species strains are marked with an " * ". Newly generated sequences are represented in **bold**.

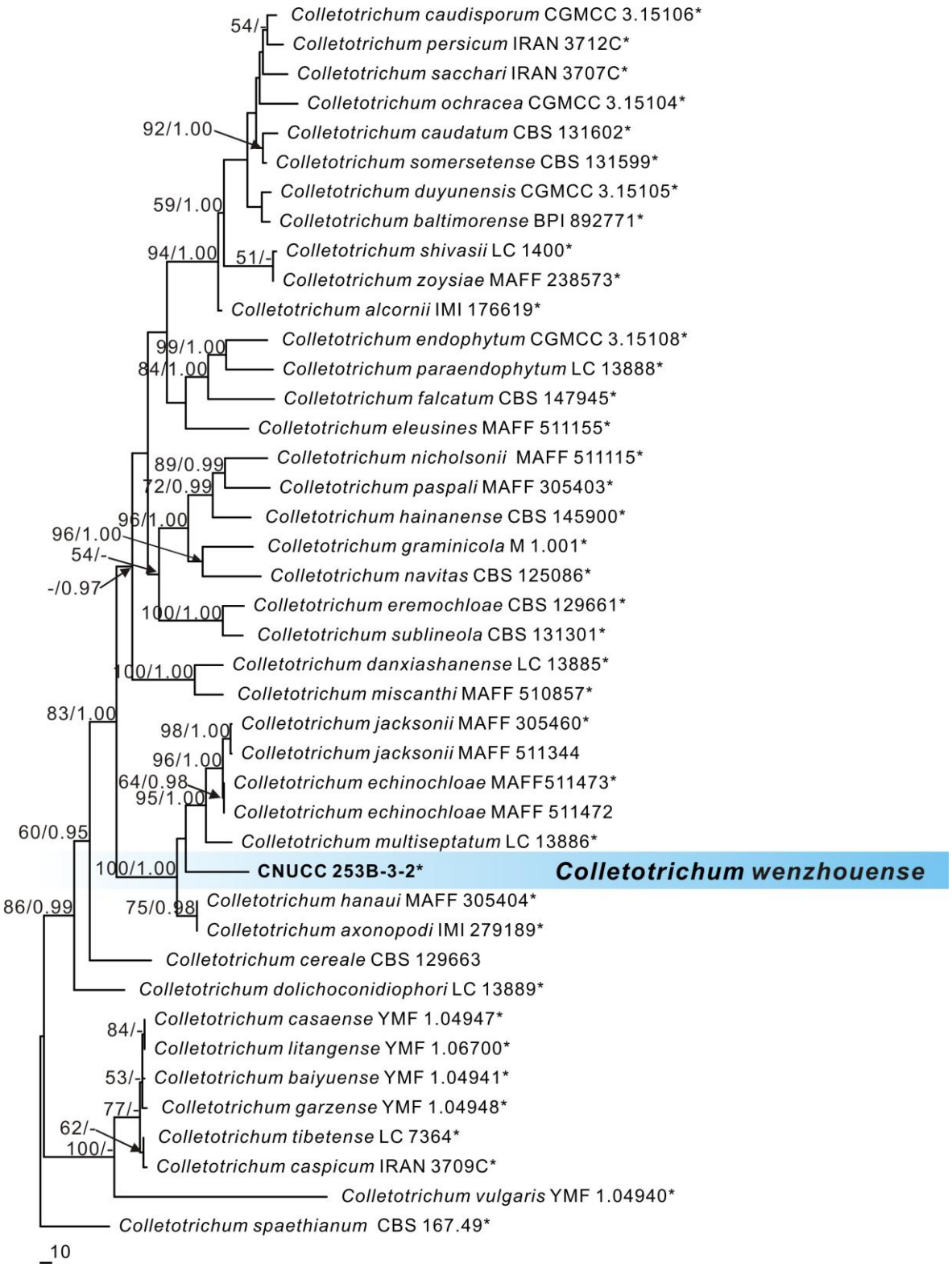


Figure 8 – Phylogenetic tree of *Colletotrichum caudatum-graminicola* species complex derived from maximum parsimony analysis of the combined *act–chs-1*–ITS–*sod2–tub* sequences, using *C. spaethianum* (CBS 167.49) as the outgroup. Maximum parsimony bootstrap values (BP > 50%) and bayesian posterior probabilities (PP > 0.95) are shown above or below the branches. Type species strains are marked with an " * ". Newly generated sequences are represented in **bold**.

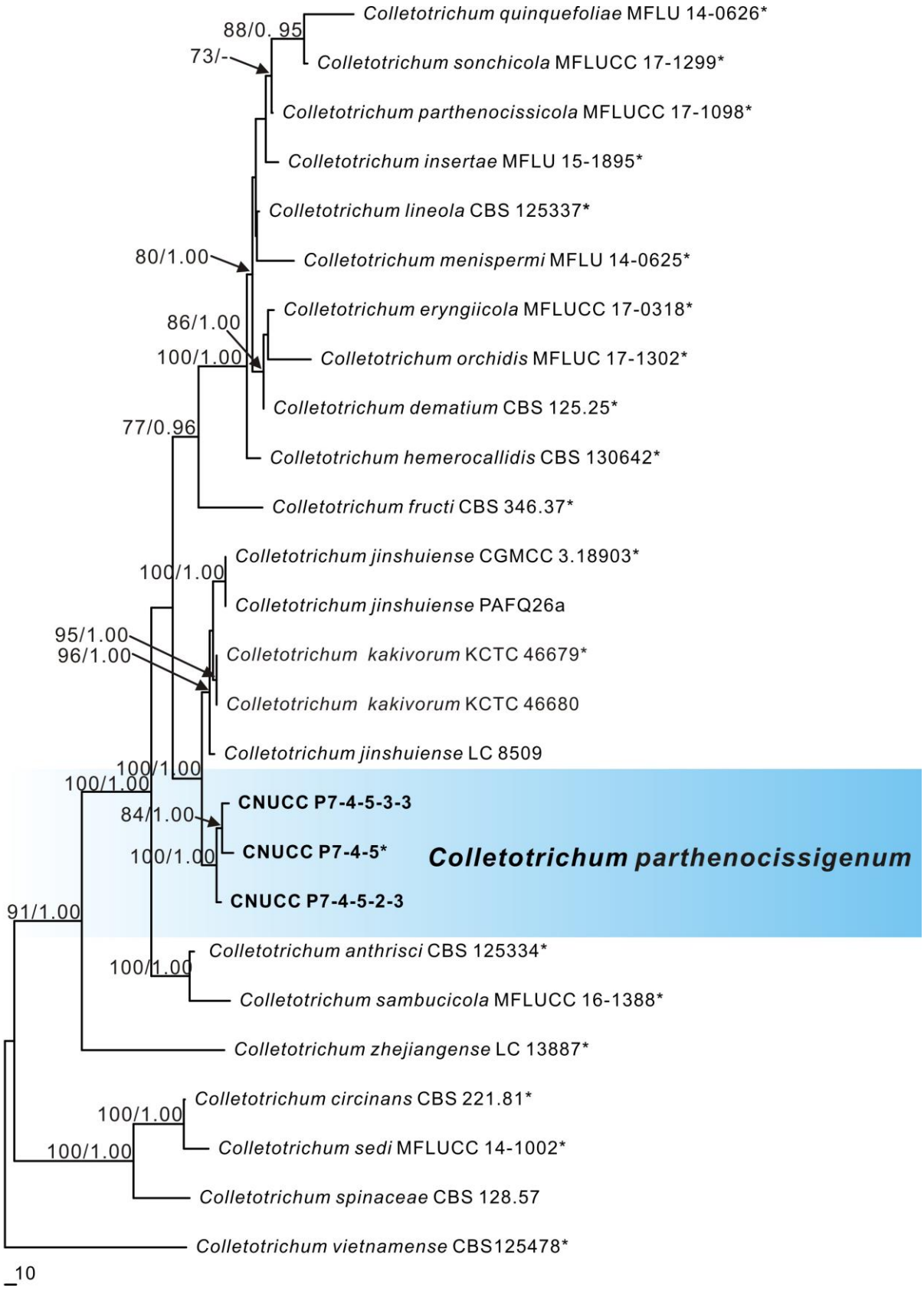


Figure 9 – Phylogenetic tree of *Colletotrichum dematium* species complex derived from maximum parsimony analysis of the combined *act–chs-1–gapdh–his3*–ITS–*tub* sequences, using *C. vietnamense* (CBS 125478) as the outgroup. Maximum parsimony bootstrap values (BP > 50%) and bayesian posterior probabilities (PP > 0.95) are shown above the branches. Type species strains are marked with an " * ". Newly generated sequences are represented in **bold**.

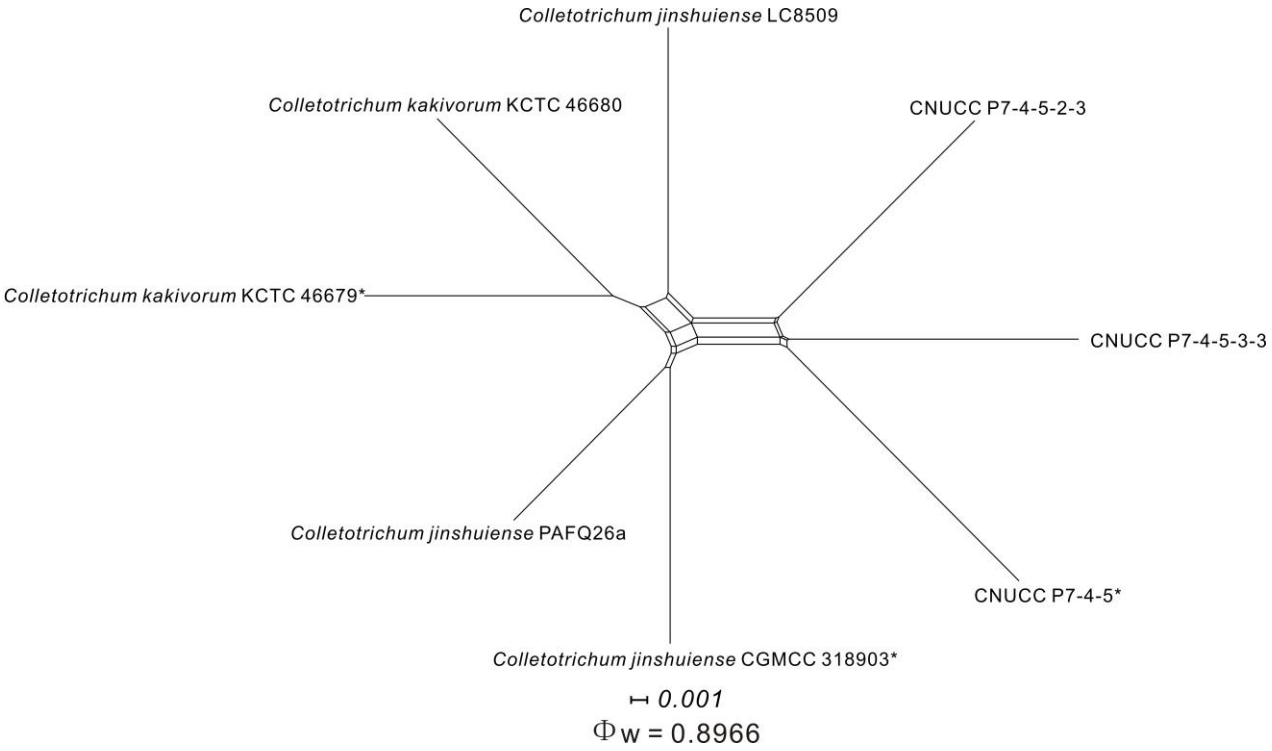


Figure 10 – The result of the pairwise homoplasy index (PHI) tests for closely related species of *Colletotrichum jinshuiense* and *C. jinshuiense* using both LogDet transformation and splits decomposition.

Taxonomy

Colletotrichum cunninghamiae Q.T. Wang, X.N. Sui & C.L. Hou, sp. nov. Fig. 23

MycoBank number: MB853832; Facesoffungi number: FoF15942

Etymology – The epithet is derived from the genus of the host plant, *Cunninghamia lanceolata*.

Typification – CHINA. Hubei Province, Xiangyang City, Longzhong Scenic Area, on leaves of *Cunninghamia lanceolata*, Feb. 2017, C.L. Hou & Q.T. Wang (holotype CAF 8000205). Ex-type CNUCC 58-57-2.

Colonies on PDA 54–58 mm diam. in 7 days, flat with entire edge, both sides are white (#ffffff), aerial mycelium sparse but dense in the margin. On SNA amended with pine needle, conidiomata acervular, scattered or gregarious, semi-immersed. *Conidial masses* very soft orange (#fae9c6), produced from conidiomata. *Vegetative hyphae* hyaline, smooth-walled, septate, branched. Setae medium brown, smooth-walled, 2-septate, 94–114 μm long, basal cells cylindrical to slightly conical, 3.5–5.5 μm diam., the tip ± acute. *Conidiophores* hyaline, solitary, septate, usually reduced to conidiogenous cells. *Conidiogenous cells* hyaline, aseptate, smooth-walled, cylindrical to ampulliform, 18.5–50 × 2.5–4.5 μm. *Conidia* hyaline, aseptate, smooth-walled, straight, cylindrical, both ends truncate or one end round and the other truncate, 15.0–19.0 × 3.5–4.5 μm (av. ± SD = 17.1 ± 0.9 × 4.0 ± 0.2 μm), L/W ratio = 4.2. *Appressoria* single, pale brown to medium brown, ellipsoidal, subglobose or irregular outline, with entire or undulate margin, 5.0–8.5 × 3.5–7.5 μm (av. ± SD = 7.0 ± 1.0 × 5.7 ± 0.8 μm), L/W ratio = 1.2.

Other specimens examined – CHINA. Hubei Province, Xiangyang City, Longzhong Scenic area, on leaves of *Cunninghamia lanceolata*, Feb. 2017, C.L. Hou & Q.T. Wang, living culture CNUCC 58-61-2.

Notes – This species is phylogenetically related to *Colletotrichum higginsianum* Sacc., *C. vignae* Damm, *C. bryoniicola* Damm, *C. fuscum* Laubert, and *Colletotrichum antirrhinicola* Damm in the *C. destructivum* species complex. For morphology, *Colletotrichum cunninghamiae*

differs from the closest species *C. higginsianum* in producing shorter conidia than the latter (15.0–19.0 µm vs. 19–20.5 µm) (Damm et al. 2014). Although in morphology, this species is

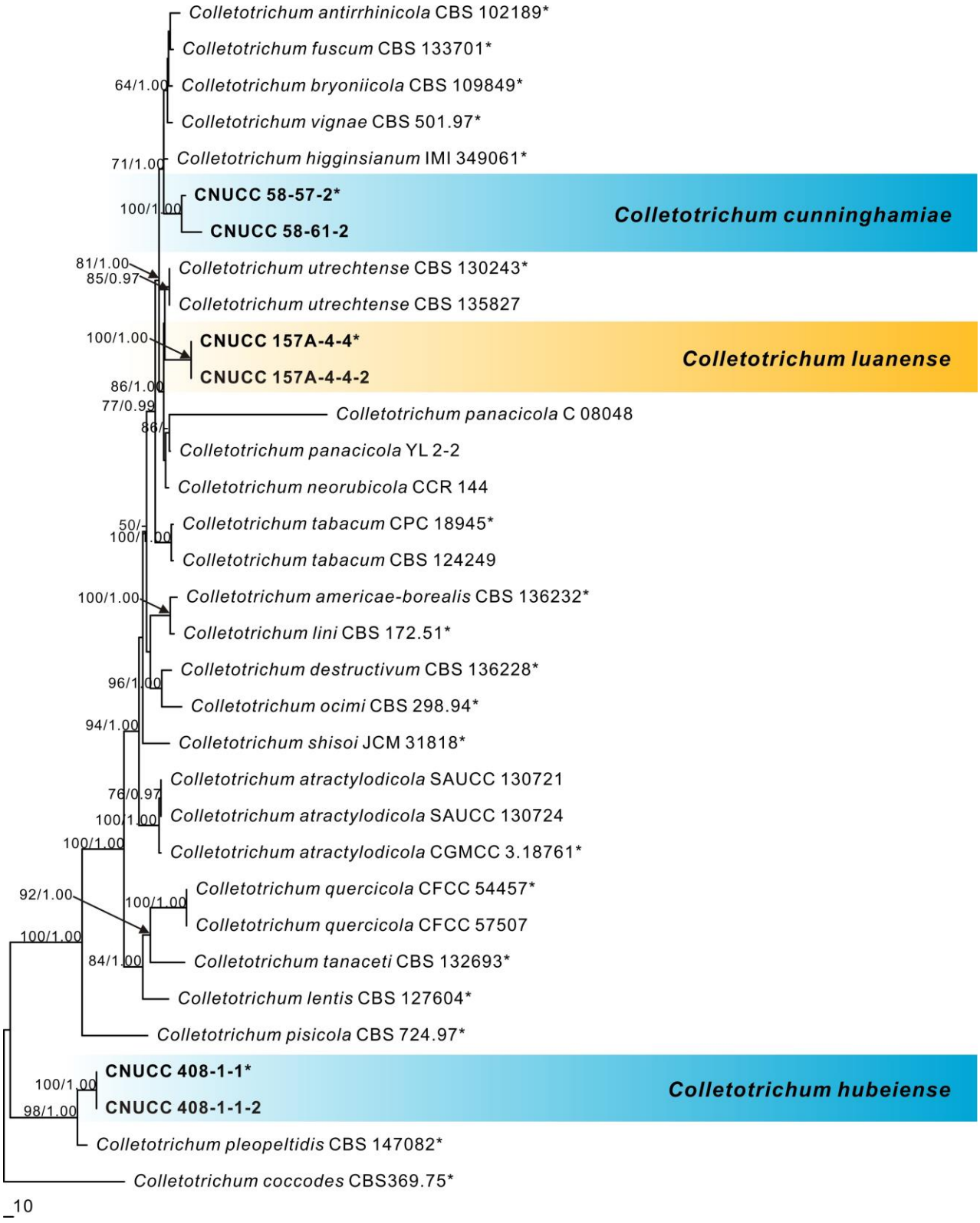


Figure 11 – Phylogenetic tree of *Colletotrichum destructivum* species complex derived from maximum parsimony analysis of the combined *act–chs-1–gapdh–his3*–ITS–*tub2* sequences, using *C. coccodes* CBS 369.75 as outgroup. Maximum parsimony bootstrap values (BP > 50%) and bayesian posterior probabilities (PP > 0.95) are shown above or below the branches. Type species strains are noted with an " * ". Newly generated sequences are represented in **bold**.

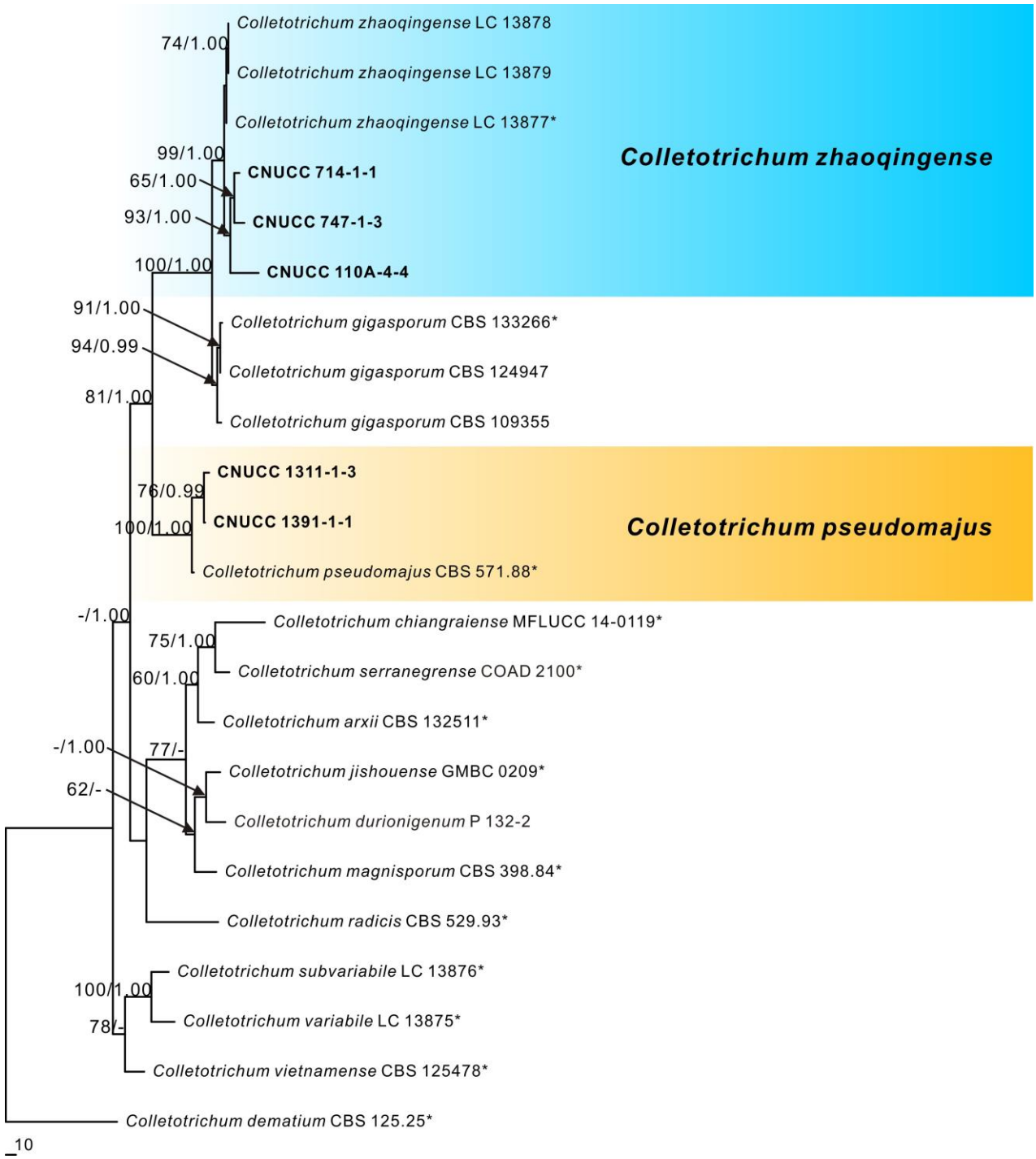


Figure 12 – Phylogenetic tree of *Colletotrichum gigasporum* species complex derived from maximum parsimony analysis of the combined ITS–*gapdh*–*chs-1*–*act*–*tub2* sequences, using *C. dematium* CBS 125.25 as outgroup. Maximum parsimony bootstrap values (BP > 50%) and bayesian posterior probabilities (PP > 0.95) are shown above the branches. Type species strains are noted with an " * ". Newly generated sequences are represented in **bold**.

similar with *Colletotrichum vignae* (Damm et al. 2014), *C. bryoniicola* (Damm et al. 2014), *C. fuscum* (Damm et al. 2014), and *C. antirrhinicola* (Damm et al. 2014), the sequence similarities of *act*, *chs-1*, *gapdh*, and *his3* are very low (*C. cunninghamiae* to *C. vignae*: *act* 97.88%, *chs-1* 98.47%, *gapdh* 96.18%, *his3* 97.81%, to *C. bryoniicola*: *act* 98.31%, *chs-1* 98.09%, *gapdh* 96.82%, *his3* 97.81%, to *C. fuscum*: *chs-1* 98.47%, *gapdh* 96.18%, *his3* 97.54%, ITS 99.09%, and to *C. antirrhinicola*: *act* 98.31%, *chs-1* 98.47%, *gapdh* 95.57%, *his3* 97.54%).

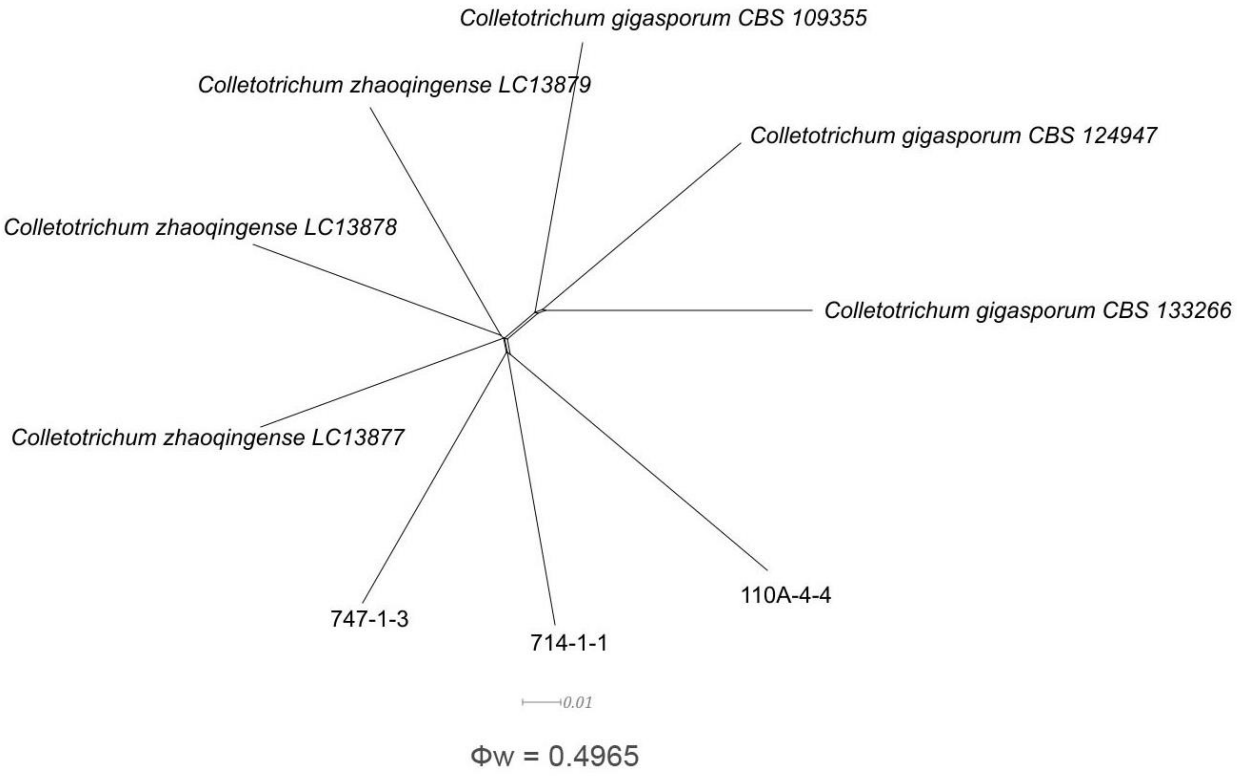


Figure 13 – The result of the pairwise homoplasy index (PHI) tests for closely related species of *Colletotrichum zhaoqingense* and *C. gigasporum* using both LogDet transformation and splits decomposition.

Colletotrichum guiyangense Q.T. Wang, M.J. Guo & C.L. Hou, sp. nov. Fig. 24

MycoBank number: MB853885; Facesoffungi number: FoF15943

Etymology – Referring to the Guiyang City where the host plants were collected.

Typification – CHINA. Guizhou Province, Guiyang City, Xifeng County, on leaves of *Camellia sinensis*, Aug. 2021, C.L. Hou & Q.T. Wang (holotype CAF 8000206). Ex-type CNUCC 823-1-1-1.

Colonies on PDA 58–64 mm diam. in 7 days, flat with entire edge, dark grayish lime green (#a2a4a2), with white (#ffffff) margin, aerial mycelium dense, reverse very dark (mostly black) lime green (#002700) in the center, grayish yellow (#b9b9ad) towards margin, with white margin. On CMA, conidiomata not developed, conidiophores formed directly on hyphae. *Vegetative hyphae* hyaline to pale brown, smooth-walled, septate, branched. *Setae* not observed. *Conidiophores* hyaline, solitary, usually reduced to conidiogenous cells. *Conidiogenous cells* hyaline, aseptate, smooth-walled, ampulliform to cylindrical, 15.5–35.5 × 2.0–3.0 μm. *Conidia* hyaline, aseptate, smooth-walled, slightly narrower in the middle, oblong-ovoid, the base is wider than the top, 11.5–16.5 × 4.0–5.5 μm (av. ± SD = 14.2 ± 1.2 × 4.6 ± 0.3 μm), L/W ratio = 3.1. *Appressoria* single or gregarious, pale brown to medium brown, ellipsoidal or irregularly shaped, 8.5–14 × 4.5–7.5 μm (av. ± SD = 11 ± 1.7 × 5.8 ± 0.6 μm), L/W ratio = 1.9. On CMA with pine needle, ascomata ellipsoidal, gregarious, light brown to slightly desaturated orange (#d5a87a), outer wall composed of pale brown to medium brown angular cells, 8–18.5 μm diam. *Asci* cylindrical to obclavate, hyaline, 42–77 × 7–10 μm, 8-spored. *Ascospores* uniseriately or irregularly arranged, hyaline, smooth-walled, aseptate, allantoid with rounded ends, slightly curved, 13–18 × 4.5–6 μm (av. ± SD = 15.6 ± 1.4 × 5.3 ± 0.3 μm), L/W ratio = 2.9.

Other specimens examined – CHINA. Guizhou Province, Guiyang City, Xifeng County, on leaves of *Camellia sinensis*, Aug. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 823-1-1-2.

Notes – This species belongs to the *Colletotrichum gloeosporioides* species complex, and is characterized by its oblong-ovoid conidia. BLASTn search of this species sequences in the NCBI GenBank revealed low sequence similarities with other species in *apmat*, *gapdh*, and *gs*, the closest matches of *apmat*, *gapdh*, and *gs* sequences are *Colletotrichum arecicola* X.R. Cao, H.Y. Che & D.Q. Luo (98.39%), *C. arecicola* (97.61%), and *C. cigarro* (B.S. Weir & P.R. Johnst.) A. Cabral & P. Talhinhas (98.53%), respectively.

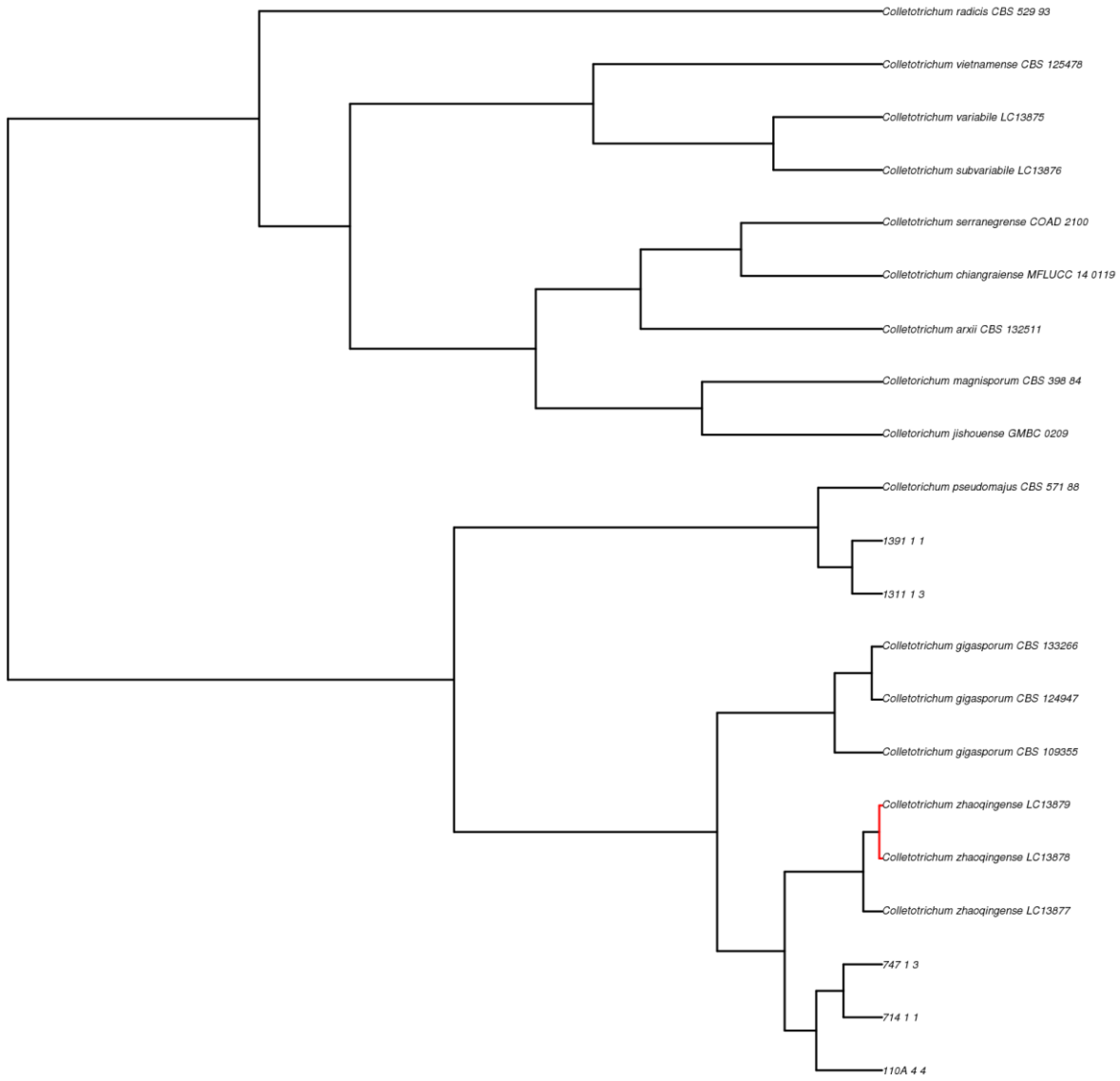


Figure 14 – The clustering result based on the single-threshold method of GMYC. Putative species clusters are indicated using transitions between black-colored to red-colored branches. The inter- and intraspecific portions of the tree are divided with a vertical line.

Colletotrichum hubeiense X.N. Sui, M.J. Guo & C.L. Hou, sp. nov. Fig. 25

MycoBank number: MB853886; Facesoffungi number: FoF15936

Etymology – Referring to the Hubei Province where the host plants were collected.

Typification – CHINA. Hubei Province, Shennongjia Forestry District, on leaves of *Lindera glauca* (Siebold & Zucc.) Blume, May 2019, C.L. Hou & Q.T. Wang (holotype CAF 8000207). Ex-type CNUCC 408-1-1.

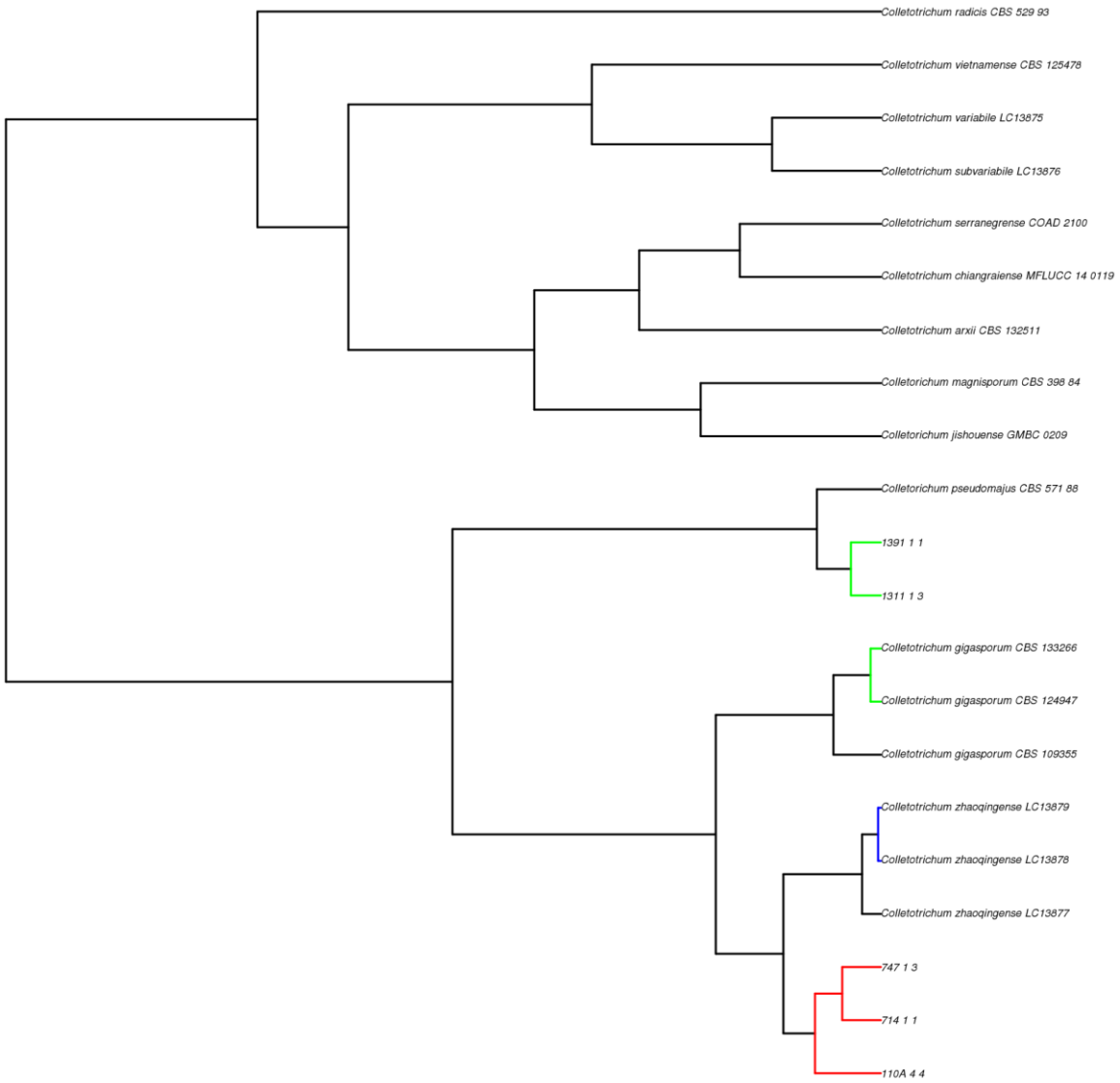


Figure 15 – The clustering result based on the multi-threshold method of GMYC. Putative species clusters are indicated using transitions between black-colored to red-colored branches. The inter- and intraspecific portions of the tree are divided with a vertical line.

Colonies on PDA 43–50 mm diam. in 7 days, flat with entire edge, white (#ffffff) to grayish yellow (#b3af98), aerial mycelium dense, reverse very dark lime green (#041004) in the center, grayish yellow (#b3af98) to margin, with white (#ffffff) margin. On PDA, conidiomata scattered or gregarious, black. *Conidial masses* grayish yellow (#bfbfb5), produced from conidiomata. *Vegetative hyphae* hyaline, smooth-walled, septate, branched. Setae pale brown, smooth-walled, 2–3-septate, 116–242 µm long, basal cells cylindrical, 5.0–6.0 µm diam., the tip ± acute. *Conidiophores* solitary or branched, septate, hyaline to pale brown. *Conidiogenous cells* hyaline to pale brown, aseptate, smooth-walled, ampulliform to cylindrical, 21–56 × 3.0–4.0 µm. Conidia hyaline, aseptate, smooth-walled, straight, cylindrical, one end round and the other truncate, 15–19.5 × 4.5–5.0 µm (av. ± SD = 17.1 ± 1.0 × 4.7 ± 0.1 µm), L/W ratio = 3.6. *Appressoria* single, pale brown to medium brown, mostly irregularly shaped, with undulate to lobate margin, sometimes elliptical with an entire margin, 9.5–18 × 5.5–7.0 µm (av. ± SD = 13.6 ± 3.0 × 6.3 ± 0.5 µm), L/W ratio = 2.2.

Other specimens examined – CHINA. Hubei Province, Shennongjia Forestry District, on leaves of *Lindera glauca*, May 2019, C.L. Hou & Q.T. Wang (holotype CAF 8000207). Ex-type culture CNUCC 408-1-1-2.

Notes – *Colletotrichum hubeiense* is phylogenetically related to *C. pleopeltidis*, but shares low sequences similarities at *act* (94.21%), *chs-1* (95.83%), and ITS (97.51%). Morphologically, *C. hubeiense* differs from *C. pleopeltidis* in producing shorter conidia (15–19.5 μm vs. 19–23μm) (Crous et al. 2021).

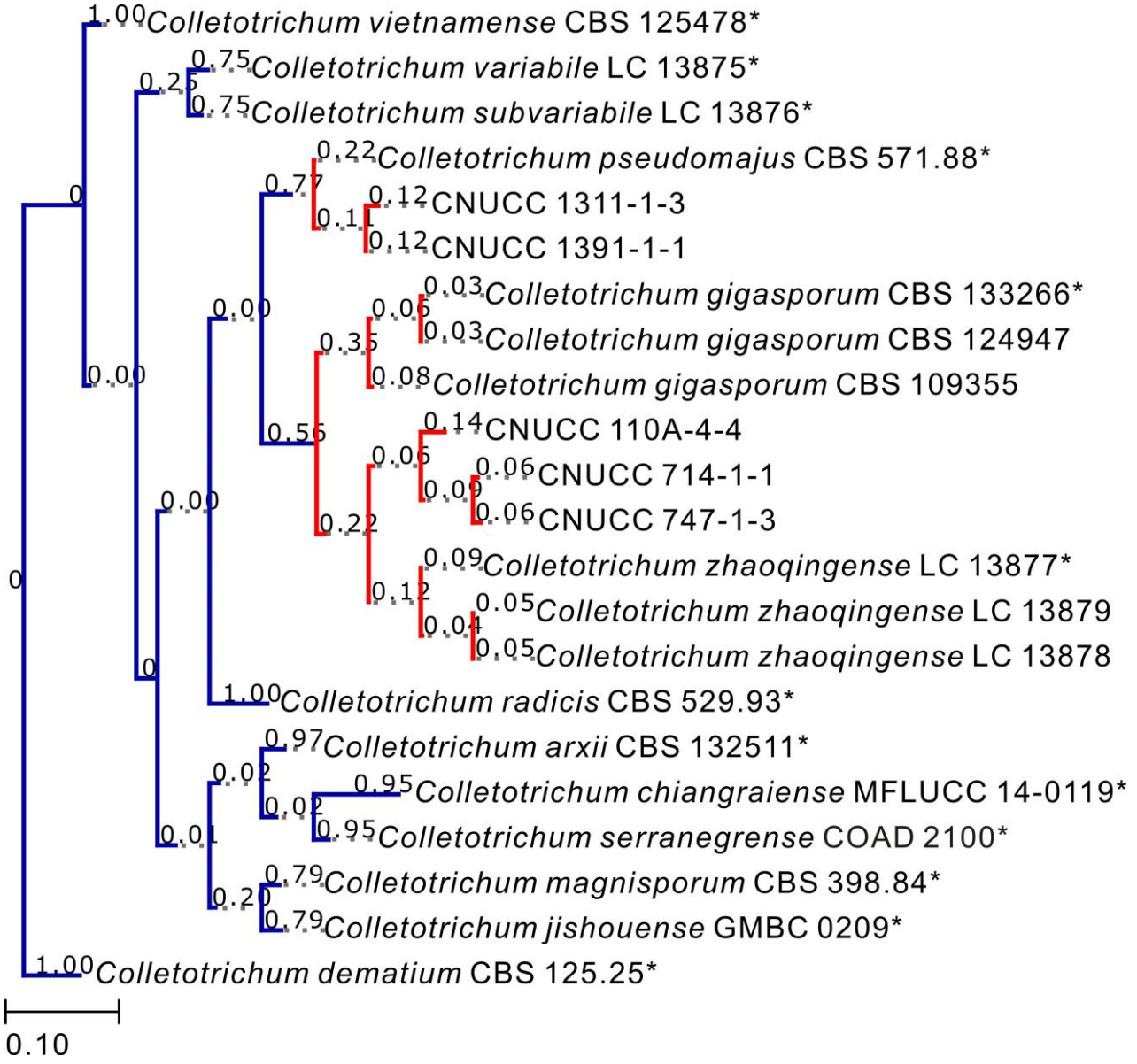


Figure 16 – Results of the bPTP analysis based on the ML topologies. Putative species clusters are indicated using transitions between blue-colored to red-colored branches.

Colletotrichum jixiense X.N. Sui, M.J. Guo & C.L. Hou, sp. nov. Fig. 26

MycoBank number: MB853887; Facesoffungi number: FoF15937

Etymology – Referring to the Jixi County in Anhui Province where the host plants were collected.

Typification – CHINA. Anhui Province, Xuancheng City, Jixi County, on leaves of *Cunninghamia lanceolata*, Oct. 2016, C.L. Hou & Q.T. Wang (holotype CAF 8000208). Ex-type CNUCC 5-21-2-1.

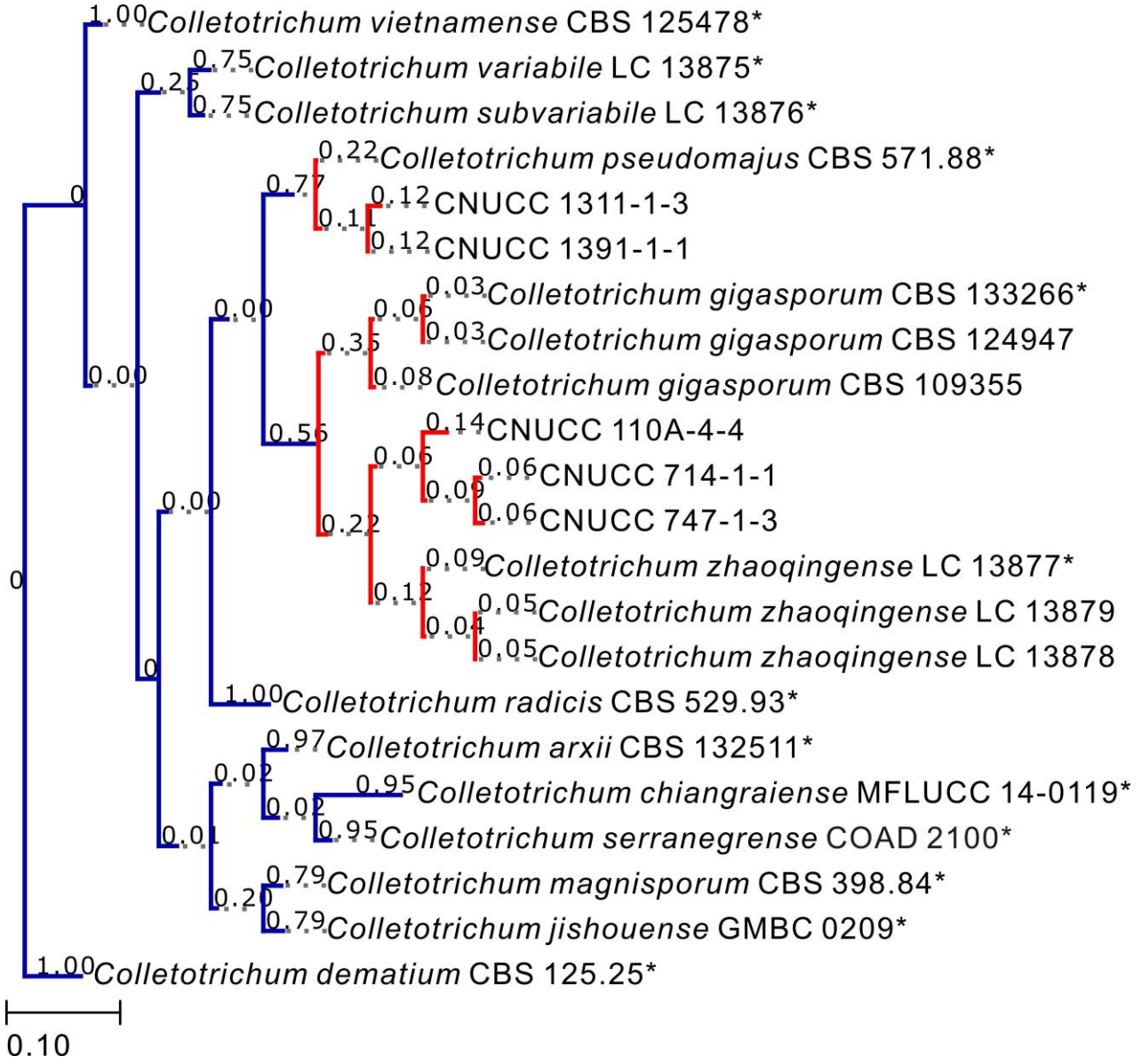


Figure 17 – Results of the bPTP analysis based on the BI. Putative species clusters are indicated using transitions between blue-colored to red-colored branches.

Colonies on PDA 50–55 mm diam. in 7 days, flat with entire edge, white (#ffffff) in the center, dark grayish yellow (#aeaca0) towards margin, with white margin, aerial mycelium dense, reverse white in the center, very light orange (#ffd589) to grayish yellow (#d1d0c9) towards margin, with white margin. On OA, conidiomata not developed, conidiophores formed directly on hyphae. *Vegetative hyphae* hyaline, smooth-walled, septate, branched. Setae not observed. *Conidiophores* hyaline, solitary, usually reduced to conidiogenous cells. *Conidiogenous cells* hyaline, aseptate, smooth-walled, ampulliform, 6.5–11.5 × 2.0–3.0 µm. *Conidia* hyaline, aseptate, smooth-walled, straight, ellipsoidal to cylindrical, both ends rounded, 12.0–15.0 × 5.5–7.0 µm (av. ± SD = 13.4 ± 0.8 × 6.2 ± 0.4 µm), L/W ratio = 2.2. *Appressoria* single or gregarious, medium brown to dark brown, ellipsoidal or irregularly shaped, with entire or lobed margin, 8.0–12 × 5.5–7.5 µm (av. ± SD = 9.5 ± 1.1 × 6.6 ± 0.5 µm), L/W ratio = 1.4.

Other specimens examined – CHINA. Anhui Province, Xuancheng City, Jixi County, on leaves of *Cunninghamia lanceolata*, Oct. 2016, C.L. Hou & Q.T. Wang, living culture CNUCC 5-21-2-2.

Notes – *Colletotrichum jixiense* belongs to the *C. gloeosporioides* species complex. In the six-locus phylogenetic tree, *Colletotrichum jixiense* has a close relationship with *C. perseae*

G. Sharma & S. Freeman. In the two-locus phylogenetic tree, this species forms an independent clade with high support (MPB = 100, PP = 1.00). However, the sequence similarities of *act* and *gapdh* of this species with *Colletotrichum perseae* are very low, with 96.61% similarity for the *act* gene and 98.70% similarity for the *gapdh* gene. For morphology, the conidia of *C. jixiense* (12.0–15.0 μm) are shorter than those of *C. perseae* (13.0–19.0 μm) (Sharma et al. 2017).

Colletotrichum luanense Q.T. Wang, X.N. Sui & C.L. Hou, sp. nov. Fig. 27

MycoBank number: MB853888; Facesoffungi number: FoF15938

Etymology – Referring to the Lu'an City where the host plants were collected.

Typification – CHINA. Anhui Province, Lu'an City, Shucheng County, on leaves of *Camellia sinensis*, May 2018, C.L. Hou & Q.T. Wang (holotype CAF 8000209). Ex-type CNUCC 157A-4-4.

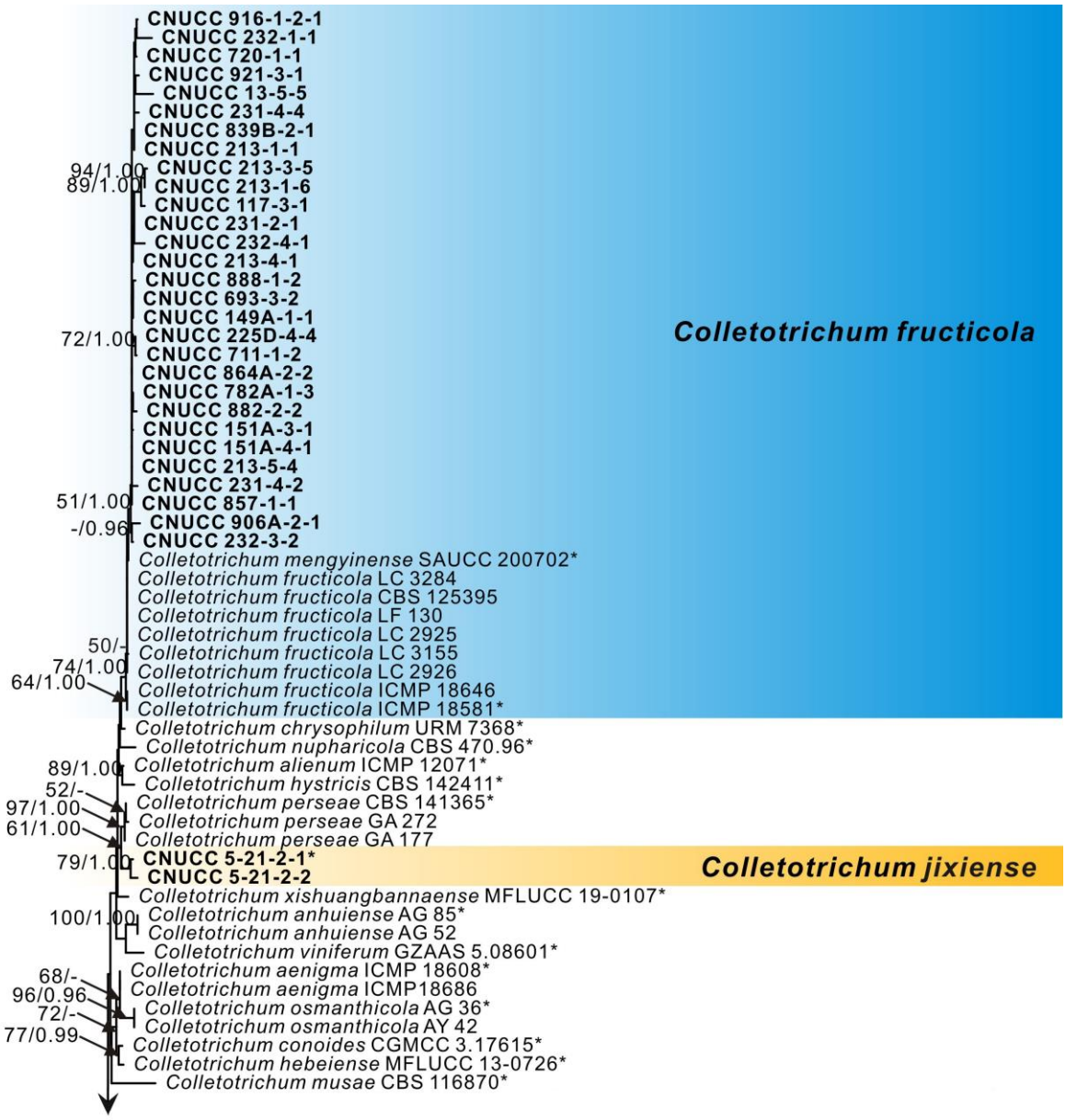


Figure 18 – Phylogenetic tree of *Colletotrichum gloeosporioides* species complex derived from maximum parsimony analysis of the combined *act–tub2–cal–chs-1–gapdh*–ITS sequences, using *C. boninense* (CBS 123755) as the outgroup. Maximum parsimony bootstrap values (BP > 50%) and bayesian posterior probabilities (PP > 0.95) are shown above or below the branches. Type species strains are noted with an " * ". Newly generated sequences are represented in **bold**.

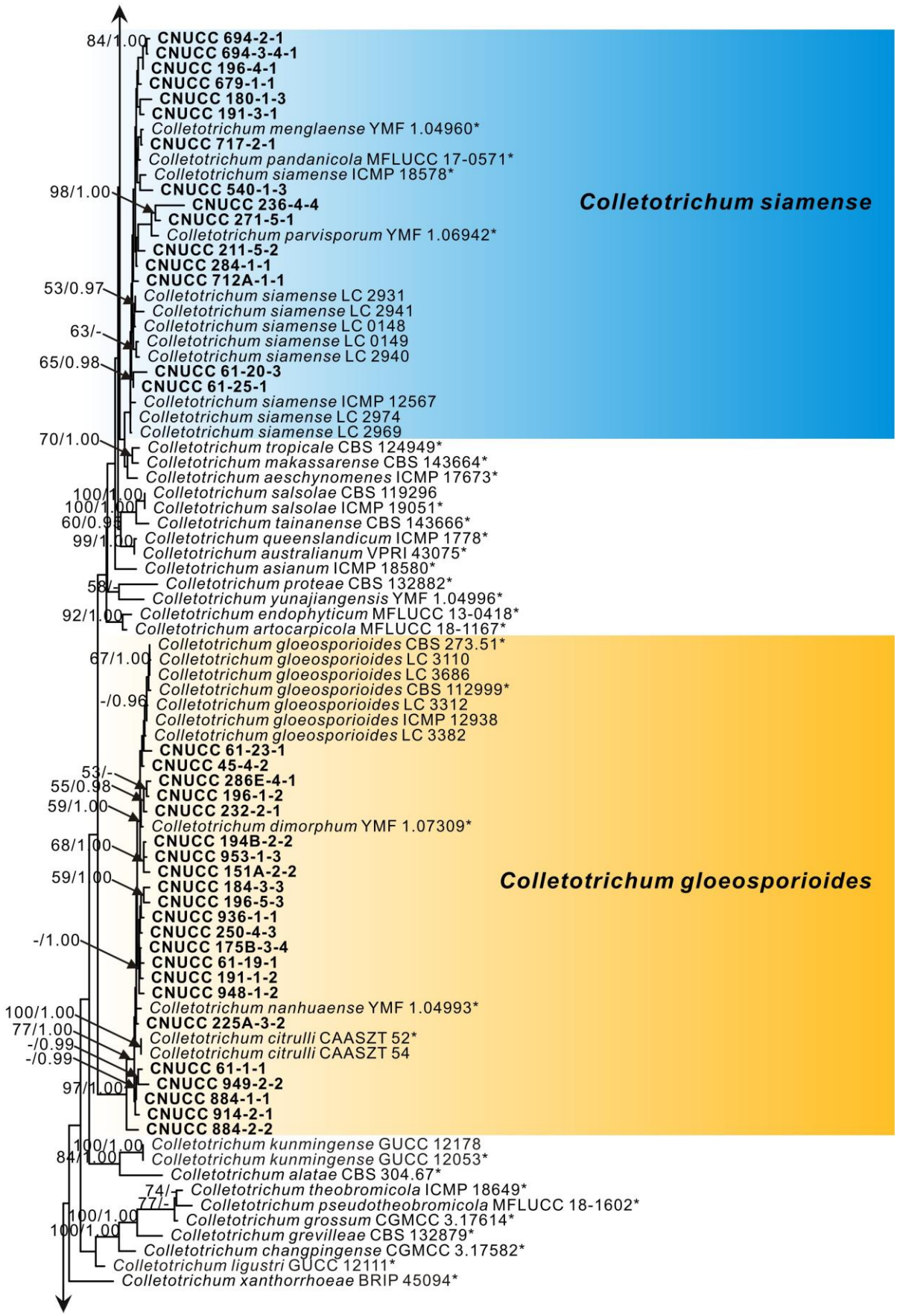


Figure 18 – Continued.

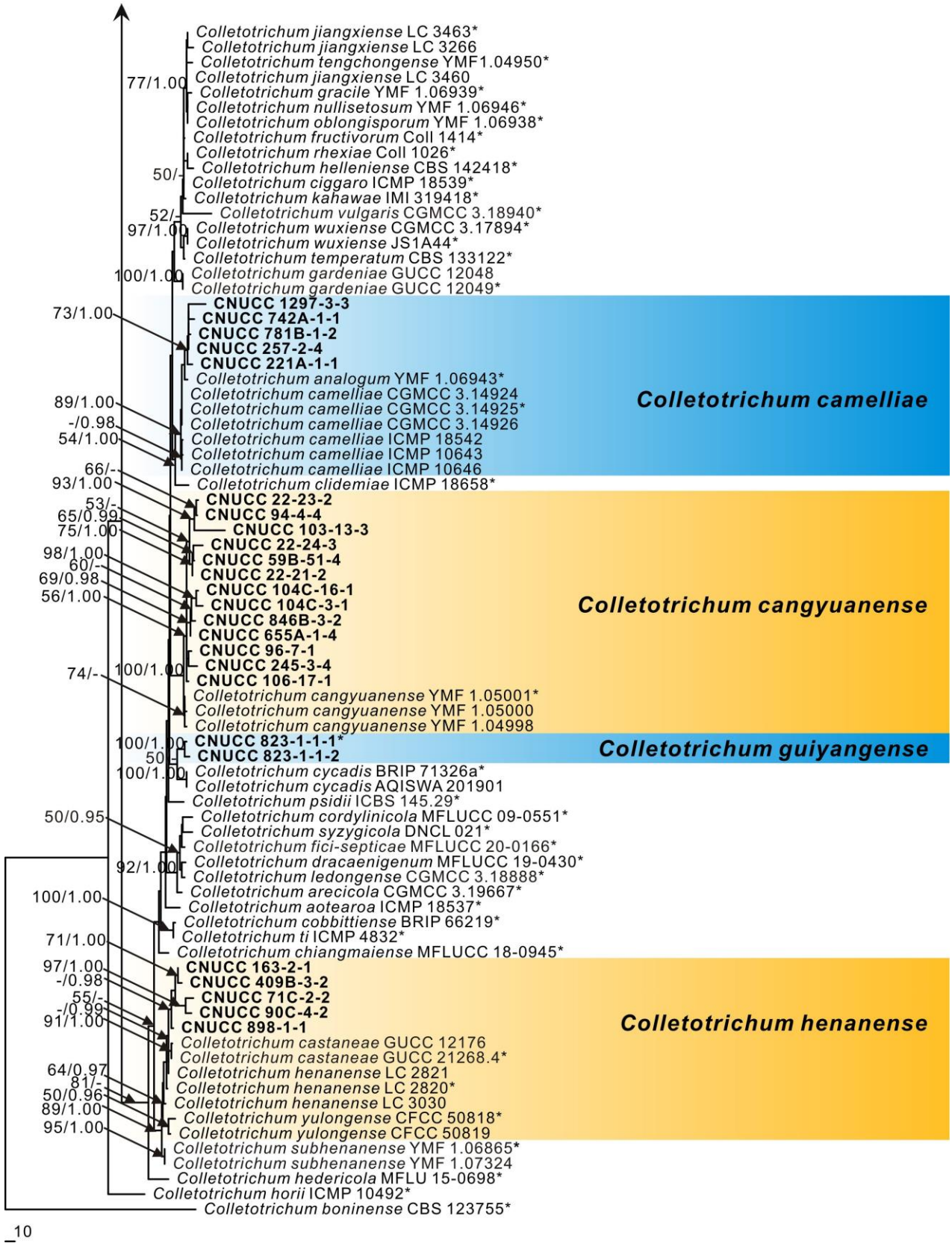


Figure 18 – Continued.

Colonies on PDA 48–63 mm diam. in 7 days, flat with entire edge, whole white (#ffffff), aerial mycelium dense, reverse olive tone (#1e1900) in the center and white (#ffffff) towards margin. On CMA amended with pine needle, conidiomata not developed, conidiophores formed directly on

hyphae. *Vegetative hyphae* hyaline, smooth-walled, septate, branched, with very light orange (#fff8eb) conidial mass. *Setae* not observed. *Conidiophores* hyaline, usually reduced to conidiogenous cells. *Conidiogenous cells* hyaline, aseptate, smooth-walled, cylindrical to ampulliform, 8.5–30 × 2.5–5.5 µm. *Conidia* hyaline, aseptate, smooth-walled, straight, cylindrical, one end round and the other slightly acute, 12–16.5 × 4–4.5 µm (av. ± SD = 14.2 ± 1.0 × 4.2 ± 0.2 µm), L/W ratio = 3.4. *Appressoria* single, pale brown to medium brown, irregularly shaped, with entire undulate or lobed margin, 7.5–13.5 × 3.5–10.5 µm (av. ± SD = 10.5 ± 1.9 × 6.6 ± 2.1 µm), L/W ratio = 1.6.

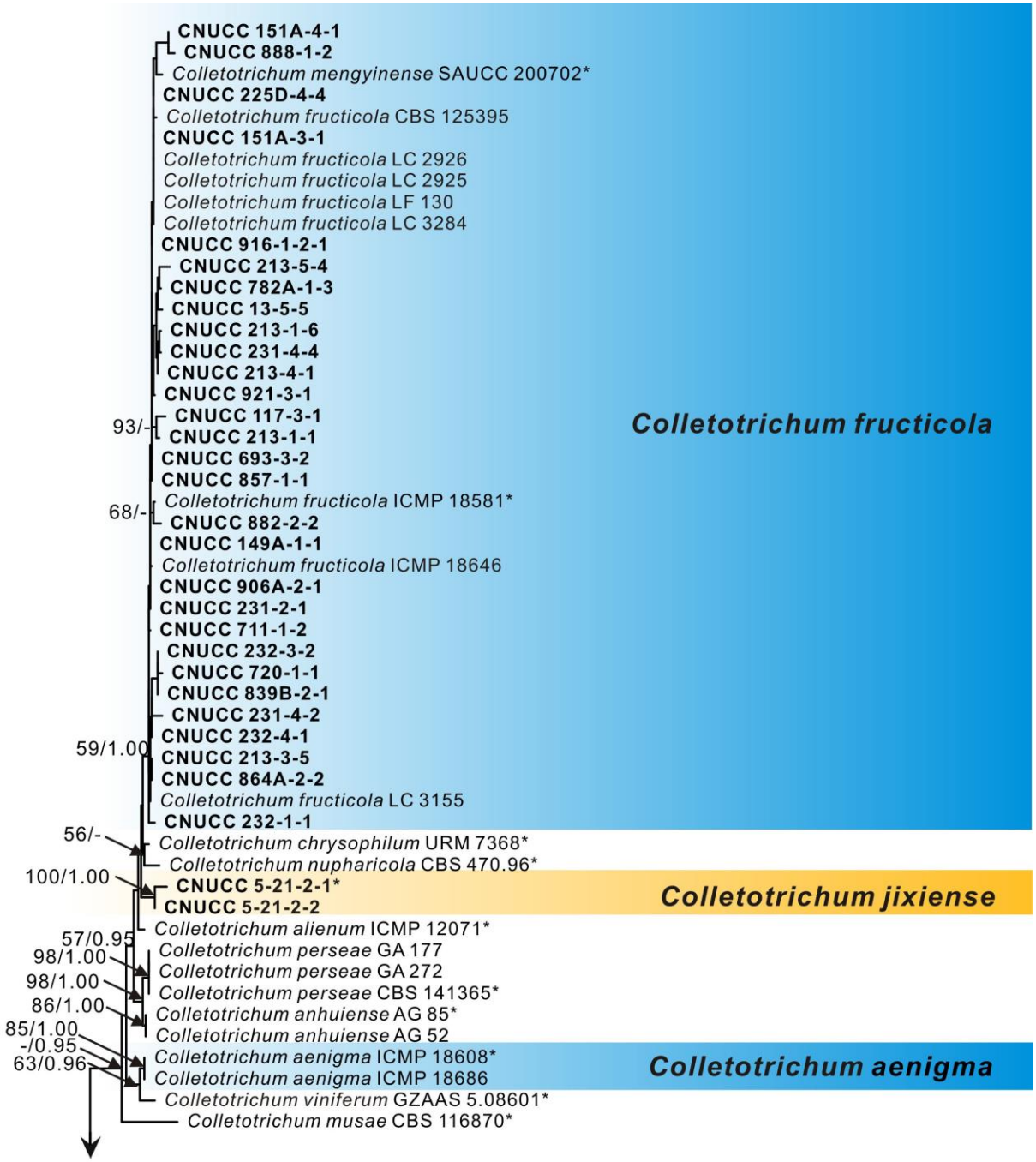


Figure 19 – Phylogenetic tree of *C. gloeosporioides* species complex derived from maximum parsimony analysis of the combined *apmat–gs* sequences, using *Colletotrichum xanthorrhoeae* ICMP 17903 as outgroup. Maximum parsimony bootstrap values (BP > 50%) and bayesian posterior probabilities (PP > 0.95) are shown above or below the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.

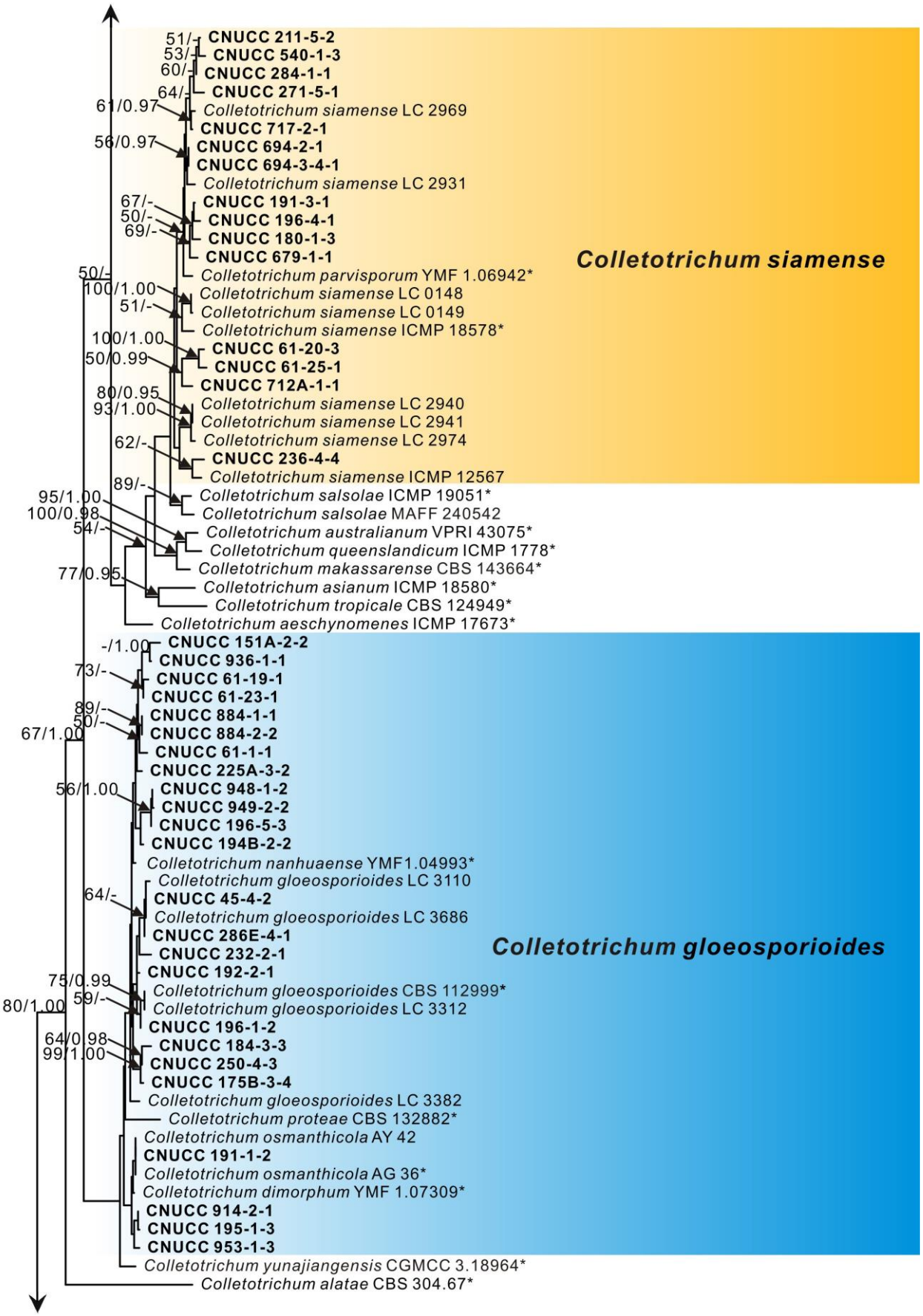


Figure 19 – Continued.

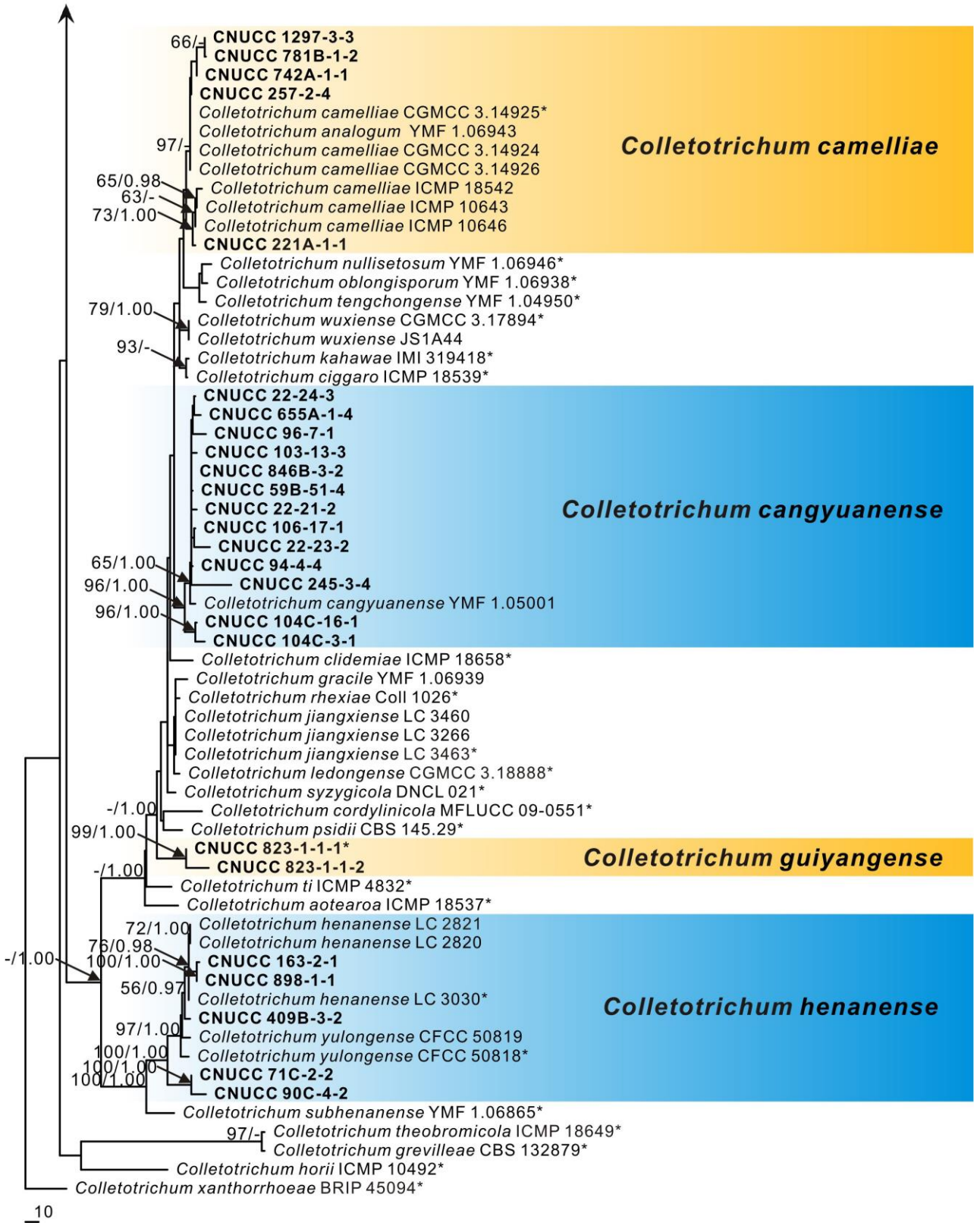


Figure 19 – Continued.

Other specimens examined – CHINA. Anhui Province, Lu'an City, Shucheng County, on leaves of *Camellia sinensis*, May 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 157A-4-4-2.

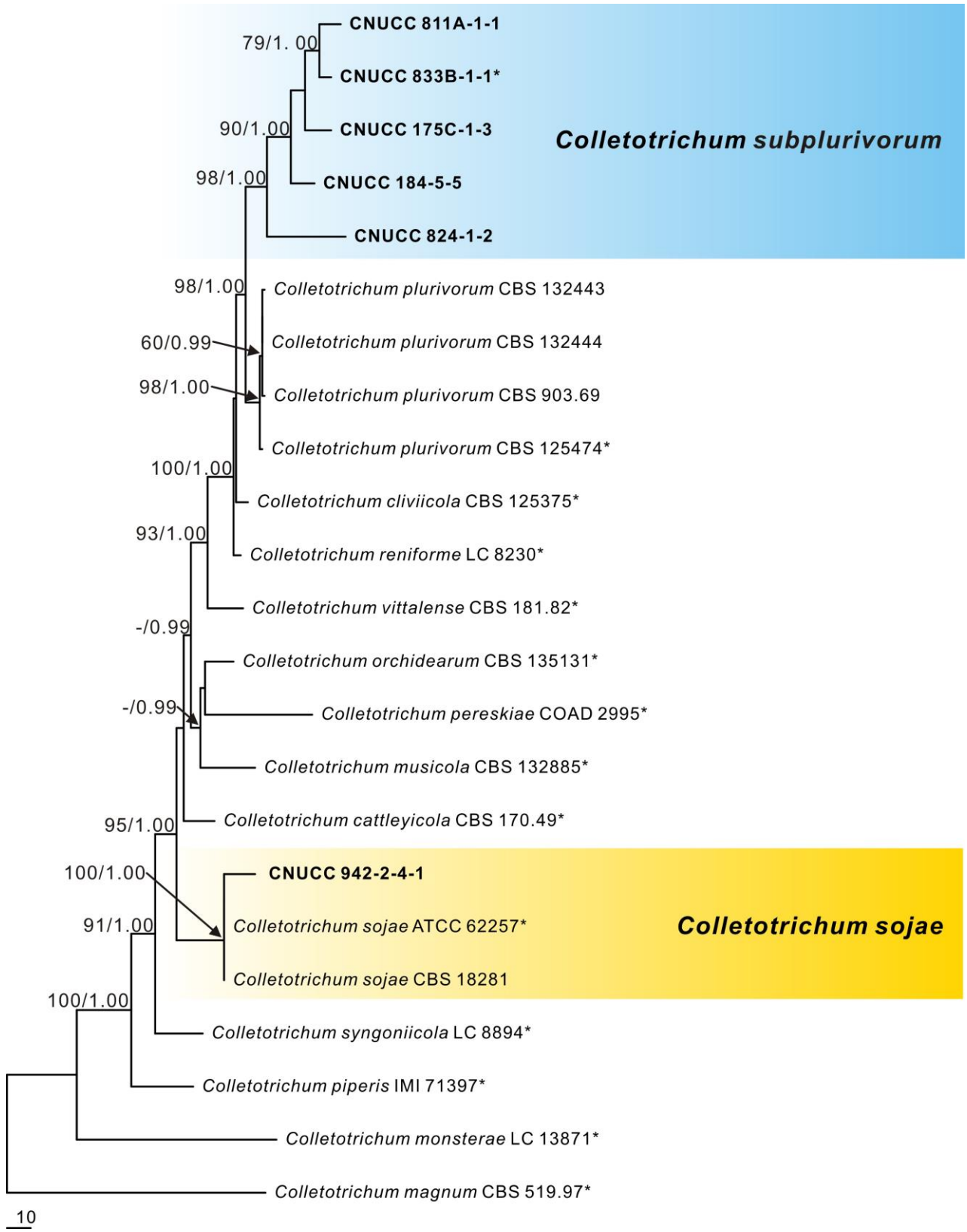


Figure 20 – Phylogenetic tree of *Colletotrichum orchidearum* species complex derived from maximum parsimony analysis of the combined *act–chs-1–gapdh–his3*–ITS–*tub* sequences, using *C. magnum* (CBS 519.97) as the outgroup. Maximum parsimony bootstrap values (BP > 50%) and bayesian posterior probabilities (PP > 0.95) are shown above the branches. Type species strains are noted with an " * ". Newly generated sequences are represented in **bold**.

Notes – *Colletotrichum luanense* is phylogenetically related to *C. panacicola*, *C. neorubicola*, and *C. utrechtense* in the *C. destructivum* species complex. However, the sequence similarities of *act* and *gapdh* of type strain are low, which are 97.99%–98.40% and 98.09%–98.73%, respectively. For morphology, although the conidia of these four species are cylindrical, the conidial length of *Colletotrichum luanense* is significantly smaller than those of the other three species (*C. neorubicola* 7.5–20.5 μm, *C. panacicola* 17.0–22.1 μm, *C. utrechtense* 14.8–23.5 μm) (Liu et al. 2020a, Liu et al. 2020b, Damm et al. 2014).

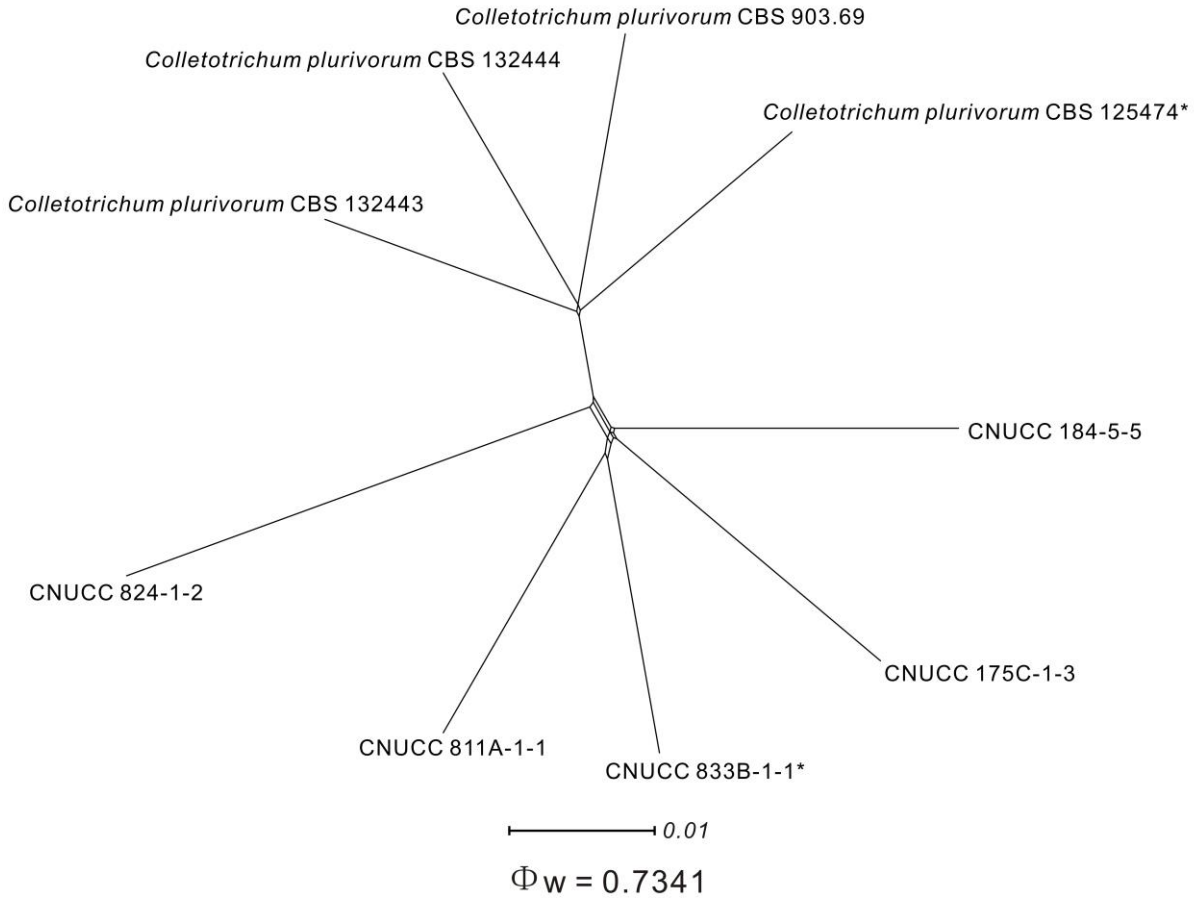


Figure 21 – The result of the pairwise homoplasy index (PHI) tests for *Colletotrichum plurivorum* and closely related species of *C. plurivorum* using both LogDet transformation and splits decomposition.

Colletotrichum parthenocissigenum Q.T. Wang, M.J. Guo & C.L. Hou, sp. nov. Fig. 28

MycoBank number: MB853889; Facesoffungi number: FoF15939

Etymology – The species epithet is derived from the family of the host plant, *Parthenocissus tricuspidate*.

Typification – CHINA. Anhui Province, Jingde City, Yunle County, on leaves of *Parthenocissus tricuspidata*, Apr. 2016, C.L. Hou & Q.T. Wang (holotype CAF 8000210). Ex-type CNUCC P7-4-5.

Colonies on PDA 48–49 mm diam. in 7 days, flat with entire edge, both sides are white (#ffffff), aerial mycelium dense. On OA amended with pine needle, conidiomata scattered, black, with setae. *Vegetative hyphae* hyaline to pale brown, smooth-walled, septate, branched. *Setae* dark brown, mostly 3–4-septate, 89–123 μm long, basal cells cylindrical or conical, smooth-walled, 5.5–7.5 μm diam., tip acute. *Conidiophores* formed from a cushion of roundish to angular medium brown cells, usually reduced to conidiogenous cells. *Conidiogenous cells* hyaline, aseptate, smooth-

walled, ampulliform, 13–18 × 3–4.5 µm. *Conidia* hyaline, aseptate, smooth-walled, reniform, with acute ends, or one end acute and the other rounded, 12–16 × 4–5.5 µm (av. ± SD = 13.9 ± 1.5 × 5 ± 0.4 µm), L/W ratio = 2.8. *Appressoria* single, pale to medium brown, clavate or irregularly shaped, with an entire margin, sometimes undulate, 10–17 × 4–6.5 µm (av. ± SD = 13.4 ± 2.2 × 5.4 ± 0.7 µm), L/W ratio = 2.5.

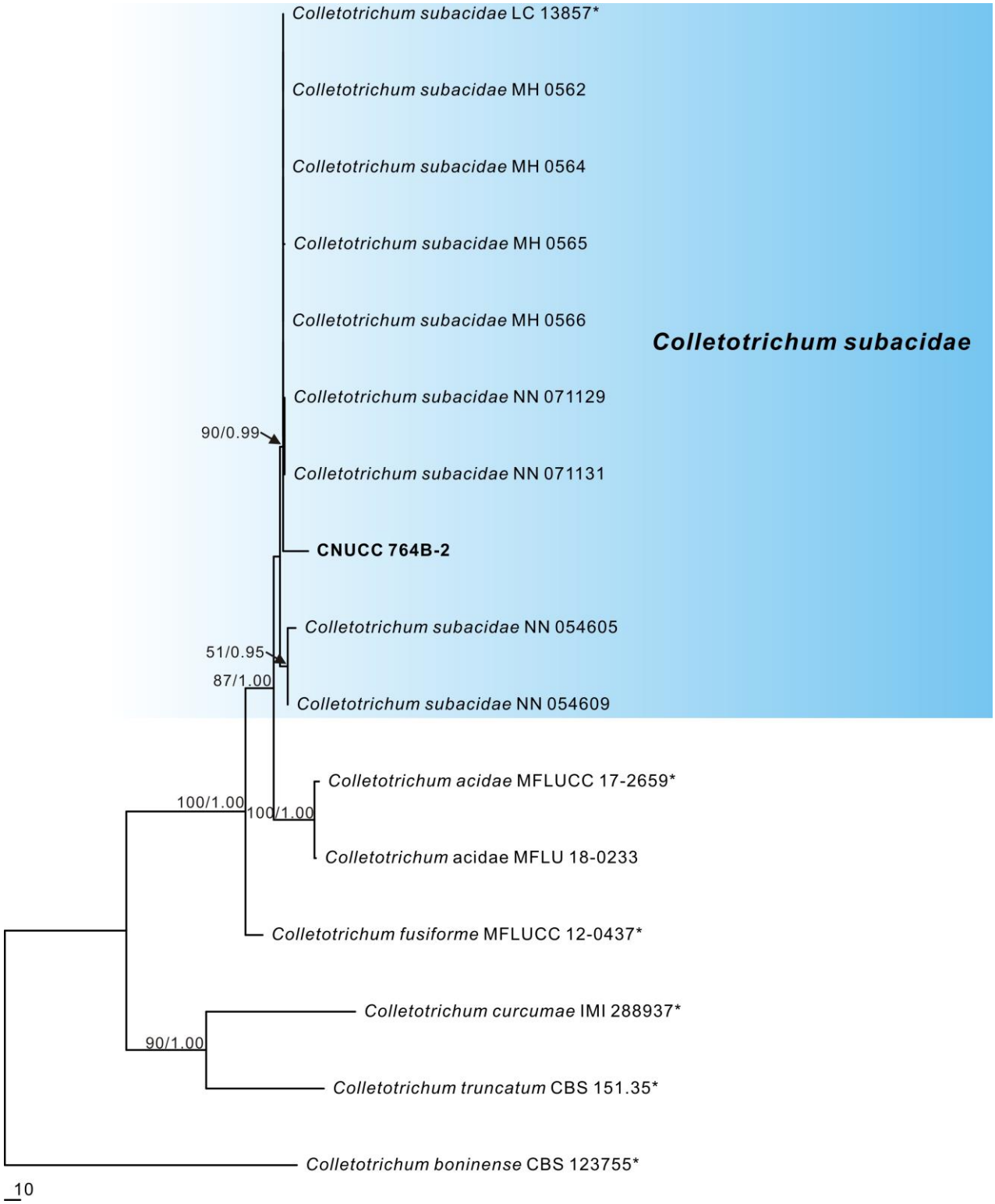


Figure 22 – Phylogenetic tree of *Colletotrichum truncatum* species complex derived from maximum parsimony analysis of the combined *act–chs-1–gapdh–his3*–ITS–*tub* sequences, using *C. boninense* CBS 123755 as outgroup. Maximum parsimony bootstrap values (BP > 50%) and

bayesian posterior probabilities (PP > 0.95) are shown above the branches. Type species strains are marked with an " * ". Newly generated sequences are represented in **bold**.

Other specimens examined – CHINA. Anhui Province, Jingde City, Yunle County, on leaves of *Parthenocissus tricuspidate*, Apr. 2016, C.L. Hou & Q.T. Wang, living culture CNUCC P7-4-5-2-3 and CNUCC P7-4-5-3-3.

Notes – This species forms a sister clade with *Colletotrichum jinshuiense* and *C. kakiivorum* H.Y. Jung & S.Y. Lee with a high support value (MBP = 100, PP = 1.00) (Fig. 9). It is worth mentioning that *Colletotrichum kakiivorum* has been treated as a synonym of *C. jinshuiense* in Liu et al (2022). Although *Colletotrichum parthenocissigenum* is closely related to *C. jinshuiense*, the sequence similarities of *act*, *gapdh*, and *tub2* is low, which are 98.68%, 98.39%, and 98.99%, respectively. And PHI test indicates that there is no significant recombination between these two specie (Φw = 0.8966) (Fig. 10). For morphology, although both species have curved conidia, the conidia of *Colletotrichum parthenocissigenum* were significantly shorter than that of *C. jinshuiense* (12–16 μm vs. 25–29.5 μm) (Fu et al. 2019).

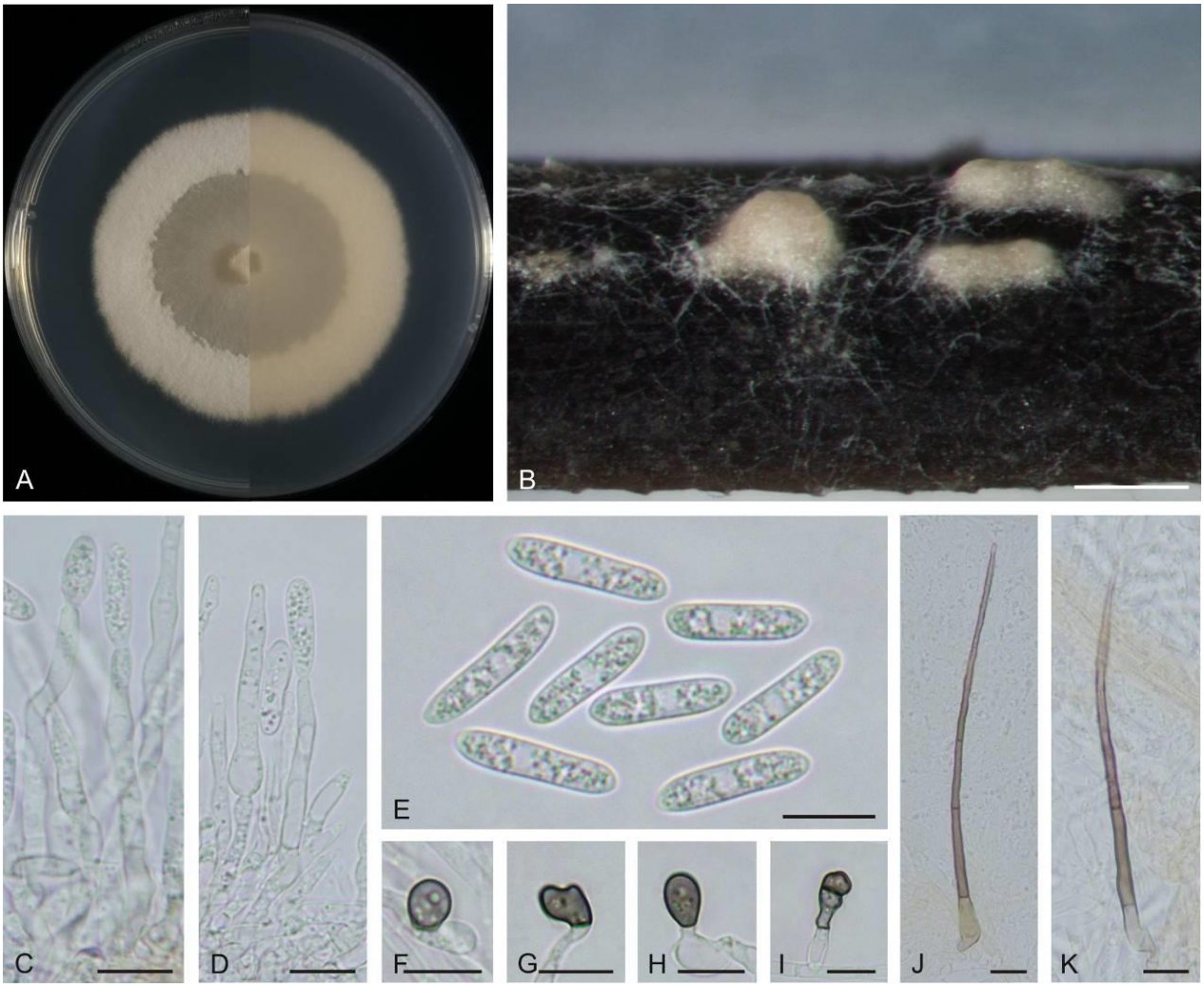


Figure 23 – *Colletotrichum cunninghamiae* (CNUCC 58-57-2, ex-type). A Front (left) and back (right) views of 7-d-old PDA culture. B Conidiomata on pine needle. C–D Conidiogenous cells. E Conidia. F–I Appressoria. J–K Setae. A from PDA. B–K from SNA with pine needle. Scale bars: B = 200 μm, C–K = 10 μm.

Colletotrichum subplurivorum Q.T. Wang, X.N. Sui, M.J. Guo & C.L. Hou, sp. nov. Fig. 29

MycoBank number: MB853890; Facesoffungi number: FoF15940

Etymology – Named to reflect its close phylogenetic relationship with *C. plurivorum*.

Typification – CHINA. Guizhou Province, Guiyang City, Xifeng County, on leaves of *Camellia oleifera*, Aug. 2021, C.L. Hou & Q.T. Wang (holotype CAF 8000211). Ex-type CNUCC 833B-1-1.



Figure 24 – *Colletotrichum guiyangense* (CNUCC 823-1-1, ex-type). A Front (left) and back (right) views of 7-d-old PDA culture. B Ascomata on pine needle. C Ascomata wall. D–E Asci. F Ascospores. G–H Conidiogenous cells. I Conidia. J–M Appressoria. A from PDA. B–F from CMA with pine needle. G–M from CMA. Scale bars: B = 200 μm, C–N = 10 μm.

Colonies on PDA 57–60 mm diam. in 7 days, flat with entire edge, very dark grayish orange (#67635d) in the center, very soft orange (#ddc8a3) towards margin, with white (#ffffff) margin, aerial mycelium dense, reverse very dark lime green (#002700) in the center, very soft orange

towards margin, with white margin. On PDA, conidiomata scattered or confluent, black. *Conidial masses* grayish orange (#ccc3ba), produced from conidiomata. *Vegetative hyphae* hyaline to pale brown, smooth-walled, septate, branched. Setae not observed. *Conidiophores* solitary or branched, septate, hyaline to pale brown, usually reduced to conidiogenous cells. *Conidiogenous cells* hyaline to pale brown, aseptate, smooth-walled, ampulliform to cylindrical, 18.5–41 × 3.5–5.0 μm. *Conidia* hyaline, aseptate, smooth-walled, straight or slightly curved, cylindrical, both ends rounded, 17.5–21.5 × 5.5–7.0 μm (av. ± SD = 19.6 ± 1.0 × 6.1 ± 0.3 μm), L/W ratio = 3.2. *Appressoria* single, pale brown to medium brown, ellipsoidal, subglobose or irregular outline, with entire or undulate margin, 5.5–13.0 × 3.5–8.5 μm (av. ± SD = 7.6 ± 2.0 × 5.5 ± 1.1 μm), L/W ratio = 1.4.

Other specimens examined – CHINA. Guizhou Province, Guiyang City, Xifeng County, on leaves of *Camellia sinensis*, 27 Aug. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 811A-1-1; *ibid.*, on leaves of *Camellia sinensis*, 27 Aug. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 824-1-2; *ibid.*, Zhejiang Province, Huzhou City, Deqing County, Mogan Mountain, on leaves of *Camellia sinensis*, Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 175C-1-3; *ibid.*, Zhejiang Province, Huzhou City, Deqing County, Mogan Mountain, on leaves of *Diospyros kaki* var. *silvestris* Makino, 2 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 184-5-5.

Notes – *Colltotrichum subplurivorum* is phylogenetically related *C. plurivorum*, but sequence similarities of *act*, *chs-1*, *gapdh* is low, which are 97.89%, 98.12%, and 98.2%, respectively. PHI test indicates that there is no significant recombination between these two species (Φw = 0.7341) (Fig. 21). For morphology, the conidia length of *Colltotrichum subplurivorum* is much longer than that of *C. plurivorum* (18.5–41 μm vs. 7–19 × 4–5.5 μm) (Damm et al. 2019).

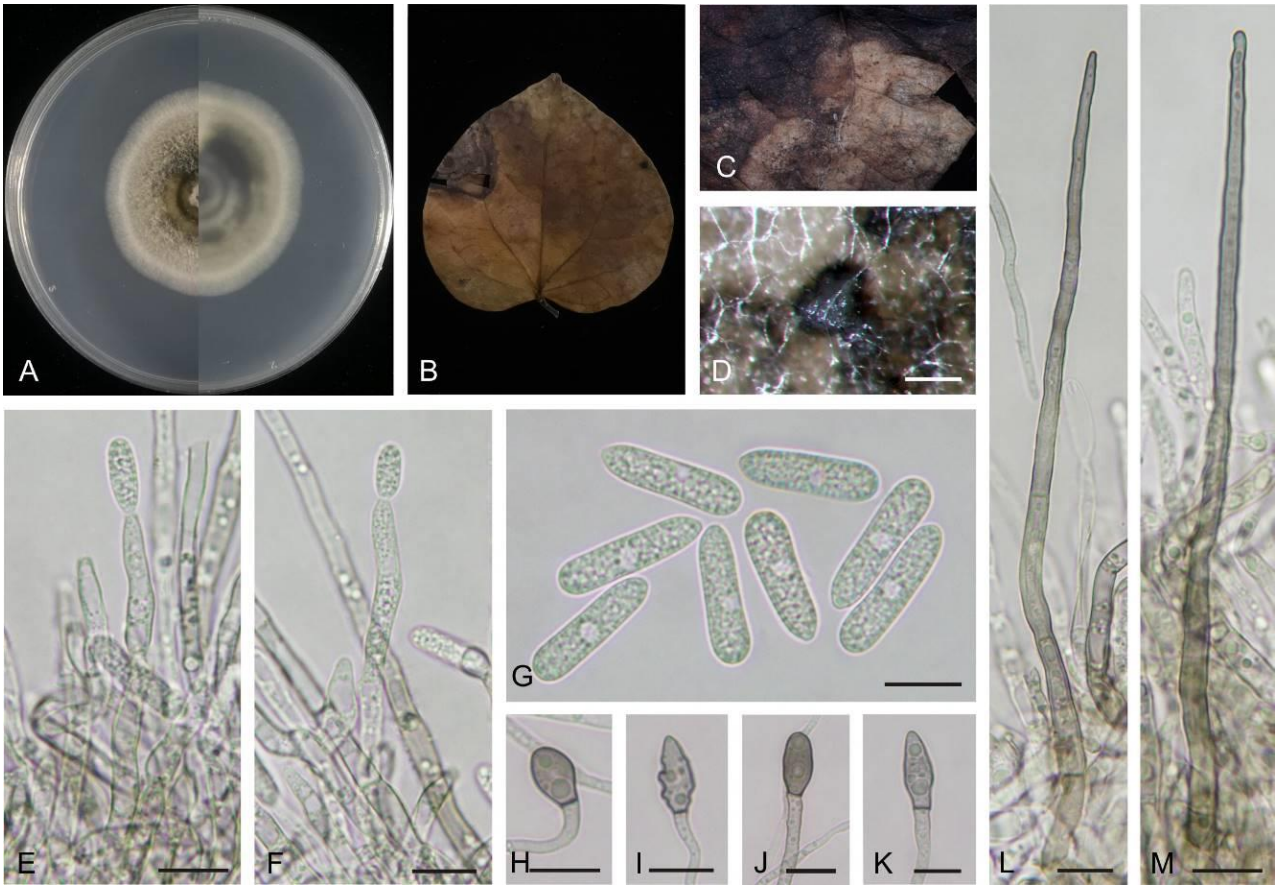


Figure 25 – *Colletotrichum hubeiense* (CNUCC 408-1-1, ex-type). A Front (left) and back (right) views of 7-d-old PDA culture. B–C Symptoms on a leaf of *Lindera glauca*. D Conidiomata. E–F Conidiogenous cells. G Conidia. H–K Appressoria. L–M Setae. A, D–M from PDA. Scale bars: D = 200 μm, E–M = 10 μm.

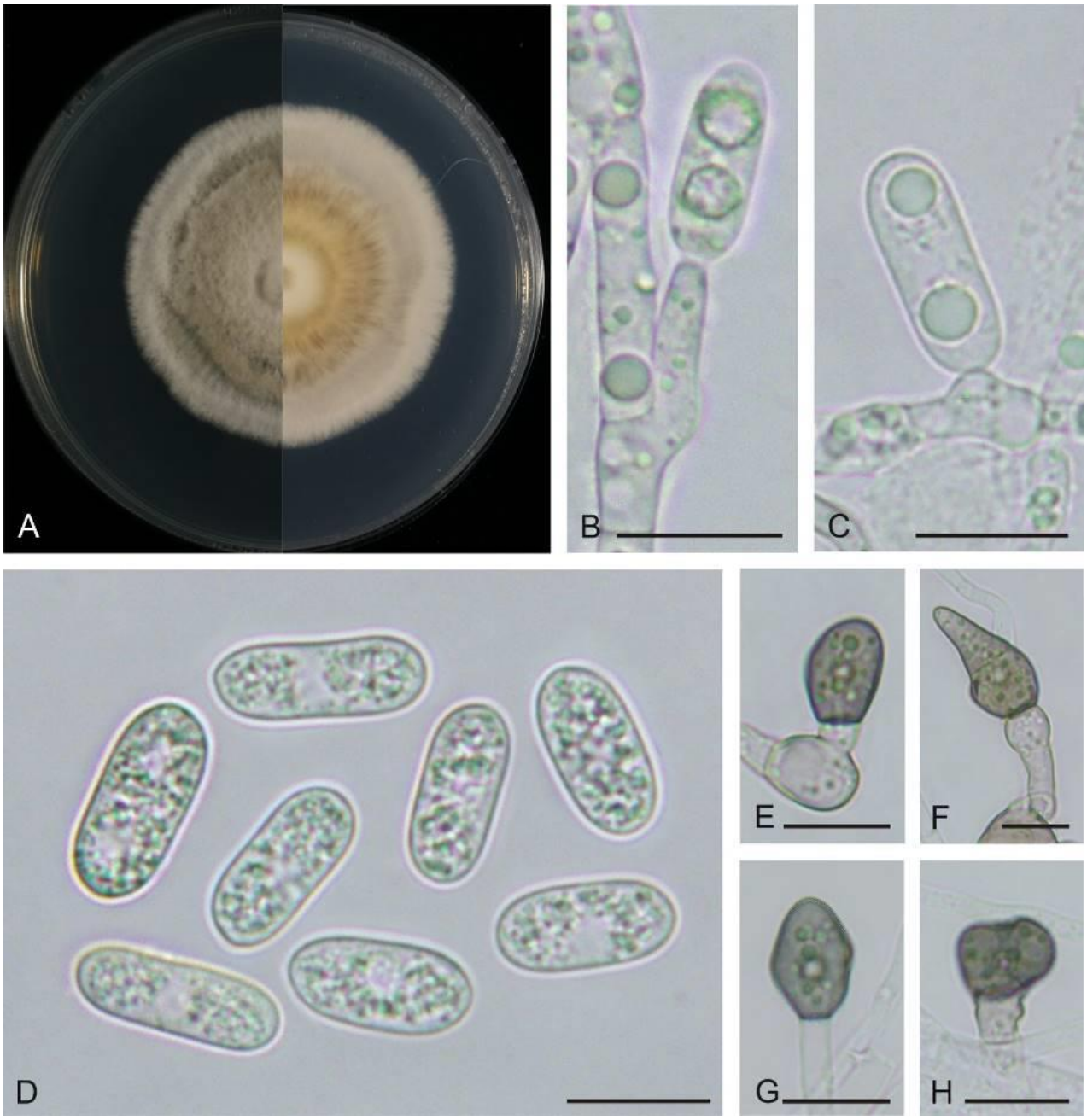


Figure 26 – *Colletotrichum jixiense* (CNUCC 5-21-2-1, ex-type). A Front (left) and back (right) views of 7-d-old PDA culture. B–C Conidiogenous cells. D. Conidia. E–H Appressoria. A from PDA. B–H from OA. Scale bars: B–H = 10 μm.

Colletotrichum wenzhouense Q.T. Wang & C.L. Hou, sp. nov. Fig. 30

MycoBank number: MB853891; Facesoffungi number: FoF15941

Etymology – Referring to the Wenzhou City where the host plants were collected.

Typification – CHINA. Zhejiang Province, Wenzhou City, Rui'an County, on leaves of *Camellia oleifera*, Nov. 2018, C.L. Hou & Q.T. Wang (holotype CAF 8000212). Ex-type CNUCC 253B-3-2.

Colonies on PDA 64–65 mm diam. in 7 days, flat with entire edge, whole white (#ffffff), aerial mycelium dense, reverse strong orange (#cc5100) in the center and pale orange (#ffe3b1) towards margin. On MEA, conidiomata not developed, conidiophores formed directly on hyphae. *Vegetative hyphae* hyaline, smooth-walled, septate, branched. *Setae* not observed. *Conidiophores* hyaline, solitary, usually reduced to conidiogenous cells. *Conidiogenous cells* hyaline, aseptate, smooth-walled, ampulliform, 5.5–15 × 2.5–4 μm. *Conidia* hyaline, aseptate, smooth-walled,

falcate, apex rounded to ± acute, base truncate, 20–33.5 × 4–5.5 μm (av. ± SD = 25.3 ± 3.2 × 4.8 ± 0.4 μm), L/W ratio = 5.3. *Appressoria* single or gregarious, medium brown to dark brown, fist-shaped, or irregularly shaped, with entire or undulate margin, 8–14 × 6–11 μm (av. ± SD = 11.1 ± 1.5 × 8.6 ± 1.1 μm), L/W ratio = 1.3.

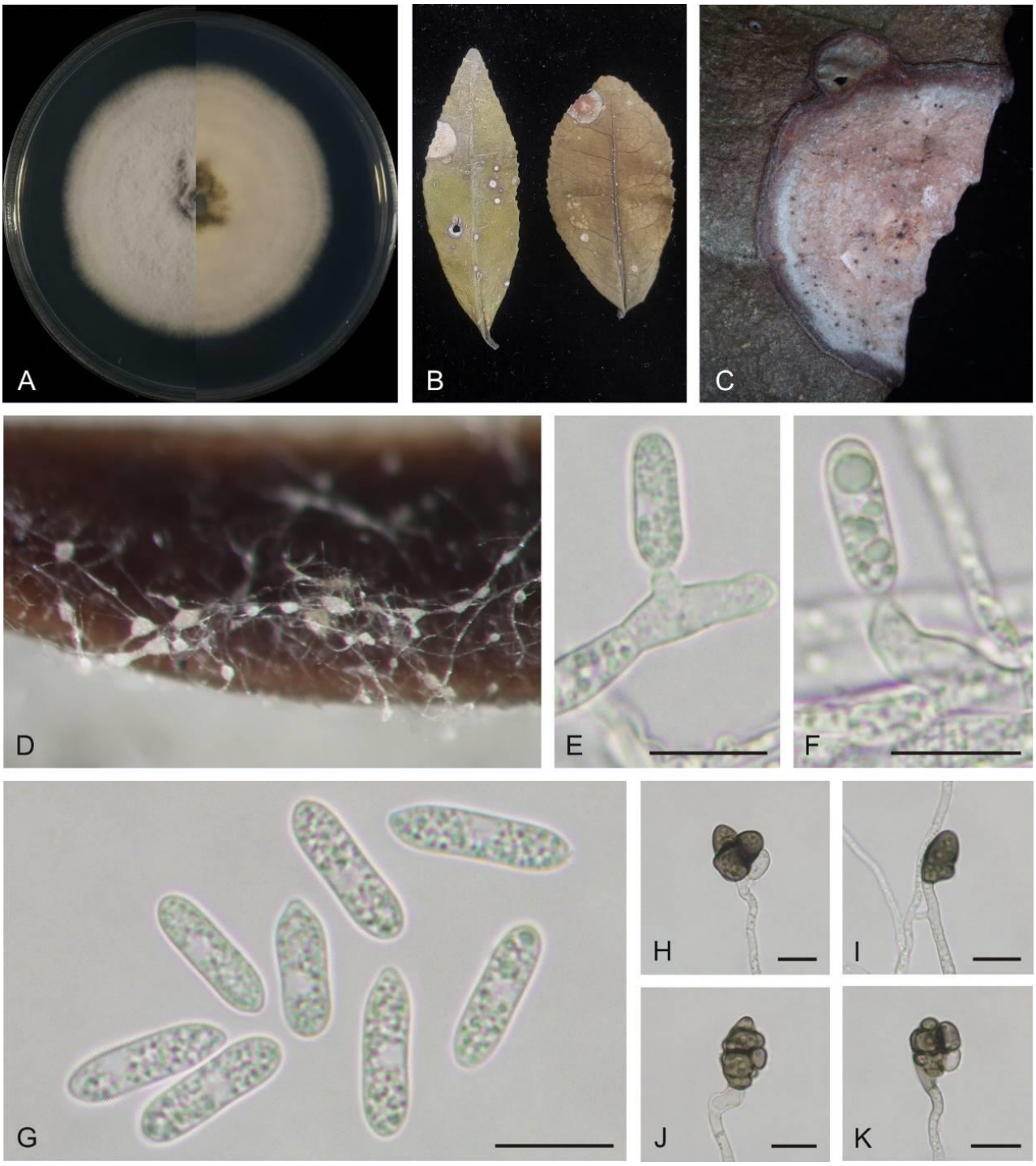


Figure 27 *Colletotrichum luanense* (CNUCC 157A-4-4, ex-type). A Front (left) and back (right) views of 7-d-old PDA culture. B–C Symptoms on a leaf of *Camellia sinensis*. D Conidial masses on aerial mycelium. E–F Conidiogenous cells. G Conidia. H–K Appressoria. A from PDA. D from CMA with pine needle. Scale bars: D = 200 μm, E–K = 10 μm.

Notes – This species is phylogenetically related to *Colletotrichum multiseptatum*, *C. echinochloae*, and *C. jacksonii* in the *C. caudatum-graminicola* species complex, but shares low

sequences similarity at ITS (98%) and even lower sequences similarity at *sod2* (95%–96%). Morphologically, the conidia lengths of *Colletotrichum multiseptatum* (Liu et al. 2022), *C. echinochloae* (Moriwaki & Tsukiboshi 2009), and *C. jacksonii* (Crouch et al. 2009a) are all less than 26 μm, while that is longer in *C. wenzhouense* (20–33.5 μm) than those three species.

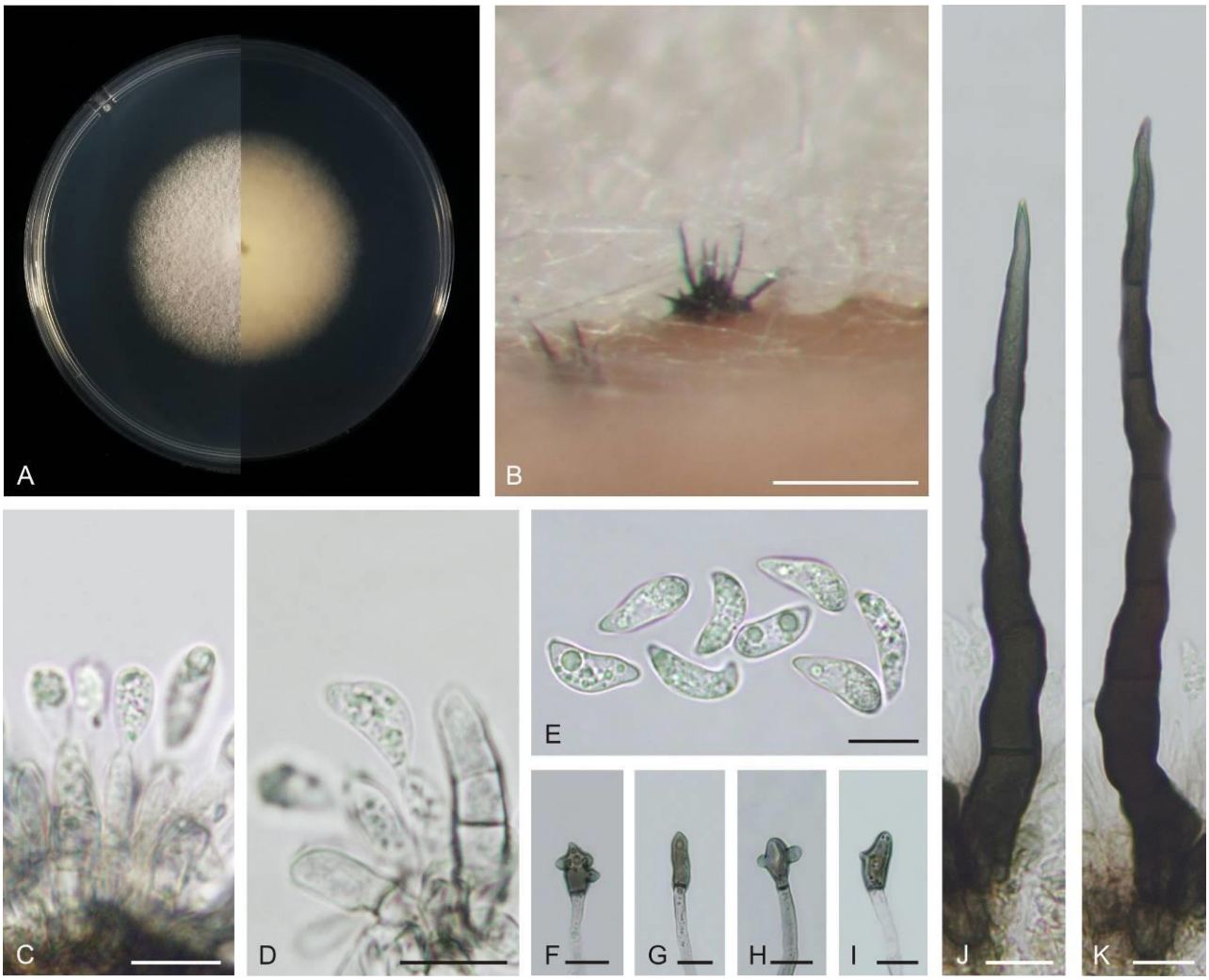


Figure 28 – *Colletotrichum parthenocissigenum* (CNUCC P7-4-5, ex-type). A Front (left) and back (right) views of 7-d-old PDA culture. B Conidiomata on pine needle. C–D Conidiogenous cells. E Conidia. F–I Appressoria. J–K Setae. A from PDA. B–K from OA with pine needle. Scale bars: B = 200 μm, C–K = 10 μm.

Colletotrichum camelliae Massee, Bull. Misc. Inf., Kew (nos 151-152): 91 (1899) Fig. 31
≡ *Colletotrichum analogum* Z.F. Yu, Journal of Fungi 8: 11 (2022)

Colonies on PDA 46–54 mm diam. in 7 days, flat with entire edge, aerial mycelium dense, dark grayish orange (#c9c9b5) covers with white (#ffffff) aerial mycelium, with white margin, reverse very dark (mostly black) cyan (#000c07) in the center and white towards margin. On PDA, conidiomata scattered or gregarious, black. *Conidial masses* very pale orange (#fff1d8), produced from conidiomata. *Vegetative hyphae* hyaline, smooth-walled, septate, branched. *Setae* not observed. *Conidiophores* formed from a cushion of roundish to angular dark brown cells, solitary or branched, septate, medium brown. *Conidiogenous cells* hyaline, aseptate, smooth-walled, cylindrical to subcylindrical, 12.5–28.5 × 3–4 μm. *Conidia* hyaline, aseptate, smooth-walled, straight, cylindrical, both ends rounded, 16–18 × 5.5–6.5 μm (av. ± SD = 17.0 ± 0.6 × 6.1 ± 0.3 μm), L/W ratio = 2.8. *Appressoria* single, sometimes in loose group, medium brown, clavate,

subelliptical, or irregular outline with a crenate or lobed margin, 7.0–13.0 × 4.5–7.0 μm (av. ± SD = 9.3 ± 1.8 × 5.8 ± 0.8 μm), L/W ratio = 1.6.

Other specimens examined – CHINA. Zhejiang Province, Jinhua City, on leaves of *Camellia chekiangoleosa* Hu, 3 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CFCC 59258; *ibid.*, Wenzhou City, Rui'an County, on leaves of *Camellia sinensis*, 4 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 257-2-4; *ibid.*, Anhui Province, Xuancheng City, Jingde County, on leaves of *Camellia oleifera*, May 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 1297-3-3; *ibid.*, Guangxi Province, Guilin City, Lingchuan County, on leaves of *Camellia sinensis*, 28 May 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 742A-1-1; *ibid.*, Jiangxi Province, Leping City, on leaves of *Camellia sinensis*, 5 Aug. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 781B-1-2.

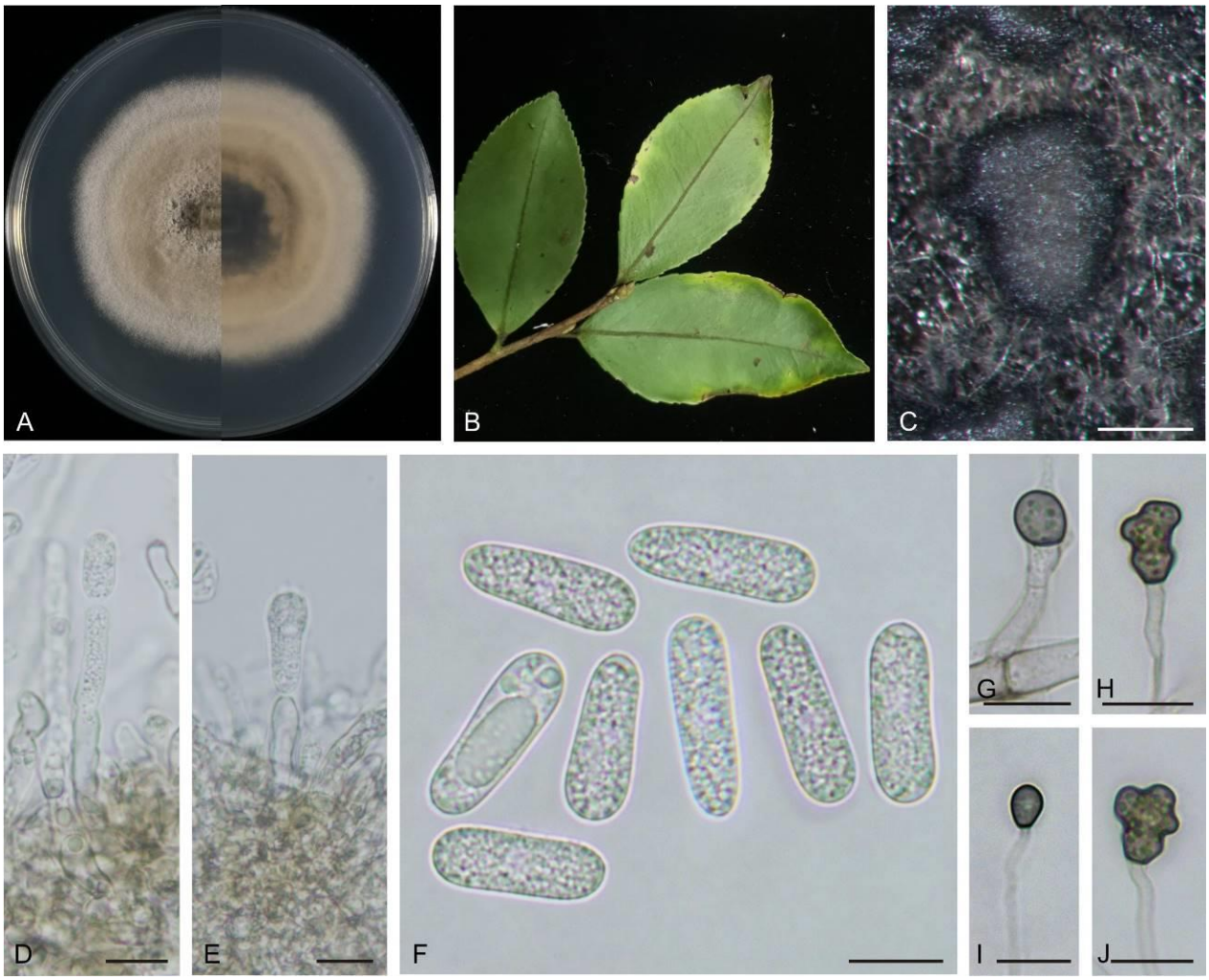


Figure 29 – *Colletotrichum subplurivorum* (CNUCC 833B-1-1, ex-type). A Front (left) and back (right) views of 7-d-old PDA culture. B Symptoms on a leaf of *Camellia oleifera*. C Conidiomata. D–E Conidiogenous cells. F Conidia. G–J Appressoria. A from PDA. C–J from OA. Scale bars: C = 200 μm, D–J = 10 μm.

Notes – The type strains of *Colletotrichum analogum* and *C. camelliae* are clustered in one clade. And the type strain of *C. analogum* and *C. camelliae* have high sequence similarities, which are *act* 100.00%, *apmat* 99.54%, *gapdh* 100%, ITS 99.21%, and *tub2* 100%. For morphology, Yu et al. (2022) considered that the conidia of *C. analogum* is narrower than that of *C. camelliae* (Liu et al. 2015). However, the conidia size of *C. analogum* (15–20 × 5–6.5 μm) is within the conidia size range of *C. camelliae* (Liu et al. 2015). Based on morphology analysis combined with multi-locus phylogenetic analysis, *C. analogum* is considered conspecific to *C. camelliae*, and treated as a

synonym of *C. camelliae*. *Colletotrichum camelliae* was reduced to synonym of *Colletotrichum coccodes* (Wallr.) S. Hughes in Index Fungorum, but the epitype strain of *C. camelliae* is far away from the neotype strain of *C. coccodes* in phylogenetic tree. Although these two species lack molecular data of holotype strains, they are currently widely accepted (Jayawardena et al. 2021) and supported by the data from other type materials. Therefore, the treatment of synonym of *C. camelliae* by Index Fungorum was not accepted in this study.

Colletotrichum camelliae could infect various species of *Camellia*, such as *Ca. japonica*, *Ca. oleifera*, *Ca. sasanqua*, *Ca. sinensis*, and *Ca. chekiangoleosa*. However, this species has been isolated only from *Camellia* spp., indicating that there may be a special infection mechanism between *C. camelliae* and *Camellia* spp., which requires further study.

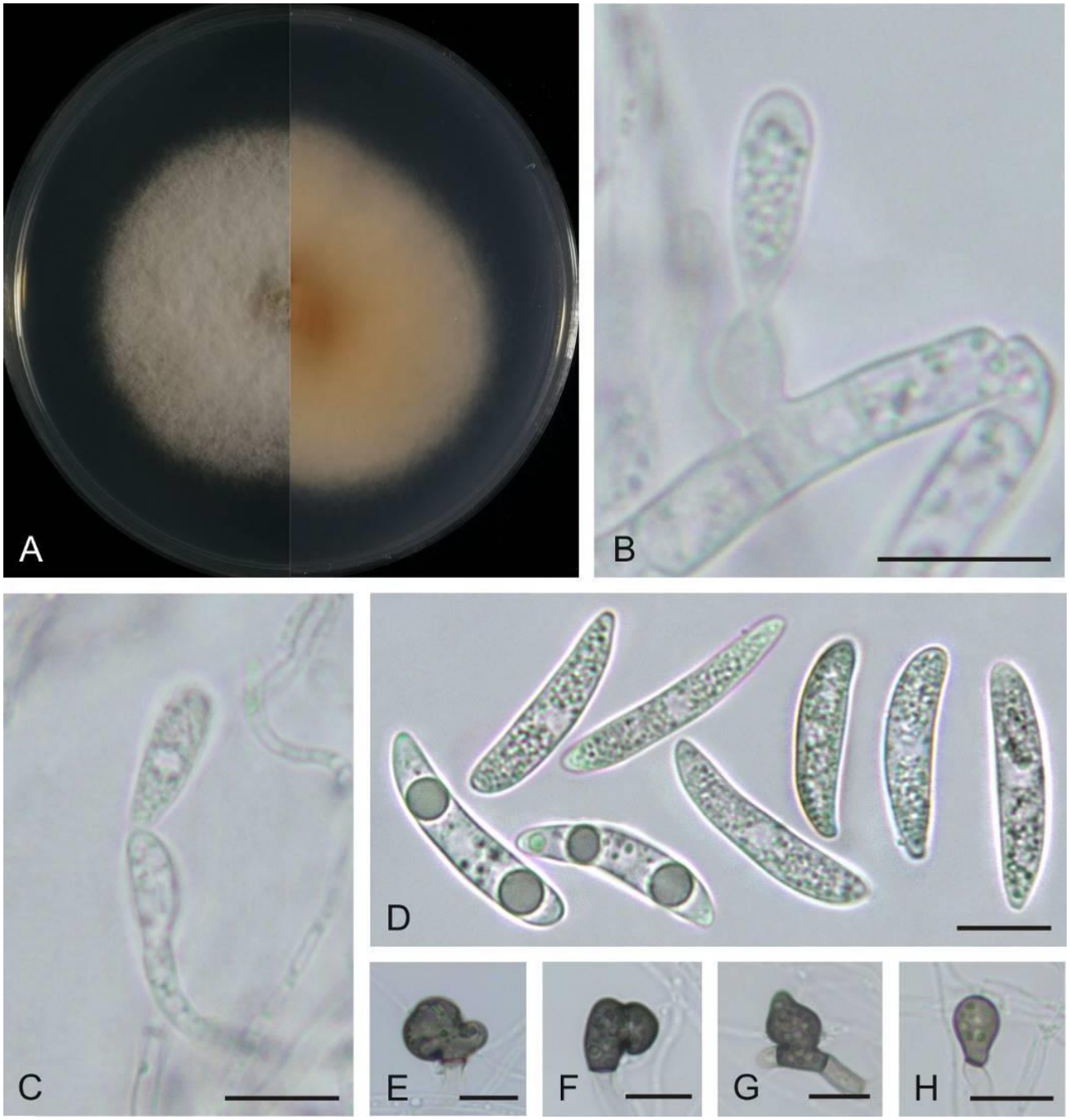


Figure 30 – *Colletotrichum wenzhouense* (CNUCC 253B-3-2, ex-type). A Front (left) and back (right) views of 7-d-old PDA culture. B−C Conidiogenous cells. D Conidia. E−H Appressoria. A from PDA. B–H from MEA. Scale bars: B−H = 10 μm.

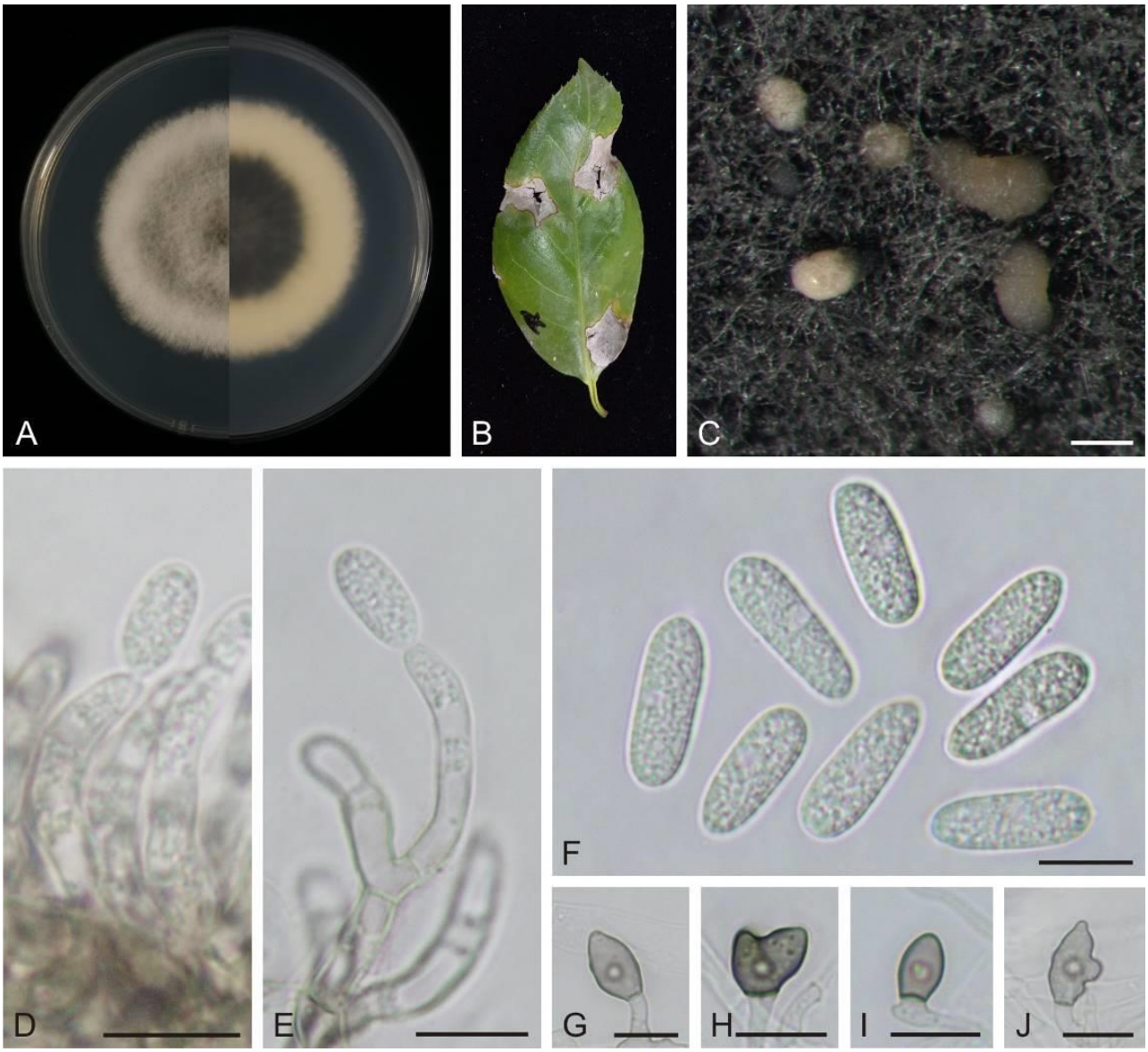


Figure 31 – *Colletotrichum camelliae* (Strains CFCC 59258). A Front (left) and back (right) views of 7-d-old PDA culture. B Symptoms on a leaf of *Camellia chekiangoleosa*. C Conidiomata. D–E Conidiogenous cells. F Conidia. G–J Appressoria. A, C–J from PDA. Scale bars: C = 200 μm, D–J = 10 μm.

Colletotrichum fructicola Prihast., L. Cai & K.D. Hyde, Fungal Diversity 39: 96 (2009) Fig. 32

≡ *Colletotrichum mengyinense* T.C. Mu, J.W. Xia, X.G. Zhang & Z. Li, MycoKeys 85: 66 (2021)

Colonies on PDA 42–54 mm diam. in 7 days, flat with entire edge, white (#ffffff) to grayish yellow (#c9c9b5), aerial mycelium sparse but dense at margin, reverse dark grayish orange (#a0937f) with white (#ffffff) margin. On PDA, conidiomata gregarious, black. *Conidial masses* vivid orange (#ffb733), produced from conidiomata. *Vegetative hyphae* hyaline, smooth-walled, septate, branched. Setae not observed. *Conidiophores* formed from a cushion of roundish to angular light brown cells, solitary or branched, aseptate, hyaline. *Conidiogenous cells* hyaline, aseptate, smooth-walled, cylindrical to ampulliform, 12.5–27.5 × 2.5–3 μm. *Conidia* hyaline, aseptate, smooth-walled, subcylindrical, both ends rounded, 13–17.5 × 4.5–5.5 μm (av. ± SD = 15.7 ± 1.0 × 5.2 ± 0.2 μm), L/W ratio = 3.0. *Appressoria* gregarious, pale to medium brown, bulb or clavate in shape, 6.0–8.0 × 3.5–5.0 μm (av. ± SD = 6.8 ± 0.6 × 4.2 ± 0.4 μm), L/W ratio = 1.6.

Other specimens examined – CHINA. Henan Province, Xinyang City, on leaves of *Camellia oleifera*, 12 Oct. 2021, living culture CNUCC 888-1-2; *ibid.*, on leaves of *Camellia oleifera*, 12 Oct. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 921-3-1; *ibid.*, on leaves of *Camellia oleifera*, 12 Oct. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 882-2-2; *ibid.*, on leaves of *Camellia sinensis*, 12 Oct. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 916-1-2-1; *ibid.*, on leaves of *Camellia sinensis*, 12 Oct. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 906A-2-1; *ibid.*, Guangshan County, on leaves of *Camellia oleifera*, 11 Oct. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 857-1-1; *ibid.*, Guangshan County, on leaves of *Camellia oleifera*, 11 Oct. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 213-5-4; *ibid.*, Guangshan County, on leaves of *Camellia oleifera*, 11 Oct. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 213-1-6; *ibid.*, Guangshan County, on leaves of *Camellia oleifera*, 11 Oct. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 213-3-5; *ibid.*, Guangshan County, on leaves of *Camellia oleifera*, 11 Oct. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 864A-2-2; *ibid.*, Zhejiang Province, Jinhua City, on leaves of *Vernicia montana* Lour., 2 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 213-1-1; *ibid.*, Zhejiang Province, Jinhua City, on leaves of *Vernicia montana*, 2 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 213-4-1; *ibid.*, Zhejiang Province, Jinhua City, on leaves of *Lauraceae* sp., 3 Nov. 2018, C.L. Hou & Q.T. Wang, C.L. Hou & Q.T. Wang, living culture CNUCC 231-2-1; *ibid.*, Zhejiang Province, Jinhua City, on leaves of *Lauraceae* sp., 3 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 231-4-2; *ibid.*, Zhejiang Province, Jinhua City, on leaves of *Lauraceae* sp., 3 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 231-4-4; *ibid.*, Zhejiang Province, Jinhua City, on leaves of *Lauraceae* sp., 3 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 232-1-1; *ibid.*, Zhejiang Province, Jinhua City, on leaves of *Lauraceae* sp., 3 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 232-3-2; *ibid.*, Zhejiang Province, Jinhua City, on leaves of *Lauraceae* sp., 3 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 232-4-1; *ibid.*, Zhejiang Province, Jinhua City, on leaves of *Lauraceae* sp., 3 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 225D-4-4; *ibid.*, Anhui Province, Huangshan City, She County, on leaves of *Camellia oleifera*, May 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 149A-1-1; *ibid.*, Anhui Province, Lu'an City, Shucheng County, on leaves of *Osmanthus fragrans* Lour., 15 May 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 151A-4-1; *ibid.*, Anhui Province, Lu'an City, Huoshan County, on leaves of *Paulownia fortunei*, 22 Nov. 2016, C.L. Hou & Q.T. Wang, living culture CNUCC 13-5-5; *ibid.*, Anhui Province, Lu'an City, Shucheng County, on leaves of *Osmanthus fragrans*, 15 May 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 151A-3-1; *ibid.*, Anhui Province, Xuancheng City, Jingde County, on leaves of *Akebia trifoliata*, 13 May 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 117-3-1; *ibid.*, Jiangxi Province, Xinyu City, Fenyi County, on leaves of *Schima superba* Gardn. et Champ. 22 Apr. 2021, living culture CNUCC 693-3-2; *ibid.*, Jiangxi Province, Leping City, on leaves of *Camellia sinensis*, 5 Aug. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 782A-1-3; *ibid.*, Guangxi Province, Guilin City, Lingchuan County, on leaves of *Lauraceae* sp., 28 May 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 711-1-2; *ibid.*, Guangxi Province, Guilin City, Lingchuan County, on leaves of *Lauraceae* sp. 28 May 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 720-1-1; *ibid.*, Guizhou Province, Guiyang City, Xifeng County, on leaves of *Camellia oleifera*, 27 Aug. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 839B-2-1.

Notes – *Colletotrichum fructicola* has a wide host range and has been reported from 57 genera of plants in China, most of which are fruit trees. This is the first time that *C. fructicola* was reported on the plants of *Vernicia montana*, *Cinnamomum camphora*, *Paulownia fortunei*, *Osmanthus fragrans*, and *Schima superba* in the world. Given the distant relationship among these plants, it implies that *C. fructicola* possesses the capacity to infect various types of forest trees, emphasizing the significance of effectively preventing and controlling the spread of *C. fructicola*. *Colletotrichum mengyinense*, a single-strain species closely related to *C. fructicola*, was published as a new species by Mu et al. (2021) based on the results of multi-locus phylogenetic tree, differences in the number of bases and the size of conidia. In this study, with more stains added in the multi-locus phylogenetic analysis, the type strain of *C. mengyinense* is clustered within the

C. fructicola clade (Figs 18, 19). Furthermore, the sequence similarities of the type strains of two species are 96.62% for *act*, 100.00% for *chs-1*, 98.39% for *gapdh*, 99.32% for ITS, 100% for *tub2*, 99.18% for *apmat*, 100.00% for *cal*, and 99.21% for *gs*, respectively. Although the sequence similarities of *act* and *gapdh* are low, *C. mengyinense* also clustered within the *C. fructicola* clade in the single gene phylogenetic trees (Supplementary Figs 11, 12, 13, 14, 15, 16). In morphology, the conidia of *C. mengyinense* are slightly longer than those of *C. fructicola* (12.5–15.7 μm vs. 9.7–14.0 μm) (Mu et al. 2021, Prihast. et al. 2009), but several studies showed that the conidia size varied in different strains of *C. fructicola* (Liu et al. 2015, de Silva et al. 2019, this study). Therefore, based on the results of multi-locus phylogenetic analysis and morphology analysis, *C. mengyinense* is considered conspecific to *C. fructicola*, and treated as synonyms of *C. fructicola* in this study.

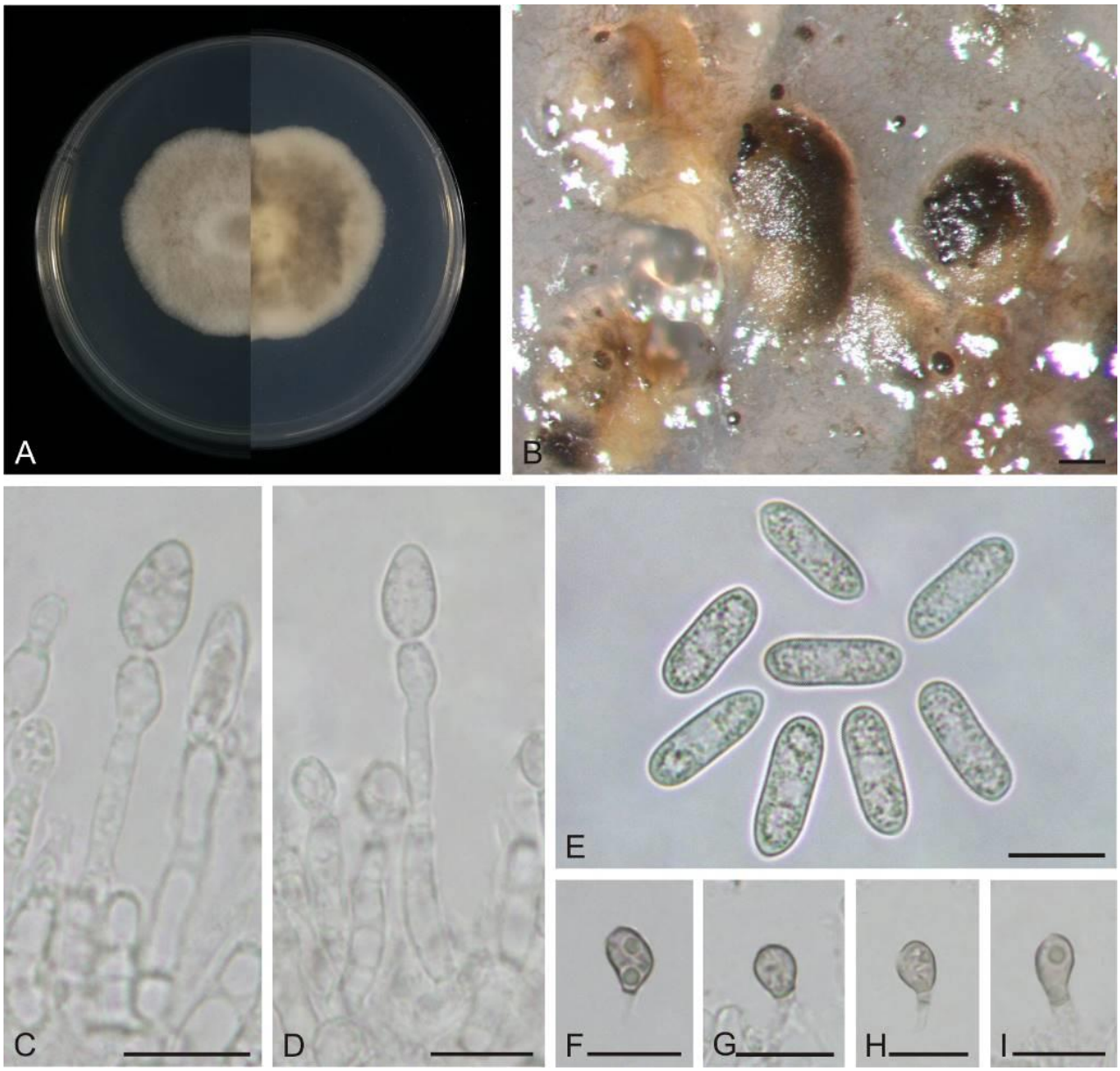


Figure 32 – *Colletotrichum fructicola* (Strains CNUCC 711-1-2). A Front (left) and back (right) views of 7-d-old PDA culture. B Conidiomata. C–D Conidiogenous cells. E Conidia. F–I Appressoria. A–I from PDA. Scale bars: B = 200 μm C–I = 10 μm.

Colletotrichum gloeosporioides (Penz.) Penz. & Sacc., Atti Inst. Veneto Sci. lett., ed Arti, Sér. 6 2(5): 670 (1884) Fig. 33

≡ *Colletotrichum citrulli* Z. Guo, H. J. Wu, B. Peng, C.X. Luo, Q.S. Gu, Journal of Fungi 8(8) (2022)

Colonies on PDA 61–80 mm diam. in 7 days, flat with entire edge, very dark (mostly black) yellow (#1f2700) with white (#ffffff) margin, aerial mycelium dense, reverse very dark (mostly black) green (#071400) in the center and white (#ffffff) towards margin. On PDA, conidiomata scattered or gregarious, black. *Conidial masses* light orange (#ffc862), produced from conidiomata. *Vegetative hyphae* hyaline to pale brown, smooth-walled, septate, branched. *Setae* medium to dark brown, 3–4-septate, 83–110 μm long, basal cells cylindrical or cylindric-conical, smooth-walled, 3.0–4.5 μm diam, tip acute. *Conidiophores* formed from a cushion of roundish to angular medium brown cells, usually reduced to conidiogenous cells. *Conidiogenous cells* hyaline, aseptate or 1-septate, smooth-walled, cylindrical to subcylindrical, 19.5–27 × 2.5–3 μm. *Conidia* hyaline, aseptate, smooth-walled, straight, subcylindrical, both ends rounded, 13.5–17 × 5–6 μm (av. ± SD = 15 ± 0.9 × 5.4 ± 0.2 μm), L/W ratio = 2.8. *Appressoria* single, medium brown, variable in shape, subelliptical, clavate, or irregular outline with a crenate or lobed, 9.0–15 × 4–7.5 μm (av. ± SD = 11.8 ± 1.7 × 5.8 ± 0.9 μm), L/W ratio = 2.0.

Other specimens examined – CHINA. Zhejiang Province, Huzhou City, Deqing County, Mogan Mountain, on leaves of *Camellia sinensis*, 2 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 175B-3-4; *ibid.*, on leaves of *Diospyros kaki* var. *silvestris*, 2 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 184-3-3; *ibid.*, on leaves of *Parthenocissus tricuspidata*, 2 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 191-1-2; *ibid.*, host unknown, 2 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 192-2-1; *ibid.*, on leaves of *Akebia quinata* (Thunb. ex Houtt.) Decne., 2 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 194B-2-2; *ibid.*, host unknown, 2 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 195-1-3; *ibid.*, on leaves of *Litsea cubeba* (Lour.) Pers., 2 Nov. 2018, C.L. Hou & Q.T. Wang, living cultures CNUCC 196-1-2, CNUCC 196-5-3; *ibid.*, on leaves of *Cunninghamia lanceolata*, 2 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 250-4-3; *ibid.*, Jinhua City, on leaves of *Camellia oleifera*, 3 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 225A-3-2; *ibid.*, Jinhua City, on leaves of *Lauraceae* sp., 3 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 232-2-1; *ibid.*, Wenzhou City, Rui'an County, on leaves of *Citrus reticulata* cv. *'Hong Mei Ren'*, 4 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 286E-4-1; *ibid.*, Henan Province, Xinyang City, on leaves of *Camellia oleifera*, 12 Oct. 2021, C.L. Hou & Q.T. Wang, living cultures CNUCC 884-1-1, CNUCC 884-2-2; *ibid.*, Henan Province, Xinyang City, on leaves of *Dalbergia hupeana* Hance, 12 Oct. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 914-2-1; *ibid.*, Henan Province, Kaifeng City, Lankao County, on leaves of *Paulownia fortunei*, 14 Oct. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 936-1-1; *ibid.*, Henan Province, Kaifeng City, Lankao County, on leaves of *Cercis chinensis* Bunge, 14 Oct. 2021, C.L. Hou & Q.T. Wang, living cultures CNUCC 948-1-2, CNUCC 953-1-3; *ibid.*, Henan Province, Kaifeng City, Lankao County, on leaves of *Paulownia fortunei*, 14 Oct. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 949-2-2; *ibid.*, Anhui Province, Lu'an City, Shucheng County, on leaves of *Osmanthus fragrans*, May 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 151A-2-2; *ibid.*, Yunnan Province, Pu'er City, on leaves of *Camellia sinensis* var. *assamica* (J. W. Masters) Kitamura, 2 Jan. 2017, C.L. Hou & Q.T. Wang, living culture CNUCC 45-4-2; *ibid.*, Hubei Province, Wuhan City, Huazhong Agricultural University, on leaves of *Cunninghamia lanceolata*, 9 Feb. 2017, C.L. Hou & Q.T. Wang, living cultures CNUCC 61-1-1, CNUCC 61-19-1, CNUCC 61-23-1.

Notes – The host range of *Colletotrichum gloeosporioides* is very wide, including nearly 124 genera of herbs and woody plants with medicinal, edible, landscaping and ornamental values. This study is the first time that *C. gloeosporioides* was reported on the plants of the genera *Cercis* and *Litsea*, as well as *Camellia sinensis* var. *assamica* worldwide.

In the two-locus and six-locus phylogenetic trees of *Colletotrichum gloeosporioides* species complex, the type strains of *C. citrulli* clustered into the *C. gloeosporioides* clade (Figs 18, 19). And these three species have high sequence similarities with *C. gloeosporioides*, which are *C. citrulli* (*act* 99.54%, *chs-1* 100.00%, *gapdh* 96.54%, ITS 99.23%, *tub2* 99.80%) respectively.

Although the sequence similarity of *gapdh* of *C. citrulli* is low (*gapdh* 97.30%), these species is clustered in *C. gloeosporioides* clade with high support values in the *gapdh* phylogenetic tree. For morphology, the shape of conidia and appressoria of *C. citrulli* (Guo et al. 2022) are similar with those of *C. gloeosporioides* (Zhang et al. 2023), and also the size of conidia (*C. gloeosporioides* 15–19 × 4–7 μm, *C. citrulli* 14–17.5 × 4–6 μm). Therefore, based on morphology analysis combined with the multi-locus phylogenetic analysis, *C. citrull* is considered conspecific to *C. gloeosporioides*, and treated as synonyms of *C. gloeosporioides*.

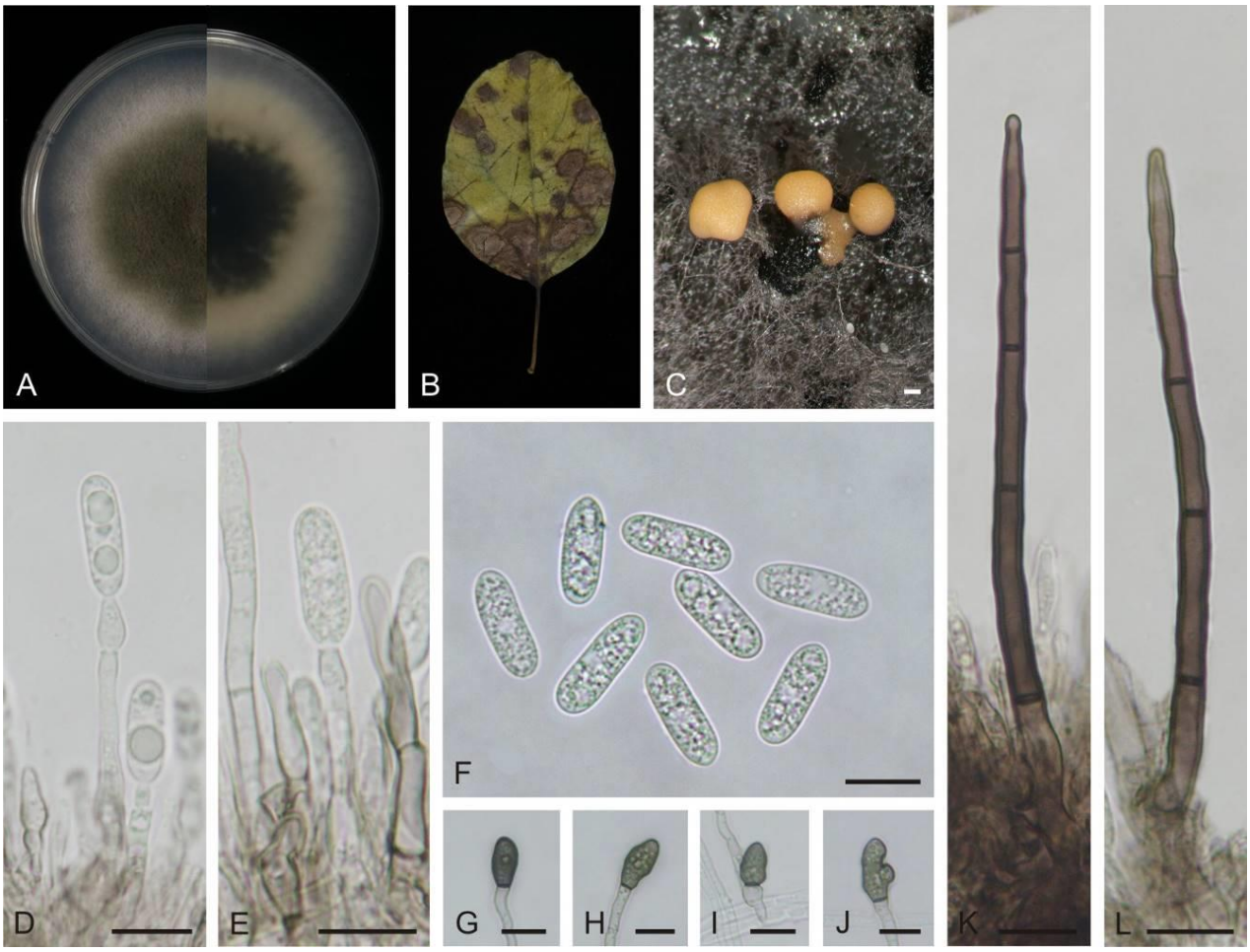


Figure 33 – *Colletotrichum gloeosporioides* (Strains CNUCC 184-3-3). A Front (left) and back (right) views of 7-d-old PDA culture. B Symptoms on a leaf of *Diospyros kaki* var. *silvestris*. C Conidiomata. D–E Conidiogenous cells. F Conidia. G–J Appressoria. K–L Setae. A, C–L from PDA. Scale bars: C = 200 μm, E–L = 10 μm.

Colletotrichum henanense F. Liu & L. Cai, Persoonia 35: 80 (2015) Fig. 34
≡ *Colletotrichum yulongense* C.L. Hou & X.T. Liu, Phytotaxa 394(4): 293 (2019)

Colonies on PDA 53–68 mm diam. in 7 days, flat with entire edge, both sides are white (#ffffff), aerial mycelium sparse but dense in the margin. On PDA, conidiomata gregarious, black. *Conidial masses* bright orange (#dca43d), produced from conidiomata. *Vegetative hyphae* hyaline, smooth-walled, septate, branched. *Setae* not observed. *Conidiophores* formed from a cushion of roundish medium brown cells, solitary or branched, septate, pale brown. *Conidiogenous cells* hyaline, aseptate, smooth-walled, cylindrical to ampulliform, 12.5–27.5 × 2.5–4 μm. *Conidia* hyaline, aseptate, smooth-walled, cylindrical, both ends rounded, 15–21 × 4.5–5.5 μm (av. ± SD = 17.7 ± 1.4 × 4.9 ± 0.3 μm), L/W ratio = 3.6. *Appressoria* single, sometimes in loose group, pale to medium brown, clavate or elliptical, with entire margin, 5.5–11.0 × 4.0–5.5 μm (av. ± SD = 7.8 ± 1.5 × 4.6 ± 0.5 μm), L/W ratio = 1.7.

Other specimens examined – CHINA. Anhui Province, Lu'an City, Shucheng County, on leaves of *Camellia oleifera*, 24 Feb. 2017, C.L. Hou & Q.T. Wang, living culture CNUCC 71C-2-2; *ibid.*, on leaves of *Camellia sinensis*, 24 Feb. 2017, C.L. Hou & Q.T. Wang, living culture CNUCC 90C-4-2. CHINA. Hubei Province, Yichang City, Shennongjia Forestry Area, on leaves of *Camellia sinensis*, Jul. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 163-2-1; *ibid.*, Shennongjia Forest Region, on leaves of *Camellia sinensis*, 7 May 2019, C.L. Hou & Q.T. Wang, living culture CNUCC 409B-3-2; *ibid.*, Henan Province, Xinyang, on leaves of *Camellia sinensis*, 12 Oct. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 898-1-1; *ibid.*, Yunnan Province, Lijiang City, Yulong County, on leaves of *Vaccinium dunalianum* var. *urophyllum* Rehd.et Wils., 20 Jul. 2013, C.L. Hou & Q.T. Wang, living cultures CFCC 50818 and CFCC 50819.

Notes – *Colletotrichum yulongense* was initially considered close to *C. henanense*. In Wang et al. (2019c), the appressoria of *C. yulongense* is longer than those of *C. henanense*, and the result of PHI analysis showed that there is no significant recombination between these two species (Φw = 1), thus *C. yulongense* was described as a new species. However, in this study, with more *C. henanense* strains included in the analysis, both six-locus tree (Fig. 18) and two-locus tree (Fig. 19), all *C. yulongense* strains clustered with the type strain of *C. henanense*. Liu et al. (2015) indicated that the analyses combining *apmat* and *gs* gene was very effective in species delimitation in the *C. gloeosporioides* complex. However, Wang et al. (2019c) did not utilize *apmat* and *gs* genes for their analysis. In this study, the *apmat* gene of *C. yulongense* was sequenced, and the result of *apmat-gs* phylogenetic analysis showed that *C. yulongense* clustered with *C. henanense*. And the sequence similarities between *C. yulongense* and *C. henanense* are very high, which are *act* 99.19%, *apmat* 99.58%, *gapdh* 98.59%, ITS 99.62%, *tub2* 99.54%, cal 99.72%, and *gs* 98.89%, respectively. For morphology, the conidia of *C. yulongense* (Wang et al. 2019c) and *C. henanense* (Liu et al. 2015) are similar in shape and size. Therefore, based on morphology analysis combined with multi-locus phylogenetic analysis, *C. yulongense* is considered conspecific to *C. henanense*, and treated as a synonym of *C. henanense*.

Colletotrichum henanense has been reported only in China, on *Camellia* spp. and *Cirsium japonicum*. The isolates obtained in this study were also isolated from *Camellia oleifera* and *Ca. sinensis*. And as *C. yulongense* was treated as a synonym of *C. henanense*, the host range of *C. henanense* has been expanded accordingly. These indicated that *C. henanense* may be the dominant parasite of *Camellia* spp., but *C. henanense* may also have a wider host range.

Colletotrichum karsti Y.L. Yang, Z.Y. Liu, K.D. Hyde & L. Cai, Cryptogonia Mycologia 32(3): 241 (2011) Fig. 35

≡ *Colletotrichum spicati* Z.F. Yu, Journal of Fungi 8(1): 16 (2022)

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

Colonies on PDA 54–63 mm diam. in 7 days, flat with entire edge, pale white (#ffffff), aerial mycelium dense, reverse white (#ffffff). On PDA, conidiomata scattered or gregarious, black. *Conidial masses* vivid orange (#ffae1a), produced from conidiomata. *Vegetative hyphae* hyaline, smooth-walled, septate, branched. *Setae* not observed. *Conidiophores* hyaline, solitary, usually reduced to conidiogenous cells. *Conidiogenous cells* hyaline, septate, smooth-walled, cylindrical to ampulliform, 12–35 × 3.0–5.0 μm. *Conidia* hyaline, aseptate, smooth-walled, straight, cylindrical, both ends rounded, sometimes with a prominent hilum, 12.5–15.5 × 5.5–6.5 μm (av. ± SD = 13.8 ± 0.8 × 6.0 ± 0.3 μm), L/W ratio = 2.3. *Appressoria* single, pale to medium brown, sub-ellipsoidal to bullet-shaped, smooth-walled to undulate, 8.5–13.5 × 6.0–9.0 μm (av. ± SD = 11.1 ± 1.5 × 7.0 ± 0.8 μm), L/W ratio = 1.6.

Other specimens examined – CHINA. Guangxi Province, Guilin City, Lingchuan County, on leaves of *Cunninghamia lanceolata*, 28 May 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 731B-1-3; *ibid.*, on leaves of *Camellia oleifera*, 28 May 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 770A-2-1; *ibid.*, on leaves of *Camellia oleifera*, 28 May 2021, C.L. Hou & Q.T. Wang, living cultures CNUCC 777-3-1, CNUCC 778-1; *ibid.*, Zhejiang Province, Deqing County, Mogan Mountain, on leaves of *Cleyera japonica* Thunb., 2 Nov. 2018, C.L. Hou & Q.T. Wang,

living culture CNUCC 181B-4-4; *ibid.*, Zhejiang Province, Jinhua City, on leaves of *Camellia oleifera*, 2 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 207-1-1; *ibid.*, Henan Province, Xinyang, on leaves of *Camellia sinensis*, 12 Oct. 2021, C.L. Hou & Q.T. Wang, living culture 904-2-3; *ibid.*, Henan Province, Xinyang City, on leaves of *Dalbergia hupeana*, 12 Oct. 2021, C.L. Hou & Q.T. Wang, living cultures 914-1-2, 914-2-1; *ibid.*, Anhui Province, Lu'an City, Shucheng County, on leaves of *Cunninghamia lanceolata*, Feb. 2017, C.L. Hou & Q.T. Wang, living culture CNUCC 96-13-3; *ibid.*, Fujian Province, Quanzhou City, Anxi County, on leaves of *Camellia oleifera*, 1 Feb. 2018, living culture CNUCC 104A-3-1; *ibid.*, Yunnan Province, Kunming, Xishan Scenic Area, on leaves of *Fagopyrum gracilipes* (Hemsl.) Damm. ex Diels, 8 Aug. 2019, C.L. Hou & Q.T. Wang, living culture CNUCC 451-2-1; *ibid.*, Hubei Province, Wuhan City, Huazhong Agricultural University, on leaves of *Cunninghamia lanceolata*, 9 Feb. 2017, C.L. Hou & Q.T. Wang, living culture CNUCC 61-24-1.

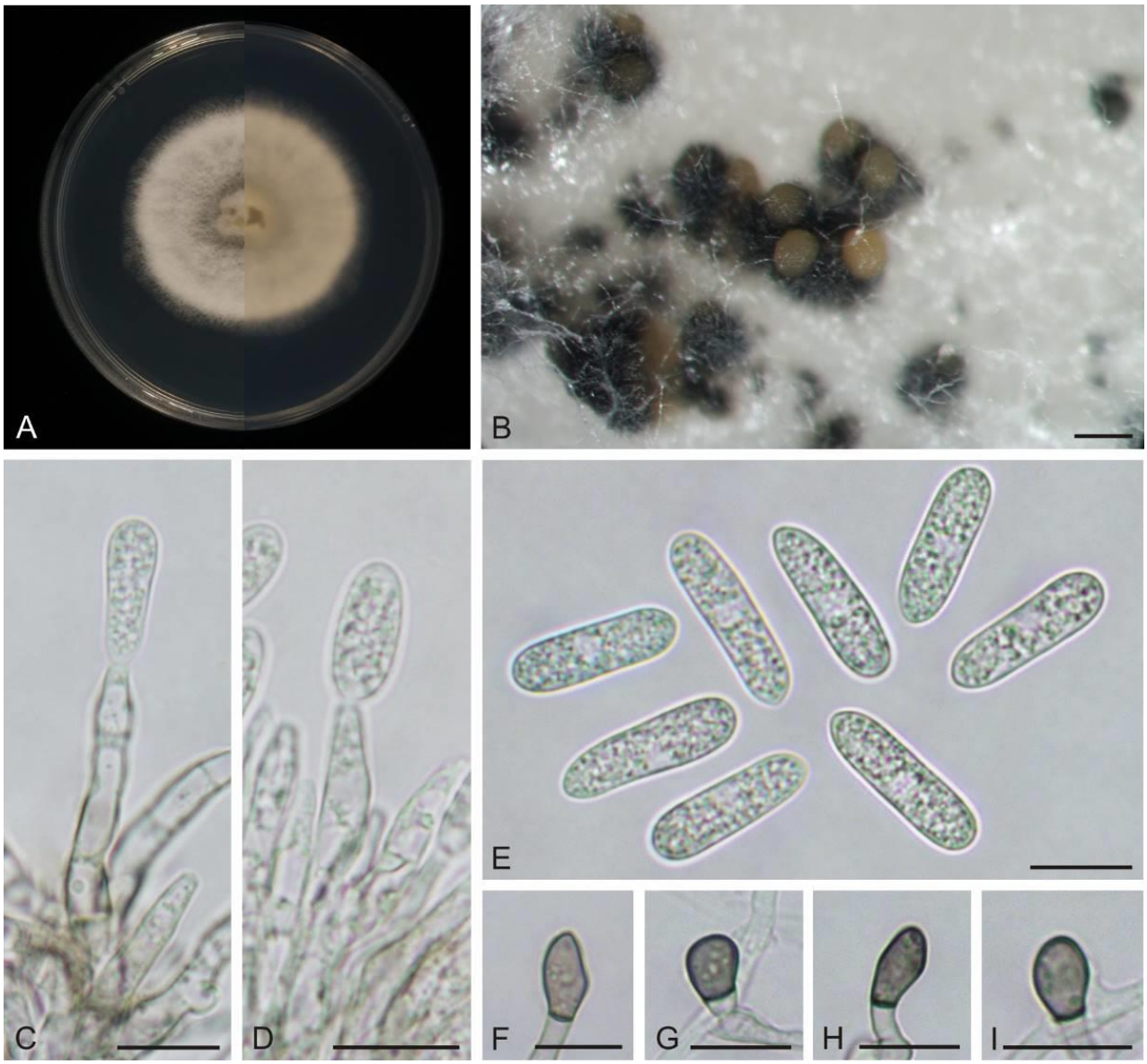


Figure 34 – *Colletotrichum henanense* (Strains CNUCC 71C-2-2). A Front (left) and back (right) views of 7-d-old PDA culture. B Conidiomata. C–D Conidiogenous cells. E Conidia. F–I Appressoria. A–I from PDA. Scale bars: B = 200 μm, C–I = 10 μm.

Notes – *Colletotrichum karsti* has a wide host range and has been reported on many economically important herbaceous and woody plants in China, such as the species of *Camellia* and

Citrus, as well as *Nicotiana tabacum*, *Capsicum annuum* L., and *Taxus wallichiana* var. *mairei* (Lemee & H. Léveillé) L. K. Fu & Nan Li, etc. This is the first time that *C. karsti* is reported on the species of *Fagopyrum* and *Cleyera* worldwide.

The type strains of *C. spicati* and *C. celtidis* clustered in the *C. karsti* clade. The sequence similarities of *chs-1*, ITS, and *tub2* between *C. karsti* and *C. spicati*, as well as between *C. karsti* and *C. celtidis*, are all above 99%. In the single-locus phylogenetic tree of act, *C. karsti* formed multiple clades, and *C. spicati* and *C. celtidis* were clustered in different clades of *C. karsti*. In morphology, the conidia of *C. spicati* (Yu et al. 2022), *C. celtidis* (Tennakoon et al. 2021), and *C. karsti* (Yang et al. 2011) are all cylindrical and the size are also very similar. Thus, *C. spicati* and *C. celtidis* are considered conspecific to *C. karsti*, and treated as synonyms of *C. karsti* in this study.

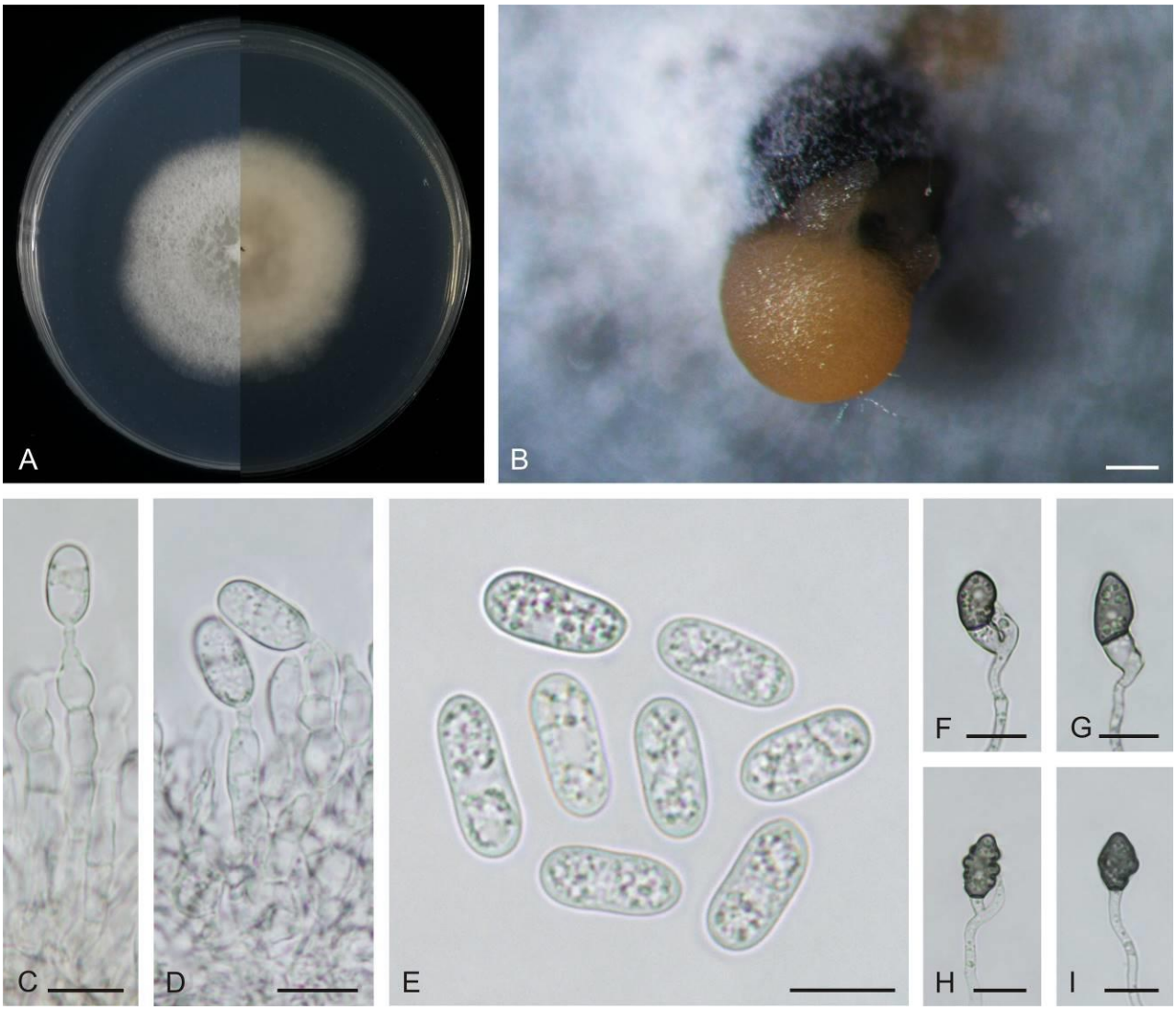


Figure 35 – *Colletotrichum karsti* (Strain CNUCC 778-1-1). A Front (left) and back (right) views of 7-d-old PDA culture. B Conidiomata. C–D Conidiogenous cells. E Conidia. F–I Appressoria. A–I from PDA. Scale bars: B = 200 μm, C–I = 10 μm.

Colletotrichum nymphaeae (Pass.) Aa, Netherlands Journal of Plant Pathology, 84(3): 110 (1978) Fig. 36

≡ *Colletotrichum simulanticitri* Z.F. Yu, Journal of Fungi 8(2): 24 (2022)

Colonies on PDA 45–59 mm diam. in 7 days, flat with entire edge, pale white (#ffffff), aerial mycelium dense, reverse very dark orange (#644e25) in the centre and white (#ffffff) towards margin. On SNA amended with pine needle, conidiomata scattered or gregarious, black. *Conidial*

masses pale orange (#ffdc9d), produced from conidiomata. *Vegetative hyphae* hyaline, smooth-walled, septate, branched. Setae not observed. *Conidiophores* pale brown, solitary or gregarious, usually reduced to conidiogenous cells. *Conidiogenous cells* hyaline, aseptate or 1-septate, smooth-walled, cylindrical to ampulliform, 9–30 × 2–3.5 μm. *Conidia* hyaline, aseptate, smooth-walled, straight, cylindrical to fusiform, both ends acute or one end rounded and one end acute, 10–12.5 × 5.5–6.5 μm (av. ± SD = 11.2 ± 0.8 × 6.0 ± 0.3 μm), L/W ratio = 1.9. *Appressoria* single, medium brown, globose to ellipsoidal, the edge entire, 6.0–10.5 × 4.5–7.0 μm (av. ± SD = 7.4 ± 1.0 × 5.6 ± 0.7 μm), L/W ratio = 1.3.

Other specimens examined – CHINA. Guizhou Province, Guiyang City, Xifeng County, on leaves of *Camellia sinensis*, 27 Aug. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 815-1-1; *ibid.*, on leaves of *Camellia sinensis*, 27 Aug. 2021, C.L. Hou & Q.T. Wang, living cultures CNUCC 819B-2-2, CNUCC 820A-2-2; *ibid.*, Wen'an County, on leaves of *Fatsia japonica* (Thunb.) Decne. et Planch., 20 Aug. 2019, C.L. Hou & Q.T. Wang, living culture CNUCC 469-3-1; *ibid.*, Zhejiang Province, Jinhua City, on leaves of *Carya cathayensis* Sarg., 3 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 234-3-4; *ibid.*, Guangxi Province, Guilin City, Xing'an County, on leaves of *Camellia oleifera*, 28 May 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 766B-1-3; *ibid.*, Hubei Province, Yichang City, Shennongjia Forestry Area, on leaves of *Camellia sinensis*, Jul. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 163-2-2-1.

Notes – *Colletotrichum nymphaeae* has a wide host range and has been discovered on important economic forest and fruit trees in China such as the plants of *Camellia*, *Carya*, *Citrus*, and *Eriobotrya*.The type strains of *C. simulanticitri* and *C. nymphaeae* clustered together with high support values in the phylogenetic tree of *C. acutatum* complex (MBP = 100, PP = 1.00) (Fig. 1). The sequence similarities of *act*, *chs-1*, *gapdh*, and ITS between the type strains of *C. simulanticitri* and *C. nymphaeae* are 99.59%, 100%, 99.19%, and 99.26% respectively. For morphology, *C. simulanticitri* and *C. nymphaeae* both could produce cylindrical and at least one acute end conidia, as well as clavate appressoria (Yu et al. 2022). The conidia of the strain YMF 107312 of *C. simulanticitri* are slightly shorter than those of strain CBS 515.78 of *C. nymphaeae* (10–13.5 μm vs. 14–18.5 μm), but similar with those of strain CBS 173.51of *C. nymphaeae* (10–13.5 μm vs. 10–14.5 μm) (Damm et al. 2012). Moreover, Damm et al. (2012) showed that the morphological characteristics of *C. nymphaeae* strains have slightly differences. Therefore, based on morphology combined with multigene phylogenetic analysis, *C. simulanticitri* is considered conspecific to *C. nymphaeae* and treated as a synonym of *C. nymphaeae*.

Colletotrichum aenigma B.S. Weir & P.R. Johnst., Studies in Mycology. 73: 135 (2012)

Holotype – ISRAEL, from *Persea americana*, S. Freeman, holotype PDD 102233; ex-type ICMP 18608 (Weir et al. 2012).

Other specimens examined – CHINA. Henan Province, Xinyang City, on leaves of *Camellia oleifera*, 12 Oct. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 883-1-2; *ibid.*, on leaves of *Camellia sinensis*, 12 Oct. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 908B-1-2; *ibid.*, Kaifeng City, Lankao County, on leaves of *Paulownia fortunei*, 14 Oct. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 956-1-2.

Notes – This species was described and illustrated in detail by Weir et al. (2012). *Colletotrichum aenigma* has a wide range of hosts, including herbaceous plants, shrubs, and trees, and many of them have high economic value, such as *Vigna unguiculata* (L.) Walp. and the species in *Capsicum*, *Vitis*, *Pyrus*, and *Camellia*. This is the first time that *C. aenigma* is reported on the species of *Paulownia* worldwide.

Colletotrichum bambusicola C.L. Hou & Q.T. Wang, Mycologia 113: 450–458 (2021)

Holotype – CHINA. Guangxi Zhuang Autonomous Region, from seeds of *Phyllostachys edulis* (Carriere) J. Houzeau, Sep. 2016, C.L. Hou & Q.T. Wang, holotype CAF80001, ex-type CFCC 54250 = ACCC 39709 = CNUCC 307307 (Wang et al. 2021).

Other specimens examined – CHINA. Guangxi Province, on seeds of *Phyllostachys edulis*, Mar. 2016, C.L. Hou & Q.T. Wang, living cultures CNUCC 305200, CNUCC 305203, CNUCC 305286, CNUCC 306122, CNUCC 30613, CNUCC 30893, CNUCC 30910, CNUCC 310192; *ibid.*, Hunan Province, Yongzhou City, Shuangpai County, on leaves of *Coptosapelta diffusa* (Champ. ex Benth.) Van Steenis, 20 Apr. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 618-3-2.

Notes – This species was described and illustrated in detail by Wang et al. (2021). *Colletotrichum bambusicola* was only discovered on Bambusoideae originally, and considered that may have host preference to bamboo. With the expansion of the sampling range, Liu et al. (2022) isolated this species from *Petasites hybridus* (Asteraceae) and *Patrinia villosa* (Valerianaceae). This is the first time that this species was reported on the host *Coptosapelta diffusa*, indicating that it may have a wide host range.

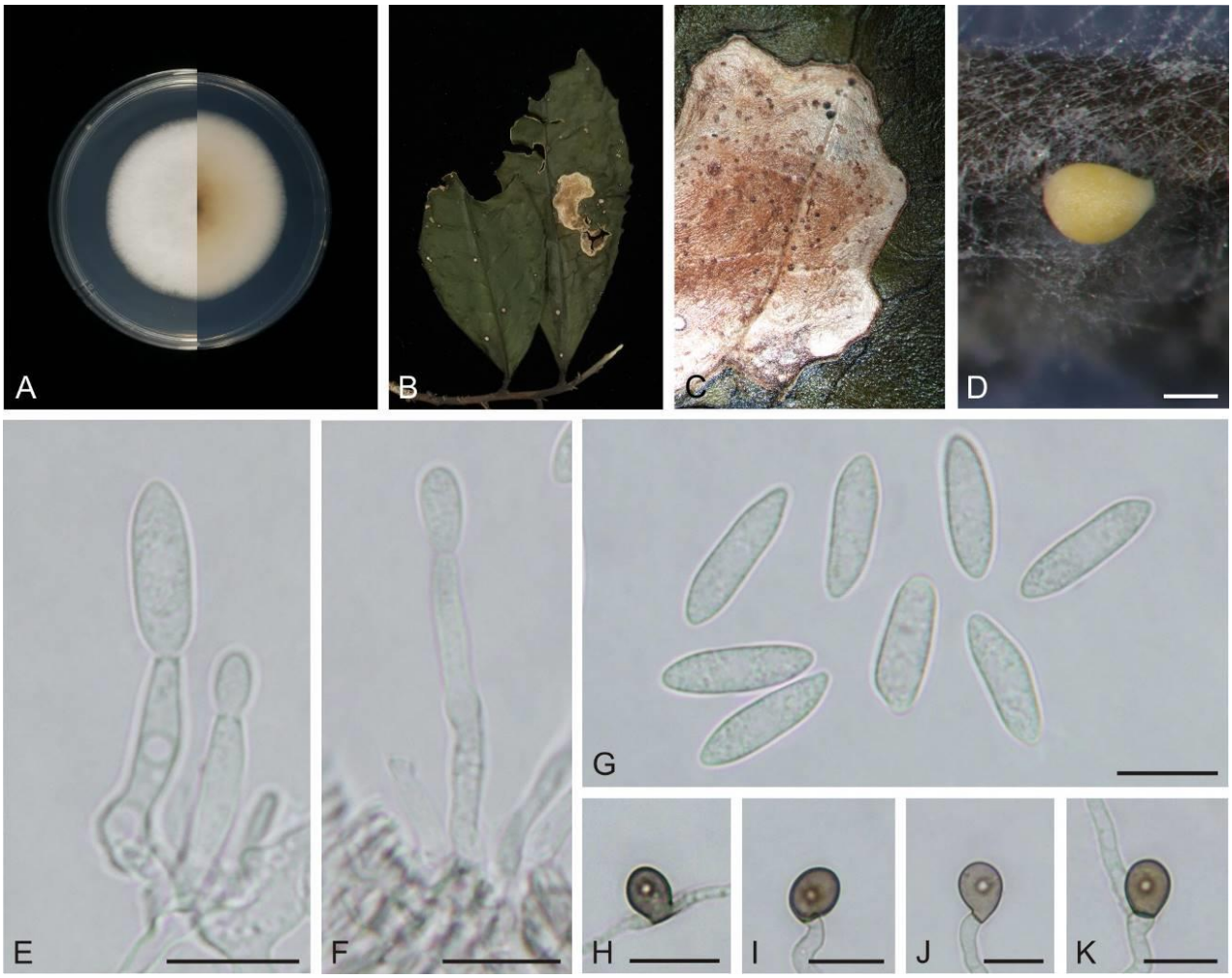


Figure 36 – *Colletotrichum nymphaeae* (Strains CNUCC 163-2-2-1). A Front (left) and back (right) views of 7-d-old PDA culture. B–C Symptoms on a leaf of *Camellia sinensis*. D Conidiomata on pine needle. E–F Conidiogenous cells. G Conidia. H–K Appressoria. A from PDA. D–K from SNA with pine needle. Scale bars: D = 200 μm, E–K = 10 μm.

Colletotrichum cangyuanense Z.F. Yu, Journal of Fungi 8(2): 12 (2022)

Holotype – CHINA, Yunnan province, Cangyuan county, isolated as an endophyte from *Ageratina adenophora* (Sprengel) R. M. King & H. Robinson, Aug. 2016, Han-Bo Zhang, holotype YMF 1.05001, ex-type CGMCC3.18969 (Yu et al. 2022).

Other specimens examined – CHINA. Fujian Province, Wuyishan City, on leaves of *Cunninghamia lanceolata*, 21 Apr. 2017, C.L. Hou & Q.T. Wang, living culture CNUCC 103-13-3;

ibid., Quanzhou City, Anxi County, on leaves of *Camellia oleifera*, 1 Feb. 2018, C.L. Hou & Q.T. Wang, living cultures CNUCC 104C-3-1, CNUCC 104C-16-1; *ibid.*, Longyan City, on leaves of *Cunninghamia lanceolata*, 21 Apr. 2017, C.L. Hou & Q.T. Wang, living cultures 106-17, 106-17-1; *ibid.*, Sichuan Province, Leshan City, Muchuan County, on leaves of *Cunninghamia lanceolata*, 5 Dec. 2016, C.L. Hou & Q.T. Wang, living cultures CNUCC 22-21-2, CNUCC 22-23-2, CNUCC 22-24-3; *ibid.*, Zhejiang Province, Jinhua City, on leaves of *Cunninghamia lanceolata*, 3 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 245-3-4; *ibid.*, Guizhou Province, Tongren City, on leaves of *Cunninghamia lanceolata*, 7 Feb. 2017, C.L. Hou & Q.T. Wang, living culture CNUCC 59B-51-4; *ibid.*, Jiangxi Province, Xinyu City, Fenyi County, on leaves of *Cunninghamia lanceolata*, 22 Apr. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 655A-1-4; *ibid.*, Anhui Province, Lv'an City, Shucheng County, on leaves of *Cunninghamia lanceolata*, 24 Feb. 2017, C.L. Hou & Q.T. Wang, living cultures CNUCC 94-4-4, CNUCC 96-7-1.

Notes – This species was described and illustrated in detail by Yu et al. (2022). *Colletotrichum cangyuanense* was originally isolated as endophyte from herbaceous plants, *Ageratina adenophora* (Yu et al. 2022), but it was isolated as the major pathogenic fungus from the woody plant *Cunninghamia lanceolata* in He et al. (2022). This is the first time that *C. cangyuanense* was reported on the species of *Camellia*, which indicated that *C. cangyuanense* may have multiple lifestyles and a wide host range. But in this study, the isolates of this species were all obtained from *Cunninghamia lanceolata* in different provinces of China except the isolates CNUCC 104C-3-1 and CNUCC 104C-16-1, which indicated that this species may be the main pathogen of China for anthracnose and needs more attention in the prevention.

Colletotrichum fioriniae (Marcelino & Gouli) Pennycook, Mycotaxon 132(1): 150 (2017)

Holotype – New York, from mummified adult *Fiorinia externa* Ferris (Insecta, Diaspididae), 2005, J. Marcelino & S. Gouli, ex-type, CBS 128517 = ARSEF 10222 (Pennycook et al. 2017).

Other specimens examined – CHINA. Anhui Province, Lu'an City, Huoshan County, on leaves of *Camellia oleifera*, Nov. 2016, C.L. Hou & Q.T. Wang, living culture CNUCC 10-4-3; *ibid.*, Shucheng County, on leaves of *Camellia oleifera*, 15 May 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 154-3-4; *ibid.*, Shucheng County, on leaves of *Camellia sinensis*, 24 Feb. 2017, C.L. Hou & Q.T. Wang, living culture CNUCC 90B-1-1; *ibid.*, Xuancheng City, Jingde County, on leaves of *Camellia sinensis*, 13 May 2018, C.L. Hou & Q.T. Wang, living cultures CNUCC 111B-1-4, CNUCC 111B-2-1; *ibid.*, Xuancheng City, Jingde County, on leaves of *Akebia trifoliata* (Thunb.) Koidz., 13 May 2018, C.L. Hou & Q.T. Wang, living cultures CNUCC 117-2-1, CNUCC 117-3-2; *ibid.*, Xuancheng City, Jingde County, on leaves of *Camellia sinensis*, 2 May 2018, C.L. Hou & Q.T. Wang, living cultures CNUCC 1297-3-2; *ibid.*, Huangshan City, on leaves of *Ilex latifolia* Thunb., 28 Apr. 2019, C.L. Hou & Q.T. Wang, living culture CNUCC 440B-2-2; *ibid.*, Chizhou City, Qingyang County, on leaves of *Cunninghamia lanceolata*, 21 Apr. 2015, C.L. Hou & Q.T. Wang, living cultures CNUCC 50905-1, CNUCC 440B-2-2; *ibid.*, Hunan Province, Yongzhou City, Shuangpai County, on leaves of *Rhododendron simsii* Planch., 20 Apr. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 610-2-2; *ibid.*, Hunan Province, Yongzhou City, Shuangpai County, on leaves of *Castanopsis eyrei* (Champ. ex Benth.) Tutch., 20 Apr. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 612A-3-1; *ibid.*, Hunan Province, Yongzhou City, Shuangpai County, on leaves of *Camellia sinensis*, 20 Apr. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 629-1-3; *ibid.*, Guangxi Province, Guilin City, Lingchuan County, on leaves of *Cinnamomum camphora*, 28 May 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 713A-1-1; *ibid.*, Guangxi Province, Guilin City, Lingchuan County, on leaves of *Cinnamomum camphora*, 28 May 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 716B-2-2; *ibid.*, Guangxi Province, Guilin City, Xing'an County, on leaves of *Camellia oleifera*, 28 May 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 762B-1-1; *ibid.*, Fujian Province, Quanzhou City, on leaves of *Camellia oleifera*, 1 Feb. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 104A-7-4; *ibid.*, Fujian Province, Sanming City, Youxi County, on leaves of *Cunninghamia lanceolata*, 21 Apr. 2017, C.L. Hou & Q.T. Wang, living culture CNUCC 110-4-1; *ibid.*, Zhejiang Province, Huzhou

City, Deqing County, Mogan Mountain, on leaves of *Diospyros kaki* var. *silvestris*, 2 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 184-3-2; *ibid.*, Zhejiang Province, Wenzhou City, Rui'an County, on leaves of *Camellia oleifera*, 4 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 265A-1-1; *ibid.*, Hubei Province, Yichang City, on leaves of *Camellia sinensis*, 24 Jul. 2018, C.L. Hou & Q.T. Wang, living cultures CNUCC 163-1-1, CNUCC 163-1-2; *ibid.*, Hubei Province, Shennongjia Forest Region, on leaves of *Camellia oleifera*, 7 May 2019, C.L. Hou & Q.T. Wang, living culture CNUCC 349-4-1; *ibid.*, Henan Province, Xinyang City, Siwang Mountain, host *Camellia sinensis*, 12 Oct. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 916-1-1; *ibid.*, Henan Province, Kaifeng City, Lankao County, host *Paulownia fortunei* (Seem.) Hemsl., 14 Oct. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 957-2-1; *ibid.*, Guizhou Province, Guiyang City, Xifeng County, on leaves of *Camellia oleifera*, 27 Aug. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 839A-2-1.

Notes – In Damm et al. (2012), the clade of *Colletotrichum fioriniae* formed two subclades with low support values, which failed to support them as two species. Thus, Damm et al. (2012) considered the segregation of *C. fioriniae* clades as intraspecific heterogeneity. Chen et al. (2022) constructed multi-locus phylogenetic tree using their own strains and the *C. fioriniae* strains selected from Damm et al. (2012). The results indicated that *C. fioriniae* clade formed two subclades with high support values. The PHI test indicates that there is no significant recombination between these two subclades (Φw = 0.15), therefore Chen et al. treated the subclade which not contained the type strain of *C. fioriniae* as a new species, named *C. orientalis*. Zhang et al. (2023) compared sequence similarity and the shape and size of spores and concluded that *C. orientalis* and *C. fioriniae* belong to the same species. More isolates of *C. fioriniae* are included in the multi-locus phylogenetic analysis in the present study, and although the *C. fioriniae* clade still formed two subclades, the support values of these two subclades are very low, which is consistent with Damm et al. (2012). The value of PHI test (Φw = 0.1927) (Fig. 2) has no significant increasing. Furthermore, the sequences similarities of type strain of *C. orientalis* and *C. fioriniae* are very high, consistent with the result of zhang et al. (*act* 99.10%, *chs-1* 99.29%, *gapdh* 99.21%, ITS 100.00%, and *tub2* 99.39%, respectively). Based on multi-locus phylogenetic analysis, combined with morphology analysis, PHI test, GCPSR, bPTP analysis, and GMYC single threshold analysis, we prefer that the two subclades of *C. fioriniae* are due to intraspecific divergence, consider *C. orientalis* and *C. fioriniae* to be the same species.

This is the first record that *C. fioriniae* was reported on *Cunninghamia lanceolata*, *Camellia oleifera*, *Akebia trifoliata*, *Diospyros kaki* var. *silvestris*, *Castanopsis eyrei*, and *Paulownia fortunei* in the world.

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

Holotype – Denmark, from seed of *Clarkia* (syn. *Godetia*) *hybrida* cv. Kelvedon Glory 463 C in seed disinfection experiment, 17 Jun. 1943, P. Neergaard, ex-type CBS 133.44 (Zhang et al. 2023).

Other specimens examined – CHINA. Hubei Province, Yichang City, on leaves of *Camellia sinensis*, 6 May 2019, C.L. Hou & Q.T. Wang, living cultures CNUCC 354-2-1, CNUCC 354-4-2; *ibid.*, on leaves of *Camellia sinensis*, 6 May 2019, C.L. Hou & Q.T. Wang, living culture CNUCC 363A-1-1; *ibid.*, Yunnan Province, Kunming, Xishan Scenic Area, on leaves of *Fagopyrum gracilipes*, 8 Aug. 2019, C.L. Hou & Q.T. Wang, living cultures CNUCC 451-3-2, CNUCC 453-1-3; *ibid.*, Yunnan Province, Kunming, Xishan Scenic Area, on leaves of *Fagopyrum gracilipes*, 8 Aug. 2019, C.L. Hou & Q.T. Wang, living culture CNUCC 456-2-1.

Notes – This species was described and illustrated in detail by Damm et al. (2012). By comparing the morphological features, the conidia length of the isolates obtained in this study is longer than those of the ex-type strain of *C. godetiae* CBS 133.44 (14–17 μm vs. 10.5–14.5 μm), but similar to that of *C. godetiae* CBS 862.70 (14–17 μm vs. 14–19 μm). And Damm et al. (2012) also point out that there are differences between different *C. godetiae* isolates in the shape and size of conidia. Although there are many subclades in *C. godetiae* clade, the support values of these

clades are low, which indicated that there may have differentiation within *C. godetiae*, but it not reached the species level.

The host range of *C. godetiae* are wide, and this species has been reported on various herbaceous and woody plants, such as the species of *Eriobotrya japonica* and *Juglans regia*, as well as, *Fragaria*, *Vitis*, *Acer*, and *Prunus*, but have not reported in China before. This study is the first time to isolate *C. godetiae* in China, and also the first time that this species has been reported on the species of *Fagopyrum*, *Lespedeza*, *Ilex*, and *Camellia* in worldwide.

Colletotrichum pseudomajus F. Liu, L. Cai, Crous & Damm, Persoonia 33: 91 (2014)

Holotype – CHINA, Taiwan, from branch of *Camellia sinensis*, unknown collection date and collector (isolated by J. Chen), holotype CBS H-21493, ex-type CBS 571.88 (Liu et al. 2014).

Other specimens examined – CHINA. Anhui Province, Lu'an City, Shucheng County, on branches of *Camellia sinensis*, 15 May 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 1311-1-3; *ibid.*, Zhejiang Province, Wenzhou, Rui'an County, on branches of *Camellia sinensis*, 4 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC CFCC 59180.

Notes – This species was described and illustrated in detail by Liu et al. (2014). *Colletotrichum pseudomajus* is only isolated from the branches of *Camellia sinensis* currently, suggesting that it may have strong host specificity.

Colletotrichum schimae F. Liu, W.P. Wu & L. Cai, Studies in Mycology, 101: 38 (2022)

Holotype – CHINA, Hunan Province, Chenzhou, Yizhang County, Mangshan, from healthy leaves of *Schima* sp., 12 Apr. 2002, W.P. Wu, holotype HMAS 350647, ex-type culture CGMCC 3.20526 = LC13880 = NN046984 (Liu et al. 2022).

Other specimens examined – CHINA. Yunnan Province, Pu'er City, Jiangcheng County, on leaves of *Camellia sinensis* var. *assamica*, 21 Feb. 2019, C.L. Hou & Q.T. Wang, living culture CNUCC 324C-1-5-2; *ibid.*, Hunan Province, Chenzhou City, on leaves of *Ilex chinensis* Sims, 19 Jul. 2020, C.L. Hou & Q.T. Wang, living culture CNUCC 528-2-2.

Notes – This species was described and illustrated in detail by Liu et al. (2022). *Colletotrichum schimae* was previously reported only on *Schima* spp. This study is the first time that this species reported on the species of *Ilex* and *Camellia* in worldwide, which revealed that this species may have a wider host range.

Colletotrichum siamense Prihast., L. Cai & K.D. Hyde, Fungal Diversity 39: 98 (2009)

Holotype – THAILAND, Chiang Mai Province, Mae Taeng District, Mae Lod Village, Royal Agricultural Project Coffee, on berry of *Coffea arabica*, 16 Jan. 2008, H. Prihastuti, holotype MFLU 090230, ex-type ICMP 18578 = CBS 130417 (Prihastuti et al. 2009).

Other specimens examined – CHINA. Zhejiang Province, Huzhou City, Deqing County, on leaves of *Parthenocissus tricuspidata*, 2 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 191-3-1; *ibid.*, on leaves of *Lindera glauca*, 2 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 180-1-3; *ibid.*, on leaves of *Litsea cubeba*, 2 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 196-4-1; *ibid.*, Jinhua City, on leaves of *Vernicia fordii* (Hemsl.) Airy Shaw, 2 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 211-5-2; *ibid.*, Jinhua City, on leaves of *Camellia oleifera*, 3 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 225B-1-4; *ibid.*, Jinhua City, on leaves of *Machilus nanmu* (Oliver) Hemsley, 3 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 236-4-4; *ibid.*, Wenzhou City, on leaves of *Lauraceae* sp., 4 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 284-1-1; *ibid.*, Wenzhou City, on leaves of *Firmiana simplex* (L.) W. Wight, 4 Nov. 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 271-5-1; *ibid.*, Guangxi Province, Guilin City, Lingchuan County, on leaves of *Cinnamomum camphora*, 28 May 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 717-2-1; *ibid.*, Guangxi Province, Guilin City, Xing'an County, on leaves of *Camellia oleifera*, 28 May 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 766A-1-3; *ibid.*, Guangxi Province, Guilin City, Lingchuan County, on leaves of *Cinnamomum camphora*, 28 May 2021, C.L. Hou & Q.T. Wang, living

culture CNUCC 712A-1-1; *ibid.*, Jiangxi Province, Xinyu City, Fenyi County, on leaves of *Camellia oleifera*, 22 Apr. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 679-1-1; *ibid.*, Jiangxi Province, Xinyu City, Fenyi County, on leaves of *Osmanthus fragrans*, 22 Apr. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 694-2-1; *ibid.*, Jiangxi Province, Xinyu City, Fenyi County, on leaves of *Osmanthus fragrans*, 22 Apr. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 694-3-4-1; *ibid.*, Hubei Province, Wuhan City, Huazhong Agricultural University, on leaves of *Cunninghamia lanceolata*, 9 Feb. 2017, C.L. Hou & Q.T. Wang, living culture CNUCC 61-20-3; *ibid.*, Hubei Province, Wuhan City, Huazhong Agricultural University, on leaves of *Cunninghamia lanceolata*, 9 Feb. 2017, C.L. Hou & Q.T. Wang, living culture CNUCC 61-25-1; *ibid.*, Hunan Province, Changsha City, Yuelu Mountain, on leaves of *Euonymus alatus* (Thunb.) Sieb., 21 Jul. 2020, C.L. Hou & Q.T. Wang, living culture CNUCC 540-1-3; Place of collection unknown, on leaves of *Phyllostachys propinqua* McClure, time of collection unknown, C.L. Hou & Q.T. Wang, living culture CNUCC BL311-1.

Notes – This species was described and illustrated in detail by Prihastuti et al. (2009). In six-locus and two-locus phylogenetic trees, the *Colletotrichum siamense* clade not have high support values, and there are many subclades within the *C. siamense* clade (Figs 18, 19). In previous studies, some subclades were treated as different species, but Liu et al. (2016b) indicated that should be same species based on GMYC, PTP, mating experiments. However, the sequence similarity of some genes between different subclades are very low, and also have some differences in morphology.

The *Colletotrichum siamense* clade did not receive high support values in the six-locus and two-locus phylogenetic trees, and there are many subclades within the *C. siamense* clade (tree diagram). In previous studies, some subclades were treated as different species, but the study of Liu et al. (2016b) showed that these species should all be *C. siamense* by GMYC, PTP, and mating type experiments. However, this study found low sequence similarity of some genes between different subclades within this clade and slight differences in morphology. Such as strain CNUCC 191-3-1, the sequence similarities of *cal* and *gapdh* between CNUCC 191-3-1 and *C. siamense* type strain ICMP 18578 is high, which are 99.56% and 99.57%, respectively. While other genes sequence similarity is low, 98.78% for *act*, 97.67% for *chs-1*, 98.48% for *gs*, 98.43% for ITS, and 98.66% for *apmat*. For morphology, the conidia of these two species are very similar, but the appressoria of 191-3-1 is longer than that of *C. siamense* ICMP 18578 (8–11.5 μm vs. 4.7–8.3 μm) (Prihastuti et al. 2009).

The strains of *Colletotrichum parvisporum* Z.F. Yu clustered in *C. siamense* clade, and the sequence similarities between the type strains of *C. parvisporum* and *C. siamense* of *act*, *chs-1*, and *tub2* are high, which are 100.00%, 99.56%, and 99.51%, respectively. However, the sequence similarities of other genes are low, with *apmat* 97.49%, *gapdh* 98.02%, and ITS 98.96%, respectively. For morphology, the conidia of these two species are very similar, but the appressoria of *C. parvisporum* are longer than that of *C. siamense* (7.5–17 μm vs. 4.7–8.3 μm) (Yu et al. 2022). *Colletotrichum menglaense* M. Qiao & Z.F. Yu and *C. pandanicola* Tibpromma & K.D. Hyde also clustered in *C. siamense* clade, by comparing the sequence similarity of the type strain with *C. siamense*, it was found that sequence similarities of the *act*, *gapdh*, ITS, and *tub2* are over 99%, while the similarity of the *chs-1* sequence is low, with 98.21% and 97.78%, respectively. For morphology, *C. pandanicola* and *C. siamense* are closely (Mu et al. 2021), but the appressoria size of *C. menglaense* is longer and wider than that of *C. siamense* (6.7–20.0 × 4.8–11.0 μm vs. 4.7–8.3 × 3.5–5 μm) (Qiao et al. 2021). Therefore, the phylogenetic positions of the subclades of *C. siamense*, as well as *C. parvisporum*, *C. menglaense*, and *C. pandanicola* need further study.

C. siamense has a wide host range and geographical distribution (Jayawardena et al. 2021). This study is the first time that *C. siamense* is reported on *Firmiana simplex*, *Litsea cubeba*, *Lindera glauca*, and *Osmanthus fragrans*.

Colletotrichum sojae Damm & Alizadeh, Studies in Mycology, 92: 35 (2018)

Holotype – USA, Illinois, from *Glycine max*, unknown collection date, J.B. Manandhar (received from R. O'Connell as Ga. glycines, before from J.B. Sinclair), holotype CBS H-21495, ex-type ATCC 62257 = CPC 19367 (Damm et al. 2019).

Other specimens examined – CHINA. Henan Province, Kaifeng City, Lankao County, on leaves of *Paulownia fortunei*, 14 Oct. 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 942-2-4-1.

Notes – This species was described and illustrated in detail by Damm et al. (2019). *C. sojae* has only been isolated from herbaceous plants with high economic value previously, such as the species of *Capsicum* and *Panax*, as well as *Arctium lappa*, *Glycine max* and etc. This is the first time that this species has been reported on *Paulownia fortune*, and also the first time that this species has been obtained from woody plants, which indicated that the host range of this species may be wider and not limited to herbaceous plants.

Colletotrichum subacidae F. Liu, Z.Y. Ma & L. Cai, Studies in Mycology, 101: 40 (2022)

Holotype – CHINA, Guangxi, Chongzuo, Guangxi Nonggang National Nature Reserve, from *Tetrastigma obovatum* (Laws.) Gagnep., Jun. 2017, Z.Y. Ma & L.W. Hou, holotype HMAS 350635, ex-type CGMCC 3.20529 = LC13857 = LH01 (Liu et al. 2022).

Other specimens examined – CHINA. Guangxi Province, Guilin City, Xing'an County, on leaves of *Camellia oleifera*, 28 May 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 764B-2.

Notes – This species was described and illustrated in detail by Liu et al. (2022). In the multi-locus phylogenetic tree, the *Colletotrichum subacidae* clade did not have strong supports (Fig. 22). And *Colletotrichum subacidae* is very closely related to *C. acidi* Samarak. & K.D. Hyde (Fig. 22). The PHI test indicated that there is significant recombination between these two species (Φw = 0.0297) (Fig. 23). But the sequence similarities of *gapdh*, *act*, and *tub2* between these two species are 93.8%, 94.3%, and 97.6%, respectively. Furthermore, in both this study and Liu et al. (2022), *C. subacidae* formed two subclades with high support values (Fig. 22). By comparing the sequence similarities between the represent strains of these two subclades, that of *act* and *gapdh* genes are low, which are 98% and 96.90%, respectively. These indicated that this clade may contain more than one species or in the process of divergence. But need more strains to verify and further confirm the relationship between *C. subacidae* with *C. acidi*.

Colletotrichum subacidae has a wide host range and has previously been isolated from herbaceous plants such as Hosta, and woody plants such as *Tetrastigma obovatum*, *Asparagus officinalis* L., and *Ailanthus altissima* (Mill.) Swingle. This study is the first time that this species is reported on the species of *Camellia* in the world.

Colletotrichum zhaoqingense F. Liu & L. Cai, Studies in Mycology, 101: 47 (2022)

Holotype – China, Zhejiang Province, Hangzhou Botanical Garden, from dead petiole of an unidentified palm (Arecaceae), 12 Jun. 2015, W.P. Wu, holotype HMAS 350646, ex-type CGMCC 3.20536 = LC13878 = NN071035 (Liu et al. 2022).

Other specimens examined – CHINA. Guangxi Province, Guilin City, Lingchuan County, on leaves of *Cinnamomum camphora*, 28 May 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 714-1-1; *ibid.*, on leaves of *Camellia sinensis*, 28 May 2021, C.L. Hou & Q.T. Wang, living culture CNUCC 747-1-3; *ibid.*, Anhui Province, Jingde County, on leaves of *Camellia sinensis*, 13 May 2018, C.L. Hou & Q.T. Wang, living culture CNUCC 110A-4-4.

Notes – This species was described and illustrated in detail by Liu et al. (2022). In the phylogenetic tree, *Colletotrichum zhaoqingense* and *C. gigasporum* formed a strong sister relationship (MBP = 100, PP = 1.00) (Fig. 12). Liu et al. (2022) indicated that the ITS sequences similarities between these two species is 93.2%, however, in this study is 99.3%. The single-gene phylogenetic analysis of *act*, *gapdh* and *tub2* cannot distinguish these two species well (Supplementary Figs 30, 32, 34). PHI test and GMYC analysis supported that they are two species (Figs 13, 14, 15), while bPTP analysis indicated that they were one species (Figs 16, 17). Because the low sequence similarities of *chs-1* and *gapdh* between these two species, and combined with the

results of PHI and GMYC analysis, *C. zhaoqingense* and *C. gigasporum* were tentatively treated as two different species in this study. the phylogenetic relationship between these two species will be further identified by phylogenomics or obtaining more strains.

Colletotrichum zhaoqingense has been previously reported on the species of *Arecaceae* and *Carica papaya* L., and this study is the first time that this species has been identified worldwide from *Camellia* spp. and camphor plants, suggesting that *C. zhaoqingense* may have a wider host range.

Pathogenicity test

The results of pathogenicity tests revealed that the new species *Colletotrichum wenzhouense* and the new host record species *C. karsti* did not demonstrate any infection on the test plants. Similarly, the new species *C. subplurivorum* and *C. hubeiense* showed infection only on their original hosts (Fig. 37). On the other hand, the new species *Colletotrichum luanense*, *C. guiyangense*, and *C. jixiense*, as well as the new host record species *C. aenigma*, *C. fioriniae*, *C. gloeosporioides*, *C. godetiae*, *C. schimae*, *C. siamense*, and *C. subacidae*, were found to be capable of infecting both their original hosts and the three test hosts used in this study (Fig. 37).

Among the identified species, *Colletotrichum luanense* and the newly host recorded species *C. aenigma*, *C. gloeosporioides*, and *C. siamense* exhibited high infection rates and virulence (Tables 4, 5). However, *C. camelliae* was able to infect the leaves of *Ca. oleifera*, *Ca. sinensis*, *Cunninghamia lanceolata*, and *Cinnamomum camphora*, but not the branches of *Camellia sinensis*. *C. pseudomajus* can only infect the branches of *Camellia sinensis*, demonstrated tissue organ-specificity towards the branches of *Ca. sinensis* (Fig. 38).

Comparative genomic analysis of CAZymes

In this study, several species of *Colletotrichum* were selected for carbohydrate-active enzymes family annotation and comparative analysis, including *C. graminicola* (Ces.) G.W. Wilson, *C. sublineola* Henn., and *C. cereale* Manns, which are considered to have host-specificity to Poaceae (Jayawardena et al. 2016). *Colletotrichum bambusicola*, *C. guangxiense* C.L. Hou & Q.T. Wang, and *C. parabambusicola* F. Liu, W.P. Wu & L. Cai have host-specificity to Bambusoideae Nees (Wang et al. 2021). *C. camelliae* is currently only isolated from *Camellia* spp., and *C. pseudomajus* was considered to have organ specificity with branches of *Camellia* spp., while *C. fructicola* has a broad host range.

The comparative genomic analysis of CAZymes (carbohydrate-active enzymes) revealed that *Colletotrichum fructicola*, which has a wide range of hosts, possesses a larger number of CAZymes compared to species with host-specificity or host preference (Fig. 39). Furthermore, the analysis of Venn diagrams highlighted that *C. pseudomajus* possesses two specific carbohydrases, namely GT61 and AA14 (Fig. 40), which are not found in the other eight species included in the comparative analysis of CAZymes. This indicates that *C. pseudomajus* may have unique enzymatic capabilities related to carbohydrate metabolism, specifically in the GT61 and AA14 families.

DISCUSSION

The primary aim of this study is to identify the *Colletotrichum* species that are associated with anthracnose from forest plants.

The 169 strains were isolated from diseased branches and leaf tissues, or healthy leaf tissues from various important forest trees, such as *Camellia oleifera*, *Ca. sinensis*, *Cunninghamia lanceolata*, *Cinnamomum camphora*, *Parthenocissus tricuspidate*, and *Paulownia fortune*.

Based on multi-locus phylogenetic analyses and morphological characteristics, a total of 23 species of anthracnose that occur on the forest trees have been identified. These species belong to nine different *Colletotrichum* species complexes, which include the *C. acutatum*, *C. boninense*, *C. caudatum-graminicola*, *C. dematium*, *C. destructivum*, *C. gigasporum*, *C. gloeosporioides*, *C. orchidearum*, and *C. truncatum* species complexes. Among the identified species, *Colletotrichum sojae* is described for the first time on a woody plant. Additionally, eight new

species including *C. wenzhouense*, *C. luanense*, *C. hubeiense*, *C. subplurivorum*, *C. cunninghamiae*, *C. guiyangense*, *C. jixiense*, and *C. parthenocissigenum* are introduced in this study.

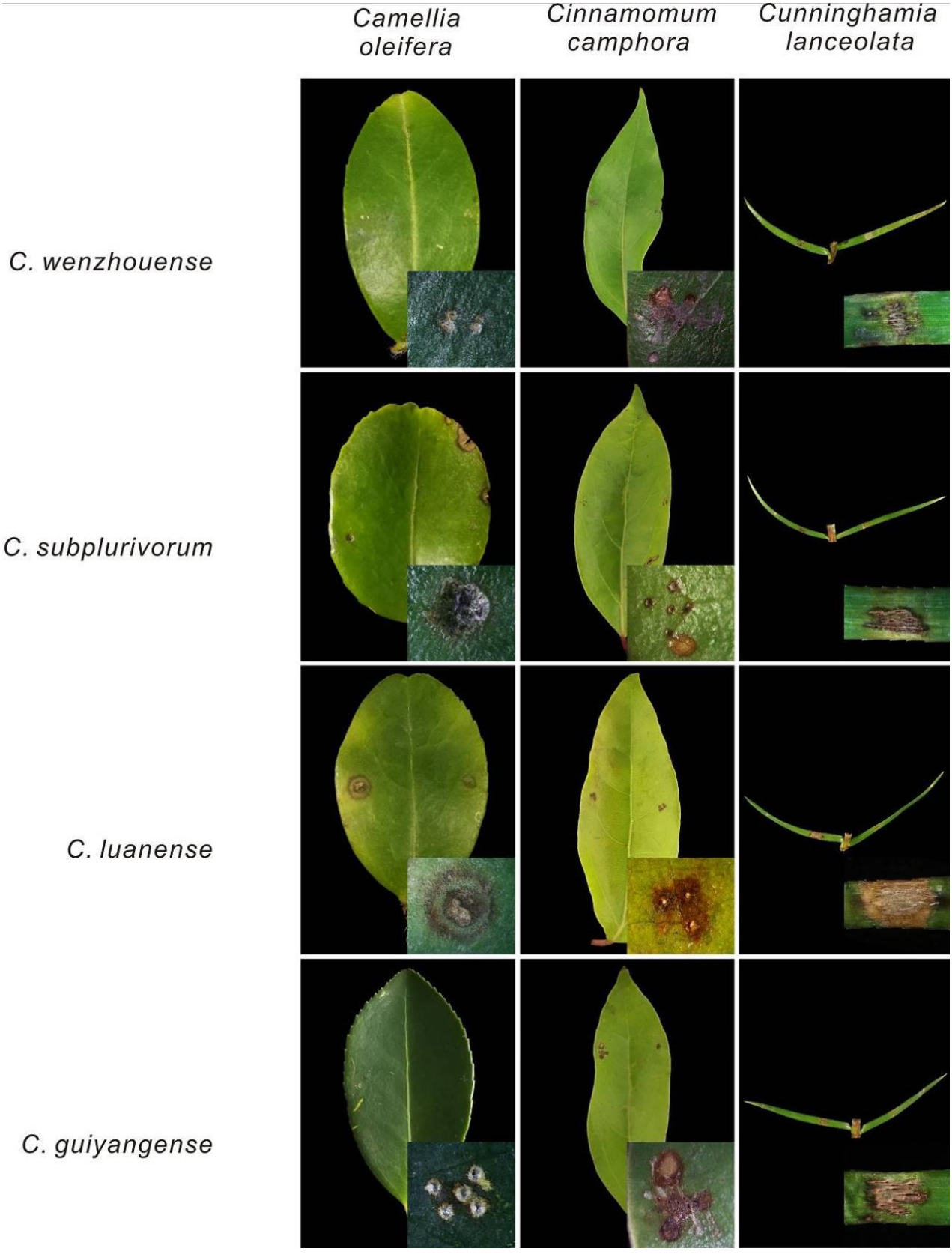


Figure 37 – Pathogenicity tests of the new species and new host recorded *Colletotrichum* species of

this study on *Camellia oleifera*, *Cinnamomum camphora*, and *Cunninghamia lanceolata* respectively. Multi-gene phylogenetic analysis is commonly used to systematically describe the

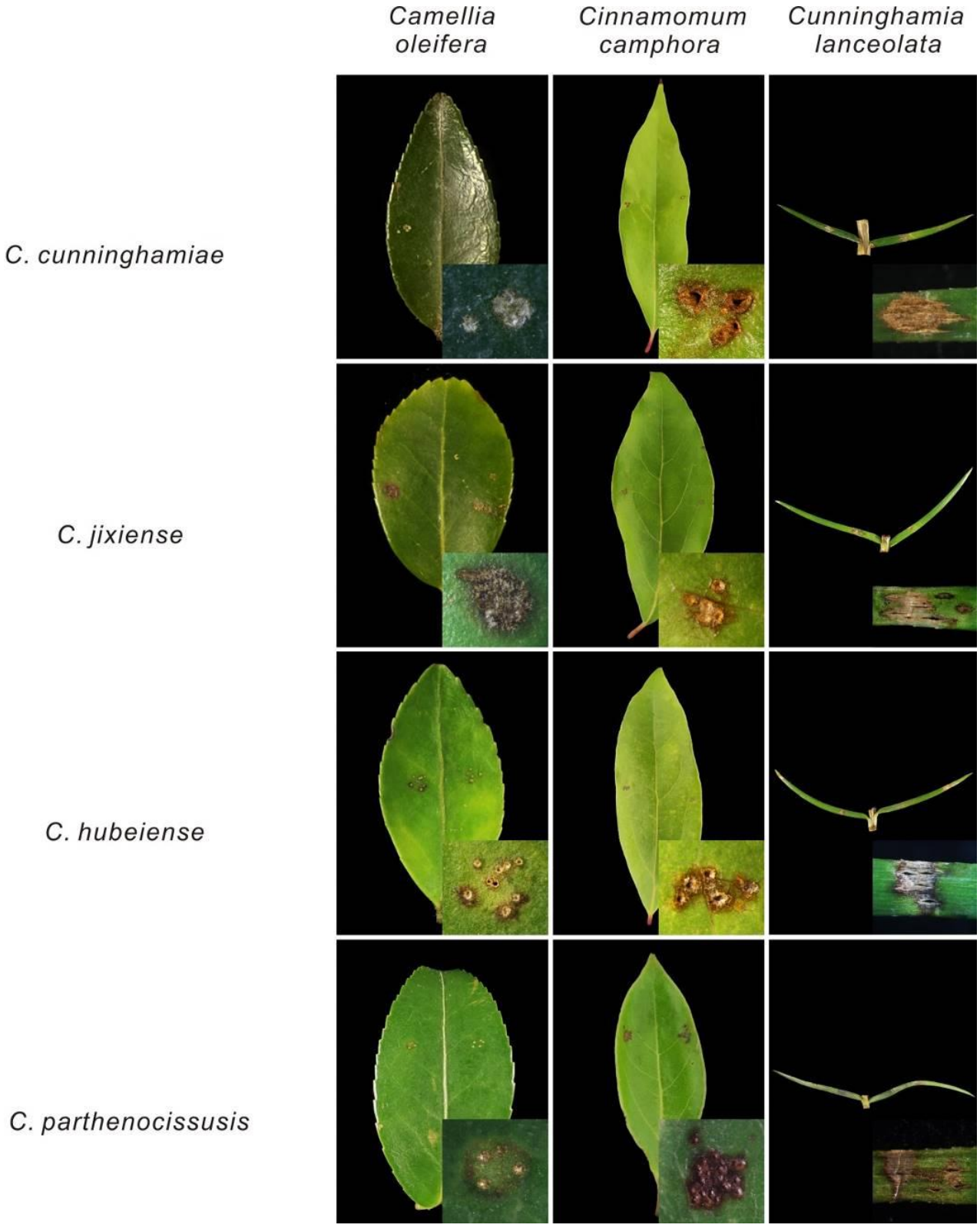


Figure 37 – Continued.

species relationships of *Colletotrichum* and serves as the basis for species identification (Crouch et al. 2006, 2009b, Damm et al. 2009, Prihastuti et al. 2009). For example, Prihastuti et al. (2009)

successfully resolved the classification of several closely related species within *Colletotrichum gloeosporioides* sensu lato using six genes (ITS, *act*, *tub2*, *cal*, *gs*, *gapdh*).

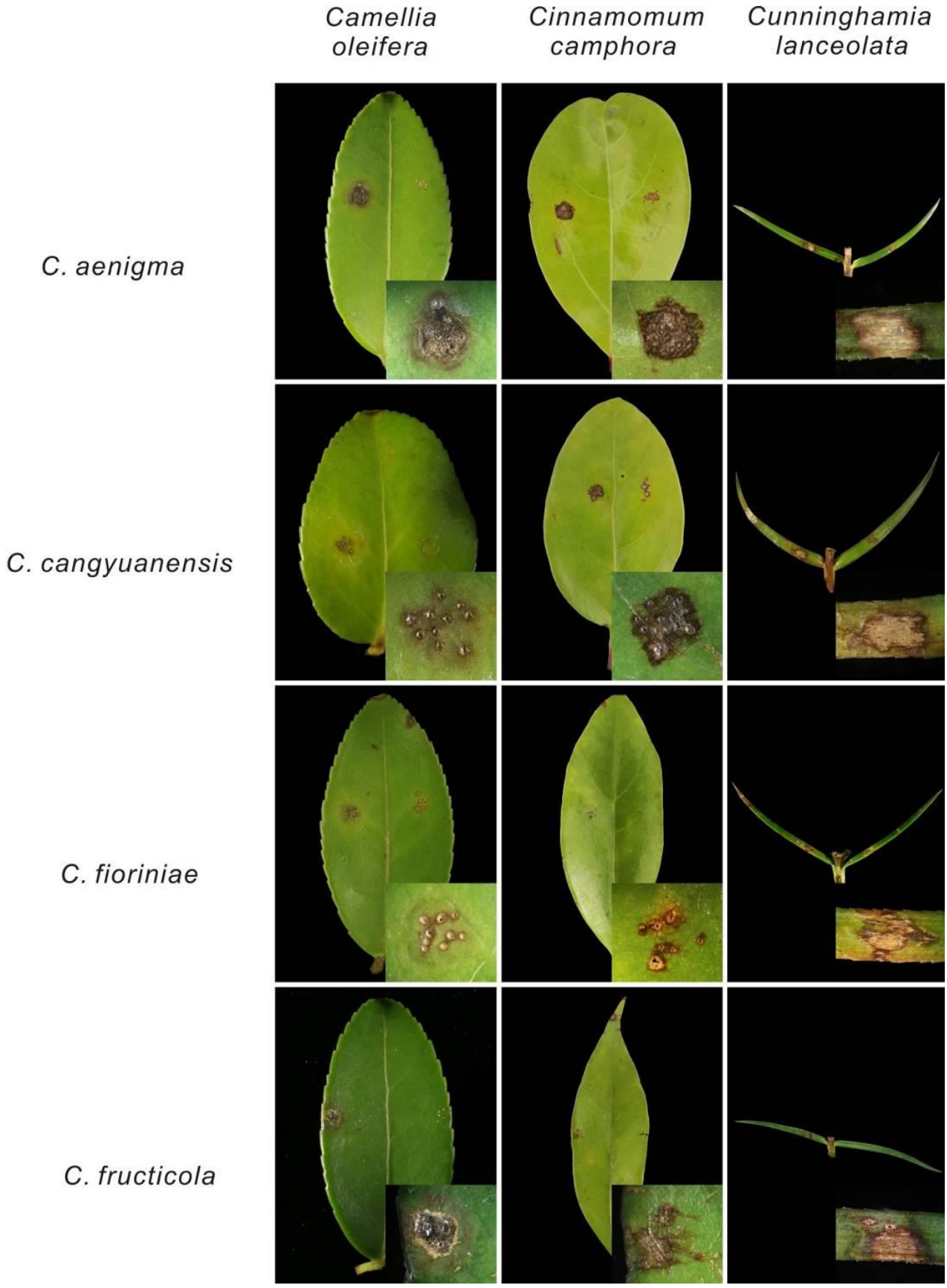


Figure 37 – Continued.

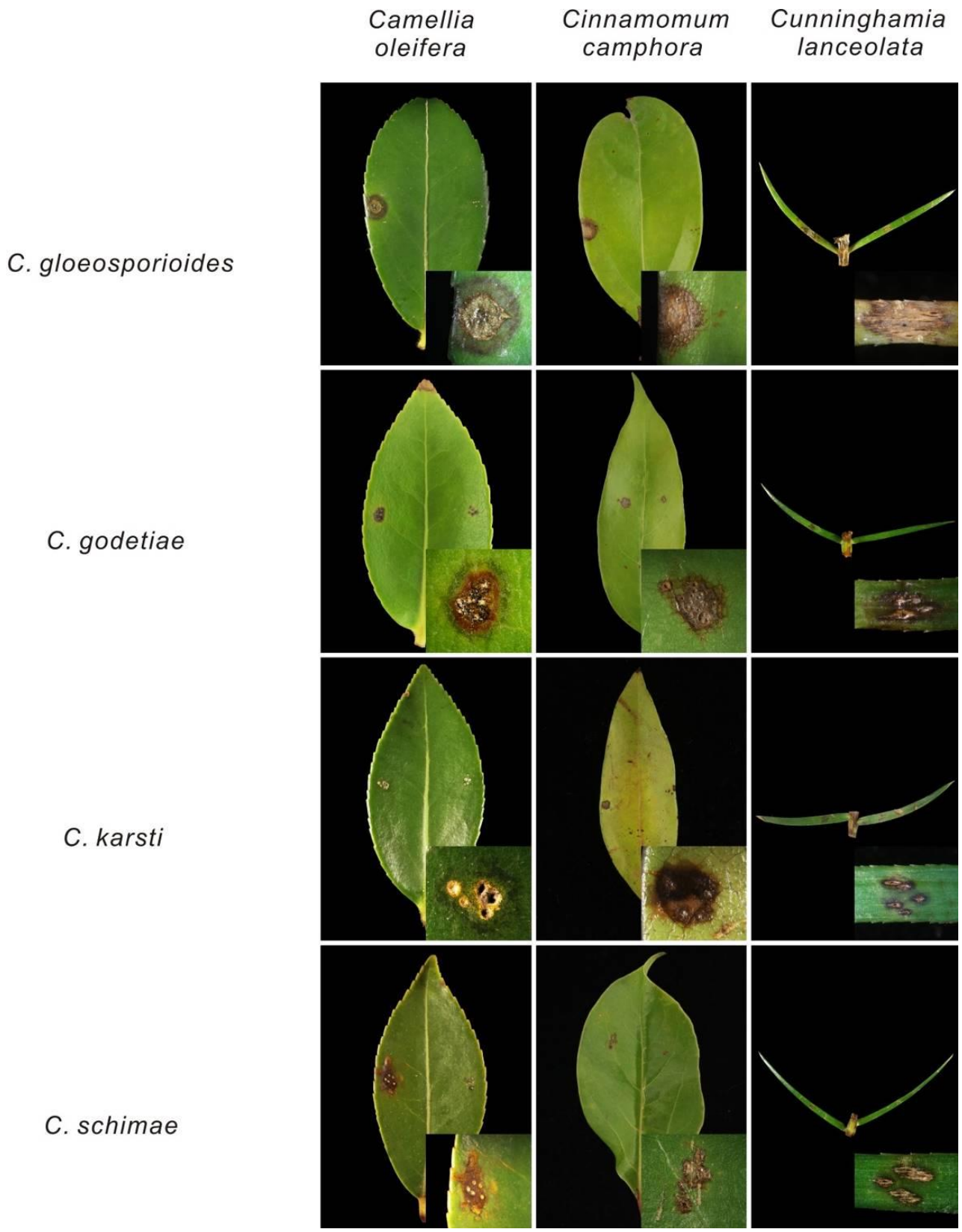


Figure 37 – Continued.

Currently, the multi-locus phylogenetic analysis of different *Colletotrichum* species complexes commonly utilizes either the ITS-*gapdh-chs-1-his3-act-tub2* or ITS-*gapdh-chs-1-act-tub2* gene region combinations (Liu et al. 2022, Jayawardena et al. 2021). However, for some species complexes, the gene combinations described above may not adequately resolve species delimitation and the inclusion of unique genetic markers is required. For example, the *sod2* gene has been found

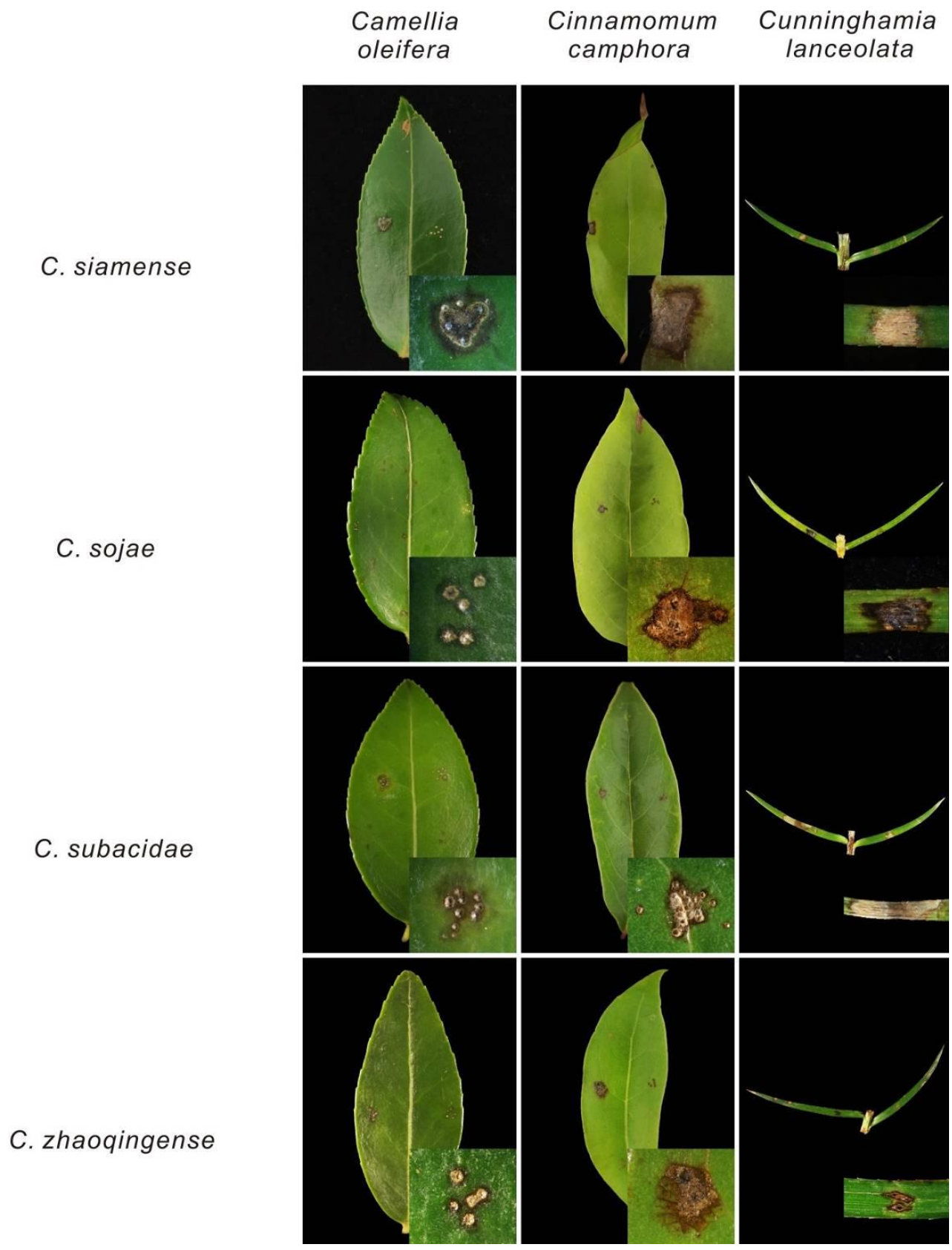


Figure 37 – Continued.

to be very effective in identifying species within the *Colletotrichum graminicola* and *C. caudatum* species complexes (Liu et al. 2022). The *apmat* and *gs* genes have been found to effectively resolve species identification within the *C. gloeosporioides* species complex. Therefore, in this study,

different gene combinations were employed for different species complexes to better identify species through nucleotide sequence analysis (Liu et al. 2015).

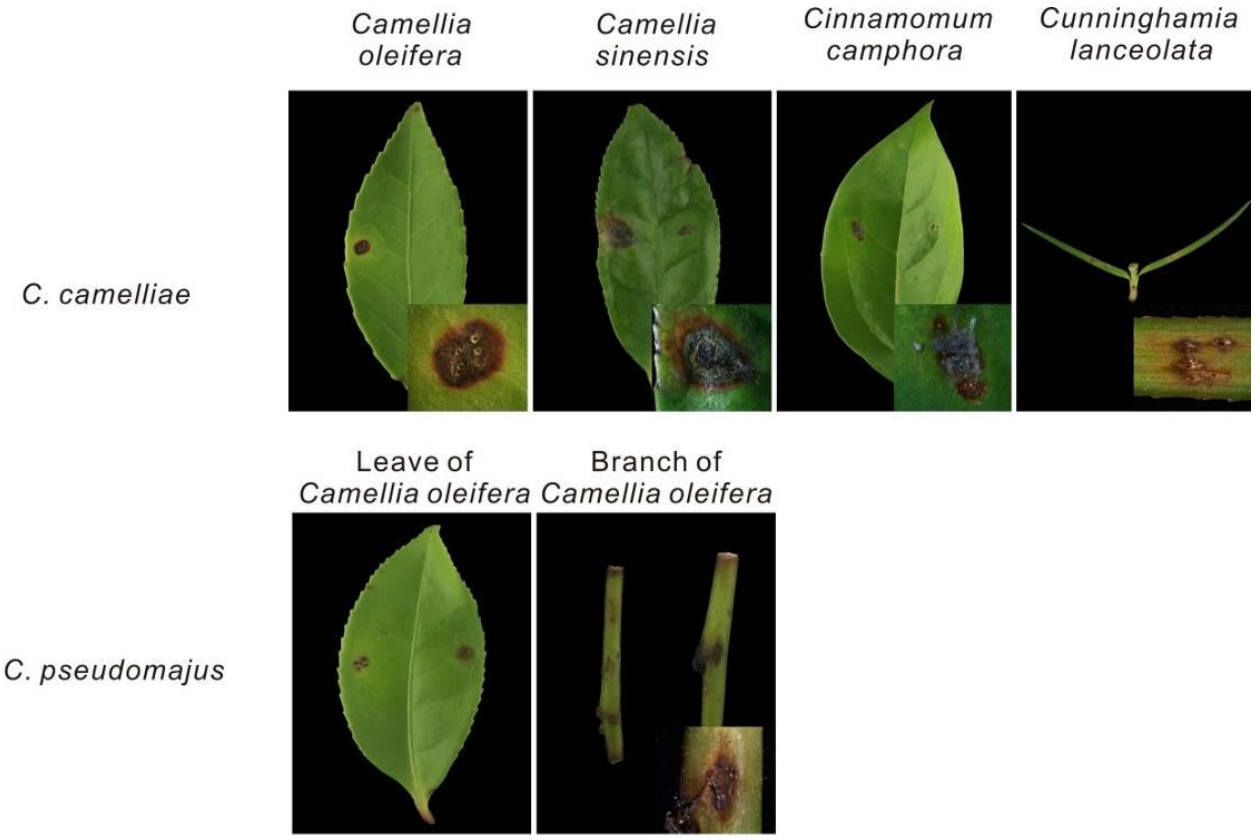


Figure 38 – Pathogenicity tests of *Colletotrichum camelliae* on *Camellia oleifera*, *Ca. sinensis*, *Cinnamomum camphora*, and *Cunninghamia lanceolata* respectively, and *C. pseudomajus* on leave of *Camellia oleifera* and branch of *Camellia oleifera*.

Subsequently, more diverse molecular identification methods have been referred to for the identification of *Colletotrichum* species, such as Genealogical concordance phylogenetic species recognition (GCPSR), PHI, GMYC, PTP (Taylor et al. 2000, Bruen et al 2006, Arrigoni et al. 2016, Renner et al. 2017). However, there are still certain species for which the taxonomic position remains uncertain using the current methods. In this study, the relationship between two closely related species, *C. subacidae* and *C. acidi*, where conflicting conclusions are obtained using methods such as GCPSR, PHI test, GMYC, bPTP analysis. Liu et al. (2016b) encountered a similar issue in their study on whether *C. siamense* s. lat. is a single species or a species complex. They found that GMYC analysis inferred *C. siamense* s. lat. as one species, while PTP analysis separated *C. siamense* s. lat. into two entities. Liu et al. (2022) constructed a phylogenomic tree using 1893 single-copy orthologous genes, and the strains of *C. siamense* clustered together in a clade with high support values. Based on the topology of the phylogenomic tree, it was shown that *C. siamense* is a single species and belongs to the *C. gloeosporioides* species complex. Therefore, to further clarify the taxonomic relationships between species, it may be necessary to employ whole-genome sequencing for comparative analysis.

In addition, some species are unclear whether are single species or species complexes. For example, *Colletotrichum pleopeltidis* is considered as a species of *C. destructivum* species complex, but it was also the base of *C. destructivum* species complex in the phylogenetic tree (Crous et al. 2021). In this study, *Colletotrichum pleopeltidis* forms a highly supported clade with new species *C. hubeiense*, and sister to other species of *C. destructivum* species complex (Fig. 11). However,

Colletotrichum pleopeltidis shares low sequence similarity with the representative species of *C. destructivum* species complex, *C. destructivum* s.str., at *act* (86.99%), *chs-1* (93.93%), and ITS (95.82%), respectively. *Colletotrichum hubeiense* also shares low sequence similarity with the species of *C. destructivum* s.str. at *chs-1* (91.98%), *his3* (89.19%), ITS (95.26%), *tub2* (88.41%),

Table 4 Incidence of the new species and new host recorded *Colletotrichum* species on leaves of host plants.

Host / Species	*Camellia oleifera*	*Cinnamomum camphora*	*Cunninghamia lanceolata*
C. bambusicola CNUCC 307307	50%	50%	/
C. guangxiense CNUCC 310138	50%	83%	/
Colletotrichum wenzhouense	/	/	/
Colletotrichum subplurivorum	33%	/	/
Colletotrichum luanense	83%	100%	100%
Colletotrichum guiyangense	50%	33%	100%
Colletotrichum cunninghamiae	/	50%	100%
Colletotrichum jixiense	100%	33%	100%
Colletotrichum hubeiense	/	83%	/
Colletotrichum parthenocissigenum	33%	33%	/
C. aenigma CNUCC 956-1-2	100%	100%	100%
C. cangyuanense CNUCC 846B-3-2	/	100%	100%
C. fioriniae CNUCC 10-4-3	100%	33%	100%
C. fructicola CNUCC 711-1-2	100%	100%	/
C. gloeosporioides CNUCC 184-3-3	100%	100%	100%
C. godetiae CNUCC 354-4-2	83%	100%	100%
C. karsti CNUCC 778-1	/	/	/
C. schimae CNUCC 324C-1-5-2	50%	100%	100%
C. sojae CNUCC 942-2-4-1	/	100%	100%
C. siamense CNUCC 191-3-1	100%	100%	100%
C. subacidae CNUCC 764B-2	83%	100%	100%
C. zhaoqingense CNUCC 747-1-3	100%	100%	/

Table 5 Lesion length on leaves of host plants inoculated with the new species and new host recorded *Colletotrichum* species of this study.

Host / Species	*Camellia oleifera*	*Cinnamomum camphora*	*Cunninghamia lanceolata*
C. bambusicola CNUCC 307307	209–250 μm	1500–3525 μm	/
C. guangxiense CNUCC 310138	1125–1188 μm	1850–3300 μm	/
Colletotrichum wenzhouense	/	/	/
Colletotrichum subplurivorum	938–1025 μm	/	/
Colletotrichum luanense	875–1250 μm	1200–1325 μm	1600–2500 μm
Colletotrichum guiyangense	250–750 μm	1050–2350 μm	1525–2275 μm
Colletotrichum cunninghamiae	/	875–1075 μm	1575–2325 μm
Colletotrichum jixiense	500–1467 μm	1367–2500 μm	2025–4700 μm
Colletotrichum hubeiense	/	1575–2400 μm	/
Colletotrichum parthenocissigenum	275–313 μm	1075–1200 μm	/
C. aenigma CNUCC 956-1-2	3950–5000 μm	3000–4050 μm	1725–2500 μm
C. cangyuanense CNUCC 846B-3-2	/	1425–2900 μm	2400–4650 μm
C. fioriniae CNUCC 10-4-3	1450–2950 μm	1400–1975 μm	2150–2475 μm
C. fructicola CNUCC 711-1-2	2050–4450 μm	1850–3100 μm	/
C. gloeosporioides CNUCC 184-3-3	4200–6250 μm	2650–4350 μm	1500–3500 μm
C. godetiae CNUCC 354-4-2	1775–2475 μm	2300–3000 μm	2225–2450 μm
C. karsti CNUCC 778-1	/	/	/
C. schimae CNUCC 324C-1-5-2	2250–6250 μm	1400–2025 μm	1075–7600 μm
C. sojae CNUCC 942-2-4-1	/	2325–2950 μm	2325–3000 μm
C. siamense CNUCC 191-3-1	1300–4500 μm	1700–3400 μm	1775–4250 μm
C. subacidae CNUCC 764B-2	2175–2450 μm	2425–2850 μm	3050–8250 μm
C. zhaoqingense CNUCC 747-1-3	550–1075 μm	1050–1975 μm	/

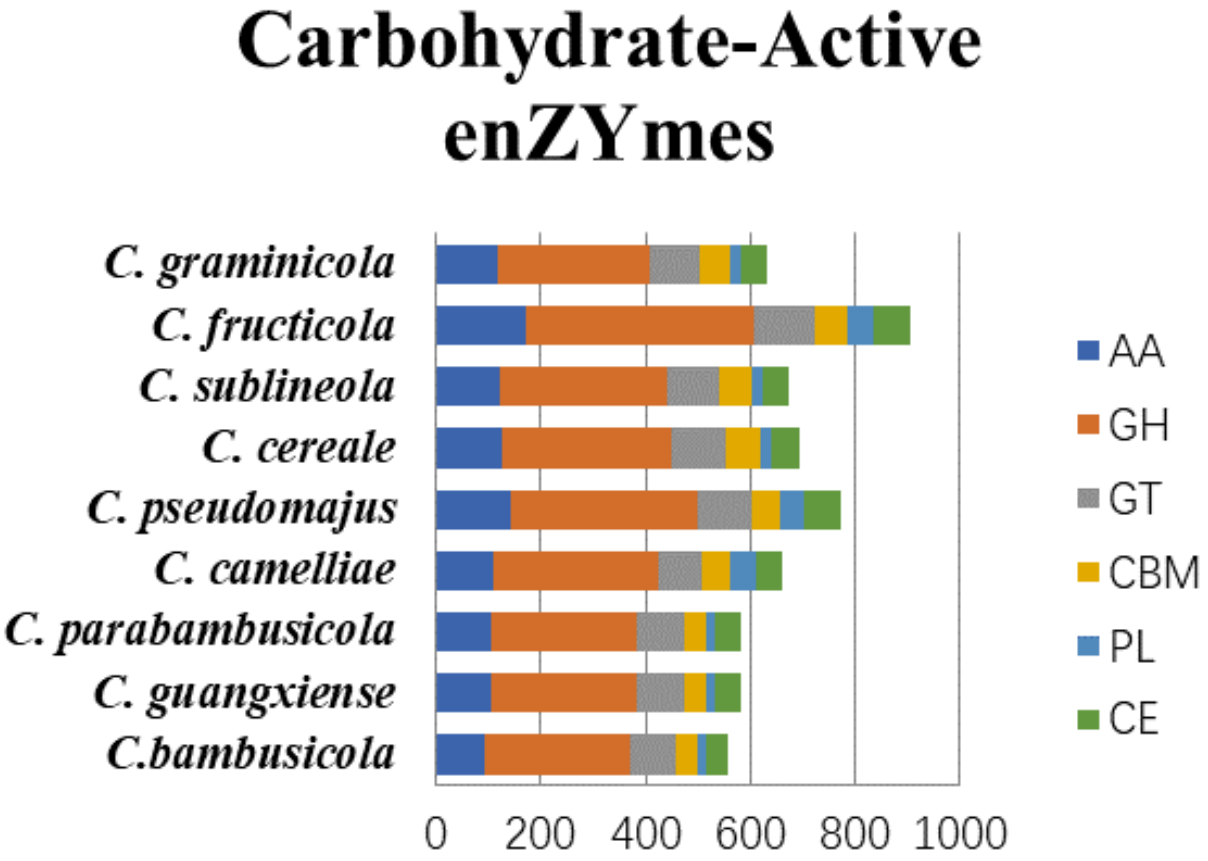


Figure 39 – The distribution of carbohydrate-active enzymes (CAZy) in the genomes used in this study. The legends on the right represent Glycoside Hydrolases (GH), Glycosyl Transferases (GT), Polysaccharide Lyases (PL), Carbohydrate Esterases (CE), Auxiliary Activities (AA), Carbohydrate-binding modules (CBM), respectively.

and *gapdh* (90.74%), respectively. Species within the same species complex should not have such low sequence similarity to each other, so the taxonomic position of these two species need to be verified further. Similarly, *Colletotrichum vulgaris* Z.F. Yu & H. Zheng, *C. garzense* Z.F. Yu & H. Zheng, *C. litangense* Qiao & Z.F. Yu, *C. casaense* Z.F. Yu & H. Zheng, *C. baiyuense* Z.F. Yu & H. Zheng, *C. caspicum* Alizadeh, Damm, F. Liu, Jav.-Nikkh. & Stukenbr., and *C. tibetense* F. Liu & L. Cai form a distinct clade with high supported values, and is the base group of *C. caudatum-graminicola* species complex. Among them, *Colletotrichum garzense* and *C. baiyuense* are considered to be single species (Zheng et al. 2022), while *C. litangense*, *C. capsicum*, and *C. tibetense* are considered to be the species of *C. caudatum-graminicola* species complex. Consequently, more confirmation of these species' taxonomic places is required. Therefore, in order to differentiate between single species and species complexs, a combination of morphological, phylogenetic, pathogenicity, and physiological characteristics should be used in polyphasic taxonomy. By matching genetic differences with morphological and biological features, *Colletotrichum* species can be identified and classified more accurately (Cai et al. 2009).

Except for *Colletotrichum* species that have high infestation rates, high infectivity, and a wide host range, such as *C. luanense*, *C. aenigma*, *C. gloeosporioides*, and *C. siamense*, that need to be paid more attention, *Colletotrichum* species that were previously recorded as endophytic fungi and with host-specificity also need to be attention. These species are likely to have diverse lifestyles and may not have highly tissue specificity. Currently, *Colletotrichum camelliae* is only isolated from plants of the *Camellia* spp. However, in this study *Colletotrichum camelliae* was also able to infect leaves of *Cinnamomum camphora* and *Cunninghamia lanceolata*, without showing

hostspecificity towards *Camellia* spp, more detailed investigation is need to explain the reasons behind this phenomenon.

Colletotrichum pseudomajus has only been isolated from the branches of *Camellia* spp. (Liu et al. 2014), and the pathogenicity test in this study indicated that *C. pseudomajus* could only infect the branches of *Ca. sinensis*., but not the leaves of *Ca. oleifera*, *Ca. sinensis*, *Cunninghamia lanceolata*, and *Cinnamomum camphora*. Therefore, *Colletotrichum pseudomajus* is considered to have host-specificity to the branches of *Camellia sinensis*. Comparative genomic analysis revealed that *Colletotrichum pseudomajus* has two specific carbohydrases, GT61 and AA14. Most family members of GT61 are xylan arabinosyltransferases (XATs), which mediate the 3-O-arabinosylation of xylan. The family AA14 involve in the process of cellulose degradation into C1-oxidized xylotriose. This may be the reason that the *Colletotrichum pseudomajus* has host-specificity to the branches of *Camellia sinensis*.

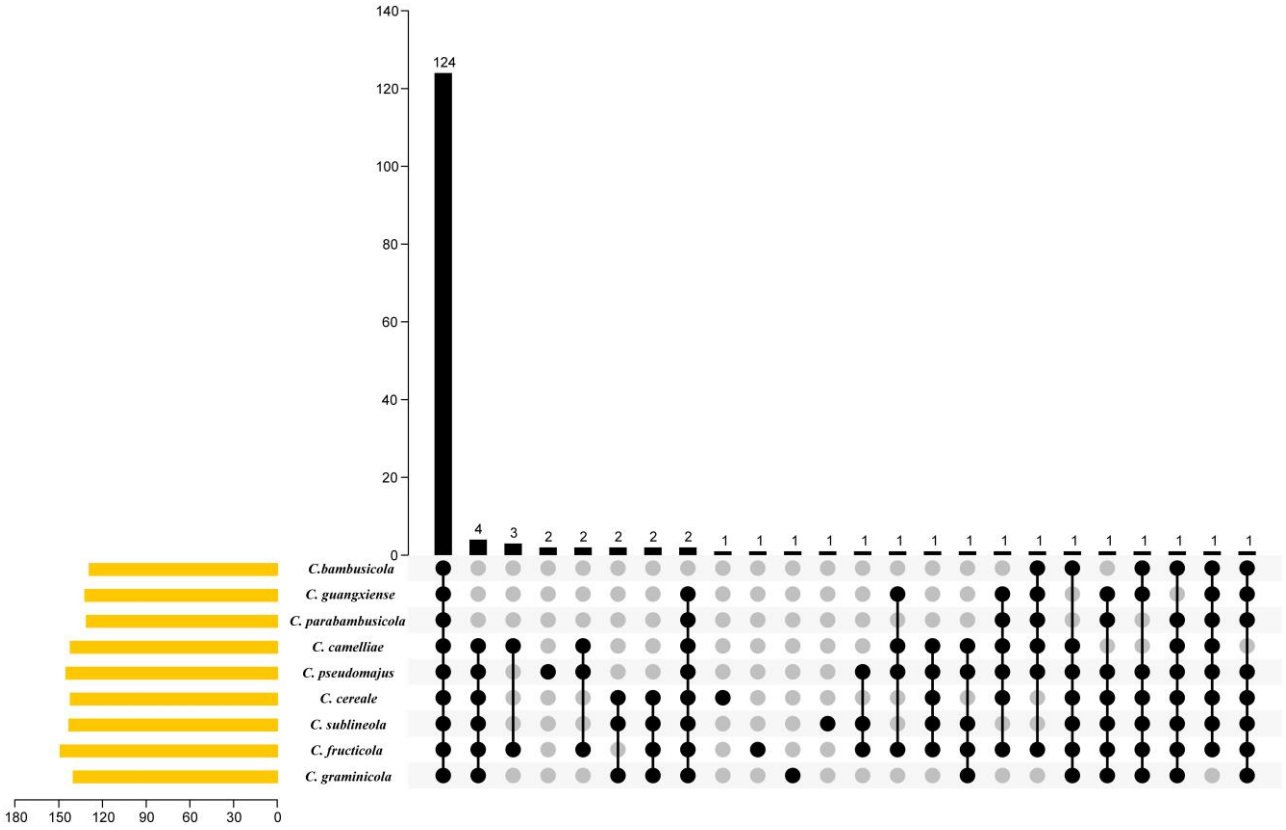


Figure 40 – Venn of the carbohydrate-active enzymes (CAZy) gene family of the *Colleotrichum* strains used in this study.

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Supplementary Table 1 Isolates and GenBank accession numbers used in the phylogenetic analyses of *C. acutatum* species complex.

Species name	Strains[1]	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*his3*
C. abscissum	COAD 1877	Holotype	*Citrus sinensis* cv. *Pera*	Brazil	KP843126	KP843129	KP843132	KP843141	KP843135	KP843138
C. acerbum	CBS 128530 = ICMP 12921 = PRJ 1199.3	Holotype	*Malus domestica*	New Zealand	JQ948459	JQ948790	JQ949120	JQ949780	JQ950110	JQ949450
C. acutatum	CBS 112996 = ATCC 56816 = STE-U 5292	Holotype	*Carica papaya*	Australia	JQ005776	JQ948677	JQ005797	JQ005839	JQ005860	JQ005818
C. arboricola	CBS 144795 = SAG 53350-12	Holotype	*Fuchsia magellanica*	Chile	MH817944	MH817950	/	MH817956	MH817962	/
C. australe	CBS 116478 = HKUCC 2616	Holotype	*Trachycarpus fortunei*	South Africa	JQ948455	JQ948786	JQ949116	JQ949776	JQ950106	JQ949446
C. australisinense	GX 1655 = CGMCC 3.18886	ex-type	*Hevea brasiliensis*	China	MG20962	MG241962	MG241981	MG241947	MG209645	/
C. bannaense	YNML 52 = CGMCC 3.18887	ex-type	*Hevea brasiliensis*	China	MG209638	MG242006	MG241996	MG242002	MG209660	/
C. brisbanense	CBS 292.67= DPI 11711	Holotype	*Capsicum annuum*	Australia	JQ948291	JQ948621	JQ948952	JQ949612	JQ949942	JQ949282
C. cairnsense	BRIP 63642	Holotype	*Capsicum annuum*	Australia	KU923672	KU923704	KU923710	KU923716	KU923688	KU923722
C. carthami	SAPA 100011	Epitype	*Carthamus tinctorium*	Japan	AB696998	/	/	/	AB696992	/
C. chrysanthemi	IMI 364540 = CPC 18930		*Chrysanthemum coronarium*	China	JQ948273	JQ948603	JQ948934	JQ949594	JQ949924	JQ949264
C. cosmi	CBS 853.73 = PD 73/856	Holotype	*Cosmos* sp.	Netherlands	JQ948274	JQ948604	JQ948935	JQ949595	JQ949925	JQ949265
C. costaricense	CBS 330.75	Holotype	*Coffea arabica* cv. *Typica, berry*	Costa Rica	JQ948180	JQ948510	JQ948841	JQ949501	JQ949831	JQ949171
C. cuscutae	IMI 304802 = CPC 18873	Holotype	*Cuscuta* sp.	Dominica	JQ948195	JQ948525	JQ948856	JQ949516	JQ949846	JQ949186
C. eriobotryae	GLMC 1935	Holotype	*Eriobotrya japonica*	China, Taiwan	MF772487	MF795423	MN191653	MN191648	MF795428	/
C. filicis	CBS 101611	Holotype	unidentified fern (Pteridophyta)	Costa Rica	JQ948196	JQ948526	JQ948857	JQ949517	JQ949847	JQ949187

Supplementary Table 1 Continued.

Species name	Strains[1]	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*his3*
C. fioriniae	CBS 128517 = ARSEF 10222 = ERL 1257 = EHS 58	Holotype	*Fiorinia externa*	USA	JQ948292	JQ948622	JQ948953	JQ949613	JQ949943	JQ949283
C. fioriniae	ATCC 12097 = CPC 19392		*Rhododendron* sp.	USA	JQ948307	JQ948637	JQ948968	JQ949628	JQ949958	JQ949298
C. fioriniae	CBS 167.86		*Myriophyllum spicatum*	USA	JQ948324	JQ948654	JQ948985	JQ949645	JQ949975	JQ949315
C. fioriniae	CBS 200.35		*Rubus* sp.	USA	JQ948293	JQ948623	JQ948954	JQ949614	JQ949944	JQ949284
C. fioriniae	CBS 293.67 = DPI 13120		*Persea americana*	Australia	JQ948310	JQ948640	JQ948971	JQ949631	JQ949961	JQ949301
C. fioriniae	CBS 786.86		*Malus sylvestris*	Italy	JQ948303	JQ948633	JQ948964	JQ949624	JQ949954	JQ949294
C. fioriniae	CBS 112995 = STE-U 5287		*Malus domestica*	USA	JQ948298	JQ948628	JQ948959	JQ949619	JQ949949	JQ949289
C. fioriniae	CBS 119186 = MEP 1325		*Vaccinium* sp.	New Zealand	JQ948312	JQ948642	JQ948973	JQ949633	JQ949963	JQ949303
C. fioriniae	CBS 124962		*Solanum lycopersicum*	USA	JQ948319	JQ948649	JQ948980	JQ949640	JQ949970	JQ949310
C. fioriniae	CBS 124963		*Solanum lycopersicum*	USA	JQ948320	JQ948650	JQ948981	JQ949641	JQ949971	JQ949311
C. fioriniae	CBS 125396 = GJS 08-140A		*Malus domestica*	USA	JQ948299	JQ948629	JQ948960	JQ949620	JQ949950	JQ949290
C. fioriniae	CBS 125956 = NB 112		*Penstemon* sp.	Netherlands	JQ948321	JQ948651	JQ948982	JQ949642	JQ949972	JQ949312
C. fioriniae	CBS 126509 = PD 92/1060		*Parthenocissus* sp.	Netherlands	JQ948316	JQ948646	JQ948977	JQ949637	JQ949967	JQ949307
C. fioriniae	CBS 126526 = PD 93/1373 = BBA 70343		*Primula* sp.	Netherlands	JQ948323	JQ948653	JQ948984	JQ949644	JQ949974	JQ949314
C. fioriniae	CBS 127600 = BRIP 20127a		*Persea americana*	Australia	JQ948308	JQ948638	JQ948969	JQ949629	JQ949959	JQ949299
C. fioriniae	CBS 127601 = BRIP 28761a		*Mangifera indica*	Australia	JQ948311	JQ948641	JQ948972	JQ949632	JQ949962	JQ949302

Supplementary Table 1 Continued.

Species name	Strains[1]	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*his3*
C. fioriniae	CBS 128498 = ICMP 17991 = PRJ 10.207		*Actinidia* sp.	New Zealand	JQ948337	JQ948667	JQ948998	JQ949658	JQ949988	JQ949328
C. fioriniae	CBS 128529 = ICMP 1701 = PRJ 659		*Fragaria* × *ananassa*	New Zealand	JQ948331	JQ948661	JQ948992	JQ949652	JQ949982	JQ949322
C. fioriniae	CBS 129930 = 2.7.3(T1326) = ICMP 1791		*Malus domestica*	New Zealand	JQ948304	JQ948634	JQ948965	JQ949625	JQ949955	JQ949295
C. fioriniae	CBS 126381		*Malus domestica* cv. *Junami*	New Zealand	JQ948302	JQ948632	JQ948963	JQ949623	JQ949953	JQ949293
C. fioriniae	CBS 129940		*Grevillea* sp.	Germany	JQ948335	JQ948665	JQ948996	JQ949656	JQ949986	JQ949326
C. fioriniae	CBS 129941		*Grevillea* sp.	Germany	JQ948336	JQ948666	JQ948997	JQ949657	JQ949987	JQ949327
C. fioriniae	CBS 129946 = PT 170 = RB 021		*Olea europaea*	Portugal	JQ948342	JQ948672	JQ949003	JQ949663	JQ949993	JQ949333
C. fioriniae	CBS 129947 = CR 46 = RB 022		*Vitis vinifera*	Portugal	JQ948343	JQ948673	JQ949004	JQ949664	JQ949994	JQ949334
C. fioriniae	IMI 324991 = CPC 18878		*Piper nigrum*	Unknown	JQ948338	JQ948668	JQ948999	JQ949659	JQ949989	JQ949329
C. fioriniae	IMI 345575 = CPC 18888		*Fragaria* × *ananassa*	New Zealand	JQ948332	JQ948662	JQ948993	JQ949653	JQ949983	JQ949323
C. fioriniae	IMI 345578 = CPC 19393 = RB 148		*Fragaria* × *ananassa*	New Zealand	JQ948334	JQ948664	JQ948995	JQ949655	JQ949985	JQ949325
C. fioriniae	IMI 345583 = CPC 18889		*Fragaria* × *ananassa*	New Zealand	JQ948333	JQ948663	JQ948994	JQ949654	JQ949984	JQ949324
C. fioriniae	IMI 363003 = CPC 18928		*Camellia reticulata*	China	JQ948339	JQ948669	JQ949000	JQ949660	JQ949990	JQ949330
C. fioriniae	CNUCC 10-4-3		*Camellia oleifera*	China	PP809315	PP832104	PP843037	PP824731	PP832182	PP832143
C. fioriniae	CNUCC 104A-7-4		*Camellia oleifera*	China	PP809316	PP832105	PP843038	PP824732	PP832183	PP832144
C. fioriniae	CNUCC 110-4-1		*Camellia sinensis*	China	PP809317	PP832106	PP843039	PP824733	PP832184	PP832145

Supplementary Table 1 Continued.

Species name	Strains[1]	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*his3*
C. fioriniae	CNUCC 111B-1-4		*Camellia sinensis*	China	PP809353	PP832107	PP843040	PP824734	PP832185	PP832146
C. fioriniae	CNUCC 111B-2-1		*Camellia sinensis*	China	PP809318	PP832108	PP843041	PP824735	PP832186	PP832147
C. fioriniae	CNUCC 117-2-1		*Akebia trifoliata*	China	PP809319	PP832109	PP843042	PP824736	PP832187	PP832148
C. fioriniae	CNUCC 117-3-2		*Akebia trifoliata*	China	PP809320	PP832110	PP843043	PP824737	PP832188	PP832149
C. fioriniae	CNUCC 1297-3-2		*Camellia sinensis*	China	PP809321	PP832111	PP843044	PP824738	PP832189	PP832150
C. fioriniae	CNUCC 154-3-4		*Camellia oleifera*	China	PP809322	PP832112	PP843045	PP824739	PP832190	PP832151
C. fioriniae	CNUCC 163-1-1		*Camellia sinensis*	China	PP809323	PP832113	PP843046	PP824740	PP832191	PP832152
C. fioriniae	CNUCC 163-1-2		*Camellia sinensis*	China	PP809324	PP832114	PP843047	PP824741	PP832192	PP832153
C. fioriniae	CNUCC 184-3-2		*Diospyros kaki* var. *silvestris*	China	PP809326	PP832116	PP843049	PP824743	PP832194	PP832155
C. fioriniae	CNUCC 265A-1-1		*Camellia oleifera*	China	PP809327	PP832117	PP843050	PP824744	PP832195	PP832156
C. fioriniae	CNUCC 349-4-1		*Camellia oleifera*	China	PP809329	PP832119	PP843052	PP824746	PP832197	PP832158
C. fioriniae	CNUCC 440B-2-2		*Ilex latifolia*	China	PP809333	PP832122	PP843056	PP824750	PP832201	PP832162
C. fioriniae	CNUCC 50905		*Cunninghamia lanceolata*	China	PP809336	PP832125	PP843059	PP824753	PP832204	PP832165
C. fioriniae	CNUCC 610-2-2		*Rhododendron simsii*	China	PP809338	PP832127	PP843061	PP824755	PP832206	PP832167
C. fioriniae	CNUCC 612A-3-1		*Castanopsis eyrei*	China	PP809339	PP832128	PP843062	PP824756	PP832207	PP832168
C. fioriniae	CNUCC 629-1-3		*Camellia sinensis*	China	PP809340	PP832129	PP843063	PP824757	PP832208	PP832169
C. fioriniae	CNUCC 713A-1-1		*Cinnamomum camphora*	China	PP809341	PP832130	PP843064	PP824758	PP832209	PP832170
C. fioriniae	CNUCC 716B-2-2		*Cinnamomum camphora*	China	PP809342	PP832131	PP843065	PP824759	PP832210	PP832171

Supplementary Table 1 Continued.

Species name	Strains[1]	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*his3*
C. fioriniae	CNUCC 762B-1-1		*Camellia oleifera*	China	PP809343	PP832132	PP843066	PP824760	PP832211	PP832172
C. fioriniae	CNUCC 839A-2-1		*Camellia oleifera*	China	PP809348	PP832137	PP843071	PP824765	PP832216	PP832177
C. fioriniae	CNUCC 90B-1-1		*Camellia sinensis*	China	PP809349	PP832138	PP843072	PP824766	PP832217	PP832178
C. fioriniae	CNUCC 916-1-1		*Camellia sinensis*	China	PP809352	PP832141	PP843075	PP824769	PP832220	PP832181
C. fioriniae	CNUCC 957-2-1		*Paulownia fortunei*	China	PP809350	PP832139	PP843073	PP824767	PP832218	PP832179
C. godetiae	CBS 133.44	Holotype	*Clarkia hybrida* cv. *Kelvon Glory*	Denmark	JQ948402	JQ948733	JQ949063	JQ949723	JQ950053	JQ949393
C. godetiae	CBS 796.72		*Aeschynomene virginica*	USA	JQ948407	JQ94873	JQ949068	JQ949728	JQ950058	JQ949398
C. godetiae	CBS 131332		*Agrimonia eupatoria*	Austria	JQ948429	JQ948760	JQ949090	JQ949750	JQ950080	JQ949420
C. godetiae	CBS 126512 = PD 88/958		Bonzai, sunken	Netherlands	JQ948412	JQ948743	JQ949073	JQ949733	JQ950063	JQ949403
C. godetiae	IMI 351248 = CPC 18894		*Ceanothus* sp.	UK	JQ948433	JQ948764	JQ949094	JQ949754	JQ950084	JQ949424
C. godetiae	CBS 862.70		*Sambucus nigra*	Netherlands	JQ948437	JQ948768	JQ949098	JQ949758	JQ950088	JQ949428
C. godetiae	CBS 129911 = CPC 15124		*Podocarpus* sp.	South Africa	JQ948434	JQ948765	JQ949095	JQ949755	JQ950085	JQ949425
C. godetiae	CBS 126503 = PD 88/859 = BBA 70342		*Fragaria* × *ananassa*	UK	JQ948420	JQ948751	JQ949081	JQ949741	JQ950071	JQ949411
C. godetiae	CBS 130251 = OL 10 = IMI 398854		*Olea europaea*	Italy	JQ948413	JQ948744	JQ949074	JQ949734	JQ950064	JQ949404
C. godetiae	CBS 130252 = IMI 398855 = OL 20		*Olea europaea*	Italy	JQ948414	JQ948745	JQ949075	JQ949735	JQ950065	JQ949405
C. godetiae	CBS 131331		*Juglans regia*, leaf spot	Austria	JQ948404	JQ948735	JQ949065	JQ949725	JQ950055	JQ949395

Supplementary Table 1 Continued.

Species name	Strains[1]	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*his3*
C. godetiae	IMI 345026 = CPC 18882		*Fragaria* × *ananassa*	Spain	JQ948424	JQ948755	JQ949085	JQ949745	JQ950075	JQ949415
C. godetiae	CNUCC 354-2-1		*Camellia sinensis*	China	PP809330	PP832120	PP843053	PP824747	PP832198	PP832159
C. godetiae	CNUCC 354-4-2		*Camellia sinensis*	China	PP809331	PP832142	PP843054	PP824748	PP832199	PP832160
C. godetiae	CNUCC 363A-1-1		*Ilex cornuta*	China	PP809332	PP832121	PP843055	PP824749	PP832200	PP832161
C. godetiae	CNUCC 456-2-1		*Lespedeza bicolor*	China	PP809334	PP832123	PP843057	PP824751	PP832202	PP832163
C. guajavae	IMI 350839	Holotype	*Psidium guajava*	India	JQ948270	JQ948600	JQ948931	JQ949591	JQ949921	JQ949261
C. indonesiense	CBS 127551	Holotype	*Eucalyptus* sp.	Indonesia	JQ948288	JQ948618	JQ948949	JQ949609	JQ949939	JQ949279
C. javanense	CBS 144963a	Holotype	*Capsicum annuum*	Indonesia	MH846576	MH846572	MH846573	MH846575	MH846574	MH846571
C. johnstonii	CBS 128532	Holotype	*Solanum lycopersicum*	New Zealand	JQ948444	JQ948775	JQ949105	JQ949765	JQ950095	JQ949435
C. kinghornii	CBS 198.35	Holotype	*Phormium* sp.	UK	JQ948454	JQ948785	JQ949115	JQ949775	JQ950105	JQ949445
C. kniphofiae	CBS 143496	Holotype	*Kniphofia uvaria*	UK	MH107884	MH107998	MH107990	MH107975	MH108037	/
C. kniphofiae	CPC 30168		*Kniphofia uvaria*	UK	MH107885	/	/	/	/	/
C. laticiphilum	CBS 112989 = IMI 383015 = STE-U 5303	Holotype	*Hevea brasiliensis*	India	JQ948289	JQ948619	JQ948950	JQ949610	JQ949940	JQ949280
C. lauri	MFLUCC 17-0205 = IT 2505_1a	Holotype	*Laurus nobilis*	Italy	KY514347	KY514344	KY514341	KY514338	KY514350	/
C. lauri	MFLUCC 17-0206		*Laurus nobilis*	Italy	KY514348;	KY514245	KY514342	KY514339	KY514351.	/
C. limetticola	CBS 114.14	Epitype	*Citrus aurantifolia*	USA, Florida	JQ948193	JQ948523	JQ948854	JQ949514	JQ949844	JQ949184
C. lupini	CBS 109225	Neotype	*Lupinus albus*	Ukraine	JQ948155	JQ948485	JQ948816	JQ949476	JQ949806	JQ949146
C. melonis	CBS 159.84	Holotype	*Cucumis melo*	Brazil	JQ948194	JQ948524	JQ948855	JQ949515	JQ949845	JQ949185

Supplementary Table 1 Continued.

Species name	Strains[1]	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*his3*
C. miaoliense	NTUCC 20-001-1	Holotype	*Fragaria* × *ananassa*	China, Taiwan	MK908419	MK908470	MK908522	MK908573	MK908624	/
C. nymphaeae	CBS 515.78	Epitype	*Nymphaea alba*	Netherlands	JQ948197	JQ948527	JQ948858	JQ949518	JQ949848	JQ949188
C. nymphaeae	CBS 126504 = C 105		*Fragaria* × *ananassa*	South Africa	JQ948265	JQ948595	JQ948926	JQ949586	JQ949916	JQ949256
C. nymphaeae	CBS 112202		*Fragaria* sp.	Spain	JQ948234	JQ948564	JQ948895	JQ949555	JQ949885	JQ949225
C. nymphaeae	CBS 173.51		*Mahonia aquifolium*	Italy	JQ948200	JQ948530.	JQ948861	JQ949521	JQ949851	JQ949191
C. nymphaeae	CBS 119294 = MEP 1534		*Leucaena* sp.	Mexico	JQ948205	JQ948535	JQ948866	JQ949526	JQ949856	JQ949196
C. nymphaeae	CBS 516.78 = IAM 14670		*Nuphar luteum*	Netherlands	JQ948198	JQ948528	JQ948859	JQ949519	JQ949849	JQ949189
C. nymphaeae	CBS 526.77		*Nymphaea alba*	Netherlands	JQ948199	JQ948529	JQ948860	JQ949520	JQ949850	JQ949190
C. nymphaeae	CBS 129926 = CPC 18719		Litter	Thailand	JQ948216	JQ948546	JQ948877	JQ949537	JQ949867	JQ949207
C. nymphaeae	IMI 301119 = CPC 18872		*Fragaria vesca*	Kenya	JQ948266	JQ948596	JQ948927	JQ949587	JQ949917	JQ949257
C. nymphaeae	IMI 360386 = CPC 18925		*Pelargonium graveolens*	India	JQ948206	JQ948536	JQ948867	JQ949527	JQ949857	JQ949197
C. nymphaeae	CBS 100064		*Anemone* sp.	Netherlands	JQ948224	JQ948554	JQ948885	JQ949545	JQ949875	JQ949215
C. nymphaeae	CBS 113004 = STE-U 4458		*Protea* sp.	South Africa	JQ948210	JQ948540	JQ948871	JQ949531	JQ949861	JQ949201
C. nymphaeae	CBS 122121 = AR 4457		*Fragaria* × *ananassa*, cv. *Redchief*	Bulgaria	JQ948237	JQ948567	JQ948898	JQ949558	JQ949888	JQ949228
C. nymphaeae	CBS 125958 = NB 155		*Fragaria* × *ananassa*	Netherlands	JQ948245	JQ948575	JQ948906	JQ949566	JQ949896	JQ949236
C. nymphaeae	CBS 126370 = PD 92/790		*Fragaria* × *ananassa*	USA	JQ948257	JQ948587	JQ948918	JQ949578	JQ949908	JQ949248
C. nymphaeae	CNUCC 163-2-2-1		*Camellia sinensis*	China	PP809325	PP832115	PP843048	PP824742	PP832193	PP832154
C. nymphaeae	CNUCC 234-3-4		*Carya cathayensis*	China	PP809351	PP832140	PP843074	PP824768	PP832219	PP832180
C. nymphaeae	CNUCC 469-3-1		*Fatsia japonica*	China	PP809335	PP832124	PP843058	PP824752	PP832203	PP832164

Supplementary Table 1 Continued.

Species name	Strains[1]	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*his3*
C. nymphaeae	CNUCC 766B-1-3		*Camellia oleifera*	China	PP809334	PP832133	PP843067	PP824761	PP832212	PP832173
C. nymphaeae	CNUCC 815-1-1		*Camellia sinensis*	China	PP809345	PP832134	PP843068	PP824762	PP832213	PP832174
C. nymphaeae	CNUCC 819B-2-2		*Camellia sinensis*	China	PP809346	PP832135	PP843069	PP824763	PP832214	PP832175
C. nymphaeae	CNUCC 820A-2-2		*Camellia sinensis*	China	PP809347	PP832136	PP843070	PP824764	PP832215	PP832176
C. orientalis	F10PGBYS1		*Malus* × *domestica*	China	KF772134	KF772104	KF772074	KF772044	KF772164	/
C. orientalis	F10PGBYS2		*Malus* × *domestica*	China	KF772135	KF772105	KF772075	KF772045	KF772165	/
C. orientalis	F10PGBYS3		*Malus* × *domestica*	China	KF772136	KF772106	KF772076	KF772046	KF772166	/
C. orientalis	F10PGBYS4		*Malus* × *domestica*	China	KF772137	KF772107	KF772077	KF772047	KF772167	/
C. orientalis	F10PGBYS7		*Malus* × *domestica*	China	KF772138	KF772108	KF772078	KF772048	KF772168	/
C. orientalis	F10PGBYS8		*Malus* × *domestica*	China	KF772139	KF772109	KF772079	KF772049	KF772169	/
C. orientalis	F10PGBYS10		*Malus* × *domestica*	China	KF772140	KF772110	KF772080	KF772050	KF772170	/
C. paranaense	CBS 134729	Holotype	*Malus domestica*	Paraná	KC204992	KC205026	KC205043	KC205077	KC205060	KC205004
C. paxtonii	IMI 165753 = CPC 18868	Holotype	*Musa* sp.	Saint Lucia	JQ948285	JQ948615	JQ948946	JQ949606	JQ949936	JQ949276
C. pedunculi	MYJ 201 = BCRC FU31310	Holotype	*Mangifera indica*	China	MN809388	MN82068	MN820676	MN820668	MN810342	MN820692
C. phormii	CBS 118194 = AR 3546	Epitype	*Phormium* sp.	Germany	JQ948446	JQ948777	JQ949107	JQ949767	JQ950097	JQ949437
C. pyricola	CBS 128531 = ICMP 12924 = PRJ 977.1	Holotype	*Pyrus communis*	New Zealand	JQ948445	JQ948776	JQ949106	JQ949766	JQ950096	JQ949436
C. rhombiforme	CBS 129953 = PT 250 = RB 011	Holotype	*Olea europaea*	Portugal	JQ948457	JQ948788	JQ949118	JQ949778	JQ950108	JQ949448

Supplementary Table 1 Continued.

Species name	Strains[1]	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*his3*
C. roseum	CBS 145754	Holotype	*Lapageria rosea*	Chile	MK903611	MK903603	/	MK903604	MK903607	/
C. salicis	CBS 607.94	Epitype	*Salix* sp.	Netherlands	JQ948460	JQ948791	JQ949121	JQ949781	JQ950111	JQ949451
C. schimae	LC 13880 = NN 046984	Holotype	*Schima* sp.	China	MZ595885	MZ664105	MZ799347	MZ66418	MZ674003	MZ673905
C. schimae	LC 13881 = NN 047247		*Schima* sp.	China	MZ595887	MZ664106	MZ799348	MZ664185	MZ674005	MZ673907
C. schimae	CNUCC 324C-1-5-2		*Camellia sinensis* var. *assamica*	China	PP809328	PP832118	PP843051	PP824745	PP832196	PP832157
C. schimae	CNUCC 528-2-2		*Ilex chinensis*	China	PP809337	PP832126	PP843060	PP824754	PP832205	PP832166
C. scovillei	CBS 126529 = PD 94/921-3 = BBA 70349	Holotype	*Capsicum* sp.	Indonesia	JQ948267	JQ948597	JQ948928	JQ949588	JQ949918	JQ949258
C. simmondsii	CBS 122122 = BRIP 28519	Holotype	*Carica papaya*	Australia	JQ948276	JQ948606	JQ948937	JQ949597	JQ949927	JQ949267
C. simulanticitri	YMF 1.07302	Holotype	*Betula* spp.	China	OK030878	OK513680	OK513577	OK513615	/	/
C. simulanticitri	YMF 1.07308		*Ageratina adenophora*	China	OK030880	OK513682	OK513579	OK513617	/	/
C. simulanticitri	YMF 1.07312		*Ageratina adenophora*	China	OK030879	OK513681	OK513578	OK513616	/	/
C. sloanei	IMI 364297 = CPC 18929	Holotype	*Theobroma cacao*	Malaysia	JQ948287	JQ948617	JQ948948	JQ949608	JQ949938	JQ949278
C. speciosum	YMF 1.07301		*Ageratina adenophora*	China	OK030881	/	/	/	/	/
C. subsalicis	CQ 1168 = LC 13863	Holotype	*Populus alba*	China	MZ852849	/	MZ799346	MZ664128	MZ673953	MZ673836
C. tamarilloi	CBS 129814 = T.A.6	Holotype	*Solanum betaceum*	Colombia	JQ948184	JQ948514	JQ948845	JQ949505	JQ949835	JQ949175
C. walleri	CBS 125472 = BMT(HL) 19	Holotype	*Coffea* sp.	Vietnam	JQ948275	JQ948605	JQ948936	JQ949596	JQ949926	JQ949266
C. wanningense	CGMCC 3.18936	Holotype	Rubber tree	China	MG830462	MG830318	MG830302	MG830270	MG830286	/

Supplementary Table 2 Isolates and GenBank accession numbers used in the phylogenetic analyses of *C. boninense* species complex.

Species name	Strains[1]	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*his3*	*cal*
C. annellatum	CBS 129826 = CH 1	Holotype	*Hevea indica*	Colombia	JQ005222	JQ005309	JQ005396	JQ005570	JQ005656	JQ005483	JQ005743
C. beeveri	CBS 128527 = ICMP 18594	Holotype	*Brachyglottis repanda*	New Zealand	JQ005171	JQ005258	JQ005345	JQ005519	JQ005605	JQ005432	JQ005692
C. boninense	CBS 123755 = MAFF 305972	Holotype	*Crinum asiaticum* var. *sinicum*	Japan	JQ005153	JQ005240	JQ005327	JQ005501	JQ005588	JQ005414	JQ005674
C. boninense	CBS 123756 = MAFF 306094		*Crinum asiaticum* var. *sinicum*	Japan	JQ005154	JQ005241	JQ005328	JQ005502	JQ005589	JQ005415	JQ005675
C. boninense	CBS 128547 = ICMP 10338		*Camellia* sp.	New Zealand	JQ005159	JQ005246	JQ005333	JQ005507	JQ005593	JQ005420	JQ005680
C. brasiliense	CBS 128501 = ICMP 18607 = PAS 12	Holotype	*Passiflora edulis*	Brazil	JQ005235	JQ005322	JQ005409	JQ005583	JQ005669	JQ005496	JQ005756
C. brassicicola	CBS 101059 = LYN 16331	Holotype	*Brassica oleracea* var. *gemmifera*	New Zealand	JQ005172	JQ005259	JQ005346	JQ005520	JQ005606	JQ005433	JQ005693
C. bromeliacearum	LC 0951	Holotype	Bromeliad	China	MZ595832	MZ664077	MZ799267	MZ664130	MZ673956	MZ673843	/
C. camelliae-japonicae	CGMCC 3.18118 = LC 6416	Holotype	*Camellia japonica*	China	KX853165	KX893584	MZ799271	KX893576	KX893580	MZ673859	/
C. catinaense	CBS 142417 = CPC 27978	Holotype	*Citrus reticulata*	Italy	KY856400	KY856224	KY856136	KY855971	KY856482	KY856307	KY856053
C. celtidis	MFLUCC 20-0177	Holotype	*Celtis formosana*	China, Taiwan	MW114362	/	MW177696	MW151580	MW148274	/	/
C. celtidis	NCYU 19-0241		*Celtis formosana*	China, Taiwan	MW114363	/	MW177697	MW151581	MW148275	/	/
C. chamaedoreae	LC 13868 = NN 052885	Holotype	*Chamaedorea erumpens*	China	MZ595890	MZ664084	MZ799274	MZ664188	MZ674008	MZ673910	/
C. chongqingense	CS 0612 (CB6-1)	ex-type	*Camellia sinensis*	China	MG602060	MG602022	MT976117	MT976107	MG602044	/	MT976097
C. citricola	ZJUC 34 = CBS 134228 = CGMCC 3.15227	Holotype	*Citrus unshiu*	China	KC293576	KC293736	KY856140	KC293616	KC293656	/	KC293696

Supplementary Table 2 Continued.

Species name	Strains[1]	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*his3*	*cal*
C. cliviigenum	CPC 38800 = CBS 146825	Holotype	*Clivia* sp.	South Africa	MZ064415	MZ078178	MZ078161	MZ078143	MZ078260	MZ078180	/
C. colombiense	CBS 129818	Holotype	*Passiflora edulis*	Colombia	JQ005174	JQ005261	JQ005348	JQ005522	JQ005608	JQ005435	JQ005695
C. condaoense	CBS 134299	Holotype	*Ipomoea pes-caprae*	Vietnam	MH229914	MH229920	MH229926	/	MH229923	MH229927	/
C. constrictum	CBS 128504 = ICMP 12941	Holotype	*Citrus limon*	New Zealand	JQ005238	JQ005325	JQ005412	JQ005586	JQ005672	JQ005499	JQ005759
C. cymbidiicola	IMI 347923	Holotype	*Cymbidium* sp.	Australia	JQ005166	JQ005253	JQ005340	JQ005514	JQ005600	JQ005427	JQ005687
C. dacrycarpi	CBS 130241 = ICMP 19107	Holotype	*Dacrycarpus dacrydioides*	New Zealand	JQ005236	JQ005323	JQ005410	JQ005584	JQ005670	JQ005497	JQ005757
C. diversum	LC 11292 = CQ 775	Holotype	*Philodendron selloum*	China	MZ595844	MZ664081	MZ799272	MZ664142	MZ673965	MZ673864	/
C. doitungense	MFLUCC 14-0128	Holotype	*Dendrobium* sp.	Thailand	MF448524	MH049480	/	MH376385	MH351277	/	/
C. feijoicola	CBS 144633	Holotype	*Acca sellowiana*	Portugal	MK876413	MK876475	/	MK876466	MK876507	/	/
C. fici	MFLU 18-2615	Holotype	*Ficus ampelas*	China, Taiwan	MW114364	/	MW177698	MW151582	/	/	/
C. hippeastri	CBS 125376 = CSSG 1	Holotype	*Hippeastrum vittatum*	China	JQ005231	JQ005318	JQ005405	JQ005579	JQ005665	JQ005492	JQ005752
C. karsti	CGMCC 3.14194 = CORCG 6	Holotype	*Vanda* sp.	China	HM585409	HM585391	HM582023	HM581995	HM585428	/	HM582013
C. karsti	CBS 127597 = BRIP 29085a		*Diospyros australis*	Australia	JQ005204	JQ005291	JQ005378	JQ005552	JQ005638	JQ005465	JQ005725
C. karsti	CBS 486.97		*Lupinus albus*, cv. *Lu Blanc*	Germany	JQ005182	JQ005269	JQ005356	JQ005530	JQ005616	JQ005443	JQ005703
C. karsti	CBS 508.97 = LARS 168		*Stylosanthes sympodialis*	Australia	JQ005193	JQ005280	JQ005367	JQ005541	JQ005627	JQ005454	JQ005714
C. karsti	BRIP 28443a = CBS 127596		*Mangifera indica*	Australia	JQ005203	JQ005290	JQ005377	JQ005551	JQ005637	JQ005464	JQ005724
C. karsti	CBS 106.91		*Carica papaya*	Brazil	JQ005220	JQ005307	JQ005394	JQ005568	JQ005654	JQ005481	JQ005741

Supplementary Table 2 Continued.

Species name	Strains[1]	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*his3*	*cal*
C. karsti	CBS 861.72		*Bombax aquaticum*	Brazil	JQ005184	JQ005271	JQ005358	JQ005532	JQ005618	JQ005445	JQ005705
C. karsti	CBS 110779		*Eucalyptus grandis*	South Africa	JQ005198	JQ005285	JQ005372	JQ005546	JQ005632	JQ005459	JQ005719
C. karsti	CBS 112762 = STE-U 3000		*Leuco-spermum* sp.	Australia	JQ005213	JQ005300	JQ005387	JQ005561	JQ005647	JQ005474	JQ005734
C. karsti	CBS 112982 = STE-U 2289		*Protea cynaroides*	Zimbabwe	JQ005183	JQ005270	JQ005357	JQ005531	JQ005617	JQ005444	JQ005704
C. karsti	CBS 113087 = STE-U 5288		*Malus* sp.	USA	JQ005181	JQ005268	JQ005355	JQ005529	JQ005615	JQ005442	JQ005702
C. karsti	CBS 118401		*Pachira* sp.	China	JQ005192	JQ005279	JQ005366	JQ005540	JQ005626	JQ005453	JQ005713
C. karsti	CBS 124951		*Theobroma cacao*	Panama	JQ005180	JQ005267	JQ005354	JQ005528	JQ005614	JQ005441	JQ005701
C. karsti	CBS 124956		*Zamia obliqua*	Panama	JQ005216	JQ005303	JQ005390	JQ005564	JQ005650	JQ005477	JQ005737
C. karsti	CBS 124969 = LCM 232		*Quercus salicifolia*	Panama	JQ005179	JQ005266	JQ005353	JQ005527	JQ005613	JQ005440	JQ005700
C. karsti	CBS 125468		*Coffea* sp.	Vietman	JQ005197	JQ005284	JQ005371	JQ005545	JQ005631	JQ005458	JQ005718
C. karsti	CBS 127536 = STE-U 196		*Eucalyptus grandis*	South Africa	JQ005201	JQ005288	JQ005375	JQ005549	JQ005635	JQ005462	JQ005722
C. karsti	CBS 127552		*Eugenia uniflora*	Brazil	JQ005217	JQ005304	JQ005391	JQ005565	JQ005651	JQ005478	JQ005738
C. karsti	CBS 127591		*Sapium integerrimium*	Australia	JQ005186	JQ005273	JQ005360	JQ005534	JQ005620	JQ005447	JQ005707
C. karsti	CBS 127595		*Musa banksii*	Australia	JQ005178	JQ005265	JQ005352	JQ005526	JQ005612	JQ005439	JQ005699
C. karsti	CBS 128500 = ICMP 18585		*Annona cherimola*	New Zealand	JQ005202	JQ005289	JQ005376	JQ005550	JQ005636	JQ005463	JQ005723
C. karsti	CBS 128524 = ICMP 18588		*Citrullus lanatus*	New Zealand	JQ005195	JQ005282	JQ005369	JQ005543	JQ005629	JQ005456	JQ005716
C. karsti	CBS 128540 = STE-U 698		*Triticum* sp.	South Africa	JQ005210	JQ005297	JQ005384	JQ005558	JQ005644	JQ005471	JQ005731
C. karsti	CBS 129822 = G 7		*Passiflora edulis*	Colombia	JQ005218	JQ005305	JQ005392	JQ005566	JQ005652	JQ005479	JQ005739
C. karsti	CBS 129824 = B 1		*Musa* sp.	Colombia	JQ005215	JQ005302	JQ005389	JQ005563	JQ005649	JQ005476	JQ005736
C. karsti	CBS 129833		*Musa* sp.	Mexico	JQ005175	JQ005262	JQ005349	JQ005523	JQ005609	JQ005436	JQ005696

Supplementary Table 2 Continued.

Species name	Strains[1]	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*his3*	*cal*
C. karsti	CBS 129834		*Musa* sp.	Mexico	JQ005176	JQ005263	JQ005350	JQ005524	JQ005610	JQ005437	JQ005697
C. karsti	CBS 130235		*Gossypium hirsutum*	Germany	JQ005190	JQ005277	JQ005364	JQ005538	JQ005624	JQ005451	JQ005711
C. karsti	MAFF 306204 = ICMP 18597		*Clivia miniata*	Japan	JQ005196	JQ005283	JQ005370	JQ005544	JQ005630	JQ005457	JQ005717
C. karsti	ICMP 18598 = MAFF 305973		*Passiflora edulis*	Japan	JQ005194	JQ005281	JQ005368	JQ005542	JQ005628	JQ005455	JQ005715
C. karsti	CNUCC 104A-3-1		*Camellia oleifera*	China	PP814845	PP838424	PP838413	PP820742	PP889539	PP841638	PP838402
C. karsti	CNUCC 181B-4-4		*Cleyera japonica*	China	PP814846	PP838425	PP838414	PP820743	PP889540	PP841639	PP838403
C. karsti	CNUCC 207-1-1		*Camellia oleifera*	China	PP814847	PP838426	PP838415	PP820744	PP889541	PP841640	PP838404
C. karsti	CNUCC 61-24-1		*Cunninghamia lanceolata*	China	PP814848	PP838427	PP838416	PP820745	PP889542	PP841641	PP838405
C. karsti	CNUCC 731B-1-3		*Cunninghamia lanceolata*	China	PP814849	PP838428	PP838417	PP820746	PP889543	PP841642	PP838406
C. karsti	CNUCC 770A-2-1		*Camellia oleifera*	China	PP814850	PP838434	PP838418	PP820747	PP889544	PP841643	PP838407
C. karsti	CNUCC 777-3-1		*Camellia oleifera*	China	PP814851	PP838429	PP838419	PP820748	PP889545	PP841644	PP838408
C. karsti	CNUCC 778-1		*Camellia oleifera*	China	PP814852	PP838430	PP838420	PP820749	PP889546	PP841645	PP838409
C. karsti	CNUCC 904-2-3		*Camellia sinensis*	China	PP814853	PP838431	PP838421	PP820750	PP889547	PP841646	PP838410
C. karsti	CNUCC 914-1-2		*Dalbergia hupeana*	China	PP814854	PP838432	PP838422	PP820751	PP889548	PP841647	PP838411
C. karsti	CNUCC 96-13-3		*Cunninghamia lanceolata*	China	PP814855	PP838433	PP838423	PP820752	/	PP841648	PP838412
C. limonicola	CBS 142410 = CPC 31141	Holotype	*Citrus limon*	Malta, Gozo	KY856472	KY856296	KY856213	KY856045	KY856554	KY856388	KY856125
C. novae-zelandiae	CBS 128505 = ICMP 12944	Holotype	*Capsicum annuum*	New Zealand	JQ005228	JQ005315	JQ005402	JQ005576	JQ005662	JQ005489	JQ005749
C. oncidii	CBS 129828	Holotype	*Oncidium* sp.	Germany	JQ005169	JQ005256	JQ005343	JQ005517	JQ005603	JQ005430	JQ005690

Supplementary Table 2 Continued.

Species name	Strains[1]	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*his3*	*cal*
C. parsonsiae	CBS 128525 = ICMP 18590	Holotype	*Parsonsia capsularis*	New Zealand	JQ005233	JQ005320	JQ005407	JQ005581	JQ005667	JQ005494	JQ005754
C. petchii	CBS 378.94	Holotype	*Dracaena marginata*	Italy	JQ005223	JQ005310	JQ005397	JQ005571	JQ005657	JQ005484	JQ005744
C. phyllanthi	CBS 175.67 = MACS 271	Holotype	*Phyllanthus acidus*	India	JQ005221	JQ005308	JQ005395	JQ005569	JQ005655	JQ005482	JQ005742
C. spicati	YMF 1.04942	Holotype	*Myriophyllum spicatum*	China	OL842171	OL981266	OL981292	OL981240	OL981226	/	/
C. spicati	F 6		*Potamogeton wrightii*	China	OL842172	OL981267	OL981293	OL981241	OL981227	/	/
C. torulosum	CBS 128544 = ICMP 18586	Holotype	*Solanum melongena*	New Zealand	JQ005164	JQ005251	JQ005338	JQ005512	JQ005598	JQ005425	JQ005685
C. watphraense	MFLUCC 14-0123	Holotype	*Dendrobium* sp.	Thailand	MF448523	MH049479	/	MH376384	MH351276	/	/
C. wuxuhaiense	YMF 1.04951	Holotype	*Potamogeton crispu*	China	OL842173	OL981268	OL981294	OL981242	OL981228	/	/
C. wuxuhaiense	F 34		*Potamogeton pectinatus*	China	OL842175	OL981270	OL981296	OL981244	OL981230	/	/

Supplementary Table 3 Isolates and GenBank accession numbers used in the phylogenetic analyses of *C. caudatum-graminicola* species complex.

Species name	Strains[1]	Type	Host	Country	ITS	*chs-1*	*act*	*tub2*	*sod2*
C. alcornii	IMI 176619	Holotype	*Imperata cylindrica* var. *major*	Australia	JX076858	/	/	/	/
C. axonopodi	IMI 279189	Holotype	*Axonopus affinis*	Australia	MN521699	/	/	/	/
C. baiyuense	YMF 1.04941	Holotype	*Hippuris vulgaris*	China	OL842184	OL981305	OL981253	/	/
C. baltimorense	BPI 892771 = SD-11	Holotype	*Sorghastrum nutans*	USA	JX076866	/	/	/	/
C. casaense	YMF 1.04947	Holotype	*Hippuris vulgaris*	China	OL842180	OL981301	OL981249	/	/
C. caspicum	IRAN 3709C = UTFC 365	Holotype	*Cyperaceae*	Iran	MW741443	/	/	MW740344	MW822612
C. caudatum	CBS 131602 = BPI 892767 = NY07-CC04	Epitype	*Sorghastrum nutans* cv. Rumsey	USA	JX076860	/	/	/	/
C. caudisporum	CGMCC 3.15106 = LC 2311	Holotype	*Bletilla ochracea*	China	JX625162	MZ799318	KC843526	JX625190	MZ674035
C. cereale	CBS 129663 = KS20BIG		*Bromus inermis*	USA	JQ005774	JQ005795	JQ005837	JQ005858	DQ133277
C. danxiashanense	LC 13885 = NN 055218	Holotype	*Miscanthus* sp.	China	MZ595898	MZ799330	MZ664196	MZ674016	MZ674042

Supplementary Table 3 Continued.

Species name	Strains[1]	Type	Host	Country	ITS	*chs-1*	*act*	*tub2*	*sod2*
C. dolichoconidiophori	LC 13889 = NN 054966	Holotype	*Dracaena sanderana*	China	MZ595896	MZ799329	MZ664194	MZ674014	MZ674041
C. duyunensis	CGMCC 3.15105 = LC 2307	Holotype	*Bletilla ochracea*	China	JX625160	MZ799320	KC843530	JX625187	MZ674034
C. echinochloae	MAFF 511473	Holotype	*Echinochloa esculenta*	Japan	AB439811	/	/	/	AB440153
C. echinochloae	MAFF 511472		*Echinochloa utilis*	Japan	AB439810	/	/	/	AB440152
C. eleusines	MAFF 511155	Epitype	*Eleusine indica*	Japan	JX519218	JX519226	JX519234	JX519243	EU554234
C. endophytum	CGMCC 3.15108 = LC 2338	Holotype	*Bletilla ochracea*	China	JX625177	MZ799327	KC843533	JX625206	MZ674036
C. eremochloae	CBS 129661	Holotype	*Echinochloa ophiuroides*	USA	JX519220	JX519228	JX519236	JX519245	JQ478449
C. falcatum	CBS 147945 = CGMCC 3.14187	Neotype	*Saccharum offcinarum*	Indonesia	JQ005772	JQ005793	JQ005835	JQ005856	/
C. garzense	YMF 1.04948	Holotype	*Hippuris vulgaris*	China	OL842185	OL981306	OL981254	/	/
C. graminicola	M 1.001 = CBS 130836	Epitype	*Zea mays*	USA	JQ005767	JQ005788	JQ005830	JQ005851	MZ674031
C. hainanense	CBS 145900	Holotype	*Axonopus compressus*	China	KY242705	/	/	/	KY242711
C. hanaui	MAFF 305404	Holotype	*Digiaria ciliaris*	Japan	JX519217	JX519225	/	JX519242	EU554205
C. jacksonii	MAFF 305460	Holotype	*Echinochloa esculenta*	Japan	JX519216	JX519224	JX519233	JX519241	EU554212
C. jacksonii	MAFF 511344		*Echinochloa esculenta*	Japan	EU554133	/	/	/	EU554236
C. litangense	YMF 1.06700	Holotype	*Hippuris vulgaris*	China	MW722955	/	/	MW776748	MW776746
C. miscanthi	MAFF 510857	Holotype	*Miscanthus sinensis*	Japan	JX519221	JX519229	JX519237	JX519246	EU554224
C. multiseptatum	LC 13886 = NN 055357	Holotype	Grass	China	MZ595901	MZ799331	MZ664199	MZ674019	MZ674043
C. navitas	CBS 125086	Holotype	*Panicum virgatum*	USA	JQ005769	JQ005790	JQ005832	JQ005853	GQ919073
C. nicholsonii	MAFF 511115	Holotype	*Paspalum dilatatum*	Japan	JQ005770	JQ005791	JQ005833	JQ005854	EU554229
C. ochracea	CGMCC 3.15104 = LC 2303	Holotype	*Bletilla ochracea*	China	NR163524	MZ799317	KC843527	JX625183	MZ674033
C. paraendophytum	LC 13888 = NN 054963	Holotype	Grass	China	MZ595895	MZ799328	MZ664193	MZ674013	MZ674040
C. paspali	MAFF 305403	Holotype	*Paspalum notatum*	Japan	JX519219	JX519227	JX519235	JX519244	EU554204
C. persicum	IRAN 3712C = UTFC 370 = CBS 148574 = DSM 113400 = GLMC 2645	Holotype	*Phragmites australis*	Iran	MW741433	/	MW822655	MW740367	MW822604

Supplementary Table 3 Continued.

Species name	Strains[1]	Type	Host	Country	ITS	*chs-1*	*act*	*tub2*	*sod2*
C. sacchari	IRAN 3707C = UTFC 363 = CBS 148575 = DSM 113401 = GLMC 2647	Holotype	*Saccharum spontaneum*	Iran	MW741431	/	MW822656	MW740368	MW822602
C. shivasii	LC 1400 = BRIP 15842a	Holotype	*Themeda thriandra*	Australia	MZ595836	MZ799316	MZ664134	MZ673957	MZ674032
C. somersetense	CBS 131599 = JAC 11-11	Holotype	*Sorghastrum nutans*	USA	JX076862	/	/	/	JX076862
C. sublineola	CBS 131301 = S3.001	Epitype	*Sorghum vulgare*	Burkina Faso	JQ005771	JQ005792	JQ005834	JQ005855	DQ132051
C. tibetense	LC 7364	Holotype	*Pocaceae*	China	MZ595840	MZ799339	MZ664138	MZ673961	MZ674037
C. vulgaris	YMF 1.04940	Holotype	*Hippuris vulgaris*	China	NR176189	OL981291	OL981239	/	/
C. wenzhouense	**CNUCC 253B-3-2**	**Holotype**	***Camellia oleifera***	**China**	**PP814984**	**PP831942**	**PP831941**	**PP831944**	**PP831943**
C. zoysiae	MAFF 238573	Holotype	*Zoysia tenuifolia*	Japan	JX076871	/	/	/	/

Supplementary Table 4 Isolates and GenBank accession numbers used in the phylogenetic analyses of *C. dematium* species complex.

Species name	Strains[1]	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*his3*
C. anthrisci	CBS 125334	Holotype	*Anthriscus sylvestris*	Netherlands	GU227845	GU228237	GU228335	GU227943	GU228139	GU228041
C. circinans	CBS 221.81	Epitype	*Allium cepa*	Serbia	GU227855	GU228247	GU228345	GU227953	GU228149	GU228051
C. dematium	CBS 125.25	Epitype	*Eryngium campestre*	France	GU227819	GU228211	GU228309	GU227917	GU228113	GU228015
C. eryngiicola	MFLUCC 17-0318	Holotype	*Eryngium*	Russia	KY792726	KY792723	KY792720	KY792717	KY792729	/
C. fructi	CBS 346.37	Epitype	*Malus sylvestris*	USA	GU227844	GU228236	GU228334	GU227942	GU228138	GU228040
C. hemerocallidis	CBS 130642 = CDLG 5 = CGMCC 3.14971	Holotype	*Hemerocallis fulva* var. *kwanso*	China	JQ400005	JQ400012	JQ399998	JQ399991	JQ400019	/
C. insertae	MFLU 15-1895	Holotype	*Parthenocissus inserta*	Russia	KX618686	KX618684	KX618683	KX618682	KX618685	/
C. jinshuiense	CGMCC 3.18903 = PAFQ 26	Holotype	*Pyrus pyrifolia* cv. *Jinshui*	China	MG748077	MG747995	MG747913	MG747767	MG748157	/
C. jinshuiense	PAFQ 26a		*Pyrus pyrifolia* cv. Jinshui	China	MG874830	MG874822	MG874814	MG874807	MG874838	/

Supplementary Table 4 Continued.

Species name	Strains[1]	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*his3*
C. jinshuiense	LC 8509 = M 333		*Dioscorea zingiberensis*	China	MZ595860	MZ664123	MZ799341	MZ664158	MZ673981	MZ673880
C. kakivorum	KCTC 46679	Holotype	*Diospyros kaki*	Korea	LC324781	LC324787	LC324783	LC324785	LC324791	LC324789
C. kakivorum	KCTC 46680		*Diospyros kaki*	Korea	LC324782	LC324788	LC324784	LC324786	LC324792	LC324790
C. lineola	CBS 125337	Epitype	*Apiaceae* sp.	Czech Republic	GU227829	GU228221	GU228319	GU227927	GU228123	GU228025
C. menispermi	MFLU 14-0625	Holotype	*Menispermum dauricum*	Russia	KU242357	KU242356	KU242355	KU242353	KU242354	/
C. orchidis	MFLUCC 17-1302	Holotype	*Orchis* sp.	Italy	MK502144	MK496857	MK496855	MK496853	MK496859	/
C. parthenocissicola	MFLUCC 17-1098	Holotype	*Parthenocissus quinquefolia*	Russia	MK629452	MK639362	MK639356	MK639358	MK639360	/
C. parthenocissigenum	**CNUCC P7-4-5**	**Holotype**	***Parthenocissus tricuspidata***	China	**PP860044**	**PP849733**	**PP849730**	**PP849727**	**PP849736**	**PP849739**
C. parthenocissigenum	**CNUCC P7-4-5-2-3**		***Parthenocissus tricuspidata***	China	**PP860045**	**PP849734**	**PP849731**	**PP849728**	**PP849737**	**PP849740**
C. parthenocissigenum	**CNUCC P7-4-5-3-3**		***Parthenocissus tricuspidata***	China	**PP860043**	**PP849732**	**PP849729**	**PP849726**	**PP849735**	**PP849738**
C. quinquefoliae	MFLU 14-0626	Holotype	*Parthenocissus quinquefolia*	Russia	KU236391	KU236390	/	KU236389	KU236392	/
C. sambucicola	MFLUCC 16-1388	Holotype	*Sambucus ebulus*	Italy	KY098781	KY098780	KY098779	KY098778	KY098782	/
C. sedi	MFLUCC 14-1002	Holotype	*Sedum* sp.	Russia	KM974758	KM974755	KM974754	KM974756	KM974757	/
C. sonchicola	MFLUCC 17-1299 = IT 3115a	Holotype	*Sonchus* sp.	Italy	KY962757	KY962754	KY962751	KY962748	/	/
C. spinaceae	CBS 128.57		*Spinacia oleracea*	Netherlands	GU227847	GU228239	GU228337	GU227945	GU228141	GU228043
C. zhejiangense	LC 13887 = NN 076215	Holotype	On dead leaves of unidentified tree	China	MZ595912	MZ664124	MZ799342	MZ664210	MZ674030	MZ673932

Supplementary Table 5 Isolates and GenBank accession numbers used in the phylogenetic analyses of *C. destructivum* species complex.

Species name	Strains[1]	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*his3*
C. americae-borealis	CBS 136232	Holotype	*Medicago sativa*	USA	KM105224	KM105579	KM105294	KM105434	KM105504	KM105364
C. antirrhinicola	CBS 102189	Holotype	*Antirrhinum majus*	New Zealand	KM105180	KM105531	KM105250	KM105390	KM105460	KM105320
C. atractylodicola	CGMCC 3.18761 = SAUCC 1307	Holotype	*Atractylodes chinensis*	China	KR149280	KR259334	KR259333	KR132243	KU058178	/
C. atractylodicola	SAUCC130721		*Atractylodes chinensis*	China	KU289190	KU289205	KU289200	KU289195	KU289210	/
C. atractylodicola	SAUCC130724		*Atractylodes chinensis*	China	KU289191	KU289206	KU289201	KU289196	KU289211	/
C. bryoniicola	CBS 109849	Holotype	*Bryonia dioica*	Netherlands	KM105181	KM105532	KM105251	KM105391	KM105461	KM105321
C. cunninghamiae	**CNUCC 58-57-2**	**Holotype**	***Cunninghamia lanceolata***	**China**	**PP812213**	**PP831925**	**PP820670**	**PP820664**	**PP831937**	**PP831931**
C. cunninghamiae	**CNUCC 58-61-2**		***Cunninghamia lanceolata***	**China**	**PP812214**	**PP831926**	**PP820671**	**PP820665**	**PP831938**	**PP831932**
C. destructivum	CBS 136228	Epitype	*Trifolium hybridum*	USA	KM105207	KM105561	KM105277	KM105417	KM105487	KM105347
C. fuscum	CBS 133701	Epitype	*Digitalis lanata*	Germany	KM105174	KM105524	KM105244	KM105384	KM105454	KM105314
C. higginsianum	IMI 349061 = CPC 19379	Epitype	*Brassica chinensis*	Trinidad and	KM105184	KM105535	KM105254	KM105394	KM105464	KM105324
C. hubeiense	**CNUCC 408-1-1**	**Holotype**	***Lindera glauca***	**China**	**PP812212**	**PP831924**	**PP820669**	**PP820663**	**PP831936**	**PP831930**
C. hubeiense	**CNUCC 408-1-1-2**		***Lindera glauca***	**China**	**PP812216**	**PP831928**	**PP820673**	**PP820667**	**PP831940**	**PP831934**
C. lentis	CBS 127604 = DAOM 235316 = CT21	Holotype	*Lens culinaris*	Canada	JQ005766	KM105597	JQ005787	JQ005829	JQ005850	JQ005808
C. lini	CBS 172.51	Epitype	*Linum usitatissimum*	Netherlands	JQ005765	KM105581	JQ005786	JQ005828	JQ005849	JQ005807
C. luanense	**CNUCC 157A-4-4**	**Holotype**	***Camellia sinensis***	**China**	**PP812211**	**PP831923**	**PP820668**	**PP820662**	**PP831935**	**PP831929**
C. luanense	**CNUCC 157A-4-4-2**		***Camellia sinensis***	**China**	**PP812215**	**PP831927**	**PP820672**	**PP820666**	**PP831939**	**PP831933**

Supplementary Table 5 Continued.

Species name	Strains[1]	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*his3*
C. neorubicola	CCR144		*Bubus idaeus*	China	MK529906	MK547520	MK547526	MK547523	MN186400	/
C. ocimi	CBS 298.94	Holotype	*Ocimum basilicum*	Italy	KM105222	KM105577	KM105292	KM105432	KM105502	KM105362
C. panacicola	C08048		*Panax ginseng*	China	GU935867	GU935847	/	GU944757	GU935887	/
C. panacicola	YL2-2		*Panax ginseng*	China	MN685228	MN894870	MN894862	MN894854	MN894877	/
C. pisicola	CBS 724.97 = LARS 60	Holotype	*Pisum sativum*	USA	KM105172	KM105522	KM105242	KM105382	KM105452	KM105312
C. pleopeltidis	CBS 147082 (CPC 39342)	Holotype	*Pleopeltis* sp.	South Africa	MW883412	/	MW890035	MW890024	/	/
C. quercicola	CFCC 54457	ex-type	*Quercus variabilis*	China	ON692810	ON755052	ON75504	ON755044	ON755056	/
C. quercicola	CFCC 57507		*Quercus variabilis*	China	ON692811	ON755053	ON755049	ON755045	ON755057	/
C. shisoi	JCM 31818	Holotype	*Perilla frutescens* var. *crispa*	Japan	MH660930	MH660931	MH660929	MH660928	MH660932	/
C. tabacum	CPC 18945 = N150	Neotype	*Nicotiana tabacum*	Canada	KM105204	KM105557	KM105274	KM105414	KM105484	KM105344
C. tabacum	CBS 124249 = MUCL 44942		*Centella asiatica*	Madagascar	KM105206	KM105560	KM105276	KM105416	KM105486	KM105346
C. tanaceti	CBS 132693 = UM01 = BRIP 57314	Holotype	*Tanacetum cinerariifolium*	Ulverstone	JX218228	JX218243	JX259268	JX218238	JX218233	/
C. utrechtense	CBS 130243	Holotype	*Trifolium pratense*	Netherlands	KM105201	KM105554	KM105271	KM105411	KM105481	KM105341
C. utrechtense	CBS 135827		*Trifolium pratense*	Netherlands	KM105202	KM105555	KM105272	KM105412	KM105482	KM105342
C. vignae	CBS 501.97 = LARS 56	Holotype	*Vigna unguiculata*	Nigeria	KM105183	KM105534	KM105253	KM105393	KM105463	KM105323

Supplementary Table 6 Isolates and GenBank accession numbers used in the phylogenetic analyses of *C. gigasporum* species complex.

Species name	Strain	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*
C. arxii	CBS 132511 = Paphi 2-1	Holotype	*Paphiopedilum* sp.	Germany	KF687716	KF687843	KF687780	KF687802	KF687881
C. chiangraiense	MFLUCC 14-0119	Holotype	*Dendrobium* sp.	Thailand	MF448522	/	/	MH376383	MH351275
C. durionigenum	P132-2 = MFLUCC 22-0111	Holotype	On durian rotting fruit	Thailand	OP740244	OP744505	OP744504	OP744503	OP744506
C. gigasporum	CBS 133266 = MUCL 44947	Holotype	*Centella asiatica*	Madagascar	KF687715	KF687822	KF687761	/	KF687866
C. gigasporum	CBS 109355 = FMR 6728		*Homo sapiens*	Brazil	KF687729	KF687827	KF687774	KF687798	KF687870
C. gigasporum	CBS 124947		*Theobromae cacao*	Panama	KF687731	KF687828	KF687763	KF687786	KF687871
C. jishouense	GMBC 0209	Holotype	*Nothapodytes pittosporoides*	China	MH482929	MH681658	/	MH708135	MH727473
C. magnisporum	CBS 398.84	Holotype	Unknown	unknown	KF687718	KF687842	KF687782	KF687803	KF687882
C. pseudomajus	CBS 571.88	Holotype	*Camellia sinensis*	Taiwan	KF687722	KF687826	KF687779	KF687801	KF687883
C. pseudomajus	CNUCC 1311-1-3		*Camellia oleifera*	China	PP818931	PP830956	PP830946	PP830951	PP830961
C. pseudomajus	CNUCC 1391-1-1		*Camellia sinensis*	China	PP818932	PP830957	PP830947	PP830952	PP830962
C. radicis	CBS 529.93	Holotype	Unknown	Costa Rica	KF687719	KF687825	KF687762	KF687785	KF687869
C. serranegrense	COAD 2100	Holotype	*Cattleya jongheana*	Brazil	KY400111	/	KY407894	KY407892	KY407896
C. subvariabile	LC 13876 = NN 040649	Holotype	Unknown plant	China	MZ595883	MZ664054	MZ799343	MZ664181	MZ674001
C. variabile	LC 13875 = NN 040656	Holotype	Unknown plant	China	MZ595884	MZ664055	MZ799344	MZ664182	MZ674002
C. vietnamense	CBS 125478 = LD 16(L2)	Holotype	*Coffea* sp.	Vietnam	KF687721	KF687832	KF687769	KF687792	KF687877
C. zhaoqingense	LC 13877 = NN 058985	Holotype	On dead petiole of palm	China	MZ595905	MZ664065	MZ799304	MZ664203	MZ674023
C. zhaoqingense	LC 13878 = NN 071035		On dead petiole of palm	China	MZ595906	MZ664066	MZ799305	MZ664204	MZ674024
C. zhaoqingense	LC 13879 = NN 071036		On dead petiole of palm	China	MZ595907	MZ664067	MZ799306	MZ673927	MZ664205
C. zhaoqingense	CNUCC 110A-4-4		*Camellia sinensis*	China	PP818930	PP830955	PP830945	PP830950	PP830960
C. zhaoqingense	CNUCC 714-1-1		*Cinnamomum camphora*	China	PP818933	PP830958	PP830948	PP830953	PP830963
C. zhaoqingense	CNUCC 747-1-3		*Camellia sinensis*	China	PP818934	PP830959	PP830949	PP830954	PP830964

Supplementary Table 7 Isolates and GenBank accession numbers used in the phylogenetic analyses of *C. gloeosporioides* species complex.

Species name	Strain	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*cal*	*apmat*	*gs*
C. aenigma	ICMP 18608	Holotype	*Persea americana*	Israel	JX010244	JX010044	JX009774	JX009443	JX010389	JX009683	KM360143	JX010078
C. aenigma	ICMP 18686		*Persea americana*	Israel	JX010243	JX009913	JX009789	JX009519	JX010390	JX009684	/	JX010079
C. aeschynomenes	ICMP 17673 = ATCC 201874	Holotype	*Aeschynomene virginica*	USA	JX010176	JX009930	JX009799	JX009483	JX010392	JX009721	KM360145	JX010081
C. alatae	CBS 304.67 = ICMP 17919	Holotype	*Dioscorea alata*	India	JX010190	JX009990	JX009837	JX009471	JX010383	JX009738	KC888932	JX010065
C. alienum	ICMP 12071	Holotype	*Malus domestica*	New Zealand	JX010251	JX010028	JX009882	JX009572	JX010411	JX009654	KM360144	JX010101
C. analogum	YMF 1.06943		*Ageratina adenophora*	China	OK030860	OK513663	OK513559	OK513599	OK513629	/	PP498774	/
C. anhuiense	AG 52		*Osmanthus fragrans*	China	OL772737	OL854172	OL854158	OM100918	OL854186	OL854147	OM100932	/
C. anhuiense	AG 85	Holotype	*Osmanthus fragrans*	China	OL772736	OL854171	OL854157	OM100917	OL854185	OL854146	OM100931	/
C. aotearoa	ICMP 18537	Holotype	*Coprosma* sp.	New Zealand	JX010205	JX010005	JX009853	JX009564	JX010420	JX009611	KC888930	JX010113
C. arecicola	CGMCC 3.19667	Holotype	*Areca catechu*	China	MK914635	MK935455	MK935541	MK935374	MK935498	/	/	/
C. artocarpicola	MFLUCC 18-1167	Holotype	*Artocarpus heterophyllus*	Thailand	MN415991	MN435568	MN435569	MN435570	MN435567	/	/	/
C. asianum	ICMP 18580 = CBS 130418	Holotype	*Coffea arabica*	Thailand	FJ972612	JX010053	JX009867	JX009584	JX010406	FJ917506	FR718814	JX010096
C. australianum	VPRI 43075 = UMC 002	Holotype	*Citrus sinensis*	Australia	MG572138	MG572127	MW091987	MN442109	MG572149	/	MG572171	MG572160
C. camelliae	CGMCC 3.14925 = LC 1364	Epitype	*Camellia sinensis*	China	KJ955081	KJ954782	/	KJ954363	KJ955230	KJ954634	KJ954497	KJ954932
C. camelliae	ICMP 18542 = LF 899 = LC 3669		*Camellia sasanqua*	USA	JX010223	JX009994	/	JX009488	JX010429	JX009628	KJ954627	JX010118
C. camelliae	ICMP 10643 = LF 897 = LC 3667		*Camellia* × *williamsii*	UK	JX010224	JX009908	/	JX009540	JX010436	JX009630	KJ954625	JX010119
C. camelliae	ICMP 10646 = LF 898 = LC 3668		*Camellia sasanqua*	USA	JX010225	JX009993	/	JX009563	JX010437	JX009629	KJ954626	JX010117
C. camelliae	CGMCC 3.14924 = LC 1363		*Camellia sinensis*	China	KJ955080	KJ954781	/	KJ954362	KJ955229	KJ954633	KJ954496	KJ954931

Supplementary Table 7 Continued.

Species name	Strain	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*cal*	*apmat*	*gs*
C. camelliae	CGMCC 3.14926 = LC 1365		*Camellia sinensis*	China	KJ955082	KJ954783	/	KJ954364	KJ955231	KJ954635	KJ954498	KJ954933
C. camelliae	CNUCC 1297-3-3		*Akebia trifoliata*	China	PP843248	PP849748	PP841656	PP922828	PP886097	PP854725	PP856623	PP841316
C. camelliae	CNUCC 221A-1-1		*Camellia Chekiang-oleosa*	China	PP843272	PP849772	PP841680	PP922852	PP890412	PP854749	PP855438	PP841340
C. camelliae	CNUCC 257-2-4		*Camellia sinensis*	China	PP843285	PP849785	PP841693	PP922865	PP890425	PP854762	PP855451	PP841353
C. camelliae	CNUCC 742A-1-1		*Camellia sinensis*	China	PP843306	PP849806	PP841714	PP922886	PP870976	PP854782	PP861121	PP841375
C. camelliae	CNUCC 781B-1-2		*Camellia sinensis*	China	PP843307	PP849807	PP841715	PP922887	PP870977	PP854783	PP861122	PP841376
C. cangyuanense	YMF 1.04998		*Ageratina adenophora*	China	OK030865	OK513668	OK513564	OK513604	OK513634	/	/	/
C. cangyuanense	YMF 1.05000		*Ageratina adenophora*	China	OK030863	OK513666	OK513562	OK513602	OK513632	/	/	/
C. cangyuanense	YMF 1.05001		*Ageratina adenophora*	China	OK030864	OK513667	OK513563	OK513603	OK513633	/	PP498775	/
C. cangyuanense	CNUCC 103-13-3		*Camellia oleifera*	China	PP843243	PP849743	PP841651	PP922823	PP886092	PP854806	PP856618	PP841311
C. cangyuanense	CNUCC 104C-16-1		*Camellia oleifera*	China	PP843244	PP849744	PP841652	PP922824	PP886093	PP854721	PP856619	PP841312
C. cangyuanense	CNUCC 104C-3-1		*Camellia oleifera*	China	PP843245	PP849745	PP841653	PP922825	PP886094	PP854722	PP856620	PP841313
C. cangyuanense	CNUCC 106-17-1		*Camellia sinensis*	China	PP843246	PP849746	PP841654	PP922826	PP886095	PP854723	PP856621	PP841314
C. cangyuanense	CNUCC 22-21-2		*Cunninghamia lanceolata*	China	PP843269	PP849769	PP841677	PP922849	PP890409	PP854746	PP856644	PP841337
C. cangyuanense	CNUCC 22-23-2		*Cunninghamia lanceolata*	China	PP843270	PP849770	PP841678	PP922850	PP890410	PP854747	PP856645	PP841338
C. cangyuanense	CNUCC 22-24-3		*Cunninghamia lanceolata*	China	PP843271	PP849771	PP841679	PP922851	PP890411	PP854748	PP856646	PP841339
C. cangyuanense	CNUCC 245-3-4		*Cunninghamia lanceolata*	China	PP843283	PP849783	PP841691	PP922863	PP890423	PP854760	PP855449	PP841351
C. cangyuanense	CNUCC 59B-51-4		*Cunninghamia lanceolata*	China	PP843292	PP849792	PP841700	PP922872	PP890430	PP854807	PP855458	PP841361

Supplementary Table 7 Continued.

Species name	Strain	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*cal*	*apmat*	*gs*
C. cangyuanense	CNUCC 655A-1-4		*Cunninghamia lanceolata*	China	PP843296	PP849796	PP841704	PP922876	PP890434	PP854772	PP855462	PP841365
C. cangyuanense	CNUCC 846B-3-2		*Cunninghamia lanceolata*	China	PP843310	PP849810	PP841718	PP922890	PP870980	PP854786	PP861125	/
C. cangyuanense	CNUCC 94-4-4		*Cunninghamia lanceolata*	China	PP843323	PP849823	PP841731	PP922903	PP870993	PP854799	PP861138	PP841391
C. cangyuanense	CNUCC 96-7-1		*Cunninghamia lanceolata*	China	PP843260	PP849827	PP841735	PP922907	PP870997	PP854803	PP861142	PP841393
C. castaneae	GUCC 12176		*Castanea mollissima*	China	OP722990	OP737972	OP715777	OP715811	OP720867	/	/	/
C. castaneae	GUCC 21268.4	Holotype	*Castanea mollissima*	China	OP722991	OP737973	OP715778	OP715812	OP720868	/	/	/
C. changpingense	CGMCC 3.17582 = SA 0016 = MFLUCC 15-0022	Holotype	Fragaria × ananass	China	KP683152	KP852469	KP852449	KP683093	KP852490	/	/	/
C. chiangmaiense	MFLUCC 18-0945	Holotype	*Magnolia garrettii*	Thailand	MW346499	MW548592	MW623653	MW655578	/	/	/	/
C. chrysophilum	URM 7368 = CMM 4268	Holotype	*Musa* sp.	Brazil	KX094252	KX094183	KX094083	KX093982	KX094285	KX094063	KX094325	KX094204
C. ciggaro	ICMP 18539	Holotype	*Olea europaea*	Australia	JX010230	JX009966	JX009800	JX009523	JX010434	JX009635	/	JX010132
C. citrulli	CAASZT 54		*Citrullus lanatu*	China	MZ475134	OL456686	OL901154	OL449284	OL456645	/	/	/
C. citrulli	CAASZT 52	Holotype	*Citrullus lanatu*	China	MZ475133	OL456685	OL901153	OL449283	OL456644	/	/	/
C. clidemiae	ICMP 18658	Holotype	*Clidemia hirta*	USA, Hawaii	JX010265	JX009989	JX009877	JX009537	JX010438	JX009645	KC888929	JX010129
C. cobbittiense	BRIP 66219	Holotype	*Cordyline stricta* × *C. australis*	Australia	MH087016	MH094133	MH094135	MH094134	MH094137	/	/	/
C. conoides	CGMCC 3.17615 = CAUG 17 = LC 6226	Holotype	*Chili pepper*	China	KP890168	KP890162	KP890156	KP890144	KP890174	KP890150	/	/
C. cordylinicola	MFLUCC 09-0551 = ICMP 18579	Holotype	*Cordyline fruticosa*	Thailand	JX010226	JX009975	JX009864	HM470235	JX010440	HM470238	JQ899274	JX010122
C. cycadis	BRIP 71326a	Holotype	*Cycas revoluta*	China	MT439915	MT439919	MT439917	/	MT439921	/	/	/
C. cycadis	AQISWA 201901		*Cycas revoluta*	China	MT439916	MT439920	MT439918	/	MT439922	/	/	/

Supplementary Table 7 Continued.

Species name	Strain	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*cal*	*apmat*	*gs*
C. dimorphum	YMF 1.07309	Holotype	*Ageratina adenophora*	China	OK030867	OK513670	OK513566	OK513606	OK513636	/	PP498776	/
C. dracaenigenum	MFLUCC 19-0430	Holotype	*Dracaena* sp.	Thailand	MN921250	MT215577	MT215575	MT313686	/	/	/	/
C. endophyticum	MFLUCC 13-0418 = LC 0324	Holotype	*Pennisetum purpureum*	Thailand	KC633854	KC832854	MZ799261	KF306258	MZ673954	KC810018	/	/
C. fici-septicae	MFLUCC 20-0166	Holotype	*Ficus septica*	China, Taiwan	MW114367	MW183774	MW177701	MW151585	/	/	/	/
C. fructicola	ICMP 18581 = BPDI 16 = CBS 130416	Holotype	*Coffea arabica*	Thailand	JX010165	JX010033	JX009866	FJ907426	JX010405	FJ917508	JQ807838	JX010095
C. fructicola	ICMP 18646 = CBS 125397 = MTCC 10906		*Tetragastris panamensis*	Panama	JX010173	JX010032	JX009874	JX009581	JX010409	JX009674	/	JX010099
C. fructicola	LF 130 = LC 2923		*Camellia sinensis*	China	KJ955083	KJ954784	/	KJ954365	KJ955232	KJ954636	KJ954499	KJ954934
C. fructicola	CBS 125395 = ICMP 18645		*Coffea arabica*	Thailand	KJ955084	KJ954785	/	KJ954366	KJ955233	KJ954637	KJ954500	KJ954935
C. fructicola	LC 2925 = LF 132 (ICMP 18581/BPDI16)		*Camellia sinensis*	China	KJ955085	KJ954786	/	KJ954367	KJ955234	KJ954638	KJ954501	KJ954936
C. fructicola	LC 2926 = LF 133(ICMP 18581/BPDI16)		*Camellia sinensis*	China	KJ955086	KJ954787	/	KJ954368	KJ955235	KJ954639	KJ954502	KJ954937
C. fructicola	LC 3155 = LF 364 (ICMP 18581/BPDI16)		*Camellia sinensis*	China	KJ955143	KJ954844	/	KJ954422	KJ955291	KJ954696	KJ954557	KJ954994
C. fructicola	LC 3284 = LF 506 (ICMP 18581/BPDI16)		*Camellia sinensis*	China	KJ955156	KJ954857	/	KJ954433	KJ955303	KJ954708	KJ954567	KJ955007
C. fructicola	CNUCC 117-3-1		*Akebia trifoliata*	China	PP843247	PP849747	PP841655	PP922827	PP886096	PP854724	PP856622	PP841315
C. fructicola	CNUCC 149A-1-1		*Camellia oleifera*	China	PP843250	PP849750	PP841658	PP922830	PP886099	PP854727	PP856625	PP841318
C. fructicola	CNUCC 151A-3-1		*Osmanthus fragrans*	China	PP843252	PP849752	PP841660	PP922832	PP886101	PP854729	PP856627	PP841320
C. fructicola	CNUCC 151A-4-1		*Osmanthus fragrans*	China	PP843253	PP849753	PP841661	PP922833	PP886102	PP854730	PP856628	/

Supplementary Table 7 Continued.

Species name	Strain	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*cal*	*apmat*	*gs*
C. fructicola	CNUCC 213-1-1		*Vernicia montana*	China	PP843264	PP849764	PP841672	PP922844	PP890404	PP854741	PP856639	PP841332
C. fructicola	CNUCC 213-1-6		*Vernicia montana*	China	PP843265	PP849765	PP841673	PP922845	PP890405	PP854742	PP856640	PP841333
C. fructicola	CNUCC 213-3-5		*Vernicia montana*	China	PP843266	PP849766	PP841674	PP922846	PP890406	PP854743	PP856641	PP841334
C. fructicola	CNUCC 213-4-1		*Vernicia montana*	China	PP843267	PP849767	PP841675	PP922847	PP890407	PP854744	PP856642	PP841335
C. fructicola	CNUCC 213-5-4		*Vernicia montana*	China	PP843268	PP849768	PP841676	PP922848	PP890408	PP854745	PP856643	PP841336
C. fructicola	CNUCC 225D-4-4		*Camellia oleifera*	China	PP843274	PP849774	PP841682	PP922854	PP890414	PP854751	PP855440	PP841342
C. fructicola	CNUCC 231-2-1		*Cinnamomum camphora*	China	PP843275	PP849775	PP841683	PP922855	PP890415	PP854752	PP855441	PP841343
C. fructicola	CNUCC 231-4-2		*Cinnamomum camphora*	China	PP843276	PP849776	PP841684	PP922856	PP890416	PP854753	PP855442	PP841344
C. fructicola	CNUCC 231-4-4		*Cinnamomum camphora*	China	PP843277	PP849777	PP841685	PP922857	PP890417	PP854754	PP855443	PP841345
C. fructicola	CNUCC 232-1-1		*Cinnamomum camphora*	China	PP843278	PP849778	PP841686	PP922858	PP890418	PP854755	PP855444	PP841346
C. fructicola	CNUCC 232-3-2		*Cinnamomum camphora*	China	PP843280	PP849780	PP841688	PP922860	PP890420	PP854757	PP855446	PP841348
C. fructicola	CNUCC 232-4-1		*Cinnamomum camphora*	China	PP843281	PP849781	PP841689	PP922861	PP890421	PP854758	PP855447	PP841349
C. fructicola	CNUCC 693-3-2		*Schima superba*	China	PP843298	PP849798	PP841706	PP922878	PP870968	PP854774	PP855464	PP841367
C. fructicola	CNUCC 711-1-2		*Cinnamomum camphora*	China	PP843301	PP849801	PP841709	PP922881	PP870971	PP854777	PP855467	PP841370
C. fructicola	CNUCC 720-1-1		*Cinnamomum camphora*	China	PP843305	PP849805	PP841713	PP922885	PP870975	PP854781	PP861120	PP841374
C. fructicola	CNUCC 782A-1-3		*Camellia sinensis*	China	PP843308	PP849808	PP841716	PP922888	PP870978	PP854784	PP861123	PP841377
C. fructicola	CNUCC 839B-2-1		*Camellia oleifera*	China	PP843309	PP849809	PP841717	PP922889	PP870979	PP854785	PP861124	PP841379
C. fructicola	CNUCC 857-1-1		*Camellia oleifera*	China	PP843311	PP849811	PP841719	PP922891	PP870981	PP854787	PP861126	PP841380
C. fructicola	CNUCC 864A-2-2		*Camellia oleifera*	China	PP843312	PP849812	PP841720	PP922892	PP870982	PP854788	PP861127	/

Supplementary Table 7 Continued.

Species name	Strain	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*cal*	*apmat*	*gs*
C. fructicola	CNUCC 882-2-2		*Camellia oleifera*	China	PP843313	PP849813	PP841721	PP922893	PP870983	PP854789	PP861128	PP841381
C. fructicola	CNUCC 888-1-2		*Camellia oleifera*	China	PP843316	PP849816	PP841724	PP922896	PP870986	PP854792	PP861131	PP841384
C. fructicola	CNUCC 906A-2-1		*Camellia sinensis*	China	PP843318	PP849818	PP841726	PP922898	PP870988	PP854794	PP861133	PP841386
C. fructicola	CNUCC 916-1-2-1		*Camellia sinensis*	China	PP843320	PP849820	PP841728	PP922900	PP870990	PP854796	PP861135	PP841388
C. fructicola	CNUCC 921-3-1		*Camellia sinensis*	China	PP843321	PP849821	PP841729	PP922901	PP870991	PP854797	PP861136	PP841389
C. fructicola	CNUCC 13-5-5		*Paulownia fortunei*	China	PP843249	PP849749	PP841657	PP922829	PP886098	PP854726	PP856624	PP841317
C. fructivorum	Coll 1414 = BPI 884103 = CBS 133125	Holotype	*Vaccinium macrocarpon*	Burling-ton	JX145145	MZ664047	MZ799259	MZ664126	JX145196	/	/	/
C. gardeniae	GUCC 12048		*Gardenia jasminoides*	China	OP722989	OP737962	OP715765	OP715800	OP720857	/	/	/
C. gardeniae	GUCC 12049	Holotype	*Gardenia jasminoides*	China	OP722995	OP737963	OP715766	OP715801	OP720858	/	/	/
C. gloeosporioides	CBS 112999 = IMI 356878 = ICMP 17821	Epitype	*Citrus sinensis*	Italy	JQ005152	JQ005239	JQ005326	JQ005500	JQ005587	JQ005673	JQ807843	JX010085
C. gloeosporioides	ICMP 12938		*Citrus sinensis*	New Zealand	JX010147	JX009935	JX009746	JX009560	/	JX009732	/	/
C. gloeosporioides	CBS 273.51 = ICMP 19121	Holotype	*Citrus limon*	Italy	JX010148	JX010054	JX009903	JX009558	/	JX009745	/	/
C. gloeosporioides	LC 3110 = LF 318		*Camellia sinensis*	China	KJ955127	KJ954828	/	KJ954407	KJ955275	KJ954680	KJ954541	KJ954978
C. gloeosporioides	LC 3312 = LF 534		*Camellia sinensis*	China	KJ955158	KJ954859	/	KJ954434	KJ955305	KJ954710	KJ954569	KJ955009
C. gloeosporioides	LC 3382 = LF 604		*Camellia sinensis*	China	KJ955176	KJ954877	/	KJ954450	KJ955323	KJ954728	KJ954584	KJ955026
C. gloeosporioides	LC 3686 = LF 916		*Camellia sinensis*	China	KJ955226	KJ954927	/	KJ954493	KJ955371	KJ954777	KJ954629	KJ955076
C. gloeosporioides	CNUCC 151A-2-2		*Osmanthus fragrans*	China	PP843251	PP849751	PP841659	PP922831	PP886100	PP854728	PP856626	PP841319
C. gloeosporioides	CNUCC 175B-3-4		*Camellia sinensis*	China	PP843255	PP849755	PP841663	PP922835	PP886104	PP854732	PP856630	PP841378

Supplementary Table 7 Continued.

Species name	Strain	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*cal*	*apmat*	*gs*
C. gloeosporioides	CNUCC 184-3-3		*Diospyros kaki* var. *silvestris*	China	PP843257	PP849757	PP841665	PP922837	PP886106	PP854734	PP856632	PP841323
C. gloeosporioides	CNUCC 191-1-2		*Partheno-cissus tricuspidata*	China	PP843258	PP849758	PP841666	PP922838	PP886107	PP854735	PP856633	PP841324
C. gloeosporioides	CNUCC 194B-2-2		*Akebia quinata*	China	PP843241	PP849741	PP841649	PP922821	PP886090	PP854719	PP856616	PP841310
C. gloeosporioides	CNUCC 196-1-2		*Litsea cubeba*	China	PP843331	PP849831	PP841668	/	PP886108	PP854737	PP861146	PP841328
C. gloeosporioides	CNUCC 196-5-3		*Litsea cubeba*	China	PP843262	PP849762	PP841670	PP922842	PP890402	PP854739	PP856637	PP841330
C. gloeosporioides	CNUCC 225A-3-2		*Camellia oleifera*	China	PP843273	PP849773	PP841681	PP922853	PP890413	PP854750	PP855439	PP841341
C. gloeosporioides	CNUCC 232-2-1		*Cinnamomum camphora*	China	PP843279	PP849779	PP841687	PP922859	PP890419	PP854756	PP855445	PP841347
C. gloeosporioides	CNUCC 250-4-3		*Cunninghamia lanceolata*	China	PP843284	PP849784	PP841692	PP922864	PP890424	PP854761	PP855450	PP841352
C. gloeosporioides	CNUCC 286E-4-1		*Citrus reticulata* cv. '*Hong Mei Ren*'	China	PP843288	PP849788	PP841696	PP922868	PP890427	PP854765	PP855454	PP841356
C. gloeosporioides	CNUCC 61-19-1		*Cunninghamia lanceolata*	China	PP843294	PP849794	PP841702	PP922874	PP890432	PP854770	PP855460	PP841363
C. gloeosporioides	CNUCC 61-23-1		*Cunninghamia lanceolata*	China	PP843295	PP849795	PP841703	PP922875	PP890433	PP854771	PP855461	PP841364
C. gloeosporioides	CNUCC 884-1-1		*Camellia oleifera*	China	PP843314	PP849814	PP841722	PP922894	PP870984	PP854790	PP861129	PP841382
C. gloeosporioides	CNUCC 884-2-2		*Camellia oleifera*	China	PP843315	PP849815	PP841723	PP922895	PP870985	PP854791	PP861130	PP841383
C. gloeosporioides	CNUCC 914-2-1		*Dalbergia hupeana*	China	PP843242	PP849742	PP841650	PP922822	PP886091	PP854720	PP856617	/
C. gloeosporioides	CNUCC 936-1-1		*Paulownia fortunei*	China	PP843322	PP849822	PP841730	PP922902	PP870992	PP854798	PP861137	PP841390
C. gloeosporioides	CNUCC 948-1-2		*Cercis chinensis*	China	PP843324	PP849824	PP841732	PP922904	PP870994	PP854800	PP861139	/
C. gloeosporioides	CNUCC 949-2-2		*Paulownia fortunei*	China	PP843325	PP849825	PP841733	PP922905	PP870995	PP854801	PP861140	/
C. gloeosporioides	CNUCC 953-1-3		*Cercis chinensis*	China	PP843326	PP849826	PP841734	PP922906	PP870996	PP854802	PP861141	PP841392

Supplementary Table 7 Continued.

Species name	Strain	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*cal*	*apmat*	*gs*
C. gloeosporioides	CNUCC 45-4-2		*Camellia sinensis* var. *assamica*	China	PP843290	PP849790	PP841698	PP922870	PP890429	PP854767	PP855456	PP841358
C. gloeosporioides	CNUCC 61-1-1		*Cunninghamia lanceolata*	China	PP843293	PP849793	PP841701	PP922873	PP890431	PP854769	PP855459	PP841362
C. gracile	YMF 1.06939	Holotype	*Ageratina adenophora*	China	OK030868	OK513671	OK513567	OK513607	OK513637	/	PP498777	PP498788
C. grevilleae	CBS 132879 = CPC 15481	Holotype	*Grevillea* sp.	Italy	KC297078	KC297010	KC296987	KC296941	KC297102	KC296963	/	KC297033
C. grossum	CGMCC 3.17614 = CAUG 7 = LC 6227	Holotype	Chili pepper	China	KP890165	KP890159	KP890153	KP890141	KP890171	KP890147	/	/
C. guiyangense	**CNUCC 823-1-1-1**	**Holotype**	***Camellia sinensis***	**China**	**PP812207**	**PP819551**	**PP819547**	**PP830762**	**PP830770**	**PP830766**	**PP830774**	**PP830758**
C. guiyangense	**CNUCC 823-1-1-2**		***Camellia sinensis***	**China**	**PP812208**	**PP819552**	**PP819548**	**PP830763**	**PP830771**	**PP830767**	**PP830775**	**PP830759**
C. hebeiense	MFLUCC 13-0726	Holotype	*Vitis vinifera*	China	KF156863	KF377495	KF289008	KF377532	KF288975	/	/	/
C. hedericola	MFLU 15-0689	Holotype	*Hedera helix*	Italy	MN631384	/	MN635794	MN635795	/	/	/	/
C. helleniense	CBS 142418=CPC 26844	Holotype	*Poncirus trifoliata*	Greece, Arta	KY856446	KY856270	KY856186	KY856019	KY856528	KY856099	/	/
C. henanense	LC 3030 = CGMCC 3.17354 = LF 238	Holotype	*Camellia sinensis*	China	KJ955109	KJ954810	MZ799256	KM023257	KJ955257	KJ954662	KJ954524	KJ954960
C. henanense	LC 2821 = LF 25		*Cirsium japonicum*	China	KM610183	KM610179	/	KM610173	KM610185	KM610177	KM610175	KM610181
C. henanense	LC 2820 = LF 24		*Cirsium japonicum*	China	KM610182	KM610178	/	KM610172	KM610184	KM610176	KM610174	KM610180
C. henanense	CNUCC 163-2-1		*Camellia sinensis*	China	PP843254	PP849754	PP841662	PP922834	PP886103	PP854731	PP856629	PP841321
C. henanense	CNUCC 409B-3-2		*Camellia sinensis*	China	PP843289	PP849789	PP841697	PP922869	PP890428	PP854766	PP855455	PP841357
C. henanense	CNUCC 71C-2-2		*Cinnamomum camphora*	China	PP843304	PP849804	PP841712	PP922884	PP870974	PP854780	PP861119	PP841373
C. henanense	CNUCC 898-1-1		*Camellia sinensis*	China	PP843317	PP849817	PP841725	PP922897	PP870987	PP854793	PP861132	PP841385

Supplementary Table 7 Continued.

Species name	Strain	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*cal*	*apmat*	*gs*
C. henanense	CNUCC 90C-4-2		*Camellia sinensis*	China	PP843319	PP849819	PP841727	PP922899	PP870989	PP854795	PP861134	PP841387
C. horii	ICMP 10492 = NBRC 7478	Neotype	*Diospyros kaki*	Japan	GQ329690	GQ329681	JX009752	JX009438	JX010450	JX009604	JQ807840	JX010137
C. hystricis	CBS 142411 = CPC 28153	Holotype	*Citrus hystrix*	Italy, Catania	KY856450	KY856274	KY856190	KY856023	KY856532	KY856103	/	/
C. jiangxiense	LC 3463 = CGMCC 3.17363 = LF 687	Holotype	*Camellia sinensis*	China	KJ955201	KJ954902	/	KJ954471	KJ955348	KJ954752	KJ954607	KJ955051
C. jiangxiense	LC 3266 = CGMCC 3.17361 = LF 488		*Camellia sinensis*	China	KJ955149	KJ954850	MZ799257	KJ954427	OK236389	KJ954701	KJ954561	KJ955000
C. jiangxiense	LC 3460 = CGMCC 3.17362 = LF 684		*Camellia sinensis*	China	KJ955198	KJ954899	/	KJ954469	KJ955345	KJ954749	KJ954604	KJ955048
C. jixiense	**CNUCC 5-21-2-1**	**Holotype**	***Cunninghamia lanceolata***	**China**	**PP812209**	**PP819553**	**PP819549**	**PP830764**	**PP830772**	**PP830768**	**PP830776**	**PP830760**
C. jixiense	**CNUCC 5-21-2-2**		***Cunninghamia lanceolata***	**China**	**PP812210**	**PP819554**	**PP819550**	**PP830765**	**PP830773**	**PP830769**	**PP830777**	**PP830761**
C. kahawae	IMI 319418 = ICMP 17816	Holotype	*Coffea arabica*	Kenya	JX010231	JX010012	JX009813	JX009452	JX010444	JX009642	JQ894579	JX010130
C. kunmingense	GUCC 12053	Holotype	*Ophiopogon japonicus*	China	OP722975	OP737965	OP715769	OP715804	OP720861	/	/	/
C. kunmingense	GUCC 12178		*Ophiopogon japonicus*	China	OP722974	OP784058	OP715770	OP715805	/	/	/	/
C. ledongense	CGMCC 3.18888	Holotype	*Hevea brasiliensis*	China	MG242009	MG242017	MG242019	MG242015	MG242011	MG242013	/	MG242021
C. ligustri	GUCC 12111	Holotype	*Ilex chinensis*	China	OP722988	OP737968	OP715773	OP740216	OP720864	/	/	/
C. makassarense	CBS 143664	Holotype	*Capsicum annuum*	Indonesia	MH728812	MH728820	MH805850	MH781480	MH846563	/	MH728831	MH748264
C. menglaense	YMF 1.04960	Holotype	Air	China	MH023505	MH023507	MH023508	MH023506	/	/	/	/
C. mengyinense	SAUCC 200702	Holotype	*Rosa chinensis*	China	MW786742	PP498786	MW883686	MW883695	MW888970	MW922538	PP498772	MW888961

Supplementary Table 7 Continued.

Species name	Strain	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*cal*	*apmat*	*gs*
C. musae	CBS 116870 = ICMP 19119	Epitype	*Musa* sp.	USA	HQ596292	HQ596299	JX009896	HQ596284	HQ596280	JX009742	KC888926	JX010103
C. nanhuaense	YMF 1.04993	Holotype	*Ageratina adenophora*	China	OK030870	OK513673	OK513569	OK513609	OK513639	/	PP498778	/
C. nullisetosum	YMF 1.06946	Holotype	*Mangifera indica*	China	OK030872	OK513675	OK513571	OK513611	OK513641	/	PP498779	PP498789
C. nupharicola	CBS 470.96 = ICMP 18187	Holotype	*Nuphar lutea* subsp. *polysepala*	USA	JX010187	JX009972	JX009835	JX009437	JX010398	JX009663	JX145319	JX010088
C. oblongisporum	YMF 1.06938	Holotype	*Ageratina adenophora*	China	OK030874	OK513677	OK513573	/	OK513643	/	PP498780	PP798790
C. osmanthicola	AG 36	Holotype	*Osmanthus fragrans*	China	OL772733	OL854168	OL854154	OM100914	OL854182	OL854143	OM100928	/
C. osmanthicola	AY 42		*Osmanthus fragrans*	China	OL772734	OL854169	OL854155	OM100915	OL854183	OL854144	OM100929	/
C. pandanicola	MFLUCC 17-0571	Holotype	*Pandanaceae*	Thailand	MG646967	MG646934	MG646931	MG646938	MG646926	/	/	/
C. parvisporum	YMF 1.06942		*Ageratina adenophora*	China	OK030876	OK513679	OK513575	OK513613	OK513645	/	PP498781	/
C. perseae	CBS 141365 = GA100	Holotype	Avocado	Israel	KX620308	KX620242	MZ799260	KX620145	KX620341	KX620206	KX620177	KX620275
C. perseae	GA 177		Avocado	Israel	KX620311	KX620245	/	KX620148	KX620344	KX620209	KX620180	KX620278
C. perseae	GA 272 = CBS 141366		Avocado	Israel	KX620321	KX620255	/	KX620158	KX620354	KX620220	KX620188	KX620287
C. proteae	CBS 132882 = CPC 14859	Holotype	*Protea* sp.	South Africa	KC297079	KC297009	KC296986	KC296940	KC297101	KC296960	/	KC297032
C. pseudotheobromicola	MFLUCC 18-1602	Holotype	*Prunus avium*	China	MH817395	MH853675	MH853678	MH853681	MH853684	/	/	/
C. psidii	CBS 145.29 = ICMP 19120	Authentic strain	*Psidium* sp.	Italy	JX010219	JX009967	JX009901	JX009515	JX010443	JX009743	KC888931	JX010133
C. queenslandicum	ICMP 1778	Epitype	*Carica papaya*	Australia	JX010276	JX009934	JX009899	JX009447	JX010414	JX009691	KC888928	JX010104
C. rhexiae	Coll 1026 = BPI 884112 = CBS 133134	Epitype	*Rhexia virginica*	USA	JX145128	MZ664046	MZ799258	MZ664127	JX145179	/	JX145290	/
C. salsolae	ICMP 19051	Holotype	*Salsola tragus*	Hungary	JX010242	JX009916	JX009863	JX009562	JX010403	JX009696	KC888925	JX010093
C. salsolae	MAFF 240542		*Carica papaya*	Japan	/	/	/	/	/	/	LC217757	/

Supplementary Table 7 Continued.

Species name	Strain	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*cal*	*apmat*	*gs*
C. salsolae	CBS 119296 = ICMP 18693		*Glycine max*	Hungary	JX010241	JX009917	JX009791	JX009559	/	JX009695	/	/
C. siamense	ICMP 12567		*Persea americana*	Australia	JX010250	JX009940	JX009761	JX009541	JX010387	JX009697	/	JX010076
C. siamense	ICMP 18578 = CBS 130417	Holotype	*Coffea arabica*	Thailand	JX010171	JX009924	JX009865	FJ907423	JX010404	/	JQ899289	/
C. siamense	LC 0148		*Camellia* sp.	China	KJ955078	KJ954779	/	KJ954360	KJ955227	KJ954631	KJ954494	KJ954929
C. siamense	LC 0149		*Camellia* sp.	China	KJ955079	KJ954780	/	KJ954361	KJ955228	KJ954632	KJ954495	KJ954930
C. siamense	LC 2931 = CGMCC 3.17353 = LF 139		*Camellia* sp.	China	KJ955087	KJ954788	/	KJ954369	KJ955236	KJ954640	KJ954503	KJ954938
C. siamense	LC 2940 = LF 148		*Camellia* sp.	China	KJ955088	KJ954789	/	KJ954370	KJ955237	KJ954641	KJ954504	KJ954939
C. siamense	LC 2941 = LF 149		*Camellia* sp.	China	KJ955089	KJ954790	/	KJ954371	KJ955238	KJ954642	KJ954505	KJ954940
C. siamense	LC 2969 = LF 177		*Camellia oleifera*	China	KJ955092	KJ954793	/	KJ954374	KJ955241	KJ954645	KJ954508	KJ954943
C. siamense	LC 2974 = LF 182		*Camellia* sp.	China	KJ955093	KJ954794	/	KJ954375	KJ955242	KJ954646	KJ954509	KJ954944
C. siamense	CNUCC 180-1-3		*Lindera glauca*	China	PP843256	PP849756	PP841664	PP922836	PP886105	PP854733	PP856631	PP841322
C. siamense	CNUCC 191-3-1		*Partheno-cissus tricuspidata*	China	PP843259	PP849759	PP841667	PP922839	/	PP854736	PP856634	PP841325
C. siamense	CNUCC 196-4-1		*Litsea cubeba*	China	PP843261	PP849760	PP841669	PP922912	PP886109	PP854738	PP856636	PP841329
C. siamense	CNUCC 211-5-2		*Vernicia fordii*	China	PP843263	PP849763	PP841671	PP922843	PP890403	PP854740	PP856638	PP841331
C. siamense	CNUCC 236-4-4		*Machilus nanmu*	China	PP843282	PP849782	PP841690	PP922862	PP890422	PP854759	PP855448	PP841350
C. siamense	CNUCC 271-5-1		*Firmiana simplex*	China	PP843286	PP849786	PP841694	PP922866	PP890426	PP854763	PP855452	PP841354
C. siamense	CNUCC 284-1-1		Lauraceae sp.	China	PP843287	PP849787	PP841695	PP922867	/	PP854764	PP855453	PP841355
C. siamense	CNUCC 540-1-3		*Euonymus alatus*	China	PP843291	PP849791	PP841699	PP922871	/	PP854768	PP855457	PP841360
C. siamense	CNUCC 61-20-3		*Cunninghamia lanceolata*	China	PP843328	PP849828	PP841736	PP922908	PP870998	PP854804	PP861143	PP841394
C. siamense	CNUCC 61-25-1		*Cunninghamia lanceolata*	China	PP843329	PP849829	PP841737	PP922909	PP870999	PP854805	PP861144	PP841322

Supplementary Table 7 Continued.

Species name	Strain	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*cal*	*apmat*	*gs*
C. siamense	CNUCC 679-1-1		*Camellia oleifera*	China	PP843297	PP849797	PP841705	PP922877	PP870967	PP854773	PP855463	PP841366
C. siamense	CNUCC 694-2-1		*Osmanthus fragrans*	China	PP843299	PP849799	PP841707	PP922879	PP870969	PP854775	PP855465	PP841368
C. siamense	CNUCC 694-3-4-1		*Osmanthus fragrans*	China	PP843300	PP849800	PP841708	PP922880	PP870970	PP854776	PP855466	PP841369
C. siamense	CNUCC 712A-1-1		*Cinnamomum camphora*	China	PP843302	PP849802	PP841710	PP922882	PP870972	PP854778	PP855468	PP841371
C. siamense	CNUCC 717-2-1		*Cinnamomum camphora*	China	PP843303	PP849803	PP841711	PP922883	PP870973	PP854779	PP861118	PP841372
C. subhenanense	YMF 1.07324		*Ageratina adenophora*	China	OK030884	OK513685	OK513582	OK513619	OK513648	/	/	/
C. subhenanense	YMF 1.06865	Holotype	*Ageratina adenophora*	China	OK030883	OK513684	OK513581	OK513618	OK513647	/	PP498782	/
C. syzygicola	DNCL 021 = MFLUCC 10-0624	Holotype	*Syzygium samarangense*	Thailand	KF242094	KF242156	/	KF157801	KF254880	KF254859	/	KF242125
C. tainanense	CBS 143666	Holotype	*Capsicum annuum*	Taiwan	MH728818	MH728823	MH805845	MH781475	MH846558	/	/	/
C. temperatum	CBS 133122 = Coll883 = BPI 884100	Holotype	*Vaccinium macrocarpon*	USA	JX145159	MZ664045	MZ799254	MZ664125	JX145211	/	/	/
C. tengchongense	YMF 1.04950	Holotype	*Isoetes sinensis*	China	OL842169	OL981264	OL981290	PP498771	PP498785	PP498784	PP498773	PP498787
C. theobromicola	ICMP 18649 = CBS 124945	Neotype	*Theobroma cacao*	Panama	JX010294	JX010006	JX009869	JX009444	JX010447	JX009591	KC790726	JX010139
C. ti	ICMP 4832	Holotype	*Cordyline* sp.	New Zealand	JX010269	JX009952	JX009898	JX009520	JX010442	JX009649	KM360146	JX010123
C. tropicale	CBS 124949 = ICMP 18653	Holotype	*Theobroma cacao*	Panama	JX010264	JX010007	JX009870	JX009489	JX010407	JX009719	KC790728	JX010097
C. viniferum	GZAAS 5.08601 = yg1	Holotype	*Vitis vinifera* cv. *Shuijing*	China	JN412804	JN412798	/	JN412795	JN412813	JQ309639	/	JN412787
C. vulgaris	CGMCC 3.18940 = YMF 1.04940	Holotype	*Hippuris vulgaris*	China	OL842170	OL981265	OL981291	OL981239				
C. wuxiense	CGMCC 3.17894 = JS1A32	Holotype	*Camellia sinensis*	China	KU251591	KU252045	KU251939	KU251672	KU252200	KU251833	KU251722	KU252101
C. wuxiense	JS1A44		*Camellia sinensis*	China	KU251592	KU252046	KU251940	KU251673	KU252201	KU251834	/	KU252102

Supplementary Table 7 Continued.

Species name	Strain	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*cal*	*apmat*	*gs*
C. xanthorrhoeae	BRIP 45094 = ICMP 17903 = CBS 127831	Holotype	*Xanthorrhoea preissii*	Australia	JX010261	JX009927	JX009823	JX009478	JX010448	JX009653	KC790689	JX010138
C. xishuangbannaense	MFLUCC 19-0107	Holotype	*Magnolia liliifera*	China	MW346469	MW537586	MW660832	MW652294	/	/	/	/
C. yulongense	CNUCC CFCC 50818		*Vaccinium dunalianum* var. *urophyllum*	China	MH751507	MK108986	MH793605	MH777394	MK108987	MH793604	PP861147	MK108988
C. yulongense	CNUCC CFCC 50819		*Vaccinium dunalianum* var. *urophyllum*	China	MK108994	MK108992	MK108991	MK108989	MK108993	MK108990	PP861148	MK108995
C. yunajiangensis	YMF 1.04996 = CGMCC 3.18964	Holotype	*Ageratina adenophora*	China	OK030885	OK513686	OK513583	OK513620	OK513649	/	PP498783	/

Supplementary Table 8 Isolates and GenBank accession numbers used in the phylogenetic analyses of *C. orchidearum* species complex.

Species name	Strains	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*his3*
C. cattleyicola	CBS 170.49	Holotype	*Cattleya* sp.	Belgium	MG600758	MG600819	MG600866	MG600963	MG601025	MG600905
C. cliviicola	CBS 125375	Holotype	*Clivia miniata*	China	MG600733	MG600795	MG600850	MG600939	MG601000	MG600892
C. monsterae	LC 13871 = NN 055214	Holotype	*Monstera deliciosa*	China	MZ595897	MZ664121	MZ799351	MZ664195	MZ674015	MZ673917
C. musicola	CBS 132885	Holotype	*Musa* sp.	Mexico	MG600736	MG600798	MG600853	MG600942	MG601003	MG600895
C. orchidearum	CBS 135131	Epitype	*Dendrobium nobile*	Netherlands	MG600738	MG600800	MG600855	MG600944	MG601005	MG600897
C. pereskiae	COAD 2995	Ex-type	*Pereskia aculeata*	Brazil	MZ262421	MZ265337	MZ265335	MZ265333	MZ265341	MZ265339
C. piperis	IMI 71397 = CPC 21195	Epitype	*Piper nigrum*	Malaysia	MG600760	MG600820	MG600867	MG600964	MG601027	MG600906
C. plurivorum	CBS 125474	Holotype	*Coffea* sp.	Vietnam	MG600718	MG600781	MG600841	MG600925	MG600985	MG600887
C. plurivorum	CBS 132443		*Gossypium* sp.	Brazil	MG600719	MG600782	MG600842	MG600926	MG600986	MG600888
C. plurivorum	CBS 132444		*Gossypium* sp.	Brazil	MG600720	MG600783	MG600843	MG600927	MG600987	MG600987
C. plurivorum	CBS 903.69		*Phaseolus lunatus*	Benin	MG600721	MG600784	MG600844	MG600928	MG600988	MG600890

Supplementary Table 8 Continued.

Species name	Strains	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*his3*
C. reniforme	LC 8230 = M 41	Holotype	*Smilax cocculoides*	China	MZ595847	MZ664110	MZ799290	MZ664145	MZ673968	MZ673867
C. sojae	ATCC 62257	Holotype	*Glycine max*	USA	MG600749	MG600810	MG600860	MG600954	MG601016	MG600899
C. sojae	CBS 18281		*Glycine max*	Serbia	MG600754	MG600815	MG600865	MG600959	MG601021	MG600904
C. syngoniicola	LC 8894 = M 745	Holotype	*Syngonium* sp.	China	MZ595863	MZ664117	MZ799296	MZ664161	MZ673982	MZ673883
C. vittalense	CBS 181.82	Holotype	*Theobroma cacao*	India	MG600734	MG600796	MG600851	MG600940	MG601001	MG600893
C. subplurivorum	**CNUCC 184-5-5**		***Diospyros kaki* var. *silvestris***	**China**	PP840578	PP841300	PP841285	PP841280	PP841295	PP841290
C. subplurivorum	**CNUCC 175C-1-3**		***Camellia sinensis***	**China**	PP840579	PP841301	PP841286	PP841281	PP841296	PP841291
C. subplurivorum	**CNUCC 811A-1-1**		***Camellia sinensis***	**China**	PP840580	PP841302	PP841287	PP841282	PP841297	PP841292
C. subplurivorum	**CNUCC 824-1-2**		***Camellia sinensis***	**China**	PP840581	PP841303	PP841288	PP841283	PP841298	PP841293
C. subplurivorum	**CNUCC 833B-1-1**	**Holotype**	***Camellia oleifera***	**China**	PP840582	PP841304	PP841289	PP841284	PP841299	PP841294
C. sojae	CNUCC 942-2-4-1		*Paulownia fortunei*	China	PP838322	PP841307	PP841306	PP841305	PP841309	PP841308

Supplementary Table 9 Isolates and GenBank accession numbers used in the phylogenetic analyses of *C. truncatum* species complex.

Species name	Strains	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*his3*
C. acidae	MFLUCC 17-2659	Holotype	*Phyllanthus acidus*	Thailand	MG996505	MH003691	MH003694	MH003697	MH003700	/
C. acidae	MFLU 18-0233		*Phyllanthus acidus*	Thailand	MG996506	MH003692	MH003695	MH003698	MH003701	/
C. curcumae	IMI 288937	Epitype	*Curcuma longa*	India	GU227893	GU228285	GU228383	GU227991	GU228187	GU228089
C. fusiforme	MFLUCC 12-0437	Holotype	Dead leaves	Thailand	KT290266	KT290255	KT290253	KT290251	KT290256	/
C. subacidae	LC 13857 = LH 01	Holotype	*Tetrastigma obovatum*	China	MZ595846	MZ664068	MZ799307	MZ664144	MZ673967	MZ673866
C. subacidae	NN 054605		*Asparagus offcinalis*	China	MZ595893	MZ664075	MZ664191	MZ664191	MZ674011	MZ673913
C. subacidae	MH 0562		*Tetrastigma obovatum*	China	MZ595872	MZ664069	MZ799313	MZ664170	MZ673991	MZ673892

Supplementary Table 9 Continued.

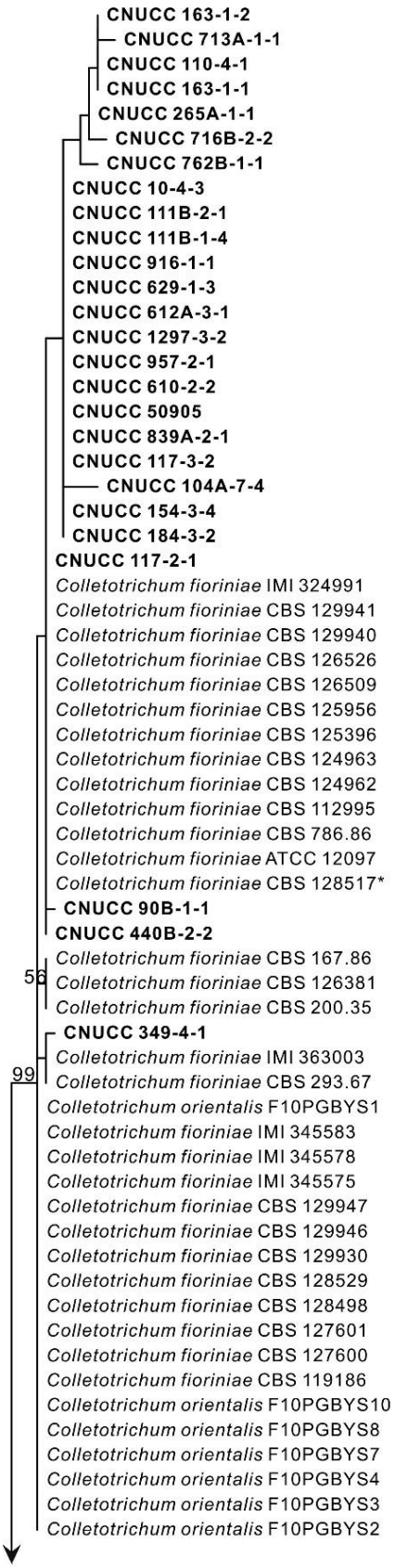
Species name	Strains	Type	Host	Country	ITS	*gapdh*	*chs-1*	*act*	*tub2*	*his3*
C. subacidae	MH 0564		*Tetrastigma obovatum*	China	MZ595873	MZ664074	MZ799308	MZ664171	MZ673992	MZ673893
C. subacidae	MH 0565		*Tetrastigma obovatum*	China	MZ595874	MZ664073	MZ799315	MZ664172	MZ673993	MZ673894
C. subacidae	MH 0566		*Tetrastigma obovatum*	China	MZ595875	MZ664070	MZ799314	MZ664173	MZ673994	MZ673895
C. subacidae	NN 054609		*Hosta* sp.	China	MZ595894	MZ664076	MZ799310	MZ664192	MZ674012	MZ673914
C. subacidae	NN 071129		*Ailanthus altissima*	China	MZ595909	MZ664071	MZ799311	MZ664207	MZ674027	MZ673929
C. subacidae	NN 071131		*Ailanthus altissima*	China	MZ595910	MZ664072	MZ799312	MZ664208	MZ674028	MZ673930
C. truncatum	CBS 151.35	Epitype	*Phaseolus lunatus*	USA	GU227862	GU228254	GU228352	GU227960	GU228156	GU228058
C. subacidae	CNUCC 764B-2		*Camellia oleifera*	China	PP830006	PP830967	PP830966	PP830965	PP830969	PP830968

Supplementary Table 10 The basic information of genome sequences downloaded from JGI.

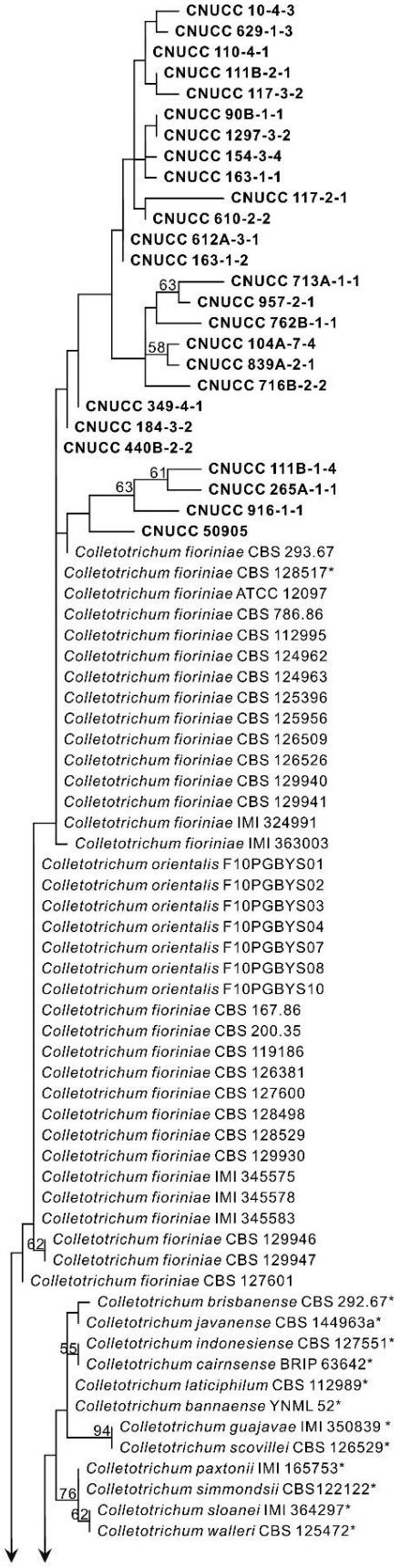
Species	Project Name	Principal Investi-gator	Product Name	Status	Status Date	User Program	Proposal	JGI Project Id	Taxonomy ID	NCBI Project Id	SRA	Sequencing Project ID	Analysis project ID
C. cereale	*Colletotrichum cereale* CBS 129662 Annotated Standard Draft	Jo Anne Crouch joanne.crouch@ars.usda.gov	Fungal Annotated Standard Draft	Complete	2017/1/25	CSP 2012	Genomic signatures of pathogenicity and endophytism in five species of grass-associated *Colletotrichum* impacting the health and production of bioenergy feedstocks, agriculture and the environment1043099	1043096	343994	403325 262440	SRP117842 SRP092693	1043098 1043097	1043101 1043100 1043099
C. sublineola	*Colletotrichum sublineola* CBS 131301 Annotated Standard Draft	Jo Anne Crouch joanne.crouch@ars.usda.gov	Fungal Annotated Standard Draft	Complete	2013/7/2	CSP 2012	Genomic signatures of pathogenicity and endophytism in five species of grass-associated *Colletotrichum* impacting the health and production of bioenergy feedstocks, agriculture and the environment	1006164	1173701	262379 262370	SRP096076 SRP084029	1006166 1006165	/

Supplementary Table 11 The basic information of genome sequences downloaded from GenBank.

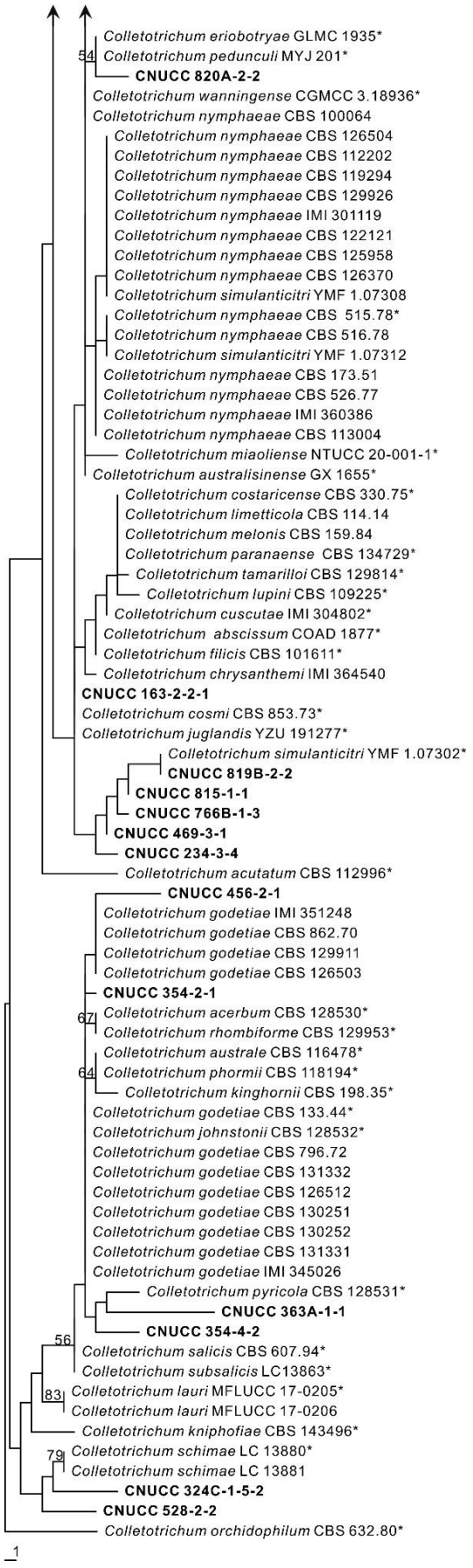
Species	Strain number	Taxonomy id	Assembly Name	Assembly Accession	Level	Contig N50	Total length	Size (Mb)	GC content	Submission Date	BioSample
C. fructicola	CGMCC3.17371	690256	ASM977102v1	GCA_009771025.1	Contig	905 947	58 056 435	58.06	53.20%	2019/12/18	SAMN11398962
C. graminicola	M1.001	31870	C_graminicola_M1_001_V	GCA_029226625.1	Scaffold	228 959	51 644 307	51.64	45.95%	2010/10/12	SAMN31693333



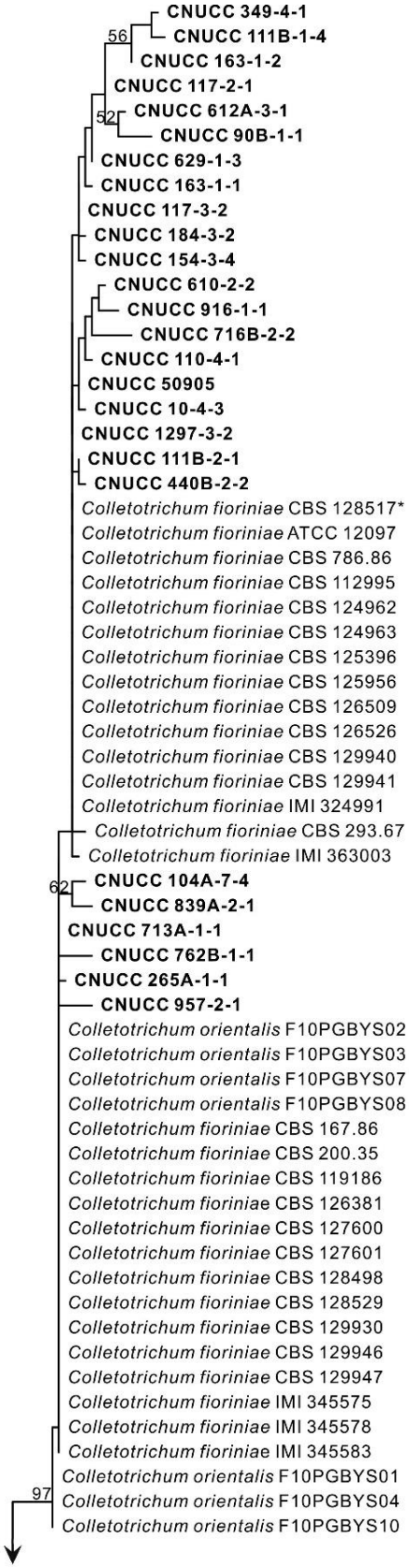
Supplementary Figure 1 – Phylogenetic tree of *C. acutatum* species complex derived from maximum parsimony analysis of *act* sequences, using *Colletotrichum orchidophilum* CBS 632.80 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



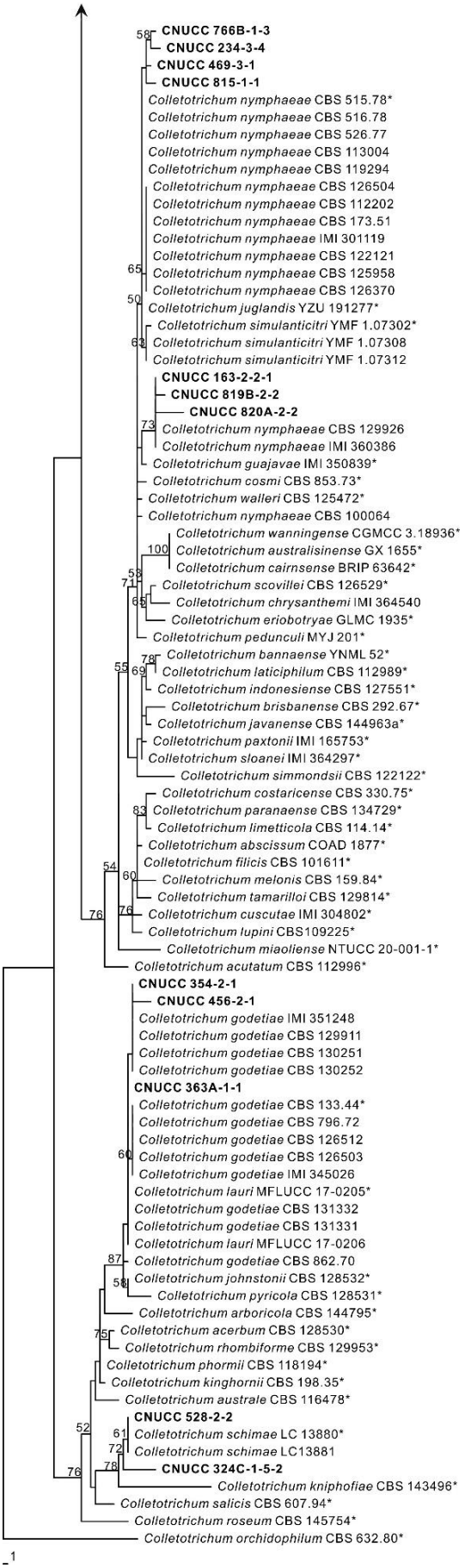
Supplementary Figure 2 – Phylogenetic tree of *C. acutatum* species complex derived from maximum parsimony analysis of *chs* sequences, using *Colletotrichum orchidophilum* CBS 632.80 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



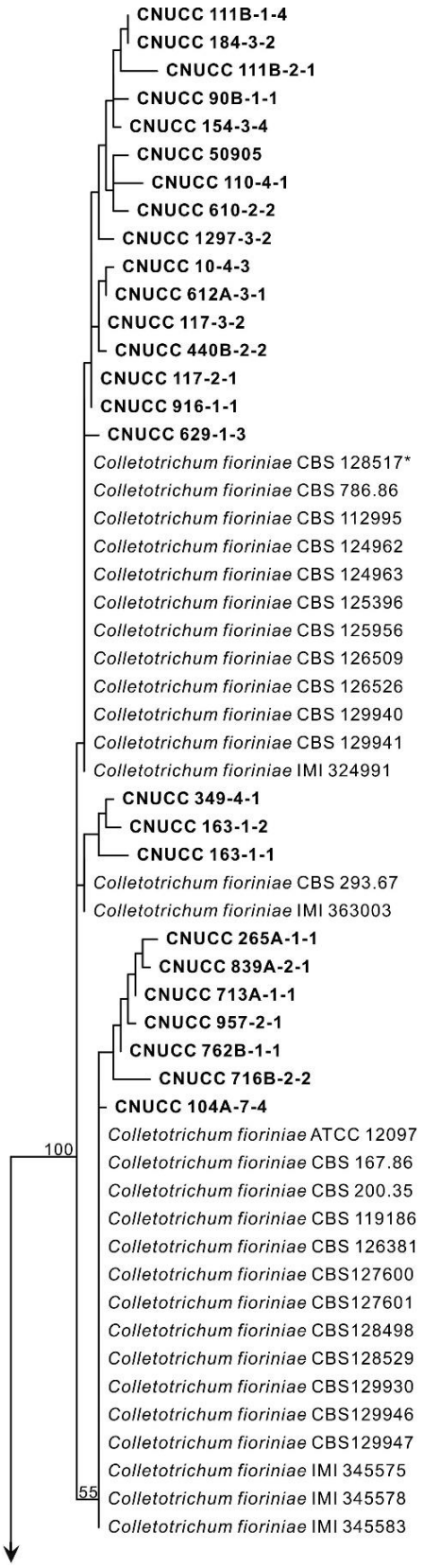
Supplementary Figure 2 – Continued.



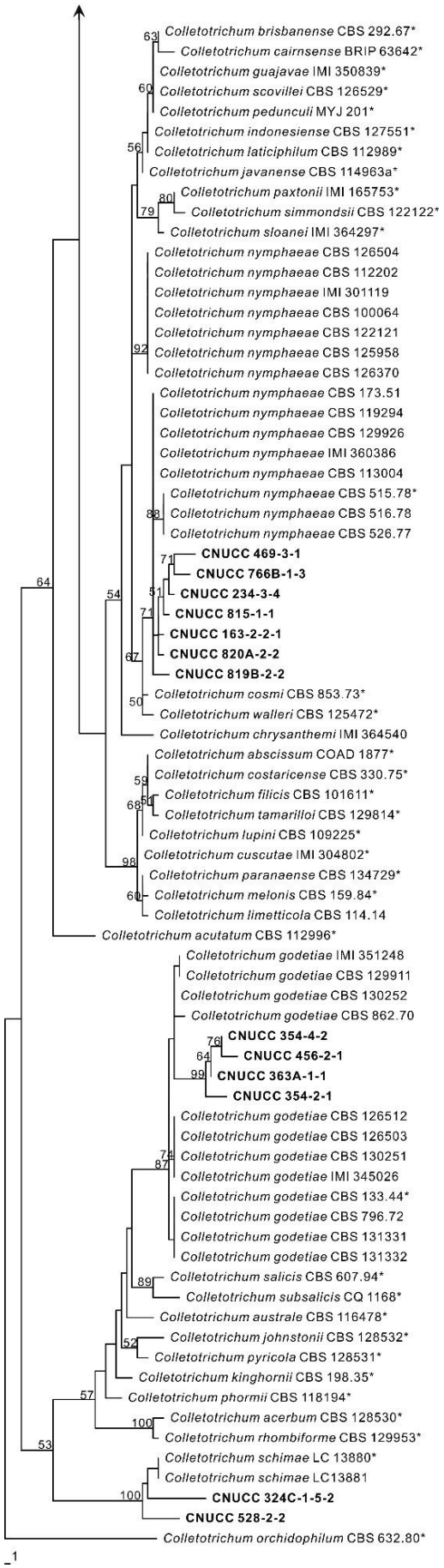
Supplementary Figure 3 – Phylogenetic tree of *C. acutatum* species complex derived from maximum parsimony analysis of *gapdh* sequences, using *Colletotrichum orchidophilum* CBS 632.80 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



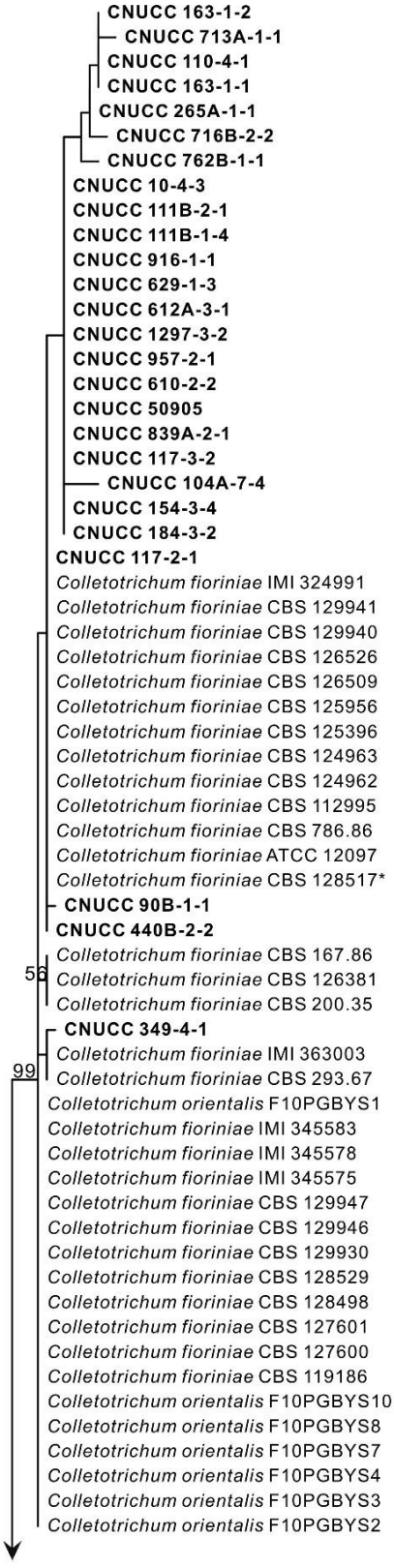
Supplementary Figure 3 – Continued.



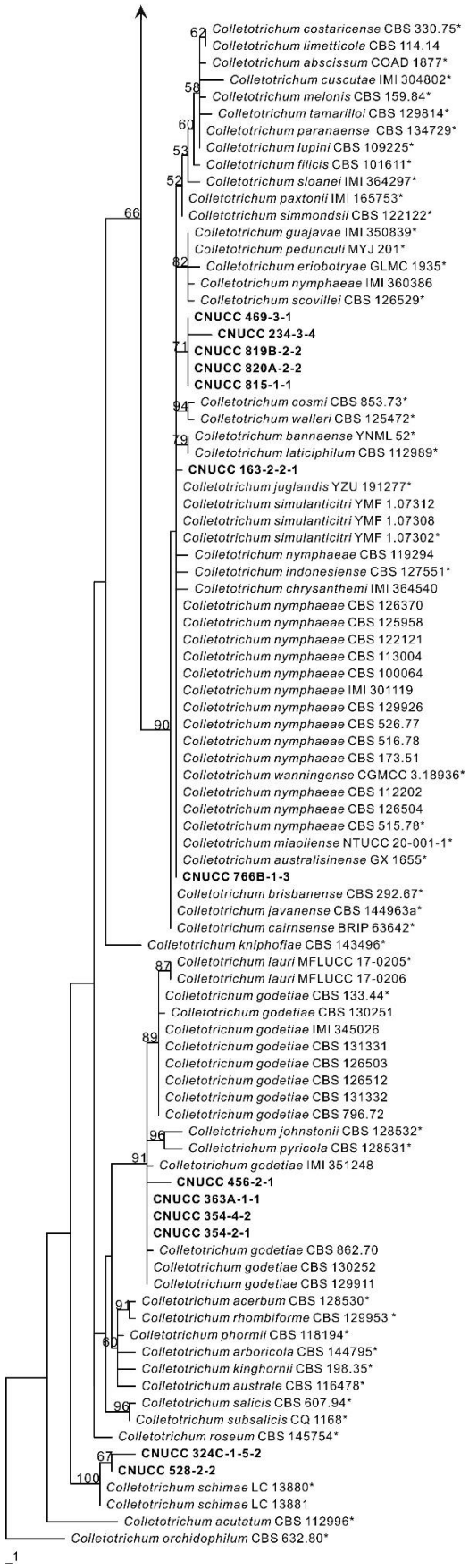
Supplementary Figure 4 – Phylogenetic tree of *C. acutatum* species complex derived from maximum parsimony analysis of *his* sequences, using *Colletotrichum orchidophilum* CBS 632.80 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



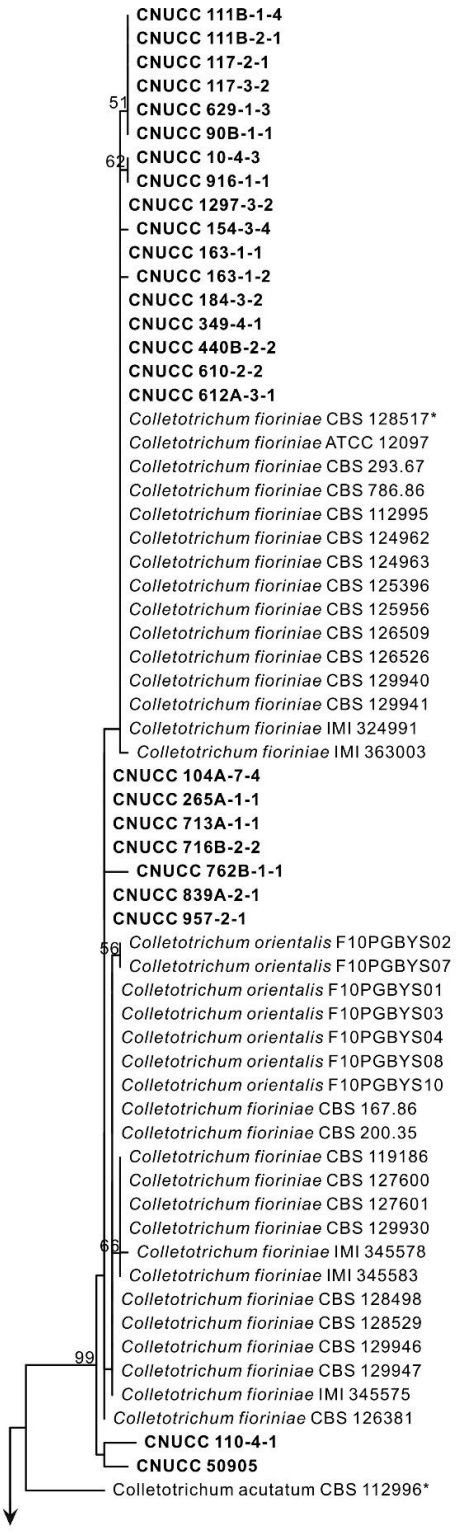
Supplementary Figure 4 – Continued.



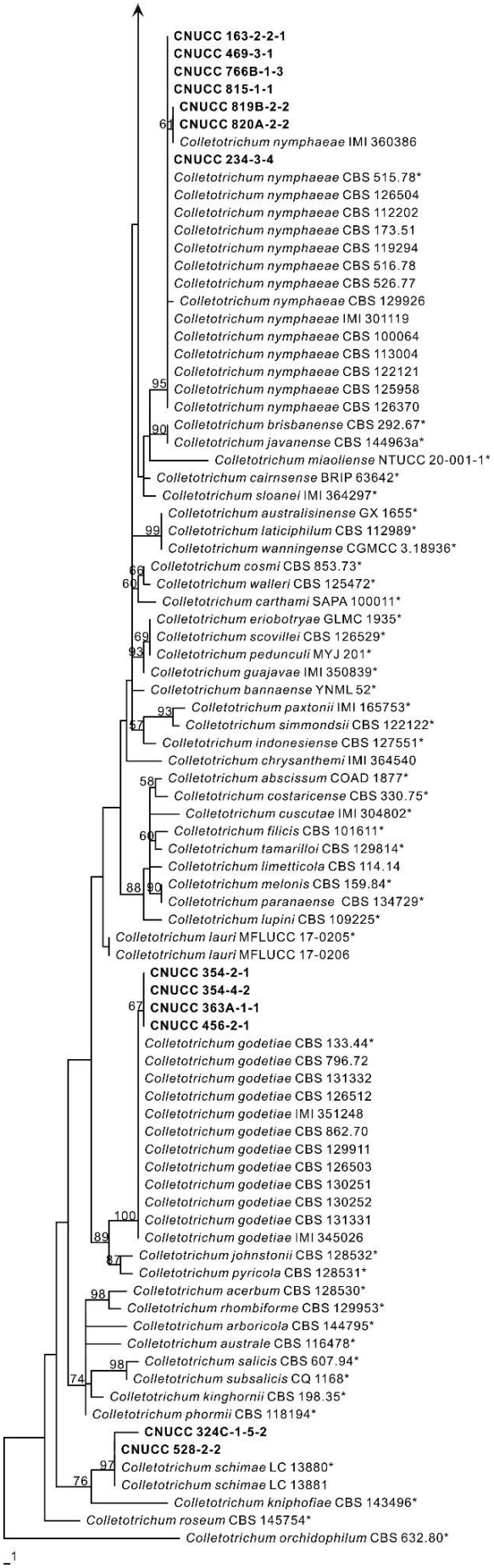
Supplementary Figure 5 – Phylogenetic tree of *C. acutatum* species complex derived from maximum parsimony analysis of ITS sequences, using *Colletotrichum orchidophilum* CBS 632.80 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



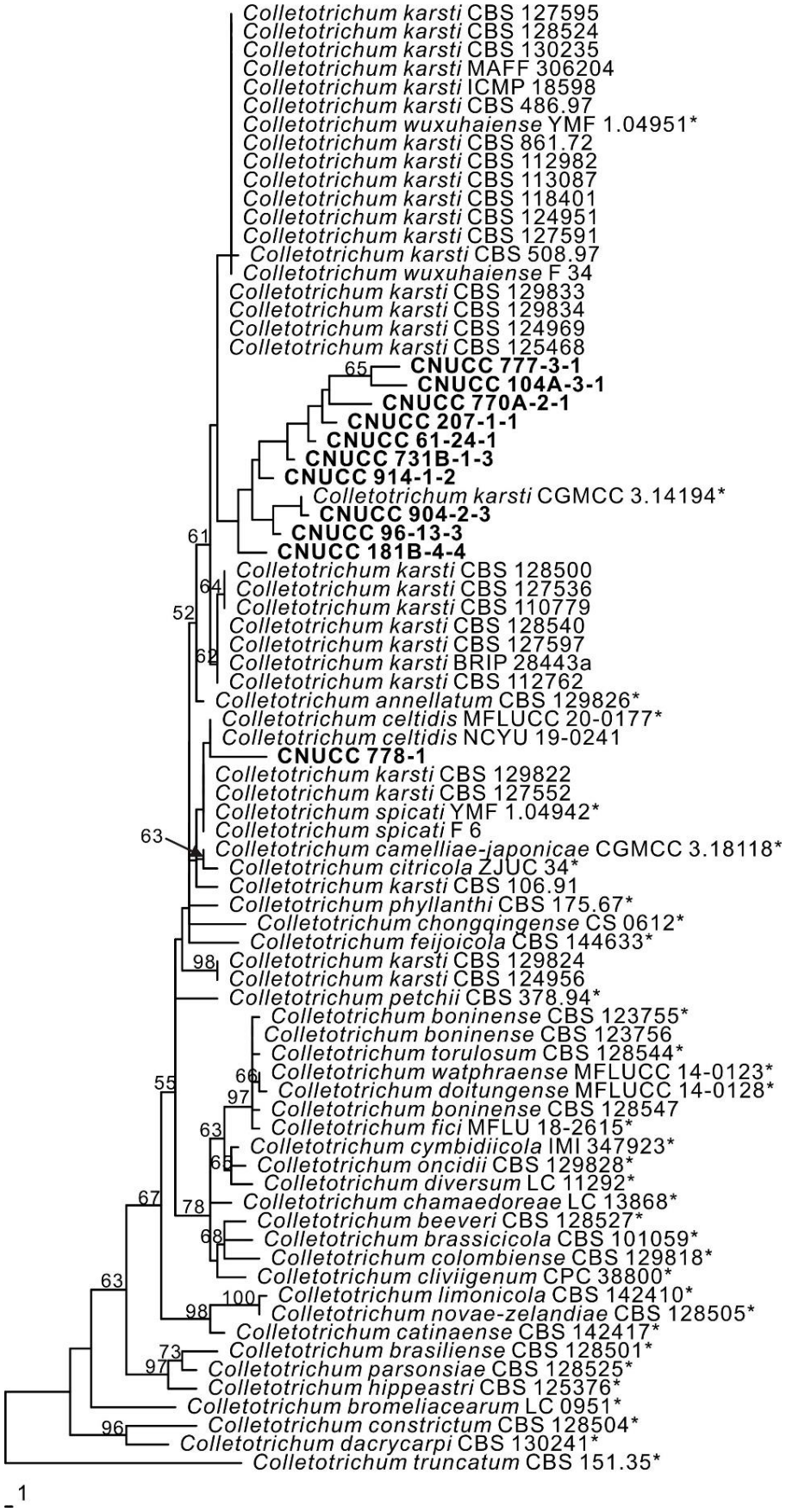
Supplementary Figure 5 – Continued.



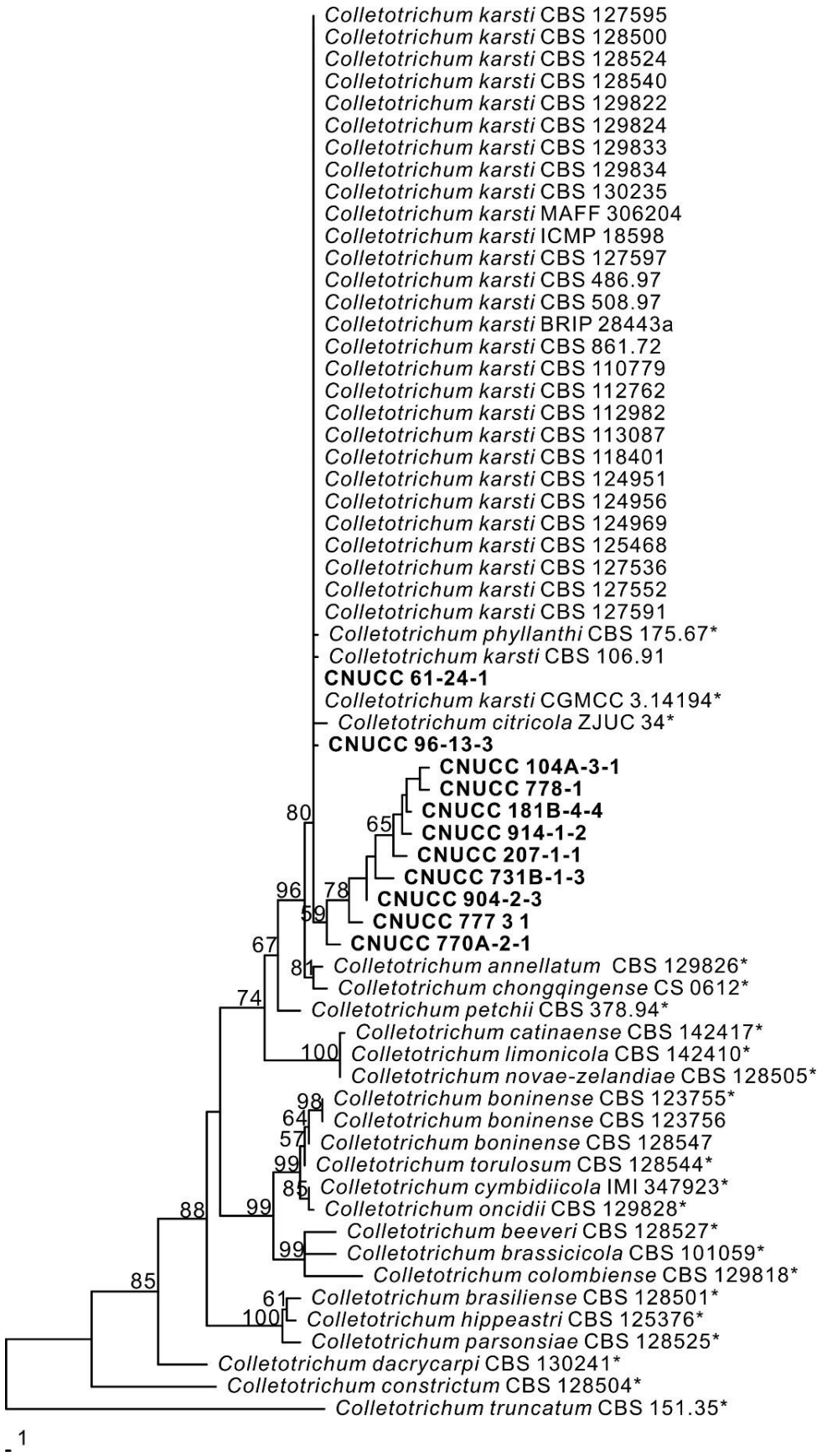
Supplementary Figure 6 – Phylogenetic tree of *C. acutatum* species complex derived from maximum parsimony analysis of *tub* sequences, using *Colletotrichum orchidophilum* CBS 632.80 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



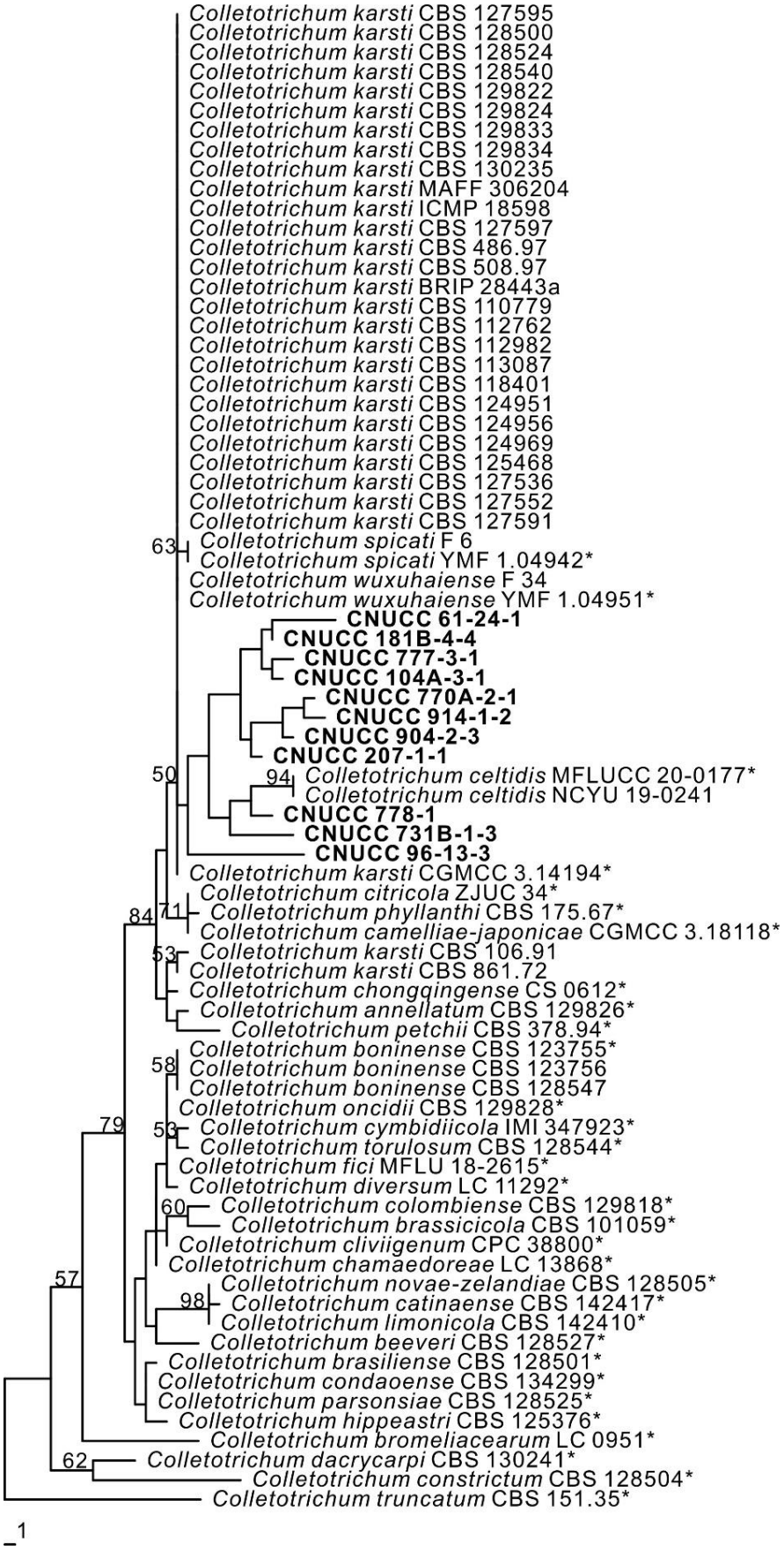
Supplementary Figure 6 – Continued.



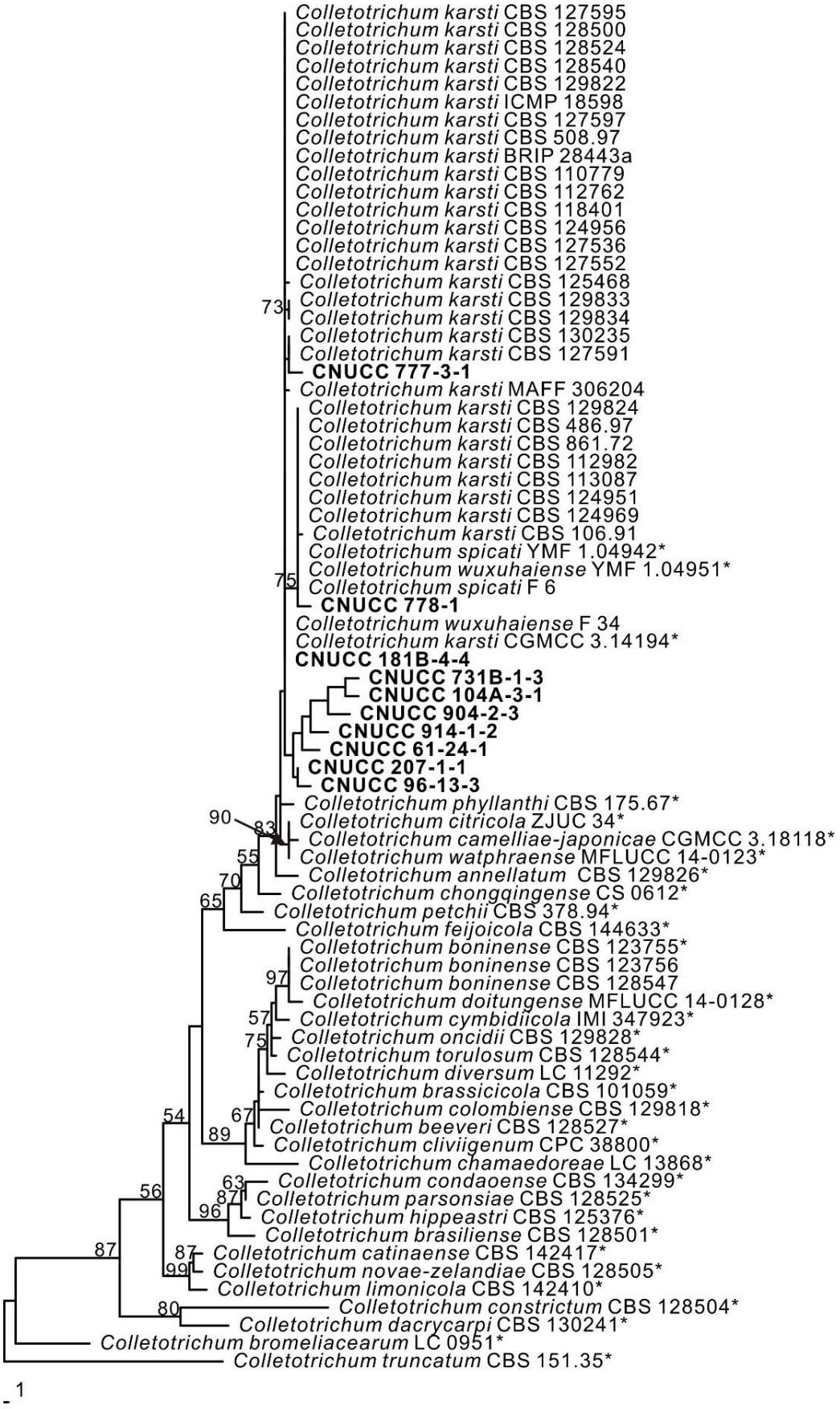
Supplementary Figure 7 – Phylogenetic tree of *C. boninense* species complex derived from maximum parsimony analysis of *act* sequences, using *Colletotrichum truncatum* CBS 151.35 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



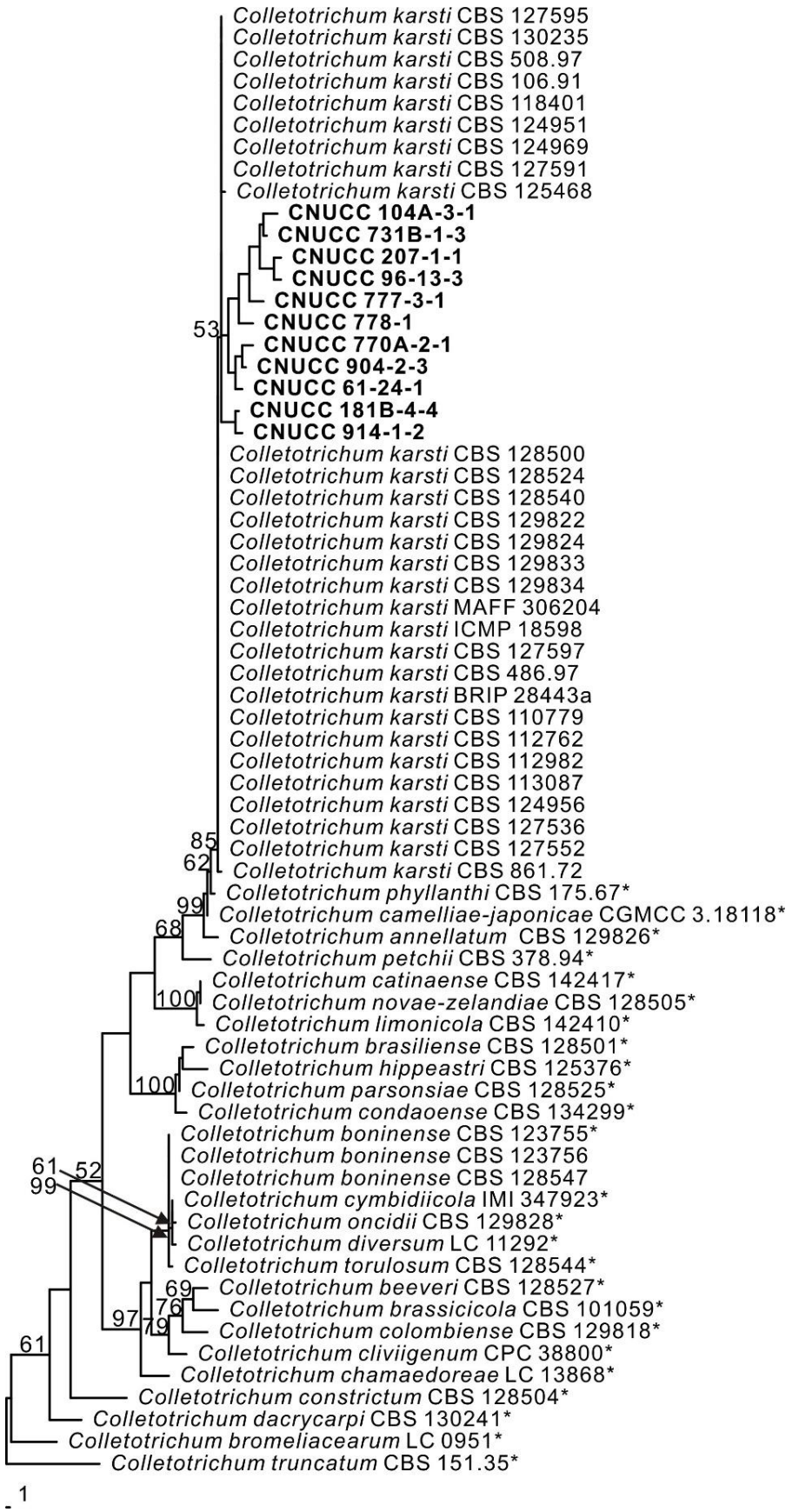
Supplementary Figure 8 – Phylogenetic tree of *C. boninense* species complex derived from maximum parsimony analysis of *cal* sequences, using *Colletotrichum truncatum* CBS 151.35 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



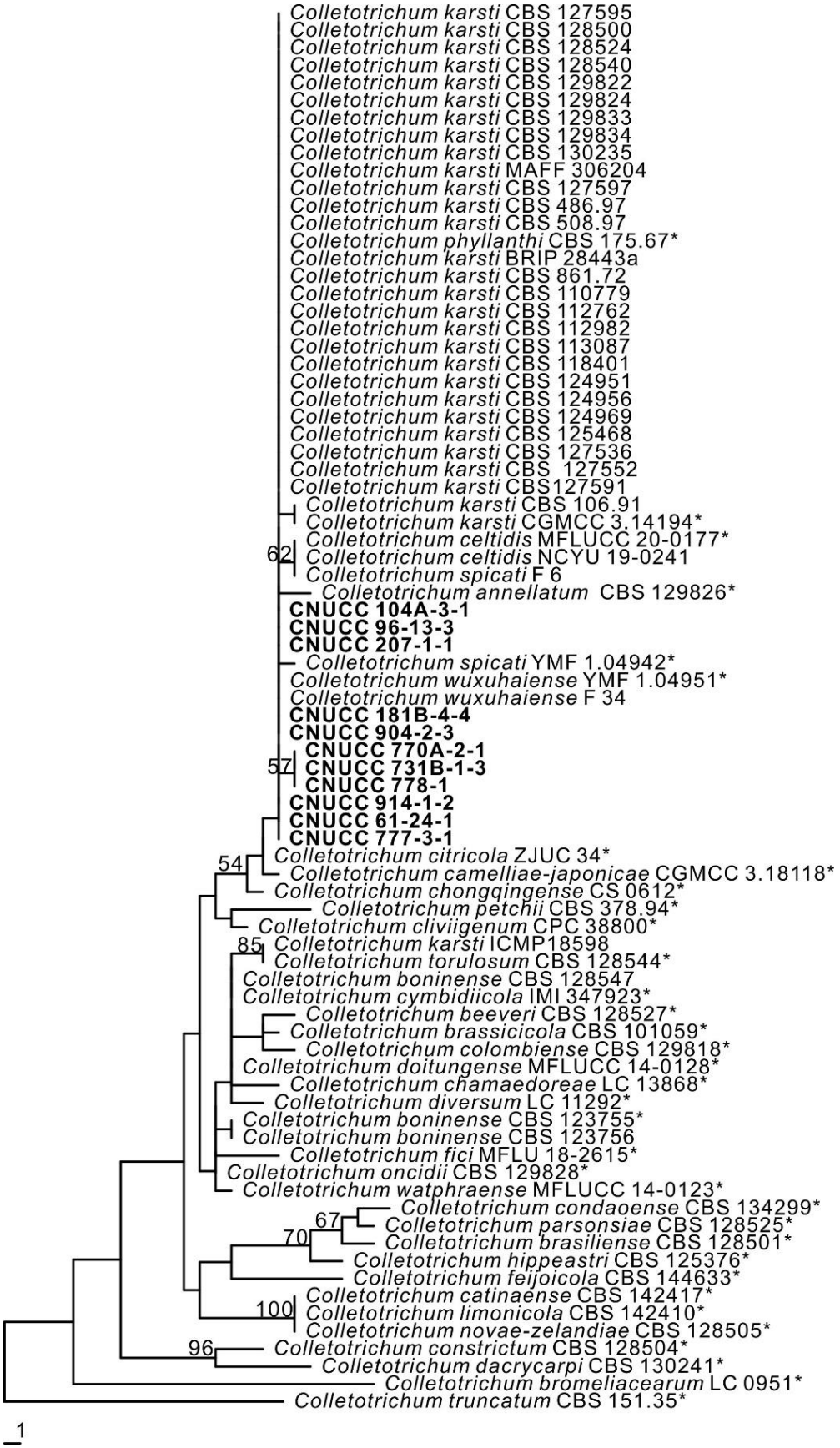
Supplementary Figure 9 – Phylogenetic tree of *C. boninense* species complex derived from maximum parsimony analysis of *chs* sequences, using *Colletotrichum truncatum* CBS 151.35 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



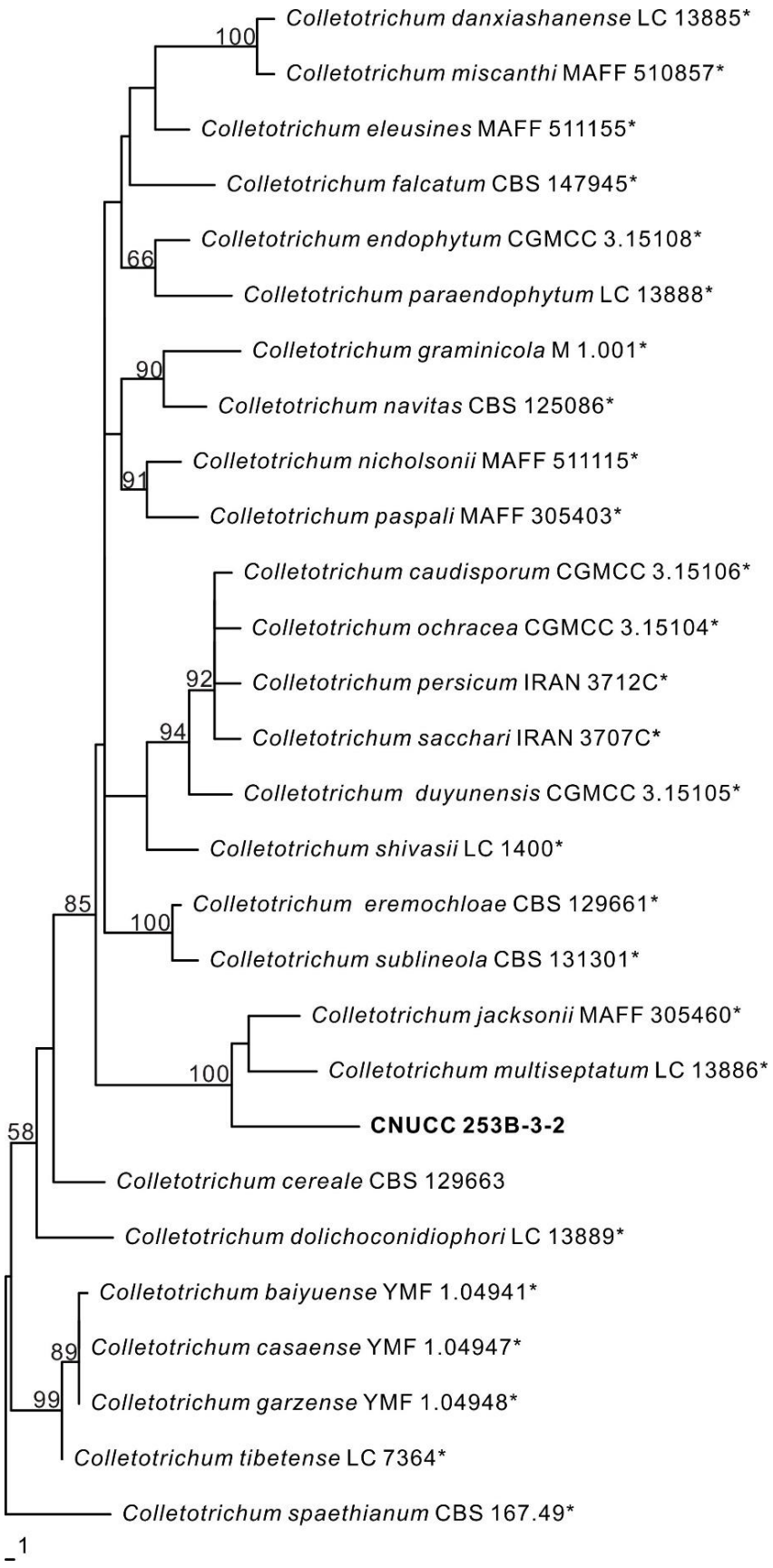
Supplementary Figure 10 – Phylogenetic tree of *C. boninense* species complex derived from maximum parsimony analysis of *gapdh* sequences, using *Colletotrichum truncatum* CBS 151.35 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



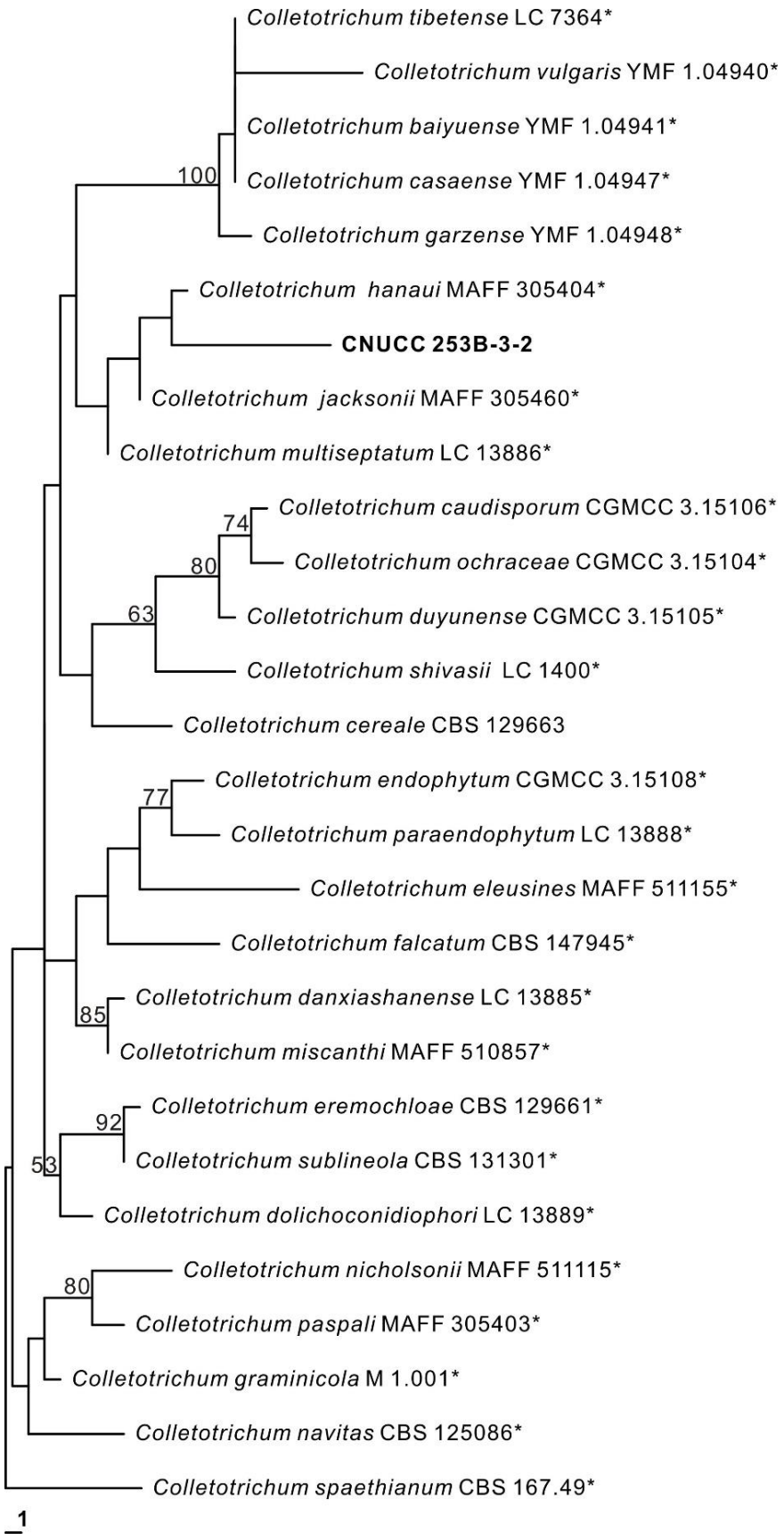
Supplementary Figure 11 – Phylogenetic tree of *C. boninense* species complex derived from maximum parsimony analysis of *his* sequences, using *Colletotrichum truncatum* CBS 151.35 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



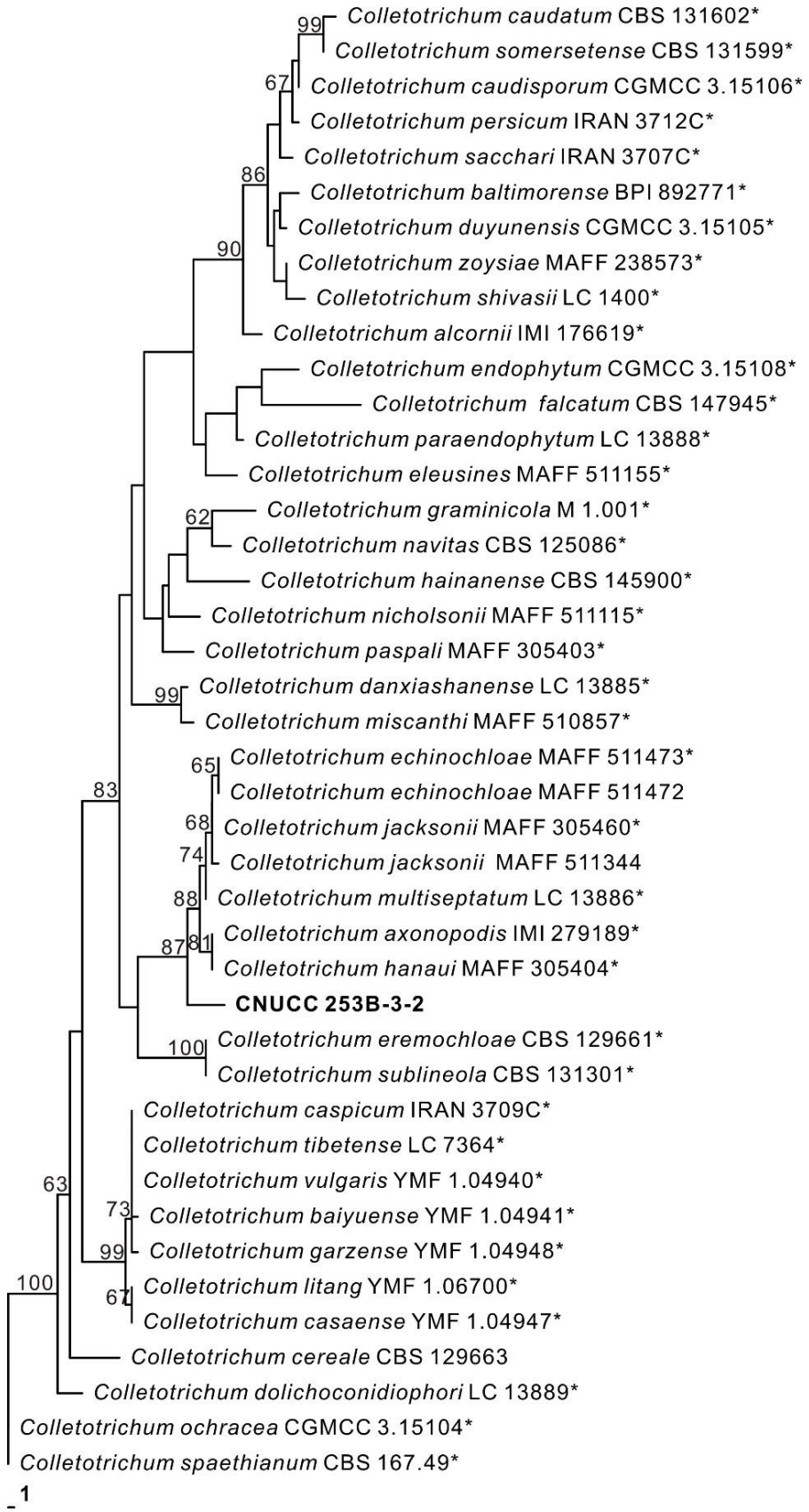
Supplementary Figure 12 – Phylogenetic tree of *C. boninense* species complex derived from maximum parsimony analysis of ITS sequences, using *Colletotrichum truncatum* CBS 151.35 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



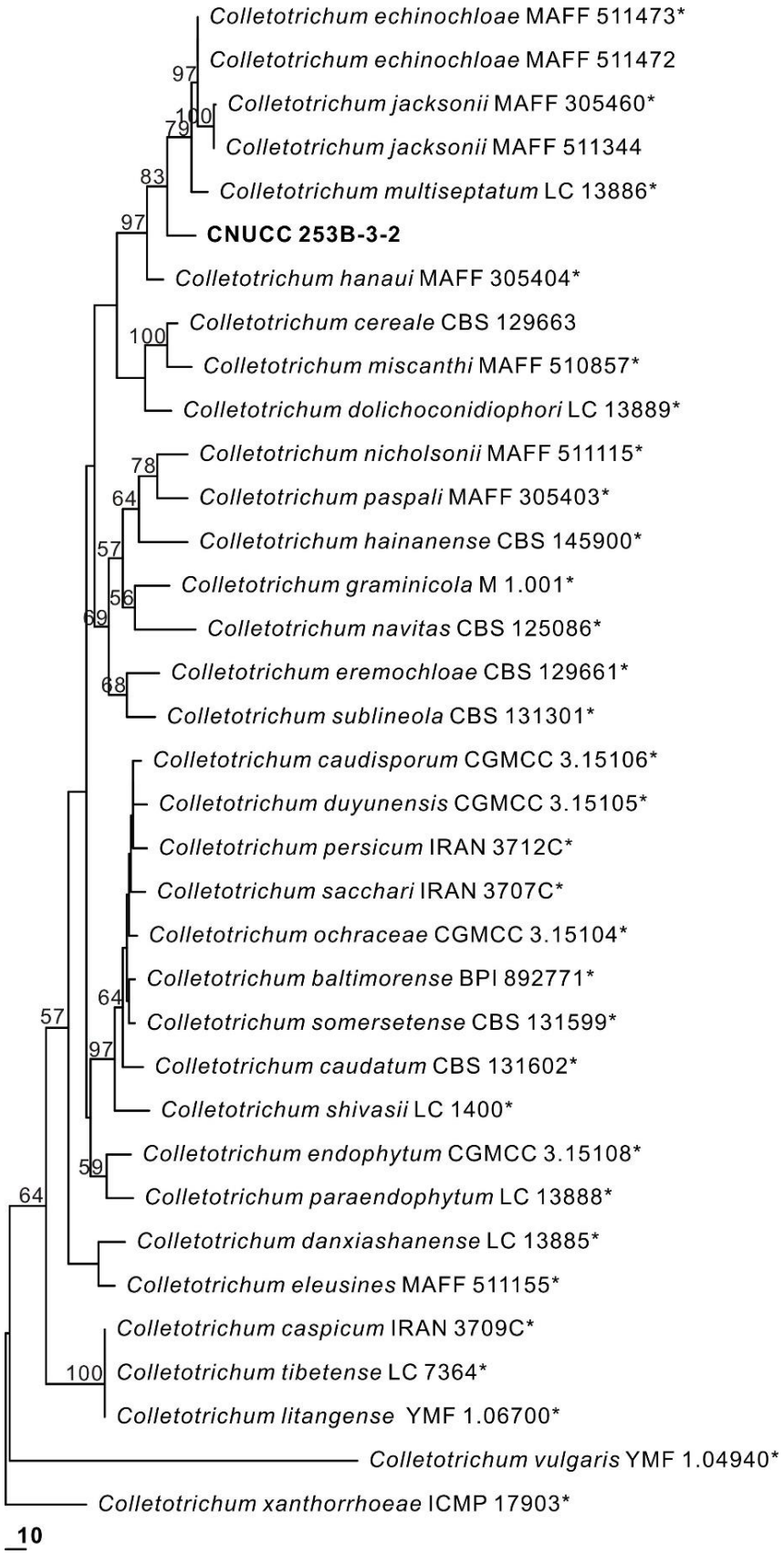
Supplementary Figure 13 – Phylogenetic tree of *C. caudatum-graminicola* species complex derived from maximum parsimony analysis of *act* sequences, using *Colletotrichum spaethianum* CBS 167.49 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



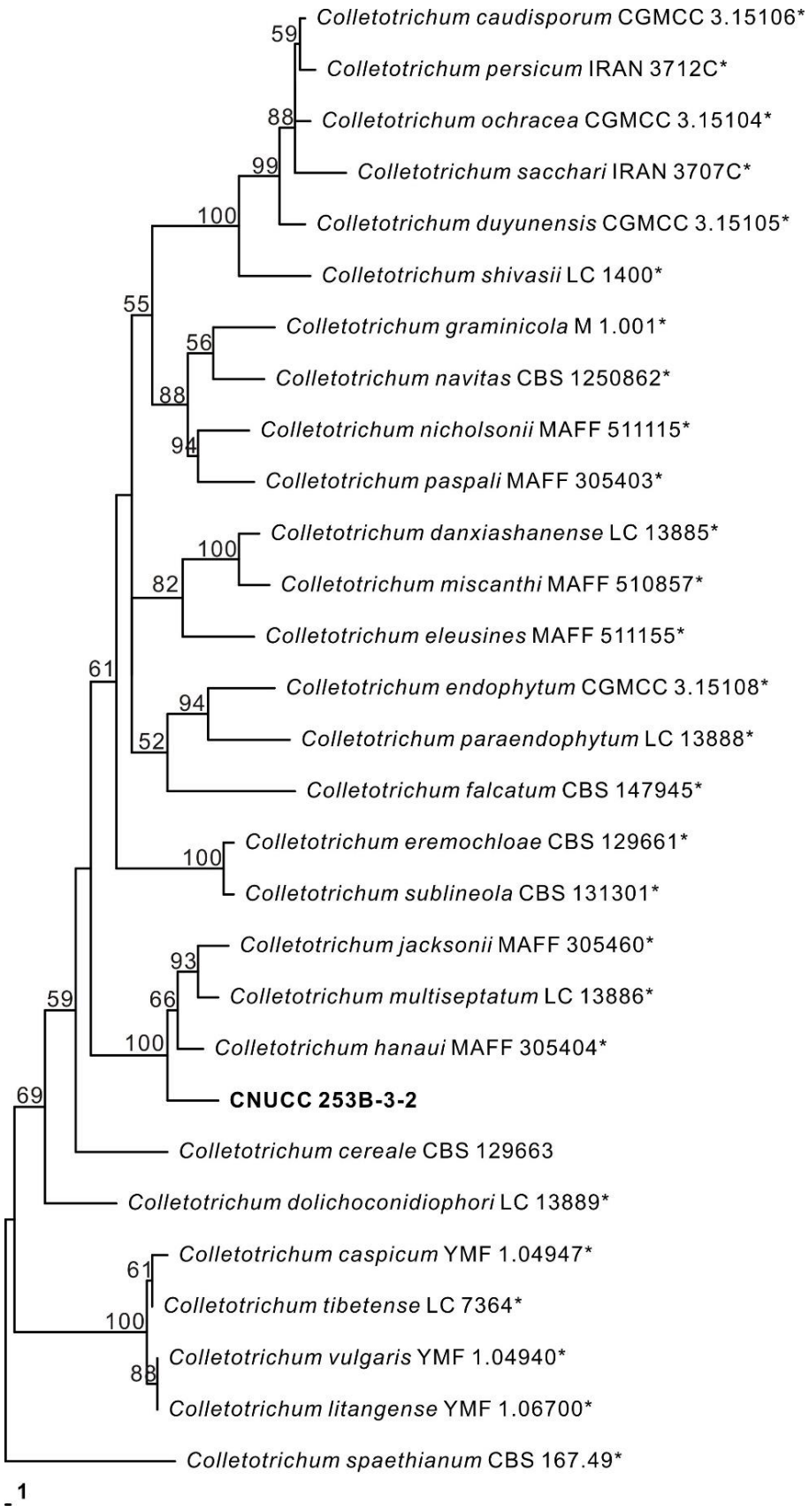
Supplementary Figure 14 – Phylogenetic tree of *C. caudatum-graminicola* species complex derived from maximum parsimony analysis of *chs* sequences, using *Colletotrichum spaethianum* CBS 167.49 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



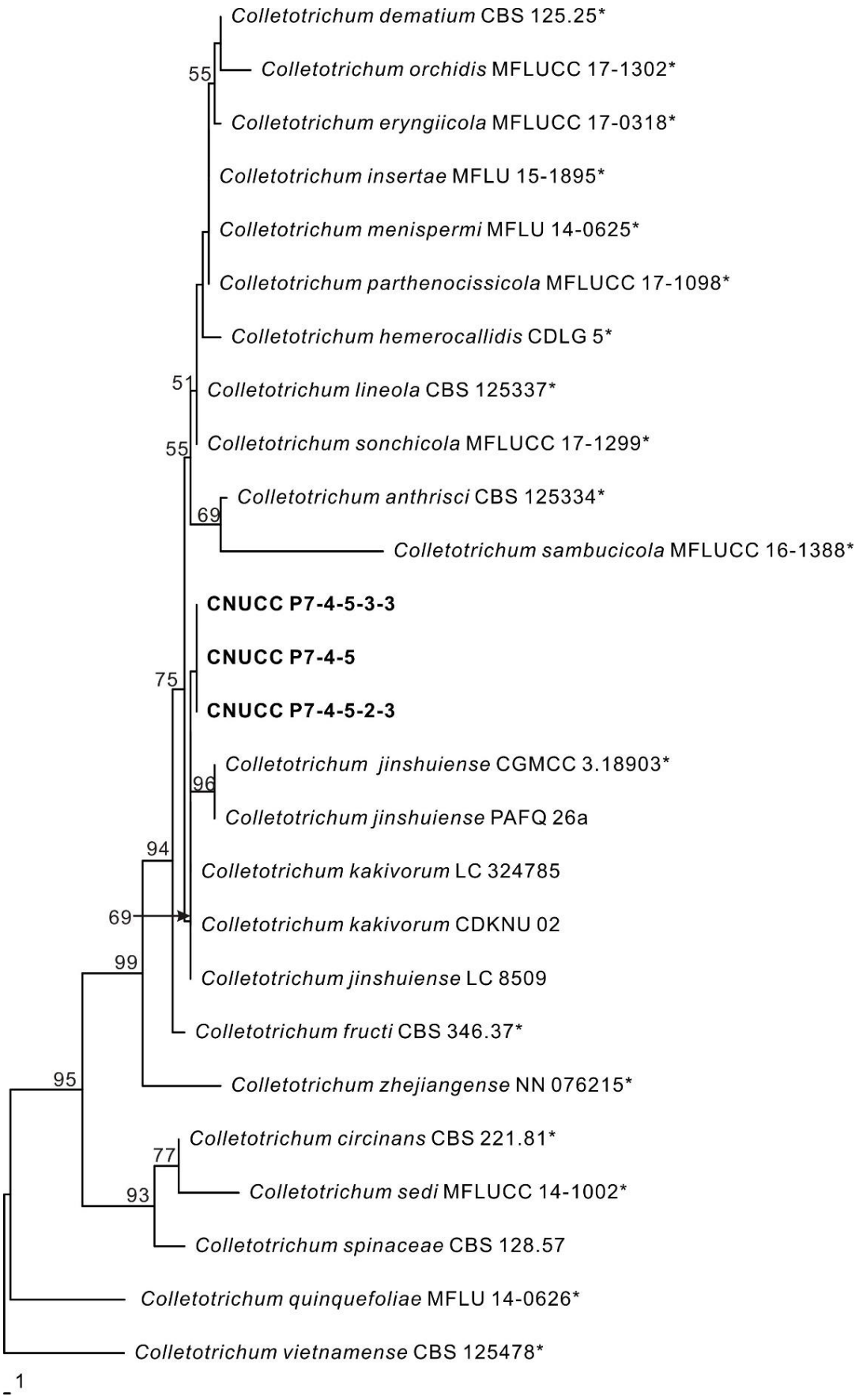
Supplementary Figure 15 – Phylogenetic tree of *C. caudatum-graminicola* species complex derived from maximum parsimony analysis of ITS sequences, using *Colletotrichum spaethianum* CBS 167.49 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



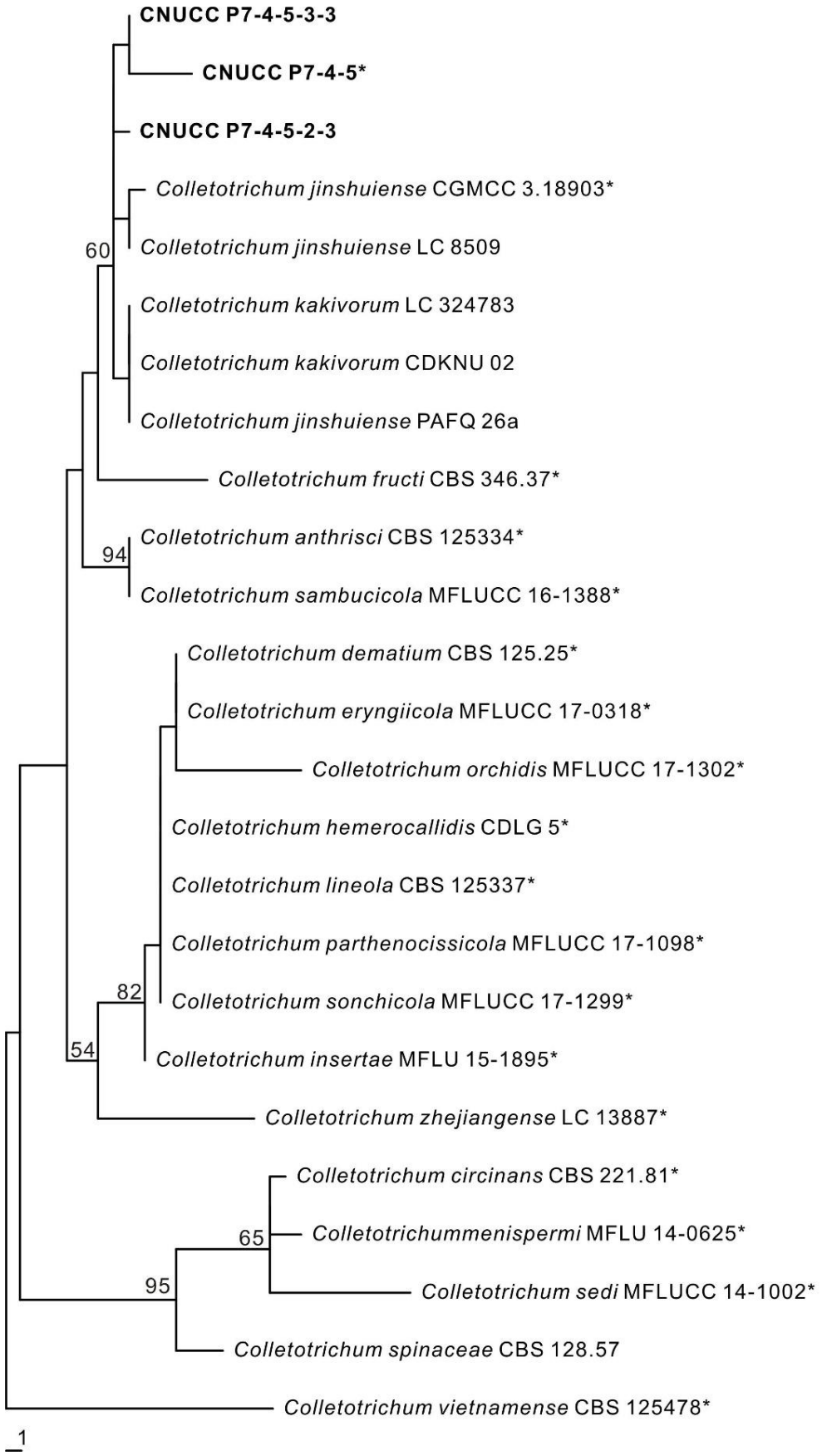
Supplementary Figure 16 – Phylogenetic tree of *C. caudatum-graminicola* species complex derived from maximum parsimony analysis of *sod* sequences, using *Colletotrichum spaethianum* CBS 167.49 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



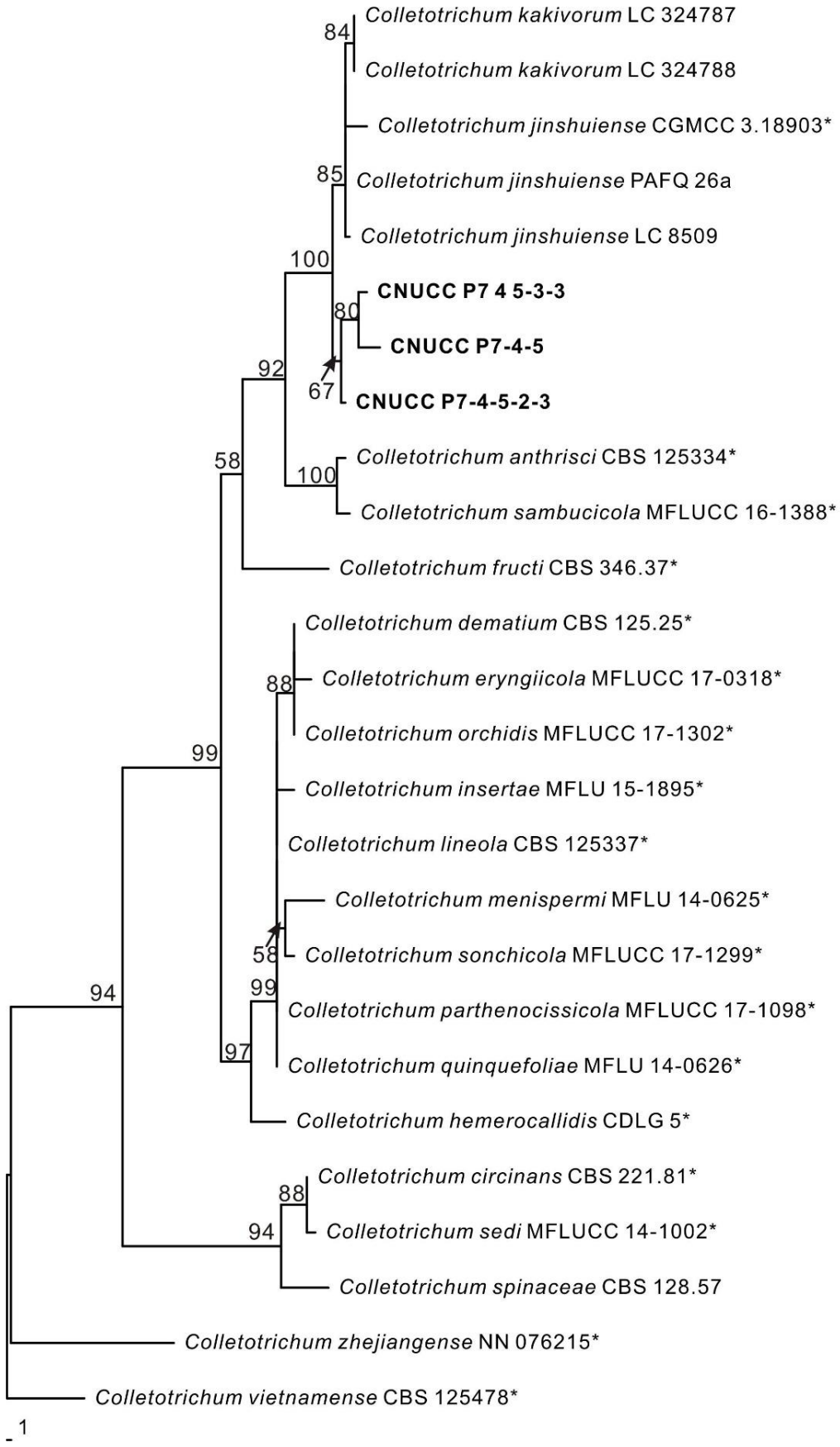
Supplementary Figure 17 – Phylogenetic tree of *C. caudatum-graminicola* species complex derived from maximum parsimony analysis of *tub* sequences, using *Colletotrichum spaethianum* CBS 167.49 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



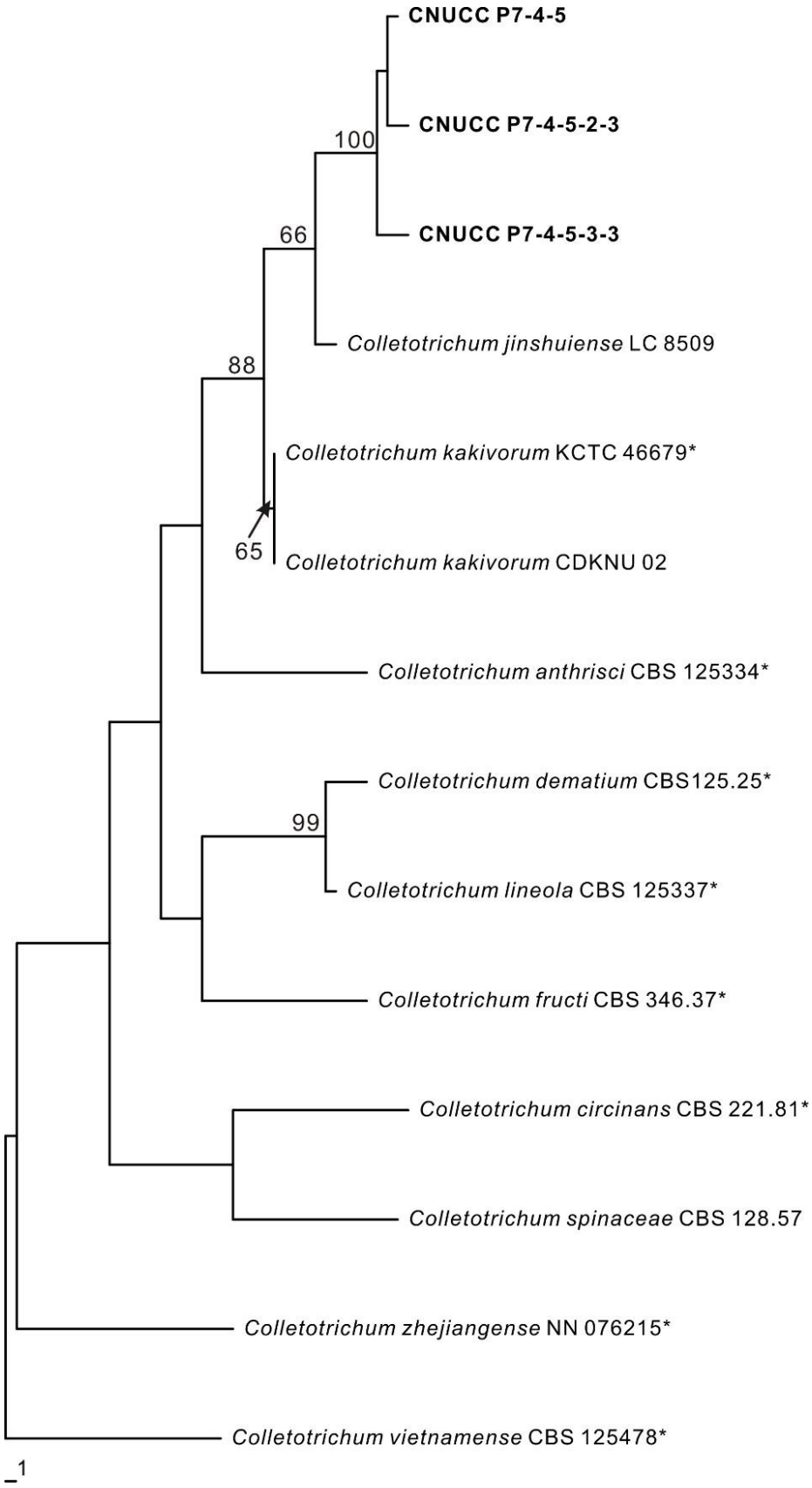
Supplementary Figure 18 – Phylogenetic tree of *C. dematium* species complex derived from maximum parsimony analysis of *act* sequences, using *Colletotrichum vietnamense* CBS 125478 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



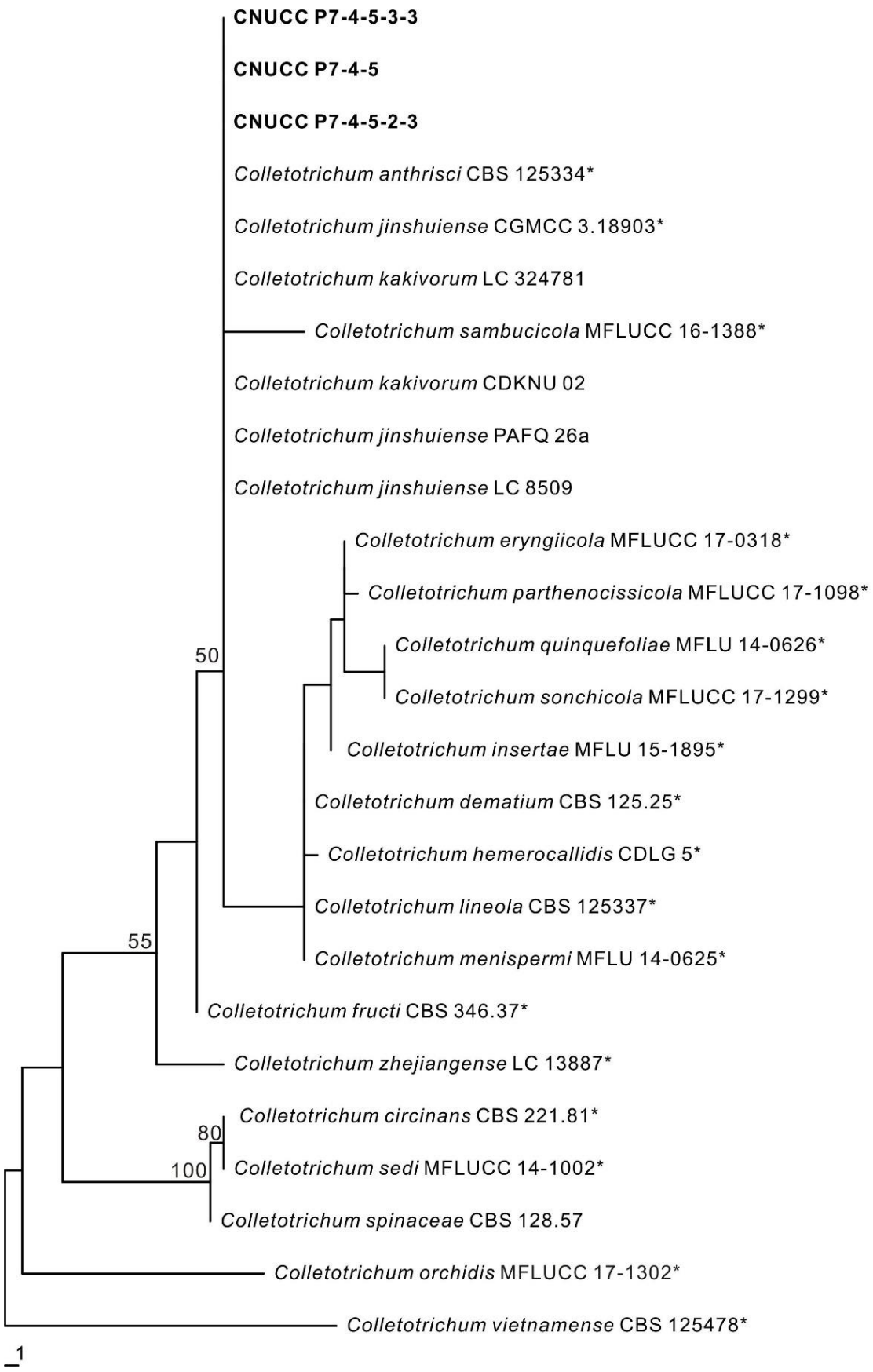
Supplementary Figure 19 – Phylogenetic tree of *C. dematium* species complex derived from maximum parsimony analysis of *chs* sequences, using *Colletotrichum vietnamense* CBS 125478 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



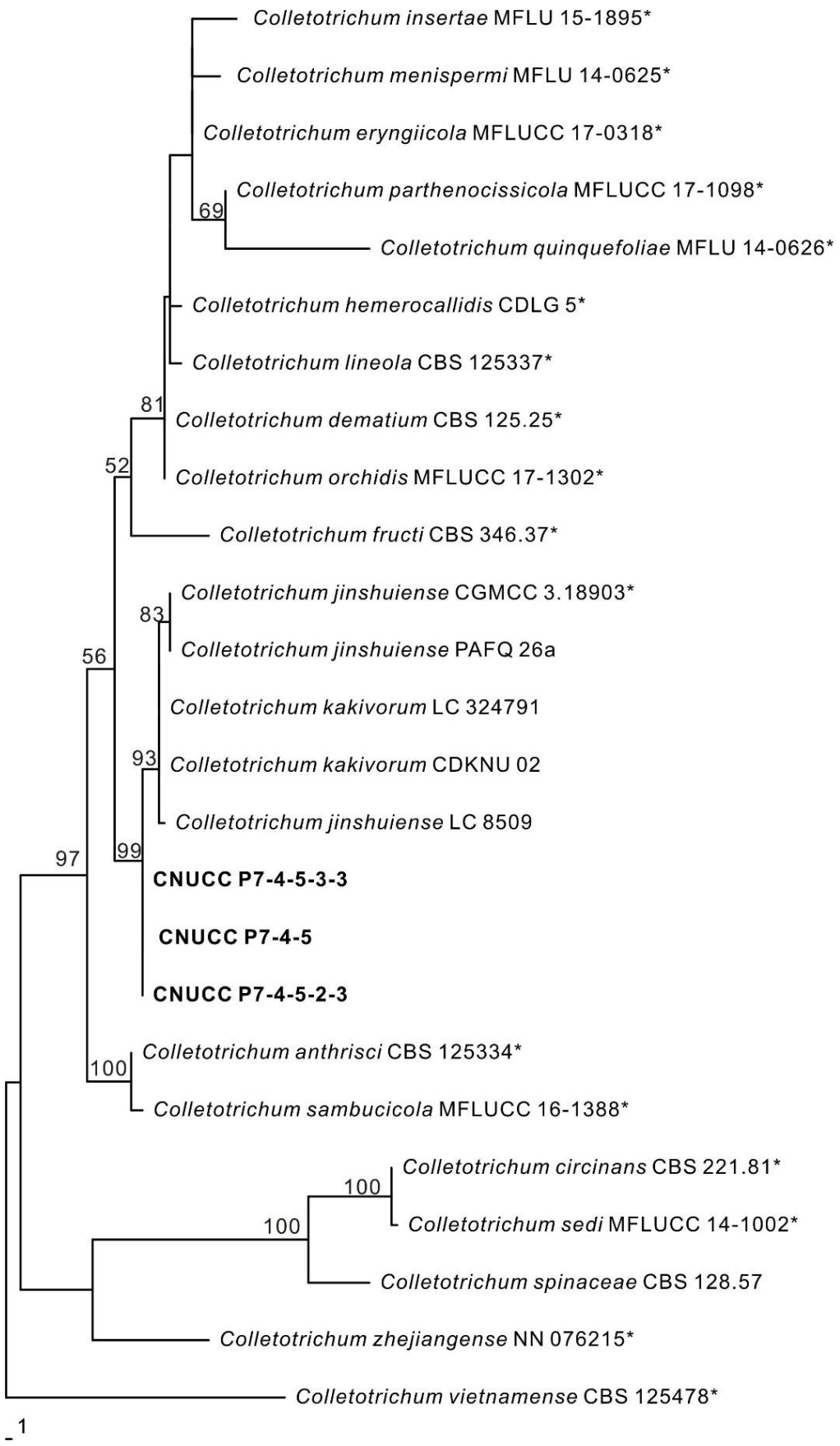
Supplementary Figure 20 – Phylogenetic tree of *C. dematium* species complex derived from maximum parsimony analysis of *gapdh* sequences, using *Colletotrichum vietnamense* CBS 125478 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



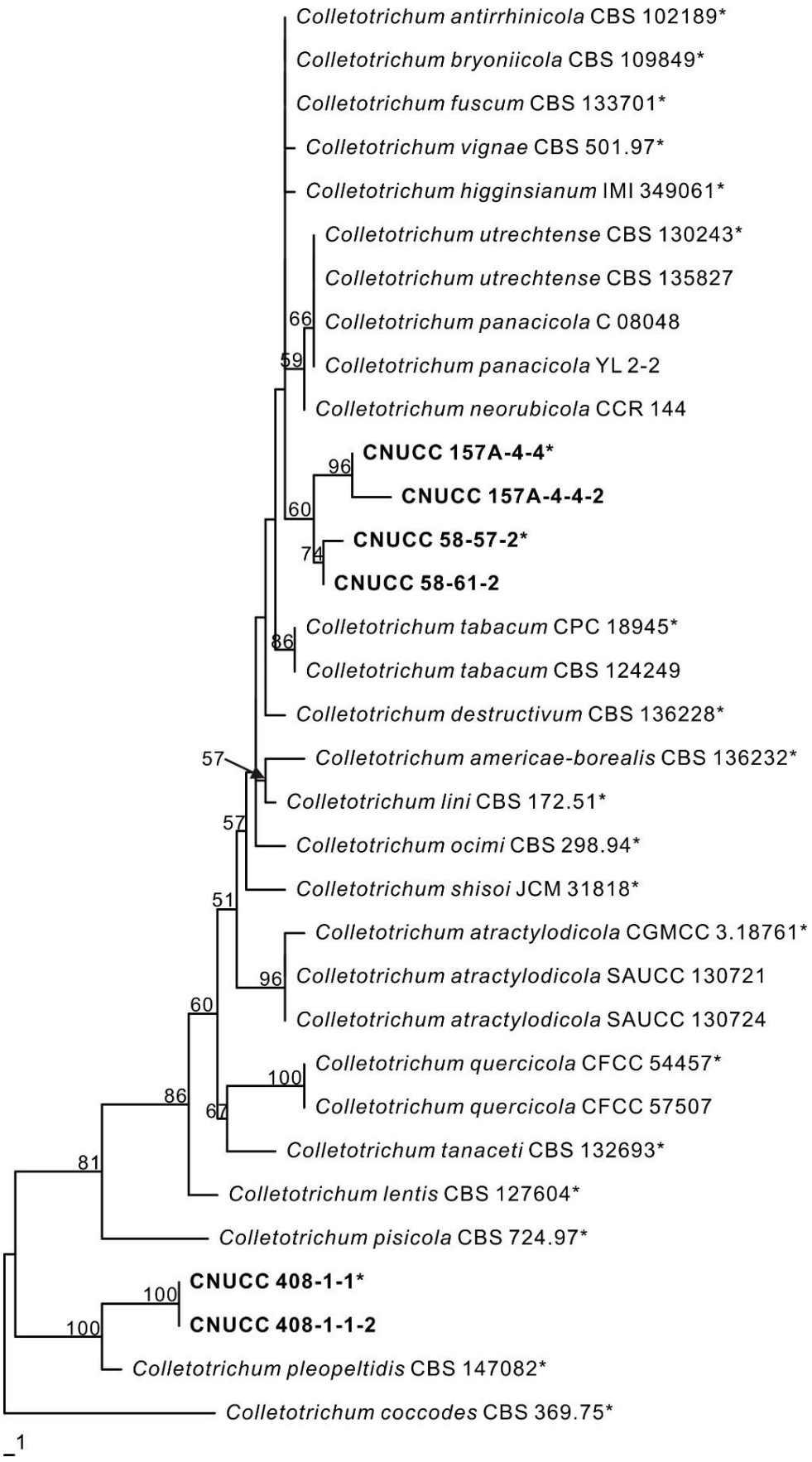
Supplementary Figure 21 – Phylogenetic tree of *C. dematium* species complex derived from maximum parsimony analysis of *his* sequences, using *Colletotrichum vietnamense* CBS 125478 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



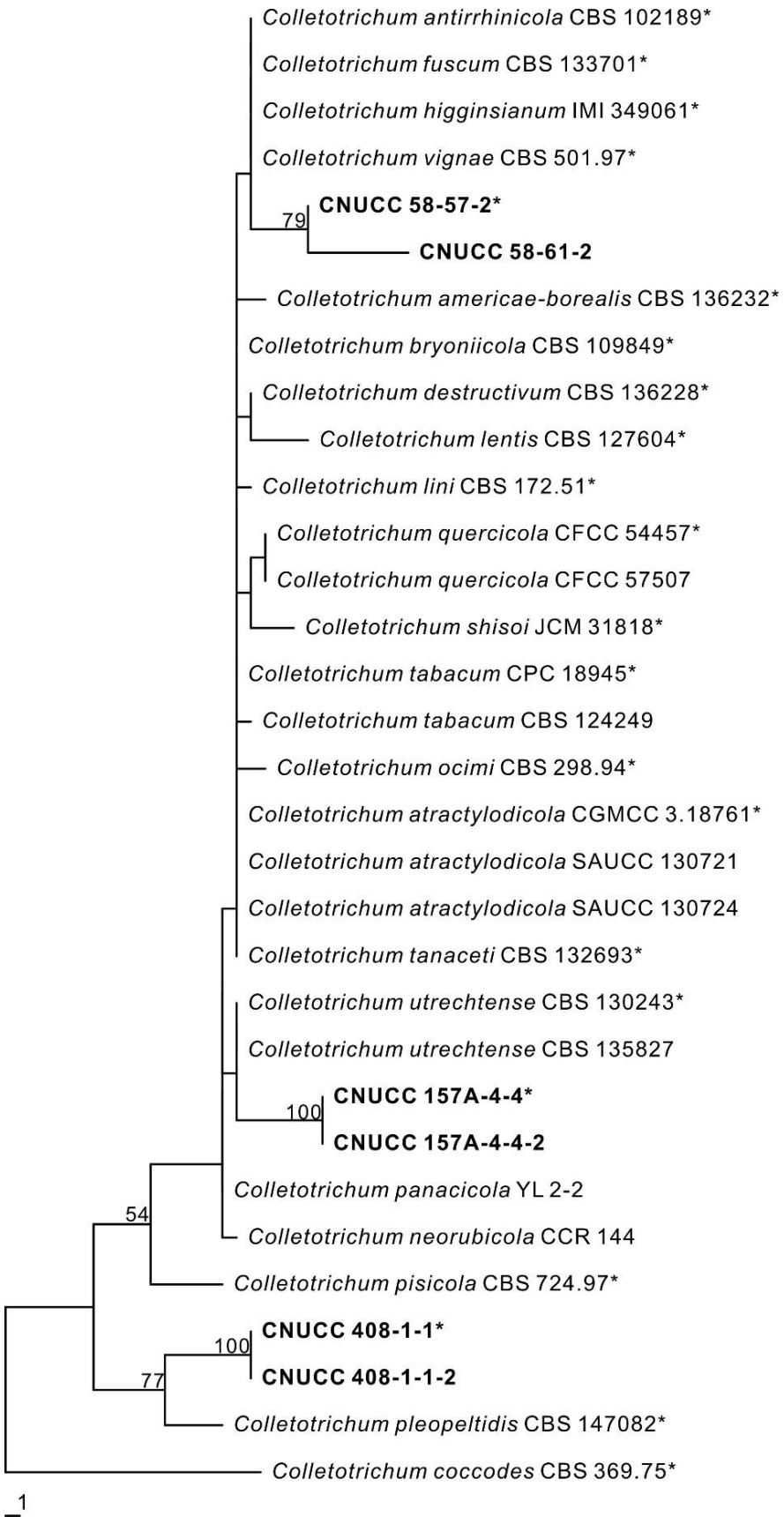
Supplementary Figure 22 – Phylogenetic tree of *C. dematium* species complex derived from maximum parsimony analysis of ITS sequences, using *Colletotrichum vietnamense* CBS 125478 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



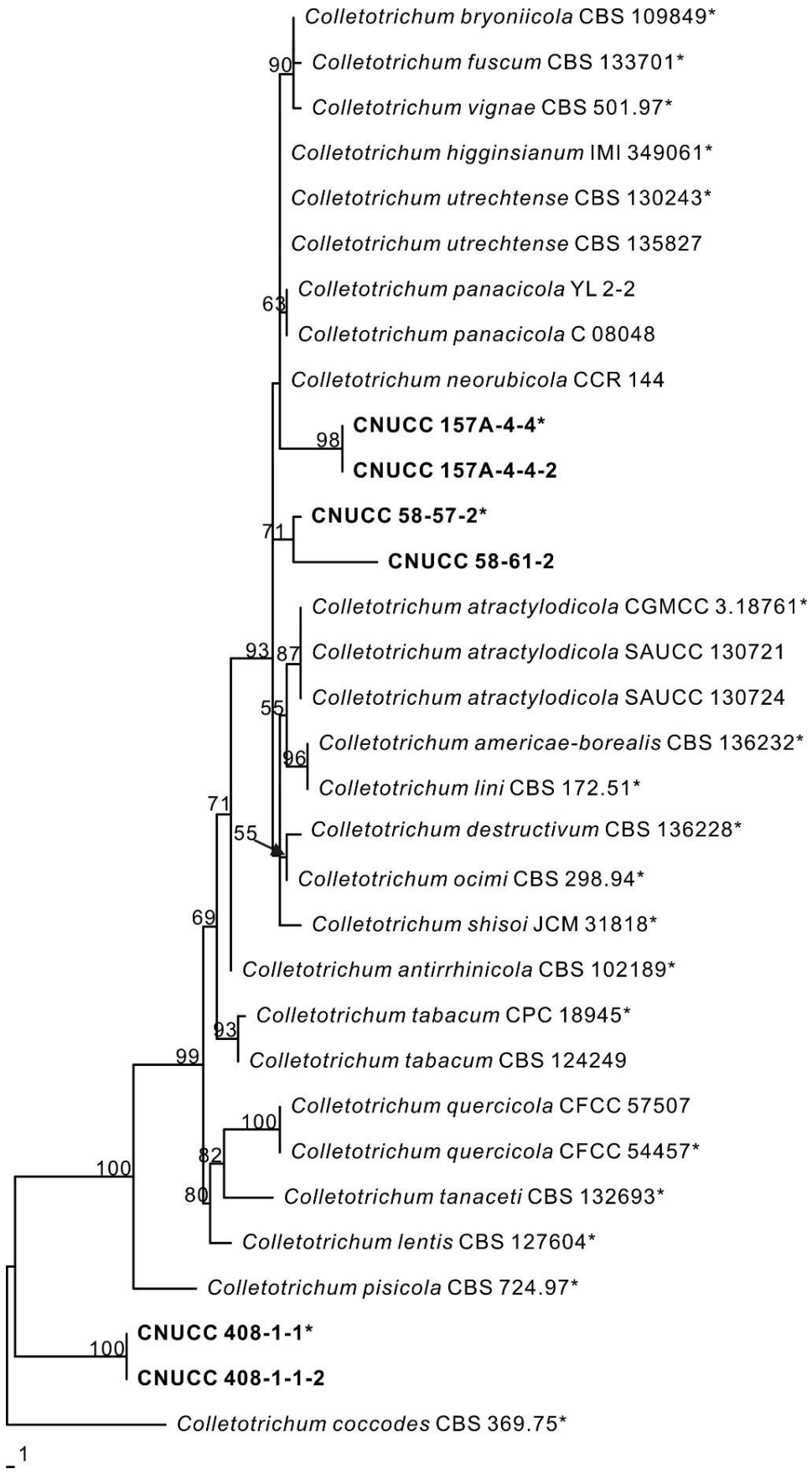
Supplementary Figure 23 – Phylogenetic tree of *C. dematium* species complex derived from maximum parsimony analysis of *tub* sequences, using *Colletotrichum vietnamense* CBS 125478 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



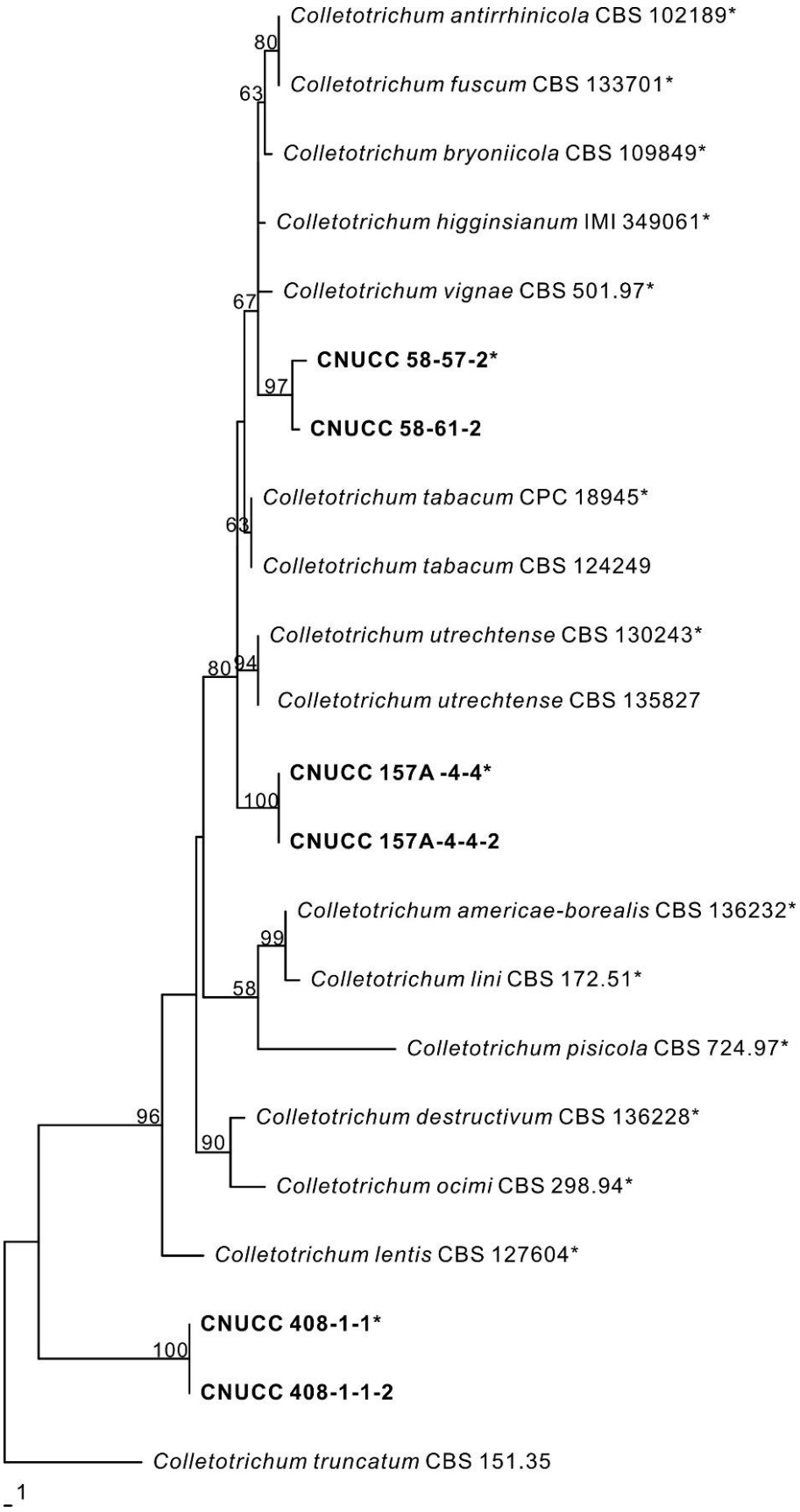
Supplementary Figure 24 – Phylogenetic tree of *C. destructivum* species complex derived from maximum parsimony analysis of *act* sequences, using *Colletotrichum coccodes* CBS 369.75 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



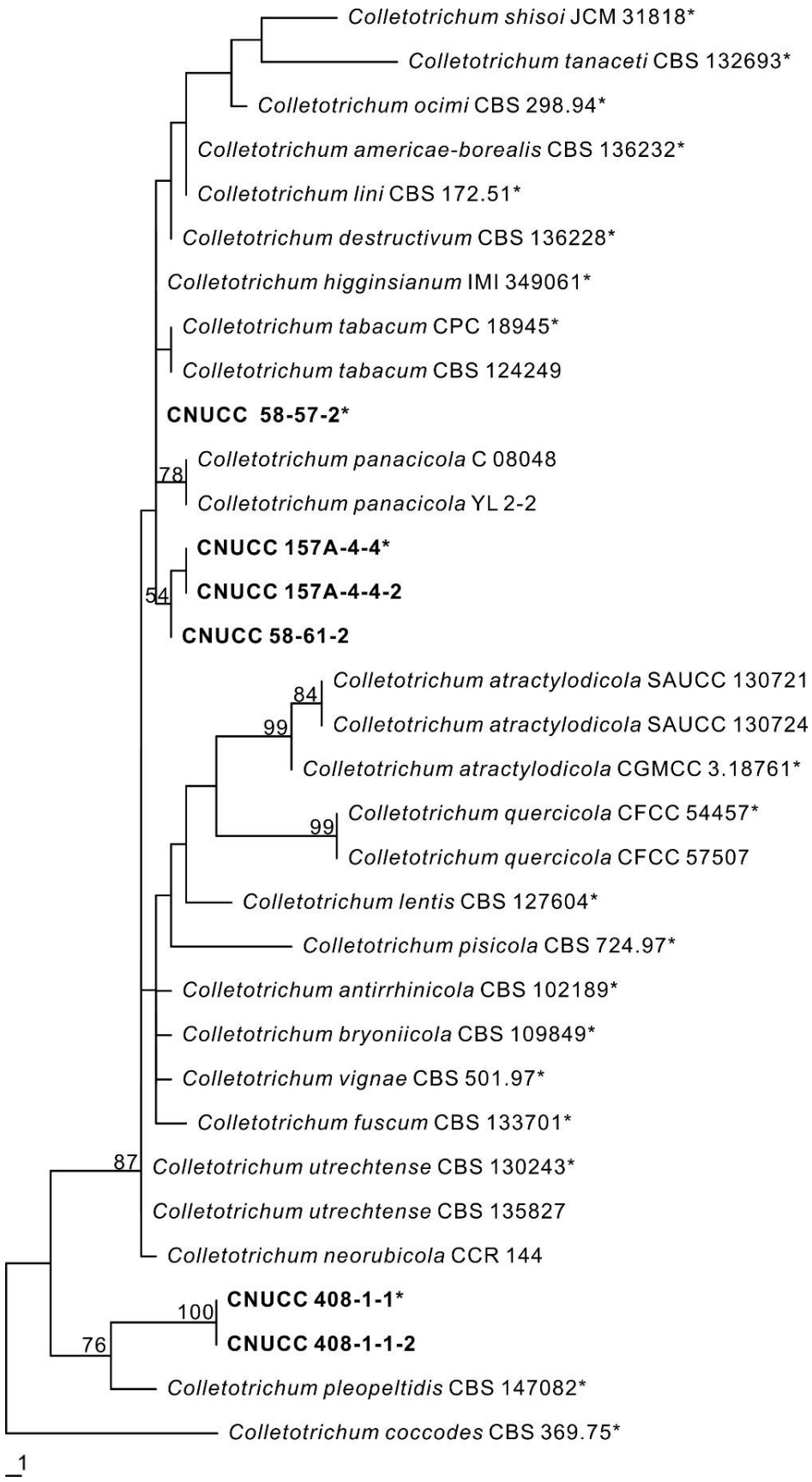
Supplementary Figure 25 – Phylogenetic tree of *C. destructivum* species complex derived from maximum parsimony analysis of *chs* sequences, using *Colletotrichum coccodes* CBS 369.75 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



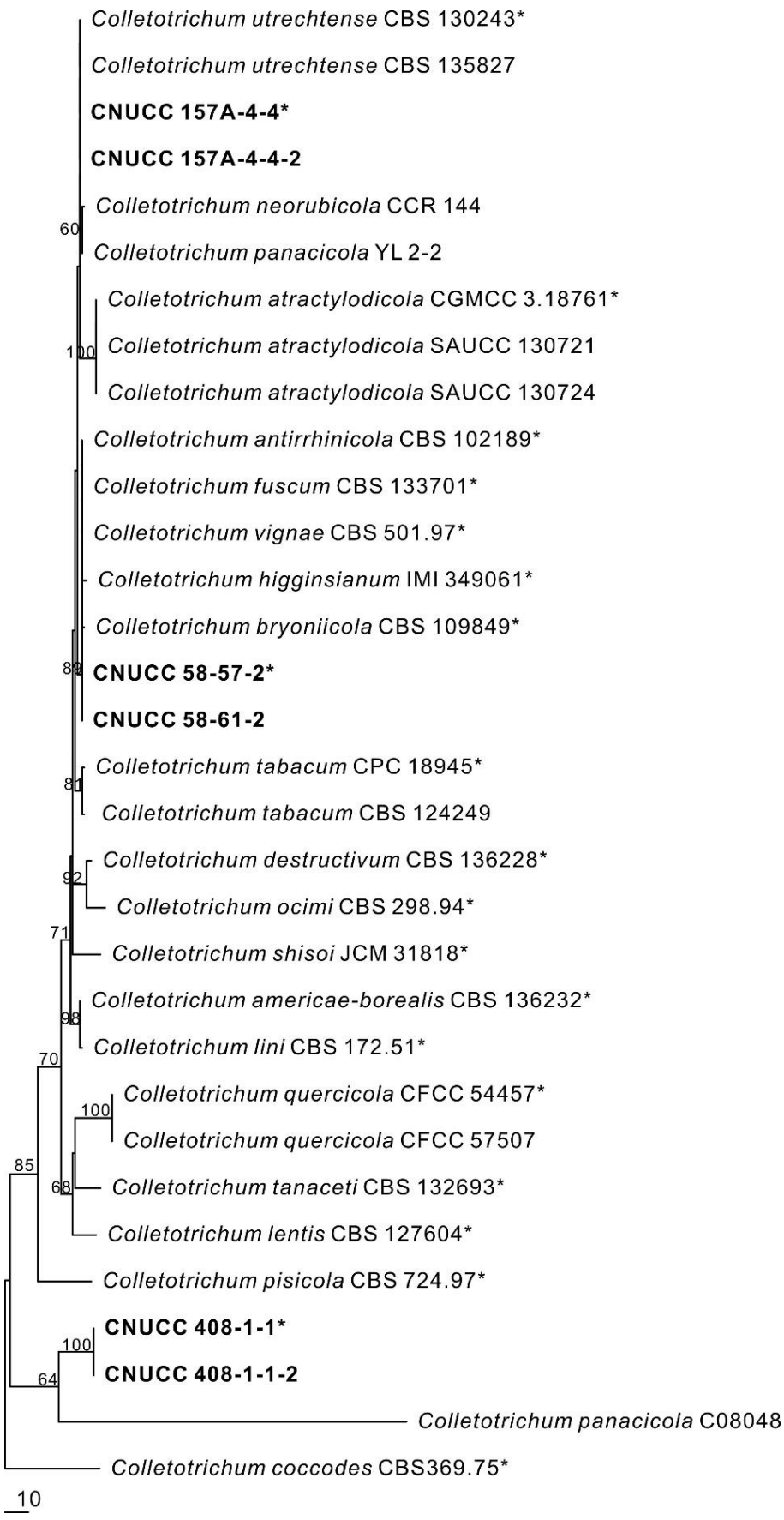
Supplementary Figure 26 – Phylogenetic tree of *C. destructivum* species complex derived from maximum parsimony analysis of *gapdh* sequences, using *Colletotrichum coccodes* CBS 369.75 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



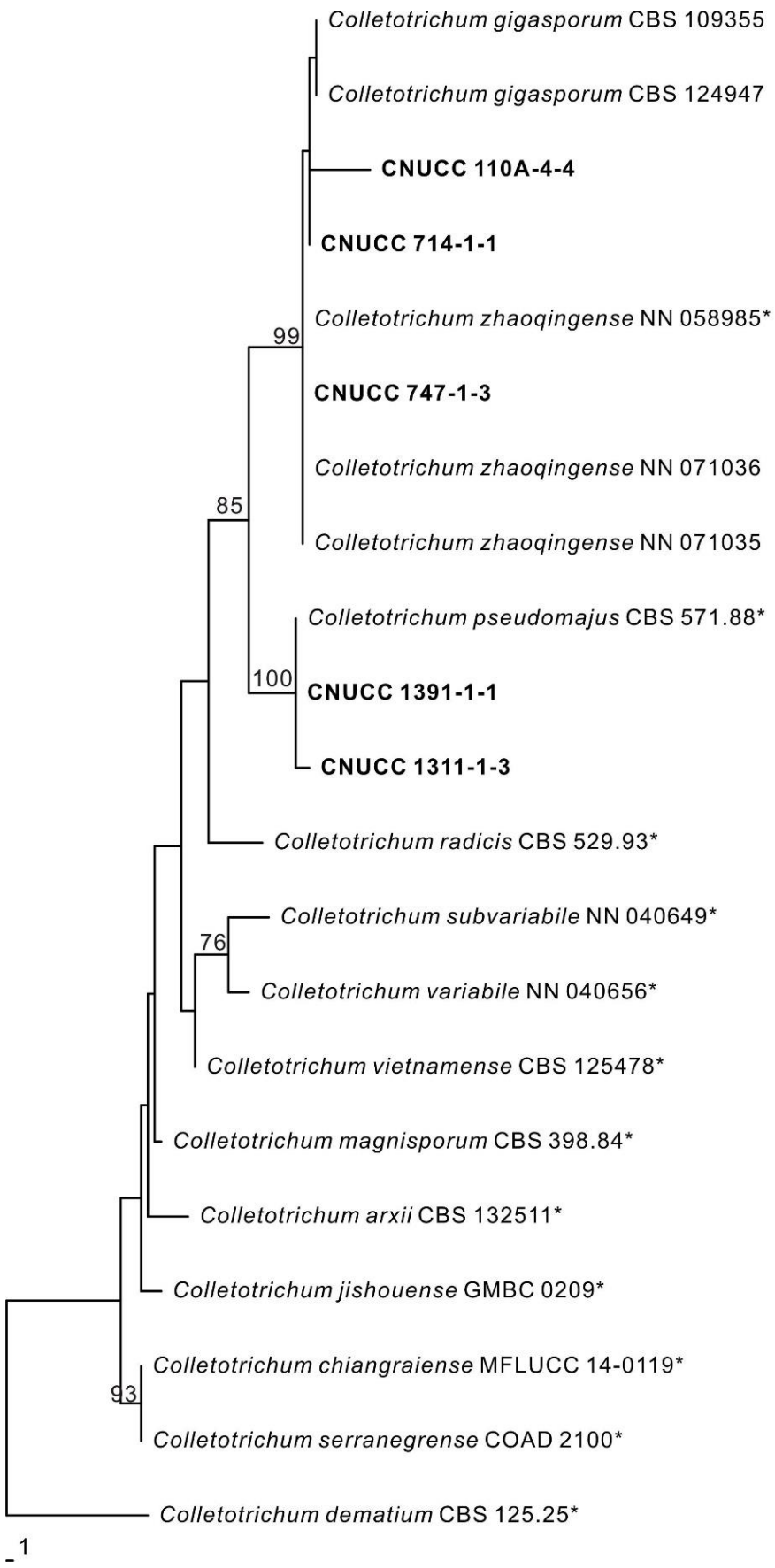
Supplementary Figure 27 – Phylogenetic tree of *C. destructivum* species complex derived from maximum parsimony analysis of *his* sequences, using *Colletotrichum coccodes* CBS 369.75 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



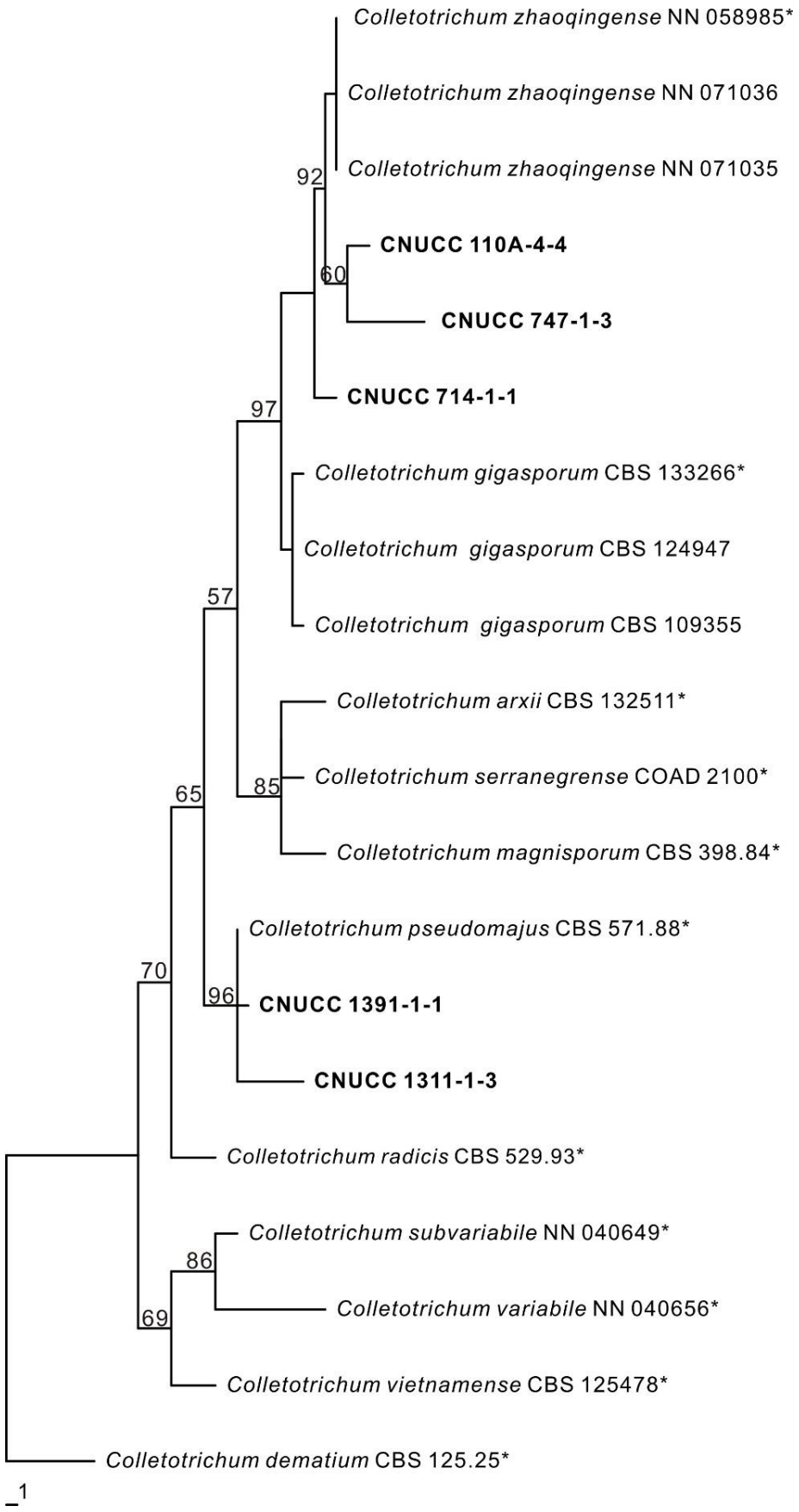
Supplementary Figure 28 – Phylogenetic tree of *C. destructivum* species complex derived from maximum parsimony analysis of ITS sequences, using *Colletotrichum coccodes* CBS 369.75 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



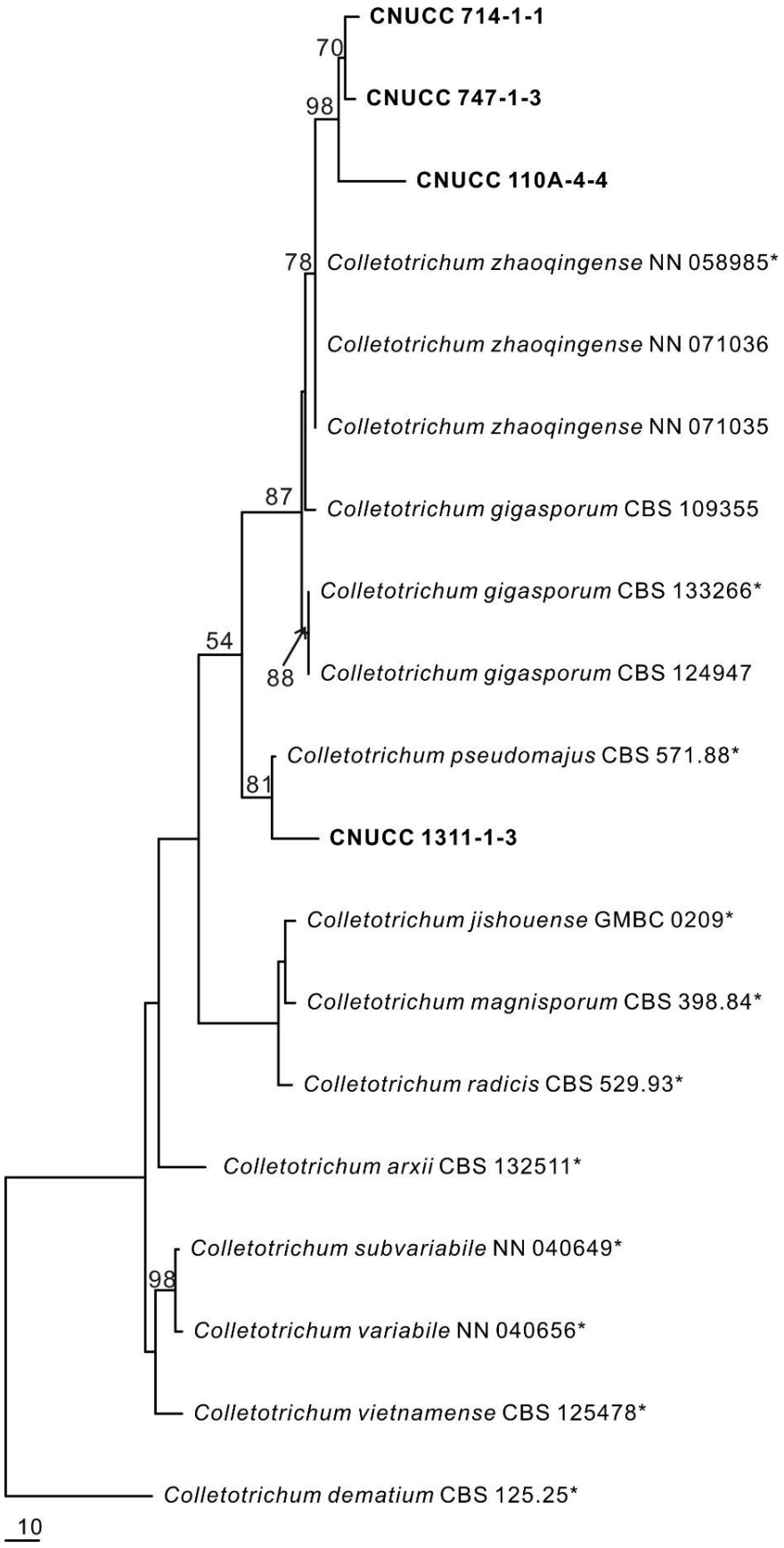
Supplementary Figure 29 – Phylogenetic tree of *C. destructivum* species complex derived from maximum parsimony analysis of *tub* sequences, using *Colletotrichum coccodes* CBS 369.75 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



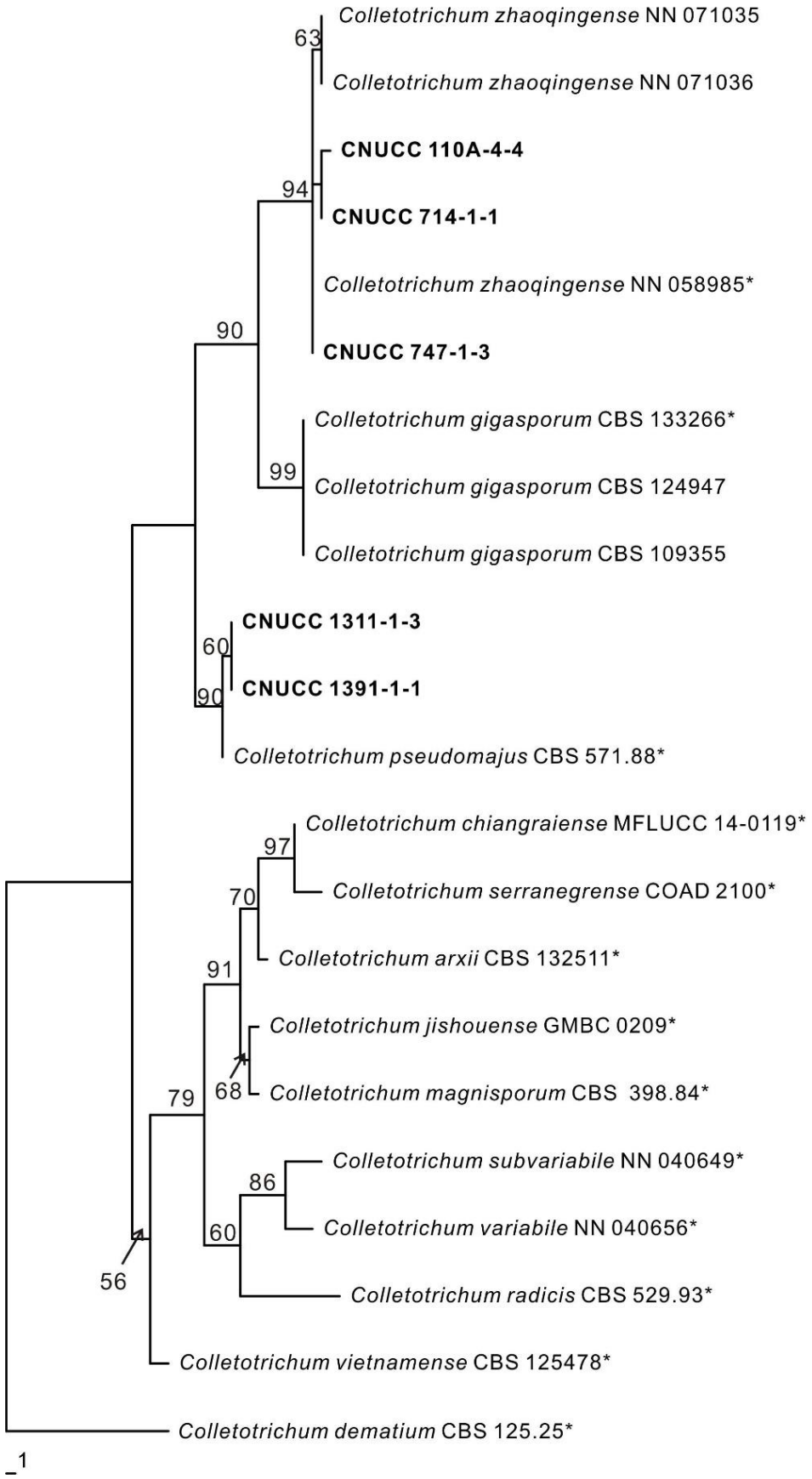
Supplementary Figure 30 – Phylogenetic tree of *C. gigasporum* species complex derived from maximum parsimony analysis of *act* sequences, using *Colletotrichum dematium* CBS 125.25 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



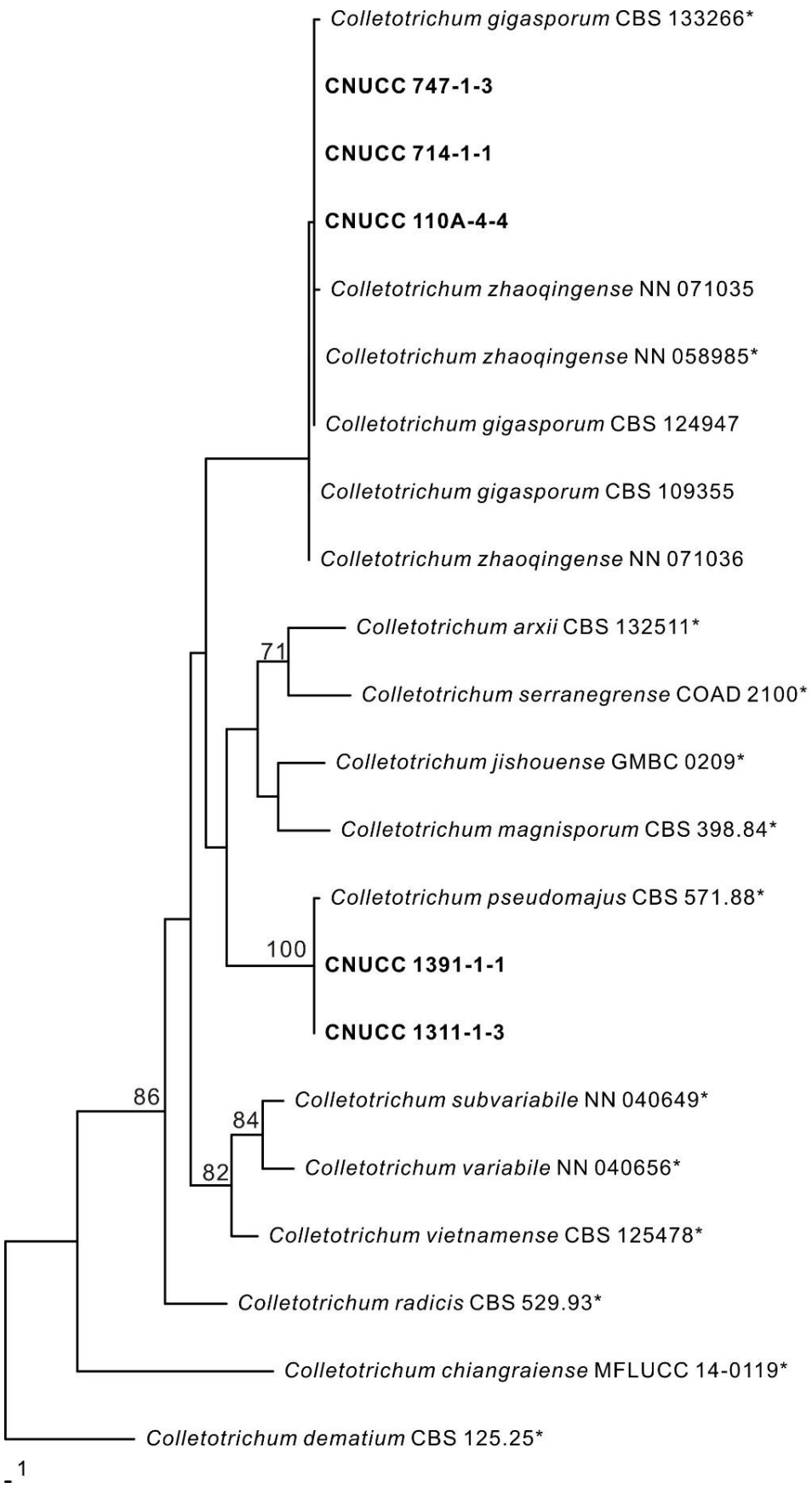
Supplementary Figure 31 – Phylogenetic tree of *C. gigasporum* species complex derived from maximum parsimony analysis of *chs* sequences, using *Colletotrichum dematium* CBS 125.25 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



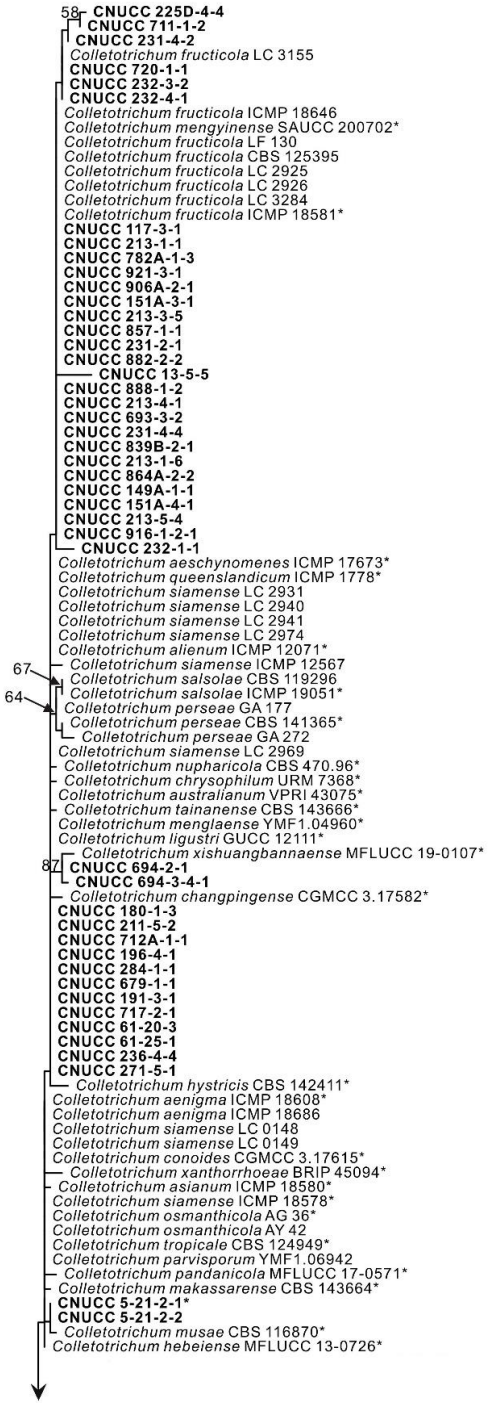
Supplementary Figure 32 – Phylogenetic tree of *C. gigasporum* species complex derived from maximum parsimony analysis of *gapdh* sequences, using *Colletotrichum dematium* CBS 125.25 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



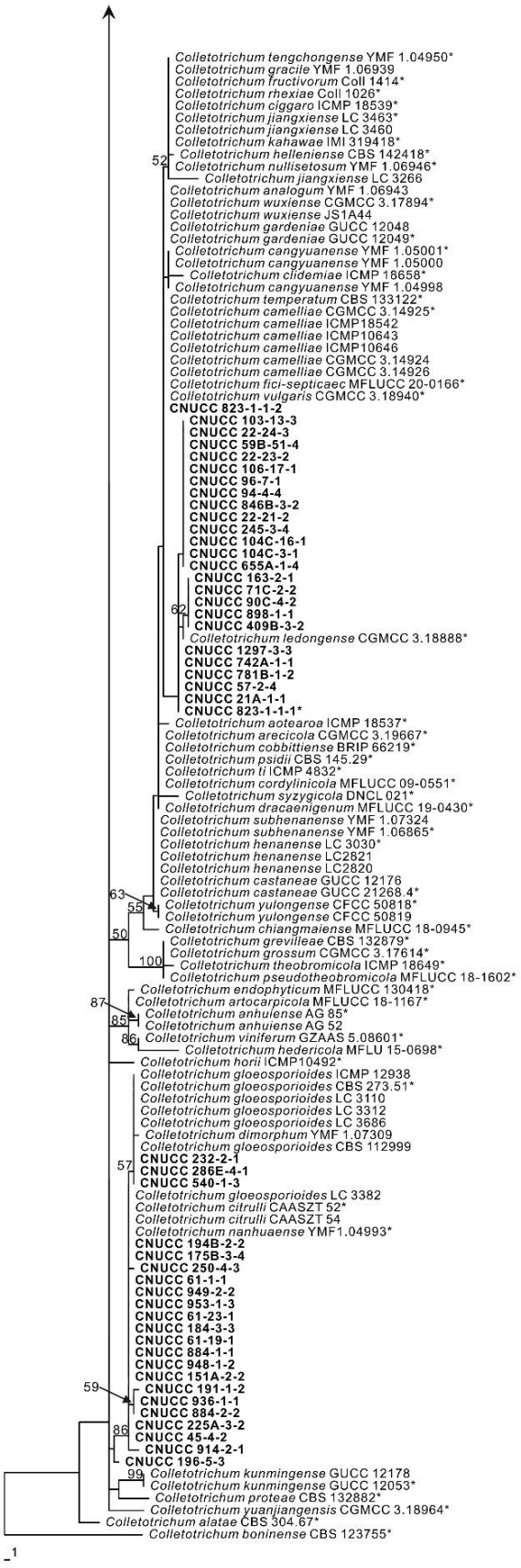
Supplementary Figure 33 – Phylogenetic tree of *C. gigasporum* species complex derived from maximum parsimony analysis of ITS sequences, using *Colletotrichum dematium* CBS 125.25 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



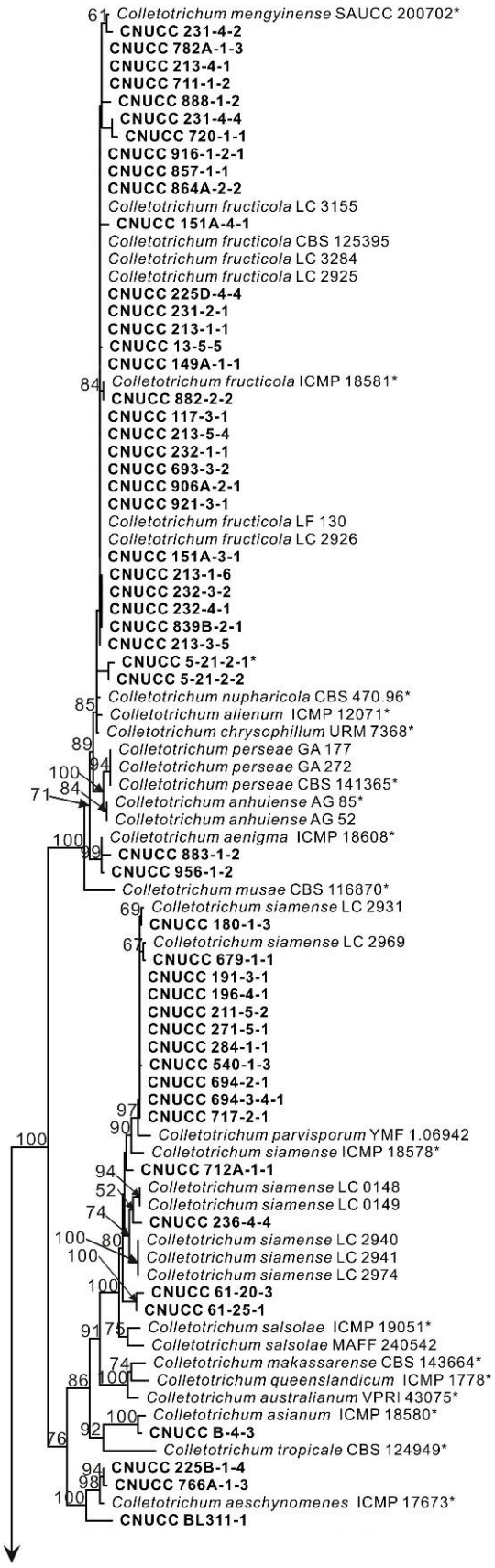
Supplementary Figure 34 – Phylogenetic tree of *C. gigasporum* species complex derived from maximum parsimony analysis of *tub* sequences, using *Colletotrichum dematium* CBS 125.25 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



Supplementary Figure 35 – Phylogenetic tree of *C. gloeosporioides* species complex derived from maximum parsimony analysis of *act* sequences, using *Colletotrichum boninense* CBS 123755 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.

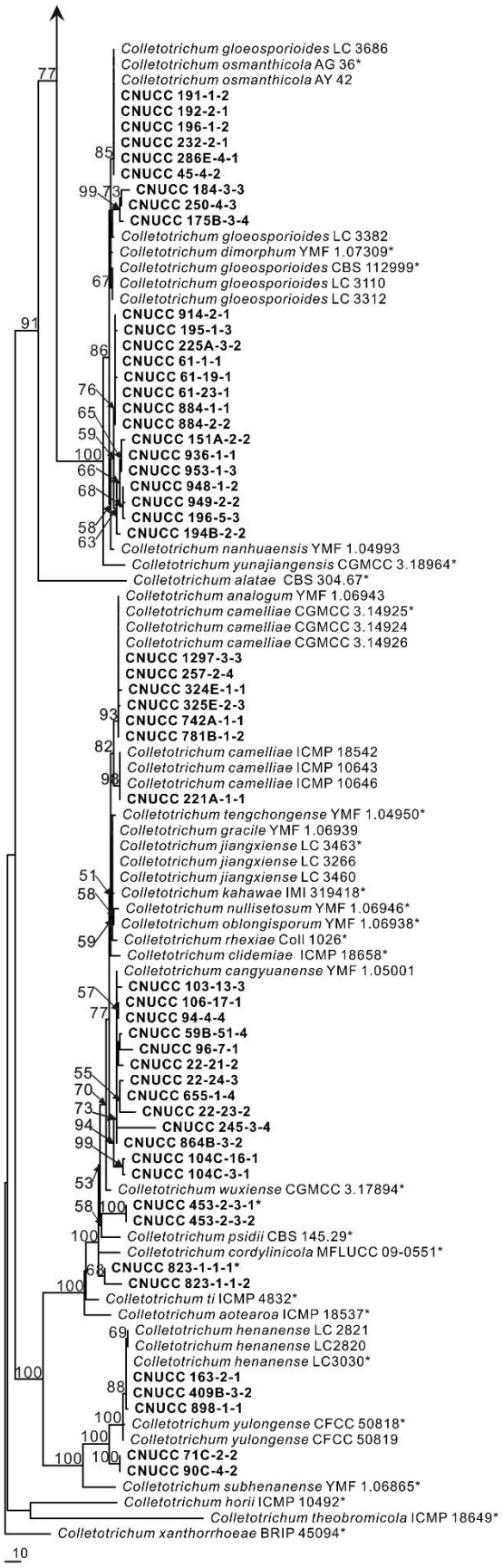


Supplementary Figure 35 – Continued.

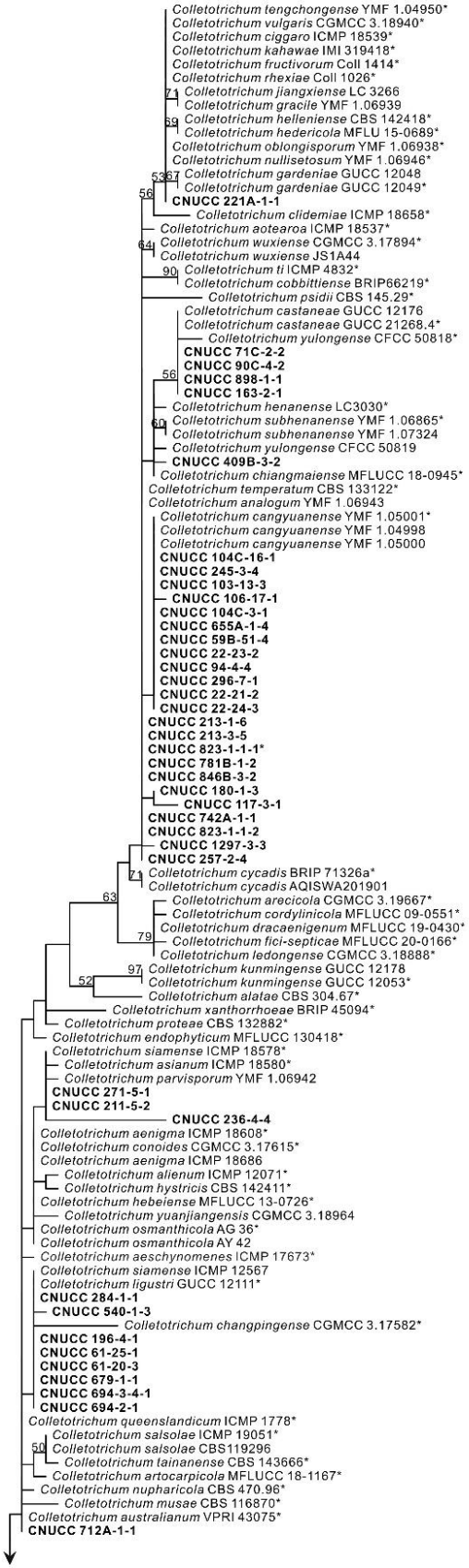


Supplementary Figure 36 – Phylogenetic tree of *C. gloeosporioides* species complex derived from maximum parsimony analysis of *apmat* sequences, using *Colletotrichum boninense* CBS 123755 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the

branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.

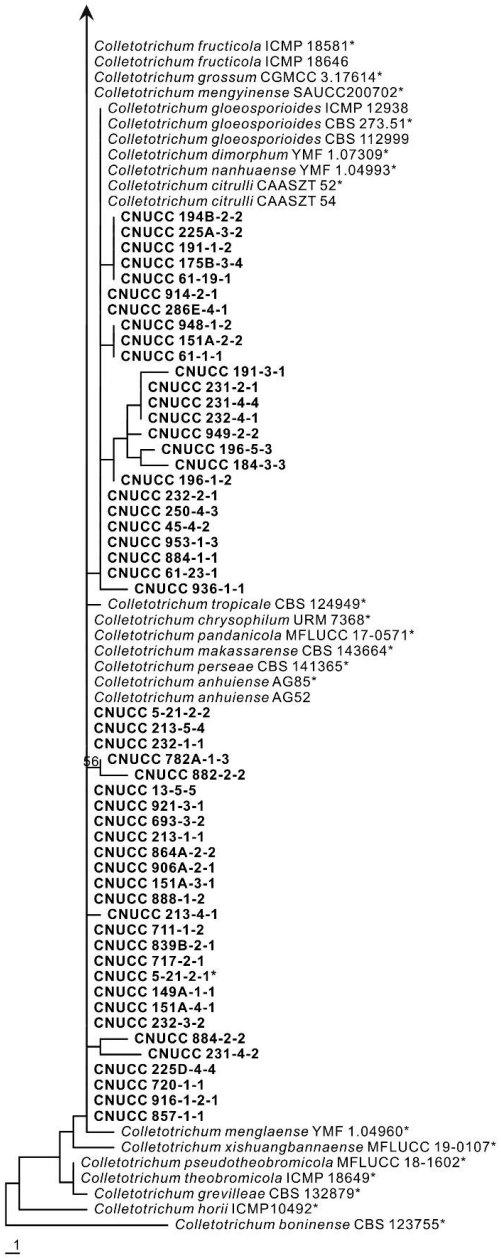


Supplementary Figure 36 – Continued.

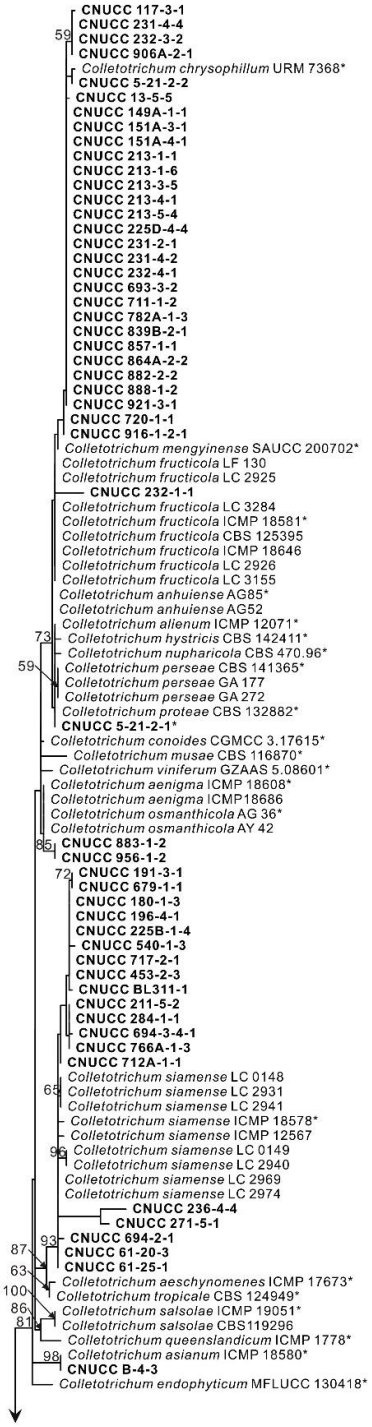


Supplementary Figure 37 – Phylogenetic tree of *C. gloeosporioides* species complex derived from maximum parsimony analysis of *chs* sequences, using *Colletotrichum boninense* CBS 123755

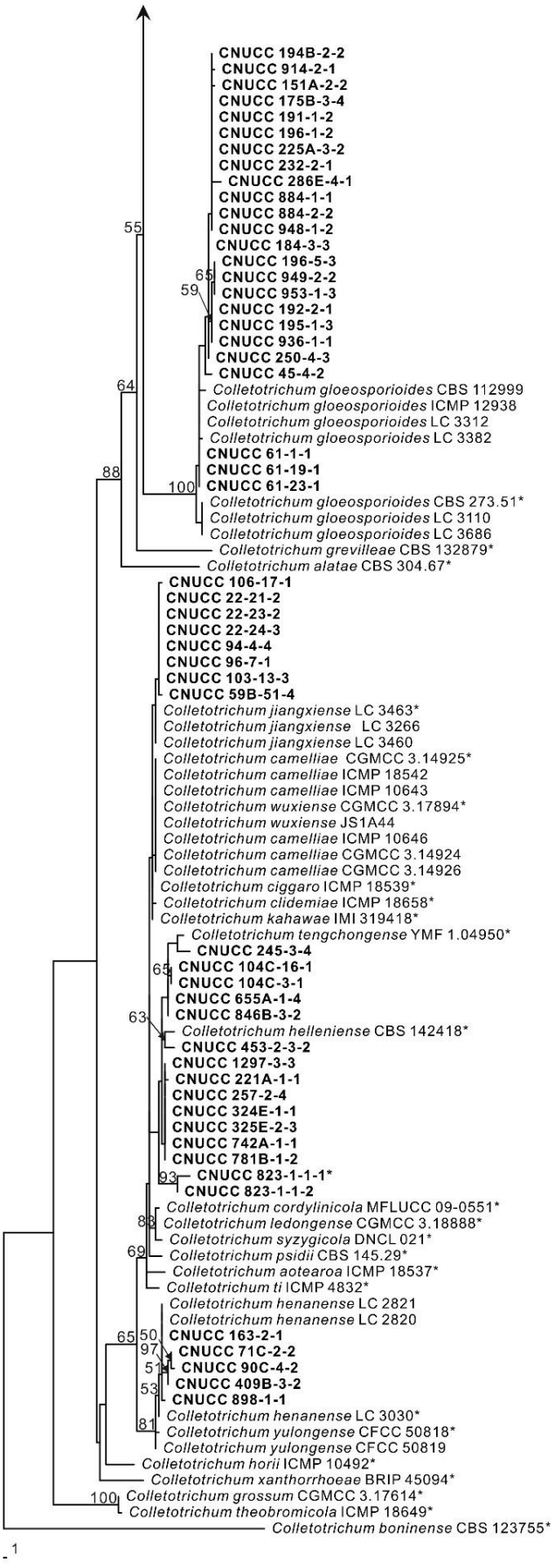
as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



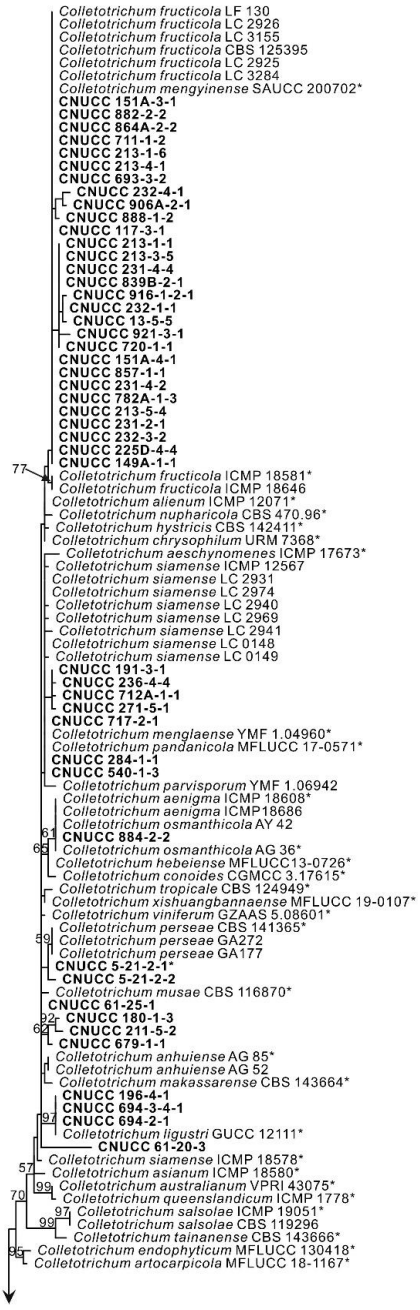
Supplementary Figure 37 – Continued.



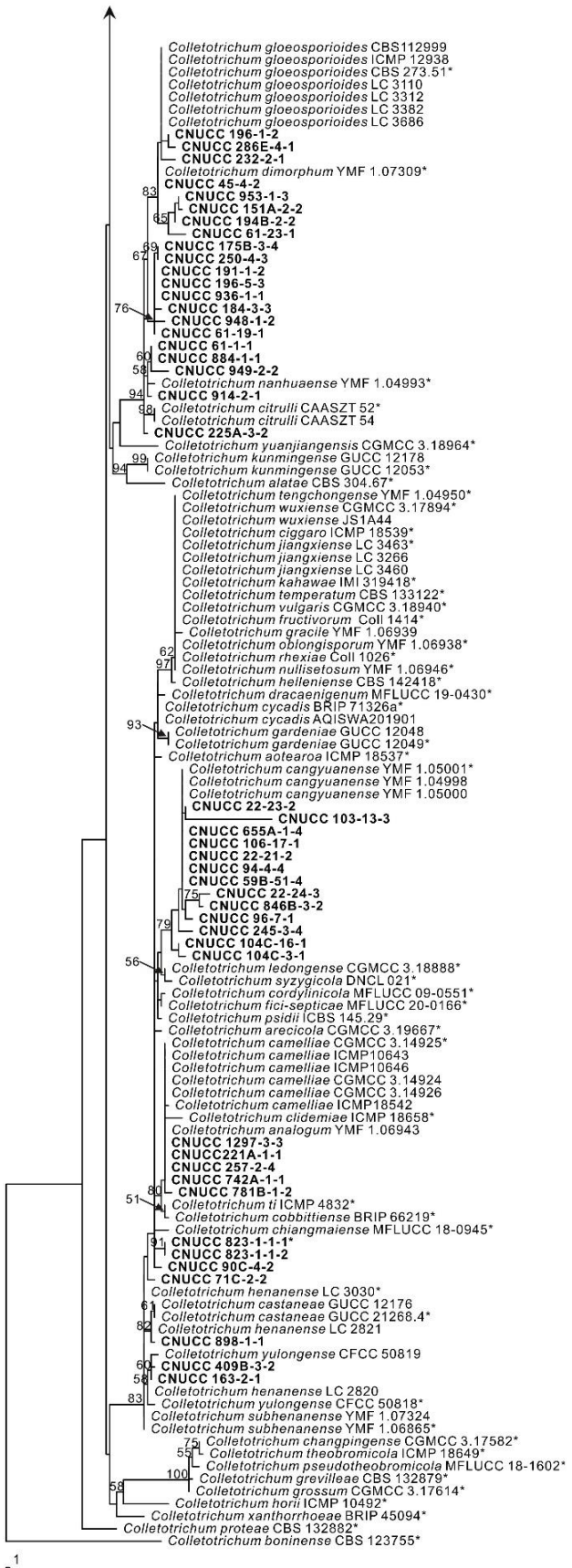
Supplementary Figure 38 – Phylogenetic tree of *C. gloeosporioides* species complex derived from maximum parsimony analysis of *cal* sequences, using *Colletotrichum boninense* CBS 123755 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



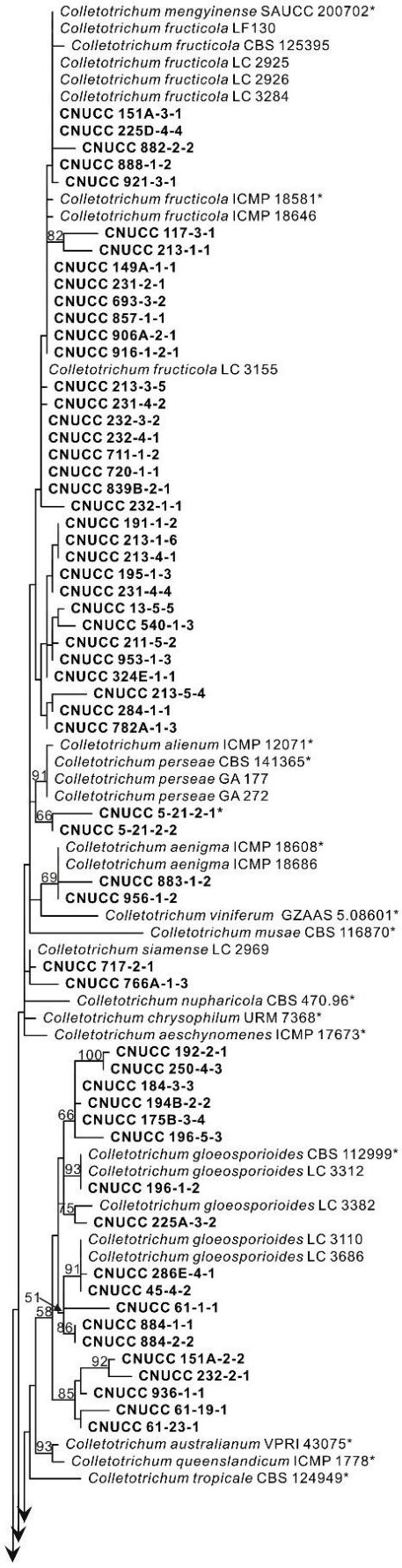
Supplementary Figure 38 – Continued.



Supplementary Figure 39 – Phylogenetic tree of *C. gloeosporioides* species complex derived from maximum parsimony analysis of *gapdh* sequences, using *Colletotrichum boninense* CBS 123755 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.

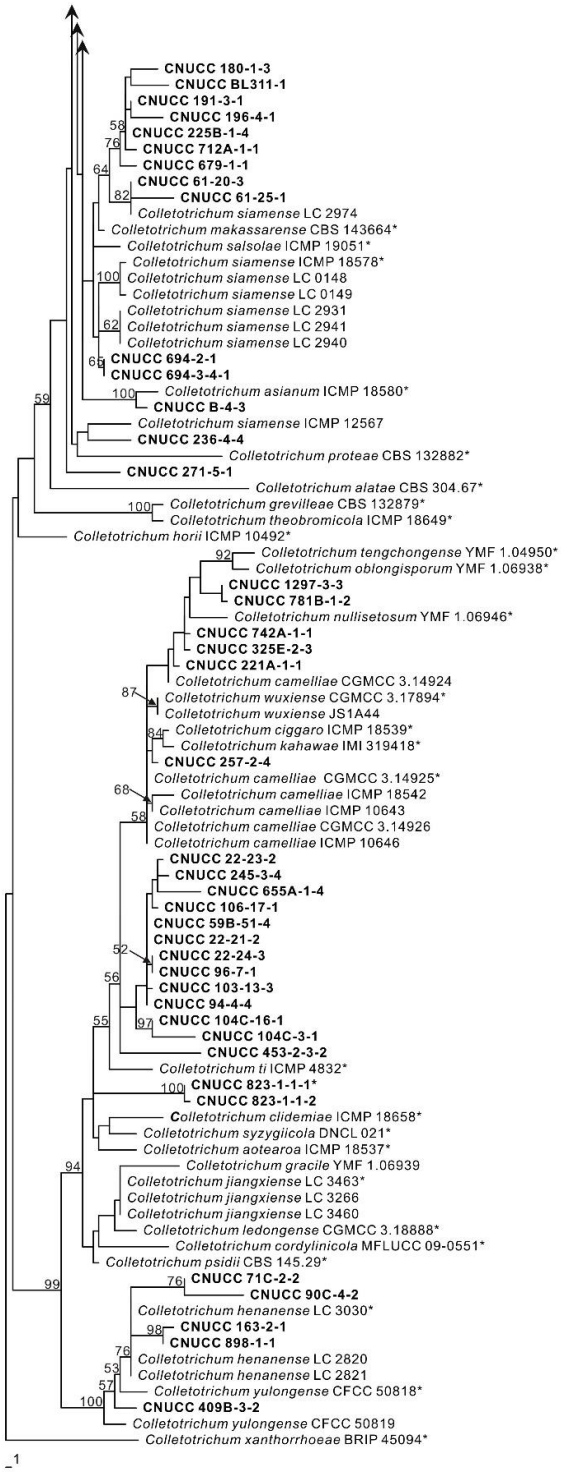


Supplementary Figure 39 – Continued.

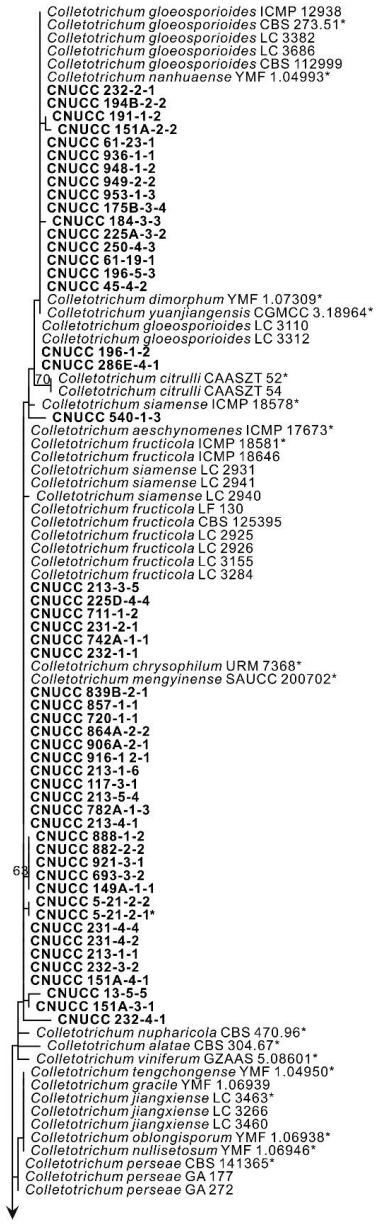


Supplementary Figure 40 – Phylogenetic tree of *C. gloeosporioides* species complex derived from maximum parsimony analysis of *gs* sequences, using *Colletotrichum boninense* CBS 123755

as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



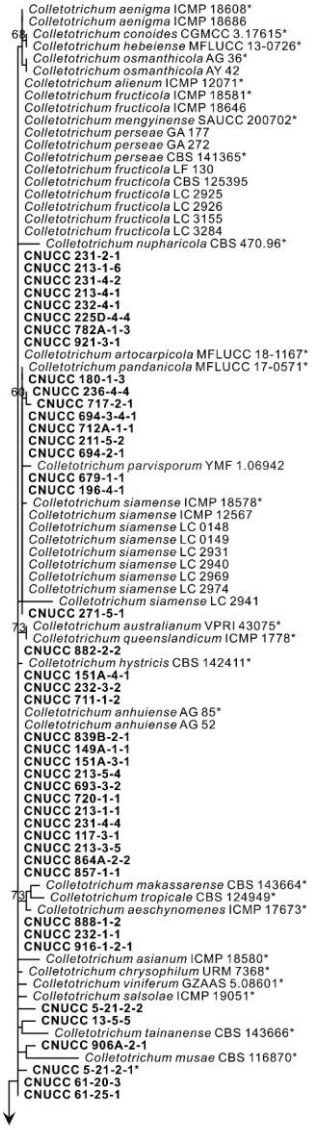
Supplementary Figure 40 – Continued.



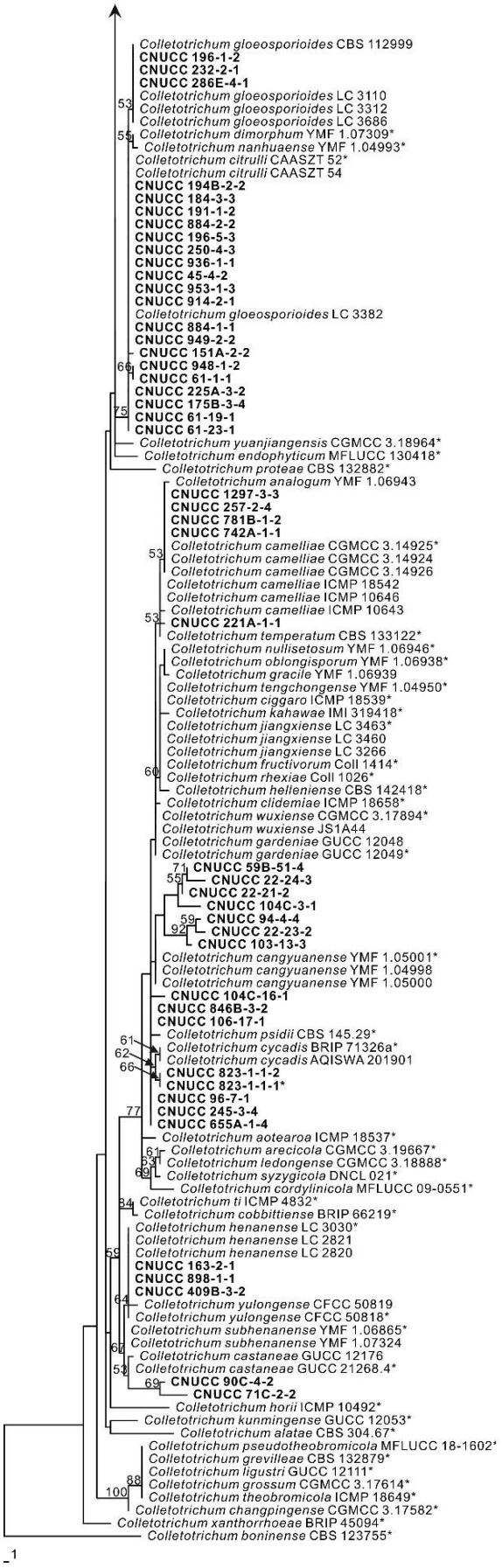
Supplementary Figure 41 – Phylogenetic tree of *C. gloeosporioides* species complex derived from maximum parsimony analysis of ITS sequences, using *Colletotrichum boninense* CBS 123755 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



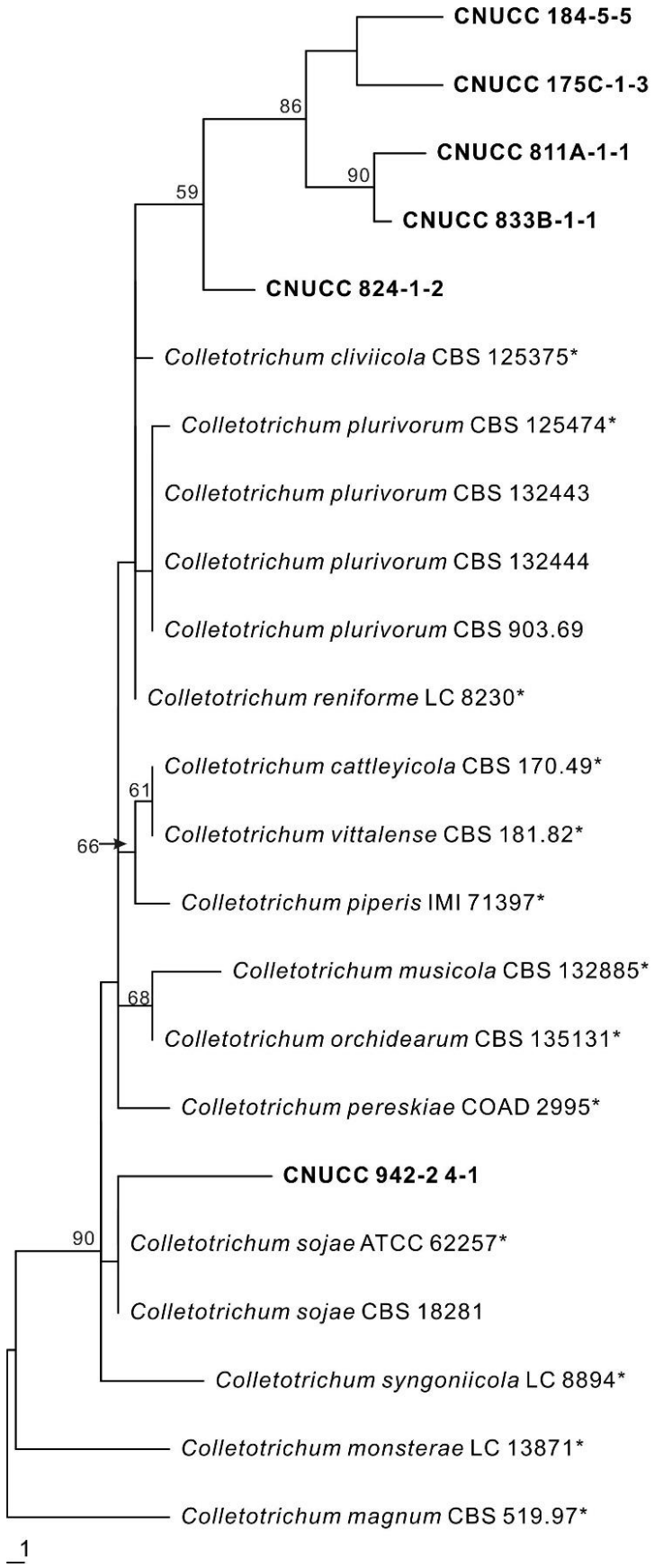
Supplementary Figure 41 – Continued.



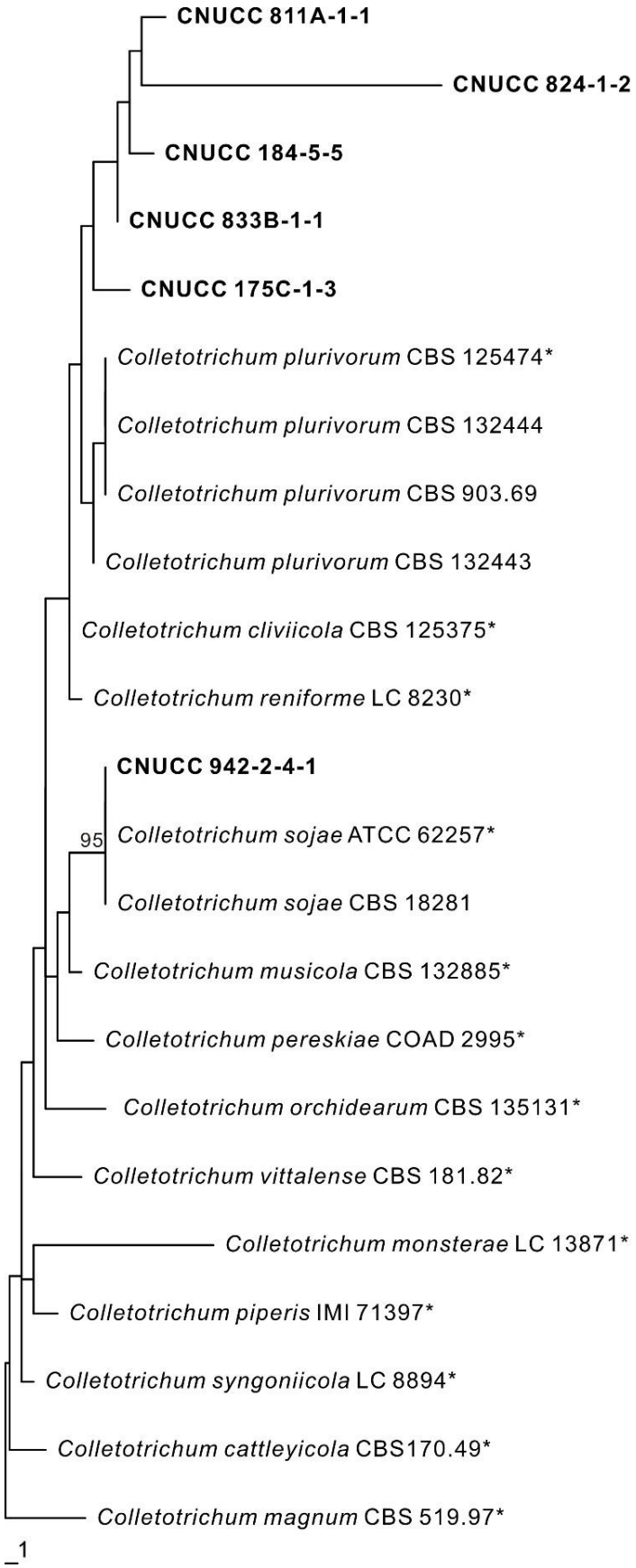
Supplementary Figure 42 – Phylogenetic tree of *C. gloeosporioides* species complex derived from maximum parsimony analysis of *tub* sequences, using *Colletotrichum boninense* CBS 123755 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



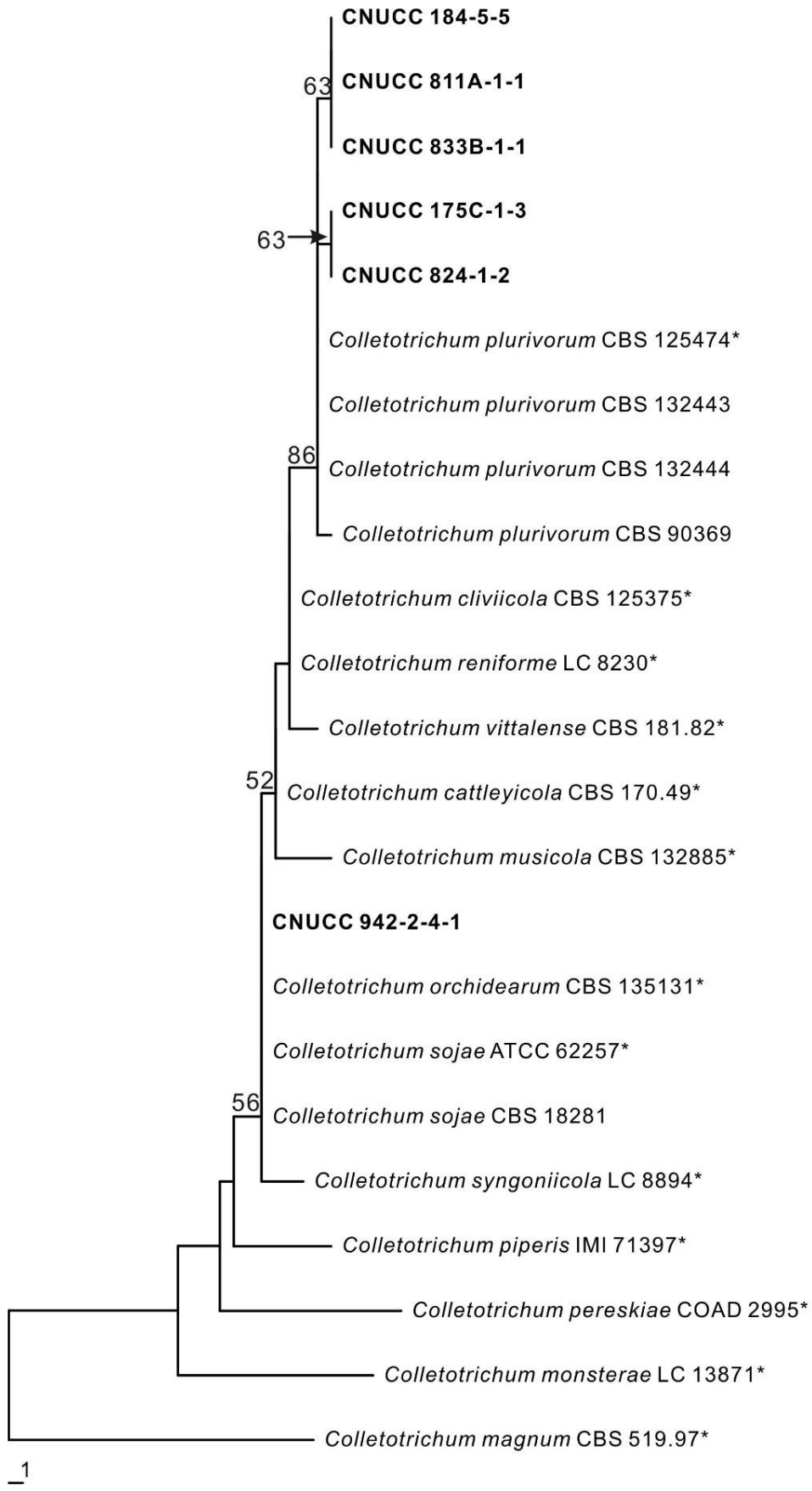
Supplementary Figure 42 – Continued.



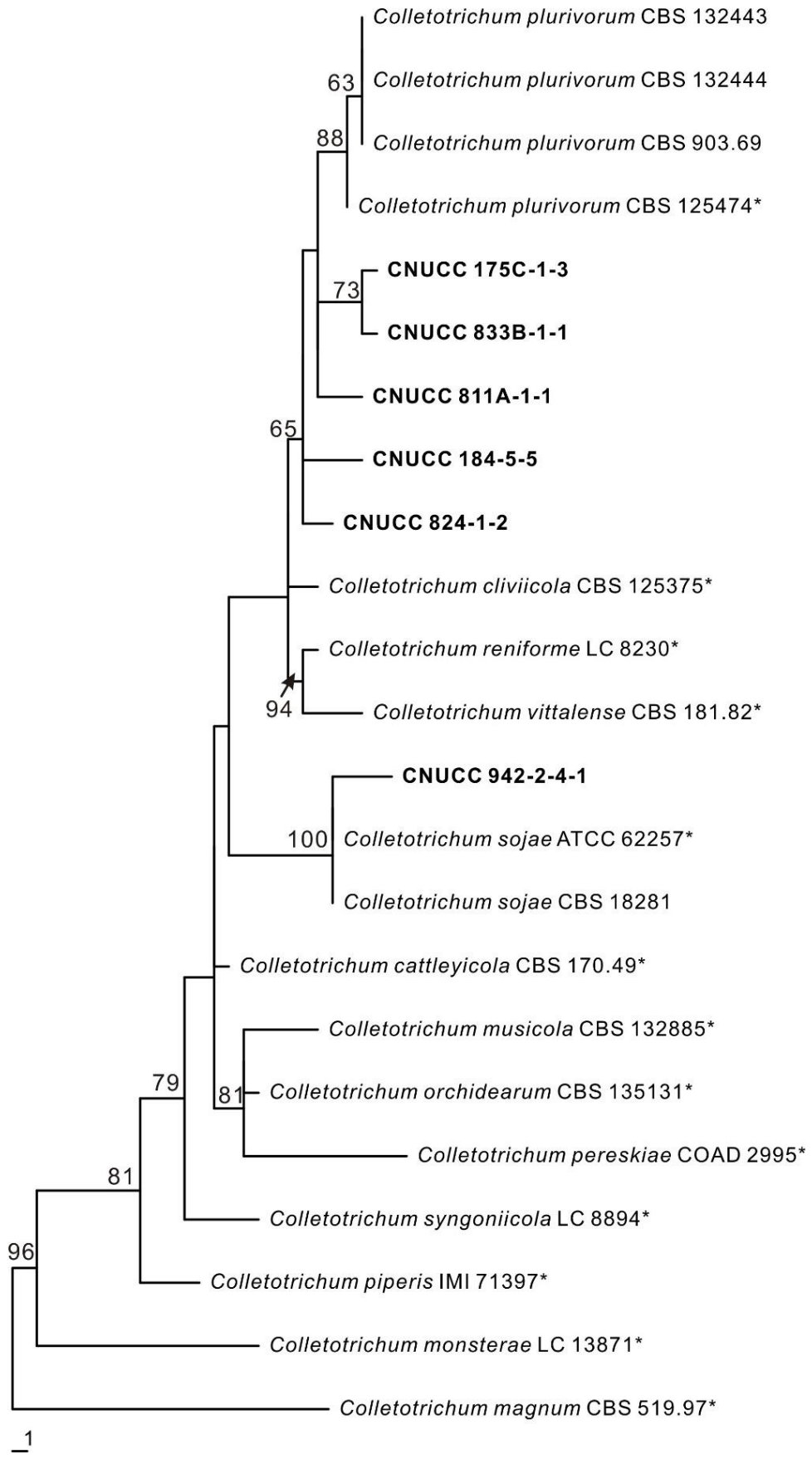
Supplementary Figure 43 – Phylogenetic tree of *C. orchidearum* species complex derived from maximum parsimony analysis of *act* sequences, using *Colletotrichum magnum* CBS 519.97 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



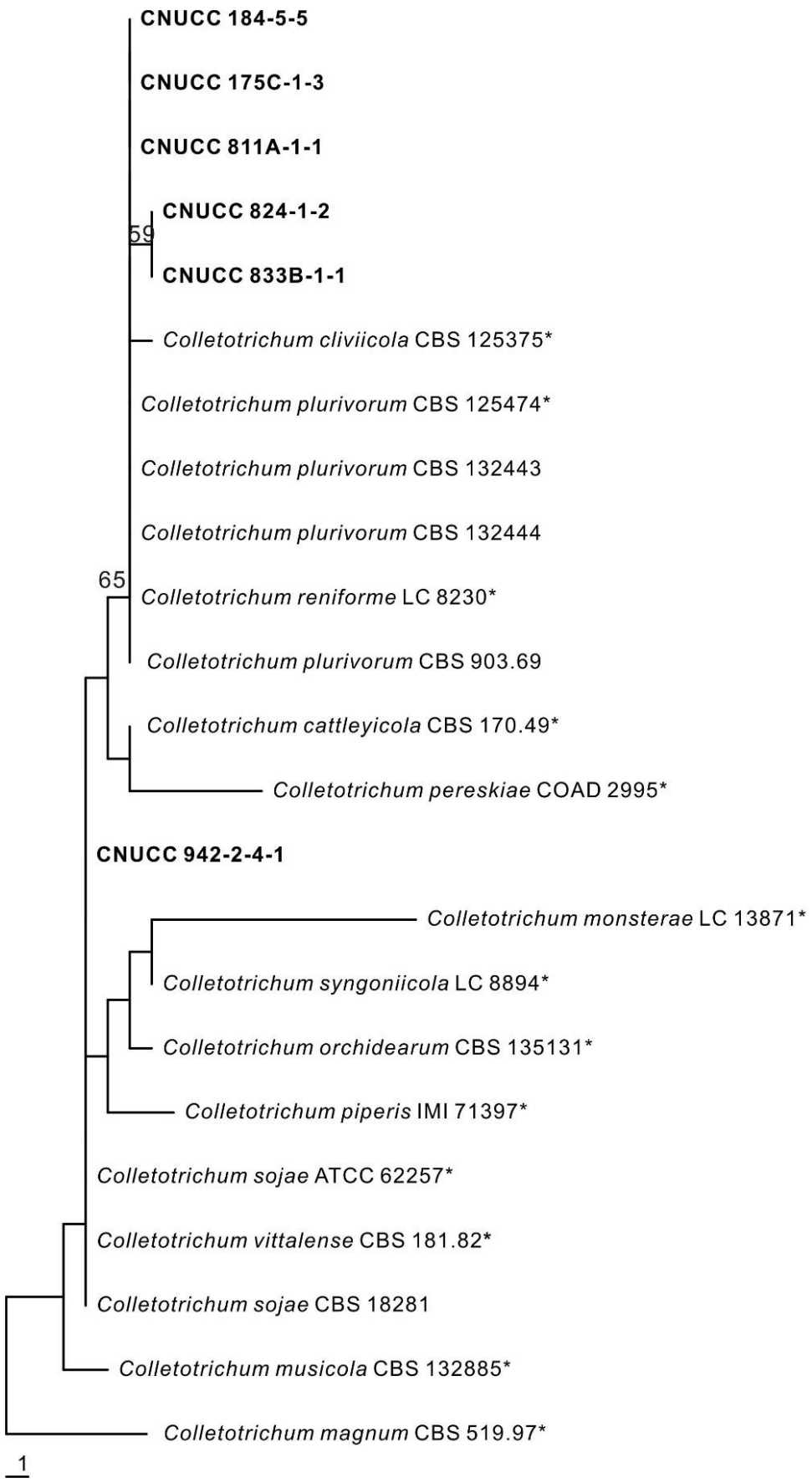
Supplementary Figure 44 – Phylogenetic tree of *C. orchidearum* species complex derived from maximum parsimony analysis of *chs* sequences, using *Colletotrichum magnum* CBS 519.97 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



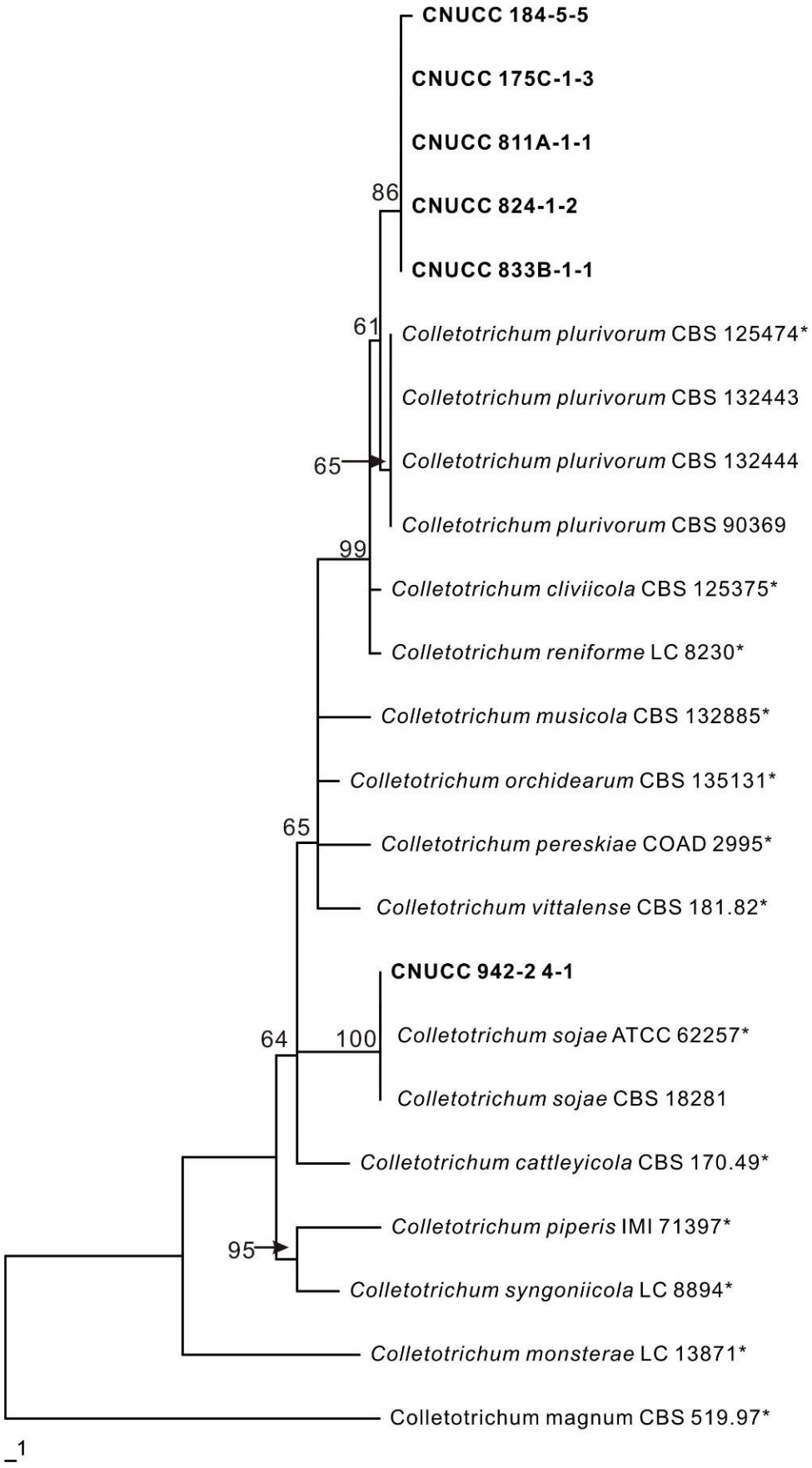
Supplementary Figure 45 – Phylogenetic tree of *C. orchidearum* species complex derived from maximum parsimony analysis of *gapdh* sequences, using *Colletotrichum magnum* CBS 519.97 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



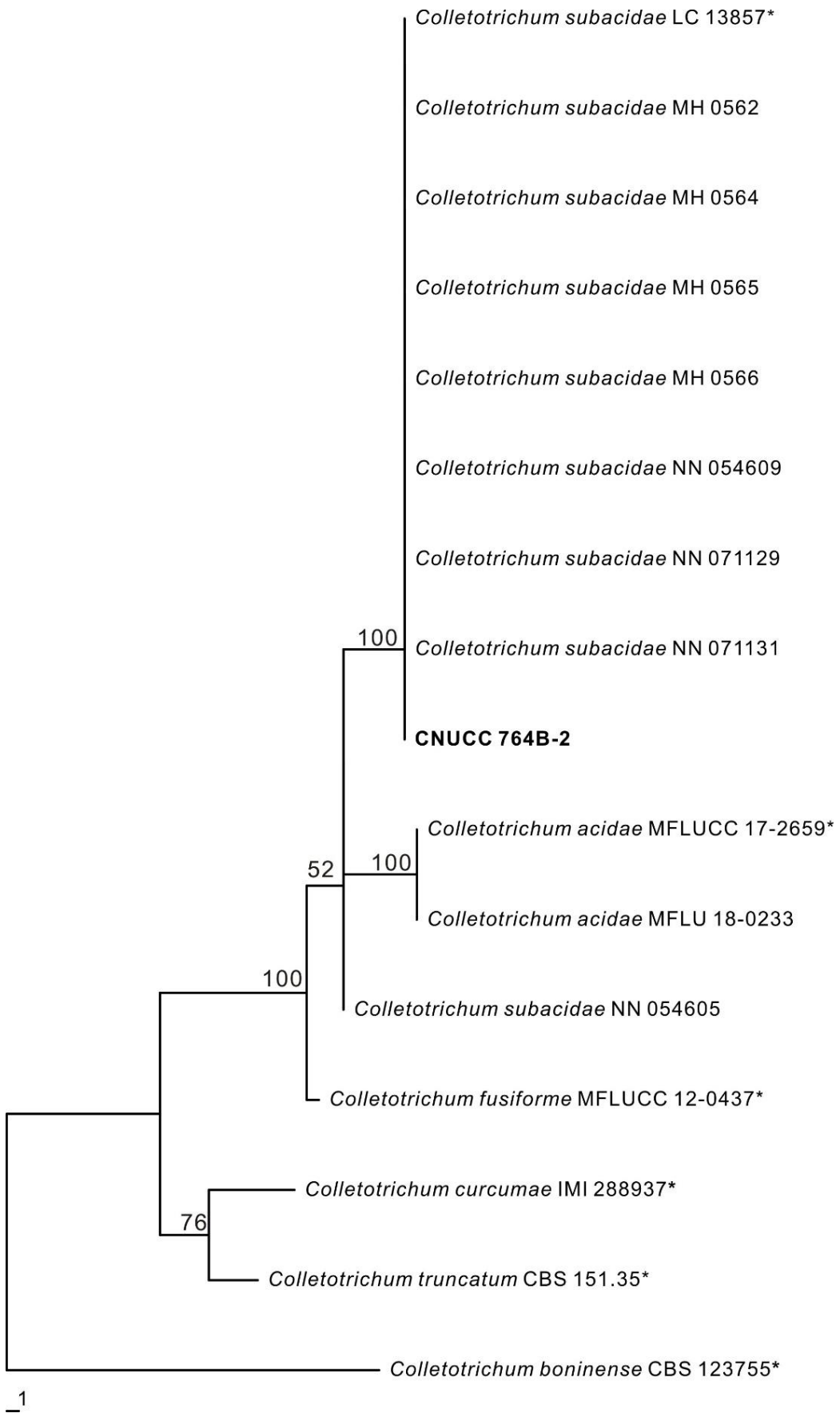
Supplementary Figure 46 – Phylogenetic tree of *C. orchidearum* species complex derived from maximum parsimony analysis of *his* sequences, using *Colletotrichum magnum* CBS 519.97 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



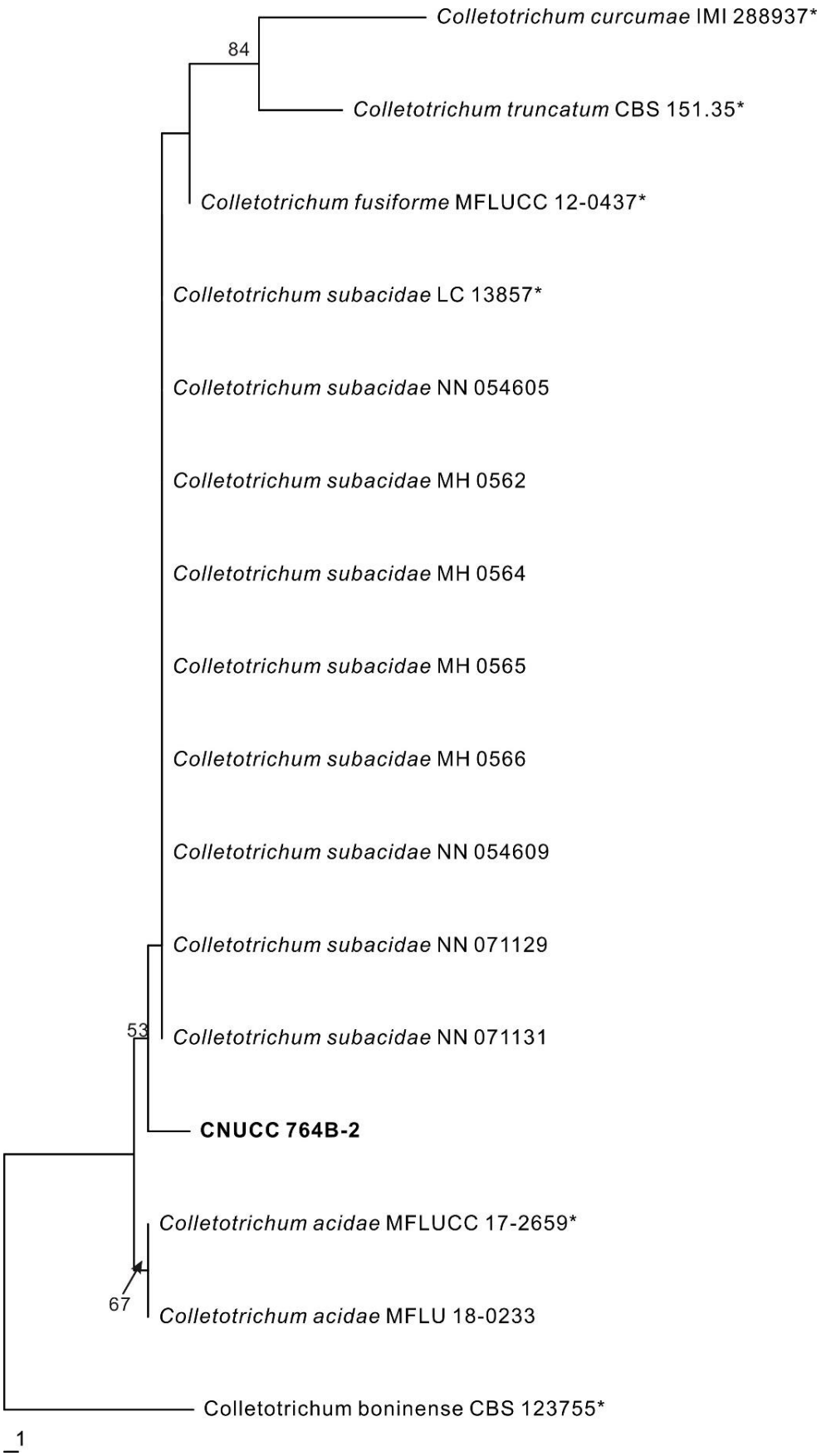
Supplementary Figure 47 – Phylogenetic tree of *C. orchidearum* species complex derived from maximum parsimony analysis of ITS sequences, using *Colletotrichum magnum* CBS 519.97 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



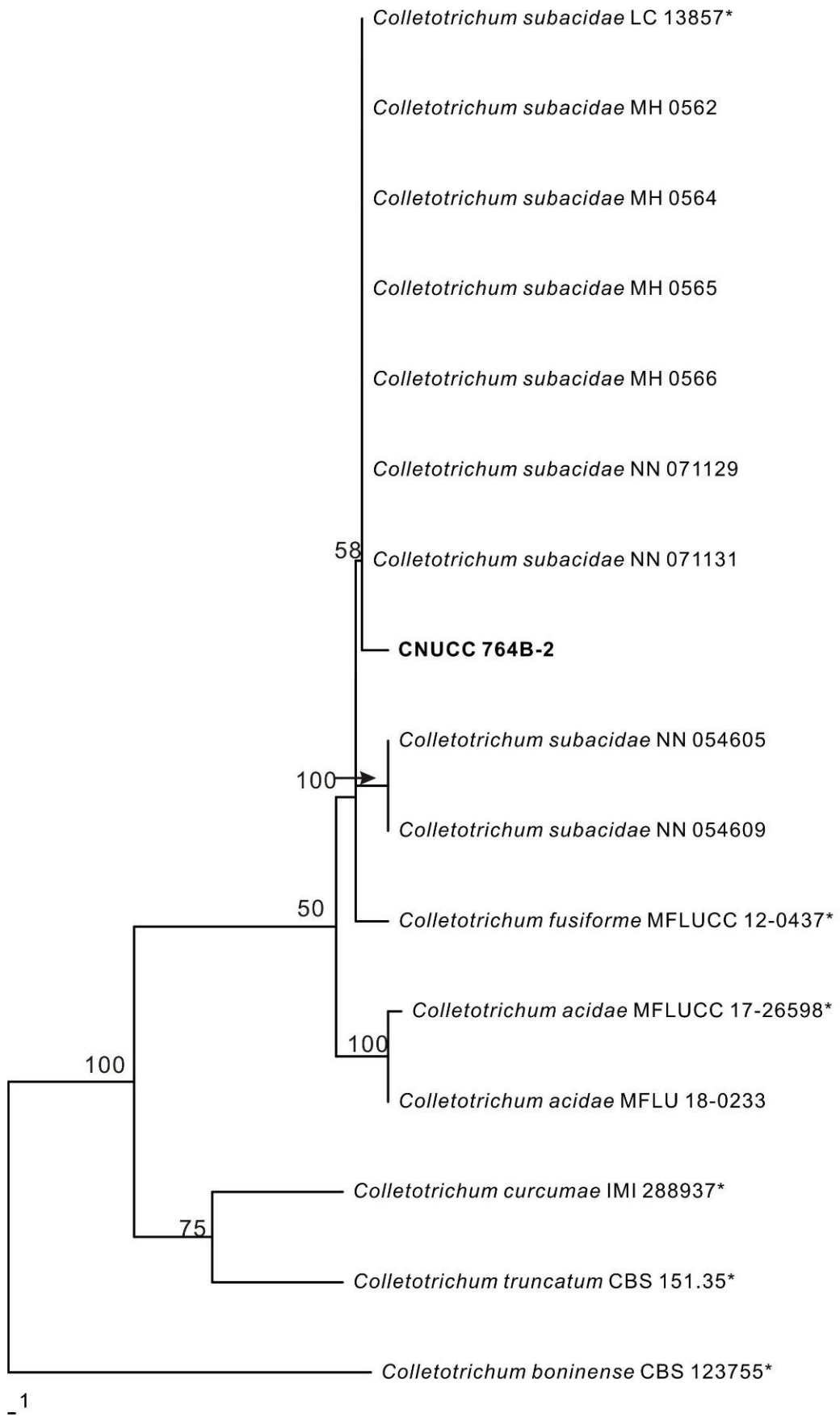
Supplementary Figure 48 – Phylogenetic tree of *C. orchidearum* species complex derived from maximum parsimony analysis of *tub* sequences, using *Colletotrichum magnum* CBS 519.97 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



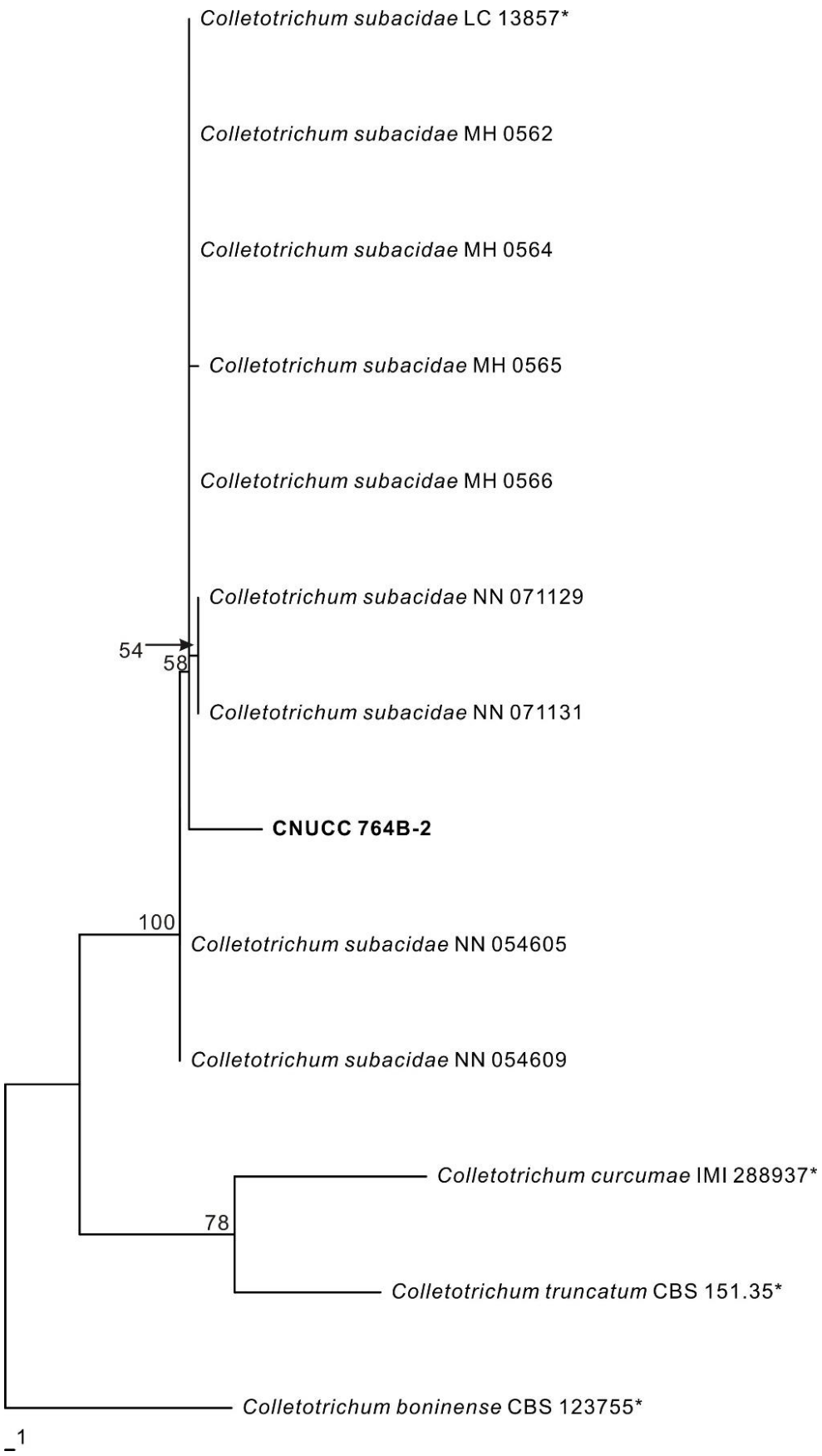
Supplementary Figure 49 – Phylogenetic tree of *C. truncatum species* complex derived from maximum parsimony analysis of *act* sequences, using *Colletotrichum boninense* CBS 123755 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



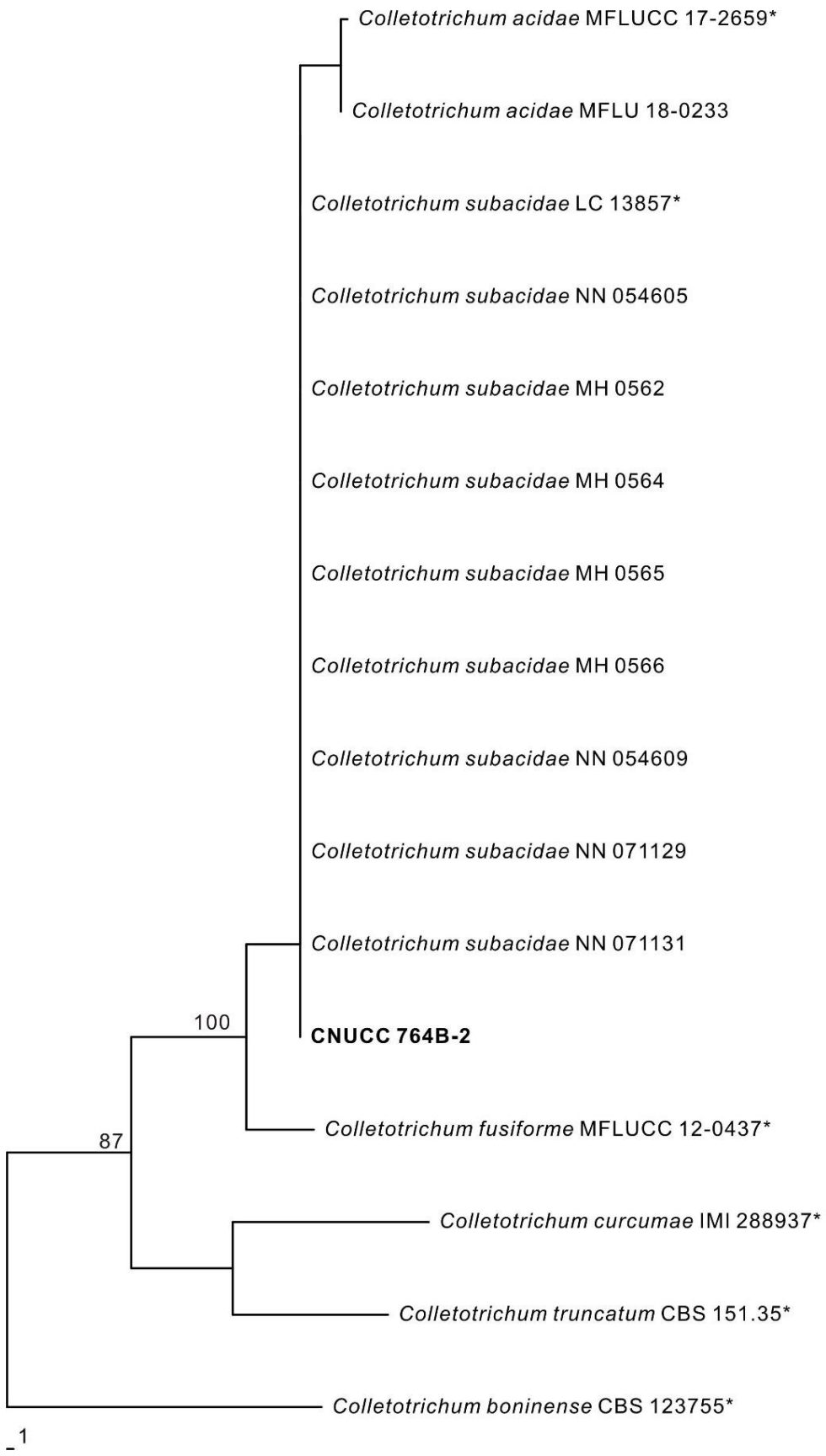
Supplementary Figure 50 – Phylogenetic tree of *C. truncatum species* complex derived from maximum parsimony analysis of *chs* sequences, using *Colletotrichum boninense* CBS 123755 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



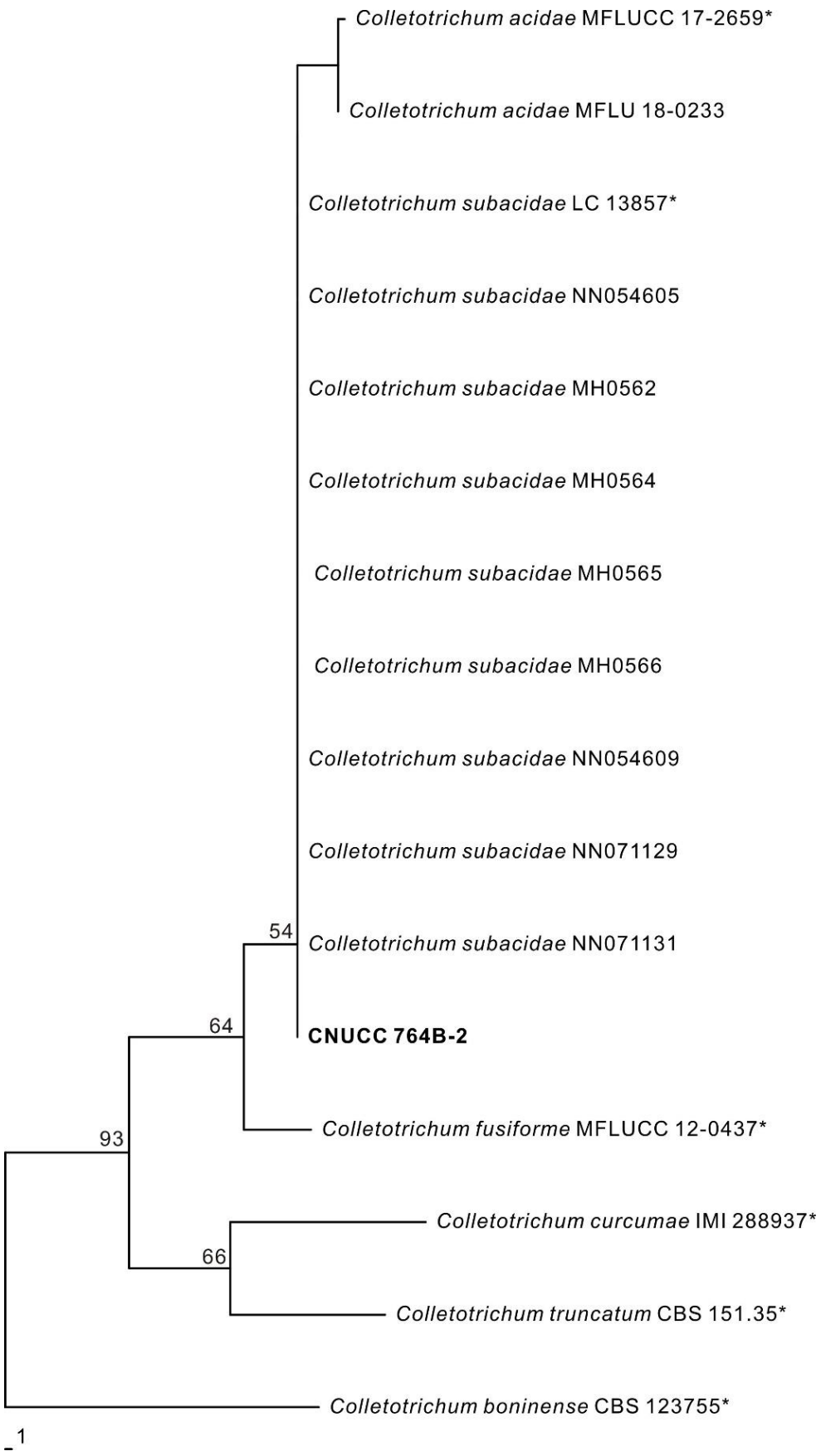
Supplementary Figure 51 – Phylogenetic tree of *C. truncatum species* complex derived from maximum parsimony analysis of *gapdh* sequences, using *Colletotrichum boninense* CBS 123755 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



Supplementary Figure 52 – Phylogenetic tree of *C. truncatum species* complex derived from maximum parsimony analysis of *his* sequences, using *Colletotrichum boninense* CBS 123755 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



Supplementary Figure 53 – Phylogenetic tree of *C. truncatum species* complex derived from maximum parsimony analysis of ITS sequences, using *Colletotrichum boninense* CBS 123755 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.



Supplementary Figure 54 – Phylogenetic tree of *C. truncatum species* complex derived from maximum parsimony analysis of *tub* sequences, using *Colletotrichum boninense* CBS 123755 as outgroup. Maximum parsimony bootstrap values (BP>50%) are shown above the branches. Type species strains are designated by " * ". Newly generated sequences are represented in **bold**.