



Notes on currently accepted species of *Colletotrichum*

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Abstract

Colletotrichum is an economically important plant pathogenic genus worldwide, but can also have endophytic or saprobic lifestyles. The genus has undergone numerous revisions in the past decades with the addition, typification and synonymy of many species. In this study, we provide an account of the 190 currently accepted species, one doubtful species and one excluded species that have molecular data. Species are listed alphabetically and annotated with their habit, host and geographic distribution, phylogenetic position, their sexual morphs and uses (if there are any known). There are eleven species complexes in *Colletotrichum* and 23 singleton species. The main characters of each species complex are detailed with illustrations. Phylogenetic trees are provided for the whole genus and each species complex. Genes and combination of genes that can be used for identification of the species complexes are suggested. Specific genes that can be used in species identification are given when possible.

Key words – *Glomerellaceae* – nomenclature – phylogeny – species complex – taxonomy

Introduction

The genus *Colletotrichum* was introduced by Corda (1831) and belongs to the family *Glomerellaceae* (Glomerellales, Sordariomycetes), and is the sole member of this family (Réblová et al. 2011, Maharachchikumbura et al. 2015, 2016). Species of this genus are important pathogens, some are endophytes as well as saprobes (Cannon et al. 2012, Hyde et al. 2014, Jayawardena et al. 2016a).

At the time of the first monographic treatment of *Colletotrichum* (von Arx 1957), around 750 names existed (Cannon et al. 2012). Von Arx (1957) reduced this to 11 taxa based on morphological characters. Sutton (1980) accepted 22 species, while Sutton (1992) accepted 39 species based on morphological and cultural characteristics. Hyde et al. (2009b) provided the first comprehensive overview of this genus with 66 names in common use and 19 doubtful names and also highlighted the need to revise this genus by using molecular methods (Hyde et al. 2009a). This

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was the beginning of the still ongoing revision of the genus based on multi-locus sequence data in which several species were revised and typified or newly described and several species complexes were detected (Cannon et al. 2012, Damm et al. 2009, 2012a, b, 2013, 2014, Weir et al. 2012, Crouch et al. 2009a, 2014, Hyde et al. 2014, Liu et al. 2015a). Index Fungorum (2016) lists 820 epithets (www.indexfungorum.org; accessed 7th August 2016) under *Colletotrichum*, but only less than 200 names are currently accepted (Hyde et al. 2014).

Misidentification of *Colletotrichum* species is a frequent mistake that happens due to few distinctive morphological characters available for identification. Misunderstanding of their host specific nature has also led to misapplication and misidentification of species (Cannon et al. 2012). Many older *Colletotrichum* names lack type specimens and authentic living strains for molecular analysis. This tends to get in the way of reconstructing a natural classification system for *Colletotrichum* (Cai et al. 2009, Hyde et al. 2009a,b, Cannon et al. 2012). Epi- or neotypes of the *Colletotrichum* species are being designated to preserve the current application of names according to the International Code of Nomenclature for Algae, Fungi and Plants (Hawksworth 2011). Before assigning an epitype for a species, the fresh collection needs to be carefully compared to the type material, if preserved. An epitype should have morphological characteristics similar to the holotype or the original description and originate from the same geographical region and host (Ariyawansa et al. 2014). Once an epitype is designated, questions of species diversity of this genus can be addressed on the basis of the DNA sequence data of the ex-epitype strain.

Currently, researchers strongly recommend the application of a polyphasic approach, including the analysis of geographical, ecological, morphological and genetic data in order to establish a natural classification system for the genus *Colletotrichum* (Cai et al. 2009). For species delimitation within this genus, phylogenetic analysis based on concatenated loci and the application of the Genealogical Concordance Phylogenetic Species Recognition (GCPSR) have proven to be powerful tools (Cannon et al. 2012, Liu et al. 2016). Coalescent-based species delimitation methods can be used to infer the dynamic of divergence, evolutionary process and the relationships among species (McCormack et al. 2009, Liu et al. 2016).

Most of the species in this genus are important phytopathogens, while some are endophytes and saprobes. The basis of the current study for the lifestyles is that if a fungus was isolated from a diseased tissue (fruit, leaf and stem) it is referred to as a pathogen; if a fungus was isolated from a healthy tissue it is considered as an endophyte and if a fungus was isolated from a dead plant matter is considered as a saprobe.

This study uses Cannon et al. (2012) as the starting point for the accepted species, as well as published records since that study. An overview of the currently accepted species in the genus with their hosts, geographic distribution, phylogenetic position, sexual morphs as well as their uses (if there are any known) is provided. The main characters of each species complex are illustrated. Phylogenetic trees are provided for the whole genus and the species complexes. Genes necessary to distinguish the species within the different species complexes are also provided when possible.

Material and Methods

This study deals with the species included in Cannon et al. (2012) and newly described species after this publication. The USDA fungal databases (Farr & Rossman 2016) have been used in order to gather information on host association and geographic distribution. Additional, new disease reports were also included.

Morphology

Conidial and appresorial characters of different species complexes were focused in this study. Photo plates were created from the photos provided by U. Damm and F. Liu. Line diagrams were drawn where necessary, using transparent drawing papers and drawing pens.

Phylogenetic Analysis

Actin (ACT), β -tubulin2 (TUB2), chitin synthase (CHS-1), DNA lyase (*Apn2*), glyceraldehyde-3-phosphate dehydrogenase (GAPDH), glutamine synthetase (GS), histone 3

(HIS3), internal transcribed spacers (ITS), manganese-superoxide dismutase (SOD2), mating type gene (Mat1), and Apn2/MAT1GS (*Ap/Mat*) sequences of each accepted species were downloaded, if available, from NCBI GenBank (<https://www.ncbi.nlm.nih.gov/genbank/>). A backbone phylogenetic tree of the whole genus and separate phylogenetic trees of the species complexes were constructed.

Single gene regions were aligned using Clustal X1.81 (Thompson et al. 1997) and combined using BioEdit v.7.0.9.0 (Hall 1999). Further alignment of the sequences was done using default settings of MAFFT v.7 (Kato & Toh 2008; <http://mafft.cbrc.jp/alignment/server/>) and manual adjustment was conducted using BioEdit where necessary. Maximum Parsimony analysis (MP) was performed using PAUP (Phylogenetic Analysis Using Parsimony) v. 4.0b10 (Swofford 2002) to obtain the most parsimonious trees. Gaps were treated as missing data and ambiguously aligned regions were excluded. Trees were inferred using the heuristic search option with Tree Bisection Reconnection branch swapping and 1000 random sequence additions. Maxtrees were set up to 5000, branches of zero length were collapsed and all multiple parsimonious trees were saved. Descriptive tree statistics for parsimony (tree length, consistency index, retention index, rescaled consistency index, and homoplasy index) were calculated for trees generated under different optimality criteria. The robustness of the most parsimonious trees was evaluated by 1000 bootstrap replications resulting from maximum parsimony analysis (Hillis & Bull 1993). Kishino-Hasegawa tests (Kishino & Hasegawa 1989) were performed in order to determine whether trees were significantly different.

A maximum likelihood analysis was performed for the whole genus in raxmlGUIv.0.9b2 (Silvestro & Michalak 2010). Rapid bootstrapping with 1000 non parametric bootstrapping iterations, using the general time reversible model (GTR) with a discrete gamma distribution, was set as the search strategy.

Bayesian inference (BI) was used in addition to construct the phylogenies using Mr. Bayes v.3.1.2 (Ronquist et al. 2003). MrModeltest v. 2.3 (Nylander 2004) was used to carry out statistical selection of best-fit model of nucleotide substitution and was incorporated into the analysis. Six simultaneous Markov chains were run for 1 000 000 generations and trees were sampled every 100th generation. The 2000 trees representing the burn-in phase of the analyses, were discarded and the remaining 8000 trees used for calculating posterior probabilities (PP) in the majority rule consensus tree. The fungal strains that were used for this study are listed in Table 1 with details of type cultures and sequence data.

Results and Discussion

The *Colletotrichum* names that are currently accepted are listed alphabetically below, with notes of the authorities and publication details, habits, hosts, geographical distribution, uses and sexual morphs (if there are any) as well as systematic position. The 190 accepted names are also listed in Table 1. Liu et al. (2016) emphasized on the importance of using polyphasic approaches such as genealogical concordance phylogenetic species recognition (GCPSR) and coalescent methods when describing new species in morphologically conserved genera. A backbone tree of the genus *Colletotrichum* comprising 189 species using five gene regions have been constructed (Fig. 1). However, several species have been excluded from this analysis due to the lack of sequences. All the species complexes can be distinguished effectively from each other by using ITS sequence data alone. Species within species complexes can be resolved with the use of additional genes are mentioned with the different complexes.

Acutatum species complex

This species complex consists of 34 species that include *C. acutatum* and its close relatives. Members of this species complex often cause fruit rots (Damm et al. 2012b). Most species within this complex have conidia with at least one acute end (Fig. 2) (Damm et al. 2012b). A combined gene analysis for this complex using ITS, GAPDH, CHS-1, HIS3, ACT and TUB2 sequences is

given in Fig. 3. In order to differentiate species within this complex effectively, use of both TUB2 and GAPDH are recommended (Damm et al. 2012b).

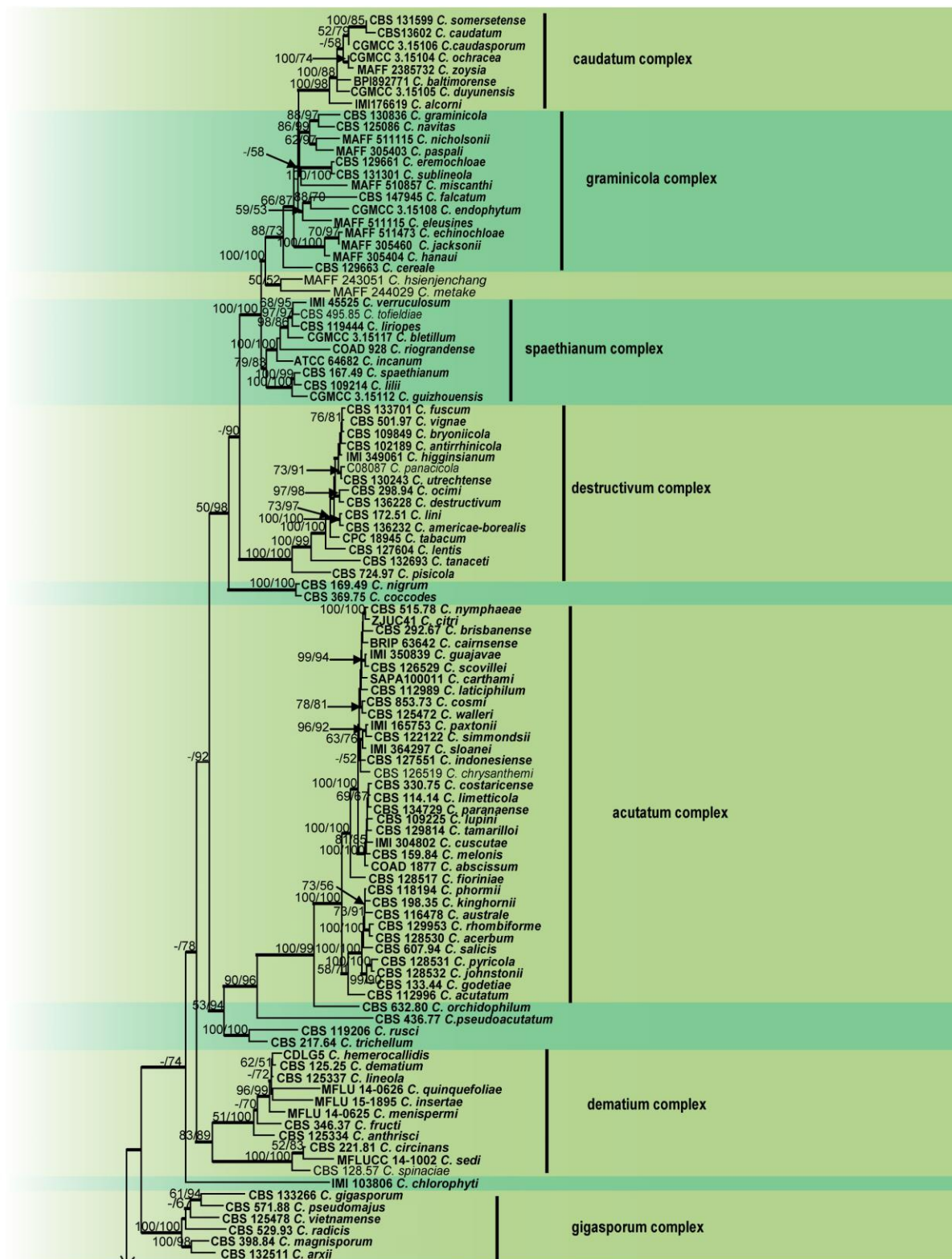


Fig. 1 One of the 100 most parsimonious trees obtained from a heuristic search of combined ITS, GAPDH, CHS-1, ACT and TUB2 sequence data of the genus *Colletotrichum*. Parsimony and likelihood bootstrap support values $\geq 50\%$ are indicated at the nodes and branches with Bayesian posterior probabilities above 0.80 are given in bold. The ex-type strains are in bold. The tree is rooted with *Monilochaetes infuscans* CBS 869.96

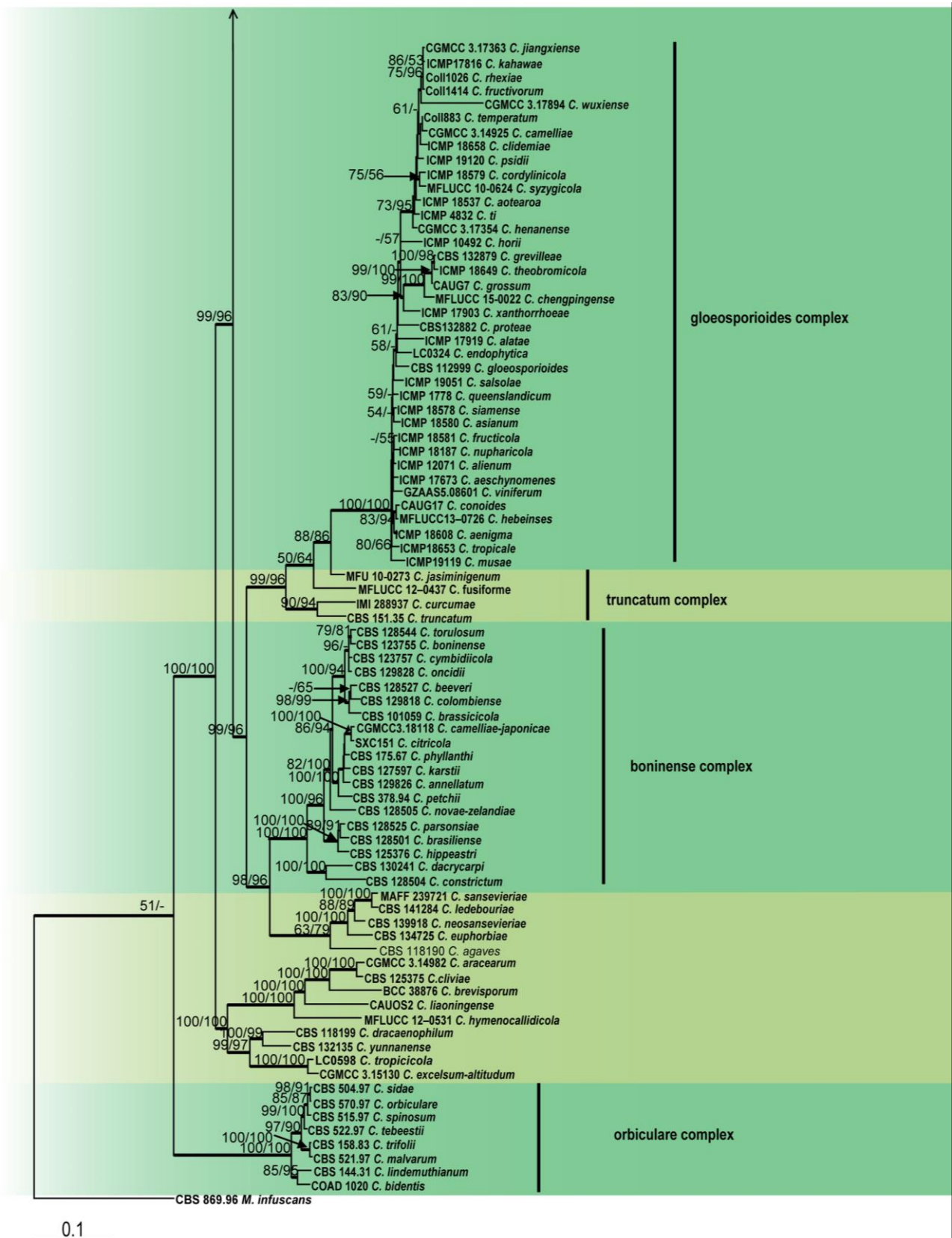


Fig. 1 (continued)
Species complexes

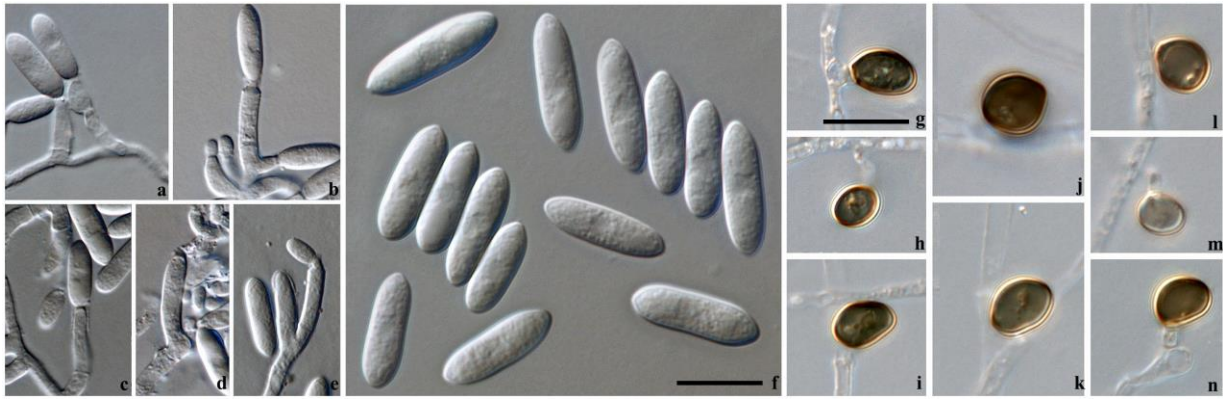


Fig. 2 *Colletotrichum acutatum* (from ex-type strain CBS 112996, on SNA) a–e. Conidiophores f. Conidia g–n. Appressoria. Scale bars: f, g = 10µm; scale bar of f and g applies to a–n (Courtesy of U. Damm).

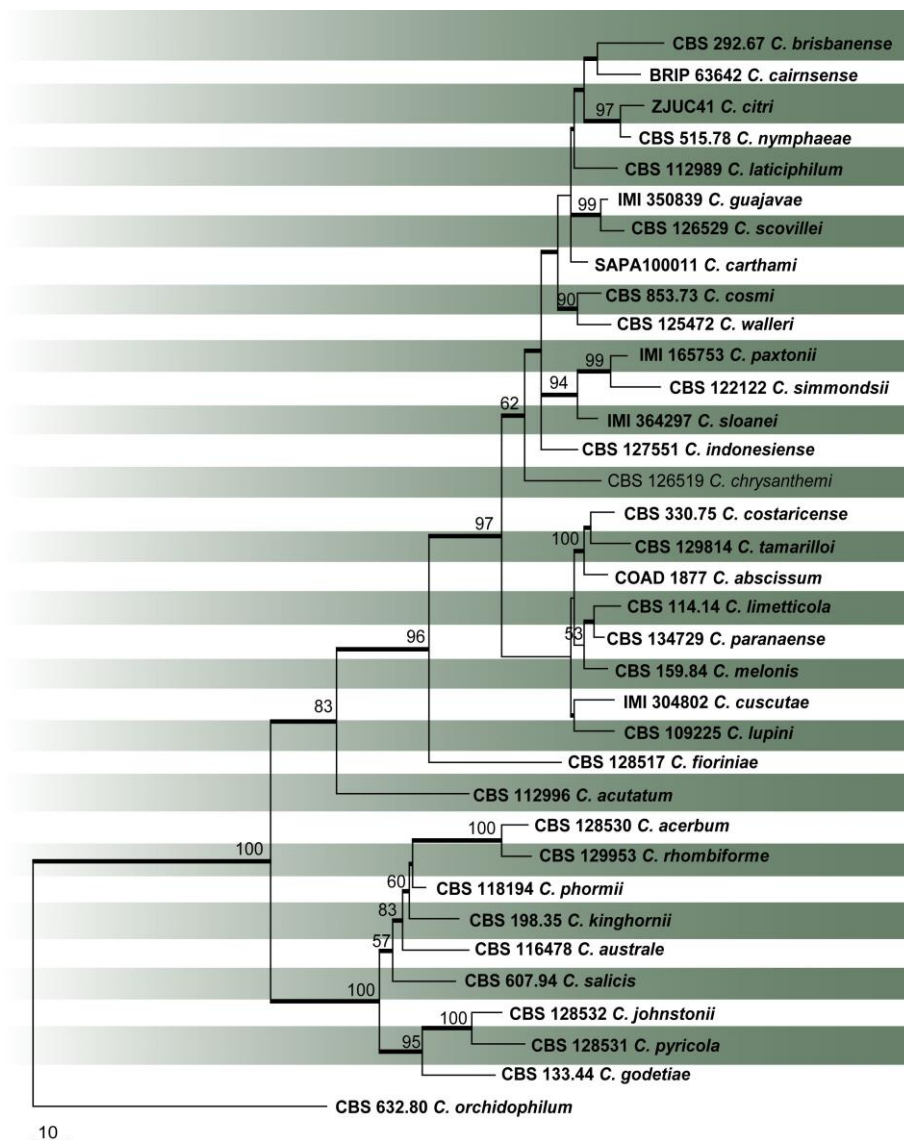


Fig. 3 One of the eight most parsimonious trees obtained from a heuristic search of combined ITS, GAPDH, CHS-1, HIS3, ACT and TUB2 sequence data of taxa from the *acutatum* species complex. Parsimony bootstrap support values above 50 % are indicated at the nodes and branches with Bayesian posterior probabilities above 0.95 are given in bold. The ex-type strains are in bold. The tree is rooted with *C. orchidophilum* CBS 632.80.

Boninense species complex

This species complex is defined as a collective of *C. boninense* and 18 closely related species with three main subclades containing 14, three and two species, respectively. Typical characters of species in this complex are the conidia that have a prominent basal scar as well as the conidiogenous cells with rather prominent periclinal thickening that sometimes extend to form a new conidiogenous locus (Damm et al. 2012a). Species of this complex are pathogens or endophytes (Damm et al. 2012a). A combined analysis of ITS, GAPDH, CHS-1, ACT, HIS3, TUB2 and CAL sequence of this species complex is given in Fig. 5. All species within this complex can be recognized with GAPDH alone (Damm et al. 2012a).



Fig. 4 *Colletotrichum boninense* (from ex-type strain CBS 123755, on SNA) a. Conidiophores b. Conidia c–h. Appressoria. Scale bars: b, c = 10µm; scale bar of b and c applies to a–h (Courtesy of U. Damm).

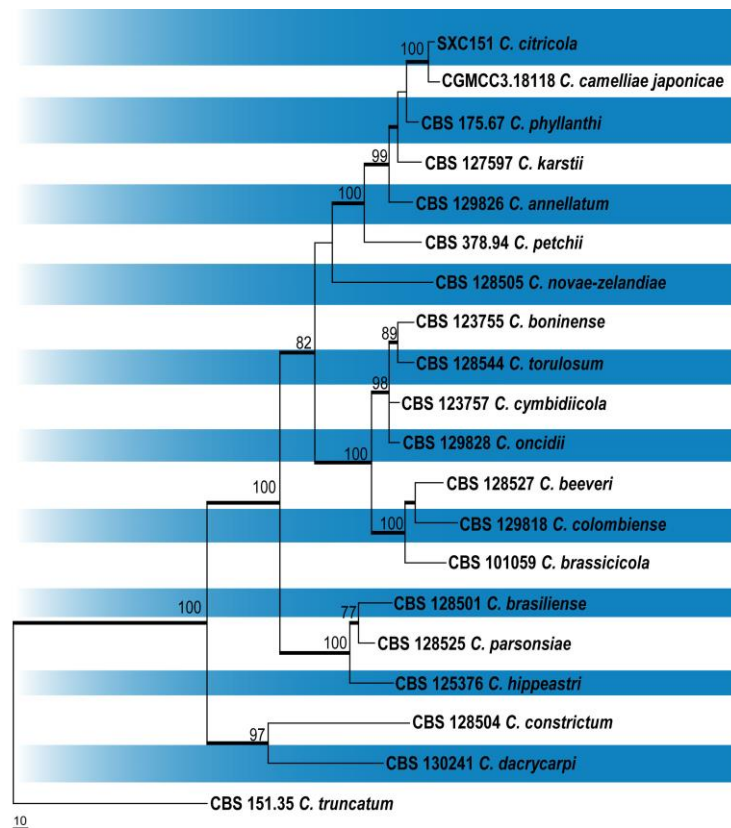


Fig. 5 The most parsimonious tree obtained from a heuristic search of combined ITS, GAPDH, CHS-1, ACT, HIS3, TUB2 and CAL sequence data of taxa from the boninense species complex. Parsimony bootstrap support values above 50 % are indicated at the nodes and branches with Bayesian posterior probabilities above 0.95 are given in bold. The ex-type strains are in bold. The tree is rooted with *C. truncatum* CBS 151.35.

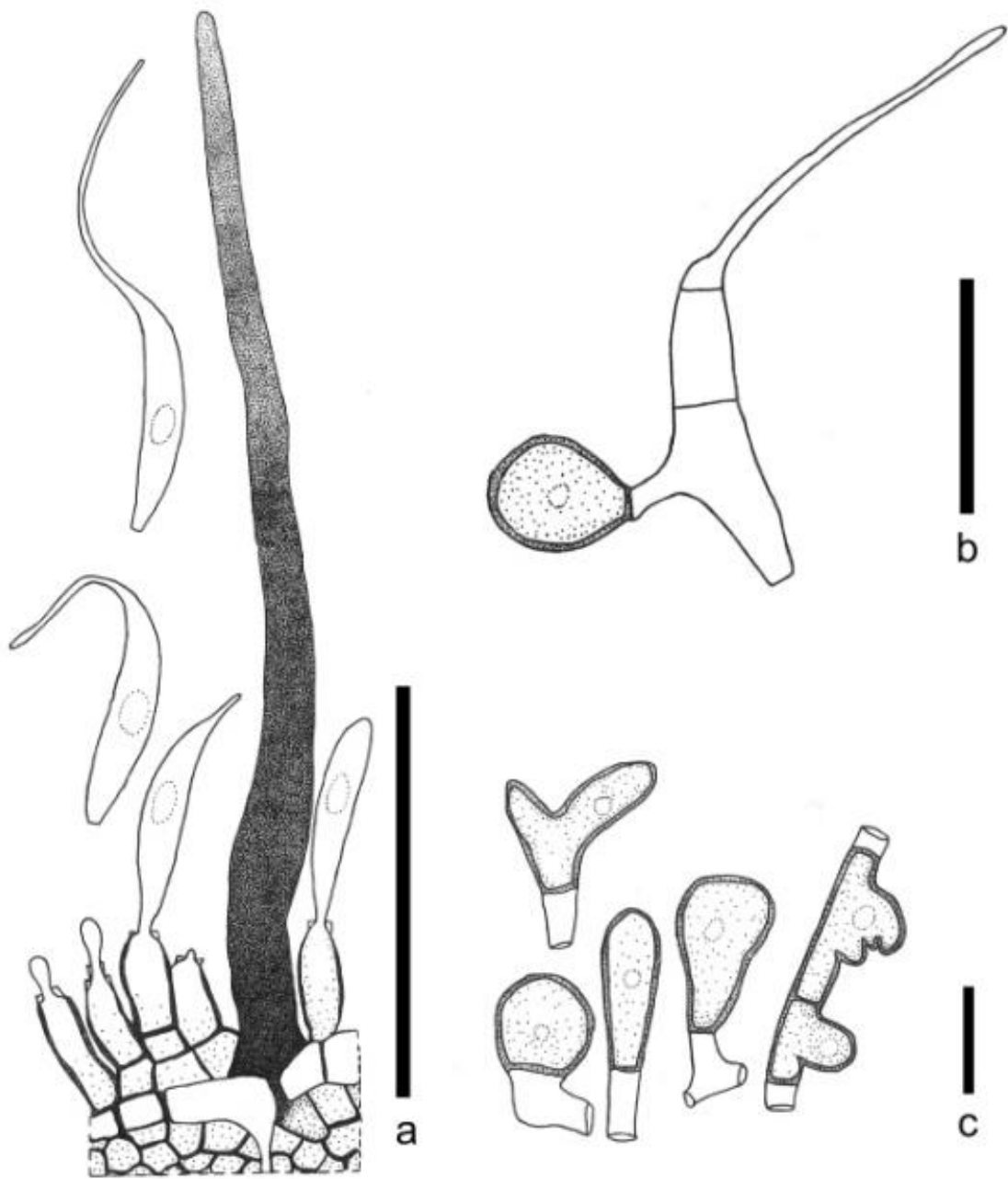


Fig. 6 *Colletotrichum caudatum* redrawn from NagRaj (1993). a. Seta with conidiogenous cells and developing conidia b. Germinating conidium c. Appressoria. Scale bars: a,b = 20 μ m, c = 5 μ m.

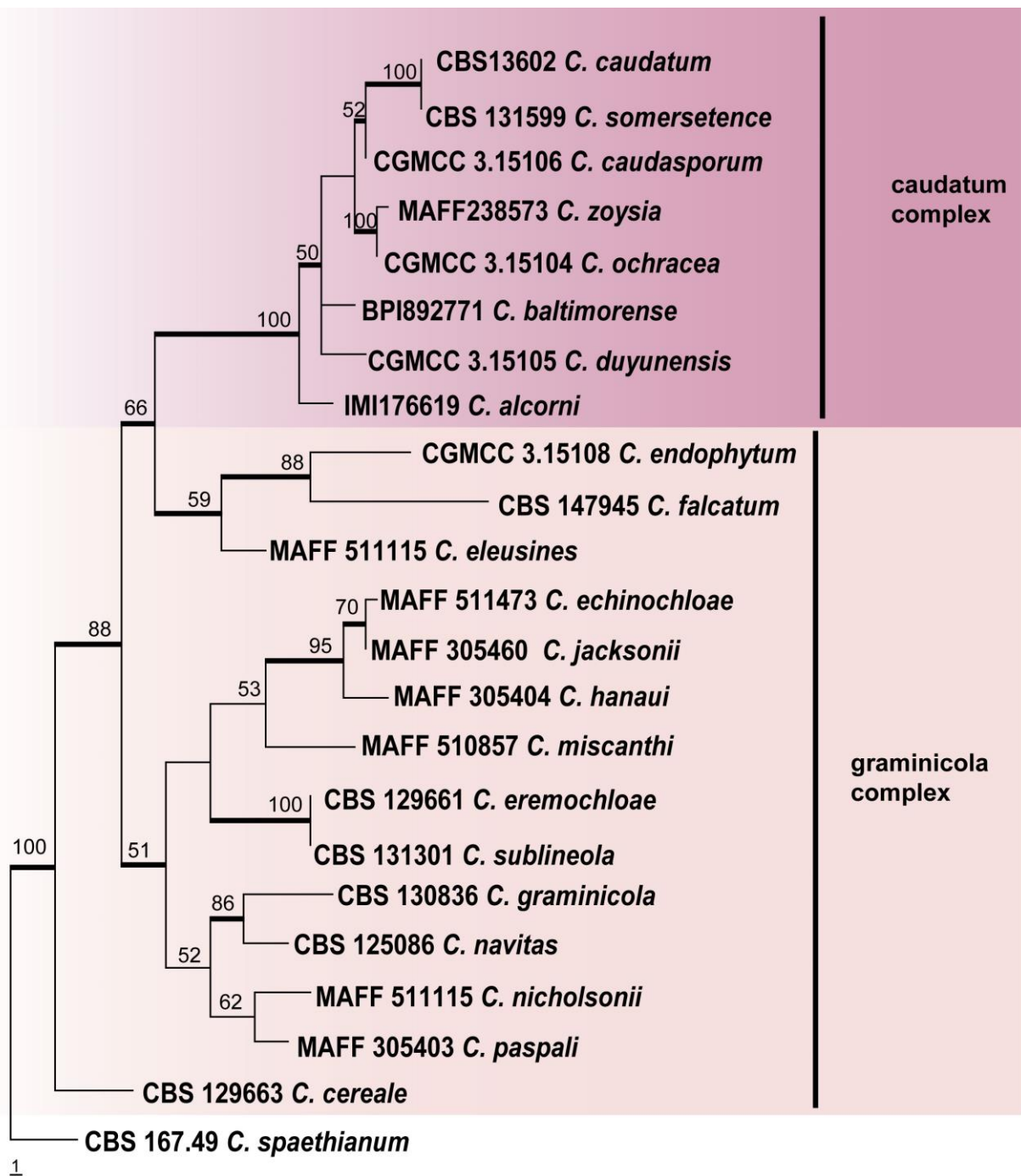


Fig. 7 The most parsimonious tree obtained from a heuristic search of ITS sequence data of taxa from the caudatum and graminicola species complex. Parsimony bootstrap support values above 50 % are indicated at the nodes and branches with Bayesian posterior probabilities above 0.95 are given in bold. The ex-type strains are in bold. The tree is rooted with *C. spaethianum* CBS 167.49.

Caudatum species complex

This species complex is defined as a collective of *C. caudatum* and seven closely related species. This complex can be distinguished by the presence of a filiform appendage at the apex of the conidium (Fig. 6) (Crouch 2014). A phylogenetic tree using ITS for the species of caudatum and graminicola species complexes has been constructed (Fig. 7). According to this phylogenetic tree, three species; *C. caudasporum*, *C. duyunensis* and *C. ochracea* which were previously identified to be in the graminicola species complex, clustered with the caudatum species complex.

However, further studies are needed to clarify whether to combine this complex with graminicola complex or to keep it as it is. Except for *C. ochracea*, the other two species agree with the morphology of the caudatum species complex. According to Fig. 7 caudatum complex appears to be a specific branch within the graminicola complex.

Dematium species complex

The dematium species complex includes *C. dematium* and ten closely related species. Species of this complex appear to be characteristic of temperate climates (Cannon et al. 2012). The type species of *Colletotrichum*, *C. lineola*, belongs in this species complex (Damm et al. 2009). There are two subclades within this complex. One clade comprises eight saprobic taxa, while the other comprises two pathogenic taxa and *C. sedi* being a saprobe. Typical are the conidia with an almost straight central part that bent abruptly to the apex and the truncate base, which gives them an almost angular shape (Fig. 8) (Damm et al. 2009). A combined gene analysis of ITS, GAPDH, CHS-1, ACT and TUB2 sequences of this species complex is shown in Fig. 9.



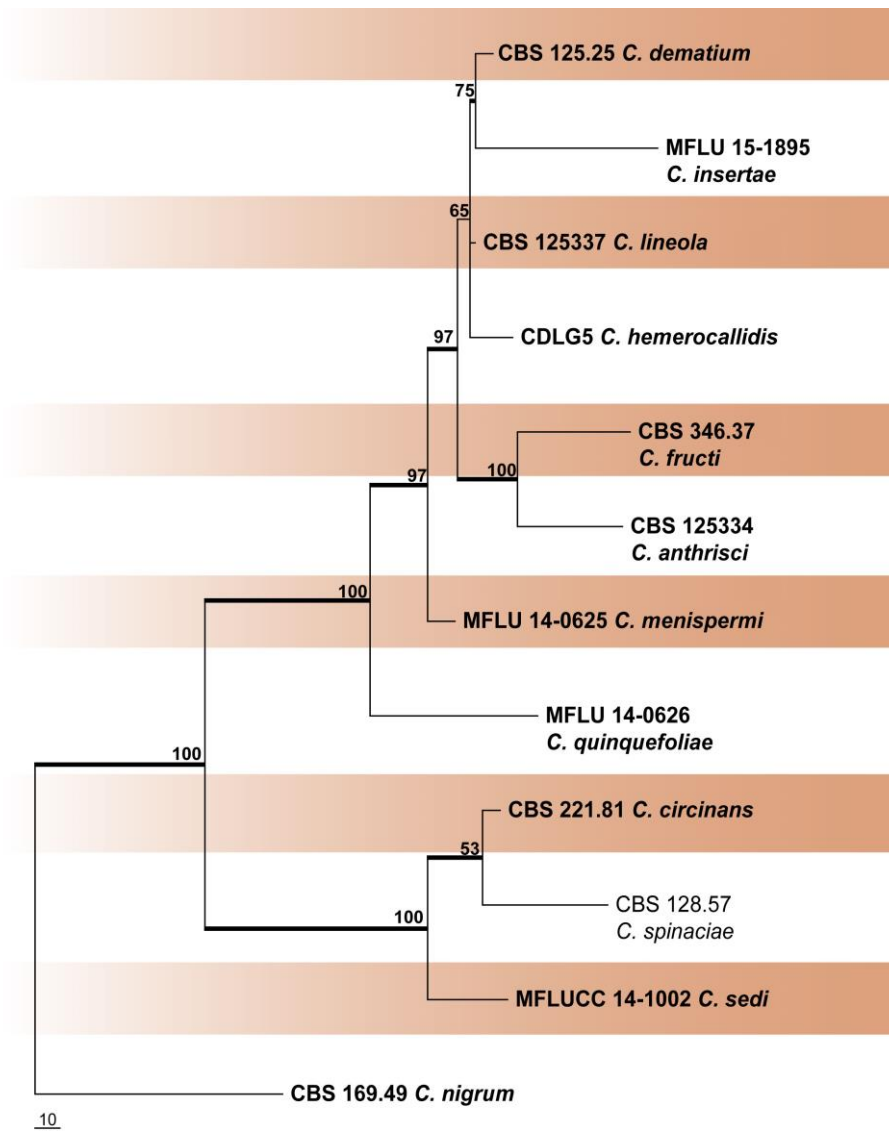
Fig. 8 *Colletotrichum dematium* (from ex-type strain CBS 125.25, on SNA) a–b. Conidiophores c. Conidia d–i. Appressoria. Scale bars: c, d = 10 μ m; scale bar of c and d applies to a–i (Courtesy of U. Damm).

Destructivum species complex

The destructivum species complex is a collective of *C. destructivum* and 14 closely related species that are mainly plant pathogens (Damm et al. 2014). The lifestyle of all species in this complex that had been examined in vivo is hemibiotrophic (Damm et al. 2014). O'Connell et al. (2012) showed that the destructivum species complex is monophyletic and distinct from other *Colletotrichum* species complexes. Species of this complex are characterized by conidia that are slightly curved due to their unilaterally tapering ends and by small inconspicuous acervuli with rather effuse growth (Fig. 10) (Damm et al. 2014). A combined analysis of ITS, GAPDH, CHS-1, HIS3, ACT and TUB2 sequences is given in Fig. 11. According to Damm et al. (2014) all species can be identified by a combination of TUB2 and GAPDH sequences.

Gigasporum species complex

The gigasporum species complex consists of *C. gigasporum* and five closely related species and is characterised by the formation of large (> 20 μ m) conidia (Fig. 12) (Liu et al. 2014). Species of this complex can be either pathogens or endophytes. A combined analyses of ACT, CHS-1, GAPDH, ITS and TUB2 sequences of this complex is given in Fig. 13. All species within this complex can be identified by any of these five genes (Liu et al. 2014).



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Fig. 9 One of the two most parsimonious trees obtained from a heuristic search of combined ITS, GAPDH, CHS-1, ACT and TUB2 sequence data of taxa from the dematium species complex. Parsimony bootstrap support values above 50 % are indicated at the nodes and branches with Bayesian posterior probabilities above 0.95 are given in bold. The ex-type strains are in bold. The tree is rooted with *C. nigrum* CBS 169.49.



Fig. 10 *Colletotrichum destructivum* (from ex-type strain CBS 136228, on SNA) a–b. Conidiophores c. Conidia d–i. Appressoria. Scale bars: c, d = 10µm; scale bar of c and d applies to a–i (Courtesy of U. Damm).

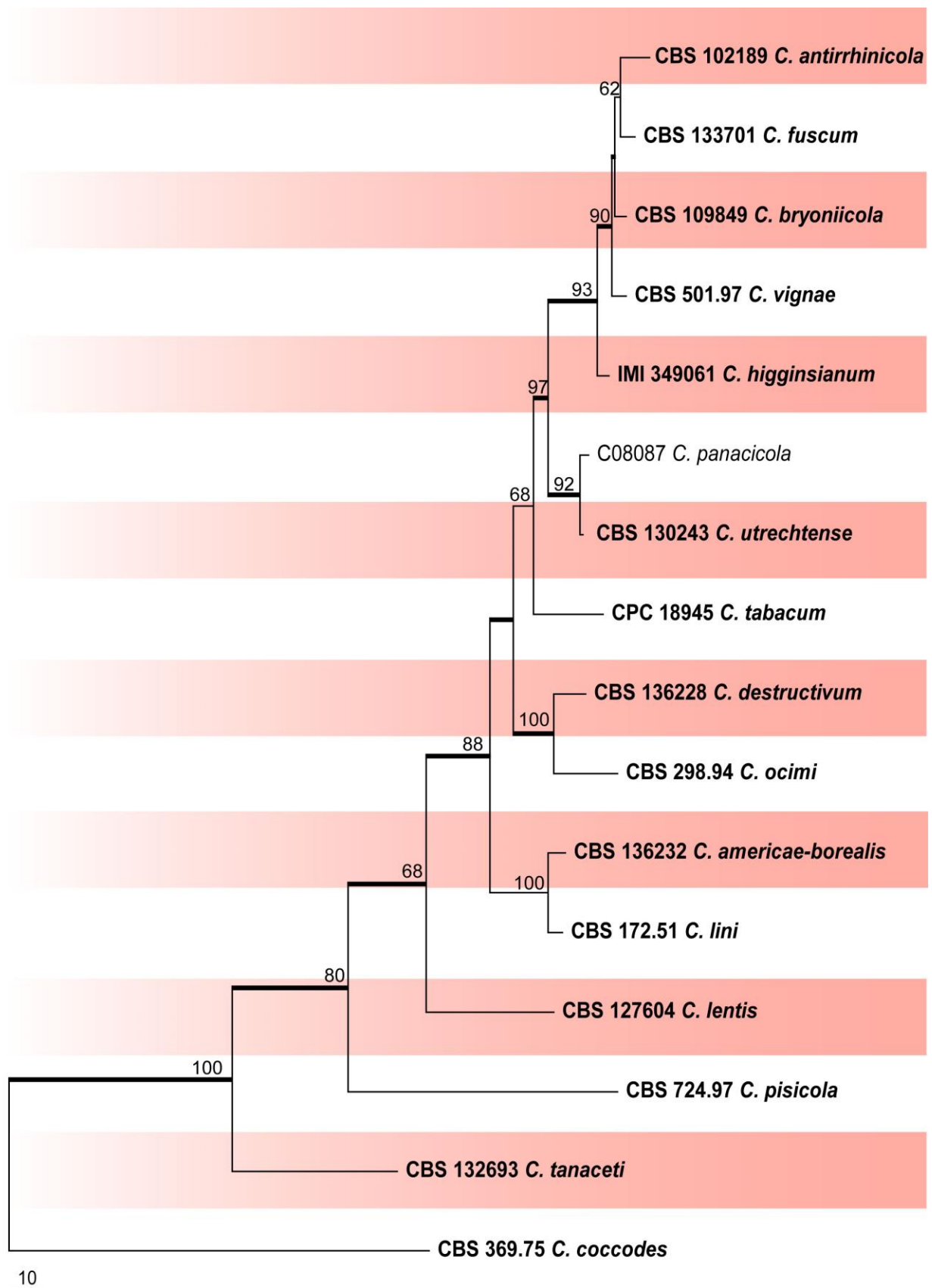


Fig. 11 One of the two most parsimonious trees obtained from a heuristic search of combined ITS, GAPDH, CHS-1, HIS3, ACT and TUB2 sequence data of taxa from the destructivum species complex. Parsimony bootstrap support values above 50 % are indicated at the nodes and branches with Bayesian posterior probabilities above 0.95 are given in bold. The ex-type strains are in bold. The tree is rooted with *C. coccodes* CBS 369.75.

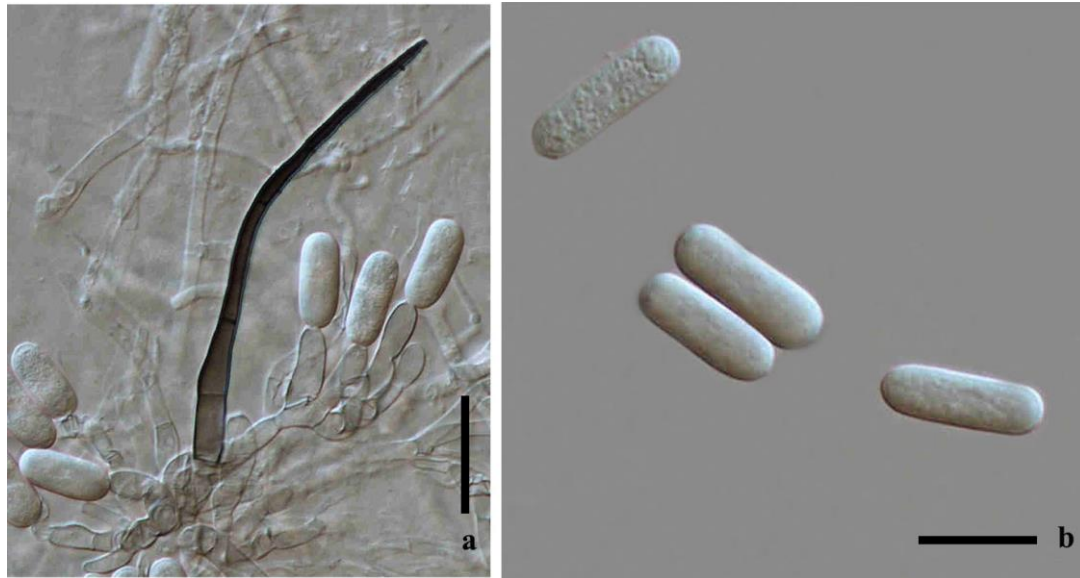


Fig. 12 *Colletotrichum gigasporum* (from strain CBS 181.52, on SNA) a. Conidiophores and a seta b. Conidia. Scale bars: a–b = 10 μ m (Courtesy of F. Liu).

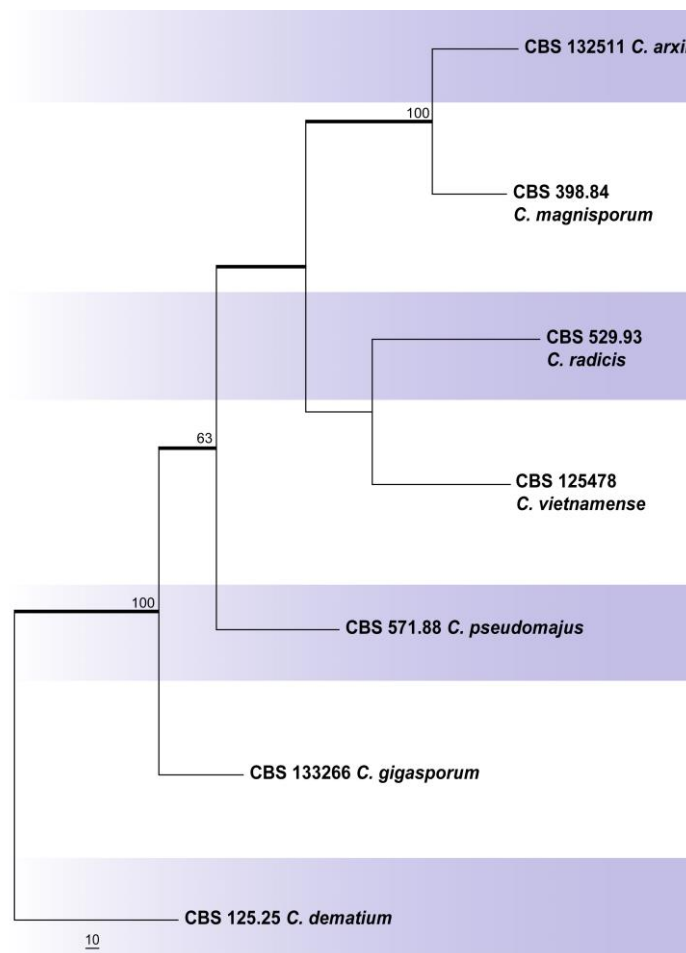


Fig. 13 One of the two most parsimonious trees obtained from a heuristic search of combined ACT, CHS-1, GAPDH, ITS and TUB2 sequence data of taxa from the gigasporum species complex. Parsimony bootstrap support values above 50 % are indicated at the nodes and branches with Bayesian posterior probabilities above 0.95 are given in bold. The ex-type strains are in bold. The tree is rooted with *C. dematium* CBS 125.25.

Gloeosporioides species complex

The gloeosporioides species complex is a collective of *C. gloeosporioides* and 37 closely related species (Fig. 14). This species complex mainly consists of plant pathogens (Weir et al. 2012), but some species were isolated as endophytes (Liu et al. 2015a). Conidia of this species complex are cylindrical with rounded ends tapering slightly towards the base (Fig. 13) (Weir et al. 2012). Based on the multigene phylogeny, Weir et al. (2012) recognized two subclades within the species complex, namely kahawae and musae (Fig. 15). A combination of *ApMat* and GS sequences can be used to distinguish the species within this complex (Liu et al. 2015a). A phylogenetic tree constructed using *ApMat* gene alone for this complex is given in Fig. 16.

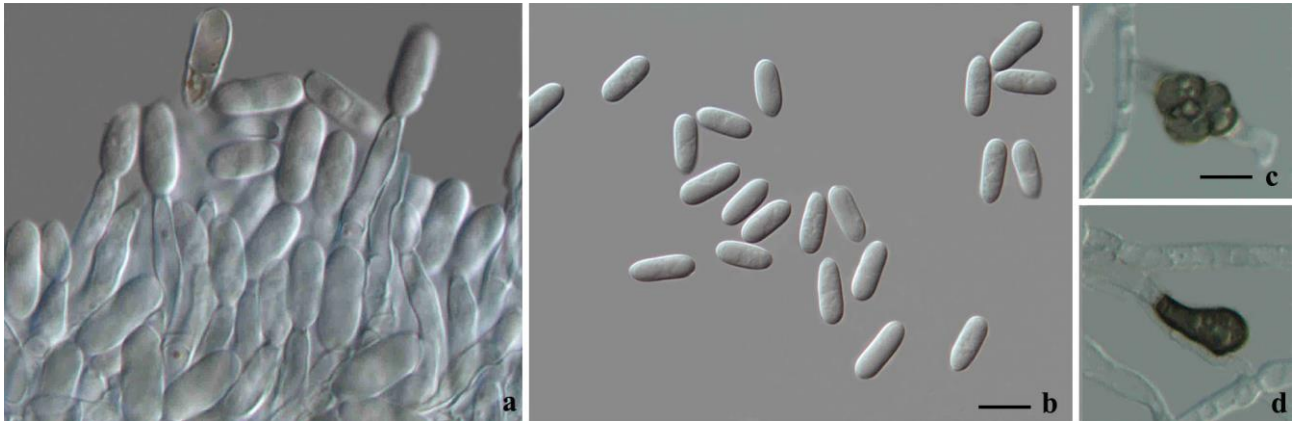


Fig. 14 *Colletotrichum gloeosporioides* (from strain CGMCC 3.17360, on SNA). a. Conidiogenous cells b. Conidia c–d. Appressoria. Scale bars: b, c = 10 μ m; scale bar of b and c applies to a–d (Courtesy of F. Liu).

Graminicola species complex

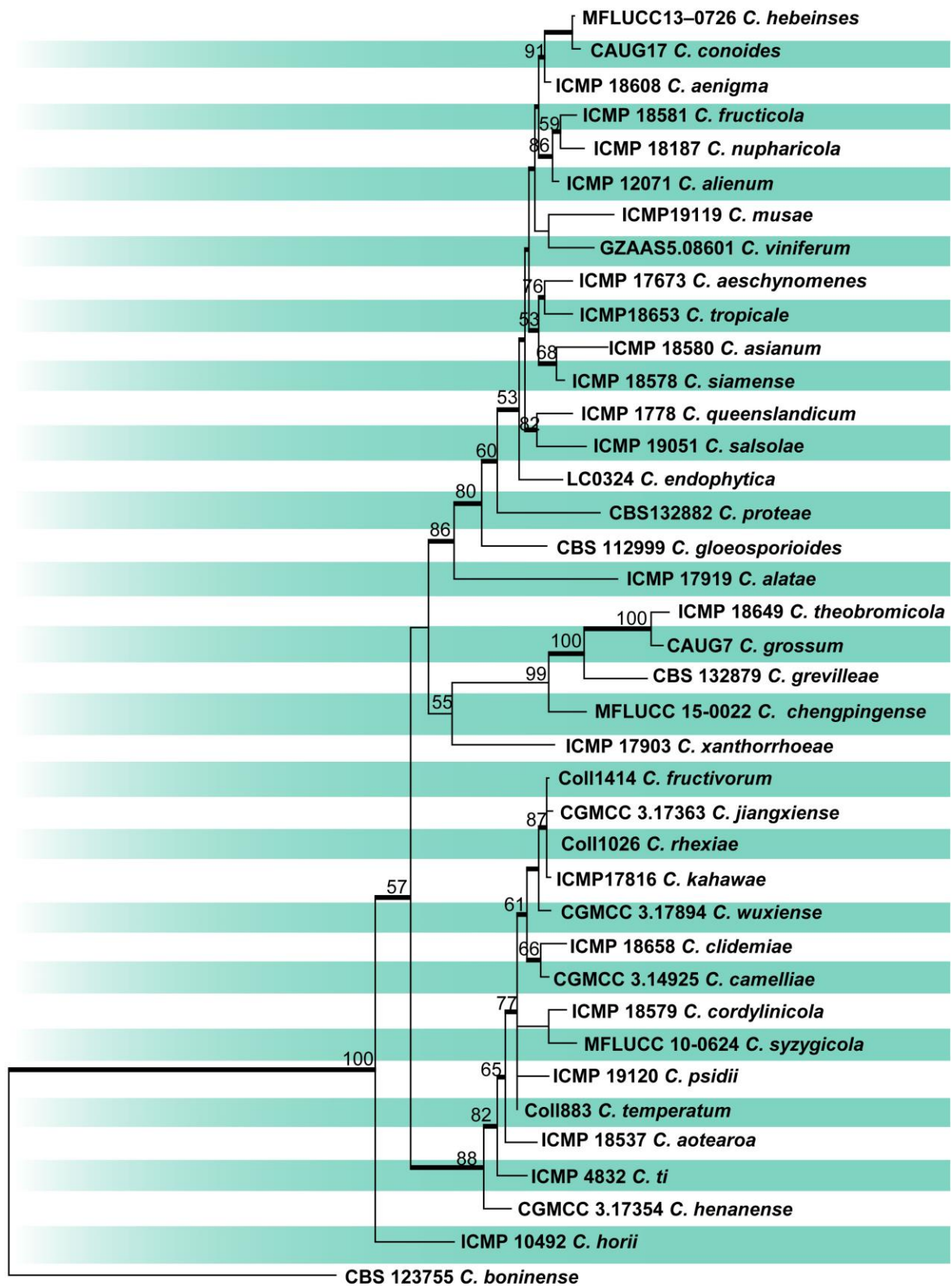
The graminicola species complex includes *C. graminicola* and 14 closely related species that are only associated with certain grasses (*Poaceae*) and form a monophyletic clade (Cannon et al. 2012). Species are characterized by widely falcate conidia (Fig. 17) (Crouch et al. 2009a). Several species of this complex are important pathogens. Results of a combined analysis of ITS, GAPDH, CHS-1, ACT and TUB2 sequence data are presented in Fig. 18.

Orbiculare species complex

The orbiculare species complex includes *C. orbiculare* and seven closely related species that are plant pathogens and are restricted to specific herbaceous host genera or species (Damm et al. 2013). The lifestyle of these species has been characterized as hemibiotrophic (Goodwin 2001, Damm et al. 2013). Members of the orbiculare species complex form conidia that are straight and relatively broad and short. Appressoria of these species are small and simple in outline (Fig. 19) (Damm et al. 2013). Results of a combined analysis of ITS, GAPDH, CHS-1, ACT, HIS3, TUB2 and GS sequence data are presented in Fig. 20. All species in this complex can be identified based on GS sequences alone (Damm et al. 2013).

Spaethianum species complex

The spaethianum species complex includes *C. spaethianum* and nine closely related species. Species in this species complex form complex appressoria (Fig. 21) (Damm et al. 2009). A multigene analysis comprised of ITS, GAPDH, CHS-1, ACT, HIS3 and TUB2 is given in Fig. 22.



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Fig. 15 One of the ten most parsimonious trees obtained from a heuristic search of combined ACT, TUB2, CAL, CHS-1, GAPDH and ITS sequence data for taxa from the gloeosporioides species complex. Parsimony bootstrap support values above 50 % are indicated at the nodes and branches with Bayesian posterior probabilities above 0.90 are given in bold. The ex-type strains are in bold. The tree is rooted with *C. boninense* CBS 123755.

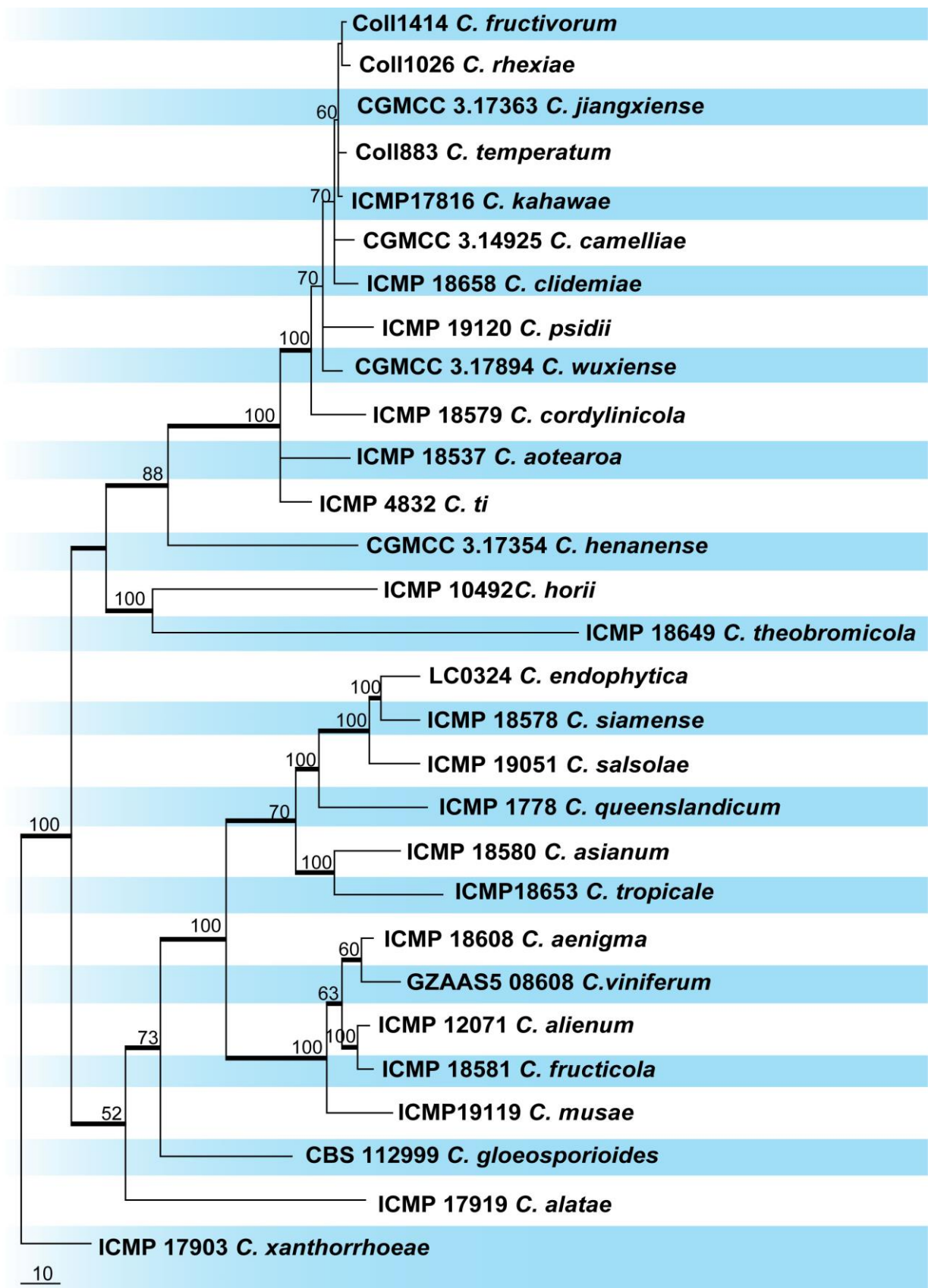


Fig. 16 One of the two most parsimonious trees obtained from a heuristic search of *Apmat* sequence data of taxa from the gloeosporioides species complex. Parsimony bootstrap support values above 50 % are indicated at the nodes and branches with Bayesian posterior probabilities above 0.80 are given in bold. The ex-type strains are in bold. The tree is rooted with *C. xanthorrhoeae* ICMP 17903.

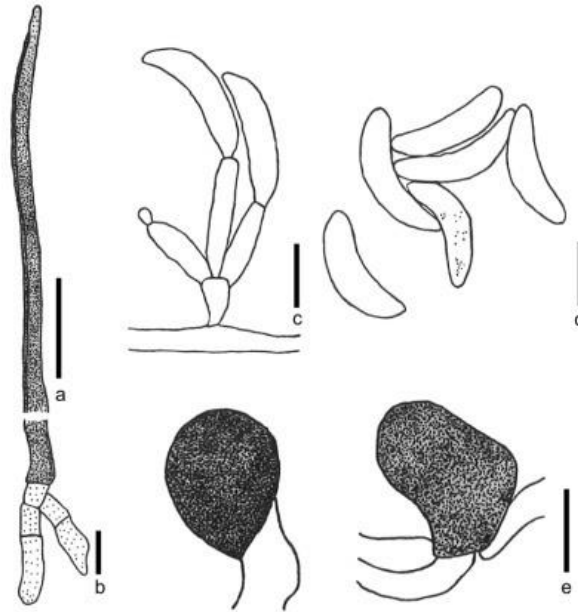


Fig. 17 *Colletotrichum graminicola* redrawn from Politis (1975) and Panaccione et al. (1989). a. Tip of a seta b. Base of a seta c. Conidiogenous cells d. Conidia e. Appressoria. Scale bars: a, b = 20 μ m, c = 5 μ m.

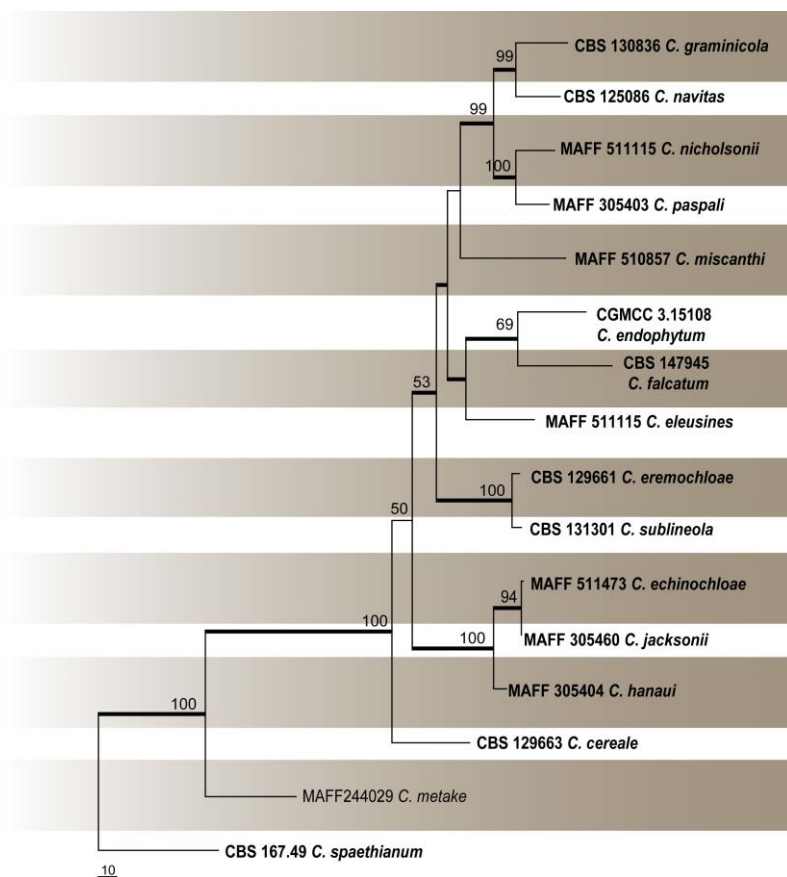


Fig. 18 One of the two most parsimonious trees obtained from a heuristic search of combined ITS, GAPDH, CHS-1, ACT and TUB2 sequence data of taxa from the *graminicola* species complex. Parsimony bootstrap support values above 50 % are indicated at the nodes and branches with Bayesian posterior probabilities above 0.95 are given in bold. The ex-type strains are in bold. The tree is rooted with *C. spaethianum* CBS 167.49.



Fig. 19 *Colletotrichum orbiculare* (a, d–h from ex-type strain CBS 570.97, b–c from strain CBS 133196, on SNA) a–c. Conidiophores d. Conidia e–h. Appressoria. Scale bars: d, e = 10µm; scale bar of d and e applies to a–h (Courtesy of U. Damm).

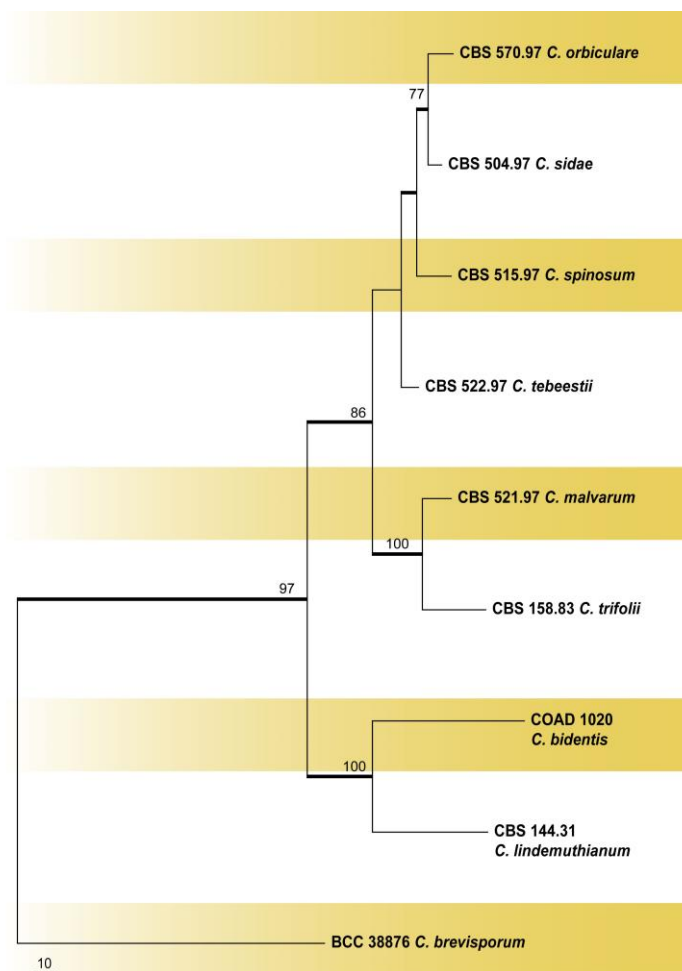


Fig. 20 One of the two most parsimonious trees obtained from a heuristic search of combined ITS, GAPDH, CHS-1, ACT, HIS3, TUB2 and GS sequence data of taxa from the orbiculare species complex. Parsimony bootstrap support values above 50 % are indicated at the nodes and branches with Bayesian posterior probabilities above 0.90 are given in bold. The ex-type strains are in bold. The tree is rooted with *C. brevisporum* BCC 38876.

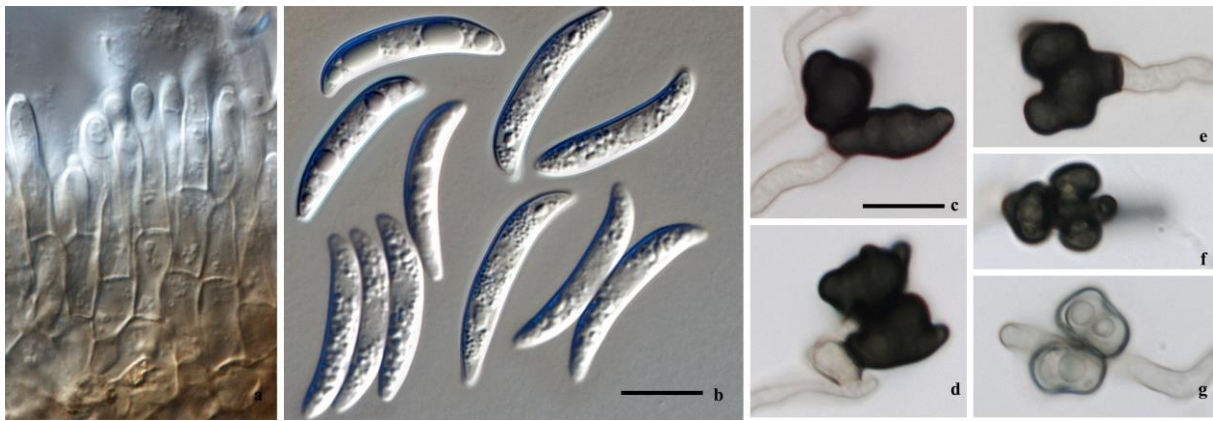


Fig. 21 *Colletotrichum spaethianum* (a, c–g from CBS 1100063, b from ex-type strain CBS 167.49, on SNA) a. Conidiophores b. Conidia c–g. Appressoria. Scale bars: a–c = 10 μ m (Courtesy of U. Damm).

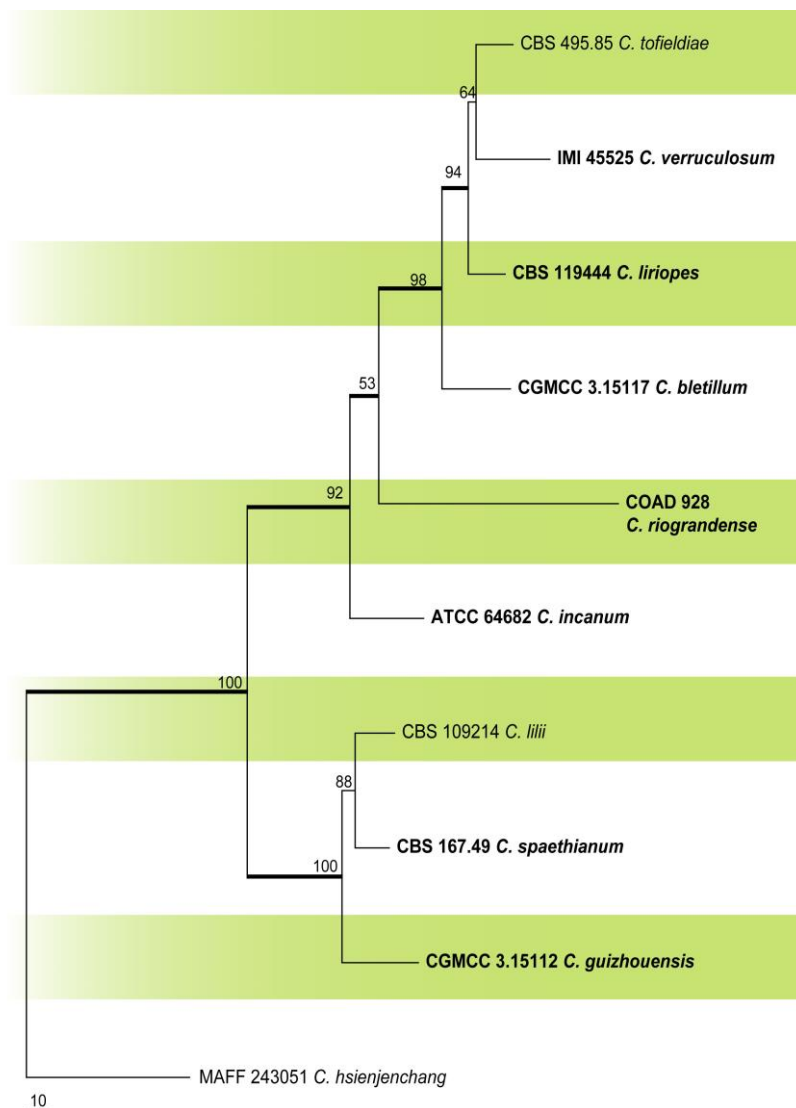


Fig. 22 The most parsimonious tree obtained from a heuristic search of combined ITS, GAPDH, CHS-1, ACT, HIS3 and TUB2 sequence data of taxa from the *spaethianum* species complex. Parsimony bootstrap support values above 50 % are indicated at the nodes and branches with Bayesian posterior probabilities above 0.95 are given in bold. The ex-type strains are in bold. The tree is rooted with *C. hsienjenchang* MAFF 243051.

Truncatum species complex

The truncatum species complex includes *C. truncatum* and three closely related species that are pathogens (Damm et al. 2009, Wikee et al. 2011). This complex can be distinguished by their curved conidia with truncated base and acute, more strongly curved apex. Presence of appressoria in groups and dense clusters is also characteristic (Fig. 23) (Damm et al. 2009). A combined analysis of ITS, GAPDH, CHS-1, ACT, HIS3 and TUB2 sequences is given in Fig. 24.



Fig. 23 *Colletotrichum truncatum* (a–c from ex-type strain CBS 151. 35, d–f from strain CBS 120709, on SNA). a. Tip of the seta b. Base of the seta c. Conidiophores d. Conidia e. Appressoria. Scale bars: a,e = 10 μ m (Courtesy of U. Damm).

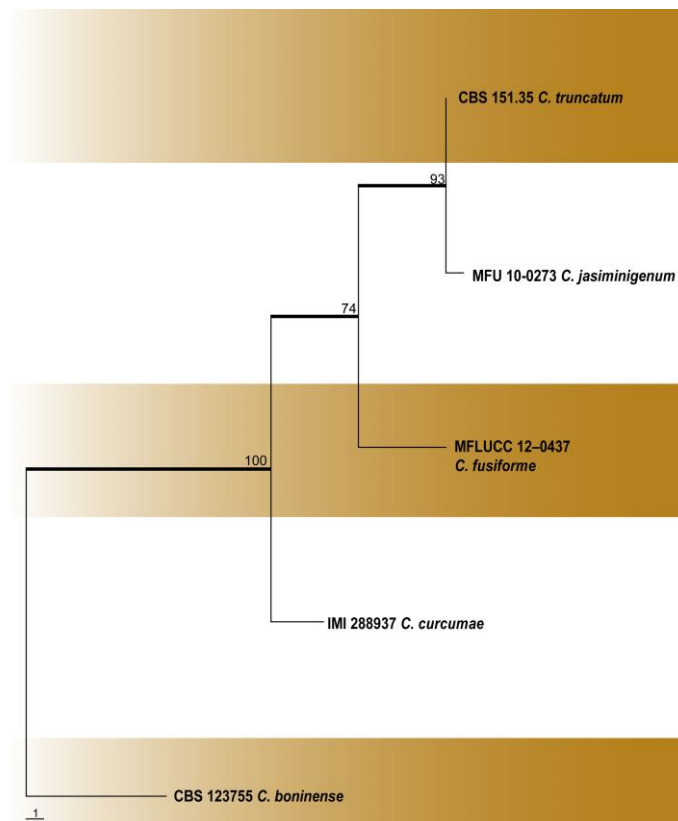


Fig. 24 The most parsimonious tree obtained from a heuristic search of combined ITS, GAPDH, CHS-1, ACT, HIS3 and TUB2 sequence data of taxa from the truncatum species complex. Parsimony bootstrap support values above 50 % are indicated at the nodes and branches with Bayesian posterior probabilities above 0.95 are given in bold. The ex-type strains are in bold. The tree is rooted with *C. boninense* CBS 123755.

Other taxa

There are several species that do not belong to any of these species complexes. These species are referred in this paper as singleton species, following the term used in Hyde et al. (2014).

Accepted species of *Colletotrichum* with notes

1. *Colletotrichum abscissum* Pinho & O.L. Pereira, *Persoonia*, *Mol. Phyl. Evol. Fungi* 34: 237 (2015)

This species has been recorded as a pathogen on *Citrus sinensis* causing postbloom fruit drop disease and on *Psidium guajava* in Brazil and the USA (Crous et al. 2015, Bragança et al. 2016). *Colletotrichum abscissum* belongs to the acutatum species complex and is phylogenetically closely related to *C. tamarilloi* and *C. costaricense* (Crous et al. 2015).

2. *Colletotrichum acerbum* Damm, P.F. Cannon & Crous, *Stud. Mycol.* 73: 43 (2012)

This taxon causes bitter rot of *Malus domestica* in New Zealand and seems to be endemic (Damm et al. 2012b). *Colletotrichum acerbum* belongs to the acutatum species complex and is a sister taxon to *C. rhombiforme* (Damm et al. 2012b). According to Damm et al. (2012b) this species can distinguished most effectively with TUB2 and ITS.

3. *Colletotrichum acutatum* J.H Simmonds, *Queensland J. agric. Anim. Sci.* 22: 458 (1965)

This taxon mainly causes fruit rots on a wide range of plants including the families *Anacardiaceae*, *Apocynaceae*, *Campanulaceae*, *Caricaceae*, *Fabaceae*, *Oleaceae*, *Pinaceae*, *Plumbaginaceae*, *Polemoniaceae*, *Proteaceae*, *Ranunculaceae*, *Rosaceae*, *Rubiaceae*, and *Solanaceae* worldwide (Damm et al. 2012b). *Colletotrichum acutatum* is the representative species of the acutatum species complex, and can be separated with the use of any of the genes (ITS, GAPDH, CHS-1, HIS3, ACT or TUB2) used in Damm et al. (2012b).

4. *Colletotrichum aenigma* B. Weir & P.R. Johnst., *Stud. Mycol.* 73: 135 (2012)

This species belongs to the gloeosporioides species complex and has been recorded as a pathogen on *Camellia sinensis* in China (Wang et al. 2016), *Persea americana* in Israel, *Pyrus pyrifolia* in Japan (Weir et al. 2012), *Olea europaea* in Italy, *Poplar* sp. in China and the USA, and on *Vitis vinifera* in China (Schena et al. 2014, Yan et al. 2015). *Colletotrichum aenigma* can be distinguished with the use of TUB2 or GS gene sequences (Weir et al. 2012).

5. *Colletotrichum aeshynomenes* B. Weir & P.R. Johnst., *Stud. Mycol.* 73: 135 (2012)

Colletotrichum aeshynomenes has been recorded only from the USA and is a pathogen of *Aeshynomene virginica* (Weir et al. 2012). It belongs to the musae clade of the gloeosporioides species complex and is genetically close to *C. siamense*. This species can be distinguished with the use of TUB2, GAPDH or GS gene sequences (Weir et al. 2012). *Colletotrichum aeshynomenes* has been developed as a weed control agent named “Collego” (Ditmore et al. 2008).

6. *Colletotrichum agaves* Cavara, *Fung. Long. Exsicc.* 3: no. 100 (1892)

It has been recorded as a pathogen on *Agave* species in Cuba, El Salvador, Haiti, Italy, Jamaica, Mexico, the Netherlands and the USA (Farr et al. 2006). ITS sequence data show this taxon to be a distinctive singleton species and can be easily distinguished from the other *Colletotrichum* species on *Agavaceae* by the conidiomata with numerous black setae (Farr et al. 2006).

7. *Colletotrichum alatae* B. Weir & P.R. Johnst., *Stud. Mycol.* 73: 135 (2012)

Colletotrichum alatae has been recorded from India and Nigeria as a pathogen of Yam (*Dioscorea alata*) (Weir et al. 2012). This species belongs to the gloeosporioides species complex. ITS sequence data can distinguish *C. alatae* from all other taxa (Weir et al. 2012).

8. *Colletotrichum alcornii* J.A. Crouch, *IMA Fungus* 5(1):27 (2014)

This taxon is known as a pathogen on *Imperata cylindrica* and *Bothriochloa bladhii* in Australia and belongs to the caudatum species complex (Crouch 2014). This species can be identified using any of the gene regions (*Apn2*, ITS, *Sod2*, *Mat/Apn2*) used in Crouch (2014).

9. *Colletotrichum alienum* B. Weir & P.R. Johnst., *Stud. Mycol.* 73: 139 (2012)

This species is known from a wide range of introduced fruit crops such as *Banksia dryandroides*, *Camellia sinensis*, *Diospyros kaki*, *Grevillea* sp., *Leucospermum* sp., *Malus domestica*, *Nerium*

oleander, *Persea americana*, *Protea* sp., *Serruria* sp. and *Telopea* sp. in Australia, China, Hawaii, New Zealand, Portugal, South Africa and Zimbabwe (Weir et al. 2012, Crous et al. 2013a, Liu et al. 2013b, 2015a, Schena et al. 2014). *Colletotrichum alienum* cannot be distinguished by morphological characters; ITS sequences do not separate it from *C. siamense* isolates. This taxon is best distinguished using CAL or GS gene regions (Weir et al. 2012, Liu et al. 2015a). It belongs to the gloeosporioides species complex.

10. *Colletotrichum americae-borealis* Damm, in Damm, O'Connell, Groenewald & Crous, Stud. Mycol. 79: 55 (2014)

This taxon belongs to the destructivum species complex and has been recorded only as a pathogen on *Medicago sativa* in the USA (Damm et al. 2014). Conidial shape of this species is similar to the conidia of *C. lini*, but it differs in having more complex appressoria. In contrast with most species of the destructivum complex, setae of this species are very abundant (Damm et al. 2014). TUB2, CHS-1, HIS3 and ACT sequence data can be used to distinguish it from other species in the destructivum complex (Damm et al. 2014).

11. *Colletotrichum annellatum* Damm, P.F. Cannon & Crous, Stud. Mycol. 73: 6 (2012)

This species has been recorded from *Hevea* sp. in Colombia. As its name suggests, *C. annellatum* produces conidiogenous cells that have annellid-like proliferations (Damm et al. 2012a). It belongs to the boninense species complex and is sister to the clade that contains *C. citricola*, *C. karstii* and *C. phyllanthi* (Damm et al. 2012a).

12. *Colletotrichum anthrisci* Damm, P.F. Cannon & Crous, in Damm, Woudenberg, Cannon & Crous, Fungal Diversity 39: 56 (2009)

Colletotrichum anthrisci is only known from *Anthriscus sylvestris* in the Netherlands (Damm et al. 2009). It belongs to the dematium species complex and has angular conidia, in which the apex is strongly pointed (Damm et al. 2009). This species differs from other species in this complex in having a constricted base of setae and very long, navicular appressoria (Damm et al. 2009, Yang et al. 2012a). *Colletotrichum anthrisci* has been found in association with stem lesions, as well as on dead stems of *Anthriscus sylvestris*.

13. *Colletotrichum antirrhinicola* Damm, in Damm, O'Connell, Groenewald & Crous, Stud. Mycol. 79: 56 (2014)

It is only known from a leaf of *Antirrhinum majus* in New Zealand (Damm et al. 2014). *Colletotrichum antirrhinicola* belongs to the destructivum complex and can be identified by its unique GAPDH and ITS sequence data.

14. *Colletotrichum aotearoa* B. Weir & P.R. Johnst., Stud. Mycol. 73: 139 (2012)

Colletotrichum aotearoa is known from Australia, India, Taiwan and New Zealand (Weir et al. 2012, Liu et al. 2013b, Sharma et al. 2015, Hsiao et al. 2016). It is common on taxonomically diverse native plants (*Banksia marginata*, *Bredia oldhamii*, *Coprosma* sp., *Dacrydium dacrydioides*, *Knightia* sp., *Musa* sp., *Podocarpus totara* and *Vitex lucens*) as a pathogen causing fruit rot and also as an endophyte on naturalized weeds (*Boehmeria* sp.) (Weir et al. 2012, Liu et al. 2013b, Tao et al. 2013, Sharma et al. 2015, Hsiao et al. 2016). An endophytic strain (BCRC 09F0161) of this species from leaves of *Bredia oldhamii*, is capable of producing 18 secondary metabolites (Hsiao et al. 2016). *Colletotrichum aotearoa* belongs to the kahawae clade of the gloeosporioides species complex. This species is morphologically indistinguishable from *C. kahawe* subsp. *ciggaro*. It can be phylogenetically distinguished with TUB2, CAL, GS and GAPDH sequence data (Weir et al. 2012). Sharma et al. (2015) showed that this species can be well-resolved from other species of the gloeosporioides complex with the *ApMat* gene region.

15. *Colletotrichum aracearum* LW. Hou & L. Cai, Mycosphere 7(8): 1115 (2016)

This species has been recorded from *Monstera delociosa* and *Philodendron selloum* in China (Hou et al. 2016). It is a singleton species with close affinity to *C. cliviae*. Sexual morph of this species has been observed.

16. *Colletotrichum arxii* F. Liu, L. Cai, Crous & Damm, Persoonia, Mol. Phyl. Evol. Fungi 33: 87 (2014)

This species is known as an endophyte on *Oncidium excavatum* in the Netherlands and on *Paphiopedilum* sp. in Germany (Liu et al. 2014). *Colletotrichum arxii* belongs to the gigasporum species complex and can be identified with ITS and TUB2 sequences.

17. *Colletotrichum asianum* Prihastuti, L. Cai & K.D. Hyde, Fungal Diversity 39: 96 (2009)

This taxon is known as a pathogen of *Mangifera indica* in Australia (Rojas et al. 2010), Brazil (Lima et al. 2013, Veira et al. 2014a), Colombia (Afanador-Kafuri et al. 2003, Hoz et al. 2016), Ghana (Honger et al. 2014), India (Liu et al. 2015a), Japan, Malaysia, Panama, the Philippines, South Africa, Sri Lanka and Thailand. It is also reported to cause anthracnose on *Capsicum annuum* in Laos (Phoulivong et al. 2010) and reported as a pathogen of *Coffea arabica* in Thailand (Weir et al. 2012, Krishnapillai & Wijeratnam 2014, Sharma et al. 2013, 2015, Zakaria et al. 2015). *Colletotrichum asianum* belongs to the gloeosporioides species complex (Weir et al. 2012). This species can be distinguished by all other taxa using ITS or any of the genes tested (ACT, TUB2, CAL, CHS-1, GAPDH) in Weir et al. (2012).

18. *Colletotrichum australe* Damm, P.F. Cannon & Crous, Stud. Mycol. 73: 57 (2012)

This species is a pathogen on *Trachycarpus fortunei* in Australia and *Hakea* sp. in South Africa (Damm et al. 2012b). It belongs to the acutatum species complex and can be distinguished with ITS, TUB2, ACT and HIS3 sequences; most effectively with HIS3 (Damm et al. 2012b).

19. *Colletotrichum axonopodi* J.A. Crouch, B.B. Clarke, J.F. White & B.I. Hillman, Mycologia 101(5): 727 (2009)

This species has a unique association with the temperate grass, *Axonopus* and has been reported as a pathogen on *Axonopus* in Australia and Honduras, Georgia and Louisiana states of the USA (Crouch et al. 2009a). It is morphologically similar to other *Colletotrichum* species associated with grasses and is sister to the clade that contains *C. echinocloae*, *C. hanau* and *C. jacksonii* belonging to the graminicola complex (Crouch et al. 2009a).

20. *Colletotrichum baltimoreense* J.A. Crouch, IMA Fungus 5(1): 27 (2014)

This taxon has only been recorded as a pathogen on leaves of *Sorghastrum nutans* in the USA (Crouch 2014). *Colletotrichum baltimoreense* belongs to the caudatum species complex. This species can be identified using any of the gene regions (*Apn2*, ITS, *Sod2*, *Mat/Apn2*) used in Crouch (2014).

21. *Colletotrichum beeveri* Damm, P.F. Cannon, Crous, P.R. Johnst & B. Weir, Stud. Mycol. 73: 9 (2012)

This species has been recorded as a pathogen of *Brachyglottis repanda* in New Zealand (Damm et al. 2012a), as well as an endophyte of *Pleione bulbocodioides* and possibly also of *Podocarpaceae* in China (Damm et al. 2012a, Yang et al. 2011). *Colletotrichum beeveri* belongs to the boninense species complex and forms a sister group to *C. brassicicola* and *C. colombiense* (Damm et al. 2012a). It can be distinguished by any of the gene regions used in Damm et al. (2012a) except for ITS and GAPDH.

22. *Colletotrichum bidentis* Damm, Guatimosim & Vieira, Fungal Diversity 61: 34 (2013)

This species is pathogenic on *Bidentis* sp. in Brazil and belongs to the orbiculare species complex. This taxon can be distinguished from the other species in the orbiculare species complex by its slightly curved conidia and setae with a conspicuous white tip (Damm et al. 2013) and it can be distinguished with the use of GS or GAPDH gene sequences.

23. *Colletotrichum bletillae* G. Tao, Zuo Y. Liu & L. Cai [as 'bletillum'], in Tao, Liu, Liu, Gao & Cai, Fungal Diversity 61: 144 (2013)

This species is an endophyte of *Bletilla ochracea* in China, and belongs to the spaethianum species complex (Tao et al. 2013). *Colletotrichum bletillum* closely related to *C. liriopes* (Tao et al. 2013). It can be distinguished by any of the gene regions (ITS, ACT, GAPDH and TUB2) used in Tao et al. (2013).

24. *Colletotrichum boninense* Moriwaki, Toy. Sato & Tsuki, Mycoscience 44: 48 (2003)

Colletotrichum boninense is a pathogen and an endophyte, occurring on a high diversity of host plants belonging to *Amaryllidaceae*, *Annonaceae*, *Bignoniaceae*, *Lauraceae*, *Olivaceae*, *Orchidaceae*, *Piperaceae*, *Podocarpaceae*, *Protaceae*, *Rubiaceae*, *Rutaceae*, *Solanaceae* and

Theaceae (Silva-Rojas et al. 2011, Diao et al. 2013, Feritas et al. 2013, Peng et al. 2012, Tao et al. 2013, Afanador-Kafuri et al. 2014, Alvarez et al. 2014, Mosca et al. 2014). Ascospores of this species are uniform with rounded ends, becoming brown and septate with age (Damm et al. 2012a). It is the reference species of the boninense species complex.

25. *Colletotrichum brasiliense* Damm, P.F. Cannon, Crous & Massola, Stud. Mycol. 73: 11 (2012) This species is only known as a pathogen on *Passiflora edulis* in Brazil (Tozze et al. 2010). *Colletotrichum brasiliense* belongs to the boninense species complex and is closely related to *C. parsoniae* and *C. hippeastri* (Damm et al. 2012a). This taxon can be distinguished from the other species with the use of ACT, GAPDH, ITS and TUB2 sequences (Damm et al. 2012a).

26. *Colletotrichum brassicicola* Damm, P.F. Cannon & Crous, Stud. Mycol. 73: 14 (2012) The taxon has been reported from leaf spots of *Brassica oleraceae* in New Zealand (Damm et al. 2012a) and from *Rubus glaucus* in Colombia (Afanador-Kafuri et al. 2014). It belongs to the boninense species complex and is distinct in having very short conidia and longer asci and ascospores compared to the other species with known sexual morphs in the complex (Damm et al. 2012a). It can be distinguished by any of the gene regions used in Damm et al. (2012a) except for ITS and GAPDH.

27. *Colletotrichum brevisporum* Noireung, Phouliv., L. Cai & K.D. Hyde, Cryptog. Mycol. 33(3): 350 (2012)

This species is a pathogen on *Carica papaya* and *Sechium edule* in Brazil (Vieira et al. 2013, Bezerra et al. 2016), *Citrus medica* in China (Peng et al. 2012), and *Neoregelia* sp. and *Pandanus pygmaeus* in Thailand (Liu et al. 2014). *Colletotrichum brevisporum* has been recorded as an endophyte of *Lycium chinense* in Korea (Paul et al. 2014). It is a singleton species. This taxon forms a sister group to *C. cliviae* (Noireung et al. 2012, Hyde et al. 2014).

28. *Colletotrichum brisbanense* Damm, P.F. Cannon & Crous, Stud. Mycol. 73: 59 (2012)

This pathogenic species is known to cause fruit rot in *Capsicum annuum* in Australia. It differs from *C. scovillei*, another anthracnose pathogen of *Capsicum annuum*, in appressoria size (Damm et al. 2012b). *Colletotrichum brisbanense* belongs to the acutatum species complex and can be distinguished effectively with the use of TUB2 and GAPDH (Damm et al. 2012b).

29. *Colletotrichum bryoniicola* Damm, in Damm, O'Connell, Groenewald & Crous, Stud. Mycol. 79: 57 (2014)

It is a saprobe known from decaying leaves of *Bryonia dioica* in the Netherlands (Damm et al. 2014). *Colletotrichum bryoniicola* belongs to the destructivum species complex and can be distinguished from closely related species by its ITS, GAPDH, HIS3 and TUB2 sequence data, as well as by its broader conidia ($\geq 4\mu\text{m}$ on SNA) and distinct conidiogenous cells (Damm et al. 2014).

30. *Colletotrichum cairnsense* D.D. De Silva, R. Shivas & P.W.J Taylor, Plant pathology [http://doi: 10.1111/ppa.12572](http://doi:10.1111/ppa.12572) (2016)

It is a pathogen of *Capsicum annuum* in Australia and belongs to the acutatum species complex (De Silva et al. 2016). This species can be distinguish from the other species of the acutatum complex with GAPDH and TUB2 sequence data.

31. *Colletotrichum camelliae* Masee, Bull. Misc. Inf., Kew: 91 (1899)

This taxon is responsible for causing twig blight and brown blight of *Camellia* sp. in China, Sri Lanka, the UK and the USA (Liu et al. 2015a, Wang et al. 2016). *Colletotrichum camelliae* belongs to the kahawae clade within the gloeosporioides complex and can be distinguished with the use of GS and ApMat gene sequences. *Glomerella cingulata* "f. sp. *camelliae*" has been synonymized with *C. camelliae* (Liu et al. 2015a).

32. *Colletotrichum camelliae-japonicae* LW. Hou & L. Cai, Mycosphere 7(8): 1117 (2016)

This species is a pathogen on *Camellia japonica*. It was isolated from *C. japonica* imported from Japan (Hou et al. 2016). *C. camelliae-japonicae* belongs in the boninense species complex. Sexual morph of this species has been observed.

33. *Colletotrichum carthami* (Fukui) S. Uematsu, Kageyama, Moriwaki & Toy. Sato, J. Gen. Pl. Path. 78(5): 326 (2012)

This species is known to be pathogenic on *Calendula officinalis* in Italy, Japan (Baroncelli et al. 2015a) and on *Carthamus tinctorius* causing leaf blight, in Japan (Uematsu et al. 2012), as well as on *Chrysanthemum coronarium* var. *spatiosum* in Korea (Uematsu et al. 2012). *Colletotrichum carthami* belongs in the acutatum species complex (Damm et al. 2012b).

34. *Colletotrichum caudatum* (Peck ex Sacc.) Peck, Bull. N.Y. St. Mus. 131: 81 (1909)

The distribution of this species is limited to *Sorghastrum nutans* in the mid-Atlantic states of the USA (Crouch 2014). This taxon belongs to the caudatum species complex and is the representative species of the complex (Crouch 2014). This species can be identified using any of the gene regions (*Apn2*, ITS, *Sod2*, *Mat/Apn2*) used in Crouch (2014).

35. *Colletotrichum caudasporum* G. Tao, Zuo Y. Liu & L. Cai [as 'caudasporum'], in Tao, Liu, Liu, Gao & Cai, Fungal Diversity 61: 149 (2013)

This taxon is an endophyte of *Bletilla ochraceae* in China (Tao et al. 2013). *Colletotrichum caudasporum* belongs to the caudatum species complex (this paper). It can be distinguished with the ITS sequences data.

36. *Colletotrichum cereale* Manns, in Selby & Manns, Proc. Indiana Acad. Sci.: 111 (1908)

It is a pathogen of grasses (*Poaceae*) of the subfamily Pooideae in Germany, Japan, New Zealand, the Netherlands and the USA (Young et al. 2008, Crouch & Inguagiato 2009, Beirn et al. 2014) and an endophyte of *Bletilla* (*Orchidaceae*) in China (Tao et al. 2013). This species belongs to the graminicola species complex (Cannon et al. 2012, Hyde et al. 2014).

37. *Colletotrichum chengpingense* G. Zhang, Jayawardena & KD Hyde, in Jayawardena et al., Mycosphere 7(8): 1155 (2016)

It is a pathogen on *Fragaria* × *ananassa* in China, belonging to the gloeosporioides species complex (Jayawardena et al. 2016b). This species can be distinguished from its closely related species with any of the gene regions used in Jayawardena et al. (2016b).

38. *Colletotrichum chlorophyti* S. Chandra & Tandon [as 'chlorophytumi'], Curr. Sci. 34: 565 (1965)

This species is a pathogen on *Chlorophytum* sp. in India (Damm et al. 2009), *Glycine max* in the USA (Yang et al. 2012b) and *Stylosanthes hamata* in Australia (Damm et al. 2009). *Colletotrichum chlorophyti* has curved conidia and can be distinguished from other species with curved conidia as it has dark brown chlamydospores in chains and clusters (Damm et al. 2009). This is a singleton species (Cannon et al. 2012, Hyde et al. 2014).

39. *Colletotrichum chrysanthemi* (Hori) Sawada, Rep. Govt Res. Inst. Dep. Agric., Formosa 85: 81 (1943)

This taxon is a pathogen on *Chrysanthemum coronarium* in China, Japan and the Netherlands causing vascular discoloration and leaf spots (Damm et al. 2012b). It also causes anthracnose on *Carthamus tinctorius* in Italy (Baroncelli et al. 2015a). This species belongs to the acutatum species complex and differs from all the other species in the complex in having very short, conidia with acute ends and can be phylogenetically best separated with TUB2, GAPDH and HIS3 (Damm et al. 2012b).

40. *Colletotrichum circinans* (Berk.) Voglino, Annali R. Accad. Agric. Torino 49: 175 (1907)

This species is common in temperate regions as an anthracnose pathogen on *Allium* sp. It is also a pathogen on *Anthriscus sylvestris* (Germany), *Beta vulgaris* (New Zealand), and *Viola hirta* (Czech Republic) (Damm et al. 2009). *Colletotrichum spinaciae* is the sister taxon of this species. When compared with *C. spinaciae*, conidia of *C. circinans* are more strongly curved towards the truncate base and acute apex as well as dark brown, concolored seate that are often constricted and sometimes inflated above the constriction (Damm et al. 2009). It is a member of the dematium species complex (Cannon et al. 2012, Hyde et al. 2014).

41. *Colletotrichum citri* F. Huang, L. Cai, K.D. Hyde & Hong Y. Li, in Huang, Chen, Hou, Fu, Cai, Hyde & Li, Fungal Diversity 61(1): 69 (2013)

It is known on *Citrus aurantifolia* in China causing anthracnose (Huang et al. 2013) and belongs to the acutatum species complex. Huang et al. (2013) mentioned that this species is not common on *Citrus*.

42. *Colletotrichum citricola* F. Huang, L. Cai, K.D. Hyde & Hong Y. Li, in Huang, Chen, Hou, Fu, Cai, Hyde & Li, *Fungal Diversity* 61(1): 67 (2013)

This species has only been reported as a saprobe from *Citrus unshiu* in China and belongs to the boninense species complex (Huang et al. 2013). *Colletotrichum citricola* differs from its sister taxon *C. phyllanthi* in having wider conidia (5.9–6.9 µm) (Huang et al. 2013).

43. *Colletotrichum clidemiae* B.S. Weir & P.R. Johnst., in Weir, Johnston & Damm, *Stud. Mycol.* 73: 148 (2012)

This species causes leaf spots on *Clidemia hirta*, *Vitis* sp. and *Quercus* sp. in the USA and belongs to the kahawae clade within the gloeosporioides species complex (Weir et al. 2012). *Colletotrichum clidemiae* can be distinguished by ACT, GAPDH or GS sequence data (Weir et al. 2012). *ApMat* sequence data can also be used to distinguish this species within the complex (in this study).

44. *Colletotrichum cliviae* Yan L. Yang, Zuo Y. Liu, K.D. Hyde & L. Cai, in Yang, Liu, Cai, Hyde, Yu & McKenzie, *Fungal Diversity* 39: 133 (2009)

This taxon causes anthracnose on leaves of *Arundina graminifolia*, *Camellia sinensis*, *Clivia miniata* and *Cymbidium hookerianum* in China (Yang et al. 2009, 2011, Wang et al. 2016) and on *Cattleya* sp., *Calamus thwaitesii*, *Phaseolus* sp. and *Saccharum* sp. in India (Chowdappa et al. 2014). It is also an endophyte on *Camellia sinensis* and *Mangifera indica* in Brazil (Vieira et al. 2014a, Liu et al. 2015a). *Colletotrichum cliviae* forms a monophyletic lineage that is not closely related to any established clade; therefore it is a singleton species (Cannon et al. 2012, Hyde et al. 2014).

45. *Colletotrichum coccodes* (Wallr.) S. Hughes, *Can. J. Bot.* 36: 754 (1958)

This species is known as a pathogen on a wide range of plant families including *Amaranthaceae*, *Amaryllidaceae*, *Apiaceae*, *Araceae*, *Araliaceae*, *Arecaceae*, *Asteraceae*, *Cucurbitaceae*, *Euphorbiaceae*, *Fabaceae*, *Iridaceae*, *Lamiaceae*, *Malvaceae*, *Moraceae*, *Myrtaceae*, *Poaceae*, *Solanaceae* and *Theaceae* worldwide (Liu et al. 2011, Liu et al. 2013b, Garibaldi et al. 2015). It is a singleton species.

46. *Colletotrichum colombiense* Damm, P.F. Cannon & Crous, *Stud. Mycol.* 73: 16 (2012)

Colletotrichum colombiense is an endophyte of *Passiflora edulis* in Colombia. It belongs to the boninense species complex and forms a sister group to *C. beeveri* (Damm et al. 2012a).

47. *Colletotrichum conoides* Y.Z. Diao, C. Zhang, L. Cai & X.L. Liu, *Persoonia* 38: 27 (2017)

This is a pathogen of *Capsicum annuum* var. *conoides* in China. It belongs to the gloeosporioides species complex (Diao et al. 2017). *Colletotrichum conoides* can be distinguished with the use of GAPDH, ACT and TUB2 sequence data.

48. *Colletotrichum constrictum* Damm, P.F. Cannon, Crous, P.R. Johnst & B. Weir, *Stud. Mycol.* 73: 17 (2012)

This species belongs to the boninense species complex. It causes fruit rots of *Citrus limon* and *Solanum betacum* in New Zealand (Damm et al. 2012a). It differs from all other species in this complex by having broader ascospores with a lower L/W ratio (Damm et al. 2012a). This species can be identified with the use of any of the genes used in Damm et al. (2012a).

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

This taxon is a pathogen on *Cordyline* sp. in Thailand (Sharma et al. 2014) and in the USA and *Eugenia* sp. in Laos (Weir et al. 2012). Phoulivong et al. (2011) reported that the isolate from *Eugenia* was not pathogenic to *Cordyline* and vice versa. *Colletotrichum cordylinicola* belongs to the gloeosporioides species complex. ITS sequence can separate this species from all other species of this complex (Weir et al. 2012).

50. *Colletotrichum cosmi* Damm, P.F. Cannon & Crous, *Stud. Mycol.* 73: 61 (2012)

Colletotrichum cosmi is a pathogen on the seeds of *Cosmos* sp. in the Netherlands and belongs to the acutatum species complex (Damm et al. 2012b). It can be distinguished with all loci used in Damm et al. (2012b), best with GAPDH and HIS3.

51. *Colletotrichum costaricense* Damm, P. F. Cannon & Crous, *Stud. Mycol.* 73: 63 (2012)

This species is pathogenic/endophytic on *Coffea* sp. in Costa Rica and belongs to the acutatum species complex (Damm et al. 2012b). It can be differentiated from other species with TUB2, GAPDH and ACT sequences, most effectively with TUB2 sequence data (Damm et al. 2012b).

52. *Colletotrichum curcumae* (Syd. & P. Syd.) E.J. Butler & Bisby, Fungi of India: 153 (1931)

This taxon is a pathogen only on *Curcuma longa* in India (Damm et al. 2009) and belongs to the truncatum species complex (Cannon et al. 2012). *Colletotrichum curcumae* differs from all other species in producing large, brown, flattened stromata with straight setae that are aggregated in the centre, and with sparse sporulation (Damm et al. 2009).

53. *Colletotrichum cuscutae* Damm, P.F. Cannon & Crous, Stud. Mycol. 73: 64 (2012)

Colletotrichum cuscutae was recorded as a pathogen of *Cuscuta* sp. in Dominica. This species belongs to the acutatum species complex and can be identified using all the genes studied in Damm et al. (2012a) except for ITS; most effectively by TUB2 and ACT sequence data.

54. *Colletotrichum cymbidiicola* Damm, P.F. Cannon, Crous, P.R. Johnst. & B. Weir, Stud. Mycol. 73: 19 (2012)

This species is a pathogen on *Cymbidium* sp. in Australia, India, Japan and New Zealand (Damm et al. 2012a, Chowdappa et al. 2014). *Colletotrichum cymbidiicola* belongs to the boninense complex and is a sister group to *C. oncidii* (Damm et al. 2012a). It is apparently host-specific at plant genus level (Damm et al. 2012a).

55. *Colletotrichum dacrycarpi* Damm, P.F. Cannon, Crous, P.R. Johnst. & B. Weir, Stud. Mycol. 73: 19 (2012)

This taxon is an endophyte of *Dacrycarpus* sp. in New Zealand. Conidia of this species are produced within closed fruiting bodies with walls that rupture. *Colletotrichum dacrycarpi* belongs to the boninense species complex and can be identified using ITS sequence data as well as the other gene regions used in Damm et al. (2012a).

56. *Colletotrichum dematium* (Pers.) Grove, J. Bot., Lond. 56: 341 (1918)

This species occurs as a pathogen, endophyte as well as a saprobe. It has been recorded as a saprobe of *Apiaceae* in the Czech Republic and *Eryngium campestre* in France, as a pathogen of *Genista tinctoria* in the Czech Republic, *Solanum tuberosum* in Australia (Damm et al. 2009), *Bidens pilosa* in Cuba, Venezuela and West Indies, (Farr & Rossman 2016) and as an endophyte on *Vitis vinifera* in South Africa (Damm et al. 2009). This taxon is characterized by the angular shape of its conidia, the production of red pigments in fresh cultures and by its well developed sclerotium-like conidiomata (Damm et al. 2009).

57. *Colletotrichum destructivum* O'Gara, Mycologia 7(1): 38 (1915)

Colletotrichum destructivum is a pathogen on hosts in *Asteraceae*, *Convolvulaceae*, *Fabaceae*, *Magnoliaceae*, *Menispermaceae*, *Lamiaceae*, *Poaceae*, *Polygonaceae* and *Solanaceae* worldwide (Damm et al. 2014) as well as an endophyte of *Bletilla ochraceae* in China (Tao et al. 2013). *Colletotrichum destructivum* belongs to the destructivum species complex and can be distinguished by ITS, HIS3, ACT and TUB2 sequence data (Damm et al. 2014).

58. *Colletotrichum dracaenophilum* D.F. Farr & M.E. Palm, in Farr, Aime, Rossman & Palm, Mycol. Res. 110(12): 1401 (2006)

This species causes leaf anthracnose of *Dracaena* sp. in Bulgaria, China and Egypt (Farr et al. 2006, Morsy & Elshahawy 2016). It is a singleton species with close affinity to *C. yunnanense* (Farr et al. 2006, Hyde et al. 2014).

59. *Colletotrichum duyunensis* G. Tao, Zuo Y. Liu & L. Cai, in Tao, Liu, Liu, Gao & Cai, Fungal Diversity 61: 149 (2013)

This taxon is an endophyte on *Bletilla ochracea* in China (Tao et al. 2013). It belongs to the caudatum species complex (this paper). This species can be distinguished from *C. caudasporum* by its longer conidial appendages (Tao et al. 2013).

60. *Colletotrichum echinichloae* Moriwaki & Tsukib., Mycoscience 50(4): 275 (2009)

It causes leaf blight and leaf spot on *Echinichloa esculenta* in Japan (Moriwaki & Tsukiboshi 2009). *Colletotrichum echinichloae* belongs to the graminicola species complex and is a sister taxon to *C. jacksonii* (Hyde et al. 2014).

61. *Colletotrichum eleusines* Pavgi & U.P. Singh [as 'eleusinis'], Mycopath. Mycol. appl. 27: 85 (1965)

This species is a pathogen on *Eleusine indica* in India, Japan and the USA (Crouch et al. 2009a) and belongs to the graminicola species complex (Cannon et al. 2012, Hyde et al. 2014). It is morphologically indistinguishable from the other closely related falcate-spored, grass inhabiting *Colletotrichum* species, but ITS, SOD2, *Apr2* and *Mat1* sequence data can be used to distinguish this species (Crouch et al. 2009a).

62. *Colletotrichum endophytica* Manamgoda, Udayanga, L. Cai & K.D. Hyde, in Manamgoda, Udayanga, Cai, Chukeatirote & Hyde, Fungal Diversity 61:110 (2013)

This is an endophytic species on healthy leaves of *Pennisetum purpureum* in Thailand (Manamgoda et al. 2013) and was also found as a saprobe on an undetermined wild fruit in Thailand (Udayanga et al. 2013). Wang et al. (2016) recorded this taxon as a pathogen on *Camellia sinensis*. *Colletotrichum endophytica* belongs to the gloeosporioides species complex and placed in between the musae and kahawae clades (Manamgoda et al. 2013).

63. *Colletotrichum endophytum* G. Tao, Zuo Y. Liu & L. Cai, in Tao, Liu, Liu, Gao & Cai, Fungal Diversity 61(1): 152 (2013)

It is an endophyte on *Bletilla ochracea* in China (Tao et al. 2013). This species belongs to the graminicola species complex (Hyde et al. 2014) and is a sister taxon of *C. falcatum*. *Colletotrichum endophytum* has shorter conidia (8.5–21.5×3–5 µm) than *C. falcatum* (15.5–26.5×4–5 µm). *Colletotrichum endophytum* also produces relatively abundant seta and more strongly falcate conidia than *C. falcatum* (Tao et al. 2013).

64. *Colletotrichum eremochloae* J.A. Crouch & Tomaso-Pet., Mycologia 104(5): 1092 (2012)

This species belongs to the graminicola species complex and has been recorded as a pathogen of *Eremochloa ophiuroides* in China and the USA (Crouch & Tomaso-Peterson 2012).

65. *Colletotrichum euphorbiae* Damm & Crous, in Crous et al., Persoonia, Mol. Phyl. Evol. Fungi 31: 203 (2013)

This species is a pathogen on leaves of *Euphorbia* sp. in South Africa. *Colletotrichum euphorbiae* forms cylindrical to clavate conidia with one end rounded and one end truncate that are larger (> 20 µm) than those of *C. sansevieriae* and species in the orbiculare complex, which have similar shapes, often in closed fruiting bodies (Crous et al. 2013b). It is a singleton species.

66. *Colletotrichum excelsum-altitudinum* G. Tao, Zuo Y. Liu & L. Cai [as 'excelsum-altitudinum'], in Tao, Liu, Liu, Gao & Cai, Fungal Diversity 61: 152 (2013)

This taxon is an endophyte of *Bletilla ochracea* in China, and a singleton species with close affinity to *C. tropicicola* (Tao et al. 2013).

67. *Colletotrichum falcatum* Went, Archiv, voor de Java Suekerrind. 1: 265 (1893)

It is a pathogen of *Saccharum officinarum* (*Poaceae*) in Australia, Indonesia, Japan, the Netherlands and Thailand (Cai et al. 2009, Crouch et al. 2009a, Crouch 2014, Prihastuti et al. 2009, 2010). It belongs to the graminicola species complex (Cannon et al. 2012).

68. *Colletotrichum fioriniae* (Marcelino & Gouli) R.G. Shivas & Y.P. Tan, Fungal Diversity 39: 117 (2009)

Colletotrichum fioriniae causes fruit rot and leaf spots on *Acacia acuminata*, *Actinidia chinensis*, *Anemone* sp., *Berberis* sp., *Camellia reticulata*, *Camellia sinensis*, *Carica papaya*, *Cinnamomum subavenium*, *Coffea arabica*, *Cyclamen* sp. *Fragaria*×*ananassa*, *Grevillea* sp., *Kalmia* sp., *Liriodendron tulipifera*, *Magnolia* sp., *Malus* sp., *Olea europea*, *Parthenocissus* sp., *Penstemon* sp., *Persea americana*, *Piper nigrum*, *Primula* sp., *Pyrus* sp., *Rhododendron* sp., *Rubus* sp., *Solanum lycopersicum*, *Toxicodendron radicans*, *Tulipa* sp., *Vaccinium* sp. and *Vitis vinifera* in Australia, China, Germany, Hawaii, Italy, the Netherlands, New Zealand, the UK and the USA (Shivas & Tan 2009, Sun et al. 2012, Damm et al. 2012b, Baroncelli et al. 2015b, Kasson et al. 2014, Kou et al. 2014, Munda 2014, Liu et al. 2015a, Wang et al. 2016). This species is also an endophyte of *Mangifera indica* in Australia. *Colletotrichum fioriniae* is pathogenic on the hemlock scale insect, *Fiorinia extrerna*, in the USA (Marcelino et al. 2008). It belongs to the acutatum species complex and can be distinguished using any of the gene sequences mentioned in Damm et al. (2012b).

Kasson et al. (2014) have shown that *C. fioriniae* can be used as a mycoherbicide against Eastern Poison Ivy (*Toxicodendron radicans*).

69. *Colletotrichum fructi* (F.Stevans & J.G. Hall) Sacc. [as ‘fructus’], Syll. fung. (Abellini) 22: 1201 (1913)

This species belongs to the dematium species complex (Cannon et al. 2012) and is a pathogen on *Malus sylvestris* in the USA (Damm et al. 2009). This taxon is slow growing and has been mentioned very rarely in the literature (Damm et al. 2009).

70. *Colletotrichum fructicola* Prihastuti, L. Cai & K.D. Hyde, Fungal Diversity 39: 96 (2009)

Colletotrichum fructicola was originally reported from coffee berries in Thailand (Prihastuti et al. 2009). It has a wide host range and geographical distribution including *Arachis* sp. (*Fabaceae*), *Citrus bergamia* (*Rutaceae*) in China (Peng et al. 2012), *Cymbopogon citrates* (*Poaceae*) in Thailand (Manamgoda et al. 2013), *Dioscorea alata* in Nigeria, *Ficus* sp. (*Dioscoreaceae*) in Germany, *Fragaria xananassa* (*Rosaceae*) in Canada and the USA, *Limonium* sp. (*Plumbaginaceae*) in Israel, *Malus domestica* (*Rosaceae*) in Australia, Brazil and Uruguay (Weir et al. 2012, Velho et al. 2015), *Mangifera indica* (*Anacardiaceae*) in India and Brazil (Liu et al. 2015a, Viera et al. 2014), *Persea americana* (*Lauraceae*) in Australia, *Pyrus pyrifolia* (*Rosaceae*) in Japan, *Theobroma cacao* (*Malvaceae*) and *Tetragastris panamensis* (*Burseraceae*) in Panama, *Pennisetum purpureum* (*Poaceae*) in Thailand (Manamgoda et al. 2013), and *Camellia sinensis* (Wang et al. 2016), *Rubus glaucus* (*Rosaceae*) and *Vitis vinifera* (*Vitaceae*) in China (Peng et al. 2013) (Yang et al. 2009, Afanador-Kafuri et al. 2014). This species also occurs as an endophyte. *Colletotrichum fructicola* belongs to the musae clade in the gloeosporioides species complex. ITS sequences do not separate this taxon from *C. aeshynomenes*. However, these species can be distinguished by GS or SOD2 sequences (Weir et al. 2012).

71. *Colletotrichum fructivorum* V.P. Doyle, P.V. Oudem. & S.A. Rehner, PLoS ONE 7(12): e51392, 12 (2012)

This taxon is pathogenic to *Vaccinium* sp. in Canada, Colombia and the USA (Doyle et al. 2013). Doyle et al. (2013) reported this species as an endophyte on *Rhexia virginica* and *Vaccinium macrocarpon* in the USA. It belongs to the gloeosporioides species complex (Doyle et al. 2013, Hyde et al. 2014).

72. *Colletotrichum fuscum* Laubert, Gartenwelt 31: 675 (1927)

This species causes anthracnose on *Digitalis* sp. Germany and the Netherlands (Damm et al. 2014). *Colletotrichum fuscum* belongs to the destructivum species complex. It can be distinguished from the other species in the complex by GAPDH sequence data, but has only one nucleotide difference from *C. bryoniicola* (Damm et al. 2014).

73. *Colletotrichum fusiforme* Jayawardena, Bhat, Tangthirasunun & K.D. Hyde, in Ariyawansa et al., Fungal Diversity 75(1): 158 (2015)

Colletotrichum fusiforme belongs to the truncatum species complex and was isolated from a dead leaf of an undetermined host in Thailand. *Colletotrichum curcumae* is a sister taxon of this species (Ariyawansa et al. 2015).

74. *Colletotrichum gigasporum* E.F. Rakotoniriana & F. Munaut, in Rakotoniriana, Scauflaire, Rabemanantsoa, Urveg-Ratsimamanga, Corbisier, Quetin-Leclercq, Declerck & Munaut, Mycol. Progr. 12(2): 407 (2013)

This species is a pathogen of *Acacia auriculiformis* in Thailand, *Centella asiatica* in Madagascar, *Coffea* sp. in Vietnam, *Diospyros kaki* and *Musa* sp. in Japan, *Persea americana* in Sri Lanka, *Theobroma cacao*, *Trichilia tuberculata* and *Viola surinamensis* in Panama and *Solanum betaceum* in New Zealand (Rakotoniriana et al. 2013, Liu et al. 2014, Wijesundera et al. 2015). *Colletotrichum thailandicum* has been synonymized with this taxon (Liu et al. 2014). *Colletotrichum gigasporum* belongs to the gigasporum species complex and is characterized by large conidia. This species had also been isolated from a phaeohyphomycotic cyst of a human (Liu et al. 2014). It can be distinguished with all loci (ITS, ACT, TUB2, CHS-1 and GAPDH) used in Liu et al. (2014).

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

Colletotrichum gloeosporioides is mainly a pathogen of *Citrus* sp., but also occurs on *Carya illinoensis* (Australia), *Ficus* sp. (New Zealand), *Mangifera* sp. (China and South Africa), *Solanum betaceum* (Colombia), *Purseraria* sp. (USA) and *Vitis vinifera* (China and the USA) (Phoulivong et al. 2010, Peng et al. 2012, Weir et al. 2012, Hoz et al. 2016, Rhaiem & Taylor 2016). Previously, about 600 species were synonymised with this species (von Arx 1957) and consequently, numerous taxa were named as *C. gloeosporioides*, and thus it has a wide host range in many publications (Farr & Rossman 2016). Weir et al. (2012) did a comprehensive study on *C. gloeosporioides* and related species, resolving most of the species under the name of *C. gloeosporioides*. ITS gene region separates this group from all other species.

76. *Colletotrichum godetiae* Neerg., Friesia 4(1–2): 72 (1950) [1949–50]

This species was initially described from seeds of *Clarkia* (syn. *Godetia*) and causes leaf spots, fruit rots, die back and stem end rots of many hosts in the families of *Adoxaceae*, *Anacardiaceae*, *Berberidaceae*, *Fabaceae*, *Juglandaceae*, *Myrtaceae*, *Oleaceae*, *Onagraceae*, *Podocarpaceae*, *Rosaceae*, *Rhamnaceae*, *Rutaceae*, *Solanaceae* and *Vitaceae* worldwide (Damm et al. 2012b, Afanador-Kafuri et al. 2014, Baroncelli et al. 2014, 2015b, Mosca et al. 2014, Munda 2014, Talhinhos et al. 2015). It has been also recorded as a saprobe of *Laurus nobilis* (Damm et al. 2012b). *Colletotrichum godetiae* belongs to the acutatum species complex and can be separated from the other species of this complex by all genes used in Damm et al. (2012b) except CHS-1; TUB2, ACT and HIS3 sequences separate this species best.

77. *Colletotrichum graminicola* (Ces.) G.W. Wilson, Phytopathology 4: 110 (1914)

Colletotrichum graminicola is a pathogen of *Zea mays* (Crouch et al. 2009a), belonging to the graminicola complex (Cannon et al. 2012). Whole-genome sequencing of this species has been completed (O'Connell et al. 2012). It has been known to be pathogenic on humans (Ritterband et al. 1997).

78. *Colletotrichum grevilleae* F. Liu, Damm, L. Cai & Crous, Fungal Diversity 61: 98 (2013)

This species is a pathogen of *Grevillea* sp. in Italy (Liu et al. 2013b). *Colletotrichum grevilleae* belongs to the gloeosporioides species complex and has a close affinity with *C. theobromicola*. However, these species can be distinguished based on CAL and GAPDH sequence data (Liu et al. 2013b).

79. *Colletotrichum grossum* Y.Z. Diao, C. Zhang, L. Cai & X.L. Liu, Persoonia 38: 29 (2017)

It is a pathogen on *Capsicum annuum* var. *grossum* in China (Diao et al. 2017). *Colletotrichum grossum* belongs to the gloeosporioides species complex and is phylogenetically closely related to *C. theobromicola*. This species can be distinguished with the use of GAPDH, ACT and TUB2 sequence data.

80. *Colletotrichum guajavae* Damm, P.F. Cannon & Crous, Stud. Mycol. 73: 69 (2012)

This taxon is a pathogen of *Psidium guajavae* in India, and belongs to the acutatum species complex (Damm et al. 2012b). It can be distinguished from other species by TUB2, ACT and GAPDH sequence data; most effectively by GAPDH (Damm et al. 2012b).

81. *Colletotrichum guizhouensis* G. Tao, Zuo Y. Liu & L. Cai, in Tao, Liu, Liu, Gao & Cai, Fungal Diversity 61: 152 (2013)

Colletotrichum guizhouensis is an endophyte of *Bletilla ochracea* (Tao et al. 2013) and *Phlegmariurus phlegmaria* in China (Zhang et al. 2015). It belongs to the spaethianum species complex and is a sister taxon to *C. spaethianum* (Hyde et al. 2014). Zhang et al. (2015) showed that this species is capable of producing Huperzine A.

82. *Colletotrichum hanau* J.A. Crouch, B.B. Clarke, J.F. White & B.I. Hillman, Mycologia 101(5): 728 (2009)

This species has a unique association with grasses in the genus *Digitaria* and has been reported in China, Japan and the USA (Crouch et al. 2009a,b, Cannon et al. 2012). *Colletotrichum hanau* is a pathogen belonging to the graminicola species complex (Cannon et al. 2012). Nucleotide polymorphisms in ITS, SOD2, *Apn2* and *Mat1* can be used to differentiate this taxon (Crouch et al.

2009a). Zhao et al. (2013) showed that this species can be used as a bio-control agent on *Digitaria sanguinalis*.

83. *Colletotrichum hebeiense* X.H. Li, Y. Wang, K.D. Hyde, M.M.R.S. Jayawardena & J.Y. Yan, in Yan, Jayawardena, Goonasekara, Wang, Zhang, Liu, Huang, Wang, Shang, Peng, Bahkali, Hyde & Li, *Fungal Diversity* 71: 241 (2015)

This is a pathogen on *Vitis vinifera* in China. It belongs to the gloeosporioides species complex and has a close affinity to *C. aenigma* (Yan et al. 2015).

84. *Colletotrichum hemerocallidis* Yan L. Yang, Zuo Y. Liu, K.D. Hyde & L. Cai, *Tropical Plant Pathology* 37(3): 170 (2012)

This taxon was isolated from a dead stalk of *Hemerocallis* sp. in Canada and China (Damm et al. 2009, Yang et al. 2012a). It is a member of the dematium species complex (Hyde et al. 2014).

85. *Colletotrichum henanense* F. Liu & L. Cai, in Liu, Weir, Damm, Crous, Wang, Liu, Zhang & Cai, *Persoonia, Mol. Phyl. Evol. Fungi* 35: 80 (2015)

Colletotrichum henanense is a pathogen known on *Camillia sinensis* and *Cirsium japonicum* in China. This taxon belongs to the gloeosporioides species complex and can be distinguished by TUB2, *ApMat* and GS sequence data (Liu et al. 2015a).

86. *Colletotrichum higginsianum* Sacc., in Higgins, *Riv. Accad. di Padova* 33: 161 (1917)

Colletotrichum higginsianum causes anthracnose on a wide range of *Brassicaceae* hosts in Italy, Japan, Korea, Trinidad and Tobago and the USA (Damm et al. 2014). This species belongs to the destructivum species complex and can be distinguished with TUB2 and ITS sequence data (Damm et al. 2014). Whole-genome sequencing of this species has been completed (O'Connell et al. 2012).

87. *Colletotrichum hippeastri* Yan L. Yang, Zuo Y. Liu, K. D. Hyde & L. Cai, *Fungal Diversity* 39: 133 (2009)

This taxon is an endophyte on leaves of *Hippeastrum* sp. in China and the Netherlands (Damm et al. 2012a). *Colletotrichum hippeastri* is an outlying species in the boninense clade and can be distinguished from related species by any of the loci used in the study of Damm et al. (2012a).

88. *Colletotrichum horii* B. Weir & P.R. Johnst., *Mycotaxon* 111: 211 (2010)

Colletotrichum horii is associated with fruit and stem disease of *Diospyros kaki* in Brazil, China, Japan and New Zealand (Weir & Johnston 2010, Weir et al. 2012, De Mio et al. 2015). *Colletotrichum horii* belongs to the gloeosporioides species complex and ITS gene region distinguishes it from all other species (Weir et al. 2012).

89. *Colletotrichum hsienjenchang* I. Hino & Hidaka, *Bull. Miyazaki Coll. Agric. Forest.* 6: 93-99 (1934)

This species is a pathogen only on *Phyllostachys* sp. in Japan (Sato et al. 2012). Combined phylogenetic analysis of ITS, CHS, ACT and HIS3 places this taxon as a singleton species closely related to *C. metake* (in this study). Sato et al. (2012) mentioned it as a rare species. In order to fix the name of this species, it still needs to be epytified.

90. *Colletotrichum hymenocallidicola* Chethana, Tangthir., Jayawardena. & K.D. Hyde, in Ariyawansa et al., *Fungal Diversity* 75(1): 160 (2015)

This taxon is a pathogen on *Hymenocallis* sp. in Thailand. It appears as a singleton species with close affinity to *C. brevisporum*. (Ariyawansa et al. 2015).

91. *Colletotrichum incanum* H.C. Yang, J.S. Haudenshield & G.L. Hartman, *Mycologia* 106(1): 38 (2014)

It is a pathogen on *Glycine max* and *Solanum lycopersicum* in the USA and on *Phaseolus vulgaris* in Canada (Yang et al. 2014, Hacquard et al. 2016), *Raphanus sativus* in Japan (Sato et al. 2005) and can also infect *Arabidopsis thaliana* (Hacquard et al. 2016). *Colletotrichum incanum* belongs to the spaethianum species complex (Hyde et al. 2014).

92. *Colletotrichum indonesiense* Damm, P.F. Cannon & Crous, *Stud. Mycol.* 73: 71 (2012)

This taxon causes leaf spots on *Eucalyptus* sp. in Indonesia (Damm et al. 2012b). It belongs to the acutatatum species complex and can be separated from other species by TUB2, ACT, GAPDH and CHS-1 sequences; most effectively with TUB2.

93. *Colletotrichum insertae* Jayawardena, Bulgakov & K.D. Hyde, in Hyde et al., Fungal Diversity 80: 176 (2016)

It is a saprobic on dying twigs and leaves of *Parthenocissus inserta* in Russia. *Colletotrichum insertae* falls within the dematium species complex.

94. *Colletotrichum jacksonii* J.A. Crouch, B.B. Clarke, J.F. White & B.I. Hillman, Mycologia 101(5): 729 (2009)

It is a pathogen of the genus *Echinochloa* in Japan and the USA (Crouch et al. 2009a). *Colletotrichum jacksonii* belongs to the graminicola species complex.

95. *Colletotrichum jasminigenum* Wikee, K.D. Hyde, L. Cai & McKenzie, in Wikee, Cai, Pairin, McKenzie, Su, Chukeatirote, Thi, Bahkali, Moslem, Abdelsalam & Hyde, Fungal Diversity 46(1): 174 (2011)

Colletotrichum jasminigenum belongs to the truncatum species complex and is known only from *Jasminium sambac* in Vietnam (Wikee et al. 2011, Hyde et al. 2014).

96. *Colletotrichum jiangxiense* F. Liu and L. Cai, Persoonia 35: 82 (2015)

This species is a pathogen as well as an endophyte on *Camellia sinensis* in China. It belongs to the gloeosporioides species complex and is closely related to *C. kahawae* s.l.. *Colletotrichum jiangxiense* can be distinguished by GS gene sequences (Liu et al. 2015a).

97. *Colletotrichum johnstonii* Damm, P.F. Cannon & Crous, Stud. Mycol. 73: 72 (2012)

This species is a pathogen on *Citrus* sp. and *Solanum lycopersicum*, and is thought to be endemic to New Zealand. It belongs to the acutatum species complex and can be differentiated from other species by ACT, HIS3, TUB2 and GAPDH, most effectively with ACT gene sequences (Damm et al. 2012b).

98. *Colletotrichum kahawae* J.M Waller & Bridge, Mycol. Res. 97(8): 993 (1993)

Colletotrichum kahawae belongs to the gloeosporioides species complex and consists of two subspecies namely *C. kahawae* subsp. *kahawae*, which is known only from *Coffea* sp. in Africa (Waller et al. 1993) and *C. kahawae* subsp. *ciggaro* which has a wide host range and wide geographic distribution (Weir et al. 2012). *Colletotrichum kahawae* subsp. *kahawae* is important in bio-security (Weir et al. 2012). The two subspecies can be distinguished by GS sequences as *C. kahawae* subsp. *kahawae* has a 22 bp deletion and a single C to T transition (Weir et al. 2012). *Colletotrichum kahawae* subsp. *kahawae* cannot utilize citrate or tartrate, while *C. kahawae* subsp. *ciggaro* can utilize both of these carbon sources (Weir & Johnston 2010).

99. *Colletotrichum karstii* Y.L. Yang, Zuo Y. Liu, K.D. Hyde & L. Cai, Cryptog. Mycol. 32(3): 241 (2011)

This taxon was first reported from orchids and is also known from many other host plants causing anthracnose, including *Annona cherimola*, *Anthurium* sp., *Bombax aquaticum*, *Camellia* sp., *Capsicum annuum*, *Carica papaya*, *Citrus* sp., *Clivia miniata*, *Coffea* sp., *Cucumis melo*, *Diospyros australis*, *Eucalyptus grandis*, *Malus domestica*, *Olea europaea*, *Pistacia vera*, *Rubus glaucus* and also on *Bletilla ochracea*, *Mangifera indica*, *Quercus salicifolia*, *Theobroma cacao* and *Zamia obliqua* as an endophyte (Damm et al. 2012a, Yang et al. 2011, Peng et al. 2012, Tao et al. 2013, Afanador-Kafuri et al. 2014, Schena et al. 2014, Velho et al. 2015, Wang et al. 2016). *Colletotrichum karstii* belongs to the boninense species complex and is the most common and geographically distributed species within the complex (Damm et al. 2012a). This species can be identified with the use of any of the genes used in Damm et al. (2012a).

100. *Colletotrichum kinghornii* Damm, P.F. Cannon & Crous, Stud. Mycol. 73: 73 (2012)

This species is a pathogen of *Phormium* sp. in the UK (Damm et al. 2012b). It belongs to the acutatum species complex and can be effectively separated from other species with the use of HIS3 sequence data (Damm et al. 2012b).

101. *Colletotrichum laticiphilum* Damm, P.F. Cannon & Crous, Stud. Mycol. 73: 74 (2012)

Colletotrichum laticiphilum causes anthracnose of *Hevea brasiliensis* in Colombia, and belongs to the acutatum species complex (Damm et al. 2012b). It can be differentiated most effectively from other species by TUB2 sequences (Damm et al. 2012b).

102. *Colletotrichum ledebouriae* Crous & M.J. Wingf, Persoonia 36: 331(2016)

This taxon causes anthracnose on *Ledebouria floridunda* in South Africa (Crous et al. 2016). It is closely related to *C. sansevieriae*. Conidia of *C. sansevieriae* are larger (12.5–32.5 × 2.8–8.8 µm) (Nakamura et al. 2006) than those of *C. ledebouriae* and overlap with those of *C. neosansevieriae* (18–22 × 5–6 µm) (Crous et al. 2015). It is a singleton species.

103. *Colletotrichum lentis* Damm, in Damm, O'Connell, Groenewald & Crous, *Stud. Mycol.* 79: 65 (2014)

This taxon is a pathogen of *Lens culinaris* in Canada and on *Vicia sativa* in China (Damm et al. 2014, Xu & Li 2015) and was first described as "*Glomerella truncata*" (Armstrong-Cho & Banniza 2006). *Colletotrichum lentis* belongs to the destructivum species complex (Damm et al. 2014).

104. *Colletotrichum liaoningense* Y.Z. Diao, C. Zhang, L. Cai & X.L. Liu, *Persoonia* 38: 34 (2017)

This taxon is a pathogen on *Capsicum annuum* var. *conoides* in China (Diao et al. 2017). *Colletotrichum liaoningense* is a singleton species and phylogenetically most closely related to *C. brevisporum*. This species can be distinguished with the use of GAPDH and TUB2 sequence data.

105. *Colletotrichum lilii* Plakidas ex Boerema & Hamers, *Neth. J. Pl. Path.* 94 (suppl.1): 12 (1988)

This taxon is pathogenic to *Lilium* sp. causing black scale disease of bulbs in Japan and the Netherlands (Damm et al. 2009). *Colletotrichum lilii* belongs to the spaethianum species complex (Hyde et al. 2014).

106. *Colletotrichum limeticola* (R.E. Clausen) Damm, P.F. Cannon & Crous, *Stud. Mycol.* 73: 76 (2012)

It is pathogenic to *Citrus aurantifolia* in Cuba and the USA (Damm et al. 2012b). This taxon belongs to the acutatum species complex and can be separated from the other species of this complex by TUB2, GAPDH and HIS3, most effectively distinguished by TUB2 sequence data (Damm et al. 2012b).

107. *Colletotrichum lindemuthianum* (Sacc. & Magnus) Briosi & Cavara, *Funghi Parass. Piante Colt. od Utili, Fasc. 2: no. 50* (1889)

This species belongs to the orbiculare species complex and is a pathogen restricted to *Phaseolus vulgaris* and *P. coccineus* (*Fabaceae*) (Damm et al. 2013, Liu et al. 2013a).

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

Colletotrichum lineola is the type species of the genus *Colletotrichum* and was primarily observed on a dead stem of an unknown host of *Apiaceae* in the Czech Republic (Corda 1831). *Colletotrichum lineola* is also reported on dead stems of *Anthriscus* sp., *Allium giganteum* and *Heracleum* sp. in the Netherlands, on petioles of *Fragaria* sp. in Canada, on rotten fruit of *Prunus domestica* in Czech Republic (Damm et al. 2009). *Colletotrichum lineola* is pathogenic on *Clarkia elegans*, *Trillium* sp. in the USA, *Astrantia major* in Zimbabwe, *Tussilago farfara*, *Euphorbia egula* in Canada, *Lupinus polyphyllus* in Germany, and *Symplocarpus foetidus* in the USA (Damm et al. 2009). It belongs to the dematium species complex (Cannon et al. 2012, Hyde et al. 2014) and is characterized by small, compressed acervuli, emerging in rows/lines (Damm et al. 2009).

109. *Colletotrichum lini* (Westerd.) Tochinai, *J. Coll. agric., Hokkaido Imp. Univ.* 14(4): 176 (1926)

Colletotrichum lini is a pathogen of *Linum* sp., *Medicago sativa*, *Nigella* sp., *Raphanus raphanistrum*, *Taraxacum* sp., *Teucrium scorodonia* and *Trifolium* sp. in France, Germany, Ireland, the Netherlands, New Zealand, Tunisia, the UK and the USA (Damm et al. 2014). *Colletotrichum lini* belongs to the destructivum species complex and can be distinguished by CHS-1, ACT, HIS3 and TUB2 gene regions. Damm et al. (2014) has synonymized *C. linicola* under this species.

110. *Colletotrichum liriopes* Damm, P.F. Cannon & Crous, in Damm, Woudenberg, Cannon & Crous, *Fungal Diversity* 39: 71 (2009)

This taxon is known to cause anthracnose on *Eria coronaria* in China (Yang et al. 2011), *Liriope muscari* in Mexico (Damm et al. 2009) and *Rohdea japonica* in Korea (Kwon & Kim 2013). Tao et al. (2013) reported this species as an endophyte of *Bletilla ochracea* in China. Also, Yang et al. (2011) reported that *C. liriopes* occurs as an endophyte on *Peione bulbocodioides* in China and

isolated this species from a dead stalk of *Hemerocallis fulva* in China. *Colletotrichum liriopes* belongs to the spaethanium species complex (Cannon et al. 2012).

111. *Colletotrichum lupini* (Bondar) Damm, P.F. Cannon & Crous, Stud. Mycol. 73: 78 (2012)

It is a pathogen on *Camellia* sp. (UK), *Cinnamomum verum* (Portugal), *Lupinus* sp. (Australia, Austria, Bolivia, Canada, Costa Rica, France, Germany, Korea, Netherlands, Poland, South Africa, USA and Ukraine), and *Manihot utilissima* (Ruwanda) (Damm et al. 2012b, Han et al. 2014, Roskopf et al. 2014). It belongs to the acutatum species complex, and can be differentiated effectively from other species by all genes used in Damm et al. (2012b) except for ACT; most effectively with TUB2.

112. *Colletotrichum magnisporum* F. Liu, L. Cai, Crous & Damm, Persoonia, Mol. Phyl. Evol. Fungi 33: 91 (2014)

This species belongs to the gigasporum species complex and was isolated from an unknown source. *Colletotrichum magnisporum* is phylogenetically close to *C. arxii* and can be differentiated by all loci used in Liu et al. (2014), including ITS. Based on ITS sequence comparison, it occurs on *Coffea* in USA (Hawaii) and on *Rhipidoctadum* (*Poaceae*) and a tropical woody plant in Panama (Vega et al. 2010, Higgins et al. 2011, Higginbotham et al. 2013).

113. *Colletotrichum malvarum* (A. Braun & Casp.) SouthW., J. Mycol. 6(3): 116 (1891)

It is a pathogen on *Malvaceae* in Germany, Korea, the UK and belongs to the orbiculare species complex (Kim et al. 2008, Damm et al. 2013). This species is one of the slowest growing species in the orbiculare species complex (Damm et al. 2013). *Colletotrichum malvarum* is closely related to *C. trifolii* and can be separated using the GS sequence data (Damm et al. 2013).

114. *Colletotrichum melonis* Damm, P.F. Cannon & Crous, Stud. Mycol. 73: 80 (2012)

This species is pathogenic to *Cucumis melo* in Brazil, *Malus domestica* in Brazil and Uruguay (Bragança et al. 2016, Velho et al. 2015) and belongs to the acutatum species complex (Damm et al. 2012b). This species can be differentiated with the use of the GAPDH, ACT and HIS3 gene sequences; most effectively with GAPDH (Damm et al. 2012b).

115. *Colletotrichum menispermii* Chethana, Jayawardena, Bulgakov & K.D. Hyde, in Li et al., Fungal Diversity 78: 80 (2016)

This taxon is a saprobe on *Menispermum dahuricum* in Russia (Li et al. 2016). *Colletotrichum menispermii* belongs to the dematium species complex.

116. *Colletotrichum metake* Sacc., Annls mycol. 6(6): 557 (1908)

This species is known only as a pathogen on *Pleioblastus simoni* in Japan (Sato et al. 2012). Morphologically this species has falcate conidia, and ITS sequence data alone can be used to identify this species. It is a singleton species, closely related to *C. hsienjenchang* (in this study). However, further studies are needed to confirm the position of this species. Sato et al. (2012) mentioned it as a rare species. In order to fix the name of this species, it still needs to be epitypified.

117. *Colletotrichum miscanthi* J.A. Crouch, B.B. Clarke, J.F. White & B.I. Hillman, Mycologia 101(5): 729 (2009)

This species has an association with the genus *Miscanthus* (Crouch et al. 2009a) in Japan. Tao et al. (2013) reported it as an endophyte on *Bletilla ochracea* in China. It belongs to the graminicola species complex (Hyde et al. 2014).

118. *Colletotrichum musae* (Berk. & M. A. Curtis) Arx, Verh. K. ned. Akad. Wet., tweede sect. 51(3): 107 (1957)

Colletotrichum musae is known to be associated with fruit lesions of *Musa* sp. in many countries and belongs to the gloeosporioides species complex (Su et al. 2011, Sakinah et al. 2014, Sharma et al. 2015, Weir et al. 2012). It has been recognized as an endophyte on *Musa acuminata* in Thailand (Tao et al. 2013). ITS sequence data can be used to separate *C. musae* from all other species (Weir et al. 2012).

119. *Colletotrichum navitas* J.A. Crouch, Mycol. Res. 113(12): 1417 (2009)

This taxon belongs to the graminicola species complex and is only known as a pathogen on *Panicum* sp. in the USA (Crouch et al. 2009b).

120. *Colletotrichum neosansevieriae* Crous & N.A. van der Merwe, *Persoonia*, Mol. Phyl. Evol. Fungi 34: 221 (2015)

It is a pathogen on leaves of *Sansevieria trifasciata* in South Africa (Crous et al. 2015). This is a singleton species, and morphologically similar to *C. sansevieriae*. However, this species is phylogenetically distinct from *C. sansevieriae*.

121. *Colletotrichum nicholsonii* J.A. Crouch, B.B. Clarke, J.F. White & B.I. Hillman, *Mycologia* 101(5): 730 (2009)

This taxon causes anthracnose on *Paspalum* sp. in Japan and New Zealand (Crouch et al. 2009a). *Colletotrichum nicholsonii* belongs to the graminicola species complex (Cannon et al. 2012).

122. *Colletotrichum nigrum* Ellis & Halst., in Halsted, New Jersey Agric. Coll. Exp. Sta. Bull.: 297 (1895)

This species is a well-known pathogen of *Capsicum* sp., *Cichorium intybus*, *Fragaria* sp., *Helianthus tuberosus*, *Lens culinaris*, *Lycopersicon esculentum* and *Solanum* sp. worldwide (Liu et al. 2013a). *Colletotrichum nigrum* is a singleton species with a close affinity to *C. coccodes* and can be identified using ITS gene sequence (Liu et al. 2013a, Cannon et al. 2012).

123. *Colletotrichum novae-zelandiae* Damm, P.F. Cannon, Crous, P.R. Johnst. & B. Weir, *Stud. Mycol.* 73: 25 (2012)

This species belongs to the boninense species complex (Damm et al. 2012a). *Colletotrichum novae-zelandiae* is only known from New Zealand and has been isolated from fruit rots of *Capsicum* sp. and *Citrus* sp. (Damm et al. 2012a).

124. *Colletotrichum nupharicola* D.A. Johnson, Carris & J.D. Rogers, *Mycol. Res.* 101(6): 647 (1997)

This species is a pathogen known only in the USA, on the aquatic plants *Nuphar* and *Nymphaea* sp. (Johnson et al. 1997). *Colletotrichum nupharicola* belongs to the gloeosporioides species complex and is closely related to *C. fruticola* and *C. alienum* within the musae clade (Weir et al. 2012). ITS sequence can separate this from all other species.

125. *Colletotrichum nymphaeae* (Pass.) Aa, *Netherlands Journal of Plant Pathology*, Supplement 1 84(3): 110 (1978)

This taxon is a pathogen of *Anemone* sp. (Israel, Italy, and the Netherlands), *Capsicum* sp. (Indonesia and Zimbabwe), *Fragaria* × *ananassa* (Bulgaria, Canada, France, Israel, Italy, Netherlands, South Africa, Spain, Switzerland, UK and the USA), *Leucaena* sp. (Mexico), *Malus domestica* (Brazil and Uruguay), *Nuphar luteum* (Netherlands), *Nymphaea alba* (Netherlands), *Oenothera* sp. (Netherlands), *Olea europaea* (Portugal), *Pelargonium graveolens* (India), *Photinia* sp. (UK), *Protea* sp. (Australia and South Africa), *Phaseolus* sp. (Netherlands) and *Vitis vinifera* (China) (Damm et al. 2012b, Velho et al. 2014, 2015, Baroncelli et al. 2015b, Talhinas et al. 2015, Liu et al. 2016). It has also been recorded as a saprobe from litter in Thailand (Damm et al. 2012b). *Colletotrichum nymphaeae* belongs to the acutatum species complex and can be separated from other species by analysis of TUB2 sequence data (Damm et al. 2012b).

126. *Colletotrichum ochraceae* G. Tao, Zuo Y. Liu & L. Cai [as 'ochracea'], in Tao, Liu, Liu, Gao & Cai, *Fungal Diversity* 61: 156 (2013)

This taxon is an endophyte of *Bletilla ochracea* in China (Tao et al. 2013). It belongs to the cadatum species complex. *Colletotrichum ochraceae* can be identified from the other species of this complex as it lacks conidial appendages.

127. *Colletotrichum ocimi* Damm, in Damm, O'Connell, Groenewald & Crous, *Stud. Mycol.* 79: 70 (2014)

This species causes anthracnose on leaves and stems of *Ocimum basilicum* in Italy (Damm et al. 2014). *Colletotrichum ocimi* belongs to the destructivum complex. It forms conidiogenous cells that are often covered by a mucoid sheath and can be identified by its unique ITS, CHS-1, HIS3, ACT and TUB2 sequences (Damm et al. 2014).

128. *Colletotrichum oncidii* Damm, P.F. Cannon & Crous, *Stud. Mycol.* 73: 26 (2012)

Colletotrichum oncidii has been recorded as an endophyte in leaves of *Oncidium* sp. in Germany and belongs to the boninense species complex (Damm et al. 2012a). It forms a sister group to *C. cymbidiicola*.

129. *Colletotrichum orbiculare* Damm, P.F. Cannon & Crous, in Damm, Cannon, Liu, Barreto, Guatimosim & Crous, Fungal Diversity 61: 39 (2013)

This taxon is a pathogen of *Benincasa hispida* (*Cucurbitaceae*) in Australia, *Cucumis melo* in Japan, *Cucumis sativus* in Japan, the UK, and the Netherland. *Colletotrichum orbiculare* belongs to the orbiculare species complex and is closely related to *C. sidae*, *C. spinosum* and *C. tebeestii* (Damm et al. 2013). This species can be separated from other species with its unique GS, ACT and HIS3 sequence data (Damm et al. 2013).

130. *Colletotrichum orchidophilum* Damm, P.F. Cannon & Crous, in Damm, Cannon, Woudenberg, & Crous, Stud. Mycol. 73: 83 (2012)

It is pathogenic or endophytic to *Orchidaceae* (*Ascocenda* sp., *Cycnoches aureum*, *Dendrobium* sp. and *Phalaenopsis* sp.) (Damm et al. 2012). It clusters basal to the acutatum species complex, and is a singleton species. *Colletotrichum orchidophilum* can be distinguished by its very narrow cylindrical conidia and uniformly shaped, dark brown, pyriform to spathulate appressoria (Damm et al. 2012b).

131. *Colletotrichum panacicola* Uyeda & S. Takim., in Takimoto, Chosen Nokai-ho 14: 24 (1919)

This species causes anthracnose on *Panax* sp. in China, Japan, Korea and Russia (Damm et al. 2014). *Colletotrichum panacicola* belongs to the destructivum species complex and has pyriform, olive appressoria (Damm et al. 2014). It can be identified by ITS and GAPDH sequences (Damm et al. 2014).

132. *Colletotrichum paranaense* C.A.D. Bragança & Damm, Fungal Biology 120: 555 (2016)

This species is a pathogen of *Caryocar brasiliense*, *Malus domestica* and *Prunus persica* in Brazil (Bragança et al. 2016). It belongs to the acutatum species complex and can be identified by its unique TUB2 and HIS3 sequence data.

133. *Colletotrichum parsoniae* Damm, P.F. Cannon, Crous, P.R. Johnst. & B. Weir, in Damm, Cannon, Woudenberg, Johnston, Weir, Tan, Shivas & P.Crous, Stud. Mycol. 73: 27 (2012)

This taxon is an endophyte of *Bletilla ochracea* in China (Tao et al. 2013) and *Parsonia caspularis* in New Zealand (Damm et al. 2012a). It belongs to the boninense species complex (Damm et al. 2012a).

134. *Colletotrichum paspali* J.A. Crouch, B.B. Clarke, J.F. White & B.I. Hillman, Mycologia 101(5): 730 (2009)

It causes anthracnose on *Paspalum notatum* in Japan (Crouch et al. 2009a). This species belongs to the graminicola species complex (Cannon et al. 2012).

135. *Colletotrichum paxtonii* Damm, P.F. Cannon & Crous, in Damm, Cannon, Woudenberg, & Crous, Stud. Mycol. 73: 85 (2012)

This species is known from *Musa* sp. as a pathogen in Saint Lucia, belongs to the acutatum species complex, and can be separated from other species with the analysis of GAPDH or TUB2 sequence data; most effectively with TUB2 (Damm et al. 2012b).

136. *Colletotrichum petchii* Damm, P.F. Cannon & Crous, in Damm, Cannon, Woudenberg, Johnston, Weir, Tan, Shivas & P.Crous, Stud. Mycol. 73: 29 (2012)

This species is recorded as a pathogen from *Dracaena* sp. in China, Italy and the Netherlands. *Colletotrichum petchii* is a member of the boninense species complex (Damm et al. 2012b).

137. *Colletotrichum phormii* (Henn.) D.F. Farr & Rossman, in Farr, Aime, Rossman & Palm, Mycol. Res. 110(12): 1403 (2006)

This taxon has been reported as a pathogen from *Phormium* sp. in Germany, New Zealand, South Africa and the UK (Damm et al. 2012b). It belongs to the acutatum species complex and is closely related to *C. salicis*. It can be separated from other species by TUB2, GAPDH, HIS3 and ACT sequences; most effectively with HIS3 (Damm et al. 2012b).

138. *Colletotrichum phyllanthi* (H.S. Pai) Damm, P.F. Cannon & Crous, in Damm, Cannon, Woudenberg, Johnston, Weir, Tan, Shivas & P.Crous, Stud. Mycol. 73: 31 (2012)

It is a pathogen and an endophyte of *Phyllanthus acidus* in India and belongs to the boninense species complex (Damm et al. 2012b).

139. *Colletotrichum pisicola* Damm, in Damm, O'Connell, Groenewald & Crous, Stud. Mycol. 79: 71 (2014)

This species is a pathogen only of *Pisum* sp. in the USA. *Colletotrichum pisicola* is characterized by distinctly curved conidia with few, short, pale brown setae with rounded tips. It is the basal species of the destructivum species complex (Damm et al. 2014). The sequences of all loci studied in Damm et al. (2014) are unique for this species.

140. *Colletotrichum proteae* F. Liu, Damm, L. Cai & Crous, Fungal Diversity 61: 100 (2013)

It is a pathogen only on *Protea* sp. in South Africa. Even though, the conidia of *C. proteae* resemble the acutatum species complex, phylogenetically this species clusters in the gloeosporioides species complex with a close affinity to *C. gloeosporioides* (Liu et al. 2013b, Cannon et al. 2012).

141. *Colletotrichum pseudoacutatum* Damm, P.F Cannon & Crous, in Damm, Cannon, Woudenberg, & Crous, Stud. Mycol. 73: 91 (2012)

This taxon is only known from *Pinus radiata* in Chile. It is basal to the acutatum species complex and considered as a singleton species (Cannon et al. 2012, Hyde et al. 2014).

142. *Colletotrichum pseudomajus* F. Liu, L. Cai, Crous & Damm, Persoonia, Mol. Phyl. Evol. Fungi 33: 91 (2014)

Colletotrichum pseudomajus is an endophyte only known on *Camellia sinensis* in Taiwan and belongs to the gigasporum species complex (Liu et al. 2014).

143. *Colletotrichum psidii* Curzi, Atti Ist. bot. R. Univ. Pavia, 3 Sér. 3(3): 207 (1927)

Only one isolate is available for this species that is known as a pathogen of *Psidium* in Italy, but it is well separated from all other species by its ITS sequence (Weir et al. 2012). *Colletotrichum psidii* belongs to the kahawae clade within gloeosporioides species complex (Weir et al. 2012).

144. *Colletotrichum pyricola* Damm, P.F. Cannon & Crous, in Damm, Cannon, Woudenberg, & Crous, Stud. Mycol. 73: 94 (2012)

This species is known only from New Zealand causing fruit rot of *Pyrus communis* (Damm et al. 2012b). It belongs to the acutatum species complex and can be identified with its unique ACT, TUB2, CHS-1, GAPDH and HIS3 sequences (Damm et al. 2012b).

145. *Colletotrichum queenslandicum* B. Weir & P.R. Johnst., in Weir, Johnston & Damm, Stud. Mycol. 73: 164 (2012)

This is a pathogen, known from *Capsicum* sp., *Carica papaya* and *Persea americana* in Australia, from *Coffea* sp. in Fiji and *Olea europaea* in Montenegro (Weir et al. 2012, Schena et al. 2014, De Silva et al. 2016). *Colletotrichum queenslandicum* belongs to the musae clade within the gloeosporioides species complex. It can be best distinguished with the use of TUB2, GAPDH and GS sequences (Weir et al. 2012).

146. *Colletotrichum quinquefoliae* Jayawardena, Bulgakov & K.D. Hyde, in Li et al. Fungal Diversity 78: 83 (2016)

This taxon is a saprobe and a weak pathogen on *Parthenocissus quinquefolia* in Russia. It belongs to the dematium species complex (Li et al. 2016).

147. *Colletotrichum radialis* F. Liu, L. Cai, Crous & Damm, Persoonia, Mol. Phyl. Evol. Fungi 33: 93 (2014)

Colletotrichum radialis belongs to the gigasporum species complex. *Colletotrichum radialis* has been isolated from a root of an undetermined host in Costa Rica (Liu et al. 2014).

148. *Colletotrichum rhexiae* Ellis & Everh., Proc. Acad. nat. Sci. Philad. 46: 372 (1894)

This species is a pathogen of *Rhexia* sp. in the USA as well as a fruit endophyte on *Vaccinium macrocarpon* in the USA (Doyle et al. 2013). *Colletotrichum rhexiae* belongs to the kahawae clade within the gloeosporioides species complex (Hyde et al. 2014).

149. *Colletotrichum rhombiforme* Damm, P.F. Cannon & Crous, in Damm, Cannon, Woudenberg, & Crous, Stud. Mycol. 73: 95 (2012)

Colletotrichum rhombiforme is a pathogen of *Olea europaea* (Portugal) and *Vaccinium macrocarpum* (USA) and belongs to the acutatum species complex (Damm et al. 2012b). It can be distinguished by its rhomboidal ascospores. This species can be separated from other species by all the sequences studied in Damm et al. (2012b) except CHS-1; best identified with TUB2 and ITS sequence data.

150. *Colletotrichum riograndense* D.M. Macedo, R.W. Barreto, O.L. Pereira & B.S. Weir, in Macedo, Pereira, Hora Jr., Weir & Barreto *Australasian Plant Pathology* 45: 49 (2016)

This taxon is a pathogen on *Tradescantia* viz. *fluminensis* in Brazil and a member of the spaethianum species complex. *Colletotrichum riograndense* is closely related to *C. bletillum* and *C. incanum* (Macedo et al. 2016).

151. *Colletotrichum rusci* Damm, P.F. Cannon & Crous, in Damm, Woudenberg, Cannon & Crous, *Fungal Diversity* 39: 72 (2009)

This species is a pathogen of *Ruscus* sp. in Italy (Damm et al. 2009). It is a singleton species and phylogenetically close to *C. trichellum* (Cannon et al. 2012).

152. *Colletotrichum salicis* (Fuckel) Damm, P.F. Cannon & Crous, in Damm, Cannon, Woudenberg, & Crous, *Stud. Mycol.* 73: 97 (2012)

This species is a pathogen on *Acer platanoides* (USA), *Fragaria × ananassa* (New Zealand), *Malus domestica* (Germany, New Zealand), *Populus* sp. (Netherlands, New Zealand), *Pyrus pyrifolia* (New Zealand), *Salix* sp. (Germany, Netherlands, New Zealand and UK) and *Solanum lycopersicum* (Germany) (Damm et al. 2012b). It belongs to the acutatum species complex and can be distinguished with HIS3, TUB2, GAPDH and ACT (Damm et al. 2012b). Sexual morph of this species has been identified as *Glomerella salicis* (Damm et al. 2012b).

153. *Colletotrichum salsolae* B. Weir & P.R. Johnst., in Weir, Johnston & Damm, *Stud. Mycol.* 73: 164 (2012)

It is known to be pathogenic on *Salsola* sp. in Hungary (Schwarczinger et al. 1998). *Colletotrichum salsolae* belongs to the musae clade within the gloeosporioides species complex and can be distinguished using TUB2 and GAPDH (Weir et al. 2012).

154. *Colletotrichum sansevieriae* Miho Nakam. & Ohzono, in Nakamura, Ohzono, Iwai & Arai, *J. Gen. Pl. Path.* 72(4): 253 (2006)

It is known only on *Sansevieria* sp. in Australia, Japan, Korea and the USA (Nakamura et al. 2006, Aldaoud et al. 2011, Palmateer et al. 2012, Park et al. 2013, Liu et al. 2014). It is a singleton species closely related to *C. ledebouriae* (Crous et al. 2013b)

155. *Colletotrichum scovillei* Damm, P.F. Cannon & Crous, in Damm, Cannon, Woudenberg, & Crous, *Stud. Mycol.* 73: 100 (2012)

It causes diseases of *Capsicum* sp. (Brazil, China, Indonesia, Taiwan and Thailand), and belongs to the acutatum species complex (Damm et al. 2012b, Caires et al. 2014, Baroncelli et al. 2015b, Hao et al. 2016). Use of TUB2, GAPDH and ACT sequence data can distinguish *C. scovillei* from other species of the acutatum species complex; with GAPDH being most effective.

156. *Colletotrichum sedi* Jayawardena, Bulgakov & K.D. Hyde, in Liu et al., *Fungal Diversity* 72:27 (2015)

This species is a saprobe on *Sedum* sp. in Russia and belongs to the dematium species complex (Liu et al. 2015b). *Colletotrichum sedi* is a sister taxon to *C. circinans* and *C. spinaciae* and produces appressoria in small groups or short chains and smaller conidia.

157. *Colletotrichum siamense* Phoulivong, L. Cai & K.D. Hyde, in Prihastuti, Cai, Chen, McKenzie & Hyde, *Fungal Diversity* 39: 98 (2009)

Colletotrichum siamense was considered to be a species complex, in which the cryptic species can be resolved using the *ApMat* marker (Sharma et al. 2015). However, Liu et al. (2016) showed using the Genealogical Concordance Phylogenetic Species Recognition (GCPSR) that it is not a species complex and the earlier described species *C. communis*, *C. dianesei*, *C. endomangiferae*, *C. hymenocallidis*, *C. jasmini-sambac*, *C. melanocaulon* and *C. murrayae* were synonymised with *C. siamense*. It occurs as a pathogen on a wide range of hosts and has a worldwide occurrence including *Capsicum* sp., *Olea europaea*, *Persea americana*, *Pistacia vera* in Australia (Weir et al.

2012, Schena et al. 2014, De Silva et al. 2016), *Mangifera indica* in Brazil and Colombia (Lima et al. 2013, Sharma et al. 2015, Hoz et al. 2016), *Camellia sinensis*, *Citrus* sp., *Hymenocallis* sp., *Jasminum sambac* and *Murraya* sp. in China (Yang et al. 2009, Wikee et al. 2011, Peng et al. 2012, Wang et al. 2016), *Bauhinia variegata*, *Cassia fusciculata*, *Citrus* sp., *Cocos nucifera*, *Ficus elastic*, *Mangifera indica*, *Psidium guajava* and *Saraca indica* in India (Lima et al. 2013, Liu et al. 2015a, Sharma et al. 2015), *Citrus*, *Murraya* sp. and on Strawberry in Italy (Peng et al. 2012), *Dioscorea rotunda*, *Commelina* sp. from Nigeria, *Carica papaya* from South Africa, *Coffea Arabica*, *Capsicum annuum*, *Pennisetum purpureum*, and *Cymbopogon citrates* in Thailand (Manamgoda et al. 2013), *Fragaria* × *ananassa*, *Malus domestica* *Vaccinium macrocarpon*, *Vitis vinifera* from the USA (Weir et al. 2012, Doyle et al. 2013) and *Jasminium sambac* in Vietnam (Prihastuti et al. 2009, Wikee et al. 2011). *Colletotrichum siamense* can be identified with the use of CAL or TUB sequence data (Weir et al. 2012).

158. *Colletotrichum sidae* Damm & P.F. Cannon, in Damm, Cannon, Liu, Barreto, Guatimosim & Crous, Fungal Diversity 61: 44 (2013)

This species is a pathogen on *Sida spinosa* (Prickly sida) in the USA and belongs to the orbiculare species complex (Damm et al. 2013). It can be distinguished with GS and ITS sequences.

159. *Colletotrichum simmondsii* R.G. Shivas & Y.P. Tan, Fungal Diversity 39:119 (2009)

It is a pathogen on *Capsicum* sp., *Carica papaya* (Australia), *Cyclamen* sp. (Netherlands), *Fragaria* × *ananassa* (Australia), *Mangifera indica* (Australia), *Murraya* sp. (China) and *Protea cynaroides* (USA) (Damm et al. 2012b, Peng et al. 2012, De Silva et al. 2016). *Colletotrichum simmondsii* is also a stem endophyte of *Actinidia chinensis* in Australia (Shivas & Tan 2009). This species belongs to the acutatum species complex and can be distinguished with the analysis of GAPDH and TUB2 sequence data; with effectively by TUB2 gene (Damm et al. 2012b).

160. *Colletotrichum sloanei* Damm, P.F. Cannon & Crous, in Damm, Cannon, Woudenberg, & Crous, Stud. Mycol. 73: 103 (2012)

It is known as an endophyte of *Theobroma cacao* in Malaysia. This species belongs to the acutatum species complex and can be distinguished with the use of TUB2, ACT and HIS3 sequence data (Damm et al. 2012b).

161. *Colletotrichum somersetense* J.A. Crouch, IMA Fungus 5(1):27 (2014)

This species is a pathogen on leaves of *Sorghastrum nutans* in the USA (Crouch 2014). *Colletotrichum somersetense* belongs to the caudatum species complex. It can be identified using any of the gene regions (*Apn2*, ITS, *Sod2*, *Mat/Apn2*) used in Crouch (2014).

162. *Colletotrichum spaethianum* (Allesch.) Damm, P.F. Cannon & Crous, in Damm, Woudenberg, Cannon & Crous, Fungal Diversity 39: 74 (2009)

Colletotrichum spaethianum has been recorded as a saprobe on dead stems of *Hosta sieboldiana* in Germany, *Hymenocallis americana* and *Peucedanum praeruptorum* in China (Damm et al. 2009, Yang et al. 2009, Guo et al. 2013) and as a pathogen of *Allium fistulosum* in Brazil, *Hermerocallis* sp. in Brazil and New Zealand and *Lillium* sp. in Korea (Damm et al. 2009, Vieira et al. 2014b, Cheon & Jeon 2016, Santana et al. 2016). It belongs to the spaethianum species complex (Cannon et al. 2012) and can be distinguished by its setae that have usually acute tips and cylindrical to conical bases and by its appressoria that are irregular in outline and more or less lobed (Damm et al. 2009).

163. *Colletotrichum spinaciae* Ellis & Halst., J. Mycol. 6(1): 34 (1890)

This taxon is a pathogen on *Spinacea* sp. in Germany, Italy, the Netherlands and Turkey (Damm et al. 2009, Yang et al. 2009, Kurt et al. 2016), *Chenopodium album* in the USA, *Portulaca oleracea* in Canada and *Medicago sativa* in the Netherlands (Damm et al. 2009). On hosts other than spinach it develops only weak symptoms (von Arx 1957). It belongs to the dematium species complex (Cannon et al. 2012).

164. *Colletotrichum spinosum* Damm & P.F. Cannon, in Damm, Cannon, Liu, Barreto, Guatimosim & Crous, Fungal Diversity 61: 46 (2013)

This species causes seed blight and stem anthracnose of *Xanthium spinosum* in Argentina and Australia (Damm et al. 2013). It belongs to the orbiculare species complex and can be identified effectively based on GAPDH, HIS3, TUB2 and GS sequences data.

165. *Colletotrichum sublineola* Henn. ex Sacc. & Trotter, Syll. fung. (Abellini) 22: 1206 (1913)

It is known only as a pathogen of *Sorghum* sp. in Togo and the USA (Crouch & Tomaso-Peterson 2012). *Colletotrichum sublineola* is a member of the graminicola species complex (Cannon et al. 2012). It can be distinguished by *Apn2*, *Apn2/Mat1* and SOD2 sequence data (Crouch & Tomaso-Peterson 2012).

166. *Colletotrichum syzygiicola* Udayanga, Manamgoda & K.D. Hyde [as 'syzygicola'], in Udayanga, Manamgoda, Liu, Chukeatirote & Hyde, Fungal Diversity 61: 173 (2013)

This species belongs to the gloeosporioides species complex and causes anthracnose of *Citrus aurantifolia* and *Syzygium samarangense* in Thailand (Udayanga et al. 2013).

167. *Colletotrichum tabacum* Böning, Prakt. Bl. Pflanzenbau Pflanzenschutz 10: 89 (1932)

This taxon causes anthracnose of *Nicotiana* sp. in France, India, Germany, and Zimbabwe as well as on *Centella asiatica* in Madagascar (Damm et al. 2014). It belongs to the destructivum species complex and can be distinguish by its appressoria with a distinct penetration pore with a dark halo (Damm et al. 2014). *Colletotrichum tabacum* is distinguished from the other species in the destructivum complex by all the loci studied by Damm et al. (2014).

168. *Colletotrichum tamarilloi* Damm, P.F. Cannon & Crous, in Damm, Cannon, Woudenberg, & Crous, Stud. Mycol. 73: 105 (2012)

Colletotrichum tamarilloi belongs to the acutatum species complex and occurs as a pathogen on *Solanum betaceum* in Colombia (Damm et al. 2012a, Hoz et al. 2016). This species can be separated from other species using CHS-1, HIS3, TUB2 and GAPDH sequences; most effectively by GAPDH sequence data (Damm et al. 2012a).

169. *Colletotrichum tanacetii* M. Barimani, S.J. Pethybridge, N. Vaghefi, F.S. Hay & P.W.J. Taylor, Pl. Path. 62(6): 1248–1257 (2013)

It is a pathogen, only known from *Tanacetum cinerariifolium* in Australia and Tasmania (Barimani et al. 2013, Damm et al. 2014). *Colletotrichum tanacetii* belongs to the destructivum species complex (Damm et al. 2014).

170. *Colletotrichum tebeesti* Damm & P.F. Cannon, in Damm, Cannon, Liu, Barreto, Guatimosim & Crous, Fungal Diversity 61: 48 (2013)

This taxon belongs to the orbiculare species complex and is known as a pathogen on *Malva pusilla* in Canada (Damm et al. 2014). *Colletotrichum tebeestii* can be differentiated from the other species in the orbiculare species complex by using GAPDH sequence data.

171. *Colletotrichum temperatum* V. Doyle, P.V. Oudem. & S.A. Rehner, PLoS ONE 7(12): e51392, 17 (2012)

This species is a pathogen on *Vaccinium macrocarpon* as well as a stem endophyte on *V. macrocarpon* in the USA. *Colletotrichum temperatum* belongs to the gloeosporioides species complex (Doyle et al. 2013).

172. *Colletotrichum theobromicola* Delacr., Bull. Soc. mycol. Fr. 21: 191 (1905)

Colletotrichum theobromicola is broadly distributed as a pathogen in tropical and subtropical regions on a wide range of hosts including *Acca* sp., *Annona* sp., *Limonium* sp., *Mangifera indica*, *Olea* sp., *Stylosanthes* sp., *Theobroma cacao*, *Quercus* sp. (Weir et al. 2012, Schena et al. 2014, Sharma et al. 2015, Hoz et al. 2016). *Colletotrichum theobromicola* is also known as a pathogen of strawberry runners; previously known as *C. fragaria*, which has been synonymized with *C. theobromicola* by Weir et al. (2012). It belongs to the gloeosporioides species complex and ITS sequence can be used to distinguish this species from all other taxa.

173. *Colletotrichum ti* B. Weir & P.R. Johnst., in Weir, Johnston & Damm, Stud. Mycol. 73: 171 (2012)

This species is a leaf pathogen of *Cordyline* sp. in New Zealand. *Colletotrichum ti* belongs to the kahawae clade within the gloeosporioides species complex (Weir et al 2012). TUB2 and GAPDH sequences can be used to distinguish this taxon (Weir et al 2012).

174. *Colletotrichum tofieldiae* (Pat.) Damm, P.F. Cannon & Crous, in Damm, Woudenberg, Cannon & Crous, *Fungal Diversity* 39: 77 (2009)

This taxon occurs on many host plants including *Agapanthus* sp. in Portugal, *Dianthus* sp. in the UK, *Lupinus* sp. and *Semele gayae* in Germany, and *Tofieldia* sp. in Switzerland and in China (Damm et al. 2009, Hacquard et al. 2016). This species has also been collected as a leaf endophyte of *Bletilla ochracea* in China (Tao et al. 2013) and as a beneficial root endophyte of *Arabidopsis thaliana* in Spain (Hacquard et al. 2016). *Colletotrichum tofieldiae* belongs to the spaethianum species complex (Cannon et al. 2012).

175. *Colletotrichum torulosum* Damm, P.F. Cannon, Crous, P.R. Johnst. & B. Weir, in Damm, Cannon, Woudenberg, Johnston, Weir, Tan, Shivas & P.Crous, *Stud. Mycol.* 73: 32 (2012)

This taxon is an endophyte of *Solanum melongena* and a pathogen of *Passiflora edulis* in New Zealand and is characterized by highly convoluted appressoria (Damm et al. 2012a). *Colletotrichum torulosum* belongs to the boninense species complex (Damm et al. 2012a).

176. *Colletotrichum trichellum* (Fr.) Duke, *Trans. Br. mycol. Soc.* 13(3–4): 173 (1928)

This species occurs as a pathogen on *Hedera* sp. worldwide (Damm et al. 2009, Hyde et al. 2009). It is a singleton species with close affinity to *C. rusci* (Cannon et al. 2012).

177. *Colletotrichum trifolii* Bain, in Bain & Essary, *J. Mycol.* 12(5): 193 (1906)

This species is a pathogen on *Medicago sativa* and *Trifolium pratense* in the USA and on *Malva sylvestris* in China (Damm et al. 2014, Samac et al. 2014, Zhou et al. 2014). *Colletotrichum trifolii* belongs to the orbiculare species complex and has darker and often knobby setae than the other species in this complex (Damm et al. 2014). It is closely related to *C. malvarum* and can be distinguished with GS sequences.

178. *Colletotrichum tropicale* E.I. Rojas, S.A. Rehner & Samuels, *Mycologia* 102(6): 1331 (2010)

It has been recorded from hosts in tropical America including *Annona muricata* (*Annonaceae*), *Cordia alliodora* (*Boraginaceae*), *Trichilia tuberculata* (*Meliaceae*), *Viola surinamensis* (*Myristicaceae*), and as leaf endophyte of *Theobroma cacao* (*Malvaceae*) (Rojas et al. 2010), *Litchi chinensis* (*Sapindaceae*) in Japan (Weir et al. 2012) and *Pennisetum purpureum* in Thailand (Manamgoda et al. 2013). *Colletotrichum tropicale* belongs to the gloeosporioides species complex and can be distinguished using TUB2, CHS-1, GS or SOD2 sequences (Weir et al. 2012).

179. *Colletotrichum tropicicola* Phouliv., Noireung, L. Cai & K.D. Hyde, *Cryptog. Mycol.* 33(3): 353 (2012)

This species is an endophyte of *Citrus maxima* and *Paphiopedilum bellatulum* in Thailand (Noireung et al. 2012). It is a singleton species with close affinity to *C. excelsum-altitudinum*.

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

This taxon has a wide host range including the families *Amaranthaceae*, *Amaryllidaceae*, *Apocynaceae*, *Asteraceae*, *Basellaceae*, *Brassicaceae*, *Cactaceae*, *Caricaceae*, *Convolvulaceae*, *Cyperaceae*, *Euphorbiaceae*, *Fabaceae*, *Malvaceae*, *Nyctaginaceae*, *Oleaceae*, *Piperaceae*, *Plumbaginaceae*, *Poaceae*, *Polygonaceae*, *Rosaceae*, *Solanaceae* and *Theaceae* (Damm et al. 2009, De Silva et al. 2016, He et al. 2016, Wang et al. 2016). It belongs to the truncatum species complex (Cannon et al. 2012). *Colletotrichum truncatum* is associated with symptoms of leaf tip die-back, foliar blight and leaf spots (Shenoy et al. 2007). The taxon is also known to be pathogenic to humans (Damm et al. 2009, Squizzato et al. 2015). *Colletotrichum aciculare* which was introduced in Ariyawansa et al. 2015 is also synonymized under this species, due to the high morphological and phylogenetic similarities (This study).

181. *Colletotrichum utrechtense* Damm, in Damm, O'Connell, Groenewald & Crous, *Stud. Mycol.* 79: 77 (2014)

This species is a pathogen on *Trifolium pratense* in the Netherlands and belongs to the destructivum species complex (Damm et al. 2014). *Colletotrichum utrechtense* can be distinguished by CHS-1, HIS3 and TUB2 sequence data (Damm et al. 2014).

182. *Colletotrichum verruculosum* Damm, P.F. Cannon & Crous, in Damm, Woudenberg, Cannon & Crous, *Fungal Diversity* 39: 81 (2009)

This species is known on *Crotalaria juncea* from Zimbabwe (Damm et al. 2009). *Colletotrichum verruculosum* belongs to the spaethianum species complex (Cannon et al. 2012).

183. *Colletotrichum vietnamense* F. Liu, L. Cai, Crous & Damm, Persoonia, Mol. Phyl. Evol. Fungi 33: 93 (2014)

This species is a pathogen on *Coffea* sp. in Vietnam and belongs to the gigasporum species complex (Liu et al. 2014).

184. *Colletotrichum vignae* Damm, in Damm, O'Connell, Groenewald & Crous, Stud. Mycol. 79: 78 (2014)

Colletotrichum vignae is known from *Vigna unguiculata* in Nigeria causing anthracnose and belongs to the destructivum species complex (Damm et al. 2014). It is one of the slowest growing species in the destructivum species complex and can be identified by its ITS, GAPDH, HIS3 and ACT sequences (Damm et al. 2014).

185. *Colletotrichum viniferum* L.J. Peng, L. Cai, K.D. Hyde & Z-Y. Ying, Mycoscience 54(1): 36 (2013)

It has been identified as a pathogen on *Vitis vinifera* in China (Peng et al. 2013, Yan et al. 2015). *Colletotrichum viniferum* belongs to the gloeosporioides species complex (Peng et al. 2013).

186. *Colletotrichum walleri* Damm, P.F. Cannon & Crous, in Damm, Cannon, Woudenberg, & Crous, Stud. Mycol. 73: 106 (2012)

This species is an endophyte of *Coffea arabica* in Vietnam and belongs to the acutatum species complex (Damm et al. 2012b). It is easily distinguished by using HIS3 and ITS sequence data.

187. *Colletotrichum wuxiense* Y.C. Wang, X.C. Wang & Y.J. Yang, Scientific Reports 6 (no:35287): 8 (2016)

It is a pathogen on leaves of *Camellia sinensis* in China. This species belongs in the gloeosporioides species complex (Wang et al. 2016). *Colletotrichum wuxiense* can be distinguished from the other members of the complex by its concatenated *ApMat* and GS sequence data.

188. *Colletotrichum xanthorrhoeae* R.G. Shivas, Bathgate & Podger, Mycol. Res. 102 (3): 280 (1998)

This species is a pathogen on *Xanthorrhoea preissii* causing leaf spot in Australia (Shivas et al. 1998). *Colletotrichum xanthorrhoeae* belongs to gloeosporioides species complex and ITS sequence can be used to identify this species (Weir et al. 2012).

189. *Colletotrichum yunnanense* Xiao Ying Liu & W.P. Wu, in Liu, Xie & Duan, Mycotaxon 100: 139 (2007)

This species is a leaf endophyte on *Buxus* sp. in China (Liu et al. 2007, Xia-Ying et al. 2007). *Colletotrichum yunnanense* is a singleton species and closely related to *C. dracaenophilum* (Cannon et al. 2012, Hyde et al. 2014).

190. *Colletotrichum zoysiae* J.A. Crouch, IMA Fungus 5(1):27 (2014)

This taxon belongs to the caudatum species complex and has been recorded as a pathogen on *Zoysia tenuifolia* only in Japan (Crouch 2014). It can be identified using any of the gene regions (*Apn2*, ITS, *Sod2*, *Mat/Apn2*) used in Crouch (2014).

Doubtful species

Colletotrichum phaseolorum S. Takim., Ann. phytopath. Soc. Japan 5: 21 (1934)

This taxon is a pathogen of *Phaseolus radiatus* var. *aureus* and on *Vigna sinensis* in Japan (Damm et al. 2009). *Colletotrichum phaseolorum* is a singleton species, phylogenetically close to *C. chlorophyti* (Damm et al. 2009, Hyde et al. 2014). However, as it has two ex-type strains belonging to two different species, we consider this species as a doubtful species.

Excluded species

Colletotrichum corchori-capsularis X.P. Niu, H. Gao, J.M. Qi, M.C. Chen & J.G. Su [as 'corchorum-capsularis'], Scientific Reports 6 (no. 25179): 4 (2016)

Colletotrichum corchorum-capsularis belongs to the *truncatum* species complex. This is a pathogen on *Corchorus capsularis* in China (Niu et al. 2016). However, as the authors have not listed an authentic dried type specimen, this species cannot be accepted as an authentic species.

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Table 1 GenBank accession Numbers of the accepted *Colletotrichum* species

Species Name	Isolate No	GenBank Accession Numbers											
		ITS	GAPDH	CHS-1	HIS3	ACT	TUB2	CAL	GS	SOD2	ApMat	Apn2	Mat1
<i>C. abscissum</i>	COAD 1877*	KP84312 6	KP84312 9	KP843132	KP843138	KP843141	KP843135	-	-	-	-	-	-
<i>C. acerbum</i>	CBS 128530*	JQ94845 9	JQ94879 0	JQ949120	JQ949450	JQ949780	JQ950110	-	-	-	-	-	-
<i>C. acutatum</i>	CBS 112996*	JQ00577 6	JQ94867 7	JQ005797	JQ005818	JQ005839	JQ005860	-	-	-	-	-	-
<i>C. aenigma</i>	ICMP 18608*	JX01024 4	JX01004 4	JX009774	-	JX009443	JX010389	JX009683	JX01007 8	JX01031 1	KM36014 3	-	-
<i>C. aeshynomenes</i>	ICMP 17673*	JX01017 6	JX00993 0	JX009799	-	JX009483	JX010392	JX009721	JX01008 1	JX01031 4	-	-	-
<i>C. agaves</i>	CBS 118190	DQ2862 21	-	-	-	-	-	-	-	-	-	-	-
<i>C. alatae</i>	ICMP 17919*	JX01019 0	JX00999 0	JX009837	-	JX009471	JX010383	JX009738	JX01006 5	JX01030 5	KC88893 2	-	-
<i>C. alienum</i>	ICMP 12071*	JX01025 1	JX01002 8	JX009882	-	JX009572	JX010411	JX009654	JX01010 1	JX01033 3	KM36014 4	-	-
<i>C. alcornii</i>	IMI 1766192*	JX07685 8	-	-	-	-	-	-	-	-	-	-	-
<i>C. americanae-borealis</i>	CBS 136232*	KM1052 24	KM1055 79	KM10529 4	KM105364	KM10543 4	KM105504	-	-	-	-	-	-
<i>C. annellatum</i>	CBS 129826*	JQ00522 2	JQ00530 9	JQ005396	JQ005483	JQ005570	JQ005656	JQ005743	-	-	-	-	-
<i>C. anthrisci</i>	CBS 125334*	GU2278 45	GU2282 37	GU22833 5	-	GU227943	GU228139	-	-	-	-	-	-

Species Name	Isolate No	GenBank Accession Numbers											
		ITS	GAPDH	CHS-1	HIS3	ACT	TUB2	CAL	GS	SOD2	ApMat	Apn2	Mat1
<i>C. antirrhinicola</i>	CBS 102189*	KM1051 80	KM1055 31	KM10525 0		KM10539 0	KM105460	-	-	-	-	-	-
<i>C. aotearoa</i>	ICMP 18537*	JX01020 5	JX01000 5	JX009853	-	JX009564	JX010420	JX009611	3	JX01011 5	JX01034 0	KC88893	-
<i>C. aracearum</i>	CGMCC 3.14982*	KX8531 67	KX8935 86	-	-	KX893578	KX893582	-	-	-	-	-	-
<i>C. arxii</i>	CBS 132511*	KF68771 6	KF68784 3	KF687780	-	KF687802	KF687881	KF687819	6	KF68775	-	-	-
<i>C. asianum</i>	ICMP 18580*	FJ97261 2	JX01005 3	JX009867	-	JX009584	JX010406	FJ917506	6	JX01009 8	JX01032 FR718814	-	-
<i>C. australe</i>	CBS 116478*	JQ94845 5	JQ94878 6	JQ949116	JQ949446	JQ949776	JQ950106	-	-	-	-	-	-
<i>C. axonopodi</i>	IMI 279189*	EU55408 6	-	-	-	-	-	-	-	-	-	-	-
<i>C. baltimorense</i>	BPI892771*	JX07686 6	-	-	-	-	-	-	-	JX07688 6	-	JX0769 27	JX076905
<i>C. beeveri</i>	CBS 128527*	JQ00517 1	JQ00525 8	JQ005345	JQ005432	JQ005519	JQ005605	JQ005692	-	-	-	-	-
<i>C. bidentis</i>	COAD 1020*	KF17848 1	KF17850 6	KF178530	KF178554	KF178578	KF178602	-	KF17862 7	-	-	-	-
<i>C. bletillum</i>	CGMCC 3.15117*	JX62517 8	KC8435 06	-	-	KC843542	JX625207	-	-	-	-	-	-
<i>C. boninense</i>	CBS 123755*	JQ00515 3	JQ00524 0	JQ005327	JQ005414	JQ005501	JQ005588	JQ005674	-	-	-	-	-
<i>C. brasiliense</i>	CBS 128501*	JQ00523 5	JQ00532 2	JQ005409	JQ005496	JQ005583	JQ005669	JQ005756	-	-	-	-	-
<i>C. brassicola</i>	CBS 101059*	JQ00517	JQ00525	JQ005346	JQ005433	JQ005520	JQ005606	JQ005693	-	-	-	-	-

Species Name	Isolate No	GenBank Accession Numbers											
		ITS	GAPDH	CHS-1	HIS3	ACT	TUB2	CAL	GS	SOD2	ApMat	Apn2	Mat1
		2	9										
<i>C. brevisporum</i>	BCC 38876*	JN05023 8	JN05022 7	KF687760	-	JN050216	JN050244	-	-	-	-	-	-
<i>C. brisbanense</i>	CBS 292.67*	JQ94829 1	JQ94862 1	JQ948952	JQ949282	JQ949612	JQ949942	-	-	-	-	-	-
<i>C. bryoniicola</i>	CBS 109849*	KM1051 81	KM1055 32	KM10525 1	KM105321	KM10539 1	KM105461	-	-	-	-	-	-
<i>C. cairnsense</i>	BRIP 63642*	KU9236 72	KU9237 04	KU92371 0	KU923722	KU923716	KU923688	-	-	-	-	-	-
<i>C. camelliae</i>	CGMCC 3.14925*	KJ95508 1	KJ95478 2	-	-	KJ954363	KJ955230	KJ954634	KJ95493 2	-	KJ954497	-	-
<i>C. camelliae-japonicae</i>	CGMCC3.18118 *	KX8531 65	KX8935 84	-	-	KX893576	KX893580	-	-	-	-	-	-
<i>C. carthami</i>	SAPA100011*	AB6969 98	-	-	-	-	AB696992	-	-	-	-	-	-
<i>C. caudatum</i>	CBS13602*	JX07686 0	-	-	-	-	-	-	-	JX07687 8	-	JX0769 32	JX076893
<i>C. caudasporum</i>	CGMCC 3.15106*	JX62516 2	KC8435 12	-	-	KC843526	JX625190	-	-	-	-	-	-
<i>C. cereale</i>	CBS 129663*	JQ00577 4	-	JQ005795	JQ005816	JQ005837	JQ005858	-	-	-	-	-	-
<i>C. chengpingense</i>	MFLUCC 15- 0022*	KP68315 2	KP85246 9	KP852449	-	KP683093	KP852490	-	-	-	-	-	-
<i>C. chlorophyti</i>	IMI 103806*	GU2278 94	GU2282 86	GU22838 4	-	GU227992	GU228188	-	-	-	-	-	-
<i>C. chrysanthemi</i>	CBS 126518*	JQ94827 1	JQ94860 1	JQ948932	JQ949262	JQ949592	JQ949922	-	-	-	-	-	-

Species Name	Isolate No	GenBank Accession Numbers											
		ITS	GAPDH	CHS-1	HIS3	ACT	TUB2	CAL	GS	SOD2	ApMat	Apn2	Mat1
<i>C. circinans</i>	CBS 221.81*	GU2278 55	GU2282 47	GU22834 5	-	GU227953	GU228149	-	-	-	-	-	-
<i>C. citri</i>	ZJUC41*	KC2935 81	KC2937 41	-	-	KC293621	KC293661	KC29370 1	KC2937 81	-	-	-	-
<i>C. citricola</i>	SXC151*	KC2935 76	KC2937 36	KC293792	-	KC293616	KC293656	KC29369 6	KC2937 76	-	-	-	-
<i>C. clidemiae</i>	ICMP 18658*	JX01026 5	JX00998 9	JX009877	-	JX009537	JX010438	JX009645	JX01012 9	JX01035 6	KC88892 9	-	-
<i>C. cliviae</i>	CBS 125375*	GQ4856 07	GQ8567 56	GQ85672 2	-	GQ856777	GQ849440	-	-	-	-	-	-
<i>C. coccodes</i>	CBS 369.75*	HM1716 79	HM1716 73	JX546681	-	HM17166 7	JX546873	-	-	-	-	-	-
<i>C. colombiense</i>	CBS 129818*	JQ00517 4	JQ00526 1	JQ005348	JQ005435	JQ005522	JQ005608	JQ005695	-	-	-	-	-
<i>C. conoides</i>	CAUG17*	KP89016 8	KP89016 2	KP890156	-	KP890144	KP890174	KP890150	-	-	-	-	-
<i>C. constrictum</i>	CBS 128504*	JQ00523 8	JQ00532 5	JQ005412	JQ005499	JQ005586	JQ005672	JQ005759	-	-	-	-	-
<i>C. cordylinicola</i>	ICMP 18579*	JX01022 6	JX00997 5	JX009864	-	HM47023 5	JX010440	HM47023 8	JX01012 2	JX01036 1	JQ899274	-	-
<i>C. cosmi</i>	CBS 853.73*	JQ94827 4	JQ94860 4	JQ948935	JQ949265	JQ949595	JQ949925	-	-	-	-	-	-
<i>C. costaricense</i>	CBS 330.75*	JQ94818 1	JQ94851 1	JQ948842	JQ949172	JQ949502	JQ949832	-	-	-	-	-	-
<i>C. curcumae</i>	IMI 288937*	GU2278 93	GU2282 85	GU22838 3	GU228089	GU227991	GU228187	-	-	-	-	-	-
<i>C. cuscutae</i>	IMI 304802*	JQ94819	JQ94852	JQ948856	JQ949186	JQ949516	JQ949846	-	-	-	-	-	-

Species Name	Isolate No	GenBank Accession Numbers											
		ITS	GAPDH	CHS-1	HIS3	ACT	TUB2	CAL	GS	SOD2	ApMat	Apn2	Mat1
		5	5										
<i>C. cymbidiicola</i>	IMI 347923*	JQ00516 6	JQ00525 3	JQ005340	JQ005427	JQ005514	JQ005600	JQ005687	-	-	-	-	-
<i>C. dacrycarpi</i>	CBS 130241*	JQ00523 6	JQ00532 3	JQ005410	JQ005497	JQ005584	JQ005670	JQ005757	-	-	-	-	-
<i>C. dematium</i>	CBS 125.25*	GU2278 19	GU2282 11	GU22830 9	GU228015	GU227917	GU228113	-	-	-	-	-	-
<i>C. destructivum</i>	CBS 136228*	KM1052 07	KM1055 61	KM10527 7	KM105347	KM10541 7	KM105487	-	-	-	-	-	-
<i>C. dracaenophilum</i>	CBS 118199*	JX51922 2	JX54670 7	JX519230	-	JX519238	JX519247	-	-	-	-	-	-
<i>C. duyunensis</i>	CGMCC 3.15105*	JX62516 0	KC8435 15	-	-	KC843530	JX625187	-	-	-	-	-	-
<i>C. echinochloae</i>	MAFF 511473*	AB4398 11	-	-	-	-	-	-	-	-	-	-	-
<i>C. eleusines</i>	MAFF 511155*	JX51921 8	-	-	-	JX519234	JX519243	-	-	-	-	-	-
<i>C. endophytica</i>	MFLUCC 13- 0418*	KC6338 54	KC8328 54	-	-	KF306258	-	KC81001 8	-	-	-	-	-
<i>C. endophytum</i>	CGMCC 3.15108*	JX62517 7	KC8435 21	-	-	KC843533	JX625206	-	-	-	-	-	-
<i>C. eremochloae</i>	CBS 129661*	JX51922 0	-	-	-	JX519236	JX519245	-	-	-	-	-	-
<i>C. euphorbiae</i>	CBS 134725*	KF77714 6	KF77713 1	KF777128	KF777134	KF777125	KF777247	-	-	-	-	-	-
<i>C. excelsum- altitudum</i>	CGMCC 3.15130*	HM7518 15	KC8435 02	-	-	KC843548	JX625211	-	-	-	-	-	-

Species Name	Isolate No	GenBank Accession Numbers											
		ITS	GAPDH	CHS-1	HIS3	ACT	TUB2	CAL	GS	SOD2	ApMat	Apn2	Mat1
<i>C. falcatum</i>	CBS 147945*	JQ005772		JQ005793	JQ005814	JQ005835	JQ005856	-	-	-	-	-	-
<i>C. fioriniae</i>	CBS 128517*	JQ948292	JQ948622	JQ948953	JQ949283	JQ949613	JQ949943	-	-	-	-	-	-
<i>C. fructi</i>	CBS 346.37*	GU227844	GU228236	GU228334	-	GU227942	GU228138	-	-	-	-	-	-
<i>C. fructicola</i>	ICMP 18581*	JX010165	JX010033	JX009866	-	FJ907426	JX010405	FJ917508	JX010095	JX010327	JQ807838	-	-
<i>C. fructivorum</i>	Coll1414 *	JX145145	-	-	-	-	JX145196	-	-	-	JX145300	-	-
<i>C. fuscum</i> *	CBS 133701*	KM105174	KM105524	KM105244	KM105314	KM105384	KM105454	-	-	-	-	-	-
<i>C. fusiforme</i>	MFLUCC 12-0437*	KT290266	KT290255	KT290253	-	KT290251	KT290256	-	-	-	-	-	-
<i>C. gigasporum</i>	CBS 133266*	KF687715	KF687822	KF687761	KF687844	-	KF687866	-	-	-	-	-	-
<i>C. gloeosporioides</i>	CBS 112999*	JQ005152	JQ005239	JQ005326	JQ005413	JQ005500	JQ005587	JQ005673	JX010085	JX010365	JQ807843	-	-
<i>C. godetiae</i>	CBS 133.44*	JQ948402	JQ948733	JQ949063	JQ949393	JQ949723	JQ950053	-	-	-	-	-	-
<i>C. graminicola</i>	CBS 130836*	JQ005767	-	JQ005788	-	JQ005830	JQ005851	-	-	-	-	-	-
<i>C. grevilleae</i>	CBS 132879*	KC297078	KC297010	KC296987	-	KC296941	KC297102	KC296963	-	-	-	-	-
<i>C. grossum</i>	CAUG7*	KP890165	KP890159	KP890153	-	KP890153	KP890171	KP890147	-	-	-	-	-
<i>C. guajavae</i>	IMI 350839*	JQ94827	JQ94860	JQ948931	JQ949261	JQ949591	JQ949921	-	-	-	-	-	-

Species Name	Isolate No	GenBank Accession Numbers											
		ITS	GAPDH	CHS-1	HIS3	ACT	TUB2	CAL	GS	SOD2	ApMat	Apn2	Mat1
		0	0										
<i>C. guizhouensis</i>	CGMCC 3.15112*	JX62515 8	KC8435 07	-	-	KC843536	JX625185	-	-	-	-	-	-
<i>C. hanau</i>	MAFF 3054042*	JX51921 7	-	JX519225	-	-	JX519242	-	-	-	-	-	-
<i>C. hebeiense</i>	MFLUCC13-0726*	KF15686 3	KF37749 5	KF289008	-	KF377532	KF288975	-	-	-	-	-	-
<i>C. hemerocallidis</i>	CDLG5*	JQ40000 5	JQ40001 2	JQ399998	-	JQ399991	JQ400019	KJ781319	-	-	-	-	-
<i>C. henanense</i>	CGMCC 3.17354*	KJ95510 9	KJ95481 0	-	-	KM02325 7	KJ955257	KJ954662	KJ95496 0	-	KJ954524	-	-
<i>C. higginsianum</i>	IMI 349061 *	KM1051 84	KM1055 35	KM10525 4	KM105324	KM10539 4	KM105464	-	-	-	-	-	-
<i>C. hippeastri</i>	CBS 125376*	JQ00523 1	JQ00531 8	JQ005405	JQ005492	JQ005579	JQ005665	JQ005752	-	-	-	-	-
<i>C. horii</i>	ICMP 10492*	GQ3296 90	GQ3296 81	JX009752	-	JX009438	JX010450	JX009604	JX01013 7	JX01037 0	JQ807840	-	-
<i>C. hsienjenchang</i>	MAFF 243051	AB7388 55	-	AB738846	AB738847	AB738845	-	-	-	-	-	-	-
<i>C. hymenocallidicola</i>	MFLUCC 12-0531*	KT29026 4	KT29026 3	KT290262	-	-	-	-	-	-	-	-	-
<i>C. incanum</i>	ATCC 64682*	KC1107 89	KC1108 07	-	KC110798	KC110825	KC110816	-	-	-	-	-	-
<i>C. indonesiense</i>	CBS 127551*	JQ94828 8	JQ94861 8	JQ948949	JQ949279	JQ949609	JQ949939	-	-	-	-	-	-
<i>C. jacksonii</i>	MAFF 3054602*	JX51921 6	-	JX519224	-	JX519233	JX519241	-	-	-	-	-	-

Species Name	Isolate No	GenBank Accession Numbers											
		ITS	GAPDH	CHS-1	HIS3	ACT	TUB2	CAL	GS	SOD2	ApMat	Apn2	Mat1
<i>C. jasiminigenum</i>	MFLUCC 10-0273*	HM131513	HM131499	-	-	HM131508	HM153770	-	-	-	-	-	-
<i>C. jiangxiense</i>	CGMCC 3.17363*	KJ955201	KJ954902	-	-	KJ954471	KJ955348	KJ954752	KJ955051	-	KJ954607	-	-
<i>C. johnstonii</i>	CBS 128532*	JQ948444	JQ948775	JQ949105	JQ949435	JQ949765	JQ950095	-	-	-	-	-	-
<i>C. kahawae</i>	ICMP 17816*	JX010231	JX010012	JX009813	-	JX009452	JX010444	JX009642	JX010130	JX010350	JQ894579	-	-
<i>C. karstii</i>	CBS 127597*	JQ005204	JQ005204	JQ005378	JQ005465	JQ005552	JQ005638	JQ005725	-	-	-	-	-
<i>C. kinghornii</i>	CBS 198.35*	JQ948454	JQ948785	JQ949115	JQ949445	JQ949775	JQ950105	-	-	-	-	-	-
<i>C. lacticiphilum</i>	CBS 112989*	JQ948289	JQ948619	JQ948950	JQ949280	JQ949610	JQ949940	-	-	-	-	-	-
<i>C. liaoningense</i>	CAUOS2*	KP890104	KP890135	KP890127	-	KP890097	KP890111	KP890119	-	-	-	-	-
<i>C. lilii</i>	CBS 109214	GU227810	GU228202	-	-	GU227908	GU228104	-	-	-	-	-	-
<i>C. limetticola</i>	CBS 114.14*	JQ948193	JQ948523	JQ948854	JQ949184	JQ949514	JQ949844	-	-	-	-	-	-
<i>C. lindemuthianum</i>	CBS 144.31*	JQ005779	JX546712	JQ005800	JQ005821	JQ005842	JQ005863	-	KF178643	-	-	-	-
<i>C. lentis</i>	CBS 127604*	JQ005766	KM105597	JQ005787	JQ005808	JQ005829	JQ005850	-	-	-	-	-	-
<i>C. ledebouriae</i>	CBS 141284*	KX228254	-	-	KX228365	KX228357	-	-	-	-	-	-	-
<i>C. lineola</i>	CBS 125337*	GU2278	GU2282	GU22831	-	GU227927	GU228123	-	-	-	-	-	-

Species Name	Isolate No	GenBank Accession Numbers											
		ITS	GAPDH	CHS-1	HIS3	ACT	TUB2	CAL	GS	SOD2	ApMat	Apn2	Mat1
		29	21	9									
<i>C. lini</i>	CBS 172.51*	JQ00576 5	KM1055 81	JQ005786	JQ005807	JQ005828	JQ005849	-	-	-	-	-	-
<i>C. liriopes</i>	CBS 119444*	GU2278 04	GU2281 96	GU22829 4	-	GU227902	GU228098	-	-	-	-	-	-
<i>C. lupini</i>	CBS 109225*	JQ94815 5	JQ94848 5	JQ948816	JQ949146	JQ949476	JQ949806	-	-	-	-	-	-
<i>C. magnisporum</i>	CBS 398.84*	KF68771 8	KF68784 2	KF687782	KF687865	KF687803	KF687882	-	KF68774 2	-	-	-	-
<i>C. malvarum</i>	CBS 521.97*	KF17848 0	KF17850 4	KF178529	KF178553	KF178577	KF178601	-	KF17862 6	-	-	-	-
<i>C. melonis</i>	CBS 159.84*	JQ94819 4	JQ94852 4	JQ948855	JQ949185	JQ949515	JQ949845	-	-	-	-	-	-
<i>C. menispermi</i>	MFLU 14- 0625*	KU2423 57	KU2423 56	KU24235 5	-	KU242353	KU242354	-	-	-	-	-	-
<i>C. metake</i>	MAFF 244029*	AB7388 59	(Sequences available at http://www.gene.affrc.go.jp/databases-micro_search_en.php)										
<i>C. miscanthi</i>	MAFF 510857*	JX51922 1	-	-	-	JX519237	JX519246	-	-	-	-	-	-
<i>C. musae</i>	ICMP 19119*	JX01014 6	JX01005 0	JX009896	-	JX009433	HQ596280	JX009742	JX01010 3	JX01033 5	KC88892 6	-	-
<i>C. navitas</i>	CBS 1250862*	JQ00576 9	-	JQ005790	JQ005811	JQ005832	JQ005853	-	-	-	-	-	-
<i>C. neosansevieriae</i>	CBS 139918*	KR4767 47	KR4767 91	-	KR476792	KR476790	KR476797	-	-	-	-	-	-
<i>C. nicholsonii</i>	MAFF 5111152*	JQ00577 0	-	JQ005791	JQ005812	JQ005833	JQ005854	-	-	-	-	-	-

Species Name	Isolate No	GenBank Accession Numbers											
		ITS	GAPDH	CHS-1	HIS3	ACT	TUB2	CAL	GS	SOD2	ApMat	Apn2	Mat1
<i>C. nigrum</i>	CBS 169.49*	JX54683 8	JX54674 2	JX546693	-	JX546646	JX546885	-	-	-	-	-	-
<i>C. novae-zelandiae</i>	CBS 128505*	JQ00522 8	JQ00531 5	JQ005402	JQ005489	JQ005576	JQ005662	JQ005749	-	-	-	-	-
<i>C. nupharicola</i>	ICMP 18187*	JX01018 7	JX00997 2	JX009835	-	JX009437	JX010398	JX009663	JX01008 8	JX01032 0	-	-	-
<i>C. nymphaeae</i>	CBS 515.78*	JQ94819 7	JQ94852 7	JQ948858	JQ949188	JQ949518	JQ949848	-	-	-	-	-	-
<i>C. ochracea</i>	CGMCC 3.15104*	JX62516 8	KC8435 13	-	-	KC843527	JX625183	-	-	-	-	-	-
<i>C. ocimi</i>	CBS 298.94*	KM1052 22	KM1055 77	KM10529 2	KM105362	KM105432	KM105502	-	-	-	-	-	-
<i>C. oncidii</i>	CBS 129828*	JQ00516 9	JQ00525 6	JQ005343	JQ005430	JQ005517	JQ005603	JQ005690	-	-	-	-	-
<i>C. orbiculare</i>	CBS 570.97*	KF17846 6	KF17849 0	KF178515	KF178539	KF178563	KF178587	-	KF17861 1	-	-	-	-
<i>C. orchidophilum</i>	CBS 632.80*	JQ94815 1	JQ94848 1	JQ948812	JQ949142	JQ949472	JQ949802	-	-	-	-	-	-
<i>C. panacicola</i>	C08048	GU9358 67	GU9358 47	-	-	-	-	-	-	-	-	-	-
<i>C. paranaense</i>	CBS 134729*	KC2049 92	KC2050 26	KC20504 3	KC205004	KC205077	KC205060	-	-	-	-	-	-
<i>C. parsonsiae</i>	CBS 128525*	JQ00523 3	JQ00532 0	JQ005407	JQ005494	JQ005581	JQ005667	JQ005754	-	-	-	-	-
<i>C. paspali</i>	MAFF 3054032*	JX51921 9	-	JX519227	-	JX519235	JX519244	-	-	-	-	-	-
<i>C. paxtonii</i>	IMI 165753*	JQ94828	JQ94861	JQ948946	JQ949276	JQ949606	JQ949936	-	-	-	-	-	-

Species Name	Isolate No	GenBank Accession Numbers											
		ITS	GAPDH	CHS-1	HIS3	ACT	TUB2	CAL	GS	SOD2	ApMat	Apn2	Mat1
		5	5										
<i>C. petchii</i>	CBS 378.94*	JQ00522 3	JQ00531 0	JQ005397	JQ005484	JQ005571	JQ005657	JQ005744	-	-	-	-	-
<i>C. phormii</i>	CBS 118194*	JQ94844 6	JQ94877 7	JQ949107	JQ949437	JQ949767	JQ950097	-	-	-	-	-	-
<i>C. phyllanthi</i>	CBS 175.67*	JQ00522 1	JQ00530 8	JQ005395	JQ005482	JQ005569	JQ005655	JQ005742	-	-	-	-	-
<i>C. pisicola</i>	CBS 724.97*	KM1051 72	KM1055 22	KM10524 2	KM105312	KM105382	KM105452	-	-	-	-	-	-
<i>C. proteae</i>	CBS 132882*	KC2970 79	KC2970 09	KC29698 6	-	KC296940	KC297101	KC29696 0	-	-	-	-	-
<i>C. pseudoacutatum</i>	CBS 436.77*	JQ94848 0	JQ94881 1	JQ949141	JQ949471	JQ949801	JQ950131	-	-	-	-	-	-
<i>C. pseudomajus</i>	CBS 571.88*	KF68772 2	KF68782 6	KF687779	KF687864	KF687801	KF687883	KF687807	KF68774 4	-	-	-	-
<i>C. psidii</i>	ICMP 19120*	JX01021 9	JX00996 7	JX009901	-	JX009515	JX010443	JX009743	JX01013 3	JX01036 6	KC88893 1	-	-
<i>C. pyricola</i>	CBS 128531*	JQ94844 5	JQ94877 6	JQ949106	JQ949436	JQ949766	JQ950096	-	-	-	-	-	-
<i>C. queenslandicum</i>	ICMP 1778*	JX01027 6	JX00993 4	JX009899	-	JX009447	JX010414	JX009691	JX01010 4	JX01033 6	KC88892 8	-	-
<i>C. quinquefoliae</i>	MFLU 14-0626*	KU2363 91	KU2363 90	-	-	KU236389	KU236392	-	-	-	-	-	-
<i>C. radialis</i>	CBS 529.93*	KF68771 9	KF68782 5	KF687762	KF687847	KF687785	KF687869	KF687806	KF68774 3	-	-	-	-
<i>C. rhombiforme</i>	CBS 129953*	JQ94845 7	JQ94878 8	JQ949118	JQ949448	JQ949778	JQ950108	-	-	-	-	-	-

Species Name	Isolate No	GenBank Accession Numbers											
		ITS	GAPDH	CHS-1	HIS3	ACT	TUB2	CAL	GS	SOD2	ApMat	Apn2	Mat1
<i>C. riograndense</i>	COAD 928 *	KM6552 99	KM6552 98	KM65529 7	-	KM655295	KM65530	KM65529 6	-	-	-	-	-
<i>C. rusci</i>	CBS 119206*	GU2278 18	GU2282 10	GU22830 8	-	GU227916	GU228112	-	-	-	-	-	-
<i>C. salicis</i>	CBS 607.94*	JQ94846 0	JQ94879 1	JQ949121	JQ949451	JQ949781	JQ950111	-	-	-	-	-	-
<i>C. salsolae</i>	ICMP 19051*	JX01024 2	JX00991 6	JX009863	-	JX009562	JX010403	JX009696	JX01009 3	JX01032 5	KC88892 5	-	-
<i>C. sansevieriae</i>	MAFF 239721 *	AB2129 91	(Sequences available at http://www.gene.affrc.go.jp/databases-micro_search_en.php)										
<i>C. scovillei</i>	CBS 126529*	JQ94826 7	JQ94859 7	JQ948928	JQ949258	JQ949588	JQ949918	-	-	-	-	-	-
<i>C. sedi</i>	MFLUCC 14- 1002*	KM9747 58;	KM9747 55	KM97475 4	-	KM974756	KM974757	-	-	-	-	-	-
<i>C. siamense</i>	ICMP 18578*	JX01017 1	JX00992 4	JX009865	-	FJ907423	JX010404	FJ917505	JX01009 4	JX01032 6	JQ899289	-	-
<i>C. sidae</i>	CBS 504.97*	KF17847 2	KF17849 7	KF178521	KF178545	KF178569	KF178593	-	KF17861 8	-	-	-	-
<i>C. simmondsii</i>	CBS 122122*	JQ94827 6	JQ94860 6	JQ948937	JQ949267	JQ949597	JQ949927	-	-	-	-	-	-
<i>C. sloanei</i>	IMI 364297*	JQ94828 7	JQ94861 7	JQ948948	JQ949278	JQ949608	JQ949938	-	-	-	-	-	-
<i>C. somersetense</i>	CBS 131599*	JX07686 2	-	-	-	-	-	-	-	JX07688 0	-	JX0769 18	JX076895
<i>C. spaethianum</i>	CBS 167.49*	GU2278 07	GU2281 99	GU22829 7	GU228003	GU227905	GU228101	-	-	-	-	-	-
<i>C. spinaceae</i>	CBS 128.57*	GU2278	GU2282	GU22833	GU228043	GU227945	GU228141	-	-	-	-	-	-

Species Name	Isolate No	GenBank Accession Numbers											
		ITS	GAPDH	CHS-1	HIS3	ACT	TUB2	CAL	GS	SOD2	ApMat	Apn2	Mat1
		47	39	7									
<i>C. spinosum</i>	CBS 515.97*	KF17847 4	KF17849 8	KF178523	KF178547	KF178571	KF178595	-	KF17862 0	-	-	-	-
<i>C. sublineola</i>	CBS 131301*	JQ00577 1	-	JQ005792	JQ005813	JQ005834	JQ005855	-	-	-	-	-	-
<i>C. syzygicola</i>	MFLUCC10- 0624*	KF24209 4	KF24215 6	-	-	KF157801	KF254880	KF254859	-	-	-	-	-
<i>C. tabacum</i>	CPC 18945*	KM1052 04	KM1055 57	KM10527 4	KM105344	KM105414	KM105484	-	-	-	-	-	-
<i>C. tamarilloi</i>	CBS 129814*	JQ94818 4	JQ94851 4	JQ948845	JQ949175	JQ949505	JQ949835	-	-	-	-	-	-
<i>C. tanacetii</i>	CBS 132693*	JX21822 8	JX21824 3	JX259268	-	JX218238	JX218233	-	-	-	-	-	-
<i>C. tebestii</i>	CBS 522.97*	KF17847 3	KF17850 5	KF178522	KF178546	KF178570	KF178594	-	KF17861 9	-	-	-	-
<i>C. temperatum</i>	Coll883 *	JX14515 9	-	-	-	-	JX145211	-	-	-	JX145298	-	-
<i>C. theobromicola</i>	ICMP 18649*	JX01029 4	JX01000 6	JX009869	-	JX009444	JX010447	JX009591	JX01013 9	JX01037 2	KC79072 6	-	-
<i>C. ti</i>	ICMP 4832*	JX01026 9	JX00995 2	JX009898	-	JX009520	JX010442	JX009649	JX01012 3	JX01036 2	KM36014 6	-	-
<i>C. tofieldiae</i>	CBS 495.85	GU2278 01	GU2281 93	GU22829 1	-	GU227899	GU228095	-	-	-	-	-	-
<i>C. torulosum</i>	CBS 128544*	JQ00516 4	JQ00525 1	JQ005338	JQ005425	JQ005512	JQ005512	JQ005512	-	-	-	-	-
<i>C. trichellum</i>	CBS 217.64*	GU2278 12	GU2282 04	GU22830 2	-	GU227910	GU228106	-	-	-	-	-	-

Species Name	Isolate No	GenBank Accession Numbers											
		ITS	GAPDH	CHS-1	HIS3	ACT	TUB2	CAL	GS	SOD2	ApMat	Apn2	Mat1
<i>C. trifolii</i>	CBS 158.83*	KF17847 8	KF17850 2	KF178527	KF178551	KF178575	KF178599	-	KF17862 4	-	-	-	-
<i>C. tropicale</i>	ICMP 18653*	JX01026 4	JX01000 7	JX009870	-	JX009489	JX010407	JX009719	JX01009 7	JX01032 9	KC79072 8	-	-
<i>C. tropicicola</i>	LC0598*	JN05024 0	JN05022 9	-	-	JN050218	JN050246	-	-	-	-	-	-
<i>C. truncatum</i>	CBS 151.35*	GU2278 62	GU2282 54	GU22835 2	-	GU227960	GU228156	-	-	-	-	-	-
<i>C. utrechtense</i>	CBS 130243*	KM1052 01	KM1055 54	KM10527 1	KM105341	KM105411	KM105481	-	-	-	-	-	-
<i>C. verruculosum</i>	IMI 45525*	GU2278 06	GU2281 98	GU22829 6	-	GU227904	GU228100	-	-	-	-	-	-
<i>C. vietnamense</i>	CBS 125478*	KF68772 1	KF68783 2	KF687769	KF687855	KF687792	KF687877	KF687816	KF68775 3	-	-	-	-
<i>C. vignae</i>	CBS 501.97*	KM1051 83	KM1051 83	KM10525 3	KM105323	KM105393	KM105463	-	-	-	-	-	-
<i>C. viniferum</i>	GZAAS5.08601 *	JN41280 4	JN41279 8	-	-	JN412795	JN412813	JQ309639	-	-	-	-	-
	GZAAS5.08608 *	-	-	-	-	-	-	-	-	-	KJ623242	-	-
<i>C. wuxiense</i>	CGMCC 3.17894*	KU2515 91	KU2520 45	KU25193 9	-	KU251672	KU252200	KU25183 3	KU2521 01	-	KU25172 2	-	-
<i>C. walleri</i>	CBS 125472*	JQ94827 5	JQ94860 5	JQ948936	JQ949266	JQ949596	JQ949926	-	-	-	-	-	-
<i>C. xanthorrhoeae</i>	ICMP 17903*	JX01026 1	JX00992 7	JX009823	-	-	JX010448	JX009653	JX01013 8	JX01036 9	KC79068 9	-	-
<i>C. yunnanense</i>	CBS 132135*	JX54680	JX54670	JX519231	-	-	JX519248	-	-	-	-	-	-

Species Name	Isolate No	GenBank Accession Numbers												
		ITS	GAPDH	CHS-1	HIS3	ACT	TUB2	CAL	GS	SOD2	ApMat	Apn2	Mat1	
		4	6											
<i>C. zoysia</i>	MAFF 2385732*	JX07687 1	-	-	-	-	-	-	-	-	-	-	JX0769 22	JX076899

ATCC: American Type Culture Collection; BCC: BIOTEC Culture Collection, National Center for Genetic Engineering and Biotechnology (BIOTEC), Khlong Luang, Pathumthani, Thailand; BRIP: Plant Pathology Herbarium, Department of Employment, Economic, Development and Innovation, Queensland, Australia; CBS: Culture collection of the Centraalbureau voor Schimmelcultures, Fungal Biodiversity Centre, Utrecht, The Netherlands; CGMCC: China General Microbiological Culture Collection; COAD: Coleção Octávio Almeida Drummond, Viçosa, Brazil; CPC: Working collection of Pedro W. Crous, housed at CBS; IMI: Culture collection of CABI Europe UK Centre, Egham, UK; LC: Working collection of Lei Cai, housed at CAS, China; MAFF: MAFF GeneBank Project, Ministry of Agriculture, Forestry and Fisheries, Tsukuba, Japan; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Rai, Thailand; MFLU: Herbarium of Mae Fah Luang University, Chiang Rai, Thailand; ICMP: International Collection of Microorganisms from Plants, Auckland, New Zealand; NBRC: Culture Collection of the Biological Resource Center, National Institute of Technology and Evaluation, Kisarazu, Japan. * ex-type strains.