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1 *Colletotrichum* species and complexes: geographic distribution, host range and 2 conservation status

3 Pedro Talhinhos^{1,*} and Riccardo Baroncelli²

4 1 Universidade de Lisboa, Instituto Superior de Agronomia, Linking Landscape, Environment, Agriculture and Food
5 (LEAF), Lisbon, Portugal; ORCID 0000-0001-6694-7502

6 2 University of Bologna, Department of Agricultural and Food Sciences (DISTAL), Bologna, Italy; ORCID 0000-0002-
7 5878-1159

8 * Correspondence should be addressed to P.T. (ptalhinhos@isa.ulisboa.pt)

9

10 **Abstract**

11 The taxonomy of the genus *Colletotrichum* has undergone tremendous changes over the last decade,
12 with over 200 species being currently recognised and species complexes being informally used to
13 cluster those species. Many of these species are important plant pathogens, some rather polyphagous
14 and others host-specific, but several occur seldomly and some may in fact be ecologically endangered.
15 Based mainly on literature from the past decade, in this work we review the occurrence, geographic
16 distribution and host spectrum of currently recognised *Colletotrichum* species under phylogenetic,
17 pathological/agronomic and ecological perspectives, providing two lists, one arranged by
18 *Colletotrichum* species and species complexes, and the other by hosts. A total of 257 species are listed
19 and grouped into 15 species complexes. In this work we have recorded 1353 unique host species-
20 *Colletotrichum* species association records from 720 hosts, with the Fabaceae as the family with
21 higher number of hosts (52 host species) but with the Rosaceae as the family with the highest number
22 of host species-*Colletotrichum* species association records (118 association records). According to
23 occurrence data, 88 species are common in nature, 128 were considered as data deficient and 41 are
24 threatened, some of which are likely extinct from nature and preserved only in culture collections.
25 Several species are relevant plant pathogens, in some cases geographically confined and thus of
26 potential quarantine relevance. Based on the major changes that occurred on *Colletotrichum*
27 taxonomy over the last decade, this work provides a comprehensive overview of occurrence data of
28 *Colletotrichum* species, compiling host range and geographical distribution, with relevance for plant
29 pathology and conservation mycology. The current taxonomic framework in *Colletotrichum* is
30 revealing numerous species but poses challenges to the employment of standard criteria for the
31 evaluation of biological conservation of these fungi. We advocate that conservation mycology and
32 taxonomy should find common routes simultaneously enabling the correct delimitation of species of
33 *Colletotrichum* and the implementation of feasible criteria for the evaluation of conservation. The
34 employment of new technologies, such whole genome sequencing (WGS), will help and support the

35 description of new species and to gain a better understanding of the genetic bases of speciation
36 processes.

37

38 **Keywords**

39 *Colletotrichum*; species complex; taxonomy; host range; geographic distribution; conservation
40 mycology

41

42 **Declarations**

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45

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53

54 1. *COLLETORICHUM* TAXONOMY AND IMPORTANCE

55 Many species belonging to the genus *Colletotrichum* are implicated in plant diseases, generally
56 referred to as anthracnose, on a wide range of hosts, and these pathogens are characterised by a
57 worldwide distribution and global relevance (Dean et al. 2012). Common hosts include many
58 dicotyledonous plants such as strawberry, apple, citrus, and stone fruits, and major cereals such as
59 maize and sorghum. Diseases on ferns and pines have also been reported. Anthracnose symptoms
60 include dark necrotic lesions, which are oval or angular. Plant parts can be superficially affected at
61 all stages of development, from seedlings to mature plants. Various *Colletotrichum* species are also
62 important post-harvest pathogens due to their ability to undergo a non-pathogenic phase (Bailey and
63 Jegger 1992). *Colletotrichum* species are characterised by a distinctive hemibiotrophic lifestyle (also
64 known to occur in other fungal species, e.g. *Magnaporthe*). Fungi belonging to this genus initially
65 infect through a brief biotrophic phase, associated with large intracellular primary hyphae. The fungus
66 later switches to a necrotrophic phase, associated with narrower secondary hyphae that spread
67 throughout the host tissue (De Silva et al. 2017b). Biomolecular processes that regulate this lifestyle
68 have long been studied by the scientific community, especially those related to the switch from
69 biotrophy to necrotrophy (O'Connell et al. 2012). Beside the economic impact of *Colletotrichum*

70 species, this genus encompasses a wide diversity of important traits such as host range and host
71 preference, mode of reproduction and differences in the strategy used to infect their hosts. In addition
72 to being plant pathogens, *Colletotrichum* members can be plant endophyte and growth promoters,
73 entomopathogens and opportunistic human pathogens. The genus contains a tremendous biological
74 diversity within a group of closely related species, and this makes it a perfect model to study the
75 molecular and genetic factors associated with biological traits.

76 The most recent formal description of the genus *Colletotrichum* is given by Jayawardena et
77 al. (2020), providing, along with Marín-Felix et al. (2017), notes on morphology and cultural
78 characteristics and information on standardised media and cultivation conditions. *Colletotrichum* was
79 established in 1837, by Corda (Sutton 1992). Von Arx (1957) thoroughly revised the genus, reducing
80 around 750 species to 11 taxa, which gradually increased. In 2000 the number of species was updated
81 with morphological, cultural and pathogenicity studies and around 40 were accepted (Cannon et al.
82 2000). *Colletotrichum* species are mainly asexual, but some have a teleomorph that can be either
83 homothallic or heterothallic. The MAT1-1/2 system in *Colletotrichum* species is not typical as that
84 in most ascomycetes, as *Colletotrichum* fungi are capable of sexual reproduction while using only
85 the *MAT1-2-1* gene (Menat et al. 2016; Liang et al. 2021; Wilson et al. 2021). The genus
86 *Colletotrichum* is the single genus in the Glomerellaceae family. Other members of the Glomerellales,
87 namely in the families Australiascaceae, Reticulascaceae and Plectosphaerellaceae (Réblová et al.
88 2011; Giraldo and Crous 2019), are far less frequently reported, with *Colletotrichum* representing
89 over 78% of the occurrences of Glomerellales recorded in GBIF database (www.gbif.org).

90 The advent of molecular systematics, at first based on ITS, and subsequently on multilocus sequence
91 typing (MLST) approach, has accelerated the elucidation of phylogenetic relationships of
92 *Colletotrichum* members. ITS is generally used to resolve species complexes within the genus
93 (Jayawardena et al. 2016a; Marín-Felix et al. 2017). ITS is also sufficient to identify some species in
94 the genus (e.g. *C. graminicola* and species in the gigasporum complex; Liu et al. 2014; Cuevas-
95 Fernández et al. 2019). However, the delimitation of most *Colletotrichum* species requires additional
96 use of a combination of sequences from some of the *act*, *ApMat*, *apn2*, *cal*, *chs-1*, *gapdh*, *gs*, *his3*,
97 *sod2* or *tub2* genes (Jayawardena et al. 2016a, 2020, 2021; Marín-Felix et al. 2017). In fact,
98 *Colletotrichum*, along with genera such as *Alternaria*, *Aspergillus*, *Cladosporium*, *Fusarium* and
99 *Penicillium*, is recognised as an example of insufficient resolution of ITS for species delimitation
100 (Lücking et al. 2020). However, the usefulness of such additional genes varies strongly in different
101 species complexes in the genus (Jayawardena et al. 2016a). The *ApMat* gene shows high resolution
102 to distinguish species in the gloeosporioides complex, but it has been of little or no use in other
103 complexes (Silva et al. 2012b; Sharma et al. 2015). In this study the phylogeny of *Colletotrichum* is

104 constructed (Figure 1) using the type strains of 252 species and five genetic loci (*act*, *chs-1*, *gapdh*,
105 ITS and *tub2* (Supplementary data 1, 'sequences' tab).

106

107 **Figure 1**

108

109 2. ACCEPTED SPECIES OF *COLLETOTRICHUM* AND SPECIES COMPLEXES

110

111 As of June 2021, Index Fungorum lists 928 taxa in the genus *Colletotrichum*, 806 at the rank of
112 species and the remaining 113 as diverse infra-specific taxa, mostly at the *formae* and *varietas* ranks.
113 *Colletotrichum lineola* was the first species described in the genus, in 1831. The vast majority of
114 *Colletotrichum* taxa (638 taxa) was described between 1888 and 1975 (Figure 2), representing on
115 average 7.3 taxa per year. One taxon per year was described on average in the 1976-2008 period, but
116 since 2009 another 230 taxa were described (228 species; 18.3 taxa per year on average, peaking in
117 2012 with 58 taxa).

118

119 **Figure 2**

120

121 Literature published in the past 10 years (approximately 800 articles, of which 353 are Plant Disease
122 Notes published in the journal Plant Disease) were scrutinised for occurrence data of *Colletotrichum*
123 species. Occurrence data was only recorded when species names were unambiguous according to
124 modern criteria, namely considering the literature that defined and delimited each complex: *acutatum*
125 (Damm et al. 2012a); *agaves* (Bhunjun et al. 2021); *boninense* (Damm et al. 2012b); *caudatum*
126 (Crouch 2014); *dematium* (Cannon et al. 2012); *destructivum* (Cannon et al. 2012); *dracaenophilum*
127 (Damm et al. 2019); *gigasporum* (Liu et al. 2014); *gloeosporioides* (Weir et al. 2012); *graminicola*
128 (Cannon et al. 2012); *magnum* (Damm et al. 2019); *orbiculare* (Cannon et al. 2012); *orchidearum*
129 (Damm et al. 2019); *spaethianum* (Cannon et al. 2012); *truncatum* (Cannon et al. 2012). Previous
130 check-lists were also considered (Jayawardena et al. 2016a, 2021; Marín-Felix et al. 2017). Fungal
131 names were checked and used following Index Fungorum (www.indexfungorum.org). Similarly,
132 plant names were checked and used according to Plants of the World Online
133 (www.plantsoftheworldonline.org). Occurrences were recorded on a table, under the following
134 parameters: fungal species; host species (and type of interaction, when known); location; date;
135 reference. Location information was used for georeferencing, as previously described (Talhinhas et
136 al. 2019) and occurrence maps were prepared using MapChart (<https://mapchart.net>).

137

138 Adapting as much as possible the criteria defined by Dahlberg and Mueller (2011) for Mycological
139 Conservation and considering also Blackwell and Vega (2018), we considered as threatened the
140 species identified once or very few times and that were identified either in conditions that impair
141 conducting surveys (e.g., identified on hosts that are not clearly defined, such as hosts with no species
142 given) or on hosts that are recurrently subject of surveys (e.g., chilli, citrus, coffee, mango,
143 strawberry) from which other species of *Colletotrichum* are recorded instead. Other species seldomly
144 reported were considered as ‘data deficient’. Species recorded from multiple hosts and/or locations
145 were considered as common.

146

147 **2.1 The acutatum species complex**

148 Before the massive use of genetic information in taxonomy, *Colletotrichum acutatum* was considered
149 as a single but morphologically and phylogenetically diverse species (Lardner et al. 1999), originally
150 described from diseased tissues of *Carica papaya*, *Capsicum frutescens* and *Delphinium ajacis* in
151 Australia by Simmonds (1965). Due to the high diversity of *C. acutatum*, several intra-specific
152 groupings were established based on morphological, physiological, sexual, and molecular data (as
153 revised by Sreenivasaprasad and Talhinhos 2005). Gradually, separate species were recognised as
154 part of the acutatum complex, e.g. *C. lupini* (Nirenberg et al. 2002), *C. phormii* (Farr et al. 2006), *C.*
155 *simmondsii* and *C. fioriniae* (Shivas and Tan 2009). The revision of the taxonomy performed by
156 Damm et al. (2012a) was a landmark in the classification in which thirty-one species were accepted
157 as member of the acutatum complex, of which 21 were newly described. To date, 41 species have
158 been described (Figure 3).

159 In phylogenetic terms (Figure 3), the acutatum species complex can be divided in six clades with
160 some degree of geographic structure. Whereas the lupini clade (comprising *C. abcissum*, *C.*
161 *costaricense*, *C. cuscudae*, *C. limetticola*, *C. lupini*, *C. melonis*, *C. paranaense* and *C. tamarilloi*)
162 shows clear evidence of neotropical origin (in spite of the global distribution of *C. lupini*), fungi in
163 the nymphaeae clade (comprising *C. brisbanense*, *C. cairnsense*, *C. carthami*, *C. chrysanthemi*, *C.*
164 *cosmi*, *C. eriobotryae*, *C. guajavae*, *C. indonesiense*, *C. javanense*, *C. laticiphilum*, *C. miaoliense*, *C.*
165 *nymphaeae*, *C. paxtonii*, *C. scovillei*, *C. simmondsii*, *C. sloanei*, *C. walleri* and *C. wanningense*) occur
166 mostly in Asia and Oceania (in spite of the global distribution of *C. nymphaeae*) and those in the
167 godetiae clade (comprising *C. acerbum*, *C. arboricola*, *C. australe*, *C. godetiae*, *C. johnstonii*, *C.*
168 *kinghornii*, *C. lauri*, *C. phormii*, *C. pyricola*, *C. rhombiforme* and *C. salicis*) are from multiple
169 locations (with *C. godetiae* presenting global distribution). Two relevant but singleton clades are the
170 acutatum and fioriniae clades, comprising *C. acutatum* and *C. fioriniae* respectively. Whereas they
171 are both of global distribution, *C. acutatum* appears to have originated from Oceania (or perhaps from
172 the Indian Ocean basin) and *C. fioriniae* from the Northern Hemisphere.

173 Members of the acutatum species complex have been associated with 171 plant species belonging to
174 129 genera (Supplementary data 1) and the vast majority of those species (90.9%) belong are dicots
175 whereas only a small proportion are monocots and gymnosperms (5.3% and 1.6% respectively).
176 Interestingly the acutatum complex is known to comprise the only *Colletotrichum* entomopathogenic
177 species as *C. fioriniae* is pathogenic towards *Fiorinia externa* (elongate hemlock scale; Marcelino et
178 al. 2008) and *C. nymphaeae* is pathogenic on *Praelongorthezia praelonga* (citrus orthezia; Mascarin
179 et al. 2016).

180 Whereas most of the species within the complex are polyphagous, some show a strong specialisation
181 towards one or a limited group of hosts; e.g. *C. lupini* is highly specialised toward *Lupinus* spp.
182 (Talhinhas et al. 2016). Species from the acutatum complex have been suggested as a model system
183 for the study of fungal evolution on a fine scale because of their different host range and host
184 preference, reproduction mode, and various living strategy (Baroncelli et al. 2017). Several species
185 in the complex present limited geographical distribution or host range but some, such as *C. acutatum*,
186 *C. fioriniae*, *C. godetiae* and *C. nymphaeae*, are of global distribution and multiple hosts. Whereas *C.*
187 *godetiae* and *C. nymphaeae* have a plethora of other species in their phylogenetic vicinity, both *C.*
188 *fioriniae* and *C. acutatum* are not accompanied by any other species in their tree branches. Given the
189 vast amount of data for organisms in any of these four clades, it is unlikely that such differences are
190 due to sampling bias and thus such differences could suggest diverse reproduction strategies that may
191 have shaped different patterns of evolution (wide diversification in the nymphaeae and godetiae
192 clades, as well as in the lupini one, and low diversity in the acutatum and fioriniae clades).

193

194 **Figure 3**

195

196 *Colletotrichum abscissum* Pinho and O.L. Pereira, *Persoonia* **34**: 237 (2015)

197

198 *Colletotrichum abscissum* is the causal agent of citrus Post-Bloom Fruit Drop (Crous et al. 2015).
199 The fungus is restricted to *Citrus* spp. (Rutaceae) and to the American continent (Crous et al. 2015;
200 Bragança et al. 2016; Silva et al. 2017a) and is thus a potential quarantine organism, namely in citrus
201 producing areas.

202

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

204

205 This species is based on a specimen collected from apple (*Malus domestica*, Rosaceae) in New
206 Zealand in 1987 (Damm et al. 2012a). The fungus has not been detected thereafter, in spite of further
207 research on apple bitter rot in New Zealand, as discussed by Damm et al. (2012a). This species could

208 be endangered or even extinct from nature, particularly as other species of *Colletotrichum* inhabit the
209 same ecosystem, causing apple bitter rot.

210

211 *Colletotrichum acutatum* J.H Simmonds, *Qld. J. Agric. Anim. Sci.* **22**: 458 (1965)

212

213 *Colletotrichum acutatum* was originally described from Australia from diverse hosts and underwent
214 several delimitations over time. Hosts harbouring *C. acutatum* sensu Damm et al. (2012a) include: in
215 the Amaryllidaceae, *Allium cepa* (Lopes et al. 2021); in the Anacardiaceae, *Mangifera indica* and
216 *Pistacia vera* (Shivas et al. 2016); in the Apocynaceae, *Nerium oleander* (Mosca et al. 2014); in the
217 Caricaceae, *Carica papaya* (Damm et al. 2012a); in the Euphorbiaceae, *Hevea brasiliensis*
218 (Hunupolagama et al. 2017); in the Fabaceae, *Aspalathus linearis* (Damm et al. 2012a) and *Vicia faba*
219 (Shivas et al. 2016); in the Fagaceae, *Castanea sativa* (Gaffuri et al. 2017); in the Juglandaceae,
220 *Juglans regia* (He et al. 2019); in the Myrtaceae, *Acca sellowiana* (Camele et al. 2018) and *Psidium*
221 *guajava* (Liu et al. 2021b); in the Oleaceae, *Olea europaea* (Mosca et al. 2014; Chattaoui et al. 2016;
222 Shivas et al. 2016; Iliadi et al. 2018; Talhinhos et al. 2018; Cara et al. 2021); in the Pinaceae, *Pinus*
223 *radiata* (Damm et al. 2012a); in the Plumbaginaceae, *Limonium* sp. (Baroncelli et al. 2015); in the
224 Proteaceae, *Grevillea* sp., *Hakea sericea* and *Leucadendron* sp. (Damm et al. 2012a); in the
225 Punicaceae, *Punica granatum* (Mincuzzi et al. 2017); in the Ranunculaceae, *Anemone* sp. (Shivas et
226 al. 2016); in the Rosaceae, *Fragaria* × *ananassa* (Damm et al. 2012a), *Malus domestica* (Shivas et
227 al. 2016), *Prunus dulcis* (López-Moral et al. 2017) and *Pyrus pyrifolia* (Baroncelli et al. 2015); in the
228 Rubiaceae, *Coffea arabica* (Damm et al. 2012a); in the Rutaceae, *Boronia megastigma* (Shivas et al.
229 2016), *Citrus limon* and *C. sinensis* (Guarnaccia et al. 2017); in the Solanaceae, *Solanum*
230 *lycopersicum* (Liu et al. 2021b); in the Theaceae, *Camellia sinensis* (Chen et al. 2016a). Recorded
231 mostly from Oceania and Africa in multiple hosts, *Colletotrichum acutatum* seems to be expanding
232 to the Mediterranean region on several fruit crops, whereas it is virtually absent from the American
233 continent (Supplementary data 2, panel A).

234

235 *Colletotrichum arboricola* M. Zapata, M.A. Palma and Piont., *Persoonia* **41**: 353 (2018)

236

237 *Colletotrichum arboricola* was recorded from *Fuchsia magellanica* (Onagraceae) leaves in 2012 in
238 Chile (Crous et al. 2018a) but the authors note that the fungus was subsequently detected in different
239 arboreal hosts in the area. Although pathogenicity has not been confirmed, this fungus may cause
240 concern to this widely used ornamental host, although its distribution and host range are still poorly
241 known.

242

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

244

245 There are no further records for this species besides the two isolates, collected from *Trachycarpus*
246 *fortunei* (Areceaceae) in Australia in 2011 and *Hakea* sp. (Proteaceae) in South Africa in 1998,
247 originally used in the species description (Damm et al. 2012a). The current conservation status of this
248 species requires further investigation.

249

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

251

252 There is a single isolate of *C. brisbanense*, collected from chilli (*Capsicum annuum*) in Australia in
253 1955 (Damm et al. 2012a). There are hundreds of reports of *Colletotrichum* on *Capsicum* spp. in the
254 last decade, with over 30 different species of *Colletotrichum* associated, none of which corresponding
255 to *C. brisbanense*, in spite of surveys conducted in Australia (Shivas et al. 2016). *Colletotrichum*
256 *brisbanense* may well be extinct from nature.

257

258 *Colletotrichum cairnsense* D.D. De Silva, R. Shivas and P.W.J Taylor, *Plant Pathol.* **66**: 254 (2017)

259

260 There is a single isolate of *C. cairnsense*, collected from chilli (*Capsicum annuum*) in Australia in
261 2015 (De Silva et al. 2017a). The current conservation status of this species is unknown and of
262 concern.

263

264 *Colletotrichum carthami* (Fukui) S. Uematsu, Kageyama, Moriwaki and Toy. Sato, *J. Gen. Plant*
265 *Pathol.* **78**: 326 (2012)

266

267 *Colletotrichum carthami* is known from the Asteraceae *Calendula officinalis*, *Carthamus tinctorius*
268 and *Glebionis coronaria* (= *Chrysanthemum coronarium*) from Italy, Japan and Korea (Damm et al.
269 2012a; Uematsu et al. 2012; Baroncelli et al. 2015; Sato et al. 2015). This fungus may be specific of
270 Asteraceae.

271

272 *Colletotrichum chrysanthemi* (Hori) Sawada, *Rep. Govt. Res. Inst. Dep. Agric., Formosa* **85**: 81
273 (1943)

274

275 *Colletotrichum chrysanthemi* is a pathogen of Asteraceae (*Glebionis coronaria* and *Carthamus*
276 *tinctorius*), recorded from Europe and China (Damm et al. 2012a; Baroncelli et al. 2015). Further

277 research may shed light on the relative importance of the different species of *Colletotrichum*
278 associated with these hosts.

279

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

281

282 The species *Colletotrichum cosmi* was described based on an isolate collected from *Cosmos* sp.
283 (Asteraceae) in the Netherlands prior to 1973 (Damm et al. 2012a). Although Damm et al. (2012a)
284 discusses the possibility of the fungus being present on *Cosmos* spp. in India, Korea and Japan, no
285 other fungi have been so far assigned to this species, rendering the conservation status of this species
286 of great concern.

287

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

289

290 The species *Colletotrichum costaricense* was described based on two isolates collected from berries
291 and twigs of *Coffea* sp. (Rubiaceae) in Costa Rica prior to 1978 (Damm et al. 2012a). No other fungi
292 have been assigned ever since to this species, rendering its conservation status of great concern,
293 particularly as numerous species of *Colletotrichum* occur on coffee plants and despite numerous
294 surveys conducted on this host.

295

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

297

298 The species *Colletotrichum cuscutae* was described based on a single isolate collected from *Cuscuta*
299 sp. (Convolvulaceae) in Dominica in 1986 (Damm et al. 2012a). No other fungi have been assigned
300 ever since to this species. *Colletotrichum* has been reported on *Cuscuta* from different parts of the
301 world, but such isolates have not been characterised in modern terms. Only recently *C. fioriniae* was
302 identified associated with *Cuscuta* sp. in the USA (Liu et al. 2021b). The conservation status of this
303 species is thus of great concern.

304

305 *Colletotrichum eriobotryae* Damm and C.J. Huang, *Mycol. Prog.* **19**: 367 (2020)

306

307 *Colletotrichum eriobotryae* was recently recorded as a pathogen of loquat (*Eriobotrya japonica*,
308 Rosaceae) in China (Taiwan) (Damm et al. 2020). Although *C. eriobotryae* showed to be the
309 prevalent pathogen in that study, several species of *Colletotrichum* have been associated to loquat
310 anthracnose, suggesting further studies to ascertain the geographic distribution, host range and
311 pathological relevance of *C. eriobotryae*.

312

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

314

315 *Colletotrichum fioriniae* is a cosmopolitan fungus, found in all continents and in a wide range of host
316 plants, but mostly occurring in temperate regions (Supplementary data 2, panel B). *Colletotrichum*
317 *fioriniae* typically occurs along other *Colletotrichum* species associated to anthracnose symptoms,
318 often being a less frequent and/or less virulent population. However, several reports consistently place
319 *C. fioriniae* as the most frequently isolated fungus associated with apple bitter rot, namely in Europe
320 and North America (Munda 2014; Munir et al. 2016; Nodet et al. 2016; Grammen et al. 2019).
321 *Colletotrichum fioriniae* is known from: *Actinidia* sp. (Damm et al. 2012a) (Actinidiaceae); *Allium*
322 *cepa* (Liu et al. 2021b) (Amaryllidaceae); *Mangifera indica* (Damm et al. 2012a), *Pistacia vera*
323 (Lichtemberg et al. 2017) and *Toxicodendron radicans* (Kasson et al. 2014) (Anacardiaceae); *Annona*
324 *cherimola* (Liu et al. 2021b) (Annonaceae); *Apium graveolens* (Liu et al. 2021b) (Apiaceae); *Ilex*
325 *verticillata* (Lin et al. 2018a) and *I. integra* (Woo et al. 2021) (Aquifoliaceae); *Berberis* sp. (Damm
326 et al. 2012a) and *B. aquifolium* (as *Mahonia aquifolium*) (Garibaldi et al. 2020; Guarnaccia et al.
327 2021) (Berberidaceae); *Corylus avellana* (Sezer et al. 2017) (Betulaceae); *Cuscuta* sp. (Liu et al.
328 2021b) (Convolvulaceae); *Cucurbita* sp. (Liu et al. 2021b) (Cucurbitaceae); *Kalmia* sp. (Damm et al.
329 2012a), *Rhododendron yedoense* (Sultana et al. 2018), *Vaccinium corymbosum* (Damm et al. 2012a;
330 Eaton et al. 2021; Liu et al. 2021b), *V. macrocarpon* (Liu et al. 2021b) and *V. myrtilus* (Mosca et al.
331 2014) (Ericaceae); *Vernicia montana* (Zhang et al. 2021c) (Euphorbiaceae); *Acacia acuminata*
332 (Shivas et al. 2016) (Fabaceae); *Fagus sylvatica* (Pszczółkowska et al. 2017) (Fagaceae);
333 *Myriophyllum spicatum* (Damm et al. 2012a) (Haloragaceae); *Juglans regia* (Zhu et al. 2015; Varjas
334 et al. 2019) (Juglandaceae); *Origanum vulgare* (Guarnaccia et al. 2019) and *Salvia leucantha*
335 (Garibaldi et al. 2016c) (Lamiaceae); *Persea americana* (Damm et al. 2012a) (Lauraceae); *Tulipa* sp.
336 (Damm et al. 2012a) (Liliaceae); *Liriodendron tulipifera*, *Magnolia* sp. (Damm et al. 2012a) and *M.*
337 *champaca* (as *Michelia champaca*) (Zhang et al. 2018a) (Magnoliaceae); *Ficus virens* (Xue et al.
338 2017) and *Morus alba* (Xue et al. 2019) (Moraceae); *Acca sellowiana* (Crous et al. 2019a)
339 (Myrtaceae); *Olea europaea* (Damm et al. 2012a; Mosca et al. 2014; Talhinhos et al. 2018; Moreira
340 et al. 2021) (Oleaceae); *Paeonia* sp. (Liu et al. 2021b) (Paeoniaceae); *Pinus radiata* (Baroncelli et al.
341 2015) (Pinaceae); *Piper nigrum* (Damm et al. 2012a) (Piperaceae); *Penstemon* sp. (Damm et al.
342 2012a) (Plantaginaceae); *Cyclamen* sp. and *Primula* sp. (Damm et al. 2012a) (Primulaceae); *Grevillea*
343 sp. (Damm et al. 2012a) (Proteaceae); *Punica granatum* (Xavier et al. 2019) (Punicaceae); *Cydonia*
344 *oblonga* (Liu et al. 2021b), *Fragaria* × *ananassa* (Damm et al. 2012a; Baroncelli et al. 2015), *Malus*
345 *domestica* (Damm et al. 2012a; Kou et al. 2014; Munda 2014; Nodet et al. 2016; Oo et al. 2018;
346 Grammen et al. 2019), *Prunus armeniaca* (Eaton et al. 2021), *P. dulcis* (Liu et al. 2021b), *P. persica*

347 (Lee et al. 2018), *Pyrus communis* (Da Lio et al. 2017; Fu et al. 2019; Pavlović et al. 2019), *P.*
348 *pyrifolia* (Damm et al. 2012a; Fu et al. 2019; Pavlović et al. 2019; Liu et al. 2021b) and *Rubus idaeus*
349 (Schoeneberg and Hu 2020) (Rosaceae); *Coffea arabica* (Damm et al. 2012a) (Rubiaceae); *Acer*
350 *negundo* (Liu et al. 2021b) and *Litchi chinensis* (Ling et al. 2021) (Sapindaceae); *Ailanthus altissima*
351 (Hyde et al. 2017) (Simaroubaceae); *Capsicum annuum* (Diao et al. 2017), *Lycium barbarum* (Liu et
352 al. 2016a), *L. chinense* (Oo et al. 2016), *Solanum lycopersicum* (Damm et al. 2012a; Chechi et al.
353 2019) and *S. melogena* (Xu et al. 2018a) (Solanaceae); *Camellia sinensis* (Wang et al. 2016)
354 (Theaceae); *Parthenocissus* sp. (Damm et al. 2012a) (Vitaceae); *Fiorinia externa* (elongate hemlock
355 scale insect) (Marcelino et al. 2008).

356

357 *Colletotrichum godetiae* Neerg., *Friesia* **4**: 72 (1950)

358

359 *Colletotrichum godetiae* is known from a large number of hosts and locations, with emphasis in
360 Europe (Damm et al. 2012a; Jayawardena et al. 2016a) on almond, apple, peach, olive and strawberry
361 (Supplementary data 2, panel C). It is known from: *Sambucus nigra* (Damm et al. 2012a)
362 (Adoxaceae); *Schinus molle* (Damm et al. 2012a) (Anacardiaceae); *Berberis aquifolium* (as *Mahonia*
363 *aquifolium*) (Damm et al. 2012a) (Berberidaceae); *Cornus mas* (Tóth et al. 2017) (Cornaceae);
364 *Aeschynomene indica* (Damm et al. 2012a) (Fabaceae); *Juglans regia* (Damm et al. 2012a; Varjas et
365 al. 2021) (Juglandaceae); *Laurus nobilis* (Damm et al. 2012a) and *Persea americana* (Hernández-
366 Lauzardo et al. 2015) (Lauraceae); *Olea europaea* (Damm et al. 2012a; Mosca et al. 2014; Talhinhos
367 et al. 2018) (Oleaceae); *Clarkia hybrida* (Damm et al. 2012a) (Onagraceae); *Ugni molinae* (Damm et
368 al. 2012a) (Myrtaceae); *Podocarpus* sp. (Damm et al. 2012a) (Podocarpaceae); *Helleborus* sp.
369 (Shivas et al. 2016) (Ranunculaceae); *Ceanothus* sp. (Damm et al. 2012a) (Rhamnaceae); *Citrus*
370 *aurantium* (Damm et al. 2012a; Guarnaccia et al. 2017) (Rutaceae); *Agrimonia eupatoria* (Damm et
371 al. 2012a), *Cydonia oblonga* (Živković et al. 2014), *Eriobotrya japonica* (Juárez-Vázquez et al.
372 2019), *Fragaria* × *ananassa* (Damm et al. 2012a; Grammen et al. 2019), *Malus domestica* (Baroncelli
373 et al. 2014; Shivas et al. 2016; Wenneker et al. 2016; Grammen et al. 2019), *Prunus avium* (Damm
374 et al. 2012a; Grammen et al. 2019), *P. cerasus* (Damm et al. 2012a), *P. dulcis* (Damm et al. 2012a;
375 López-Moral et al. 2017; Liu et al. 2021b), *Rubus glaucus* (Afanador-Kafuri et al. 2014) and *R. idaeus*
376 (Damm et al. 2012a) (Rosaceae); *Solanum betaceum* (Damm et al. 2012a) (Solanaceae);
377 *Parthenocissus* sp. (Damm et al. 2012a) and *Vitis vinifera* (Damm et al. 2012a; Zapparata et al. 2017)
378 (Vitaceae).

379

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

381

382 *Colletotrichum guajavae* was designated based on an isolate collected from *Psidium guajava*
383 (Myrtaceae) in India at an unknown date (Damm et al. 2012a). The species was subsequently
384 identified as one of the causal agents of anthracnose on leaves of small cardamom (*Elettaria*
385 *cardamomum*, Zingiberaceae) in India in 2011 (Chethana et al. 2016). The pathological status of *C.*
386 *guajavae* and its geographical distribution requires further investigation. As causal agent of small
387 cardamom anthracnose, the pathogen may be of quarantine relevance.

388

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

390

391 There is a single record of *Colletotrichum indonesiense*, obtained from leaf spots developing after
392 herbicide treatment of an undesignated species of *Eucalyptus* (Myrtaceae) in Indonesia in 2008
393 (Damm et al. 2012a). Although *Colletotrichum* records on eucalypts are seldom, the circumstances
394 of the discovery of *C. indonesiense* and the lack of additional records for this taxon raise serious
395 concerns on its conservation status.

396

397 *Colletotrichum javanense* D.D. De Silva, P.W. Crous and P.W.J. Taylor, *IMA Fungus* **10**: 8 (2019)

398

399 *Colletotrichum javanense* is based on a single isolate, obtained from a chilli (*Capsicum annuum*,
400 Solanaceae) fruit in Indonesia in 2014 (De Silva et al. 2019). The high number of species of
401 *Colletotrichum* occurring on *Capsicum* raises serious concerns on the conservation status of *C.*
402 *javanense*, prompting for further surveys to ascertain its distribution and prevalence. As this fungus
403 was shown to be highly virulent to chilli (De Silva et al. 2019), it may turn out to become a fungus of
404 quarantine relevance.

405

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

407

408 *Colletotrichum johnstonii* was described based on two isolates collected in New Zealand, from fruit
409 rot in *Citrus* sp. and tomato (*Solanum lycopersicum*) in 1989 and 1990, respectively (Damm et al.
410 2012a). Recently Liu et al. (2021b) associated an additional fungus to this species, isolated from
411 groundnut (*Arachis hypogaea*, Fabaceae), at an unknown location and date. No further occurrences
412 of *C. johnstonii* have been reported which, along the large number of species of *Colletotrichum*
413 known from each host, raises serious concern on the conservation status of this taxon.

414

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

416

417 *Colletotrichum kinghornii*, described based on a single isolate collected from *Phormium tenax*
418 (Xanthorrhoeaceae) in the UK in 1935 (Damm et al. 2012a), has been recently identified on *Ph.*
419 *cookianum* in New Zealand (Crous et al. 2021). The scarcity of records suggests that the fungus is
420 rare, although the employment of the host plant as an ornamental raises caution of possible quarantine
421 implications.

422

423 *Colletotrichum kniphofiae* Crous and Denman, *Fungal Syst. Evol.* **1**: 180 (2018)

424

425 *Colletotrichum kniphofiae* was recently described based on an isolate collected from *Kniphofia uvaria*
426 (Xanthorrhoeaceae) dead leaves in the UK in 2016 (Crous et al. 2018b). Nothing is known about its
427 ecology or pathology and no other species of *Colletotrichum* have been reported from *K. uvaria*,
428 although *C. spaethianum* has been reported from *K. northiae* (Sato et al. 2015). The conservation
429 status of *C. kniphofiae* is therefore of great uncertainty.

430

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

432

433 The species *Colletotrichum laticiphilum* was described to accommodate fungi isolated from
434 anthracnose symptoms on rubber tree (*Hevea brasiliensis*, Euphorbiaceae) leaves in Colombia and
435 India (Damm et al. 2012a). The fungus was subsequently identified in Sri Lanka in 2012 also
436 associated to anthracnose of rubber tree (Hunupolagama et al. 2017), suggesting that this fungus may
437 be host specific. Several species of *Colletotrichum* occur on rubber tree, prompting further studies to
438 analyse the pathological relevance and conservation status of *C. laticiphilum*.

439

440 *Colletotrichum lauri* Jayawardena, Camporesi and K.D. Hyde, *Fungal Divers.* **87**: 148 (2017)

441

442 The species *Colletotrichum lauri* was described to accommodate an isolate obtained from dead leaves
443 of laurel (*Laurus nobilis*, Lauraceae) collected in Italy in 2015 (Hyde et al. 2017). There are no other
444 reports of this fungus worldwide and there are other species of *Colletotrichum* reported from laurel,
445 raising serious concern about the conservation status of *C. lauri*.

446

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

448

449 The species *Colletotrichum limeticola* is based on fungi isolated from wither tip symptoms on sour
450 lime (*Citrus aurantiifolia*, Rutaceae) in Cuba and the USA (Damm et al. 2012a), but such records are
451 dated from the 1910s, and no further occurrences have been recorded ever since on citrus, although

452 several species of *Colletotrichum* are known from these hosts. However, *C. limetticola* was recently
453 found in Brazil causing Glomerella leaf spot on apples, showing low prevalence but high virulence
454 (Moreira et al. 2019a). Both hosts are subject of numerous studies concerning the identification of
455 *Colletotrichum*, hence the scarcity of records of *C. limetticola* raise concern on its conservation status.

456

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

458

459 *Colletotrichum lupini* is the lupin anthracnose pathogen, reported from different parts of the world
460 (Supplementary data 2, panel D) on several species of *Lupinus* (Fabaceae), including *L. albus*, *L.*
461 *angustifolius*, *L. consentinii*, *L. hartwegii*, *L. luteus*, *L. mutabilis* and *L. polyphyllus* (Talhinhas et al.
462 2016). It is thus a host-specific pathogen of global distribution and common occurrence, although it
463 has been sporadically reported from other hosts.

464

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

466

467 The taxon *Colletotrichum melonis* was described to accommodate a fungus isolated from melon
468 (*Cucumis melo*, Cucurbitaceae) in Brazil prior to 1984 (Damm et al. 2012a). Although there are no
469 further reports of *Colletotrichum melonis* from melon, the fungus was subsequently reported from
470 persimmon (*Diospyros kaki*, Ebenaceae) in Brazil (Carraro et al. 2019) and from apple (*Malus*
471 *domestica*, Rosaceae) in Brazil and Uruguay (Alaniz et al. 2015; Bragança et al. 2016; Moreira et al.
472 2019a). *Colletotrichum melonis* seems to be common in Southeastern South America.

473

474 *Colletotrichum miaoliense* P.C. Chung & H.Y. Wu, in Chung, Wu, Wang, Hu, Ariyawansa, Hung,
475 Tzean & Chung, *Sci. Rep.* **10**(no. 14664): 6 (2020)

476

477 *Colletotrichum miaoliense* is known only from Taiwan, associated to strawberry anthracnose among
478 several pathogens from other species of *Colletotrichum* (Chung et al. 2020). The conservation status
479 of this fungus remains to be analysed.

480

481 *Colletotrichum nymphaeae* (Pass.) Aa, *Neth. J. Plant Pathol.*, **84**: 110 (1978)

482

483 Damm et al. (2012a) recognised *Colletotrichum nymphaeae* as a pathogen of *Anemone* sp.
484 (Ranunculaceae), *Capsicum* sp. (Solanaceae), *Fragaria × ananassa*, *Malus pumila* and *Photinia* sp.
485 (Rosaceae), *Leucaena* sp. and *Phaseolus* sp. (Fabaceae), *Berberis aquifolium* (= *Mahonia aquifolium*,
486 Berberidaceae), *Nuphar lutea* and *Nymphaea alba* (Nymphaeaceae), *Oenothera* sp. (Onagraceae),

487 *Olea europaea* (Oleaceae), *Pelargonium graveolens* (Geraniaceae) and *Protea* spp. (Proteaceae). The
488 fungus was subsequently identified from: *Actinidia arguta* (Actinidiaceae) in Korea (Kim et al. 2018);
489 *Allium cepa* (Amaryllidaceae) in Brazil (Lopes et al. 2021); *Apium graveolens* (Apiaceae) in Japan
490 (Yamagishi et al. 2015); *Camellia oleifera* (Theaceae) in China (Li and Li 2020); *Campanula*
491 *rapunculoides* (Campanulaceae) in Italy (Guarnaccia et al. 2021); *Carya illinoensis* (Juglandaceae)
492 in Brazil and China (Poletto et al. 2019; Zhang et al. 2019a); *Citrus aurantifolia* (as *Colletotrichum*
493 *citri*; Damm et al. 2020) and *Citrus limon* (Rutaceae) in China and Australia respectively (Huang et
494 al. 2013; Shivas et al. 2016); *Cyclamen persicum* (Primulaceae) in Italy (Mosca et al. 2014);
495 *Diospyros kaki* (Ebenaceae) in Brazil and Korea (Carraro et al. 2019; Hassan et al. 2019a); *Eriobotrya*
496 *japonica* (Rosaceae) in China (Wu et al. 2018); *Hevea brasiliensis* (Euphorbiaceae) in Sri Lanka
497 (Hunupolagama et al. 2017); *Ilex verticillata* × *I. serrata* (Aquifoliaceae) in the USA (Lin et al.
498 2018a); *Juglans regia* (Juglandaceae) in Brazil (Savian et al. 2019); *Malus domestica* (Rosaceae) in
499 Brazil, Korea and the USA (Velho et al. 2014b; Munir et al. 2016; Oo et al. 2018); *Prunus persica*
500 and *P. salicina* (Rosaceae) in Brazil and Korea respectively (Chang et al. 2018a; Moreira et al. 2020);
501 *Psidium guajava* (Myrtaceae) in Brazil (Bragança et al. 2016); *Punica granatum* (Lythraceae) in the
502 USA (Xavier et al. 2019); *Pyrus pyrifolia* (Rosaceae) in Brazil (Moreira et al. 2019b); *Robinia*
503 *pseudoacacia* (Fabaceae) in Japan (Yamagishi et al. 2016); *Rubus corchorifolius* (Rosaceae) in China
504 (Wu et al. 2021); *Solanum lycopersicum* (Solanaceae) in the USA (Chechi et al. 2019); *Vitis vinifera*
505 (Vitaceae) in China (Liu et al. 2016b); the citrus scale insect *Praelongorthezia praelonga* (Hemiptera:
506 Ortheziidae) in Brazil as *Colletotrichum nymphaeae* var. *entomophilum* (Wynns et al. 2019). Thus,
507 *C. nymphaeae* occurs on a vast list of important agricultural crops, often as the main causal agent of
508 anthracnose (such as strawberry anthracnose). Whereas older reports were more frequent in the Old
509 World, most reports from the 2010s decade are from America, suggesting a recent spread over this
510 continent (Supplementary data 2, panel E).

511

512 *Colletotrichum paranaense* C.A.D. Bragança and Damm, *Fungal Biol.* **120**: 555 (2016)

513

514 *Colletotrichum paranaense* is known from Brazil only, associated to anthracnose symptoms in apple
515 (*Malus domestica*) and peach (*Prunus persica*) fruits, as well as from *Caryocar brasiliense*
516 (*Caryocaraceae*) (Bragança et al. 2016). In a population study, *C. paranaense* was identified in several
517 states in Brazil associated to apple Glomerella leaf spot disease, although not as the most frequent
518 pathogen (Moreira et al. 2019a). Further surveys will clarify the geographical distribution of
519 *Colletotrichum paranaense*, its pathological relevance to apple and other crops, as well as its
520 conservation status.

521

522 *Colletotrichum paxtonii* Damm, P.F. Cannon and Crous, *Stud. Mycol.* **73**: 85 (2012)

523

524 The species *Colletotrichum paxtonii* is known only from a fungus obtained from *Musa nana*
525 (Musaceae) in Saint Lucia in 1972 (Damm et al. 2012a). The inexistence of any further occurrences
526 of this species, in spite of the widespread cultivation of banana, along with the frequent occurrence
527 of other species of *Colletotrichum* in this host, suggests that *C. paxtonii* may be extinct from nature.

528

529 *Colletotrichum phormii* (Henn.) D.F. Farr and Rossman, *Mycol. Res.* **110**: 1403 (2006)

530

531 *Colletotrichum phormii* occurs on New Zealand flax (*Phormium tenax* and *Ph. colensoi*,
532 Xanthorrhoeaceae), being reported from Australia, New Zealand, South Africa, Germany, the
533 Netherlands, UK and the USA (Supplementary data 2, panel F), with reports spanning from the late
534 19th century till contemporary times (Damm et al. 2012a; Serdani et al. 2013; Baroncelli et al. 2015;
535 Shivas et al. 2016). *Colletotrichum phormii* seems to be the most common causal agent of New
536 Zealand flax anthracnose and it appears to be a relatively common fungus on this host.

537

538 *Colletotrichum pyricola* Damm, P.F. Cannon and Crous, *Stud. Mycol.* **73**: 94 (2012)

539

540 Defined originally based on an isolate collected from a pear (*Pyrus communis*, Rosaceae) fruit rot in
541 New Zealand in 1988 (Damm et al. 2012a), *Colletotrichum pyricola* was subsequently identified
542 associated to leaf and tip dieback of *Daphne odora* (Thymelaeaceae) in Australia (although collected
543 in 1983) (Shivas et al. 2016) and to leaf spots of *Embothrium coccineum* (Proteaceae) in Chile in
544 2015 (Zapata and Opazo 2017). Although reported from diverse hosts and locations, this fungus is
545 rarely recorded, prompting further studies to better ascertain its conservation status.

546

547 *Colletotrichum rhombiforme* Damm, P.F. Cannon and Crous, *Stud. Mycol.* **73**: 95 (2012)

548

549 *Colletotrichum rhombiforme* was described based on two isolates, obtained from olive (*Olea*
550 *europaea*, Oleaceae) in Portugal in 2003 (Talhinhas et al. 2005; Damm et al. 2012a) and from
551 blueberry (*Vaccinium macrocarpum*, Ericaceae) in the USA (Damm et al. 2012a). The species was
552 subsequently identified from apple (*Malus domestica*, Rosaceae) in Belgium in 2014 (Grammen et
553 al. 2019) and in China in 2016 (Wu et al. 2017) and from *Vaccinium dunalianum* var. *urophyllum* in
554 China (Wang et al. 2019b). Whereas this species seems widespread, the scarcity of its records spread
555 through several hosts suggests that further surveys are needed to ascertain its distribution,
556 pathological relevance and conservation status.

557

558 *Colletotrichum roseum* M. Zapata, M.A. Palma, M.J. Aninat and Piont., *Persoonia* **43**: 354 (2019)

559

560 The species *Colletotrichum roseum* contains isolates obtained from *Lapageria rosea* (Philesiaceae)
561 in Chile in 2018 (Crous et al. 2019a). The geographical distribution, pathological relevance and
562 conservation status of *Colletotrichum roseum* remains to be clarified.

563

564 *Colletotrichum salicis* (Fuckel) Damm, P.F. Cannon and Crous, *Stud. Mycol.* **73**: 97 (2012)

565

566 The species *Colletotrichum salicis* contains fungi occurring on diverse hosts and regions, in higher
567 latitudes than most other species of *Colletotrichum* (Supplementary data 2, panel G): *Acer*
568 *platanoides* (Sapindaceae) in the USA (Damm et al. 2012a); *Araucaria columnaris* (as *Araucaria*
569 *excelsa*, Araucariaceae) in the USA (Damm et al. 2012a); *Fragaria* × *ananassa* (Rosaceae) in
570 Belgium and New Zealand (Damm et al. 2012a; Grammen et al. 2019); *Malus domestica* (Rosaceae)
571 in Belgium, Germany and New Zealand (Damm et al. 2012a; Grammen et al. 2019); *Populus* ×
572 *canadensis* and *P. nigra* (Salicaceae) in the Netherlands and Iran respectively (Damm et al. 2012a;
573 Khodaei et al. 2019); *Pyrus pyrifolia* (Rosaceae) in New Zealand (Damm et al. 2012a);
574 *Rhododendron* sp. (Ericaceae) in Latvia (Damm et al. 2012a); *Salix* spp. (Salicaceae) in Australia,
575 New Zealand, Japan, Poland, Germany, the Netherlands and UK (Damm et al. 2012a; Shivas et al.
576 2016; Okorski et al. 2018); *Solanum lycopersicum* (Solanaceae) in Germany (Damm et al. 2012a);
577 *Vaccinium corymbosum* (Ericaceae) in Norway (Damm et al. 2012a). Although there are some recent
578 reports of *Colletotrichum salicis*, most occurrences are old, suggesting that this fungus may not be
579 very common in present days.

580

581 *Colletotrichum scovillei* Damm, P.F. Cannon and Crous, *Stud. Mycol.* **73**: 100 (2012)

582

583 *Colletotrichum scovillei* is a species associated to chilli (*Capsicum* spp., Solanaceae) anthracnose.
584 This species is known from Asia (China, Indonesia, Japan, Korea and Thailand; Damm et al. 2012a;
585 Kanto et al. 2014; Zhao et al. 2016a; Oo et al. 2017; Huo et al. 2021), but also from Brazil (Caires et
586 al. 2014) and the USA (Toporek and Keinath 2021) (Supplementary data 2, panel H). Recently it has
587 been reported in China associated to anthracnose symptoms on banana (*Musa acuminata*, Musaceae)
588 (Zhou et al. 2017), mango (*Mangifera indica*, Anacardiaceae) (Qin et al. 2019) and wampi
589 (*Clausena lansium*, Rutaceae) (Lin et al. 2020), and from Brazil associated to anthracnose
590 symptoms on onion (Lopes et al. 2021). The host range of *C. scovillei* and the pathological relevance
591 for crops other than chillies still need to be fully elucidated.

592

593 *Colletotrichum simmondsii* R.G. Shivas and Y.P. Tan, *Fungal Divers.* **39**:119 (2009)

594

595 *Colletotrichum simmondsii* sensu Damm et al. (2012a) is a fungus recorded predominantly from
596 Australia, on multiple hosts: *Actinidia chinensis* (Actinidiaceae); *Averrhoa carambola* (Oxalidaceae);
597 *Calothamnus quadrifidus* (Myrtaceae); *Capsicum annuum* (Solanaceae); *Carica papaya*
598 (Caricaceae); *Citrus reticulata* (Rutaceae); *Cyclamen* sp. (Primulaceae); *Fragaria* × *ananassa*
599 (Rosaceae); *Hevea brasiliensis* (Euphorbiaceae); *Litchi chinensis* (Sapindaceae); *Mandevilla* sp.
600 (Apocynaceae); *Mangifera indica* (Anacardiaceae); *Murraya* sp. (Rutaceae); *Nephelium lappaceum*
601 (Sapindaceae); *Protea cynaroides* (Proteaceae); *Prunus domestica* (Rosaceae); *Punica granatum*
602 (Punicaceae); *Solanum betaceum* and *S. lycopersicum* (Solanaceae); *Vaccinium corymbosum*
603 (Ericaceae) (Damm et al. 2012a; Shivas et al. 2016; Guarnaccia et al. 2017; Hunupolagama et al.
604 2017; De Silva et al. 2017a; Xavier et al. 2019). Few occurrences of *Colletotrichum simmondsii* are
605 recorded from countries other than Australia and even fewer are recent, whereas most of the recent
606 reports of the fungus are from Australia, suggesting this species to be mostly geographically confined
607 to this country (Supplementary data 2, panel I).

608

609 *Colletotrichum sloanei* Damm, P.F. Cannon and Crous, *Stud. Mycol.* **73**: 103 (2012)

610

611 *Colletotrichum sloanei* was described based on a fungus isolated from cacao (*Theobroma cacao*,
612 Malvaceae) in Malaysia in 1994 (Damm et al. 2012a). It was subsequently isolated from lychee (*Litchi*
613 *chinensis*, Sapindaceae) in Australia in 2003 (Shivas et al. 2016) and recently from apple (*Malus*
614 *domestica*, Rosaceae) and guava (*Psidium guajava*, Myrtaceae) in Indonesia in 2019 (Zhafarina et al.
615 2021). Records of *C. sloanei* are scarce and dispersed which, along with the occurrence of several
616 other species of *Colletotrichum* on its hosts, render its conservation status of concern.

617

618 *Colletotrichum tamarilloi* Damm, P.F. Cannon and Crous, *Stud. Mycol.* **73**: 105 (2012)

619

620 *Colletotrichum tamarilloi* is the causal agent of anthracnose on tamarillo (*Solanum betaceum*,
621 Solanaceae), reported from Colombia and Ecuador (Damm et al. 2012a; Pardo-De la Hoz et al. 2016;
622 Caicedo et al. 2017), although Pardo-De la Hoz et al. (2016) also reported this fungus from mango in
623 Colombia, and recently Lopes et al. (2021) reported it from onion in Brazil (Supplementary data 2,
624 panel J). *Colletotrichum tamarilloi* thus seems to be mostly a host specific fungus of common
625 occurrence on its host, but disseminating in South America.

626

627 *Colletotrichum walleri* Damm, P.F. Cannon and Crous, *Stud. Mycol.* **73**: 106 (2012)

628

629 *Colletotrichum walleri* is only known from a single isolate, obtained from coffee (*Coffea arabica*) in
630 Vietnam in an unknown date (Damm et al. 2012a). Several species of *Colletotrichum* are known from
631 coffee and there are no further records attributable to *C. walleri*, raising serious concerns about the
632 actual existence of this species in nature.

633

634 *Colletotrichum wanningense* X.R. Cao, H.Y. Che and D.Q. Luo, *Plant Dis.* **103**: 117 (2019)

635

636 *Colletotrichum wanningense* was designated based on a single isolate obtained from an asymptomatic
637 leaf of rubber tree (*Hevea brasiliensis*, Euphorbiaceae) in China in 2017 (Cao et al. 2019b).
638 Considering the large number of species of *Colletotrichum* recorded from *Hevea* and the absence of
639 any further records of *Colletotrichum wanningense*, concerns raise on the actual conservation status
640 of this species, prompting further surveys to ascertain its presence in nature.

641

642 **2.2 The Agaves species complex**

643

644 Recently described (Bhunjun et al. 2021), the agaves species complex is a well-established
645 monophyletic group of five species, *Colletotrichum agaves*, *C. ledebouriae*, *C. neosansevieriae*, *C.*
646 *euphorbiae* and *C. sansevieriae* (Figure 4), considered until recently as singletons (Jayawardena et
647 al. 2016a; Marín-Felix et al. 2017). The species complex name comes from *C. agaves* that has been
648 the first species of this group described (Farr et al. 2006). Among the species encompassed in this
649 complex, three species (*C. ledebouriae*, *C. neosansevieriae* and *C. euphorbiae*) seem to be extremely
650 rare as they have been reported only once in South Africa. *Colletotrichum agaves* has been reported
651 in several geographic regions (Italy, Mexico, USA, Cuba, Jamaica, Haiti, El Salvador) but not in the
652 past 15 years, while several records have reported *C. sansevieriae* in diverse regions of Asia and in
653 the USA. Interestingly four of the species encompassed in this complex such as *C. agaves*, *C.*
654 *ledebouriae*, *C. neosansevieriae* and *C. sansevieriae* have been reported only on hosts belonging to
655 the Asparagaceae family (Liliopsida [monocot]; Asparagales) whereas only one testimony of *C.*
656 *euphorbiae* on *Euphorbia* sp. (Magnoliopsida [eudicot], Euphorbiales, Euphorbiaceae) has been
657 reported.

658

659 **Figure 4**

660

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

662

663 As reviewed by Farr et al. (2006), most reports of *Colletotrichum agaves* are from the first half of the
664 20th century. The three most recent records are from 2002 in Mexico, from 1982 in the USA and from
665 1979 in the Netherlands on *Agave* spp. (Supplementary data 3, panel A). Other *Colletotrichum* spp.
666 occur on the Agavaceae and the current conservation status of *C. agaves* is of concern.

667

668 *Colletotrichum euphorbiae* Damm and Crous, *Persoonia* **31**: 203 (2013)

669

670 The only record of *Colletotrichum euphorbiae* is from leaves of an unspecified species of *Euphorbia*
671 collected at the Kirstenbosch Botanical Garden in South Africa in 2012 (Crous et al. 2013). There is
672 no information on the pathological status of this fungus neither on whether the host plant was present
673 as part of the botanical collection or as a weed. Considering that *Euphorbia* is a vast genus and one
674 of the most morphologically diverse in botany, the conservation status of *C. euphorbiae* can be
675 considered of extreme concern.

676

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

678

679 There is a single record of *Colletotrichum ledebouriae*, obtained from *Ledebouria floribunda*
680 (Asparagaceae) in 2014 in South Africa (Crous et al. 2016). There are no records of anthracnose on
681 this host and no further records for *C. ledebouriae*, raising serious concerns about its conservation
682 status.

683

684 *Colletotrichum neosansevieriae* Crous and N.A. van der Merwe, *Persoonia* **34**: 221 (2015)

685

686 This species is known only from a single isolate, collected in South Africa from *Sansevieria*
687 *trifasciata* (Asparagaceae) in 2014 (Crous et al. 2015). The absence of further records for this fungus
688 and the occurrence of other species of *Colletotrichum* on *Sansevieria* raises serious concerns on the
689 conservation status of *C. neosansevieriae*.

690

691 *Colletotrichum sansevieriae* Miho Nakam. and Ohzono, *J. Gen. Plant Pathol.* **72**: 253 (2006)

692

693 *Colletotrichum sansevieriae* is reported from *Sansevieria trifasciata* (Asparagaceae) in Japan since
694 1997 (Nakamura et al. 2006), in Australia since 2008 (Aldaoud et al. 2011), in the USA since 2010
695 (Palmateer et al. 2012), in Korea since 2012 (Park et al. 2013), in Iran since 2015 (Karimi et al. 2017)

696 and in Malaysia since 2015 (Kee et al. 2020) (Supplementary data 3, panel B). *Colletotrichum*
697 *sansevieriae* seems to be common and to show a high host specificity.

698

699 **2.3 The boninense species complex**

700

701 As a species, *Colletotrichum boninense* was first described in 2003 associated with *Crinum asiaticum*
702 (Amaryllidaceae) in Japan (Moriwaki et al. 2003). Historically *C. boninense* was described as a
703 pathogen and endophyte of a wide range of plant hosts worldwide until 2012 when Damm and
704 colleagues (Damm et al. 2012b) used an MLST approach on 86 strains previously identified as *C.*
705 *boninense* and other related strains revealing 18 clades and describing 17 of those as novel species.
706 Since the taxonomic revision and the description of what is now known as the boninense species
707 complex, more species have been described. Currently boninense is the third largest complex of the
708 genus encompassing 26 described species (Figure 5). Among these, half have only been reported
709 once, whereas others such as *C. boninense* and *C. cymbidiicola* have been reported several times.
710 Inside this complex *C. karsti* is by far the most cosmopolitan and polyphagous species as it has been
711 associated with more than 60 plant species worldwide. Like the acutatum and the gloeosporioides
712 species complexes, the boninense complex includes highly polyphagous species as well as species
713 that show a certain level of specialisation. For example, *C. cymbidiicola* has been reported on at least
714 eight plant hosts belonging to different genera but all of them belonging to the Orchidaceae family
715 (Liliopsida [monocot]; Orchidales). A geographic and host-range analysis of the phylogeny of the
716 boninense species complex reveal that: fungi in the clade containing *C. annellatum*, *C. camelliae-*
717 *japonicae*, *C. citricola*, *C. chongqingense*, *C. karsti* and *C. phyllanthi* occur mostly in Asia and
718 Oceania (but *C. karsti* is of global distribution); those in the clade containing *C. catinaense*, *C.*
719 *limonicola* and *C. novae-zelandiae* are associated with citrus in Mediterranean Europe and New
720 Zealand; fungi in the clade containing *C. beeveri*, *C. boninense*, *C. brassicicola*, *C. colombiense*, *C.*
721 *cymbidiicola*, *C. doitungense*, *C. oncidii* and *C. torulosum* occur mostly in Asia and Oceania, with
722 the *C. cymbidiicola* - *C. oncidii* cluster specifically from orchids; the fungi in the clade containing *C.*
723 *brasiliense*, *C. condaoense*, *C. hippeastri* and *C. parsonsiae* originate from multiple continents; the
724 clade comprising *C. constrictum* and *C. dacrycarpi*, phylogenetically basal to the complex, contains
725 fungi from New Zealand. This phylogeographic approach indicates a wider species diversity in Asia
726 and Oceania, suggesting that the complex may have originated from there.

727

728 **Figure 5**

729

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

731

732 There is a single record for *Colletotrichum annellatum*, collected from *Hevea brasiliensis* leaves in
733 Colombia in 2010, with unconfirmed pathogenicity (Damm et al. 2012b). The pathological relevance
734 and ecological status of this species remains to be analysed.

735

736 *Colletotrichum beeveri* Damm, P.F. Cannon, Crous, P.R. Johnst and B. Weir, *Stud. Mycol.* **73**: 9
737 (2012)

738

739 There is a single record for *Colletotrichum beeveri*, from *Brachyglottis repanda* (Asteraceae) in New
740 Zealand in 2006, although sequence similarity suggests its occurrence as endophyte on *Pleione*
741 *bulbocodioides* (Orchidaceae) in China and on Podocarpaceae in New Zealand (Damm et al. 2012b).
742 The current conservation status of this species is therefore of concern.

743

744 *Colletotrichum boninense* Moriwaki, Toy. Sato and Tsukib., *Mycoscience* **44**: 48 (2003)

745

746 *Colletotrichum boninense* is recorded from several hosts, often as endophyte, mostly in Asia and
747 Oceania (Damm et al. 2012b) (Supplementary data 4, panel A), including *Crinum asiaticum* var.
748 *sinicum* (Amaryllidaceae; Damm et al. 2012b), *Tecomanthe speciosa* (Bignoniaceae; Damm et al.
749 2012b), *Vriesea imperialis* (as *Alcantarea imperialis*) (Bromeliaceae; Meneses et al. 2019), *Manihot*
750 *esculenta* (Euphorbiaceae; Hyde et al. 2018), *Eucalyptus robusta* (Myrtaceae; Zhang and Zhu 2018),
751 *Bletilla ochracea* and *Dendrobium* sp. (Orchidaceae; Tao et al. 2013; Hyde et al. 2018), *Dacrycarpus*
752 *dacrydioides* (Podocarpaceae; Damm et al. 2012b), *Leucospermum* sp. (Proteaceae; Damm et al.
753 2012b), *Coptis chinensis* (Ranunculaceae; Ding et al. 2020); *Capsicum frutescens*, *Solanum betaceum*
754 and *S. lycopersicum* (Solanaceae; Damm et al. 2012b; Diao et al. 2013; Rashid et al. 2015), *Fragaria*
755 \times *ananassa*, *Rosa chinensis* and *Rubus rosaefolius* (Rosaceae; Bi et al. 2017b; Ding et al. 2021; Zheng
756 et al. 2021a), *Coffea arabica* (Rubiaceae; Freitas et al. 2013), *Citrus medica* (Rutaceae; Guarnaccia
757 et al. 2017) and *Camellia sinensis* (Theaceae; Liu et al. 2015b).

758

759 *Colletotrichum brasiliense* Damm, P.F. Cannon, Crous and Massola, *Stud. Mycol.* **73**: 11 (2012)

760

761 A single isolate is known for *Colletotrichum brasiliense*, collected in Brazil in 2006 from *Passiflora*
762 *edulis* fruits (Damm et al. 2012b). Additional species of *Colletotrichum* are known from passionfruit
763 (Damm et al. 2012b), raising concern on the conservation status of *C. brasiliense*.

764

765 *Colletotrichum brassicicola* Damm, P.F. Cannon and Crous, *Stud. Mycol.* **73**: 14 (2012)

766

767 There are only two known isolates for this species, collected respectively in New Zealand on *Brassica*
768 *oleracea* var. *gemmifera* in an unknown date prior to 1998 (Damm et al. 2012b) and in Colombia on
769 *Rubus glaucus* in 2008 (Afanador-Kafuri et al. 2014). Both plant species host several other species
770 of *Colletotrichum*, therefore the pathological relevance and conservation status of *C. brassicicola*
771 remains to be clarified.

772

773 *Colletotrichum camelliae-japonicae* LW. Hou and L. Cai, *Mycosphere* **7**: 1117 (2016)

774

775 *Colletotrichum camelliae-japonicae* was reported only once, in 2013, on *Camellia japonica* plants
776 from Japan (Hou et al. 2016). The conservation status of this pathogen is unknown and of concern.

777

778 *Colletotrichum catinaense* Guarnaccia and Crous, *Persoonia* **39**: 32 (2017)

779

780 This species is known from *Citrus sinensis* (fruit tear-stain) and *C. reticulata* (leaf lesion) collected
781 in 2015 in Portugal and Italy (Guarnaccia et al. 2017). As several species of *Colletotrichum* are found
782 on *Citrus* spp. (Huang et al. 2013; Ramos et al. 2016; Douanla-Meli and Unger 2017; Guarnaccia et
783 al. 2017; Silva et al. 2017a; Uysal and Kurt 2019), the pathological relevance and conservation status
784 of *Colletotrichum catinaense* need to be further investigated.

785

786 *Colletotrichum chongqingense* Y.J. Chen, *Plant Dis.* in press (2021) DOI: 10.1094/PDIS-09-20-
787 1912-RE

788

789 The species *Colletotrichum chongqingense* was described based on a single isolate associated to
790 anthracnose symptoms on *Camellia sinensis* (Theaceae) leaves in China, isolated in 2017 (Wan et al.
791 2021). Considering the vast number of species of *Colletotrichum* known from tea plants, the
792 pathological relevance and conservation status of *C. chongqingense* are much uncertain.

793

794 *Colletotrichum citricola* F. Huang, L. Cai, K.D. Hyde and Hong Y. Li, *Fungal Divers.* **61**: 67 (2013)

795

796 Initially described as an endophyte of *Citrus unchiu* collected in 2012 in China (Huang et al. 2013),
797 *Colletotrichum citricola* was subsequently isolated from anthracnose symptoms on leaves of *Pyrus*
798 *pyrifolia* in 2015 in China (Fu et al. 2019) and from healthy *Dendrobium* sp. plants in Thailand (Ma
799 et al. 2018). All three host plants harbor other species of *Colletotrichum*, rendering the pathologic
800 relevance of *C. citricola* uncertain and its conservation status of concern.

801

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

803

804 *Colletotrichum colombiense* is based on an isolate collected from *Passiflora edulis* in Colombia in
805 2010 (Damm et al. 2012b). Additional isolates obtained from *Passiflora* sp. in Colombia may also
806 belong to *C. colombiense*, as discussed by Damm et al. (2012b). Nevertheless, given that there are
807 several species of *Colletotrichum* occurring on *Passiflora*, the conservation status of *C. colombiense*
808 is uncertain.

809

810 *Colletotrichum condaoense* Damm, *Persoonia* **40**: 240 (2018)

811

812 *Colletotrichum condaoense* is based on an isolate collected from *Ipomoea pes-caprae*
813 (Convolvulaceae) in Vietnam in 2012 (Crous et al. 2018c). No other species of *Colletotrichum* have
814 been reported on this host species. The host is widespread in tropical coastal areas, suggesting that
815 the conservation status of *C. condaoense* should be investigated.

816

817 *Colletotrichum constrictum* Damm, P.F. Cannon, Crous, P.R. Johnst and B. Weir, *Stud. Mycol.* **73**:
818 17 (2012)

819

820 *Colletotrichum constrictum* is composed of two strains, collected in New Zealand in 1988 from
821 diseased lemon (*Citrus limon*) and tamarillo (*Solanum betaceum*) fruits, and presumably also of
822 strains collected from *Passiflora edulis* and *P. mollissima* also in New Zealand (Damm et al. 2012b).
823 No new strains have been assigned to *C. constrictum* for over 30 years which, together with the fact
824 that all hosts harbor several species of *Colletotrichum*, render the conservation status of the species
825 of great concern.

826

827 *Colletotrichum cymbidiicola* Damm, P.F. Cannon, Crous, P.R. Johnst. and B. Weir, *Stud. Mycol.* **73**:
828 19 (2012)

829

830 *Colletotrichum cymbidiicola* is known from *Cymbidium* (Orchidaceae) in Australia, New Zealand,
831 Japan and India (Supplementary data 4, panel B) with endophytic behavior (Damm et al. 2012b), but
832 also from the orchids *Bulbophyllum hirtum*, *Callostylis bambusifolia*, *Coelogyne* sp., *Dendrobium*
833 *fimbriatum*, *Liparis viridiflora*, *Oncidium sphacealatum* and *Pinalia amica* in India causing
834 anthracnose (Chowdappa et al. 2014). Considering the vast amount of species of *Colletotrichum*
835 occurring on Orchidaceae, the conservation status of *C. cymbidiicola* prompts for caution.

836

837 *Colletotrichum dacrycarpi* Damm, P.F. Cannon, Crous, P.R. Johnst. and B. Weir, *Stud. Mycol.* **73**:
838 19 (2012)

839

840 *Colletotrichum dacrycarpi*, a morphologically and phylogenetically atypical *Colletotrichum* species,
841 is known only from a single isolate collected as an endophyte on a *Dacrycarpus dacrydioides*
842 (Podocarpaceae) leaf in New Zealand in 2009 (Damm et al. 2012b). There are no other records of
843 *Colletotrichum* on *Dacrycarpus*, stressing that the conservation status of *C. dacrycarpi* is of great
844 concern.

845

846 *Colletotrichum doitungense* X.Y. Ma, K.D. Hyde and Jayawardena, *MycKeys* **43**: 23 (2018)

847

848 *Colletotrichum doitungense* is known from a single isolate collected epiphytically on *Dendrobium*
849 sp. (Orchidaceae) in Thailand in 2013 (Ma et al. 2018). Considering the vast amount of species of
850 *Colletotrichum* occurring on Orchidaceae, the conservation status of *C. doitungense* is of great
851 concern.

852

853 *Colletotrichum feijoicola* Guarnaccia and Damm, *Persoonia* **42**: 291 (2019)

854

855 *Colletotrichum feijoicola* has recently been reported based on a single isolate, collected from *Acca*
856 *sellowiana* (Myrtaceae) leaf spots from the Azores islands (Portugal) in 2017 (Crous et al. 2019b).
857 Considering that several species of *Colletotrichum* have been reported from *Acca sellowiana*, the
858 conservation status of *C. feijoicola* is of concern.

859

860 *Colletotrichum hippeastri* Yan L. Yang, Zuo Y. Liu, K. D. Hyde and L. Cai, *Fungal Divers.* **39**: 133
861 (2009)

862

863 The species *Colletotrichum hippeastri* was designated to accommodate fungi isolated from
864 *Hippeastrum* (Amaryllidaceae) hosts in Brazil, China and the Netherlands (Damm et al. 2012b).
865 Reports of anthracnose are scarce on *Hippeastrum* and no additional occurrences of *C. hippeastri*
866 have been described, raising concern on the conservation status of this species.

867

868 *Colletotrichum karsti* Y.L. Yang, Zuo Y. Liu, K.D. Hyde and L. Cai, *Cryptog. Mycol.* **32**: 241 (2011)

869

870 Damm et al. (2012b) recognised *Colletotrichum karsti* from a number of hosts and regions
871 (Supplementary data 4, panel C), including *Annona cherimola*, *Anthurium* sp., *Capsicum annuum*,
872 *Carica papaya*, *Citrullus lanatus*, *Citrus* spp., *Clivia miniata*, *Coffea* spp., *Cucumis melo*, *Diospyros*
873 spp., *Eucalyptus grandis*, *Eugenia uniflora*, *Gossypium hirsutum*, *Leucospermum* sp., *Lupinus albus*,
874 *Malus* sp., *Mangifera indica*, *Musa* sp., *Pachira aquatica* (as *Bombax aquaticum*), *Passiflora edulis*,
875 *Quercus salicifolia*, *Sclerocroton integerrimus*, *Solanum betaceum*, *S. lycopersicum*, *Stylosanthes*
876 spp., *Synsepalum dulcificum*, *Theobroma cacao*, *Triticum* sp., and *Zamia obliqua*, along with orchid
877 species, from where it was initially described (Youlian et al. 2011). The species was subsequently
878 identified on *Alocasia macrorrhizos* and *Areca catechu* (Araceae) in China (He et al. 2014; Cao et al.
879 2020), *Bletilla ochracea* (Orchidaceae) in China (Tao et al. 2013), *Camellia* spp. (Theaceae) in China
880 and Italy (Schena et al. 2014; Wang et al. 2016; Jiang and Li 2018), *Carissa macrocarpa* (= *C.*
881 *grandiflora*; Apocynaceae) in Spain (García-Lopez et al. 2021), *Dendrobium nobile* (Orchidaceae) in
882 Mexico (Fernández-Herrera et al. 2020), *Dracaena braunii* (as *D. sanderiana*, Asparagaceae) in
883 China (Li et al. 2018a), *Elettaria cardamomum* (Zingiberaceae) in India (Chethana et al. 2016), *Fatsia*
884 *japonica* (Araliaceae) in China (Xu et al. 2021), *Fragaria* × *ananassa* in Brazil (Soares et al. 2021),
885 *Hevea brasiliensis* (Euphorbiaceae) in China (Cai et al. 2016a), *Hylocereus undatus* (Cactaceae) in
886 Brazil (Nascimento et al. 2019b), *Litchi chinensis* (Sapindaceae) in China (Zhao et al. 2021c), *Malus*
887 *domestica* (Rosaceae) in Brazil and Uruguay (Velho et al. 2014a, 2015), cassava (*Manihot esculenta*,
888 Euphorbiaceae) in China (Liu et al. 2019a), *Morus alba* (Moraceae) in China (Xue et al. 2019),
889 *Nandina domestica* (Berberidaceae) in China (Li et al. 2018b), olive (*Olea europaea*, Oleaceae) in
890 Italy (Schena et al. 2014), avocado (*Persea americana*, Lauraceae) in Israel and Mexico (Velázquez-
891 del Valle et al. 2016; Sharma et al. 2017), *Pistacia vera* (Anacardiaceae) in Italy and the USA (Schena
892 et al. 2014; Lichtemberg et al. 2017), *Pyrus pyrifolia* (Rosaceae) in China (Fu et al. 2019), *Rubus*
893 *glaucus* (Rosaceae) in Colombia (Afanador-Kafuri et al. 2014), *Taxus wallichiana* (Taxaceae) in
894 China (Xu et al. 2019), *Vaccinium* sp. (Ericaceae) in Brazil (Rios et al. 2015) and *Vellozia gigantea*
895 (Velloziaceae) in Brazil (Ferreira et al. 2017). *Colletotrichum karsti* is thus a cosmopolitan fungus,
896 inhabiting a vast array of plant hosts.

897

898 *Colletotrichum limonicola* Guarnaccia and Crous, *Persoonia* **39**: 32 (2017)

899

900 *Colletotrichum limonicola* is known only from a single record, obtained from wither-tip twigs of
901 lemon (*Citrus limon*, Rutaceae) in Malta in 2016 (Guarnaccia et al. 2017). Considering that there are
902 numerous species of *Colletotrichum* occurring on citrus, the conservation status of *C. limonicola* is
903 of great concern.

904

905 *Colletotrichum novae-zelandiae* Damm, P.F. Cannon, Crous, P.R. Johnst. and B. Weir, *Stud. Mycol.*
906 **73**: 25 (2012)

907

908 *Colletotrichum novae-zelandiae* is known only from three isolates collected in New Zealand from
909 chilli (*Capsicum annuum*, Solanaceae) and grapefruit (*Citrus* sp., Rutaceae) fruits in 1990 and 1988
910 respectively (Johnston and Jones 1997; Damm et al. 2012b). There are numerous species of
911 *Colletotrichum* reported from each of these hosts and there are no further occurrences of *C. novae-*
912 *zelandiae* ever since despite recent surveys, suggesting great concern on its conservation status.

913

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

915

916 *Colletotrichum oncidii* is only known from an unspecified species of *Oncidium* (Orchidaceae),
917 collected in 2010 in Germany (Damm et al. 2012b). There are no further occurrences of this species
918 and there are many other species of *Colletotrichum* occurring on *Oncidium*, raising serious concerns
919 over the conservation status of *C. oncidii* and rendering very difficult the deployment of surveys to
920 ascertain its conservation status.

921

922 *Colletotrichum parsonsiae* Damm, P.F. Cannon, Crous, P.R. Johnst. and B. Weir, *Stud. Mycol.* **73**:
923 27 (2012)

924

925 There are two occurrences reported for *Colletotrichum parsonsiae*, as an endophyte on *Parsonsia*
926 *capsularis* (Apocynaceae) leaves in New Zealand in 2009 (Damm et al. 2012b) and on healthy leaves
927 of *Bletilla ochracea* (Orchidaceae) in China in 2006 (Tao et al. 2013). There are numerous species of
928 *Colletotrichum* known from *Bletilla*, whereas there are no other reports from *Parsonsia*. Considering
929 the scarcity of reports of *C. parsonsiae*, its conservation status can be considered of concern.

930

931 *Colletotrichum petchii* Damm, P.F. Cannon and Crous, *Stud. Mycol.* **73**: 29 (2012)

932

933 *Colletotrichum petchii* occurs on *Dracaena* (Asparagaceae), being reported from *D. aletriformis*, *D.*
934 *brownii*, *D. fragrans* and *D. sanderiana*, in Australia, China, Germany, Italy and the Netherlands
935 (Damm et al. 2012b; Shivas et al. 2016). Although reports of *C. petchii* range from the late 19th
936 century to current times, spanning different hosts and locations (Supplementary data 4, panel D), the
937 identification of other species of *Colletotrichum* on *Dracaena* advise periodic surveying to ascertain
938 the conservation status of this species.

939

940 *Colletotrichum phyllanthi* (H.S. Pai) Damm, P.F. Cannon and Crous, *Stud. Mycol.* **73**: 31 (2012)
941
942 Damm et al. (2012b) reported *Colletotrichum phyllanthi* based on a single, non-sporulating fungal
943 culture, obtained in 1966 in India from leaf anthracnose on *Phyllanthus acidus* (Phyllanthaceae) and
944 stressed the absence of any further reports of this fungus. Moreover, a different species, *C. acidae*,
945 clustering in the truncatum complex, has been recently reported from *Phyllanthus acidus*
946 (Samarakoon et al. 2018). However, recently *C. phyllanthi* was recorded to occur epiphytically on
947 *Carapichea ipecacuanha* (Rubiaceae) in Brazil (Ferreira et al. 2020), prompting for further surveys
948 to ascertain its distribution and hosts.
949
950 *Colletotrichum torulosum* Damm, P.F. Cannon, Crous, P.R. Johnst. and B. Weir, *Stud. Mycol.* **73**: 32
951 (2012)
952
953 *Colletotrichum torulosum* is known only from two isolates obtained in New Zealand from passionfruit
954 (*Passiflora edulis*, Passifloraceae) in 2000 and eggplant (*Solanum melogena*, Solanaceae) in 1990
955 (Damm et al. 2012b). It is possible that this species also occurs on *Kunzea ericoides* (Myrtaceae) in
956 New Zealand (Joshee et al. 2009; Damm et al. 2012b). Nevertheless, each of these three hosts harbor
957 other species of *Colletotrichum* which, along the prolonged absence of new records for this species,
958 raises concerns on the conservation status of *Colletotrichum torulosum*.
959
960 *Colletotrichum watphraense* X.Y. Ma, K.D. Hyde and Jayawardena, *MycoKeys* **43**: 35 (2018)
961
962 *Colletotrichum watphraense* was designated based on a single isolate obtained from healthy stems of
963 an unspecified species of *Dendrobium* (Orchidaceae) in Thailand in 2013 (Ma et al. 2018). The
964 occurrence of several species of *Colletotrichum* on *Dendrobium*, along with the absence of any further
965 records of this fungus, raises serious concerns about the conservation status of *C. watphraense*.
966
967 **2.4 The caudatum species complex**
968
969 *Colletotrichum caudatum* was considered as one single species pathogenic of a broad range of warm-
970 season grasses as traditional morphological approaches differentiate *C. caudatum* sensu lato from
971 other *Colletotrichum* species by the presence of a unique filiform appendage at the apex of the
972 conidium (Crouch 2014). However, multi-locus phylogenetic analyses reject the view of a single
973 species and instead have shown that isolates from different hosts were mainly segregated into
974 different lineages. Initially subdivided in five species pathogenic to grasses, the caudatum complex

975 now includes eight species (Figure 6), three of which described as endophyte of *Bletilla ochracea*
976 (Orchidaceae) (Tao et al. 2013). Based on our knowledge, members of the caudatum complex have
977 only been reported to be pathogenic or endophyte of monocot hosts. The caudatum species complex
978 is a monophyletic group of species that fit within the graminicola species complex with which shares
979 similar characteristics like the host specificity towards different lineages of monocot plants.

980

981 **Figure 6**

982

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

984

985 *Colletotrichum alcornii* is known from only two specimens, collected from *Bothriochloa bladhii* and
986 *Imperata cylindrica* var. *major* (Poaceae) in close locations in Australia in 1972/73 (Crouch 2014;
987 Shivas et al. 2016). The conservation status of this species is thus of concern.

988

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

990

991 *Colletotrichum baltimoreense* is known only from *Sorghastrum nutans* (Poaceae), collected from a
992 single location in the USA in 2011 (Crouch 2014). The pathological status of this fungus to
993 indiangrass requires investigation and its conservation status is of concern.

994

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

996

997 *Colletotrichum caudatum* is known only from *Sorghastrum nutans* (Poaceae) in the USA. It was
998 identified twice in different locations, the first in 1887 and the second in 2007 (Crouch 2014). The
999 pathological status of this fungus to indiangrass requires investigation and its ecological status is of
1000 concern.

1001

1002 *Colletotrichum caudisporum* G. Tao, Zuo Y. Liu and L. Cai, *Fungal Divers.* **61**: 149 (2013)

1003

1004 There is a single record for *Colletotrichum caudisporum*, obtained as an endophyte from *Bletilla*
1005 *ochracea* (Orchidaceae) in China in 2006 (Tao et al. 2013). Considering that there are several species
1006 of *Colletotrichum* associated to orchids, the ecological status of *C. caudisporum* is of great concern.

1007

1008 *Colletotrichum duyunense* G. Tao, Zuo Y. Liu and L. Cai, *Fungal Divers.* **61**: 149 (2013)

1009

1010 *Colletotrichum duyunense* is only known from a single isolate collected epiphytically from *Bletilla*
1011 *ochracea* (Orchidaceae) in China in 2006 (Tao et al. 2013). Considering that there are several species
1012 of *Colletotrichum* associated to orchids, the ecological status of *C. duyunense* is of great concern.

1013

1014 *Colletotrichum ochraceae* G. Tao, Zuo Y. Liu and L. Cai, *Fungal Divers.* **61**: 156 (2013)

1015

1016 The species *Colletotrichum ochraceae* was designated to accommodate two isolates identified as
1017 endophytes on *Bletilla ochracea* (Orchidaceae) in China in 2006 (Tao et al. 2013). No further
1018 occurrences of this species have been reported and several species of *Colletotrichum* occur on *Bletilla*
1019 *ochracea*, rendering the conservation status of *C. ochraceae* of high concern.

1020

1021 *Colletotrichum somersetense* J.A. Crouch, *IMA Fungus* **5**:27 (2014)

1022

1023 *Colletotrichum somersetense* is known only from *Sorghastrum nutans* (Poaceae) from the USA,
1024 collected in 2011 (Crouch 2014). There are no additional records for this fungus and there are other
1025 species of *Colletotrichum* recorded from this host, raising serious concerns about the conservation
1026 status of *C. somersetense*.

1027

1028 *Colletotrichum zoysiae* J.A. Crouch, *IMA Fungus* **5**:27 (2014)

1029

1030 *Colletotrichum zoysiae* is known only from *Zoysia tenuifolia* (Poaceae) leaves, collected in Japan in
1031 1998 (Crouch 2014). Although there are no other species of *Colletotrichum* reported from this host,
1032 the absence of any further records of *C. zoysiae* raises concern over its conservation status.

1033

1034 **2.5 The dematium species complex**

1035

1036 The dematium species complex was firstly introduced by Cannon et al. (2012) based on species
1037 designation assigned by Damm et al. (2009), as part of a study of *Colletotrichum* species with curved
1038 conidia. The type species of the genus, *C. lineola*, is part of this species complex (Damm et al. 2009).
1039 As defined initially by the authors, the dematium clade contained six species forming two clear and
1040 distinct subclades. However, the distinct separation in two clades pretty far from each other and the
1041 low support values based on the ITS sequences suggest that the two lineages are different complexes.
1042 In the past years the number of species in this complex has increased rapidly reaching 17 described
1043 lineages (Figure 7). Geographically, members of this complex are typically origin from Europe or
1044 central Asia, several of which from Russia.

1045 Members of the dematium species complex have been associated with 33 plant species belonging to
1046 31 genera belonging mainly to eudicots (27/31). *Colletotrichum dematium* has also been reported as
1047 capable of infecting human tissues such as cornea.

1048

1049 **Figure 7**

1050

1051 *Colletotrichum anthrisci* Damm, P.F. Cannon and Crous, *Fungal Divers.* **39**: 56 (2009)

1052

1053 There is a single record for *Colletotrichum anthrisci*, collected from *Anthriscus sylvestris* (Apiaceae)
1054 dead stems in the Netherlands in 2009, with unconfirmed pathogenicity (Damm et al. 2009). The host
1055 plant is widespread in temperate regions. The pathological behavior and conservation status of this
1056 species remains to be analysed.

1057

1058 *Colletotrichum circinans* (Berk.) Voglino, *Annali R. Accad. Agric. Torino* **49**: 175 (1907)

1059

1060 Besides being a pathogen of onion and other *Allium* spp., *Colletotrichum circinans* is also known
1061 from other hosts (*Anthriscus sylvestris*, *Beta vulgaris* and *Viola hirta*), in different parts of the world
1062 (Damm et al. 2009; Sato et al. 2015) (Supplementary data 5, panel A).

1063

1064 *Colletotrichum dematium* (Pers.) Grove, *J. Bot., Lond.* **56**: 341 (1918)

1065

1066 *Colletotrichum dematium* is known from several plant hosts in all continents (Supplementary data 5,
1067 panel B), either as a pathogen, a saprobe or an endophyte (Damm et al. 2009; Jayawardena et al.
1068 2016a), including reports as a human opportunistic pathogen (Valenzuela-Lopez et al. 2018; Buchta
1069 et al. 2019). Nevertheless, recent reports of *C. dematium* sensu Damm et al. (2009) are seldom [on
1070 *Polygonatum odoratum* (Asparagaceae) in Italy (Karimi et al. 2016), on *Asparagus racemosus*
1071 (Asparagaceae) and on *Hemidesmus indicus* (Apocynaceae) in India (Rather et al. 2018), on *Lycopus*
1072 *lucidus* (Lamiaceae) and on *Polygonum aviculare* (Polygonaceae) in China (Guan et al. 2016; Liu et
1073 al. 2016d) and on *Armeria maritima* (Plumbaginaceae) in Japan (Sato et al. 2015)], suggesting that
1074 the conservation status of *C. dematium* should be under survey.

1075

1076 *Colletotrichum eryngiicola* Jayaward., Bulgakov and K.D. Hyde, *Cryptog. Mycol.* **38**: 101 (2017)

1077

1078 *Colletotrichum eryngiicola* is known from a single isolate collected from *Eryngium campestre*
1079 (Apiaceae) in Russia in 2016 (Buyck et al. 2017). An additional species (*C. dematium*) has also been

1080 reported from this host, albeit both reports are very scarce, suggesting that the conservation status of
1081 *C. eryngiicola* is of concern.

1082

1083 *Colletotrichum fructi* (F. Stevans and J.G. Hall) Sacc., *Syll. fung.* (Abellini) **22**: 1201 (1913)

1084

1085 There are only two described occurrences of *Colletotrichum fructi*, both recorded in the USA on
1086 apple, in 1907 and 1937 (Damm et al. 2009). Given that several other species of *Colletotrichum* occur
1087 on apple and that many studies have been conducted on apple bitter rot pathogens worldwide, the
1088 conservation status of *C. fructi* is of great concern and this taxon may well be extinct from nature.

1089

1090 *Colletotrichum hemerocallidis* Yan L. Yang, Zuo Y. Liu, K.D. Hyde and L. Cai, *Trop. Plant Pathol.*
1091 **37**: 170 (2012)

1092

1093 *Colletotrichum hemerocallidis* is known from two isolates collected from dead stalks of *Hemerocallis*
1094 *fulva* var. *kwanso* (Xanthorrhoeaceae) in two locations in China in 2008 (Yang et al. 2012b).
1095 Considering the lack of any further reports of this fungus and the occurrence of other species of
1096 *Colletotrichum* on *Hemerocallis* spp., the conservation status of this species is of concern.

1097

1098 *Colletotrichum insertae* Jayawardena, Bulgakov and K.D. Hyde, *Fungal Divers.* **80**: 176 (2016)

1099

1100 *Colletotrichum insertae* is only known from *Parthenocissus inserta* (Vitaceae) in Russia, where it
1101 was collected in 2015 as a saprobe on dying twigs and leaves (Hyde et al. 2016). There are several
1102 species of *Colletotrichum* recorded from *Parthenocissus*, rendering the conservation status of *C.*
1103 *insertae* of serious concern.

1104

1105 *Colletotrichum jinshuiense* M. Fu and G.P. Wang, *Persoonia* **42**: 1 (2019)

1106

1107 *Colletotrichum jinshuiense* is known only from *Pyrus pyrifolia* (Rosaceae) leaves, collected in China
1108 in 2016 (Fu et al. 2019). This single occurrence, along with the high number of species of
1109 *Colletotrichum* reported from pear, calls for concern on the conservation status of *C. jinshuiense*.

1110

1111 *Colletotrichum kakiivorum* H.Y. Jung and S.Y. Lee, *Mycol. Prog.* **17**: 1113-1121 (2018)

1112

1113 *Colletotrichum kakiivorum* is known from two occurrences associated with leaf spots in persimmon
1114 (*Diospyros kaki*, Ebenaceae) in Korea in 2016 (Lee and Jung 2018). There are several species of

1115 *Colletotrichum* occurring on persimmon, including in Korea, rendering the conservation status of *C.*
1116 *kakiivorum* of concern.

1117

1118 *Colletotrichum lineola* Corda, in Sturm, *Deutschl. Fl.*, 3 Abt. (Pilze Deutschl.) **3** (12): 41 (1831)

1119

1120 *Colletotrichum lineola*, the type species of the genus *Colletotrichum*, occurs as a pathogen or as a
1121 saprobe on a large number of host plants and locations (Jayawardena et al. 2016a). In a study on
1122 *Colletotrichum* spp. with curved conidia in Japan, Sato et al. (2015) found *Colletotrichum lineola* on
1123 *Dianthus* sp. and *Saponaria officinalis* (Caryophyllaceae), *Helleborus niger* (Ranunculaceae),
1124 *Isotoma axillaris* (Campanulaceae), *Sanguisorba officinalis* (Rosaceae), *Taraxacum campyloides*
1125 (Asteraceae) and *Vigna angularis* (Fabaceae). More recently, Guarnaccia et al. (2021) reported *C.*
1126 *lineola* from *Campanula trachelium* (Campanulaceae) in Italy. *Colletotrichum lineola* is thus a
1127 common fungus worldwide, but apparently with low host preference.

1128

1129 *Colletotrichum menispermi* Chethana, Jayawardena, Bulgakov and K.D. Hyde, *Fungal Divers.* **78**:
1130 80 (2016)

1131

1132 The species *Colletotrichum menispermi* was described based on an isolate obtained from dead twigs
1133 of *Menispermum dauricum* (Menispermaceae) in Russia in 2014 (Li et al. 2016c). There are no
1134 additional records for this fungus nor other reports of *Colletotrichum* from this host, indicating that
1135 the conservation status of this fungus is of serious concern.

1136

1137 *Colletotrichum parthenocissicola* Jayawardena, Bulgakov, Huanraluek & K.D. Hyde *Fungal Divers.*
1138 **104**: 1 (2020)

1139

1140 *Colletotrichum parthenocissicola* is known only from dying and dead twigs and petioles of
1141 *Parthenocissus quinquefolia* (Vitaceae) in Russia in 2016 (Yuan et al. 2020). The absence of
1142 additional records for this species and the occurrence of other species of *Colletotrichum* on
1143 *Parthenocissus* raises severe concerns about the conservation status of *C. parthenocissicola*.

1144

1145 *Colletotrichum quinquefoliae* Jayawardena, Bulgakov and K.D. Hyde, *Fungal Divers.* **78**: 83 (2016)

1146

1147 *Colletotrichum quinquefoliae* is known only from dying and dead leafstalks, twigs and tendrils of
1148 *Parthenocissus quinquefolia* (Vitaceae) in Russia in 2014 (Li et al. 2016c). The absence of additional

1149 records for this species and the occurrence of other species of *Colletotrichum* on *Parthenocissus*
1150 raises severe concerns about the conservation status of *C. quinquefoliae*.

1151

1152 *Colletotrichum sambucicola* Jayawardena, Camporesi and K.D. Hyde, *Fungal Divers.* **83**: 131 (2017)

1153

1154 There is a single fungus known from the species *Colletotrichum sambucicola*, isolated from a dead
1155 branch of *Sambucus ebulus* (Adoxaceae) in Italy in 2016 (Tibpromma et al. 2017). There are no
1156 further references to this species and there are other species of *Colletotrichum* identified from
1157 *Sambucus*, raising serious concerns about the conservation status of *C. sambucicola*.

1158

1159 *Colletotrichum sedi* Jayawardena, Bulgakov and K.D. Hyde, *Fungal Divers.* **72**:27 (2015)

1160

1161 *Colletotrichum sedi* is known only from a single occurrence, obtained from an unspecified species of
1162 *Sedum* (Crassulaceae) in Russia in 2014 (Liu et al. 2015b). The absence of additional reports for this
1163 fungus and the occurrence of other species of *Colletotrichum* on *Sedum* raise severe concerns about
1164 the conservation status of *C. sedi*.

1165

1166 *Colletotrichum sonchicola* Jayawardena, Camporesi and K.D. Hyde, *Phytotaxa* **314**: 55 (2017)

1167

1168 The species *Colletotrichum sonchicola* was described based on a single isolate collected from dead
1169 stems of an unspecified species of *Sonchus* (Asteraceae) in Italy in 2016 (Jayawardena et al. 2017).
1170 Although no further species of *Colletotrichum* are known to inhabit *Sonchus*, the absence of any
1171 further records for *C. sonchicola* raises serious concerns about its conservation status.

1172

1173 *Colletotrichum spinaciae* Ellis and Halst., *J. Mycol.* **6**: 34 (1890)

1174

1175 Initially treated as a specific pathogen of spinach (*Spinacea oleracea*, Amaranthaceae),
1176 *Colletotrichum spinaciae* sensu Damm et al. (2009) is recognised as occurring also on *Chenopodium*
1177 *album* (Amaranthaceae), *Portulaca oleracea* (Portulacaceae) and *Medicago sativa* (Fabaceae) in
1178 Europe and North America. More recently the fungus was reported on spinach in Turkey and
1179 Australia (Kurt et al. 2016; Shivas et al. 2016) and on *Medicago sativa* in China (Wang et al. 2019c).
1180 *Colletotrichum spinaciae* thus seems to be a common fungus.

1181

1182 **2.6 The destructivum species complex**

1183

1184 The destructivum aggregate was firstly introduced by Cannon et al. (2012) as a monophyletic group
1185 of six important plant pathogenic species: *Colletotrichum destructivum*, *C. fuscum*, *C. tabacum*, *C.*
1186 *linicola*, *C. higginsianum* and *Glomerella truncata*. Two years later, Damm et al. (2014) described
1187 the destructivum species complex encompassing the six previously mentioned species (with *G.*
1188 *truncata* renamed as *C. lentis*) and 10 closely related ones. Nowadays the complex has a total of 20
1189 species (Figure 8) and among them *C. destructivum*, *C. lini* and *C. higginsianum* are the most common
1190 ones whereas the others are pretty rare.

1191 Members of the destructivum species complex have been associated with 49 plant species belonging
1192 to 41 genera; the vast majority of these (37/41, 90%) are eudicots. Beside the economic impact of
1193 these pathogens, the species belonging to the destructivum complex such as *C. higginsianum* are
1194 important model systems that have been successfully used to advance the knowledge of the molecular
1195 basis of plant pathogenicity (O'Connell et al. 2012; Bhadauria et al. 2019).

1196

1197 **Figure 8**

1198

1199 *Colletotrichum americae-borealis* Damm, *Stud. Mycol.* **79**: 55 (2014)

1200

1201 Originally described on *Medicago sativa* from the USA (Damm et al. 2014), *Colletotrichum*
1202 *americae-borealis* has recently been recorded in Iran as a pathogen on *Tragopogon graminifolius*
1203 (Asteraceae), *Convolvulus arvensis* (Convolvulaceae), *Heracleum persicum* (Apiaceae) and *Sorghum*
1204 *halepense* (Poaceae) (Khodaei et al. 2019) and in China also on *Medicago sativa* (Kemei et al. 2021),
1205 suggesting a pluricontinental distribution and polyphagous behaviour.

1206

1207 *Colletotrichum antirrhinicola* Damm, *Stud. Mycol.* **79**: 56 (2014)

1208

1209 There is a single record for *Colletotrichum antirrhinicola*, collected from snap dragon (*Antirrhinum*
1210 *majus*, Plantaginaceae) leaves in New Zealand in 1999, with unconfirmed pathogenicity (Damm et
1211 al. 2014). The host plant is of widespread use as an ornamental. The pathological behaviour and
1212 conservation status of this species remains to be analysed. Anthracnose, attributed to *Colletotrichum*
1213 pathogens, is a common disease of snap dragon, but most of the literature lacks recent reports that
1214 may establish a clear link between this disease and *C. antirrhinicola*. In 2011, Tomioka et al. (2011)
1215 analysed the causal agents of snapdragon anthracnose in Japan, but these fungi can be attributed to
1216 *C. higginsianum*.

1217

1218 *Colletotrichum atractylodicola* R.J. Zhou and H.J. Xu, *Mycol. Prog.* **17**: 393 (2018)

1219

1220 There is a single record for *Colletotrichum atractylodicola*, collected from *Atractylodes lancea* (as *A.*
1221 *chinensis*, Asteraceae) in China in 2013 (Xu et al. 2018b). There are various species of *Colletotrichum*
1222 occurring on *Atractylodes*, rendering the pathological status of *C. atractylodicola* uncertain and its
1223 conservation status of concern.

1224

1225 *Colletotrichum bryoniicola* Damm, *Stud. Mycol.* **79**: 57 (2014)

1226

1227 There are two isolates of *Colletotrichum bryoniicola*, collected from decaying leaves of *Bryonia*
1228 *cretica* subsp. *dioica* (Cucurbitaceae) in the Netherlands in 2001 (Damm et al. 2014) and from
1229 anthracnose symptoms on *Salvia nemerosa* (Lamiaceae) in Italy in 2018 (Guarnaccia et al. 2019).
1230 The pathological and conservation status of *C. bryoniicola* is uncertain and of concern.

1231

1232 *Colletotrichum destructivum* O’Gara, *Mycologia* **7**: 38 (1915)

1233

1234 *Colletotrichum destructivum* is found as a pathogen on numerous botanical families, mostly
1235 dicotyledonous, throughout the world, being recurrently reported (Supplementary data 6, panel A).
1236 Hosts of *C. destructivum* include: *Cynanchum atratum* (Apocynaceae; Miao et al. 2017); *Aster*
1237 *tataricus* and *Helianthus annuus* (Asteraceae; Cong et al. 2018; Sun and Liang 2018); *Echium*
1238 *italicum* (Boraginaceae; Khodaei et al. 2019); *Medicago sativa*, *M. scutellata* and *Trifolium* spp.
1239 (Fabaceae; Damm et al. 2014; Shivas et al. 2016; Xue et al. 2018b); *Ocimum basilicum* and *Thymus*
1240 *vulgaris* (Lamiaceae; Mosca et al. 2014; Fu et al. 2015); *Bletilla ochracea* (Orchidaceae; Tao et al.
1241 2013); *Phragmites* sp. (Poaceae; Damm et al. 2014); *Rumex crispus* (Polygonaceae; Liu et al. 2017b);
1242 *Viola odorata* (Violaceae; Katoch et al. 2017).

1243

1244 *Colletotrichum fuscum* Laubert, *Gartenwelt* **31**: 675 (1927)

1245

1246 *Colletotrichum fuscum* is known from Germany and the Netherlands on several species of *Digitalis*
1247 (Plantaginaceae) and on an unspecified species of *Heracleum* (Apiaceae) (Damm et al. 2014). It was
1248 also recently reported from Italy on *Coreopsis lanceolata* (Asteraceae) (Guarnaccia et al. 2021).
1249 There are no other species of *Colletotrichum* recorded from *Digitalis* or *Coreopsis* and additional
1250 reports of anthracnose on these hosts suggest the presence of the fungus in Poland and the UK
1251 (Zimowska et al. 2016; Cannon 2019). The apparent host specificity and relatively narrow geographic
1252 distribution of *C. fuscum* recommend caution concerning its conservation status.

1253

1254 *Colletotrichum higginsianum* Sacc., *Riv. Accad. Padova* **33**: 161 (1917)
1255
1256 Damm et al. (2014) described *Colletotrichum higginsianum* as a taxon of pathogens of Brassicaceae.
1257 Recent reports are scarce and refer to hosts other than Brassicaceae, namely *Campanula* sp.
1258 (Campanulaceae) in Iran (Khodaei et al. 2019) and *Rumex acetosa* (Polygonaceae) in China (Zhang
1259 et al. 2018b). These observations suggest that the current host range and geographical distribution of
1260 *C. higginsianum* should be further investigated (Supplementary data 6, panel B).
1261
1262 *Colletotrichum lentis* Damm, *Stud. Mycol.* **79**: 65 (2014)
1263
1264 *Colletotrichum lentis* was designated by Damm et al. (2014) to accommodate fungi infecting lentil
1265 (*Lens culinaris*, Fabaceae) occurring in Canada and Romania. The fungus was subsequently reported
1266 from common vetch (*Vicia sativa*, Fabaceae) in China (Xu and Li 2015). This fungus seems to be
1267 host specific and is commonly found causing lentil anthracnose.
1268
1269 *Colletotrichum lini* (Westerd.) Tochinai, *J. Coll. agric., Hokkaido Imp. Univ.* **14**(4): 176 (1926)
1270
1271 *Colletotrichum lini* is known from flax (*Linum usitatissimum*, Linaceae), alfalfa (*Medicago sativa*)
1272 and *Trifolium* spp. (Fabaceae), *Raphanus raphanistrum* (Brassicaceae) and *Teucrium scorodonia*
1273 (Lamiaceae) (Damm et al. 2014). Nevertheless, the fungus is infrequently reported, recommending
1274 surveys to ascertain its conservation status (Supplementary data 6, panel C).
1275
1276 *Colletotrichum neorubicola* Yu Li, J. Gao & L. P. Liu, *Mycol. Prog.* **19**:947-955 (2020)
1277
1278 This species comprises isolates obtained from *Rubus idaeus* (Rosaceae) in 2013 in China causing leaf
1279 anthracnose (Liu et al. 2020c). No additional fungi have been added to this species and several species
1280 of *Colletotrichum* are known from *Rubus* spp., rendering the conservation status of *C. neorubicola* of
1281 concern.
1282
1283 *Colletotrichum ocimi* Damm, *Stud. Mycol.* **79**: 70 (2014)
1284
1285 *Colletotrichum ocimi* is associated to anthracnose of basil (*Ocimum basilicum*, Lamiaceae), and has
1286 been reported from Italy (Damm et al. 2014; Guarnaccia et al. 2019; Cacciola et al. 2020) and
1287 Australia (Shivas et al. 2016). The knowledge on the geographic distribution of *C. ocimi* requires
1288 further investigation to ascertain its pathological relevance and ecological status.

1289

1290 *Colletotrichum orchidis* Jayaward., Camporesi and K.D. Hyde, *Mycosphere* **11**: 305 (2020)

1291

1292 *Colletotrichum orchidis* is known from a single isolate obtained from an aerial stem of an unspecified
1293 species of *Orchis* (Orchidaceae) in Italy (Hyde et al. 2020b). There are no additional records of this
1294 fungus and there are many species of *Colletotrichum* reported from orchids, raising serious concerns
1295 on the conservation status of *C. orchidis*.

1296

1297 *Colletotrichum panacicola* Uyeda and S. Takim., *Chosen Nokai-ho* **14**: 24 (1919)

1298

1299 *Colletotrichum panacicola* is associated to anthracnose on *Panax ginseng* (Araliaceae) in China,
1300 Japan, Korea and Russia (Choi et al. 2011; Damm et al. 2014). The fungus appears to be host specific
1301 and to occur in Eastern Asia.

1302

1303 *Colletotrichum pisicola* Damm, *Stud. Mycol.* **79**: 71 (2014)

1304

1305 *Colletotrichum pisicola* is known from pea (*Pisum sativum*, Fabaceae) in America (Ecuador, Mexico,
1306 Puerto Rico and the USA) (Damm et al. 2014), but all reports are old. The lack of recent occurrences
1307 of *C. pisicola* raise serious concerns about its conservation status, suggesting that this taxon may no
1308 longer occur in nature.

1309

1310 *Colletotrichum pleopeltidis* Crous & Jol. Roux, *Fungal Syst. Evol.* **7**:285 (2021)

1311

1312 *Colletotrichum pleopeltidis* is known only from a single occurrence on leaves of an unspecified
1313 species of the fern *Pleopeltis*, collected in 2015 in South Africa (Crous et al. 2021). There are no
1314 details regarding the lifestyle of this fungus and its conservation status is of concern.

1315

1316 *Colletotrichum shisoi* P. Gan, A. Tsushima, M. Kawaradani, Damm and K. Shirasu, *Sci. Rep.* **9**:
1317 13349 (2019)

1318

1319 *Colletotrichum shisoi* is known only from anthracnose symptoms in *Perilla frutescens* (Lamiaceae)
1320 in Japan, where it was collected in 2006 (Gan et al. 2019). There have been no additional reports of
1321 *C. shisoi*, raising serious concerns over the conservation status of this taxon.

1322

1323 *Colletotrichum tabacum* Böning, *Prakt. Bl. Pflanzenbau Pflanzenschutz* **10**: 89 (1932)

1324

1325 *Colletotrichum tabacum* sensu Damm et al. (2014) is a species occurring on tobacco (*Nicotiana* spp.,
1326 Solanaceae) as well as on *Centella asiatica* (Apiaceae). The latter seems to be the most recent report
1327 of this fungus, dating from 2003 from Madagascar. There are no recent reports of the occurrence of
1328 *C. tabacum* other than its use in artificial inoculation experiments, as stressed by Damm et al. (2014),
1329 raising serious concerns on the conservation status of this species.

1330

1331 *Colletotrichum tanacetii* M. Barimani, S.J. Pethybridge, N. Vaghefi, F.S. Hay and P.W.J. Taylor,
1332 *Plant Pathol.* **62**: 1248–1257 (2013)

1333

1334 *Colletotrichum tanacetii* is known to occur across the cultivation area of *Tanacetum cinerariifolium*
1335 (Asteraceae) in Australia (Barimani et al. 2013; Damm et al. 2014; Lelwala et al. 2019). The fungus
1336 appears to be host specific and may become of quarantine relevance.

1337

1338 *Colletotrichum utrechtense* Damm, *Stud. Mycol.* **79**: 77 (2014)

1339

1340 *Colletotrichum utrechtense* is known from a single isolate, obtained from leaves of *Trifolium pratense*
1341 (Fabaceae) in the Netherlands in 2011 (Damm et al. 2014). Several other species of *Colletotrichum*
1342 are known from *Trifolium* and there are no other records of *C. utrechtense*, raising serious concerns
1343 about the conservation status of this taxon.

1344

1345 *Colletotrichum vignae* Damm, *Stud. Mycol.* **79**: 78 (2014)

1346

1347 *Colletotrichum vignae* is known only from a single record obtained from cowpea (*Vigna unguiculata*,
1348 Fabaceae) in Nigeria prior to 1997 (Damm et al. 2014). The occurrence of several other species of
1349 *Colletotrichum* on *Vigna* and the absence of any other records of *C. vignae*, raise serious concerns
1350 about the conservation status of this fungal taxon, which may no longer exist in nature.

1351

1352 **2.7 The dracaenophilum species complex**

1353

1354 Together with the agaves, magnum and the orchidearum complexes, the dracaenophilum complex is
1355 one of the most recently described species complexes (Damm et al. 2019). The dracaenophilum
1356 species complex encompasses eight species distributed in the northern hemisphere (Asia, Europe and
1357 Mexico). Species belonging to this complex have been associated with nine plant species belonging
1358 to seven genera in monocots and eudicots. Due to the low number of representative isolates for each

1359 species, almost every lineage shows a certain level of specificity towards one genus, however more
1360 studies are needed to confirm the level of host preference (Figure 9).

1361

1362 **Figure 9**

1363

1364 *Colletotrichum cariniferi* X.Y. Ma, K.D. Hyde and Jayawardena, *MycKeys* **43**: 23 (2018)

1365

1366 *Colletotrichum cariniferi* is known only from *Dendrobium cariniferum* (Orchidaceae), collected from
1367 stems in Thailand in 2013 (Ma et al. 2018). The pathological relevance and conservation status of
1368 this species remains to be analysed.

1369

1370 *Colletotrichum coelogyne* Damm, *Stud. Mycol.* **92**: 1 (2019)

1371

1372 *Colletotrichum coelogyne* is known from a single isolate, obtained from *Coelogyne* sp.
1373 (Orchidaceae) leaves in Germany in 2010 (Damm et al. 2019). Another species, *C. cymbidiicola*, is
1374 also known from *Coelogyne*, raising concern on the conservation status of *C. coelogyne*.

1375

1376 *Colletotrichum dracaenophilum* D.F. Farr and M.E. Palm, *Mycol. Res.* **110**: 1401 (2006)

1377

1378 *Colletotrichum dracaenophilum* is only known from *Dracaena* (*D. sanderiana* and *D. braunii*) in
1379 Brazil, Bulgaria, Egypt, China and Australia (Macedo and Barreto 2016; Morsy and Elshahawy 2016;
1380 Shivas et al. 2016; Damm et al. 2019) (Supplementary data 7). Other species of *Colletotrichum* are
1381 known from *Dracaena*, indicating that the conservation status of *C. dracaenophilum* should be under
1382 surveillance.

1383

1384 *Colletotrichum excelsum-altitudinum* G. Tao, Zuo Y. Liu and L. Cai, *Fungal Divers.* **61**: 152 (2013)

1385

1386 *Colletotrichum excelsum-altitudinum* is only known from a single isolate collected from healthy
1387 *Bletilla ochracea* (Orchidaceae) leaves in China in 2006, along with several other species of
1388 *Colletotrichum* (Tao et al. 2013). Many species of *Colletotrichum* occur on this host and even more
1389 on orchids in general, most epiphytically, rendering the conservation status of *Colletotrichum*
1390 *excelsum-altitudinum* of great concern.

1391

1392 *Colletotrichum parallelophorum* X.Y. Ma, K.D. Hyde and Jayawardena, *MycKeys* **43**: 23 (2018)

1393

1394 This species is recorded only from an epiphytic fungus occurring on an unspecified species of
1395 *Dendrobium* (Orchidaceae) in Thailand in 2013 (Ma et al. 2018). There are no additional reports of
1396 this fungus and many other species of *Colletotrichum* occur on *Dendrobium*, raising serious concerns
1397 on the conservation status of *C. parallelophorum*.

1398

1399 *Colletotrichum tongrenense* S.X. Zhou, J.C. Kang and K.D. Hyde, *MycKeys* **49**: 1 (2009)

1400

1401 *Colletotrichum tongrenense* is known from a single isolate, obtained from symptomless leaves and
1402 stems of *Nothapodytes pittosporoides* (Icacinaceae) in China (Zhou et al. 2019). The ecological and
1403 conservation status of *Colletotrichum tongrenense* is unknown and of concern.

1404

1405 *Colletotrichum tropicicola* Phouliv., Noireung, L. Cai and K.D. Hyde, *Cryptog. Mycol.* **33**: 353
1406 (2012)

1407

1408 *Colletotrichum tropicicola* was designated based on two endophytic occurrences reported from
1409 Thailand in 2009 on leaves of *Citrus maxima* (Rutaceae) and *Paphiopedilum bellatulum*
1410 (Orchidaceae) (Noireung et al. 2012). Damm et al. (2019) identified isolates obtained from *Citrus* sp.
1411 in Mexico as belonging to *Colletotrichum tropicicola*, along with the Thai isolate from *Citrus*
1412 *maxima*, suggesting that the *Paphiopedilum bellatulum* isolate may lay in a separate, undescribed
1413 species. *Colletotrichum tropicicola* is still in a phase of delimitation, and consequently its ecological
1414 and conservation statuses need clarification.

1415

1416 *Colletotrichum yunnanense* Xiao Ying Liu and W.P. Wu, *Mycotaxon* **100**: 139 (2007)

1417

1418 *Colletotrichum yunnanense* was described based on an isolate obtained from healthy leaves of an
1419 unspecified species of *Buxus* (Buxaceae) in China in 2004 (Liu et al. 2007; Weir et al. 2012), but no
1420 additional records have been reported ever since and reports of *Colletotrichum* from *Buxus* are
1421 seldom. The current conservation status of *C. yunnanense* is therefore of concern.

1422

1423 **2.8 The gigasporum species complex**

1424

1425 The gigasporum species complex (Figure 10) was firstly described by Liu et al. (2014) encompassing
1426 six species. *Colletotrichum gigasporum* was identified and named based the formation of large (> 20
1427 µm-long) conidia distinct from other currently known *Colletotrichum* species and confirmed by
1428 multi-locus phylogenetic analyses (ITS, *act*, *tub2*, *chs-1* and *gapdh*). Recently three new members of

1429 this complex have been described: *C. serranegrense*, endophytic of *Cattleya jongheana* in Brazil
1430 (Silva et al. 2018), and *C. jishouense* and *C. chiangraiense*, endophytic species of *Nothapodytes*
1431 *pittosporoides* and *Dendrobium* sp. respectively in China (Ma et al. 2018; Zhou et al. 2019), although
1432 we exclude *C. chiangraiense* from the list of accepted species based on incongruence of the
1433 nucleotide sequence of the type strain (whereas the ITS sequence places this taxon in the boninense
1434 complex, the *act* and *tub2* sequences place it in the gigasporum complex) as detailed in section 2.18.
1435 Whereas *C. serranegrense* and *C. jishouense* have been described as members of the gigasporum
1436 species complex, *C. chiangraiense* has been described as a basal species of the boninense species
1437 complex, highlighting differences in the ITS clustering compared to the other genes. Further analyses
1438 will be needed to confirm the situation of *C. chiangraiense*. Species in the gigasporum complex have
1439 seldomly been reported (still *C. gigasporum* is the most common species), making this complex the
1440 less common of the genus.

1441

1442 **Figure 10**

1443

1444 *Colletotrichum arxii* F. Liu, L. Cai, Crous and Damm, *Persoonia* **33**: 87 (2014)

1445

1446 *Colletotrichum arxii* is known only from two isolates collected in Europe in the orchids
1447 *Paphiopedilum* sp. and *Oncidium excavatum* in 2010 and before 1956 respectively (Liu et al. 2014).
1448 There are multiple species of *Colletotrichum* inhabiting orchids, raising concern on the current
1449 conservation status of *C. arxii*.

1450

1451 *Colletotrichum gigasporum* E.F. Rakotoniriana and F. Munaut, *Mycol. Prog.* **12**: 407 (2013)

1452

1453 *Colletotrichum gigasporum* occurs on several hosts, mostly in tropical regions across the globe
1454 (Rakotoniriana et al. 2013) (Supplementary data 8). Studies targeting the analysis of population
1455 frequency of *Colletotrichum* anthracnose pathogens on diverse hosts all coincide in revealing *C.*
1456 *gigasporum* as a secondary pathogen, including on *Annona* spp. in Brazil (Costa et al. 2019), coffee
1457 in Mexico (Cristóbal-Martínez et al. 2017) and in China (Cao et al. 2019a) and mango in China (Li
1458 et al. 2019b), prompting regular surveys to ascertain the conservation status of this species.

1459

1460 *Colletotrichum jishouense* SX. Zhou, JC. Kang and K.D. Hyde, *MycKeys* **49**: 1 (2019)

1461

1462 *Colletotrichum jishouense* has been recorded only from healthy roots of *Nothapodytes pittosporoides*
1463 (Icacinaceae), in China in 2016 (Zhou et al. 2019). Further research is needed to ascertain the host
1464 and geographic distribution of this taxon, as there is concern regarding its current conservation status.

1465

1466 *Colletotrichum magnisporum* F. Liu, L. Cai, Crous and Damm, *Persoonia* **33**: 91 (2014)

1467

1468 *Colletotrichum magnisporum* is an enigmatic fungus, collected prior to 1984 from an unknown source
1469 (Liu et al. 2014). There are no additional records for this fungus, although metagenomics data suggest
1470 its occurrence in nature (Jayawardena et al. 2016a). Under these circumstances, the conservation
1471 status of *C. magnisporum* is of great concern and further surveys are needed to ascertain its occurrence
1472 on nature.

1473

1474 *Colletotrichum pseudomajus* F. Liu, L. Cai, Crous and Damm, *Persoonia* **33**: 91 (2014)

1475

1476 *Colletotrichum pseudomajus* is known only from a single isolate, collected from *Camellia sinensis*
1477 (Theaceae) in China at an unknown date (prior to 1988) (Liu et al. 2014). The absence of any further
1478 records of this species and the occurrence of several species of *Colletotrichum* on *Camellia* spp.
1479 render the conservation status of *C. pseudomajus* of serious concern, with extinction from nature as
1480 a plausible scenario for this species.

1481

1482 *Colletotrichum radialis* F. Liu, L. Cai, Crous and Damm, *Persoonia* **33**: 93 (2014)

1483

1484 There is a single isolate in the species *Colletotrichum radialis*, obtained from a root of an undetermined
1485 host in Costa Rica in 1993 (Liu et al. 2014). The scarcity of information on the ecological context of
1486 its isolation and the absence of any other records for this species hamper further surveys and strongly
1487 suggest that *Colletotrichum radialis* may be extinct from nature.

1488

1489 *Colletotrichum serranegrense* Meir. Silva & M.C.M. Kasuya, *Phytotaxa* **351**: 163 (2018)

1490

1491 This species is known only from a single location, collected in Brazil in 2015 as a root endophyte of
1492 the endangered orchid *Cattleya jongheana* (Silva et al. 2018). Several other species of *Colletotrichum*
1493 have been obtained from *Cattleya* spp., rendering the conservation status of *C. serranegrense* of
1494 concern.

1495

1496 *Colletotrichum vietnamense* F. Liu, L. Cai, Crous and Damm, *Persoonia* **33**: 93 (2014)

1497

1498 *Colletotrichum vietnamense* is known only from two isolates obtained from anthracnose symptoms
1499 on leaves of *Coffea* sp. (Rubiaceae) in Vietnam at an unknown date (Liu et al. 2014). The absence of
1500 any additional records of this taxon and the occurrence of several other species of *Colletotrichum* on
1501 *Coffea* raise serious concerns about the conservation status of *C. vietnamense*.

1502

1503 **2.9 The gloeosporioides species complex**

1504

1505 Like the acutatum complex, the gloeosporioides species complex was considered as one unique
1506 morphologically and phylogenetically diverse species. The name *Colletotrichum gloeosporioides* was
1507 firstly proposed in Penzig (1882), based on *Vermicularia gloeosporioides*, the type specimen of which
1508 was collected from *Citrus* in Italy. In the past century the term *Colletotrichum gloeosporioides* has
1509 undergone several usages and different taxonomists have kept agglomerating or dividing species
1510 under this name according with the evolution of the species concept. The revision performed by Weir
1511 et al. (2012) was a breakthrough in the taxonomy of this group and 22 species plus one subspecies
1512 were accepted as member of the gloeosporioides species complex. Nevertheless, the complex has
1513 undergone recurrent changes and several lineages have been merged and separated into novel species
1514 since then. One good example of the level of instability is provided by *C. siamense*. From 2009 to
1515 2014, seven species with close phylogenetic affinities to *C. siamense* have been described and in
1516 some cases considered as species within *C. siamense* sensu lato (Liu et al. 2016c). Whereas some of
1517 these species (i.e. *C. hymenocallidis* and *C. jasmini-sambac*) were synonymised with *C. siamense*
1518 sensu stricto based on Weir et al. (2012), other authors resurrected those names describing *C.*
1519 *siamense* as a species complex. These changes have led to substantial disagreements regarding the
1520 taxonomy of this group. Finally, Liu et al. (2015a) used multiple approaches to demonstrate the lack
1521 of recognition of any independent evolutionary lineages within *C. siamense* sensu lato as distinct
1522 species, thus rejecting the null hypothesis. To date, 57 species have been described (Figure 11) and
1523 despite significant developments, the taxonomy of this complex remains in a state of flux. Three
1524 major clades can be recognised in the complex (the theobromicola, kahawae and gloeosporioides
1525 clades), but phylogenetic distances between species vary strongly in each of these clades, mostly
1526 showing little geographical structure.

1527 Members of the gloeosporioides species complex have been associated with 283 plant species
1528 belonging to 212 genera and the majority of those species (80.6%) belong to eudicots whereas only
1529 a smaller part belongs to monocots and gymnosperms (16.1% and 2.2% respectively). Members of
1530 the gloeosporioides species complex have also been reported as opportunistic pathogens of humans
1531 (Werbel et al. 2019).

1532 Most of the species within the complex are polyphagous, but some show a strong specialisation
1533 towards one host. An example is provided by *C. kahawae* a highly aggressive and specialised
1534 pathogen of coffee, causing the devastating Coffee Berry Disease. This pathogen has the unique
1535 ability to infect green developing coffee berries and for its massive economic impact, it is ranked as
1536 a quarantine pathogen and even as a biological weapon (Australia Group 2014; Batista et al. 2017).
1537 The gloeosporioides complex is the most common and polyphagous species complex of the genus.

1538

1539 **Figure 11**

1540

1541 *Colletotrichum aenigma* B. Weir and P.R. Johnst., *Stud. Mycol.* **73**: 135 (2012)

1542

1543 *Colletotrichum aenigma* was described based only on two isolates (Weir et al. 2012), but was
1544 subsequently recognised as inhabiting multiple hosts in diverse locations, namely: *Actinidia arguta*
1545 (Actinidiaceae) in China (Wang et al. 2019a); *Aquilaria sinensis* (Thymelaeaceae) in China (Liu et al.
1546 2021a); *Camellia japonica*, *C. oleifera*, *C. sasanqua* and *C. sinensis* (Theaceae) in China (Wang et
1547 al. 2016; Chen et al. 2019a; Yang et al. 2019a; Wang et al. 2020a); *Capsicum* sp. (Solanaceae) in
1548 China (Diao et al. 2017); *Citrus sinensis* (Rutaceae) in Italy (Schena et al. 2014); *Cyclocarya paliurus*
1549 (Juglandaceae) in China (Zheng et al. 2021b); *Fragaria* × *ananassa* (Rosaceae) in China (Han et al.
1550 2016; Chen et al. 2020); *Hylocereus undatus* (Cactaceae) in Thailand (Meetum et al. 2015); *Juglans*
1551 *regia* (Juglandaceae) in China (Wang et al. 2021e); *Malus domestica* (Rosaceae) in China (Zhang et
1552 al. 2021b); *Olea europaea* (Oleaceae) in Italy (Schena et al. 2014); *Persea americana* (Lauraceae) in
1553 Israel (Weir et al. 2012; Sharma et al. 2017); *Populus* sp. (as *Colletotrichum populi*) in China (Li et
1554 al. 2012); *Pyrus bretschneideri* (Rosaceae) in China (Fu et al. 2019), *P. communis* in Italy (Mosca et
1555 al. 2014; Schena et al. 2014) and *P. pyrifolia* in China and Japan (Weir et al. 2012; Fu et al. 2019);
1556 *Sedum kamtschaticum* (Crassulaceae) in Korea (Choi et al. 2017); *Vitis vinifera* (Vitaceae) in China
1557 (Yan et al. 2015) and Korea (Kim et al. 2021). *Colletotrichum aenigma* thus seems to be a fungus in
1558 expansion, hosted by numerous agricultural crop plants (Supplementary data 9, panel A).

1559

1560 *Colletotrichum aeshynomenes* B. Weir and P.R. Johnst., *Stud. Mycol.* **73**: 135 (2012)

1561

1562 Besides being a pathogen of the weed *Aeschynomene indica* (Fabaceae) in the USA (Weir et al. 2012),
1563 *Colletotrichum aeshynomenes* was recently reported in Brazil as causing anthracnose in cacao
1564 (*Theobroma cacao*; Malvaceae) (Nascimento et al. 2019a) and in *Myrciaria dubia* (Myrtaceae)
1565 (Matos et al. 2020) and as an endophyte on *Vellozia gigantea* (Velloziaceae) (Ferreira et al. 2017), as

1566 well as from Thailand on *Manihot esculenta* (Euphorbiaceae) with unconfirmed pathogenicity
1567 (Sangpueak et al. 2018).

1568

1569 *Colletotrichum alatae* B. Weir and P.R. Johnst., *Stud. Mycol.* **73**: 135 (2012)

1570

1571 *Colletotrichum alatae* is recorded only from water yam (*Dioscorea alata*, Dioscoreaceae) from
1572 America, Africa and Asia (Weir et al. 2012; Lin et al. 2018b). It is a common and host-specific fungus.

1573

1574 *Colletotrichum alienum* B. Weir and P.R. Johnst., *Stud. Mycol.* **73**: 139 (2012)

1575

1576 *Colletotrichum alienum* is recorded as a pathogen from multiple dicotyledonous hosts in Oceania,
1577 Asia, Africa and Europe (Supplementary data 9, panel B), namely on: *Aquilaria sinensis* in China
1578 (Thymelaeaceae; Liu et al. 2020a); *Camellia sinensis* in China (Theaceae; Liu et al. 2015a);
1579 *Diospyros kaki* in New Zealand (Ebenaceae; Weir et al. 2012); *Fragaria × ananassa* in Australia
1580 (Rosaceae; Shivas et al. 2016); *Grevillea* sp. in Australia (Proteaceae; Liu et al. 2013a);
1581 *Leucadendron* sp. in Portugal and South Africa (Proteaceae; Liu et al. 2013a); *Malus domestica* in
1582 New Zealand (Rosaceae; Weir et al. 2012); *Mangifera indica* in China (Anacardiaceae; Ahmad et al.
1583 2021); *Nerium oleander* in Australia (Apocynaceae; Schena et al. 2014); *Persea americana* in
1584 Australia, New Zealand and Israel (Lauraceae; Weir et al. 2012; Sharma et al. 2017); *Protea*
1585 *cynaroides* in Portugal and South Africa (Proteaceae; Liu et al. 2013a); *Serruria* sp. in South Africa
1586 (Proteaceae; Liu et al. 2013a). Additionally, it was recently recorded in Mexico as a pathogen in
1587 mango (*Mangifera indica*; Tovar-Pedraza et al. 2020) and in Uruguay associated to olive anthracnose
1588 (Moreira et al. 2021), suggesting its spread to America.

1589

1590 *Colletotrichum aotearoa* B. Weir and P.R. Johnst., *Stud. Mycol.* **73**: 139 (2012)

1591

1592 This species is reported from numerous native angiosperms and gymnosperms from Australia and
1593 New Zealand (Supplementary data 9, panel C) either as pathogen or as endophyte (Weir et al. 2012;
1594 Liu et al. 2013a; Shivas et al. 2016), including: the Araliaceae *Meryta sinclairii*; the Berberidaceae
1595 *Berberis glaucocarpa*; the Lamiaceae *Vitex lucens*; the Loganiaceae *Geniostoma rupestre* var.
1596 *ligustrifolium*; the Meliaceae *Dysoxylum spectabile*; the Monimiaceae *Hedycarya angustifolia*; the
1597 Myrtaceae *Syzygium smithii* (as *Acmena smithii*) and *Kunzea ericoides*; the Oleaceae *Ligustrum*
1598 *lucidum*; the Podocarpaceae *Dacrycarpus dacrydioides*, *Podocarpus totara* and *Prumnopitys*
1599 *ferruginea*; the Proteaceae *Banksia marginata* and *Knightia* sp.; the Rubiaceae *Coprosma* sp.; the
1600 Violaceae *Melicytus ramiflorus*. It was also found on banana in India and classified as “slightly

1601 pathogenic” (Sharma et al. 2015). The presence of *C. aotearoa* on *Boehmeria* in China needs to be
1602 confirmed (Weir et al. 2012).

1603

1604 *Colletotrichum arecicola* X.R. Cao, H.Y. Che and D.Q. Luo, *Plant Dis.* **104**: 1369 (2020)

1605

1606 *Colletotrichum arecicola* was recently described as a leaf pathogen of *Areca catechu* in China (Cao
1607 et al. 2020). Whereas there were no previous occurrences of *Colletotrichum* reported from *Areca*
1608 hosts, that study detected several species of *Colletotrichum* occurring on *Areca catechu*, suggesting
1609 that further surveys are necessary to ascertain the pathological relevance, geographic distribution and
1610 conservation status of *C. arecicola*.

1611

1612 *Colletotrichum artocarpicola* Bhunjun, Jayawardena, Jeewon and K.D. Hyde, *Phytotaxa* **418**: 273
1613 (2019)

1614

1615 *Colletotrichum artocarpicola* was collected as a saprobe from a dead root of jackfruit (*Artocarpus*
1616 *heterophyllus*, Moraceae) in Thailand in 2018 (Bhunjun et al. 2019). The pathological and
1617 conservation status of this fungus remains to be investigated. The host plant is a widely cultivated
1618 tropical fruit tree.

1619

1620 *Colletotrichum asianum* Prihastuti, L. Cai and K.D. Hyde, *Fungal Divers.* **39**: 96 (2009)

1621

1622 *Colletotrichum asianum* is isolated recurrently and with high frequency as a pathogen of mango
1623 (*Mangifera indica*) from different parts of the world (Supplementary data 9, panel D), typically along
1624 with *C. siamense* and several other species (Li et al. 2019a,b; Tovar-Pedraza et al. 2020; Benatar et
1625 al. 2021). It was also recently reported from avocado (*Persea americana*) in Indonesia (Zhafarina et
1626 al. 2021).

1627

1628 *Colletotrichum australianum* W. Wang, D. D. De Silva, and P. W. J. Taylor, *J. Fungi* **7**:47 (2021)

1629

1630 The species *Colletotrichum australianum* was recently described to accommodate fungi found in
1631 association with citrus anthracnose in Australia, namely on *Citrus reticulata* and *C. sinensis* (Wang
1632 et al. 2021c). The species also encompasses a fungus previously identified as *Colletotrichum*
1633 *queenslandicum*, isolated from chilli (*Capsicum annuum*). The pathological relevance and host range
1634 of *C. australianum* remains to be established, but this fungus may become of quarantine relevance.

1635

1636 *Colletotrichum camelliae* Masee, *Bull. Misc. Inf., Kew*: 91 (1899)

1637

1638 *Colletotrichum camelliae* is known only from *Camellia* spp. (Wang et al. 2016; Lu et al. 2018; Win

1639 et al. 2018; He et al. 2019; Wang et al. 2020a). Besides one isolate collected in the USA in 1982 (Liu

1640 et al. 2015a), the pathogen seems to be more frequent in Asia (Supplementary data 9, panel E).

1641

1642 *Colletotrichum changpingense* G. Zhang, Jayawardena and KD Hyde, *Mycosphere* **7**: 1155 (2016)

1643

1644 There are two records for *Colletotrichum changpingense*, obtained from diseased strawberry

1645 (*Fragaria* × *ananassa*) rhizomes in China in 2011 and 2012 (Jayawardena et al. 2016b). There are

1646 multiple *Colletotrichum* species associated with strawberry plants and the pathological relevance and

1647 the ecological status of *C. changpingense* require clarification.

1648

1649 *Colletotrichum chiangmaiense* N.I. de Silva, Lumyong & K.D. Hyde, *Mycosphere* **12**(1): 192 (2021)

1650

1651 *Colletotrichum chiangmaiense* is known from a single isolate collected as an endophyte in leaves of

1652 *Magnolia garrettii* (Magnoliaceae) in 2017 in Thailand (De Silva et al. 2021). There are no further

1653 records of this fungus and other species of *Colletotrichum* are known from other *Magnolia* spp.,

1654 rendering the conservation status of this taxon of concern.

1655

1656 *Colletotrichum chrysophilum* W.A.S. Vieira, W.G. Lima, M.P.S. Câmara and V.P. Doyle, *Mycologia*

1657 **109**: 912 (2017)

1658

1659 The taxon *Colletotrichum chrysophilum* was recently described based on fungi causing anthracnose

1660 on banana plants (*Musa acuminata*) in Brazil, but also containing fungi previously assigned to *C.*

1661 *ignotum* E.I. Rojas, S.A. Rehner and Samuels, which includes endophytes of *Theobroma cacao*

1662 (Malvaceae), *Genipa americana* (Rubiaceae), *Tetragastris panamensis* (Burseraceae) and

1663 *Terpsichore taxifolia* (Polypodiaceae) from Panama and Puerto Rico (Vieira et al. 2017). The fungus

1664 was also found in Brazil as a causal agent both of cashew (*Anacardium* spp.) anthracnose (Veloso et

1665 al. 2018) and of cassava (*Manihot esculenta*) anthracnose (Machado et al. 2021a), and was also

1666 associated to banana and avocado anthracnose in Mexico (Fuentes-Aragón et al. 2020, 2021). The

1667 importance of this taxon as an avocado, banana, cassava or cashew pathogen requires further

1668 investigation. Being currently restricted to the American continent, it may become a quarantine

1669 pathogen for these crops in other continents.

1670

1671 *Colletotrichum cigarro* (B.S. Weir and P.R. Johnston) A. Cabral and P. Talhinhos, *Plants* **9**: 502
1672 (2020)

1673

1674 *Colletotrichum cigarro*, recently named by raising *C. kahawae* ssp. *cigarro* to the species rank
1675 (Cabral et al. 2020), is known from numerous hosts and regions, including the Proteaceae *Banksia*
1676 sp. and *Dryandra* sp. in Portugal (Madeira) and Spain (Weir et al. 2012; Liu et al. 2013a),
1677 *Leucospermum* sp. in the USA (Hawaii) (Weir et al. 2012) and *Toronia toru* in New Zealand (Weir et
1678 al. 2012), the Rosaceae *Dryas octopetala* in Switzerland (Weir et al. 2012), apple (*Malus domestica*)
1679 in Belgium and the USA (Grammen et al. 2019; McCulloch et al. 2020) and *Rubus glaucus* in
1680 Colombia (Afanador-Kafuri et al. 2014), the Myrtaceae *Eucalyptus grandis* in South Africa
1681 (Mangwende et al. 2020) and *Kunzea ericoides* in New Zealand (Weir et al. 2012), as well as on
1682 *Areca catechu* (Arecaceae) in China (Zhang et al. 2020d), *Citrus reticulata* (Rutaceae) in Italy
1683 (Perrone et al. 2016), *Eruca vesicaria* (as *E. sativa*, Brassicaceae) in Italy (Garibaldi et al. 2016a),
1684 *Hypericum perforatum* (Hypericaceae) in Germany (Weir et al. 2012), *Liquidambar styraciflua*
1685 (Altingiaceae) in Italy (Garibaldi et al. 2016b; Guarnaccia et al. 2021), mango (*Mangifera indica*,
1686 Anacardiaceae) in Colombia and Italy (Ismail et al. 2015; Pardo-De La Hoz et al. 2016), *Miconia* sp.
1687 (Melastomataceae) in Brazil (Weir et al. 2012), *Morus alba* (Moraceae) in China (Xue et al. 2019),
1688 olive (*Olea europaea*, Oleaceae) in Australia and Italy (Weir et al. 2012; Schena et al. 2014), avocado
1689 (*Persea americana*, Lauraceae) in Korea and New Zealand (Weir et al. 2012; Kwon et al. 2020), tree
1690 tomato (*Solanum betaceum*, Solanaceae) in Colombia (Rojas et al. 2018) and *Vaccinium*
1691 *macrocarpum* (Ericaceae) in the USA (Weir et al. 2012). *Colletotrichum cigarro* is thus a common
1692 fungus worldwide (Supplementary data 9, panel F).

1693

1694 *Colletotrichum clidemiae* B.S. Weir and P.R. Johnst., *Stud. Mycol.* **73**: 148 (2012)

1695

1696 *Colletotrichum clidemiae* is known from the USA and Panama on *Clidemia hirta* (Melastomataceae),
1697 and from the USA on *Vitis* sp. and *Quercus* sp. (Weir et al. 2012). No additional isolates have been
1698 reported since the taxon was described, indicating that the conservation status of *C. clidemiae* requires
1699 clarification.

1700

1701 *Colletotrichum cobbittiense* S. Luo, G. Dong and P. Wong, *Persoonia* **40**: 240 (2018)

1702

1703 *Colletotrichum cobbittiense* includes a single isolate collected from leaf lesions of *Cordyline stricta*
1704 × *C. australis* (Asparagaceae) in Australia in 2016 (Crous et al. 2018c). There are several species of

1705 *Colletotrichum* occurring on *Cordyline*, rendering the pathological status of *C. Cobbittiense* uncertain
1706 and its conservation status of concern.

1707

1708 *Colletotrichum conoides* Y.Z. Diao, C. Zhang, L. Cai and X.L. Liu, *Persoonia* **38**: 27 (2017)

1709

1710 The species *Colletotrichum conoides* was designated based on an isolate collected from *Capsicum*
1711 *annuum* var. *conoides* fruits in China in 2010 (Diao et al. 2017). The fungus was subsequently found
1712 associated with anthracnose symptoms on *Pyrus pyrifolia* in China in 2015 (Fu et al. 2019). Both
1713 hosts harbour numerous species of *Colletotrichum*, rendering the pathological status of *C. conoides*
1714 uncertain and its conservation status of concern.

1715

1716 *Colletotrichum cordylinicola* Phoulivong, L. Cai and K. D. Hyde, *Mycotaxon* **114**: 251 (2011)

1717

1718 *Colletotrichum cordylinicola* is known from *Cordyline* spp. (Asparagaceae) in the USA (Sharma et
1719 al. 2014) and Thailand, from *Eugenia* sp. (Myrtaceae) in Laos and from *Areca catechu* (Arecaceae)
1720 in China (Cao et al. 2020). Additional species of *Colletotrichum* are reported from these hosts,
1721 rendering the pathological status of *C. cordylinicola* uncertain and its conservation status of concern.

1722

1723 *Colletotrichum cycadis* Andjic, Maxwell & Smith, *Persoonia* **45**:251-409 (2020)

1724

1725 The species *Colletotrichum cycadis* was described based on fungi isolated from leaf spots on *Cycas*
1726 *revoluta* (Cycadaceae) plants originary from China (Crous et al. 2020). Records of *Colletotrichum*
1727 spp. on *Cycas* are seldom, but given the ornamental importance of these plants, the pathological
1728 relevance of this fungus needs to be studied.

1729

1730 *Colletotrichum dracaenigenum* Chaiwan & K.D. Hyde, *Phytotaxa* **491**:143-157 (2021)

1731

1732 *Colletotrichum dracaenigenum* was described based on a single isolate obtained in 2017 in Thailand
1733 on dead leaves of *Dracaena fragrans* (Asparagaceae) and assumed as a saprobe (Chaiwan et al. 2021).
1734 Given that there are several species of *Colletotrichum* on *Dracaena* spp., the conservation status of
1735 *C. dracaenigenum* is uncertain and of concern.

1736

1737 *Colletotrichum endophyticum* Manamgoda, Udayanga, L. Cai and K.D. Hyde, *Fungal Divers.* **61**:
1738 110 (2013)

1739

1740 *Colletotrichum endophyticum* was reported as an endophyte collected in Thailand in 2010 on
1741 *Pennisetum purpureum* (Poaceae) and on an unknown wild fruit (Manamgoda et al. 2013), and
1742 subsequently found as an endophyte on *Capsicum annuum* fruits in Thailand and in China (Diao et
1743 al. 2017; De Silva et al. 2019). Nevertheless, *C. endophyticum* was found as an anthracnose pathogen
1744 associated to *Camellia sinensis* leaves (Wang et al. 2016), to coffee (*Coffea arabica* and *C. robusta*)
1745 leaves and fruits (Cao et al. 2019a) and to mango leaves and fruits (Li et al. 2019b) in China.
1746 *Colletotrichum endophyticum* could be emerging in Southeast Asia and may be of pathological
1747 concern to the host crops (tea, coffee and mango) in which it was shown to be pathogenic. However,
1748 any of these three crops harbour a vast array of *Colletotrichum* species, suggesting attentive surveys
1749 for the presence and spread of *C. endophyticum*.

1750
1751 *Colletotrichum fructicola* Prihastuti, L. Cai and K.D. Hyde, *Fungal Divers.* **39**: 96 (2009)

1752
1753 *Colletotrichum fructicola* is a cosmopolitan fungus, found in all continents and in a wide range of
1754 host plants (Supplementary data 9, panel G), but mostly occurring in tropical and sub-tropical regions.
1755 *Colletotrichum fructicola* typically occurs along other *Colletotrichum* species associated to
1756 anthracnose symptoms, often being a less frequent and/or less virulent population. However, several
1757 reports consistently place *C. fructicola* as the most frequently isolated fungus associated with apple
1758 bitter rot in South America (Alaniz et al. 2019; Moreira et al. 2019a; Velho et al. 2019), in contrast
1759 with *C. fioriniae* as the main causal agent of this disease in North America and Europe. Other reports
1760 where *C. fructicola* was recorded as the main anthracnose pathogen are on *Annona* spp. in Brazil
1761 (Costa et al. 2019) and on *Pyrus* spp. (Fu et al. 2019), strawberry (Jayawardena et al. 2016b), tea plant
1762 (*Camellia sinensis*; Wang et al. 2016) and tea-oil tree (*Camellia oleifera*; Wang et al. 2020a) in China.

1763
1764 *Colletotrichum fructivorum* V.P. Doyle, P.V. Oudem. and S.A. Rehner, *PLoS ONE* **7**: e51392 (2012)

1765
1766 *Colletotrichum fructivorum* includes isolates obtained in the USA from fruits of cultivated *Vaccinium*
1767 *macrocarpon* and wild *V. oxycoccos* (Ericaceae) and stems of *Rhexia virginica* (Melastomataceae) in
1768 2009-2010 (Doyle et al. 2013) (Supplementary data 9, panel H). However, no further occurrences of
1769 *C. fructivorum* have been reported ever since, raising concern on its conservation status.

1770
1771 *Colletotrichum gloeosporioides* (Penz.) Penz. and Sacc., *Atti Inst. Veneto Sci. Lett., ed Arti*, Sér. 6
1772 (2): 670 (1884)

1773

1774 For over 100 years the limits of the taxon *Colletotrichum gloeosporioides* have changed several times.
1775 Following Cannon et al. (2008) and Weir et al. (2012), modern *C. gloeosporioides*, or *C.*
1776 *gloeosporioides* sensu stricto, was defined based on fungi occurring on *Citrus* spp., as well as on
1777 hosts such as *Ficus*, *Mangifera*, *Pueraria* and *Vitis*, suggesting that this taxon was not of cosmopolitan
1778 distribution (Phoulivong et al. 2010). However, in the last decade, *C. gloeosporioides* sensu stricto
1779 was recorded in a vast number of hosts and locations in addition to those hosts: okra (*Abelmoschus*
1780 *esculentus*, Malvaceae) in China (Shi et al. 2019); *Acca sellowiana* (Myrtaceae) in Brazil (Fantinel et
1781 al. 2017); *Acer coriaceifolium* (Sapindaceae) in China (Zhu et al. 2020); *Actinidia* spp.
1782 (Actinidiaceae) in China (Deng et al. 2017; Li et al. 2017a); *Akebia trifoliata* (Lardizabalaceae) in
1783 China (Pan et al. 2021); *Annona* spp. (Annonaceae) in Brazil (Costa et al. 2019), Colombia (Álvarez
1784 et al. 2014) and Italy (Schena et al. 2014); *Anoectochilus roxburghii* (Orchidaceae) in China (Chen
1785 et al. 2016b); *Areca catechu* (Arecaceae) in China (Cao et al. 2020); *Atalantia citroides* (Rutaceae)
1786 in Spain (Guarnaccia et al. 2017); *Barringtonia edulis* (Lecythidaceae) in Papua New Guinea
1787 (Buyoyu et al. 2017); *Bauhinia blakeana* (Fabaceae) in China (Li et al. 2016a); *Camellia oleifera* and
1788 *C. sinensis* (Theaceae) in China (Guo et al. 2014a; Wang et al. 2020a); chilli (*Capsicum* spp.,
1789 Solanaceae) in China (Diao et al. 2017; Li et al. 2021); *Catalpa fargesii* f. *duciouxii* (Bignoniaceae)
1790 in China (Fu et al. 2013); *Chaenomeles sinensis* (Rosaceae) in China (Ni et al. 2021); *Choerospondias*
1791 *axillaris* (Anacardiaceae) in China (Li et al. 2017b); Arabica coffee (*Coffea arabica*, Rubiaceae) in
1792 Mexico (Cristóbal-Martínez et al. 2017); *Crataegus gracilior* (Rosaceae) in Mexico (Nieto-López et
1793 al. 2018); *Cunninghamia lanceolata* (Cupressaceae) in China (Huang et al. 2019); *Cyclocarya*
1794 *paliurus* (Juglandaceae) in China (Zheng et al. 2021b); *Dendrobium officinale* (Orchidaceae) in China
1795 (Lan et al. 2016); *Elaeocarpus sylvestris* (Elaeocarpaceae) in China (Li et al. 2016b); *Elettaria*
1796 *cardamomum* (Zingiberaceae) in India (Chethana et al. 2016); loquat (*Eriobotrya japonica*,
1797 Rosaceae) in Pakistan (Naz et al. 2017); *Euonymus japonicus* (Celastraceae) in China (Huang et al.
1798 2016); *Falcataria moluccana* (as *Albizia falcataria*, Fabaceae) in China (Chen et al. 2019b);
1799 *Hymenocallis littoralis* (Amaryllidaceae) in China (Zhao et al. 2019); walnut (*Juglans regia*,
1800 Juglandaceae) in China (Wang et al. 2020b; Yang et al. 2021); *Ligustrum japonicum* (Oleaceae) in
1801 China (Shen et al. 2017); *Liriodendron chinense* × *tulipifera* (Magnoliaceae) in China (Zhu et al.
1802 2019a); *Liriope cymbidiomorpha* (Asparagaceae) in China (Yang et al. 2020); *Magnolia candolli*
1803 (Magnoliaceae) in China (De Silva et al. 2021); *Malus pumila* (Rosaceae) in Korea (Cheon et al.
1804 2016); *Mikania micrantha* (Asteraceae) in China (Zhu et al. 2019b); banana (*Musa acuminata*,
1805 Musaceae) in Ecuador, Malaysia and Pakistan (Intan Sakinah et al. 2013; Riera et al. 2019; Alam et
1806 al. 2021); olive (*Olea europaea*, Oleaceae) in Italy, Portugal and Tunisia (Mosca et al. 2014;
1807 Chattaoui et al. 2016; Talhinas et al. 2018); *Osmanthus fragrans* (Oleaceae) in China (Tang et al.
1808 2018); *Oxalis corniculata* (Oxalidaceae) in Brazil (Bellé et al. 2019); *Paeonia lactiflora*

1809 (Paeoniaceae) in China (Zhang and Dai 2017); avocado (*Persea americana*, Lauraceae) in Israel and
1810 Turkey (Akgül et al. 2016; Sharma et al. 2017); *Pouteria caimito* (Sapotaceae) in China (Duan et al.
1811 2018b); *Pteridium aquilinum* (Dennstaedtiaceae) in China (Tan et al. 2017); pomegranate (*Punica*
1812 *granatum*, Lythraceae) in the USA (Xavier et al. 2019); *Pyrus* spp. (Rosaceae) in China (Fu et al.
1813 2019); *Quercus glauca* (Fagaceae) in China (Liu et al. 2021c); *Robinia pseudoacacia* (Fabaceae) in
1814 China (Xue et al. 2018a); rose (*Rosa* sp., Rosaceae) in South Korea (Hassan et al. 2019b); *Rubia*
1815 *cordifolia* (Rubiaceae) in China (Tang and Tan 2020); *Sedum kamtschaticum* (Crassulaceae) in South
1816 Korea (Jeon and Kwak 2016); *Smilax sieboldii* (Smilacaceae) in China (Zhang et al. 2017); *Sorbaria*
1817 *sorbifolia* (Rosaceae) in China (Li et al. 2019c; Wang et al. 2021a); *Syzygium samarangense*
1818 (Myrtaceae) in Malaysia (Al-Obaidi et al. 2017); *Viburnum odoratissimum* (Adoxaceae) in China
1819 (Yang et al. 2015). *Colletotrichum gloeosporioides* sensu stricto is thus a cosmopolitan fungus
1820 (Supplementary data 9, panel I), inhabiting a wide range of host plants.

1821
1822 *Colletotrichum grevilleae* F. Liu, Damm, L. Cai and Crous, *Fungal Divers.* **61**: 98 (2013)

1823
1824 *Colletotrichum grevilleae* is known only from a single isolate collected from root and collar rot of
1825 *Grevillea* sp. (Proteaceae) in Italy in 2000 (Liu et al. 2013a). No further occurrences of *C. grevilleae*
1826 have been reported ever since and several other species of *Colletotrichum* occur on *Grevillea*, raising
1827 great concern on its conservation status.

1828
1829 *Colletotrichum grossum* Y.Z. Diao, C. Zhang, L. Cai and X.L. Liu, *Persoonia* **38**: 29 (2017)

1830
1831 The species *Colletotrichum grossum* was recently defined based on one isolate collected from
1832 *Capsicum annuum* var. *grossum* in China in 2011 (Diao et al. 2017). The fungus was recently
1833 identified on chilli in Italy (Guarnaccia et al. 2021). The scarcity of reports of *C. grossum* and the
1834 occurrence of several other species of *Colletotrichum* on chilli raise concern on the conservation
1835 status of this species.

1836
1837 *Colletotrichum hebeiense* X.H. Li, Y. Wang, K.D. Hyde, M.M.R.S. Jayawardena and J.Y. Yan,
1838 *Fungal Divers.* **71**: 241 (2015)

1839
1840 *Colletotrichum hebeiense* is defined based on two isolates obtained from grapes (*Vitis vinifera*) in
1841 two locations in China in 2009 (Yan et al. 2015). No additional occurrences of *C. hebeiense* have
1842 been recorded ever since. Considering that a vast list of species of *Colletotrichum* is known from *Vitis*
1843 spp., the conservation status of *C. hebeiense* is of serious concern.

1844

1845 *Colletotrichum hederiicola* Jayaward., Camporesi and K.D. Hyde, *Fungal Divers.* **100**: 5 (2020)

1846

1847 The species *Colletotrichum hederiicola* was recently coined to accommodate a fungus isolated as a
1848 saprobe from a dead branch of ivy (*Hedera helix*, Araliaceae) in Italy in 2014 (Hyde et al. 2020a).
1849 No further records of *C. hederiicola* are known. *Colletotrichum trichellum*, also reported from *Hedera*
1850 spp., is also seldom. The conservation status of *C. hederiicola* is therefore of great concern.

1851

1852 *Colletotrichum helleniense* Guarnaccia and Crous, *Persoonia* **39**: 32 (2017)

1853

1854 *Colletotrichum helleniense* is a taxon containing isolates associated with citrus anthracnose, namely
1855 from wither-tip twigs of *Citrus reticulata* and *C. trifoliata* (as *Poncirus trifoliata*, Rutaceae) from the
1856 same location in Greece in 2015 (Guarnaccia et al. 2017). No additional occurrences of *C. helleniense*
1857 have been recorded ever since and numerous species of *Colletotrichum* occur on citrus, rendering the
1858 conservation status of *C. helleniense* of concern.

1859

1860 *Colletotrichum henanense* F. Liu and L. Cai, *Persoonia* **35**: 80 (2015)

1861

1862 *Colletotrichum henanense* was described based on two isolates obtained in China from tea (*Camellia*
1863 *sinensis*, Theaceae) in 2012 and from *Cirsium japonicum* (Asteraceae) in 2010 (Liu et al. 2015a).
1864 Subsequently the fungus was detected also in China, causing anthracnose on *Camellia oleifera* in
1865 2016 (Li et al. 2018c). This is the single report of *Colletotrichum* on *Cirsium*, suggesting that this is
1866 not a common host of *Colletotrichum* spp. On the other hand, there are many species of
1867 *Colletotrichum* reported on *Camellia* spp., raising concerns on the conservation status of
1868 *Colletotrichum henanense*.

1869

1870 *Colletotrichum horii* B. Weir and P.R. Johnst., *Mycotaxon* **111**: 211 (2010)

1871

1872 *Colletotrichum horii* is defined based on fungal pathogens of persimmon (*Diospyros kaki*, Ebenaceae)
1873 from China, Korea, Japan and New Zealand (Weir and Johnston 2010). The fungus has subsequently
1874 been reported from Brazil associated to twig blight and defoliation (Mio et al. 2015), with further
1875 reports from Korea showing severe infections (Kwon et al. 2013; Jeon et al. 2017; An et al. 2018).
1876 *Colletotrichum horii* is apparently specific to persimmon, occurring commonly in Asia
1877 (Supplementary data 9, panel J) and may be considered a quarantine pathogen elsewhere.

1878

1879 *Colletotrichum hystricis* Guarnaccia and Crous, *Persoonia* **39**: 32 (2017)

1880

1881 The species *Colletotrichum hystricis* includes a single isolate obtained from a leaf lesion of *Citrus*

1882 *hystrix* (Rutaceae) in Italy in 2016 (Guarnaccia et al. 2017). The occurrence of multiple species of

1883 *Colletotrichum* on citrus renders the conservation status of *C. hystricis* of serious concern.

1884

1885 *Colletotrichum jiangxiense* F. Liu and L. Cai, *Persoonia* **35**: 82 (2015)

1886

1887 The species *Colletotrichum jiangxiense* was designated based on two isolates collected from tea plant

1888 (*Camellia sinensis*, Theaceae) in China in 2013 (Liu et al. 2015a). The species was subsequently

1889 identified as an endophyte on *Dendrobium* sp. (Orchidaceae) in Thailand (Ma et al. 2018) and

1890 associated to avocado (*Persea americana*, Lauraceae) anthracnose in Mexico (Ayvar-Serna et al.

1891 2021). The uncertainty about its pathological status and the occurrence of vast numbers of species of

1892 *Colletotrichum* on its hosts raise concern about the conservation status of *C. jiangxiense*.

1893

1894 *Colletotrichum kahawae* J.M Waller and Bridge, *Mycol. Res.* **97**(8): 993 (1993)

1895

1896 *Colletotrichum kahawae* is found in Africa in *Coffea* spp. (Rubiaceae), causing the Coffee Berry

1897 Disease (Waller et al. 1993; Cabral et al. 2020). This fungus has undergone a host-jump speciation

1898 process (Silva et al. 2012a) accompanied by a genome size expansion (Pires et al. 2016), becoming

1899 biologically and phylogenetically isolated from the closely related *Colletotrichum cigarro* (Cabral et

1900 al. 2020). Although common in Africa (Supplementary data 9, panel K), this pathogen is of quarantine

1901 concern in coffee growing regions in Asia and America (Batista et al. 2017).

1902

1903 *Colletotrichum makassareense* D.D. De Silva, P.W. Crous and P.W.J. Taylor, *IMA Fungus* **10**: 8

1904 (2019)

1905

1906 The taxon *Colletotrichum makassareense* was designated to accommodate a single isolate obtained

1907 from chilli (*Capsicum annuum*, Solanaceae) in Indonesia (De Silva et al. 2019). No further isolates

1908 of *Colletotrichum makassareense* have been reported and many other species of *Colletotrichum* are

1909 known from chilli, raising high concern about the conservation status of this species.

1910

1911 *Colletotrichum musae* (Berk. and M. A. Curtis) Arx and Verh. *K. ned. Akad. Wet.*, tweede sect. 51(3):

1912 107 (1957)

1913

1914 *Colletotrichum musae* is the causal agent of banana (*Musa* sp., Musaceae) anthracnose, occurring
1915 worldwide (Supplementary data 9, panel L) as a common post-harvest disease (Weir et al. 2012).

1916

1917 *Colletotrichum nupharicola* D.A. Johnson, Carris and J.D. Rogers, *Mycol. Res.* **101**: 647 (1997)

1918

1919 The species *Colletotrichum nupharicola* was described based on isolates collected from the water
1920 lilies *Nuphar lutea* and *Nymphaea odorata* (Nymphaeaceae) in the USA in the 1990s (Weir et al.
1921 2012). No further occurrences of *C. nupharicola* have been recorded thereafter, but this taxon has
1922 been reported recently from avocado (*Persea americana*, Lauraceae) in Israel (Sharma et al. 2017).
1923 The geographic distribution, pathological relevance and conservation status of *C. nupharicola* are
1924 thus unknown and require further investigation.

1925

1926 *Colletotrichum pandanicola* Tibpromma and K.D. Hyde, *MycKeys* **33**: 25 (2018)

1927

1928 This species is recorded only from an epiphytic fungus occurring on leaves on an unspecified species
1929 of *Pandanus* (Pandaneaceae) in Thailand in 2016 (Tibpromma et al. 2018). There are no additional
1930 reports of this fungus and other species of *Colletotrichum* occur on *Pandanus*, raising serious
1931 concerns on the conservation status of *C. pandanicola*.

1932

1933 *Colletotrichum perseae* G. Sharma and S. Freeman, *Sci. Rep.* **17**: 15839 (2017)

1934

1935 *Colletotrichum perseae* was reported from several locations in Israel in 2014, among several other
1936 species of *Colletotrichum*, as the prevailing pathogen associated to leaf spots and fruit rot of avocado
1937 (*Persea americana*, Lauraceae) (Sharma et al. 2017). The fungus was recently detected in New
1938 Zealand, also associated to mango anthracnose (Hofer et al. 2021). The pathological relevance of *C.*
1939 *perseae* to avocado cultivation remains to be analysed, suggesting that it may be considered a
1940 quarantine pathogen.

1941

1942 *Colletotrichum proteae* F. Liu, Damm, L. Cai and Crous, *Fungal Divers.* **61**: 100 (2013)

1943

1944 *Colletotrichum proteae* is known from a single isolate, collected from an unspecified species of
1945 *Protea* (Proteaceae) in South Africa in 2008 (Liu et al. 2013a). Its pathological condition is not known
1946 and there are several other species of *Colletotrichum* occurring on *Protea* and on Proteaceae, which
1947 raises severe concerns about the conservation status of *C. proteae*.

1948

1949 *Colletotrichum pseudotheobromicola* Chethana, Yan, Li and K.D. Hyde, *Mycosphere* **10**: 518 (2019)

1950

1951 *Colletotrichum pseudotheobromicola* has been recently named to accommodate a fungus associated

1952 to leaf spots of *Prunus avium* (Rosaceae) in China (Chetana et al. 2019). This is the single report of

1953 this species and there are numerous species of *Colletotrichum* occurring on *Prunus* (and even

1954 specifically on *P. avium*), suggesting that the pathological relevance and the conservation status of

1955 *C. pseudotheobromicola* require further investigation.

1956

1957 *Colletotrichum psidii* Curzi, *Atti Ist. bot. R. Univ. Pavia*, 3 Sér. **3**: 207 (1927)

1958

1959 *Colletotrichum psidii* is known from a single occurrence, collected from guava (*Psidium* sp.,

1960 Myrtaceae) in Italy, prior to 1927 (Weir et al. 2012). The only available culture in collection is

1961 reported as sterile (Weir et al. 2012). The absence of any further records of this species, along with

1962 the occurrence of several other species of *Colletotrichum* on guava, suggests that *Colletotrichum*

1963 *psidii* may be extinct.

1964

1965 *Colletotrichum queenslandicum* B. Weir and P.R. Johnst., *Stud. Mycol.* **73**: 164 (2012)

1966

1967 *Colletotrichum queenslandicum* was originally described from papaya (*Carica papaya*, Caricaceae)

1968 and avocado (*Persea americana*, Lauraceae) in Australia and from cashew (*Anacardium occidentale*,

1969 Anacardiaceae) in Brazil (Veloso et al. 2018) and coffee (*Coffea* sp., Rubiaceae) in Fiji (Weir et al.

1970 2012). It was subsequently reported from persian lime (*Citrus × latifolia*, Rutaceae) in the USA

1971 (Kunta et al. 2018), from *Licania tomentosa* (Chrysobalanaceae) in Brazil (Lisboa et al. 2018), from

1972 lychee (*Litchi chinensis*, Sapindaceae) in Australia (Anderson et al. 2013; Shivas et al. 2016), from

1973 mango (*Mangifera indica*, Anacardiaceae) in Australia (Shivas et al. 2016), from *Nephelium*

1974 *lappaceum* (Sapindaceae) in Puerto Rico (Serrato-Diaz et al. 2017), from olive (*Olea europaea*,

1975 Oleaceae) in Montenegro (Schena et al. 2014) and from passionfruit (*Passiflora edulis*,

1976 Passifloraceae) in Australia (Shivas et al. 2016). Such recent reports of *C. queenslandicum*, besides

1977 confirming this as a common fungus in Australia, revealed its presence in America and Europe

1978 (Supplementary data 9, panel M), associated to woody agricultural crops. The pathological relevance

1979 and the host range of *C. queenslandicum* should be analysed, namely in a quarantine perspective.

1980

1981 *Colletotrichum rhexiae* Ellis and Everh., *Proc. Acad. nat. Sci. Philad.* **46**: 372 (1894)

1982

1983 *Colletotrichum rhexiae* is known from *Rhexia virginica* (Melastomataceae) leaf and stem lesions and
1984 from *Vaccinium macrocarpon* (Ericaceae) fruit lesions in the USA (Doyle et al. 2013). No additional
1985 reports of this species have occurred, suggesting that it is geographically confined and that it may not
1986 occur on major agricultural crops. Further surveys would improve current knowledge on the
1987 conservation status of *C. rhexiae*.

1988

1989 *Colletotrichum salsolae* B. Weir and P.R. Johnst., *Stud. Mycol.* **73**: 164 (2012)

1990

1991 *Colletotrichum salsolae* is known from *Salsola kali* subsp. *tragus* (Amaranthaceae), occurring
1992 throughout the geographic range of the host (Weir et al. 2012). Recently, the fungus was reported as
1993 a causal agent of anthracnose on papaya (*Carica papaya*, Caricaceae) fruits in India, along with
1994 *Colletotrichum gloeosporioides* (Saini et al. 2017a).

1995

1996 *Colletotrichum siamense* Phoulivong, L. Cai and K.D. Hyde, *Fungal Divers.* **39**: 98 (2009)

1997

1998 Liu et al. (2016c) synonymised several species (namely *Colletotrichum communis*, *C. dianesei*, *C.*
1999 *endomangiferae*, *C. hymenocallidis*, *C. jasmini-sambac* and *C. murrayae*) to *C. siamense*, thus
2000 recognising its occurrence on multiple hosts, to which add additional recent reports. *Colletotrichum*
2001 *siamense* is thus known from *Alocasia macrorrhizos* (Araceae), *Alpinia purpurata* (Zingiberaceae),
2002 *Amorphophallus paeoniifolius* (Araceae), *Anacardium occidentale*, *A. humile* and *A. othonianum*
2003 (Anacardiaceae), *Annona muricata* (Annonaceae), *Areca catechu* (Arecaceae), *Artocarpus*
2004 *heterophyllus* and *A. sericicarpus* (Moraceae), *Azadirachta indica* (Meliaceae), *Bauhinia forficata*
2005 and *B. variegata* (Fabaceae), *Camellia chrysantha*, *C. oleifera* and *C. sinensis* (Theaceae), *Capsicum*
2006 *annuum*, *C. chinensis* and *C. frutescens* (Solanaceae), *Carica papaya* (Caricaceae), *Carya illinoensis*
2007 (Juglandaceae), *Cassia fistula* (Fabaceae), *Cercis chinensis* (Fabaceae), *Cinnamomum kotoense*
2008 (Lauraceae), *Citrus limon*, *C. pennivesiculata*, *C. reticulata* and *C. sinensis* (Rutaceae), *Cocos*
2009 *nucifera* (Arececeae), *Coffea arabica* and *C. canephora* (Rubiaceae), *Commelina* sp.
2010 (Commelinaceae), *Corchorus capsularis* (Malvaceae), *Cornus hongkongensis* (Cornaceae), *Cycas*
2011 *debaensis* (Cycadaceae), *Cymbopogon citratus* (Poaceae), *Datura metel* (Solanaceae),
2012 *Dieffenbachia* sp. (Araceae), *Dionaea muscipula* (Droseraceae), *Dioscorea cayennensis* ssp.
2013 *rotundata* (Dioscoreaceae), *Diospyros kaki* (Ebenaceae), *Dypsis lutescens* (as *Chrysalidocarpus*
2014 *lutescens*, Arececeae), *Elettaria cardamomum* (Zingiberaceae), *Ensete superbum* (Musaceae),
2015 *Eriobotrya japonica* (Rosaceae), *Euonymus japonicus* (Celastraceae), *Ficus carica* and *F. elastica*
2016 (Moraceae), *Fragaria* × *ananassa* (Rosaceae), *Hevea brasiliensis* (Euphorbiaceae), *Hibiscus* sp.
2017 (Malvaceae), *Hylocereus lemairei* (as *Hylocereus polyrhizus*) and *H. undulatus* (Cactaceae),

2018 *Hymenocallis littoralis* (as *Hymenocallis americana*, Amaryllidaceae), *Iris tectorum* (Iridaceae),
2019 *Jasminum mesnyi* and *J. sambac* (Oleaceae), *Juglans regia* (Juglandaceae), *Licania tomentosa*
2020 (Chrysobalanaceae), *Liriodendron chinense* × *tulipifera* (Magnoliaceae), *Litchi chinensis*
2021 (Sapindaceae), *Macadamia integrifolia* (Proteaceae), *Machilus ichangensis* (Lauraceae), *Malus*
2022 *domestica* (Rosaceae), *Mandevilla* sp. (Apocynaceae), *Mangifera indica* (Anacardiaceae), *Manihot*
2023 *esculenta* (Euphorbiaceae), *Mentha* sp. (Lamiaceae), *Michelia alba* (Magnoliaceae), *Musa acuminata*
2024 (Musaceae), *Nelumbo nucifera* (Nelumbonaceae), *Nopalea cochenillifera* (Cactaceae), *Ocimum*
2025 *basilicum* (Lamiaceae), *Olea europaea* (Oleaceae), *Parthenocissus tricuspidata* (Vitaceae),
2026 *Pennisetum purpureum* (Poaceae), *Persea americana* (Lauraceae), *Piper nigrum* (Piperaceae),
2027 *Pistachia vera* (Anacardiaceae), *Plukenetia volubilis* (Euphorbiaceae), *Plumeria alba*
2028 (Apocynaceae), *Pongamia pinnata* (Fabaceae), *Protea cynaroides* (Proteaceae), *Prunus persica*
2029 (Rosaceae), *Psidium guajava* (Myrtaceae), *Punica granatum* (Lythraceae), *Pyrus communis* and *P.*
2030 *pyrifolia* (Rosaceae), *Rosa chinensis* (Rosaceae), *Rosmarinus officinalis* (Lamiaceae), *Salix*
2031 *matsudana* (Salicaceae), *Saraca indica* (Fabaceae), *Sarcandra glabra* (Chloranthaceae), *Sophora*
2032 *tonkinensis* (Fabaceae), *Sterculia nobilis* and *S. lanceolata* (Malvaceae), *Theobroma cacao*
2033 (Malvaceae), *Uraria picta* (Fabaceae), *Vaccinium macrocarpon* (Ericaceae), *Viola odorata*
2034 (Violaceae) and *Vitis vinifera* (Vitaceae) (Weir et al. 2012; Cheng et al. 2013; Doyle et al. 2013; Liu
2035 et al. 2013a; Manamgoda et al. 2013; Udayanga et al. 2013; Álvarez et al. 2014; Schena et al. 2014;
2036 Larran et al. 2015; Meetum et al. 2015; Sharma et al. 2015; Dwarka et al. 2016; Niu et al. 2016a;
2037 Shivas et al. 2016; Watanabe et al. 2016; Ye et al. 2016; Zhou et al. 2016; Conforto et al. 2017;
2038 Douanla-Meli and Unger 2017; Katoch et al. 2017; Kumar et al. 2017; Liu et al. 2017a; Ni et al. 2017;
2039 Prasad et al. 2017; Vieira et al. 2017; Wang et al. 2017; Chang et al. 2018b; Naik et al. 2018; Oliveira
2040 et al. 2018; Veloso et al. 2018; Xavier et al. 2018; Zhao et al. 2018; Abirami et al. 2019; Cao et al.
2041 2019b; Chaves et al. 2019; Cheng et al. 2019; Chou et al. 2019; Feng et al. 2019; Fu et al. 2019; Ji et
2042 al. 2019; Xavier et al. 2019; Zhang et al. 2019b; Zhu et al. 2019a; Chen et al. 2020; Prasannath et al.
2043 2020; Wang et al. 2020c; Wu 2020; Zhang et al. 2020a,b; Zhao et al. 2020; Borges et al. 2021;
2044 Carbone et al. 2021; Eaton et al. 2021; Han et al. 2021; Hofer et al. 2021; Huang et al. 2021a,b; Ismail
2045 et al. 2021a,b; Oh et al. 2021; Oo et al. 2021; Qin et al. 2021; Rodríguez-Palafox et al. 2021; Song et
2046 al. 2021; Wang et al. 2021c,d; Zhafarina et al. 2021; Zhang et al. 2021a,d; Zhao et al. 2021a).
2047 *Colletotrichum siamense* is a fungus with a very broad host range and found throughout the world
2048 (Supplementary data 9, panel N), although prevailing in Australasia and tropical America, whereas it
2049 seems to be quite rare in Europe.

2050

2051 *Colletotrichum syzygiicola* Udayanga, Manamgoda and K.D. Hyde, *Fungal Divers.* **61**: 173 (2013)

2052

2053 *Colletotrichum syzygiicola* was first described from anthracnose symptoms on *Citrus aurantifolia*
2054 (Rutaceae) and *Syzygium samarangense* (Myrtaceae) fruits collected in Thailand in 2010 (Udayanga
2055 et al. 2013). The fungus was subsequently associated to anthracnose of *Elettaria cardamomum*
2056 (Zingiberaceae) in India (Chethana et al. 2016). Records of *Colletotrichum syzygiicola* are still
2057 seldom and each of the hosts is known to harbour other species of *Colletotrichum*, raising concern on
2058 the actual occurrence of this fungus in nature.

2059

2060 *Colletotrichum tainanense* D.D. De Silva, P.W. Crous and P.W.J. Taylor, *IMA Fungus* **10**: 8 (2019)

2061

2062 *Colletotrichum tainanense* is known from a single report obtained from fruits of *Capsicum annuum*
2063 (Solanaceae) in China in 2014 (De Silva et al. 2019). There are no additional reports for this taxon
2064 and multiple species of *Colletotrichum* occur on this host, raising severe concerns about the
2065 conservation status of *C. tainanense*.

2066

2067 *Colletotrichum temperatum* V. Doyle, P.V. Oudem. and S.A. Rehner, *PLoS One* **7**: e51392 (2012)

2068

2069 *Colletotrichum temperatum* is known from two isolates collected from fruit rot and asymptomatic
2070 stems of *Vaccinium macrocarpon* (Ericaceae) in the USA in 2009 (Doyle et al. 2013). There are no
2071 further reports of this species and there are numerous other species of *Colletotrichum* recorded on
2072 *Vaccinium*, raising serious concerns about the conservation status of *C. temperatum*.

2073

2074 *Colletotrichum theobromicola* Delacr., *Bull. Soc. Mycol. Fr.* **21**: 191 (1905)

2075

2076 *Colletotrichum theobromicola*, as defined by Weir et al. (2012) following Rojas et al. (2010)
2077 description, is a fungus with a broad host range, upon the placement of *C. fragariae* and
2078 *Colletotrichum gloeosporioides* f. *stylosanthis* in synonymy to it. Thereafter, the fungus has been
2079 found on other hosts, being currently known from: *Acca sellowiana* (Myrtaceae) (Weir et al. 2012);
2080 *Aeschynomene falcata* (Fabaceae) (Shivas et al. 2016); *Allium cepa* and *A. fistulosum*
2081 (Amaryllidaceae) (Matos et al. 2017; Lopes et al. 2021); *Anacardium occidentale* (Anacardiaceae)
2082 (Veloso et al. 2018); *Annona macrophyllata* (as *A. diversifolia*), *A. muricata* and *A. squamosa*
2083 (Annonaceae) (Weir et al. 2012; Álvarez et al. 2014; Costa et al. 2019); *Buxus microphylla* var.
2084 *japonica* (Buxaceae) (Singh et al. 2015); *Campomanesia phaea* (Myrtaceae) (Santos et al. 2017);
2085 *Carapichea ipecacuanha* (Rubiaceae) (Ferreira et al. 2020); *Coffea arabica* (Rubiaceae) (Shivas et
2086 al. 2016; Cristóbal-Martínez et al. 2017); *Copernicia prunifera* (Areceaceae) (Araújo et al. 2018);
2087 *Cyclamen persicum* (Primulaceae) (Sharma et al. 2016); *Fragaria* × *ananassa* (Rosaceae) (Weir et

2088 al. 2012); *Limonium* sp. (Plumbaginaceae) (Weir et al. 2012); *Malpighia emarginata* (Malpighiaceae)
2089 (Bragança et al. 2014); *Malus domestica* (Rosaceae) (Alaniz et al. 2015; Munir et al. 2016);
2090 *Mangifera indica* (Anacardiaceae) (Sharma et al. 2013; Pardo-De la Hoz et al. 2016); *Manihot*
2091 *esculenta* (Euphorbiaceae) (Oliveira et al. 2018); *Manilkara zapota* (Sapotaceae) (Martins et al.
2092 2018); *Musa* sp. (Musaceae) (Vieira et al. 2017); *Olea europaea* (Oleaceae) (Weir et al. 2012; Lima
2093 et al. 2020; Moreira et al. 2021); *Persea americana* (Lauraceae) (Sharma et al. 2017); *Punica*
2094 *granatum* (Lythraceae) (Shivas et al. 2016; Xavier et al. 2019); *Quercus* sp. (Fagaceae) (Weir et al.
2095 2012); *Stylosanthes guianensis* and *S. viscosa* (Fabaceae) (Weir et al. 2012); *Theobroma cacao*
2096 (Malvaceae) (Rojas et al. 2010). *Colletotrichum theobromicola* is thus a predominantly tropical and
2097 sub-tropical fungus (Supplementary data 9, panel O), with a growing host range, and of pathological
2098 relevance.

2099
2100 *Colletotrichum ti* B. Weir and P.R. Johnst., *Stud. Mycol.* **73**: 171 (2012)

2101
2102 *Colletotrichum ti* is a fungus exhibiting pathogenic host specificity to *Cordyline australis*
2103 (Asparagaceae) and found only in New Zealand (Weir et al. 2012). There are other species of
2104 *Colletotrichum* known from *Cordyline* (although not from New Zealand) which, along with the
2105 absence of recent reports of *C. ti*, raise concern about the conservation status of this species.

2106
2107 *Colletotrichum tropicale* E.I. Rojas, S.A. Rehner and Samuels, *Mycologia* **102**(6): 1331 (2010)

2108
2109 Originally described as a fungus occurring as a leaf endophyte of several host species in tropical
2110 forests of Panama (Rojas et al. 2010), *Colletotrichum tropicale* has been identified from numerous
2111 hosts in many parts of the world (Supplementary data 9, panel P): *Anacardium occidentale*
2112 (Anacardiaceae) in Brazil (Veloso et al. 2018); *Annona cherimola* and *A. muricata* (Annonaceae) in
2113 Brazil, Colombia, Cuba and Panama (Rojas et al. 2010; Álvarez et al. 2014; García and Manzano
2114 2017; Costa et al. 2019); *Areca catechu* (Arecaceae) in China (Cao et al. 2020); *Capsicum annuum*
2115 and *C. frutescens* (Solanaceae) in Indonesia and Brazil respectively (De Silva et al. 2017a, 2019);
2116 *Cattleya* spp. (Orchidaceae) in Brazil (Silva-Cabral et al. 2019); *Coffea* sp. (Rubiaceae) in China (Cao
2117 et al. 2019a); *Copernicia prunifera* (Arecaceae) in Brazil (Araújo et al. 2018); *Cordia alliodora*
2118 (Boraginaceae) in Panama (Rojas et al. 2010); *Ficus binnendijkii* (Moraceae) in China (Kong et al.
2119 2020); *Licania tomentosa* (Chrysobalanaceae) in Brazil (Lisboa et al. 2018); *Litchi chinensis*
2120 (Sapindaceae) in Japan (Weir et al. 2012); *Mangifera indica* (Anacardiaceae) in Brazil, China and
2121 Mexico (Lima et al. 2013; Li et al. 2019b; Tovar-Pedraza et al. 2020); *Manihot dichotoma* and *M.*
2122 *epruinosa* (Euphorbiaceae) in Brazil (Oliveira et al. 2016); *Musa* sp. (Musaceae) in Brazil (Vieira et

2123 al. 2017); *Myrciaria dubia* (Myrtaceae) in Brazil (Matos et al. 2020); *Passiflora edulis* in Brazil (Silva
2124 et al. 2021); *Persea americana* (Lauraceae) in Mexico (Fuentes-Aragón et al. 2020); *Plinia cauliflora*
2125 (as *Myrciaria cauliflora*, Myrtaceae) in Japan (Taba et al. 2020); *Nelumbo nucifera* (Nelumbonaceae)
2126 in China (Xavier et al. 2018); *Origanum vulgare* (Lamiaceae) in Mexico (Ayvar-Serna et al. 2020);
2127 *Pennisetum purpureum* (Poaceae) in Thailand (Manamgoda et al. 2013); *Punica granatum*
2128 (Lythraceae) in Brazil (Silva-Cabral et al. 2019); *Sauropus androgynus* (Phyllanthaceae) in China
2129 (Liu et al. 2018); *Theobroma cacao* (Malvaceae) in Panama (Rojas et al. 2010); *Trichilia tuberculata*
2130 (Meliaceae) in Panama (Rojas et al. 2010); *Viola surinamensis* (Violaceae) in Panama (Rojas et al.
2131 2010); human eye (Hung et al. 2020). *Colletotrichum tropicale* is thus a cosmopolitan and
2132 polyphagous species, of contemporary widespread occurrence.

2133

2134 *Colletotrichum viniferum* L.J. Peng, L. Cai, K.D. Hyde and Z-Y. Ying, *Mycoscience* **54**: 36 (2013)

2135

2136 *Colletotrichum viniferum* was described as a pathogen of grapes (*Vitis vinifera*) in China (Peng et al.
2137 2013), where it is the most prevalent and virulent causal agent of grape anthracnose (Yan et al. 2015).
2138 The fungus was subsequently recorded from grapevine in Korea (Oo and Oh 2017a), from *Hopea*
2139 *odorata* (Dipterocarpaceae) in Bangladesh (Rashid et al. 2020) and from chilli (*Capsicum* sp.; Diao
2140 et al. 2017), strawberry (*Fragaria × ananassa*; He et al. 2019) and walnut (*Juglans regia*; He et al.
2141 2019) in China. Considering the geographical distribution currently known for this fungus
2142 (Supplementary data 9, panel Q), along with the high virulence to grapevines and the expanding host
2143 range, *Colletotrichum viniferum* should be regarded with concern regarding its pathological relevance
2144 and potential quarantine status.

2145

2146 *Colletotrichum wuxiense* Y.C. Wang, X.C. Wang and Y.J. Yang, *Sci. Rep.* **6**: 35287 (2016)

2147

2148 *Colletotrichum wuxiense* was described based on an isolate obtained from diseased leaves of *Camellia*
2149 *sinensis* (Theaceae) in China in 2014 (Wang et al. 2016) and subsequently identified associated to
2150 anthracnose symptoms on *Pyrus pyrifolia* (Rosaceae) also in China, in 2016 (Fu et al. 2019).
2151 Considering the large number of species of *Colletotrichum* known from both hosts, further surveys
2152 are important to reveal the pathological and ecological relevance of *C. wuxiense*, as well as its
2153 conservation status.

2154

2155 *Colletotrichum xanthorrhoeae* R.G. Shivas, Bathgate and Podger, *Mycol. Res.* **102**: 280 (1998)

2156

2157 *Colletotrichum xanthorrhoeae* was described based on isolates obtained from *Xanthorrhoea* spp.
2158 (*Xanthorrhoeaceae*) in Australia in the 1990s (Shivas et al. 1998; Weir et al. 2012), but no additional
2159 records have been reported ever since. The current conservation status of *C. xanthorrhoeae* is
2160 therefore of concern.

2161

2162 *Colletotrichum xishuangbannaense* N.I. de Silva, Lumyong & K.D. Hyde, *Mycosphere* **12**(1):195
2163 (2021)

2164

2165 *Colletotrichum xishuangbannaense* is known from a single isolate collected as an endophyte in leaves
2166 of *Magnolia candolli* (*Magnoliaceae*) in 2017 in China (De Silva et al. 2021). There are no further
2167 records of this fungus and other species of *Colletotrichum* are known from this and other *Magnolia*
2168 spp., rendering the conservation status of this taxon of concern.

2169

2170 *Colletotrichum yulongense* C.L. Hou and X.T. Liu, *Phytotaxa* **394**: 285 (2019)

2171

2172 *Colletotrichum yulongense* is known only from a single occurrence, as an endophyte on leaves of
2173 *Vaccinium dunalianum* var. *urophyllum* in China in 2013 (Wang et al. 2019b). There are other species
2174 of *Colletotrichum* occurring on *Vaccinium*, suggesting that the ecological and conservation status of
2175 *C. yulongense* must be clarified.

2176

2177 **2.10 The graminicola species complex**

2178

2179 Firstly described by Cannon et al. (2012) and in agreement with studies published by Crouch et al.
2180 (2009a,b), the graminicola complex is a well-defined monophyletic clade encompassing
2181 *Colletotrichum* species mainly associated with grasses and with characteristic widely falcate conidia.
2182 MLST approaches initially revealed two major subclades within the graminicola clade (Crouch et al.
2183 2009a,b). The first one is represented only by *Colletotrichum cereale*, a species associated with C3
2184 grasses as either pathogens or endophytes (Crouch et al. 2009b). The second subclade encompasses
2185 apparently host-specific species associated with C4 grasses. More recently a third clade has been
2186 recognised and described as the caudatum species complex (see the section above). Currently the
2187 graminicola complex encompasses 16 species (Figure 12) pathogenic to different lineages of Poaceae
2188 but also endophytes of Poaceae and Orchidaceae (both monocot plants). Several of the species
2189 included in the graminicola clade are of major importance, including *C. falcatum* on sugarcane, *C.*
2190 *graminicola* on maize and *C. sublineola* on *Sorghum* species. *Colletotrichum cereale* and *C.*

2191 *eremochloae* are pathogens of cultivated turfgrasses (Crouch and Beirn 2009). Beside the economic
2192 impact, the maize pathogen *C. graminicola* is an important model system (O’Connell et al. 2012).

2193

2194 **Figure 12**

2195

2196 *Colletotrichum axonopodi* J.A. Crouch, B.B. Clarke, J.F. White and B.I. Hillman, *Mycologia* **101**:
2197 727 (2009)

2198

2199 There are four records for this species, collected in the first half of the 20th century in the USA and
2200 Honduras and in 1983 in Australia, on *Axonopodus* spp. (Poaceae) (Crouch et al. 2009a). Although
2201 anthracnose of *Axonopus* was associated to *C. axonopodi* (Crouch and Beirn 2009), more recently *C.*
2202 *hainanense* was described as an additional causal agent of this disease (Zhang et al. 2020c). The
2203 current conservation status of *C. axonopodi* is therefore uncertain and of concern.

2204

2205 *Colletotrichum cereale* Manns, *Proc. Indiana Acad. Sci.*: 111 (1908)

2206

2207 Besides being a pathogen of grasses (Poaceae) throughout the world (Crouch et al. 2009a)
2208 (Supplementary data 10, panel A) (inspite of scarce records; Zhao et al. 2021b), *C. cereale* was also
2209 reported as an endophyte from *Bletilla ochracea* (Orchidaceae) in China in 2006 (Tao et al. 2013).

2210

2211 *Colletotrichum echinochloae* Moriwaki and Tsukib., *Mycoscience* **50**: 275 (2009)

2212

2213 *Colletotrichum echinochloae* is only known from *Echinochloa utilis* (Poaceae) in Japan, collected
2214 over the years (Moriwaki and Tsukiboshi 2009). This fungus seems to be host-specific and
2215 geographically-confined, suggesting its ecological status to be under survey.

2216

2217 *Colletotrichum eleusines* Pavgi and U.P. Singh, *Mycopath. Mycol. Appl.* **27**: 85 (1965)

2218

2219 *Colletotrichum eleusines* is known from few and ancient (1936 and 1977) records, collected from
2220 *Eleusine indica* (Poaceae) in the USA and Japan (Crouch et al. 2009a). No other species of
2221 *Colletotrichum* have been recorded from this host, but the lack of recent reports of *C. eleusines* raises
2222 serious concern on its conservation status.

2223

2224 *Colletotrichum endophytum* G. Tao, Zuo Y. Liu and L. Cai, *Fungal Divers.* **61**: 152 (2013)

2225

2226 *Colletotrichum endophyllum* is known only from two isolates collected from healthy leaves of *Bletilla*
2227 *ochracea* (Orchidaceae) in two locations in China in 2006 (Tao et al. 2013). No additional
2228 occurrences of *C. endophyllum* were recorded thereafter, and several species of *Colletotrichum* occur
2229 on *Bletilla* (and even more so on orchids), rendering the conservation status of *C. endophyllum* of
2230 great concern.

2231

2232 *Colletotrichum eremochloae* J.A. Crouch and Tomaso-Pet., *Mycologia* **104**: 1092 (2012)

2233

2234 *Colletotrichum eremochloae* has been recorded in the USA (including on a shipment from China in
2235 1923) in different moments during the 20th century and more recently in 2007 associated to
2236 anthracnose symptoms on *Eremochloa ophiuroides* (Poaceae) (Crouch and Tomaso-Peterson 2012).
2237 Although the fungus seems to be host specific, its seldom occurrence raises concern on its
2238 conservation status.

2239

2240 *Colletotrichum falcatum* Went, *Archiv, voor de Java Suekerrind.* **1**: 265 (1893)

2241

2242 *Colletotrichum falcatum* is the causal agent of red rot of sugarcane, found in all continents where the
2243 host plant (*Saccharum officinarum*) is cultivated (Crouch et al. 2009a) (Supplementary data 10, panel
2244 B).

2245

2246 *Colletotrichum graminicola* (Ces.) G.W. Wilson, *Phytopathology* **4**: 110 (1914)

2247

2248 *Colletotrichum graminicola* is considered a pathogen of maize (*Zea mays*, Poaceae), reported from
2249 different parts of the world (Crouch et al. 2009a) (Supplementary data 10, panel C). Recent reports
2250 are mostly from Europe, including Bosnia and Herzegovina, Portugal and Switzerland (Sukno et al.
2251 2014; Sanz-Martín et al. 2016; Cuevas-Fernández et al. 2019), but also from China (Duan et al. 2019).
2252 The fungus is also reported as a human opportunistic pathogen (Valenzuela-Lopez et al. 2018).

2253

2254 *Colletotrichum hanaui* J.A. Crouch, B.B. Clarke, J.F. White and B.I. Hillman, *Mycologia* **101**: 728
2255 (2009)

2256

2257 The species *Colletotrichum hanaui* was defined to accommodate fungi isolated from *Digitaria ciliaris*
2258 and *D. sanguinalis* (Poaceae) in the USA and Japan in the 1940s and in 1975, respectively (Crouch
2259 et al. 2009a). Although there are no other species of *Colletotrichum* recorded on *Digitaria* spp., the

2260 lack of contemporary records of *C. hanau* raises serious concerns on the conservation status of this
2261 taxon.

2262

2263 *Colletotrichum hainanense* W. Zhang and X. L. Niu, *Plant Dis.* **104**:1744 (2020)

2264

2265 *Colletotrichum hainanense* was recently named to accommodate fungi causing anthracnose of
2266 *Axonopus compressus* (Poaceae) in China in 2015 (Zhang et al. 2020c). *Colletotrichum axonopodi* is
2267 also associated to anthracnose in this host, rendering the conservation status of *C. hainanense* of
2268 concern.

2269

2270

2271 *Colletotrichum jacksonii* J.A. Crouch, B.B. Clarke, J.F. White and B.I. Hillman, *Mycologia* **101**: 729
2272 (2009)

2273

2274 *Colletotrichum jacksonii* is known from *Echinochloa esculenta* (Poaceae) in Japan and *E. crus-galli*
2275 in the USA, recorded respectively in the 1977-1985 and in the 1912-1943 periods (Crouch et al.
2276 2009a). The lack of recent records, along with the identification of a different species (*C.*
2277 *echinochloae*) more recently in Japan, raises serious concerns on the conservation status of *C.*
2278 *jacksonii*.

2279

2280 *Colletotrichum miscanthi* J.A. Crouch, B.B. Clarke, J.F. White and B.I. Hillman, *Mycologia* **101**: 729
2281 (2009)

2282

2283 Originally defined based on an isolate obtained from *Miscanthus sinensis* (Poaceae) in Japan in 1972
2284 (Crouch et al. 2009a), the fungus was detected thereafter only once, as an endophyte on *Bletilla*
2285 *ochracea* (Orchidaceae) in China in 2006 (Tao et al. 2013). *Colletotrichum miscanthi* is thus a species
2286 of elusive pathological relevance and with its conservation status of high concern.

2287

2288 *Colletotrichum navitas* J.A. Crouch, *Mycol. Res.* **113**: 1417 (2009)

2289

2290 Crouch et al. (2009b) designated the species *Colletotrichum navitas* based on numerous isolates
2291 collected from the USA on *Panicum virgatum* (Poaceae) throughout the 20th century, as well as on *P.*
2292 *crus-galli*, *P. curtisii* and *P. hemitomon*. There are no records of the fungus outside of the USA,
2293 suggesting further surveys to ascertain the geographical distribution and current conservation status
2294 of *C. navitas*.

2295

2296 *Colletotrichum nicholsonii* J.A. Crouch, B.B. Clarke, J.F. White and B.I. Hillman, *Mycologia* **101**:
2297 730 (2009)

2298

2299 *Colletotrichum nicholsonii* is known from *Paspalum dilatatum* (Poaceae) from Japan, New Zealand
2300 and the USA, with isolates collected between 1965 and 1975 (Crouch et al. 2009a). Although
2301 *Paspalum dilatatum* is a cosmopolitan plant, no additional occurrences of *C. nicholsonii* have been
2302 recorded since 1975, indicating that the current existence of this species in nature must be scrutinised.

2303

2304 *Colletotrichum paspali* J.A. Crouch, B.B. Clarke, J.F. White and B.I. Hillman, *Mycologia* **101**: 730
2305 (2009)

2306

2307 *Colletotrichum paspali* is known only from two records, collected in the 1970s, on *Paspalum notatum*
2308 (Poaceae) in Japan (Crouch et al. 2009a). There are no other species of *Colletotrichum* recorded from
2309 *Paspalum notatum*, but *C. nicholsonii* has also been recorded from *Paspalum dilatatum* in Japan.
2310 Considering the absence of recent reports of *C. paspali*, its conservation status is of serious concern.

2311

2312 *Colletotrichum sublineola* Henn. ex Sacc. and Trotter, *Syll. Fung. (Abellini)* **22**: 1206 (1913)

2313

2314 *Colletotrichum sublineola* is the sorghum (*Sorghum* spp.) anthracnose pathogen (Crouch and
2315 Tomaso-Peterson 2012). Effective records are known from Africa, America and Korea
2316 (Supplementary data 10, panel D), but the disease is known from virtually the entire sorghum
2317 cultivation area (Crouch and Tomaso-Peterson 2012; Tsedaley et al. 2016; Xavier et al. 2018; Bunker
2318 et al. 2019; Choi et al. 2021). The fungus appears to be common, but a recent review on sorghum
2319 anthracnose is lacking.

2320

2321 **2.11 The magnum species complex**

2322

2323 The magnum complex is one of the most recently described species complexes (Damm et al. 2019).
2324 Sister clade of the orchidearum complex, the magnum species complex encompasses eight accepted
2325 species (Figure 13). Whereas almost all of them have been reported only once or in one host in one
2326 country, *Colletotrichum brevisporum* seems to be a quite common species as it has been associated
2327 with at least 20 plant species belonging to 18 genera (both monocots and eudicots) in Asia, Oceania
2328 and South America. Like for other uncommon or rare species, not much is available about the host
2329 spectrum, the specificity or the lifestyle of the other members of the complex.

2330

2331 **Figure 13**

2332

2333 *Colletotrichum brevisporum* Noireung, Phouliv., L. Cai and K.D. Hyde, *Cryptog. Mycol.* **33**: 350
2334 (2012)

2335

2336 *Colletotrichum brevisporum* is recorded from several hosts in tropical and sub-tropical regions
2337 throughout the world (Damm et al. 2019) (Supplementary data 11), including: *Annona* sp.
2338 (Annonaceae) in Brazil (Costa et al. 2019); *Anthurium* sp. (Araceae) in Thailand (Damm et al. 2019);
2339 *Capsicum annuum* (Solanaceae) in China and Trinidad and Tobago (Liu et al. 2016c; Damm et al.
2340 2019; Villafana et al. 2019) and *C. chinense* and *C. frutescens* in Brazil (Almeida et al. 2017; Oliveira
2341 et al. 2017; Silva et al. 2017b; Damm et al. 2019); *Carapichea ipecacuanha* (Rubiaceae) in Brazil
2342 (Ferreira et al. 2020); *Carica papaya* (Caricaceae) in Australia, Brazil and China (Vieira et al. 2013;
2343 Shivas et al. 2016; Duan et al. 2018a; Damm et al. 2019; Liu et al. 2019c); *Citrus medica* (Rutaceae)
2344 in China (Guarnaccia et al. 2017); *Coffea* sp. (Rubiaceae) in China (Cao et al. 2019a); *Colocasia*
2345 *esculenta* (Araceae) in Mexico (Vásquez-López et al. 2019); *Glycine max* (Fabaceae) in China (Shi
2346 et al. 2021); *Lycium chinense* (Solanaceae) in Korea (Damm et al. 2019); *Momordica cochinchinensis*
2347 (Cucurbitaceae) in Thailand (Chai et al. 2018); *Neoregelia* sp. (Bromeliaceae) in Thailand (Damm et
2348 al. 2019); *Pandanus pygmaeus* (Pandanaeae) in Thailand (Damm et al. 2019); *Passiflora edulis*
2349 (Passifloraceae) in Australia and China (Shivas et al. 2016; Du et al. 2017; Qiu et al. 2021); *Sechium*
2350 *edule* (Cucurbitaceae) in Brazil (Bezerra et al. 2016).

2351

2352 *Colletotrichum cacao* Damm, in *Stud. Mycol.* **92**: 1 (2019)

2353

2354 *Colletotrichum cacao* is known from a single isolate collected as an endophyte from *Theobroma*
2355 *cacao* in Costa Rica at an unknown date (Damm et al. 2019). Several other species of *Colletotrichum*
2356 are recorded on this host, raising great concern on the current ecological status of *C. cacao*.

2357

2358 *Colletotrichum liaoningense* Y.Z. Diao, C. Zhang, L. Cai and X.L. Liu, *Persoonia* **38**: 34 (2017)

2359

2360 *Colletotrichum liaoningense* occurs on chilli (*Capsicum* sp., Solanaceae) in China (Diao et al. 2017;
2361 Damm et al. 2019), but it was recently identified in China associated to anthracnose on mango
2362 (*Mangifera indica*, Anacardiaceae) (Li et al. 2019b) and on *Solanum pseudocapsicum* (Solanaceae;
2363 Liu et al. 2021a). Both chilli and mango harbour many species of *Colletotrichum*, rendering the
2364 conservation status of *C. liaoningense* of concern.

2365

2366 *Colletotrichum lobatum* Damm, *Stud. Mycol.* **92**: 1 (2019)

2367

2368 *Colletotrichum lobatum* is known from a single isolate obtained from *Piper marginatum* f.
2369 *catalpifolium* (as *Piper catalpifolium*, Piperaceae) in Trinidad and Tobago in an unknown date
2370 (Damm et al. 2019). There are no further occurrences of *C. lobatum* recorded and several other species
2371 of *Colletotrichum* are known from *Piper* spp., raising serious concern on the conservation status of
2372 this species.

2373

2374 *Colletotrichum magnum* (S.F. Jenkins and Winstead) Rossman and W.C. Allen, *IMA Fungus* **7**:1
2375 (2016)

2376

2377 Originally defined as a pathogen of watermelon (*Citrullus lanatus*, Cucurbitaceae) (Rossman et al.
2378 2016), *Colletotrichum magnum* is seldom reported: it was identified causing anthracnose on papaya
2379 (*Carica papaya*, Caricaceae) in Mexico in 2014 (Tapia-Tussell et al. 2016) and on *Lobelia chinensis*
2380 (Campanulaceae) in China in 2014 (Li et al. 2013). Further surveys will convey additional
2381 information about the pathological relevance and conservation status of *Colletotrichum magnum*.

2382

2383 *Colletotrichum merremiae* Damm, *Stud. Mycol.* **92**: 1 (2019)

2384

2385 The species *Colletotrichum merremiae* was described based on an isolate occurring as a leaf
2386 endophyte of *Merremia umbellata* (Convolvulaceae) in Panama in 2004 (Damm et al. 2019). There
2387 are no additional records for this fungus, indicating that the conservation status of *C. merremiae* is of
2388 serious concern.

2389

2390 *Colletotrichum okinawense* Damm and Toy. Sato, *Stud. Mycol.* **92**: 1 (2019)

2391

2392 *Colletotrichum okinawense* was described based on two isolates collected from papaya (*Carica*
2393 *papaya*) stems/petioles in Brazil and in Japan in 1892 and 2007 respectively (Damm et al. 2019).
2394 However, the fungus was subsequently re-identified in Brazil in 2018 associated to papaya fruit
2395 anthracnose (Dias et al. 2020). The scarcity of reports of *Colletotrichum okinawense* along with the
2396 large number of other species of *Colletotrichum* occurring on papaya renders the pathological
2397 relevance of this species uncertain and raises concern about its conservation status.

2398

2399 *Colletotrichum panamense* Damm, *Stud. Mycol.* **92**: 1 (2019)

2400

2401 *Colletotrichum panamense* is known from a single isolate, occurring as an epiphyte on *Merremia*
2402 *umbellata* (Convolvulaceae) in Panama in 2004 (Damm et al. 2019). There are no further records for
2403 this taxon and other species of *Colletotrichum* are known from this host, casting great concern on the
2404 conservation status of *C. panamense*.

2405

2406 **2.12 The orbiculare species complex**

2407

2408 Introduced by Cannon et al. (2012) as a small aggregate of only two species, the orbiculare species
2409 complex has been widely described by Damm et al. (2013) based on MLST and morphological
2410 characters. Analysis performed by the authors resulted in nine clades that confirmed four species
2411 previously known, *Colletotrichum lindemuthianum*, *C. malvarum*, *C. orbiculare* and *C. trifolii*, and
2412 recognised four new species from weeds, namely *C. bidentis*, *C. sidae*, *C. spinosum* and *C. tebeestii*.
2413 Most of them are known for their hemibiotrophic infection strategy and as destructive pathogens
2414 either of field crops or weeds (Figure 14). While initially the species included in the orbiculare
2415 complex were considered host specific, new reports suggest that most of them are rather specialised,
2416 but not exclusive, to a group of hosts. Overall members of this complex have been associated with 19
2417 host species belonging to 16 genera, with a vast majority of eudicot hosts and only one report on
2418 *Asparagus racemosus* (Asparagaceae, monocot). *Colletotrichum lindemuthianum* is a well-known
2419 bean pathogen and the most common species of the complex, followed by *C. orbiculare*, causal agent
2420 of anthracnose of Cucurbitaceae, and *C. trifolii*, a species pathogenic of alfalfa, red clover and
2421 mallow.

2422

2423 **Figure 14**

2424

2425 *Colletotrichum bidentis* Damm, Guatimosim and Vieira, *Fungal Divers.* **61**: 34 (2013)

2426

2427 There is a single record for *Colletotrichum bidentis*, isolated from *Bidens subalternans* (Asteraceae)
2428 in Brazil in 2010 (Damm et al. 2013). *Bidens* spp. are recorded from all over the world, often as
2429 invasive weeds, but the conservation status of *C. bidentis* is of concern.

2430

2431 *Colletotrichum lindemuthianum* (Sacc. and Magnus) Briosi and Cavara, *Funghi Parass. Piante Colt.*
2432 *od Utili*, Fasc. 2: no. 50 (1889)

2433

2434 The common bean (*Phaseolus vulgaris* and *P. coccineus*, Fabaceae) anthracnose pathogen,
2435 *Colletotrichum lindemuthianum*, is found all over the world (Supplementary data 12, panel A), and it
2436 develops a singular race-dependent interaction with the host (Liu et al. 2013b; Padder et al. 2017).

2437

2438 *Colletotrichum malvarum* (A. Braun and Casp.) SouthW., *J. Mycol.* **6**: 116 (1891)

2439

2440 Only two strains were considered as belonging to *Colletotrichum malvarum* by Damm et al. (2013),
2441 obtained from *Malva* sp. and *Lavatera trimestris* (Malvaceae) in Germany and UK respectively, with
2442 several other reports of anthracnose pathogens on Malvaceae either assigned to different species or
2443 requiring further investigation. No reports of *C. malvarum* have arose ever since, laying high concern
2444 over the conservation status of this species.

2445

2446 *Colletotrichum orbiculare* Damm, P.F. Cannon and Crous, *Fungal Divers.* **61**: 39 (2013)

2447

2448 *Colletotrichum orbiculare* was newly described by Damm et al. (2013) encompassing fungi occurring
2449 on (and as important pathogens of) the Cucurbitaceae *Cucumis melo*, *Cucurbita pepo* and *Lagenaria*
2450 spp. Recently the species was also recorded from other Cucurbitaceae such as *Benincasa hispida* in
2451 Australia (Shivas et al. 2016) and watermelon (*Citrullus lanatus*) in the USA (Rennberger et al. 2018)
2452 (Supplementary data 12, panel B).

2453

2454 *Colletotrichum sidae* Damm and P.F. Cannon, *Fungal Divers.* **61**: 44 (2013)

2455

2456 *Colletotrichum sidae* is known only from *Sida spinosa* (Malvaceae) in the USA only (Damm et al.
2457 2013). The scarcity of recent reports of *Colletotrichum sidae* raises concerns on its conservation
2458 status.

2459

2460 *Colletotrichum spinosum* Damm and P.F. Cannon, *Fungal Divers.* **61**: 46 (2013)

2461

2462 Damm et al. (2013) revised literature on the occurrence of *Colletotrichum spinosum*, revealing this
2463 fungus to be common in Australia and to occur also in Argentina on *Xanthium spinosum* (Asteraceae).
2464 However, there are no recent records of this fungus, while other species of *Colletotrichum* are
2465 reported from the host, suggesting further surveys to ascertain the conservation status of *C. spinosum*.

2466

2467 *Colletotrichum tebeestii* Damm and P.F. Cannon, *Fungal Divers.* **61**: 48 (2013)

2468

2469 *Colletotrichum tebeestii* was described based on a fungus isolated from *Malva pusilla* (Malvaceae)
2470 in Canada (Damm et al. 2013). Fungi from this species were developed as mycoherbicides, but there
2471 is a lack of current reports of this fungus, raising concern about the current conservation status of this
2472 species.

2473

2474 *Colletotrichum trifolii* Bain, *J. Mycol.* **12**: 193 (1906)

2475

2476 *Colletotrichum trifolii* is known from Fabaceae (*Medicago sativa* and *Trifolium pratense*) in the USA
2477 (Damm et al. 2013; Samac et al. 2014), but also from *Malva crispa* and *M. sylvestris* (Malvaceae) in
2478 China (Zhou et al. 2014; Liu et al. 2017c) and, as an endophyte, from *Viola odorata* (Violaceae) in
2479 India (Katoch et al. 2017). Future surveys may improve the knowledge on the host range and
2480 geographic distribution of *C. trifolii*.

2481

2482 **2.13 The orchidearum species complex**

2483

2484 The orchidearum complex is the last of the four most recently described species complexes (Damm
2485 et al. 2019; Bhunjun et al. 2021). Sister clade of the magnum complex, the orchidearum species
2486 complex encompasses eight accepted species (Figure 15). Unlike the other two closely related
2487 aggregates, most of the species encompassing this complex are quite common and polyphagous.
2488 Overall members of this complex have been associated with 35 plant species belonging to 31 genera
2489 (almost the same proportion between eudicots and monocots). Interestingly several species belonging
2490 to this clade (*Colletotrichum sojae*, *C. plurivorum* and *C. musicola*) have been reported to be serious
2491 problems of an important crop such as soybean (Rogério et al. 2020).

2492

2493 **Figure 15**

2494

2495 *Colletotrichum cattleyicola* Damm and Toy. Sato, *Stud. Mycol.* **92**: 1 (2019)

2496

2497 *Colletotrichum cattleyicola* is known from unspecified species of *Cattleya* (Orchidaceae; root and
2498 stem), collected in Belgium prior to 1949 and in Japan around 2000 (Damm et al. 2019). The
2499 pathological status of *Colletotrichum cattleyicola* is unknown and its conservation status is of
2500 concern, as several other species of *Colletotrichum* are recorded on orchids.

2501

2502 *Colletotrichum cliviicola* Damm and Crous, *Stud. Mycol.* **92**: 1 (2019)

2503

2504 *Colletotrichum cliviicola*, recently described in replacement of *C. cliviae* Yan L. Yang et al., includes
2505 isolates obtained from *Clivia* spp. (Amaryllidaceae) in China in 2008 and in South Africa in 2012
2506 (Damm et al. 2019), along with isolates obtained in China from *Pennisetum americanum* × *P.*
2507 *purpureum* (Poaceae) (Han et al. 2019) and *Mangifera indica* (Li et al. 2019b) (Supplementary data
2508 13, panel A).

2509

2510 *Colletotrichum musicola* Damm, *Stud. Mycol.* **92**: 1 (2019)

2511

2512 The species *Colletotrichum musicola* was defined based on an isolate collected from *Musa* sp.
2513 (Musaceae) in Mexico in 2008 (Damm et al. 2019). Subsequently the fungus was identified associated
2514 to leaf anthracnose of taro (*Colocasia esculenta*, Araceae) in 2017, also in Mexico (Vásquez-López
2515 et al. 2019). So far restricted to Mexico, the host range of *Colletotrichum musicola* remains to be
2516 elucidated, along with its pathological relevance and conservation status.

2517

2518 *Colletotrichum orchidearum* Allesch., *Rabenh. Krypt.-Fl.*, Edn 2 (Leipzig) **1**: 563 (1903)

2519

2520 Damm et al. (2019) provide a description of *Colletotrichum orchidearum* and placed *C.*
2521 *hymenocallidicola* and *C. aracearum* as its synonyms. As such, *C. orchidearum* is known from
2522 *Dendrobium nobile* and *Eria javanica* (Orchidaceae) in the Netherlands and Germany respectively,
2523 *Epipremnum aureum*, *Monstera deliciosa* and *Philodendron bipinnatifidum* (as *P. selloum*) (Araceae)
2524 in Iran and China respectively and *Hymenocallis* sp. (Amaryllidaceae) in Thailand (Ariyawansa et al.
2525 2015; Hou et al. 2016; Damm et al. 2019). Thus, the geographic distribution (Supplementary data 13,
2526 panel B) and host range of *C. orchidearum* requires further investigation in order to clarify its
2527 conservation status.

2528

2529 *Colletotrichum piperis* Petch, *Ann. R. bot. Gdns Peradeniya* **6**: 239 (1917)

2530

2531 Damm et al. (2019) listed four isolates under *Colletotrichum piperis*, collected from *Piper betle*, *P.*
2532 *nigrum* and *P. umbellatum* (Piperaceae) in China, Malaysia, Sri Lanka and Puerto Rico, all obtained
2533 at least over 70 years ago. Although scarce, other species of *Colletotrichum* have been recorded from
2534 *Piper*, raising serious concerns about the conservation status of *Colletotrichum piperis* and suggesting
2535 that it may no longer exist in nature.

2536

2537 *Colletotrichum plurivorum* Damm, Alizadeh and Toy. Sato, *Stud. Mycol.* **92**: 1 (2019)

2538

2539 *Colletotrichum plurivorum* was recently described by Damm et al. (2019) accommodating fungi
2540 previously belonging to *C. sichuanensis* but regarding *C. cliviicola* as a distinct species, contrary to
2541 the study by Douanla-Meli et al. (2018). Other recent works added further reports of *Colletotrichum*
2542 *plurivorum*, being this species currently known from: chilli (*Capsicum annuum*, Solanaceae) in China
2543 (as *Colletotrichum sichuanensis*; Liu et al. 2016c) and Thailand (De Silva et al. 2019); papaya (*Carica*
2544 *papaya*, Caricaceae) in China and Mexico (Sun et al. 2019b; García-Estrada et al. 2020); lemon
2545 (*Citrus limon*, Rutaceae) in Vietnam (Damm et al. 2019); coffee (*Coffea* sp., Rubiaceae) in Vietnam
2546 (Damm et al. 2019); soybean (*Glycine max*, Fabaceae) in Myanmar (Zaw et al. 2020); cotton
2547 (*Gossypium* sp., Malvaceae) in Brazil (Damm et al. 2019); cassava (*Manihot esculenta*,
2548 Euphorbiaceae) in Brazil (as *Colletotrichum sichuanensis*; Oliveira et al. 2020) and China (Liu et al.
2549 2019a); *Myrianthus arboreus* (Urticaceae) in Cameroon (Damm et al. 2019); lima bean (*Phaseolus*
2550 *lunatus*, Fabaceae) in Benin and Brazil (as *C. sichuanensis*) and common bean (*P. vulgaris*) in Iran
2551 (Cavalcante et al. 2018; Damm et al. 2019); *Pyrus bretschneideri* (Rosaceae) in China (Fu et al.
2552 2019); peace lily (*Spathiphyllum wallisii*, Araceae) in Iran (Damm et al. 2019). *Colletotrichum*
2553 *plurivorum* is thus a cosmopolitan and polyphagous fungus (Supplementary data 13, panel C), found
2554 on numerous agricultural crops. The numerous recent reports suggest that this fungus may be
2555 expanding and further occurrence notices are expected to arise in the near future.

2556
2557 *Colletotrichum sojae* Damm and Alizadeh, *Stud. Mycol.* **92**: 35 (2019)

2558
2559 Specimens identified as *Colletotrichum sojae* have been collected since 1980 up to present days from
2560 soybean (*Glycine max*, Fabaceae) in Iran, Italy, Serbia, and the USA, but also from other Fabaceae
2561 such as alfalfa (*Medicago sativa*) in the USA, common bean (*Phaseolus vulgaris*) in Iran and cowpea
2562 (*Vigna unguiculata*) also in Iran (Damm et al. 2019) (Supplementary data 13, panel D). Recently the
2563 fungus was reported from *Panax quinquefolium* (Araliaceae) in China (Guan et al. 2021). Additional
2564 surveys are likely to clarify the host range, pathological relevance and geographic distribution of
2565 *Colletotrichum sojae*.

2566
2567 *Colletotrichum vittalense* Damm, *Stud. Mycol.* **92**: 38 (2019)

2568
2569 *Colletotrichum vittalense* is a taxon of obscure existence. It is known from two isolates collected
2570 nearly one century ago, one from cacao (*Theobroma cacao*) in India and the other from an unspecified
2571 Orchidaceae plant from an unknown location (Damm et al. 2019). Several species of *Colletotrichum*
2572 are known from cacao and orchids. No other fungus clustering in *C. vittalense* have been documented
2573 in spite of extensive studies on both hosts, suggesting that this taxon may be extinct.

2574

2575 **2.14 The spaethianum species complex**

2576

2577 The spaethianum species complex was first described by Cannon et al. (2012) as an aggregate
2578 containing five species, four of which are associated with petaloid monocot plants, and none appears
2579 to have economic importance. The spaethianum is as a sister group to the graminicola complex. This
2580 complex was recognised as a distinct assemblage by Damm et al. (2009) in their work on
2581 *Colletotrichum* with curved conidia associated with non-grass species. Since it was firstly introduced,
2582 more species belonging to this group have been described, reaching nine accepted species (Figure
2583 16). Overall members of this group have been associated with 37 species belonging to 28 genera,
2584 mostly monocots (65%).

2585

2586 **Figure 16**

2587

2588 *Colletotrichum bletillae* G. Tao, Zuo Y. Liu and L. Cai, *Fungal Divers.* **61**: 144 (2013)

2589

2590 There is a single record for *Colletotrichum bletillae*, collected as an endophyte from *Bletilla ochracea*
2591 (Orchidaceae) in China in 2006 (Tao et al. 2013). The authors refer 17 different endophytic
2592 *Colletotrichum* species in the host species, thus rendering the conservation status *C. bletillae* of great
2593 concern.

2594

2595 *Colletotrichum guizhouense* G. Tao, Zuo Y. Liu and L. Cai, *Fungal Divers.* **61**: 152 (2013)

2596

2597 The species *Colletotrichum guizhouense* was designated to accommodate fungi occurring as
2598 endophytes of *Bletilla ochracea* (Orchidaceae) in China (Tao et al. 2013). Subsequently the fungus
2599 was identified as an endophyte on *Huperzia phlegmaria* (= *Phlegmariurus phlegmaria*,
2600 Lycopodiaceae) in China exhibiting pharmaceutical interest. There are numerous species of
2601 *Colletotrichum* occurring on *Bletilla* spp., rendering the conservation status of *C. guizhouense* of
2602 concern.

2603

2604 *Colletotrichum incanum* H.C. Yang, J.S. Haudenshield and G.L. Hartman, *Mycologia* **106**: 38 (2014)

2605

2606 The species *Colletotrichum incanum* was defined based on isolates obtained from diseased soybean
2607 (*Glycine max*) petioles in the USA (Yang et al. 2014) and subsequently reported from *Capsicum* sp.

2608 in China (Diao et al. 2017). The current pathological relevance, geographic distribution and
2609 conservation status of *C. incanum* require further investigation.

2610

2611 *Colletotrichum lilii* Plakidas ex Boerema and Hamers, *Neth.Jl Pl. Path.* **94**: 12 (1988)

2612

2613 *Colletotrichum lilii* is recurrently found associated to the black scale disease of *Lilium* (Liliaceae)
2614 bulbs. It has been reported from the USA, the Netherlands and Japan (Damm et al. 2009), and more
2615 recently from Russia (Nikitin et al. 2018). Although seldom reported, this pathogen seems to be
2616 present in different parts of the world. Nevertheless, the presence of other species of *Colletotrichum*
2617 in *Lilium* suggests further surveys to ascertain the conservation status of *C. lilii*.

2618

2619 *Colletotrichum liriopes* Damm, P.F. Cannon and Crous, *Fungal Divers.* **39**: 71 (2009)

2620

2621 The species *Colletotrichum liriopes* was defined based on fungi isolated from *Liriope muscari*
2622 (Asparagaceae) in Mexico (Damm et al. 2009) and subsequently enlarged with fungi obtained from
2623 the Orchidaceae *Eria coronaria*, *Bletilla ochracea* and *Pleione bulbocodioides* in China (Yang et al.
2624 2012b; Tao et al. 2013), the Asteraceae *Erigeron philadelphicus* and *Laphangium affine*
2625 (= *Gnaphalium affine*) in Japan (Sato et al. 2015), the Asparagaceae *Rohdea japonica* in Japan, Korea
2626 and the USA (Kwon and Kim 2013; Sato et al. 2015; Trigiano et al. 2018), *Ophiopogon japonicus* in
2627 China (Wang and Wang 2021) and *Liriope cymbidiomorpha* and *L. spicata* in China and *L. muscari*
2628 in Korea (Oo and Oh 2017b; Chen et al. 2019c; Yang et al. 2020), as well as from *Hemerocallis fulva*
2629 (Xanthorrhoeaceae) in China (Yang et al. 2012b), *Fagopyrum esculentum* (Polygonaceae) in China
2630 (Chen et al. 2021) and *Rumex acetosa* (Polygonaceae) in Japan (Sato et al. 2015). *Colletotrichum*
2631 *liriopes* is thus a fungus that has been recurrently reported in recent years, mostly from Asparagaceae
2632 and Orchidaceae in Asia (Supplementary data 14, panel A).

2633

2634 *Colletotrichum riograndense* D.M. Macedo, R.W. Barreto, O.L. Pereira and B.S. Weir, *Australasian*
2635 *Plant Pathol.* **45**: 49 (2016)

2636

2637 *Colletotrichum riograndense* is known from a single record obtained from *Tradescantia* viz.
2638 *fluminensis* (Commelinaceae) leaves in Brazil in 2008 (Macedo et al. 2016). Although there are no
2639 other species of *Colletotrichum* recorded from *Tradescantia*, the absence of additional records of *C.*
2640 *riograndense* raises severe concerns about its conservation status.

2641

2642 *Colletotrichum spaethianum* (Allesch.) Damm, P.F. Cannon and Crous, *Fungal Divers.* **39**: 74 (2009)

2643

2644 *Colletotrichum spaethianum* is known mostly from China, Korea and Japan, but it has been reported
2645 also from Brazil, Germany and India (Supplementary data 14, panel B), from several hosts: *Allium*
2646 *fistulosum* and *A. ledebourianum* (Amaryllidaceae) (Sato et al. 2015; Santana et al. 2016; Salunkhe
2647 et al. 2018a); *Anemarrhena asphodeloides* (Asparagaceae) (Okorley et al. 2019); *Atractylodes*
2648 *japonica* (Asteraceae) (Guan et al. 2018); *Convallaria keiskei* (Asparagaceae) (Ahn et al. 2017);
2649 *Crinum latifolium* (Amaryllidaceae) (Sato et al. 2015); *Dianthus chinensis* (Caryophyllaceae) (Sato
2650 et al. 2015); *Hemerocallis citrina*, *H. flava* and *H. fulva* (Xanthorrhoeaceae) (Yang et al. 2012b;
2651 Vieira et al. 2014); *Hosta plantaginea*, *H. sieboldiana* and *H. ventricosa* (Asparagaceae) (Damm et
2652 al. 2009; Sato et al. 2015; Cheon and Jeon 2016; Sun et al. 2020a); *Hymenocallis littoralis*
2653 (Amaryllidaceae) (Yang et al. 2012b); *Iris × germanica* (Iridaceae) (Sato et al. 2015); *Kniphofia*
2654 *northiae* (Xanthorrhoeaceae) (Sato et al. 2015); *Lilium* spp. (Liliaceae) (Damm et al. 2009; Zhao et
2655 al. 2016b); *Paris polyphylla* (Melanthiaceae) (Zhong et al. 2020); *Peucedanum praeruptorum*
2656 (Apiaceae) (Guo et al. 2013); *Phaseolus vulgaris* (Fabaceae) (Yang et al. 2019b); *Polygonatum*
2657 *cyrtonema*, *P. falcatum* and *P. odoratum* (Asparagaceae) (Sato et al. 2015; Liu et al. 2020b; Ma et al.
2658 2021). Reported mostly from Asparagales hosts, it is noteworthy that records of *Colletotrichum*
2659 *spaethianum* on eudicotyledons (*Dianthus*, *Peucedanum* and *Phaseolus*) have occurred recently.

2660

2661 *Colletotrichum tofieldiae* (Pat.) Damm, P.F. Cannon and Crous, *Fungal Divers.* **39**: 77 (2009)

2662

2663 *Colletotrichum tofieldiae* has been reported either as a pathogen, a saprobe or an endophyte, on
2664 several hosts and locations (Supplementary data 14, panel C): symptomless roots of *Arabidopsis*
2665 *thaliana* (Brassicaceae) in Spain (Hacquard et al. 2016); symptomless leaves of *Bletilla ochracea*
2666 (Orchidaceae) in China (Tao et al. 2013); *Dianthus* sp. (Caryophyllaceae) in the UK (Damm et al.
2667 2009); *Grevillea crithmifolia* (Proteaceae) in Australia (Shivas et al. 2016); *Iris × germanica*
2668 (Iridaceae) in Australia (Shivas et al. 2016); dead stem of *Lupinus polyphyllus* (Fabaceae) in Germany
2669 (Damm et al. 2009); *Ornithogalum umbellatum* (Asparagaceae) in Japan (Sato et al. 2015); dead
2670 leaves of *Tofieldia* sp. and *T. calyculata* (Tofieldiaceae) in China and Switzerland respectively
2671 (Damm et al. 2009). *Colletotrichum tofieldiae* is thus a fungus with varied life styles recorded from
2672 several hosts and locations, suggesting that further studies many shed additional light on its
2673 conservation status, geographical distribution and ecological relevance.

2674

2675 *Colletotrichum verruculosum* Damm, P.F. Cannon and Crous, *Fungal Divers.* **39**: 81 (2009)

2676

2677 *Colletotrichum verruculosum* is known from a single fungus, isolated in 1951 from *Crotalaria juncea*
2678 (Fabaceae) in Zimbabwe (Damm et al. 2009). Although there are no other species of *Colletotrichum*
2679 known from *Crotalaria*, the prolonged absence of additional records of this fungus raises serious
2680 concerns about its conservation status.

2681

2682 **2.15 The truncatum species complex**

2683

2684 Introduced by Cannon et al. (2012), the truncatum complex comprised only one common species,
2685 *Colletotrichum truncatum* (syn: *C. capsici*; Damm et al. 2009), which is reported as an economically
2686 destructive pathogen of many tropical crops including legumes such as soybean and solanaceous
2687 plants. As the taxonomy of this species complex has not been revised recently and besides the fact
2688 that this complex is quite small and encompasses four species (Figure 17), its taxonomy is still
2689 confused and challenging for the most. An example is provided by *C. corchorum-capsularis*, a
2690 pathogen of *Corchorus capsularis* in China (Niu et al. 2016b): as no accurate dried type specimen
2691 was listed, this species has not been recognised as a reliable species. Another example is provided by
2692 *Colletotrichum jasminigenum*: the *cal*, *gs*, *tub2* and ITS sequences for the type strain of this species
2693 place it in the truncatum complex (no differences to *C. truncatum*) but the *act* and *gapdh* sequences
2694 place it in the gloeosporioides complex, suggesting that this species (containing a single isolate) is an
2695 artifact and does not exist (as detailed in section 2.18). Overall members of this complex have been
2696 associated with 56 species belonging to 48 genera (23% monocots and 77% eudicots). Interestingly
2697 two different species of this clade have been reported as opportunistic human pathogens, *C. truncatum*
2698 and *C. fusiforme*.

2699

2700 **Figure 17**

2701

2702 *Colletotrichum acidae* Samarak. and K.D. Hyde, *Mycosphere* **9**: 587 (2018)

2703

2704 The single isolate belonging to *Colletotrichum acidae* was obtained from a dead rachis of *Phyllanthus*
2705 *acidus* (Phyllanthaceae) in Thailand in 2017 and treated as saprobe (Samarakoon et al. 2018),
2706 although there are no studies on putative pathogenicity to its host. The host plant, gooseberry tree, is
2707 widely cultivated as a fruit tree in the tropics. The abundance, pathological relevance and
2708 conservation status of this species remains to be investigated.

2709

2710 *Colletotrichum curcumae* (Syd. and P. Syd.) E.J. Butler and Bisby, *Fungi of India*: 153 (1931)

2711

2712 The species *Colletotrichum curcumae* was designated based on two isolates collected from *Curcuma*
2713 *longa* (Zingiberaceae) in India in 1912 and 1984 (Damm et al. 2009). More recently, in 2012, the
2714 fungus was identified as the causal agent of leaf spot symptoms on *Curcuma wenyujin* in China (Li
2715 et al. 2016d). There seems to be a biunivocal relationship between *Colletotrichum curcumae* and
2716 *Curcuma*.

2717

2718 *Colletotrichum fusiforme* Jayawardena, Bhat, Tangthirasunun and K.D. Hyde, *Fungal Divers.* **75**:
2719 158 (2015)

2720

2721 *Colletotrichum fusiforme* is known from a single isolate collected in Thailand in 2012 on a dead leaf
2722 of an unknown plant (Ariyawansa et al. 2015). Hung et al. (2020) reported fungi associated with
2723 human eye keratitis similar to *C. fusiforme*, treating these as genetics variants of *C. fusiforme* or
2724 putatively as new species. Under this scenario, the conservation status of *C. fusiforme* is of great
2725 concern.

2726

2727 *Colletotrichum truncatum* (Schwein.) Andrus and W.D. Moore, *Phytopathology* **25**: 121 (1935)

2728

2729 *Colletotrichum truncatum* is most noticed as causing anthracnose of economical relevance on
2730 Fabaceae and Solanaceae (Damm et al. 2009). In the past decade, the fungus was recorded from: the
2731 Amaranthaceae *Salsola komarovii* (Sato et al. 2015); the Amaryllidaceae *Allium angulosum* and *A.*
2732 *fistulosum* (Matos et al. 2017; Salunkhe et al. 2018b), *Hippeastrum × hybridum* (Sato et al. 2015) and
2733 *Hymenocallis* sp. (Hyde et al. 2018); the Apocynaceae *Mandevilla* sp. (Watanabe et al. 2016) and
2734 *Plumeria rubra* (Sato et al. 2015); the Araceae *Alocasia macrorrhizos* (Ben et al. 2020),
2735 *Dieffenbachia* sp. and *Syngonium* sp. (Sato et al. 2015); the Asparagaceae *Dracaena braunii* (Liu et
2736 al. 2019b), *Polianthes tuberosa* (Mahadevakumar et al. 2019) and *Sansevieria* sp. (Sato et al. 2015);
2737 the Asteraceae *Dendranthema grandiflorum* (Sato et al. 2015), *Helianthus annuus* and *Xanthium*
2738 *strumarium* (as *X. occidentale*) (Shivas et al. 2016); the Basellaceae *Basella alba* (Yang et al. 2018);
2739 the Begoniaceae *Begonia × semperflorens* (Zhai et al. 2018); the Brassicaceae *Brassica rapa* (as *B.*
2740 *parachinensis*) and *B. rapa* var. *chinensis* (Sato et al. 2015; He et al. 2016); the Cactaceae *Hylocereus*
2741 *undatus* (Guo et al. 2014b; Sato et al. 2015; Ngoc et al. 2018); the Caricaceae *Carica papaya* (Sato
2742 et al. 2015; Aktaruzzaman et al. 2018; Vieira et al. 2020); the Chenopodiaceae *Chenopodium quinoa*
2743 (Pal and Testen 2021); the Cucurbitaceae *Cucumis sativus* (Sato et al. 2015); the Euphorbiaceae
2744 *Euphorbia pulcherrima* (Sato et al. 2015), *Jatropha curcas* (Ellison et al. 2015) and *Manihot*
2745 *esculenta* (Hyde et al. 2018; Machado et al. 2021b); the Fabaceae *Arachis hypogaea* (Damm et al.
2746 2009; Shivas et al. 2016; Yu et al. 2020), *Cicer arietinum* (Mahmodi et al. 2013), *Glycine max* (Sato

2747 et al. 2015; Shivas et al. 2016; Rogério et al. 2019; Zaw et al. 2020), *Stylosanthes hamata* (Shivas et
2748 al. 2016; Hyde et al. 2018) and *Vigna subterranea* and *V. unguiculata* ssp. *sesquipedalis* (Sato et al.
2749 2015; Hyde et al. 2018); the Malvaceae *Abutilon theophrasti* (Cong et al. 2020) and *Gossypium* sp.
2750 (Hyde et al. 2018); the Oleaceae *Fraxinus excelsior* (Davydenko et al. 2013); the Passifloraceae
2751 *Passiflora edulis* (Sato et al. 2015; Chen and Huang 2018); the Piperaceae *Piper betle* (Sun et al.
2752 2020b); the Polygonaceae *Fagopyrum esculentum* (Sato et al. 2015); the Rosaceae *Fragaria* ×
2753 *ananassa* (Sato et al. 2015; Bi et al. 2017a) and *Prunus persica* (Grabke et al. 2014); the Rutaceae
2754 *Citrus flamea*, *C. limon* and *C. reticulata* (Huang et al. 2013; Cheng et al. 2014; Guarnaccia et al.
2755 2017); the Saururaceae *Houttuynia cordata* (Sato et al. 2015); the Solanaceae *Capsicum annuum* and
2756 *C. frutescens* (Damm et al. 2009; Sato et al. 2015; Liu et al. 2016c; Diao et al. 2017; De Silva et al.
2757 2017a; Tariq et al. 2017; Oo and Oh 2020) and *Solanum lycopersicum* and *S. melogena* (Diao et al.
2758 2014; Sato et al. 2015; Saini et al. 2017b; Hyde et al. 2018; Almaraz-Sánchez et al. 2019); the
2759 Theaceae *Camellia sinensis* (Wang et al. 2016); the Violaceae *Viola odorata* (Katoch et al. 2017);
2760 the Vitaceae *Vitis labruscana* × *V. vinifera* (Zhang et al. 2018c); human eye (Valenzuela-Lopez et al.
2761 2018). *Colletotrichum truncatum* is thus a polyphagous and cosmopolitan fungus, with the most part
2762 of recent records being reported from Asia (Supplementary data 15).

2763

2764 **2.16 Singleton species**

2765

2766 Another 14 species of *Colletotrichum* do not cluster with any other species or species complexes and
2767 are therefore considered as singleton species.

2768

2769 *Colletotrichum bambusicola* C.L. Hou & Q.T. Wang, *Mycologia* **113**: 450-458 (2021)

2770

2771 The species *Colletotrichum bambusicola* was described based on fungi identified as endophytes on
2772 seeds of the bamboos *Brachystachyum densiflorum*, *Phyllostachys aureosulcata*, *Ph. edulis* and *Ph.*
2773 *sulphurea* on several locations in China (Wang et al. 2021b). Considering the endophytic nature of
2774 these fungi and the large number of species of *Colletotrichum* on bamboos, the conservation status
2775 of this species should be under surveillance.

2776

2777 *Colletotrichum chlorophyti* S. Chandra and Tandon, *Curr. Sci.* **34**: 565 (1965)

2778

2779 *Colletotrichum chlorophyti* is known from *Chlorophytum* sp. (Asparagaceae) in India, *Stylosanthes*
2780 *hamata* (Fabaceae) in Australia (Damm et al. 2009), soybean (*Glycine max*; Fabaceae) in the USA
2781 (Yang et al. 2012a), *Moringa oleifera* (Moringaceae) and *Atractylodes lancea* (as *A. chinensis*,

2782 Asteraceae) in China (Cai et al. 2016b; Sun et al. 2019a). *Colletotrichum chlorophyti* was also
2783 recently identified from a human eye associated to keratomycosis (Paniz-Mondolfi et al. 2021).
2784 *Colletotrichum chlorophyti* is thus a polyphagous and pluricontinental fungus (Supplementary data
2785 16, panel A), but its ecological status and pathological relevance must be further clarified.

2786

2787 *Colletotrichum citrus-medicae* Qian Zhang, Yong Wang bis, Jayawardena & K.D. Hyde, in Hyde et
2788 al., *Fungal Divers.* **103**: 219-271 (2020)

2789

2790 *Colletotrichum citrus-medicae* was recently described based on isolates collected at a single location
2791 in China, associated to spots on *Citrus medica* leaves (Hyde et al. 2020c). The vast number of species
2792 of *Colletotrichum* occurring on citrus calls for attention concerning the conservation status of *C.*
2793 *citrus-medicae*.

2794

2795 *Colletotrichum coccodes* (Wallr.) S. Hughes, *Can. J. Bot.* **36**: 754 (1958)

2796

2797 Recorded from numerous hosts in diverse families, *C. coccodes* is most noticeable as a pathogen of
2798 *Solanum tuberosum* and *S. lycopersicum*, causing potato black dot and tomato anthracnose (Liu et al.
2799 2011). Recent notices from different regions indicate its widespread presence worldwide (Çakir et al.
2800 2019; Pérez-Mora et al. 2020) (Supplementary data 16, panel B).

2801

2802 *Colletotrichum guangxiense* C.L. Hou & Q.T. Wang, *Mycologia* **113**: 450-458 (2021)

2803

2804 The species *Colletotrichum guangxiense* was described based on fungi identified as endophytes on
2805 seeds of the bamboo *Phyllostachys edulis* in China (Wang et al. 2021b). Considering the endophytic
2806 nature of this fungus and the large number of species of *Colletotrichum* on bamboos, the conservation
2807 status of this species should be under surveillance.

2808

2809 *Colletotrichum hsienjenchang* I. Hino and Hidaka, *Bull. Miyazaki Coll. Agric. Forest.* **6**: 93-99 (1934)

2810

2811 This species is associated to bamboos (*Phyllostachys* spp., Poaceae) and recorded from Japan and
2812 China since 1934, with the most recent record dating from 2011 (Sato et al. 2012). The species is
2813 considered rare, although no other species of *Colletotrichum* are recorded from *Phyllostachys*,
2814 prompting further studies on these hosts to ascertain the current distribution and conservation status
2815 of *C. hsienjenchang*.

2816

2817 *Colletotrichum metake* Sacc., *Annls Mycol.* **6**: 557 (1908)

2818

2819 *Colletotrichum metake* was described as a fungus inhabiting an unspecified bamboo species in Italy
2820 in 1908 and is currently found on the Poaceae *Pleioblastus simonii* in Japan (Sato et al. 2012) and
2821 *Chimonobambusa quadrangularis* in China (Wang et al. 2021b). The species is considered rare (Sato
2822 et al. 2012) and further surveys are important to ascertain its conservation status in the future.

2823

2824 *Colletotrichum nigrum* Ellis and Halst., in Halsted, *New Jersey Agric. Coll. Exp. Sta. Bull.*: 297
2825 (1895)

2826

2827 *Colletotrichum nigrum* was described as a pathogen of chilli (*Capsicum annuum*, Solanaceae) and
2828 subsequently reported from chicory (*Cichorium intybus*, Asteraceae), strawberry (*Fragaria ×*
2829 *ananassa*, Rosaceae), sunflower (*Helianthus tuberosus*, Asteraceae), lentil (*Lens culinaris*, Fabaceae)
2830 and tomato (*Solanum lycopersicum*, Solanaceae) in different parts of the world (Rivera et al. 2016)
2831 (Supplementary data 16, panel C). Several other species of *Colletotrichum* have been identified as
2832 causal agents of anthracnose on each of these hosts (and no reports on chicory) in recent years,
2833 whereas recent reports of *C. nigrum* are quite seldom: it was reported associated to tomato
2834 anthracnose in the USA in 2013 (Rivera et al. 2016), to autumn sage (*Salvia greggii*, Lamiaceae) in
2835 Italy in 2015 (Guarnaccia et al. 2019) and to quinoa (*Chenopodium quinoa*, Chenopodiaceae) in the
2836 USA in 2019 (Pal and Testen 2021). The current pathological relevance of *Colletotrichum nigrum* is
2837 uncertain and its conservation status is of concern.

2838

2839 *Colletotrichum orchidophilum* Damm, P.F. Cannon and Crous, *Stud. Mycol.* **73**: 83 (2012)

2840

2841 *Colletotrichum orchidophilum* was described from fungi isolated from the Orchidaceae *×Ascocenda*
2842 sp. in the USA, *Cycnoches aureum* in Panama, *Dendrobium* sp. in Thailand and the USA and
2843 *Phalaenopsis* sp. in the UK (Damm et al. 2012a; Ma et al. 2018). Such seldom reports, along with
2844 the large number of species of *Colletotrichum* occurring on orchids, raise concern on the conservation
2845 status of *C. orchidophilum*.

2846

2847 *Colletotrichum pseudoacutatum* Damm, P.F Cannon and Crous, *Stud. Mycol.* **73**: 91 (2012)

2848

2849 The species *Colletotrichum pseudoacutatum* was described based on a single isolate, obtained from
2850 *Pinus radiata* (Pinaceae) in Chile in 1976 (Damm et al. 2012a). Recently the species was rediscovered
2851 associated to anthracnose of *Syzygium jambos* (Myrtaceae) in Brazil (Soares et al. 2017). In spite of

2852 the seldom records, this recent finding suggests that the species may be currently occurring in nature
2853 at least in South America, but further studies are needed to account for its pathological relevance,
2854 geographic distribution and conservation status.

2855

2856 *Colletotrichum pyrifoliae* M. Fu and G.P. Wang, *Persoonia* **42**: 25 (2019)

2857

2858 *Colletotrichum pyrifoliae* is known only from a single isolate collected from *Pyrus pyrifolia*
2859 (Rosaceae) in China in 2016 (Fu et al. 2019). The absence of additional records for this fungus and
2860 the large number of species of *Colletotrichum* known from *Pyrus* raise high concern on the
2861 conservation status of *C. pyrifoliae*.

2862

2863 *Colletotrichum rusci* Damm, P.F. Cannon and Crous, *Fungal Divers.* **39**: 72 (2009)

2864

2865 *Colletotrichum rusci* was described based on a single isolate obtained from an unspecified species of
2866 *Ruscus* (Asparagaceae) in Italy in 2002 (Damm et al. 2009). No other species of *Colletotrichum* have
2867 been reported from *Ruscus*. The absence of any further occurrences of *C. rusci* raises severe concerns
2868 about its conservation status.

2869

2870 *Colletotrichum sydowii* Damm, *Stud. Mycol.* **86**: 99 (2017)

2871

2872 *Colletotrichum sydowii* is known from a single isolate obtained from an unspecified species of
2873 *Sambucus* (Adoxaceae) in China in 2011 (Marín-Felix et al. 2017). The absence of any further records
2874 for this fungus and the occurrence of other species of *Colletotrichum* on *Sambucus* raises serious
2875 concerns on the conservation status of *C. sydowii*.

2876

2877 *Colletotrichum trichellum* (Fr.) Duke, *Trans. Br. Mycol. Soc.* **13**: 173 (1928)

2878

2879 *Colletotrichum trichellum* is a pathogen of ivy (*Hedera* spp., Araliaceae), reported from diverse parts
2880 of the world (Damm et al. 2009; Sato et al. 2015) (Supplementary data 16, panel D), although still
2881 lacking modern taxonomic treatment (Damm et al. 2009; Cannon et al. 2012). Recent records are
2882 scarce, suggesting that the conservation status of *C. trichellum* should be better monitored.

2883

2884 **2.17 Synonymised and doubtful species of *Colletotrichum***

2885

2886 From the 805 species of *Colletotrichum* recorded in Index Fungorum, the present work lists 257
2887 species, meaning that another 548 species are pending modern treatment or have been synonymised.
2888 Table 1 lists the species described since 2009 that are not in use as they have been subsequently
2889 synonymised.

2890

2891 **Table 1**

2892

2893 Additionally, the taxon *Colletotrichum japonicum* (Hemmi) Bedlan was named to accommodate a
2894 pathogen of *Berberis aquifolium* occurring in Japan (Bedlan 2012) and presumably also in Poland
2895 and Austria (Świdarska-Burek 2021), but no molecular data is provided, and the taxon is pending
2896 modern taxonomic treatment.

2897 Also, *Colletotrichum jasminigenum*, known from a single record obtained from *Jasminum sambac*
2898 (Oleaceae) in Vietnam in 2009 (Wikee et al. 2011) and placed in the truncatum complex, was
2899 described based on ITS, *tub2*, *cal* and *gs* sequences (HM131513, HM153770, HM131494 and
2900 HM131504 GenBank references, respectively) that are similar to those of *C. truncatum*, whereas the
2901 *act* and *gapdh* sequences (HM131508 and HM131499, respectively) are similar to those of *C.*
2902 *pandanicola* (gloeosporioides complex), suggesting that *C. jasminigenum* is an artifact and that it
2903 should not be recognised as a species.

2904 Similarly, *Colletotrichum chiangraiense* reported once, from a *Dendrobium* sp. (Orchidaceae) root
2905 in Thailand in 2013 (Ma et al. 2018), along with other *Colletotrichum* species and placed by the
2906 authors in the boninense complex, is considered as an artifact, since the ITS sequence of the type
2907 strain (MF448522) places this taxon in the boninense complex, whereas the *act* (MH376383) and
2908 *tub2* (MH351275) sequences place it in the gigasporum complex.

2909

2910 **2.18 Geographical distribution of *Colletotrichum* occurrences**

2911

2912 In this work we documented 2717 occurrences of *Colletotrichum*, with 25.6% of the records in China,
2913 followed by Brazil (9.4%), Australia (8.5%) and the USA (8.1%), and then by Italy, Japan, and New
2914 Zealand (4-5% each), followed by Thailand, India and the Netherlands. By continent, Asia represents
2915 42.1% of the occurrences, followed by America (25.0%), Europe (15.6%), Oceania (12.9%) and
2916 Africa (3.6%). However, species of *Colletotrichum* are distributed differently, for example, *C.*
2917 *acutatum*, *C. simmondsii* and *C. queenslandicum* preferentially occur in Australia and *C. aotearoa* in
2918 New Zealand; *C. kahawae* is restricted to Africa; *C. abscissum*, *C. chrysophilum*, *C. fructivorum*, *C.*
2919 *tamarilloi*, *C. theobromicola* and *C. tropicale* occur mostly in America; *C. godetiae* (and to a certain
2920 extent, *C. fioriniae* and *C. nymphaeae*) occur more frequently in Europe (Table 2).

2921

2922 **Table 2**

2923

2924 3. HOST SPECIFICITY

2925

2926 *Colletotrichum* occurs mostly on dicotyledonous plants (over 77% of all host-fungus species
2927 association records), but monocotyledonous hosts are the most common in the clade grouping the
2928 caudatum, graminicola and spaethianum species complexes. *Colletotrichum* also occurs, although
2929 less frequently, on gymnosperms, ferns, mosses and animals.

2930 In this work we have recorded 1358 unique host species-*Colletotrichum* species association records
2931 from 720 hosts (Supplementary data 1, 'occurrences' tab). Two members of the gloeosporioides
2932 complex, such as *Colletotrichum siamense* and *C. gloeosporioides* are the species with the largest
2933 number of host species (Table 3), inhabiting hosts from very diverse botanical families. On the other
2934 hand, several species consistently present a high degree of host specificity. These include: in the
2935 acutatum complex, *Colletotrichum abscissum* on *Citrus sinensis*, *Colletotrichum laticiphilum* on
2936 *Hevea brasiliensis*, *C. lupini* on *Lupinus* spp., *C. phormii* on *Phormium* spp. and *C. tamarilloi* on
2937 *Solanum betaceum*; in the agaves complex, *C. agaves* on *Agave* spp. and *C. sansevieriae* on
2938 *Sansevieria trifasciata*; in the boninense complex, *C. petchii* on *Dracaena* spp.; in the destructivum
2939 complex, *C. lentis* on *Lens culinaris*, *C. ocimi* on *Ocimum basilicum* and *C. pisicola* on *Pisum*
2940 *sativum*; in the dracaenophilum complex, *C. dracaenophilum* on *Dracaena* spp.; in the
2941 gloeosporioides complex, *C. alatae* on *Dioscorea alata*, *C. arenicola* on *Areca catechu*, *C. camelliae*
2942 on *Camellia* spp., *Colletotrichum horii* on *Diospyros kaki*, *C. kahawae* on *Coffea arabica*,
2943 *Colletotrichum musae* on *Musa* spp. and *C. perseae* on *Persea americana*; in the graminicola
2944 complex, *C. eremochloae* on *Eremochloa ophiuroides*, *C. falcatum* on *Saccharum officinarum*, *C.*
2945 *graminicola* on *Zea mays* and *C. sublineola* on *Sorghum* spp.; in the orbiculare complex, *C.*
2946 *lindemuthianum* on *Phaseolus* spp.; *Colletotrichum trichellum* (singleton species) on *Hedera* spp.
2947 Many other examples are pending further records to confirm the host specificity of such fungi.
2948 Whereas some *Colletotrichum* species are specific of a given host species (e.g., *C. tamarilloi* or *C.*
2949 *laticiphilum*), others are specific of the host genus (e.g., *C. lupini* or *C. camelliae*) and others are
2950 specific at the family level, such as: in the acutatum complex, *C. carthami* and *C. chrysanthemi* on
2951 the Asteraceae; in the boninense complex, *C. cymbidiicola* on the Orchidaceae; in the graminicola
2952 complex, *C. cereale* on the Poaceae; in the orbiculare complex, *C. orbiculare* on the Cucurbitaceae;
2953 in the orchidearum complex, *C. sojae* on the Fabaceae; *C. orchidophilum* (singleton species) on the
2954 Orchidaceae.

2955

2956 **Table 3**

2957

2958 The gloeosporioides complex encompasses 516 *Colletotrichum* species-host species association
2959 records, followed by the acutatum and the boninense complexes (Table 4). The acutatum,
2960 gloeosporioides and truncatum complexes have, on average, over seven host species for each species
2961 of *Colletotrichum*, whereas the agaves, caudatum, dracaenophilum and graminicola have on average
2962 between one and two host species for each species of *Colletotrichum*. It is worth noting that most of
2963 the later complexes contain species more frequently found on monocots.

2964

2965 **Table 4**

2966

2967 The Fabaceae is the family with the largest number of species hosting *Colletotrichum* (51 host
2968 species), followed by the Poaceae (42 hosts), and then by the Orchidaceae, Asparagaceae and
2969 Rosaceae (Table 5). Nevertheless, it is in the Rosaceae that the highest number of *Colletotrichum*
2970 species-host species association records is found (118), followed by the Fabaceae (87), Solanaceae
2971 (72), Rutaceae (63) and Orchidaceae (59). The Fabaceae stand out also as the family hosting the
2972 highest number of species complexes (11), followed by the Solanaceae (10) and the Asteraceae and
2973 Orchidaceae (9 each).

2974

2975 **Table 5**

2976

2977 The Rosaceae and the Solanaceae host 41 species of *Colletotrichum* each, followed by the
2978 Orchidaceae and the Fabaceae (36 species), and then by the Poaceae and Rutaceae (Table 6). There
2979 are 880 unique association records between *Colletotrichum* species and host family, with the
2980 gloeosporioides complex representing 36.8% of such association records, followed by the acutatum
2981 complex (20.9%) and by the boninense complex (9.7%), and then by the destructivum, truncatum,
2982 spaethianum, orchidearum and dematium complexes (3-5% each). Whereas for most host families
2983 these proportions remain valid (e.g, the Anacardiaceae, Ericaceae, Lauraceae, Malvaceae, Moraceae,
2984 Myrtaceae, Oleaceae, Proteaceae, Rosaceae, Rubiaceae, Rutaceae, Solanaceae, Theaceae and
2985 Vitaceae, i.e., mostly dicots, but also the Arecaceae and Musaceae), some other families clearly have
2986 different patterns of preference concerning species complexes. The destructivum complex registers
2987 the highest number of unique species-host family association records in the Fabaceae, Asteraceae and
2988 Lamiaceae, instead of the gloeosporioides complex, whereas the destructivum and dematium
2989 complexes are the most represented in the Apiaceae. In the Euphorbiaceae, the acutatum complex is
2990 more represented than the gloeosporioides one. The situation is more heterogeneous among the

2991 monocots: the graminicola complex (followed by the caudatum complex) prevails in the Poaceae; the
2992 boninense complex is the most common in the Orchidaceae, and along with gloeosporioides in the
2993 Amaryllidaceae and with orchidearum in the Araceae; the agaves complex (along with
2994 gloeosporioides and spaethianum) is the most represented in the Asparagaceae. Although supported
2995 on limited numbers, the acutatum and boninense complexes are more frequent on the gymnosperms
2996 than the gloeosporioides complex.

2997

2998 **Table 6**

2999

3000 4. ABUNDANCE AND CONSERVATION OF *COLLETOTRICHUM* SPP.

3001 *Colletotrichum* occur on a large number of host and locations, with new host and locations frequently
3002 reported. Over the last decade, *Colletotrichum* became consolidated as the second most referred genus
3003 in terms of number of Plant Disease Notes published in the journal Plant Disease, raising from an
3004 average of 17.7 Notes per year during 2010-2015 to 48 Notes per year during 2016-2020, second only
3005 to *Fusarium* (Figure 18).

3006

3007 **Figure 18**

3008

3009 As discussed in the previous sections, several species of *Colletotrichum* occur on multiple hosts and
3010 in diverse locations, whereas others are host specific and/or geographically confined, but still are
3011 common on those hosts and/or regions. Being mostly plant pathogens, some of these fungi cause
3012 losses of economical relevance on agricultural crops, thus requiring control. Other species however
3013 are uncommon or even rare, and may incur in conservation problems. From the 257 species of
3014 *Colletotrichum* listed in this work, 101 (i.e., 39.3% of all species) have been recorded only once and
3015 another 44 have been recorded only twice, meaning that only 44.0% of the 257 species recognised
3016 have been recorded three times or more. In fact, the 10% more common species represent 67.2% of
3017 all occurrences.

3018 Many of these unfrequent species have been recorded recently and it is therefore plausible that
3019 additional occurrences arise in the future. Until then, however, such species must be regarded as
3020 potentially endangered. The number of occurrences and year of description of recent but unfrequent
3021 species are presented in Table 7. For instance, *Colletotrichum yunnanense* was described in 2007
3022 based on one occurrence but never recorded again and *C. fructivorum*, although recorded nine times,
3023 was never again documented besides its original description in 2013.

3024

3025 **Table 7**

3026

3027 In this work we have considered 88 species as common, meaning that the remaining 169 species are
3028 of seldom occurrence. Among these, we have considered 42 species as threatened, either because they
3029 have not been recorded inspite of recurrent surveys or because they are rare and have been described
3030 in circumstances that inpair conducting additional surveys. The list of the 42 species considered as
3031 threatened is presented in Table 8, arranged by species complexes and containing information related
3032 to each species.

3033

3034 **Table 8**

3035

3036 Another 127 species are treated as ‘data deficient’ (Table 9) and further surveys are needed to
3037 ascertain their conservation status, host range and geographic distribution, including unfrequent
3038 species that have been recently described along with others not recorded for decades but from hosts
3039 not commonly surveyed.

3040

3041 **Table 9**

3042

3043 Altogether, from the 257 species of *Colletotrichum*, 127 are classified as ‘data deficient’ and 42 as
3044 ‘threatened’, meaning that 169 species (65.8% of total) are not known to be firmly established in
3045 nature. The remaining 88 species are considered ‘common’ and generally occur on multiple hosts or
3046 in single hosts but in multiple locations. The relative proportion of these three categories varies
3047 according to the species complex, with threatened species representing a large fraction of the species
3048 in the orchidearum and gigasporum complexes, and common species more frequently found in the
3049 gloeosporioides, spaethianum, acutatum, orchidearum and destructivum complexes (Figure 19).

3050

3051 **Figure 19**

3052

3053 Under the current knowledge 130 *Colletotrichum* species are known only from a single country and
3054 can therefore considered as endemisms. By country, these are:

3055 -Australia – *C. brisbanense* and *C. cairnsense* (acutatum complex), *C. alcornii* (caudatum complex),
3056 *C. tanaceti* (destructivum complex) and *C. australianum*, *C. cobbittiense* and *C. xanthorrhoeae*
3057 (gloeosporioides complex);

3058 -Brazil – *C. paranaense* (acutatum complex), *C. brasiliense* (boninense complex), *C. serranegrense*
3059 (gigasporum complex), *C. bidentis* (orbiculare complex) and *C. riograndense* (spaethianum
3060 complex);

- 3061 -Canada – *C. tebeestii* (orbiculare complex);
- 3062 -Chile – *C. arboricola* and *C. roseum* (acutatum complex);
- 3063 -China – *C. eriobotryae* and *C. miaoliense* (acutatum complex), *C. chongqingense* (boninense
3064 complex), *C. caudisporum*, *C. duyunense* and *C. ochraceae* (caudatum complex), *C. hemerocallidis*
3065 and *C. jinshuiense* (dematium complex), *C. atractylodicola* and *C. neorubicola* (destructivum
3066 complex), *C. excelsum-altitudinum*, *C. tongrenense* and *C. yunnanense* (dracaenophilum complex),
3067 *C. jishouense* and *C. pseudomajus* (gigasporum complex), *C. arecicola*, *C. changpingense*, *C.*
3068 *conoides*, *C. cycadis*, *C. hebeiense*, *C. henanense*, *C. pseudotheobromicola*, *C. tainanense*, *C.*
3069 *wuxiense*, *C. xishuangbannaense* and *C. yulongense* (gloeosporioides complex), *C. endophytum* and
3070 *C. hainanense* (graminicola complex), *C. liaoningense* (magnum complex), *C. bletillae* and *C.*
3071 *guizhouense* (spaethianum complex) and *C. citrus-medicae*, *C. bambusicola*, *C. guangxiense*, *C.*
3072 *sydowii* and *C. pyrifoliae* (singleton species);
- 3073 -Colombia – *C. annellatum* and *C. colombiense* (boninense complex);
- 3074 -Costa Rica – *C. costaricense* (acutatum complex), *C. radialis* (gigasporum complex) and *C. cacao*
3075 (magnum complex);
- 3076 -Dominica – *C. cuscutae* (acutatum complex);
- 3077 -Germany – *C. oncidii* (boninense complex) and *C. coelogyne* (dracaenophilum complex);
- 3078 -Greece – *C. helleniense* (gloeosporioides complex);
- 3079 -India – *C. guajavae* (acutatum complex) and *C. vittalense* (orchidearum);
- 3080 -Indonesia – *C. indonesiense* and *C. javanense* (acutatum complex) and *C. makassarensis*
3081 (gloeosporioides complex);
- 3082 -Italy – *C. lauri* (acutatum complex), *C. sambucicola* and *C. sonchicola* (dematium complex), *C.*
3083 *orchidis* (destructivum complex), *C. grevilleae*, *C. hedericola*, *C. hystericis* and *C. psidii*
3084 (gloeosporioides complex) and *C. rusci* (singleton species);
- 3085 -Japan – *C. camelliae-japonicae* (boninense complex), *C. zoysiae* (caudatum complex), *C. shisoii*
3086 (destructivum complex) and *C. echinocloae* and *C. paspali* (graminicola complex);
- 3087 -Korea – *C. kakiivorum* (dematium complex);
- 3088 -Netherlands – *C. cosmi* (acutatum complex), *C. anthrisci* (dematium complex) and *C. utrechtense*
3089 (destructivum complex);
- 3090 -New Zealand – *C. acerbum* and *C. johnstonii* (acutatum complex), *C. beeveri*, *C. constrictum*, *C.*
3091 *dacrycarpi*, *C. novae-zelandiae* and *C. torulosum* (boninense complex), *C. antirrhinicola* (dematium
3092 complex) and *C. ti* (gloeosporioides complex);
- 3093 -Nigeria – *C. vignae* (destructivum complex);
- 3094 -Panama – *C. merremiae* and *C. panamense* (magnum complex);
- 3095 -Portugal – *C. feijoicola* (boninense complex);

- 3096 -Russia – *C. eryngiicola*, *C. insertae*, *C. menispermi*, *C. parthenocissicola*, *C. quinquefoliae* and *C.*
3097 *sedi* (dematium complex);
- 3098 -Saint Lucia – *C. paxtonii* (acutatum complex);
- 3099 -South Africa – *C. euphorbiae*, *C. ledebouriae* and *C. neosansevieriae* (agaves complex), *C.*
3100 *pleopeltidis* (destructivum complex) and *C. proteae* (gloeosporioides complex);
- 3101 -Thailand – *C. doitungense* (boninense complex), *C. cariniferi* and *C. parallelophorum*
3102 (dracaenophilum complex), *C. artocarpicola*, *C. Chiangmaiense*, *C. dracaenigenum* and *C.*
3103 *pandanicola* (gloeosporioides complex) and *C. acidae* (truncatum complex);
- 3104 -Trinidad and Tobago – *C. lobatum* (magnum complex);
- 3105 -UK – *C. kniphofiae* (acutatum complex);
- 3106 -USA – *C. baltimoreense*, *C. caudatum* and *C. somersetense* (caudatum complex), *C. fructi* (dematium
3107 complex), *C. rhexiae* and *C. temperatum* (gloeosporioides complex), *C. navitas* (graminicola
3108 complex) and *C. sidae* (orbiculare complex);
- 3109 -Vietnam – *C. walleri* (acutatum complex), *C. condaoense* (boninense complex) and *C. vietnamense*
3110 (gigasporum complex);
- 3111 -Zimbabwe – *C. verruculosum* (spaethianum complex).

3112

3113 5. CONCLUSIONS, IMPLICATIONS AND FUTURE PERSPECTIVES

3114

3115 In this work we have listed 257 species of *Colletotrichum*, clustering in 16 species complexes (some
3116 species are not assigned to any complex). Species complexes in *Colletotrichum* (as well as in other
3117 genera that have also experienced a recent rapid increase in the number of species recognised) gained
3118 high practical relevance but, anachronistically, they lack formal definition. For instance, when
3119 referring to *C. abscissum*, authors frequently use expressions such as “*Colletotrichum abscissum* of
3120 the acutatum complex”, which is a complicated and unfriendly designation. In the future, and as the
3121 phylogeny of *Colletotrichum* progresses to a mature and stable condition, species complexes may
3122 gain formal taxonomic value and become infra-generic taxa.

3123 In this work we have also highlighted difficulties and challenges regarding species delimitation and
3124 identification. Two species have been rejected as they turned out to be defined based on chimeric
3125 sequences that, once concatenated, suggested these to be novel taxa, but individually, were identical
3126 to those of previously described species. When describing new species it is fundamental that the
3127 sequence of each gene is compared to sequences of the type strains of existing species and not just
3128 the concatenated sequence of diverse genes. The employment of multiple loci in taxonomy is highly
3129 recommended (e.g., Lücking et al. 2020; Aime et al. 2021) but the examples provided here emphasise
3130 the relevance of analysing each locus individually. Chimeric multiloci sequences are quite perverse,

3131 as they affect the tree topology and, when applied, the time calibration. Depositing fungal cultures in
3132 living collections (but also providing accurate information on their substrates and collection location
3133 in nature) is fundamental for current and future understanding of these fungi (as detailed by Aime et
3134 al. 2021). It is expected that fungal whole genome sequencing (WGS) will soon become easier and
3135 cheaper, and this will allow most research laboratories to start in-house WGS projects on a daily
3136 basis. Providing genome data for type strains will soon become good practice that should be
3137 implemented when describing new species. The use of WGS will support the identification and the
3138 description of new species by:

- 3139 • extended MLST approaches such as phylogenomic analyses;
- 3140 • quantification of genetic interchange between taxonomic groups; this will also help resolve
3141 the situation of chimeric strains or hybrids (e.g. by analysing genomic portion or loci into
3142 different datasets established by congruent tree topologies;
- 3143 • time estimation of genetic isolation;
- 3144 • the identification of the genetic factors involved in important biological processes such as
3145 those linked with the speciation process.

3146 Nevertheless, strains from new species should also be characterised considering their life styles, with
3147 pathogenicity/host range/substrate usage studies being highly recommended to be included along the
3148 description of novel species.

3149 In this work we have considered a total of 2711 occurrence reports of *Colletotrichum* strains that
3150 could be confidently traced to species under current taxonomic criteria. When revising literatures
3151 from the last 10 years we were particularly careful in scrutinising the use of multilocus analyses
3152 (when necessary) for identification by comparison to sequences from the type strains of the candidate
3153 species. In several circumstances we did not considered identification reports that were based on
3154 single gene information (when more than one gene was required to identify a given species) nor those
3155 based only on BLAST identification. BLAST searches are adequate for preliminary identification of
3156 candidate target species, but then the sequence(s) of the strain to be identified should be compared to
3157 the sequences of the type strains of the several species that are phylogenetically close to the candidate
3158 target species identified in the BLAST search. A recent analysis showed that ca. 30% of ITS
3159 sequences available in nucleotide sequence databases are associated to a wrong fungal taxon
3160 (Hofstetter et al. 2019) and this holds true in the *Colletotrichum* genus (Bouffleur et al. 2021). Here
3161 (Supplemental Data 1) we present the most recent table listing species of *Colletotrichum* and the
3162 respective GenBank references for ITS, *gapdh*, *chs-1*, *act* and *tub2* sequences. Ensuring that
3163 identification of strains is performed scrupulously is fundamental for a stable and meaningful
3164 utilisation of species in *Colletotrichum*, both from taxonomical and plant pathology perspectives.

3165 Whereas conservation status of animal and plant species are of major concern, fungi have deserved
3166 much less attention, and still mostly focused on macrofungi and lichens. The IUCN Red List of
3167 Threatened species (www.iucnredlist.org) lists the conservation status of 343 fungal species (as
3168 compared to ca. 43500 plant and 76500 animal species), including 62 Ascomycota among which only
3169 seven Sordariomycetes, none of which from the Glomerellales. Microfungi, and plant pathogens in
3170 particular, are notoriously absent from such lists. The IUCN Red List system is recognised as the
3171 most authoritative for the evaluation of biological conservation and criteria have been adapted to use
3172 in fungi (Dahlberg and Mueller 2011) and Conservation Mycology has been recently recognised as a
3173 discipline within Conservation Biology (May et al. 2018), but macrofungi take most of the attention
3174 and plant pathology was clearly excluded from fungal conservation (Dahlberg et al. 2010), as fungal
3175 plant pathogens fail to meet the criteria according to which fungi can be readily integrated into
3176 conservation (Heilmann-Clausen et al. 2014). The conservation of microfungi, with emphasis on
3177 those that are not directly observable because of their endophytic or otherwise latent nature, has been
3178 subject of attention recently (Blackwell and Vega 2018). Metagenomics analyses of fungal
3179 communities in given ecosystems can provide the means to obtain abundant occurrence data
3180 (Blackwell and Vega 2018), but current approaches, based on DNA barcode genes of large
3181 phylogenetic spectrum (Hibbett et al. 2016), do not enable the discrimination of several species of
3182 *Colletotrichum*, for which specific markers are needed. In other words, under current delimitation,
3183 species of *Colletotrichum* are not directly identifiable in nature nor can be identified based on broad
3184 (i.e. ITS-based) metagenomics approaches. Ascertaining whether a species of *Colletotrichum* is
3185 threatened thus faces additional problems to those raised by Blackwell and Vega (2018). In this work
3186 we have opted to use informal classifications of the conservation status of *Colletotrichum* species as
3187 the employment of criteria as defined by Dahlberg and Mueller (2011) is not possible for most
3188 species. Recently Aime et al. (2021) provided updated guidelines on “How to publish a new fungal
3189 species or name”, among which stand the recommendation to “include multiple collections of
3190 specimens or cultured isolates when describing a new species”, in sharp contrast with the fact that
3191 145 of the currently recognised species of *Colletotrichum* (i.e., 56.4% of the 257 species) have been
3192 recorded no more than two times from nature. Conservation is structurally based on the concept of
3193 species, but the threshold for the classification of fungal species has varied strongly over the last
3194 decades, with the history of *Colletotrichum* taxonomy being paradigmatic of this. Conservation of
3195 *Colletotrichum* species is thus critically dependent on a stable taxonomic framework. Species denoted
3196 as “data deficient” in this work may in fact turn out to be common and even of pathological relevance,
3197 but further monitoring is needed, joining efforts between Conservation Mycology and Plant
3198 Pathology, an area in which the generalisation of WGS approaches may provide a decisive help. The
3199 present study, providing a comprehensive review of accepted species of *Colletotrichum* and their

3200 clustering into complexes, along with the compilation of occurrence data, provides a basis for
3201 subsequent studies linking taxonomy and conservation of *Colletotrichum* species and on the role of
3202 these fungi as plant pathogens of major agricultural crops worldwide.

3203

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3205

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5253

5254 Figure legends

5255

5256 **Figure 1.** Phylogeny of *Colletotrichum* species and complexes. Maximum-Likelihood Tree obtained by FastTree2
5257 v2.1.10 (Price et al. 2010) reconstructed from *act*, *chs-1*, *gapdh*, *ITS* and *tub2* sequence alignment of 253 reference isolates
5258 including the outgroup. The alignment was performed with MAFFT v7.450 (Katoh and Standley 2013), exported to
5259 MEGA7 (Kumar et al. 2016) and the best-fit substitution model calculated. The Markov chain Monte Carlo (MCMC)
5260 algorithm was performed to generate phylogenetic trees with Bayesian posterior probabilities for the alignment. Four
5261 MCMC chains were run simultaneously for random trees for 5,000,000 generations and sampled every 500 generations.
5262 The first 25% of trees were discarded as burn-in phase of each analysis and posterior probabilities were determined from
5263 the remaining trees. Bayesian posterior probability (obtained with MrBayes 3.2.6; Ronquist et al. 2012) and FastTree
5264 support values above 0.50/50 are reported next of the node; thicker branches represent node with BPP = 1.00 and ML =
5265 100. The scale bar represents the number of expected substitutions per site. The tree is rooted with *Monilochaetes*
5266 *infuscans*. GenBank accession numbers are listed in Supplementary file 1. Information of each species such as host range,
5267 number of reported occurrences (O), number of reported host species, O/HS ratio, level of endanger and complexes are
5268 reported on the right.

5269

5270 **Figure 2.** Number of *Colletotrichum* species and infra-specific taxa recorded in Index Fungorum according to the year
5271 of publication since 1831 by decade (panel A) and since 2000 by year (panel B).

5272

5273 **Figure 3.** Bayesian inference phylogenetic tree of the acutatum species complex and closely related singleton species.
5274 The tree was reconstructed from a combined multi-locus sequence alignment (*ITS*, *gapdh*, *chs-1*, *his3*, *act* and *tub2*). For
5275 each locus the alignment was performed with MAFFT v7.450 (Katoh and Standley 2013), exported to MEGA7 (Kumar
5276 et al. 2016) and the best-fit substitution model calculated. Phylogenetic analyses were performed with FastTree2 v2.1.10
5277 (Price et al. 2010) and MrBayes 3.2.6 (Ronquist et al. 2012). Bayesian posterior probability (BPP) and Maximum-
5278 Likelihood (ML) bootstrap values (above 0.50) are reported next to the node. The scale bar represents the number of
5279 expected substitutions per site. GenBank accession numbers are listed in Supplementary file 1.

5280

5281 **Figure 4.** Bayesian inference phylogenetic tree of the agaves species complex. The tree was reconstructed from a
5282 combined multi-locus sequence alignment (*ITS*, *gapdh*, *his3*, *act* and *tub2*). For each locus the alignment was
5283 performed with MAFFT v7.450 (Katoh and Standley 2013), exported to MEGA7 (Kumar et al. 2016) and the best-fit
5284 substitution model calculated. Phylogenetic analyses were performed with FastTree2 v2.1.10 (Price et al. 2010) and
5285 MrBayes 3.2.6 (Ronquist et al. 2012). Bayesian posterior probability (BPP) and Maximum-Likelihood (ML) bootstrap
5286 values (above 0.50) are reported next to the node. The scale bar represents the number of expected substitutions per site.
5287 GenBank accession numbers are listed in Supplementary file 1.

5288

5289 **Figure 5.** Bayesian inference phylogenetic tree of the boninense species complex. The tree was reconstructed from a
5290 combined multi-locus sequence alignment (*ITS*, *gapdh*, *chs-1*, *his3*, *act*, *cal* and *tub2*). For each locus the alignment was
5291 performed with MAFFT v7.450 (Katoh and Standley 2013), exported to MEGA7 (Kumar et al. 2016) and the best-fit
5292 substitution model calculated. Phylogenetic analyses were performed with FastTree2 v2.1.10 (Price et al. 2010) and
5293 MrBayes 3.2.6 (Ronquist et al. 2012). Bayesian posterior probability (BPP) and Maximum-Likelihood (ML) bootstrap

5294 values (above 0.50) are reported next to the node. The scale bar represents the number of expected substitutions per site.
5295 GenBank accession numbers are listed in Supplementary file 1.

5296

5297 **Figure 6.** Bayesian inference phylogenetic tree of the caudatum species complex. The tree was reconstructed from a
5298 combined multi-locus sequence alignment (ITS, *tub2*, *apn2* and *sod2*). For each locus the alignment was performed with
5299 MAFFT v7.450 (Katoh and Standley 2013), exported to MEGA7 (Kumar et al. 2016) and the best-fit substitution model
5300 calculated. Phylogenetic analyses were performed with FastTree2 v2.1.10 (Price et al. 2010) and MrBayes 3.2.6 (Ronquist
5301 et al. 2012). Bayesian posterior probability (BPP) and Maximum-Likelihood (ML) bootstrap values (above 0.50) are
5302 reported next to the node. The scale bar represents the number of expected substitutions per site. GenBank accession
5303 numbers are listed in Supplementary file 1.

5304

5305 **Figure 7.** Bayesian inference phylogenetic tree of the dematium species complex. The tree was reconstructed from a
5306 combined multi-locus sequence alignment (ITS, *gapdh*, *chs-1*, *his3*, *act* and *tub2*). For each locus the alignment was
5307 performed with MAFFT v7.450 (Katoh and Standley 2013), exported to MEGA7 (Kumar et al. 2016) and the best-fit
5308 substitution model calculated. Phylogenetic analyses were performed with FastTree2 v2.1.10 (Price et al. 2010) and
5309 MrBayes 3.2.6 (Ronquist et al. 2012). Bayesian posterior probability (BPP) and Maximum-Likelihood (ML) bootstrap
5310 values (above 0.50) are reported next to the node. The scale bar represents the number of expected substitutions per site.
5311 GenBank accession numbers are listed in Supplementary file 1.

5312

5313 **Figure 8.** Bayesian inference phylogenetic tree of the destructivum species complex. The tree was reconstructed from a
5314 combined multi-locus sequence alignment (ITS, *gapdh*, *chs-1*, *his3*, *act* and *tub2*). For each locus the alignment was
5315 performed with MAFFT v7.450 (Katoh and Standley 2013), exported to MEGA7 (Kumar et al. 2016) and the best-fit
5316 substitution model calculated. Phylogenetic analyses were performed with FastTree2 v2.1.10 (Price et al. 2010) and
5317 MrBayes 3.2.6 (Ronquist et al. 2012). Bayesian posterior probability (BPP) and Maximum-Likelihood (ML) bootstrap
5318 values (above 0.50) are reported next to the node. The scale bar represents the number of expected substitutions per site.
5319 GenBank accession numbers are listed in Supplementary file 1.

5320

5321 **Figure 9.** Bayesian inference phylogenetic tree of the dracaenophilum species complex. The tree was reconstructed from
5322 a combined multi-locus sequence alignment (ITS, *gapdh*, *chs-1*, *his3*, *act* and *tub2*). For each locus the alignment was
5323 performed with MAFFT v7.450 (Katoh and Standley 2013), exported to MEGA7 (Kumar et al. 2016) and the best-fit
5324 substitution model calculated. Phylogenetic analyses were performed with FastTree2 v2.1.10 (Price et al. 2010) and
5325 MrBayes 3.2.6 (Ronquist et al. 2012). Bayesian posterior probability (BPP) and Maximum-Likelihood (ML) bootstrap
5326 values (above 0.50) are reported next to the node. The scale bar represents the number of expected substitutions per site.
5327 GenBank accession numbers are listed in Supplementary file 1.

5328

5329 **Figure 10.** Bayesian inference phylogenetic tree of the gigasporum species complex. The tree was reconstructed from a
5330 combined multi-locus sequence alignment (ITS, *gapdh*, *chs-1*, *his3*, *act*, *tub2* and *gs*). For each locus the alignment was
5331 performed with MAFFT v7.450 (Katoh and Standley 2013), exported to MEGA7 (Kumar et al. 2016) and the best-fit
5332 substitution model calculated. Phylogenetic analyses were performed with FastTree2 v2.1.10 (Price et al. 2010) and
5333 MrBayes 3.2.6 (Ronquist et al. 2012). Bayesian posterior probability (BPP) and Maximum-Likelihood (ML) bootstrap

5334 values (above 0.50) are reported next to the node. The scale bar represents the number of expected substitutions per site.
5335 GenBank accession numbers are listed in Supplementary file 1.

5336

5337 **Figure 11.** Bayesian inference phylogenetic tree of the gloeosporioides species complex and closely related singleton
5338 species. The tree was reconstructed from a combined multi-locus sequence alignment (ITS, *gapdh*, *chs-1*, *act*, *tub2*, *cal*,
5339 *gs*, *sod2* and *ApMat*). For each locus the alignment was performed with MAFFT v7.450 (Katoh and Standley 2013),
5340 exported to MEGA7 (Kumar et al. 2016) and the best-fit substitution model calculated. Phylogenetic analyses were
5341 performed with FastTree2 v2.1.10 (Price et al. 2010) and MrBayes 3.2.6 (Ronquist et al. 2012). Bayesian posterior
5342 probability (BPP) and Maximum-Likelihood (ML) bootstrap values (above 0.50) are reported next to the node. The scale
5343 bar represents the number of expected substitutions per site. GenBank accession numbers are listed in Supplementary file
5344 1.

5345

5346 **Figure 12.** Bayesian inference phylogenetic tree of the graminicola species complex and closely related singleton species.
5347 The tree was reconstructed from a combined multi-locus sequence alignment (ITS, *chs-1*, *act*, *tub2*, *sod2* and *apn2*). For
5348 each locus the alignment was performed with MAFFT v7.450 (Katoh and Standley 2013), exported to MEGA7 (Kumar
5349 et al. 2016) and the best-fit substitution model calculated. Phylogenetic analyses were performed with FastTree2 v2.1.10
5350 (Price et al. 2010) and MrBayes 3.2.6 (Ronquist et al. 2012). Bayesian posterior probability (BPP) and Maximum-
5351 Likelihood (ML) bootstrap values (above 0.50) are reported next to the node. The scale bar represents the number of
5352 expected substitutions per site. GenBank accession numbers are listed in Supplementary file 1.

5353

5354 **Figure 13.** Bayesian inference phylogenetic tree of the magnum species complex. The tree was reconstructed from a
5355 combined multi-locus sequence alignment (ITS, *gapdh*, *chs-1*, *his3*, *act* and *tub2*). For each locus the alignment was
5356 performed with MAFFT v7.450 (Katoh and Standley 2013), exported to MEGA7 (Kumar et al. 2016) and the best-fit
5357 substitution model calculated. Phylogenetic analyses were performed with FastTree2 v2.1.10 (Price et al. 2010) and
5358 MrBayes 3.2.6 (Ronquist et al. 2012). Bayesian posterior probability (BPP) and Maximum-Likelihood (ML) bootstrap
5359 values (above 0.50) are reported next to the node. The scale bar represents the number of expected substitutions per site.
5360 GenBank accession numbers are listed in Supplementary file 1.

5361

5362 **Figure 14.** Bayesian inference phylogenetic tree of the orbiculare species complex. The tree was reconstructed from a
5363 combined multi-locus sequence alignment (ITS, *gapdh*, *chs-1*, *his3*, *act*, *tub2* and *gs*). For each locus the alignment was
5364 performed with MAFFT v7.450 (Katoh and Standley 2013), exported to MEGA7 (Kumar et al. 2016) and the best-fit
5365 substitution model calculated. Phylogenetic analyses were performed with FastTree2 v2.1.10 (Price et al. 2010) and
5366 MrBayes 3.2.6 (Ronquist et al. 2012). Bayesian posterior probability (BPP) and Maximum-Likelihood (ML) bootstrap
5367 values (above 0.50) are reported next to the node. The scale bar represents the number of expected substitutions per site.
5368 GenBank accession numbers are listed in Supplementary file 1.

5369

5370 **Figure 15.** Bayesian inference phylogenetic tree of the orchidearum species complex. The tree was reconstructed from a
5371 combined multi-locus sequence alignment (ITS, *gapdh*, *chs-1*, *his3*, *act* and *tub2*). For each locus the alignment was
5372 performed with MAFFT v7.450 (Katoh and Standley 2013), exported to MEGA7 (Kumar et al. 2016) and the best-fit
5373 substitution model calculated. Phylogenetic analyses were performed with FastTree2 v2.1.10 (Price et al. 2010) and
5374 MrBayes 3.2.6 (Ronquist et al. 2012). Bayesian posterior probability (BPP) and Maximum-Likelihood (ML) bootstrap

5375 values (above 0.50) are reported next to the node. The scale bar represents the number of expected substitutions per site.
5376 GenBank accession numbers are listed in Supplementary file 1.

5377

5378 **Figure 16.** Bayesian inference phylogenetic tree of the *spaethianum* species complex. The tree was reconstructed from a
5379 combined multi-locus sequence alignment (ITS, *gapdh*, *chs-1*, *his3*, *act* and *tub2*). For each locus the alignment was
5380 performed with MAFFT v7.450 (Katoh and Standley 2013), exported to MEGA7 (Kumar et al. 2016) and the best-fit
5381 substitution model calculated. Phylogenetic analyses were performed with FastTree2 v2.1.10 (Price et al. 2010) and
5382 MrBayes 3.2.6 (Ronquist et al. 2012). Bayesian posterior probability (BPP) and Maximum-Likelihood (ML) bootstrap
5383 values (above 0.50) are reported next to the node. The scale bar represents the number of expected substitutions per site.
5384 GenBank accession numbers are listed in Supplementary file 1.

5385

5386 **Figure 17.** Bayesian inference phylogenetic tree of the *truncatum* species complex. The tree was reconstructed from a
5387 combined multi-locus sequence alignment (ITS, *gapdh*, *chs-1*, *act* and *tub2*). For each locus the alignment was performed
5388 with MAFFT v7.450 (Katoh and Standley 2013), exported to MEGA7 (Kumar et al. 2016) and the best-fit substitution
5389 model calculated. Phylogenetic analyses were performed with FastTree2 v2.1.10 (Price et al. 2010) and MrBayes 3.2.6
5390 (Ronquist et al. 2012). Bayesian posterior probability (BPP) and Maximum-Likelihood (ML) bootstrap values (above
5391 0.50) are reported next to the node; thicker branches represent node with BPP = 1.00 and ML = 100. The scale bar
5392 represents the number of expected substitutions per site. GenBank accession numbers are listed in Supplementary file 1.

5393

5394 **Figure 18.** Number of Plant Disease Notes published in the journal Plant Disease (section “Diseases Caused by Fungi
5395 and Fungus-Like Organisms”) for the five most reported genera, by year of publication.

5396

5397 **Figure 19.** Relative and absolute frequency of the number of *Colletotrichum* species considered “common”, “data
5398 deficient” and “threatened” in each species complex.

5399

5400 Table legends

5401

5402 **Table 1.** Species of *Colletotrichum* described since 2009 that have been subsequently synonymised

5403

5404 **Table 2.** Number of occurrences of *Colletotrichum* spp. (for species with 30 or more records in this work) per continent;
5405 heatmaps (green – low; red – high) depict the relative frequency of occurrence of each species per continent

5406

5407 **Table 3.** The ten species of *Colletotrichum* with the larger number of host species (follows *C. godetiae*, *C. spaethianum*,
5408 *C. cigarro*, *C. aenigma*, *C. boninense* and *C. simmondsii*)

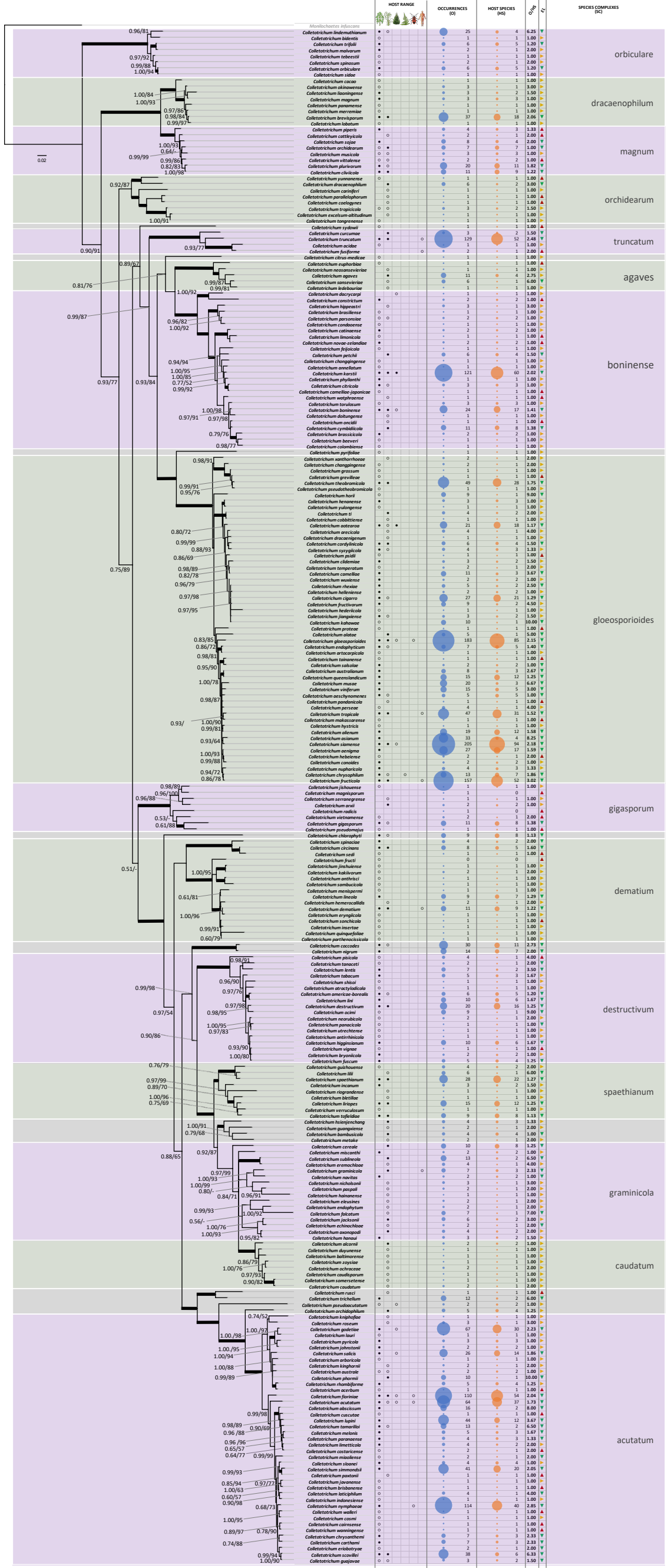
5409

5410 **Table 4.** Number of *Colletotrichum* species-host species association records by complex

5411

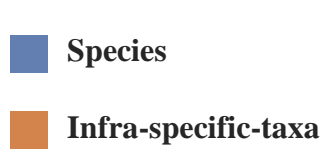
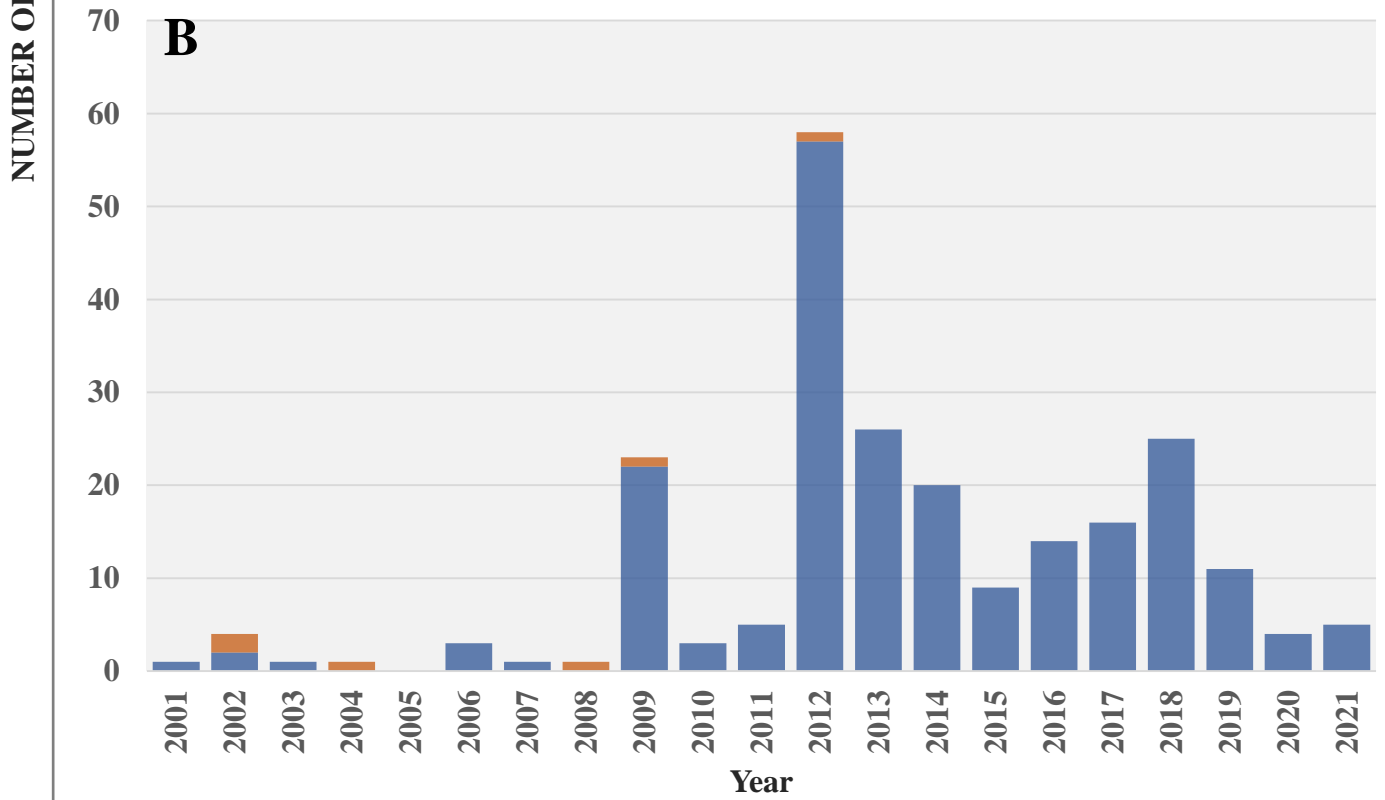
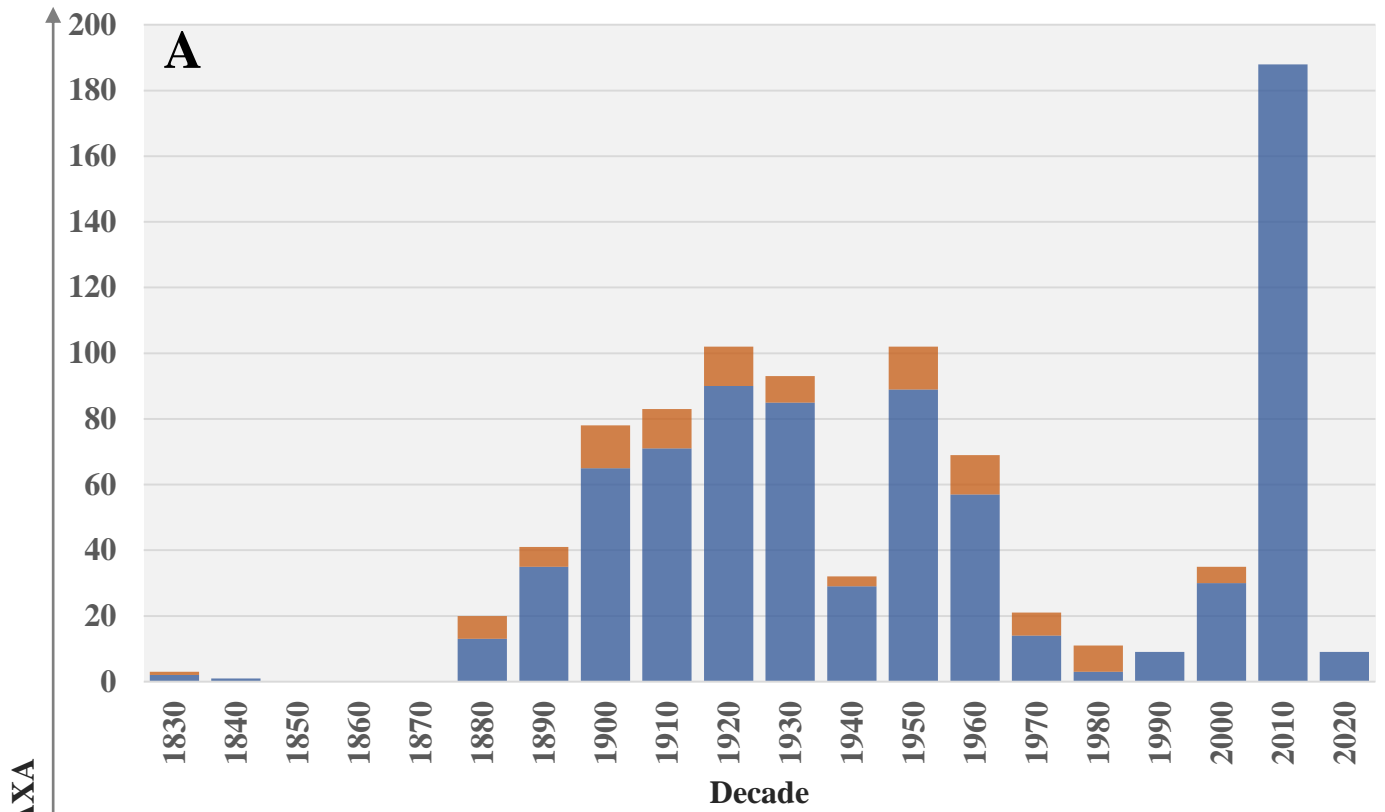
5412 **Table 5.** Number of host species, of fungus-host association records and number of *Colletotrichum* species and species
5413 complexes by host family [**footnote legend:** only families inhabited by 10 or more species of *Colletotrichum* are listed;
5414 the Araceae (11 host species and 18 fungus-host association records), the Cucurbitaceae (nine host species and 16 fungus-
5415 host association records) and the Annonaceae (five host species and 15 fungus-host association records) follow.]

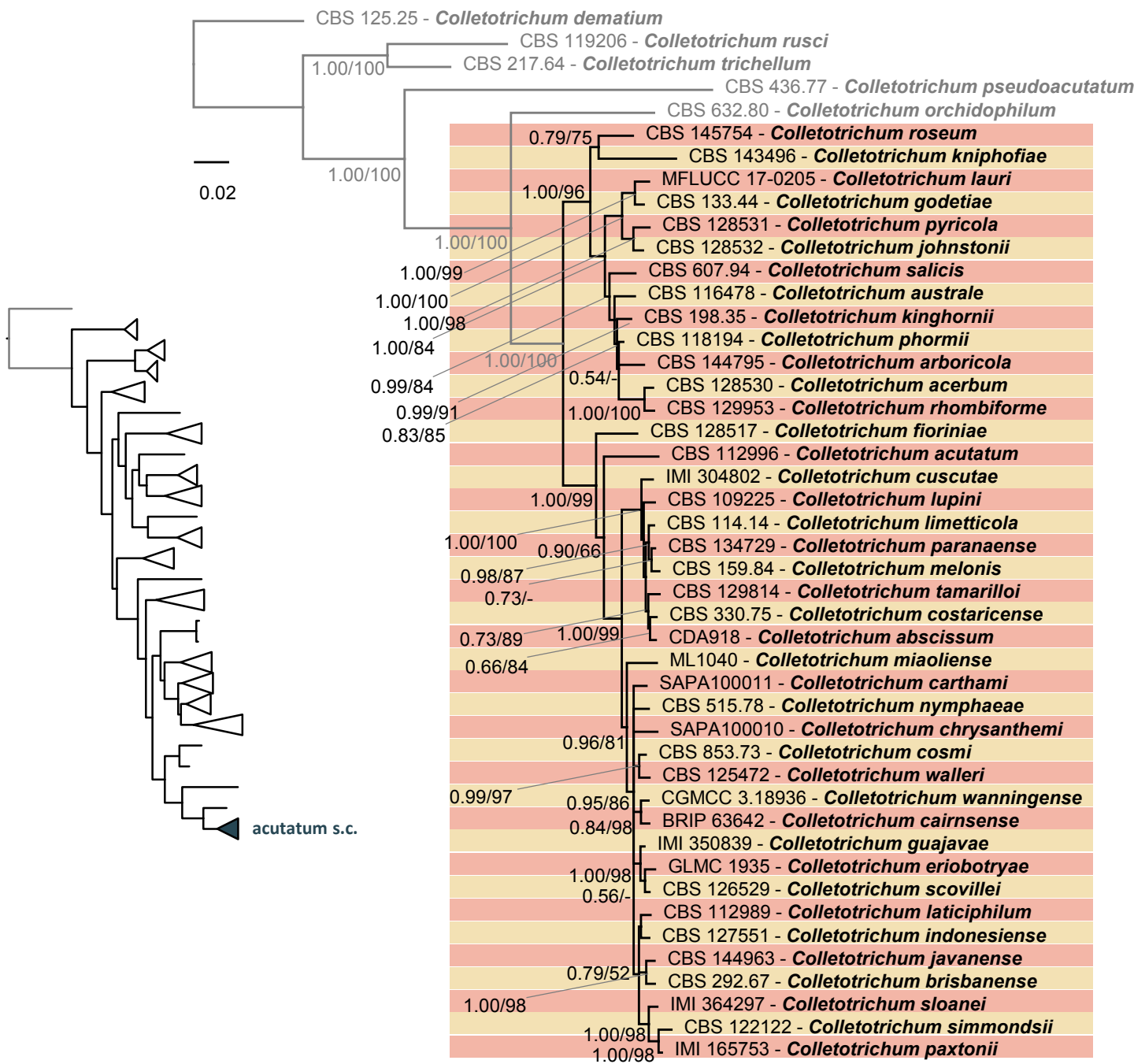
- 5416
- 5417 **Table 6.** Number of unique association records between *Colletotrichum* species and host families per species complex
- 5418 and for the most represented families
- 5419
- 5420 **Table 7.** Number of species of *Colletotrichum* recently described but seldomly reported, according to year of publication
- 5421 of the taxon and to the number of occurrences recorded in this work
- 5422
- 5423 **Table 8.** List of 42 species of *Colletotrichum* considered as threatened
- 5424
- 5425 **Table 9.** List of 127 species of *Colletotrichum* treated as ‘data deficient’

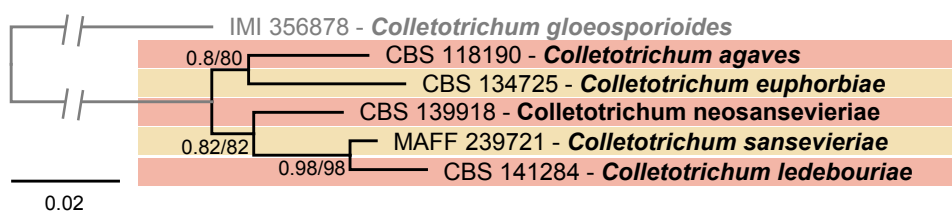
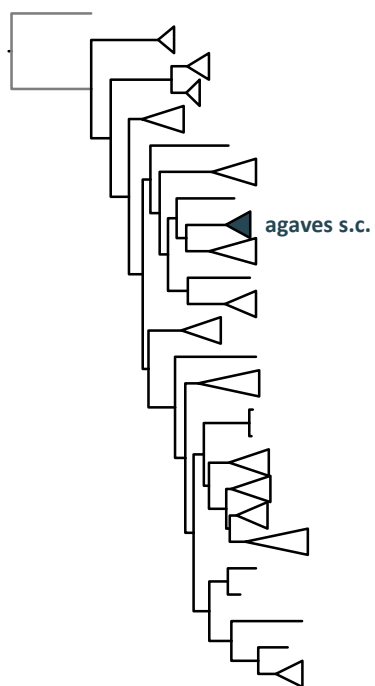


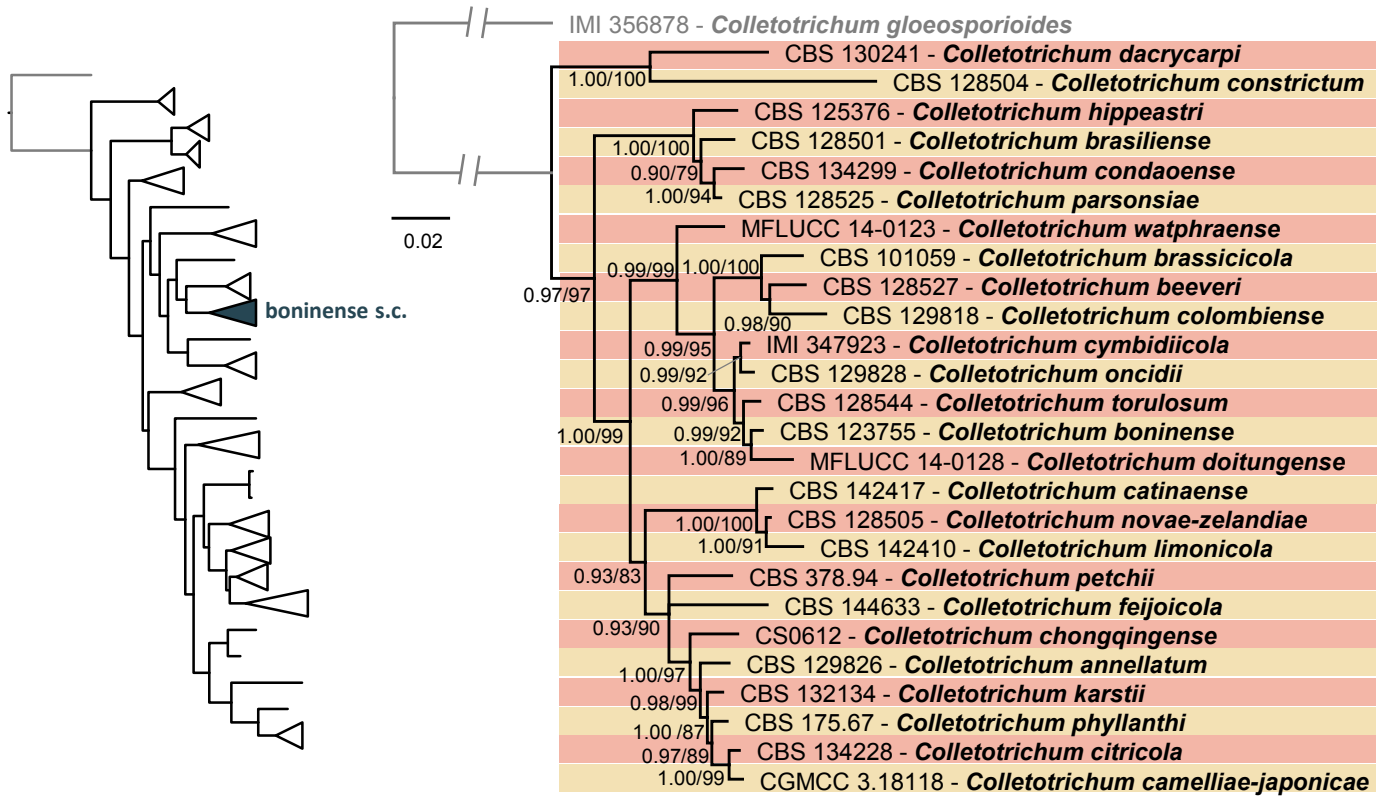
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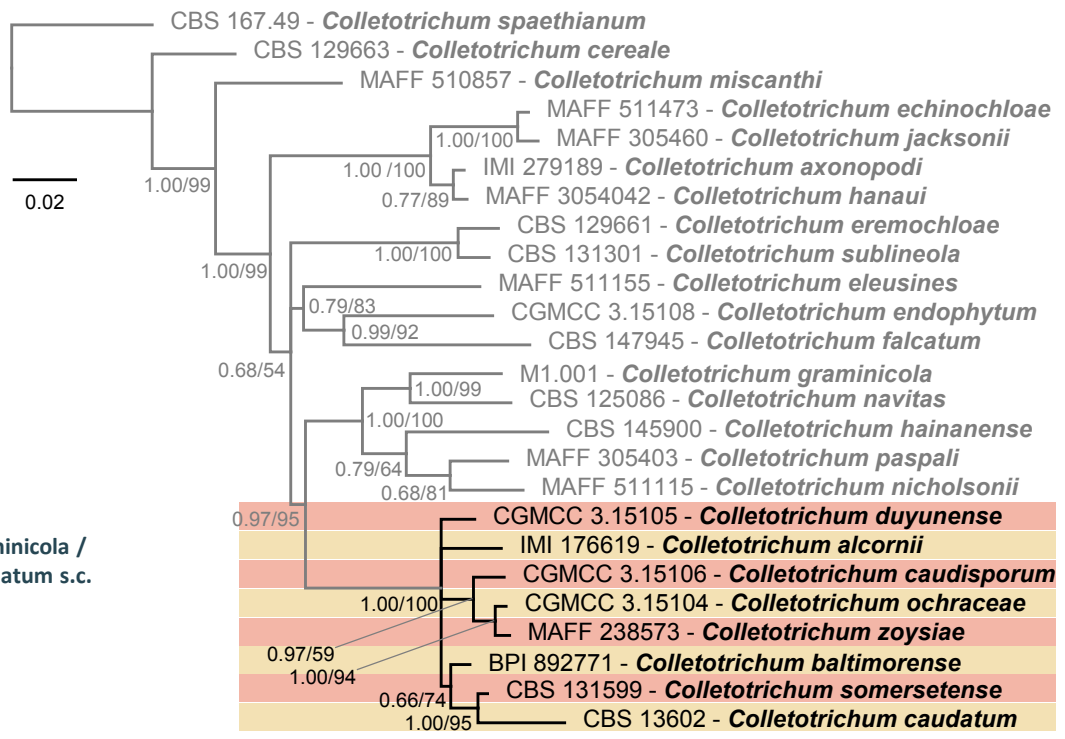
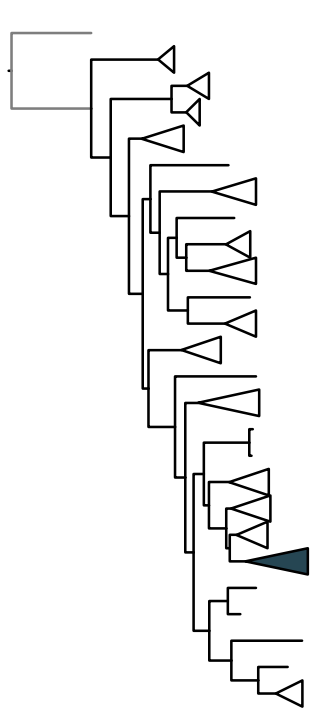
- Eudicots
- Monocots
- Gymnosperms
- Ferns
- Insects
- Humans
- Multiple species
- One species
- Number of occurrences
- Number of host species
- ▲ Threatened species
- ▲ Data deficient species
- ▲ Common species

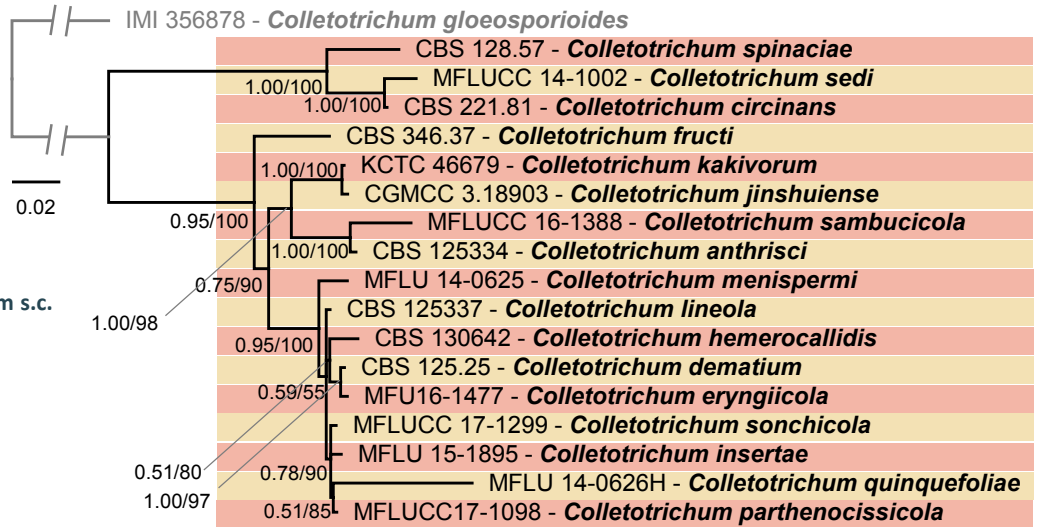
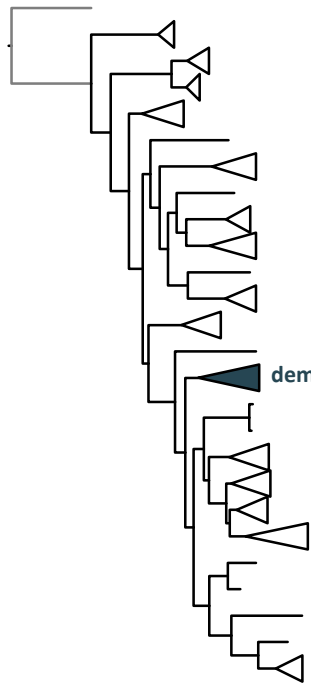


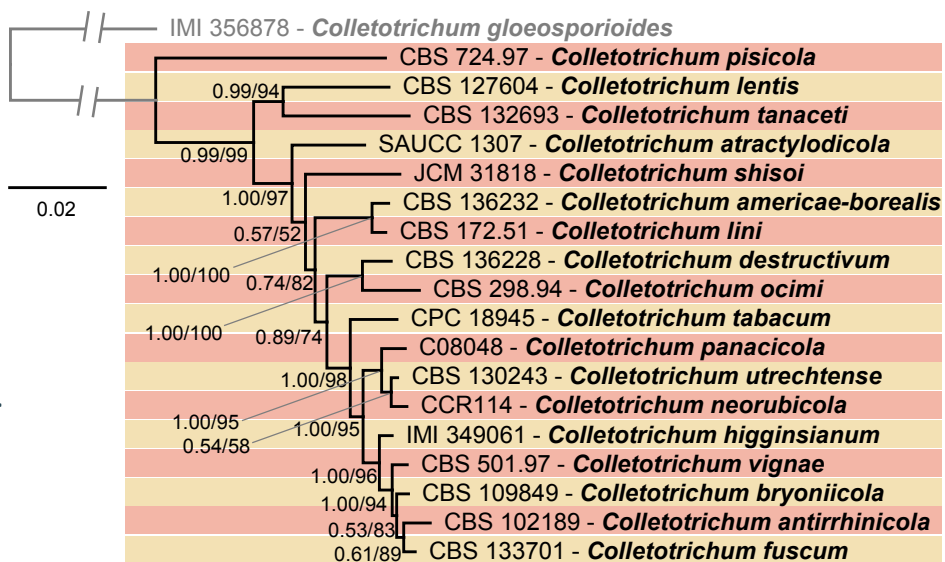


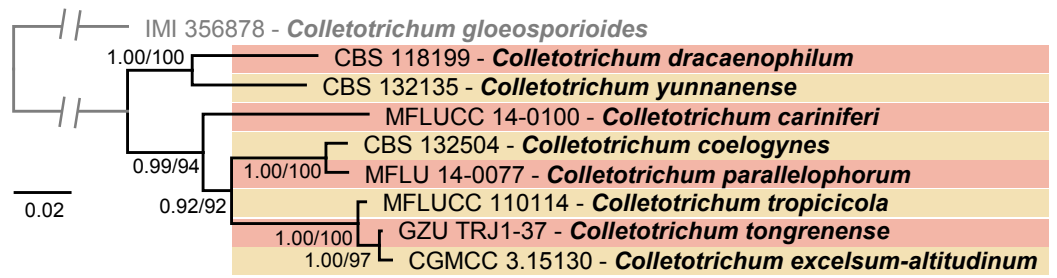
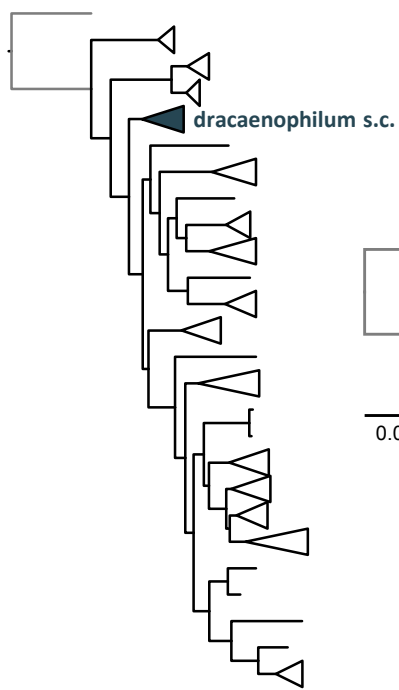


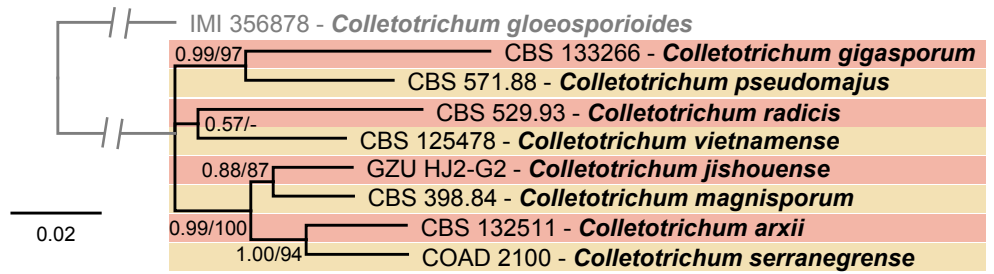
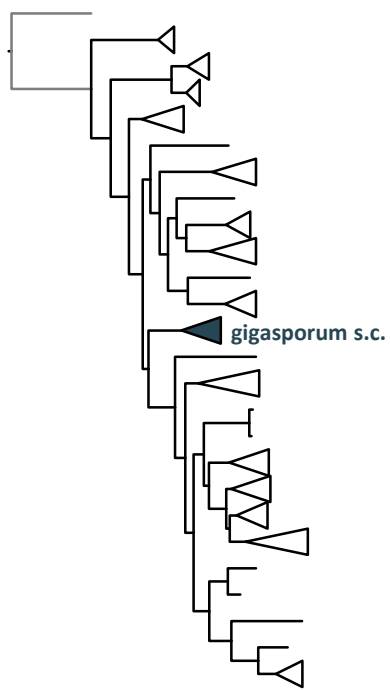


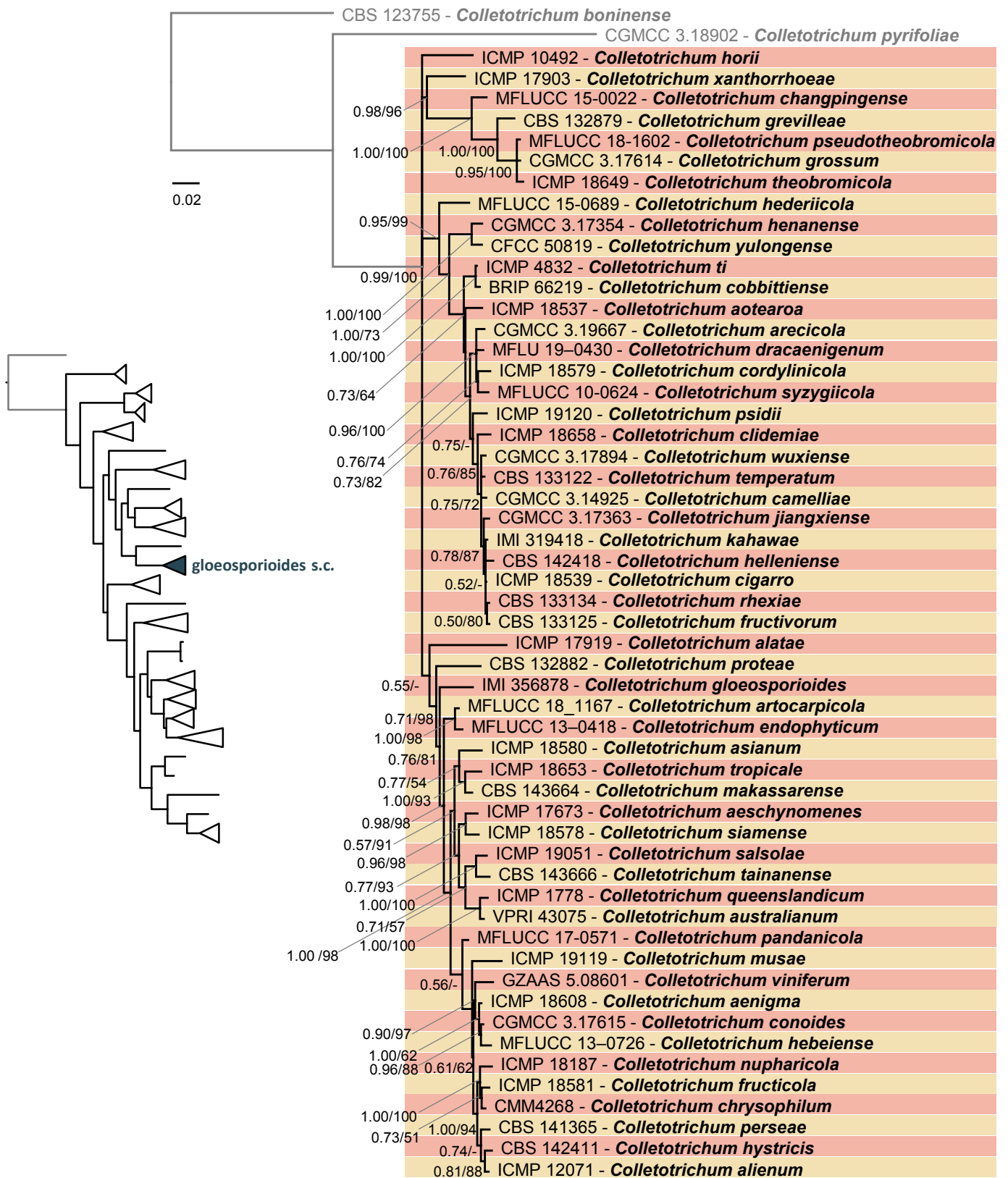


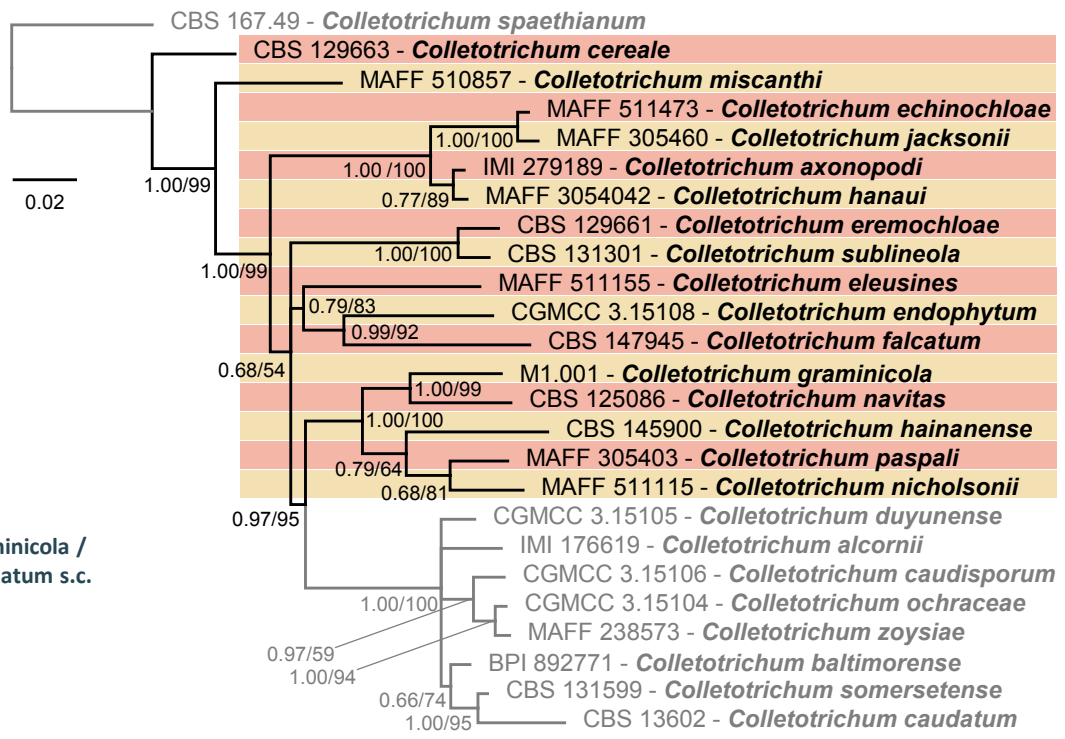
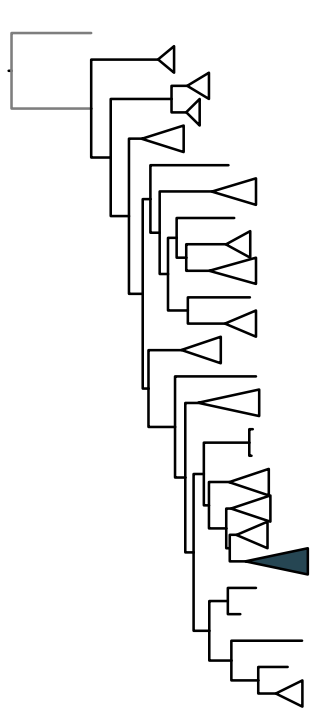


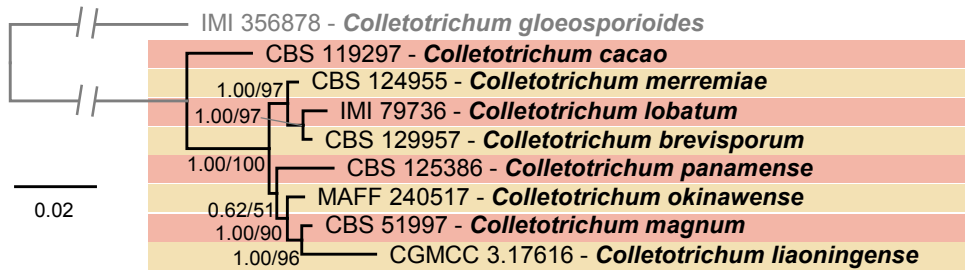
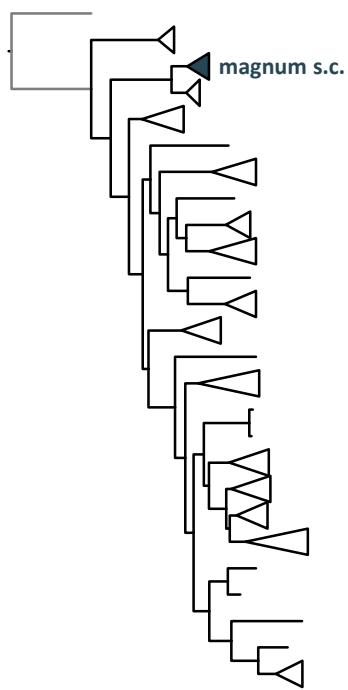


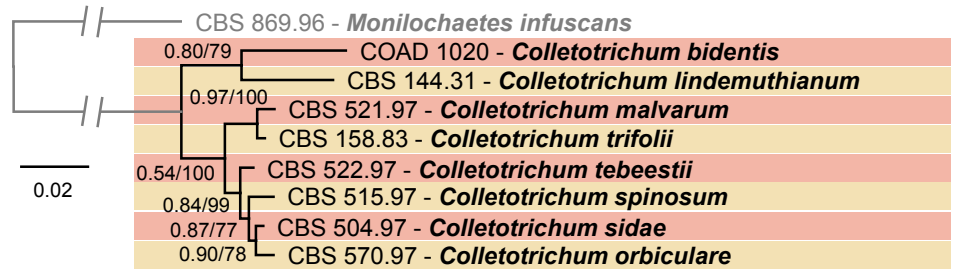
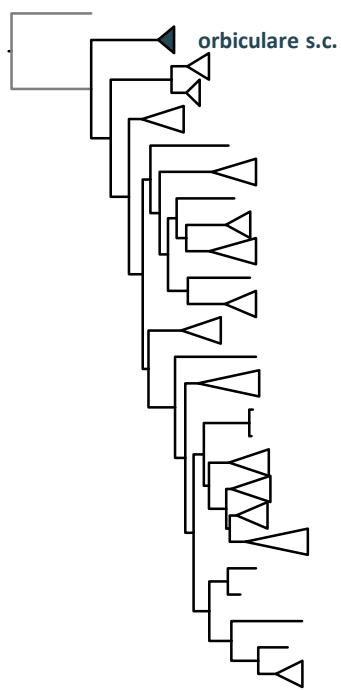


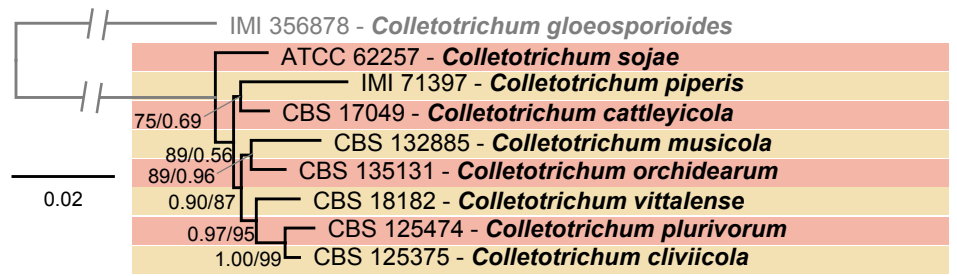
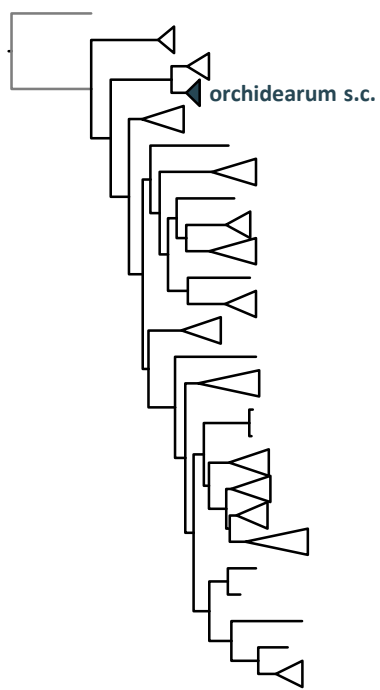


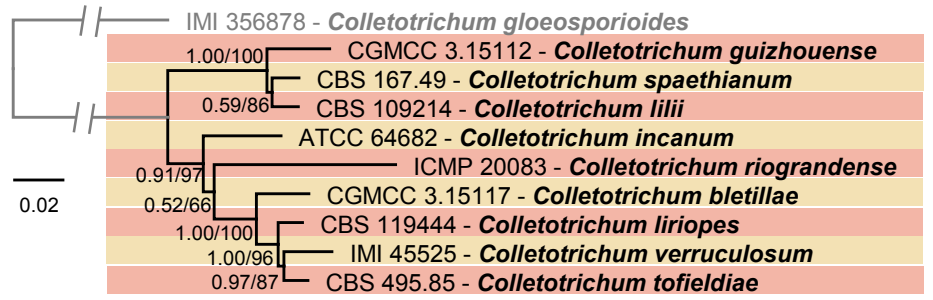
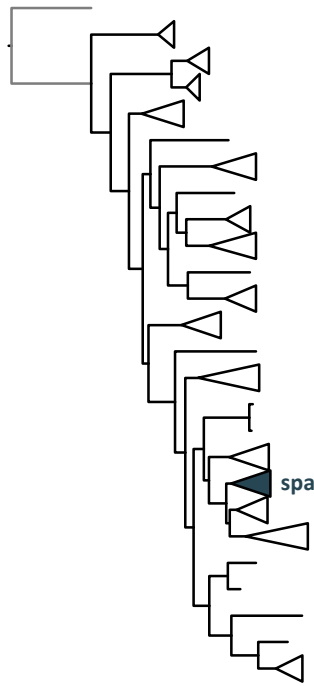


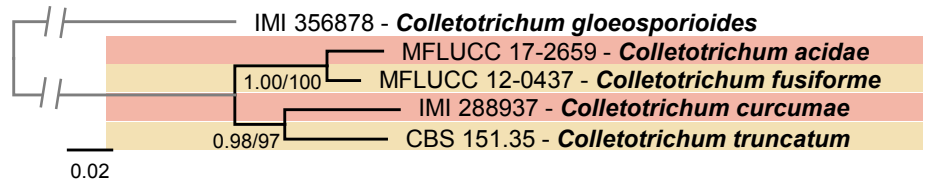
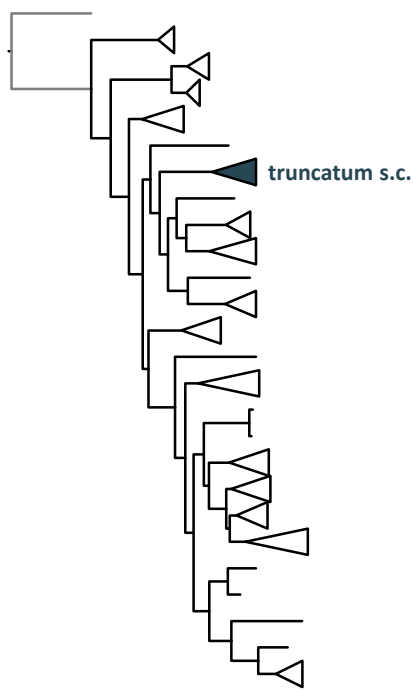


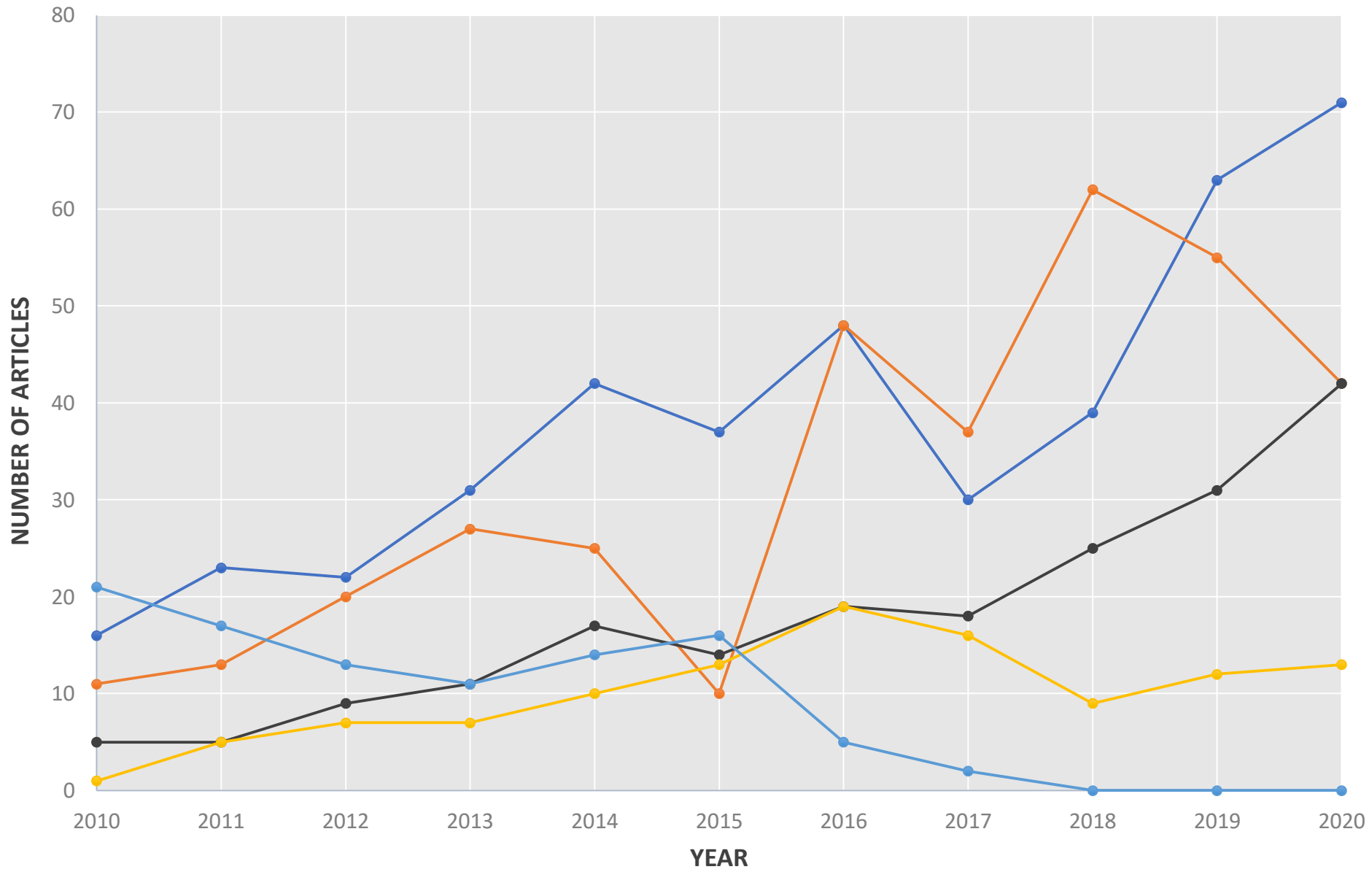




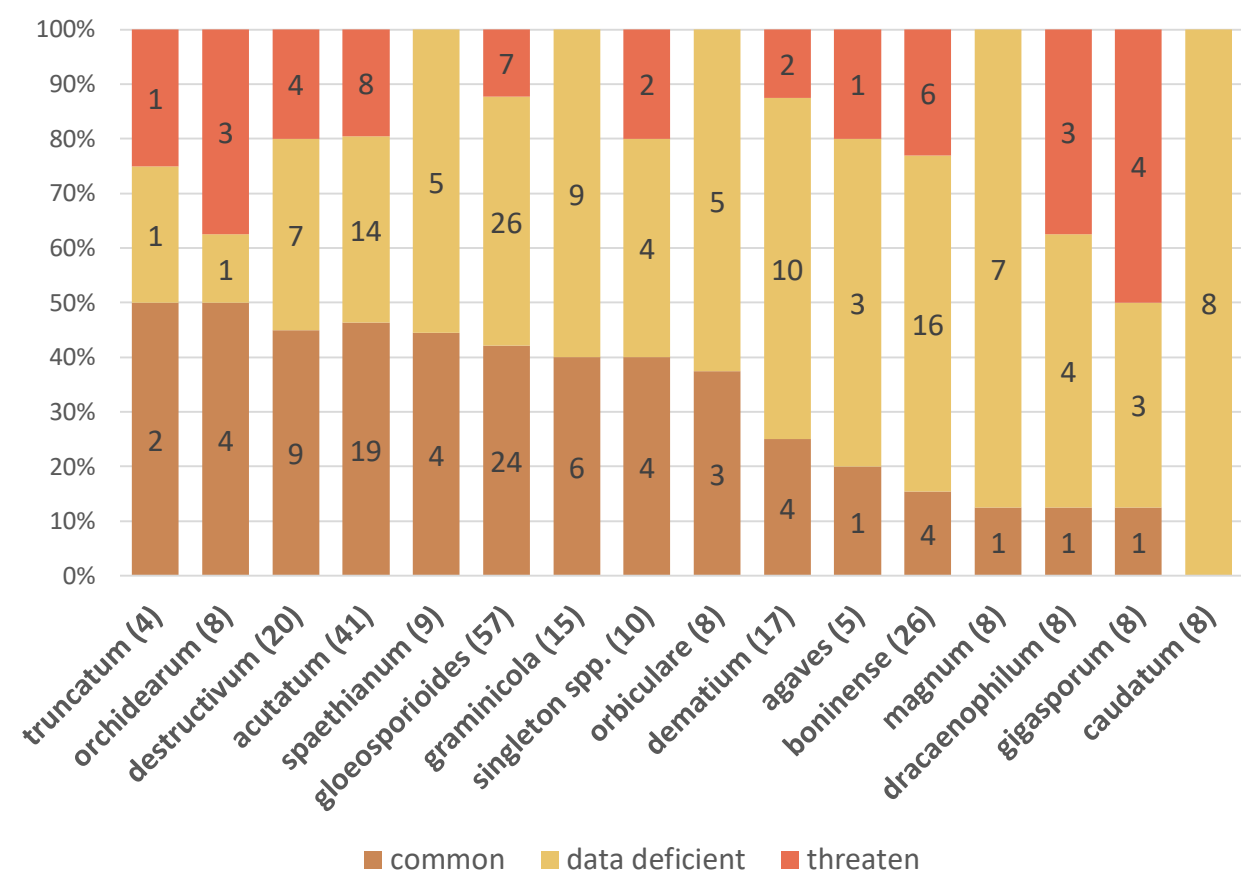








—●— *Fusarium* —●— *Colletotrichum* —●— *Alternaria* —●— *Erysiphe* —●— *Phytophthora*



■ common
 ■ data deficient
 ■ threaten

Table 1. Species of *Colletotrichum* described since 2009 that have been subsequently synonymized

Original species	Year	Current species	Reference
<i>C. aciculare</i> Jayaward., Tangthir. and K.D. Hyde	2015	<i>C. truncatum</i>	Jayawardena et al. (2016a)
<i>C. aracearum</i> L.W. Hou and L. Cai	2016	<i>C. orchidearum</i>	Damm et al. (2019)
<i>C. citri</i> F. Huang, L. Cai, K.D. Hyde and Hong Y. Li	2013	<i>C. nymphaeae</i>	Damm et al. (2020)
<i>C. clavatum</i> Agosteo, Faedda and Cacciola	2011	<i>C. godetiae</i>	Damm et al. (2012a)
<i>C. cliviae</i> Yan L. Yang, Zuo Y. Liu, K.D. Hyde and L. Cai	2009	<i>C. cliviicola</i>	Damm et al. (2019)
<i>C. communis</i> G. Sharma, Pinnaka and Shenoy	2014	<i>C. siamense</i>	Sharma et al. (2015a)
<i>C. dianesei</i> N.B. Lima, M.P.S. Câmara and Michereff	2013	<i>C. siamense</i>	Sharma et al. (2015a)
<i>C. endomangiferae</i> W.A.S. Vieira, M.P.S. Câmara and Michereff	2014	<i>C. siamense</i>	Sharma et al. (2015a)
<i>C. hymenocallidicola</i> Chethana, Tangthir., Wijayaw. and K.D. Hyde	2015	<i>C. orchidearum</i>	Damm et al. (2019)
<i>C. hymenocallidis</i> Yan L. Yang, Zuo Y. Liu, K.D. Hyde and L. Cai	2009	<i>C. siamense</i>	Liu et al. (2015a)
<i>C. ignotum</i> E.I. Rojas, S.A. Rehner and Samuels	2010	<i>C. fructicola</i>	Weir et al. (2012)
<i>C. jasmini-sambac</i> Wikee, K.D. Hyde, L. Cai and McKenzie	2011	<i>C. siamense</i>	Liu et al. (2015a)
<i>C. melanocaulon</i> V.P. Doyle, P.V. Oudem. and S.A. Rehner	2013	<i>C. siamense</i>	Sharma et al. (2015a)
<i>C. murrayae</i> Li J. Peng and K.D. Hyde	2012	<i>C. siamense</i>	Sharma et al. (2015a)
<i>C. populi</i> C.M. Tian & Zheng Li	2012	<i>C. aenigma</i>	Liu et al. (2013a)
<i>C. thailandicum</i> Phouliv., Noireung, L. Cai and K.D. Hyde	2012	<i>C. gigasporum</i>	Liu et al. (2014)

Table 2. Number of occurrences of *Colletotrichum* spp. (for species with 30 or more records in this work) per continent^a

Species	N.C. America	S. America	Africa	Europe	Asia	Oceania	Total
<i>C. siamense</i>	20	38	6	0	144	25	228
<i>C. gloeosporioides</i>	10	17	6	54	110	20	217
<i>C. fructicola</i>	11	37	2	8	113	6	176
<i>C. fioriniae</i>	43	1	1	33	36	22	134
<i>C. truncatum</i>	5	4	2	2	110	7	130
<i>C. karstii</i>	16	24	6	19	48	19	130
<i>C. nymphaeae</i>	15	26	8	39	28	6	118
<i>C. acutatum</i>	0	10	15	19	4	28	68
<i>C. godetiae</i>	5	3	1	51	3	2	65
<i>C. theobromicola</i>	12	27	0	0	5	13	56
<i>C. tropicale</i>	9	26	0	0	13	0	48
<i>C. lupini</i>	5	1	4	17	2	16	45
<i>C. scovillei</i>	1	5	0	0	36	0	42
<i>C. simmondsii</i>	2	0	0	2	2	34	40
<i>C. brevisporum</i>	2	12	0	0	22	4	40
<i>C. asianum</i>	3	8	3	0	11	9	34
<i>C. coccodes</i>	7	1	2	13	4	4	31
Total (incl. other spp.)	335	353	98	420	1144	347	2697

^aheatmaps (green – low; red – high) depict the relative frequency of occurrence of each species per continent

Table 3. The ten species of *Colletotrichum* with the larger number of host species ^a

Species	Complex	nr host species
<i>C. siamense</i>	gloeosporioides	103
<i>C. gloeosporioides</i>	gloeosporioides	87
<i>C. fioriniae</i>	acutatum	73
<i>C. karstii</i>	boninense	63
<i>C. fructicola</i>	gloeosporioides	63
<i>C. truncatum</i>	truncatum	52
<i>C. nymphaeae</i>	acutatum	42
<i>C. acutatum</i>	acutatum	40
<i>C. theobromicola</i>	gloeosporioides	31
<i>C. tropicale</i>	gloeosporioides	31

^a follows *C. godetiae*, *C. spaethianum*, *C. cigarro*, *C. aenigma*, *C. boninense* and *C. simmondsii*

Table 4. Number of *Colletotrichum* species-host species association records by complex

Complex	nr species	nr <i>Colletotrichum</i> species-host combinations	combinations/ <i>Colletotrichum</i> species ratio
acutatum	41	295	7,2
agaves	5	8	1,6
boninense	26	129	5,0
caudatum	8	9	1,1
dematium	17	37	2,2
destructivum	20	57	2,9
dracaenophilum	8	10	1,3
gigasporum	8	15	1,9
gloeosporioides	57	516	9,1
graminicola	16	31	2,0
magnum	8	30	3,8
orbiculare	8	20	2,5
orchidearum	8	41	5,1
spaethianum	9	52	5,8
truncatum	4	58	14,5

Table 5. Number of host species, of fungus-host association records and number of *Colletotrichum* species and species complexes by host family ^a

Family	nr host species	nr <i>Colletotrichum</i> species-host combinations	nr species complexes	nr <i>Colletotrichum</i> species
Rosaceae	33	118	7	41
Fabaceae	51	87	11	36
Solanaceae	14	72	10	41
Rutaceae	24	63	7	31
Orchidaceae	28	59	9	36
Poaceae	42	53	5	32
Anacardiaceae	8	42	6	23
Asparagaceae	32	42	8	20
Theaceae	6	33	5	20
Proteaceae	17	33	4	15
Myrtaceae	16	32	3	23
Asteraceae	26	30	9	22
Malvaceae	14	30	8	18
Euphorbiaceae	11	28	6	19
Rubiaceae	6	27	6	22
Amaryllidaceae	12	26	6	17
Lauraceae	6	23	3	19
Oleaceae	8	22	4	17
Ericaceae	7	19	3	11
Vitaceae	6	18	4	14
Lamiaceae	12	17	4	13
Moraceae	8	15	5	10
Musaceae	5	14	3	10
Arecaceae	5	13	3	10
Caricaceae	1	12	6	12
Apiaceae	6	12	6	12

^a only families inhabited by 10 or more species of *Colletotrichum* are listed; the Araceae (11 host species and 18 fungus-host association records), the Cucurbitaceae (nine host species and 16 fungus-host association records) and the Annonaceae (five host species and 15 fungus-host association records) follow.

Table 6. Number of unique association records between *Colletotrichum* species and host families per species complex and for the most represented families

Host family	singleton species	Species complex															Total
		acutatum	agaves	boninense	caudatum	dematum	destructivum	dracaenophilum	gigasporum	gloeosporioides	graminicola	magnum	orbiculare	orchidearum	spatheanthum	truncatum	
dicots																	
Anacardiaceae	0	6	0	1	0	0	0	0	1	13	0	1	0	1	0	0	23
Apiaceae	0	2	0	0	0	4	3	0	1	1	0	0	0	0	1	0	12
Asteraceae	2	3	0	1	0	2	5	0	0	3	0	0	2	1	2	1	22
Caricaceae	0	2	0	1	0	0	0	0	0	4	0	3	0	1	0	1	12
Ericaceae	0	4	0	1	0	0	0	0	0	6	0	0	0	0	0	0	11
Euphorbiaceae	0	7	1	3	0	0	0	0	0	6	0	0	0	1	0	1	19
Fabaceae	3	6	0	1	0	2	7	0	1	4	0	1	2	4	4	1	36
Lamiaceae	2	1	0	0	0	1	5	0	0	4	0	0	0	0	0	0	13
Lauraceae	0	4	0	1	0	0	0	0	0	14	0	0	0	0	0	0	19
Malvaceae	0	1	0	1	0	0	0	0	1	7	0	1	4	2	0	1	18
Moraceae	0	1	0	1	0	0	0	0	0	6	0	1	0	1	0	0	10
Myrtaceae	1	8	0	4	0	0	0	0	0	10	0	0	0	0	0	0	23
Oleaceae	0	6	0	1	0	0	0	0	0	8	0	0	0	0	0	1	16
Proteaceae	0	6	0	2	0	0	0	0	0	6	0	0	0	0	1	0	15
Rosaceae	4	15	0	4	0	2	1	0	0	13	0	0	0	1	0	1	41
Rubiaceae	0	4	0	3	0	0	0	0	2	11	0	1	0	1	0	0	22
Rutaceae	1	8	0	7	0	0	0	1	0	11	0	1	0	1	0	1	31
Solanaceae	2	12	0	5	0	1	1	0	0	13	0	2	1	2	1	1	41
Theaceae	0	4	0	4	0	0	0	0	1	10	0	0	0	0	0	1	20
Vitaceae	0	3	0	0	0	3	0	0	0	7	0	0	0	0	0	1	14
others (dicots)	7	60	0	20	0	14	14	2	2	107	0	8	2	4	5	13	258
monocots																	
Amaryllidaceae	1	5	0	3	0	1	0	0	0	3	0	0	0	2	1	1	17
Araceae	0	0	0	1	0	0	0	0	1	1	0	1	0	4	0	1	9
Arecaceae	0	1	0	1	0	0	0	0	0	7	0	0	0	0	0	0	10
Asparagaceae	2	0	4	2	0	1	0	1	0	5	0	0	1	0	3	1	20
Musaceae	0	2	0	1	0	0	0	0	0	7	0	0	0	0	0	0	10
Orchidaceae	1	0	0	8	3	0	2	5	2	4	3	0	0	4	4	0	36
Poaceae	5	0	0	1	5	0	2	0	0	4	14	0	0	1	0	0	37
others (monocots)	1	6	0	3	0	1	0	0	0	18	0	2	0	0	9	2	42
others																	
gymnosperms	1	4	0	4	0	0	0	0	0	4	0	0	0	0	0	0	13
others (mosses, ferns and animals)	1	3	0	0	0	1	1	0	0	6	1	0	0	0	0	2	15
Total	34	184	5	85	8	33	41	9	12	324	18	22	12	31	31	31	885

Table 8. List of 42 species of *Colletotrichum* considered as threatened

Species	Notes	References
singleton species		
<i>C. rusci</i>	endangered (one record only), from <i>Ruscus</i> sp.	Damm et al. (2009)
<i>C. sydowii</i>	highly endangered (one record only) and other species occur on the same host (<i>Sambucus</i> sp.)	Marín-Felix et al. (2017)
acutatum complex		
<i>C. acerbum</i>	possibly extinct; detection only in 1987 from <i>Malus domestica</i> and other species occur on the same host and location (New Zealand)	Lardner et al. (1999); Damm et al. (2012a)
<i>C. brisbanense</i>	possibly extinct; single detection in 1955 from <i>Capsicum annuum</i> and many other species occur on the same host and location (Australia)	Damm et al. (2012a); Shivas et al. (2016)
<i>C. cairnsense</i>	highly endangered (one record only) and many other species occur on the same host (<i>Capsicum annuum</i>)	Silva et al. (2017a)
<i>C. costaricense</i>	highly endangered (two records only), from <i>Coffea</i> sp.; last detection <1978	Damm et al. (2012a)
<i>C. cuscutae</i>	highly endangered (one record only), from <i>Cuscuta</i> sp.; single detection in 1986	Damm et al. (2012a)
<i>C. paxtonii</i>	possibly extinct; single detection in 1972 from <i>Musa</i> sp. and other species occur on the same host	Damm et al. (2012a)
<i>C. walleri</i>	highly endangered (one record only) and other species occur on the same host (<i>Coffea</i> sp.); single detection <2012	Damm et al. (2012a)
<i>C. wanningense</i>	highly endangered (one record only) and other species occur on the same host (<i>Hevea brasiliensis</i>)	Cao et al. (2019b)
agaves complex		
<i>C. euphorbiae</i>	critically endangered (one record only) and host plant (<i>Euphorbia</i> sp.) highly uncertain	Crous et al. (2013)
boninense complex		
<i>C. camelliae-japonicae</i>	highly endangered (one record only) and other species occur on the same host (<i>Camellia japonica</i>)	Hou et al. (2016)
<i>C. constrictum</i>	highly endangered (two records only) and other species occur on the same hosts (<i>Citrus limon</i> and <i>Solanum betaceum</i>); last detection in 1988	Damm et al. (2012b)
<i>C. limonicola</i>	highly endangered (one record only) and other species occur on the same host (<i>Citrus limon</i>)	Guarnaccia et al. (2017)
<i>C. novae-zelandiae</i>	possibly extinct; known from <i>Capsicum annuum</i> and <i>Citrus × paradisi</i> last detection in 1990; other species occur on the same hosts	Johnston and Jones (1997); Damm et al. (2012b)
<i>C. oncidii</i>	highly endangered (one record only) and other species occur on the same host (<i>Oncidium</i> sp.)	Damm et al. (2012b)
<i>C. watphraense</i>	highly endangered (one record only) and other species occur on the same host (<i>Dendrobium</i> sp.)	Ma et al. (2018)
dematium complex		
<i>C. fructi</i>	possibly extinct; last detection in 1937 from <i>Malus domestica</i> and other species occur on the same host and location (USA)	González et al. (2006); Damm et al. (2009)
<i>C. sedi</i>	highly endangered (one record only) and other species occur on the same host (<i>Sedum</i> sp.)	Liu et al. (2015b)
<i>C. sonchicola</i>	highly endangered (one record only), from <i>Sonchus</i> sp.	Jayawardena et al. (2017)
destructivum complex		
<i>C. orchidis</i>	highly endangered (one record only) and other species occur on the same host (<i>Orchis</i> sp.)	Hyde et al. (2020b)
<i>C. pisicola</i>	possibly extinct; known from <i>Pisum sativum</i> ; last detection in 1997	Damm et al. (2014)
<i>C. pleopeltidis</i>	endangered (one record only) and host plant (<i>Pleopeltis</i> sp.) uncertain	Crous et al. (2021)
<i>C. vignae</i>	possibly extinct; single detection <1997 and other species occur on the same host (<i>Vigna unguiculata</i>)	Damm et al. (2014)
dracaenophilum complex		
<i>C. coelogyne</i>	highly endangered (one record only) and other species occur on the same host (<i>Coelogyne</i> sp.)	Damm et al. (2019)
<i>C. paralleloporum</i>	highly endangered (one record only) and other species occur on the same host (<i>Dendrobium harveyanum</i>)	Ma et al. (2018)
<i>C. yunnanense</i>	highly endangered (one record only), from <i>Buxus</i> sp.	Damm et al. (2019)
gigasporum complex		
<i>C. magnisporum</i>	possibly extinct; single detection <1984 from unknown substrate	Liu et al. (2014)
<i>C. pseudomajus</i>	possibly extinct; single detection <1988 and many other species occur on the same host (<i>Camellia sinensis</i>) and location (China)	Liu et al. (2014)
<i>C. radicis</i>	possibly extinct; single detection in 1993 from root of an unknown plant	Liu et al. (2014)
<i>C. vietnamense</i>	highly endangered (two records only) and other species occur on the same host (<i>Coffea</i> sp.)	Liu et al. (2014)

Table 8. (cont.)

gloeosporioides complex		
<i>C. grevilleae</i>	highly endangered (one record only), from <i>Grevillea</i> sp.	Liu et al. (2013a)
<i>C. hebeiense</i>	highly endangered (two records only) and other species occur on the same host (<i>Vitis vinifera</i>)	Yan et al. (2015)
<i>C. makassarensis</i>	highly endangered (one record only) and other species occur on the same host (<i>Capsicum annuum</i>)	Silva et al. (2019a)
<i>C. pandanicola</i>	highly endangered (one record only) and other species occur on the same host (<i>Pandanus</i> sp.)	Tibpromma et al. (2018)
<i>C. perseae</i>	rare, from <i>Persea americana</i>	Sharma et al. (2017)
<i>C. proteae</i>	highly endangered (one record only) and same host plant (<i>Protea</i> sp.) uncertain	Liu et al. (2013a)
<i>C. psidii</i>	possibly extinct; single detection <1927 and other species occur on the same host (<i>Psidium</i> sp.)	Weir et al. (2012)
<i>C. tainanense</i>	highly endangered (one record only) and other species occur on the same host (<i>Capsicum annuum</i>)	Silva et al. (2019a)
orchidearum complex		
<i>C. cattleyicola</i>	highly endangered (two records only) and other species occur on the same host (<i>Cattleya</i> sp.); last detection <2000	Damm et al. (2019)
<i>C. piperis</i>	possibly extinct; from <i>Piper</i> spp.; last detection <1957	Damm et al. (2019)
<i>C. vittalense</i>	possibly extinct, from <i>Theobroma cacao</i> and an unspecified Orchidaceae; last detection <1928	Damm et al. (2019)
truncatum complex		
<i>C. fusiforme</i>	highly endangered (two records only), from an unknown plant and from human eye	Ariyawansa et al. (2015); Hung et al. (2020)

Table 9. List of 127 species of *Colletotrichum* treated as ‘data deficient’

Species	Notes	References
singleton species		
<i>C. citrus-medicae</i>	highly endangered (one record only) and other species occur on the same host (<i>Citrus medica</i>)	Hyde et al. (2020c)
<i>C. guangxiense</i>	highly endangered (two records only) and other species occur on the same host (<i>Phyllostachys edulis</i>)	Wang et al. (2021b)
<i>C. hainanense</i>	few records and other species occur on the same host (<i>Axonopus compressus</i>)	Zhang et al. (2020c)
<i>C. hsienjenchang</i>	rare, from <i>Phyllostachys</i> spp.	Sato et al. (2012)
<i>C. metake</i>	rare, from <i>Phyllostachys</i> spp.	Sato et al. (2012); Wang et al. (2021b)
<i>C. orchidophilum</i>	seldom reports and other species occur on the same hosts (orchids)	Damm et al. (2012a)
<i>C. pseudoacutatum</i>	rare, from <i>Pinus radiata</i> and <i>Syzygium jambos</i>	Damm et al. (2012a); Soares et al. (2017)
<i>C. pyrifoliae</i>	highly endangered (one record only) and other species occur on the same host (<i>Pyrus pyrifolia</i>)	Fu et al. (2019)
acutatum complex		
<i>C. arboricola</i>	recorded only from <i>Fuchsia magellanica</i> in Chile, with unprecise reference to putative additional occurrences	Crous et al. (2018a)
<i>C. australe</i>	highly endangered (two records only), from <i>Trachycarpus fortunei</i> and <i>Hakea</i> sp.	Damm et al. (2012a)
<i>C. cosmi</i>	highly endangered (one ancient record only), from <i>Cosmos</i> sp.	Damm et al. (2012a)
<i>C. indonesiense</i>	highly endangered (one record only) and other species occur on the same host (<i>Eucalyptus</i> sp.)	Damm et al. (2012a)
<i>C. javanense</i>	highly endangered (one record only) and other species occur on the same host (<i>Capsicum annuum</i>)	Silva et al. (2019a)
<i>C. johnstonii</i>	highly endangered (two records) and other species occur on the same hosts (<i>Citrus</i> sp. and <i>Solanum lycopersicum</i>); last detection in 1990	Damm et al. (2012a)
<i>C. kinghornii</i>	single detection in 1935 from <i>Phormium tenax</i> and other species occur on the same host	Damm et al. (2012a)
<i>C. kniphofiae</i>	endangered (one record only), from <i>Kniphofia uvaria</i>	Crous et al. (2018b)
<i>C. lauri</i>	highly endangered (one record only) and other species occur on the same host (<i>Laurus nobilis</i>)	Hyde et al. (2017)
<i>C. limetticola</i>	seldom reports and other species occur on the same hosts (citrus and apple)	Damm et al. (2012a); Guarnaccia et al. (2017); Moreira et al. (2019a)
<i>C. pyricola</i>	rare, from <i>Daphne odora</i> , <i>Embothrium coccineum</i> and <i>Pyrus communis</i>	Damm et al. (2012a); Shivas et al. (2016); Zapata and Opazo (2017)
<i>C. rhombiforme</i>	rare, from <i>Malus domestica</i> , <i>Olea europaea</i> and <i>Vaccinium</i> spp.	Damm et al. (2012a); Wu et al. (2017); Wang et al. (2019b)
<i>C. roseum</i>	rare, from <i>Lapageria rosea</i>	Crous et al. (2019a)
<i>C. sloanei</i>	highly endangered (two records only) and other species occur on the same hosts (<i>Theobroma cacao</i> and <i>Litchi chinensis</i>); last detection in 2003	Damm et al. (2012a); Shivas et al. (2016)
agaves complex		
<i>C. agaves</i>	rare in recent years, from Agavaceae; most records from the early 20 th century, last detection in 2002	Farr et al. (2006)
<i>C. ledebouriae</i>	endangered (one record only), from <i>Ledebouria floridunda</i>	Crous et al. (2016)
<i>C. neosansevieriae</i>	highly endangered (one recent record only) and other species occur on the same host (<i>Sansevieria trifasciata</i>)	Crous et al. (2015)

Table 9. (cont.)

boninense complex		
<i>C. annellatum</i>	highly endangered (one record only) and other species occur on the same host (<i>Hevea brasiliensis</i>)	Damm et al. (2012b)
<i>C. beeveri</i>	highly endangered (one record only), from <i>Brachyglottis repanda</i> , but may be present in other hosts	Damm et al. (2012b)
<i>C. brasiliense</i>	highly endangered (one confirmed record only) and other species occur on the same host (<i>Passiflora edulis</i>)	Damm et al. (2012b)
<i>C. brassicicola</i>	highly endangered (two records only) and other species occur on the same hosts (<i>Brassica oleracea</i> and <i>Rubus glaucus</i>)	Damm et al. (2012b); Afanador-Kafuri et al. (2014)
<i>C. catinaense</i>	endangered (two records only), from <i>Citrus</i> spp.	Guarnaccia et al. (2017)
<i>C. chongqingense</i>	highly endangered (one record only) and other species occur on the same host (<i>Camellia sinensis</i>)	Wan et al. (2021)
<i>C. citricola</i>	endangered (few records) and other species occur on the same hosts (<i>Citrus unchiu</i> , <i>Pyrus pyrifolia</i> and <i>Dendrobium</i> sp.)	Fu et al. (2019)
<i>C. colombiense</i>	highly endangered (one confirmed record only) and other species occur on the same host (<i>Passiflora edulis</i>)	Damm et al. (2012b)
<i>C. condaoense</i>	endangered (one record only), from <i>Ipomoea pes-caprae</i>	Crous et al. (2018c)
<i>C. dacrycarpi</i>	highly endangered (one record only), from <i>Dacrycarpus dacrydioides</i>	Damm et al. (2012b)
<i>C. doitungense</i>	highly endangered (one record only) and other species occur on the same host (<i>Dendrobium</i> sp.)	Ma et al. (2018)
<i>C. feijoicola</i>	highly endangered (one record only) and other species occur on the same host (<i>Acca sellowiana</i>)	Crous et al. (2019b)
<i>C. hippeastri</i>	highly endangered (few records), from <i>Hippeastrum</i> sp.; last detection in 2009	Damm et al. (2012b)
<i>C. parsonsiae</i>	rare, from <i>Bletilla ochracea</i> and <i>Parsonsia capsularis</i>	Damm et al. (2012b); Tao et al. (2013)
<i>C. phyllanthi</i>	very rare; detected once in 1966 from <i>Phyllanthus acidus</i> and recently as an epiphyte on <i>Carapichea ipecacuanha</i>	Damm et al. (2012b); Ferreira et al. (2020)
<i>C. torulosum</i>	highly endangered (few records only) and other species occur on the same hosts (<i>Passiflora edulis</i> , <i>Solanum melongena</i> and <i>Kunzea ericoides</i>); last detection in 2004	Joshee et al. (2009); Damm et al. (2012b)
caudatum complex		
<i>C. alcornii</i>	highly endangered (two records only), from <i>Bothriochloa bladhii</i> and <i>Imperata cylindrica</i> ; last detection in 1973	Crouch (2014)
<i>C. baltimoreense</i>	highly endangered (one record only) and other species occur on the same host (<i>Sorghastrum nutans</i>)	Crouch (2014)
<i>C. caudatum</i>	highly endangered (two records only) and other species occur on the same host (<i>Sorghastrum nutans</i>); last detection in 2007	Crouch (2014)
<i>C. caudisporum</i>	highly endangered (one record only) and other species occur on the same host (<i>Bletilla ochracea</i>)	Tao et al. (2013)
<i>C. duyunense</i>	highly endangered (one record only) and other species occur on the same host (<i>Bletilla ochracea</i>)	Tao et al. (2013)
<i>C. ochraceae</i>	highly endangered (two records only) and other species occur on the same host (<i>Bletilla ochracea</i>)	Tao et al. (2013)
<i>C. somersetense</i>	highly endangered (one record only) and other species occur on the same host (<i>Sorghastrum nutans</i>)	Crouch (2014)
<i>C. zoysiae</i>	highly endangered (one record only), from <i>Zoysia tenuifolia</i> ; single detection in 1998	Crouch (2014)
dematium complex		
<i>C. anthrisci</i>	highly endangered (one record only), from <i>Anthriscus sylvestris</i>	Damm et al. (2009)
<i>C. eryngiicola</i>	highly endangered (one record only) and other species occur on the same host (<i>Eryngium campestre</i>)	Buyck et al. (2017)
<i>C. hemerocallidis</i>	highly endangered (two records only) and other species occur on the same host (<i>Hemerocallis fulva</i>)	Yang et al. (2012b)
<i>C. insertae</i>	highly endangered (one record only) and other species occur on the same host (<i>Parthenocissus inserta</i>)	Hyde et al. (2016)
<i>C. jinshuiense</i>	highly endangered (one record only) and other species occur on the same host (<i>Pyrus pyrifolia</i>)	Fu et al. (2019)
<i>C. kakiivorum</i>	highly endangered (two records only) and other species occur on the same host (<i>Diospyrus kaki</i>)	Lee and Jung (2018)
<i>C. menispermii</i>	highly endangered (one record only), from <i>Menispermum dauricum</i>	Li et al. (2016c)
<i>C. parthenocissicola</i>	highly endangered (one record only) and other species occur on the same host (<i>Parthenocissus quinquefolia</i>)	Yuan et al. (2020)
<i>C. quinquefoliae</i>	highly endangered (one record only) and other species occur on the same host (<i>Parthenocissus quinquefolia</i>)	Li et al. (2016c)
<i>C. sambucicola</i>	highly endangered (one record only) and other species occur on the same host (<i>Sambucus ebulus</i>)	Tibpromma et al. (2017)

Table 9. (cont.)

destructivum complex		
<i>C. antirrhinicola</i>	highly endangered (one record only) and other species occur on the same host (<i>Antirrhinum majus</i>); single detection in 1999	Damm et al. (2014)
<i>C. atractylodicola</i>	highly endangered (one record only) and other species occur on the same host (<i>Atractylodes lancea</i>)	Xu et al. (2018b)
<i>C. bryoniicola</i>	endangered (two records only), from <i>Bryonia dioica</i> and <i>Salvia nemerosa</i>	Damm et al. (2014); Guarnaccia et al. (2019)
<i>C. neorubicola</i>	highly endangered (two records only) and other species occur on the same host (<i>Rubus idaeus</i>)	Liu et al. (2020d)
<i>C. shisoi</i>	endangered (one record only), from <i>Perilla frutescens</i>	Gan et al. (2019)
<i>C. tabacum</i>	rare, from <i>Nicotiana</i> spp. and <i>Centella asiatica</i> ; last detection in 2003	Damm et al. (2014)
<i>C. utrechtense</i>	highly endangered (one record only) and other species occur on the same host (<i>Trifolium pratense</i>)	Damm et al. (2014)
dracaenophilum complex		
<i>C. cariniferi</i>	highly endangered (one record only), from <i>Dendrobium cariniferum</i>	Ma et al. (2018)
<i>C. excelsum-altitudinum</i>	highly endangered (one record only) and other species occur on the same host (<i>Bletilla ochracea</i>)	Tao et al. (2013)
<i>C. tongrenense</i>	endangered (one record only), from <i>Nothapodytes pittosporoides</i>	Zhou et al. (2019)
<i>C. tropicicola</i>	endangered (three records only), from <i>Citrus</i> sp. and <i>Paphiopedilum bellatulum</i> ; species in state of delimitation	Noireung et al. (2012); Damm et al. (2019)
gigasporum complex		
<i>C. arxii</i>	highly endangered (two records only), from orchids	Liu et al. (2014)
<i>C. jishouense</i>	endangered (one record only), from <i>Nothapodytes pittosporoides</i>	Zhou et al. (2019)
<i>C. serranegrense</i>	highly endangered (one record only), from <i>Cattleya jongheana</i>	Silva et al. (2018)
gloeosporioides complex		
<i>C. arecicola</i>	rare, from <i>Areca catechu</i>	Cao et al. (2020)
<i>C. artocarpicola</i>	highly endangered (one record only), from <i>Artocarpus heterophyllus</i>	Bhunjun et al. (2019)
<i>C. changpingense</i>	highly endangered (two records only) and other species occur on the same host (<i>Fragaria</i> × <i>ananassa</i>)	Jayawardena et al. (2016b)
<i>C. Chiangmaiense</i>	highly endangered (one record only) and other species occur on the same host genus (<i>Magnolia</i>)	de Silva et al. (2021b)
<i>C. clidemiae</i>	rare, from <i>Clidemia hirta</i> and <i>Vitis</i> sp.	Weir et al. (2012)
<i>C. cobbittiense</i>	highly endangered (one record only) and other species occur on the same host (<i>Cordyline stricta</i> × <i>australis</i>)	Crous et al. (2018c)
<i>C. conoides</i>	highly endangered (two records only) and other species occur on the same hosts (<i>Capsicum annuum</i> var. <i>conoides</i> and <i>Pyrus pyrifolia</i>)	Diao et al. (2017); Fu et al. (2019)
<i>C. cycadis</i>	endangered (one record only), from <i>Cycas revoluta</i>	Crous et al. (2020)
<i>C. dracaenigenum</i>	highly endangered (one record only) and other species occur on the same host (<i>Dracaena</i>)	Chaiwan et al. (2021)
<i>C. fructivorum</i>	no recent reports; mostly from <i>Vaccinium</i> spp.	Doyle et al. (2013)
<i>C. grossum</i>	highly endangered (two records only) and other species occur on the same host (<i>Capsicum annuum</i>)	Diao et al. (2017); Guarnaccia et al. (2021)
<i>C. hedericola</i>	highly endangered (one record only) and other species occur on the same host (<i>Hedera helix</i>)	Hyde et al. (2020a)
<i>C. helleniense</i>	highly endangered (two records only) and other species occur on the same hosts (<i>Citrus</i> spp.)	Guarnaccia et al. (2017)
<i>C. henanense</i>	endangered (few records) and other species occur on the same hosts (<i>Camellia</i> spp. and <i>Cirsium japonicum</i>)	Liu et al. (2015a); Li et al. (2018c)
<i>C. hystricis</i>	highly endangered (one record only) and other species occur on the same host (<i>Citrus hystrix</i>)	Guarnaccia et al. (2017)
<i>C. Jiangxiense</i>	endangered (few records) and other species occur on the same host (<i>Camellia sinensis</i> and <i>Dendrobium</i> sp.)	Liu et al. (2015a); Ma et al. (2018)
<i>C. nupharicola</i>	rare, from waterlilies and <i>Persea americana</i>	Weir et al. (2012); Sharma et al. (2017)
<i>C. perseae</i>	rare, from <i>Persea americana</i>	Sharma et al. (2017)
<i>C. pseudotheobromicola</i>	highly endangered (one record only) and other species occur on the same host (<i>Prunus avium</i>)	Chethana et al. (2019)
<i>C. syzygiicola</i>	endangered (few records) and other species infected the same hosts (<i>Citrus aurantifolia</i> , <i>Elettaria cardamomum</i> and <i>Syzygium samarangense</i>)	Udayanga et al. (2013); Chethana et al. (2016)
<i>C. temperatum</i>	highly endangered (two records only) and other species occur on the same host (<i>Vaccinium macrocarpon</i>)	Doyle et al. (2013)
<i>C. ti</i>	endangered (few records) and other species occur on the same host (<i>Cordyline australis</i>); last detection in 1992	Weir et al. (2012)
<i>C. wuxiense</i>	endangered (few records) and other species occur on the same hosts (<i>Camellia sinensis</i> and <i>Pyrus pyrifolia</i>)	Wang et al. (2016a); Fu et al. (2019)
<i>C. xanthorrhoeae</i>	endangered (few records), from <i>Xanthorrhoea</i> sp.; last detection in 1994	Weir et al. (2012)
<i>C. xishuangbannaense</i>	highly endangered (one record only) and other species occur on the same host genus (<i>Magnolia</i>)	de Silva et al. (2021b)
<i>C. yulongense</i>	highly endangered (one record only) and other species occur on the same host (<i>Vaccinium dunalianum</i>)	Wang et al. (2019b)

Table 9. (cont.)

graminicola complex		
<i>C. axonopodi</i>	rare, from <i>Axonopus</i> spp.; last detection in 1983	Crouch et al. (2009a)
<i>C. eleusines</i>	highly endangered (two records only), from <i>Eleusine indica</i> ; last detection in 1977	Crouch et al. (2009a)
<i>C. endophytum</i>	highly endangered (two records only) and other species occur on the same host (<i>Bletilla ochracea</i>)	Tao et al. (2013)
<i>C. eremochloae</i>	rare, from <i>Eremochloa ophiuroides</i> ; last detection in 2007	Crouch and Tomaso-Peterson (2012)
<i>C. hanau</i>	highly endangered (few records), from <i>Digitaria</i> spp.; last detection in 1975	Crouch et al. (2009a)
<i>C. jacksonii</i>	highly endangered (few ancient records) and other species occur on the same host (<i>Echinochloa</i> spp.); last detection in 1985	Crouch et al. (2009a)
<i>C. miscanthei</i>	highly endangered (one recent record only) and other species occur on the same hosts (<i>Miscanthus sinensis</i> and <i>Bletilla ochracea</i>); last detection in 2006	Crouch et al. (2009a); Tao et al. (2013)
<i>C. nicholsonii</i>	possibly extinct; from <i>Paspalum dilatatum</i> ; last detection in 1975	Crouch et al. (2009a)
<i>C. paspali</i>	possibly extinct; from <i>Paspalum notatum</i> ; last detection in 1977	Crouch et al. (2009a)
magnum complex		
<i>C. cacao</i>	possibly extinct; single detection at an unknown (presumably ancient) date and other species occur on the same host (<i>Theobroma cacao</i>)	Damm et al. (2019)
<i>C. liaoningense</i>	endangered (few records) and other species infect the same hosts (<i>Capsicum annuum</i> and <i>Mangifera indica</i>)	Li et al. (2019b)
<i>C. lobatum</i>	possibly extinct; single detection at an unknown (presumably ancient) date and other species occur on the same host (<i>Piper catalpaefolium</i>)	Damm et al. (2019)
<i>C. magnum</i>	endangered (few records) and other species infect the same hosts (<i>Carica papaya</i> , <i>Citrullus lanatus</i> and <i>Lobelia chinensis</i>)	Li et al. (2013a); Tapia-Tussell et al. (2016); Damm et al. (2019)
<i>C. merremiae</i>	highly endangered (one record only) and other species occur on the same host (<i>Merremia umbellata</i>)	Damm et al. (2019)
<i>C. okinawense</i>	endangered (few records) and other species occur on the same host (<i>Carica papaya</i>)	Damm et al. (2019); Dias et al. (2020)
<i>C. panamense</i>	highly endangered (one record only) and other species occur on the same host (<i>Merremia umbellata</i>)	Damm et al. (2019)
orbiculare complex		
<i>C. bidentis</i>	highly endangered (one record only), from <i>Bidens subalternans</i>	Damm et al. (2013)
<i>C. malvarum</i>	highly endangered (few records), from <i>Malva</i> sp. and <i>Lavatera trimestris</i> ; last detection in 1997	Damm et al. (2013)
<i>C. sidae</i>	highly endangered (one record only), from <i>Sida spinosa</i> ; single detection in 1988	Damm et al. (2013)
<i>C. spinosum</i>	few records, from <i>Xanthium spinosum</i> only	Damm et al. (2013)
<i>C. tebeestii</i>	rare, from <i>Malva pusilla</i> ; single detection in 1982	Damm et al. (2013)
orchidearum complex		
<i>C. musicola</i>	endangered (few records), from <i>Musa</i> sp., <i>Colocasia esculenta</i> and <i>Glycine max</i>	Damm et al. (2019); Vásquez-López et al. (2019); Bouffleur et al. (2020)
spaehtianum complex		
<i>C. bletillae</i>	highly endangered (one record only) and other species occur on the same host (<i>Bletilla ochracea</i>)	Tao et al. (2013)
<i>C. guizhouense</i>	few records, from <i>Bletilla ochracea</i> and <i>Huperzia phlegmaria</i>	Tao et al. (2013); Zhang et al. (2015a)
<i>C. incanum</i>	endangered (few records) and other species occur on the same hosts (<i>Capsicum</i> sp. and <i>Glycine max</i>)	Yang et al. (2014); Diao et al. (2017)
<i>C. riograndense</i>	endangered (one record only), from <i>Tradescantia fluminensis</i>	Macedo et al. (2016)
<i>C. verruculosum</i>	possibly extinct, from <i>Crotalaria juncea</i> ; single detection in 1951	Damm et al. (2009)
truncatum complex		
<i>C. acidae</i>	highly endangered (one record only), from <i>Phyllanthus acidus</i>	Samarakoon et al. (2018)