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# *Colletotrichum* species in Australia

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**Abstract** Forty-four species of *Colletotrichum* are confirmed as present in Australia based on DNA sequencing analyses. Many of these species were identified directly as a result of two workshops organised by the Subcommittee on Plant Health Diagnostics in Australia in 2015 that covered morphological and molecular approaches to identification of *Colletotrichum*. There are several other species of *Colletotrichum* reported from Australia that remain to be substantiated by DNA sequence-based methods. This body of work aims to provide a basis from which to critically examine a number of isolates of *Colletotrichum* deposited in Australian culture collections.

**Keywords** Biosecurity · Diagnostics · Molecular methods · Phylogenetic methods · Plant pathogens · Taxonomy

## Introduction

*Colletotrichum* (Ascomycota, Sordariomycetes) is one of the most important genera of plant pathogenic fungi worldwide, having been voted as one of the top 10 fungal pathogens by 495 scientists associated with the journal *Molecular Plant Pathology* (Dean et al. 2012). Species of *Colletotrichum* affect a range of plants, often causing diseases known as anthracnose, on many field and horticultural crops (Hyde et al. 2009a). On some tropical fruits, anthracnose can cause postharvest losses of up to 100 % in the absence of control measures. *Colletotrichum* species are also common endophytes, epiphytes and saprobes (Hyde et al. 2009b).

According to Taylor et al. (2000), the three most common ways to recognize species are the morphological, biological, and phylogenetic species concepts. The morphological species

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concept has been used for fungal species descriptions and diagnoses since 1753, when Linnaeus published *Species Plantarum* (McNeill et al. 2012, art. 13). However, between the 1880s and the 1950s, hundreds of new *Colletotrichum* species were described based on thepremise that *Colletotrichum* species were host-specific. The first monograph of *Colletotrichum* was published by von Arx (1957), who accepted 11 species, based on morphological characteristics alone, disregarding the plant hosts. Later Sutton (1980) reviewed this genus and accepted 23 species, and subsequently, 39 species of *Colletotrichum* (Sutton 1992). The identification and classification of species of *Colletotrichum* has undergone a taxonomic revolution in the last decade through the application of molecular phylogenetic methods (Cai et al. 2009, Crouch et al. 2009b, Hyde et al. 2009a, b). This approach has resulted in the recognition that several single species were actually complexes or aggregates of closely related cryptic species that were morphologically indistinguishable (Cannon et al. 2012), including *C. acutatum* (Damm et al. 2012b), *C. boninense* (Damm et al. 2012a), *C. caudatum* (Crouch 2014), *C. destructivum* (Damm et al. 2014), *C. gloeosporioides* (Weir et al. 2012), *C. gigasporum* (Liu et al. 2014), *C. graminicola* (Crouch and Beirn 2009, Du et al. 2005), *C. orbiculare* (Damm et al. 2013) and *C. truncatum* (Damm et al. 2009). Several major revisions of these species complexes have resulted in the formal description of many new species of *Colletotrichum* (Cai et al. 2009, Crouch et al. 2009a, b, Crouch 2014, Damm et al. 2009, 2012a, b, 2013, 2014, Hyde et al. 2009a, b, Shivas and Tan 2009, Weir et al. 2012). Cannon et al. (2012) summarised the history of the classification of *Colletotrichum*, which currently has over 100 accepted species. The importance of using a polyphasic approach to species delimitation in *Colletotrichum*, together with a large sample size, was emphasised in a recent study (Liu et al. 2016) that showed the apparent *C. siamense* species complex (Sharma et al. 2015) was a single species.

Very little is known about the biology, pathogenicity, host range and geographical distribution of many of the recently recognised species of *Colletotrichum*. This has created a dilemma for plant pathologists. Hyde et al. (2010) first noted that there was an urgent need to reassess inventories of many plant pathogenic genera, including *Colletotrichum*, in Australia where the effectiveness of biosecurity measures relies heavily on the accuracy of specimen-based databases of plant pathogens (Shivas et al. 2006). Hyde et al. (2010) recognised that the revision of checklists must be supported by examination of herbarium specimens, living cultures and DNA libraries.

Two complementary workshops were held in Australia in 2015 as part of annual training offered to the National Plant Biosecurity Diagnosticians Network in order to ensure Australian plant biosecurity diagnosticians were introduced to taxonomic changes and diagnostic challenges that surround recent changes in the taxonomy of *Colletotrichum* species. The workshops were funded by Plant Health Australia and arranged by the Subcommittee on Plant Health Diagnostics. The first workshop introduced the species complexes with a focus on morphology and biology. The second workshop introduced molecular and phylogenetic methods as applied to DNA sequence data obtained from isolates of *Colletotrichum*. Both workshops emphasised practical methods with more than 80 isolates examined from several Australian culture collections. Information gathered from these two workshops formed the basis for an up-to-date inventory of *Colletotrichum* species in Australia based on molecular phylogenetic evidence.

## Materials and methods

### Specimens and species identification

Living cultures of 86 specimens were sourced from Australian plant pathogen culture collections, including BRIP (Queensland), DAR (New South Wales), VPRI (Victoria) and WAC (Western Australia). A literature and database search found a further 106 Australian specimens with publically accessible evidence of DNA sequence data from previous studies. This DNA sequence data was sourced from GenBank (http://www.ncbi.nlm.nih.gov) (Benson et al. 2013 ), and the Q-bank Fungi database (a reference database for mycological phytopathology, http://www.q-bank.eu/Fungi/). Confirmation that species of *Colletotrichum* occurred in Australia required that the specimen had an unambiguous DNA sequence that matched data from the ex-type specimen.

### DNA extraction, PCR amplification and DNA sequencing

Mycelia were collected from cultures grown on potato dextrose agar (Difco$^{TM}$, Becton, Dickinson and Company, New Jersey, USA) and macerated with 0.5 mm glass beads (Daintree Scientific) in a Tissue Lyser (QIAGEN). Genomic DNA was extracted with the Gentra Puregene DNA Extraction kit (QIAGEN) or with ISOLATE II Plant DNA kit (Bioline) according to the manufacturers' instructions. Gene sequences were obtained from up to four nuclear gene regions for species identifications. These are *glyceraldehyde-3-phosphate dehydrogenase* (GAPDH), *glutamine synthetase* (GS), the *internal transcribed spacer* (ITS), and *β-tubulin* 2 (TUB). Primers used in this study are shown in Table 1. Where the standard GS primers (Stephenson et al. 1997) sequenced poorly, the primers from Weir et al. (2012) were used instead. All gene regions were amplified with the Phusion High-Fidelity PCR Master Mix (New England Biolabs). The PCR products were purified with the QIAquick PCR Purification Kit (QIAGEN), and sequenced on the 3730xl DNA Analyzer (Applied Biosystems) by a commercial company (Macrogen Incorporated, Korea) using the amplifying primers. All sequences generated were assembled using Geneious v. 9.1

**Table 1** Primers used in this study, with sequences and references

| Gene | Product name | Primer | Direction | Sequence (5′-3′) | Reference |
|---|---|---|---|---|---|
| GAPDH | *Glyceraldehyde-3-phosphate dehydrogenase* | GDF | Forward | GCC GTC AAC GAC CCC TTC ATT GA | Templeton et al. 1992 |
| | | GDR | Reverse | GGG TGG AGT CGT ACT TGA GCA TGT | Templeton et al. 1992 |
| GS | *Glutamine synthetase* | GSF1 | Forward | ATG GCC GAG TAC ATC TGG | Stephenson et al. 1997 |
| | | GSF3* | Forward | TCG CCC GCA CTG CTG CAG CCG G | Weir et al. 2012 |
| | | GSR1 | Reverse | GAA CCG TCG AAG TTC CAG | Stephenson et al. 1997 |
| | | GSR2 | Reverse | GAA CCG TCG AAG TTC CAC | Weir et al. 2012 |
| ITS | *Internal transcribed spacer* | V9G | Forward | TTACGTCCCTGCCCTTTGTA | de Hoog and Gerrits van den Ende 1998 |
| | | ITS4 | Reverse | TCC TCC GCT TAT TGA TAT GC | White et al. 1990 |
| TUB | *$\beta$-tubulin 2* | T1 | Forward | AAC ATG CGT GAG ATT GTA AGT | O'Donnell and Cigelnik 1997 |
| | | Bt2b | Reverse | ACC CTC AGT GTA GTG ACC CTT GGC | Glass and Donaldson 1995 |

* The sequence given by Weir et al. (2012) has been corrected here

(Biomatters Ltd), and deposited in GenBank (Table 2, in bold). These sequences were compared against those from type specimens using BLASTn (https://blast.ncbi.nlm.nih.gov/Blast.cgi).

## Results

The names of Australian *Colletotrichum* species that were verified by DNA sequence analysis are given in the following numbered list. This list contains only species that were verified by comparison of their DNA sequence data against type specimens. The GenBank accession numbers of sequences generated in this study are provided in Table 2 (in bold font) together with reference sequences generated in other studies (Roman font).

### Australian species of *Colletotrichum* verified by DNA sequence data

1. x***Colletotrichum acutatum*** J.H. Simmonds, Queensland Journal of Agricultural and Animal Science 25: 178A (1968).

*Colletotrichum acutatum* was first described from Redlands Horticultural Research Station, Cleveland, Queensland on papaya (*Carica papaya*) by Simmonds (1965, 1968). This species has since been recognised as an important pathogen that causes anthracnose on a range of plants worldwide. However, *C. acutatum* has long been recognised as a complex of closely related species that have conidia with acute ends (Simmonds 1965). The chequered taxonomic history of *C. acutatum* was summarized by Damm et al. (2012b), who designated an epitype that has ultimately provided taxonomic stability for this species. In Australia, *C. acutatum* is widespread and known to cause diseases or be associated with disease symptoms on a range of plants, including papaya, strawberry, olives and pistachio. The literature indicates that the *C. acutatum* species complex may have a much wider host range in Australia, where it has been reported to cause diseases on avocado, tomato (Simmonds 1965), grapes (Melksham et al. 2002, Whitelaw-Weckert et al. 2007), olive (Spooner-Hart et al. 2007) and almond (McKay et al. 2009). However, many of these records require verification. *Colletotrichum acutatum* can be distinguished from other species in the *C. acutatum* species complex by any of the six genes analysed in Damm et al. (2012b). The Australian specimens of *C. acutatum* were identified based on the 100 % identity of ITS, GS and/or TUB sequences to *C. acutatum* ex-type strain CBS 112996 (Table 2).

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

*Colletotrichum alcornii* belongs to the *Colletotrichum caudatum* species complex (Crouch 2014). *Colletotrichum alcornii* is only known from two native Australian grass species in south-east Queensland. Although morphologically similar to four other species in the *C. caudatum* species complex, *C. alcornii* is easily distinguished based on ITS sequences (Crouch 2014).

3. ***Colletotrichum alienum*** B.S. Weir & P.R. Johnst., Studies in Mycology 73: 139 (2012).

*Colletotrichum alienum* belongs to the *C. gloeosporioides* species complex (Weir et al. 2012). In Australia, *C. alienum* has been reported from avocado (Weir *et al.* 2012), *Grevillea* sp. (Liu et al. 2013b), *Protea* spp. (Crous et al. 2013) and *Nerium oleander* (oleander) (Schena et al. 2014). *Colletotrichum alienum* was identified as a serious anthracnose pathogen of Proteaceae in South Africa, Europe and Australia (Liu et al. 2013b, Crous et al. 2013). *Colletotrichum alienum* is best distinguished from other

**Table 2** List of Australian species of *Colletotrichum* verified by DNA sequencing. Sequences derived from this study are in **bold**

| Species | Culture $^{a\ b}$ | Host (symptoms) | Locality (State$^{c}$, city/town) | GenBank Accessions | | | |
|---|---|---|---|---|---|---|---|
| | | | | ITS | GAPDH | GS | TUB |
| *Colletotrichum acutatum* | VPRI 10179 = BRIP 52653 | *Anemone* sp. (stem spot) | Vic, Geelong | GU183350 | | | GU183309 |
| | VPRI 10517 | *Anemone* sp. (leaf spot) | Vic, Geelong | GU183353 | | | GU183310 |
| | = BRIP 52656 | | | | | | |
| | = IMI 223120 | | | | | | |
| | WAC 12421 | *Boronia megastigma* | SA, Mt Barker | | | | |
| | = BRIP 52695 | | | | | | |
| | IMI 117617$^{HT}$ | *Carica papaya* (fruit rot) | Qld, Ormiston | AF411700 | | | |
| | BRIP 4693$^{IS}$ | | | | | | |
| | CBS 112996 | | | JQ005776 | | | |
| | = ATCC 56816 | | | | | | |
| | = ICMP 1783$^{ex\text{-}EP}$ | | | | | | |
| | WAC 5416 | *Fragaria x ananassa* (fruit rot) | WA, Wanneroo | GU183356 | | | GU183312 |
| | = BRIP 52691 | | | | | | |
| | = CBS 127602 | | | | | | |
| | BRIP 54038 | *Malus domestica* (bitter rot) | Qld, Brisbane | **KU498249** | | | |
| | CBS 111993 | *Grevillea* sp. | NSW, Mt Annari | JQ948349 | | | JQ950000 |
| | BRIP 27048 | *Mangifera indica* (fruit lesion) | Qld, Ayr | GU183326 | | | GU183307 |
| | WAC 5990 = BRIP 52692 | *Olea europaea* | WA, Kalamunda | GU183357 | | | GU183313 |
| | WAC 12568 | | WA, Perth | **KX069826** | | **KX069811** | **KX069817** |
| | = BRIP 63678 | | | | | | |
| | VPRI 41821 | *Pistacia vera* (leaf and fruit spots) | NSW, Kyalite | **KU498251** | | | **KU221358** |
| | = BRIP 62667 | | | | | | |
| | VPRI 41430 | *Pistacia vera* | | **KU498250** | | | **KU221356** |
| | = BRIP 54786 | *Pistacia vera* | | | | | |
| | VPRI 41429 | *Pistacia vera* | Vic, Robinvale | | | | **KU221357** |
| | = BRIP 54787 | | | | | | |
| | VPRI 41432 | | Vic, Nangiloc | | | | **KU221355** |
| | = BRIP 54785 | | | | | | |
| | WAC 5506 = BRIP 52690 | | WA, unknown | GU183355 | | | GU183311 |
| | IMI 336479 | | WA, Perth | JQ948367 | | | JQ950018 |
| | VPRI 16304 | *Ranunculus* sp. | Vic, Clayton South | GU183349 | | | GU183308 |
| | = BRIP 52652 | | | | | | |
| | WAC 11064 = BRIP 62860 | *Vicia faba* var. *minor* | WA, Dongara | **KX069821** | **KX069805** | **KX069808** | **KX069812** |
| *Colletotrichum alcornii* | IMI 176617$^{PT}$ | *Bothriochloa bladhii* | Qld, Toogoolawah | JX076857 | | | |
| | = BRIP 8779$^{PT}$ | | | | | | |
| | IMI 176619$^{HT}$ | *Imperata cylindrica* var. *major* | Qld, Caboolture | JX076858 | | | |
| | BRIP 8824$^{IS}$ | | | | | | |
| *Colletotrichum alienum* | DAR 25578 | *Fragaria x ananassa* (fruit rot) | NSW, Sydney | **KU498254** | **KU221344** | **KU221335** | **KU221362** |
| | = BRIP 61805 | | | | | | |
| | DAR 32071 | *Fragaria x ananassa* | NSW, Gosford | **KU498253** | | **KU221334** | **KU221361** |
| | = BRIP 61799 | | | | | | |
| | CBS 111982 | *Grevillea* sp. | NSW, unknown | KC297069 | KC296998 | KC297021 | KC297091 |
| | CBS 132880 | | | KC297075 | KC297005 | KC297022 | KC297099 |
| | F263 | *Nerium oleander* | Unknown | KC425654 | | | KC435707 |
| | DAR 37820 | *Persea americana* | NSW, Murwillumbah | JX010217 | JX010018 | JX010074 | JX010385 |
| | = IMI 313842 | | | | | | |

**Table 2** (continued)

| Species | Culture $^{a\ b}$ | Host (symptoms) | Locality (State$^{c}$, city/town) | GenBank Accessions | | | |
|---|---|---|---|---|---|---|---|
| | | | | ITS | GAPDH | GS | TUB |
| | = ICMP 18691 | | | | | | |
| *Colletotrichum aotearoa* | CBS 132448 | *Banksia marginata* (leaf spot) | Vic, Dunkeld | KC297064 | KC296997 | KC297020 | KC297089 |
| | VPRI 40656 | *Hedycarya angustifolia* (leaf spot) | Vic, Marysville | **KU498255** | **KU221340** | | **KU221363** |
| | = BRIP 62670 | | | | | | |
| *Colletotrichum asianum* | IMI 313839 | *Mangifera indica* | NSW, Sextonville | JX010192 | JQ00973 | JX010073 | JX010384 |
| | = ICMP 18696 | | | | | | |
| | BRIP 57972 | *Mangifera indica* (stem dieback) | NT, Bees Creek | KF877314 | | | |
| | BRIP 58110 | | Qld, Brisbane | | | | **KU221370** |
| | BRIP 58326b | *Mangifera indica* (stem dieback & leaf wilt) | Qld, Townsville | **KU498262** | | | **KU221371** |
| | BRIP 57882 | *Mangifera indica* (stem canker) | Qld, Narangba | **KU498261** | | | |
| | BRIP 28734 | *Mangifera indica* (anthracnose) | Qld, Gin Gin | JN191511 | | | JN191525 |
| | BRIP 28451 | *Mangifera indica* (fruit rot) | Qld, Mareeba | **KU498256** | | | |
| | BRIP 62535b | *Mangifera indica* (fruit lesion) | Qld, Tolga | **KU498263** | | | |
| *Colletotrichum australe* | CBS 131325$^{PT}$ | *Hakea* sp. | WA, Alcoa | JQ948456 | | | JQ950107 |
| *Colletotrichum axonopodi* | IMI 279189$^{HT}$ | *Axonopus fissifolius* | Qld, Peregian Beach | EU554086 | | | |
| | BRIP 14026$^{IS}$ | | | | | | |
| *Colletotrichum boninense* | CBS 112762 | *Leucospermum* sp. | NSW, Nunkeri | AY376522 | | | AY376570 |
| *Colletotrichum brevisporum* | BRIP 54898b | *Carica papaya* (fruit rot) | Qld, South Johnstone | **KU498265** | | | |
| | BRIP 43898 | *Passiflora edulis* (vascular discolouration) | Qld, Gregory River | **KU498264** | | | |
| *Colletotrichum brisbanense* | IMI 117622$^{HT}$ | *Capsicum frutescens* (fruit rot) | Qld, Brisbane | JQ948291 | JQ948621 | | JQ949942 |
| | BRIP 4684$^{IS}$ | | | | | | |
| | CBS 292.67$^{ex\text{-}IS}$ | | | | | | |
| *Colletotrichum chlorophyti* | CBS 142.79 | *Stylosanthes hamata* | Qld, Townsville | GU227895 | GU228287 | | GU228189 |
| *Colletotrichum circinans* | VPRI 42617 | *Allium porrum* | Vic, Devon Meadows | **KU612898** | **KU612899** | | |
| *Colletotrichum coccodes* | DAR 32115 = BRIP 61800 | *Fragaria x ananassa* (fruit rot) | NSW, Pimlico | **KU498266** | | | |
| | WAC 8123 = BRIP 63677 | *Iris* sp. | WA, Millendon | **KX069825** | | **KX069810** | **KX069816** |
| | VPRI 41585 = BRIP 54784 | *Solanum lycopersicum* (root rot & anthracnose) | Vic, Warragul | | | | **KU221372** |
| *Colletotrichum cymbidiicola* | IMI 34792$^{HT}$ | *Cymbidium* sp. (leaf lesion) | WA, Fremantle | JQ005166 | JQ005253 | | JQ005600 |
| *Colletotrichum dematium* | IMI 350847 | *Solanum tuberosum* | Tas, unknown | GU227825 | GU228217 | | GU228119 |
| *Colletotrichum destructivum* | UQ349 | *Medicago scutellata* | Qld, Kingsthorpe | AF451909 | | | |
| | UQ343 | *Ornithopus compressus* | Qld, Leyburn | AF451908 | | | |
| *Colletotrichum dracaenophilum* | VPRI 41774 | *Dracaena sanderiana* (stem lesion) | Vic, Narre Warren | **KU612894** | **KU612895** | | |
| | VPRI 41775 | | Vic, Vermont | **KU612896** | **KU612897** | | |
| *Colletotrichum fioriniae* | WAC 13265 | *Acacia acuminata* | WA, Manjimup | GU183320 | | | GU183268 |
| | = BRIP 52696 | | | | | | |
| | BRIP 28761 | *Mangifera indica* (endophyte) | Qld, Yarwun | GU183333 | | | GU183269 |
| | BRIP 20127 | *Persea americana* (fruit rot) | Qld, Brisbane | GU183320 | | | GU183268 |
| | BRIP 29285 | | Qld, Mt Tamborine | GU183336 | | | GU183271 |
| | BRIP 29284 | | | GU183335 | | | GU183270 |
| | BRIP 52336 | | WA, Pemberton | GU183347 | | | GU183273 |
| | BRIP 52335 | | | GU183346 | | | GU183272 |
| *Colletotrichum fructicola* | BRIP 28522 | *Persea americana* (fruit rot) | Qld, Bli Bli | JX01066 | JX009946 | | |
| | = ICMP 12568 | | | | | | |
| *Colletotrichum gloeosporioides* | DAR 76936 = ICMP 18736 | *Carya illinoinensis* | NSW, Tamworth | JX010151 | JX009976 | | |
| | F264 | *Citrus limon* | unknown | KC425621 | | | KC425696 |
| | F265 | | | KC425619 | | | KC425695 |

**Table 2** (continued)

| Species | Culture [a] [b] | Host (symptoms) | Locality (State[c], city/town) | GenBank Accessions | | | |
|---|---|---|---|---|---|---|---|
| | | | | ITS | GAPDH | GS | TUB |
| | F266 | | | KC425620 | | | KC425694 |
| | VPRI 42335 | *Citrus sinensis* | Vic, Lindenow | **KU612890** | **KU612891** | | |
| | WAC 12803 = BRIP 63680 | | WA, Gingin | **KX069827** | | | **KX069818** |
| *Colletotrichum godetiae* | VPRI 41712 = BRIP 54820 | *Helleborus* sp. (leaf spot) | Vic, Olinda | | | | **KU612889** |
| | VPRI 16247 | *Malus domestica* (fruit rot) | Vic, Mt Selby | **KU612886** | **KU612888** | | |
| *Colletotrichum kahawae* subsp. *ciggaro* | ICMP 18539$^{ex-HT}$ | *Olea europea* cv. Manzanillo | NSW, Nemingham | | | JX010132 | |
| *Colletotrichum karstii* | BRIP 29085 = CBS 127597 | *Diospyros australis* (calyx necrosis) | Qld, Palmwoods | JQ005204 | JQ005291 | | JQ005638 |
| | CBS 111998 | *Leucospermum* sp. | NSW, unknown | JQ005299 | | | JQ005646 |
| | BRIP 28443 = CBS 127596 | *Mangifera indica* (endophyte) | Qld, Brisbane | JQ005203 | JQ005290 | | JQ005637 |
| | CBS 127595 | *Musa banksii* | unknown | JQ005178 | JQ005265 | | JQ005612 |
| | CBS 127591 | *Sclerocroton integerrimus* | unknown | JQ005186 | JQ005273 | | JQ005620 |
| *Colletotrichum lupini* | WAC 10408 = BRIP 63847 | *Lupinus albus* | WA, Mingenew | **KU974988** | **KU974972** | | **KU975004** |
| | WAC 9624 = IMI 375715 | | WA, Morawa | JQ948161 | JQ948491 | | JQ949812 |
| | WAC 12999 = BRIP 63855 | | | **KU974991** | **KU974979** | | **KU975012** |
| | WAC 10361 = BRIP 63844 | | | **KU974985** | **KU974969** | | **KU975001** |
| | WAC 10359 = BRIP 63843 | | WA, Three Springs | **KU974984** | **KU974968** | | **KU975000** |
| | WAC 13001 = BRIP 63857 | | WA, Yandanooka | **KU974998** | **KU974981** | | **KU975014** |
| | WAC 12994 = BRIP 63850 | *Lupinus angustifolius* | WA, Dongara | **KU974992** | **KU974975** | | **KU975007** |
| | WAC 13000 = BRIP 63856 | *Lupinus consentinii* | WA, Badgingarra | **KU974997** | **KU974980** | | **KU975013** |
| | WAC 13003 = BRIP 63859 | | WA, Eneabba | **KU974999** | **KU974983** | | **KU975016** |
| | WAC 12997 = BRIP 63853 | | WA, Geraldton | **KU974995** | **KU974978** | | **KU975010** |
| | WAC 10425 = BRIP 63848 | | WA, Mingenew | **KU974989** | **KU974973** | | **KU975005** |
| | WAC 10427 = BRIP 63849 | | | **KU974990** | **KU974974** | | **KU975006** |
| | WAC 10404 = BRIP 63846 | | WA, Morawa | **KU974987** | **KU974971** | | **KU975003** |
| | WAC 12998 = BRIP 63854 | | WA, Mullewa | **KU974996** | | | **KU975011** |
| | WAC 10398 = BRIP 63845 | | WA, Three Springs | **KU974986** | **KU974970** | | **KU975002** |
| | WAC 12996 = BRIP 63852 | | WA, Walkaway | **KU974994** | **KU974977** | | **KU975009** |
| | WAC 13002 = BRIP 63858 | | | | **KU974982** | | **KU975015** |
| | WAC 12995 = BRIP 63851 | *Lupinus luteus* | WA, Mingenew | **KU974993** | **KU974976** | | **KU975008** |

**Table 2** (continued)

| Species | Culture [a] [b] | Host (symptoms) | Locality (State[c], city/town) | GenBank Accessions | | | |
|---|---|---|---|---|---|---|---|
| | | | | ITS | GAPDH | GS | TUB |
| *Colletotrichum musae* | BRIP 59413 | *Musa acuminata* (crown rot) | Qld, Tully | **KU498267** | | | |
| | WAC 6994 = BRIP 63674 | *Musa acuminata* (leaf spot) | WA, Carnarvon | **KX069823** | **KX069807** | | **KX069814** |
| | WAC 13307 = BRIP 63681 | | | **KX069828** | | | **KX069819** |
| | BRIP 61880b | *Musa* sp. (endophyte) | Qld, Atherton | **KU498270** | | | |
| | BRIP 61879b | | Qld, Walkamin | **KU498269** | | | |
| | DAR 30640 = BRIP 61798 | *Musa* sp. (fruit rot) | NSW, Macksville | **KU498268** | | | |
| *Colletotrichum nymphaeae* | VPRI 10347 = BRIP 54771 | *Citrus limon* (leaf spot) | Vic, unknown | | | | **KU221374** |
| | VPRI 41914 = BRIP 62666 | *Fragaria x ananassa* (plant wilt) | Vic, Heatherton | **KU498271** | **KU221346** | | **KU221376** |
| | VPRI 11206 = BRIP 54791 = IMI 260254 | *Protea compacta* (stem dieback) | Vic, Emerald | | | | **KU221375** |
| | CBS 482.82 | *Protea* sp. (leaf spot) | Vic, Burnley | JQ948213 | JQ948543 | | JQ949864 |
| | VPRI 17866 = BRIP 54770 | | Vic, Doncaster | | | | **KU221373** |
| *Colletotrichum ocimi* | BRIP 49125 | *Ocimum basilicum* (leaf spot) | Qld, Brisbane | **KU498272** | | | |
| *Colletotrichum orbiculare* | DAR 81253 = CBS 129432 | *Benincasa hispida* (leaf lesion) | NSW, Bringelly | KF178469 | KF178494 | KF178614 | KF178590 |
| *Colletotrichum petchii* | VPRI 41776 | *Dracaena sanderiana* | Vic, Blackburn | **KU612982** | **KU612893** | | |
| *Colletotrichum phormii* | WAC 15254 = BRIP 62862 | *Phormium tenax*(anthracnose) | WA, Busselton | **KU947422** | | | **KU947421** |
| *Colletotrichum pyricola* | VPRI 12013 = BRIP 62668 | *Daphne odora* (leaf and tip dieback) | Vic, Mitcham | **KU498273** | **KU221341** | | **KU221364** |
| *Colletotrichum queenslandicum* | IMI 117612$^{HT}$<br>PDD 28797$^{EP}$<br>ICMP 1778$^{ex-EP}$ | *Carica papaya* (fruit rot) | Qld, Brisbane | JX010276 | JZ009934 | JX010104 | JZ010414 |
| | ICMP 1780 | | | JX010186 | JX010010 | | |
| | BRIP 48744 | *Litchi chinensis* (anthracnose) | Qld, Mena Creek | JN191512 | | | JN191526 |
| | BRIP 57881 | *Mangifera indica* (stem canker) | Qld, Narangba | **KU498275** | **KU221348** | | **KU221378** |
| | BRIP 57981 | *Passiflora edulis* (anthracnose) | NT, Darwin | | | | KF877320 |
| | BRIP 55403 | *Persea americana* (stem dieback) | NSW, Duranbah | **KU498274** | **KU221347** | | **KU221377** |
| | ICMP 12564 = BRIP 28418 | | Qld, Home Hill | JX010184 | JX009919 | | |
| *Colletotrichum salicis* | VPRI 32546 = BRIP 60908 | *Salix alba* subsp. *vitellina* (leaf lesion) | ACT, Brindabella | **KU498279** | **KU221351** | | **KU221381** |
| | VPRI 32735 = BRIP 55537 | *Salix cinerea* (leaf lesion) | Vic, Cann River | **KU498277** | **KU221349** | | |
| | VPRI 32575 = BRIP 55536 | *Salix fragilis* (leaf lesion) | NSW, Tumut River | **KU498276** | | | **KU221379** |
| | VPRI 32736 = BRIP 55538 | *Salix purpurea* (leaf lesion) | Tas, Blackfish Creek | **KU498278** | **KU221350** | | **KU221380** |
| *Colletotrichum sansevieriae* | VPRI 41498 | *Sansevieria* sp. (anthracnose) | Vic, Cranbourne | HQ433226 | | | |
| *Colletotrichum siamense* | BRIP 57967b | *Artocarpus heterophyllus* (endophyte) | NT, Middle Point | | | | KF877321 |
| | BRIP 57977 | *Artocarpus sericicarpus* (endophyte) | NT, Bees Creek | | | | KF877322 |
| | BRIP 57970 | *Coffea arabica* (leaf lesion) | NT, Bees Creek | | | | KF877323 |
| | BRIP 57963 | *Coffea canephora* (endophyte) | NT, Middle Point | | | | KF877324 |

**Table 2** (continued)

| Species | Culture[a, b] | Host (symptoms) | Locality (State[c], city/town) | GenBank Accessions | | | |
|---|---|---|---|---|---|---|---|
| | | | | ITS | GAPDH | GS | TUB |
| | DAR 28343c<br>= BRIP 61797 | *Dionaea muscipula* (leaf blight) | NSW, Sydney | **KU498283** | | | **KU221383** |
| | BRIP 57980 | *Eriobotrya japonica* (endophyte) | NT, Bees Creek | | | | KF877327 |
| | BRIP 57979 | *Ficus carica* (endophyte) | NT, Bees Creek | | | | KF877328 |
| | F272 | *Hibiscus* sp. | unknown | KC425649 | | | KC425703 |
| | BRIP 57975 | *Mentha* sp. (leaf lesion) | NT, Bees Creek | | | | KF877329 |
| | F28 | *Olea europaea* | unknown | KC425659 | | | KC425702 |
| | ICMP 12567<br>= BRIP 19772 | *Persea americana* (fruit rot) | NSW, Murwillumbah | JX010250 | JX00940 | JX10076 | JX010387 |
| | ICMP 12565<br>= BRIP 28812 | *Persea americana* (anthracnose) | Qld, Mt Tamborine | JX010249 | JX009937 | | |
| | BRIP 57976 | *Piper nigrum* (leaf lesion) | NT, Bees Creek | | | | KF877330 |
| | ICMP 18574<br>= DAR 76934 | *Pistacia vera* | NSW, Muswellbrook | JX010270 | JX010002 | | JX010391 |
| | BRIP 57978 | *Rosmarinus officinalis* (endophyte) | NT, Bees Creek | | | | KF877331 |
| | BRIP 57966 | *Theobroma cacao* (endophyte) | NT, Middle Point | | | | KF877318 |
| *Colletotrichum simmondsii* | BRIP 24197 | *Actinidia chinensis* (stem end rot) | Qld, Mt Tamborine | GU183323 | | | GU183282 |
| | BRIP 28487 | *Averrhoa carambola* (fruit rot) | Qld, unknown | GU183328 | | | GU183286 |
| | VPRI 13891a<br>= BRIP 54772 | *Calothamnus quadrifidus* (stem lesion) | Vic, Park Orchards | | | | **KU221386** |
| | BRIP 11084<br>= CBS 294.67 | *Carica papaya* (fruit rot) | Qld, Brisbane | JQ948277 | JQ948607 | | JQ949928 |
| | BRIP 28519$^{\mathrm{HT}}$<br>= CBS 122122<br>= ICMP 17298 | *Carica papaya* (anthracnose) | Qld, Yandina | GU183331 | JQ948606 | | GU183289 |
| | BRIP 28420 | *Cyphomandra betacea* (fruit rot) | Qld, Mt Tamborine | GU183327 | | | GU183285 |
| | BRIP 4704 | *Fragaria x ananassa* (fruit rot) | Qld, Forest Glen | GU183317 | | | GU183277 |
| | BRIP 11086 = CBS 295.67 | | Qld, Nambour | GU183318 | JQ948608 | | GU183278 |
| | BRIP 4703 | | Qld, Townsville | GU183316 | | | GU183276 |
| | VPRI 10360<br>= BRIP 52654 | | Vic, Scoresby | GU183348 | | | GU183301 |
| | VPRI 10487 = BRIP 52655 | | Vic, Silvan | GU183351 | | | GU183302 |
| | WAC 2768<br>= IMI 354381 | | WA, Wanneroo | JQ948280 | JQ948610 | | JQ949931 |
| | VPRI 10449<br>= BRIP 54813<br>= CBS 132311 | *Fragaria x ananassa* (leaf spot) | unknown | | | | **KU221387** |
| | WAC 7989<br>= BRIP 52694 | | WA, Baldivis | GU183359 | | | GU183306 |
| | BRIP 39473 | *Litchi chinensis* (fruit pepper spot) | NSW, Byron Bay | GU183337 | | | GU183292 |
| | BRIP 24243 | *Litchi chinensis* (anthracnose) | Qld, Atherton | GU183324 | | | GU183283 |
| | BRIP 48724 | | Qld, Mena Creek | GU183338 | | | GU183263 |
| | BRIP 60282 | *Litchi chinensis* (endophyte) | Qld, Mareeba | **KU498285** | | | **KU221388** |
| | VPRI 15973<br>= BRIP 54768 | *Mandevilla* sp. (leaf spot) | Vic, Park Orchards | | | | **KU221385** |
| | BRIP 28832 | *Mangifera indica* (fruit rot) | Qld, Ayr | GU183334 | | | GU183291 |

**Table 2** (continued)

| Species | Culture [a] [b] | Host (symptoms) | Locality (State[c], city/town) | GenBank Accessions | | | |
|---|---|---|---|---|---|---|---|
| | | | | ITS | GAPDH | GS | TUB |
| | BRIP 28533 | *Mangifera indica* (anthracnose) | Unknown | GU183332 | | | GU183290 |
| | BRIP 24124 | *Nephelium lappaceum* (fruit rot) | Qld, Kamerunga | GU183321 | | | GU183280 |
| | BRIP 54619 | *Prunus domestica* (shoot dieback) | Qld, Lake Eacham | **KU498284** | | | **KU221384** |
| | DAR 62104<br>= BRIP 61803 | *Solanum lycopersicum* (fruit spot & rot) | NSW, Comboyne | **KU498286** | | | |
| | VPRI 11088<br>= IMI 260260<br>= BRIP 52657 | | NSW, Tweed Heads | GU183352 | | | GU183303 |
| | BRIP 62284 | *Vaccinium corymbosum* (fruit rot) | NSW, Brooklet | **KU498287** | | | |
| | BRIP 62285 | | NSW, Corindi | **KU498288** | | | |
| | VPRI 15627<br>= BRIP 52651 | | Vic, Knoxfield | GU183300 | | | |
| *Colletotrichum sloanei* | BRIP 48742 | *Litchi chinensis* (anthracnose) | Qld, Mena Creek | **KU498289** | **KU221342** | | **KU221365** |
| *Colletotrichum spinaciae* | VPRI 31994<br>= BRIP 52700<br>= CBS 125444 | *Spinacia oleracea* (leaf spot) | Vic, Cora Lynn | **KU498290** | **KU221353** | | |
| | VPRI 32005<br>= BRIP 52701<br>= CBS 125446 | | | **KU498291** | **KU221354** | | |
| *Colletotrichum spinosum* | DAR 48942$^{\mathrm{HT}}$<br>= CBS 515.97$^{\mathrm{ex\text{-}HT}}$ | *Xanthium spinosum* (stem lesion) | NSW, Coolah | KF178474 | KF178498 | KF178620 | KF178595 |
| *Colletotrichum tanaceti* | BRIP 57314$^{\mathrm{HT}}$<br>= CBS 132693$^{\mathrm{ex\text{-}HT}}$ | *Tanacetum cinerariifolium* (leaf lesion) | Tas, Scottsdale | JX218228 | JX218243 | | JX218233 |
| *Colletotrichum theobromicola* | DAR 41929<br>= BRIP 13654 | *Aeschynomene falcata* (leaf spot & stem blight) | NSW, Grafton | | | | **KU221389** |
| | DAR 25000 = BRIP 61796 | *Aeschynomene falcata* (stem lesion) | NSW, Shannon Brook | **KU498293** | | | **KU221391** |
| | BRIP 57969 | *Coffea arabica* (flower lesion) | NT, Bees Creek | KF877316 | | | |
| | BRIP 57984 | *Coffea arabica* (leaf lesion) | NT, Melville Island | KF877317 | | | |
| | BRIP 46055 | *Olea europaea* (anthracnose) | Qld, Wondai | **KU498292** | | | |
| | BRIP 58448 | *Punica granatum* (fruit rot) | Qld, Tolga | | | | **KU221390** |
| | ICMP 17958<br>= CBS 124250 | *Stylosanthes guianensis* | Qld, Samford | JX010291 | JX009948 | JX010067 | JX010381 |
| | BRIP 35000$^{\mathrm{HT}}$ [d]<br>= ICMP 17957$^{\mathrm{IS}}$<br>= CBS 124251$^{\mathrm{IS}}$ | *Stylosanthes viscosa* | Qld, Townsville | JX010289 | JX009962 | JX010063 | JX010380 |
| *Colletotrichum tofieldiae* | BRIP 63314c | *Grevillea crithmifolia* | WA, Bullsbrook | **KX069822** | | | **KX069813** |
| | WAC 7298 = BRIP 63676 | *Iris germanica* | WA, Mundaring | **KX069824** | | | **KX069815** |
| *Colletotrichum truncatum* | BRIP 12563 | *Arachis hypogaea* (leaf spot) | Qld, Gurgeena | AF451899 | | | |
| | DAR 33949b<br>= BRIP 62368 | *Glycine max* (pod blight) | NSW, Grafton | **KU498297** | | | |
| | DAR 44534 | | NSW, Herons Creek | AF451906 | | | |
| | BRIP 55638b | | unknown | **KU498294** | | | |
| | BRIP 55662b | | unknown | **KU498295** | | | |
| | BRIP 55697 | *Helianthus annuus* | Qld, Ryeford | **KU498296** | | | |
| | CBS 141.79 | *Stylosanthes hamata* | Qld, Townsville | GU227873 | GU228265 | | GU228167 |
| | DAR 67500 | *Xanthium occidentale* | NT, Mainoru Station | AF451907 | | | |

**Table 2** (continued)

| Species | Culture [a] [b] | Host (symptoms) | Locality (State[c], city/town) | GenBank Accessions | | | |
|---|---|---|---|---|---|---|---|
| | | | | ITS | GAPDH | GS | TUB |
| *Colletotrichum xanthorrhoeae* | WAC 8358$^{HT}$<br>= BRIP 45094$^{ex-HT}$<br>= CBS 127831$^{IS}$<br>= ICMP 17903$^{IS}$ | *Xanthorrhoea preissii* (leaf spot) | WA, Perth | GU048667 | JX009927 | JX010138 | JX010448 |
| | IMI 350817<br>= ICMP 17820 | *Xanthorrhoea* sp. (leaf spot) | Qld, Cunningham's Gap | JX010260 | JX010008 | | |

[a] BRIP, Queensland Plant Pathology Herbarium, Brisbane, Queensland; CBS, Centraalbureau voor Schimmelcultures, Fungal Biodiversity Centre, Utrecht, the Netherlands; DAR, NSW Plant Pathology Herbarium, Orange, NSW; ICMP, International Collection of Microorganisms from Plants, Auckland, New Zealand; IMI, Culture collection of CAB International, Wallingford, UK; PDD, New Zealand Fungal and Plant Disease Collection, New Zealand; UQ, University of Queensland, St Lucia, Queensland; VPRI, Victorian Plant Pathology Herbarium, Bundoora, Victoria; WAC, Western Australian Culture Collection, South Perth, Western Australia

[b] EP, epitype; HT, holotype; IS, isotype; PT, paratype

[c] ACT, Australian Capital Territory, NSW, New South Wales; NT, Northern Territory; Qld, Queensland; SA, South Australia; Tas, Tasmania; Vic, Victoria; WA, Western Australia

[d] holotype of *Colletotrichum gloeosporioides* f. *stylosanthis*

species in the *C. gloesporioides* species complex using GS sequences. The Australian specimens of *C. alienum* were identified based on the 99–100 % identity of GS sequences to *C. alienum* ex-type strain ICMP 12071 (Table 2).

4. ***Colletotrichum aotearoa*** B. Weir & P.R. Johnst. Studies in Mycology 73: 139 (2012).

*Colletotrichum aotearoa* belongs to the *C. gloeosporioides* species complex (Weir et al. 2012). *Colletotrichum aotearoa* was first reported from Australia on *Banksia marginata* (Liu et al. 2013b) in a study of *Colletotrichum* species on Proteaceae. *Colletotrichum aotearoa* can be distinguished from other species in the *C. gloesporioides* species complex with GAPDH, GS and/or TUB sequences (Weir et al. 2012). The Australian specimens of *C. aotearoa* were identified based on the 99–100 % identity of GS sequences to the *C. aotearoa* ex-type strain ICMP 18537 (Table 2).

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

*Colletotrichum asianum* belongs to the *C. gloeosporioides* species complex (Weir et al. 2012). In Australia, *C. asianum* has only been isolated from mango, on which it is associated with a range of disease symptoms (Weir et al. 2012; Anderson et al. 2013 as *C. gloeosporioides*, James et al. 2014). *Colletotrichum asianum* can be distinguished from other species in the *C. gloeosporioides* species complex by any of the eight genes analysed in Weir et al. (2012). The Australian specimens of *C. asianum* were identified based on the 99–100 % identity of ITS, and/or TUB sequences to *C. asianum* ex-type strain MFLU 090234 (Table 2).

6. ***Colletotrichum australe*** Damm, P.F. Cannon & Crous, Studies in Mycology 73: 57 (2012b).

*Colletotrichum australe* belongs to the *C. acutatum* species complex, and is distinguishable by either GAPDH, histone 3, ITS or TUB sequences (Damm et al. 2012b).

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

*Colletotrichum axonopodi* belongs to the *C. graminicola* species complex, which comprises predominantly grass infecting species with falcate spores (Cannon et al. 2012). *Colletotrichum axonopodi* can be identified by its unique ITS sequence and association with leaf spots on some species of *Axonopus* (Crouch et al. 2009a).

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

Damm et al. (2012a) resolved the *C. boninense* species complex with multilocus phylogenetic analyses, describing several new species. *Colletotrichum boninense* is best identified by ITS and GAPDH sequences (Damm et al. 2012a). Damm et al. (2012a) reported *C. boninense* from *Leucospermum* sp. in Australia without specimen collection details (CBS 112115). *Colletotrichum boninense* has been reported as a pathogen and an endophyte on a range of plant species worldwide (Hyde et al. 2009a).

9. ***Colletotrichum brevisporum*** Noireung, Phouliv., L. Cai & K.D. Hyde, Cryptogamie Mycologie 33: 350 (2012).

This is the first record of *C. brevisporum* in Australia. *Colletotrichum brevisporum* has been recorded as an endophyte as well as a pathogen on a range of host plant species in several tropical countries. *Colletotrichum brevisporum* can be identified based on sequence identity of ITS, GAPDH and/or TUB (Noireung et al. 2012). The Australian specimens of *C. brevisporum* have been identified based on the 100 % identity of ITS sequences to *C. brevisporum* ex-type strain BCC 38876 (Table 2).

10. ***Colletotrichum brisbanense*** Damm. P.F. Cannon & Crous, Studies in Mycology 73: 59 (2012b).

*Colletotrichum brisbanense* belongs to the *C. acutatum* species complex (Damm et al. 2012b). This species is only known from the type specimen. *Colletotrichum brisbanense* was described from one of Simmonds' (1968) paratype specimens of *C. acutatum*, which Shivas & Tan (2009) had assigned to *C. simmondsii*. GAPDH and TUB sequences clearly separate *C. brisbanense* and *C. simmondsii* (Damm et al. 2012b).

11. ***Colletotrichum chlorophyti*** S. Chandra & Tandon [as *chlorophytumi*], Current Science 34: 565 (1965).

In North America, *C. chlorophyti* has been reported as the cause of anthracnose in soybean (*Glycine max*) (Yang et al. 2012). The only Australian specimen was deposited in the CBS culture collection as *C. dematium* (Table 2). A multilocus phylogenetic analysis re-identified it as *C. chlorophyti* (Damm et al. 2009). The extent to which *C. chlorophyti* is responsible for anthracnose on *Stylosanthes hamata* in Australia is not known.

12. ***Colletotrichum circinans*** (Berk.) Voglino, Annali della Reale Academia d'Agricoltura di Torino 49: 175 (1907).

*Colletotrichum circinans* belongs to the *C. dematium* clade (Cannon et al. 2012). There are records of *C. circinans* in Australia from onion, shallot and leeks (*Allium* spp.) with smudge and bulb rot (Hall et al. 2009, Persley et al. 2010). The only Australian specimen has been identified based on the 100 % identity of ITS and GAPDH sequences to *C. circinans* ex-type strain CBS 221.81 (Table 2).

13. ***Colletotrichum coccodes*** (Wallr.) S. Hughes, Canadian Journal of Botany 36: 754 (1958).

*Colletotrichum coccodes* was recently neotypified (Liu et al. 2011), which stabilized the taxonomic concept of this species. Prior to this, *C. coccodes* was reported as the causal agent of brown root rot of tomato (Golzar 2009b) and black dot of potato (Ben-Daniel et al. 2010). Most isolates identified as *C. coccodes* in Australian culture collections require validation by molecular phylogenetic analyses. The Australian specimens have been identified based on the 100 % identity of ITS, GAPDH and/or TUB sequences to *C. coccodes* ex-type strain CBS 164.49 (Table 2).

14. ***Colletotrichum cymbidiicola*** Damm, P.F. Cannon, Crous, P.R. Johnst. & B. Weir, Studies in Mycology 73: 19 (2012a).

*Colletotrichum cymbidiicola* belongs to the *C. boninense* species complex (Damm et al. 2012a). *Colletotrichum cymbidiicola* causes anthracnose on *Cymbidium* spp. in Australia, India, Japan, New Zealand and USA (Damm et al. 2012a, Chowdappa et al. 2014, Bethke 2014), and is likely present in all countries where *Cymbidium* orchids are grown. The only Australian specimen (Table 2) is the holotype of *C. cymbidiicola* (Damm et al. 2012a).

15. ***Colletotrichum dematium*** (Pers.) Grove, Journal of Botany, British and Foreign Legion, London 56: 341 (1918).

Damm et al. (2009) designated an epitype for *C. dematium* derived from a culture isolated from a dead leaf of *Eryngium campestre* collected in France. *Colletotrichum dematium* has a wide host range with pathogenic, saprobic and endophytic strains (Damm et al. 2009). Although *C. dematium* has been claimed to cause several economically important diseases, this has rarely been demonstrated. The only Australian specimen (Table 2) was included in the study by Damm et al. (2009). Most isolates identified as *C. dematium* in Australian culture collections require validation by molecular phylogenetic analyses.

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

*Colletotrichum destructivum* is a species complex that was recently revised by Damm et al. (2014) who designated an epitype for *C. destructivum*. *Colletotrichum destructivum* can be identified by its ITS and TUB2 sequences. In Australia, two isolates from pasture legumes

(Ford et al. 2004) have ITS sequences identical to those of the epitype.

17. ***Colletotrichum dracaenophilum*** D.F. Farr & M.E. Palm, Mycological Research 110: 1401 (2006).

*Colletotrichum dracaenophilum* is a stem pathogen of *Dracaena* spp. (Farr et al. 2006). *Colletotrichum dracaenophilum* occupies a small clade that is basal to the entire genus, apart from the combined *C. orbiculare* and *C. cliviae* clade (Cannon et al. 2012). The Australian records have been identified based on the 100 % identity of ITS and GAPDH sequences to *C. dracaenophilum* ex-type strain CBS 118199 (Table 2).

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

*Colletotrichum fioriniae* belongs to the *C. acutatum* species complex. *Colletotrichum fioriniae* was originally described as an entomopathogen from a scale insect in the USA, where it has also been reported as an endophyte in several plants (Marcelino et al. 2008). In Australia, *C. fioriniae* has been reported as the cause of leaf and stem blight on *Acacia acuminata* (Golzar 2009a as *C. acutatum*) and fruit rot of avocado (Shivas and Tan 2009). *Colletotrichum fioriniae* is readily identified by any of the six genes analysed by Damm et al. (2012b).

19. ***Colletotrichum fructicola*** Prihastuti, L.Cai & K.D. Hyde, Fungal Diversity 39: 158 (2009).

*Colletotrichum fructicola* belongs to the *C. gloeosporioides* species complex (Weir et al. 2012). Little is known about the host range and pathogenicity of this species in Australia. *Colletotrichum fructicola* can be distinguished from other species in the *C. gloesporioides* species complex with GS sequences (Weir et al. 2012).

20. ***Colletotrichum gloeosporioides*** (Penz.) Penz. & Sacc., Atti del Reale Istituto Veneto di Scienze, Lettere ed Arti, Serie 6, 2: 670 (1884).

*Colletotrichum gloeosporioides* is a name well known to plant pathologists. A major revision of *Colletotrichum* by von Arx (1957) based on morphology rather than host association, reduced the number of accepted species from 750 to 11, with the vast majority reduced to synonymy with *C. gloeosporioides*. This left *C. gloeosporioides* as a biologically and genetically diverse species associated with at least 470 different host genera (Sutton 1980). Cannon et al. (2008) epitypified *C. gloeosporioides* with a specimen and living culture from *Citrus sinensis* collected from Italy. In a major revision, Weir et al. (2012) used multilocus sequence analyses to resolve the *C. gloeosporioides* species complex into a number of segregate species. The species that gives its name to this complex, *C. gloeosporioides*, was found to be commonly associated with *Citrus*, although it also occurred on other host species (Weir et al. 2012).

Although *C. gloeosporioides* has been implicated as an important pathogen of a wide range of plants in Australia, there are relatively few published records that can be verified by DNA sequence data. The situation is similar for most applications of the name *C. gloeosporioides* in much of the plant pathology literature worldwide. The extent of the problem was highlighted by Cai et al. (2009), who estimated that more than 86 % of the records of *C. gloeosporioides* in GenBank had sequences that diverged considerably from the epitype and were likely to represent other species. Further, Phoulivong et al. (2010) considered that *C. gloeosporioides* was not a common pathogen on tropical fruits. In Australia, *C. gloeosporioides* has been recorded from cultivated *Citrus* spp. (Schena et al. 2014) and pecan (Weir et al. 2012). *Colletotrichum gloeosporioides* can be distinguished from other species in the *C. gloeosporioides* species complex by any of the eight genes analysed in Weir et al. (2012). The Australian records of *C. gloeosporioides* have been identified based on the 100 % identity of ITS, GAPDH and/or TUB sequences to the *C. gloeosporioides* ex-type strain IMI 356878 (Table 2).

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

*Colletotrichum godetiae* belongs to the *C. acutatum* species complex (Damm et al. 2012b). *Colletotrichum godetiae* is recorded as a pathogen of fruit, leaves and stems of *Fragaria*, *Malus* and *Prunus*, mainly in Europe and Western Asia (Damm et al. 2012b). These are new records for Australia. *Colletotrichum godetiae* can be distinguished from other species in the *C. acutatum* species complex by any of the six genes analysed in Damm et al. (2012b). The Australian records of *C. godetiae* have been identified based on the 100 % identity of ITS and/or TUB sequences to *C. godetiae* ex-type strain CBS 133.44 (Table 2).

22. ***Colletotrichum kahawae* subsp. *ciggaro*** B. Weir & P.R. Johnst., Studies in Mycology 73: 158 (2012).

*Colletotrichum kahawae* subsp. *ciggaro* belongs to the *C. gloeosporioides* species complex (Weir et al. 2012). *Colletotrichum kahawae* subsp. *ciggaro* has a broad host range and worldwide distribution. It differs only in one gene, glutamine synthetase, from the African coffee berry disease pathogen, *C. kahawae* subsp. *kahawae*, which is not present in Australia (Weir et al. 2012). The only Australian record listed in Table 2 is the ex-type culture of *C. kahawae* subsp. *ciggaro* (Weir et al. 2012).

23. ***Colletotrichum karsti*** You L. Yang, Zuo Y. Liu, K.D. Hyde & L. Cai [as '*karstii*'], Cryptogamie Mycologie 32: 241 (2011).

*Colletotrichum karsti* belongs to the *C. boninense* species complex (Damm et al. 2012a). Due to the high variation observed in morphology and sequences, a polyphasic approach is recommended to ensure accurate identification (Damm et al. 2012a). In Australia, *C. karsti* has a wide host range, although its role as a pathogen is not known.

24. ***Colletotrichum lupini*** (Bondar) Damm, P.F. Cannon & Crous, Studies in Mycology 73: 78 (2012).

*Colletotrichum lupini* belongs to the *C. acutatum* species complex (Damm et al. 2012b). *Colletotrichum lupini* is an economically important pathogen of lupin crops worldwide, including Australia, where it was first detected in Western Australia in 1994 (Sweetingham et al. 1995, Yang and Sweetingham 1998, as *C. gloeosporioides*). *Colletotrichum lupini* has established in Western Australia, where it has spread through wild populations of blue lupins (*Lupinus cosentinii*), as well as in parts of South Australia, where it is known to occur in *Lupinus albus*. *Colletotrichum lupini* is not known to occur in the lupin growing regions in New South Wales (Anon. 2015) or Victoria (Thomas 2010). *Colletotrichum lupini* can be distinguished from other species in the *C. acutatum* species complex by most of the six genes (excluding actin) analysed by Damm et al. (2012b), with TUB providiving the best resolution. The Australian records of *C. lupini* have been identified based on the 100 % identity of ITS, GAPDH and/or TUB sequences to *C. lupini* ex-type strain CBS 109225 (Table 2).

25. ***Colletotrichum musae*** (Berk. & M.A. Curtis) Arx, Verhandelingen Koninklijke Nederlandse Akademie van Wetenschappen, Sect. 51: 107 (1957).

*Colletotrichum musae* belongs to the *C. gloeosporioides* species complex (Weir et al. 2012). Su et al. (2011) designated an epitype for *C. musae* from banana (*Musa* sp.) fruit in the USA, collected from the geographic locality of the type. In Australia, *C. musae* has been associated with several banana diseases, including anthracnose, fruit speckle, black end and crown rot (Cooke et al. 2009). However, many of these records require verification by molecular methods. *Colletotrichum musae* can be distinguished from other species in the *C. gloeosporioides* species complex by any of eight genes analysed by Weir et al. (2012). The Australian records of *C. musae* have been identified based on the 100 % identity of ITS, GAPDH and/or TUB sequences to *C. musae* ex-type strain CBS 116870 (Table 2).

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

*Colletotrichum nymphaeae* belongs to the *C. acutatum* species complex (Damm et al. 2012b). *Colletotrichum nymphaeae* was determined as the causal agent of celery stunt disease in Japan (Yamagishi et al. 2015). This raises the possibility that celery leaf curl disease in Queensland, which was attributed to *C. acutatum sensu lato* (Heaton and Dullahide 1993), may be caused by *C. nymphaeae*. *Colletotrichum nymphaeae* is easily distinguished from other species in the *C. acutatum* species complex with TUB (Damm et al. 2012b). The Australian records of *C. nymphaeae* have been identified based on the 100 % identity of TUB sequences to *C. nymphaeae* ex-type strain CBS 515.78 (Table 2).

27. ***Colletotrichum ocimi*** Damm, Studies in Mycology 79: 70 (2014).

*Colletotrichum ocimi* belongs to the *C. destructivum* species complex (Damm et al. 2014). Persley et al. (2010) reported that black spot of basil, caused by *C. ocimi* (as *C. gloeosporioides*), is a minor disease in Australia. *Colletotrichum ocimi* is easily distinguished from other species in the *C. acutatum* species complex by its unique ITS and TUB sequences (Damm et al. 2014). The Australian record of *C. ocimi* was identified based on the 100 % identity of ITS sequence to *C. ocimi* ex-type strain CBS 298.94 (Table 2).

28. ***Colletotrichum orbiculare*** Damm, P.F. Cannon & Crous, Fungal Diversity 61: 39 (2013).

*Colletotrichum orbiculare sensu* Damm et al. (2013) was recently described and pragmatically given the same name as the earlier invalid name *C. orbiculare sensu* von Arx (1957), which is well known in the plant pathology literature worldwide as a pathogen of host plants in the Cucurbitaceae. In Australia, *C. orbiculare sensu lato* has been associated with diseases on several plant species in the Asteraceae, Cucurbitaceae and Fabaceae (Auld et al. 1994 as *C. lagenarium*, Simmonds 1965, Walker et al. 1991, Persley et al. 2010). However, most of these records require verification by molecular methods. The only verified Australian specimen (Table 2) was included in the study by Damm et al. (2013)

29. ***Colletotrichum petchii*** Damm, P.F. Cannon & Crous, Studies in Mycology 73: 29 (2012a).

*Colletotrichum petchii* belongs to the *C. boninense* species complex (Damm et al. 2012a). This fungus appears to be host specific to *Dracaena* spp., which are native to Africa (Damm et al. 2012a). The Australian record of *C. petchii* was identified based on the 100 % identity of ITS and GAPDH sequences to *C. petchii* ex-type strain CBS 378.94 (Table 2).

30. ***Colletotrichum phormii*** (Henn.) D.F. Farr & Rossman, Mycological Research 110: 1403 (2006).

*Colletotrichum phormii* belongs to the *C. acutatum* complex (Damm et al. 2012b). *Colletotrichum phormii* was first reported in Australia in 2010 from Perth, WA, based on the ITS sequence of isolate WAC 12416 (Golzar and Wang 2010). However, this record cannot be verified as there is no living culture available and the sequence data was not deposited in GenBank. *Colletotrichum phormii* is separated from other species in the *C. acutatum* species complex by sequences of secondary genes, namely TUB, GAPDH, histone and actin (Damm et al. 2012b). The Australian record of *C. phormii* was identified based on the 100 % identity of TUB sequences to *C. phormii* ex-type strain CBS 118194 (Table 2).

31. ***Colletotrichum pyricola*** Damm, P.F. Cannon & Crous, Studies in Mycology 73: 94 (2012b).

*Colletotrichum pyricola* belongs to the *C. acutatum* species complex (Damm et al. 2012b). This fungus was first described from fruit rot of pear (*Pyrus communis*) in New Zealand. *Colletotrichum pyricola* can be distinguished from other species in the *C. acutatum* species complex with GAPDH and TUB (Damm et al. 2012b). The Australian record of *C. pyricola* was identified based on the 100 % identity of GAPDH and TUB sequences to *C. pyricola* ex-type strain CBS 128531 (Table 2).

32. ***Colletotrichum queenslandicum*** B. Weir & P.R. Johnst., Studies in Mycology 73: 164 (2012).

*Colletotrichum queenslandicum* belongs to the *C. gloeosporioides* species complex (Weir et al. 2012). This fungus was first described from Queensland as *C. gloeosporioides* var. *minor* Simmonds (1968), who regarded this fungus as an important cause of fruit rot in avocado and papaya, as well as a wide range of other hosts (Simmonds 1965, 1966). A new name, *C. queenslandicum*, was given to this taxon as the orthographically correct species epithet *minus* was already occupied by *C. minus* Zimm. In Australia, *C. queenslandicum* has been reported from avocado (Weir et al. 2012), lychee (Anderson et al. 2013 as *C. gloeosporioides*), passionfruit (James et al. 2014) and pawpaw (Weir et al. 2012). *Colletotrichum queenslandicum* is best distinguished from other species in the *C. gloeosporioides* species complex by GAPDH, GS or TUB sequences (Weir et al. 2012). The Australian specimens of *C. queenslandicum* were identified based on the 100 % identity of GAPDH and/or TUB sequences to *C. queenslandicum* ex-type strain ICMP 1778 (Table 2).

33. ***Colletotrichum salicis*** (Fuckel) Damm, P.F. Cannon & Crous, Studies in Mycology 73: 97 (2012b).

*Colletotrichum salicis* belongs to the *C. acutatum* species complex (Damm et al. 2012b). This fungus was first reported on *Salix* spp. from mainland Australia as *Glomerella miyabeana* (Cunnington et al. 2007), which is considered a synonym of *C. salicis* by Damm et al. (2012b). *Colletotrichum salicis* is best distinguished from other species in the *C. acutatum* species complex with GAPDH or TUB sequences (Damm et al. 2012b). The Australian specimens of *C. salicis* were identified based on the 99–100 % identity of GAPDH and/or TUB sequences to *C. salicis* ex-type strain CBS 607.94 (Table 2).

34. ***Colletotrichum sansevieriae*** Miho Nakam. & Ohzono, Journal of General Plant Pathology 72: 253 (2006).

*Colletotrichum sansevieriae* causes leaf anthracnose on *Sansevieria* spp., which are native to Africa and Asia. The only Australian specimen (Table 2) was collected in 2008 (Aldaoud et al. 2011).

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

*Colletotrichum siamense* belongs to the *C. gloeosporioides* species complex (Weir et al. 2012). In Australia, *C. siamense* has a diverse host range (Weir et al. 2012, James et al. 2014, Schena et al. 2014), although its role as a pathogen is unclear. *Colletotrichum siamense* is best distinguished from other species in the *C. gloeosporioides* species complex with TUB (Weir et al. 2012). The Australian specimens of *C. siamense* were identified based on the 100 % identity of TUB sequences to *C. siamense* ex-type strain ICMP 18578 (Table 2).

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

*Colletotrichum simmondsii* belongs to the *C. acutatum* species complex (Damm et al. 2014). In Australia, *C. simmondsii* has been associated with fruit rots of papaya, strawberry, tomato and blueberry (Shivas and Tan, 2009). *Colletotrichum simmondsii* is easily distinguished from other species in the *C. acutatum* species complex with ITS or TUB sequences (Damm et al. 2012b). The Australian specimens of *C. simmondsii* were identified based on the 100 % identity of ITS and/or TUB to *C. simmondsii* ex-type strain BRIP 28519 (Table 2).

37. ***Colletotrichum sloanei*** Damm. P.F. Cannon & Crous., Studies in Mycology 73: 103 (2012b).

*Colletotrichum sloanei* belongs to the *C. acutatum* species complex (Damm et al. 2012b). Little is known about the host range and pathogenicity of this species. *Colletotrichum sloanei* is best distinguished from other species in the *C. acutatum* species complex with GAPDH or TUB sequences (Damm et al. 2012b). The Australian specimens of *C. sloanei* were identified based on the 100 % identity of GAPDH and TUB sequences to *C. sloanei* ex-type strain IMI 364297 (Table 2).

38. ***Colletotrichum spinaciae*** Ellis & Halst., Journal of Mycology 6: 34 (1890).

*Colletotrichum spinaciae* belongs to the *C. dematium* clade (Cannon et al. 2012). In Victoria, *C. spinaciae* (as *C. dematium*) was shown to cause anthracnose on spinach when it was first detected in 2004 (Washington et al. 2006). This detection invoked a biosecurity response of interstate surveys, which found that anthracnose on spinach was widespread in eastern Australia, resulting in no further quarantine action (Washington et al. 2006). The Australian specimens of *C. spinaciae* were identified based on the 100 % identity of ITS and GAPDH sequences to *C. spinaciae* ex-epitype strain CBS 128.57 (Table 2).

39. ***Colletotrichum spinosum*** Damm & P.F. Cannon, Fungal Diversity 61:46 (2013).

*Colletotrichum spinosum* belongs to the *C. orbiculare* species complex (Damm et al. 2013). *Colletotrichum spinosum* is a common pathogen of *Xanthium spinosum* in eastern Australia, where it caused seedling blight and stem anthracnose (Veitch 1942, Butler 1951, Anderson and Walker 1962, Simmonds 1965, 1966, Walker et al. 1991). In pathogenicity tests, the ex-holotype isolate was found to be highly virulent on *Xanthium* spp. as well as some other Asteraceae, and further infected some species of Cucurbitaceae, Fabaceae and Myrtaceae (Walker et al. 1991). It has been evaluated as a mycoherbicide for the biological control of *Xanthium spinosum* in Australia (Auld et al. 1988, 1990, Auld & Say 1999). *Colletotrichum spinosum* can be easily identified based on GAPDH, GS and/or TUB2 sequences (Damm et al. 2013).

40. ***Colletotrichum tanaceti*** M. Barimani et al., Plant Pathology 62: 1252 (2013).

*Colletotrichum tanaceti* belongs to the *C. destructivum* species complex (Damm et al. 2014). *Colletotrichum tanaceti* is a serious pathogen of pyrethrum in northern Tasmania (Barimani et al. 2013). The only Australian specimen (Table 2) is the holotype of *C. tanaceti*, which was distinguished from other *Colletotrichum* spp. by GAPDH, ITS and TUB sequences (Barimani et al. 2013)

41. ***Colletotrichum theobromicola*** Delacr., Bull. Soc. Mycol. France 31: 191 (1905).

*Colletotrichum theobromicola* belongs to the *C. gloeosporioides* species complex (Weir et al. 2012). *Colletotrichum theobromicola* has been reported on several diverse host species in Australia (James et al. 2014, Schena et al. 2014). The Type A and Type B isolates of *C. gloeosporioides* f. *stylosanthis* were shown to be pathogenic on *Stylosanthes* in northern Australia (Irwin & Cameron 1978). These isolates were subsequently named *C. gloeosporioides* f. *stylosanthis* “f. sp. *guianensis*” and *C. gloeosporioides* f. *stylosanthis* “f. sp. *stylosanthis*”, respectively, by Munaut et al. (2002). Weir et al. (2012) considered these names synonyms of *C. theobromicola. Colletotrichum theobromicola* can be distinguished from other species in the *C. gloeosporioides* species complex by any of the eight genes analysed in Weir et al. (2012). The Australian specimens of *C. theobromicola* have been identified based on the 100 % identity of ITS and/or TUB sequences to *C. theobromicola* ex-type strain CBS 124945 (Table 2).

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

*Colletotrichum tofieldiae* was previously treated as a variant of *C. dematium* var. *minus*, but was confirmed as a distinct species after an epitype was designated (Damm et al. 2009). *Colletotrichum tofieldiae* has been reported as an endophyte (Tao et al. 2013, Hiruma et al. 2016). Its role as a pathogen is unknown. The Australian specimens of *C. tofieldiae* were identified based on the 100 % identity of ITS and TUB sequences to *C. tofieldiae* ex-type strain CBS 495.85 (Table 2).

43. ***Colletotrichum truncatum*** (Schwein.) Andrus & W.D. Moore, Phytopathology 25: 122 (1935).

In Australia, most records of this fungus (e.g. Ford et al. 2004) still require verification by molecular methods. Worldwide, *C. truncatum* causes anthracnose diseases of many hosts in the Solanaceae and Fabaceae (Damm et al. 2009). An epitype from *Phaseolus lunatus* in the USA was designated by Damm et al. (2009), who used multilocus phylogenetic analyses to show that *C. capsici* and *C. curvatum* were synonyms of *C. truncatum*. The Australian specimens of *C. truncatum* were identified based on the 100 % identity of ITS sequences to *C. truncatum* ex-type strain CBS 151.35 (Table 2).

44. ***Colletotrichum xanthorrhoeae*** R.G. Shivas, Bathgate & Podger, Mycological Research 102: 280 (1998).

*Colletotrichum xanthorrhoeae* belongs to the *C. gloeosporioides* species complex (Weir et al. 2012). *Colletotrichum xanthorrhoeae* was widespread in Western Australia, where it caused a leaf spot disease on *Xanthorrhoea* spp. (Shivas et al. 1998). *Colletotrichum xanthorrhoeae* can be easily identified by its distinctive morphology, very slow growth rate in culture, and its unique ITS sequence (Weir et al. 2012).

## Discussion

The species listed above have been verified by molecular phylogenetic analyses. There are several other names of *Colletotrichum* species that have been either (i) reported in the scientific literature as occurring in Australia, or (ii) listed (often unpublished) in culture collections of Australian isolates, which have yet to be verified by DNA sequence analyses. Some omissions from the Australian list of verified names are worthy of comment, in particular, *C. lindemuthianum* (Sacc. & Magnnus) Briosi & Cavara, *C. graminicola* (Ces.) G.W. Wilson and *C. sublineola* Henn. ex Sacc. & Trotter. *Colletotrichum lindemuthianum*, belongs to the *C. orbiculare* species complex (Damm et al. 2013) and is the causal agent of anthracnose of common bean (*Phaseolus vulgaris*) (Cruickshank 1966), although it has been practically eradicated from commercial production in Australia (Persley et al. 2010). The name *C. lindemuthianum* was only recently stabilised with the designation of an epitype (Liu et al. 2013a). Liu et al. (2013a) also noted that very few studies of *C. lindemuthianum* incorporated DNA sequence analysis, which is the case in Australia and explains its absence from our list. *Colletotrichum graminicola* and *C. sublineola* belong to a monophyletic clade of species with falcate conidia that are mostly host specific on grasses (Crouch et al. 2009a, b, Cannon et al. 2012). Worldwide, *C. graminicola* and *C. sublineola* are important pathogens of maize (*Zea mays*) and corn (*Sorghum* spp.), respectively (Crouch and Beirn 2009), yet rarely important in Australia (Simmonds 1966, Plant Health Australia (2001) Australian Plant Pest Database, online database http://appd.ala.org.au/ accessed 2 Sep. 2016). The graminicolous *Colletotrichum* isolates in Australian collections have yet, for the most part, to be identified and classified by molecular phylogenetic methods.

Other Australian species that remain to be verified by DNA sequence analyses include *C. acaciae* Gutner, *C. caudatum* (Peck ex Sacc.) Peck, *C. crassipes* (Speg.) Arx, *C. falcatum* Went, *C. fuscum* Laubert, *C. higginsianum* Sacc., *C. malvarum* (A. Braun & Casp.) Southw., *C. orchidearum* Allesch., *C. schizanthi* C.N. Jensen & V.B. Stewart, *C. trichellum* (Fr.) Duke, *C. trifolii* Bain, and *C. xanthii* Halst. These species require verification by DNA sequencing to confirm their presence in Australia.

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