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Genera of phytopathogenic fungi: GOPHY 1

Y. Marin-Felix[1,2*], J.Z. Groenewald[1], L. Cai[3], Q. Chen[3], S. Marincowitz[2], I. Barnes[4], K. Bensch[1,5], U. Braun[6], E. Camporesi[7,8,9], U. Damm[10], Z.W. de Beer[2], A. Dissanayake[11,12], J. Edwards[13], A. Giraldo[1,2], M. Hernández-Restrepo[1,2], K.D. Hyde[11,14], R.S. Jayawardena[11,12], L. Lombard[1], J. Luangsa-ard[15], A.R. McTaggart[16], A.Y. Rossman[17], M. Sandoval-Denis[1,18], M. Shen[19], R.G. Shivas[20], Y.P. Tan[21,22], E.J. van der Linde[23], M.J. Wingfield[2], A.R. Wood[24], J.Q. Zhang[19], Y. Zhang[19], and P.W. Crous[1,2*]

[1]*Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;* [2]*Department of Microbiology and Plant Pathology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa;* [3]*State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, Beijing 100101, PR China;* [4]*Department of Genetics, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa;* [5]*Botanische Staatssammlung München, Menzinger Straße 67, D-80638 München, Germany;* [6]*Martin-Luther-Universität, Institut für Biologie, Bereich Geobotanik und Botanischer Garten, Herbarium, Neuwerk 21, D-06099 Halle (Saale), Germany;* [7]*A.M.B. Gruppo Micologico Forlivese "Antonio Cicognani", Via Roma 18, Forlì, Italy;* [8]*A.M.B. Circolo Micologico "Giovanni Carini", C.P. 314, Brescia, Italy;* [9]*Società per gli Studi Naturalistici della Romagna, C.P. 144, Bagnacavallo (RA), Italy;* [10]*Senckenberg Museum of Natural History Görlitz, PF 300 154, 02806 Görlitz, Germany;* [11]*Center of Excellence in Fungal Research, School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand;* [12]*Institute of Plant and Environment Protection, Beijing Academy of Agriculture and Forestry Sciences, Beijing 100097, PR China;* [13]*AgriBio Centre for AgriBiosciences, Department of Economic Development, Jobs, Transport and Resources, 5 Ring Road, LaTrobe University, Bundoora, Victoria 3083, Australia;* [14]*School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand;* [15]*Microbe Interaction and Ecology Laboratory, Biodiversity and Biotechnological Resource Research Unit (BBR), BIOTEC, NSTDA 113 Thailand Science Park Phahonyothin Rd., Khlong Nueng, Khlong Luang, Pathum Thani 12120, Thailand;* [16]*Department of Plant and Soil Science, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa;* [17]*Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR 97331, USA;* [18]*Faculty of Natural and Agricultural Sciences, Department of Plant Sciences, University of the Free State, P.O. Box 339, Bloemfontein 9300, South Africa;* [19]*Institute of Microbiology, P.O. Box 61, Beijing Forestry University, Beijing 100083, PR China;* [20]*Centre for Crop Health, Institute for Agriculture and the Environment, University of Southern Queensland, Toowoomba 4350, Queensland, Australia;* [21]*Department of Agriculture & Fisheries, Biosecurity Queensland, Ecosciences Precinct, Dutton Park, Queensland 4102, Australia;* [22]*Microbiology, Department of Biology, Utrecht University, Padualaan 8, 3584 CT Utrecht, The Netherlands;* [23]*ARC – Plant Protection Research Institute, Biosystematics Division – Mycology, P. Bag X134, Queenswood 0121, South Africa;* [24]*ARC – Plant Protection Research Institute, P. Bag X5017, Stellenbosch 7599, South Africa*

**Correspondence*: Y. Marin-Felix, y.marin@westerdijkinstitute.nl; P.W. Crous, p.crous@westerdijkinstitute.nl

Abstract: Genera of Phytopathogenic Fungi (GOPHY) is introduced as a new series of publications in order to provide a stable platform for the taxonomy of phytopathogenic fungi. This first paper focuses on 21 genera of phytopathogenic fungi: *Bipolaris*, *Boeremia*, *Calonectria*, *Ceratocystis*, *Cladosporium*, *Colletotrichum*, *Coniella*, *Curvularia*, *Monilinia*, *Neofabraea*, *Neofusicoccum*, *Pilidium*, *Pleiochaeta*, *Plenodomus*, *Protostegia*, *Pseudopyricularia*, *Puccinia*, *Saccharata*, *Thyrostroma*, *Venturia* and *Wilsonomyces*. For each genus, a morphological description and information about its pathology, distribution, hosts and disease symptoms are provided. In addition, this information is linked to primary and secondary DNA barcodes of the presently accepted species, and relevant literature. Moreover, several novelties are introduced, i.e. new genera, species and combinations, and neo-, lecto- and epitypes designated to provide a stable taxonomy. This first paper includes one new genus, 26 new species, ten new combinations, and four typifications of older names.

Key words: DNA barcodes, Fungal systematics, Phytopathogenic fungi, Plant pathology, Taxonomy, Typifications.

Taxonomic novelties: New genus: *Verkleyomyces* Y. Marín & Crous; **New species:** *Bipolaris saccharicola* Y. Marín & Crous, *Bi. variabilis* Y. Marín, Y.P. Tan & Crous, *Boeremia trachelospermi* Q. Chen & L. Cai, *Calonectria ecuadorensis* L. Lombard & Crous, *Ca. longiramosa* L. Lombard & Crous, *Ca. nemoralis* L. Lombard & Crous, *Ca. octoramosa* L. Lombard & Crous, *Ca. parvispora* L. Lombard & Crous, *Ca. tucuruiensis* L. Lombard & Crous, *Cladosporium chasmanthicola* Bensch, U. Braun & Crous, *Cl. kenpeggii* Bensch, U. Braun & Crous, *Cl. welwitschiicola* Bensch, U. Braun & Crous, *Colletotrichum sydowii* Damm, *Curvularia pisi* Y. Marín & Crous, *Cu. soli* Y. Marín & Crous, *Neofusicoccum italicum* Dissanayake & K.D. Hyde, *Nm. pistaciicola* Crous, *Nm. pruni* Crous, *Pilidium septatum* Giraldo & Crous, *Pleiochaeta carotae* Hern.-Rest., van der Linde & Crous, *Plenodomus deqinensis* Q. Chen & L. Cai, *Protostegia eucleicola* Crous, *Saccharata leucospermi* Crous, *S. protearum* Crous, *Thyrostroma franseriae* Crous, *Venturia phaeosepta* Y. Zhang ter & J.Q. Zhang; **New combinations:** *Coniella hibisci* (B. Sutton) Crous, *Monilinia mumeicola* (Y. Harada et al.) Sandoval-Denis & Crous, *M. yunnanensis* (M.J. Hu & C.X. Luo) Sandoval-Denis & Crous, *Pseudopyricularia bothriochloae* (Crous & Cheew.) Y. Marín & Crous, *Puccinia dianellae* (Dietel) McTaggart & R.G. Shivas, *Pu. geitonoplesii* (McAlpine) McTaggart & R.G. Shivas, *Pu. merrilliana* (Syd. & P. Syd.) McTaggart & R.G. Shivas, *Pu. rhagodiae* (Cooke & Massee) McTaggart & R.G. Shivas, Venturia martianoffiana (Thüm.) Y. Zhang ter & J.Q. Zhang, *Verkleyomyces illicii* (X. Sun et al.) Y. Marín & Crous; **Typification: Epitypification:** *Ceratophorum setosum* Kirchn., *Coniella musaiaensis* var. *hibisci* B. Sutton, *Helminthosporium carpophilum* Lév.; **Lectotypification:** *Ceratophorum setosum* Kirchn.

INTRODUCTION

Since the advent of molecular DNA techniques, many species of phytopathogenic fungi have been shown to represent species complexes or to be included in genera that are poly- or paraphyletic (Crous *et al.* 2015b). Resolving these generic and species concepts is thus of the utmost importance for plant health and global trade in food and fibre (Crous *et al.* 2015b, 2016a). The present project focused on genera of fungi that have members causing plant diseases (phytopathogenic), links to a larger initiative called the "The Genera of Fungi project" based on Clements & Shear (1931) (www.GeneraOfFungi.org, Crous *et al.* 2014a, 2015a, Giraldo *et al.* 2017), which aims to revise the generic names of all currently accepted fungi (Kirk *et al.* 2013).

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Of the approximately 18 000 fungal genera that have thus far been described, only around 8 000 are in current use. However, the majority of these were described before the DNA era. To validate the application of these names, their type species need to be recollected and designated as epi- or neotypes with a MycoBank Typification (MBT) number to ensure traceability of the nomenclatural act (Robert *et al.* 2013). Furthermore, to move to a single nomenclature for fungi (Wingfield *et al.* 2012, Crous *et al.* 2015b), their sexual–asexual links also need to be confirmed.

The present initiative forms part of the activities of the International Subcommission for the Taxonomy of Phytopathogenic Fungi [Pedro Crous and Amy Rossman (co-chairs), of the International Committee for the Taxonomy of Fungi (www.fungaltaxonomy.org/)].

The aims of this project are to:

1. Establish a new website, www.plantpathogen.org, to host a database that will link metadata to other databases such as MycoBank, Index Fungorum, FacesofFungi, U.S. National Fungus Collections Databases, etc., and associated DNA barcodes (ITS, LSU and other loci as needed) to GenBank (Schoch *et al.* 2014).
2. Source type specimens and cultures of the type species of genera from fungaria and Biological Resource Centres (BRCs), and generate the required metadata as explained below.
3. Recollect fresh material of the type species if not already available, and as far as possible derive DNA barcodes and cultures from this material.
4. Designate type species, and type specimens of those species, for those genera where this has not been indicated in the original publications.
5. Fix the application of the type species of generic names by means of lecto-, neo-, or epitypification as appropriate, and at the same time deposit cultures in at least two Microbial Biological Resource Centres (M-BRCs) from which they would be widely available to the international research community.
6. Publish modern generic descriptions, and provide DNA barcodes for all accepted species, with reference to appropriate literature.

Authors with new submissions should ensure that all new species and typification events are registered in MycoBank (MB and MBT numbers), respectively. It is recommended that the following issues are addressed in each genus:

1. Modern generic description, and phylogenetic placement of the type species of the genus.
2. Higher order phylogeny.
3. New nomenclature merging asexual and sexual generic names (see Rossman *et al.* 2013, Johnston *et al.* 2014).
4. Description of novel taxa, with a reference collection (e.g. fungarium), and MycoBank and GenBank sequence accession numbers.
5. Name changes that result from the new phylogenetic placement.
6. Notes discussing the relevance and implications of the phylogeny, and importance of the genus.

Authored generic contributions will be combined into scientific papers to be published online in *Studies in Mycology*, and also placed in a database displayed on www.plantpathogen.org. Preference will be given to genera that include novel DNA data and/or novel species or typifications. Authors that wish to contribute to future issues of this project are encouraged to first contact Pedro Crous (p.crous@westerdijkinstitute.nl) before final submission, to ensure there is no potential overlap with activities arising from other research groups. The genera chosen in the first paper were randomly selected, based on the fact that their phylogenetic position was resolved, DNA data were available for those species known from culture, and novel species or typifications were available for inclusion.

MATERIAL AND METHODS

Isolates and morphological analysis

Descriptions of the new taxa and typifications are based on cultures obtained from the Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands (CBS), the working collection of P.W. Crous (CPC), housed at the Westerdijk Institute, Herbarium Mycologicum Academiae Sinicae (HMAS), BIOTEC Culture Collection (BCC), the Queensland Plant Pathology Herbarium (BRIP), the Chinese General Microbiological Culture Collection Center (CGMCC), the Mae Fah Luang University Culture Collection (MFLUCC), and the Victorian Plant Pathogen Herbarium (VPRI). For fresh collections, we followed the procedures previously described in Crous *et al.* (1991). Colonies were transferred to different media, i.e. carnation leaf agar (CLA), cornmeal agar (CMA), 2 % malt extract agar (MEA), 2 % potato-dextrose agar (PDA), synthetic nutrient-poor agar (SNA), oatmeal agar (OA), water agar (WA) (Crous *et al.* 2009c), autoclaved pine needles on 2 % tap water agar (PNA) (Smith *et al.* 1996), and incubated at different conditions depending on the taxon to induce sporulation (requirements of media and conditions of incubations specified in each genus). Reference strains and specimens are maintained at the BCC, CBS, CGMCC, HMAS and MFLUCC.

Vegetative and reproductive structures were mounted in clear lactic acid, Shear's mounting fluid and lactophenol cotton blue, either directly from specimens or from colonies sporulating on CLA, MEA, OA, PDA, PNA, or SNA. Sections of conidiomata were made by hand for examination purposes. For cultural characterisation, isolates were grown and incubated on different culture media and temperatures as stipulated for each genus. Colour notations were rated according to the colour charts of Rayner (1970). For some taxa, NaOH pot test was carried out on MEA cultures to detect the production of metabolite E (Boerema *et al.* 2004). Taxonomic novelties were deposited in MycoBank (www.MycoBank.org; Crous *et al.* 2004b).

DNA isolation, amplification and analyses

Fungal DNA was extracted and purified directly from the colonies or host material according to the Wizard® Genomic DNA purification kit protocol (Promega, Madison, USA). Primers and protocols for the amplification and sequencing of gene loci can be found in the bibliography related to the phylogeny presented for each genus. Phylogenetic analyses consisted of Maximum-Likelihood (ML), Bayesian Inference (BI), and Maximum Parsimony (MP). The ML was carried out using methods described by Hernández-Restrepo *et al.* (2016), and the MP using those described by Crous *et al.* (2006b). The BI was inferred as described by Hernández-Restrepo *et al.* (2016), or on the CIPRES portal (www.phylo.org) using MrBayes on XSEDE v. 3.2.6. Sequence data generated in this study were deposited in GenBank and ENA databases, and the alignments and trees in TreeBASE (http://www.treebase.org).

RESULTS

Bipolaris Shoemaker, Canad. J. Bot. 37: 882. 1959. Fig. 1.
Synonym: *Cochliobolus* Drechsler, Phytopathology 24: 973. 1934.

Classification: *Dothideomycetes*, *Pleosporomycetidae*, *Pleosporales*, *Pleosporaceae.*

Type species: *Bipolaris maydis* (Y. Nisik. & C. Miyake) Shoemaker. Neotype and ex-neotype culture: ATCC 48332, CBS 137271.

DNA barcodes (genus): LSU, ITS.

DNA barcodes (species): ITS, *gapdh*, *tef1*. Table 1. Fig. 2.

Ascomata pseudothecial, mostly globose to ellipsoidal, sometimes flask-shaped or flattened on hard substrata, brown or black, immersed, erumpent, partially embedded or superficial, free, smooth or covered with vegetative hyphae; *ostiole* central, papillate or with a sub-conical, conical, paraboloid or cylindrical neck; *ascomatal wall* comprising pseudoparenchymatous cells of equal thickness or slightly thickened at apex of the ascoma. *Hamathecium* comprising septate, filiform, branched pseudoparaphyses. *Asci* bitunicate, clavate, cylindrical-clavate or broadly fusoid, straight or slightly curved, thin-walled, fissitunicate, often becoming more or less distended prior to dehiscence, short pedicellate, rounded at apex. *Ascospores* multiseriate, filiform or flagelliform, hyaline or sometimes pale yellow or pale brown at maturity, septate, helically coiled within ascus, ascospore coiling moderate to strongly, often with a mucilaginous sheath. *Conidiophores* single, sometimes arranged in small groups, straight to flexuous or geniculate, pale to dark brown, branched, thick-walled, septate. *Conidiogenous nodes* smooth to slightly verruculose. *Conidia* canoe-shaped, fusoid or obclavate, mostly curved, hyaline, pale or dark brown, reddish brown or pale to deep olivaceous, thick-walled, smooth-walled, 3–14-distoseptate, germinating by production of one or two germination tubes by polar cells; *hila* often slightly protruding or truncate, sometimes inconspicuous; *septum* ontogeny first septum median to sub-median, second septum delimits basal cell and third delimits distal cell (adapted from Manamgoda *et al.* 2014).

Culture characteristics: Colonies on PDA white or pale grey when young, brown or dark grey when mature, fluffy, cottony, raised or convex with papillate surface, margin lobate, undulate, entire or sometimes rhizoid.

Optimal media and cultivation conditions: Sterilised *Zea mays* leaves placed on 1.5 % WA or slide cultures of PDA under near-ultraviolet light (12 h light, 12 h dark) at 25 °C to induce sporulation of the asexual morph, while for the sexual morph Sach's agar with sterilised rice or wheat straw at 25 °C is used.

Distribution: Worldwide.

Hosts: Mainly pathogens of grasses, but some also on non-grass hosts, causing devastating diseases on cereal crops in the *Poaceae*, including rice, maize, wheat and sorghum and on various other host plants. Moreover, this genus can occur on at least 60 other genera in *Anacardiaceae*, *Araceae*, *Euphorbiaceae*, *Fabaceae*, *Malvaceae*, *Rutaceae* and *Zingiberaceae* as either saprobes or pathogens.

Disease symptoms: Leaf spots, leaf blight, melting out, root rot, and foot rot, among others.

Notes: Species delimitation based on morphology alone is limited since many species have overlapping characters. Moreover, the morphology of the sexual morph is of limited value due to difficulties to induce this morph in culture, or find it in nature. The genus is morphologically similar to *Curvularia*, and distinguishing these genera can be problematic. Both genera contain species with straight or curved conidia, but in *Bipolaris* the curvature is continuous throughout the length of the conidium, while the conidia of *Curvularia* have intermediate cells inordinately enlarged which contributes to their curvature. Moreover, conidia in *Bipolaris* are usually longer than in *Curvularia*. Another morphological difference is the presence of stromata in some species of *Curvularia*, a feature not observed in species of *Bipolaris*. In order to properly delineate both genera, phylogenetic studies using ITS, *gapdh* and *tef1* sequences were recently performed (Manamgoda *et al.* 2014, 2015).

References: Ellis 1971, Sivanesan 1987 (morphology and pathogenicity); Manamgoda *et al.* 2011, Tan *et al.* 2016 (morphology, phylogeny and pathogenicity); Manamgoda *et al.* 2014 (morphology, phylogeny, pathogenicity and key of all *Bipolaris* spp.).

Bipolaris saccharicola Y. Marín & Crous, **sp. nov.** MycoBank MB820809. Fig. 3.

Etymology: Name refers to the host genus it was isolated from, *Saccharum*.

Hyphae hyaline to pale brown, branched, septate, thin-walled, 2.5–5.5 µm. *Conidiophores* arising in smalls groups, septate, straight or flexuous, smooth-walled, sometimes branched, cell walls thicker than those of vegetative hyphae, mononematous, semi- to macronematous, pale brown to brown, paler towards apex, rarely swollen at base, up to 900 µm tall. *Conidiogenous cells* smooth-walled, terminal or intercalary, subhyaline to pale brown or brown, subcylindrical to swollen, 10–27(–47) × 4–8 µm. *Conidia* verruculose, curved, rarely straight, fusiform, subhyaline to pale brown or brown, (2–)4–9(–11)-distoseptate, (30–)45–120 × 10.5–20(–21.5) µm; *hila* inconspicuous, brown, slightly protuberant, flat, darkened, slightly thickened, 2–4 µm. *Chlamydospores* and *sexual morph* not observed.

Culture characteristics: Colonies on PDA reaching 41–53 mm diam after 1 wk, moderate aerial mycelium giving a cottony

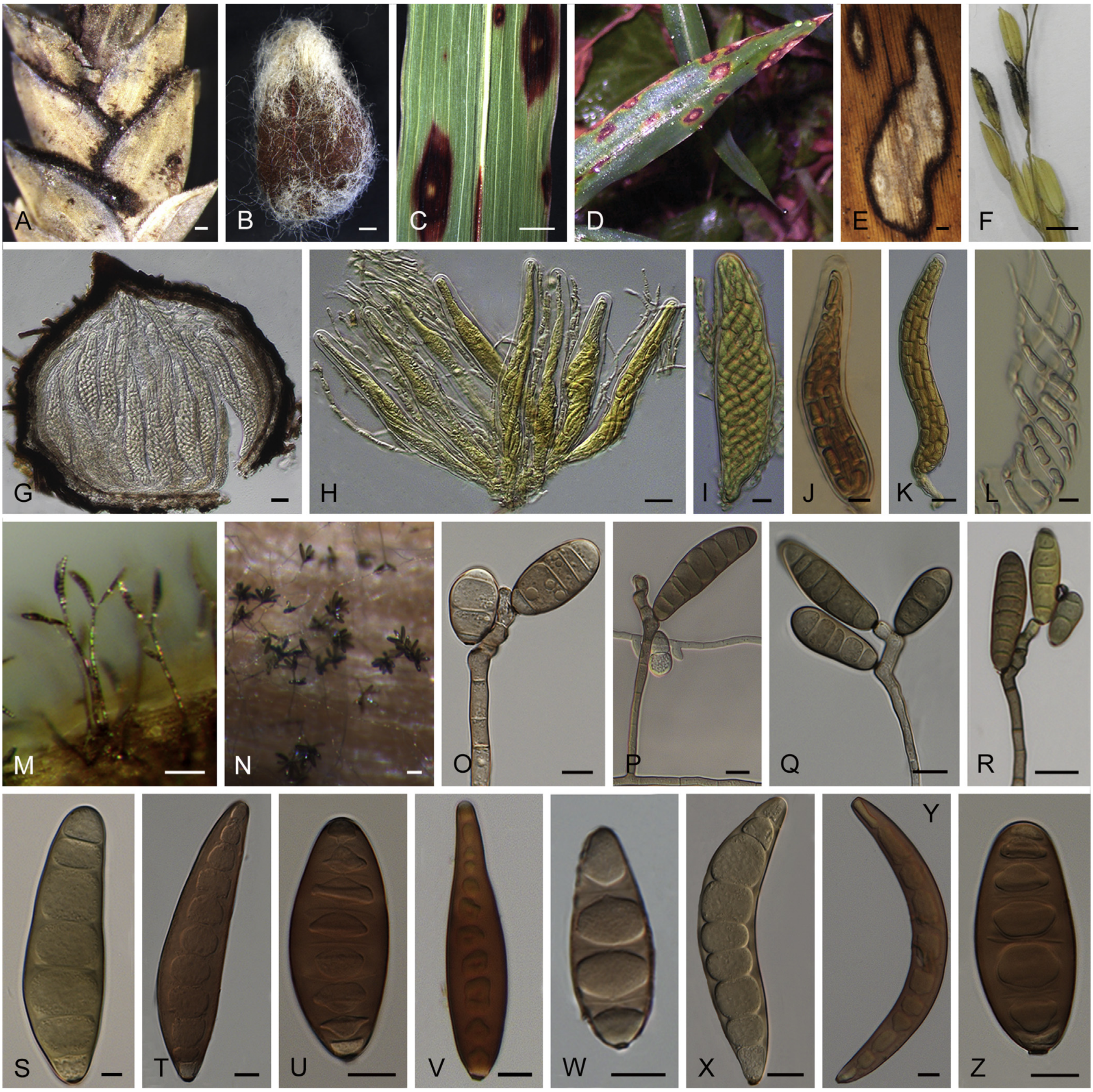


Fig. 1. *Bipolaris* spp. **A–F.** Disease symptoms. **A.** Symptoms caused by *Bipolaris eragrostiellae* (ex-type IMI 155931). **B.** Symptoms caused by *Bipolaris gossypina* (IMI 123377). **C.** Symptoms caused by *Bipolaris halepensis* (ex-type BPI 1103129). **D.** Symptoms caused by *Bipolaris microstegii*. **E.** Symptoms caused by *Bipolaris musae-sapientium* (ex-type K (M) 181466). **F.** Symptoms caused by *Bipolaris oryzae* (ex-neotype MFLUCC 10-0715). **G–L.** Sexual morphs. **G.** Ascoma of *Bipolaris luttrellii* (IMI 345516). **H–K.** Asci. **H.** *Bipolaris chloridis* (ex-type IMI 213865). **I.** *Bipolaris luttrellii* (IMI 345516). **J.** *Bipolaris maydis* (CBS 241.92). **K.** *Bipolaris microlaenae* (IMI 338218). **L.** Ascospores of *Bipolaris maydis* (CBS 241.92). **M–Z.** Asexual morphs. **M–R.** Conidiophores and conidia. **M.** *Bipolaris setariae* (BPI 880305B). **N.** *Bipolaris zeae* (ex-type IMI 202085). **O.** *Bipolaris bicolor* (CBS 690.96). **P.** *Bipolaris heveae* (CBS 241.92). **Q.** *Bipolaris sorokiniana* (ex-type CBS 110.14). **R.** *Bipolaris zeicola* (ex-type BPI 626668). **S–Z.** Conidia. **S.** *Bipolaris cookei* (ex-type BPI 428852). **T.** *Bipolaris costina* (ex-type IMI 256417). **U.** *Bipolaris crotonis* (ex-type IMI 223682). **V.** *Bipolaris gossypina* (IMI 123377). **W.** *Bipolaris obclavata* (ex-type IMI 331725). **X.** *Bipolaris oryzae* (ex-neotype MFLUCC 10-0715). **Y.** *Bipolaris salviniae* (DAR 35056). **Z.** *Bipolaris sorokiniana* (ex-type CBS 110.14). Scale bars: A, N = 100 μm; B, E, F = 500 μm; C = 1 cm; G, H = 20 μm; I–L, O–Z = 10 μm; M = 50 μm. All pictures except for D taken from Manamgoda *et al.* (2014).

appearance, margin lobate; surface olivaceous grey to olivaceous black; reverse olivaceous black.

Material examined: **Unknown country**, unknown substratum, 1926, H. Atherton (**holotype** CBS H-23114, culture ex-type CBS 155.26 = MUCL 9693); **Unknown country**, from *Saccharum officinarum*, unknown date, R.R. Nelson, CBS 324.64; CBS 325.64 = DSM 62597 = MUCL 18220 = MUCL 9694 = NRRL 5241.

Notes: This species is closely related to *Bi. maydis*. However, *Bi. saccharicola* can easily be distinguished by the absence of a sexual morph, longer conidiophores and verruculose, more prominently curved conidia. Both species can be found on the same host, *Saccharum officinarum*. Other species of *Bipolaris* isolated from this host include *Bi. cynodontis*, *Bi. sacchari*, *Bi. setariae*, *Bi. stenospila* and *Bi. yamadae* (Manamgoda *et al.* 2014). *Bipolaris saccharicola* is morphologically similar to *Bi.*

Table 1. DNA barcodes of accepted *Bipolaris* spp.

Species	**Isolates**[1]	**GenBank accession numbers**[2]			**References**
		ITS	***gapdh***	***tef1***	
Bipolaris austrostipae	BRIP 12490^{T}	KX452442	KX452408	KX452459	Tan *et al.* (2016)
Bi. axonopicola	BRIP 11740^{T}	KX452443	KX452409	KX452460	Tan *et al.* (2016)
Bi. bamagaensis	BRIP 13577^{T}	KX452445	KX452411	KX452462	Tan *et al.* (2016)
Bi. bicolor	CBS 690.96	KJ909762	KM042893	KM093776	Manamgoda *et al.* (2014)
Bi. chloridis	BRIP 10965^{T}	KJ415523	KJ415423	KJ415472	Tan *et al.* (2014)
Bi. clavata	BRIP 12530^{T}	KJ415524	KJ415422	KJ415471	Tan *et al.* (2014)
Bi. coffeana	BRIP 14845^{IsoT}	KJ415525	KJ415421	KJ415470	Tan *et al.* (2014)
Bi. cookei	AR 5185	KJ922391	KM034833	KM093777	Manamgoda *et al.* (2014)
Bi. crotonis	BRIP 14838	KJ415526	KJ415420	KJ415479	Tan *et al.* (2014)
Bi. cynodontis	CBS 109894	KJ909767	KM034838	KM093782	Manamgoda *et al.* (2014)
Bi. drechsleri	CBS 136207^{T}	KF500530	KF500533	KM093760	Crous *et al.* (2013b), Manamgoda *et al.* (2014)
Bi. gossypina	BRIP 14840^{T}	KJ415528	KJ415418	KJ415467	Tan *et al.* (2014)
Bi. heliconiae	BRIP 17186^{T}	KJ415530	KJ415417	KJ415465	Tan *et al.* (2014)
Bi. heveae	CBS 241.92	KJ909763	KM034843	KM093791	Manamgoda *et al.* (2014)
Bi. luttrellii	BRIP 14643^{IsoT}	AF071350	AF081402	–	Berbee *et al.* (1999)
Bi. maydis	CBS 137271^{NT}	AF071325	KM034846	KM093794	Berbee *et al.* (1999), Manamgoda *et al.* (2014)
Bi. microlaenae	CBS 280.91^{T}	JN601032	JN600974	JN601017	Manamgoda *et al.* (2011)
Bi. microstegii	CBS 132550^{T}	JX089579	JX089575	KM093756	Crous *et al.* (2012a), Manamgoda *et al.* (2014)
Bi. oryzae	MFLUCC 10-0715^{NT}	JX256416	JX276430	JX266585	Manamgoda *et al.* (2012c)
Bi. panici-miliacei	CBS 199.29^{LT}	KJ909773	KM042896	KM093788	Manamgoda *et al.* (2014)
Bi. peregianensis	BRIP 12790^{T}	JN601034	JN600977	JN601022	Manamgoda *et al.* (2011)
Bi. pluriseptata	BRIP 14839^{IsoT}	KJ415532	KJ415414	KJ415461	Tan *et al.* (2014)
Bi. sacchari	ICMP 6227	KJ922386	KM034842	KM093785	Manamgoda *et al.* (2014)
Bi. salkadehensis	Bi 1^{T}	AB675490	–	–	Ahmadpour *et al.* (2012b)
Bi. salviniae	BRIP 16571^{LT}	KJ415535	KJ415411	KJ415457	Tan *et al.* (2014)
Bi. saccharicola	CBS 155.26^{T}	KY905674	KY905686	KY905694	Present study
	CBS 324.64	HE792932	KY905692	KY905699	Present study da Cunha *et al.* (2012)
	CBS 325.64	KY905675	KY905687	KY905695	Present study
Bi. secalis	BRIP 14453^{IsoLT}	KJ415537	KJ415409	KJ415455	Tan *et al.* (2014)
Bi. setariae	CBS 141.31	EF452444	EF513206	–	Andrie *et al.* (2008)
Bi. shoemakeri	BRIP 15929^{T}	KX452453	KX452419	KX452470	Tan *et al.* (2016)
Bi. simmondsii	BRIP 12030^{T}	KX452454	KX452420	KX452471	Tan *et al.* (2016)
Bi. sivanesaniana	BRIP 15847^{T}	KX452455	KX452421	KX452472	Tan *et al.* (2016)
Bi. sorokiniana	CBS 110.14	KJ922381	KM034822	KM093763	Manamgoda *et al.* (2014)
Bi. subramanianii	BRIP 16226^{T}	KX452457	KX452423	KX452474	Tan *et al.* (2016)
Bi. urochloae	ATCC 58317	KJ922389	KM230396	KM093770	Manamgoda *et al.* (2014)
Bi. variabilis	CBS 127716^{T}	KY905676	KY905688	KY905696	Present study
	CBS 127736	KY905677	KY905689	–	Present study
Bi. victoriae	CBS 327.64^{T}	KJ909778	KM034811	KM093748	Manamgoda *et al.* (2014)
Bi. yamadae	CBS 202.29^{ET}	KJ909779	KM034830	KM093773	Manamgoda *et al.* (2014)
	CBS 127087 (neotype of *Bi. euphorbiae*)	KY905673	KY905685	KY905693	Present study

(*continued on next page*)

Table 1. (Continued).

Species	Isolates[1]	GenBank accession numbers[2]			References
		ITS	*gapdh*	*tef1*	
Bi. woodii	BRIP 12239^{T}	KX452458	KX452424	KX4524725	Tan *et al.* (2016)
Bi. zeae	BRIP 11512^{IsoPT}	KJ415538	KJ415408	KJ415454	Tan *et al.* (2014)
Bi. zeicola	FIP 532^{ET}	KM230398	KM034815	KM093752	Manamgoda *et al.* (2014)

[1] AR, FIP: Isolates housed in Systematic Mycology and Microbiology Laboratory, United States Department of Agriculture, Agricultural Research Service, Beltsville, Maryland, USA; Bi: Isolates housed in the Department of Plant Protection, Faculty of Agricultural Sciences and Engineering, University College of Agriculture and Natural Resources, University of Tehran, Karaj, Iran (TUPP); ATCC: American Type Culture Collection, Virginia, USA; BRIP: Queensland Plant Pathology Herbarium, Brisbane, Australia; CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; ICMP: International Collection of Micro-organisms from Plants, Landcare Research, Private Bag 92170, Auckland, New Zealand; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Ria, Thailand. $^{T, ET, IsoT, IsoLT, IsoPT, LT}$ and ^{NT} indicate ex-type, ex-epitype, ex-isotype, ex-isolectotype, ex-isoparatype, ex-lectotype and ex-neotype strains, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *gapdh*: partial glyceraldehyde-3-phosphate dehydrogenase gene; *tef1*: partial translation elongation factor 1-alpha gene.

sacchari, but *Bi. saccharicola* can be distinguished by its much longer and non-geniculate conidiophores and wider and more septate conidia.

Bipolaris variabilis Y. Marín, Y.P. Tan & Crous, **sp. nov.** MycoBank MB820810. Fig. 4.

Etymology: Name refers to the highly variable conidial morphology.

Leaf spots brown to reddish, elongated, often confluent and following veins, some with central part brown, 2.5 × 1–2 mm. *Hyphae* subhyaline to pale brown, branched, septate, thin-walled, 3–6 μm. *Conidiophores* arising in groups, septate, straight or flexuous, sometimes geniculate at upper part, smooth to verruculose, branched, cells walls thicker than those of vegetative hyphae, mononematous, semi- to macronematous, pale brown to brown, paler towards apex, slightly swollen at base, up to 1 600 μm tall. *Conidiogenous cells* smooth-walled, terminal or intercalary, proliferating sympodially, subhyaline or pale brown to brown, subcylindrical to swollen, (6.5–)8–26(–35) × 5.5–11 μm. *Conidia* verruculose, straight or slightly curved, globose, subglobose, ellipsoidal to obclavate, pale brown to brown, apical and basal cells paler than middle cells being subhyaline to pale brown, (1–)3–7(–9)-distoseptate, 13.5–77 × 10–19.5 μm; *hila* inconspicuous, slightly protuberant, flat, darkened, thickened, 3–6 μm diam. *Chlamydospores* and *sexual morph* not observed.

Culture characteristics: Colonies on PDA reaching 90 mm diam within 1 wk, with sparse to moderate aerial mycelium giving a cottony appearance, margin lobate; surface olivaceous grey to iron-grey; reverse olivaceous black.

Material examined: **Argentina**, from leaf spots on *Pennisetum clandestinum*, 28 Jul. 1986, col. M.N. Sisterna, isol. J.L. Alcorn (**holotype** CBS H-23115, culture ex-type CBS 127716 = BRIP 15349). **Brazil**, from *Pennisetum clandestinum*, Apr. 1987, J.J. Muchovej, CBS 127736 = BRIP 15702 = ATCC 62423.

Notes: *Bipolaris variabilis* can easily be distinguished based on its highly variable conidial size, shape and septation. Hitherto, this species has only been found on *Pennisetum clandestinum* in South America. Other species of *Bipolaris* can be found on *Pennisetum* spp., i.e. *Bi. bicolor*, *Bi. colocasiae*, *Bi. cynodontis*, *Bi. maydis*, *Bi. mediocris*, *Bi. sacchari*, *Bi. setariae*, *Bi. sorokiniana*, *Bi. stenospila*, *Bi. urochloae* and *Bi. zeae*; however, only *Bi. mediocris* is restricted to that host (Manamgoda *et al.* 2014). *Bipolaris mediocris* and *Bi. variabilis* are morphologically similar, but *Bi. variabilis* produces smaller, verruculose conidia. Moreover, *Bi. mediocris* is characterised by much shorter conidiophores (up to 150 μm tall), and has only been reported in Africa (Farr & Rossman 2017). *Bipolaris variabilis* is closely related to *Bi. zeae*, but the latter is characterised by shorter conidiophores (up to 370 μm tall), and less septate conidia that are less variable in shape than those of *Bi. variabilis*.

Bipolaris yamadae (Y. Nisik.) Shoemaker, Canad. J. Bot. 37: 884. 1959. Fig. 5.

Basionym: *Helminthosporium yamadae* Y. Nisik., Rept. Ohara. Inst. Agr. Research 4: 120. 1928.

Synonyms: *Drechslera yamadai* (Y. Nisik.) Subram. & B.L. Jain, Curr. Sci. 35: 355. 1966.

Helminthosporium euphorbiae Hansf., Proc. Linn. Soc. London 155: 49. 1943.

Bipolaris euphorbiae (Hansf.) J.J. Muchovej & A.O. Carvalho, Mycotaxon 35: 160. 1989.

Drechslera euphorbiae (Hansf.) M.B. Ellis, Dematiaceous Hyphomycetes (Kew): 440. 1971.

Notes: *Bipolaris euphorbiae* was originally described in *Helminthosporium* (Hansford 1943), then transferred to *Drechslera* (Ellis 1971), and finally placed in *Bipolaris* based on the bipolar germination and hilum structure (Muchovej & Carvalho 1989). In their revision of *Bipolaris*, Manamgoda *et al.* (2014) accepted this species in the genus despite the lack of molecular data. In the present study, the neotype strain of *Bi. euphorbiae* CBS 127087 (=BRIP 16567; see Fig. 5), which was designated by Muchovej & Carvalho (1989), clustered with the ex-epitype strain of *Bi. yamadae*. Both species are morphologically similar differing only in the size of the structures that are usually overlapping. Based on these data, we propose to reduce *Bi. euphorbiae* to synonymy under *Bi. yamadae*. Moreover, we emended the description of *Bi. yamadae* to include the morphology of its new synonym, as well as the new host and distribution records.

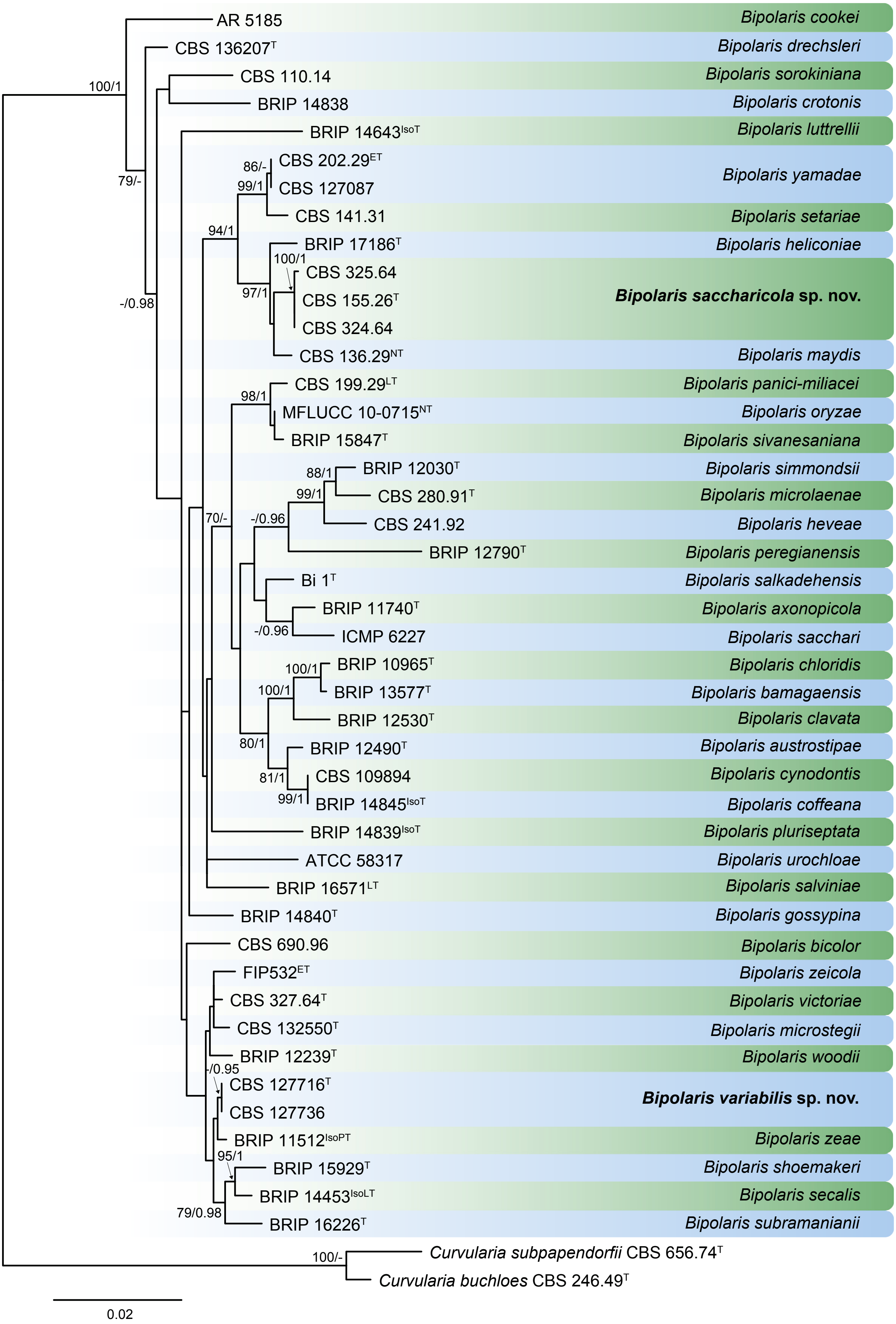

AR 5185
Bipolaris cookei
CBS 136207T
Bipolaris drechsleri
100/1
CBS 110.14
Bipolaris sorokiniana
BRIP 14838
Bipolaris crotonis
BRIP 14643IsoT
Bipolaris luttrellii
79/-
86/-
CBS 202.29ET
99/1
CBS 127087
Bipolaris yamadae
CBS 141.31
Bipolaris setariae
94/1
BRIP 17186T
Bipolaris heliconiae
100/1
CBS 325.64
CBS 155.26T
CBS 324.64
Bipolaris saccharicola sp. nov.
97/1
-/0.98
CBS 136.29NT
Bipolaris maydis
CBS 199.29LT
Bipolaris panici-miliacei
98/1
MFLUCC 10-0715NT
Bipolaris oryzae
BRIP 15847T
Bipolaris sivanesaniana
88/1
BRIP 12030T
Bipolaris simmondsii
99/1
CBS 280.91T
Bipolaris microlaenae
70/-
-/0.96
CBS 241.92
Bipolaris heveae
BRIP 12790T
Bipolaris peregianensis
Bi 1T
Bipolaris salkadehensis
BRIP 11740T
Bipolaris axonopicola
-/0.96
ICMP 6227
Bipolaris sacchari
100/1
BRIP 10965T
Bipolaris chloridis
100/1
BRIP 13577T
Bipolaris bamagaensis
BRIP 12530T
Bipolaris clavata
80/1
BRIP 12490T
Bipolaris austrostipae
81/1
CBS 109894
Bipolaris cynodontis
99/1
BRIP 14845IsoT
Bipolaris coffeana
BRIP 14839IsoT
Bipolaris pluriseptata
ATCC 58317
Bipolaris urochloae
BRIP 16571LT
Bipolaris salviniae
BRIP 14840T
Bipolaris gossypina
CBS 690.96
Bipolaris bicolor
FIP532ET
Bipolaris zeicola
CBS 327.64T
Bipolaris victoriae
CBS 132550T
Bipolaris microstegii
BRIP 12239T
Bipolaris woodii
-/0.95
CBS 127716T
CBS 127736
Bipolaris variabilis sp. nov.
BRIP 11512IsoPT
Bipolaris zeae
95/1
BRIP 15929T
Bipolaris shoemakeri
BRIP 14453IsoLT
Bipolaris secalis
79/0.98
BRIP 16226T
Bipolaris subramanianii
100/-
Curvularia subpapendorfii CBS 656.74T
Curvularia buchloes CBS 246.49T
0.02

Fig. 3. *Bipolaris saccharicola* (ex-type CBS 155.26). **A–C.** Conidiophores and conidia. **D–H.** Conidia. Scale bars: A–C = 20 μm; H applies to D–H = 10 μm.

Leaf spots on *Panicum* sp. ovoid, oblong, pale brown at margin and pale brown at centre, with an irregular concentric zone. *Hyphae* hyaline, branched, septate, anastomosing, thin-walled, 1.5–4.5 μm. *Conidiophores* arising singly or in small groups, septate, rarely branched, straight or flexuous, sometimes geniculate at upper part, smooth walled, mononematous, semi- to macronematous, olive-brown to pale brown, sometimes paler towards apex, swollen at base, 40–650 × 3–10.5 μm. *Conidiogenous cells* smooth-walled, sometimes slightly verruculose, terminal or intercalary, subhyaline to pale brown or dark brown, subcylindrical to slightly swollen, 7–30(–40) × 5.5–9.5 μm. *Conidia* smooth-walled, straight or curved, ellipsoidal, cylindrical, fusiform or obclavate, sometimes obovoid, with rounded ends, subhyaline to pale brown or olive-brown, (3–)5–7(–11)-distoseptate, 27–100(–120) × 11.5–20 μm; *hila* 2.5–4.5 μm, non or slightly protuberant, flat, darkened; *germination* at both ends.

Culture characteristics: Colonies on PDA reaching 30–65 mm diam after 1 wk, cottony, with irregular margins; surface pale olivaceous grey to olivaceous grey; reverse olivaceous black.

Distribution: Brazil, Cuba, China, India, Japan, Sudan, Tanzania, USA (IA, ID, ND, WI).

Hosts: *Panicum capillare*, *Pa. implicatum*, *Pa. maximum*, *Pa. miliaceum*, *Euphorbia* sp., *Oryza* sp., *Saccharum* sp., *Setaria plicata* (Farr & Rossman 2017).

Authors: Y. Marin-Felix, P.W. Crous & Y.P. Tan

Boeremia Aveskamp *et al.*, Stud. Mycol. 65: 36. 2010. Fig. 6.

Classification: *Dothideomycetes*, *Pleosporomycetidae*, *Pleosporales*, *Didymellaceae.*

Type species: *Boeremia exigua* (Desm.) Aveskamp *et al.* Representative strain: CBS 431.74.

DNA barcodes (genus): LSU, ITS.

DNA barcodes (species): *act*, *cal*, *rpb2*, *tef1*, *tub2*. Table 2. Fig. 7.

Fig. 2. RAxML phylogram obtained from the combined ITS (478 bp), *gapdh* (472 bp) and *tef1* (892 bp) sequences of all the accepted species of *Bipolaris.* The tree was rooted to *Curvularia buchloës* CBS 246.49 and *Curvularia subpapendorfii* CBS 656.74. The novel species described in this study are shown in **bold**. RAxML bootstrap support (BS) values above 70 % and Bayesian posterior probability scores ≥ 0.95 are shown at the nodes. GenBank accession numbers are indicated in Table 1. $^{\text{T, ET, IsoT, IsoLT, IsoPT, LT}}$ and $^{\text{NT}}$ indicate ex-type, ex-epitype, ex-isotype, ex-isolectotype, ex-isoparatype, ex-lectotype and ex-neotype strains, respectively. TreeBASE: S20877.

Fig. 4. *Bipolaris variabilis* (ex-type CBS 127716). **A–C.** Conidiophores and conidia. **D–M.** Conidia. Scale bars: A = 20 μm; B, C = 15 μm; H applies to D–H, M applies to I–M = 5 μm.

Ascomata pseudothecial, subglobose. *Asci* cylindrical or subclavate, 8-spored, biseriate. *Ascospores* ellipsoidal, 1-septate. *Conidiomata* pycnidial, variable in shape and size, mostly globose to subglobose, superficial or immersed into agar, solitary or confluent; *ostiole* non-papillate or papillate, lined internally with hyaline cells when mature; *conidiomatal wall* pseudoparenchymatous, multi-layered, outer wall brown pigmented. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* phialidic, hyaline, smooth, ampulliform to doliiform. *Conidia* variable in shape, hyaline, smooth- and thin-walled, mainly aseptate, but 1(–2)-septate larger conidia may be found (adapted from Aveskamp *et al.* 2010).

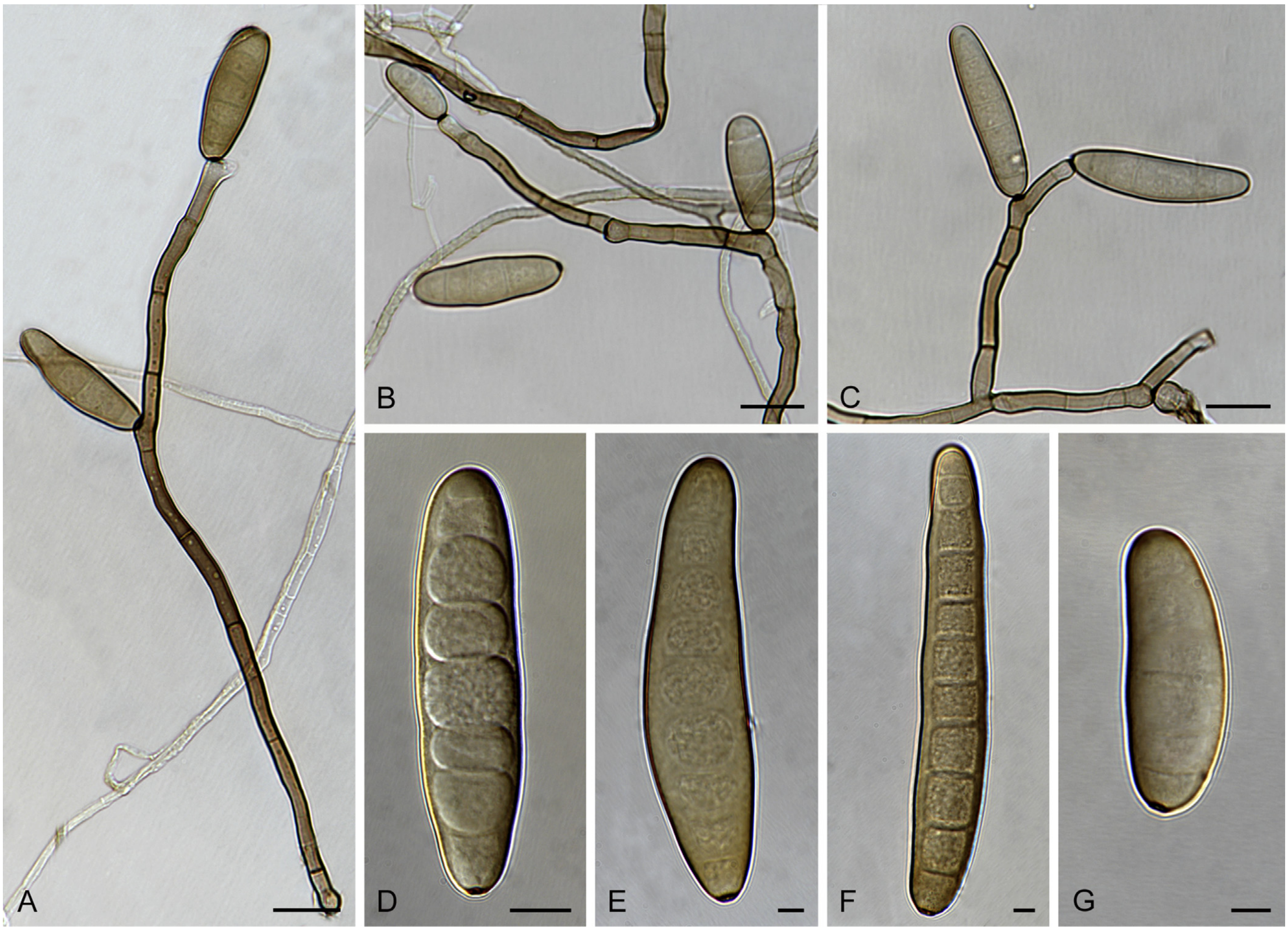


Fig. 5. *Bipolaris yamadae* (CBS 127087). **A–C.** Conidiophores and conidia. **D–G.** Conidia. Scale bars: A–C = 20 µm; D–G = 10 µm.

Culture characteristics: Colonies on OA white to dull green, grey olivaceous to olivaceous or smoke-grey, velvety, floccose to woolly, margin often regular, sometimes lobate and irregular scalloped.

Optimal media and cultivation conditions: OA or PNA at 25 °C under near-ultraviolet light (12 h light, 12 h dark) to promote sporulation.

Distribution: Worldwide.

Hosts: Seed-borne pathogens of *Phaseolus vulgaris* (*Fabaceae*) and noxious pathogens of *Coffea arabica* (*Rubiaceae*). Species on more than 200 host genera including *Amaryllidaceae*, *Apocynaceae*, *Araliaceae*, *Asteraceae*, *Caprifoliaceae*, *Chenopodiaceae*, *Crassulaceae*, *Fabaceae*, *Lamiaceae*, *Linaceae*, *Oleaceae*, *Salicaceae*, *Solanaceae*, *Ulmaceae*, *Umbelliferae*.

Disease symptoms: Leaf spots, stem lesions, black node, bulb rot, root rot, shoot dieback.

Notes: The genus *Boeremia* was established by Aveskamp *et al.* (2010) to accommodate phoma-like species that are morphologically similar and closely related to *Ph. exigua*. Taxa in this genus are characterised by having ostioles with a hyaline inner layer of cells and producing aseptate and septate conidia (Aveskamp *et al.* 2010). To date only *Bo. lycopersici* has been reported to have a sexual morph. Recently, Chen *et al.* (2015a) and Berner *et al.* (2015) further examined the phylogenetic relationships of taxa in *Boeremia* in two combined multilocus analyses, the first one based on LSU, ITS, *tub2* and *rpb2* sequences, and the second on ITS, *act*, *cal*, *tef1* and *tub2* sequences.

References: Boerema *et al.* 2004 (morphology and pathogenicity); Aveskamp *et al.* 2010, Chen *et al.* 2015a (morphology and phylogeny); Berner *et al.* 2015 (morphology, pathogenicity and phylogeny).

Boeremia trachelospermi Q. Chen & L. Cai, **sp. nov.** MycoBank MB818819. Fig. 8.

Etymology: Named for the host genus from which the holotype was collected, *Trachelospermum*.

Conidiomata pycnidial, solitary or aggregated, globose to subglobose, glabrous or with few hyphal outgrowths, superficial, with a short neck, 75–255 × 60–225 µm; *ostiole* single, papillate or non-papillate; *conidiomatal wall* pseudoparenchymatous 2–4-layered, 16.5–37 µm thick, composed of isodiametric cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* phialidic, hyaline, smooth, ampulliform to doliiform, 4.5–12.5 × 4.5–6 µm. *Conidia* variable in shape, mostly ovoid, ellipsoidal to cylindrical, smooth- and thin-walled, hyaline, mainly aseptate, occasionally 1-

Fig. 6. *Boeremia* spp. **A.** Symptoms of *Boeremia lilacis* (LC 8116) on *Ocimum* sp. **B.** Symptoms of *Boeremia exigua* var. *rhapontica* (ex-type CBS 113651) on *Rhaponticum repens*. **C.** Symptoms of *Boeremia lilacis* (LC 5178) on *Lonicera* sp. **D.** Ostiole configuration of *Boeremia exigua* var. *exigua* (CBS 431.74). **E.** Section of young pycnidium of *Boeremia exigua* var. *pseudolilacis* (ex-type CBS 101207). **F.** Conidia of *Boeremia exigua* var. *pseudolilacis* (ex-type CBS 101207). **G.** Conidia of *Boeremia exigua* var. *heteromorpha* (ex-neotype CBS 443.94). Scale bars: D–E = 20 μm; F = 5 μm; G = 10 μm. Picture B taken from Berner *et al.* (2015); D–F from Aveskamp *et al.* (2010); G from Chen *et al.* (2015a).

septate large conidia, 4.5–9.5 × 2.5–4.5 μm, with 1–8 guttules. *Conidial matrix* cream-coloured.

Culture characteristics: Colonies on OA, reaching 47–55 mm diam after 1 wk, margin regular, floccose, white, dark grey near centre; reverse white to buff, dark grey near centre. Colonies on MEA 40–60 mm diam after 1 wk, margin regular, woolly, pale olivaceous grey; reverse concolourous. Colonies on PDA, reaching 20–25 mm diam after 1 wk, margin regular, floccose, compact, white to olivaceous; reverse white to buff, olivaceous near centre. NaOH test negative.

Material examined: **USA**, on seedlings of *Trachelospermum jasminoides*, 2014, W.J. Duan (**holotype** HMAS 246706, culture ex-type CGMCC 3.18222 = LC 8105).

Notes: *Boeremia trachelospermi* represents the first report of a *Boeremia* species on *Trachelospermum* (*Apocynaceae*). Phylogenetically, it forms a distinct lineage separate from *Bo. diversispora*, the *Bo. exigua* varieties, *Bo. noackiana* and *Bo. sambuci-nigrae* (Fig. 7), and morphologically it often produces longer conidiogenous cells and conidia than the other taxa.

Authors: Q. Chen & L. Cai

Calonectria De Not., Comm. Soc. crittog. Ital. 2(fasc. 3): 477. 1867. Figs 9, 10.
Synonyms: *Cylindrocladium* Morgan, Bot. Gaz. 17: 191. 1892.
Candelospora Rea & Hawley, Proc. R. Ir. Acad., Sect. B, Biol. Sci. 13: 11. 1912.

Classification: *Sordariomycetes*, *Hypocreomycetidae*, *Hypocreales*, *Nectriaceae.*

Type species: *Calonectria pyrochroa* (Desm.) Sacc. Holotype: Italy, leaves of *Magnolia grandiflora*, Daldini (as *Ca. daldiniana*); Lectotype: France, litter of *Platanus*, Autumn. Desm., Pl. Crypt. France Ed. 2 (2) # 372 (*fide* Rossman 1979); no culture or DNA data available.

DNA barcodes (genus): LSU, ITS.

DNA barcodes (species): *cmdA*, *his3*, *tef1*, *tub2*, and *rpb2.* Table 3. Fig. 11.

Ascomata perithecial, solitary or in groups, globose to subglobose to ovoid, yellow to orange to red or red-brown to brown, turning dark red to red-brown in KOH, rough-walled; *ascomatal apex* consisting of flattened, thick-walled hyphal elements with rounded tips forming a palisade, discontinuous with warty wall, gradually becoming thinner towards ostiolar canal, and merging with outer periphyses; *ascomatal base* consisting of dark brown-red, angular cells, merging with an erumpent stroma, cells of outer wall layer continuing into pseudoparenchymatous cells of erumpent stroma. *Asci* 8-spored, clavate, tapering to a long thin stalk. *Ascospores* aggregated in upper third of ascus, hyaline, smooth, fusoid with rounded ends, straight to sinuous, unconstricted, or constricted at septa. *Megaconidiophores*, if present, borne on agar surface or immersed in agar; *stipe extensions* mostly absent; *conidiophores* unbranched, terminating in 1–3 phialides, or sometimes with a single subterminal phialide; *phialides* straight to curved, cylindrical, seemingly producing a single conidium, periclinal thickening and an inconspicuous, divergent collarette rarely visible. *Megaconidia* hyaline, smooth, frequently remaining attached to phialide, multi-septate, widest in middle, bent or curved, with a truncated base and rounded apical cell. *Macroconidiophores* consist of a stipe, a penicillate arrangement of fertile branches, a stipe extension, and a terminal vesicle; *stipe* septate, hyaline or slightly pigmented at base, smooth or finely verruculose; *stipe extensions* septate, straight to flexuous, mostly thin-walled, terminating in a thin-walled vesicle of characteristic shape. *Conidiogenous apparatus* with 0–1-septate primary branches,

Table 2. DNA barcodes of accepted *Boeremia* spp.

Species	**Isolates**[1]	**GenBank accession numbers**[2]						**References**
		ITS	***act***	***cal***	***rpb2***	***tef1***	***tub2***	
Boeremia crinicola	CBS 109.79	GU237737	KY484558	KY484571	KT389563	–	GU237489	Aveskamp *et al.* (2010), Chen *et al.* (2015a), Berner *et al.* (2015)
Bo. diversispora	CBS 102.80	GU237725	EU880861	KY484575	KT389565	KY484676	GU237492	Aveskamp *et al.* (2009b, 2010), Chen *et al.* (2015a), Berner *et al.* (2015)
Bo. exigua var. *coffeae*	CBS 109183	GU237748	KY484560	KY484576	KT389566	KY484678	GU237505	Aveskamp *et al.* (2010), Chen *et al.* (2015a), Berner *et al.* (2015)
Bo. exigua var. *exigua*	CBS 431.74	FJ427001	EU880854	KY484584	KT389569	KY484687	FJ427112	Aveskamp *et al.* (2009a, b), Chen *et al.* (2015a), Berner *et al.* (2015)
Bo. exigua var. *forsythiae*	CBS 101213	GU237723	EU880868	KY484589	KT389571	KY484692	GU237494	Aveskamp *et al.* (2009b, 2010), Chen *et al.* (2015a), Berner *et al.* (2015)
Bo. exigua var. gilvescens	CBS 101150	GU237715	KY484562	KY484591	KT389568	KY484694	GU237495	Aveskamp *et al.* (2010), Chen *et al.* (2015a), Berner *et al.* (2015)
Bo. exigua var. *heteromorpha*	CBS 443.94^{NT}	GU237866	EU880869	KY484598	KT389573	KY484700	GU237497	Aveskamp *et al.* (2009b, 2010), Chen *et al.* (2015a), Berner *et al.* (2015)
Bo. exigua var. *linicola*	CBS 116.76	GU237754	EU880880	KY484604	KT389574	KY484705	GU237500	Aveskamp *et al.* (2009b, 2010), Chen *et al.* (2015a). Berner *et al.* (2015)
Bo. exigua var. *populi*	CBS 100167^{T}	GU237707	EU880885	KY484605	–	KY484706	GU237501	Aveskamp *et al.* (2009b, 2010), Berner *et al.* (2015)
Bo. exigua var. *pseudolilacis*	CBS 101207^{T}	GU237721	EU880874	KY484609	–	KY484710	GU237503	Aveskamp *et al.* (2009b, 2010), Berner *et al.* (2015)
Bo. exigua var. *rhapontica*	CBS 113651^{T}	KY484662	KY484566	KY484612	–	KY484713	KY484760	Berner *et al.* (2015)
Bo. exigua var. *viburni*	CBS 100354	GU237711	EU880889	KY484613	KT389577	–	GU237506	Aveskamp *et al.* (2009b, 2010), Chen *et al.* (2015a), Berner *et al.* (2015)
Bo. foveata	CBS 109176	GU237742	EU880892	KY484614	KT389578	KY484714	GU237508	Aveskamp *et al.* (2009b, 2010), Chen *et al.* (2015a), Berner *et al.* (2015)
Bo. hedericola	CBS 367.91	GU237842	KY484568	KY484618	KT389579	KY484718	GU237511	Aveskamp *et al.* (2010), Chen *et al.* (2015a), Berner *et al.* (2015)
Bo. lilacis	CBS 569.79	GU237892	EU880875	KY484619	–	KY484721	GU237498	Aveskamp *et al.* (2009b, 2010), Berner *et al.* (2015)
Bo. lycopersici	CBS 378.67	GU237848	EU880898	KY484623	KT389580	KY484726	GU237512	Aveskamp *et al.* (2009b, 2010), Chen *et al.* (2015a), Berner *et al.* (2015)
Bo. noackiana	CBS 100353	GU237710	EU880881	KY484624	–	KY484727	GU237514	Aveskamp *et al.* (2009b, 2010), Berner *et al.* (2015)
Bo. sambuci-nigrae	CBS 629.68^{T}	GU237897	KY484570	KY484630	–	KY484734	GU237517	Aveskamp *et al.* (2010), Berner *et al.* (2015)
Bo. strasseri	CBS 126.93	GU237773	EU880904	KY484631	KT389584	KY484735	GU237518	Aveskamp *et al.* (2009b, 2010), Chen *et al.* (2015a), Berner *et al.* (2015)
Bo. telephii	CBS 109175	GU237741	EU880906	KY484633	KT389585	KY484737	GU237520	Aveskamp *et al.* (2009b, 2010), Chen *et al.* (2015a), Berner *et al.* (2015)
Bo. trachelospermi	CGMCC 3.18222^{T}	KY064028	–	–	KY064033	–	KY064051	Present study

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CGMCC: Chinese General Microbiological Culture Collection Center, Beijing, China. ^{T} and ^{NT} indicate ex-type and ex-neotype strains, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *act*: partial actin gene; *cal*: partial calmodulin gene; *rpb2*: partial RNA polymerase II second largest subunit gene; *tef1*: partial translation elongation factor 1-alpha gene; *tub2*: partial β-tubulin gene.

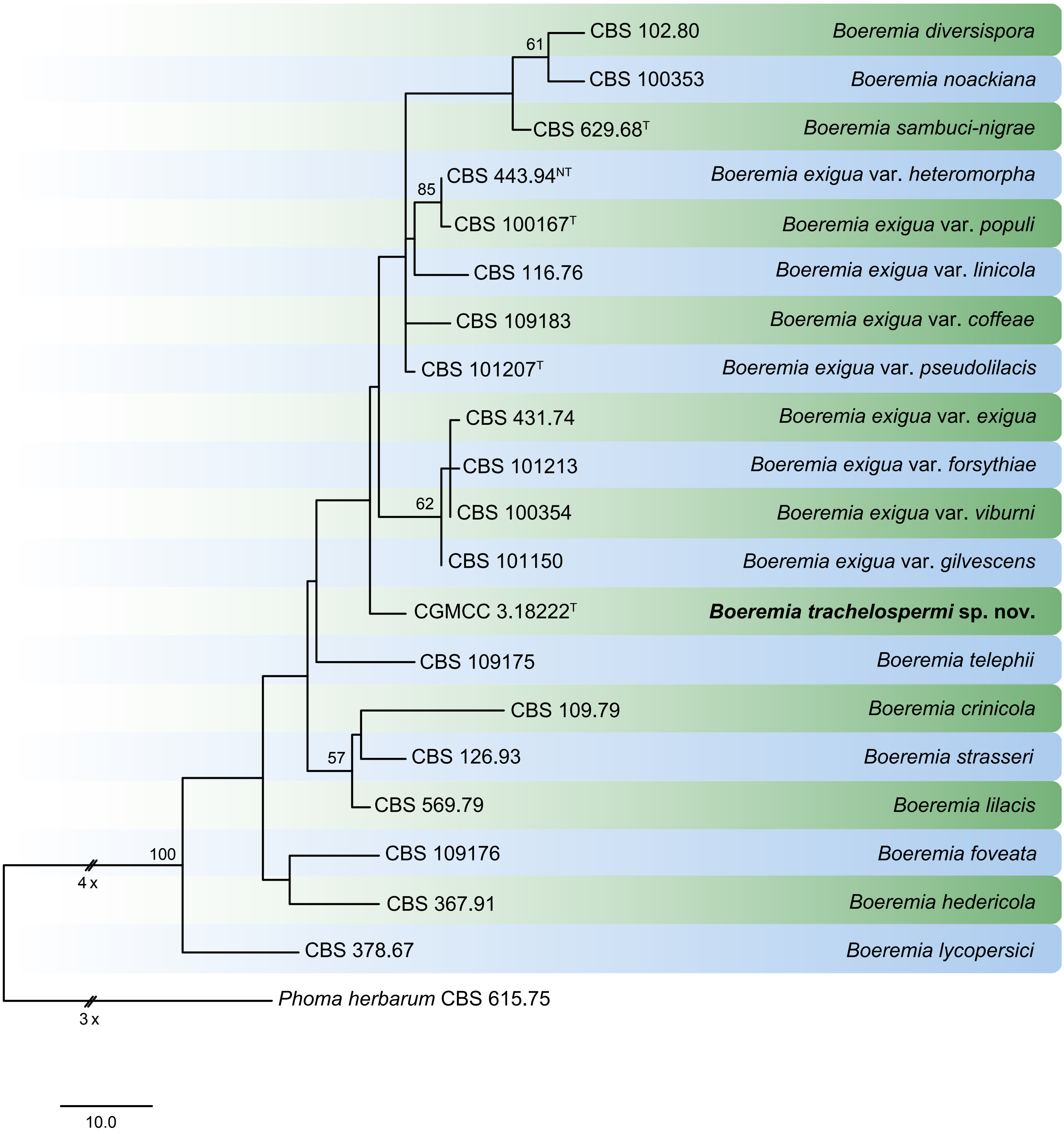


Fig. 7. Phylogenetic tree generated from a maximum parsimony analysis based on the combined LSU, ITS, *tub2* and *rpb2* sequences. Values above the branches represent parsimony bootstrap support values (> 50 %). The novel species are shown in **bold**. The tree is rooted with *Phoma herbarum* CBS 615.75. GenBank accession numbers are indicated in Table 2. ^{T} and ^{NT} indicate ex-type and ex-neotype strains, respectively. TreeBASE: S21048.

up to eight additional branches, mostly aseptate, each terminal branch producing 1–6 phialides; *phialides* cylindrical to allantoid, straight to curved, or doliiform to reniform, hyaline, aseptate, apex with minute periclinal thickening and inconspicuous divergent collarette. *Macroconidia* cylindrical, rounded at both ends, straight or curved, widest at base, middle, or first basal septum, 1- to multi-septate, lacking visible abscission scars, held in parallel cylindrical clusters by colourless slime. *Microconidiophores* consist of a stipe and a penicillate or subverticillate arrangement of fertile branches; *primary branches* 0–1-septate, subcylindrical; *secondary branches* 0–1-septate, terminating in 1–4 phialides; *phialides* cylindrical, straight to slightly curved, apex with minute periclinal thickening and marginal frill. *Microconidia* cylindrical, straight to curved, rounded at apex, flattened at base, 1(–3)-septate, held in asymmetrical clusters by colourless slime.

Culture characteristics: Colonies on MEA white to pale brick when young, becoming pale brick to dark sepia when mature, fluffy, cottony, effuse to convex with papillate surface, margin entire, undulate, lobate, or fimbriate, sometimes with abundant chlamydospores forming microsclerotia within medium.

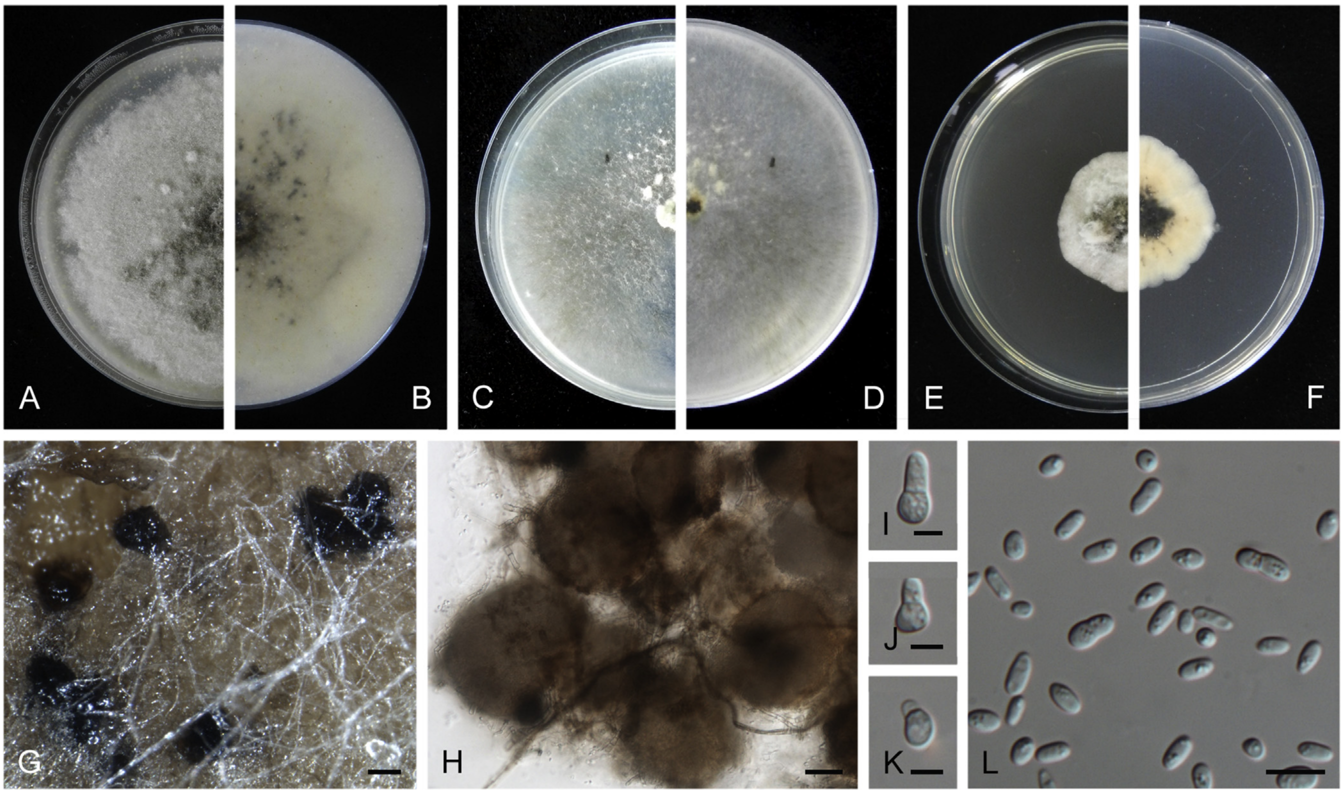


Fig. 8. *Boeremia trachelospermi* (ex-type CGMCC 3.18222). **A, B.** Colony on OA (front and reverse). **C, D.** Colony on MEA (front and reverse). **E, F.** Colony on PDA (front and reverse). **G.** Pycnidia forming on OA. H. Pycnidia. **I–K.** Conidiogenous cells. **L.** Conidia. Scale bars: G = 200 µm; H = 50 µm; I–K = 5 µm; L = 10 µm.

Optimal media and cultivation conditions: CLA to induce sporulation of the asexual morph at 25 °C, while for the sexual morph sterile toothpicks placed on SNA is used at 20 °C.

Distribution: Worldwide.

Hosts: Soil-borne pathogens of forestry, agricultural and horticultural crops representing approximately 100 plant families and 340 plant host species (Crous 2002, Lombard *et al.* 2010c).

Disease symptoms: Leaf spots, leaf and shoot blights, cutting rot, stem cankers, damping-off and root rot.

Notes: The genus *Calonectria* presently includes 151 species of which only *Ca. hederae* and *Ca. pyrochroa* are not supported by ex-type cultures and supplementary DNA barcodes. Species delimitation based on morphology alone is complicated by the large number of cryptic taxa recognised in this genus (Lombard *et al.* 2016). The perithecia of several *Calonectria* spp. are morphologically similar. The cylindrocladium-like asexual morph, the life phase most commonly found in nature, is extensively used for taxon identification, although it is complicated by the morphological overlap of some cryptic species. For accurate species delimitation, phylogenetic inference of the *cmdA*, *tef1* and *tub2* (or combinations of these) is required.

References: Crous 2002 (morphology, pathogenicity and monograph); Lombard *et al.* 2010a–d, 2015, 2016 (morphology, phylogeny and key of *Calonectria* spp.); Alfenas *et al.* 2015 (morphology and phylogeny).

Calonectria ecuadorensis L. Lombard & Crous, **sp. nov.** MycoBank MB820849. Fig. 12.

Etymology: Name refers to Ecuador, the country where this fungus was collected.

Macroconidiophores consist of a stipe bearing a penicillate arrangement of fertile branches, and a stipe extension terminating in a vesicle; *stipe* septate, hyaline, smooth, 55–70 × 6–10 µm; *stipe extension* septate, straight to flexuous, 130–280 µm long, 3–6 µm wide at apical septum, terminating in a clavate vesicle, 4–6 µm diam. *Conidiogenous apparatus* 45–90 µm wide, and 20–90 µm long; *primary branches* aseptate, 13–31 × 4–6 µm; *secondary branches* aseptate, 13–23 × 4–5 µm; *tertiary branches* aseptate, 9–15 × 3–4 µm, each terminal branch producing 2–6 phialides; *phialides* doliiform to reniform, hyaline, aseptate, 6–11 × 2–4 µm, apex with minute periclinal thickening and inconspicuous collarette. *Macroconidia* cylindrical, rounded at both ends, straight, (34–)35–39(–44) × (3–)3.5–4.5(–5) µm (av. 37 × 4 µm), 1-septate, lacking a visible abscission scar, held in parallel cylindrical clusters by colourless slime. *Mega-* and *microconidia* not observed.

Culture characteristics: Colonies moderately fast growing (35–55 mm diam) on MEA after 1 wk at room temperature; surface rosy-buff to cinnamon with sparse white woolly aerial mycelium and abundant sporulation on aerial mycelium and colony surface; reverse rosy-buff to cinnamon to sepia with abundant chlamydospores throughout medium, forming microsclerotia.

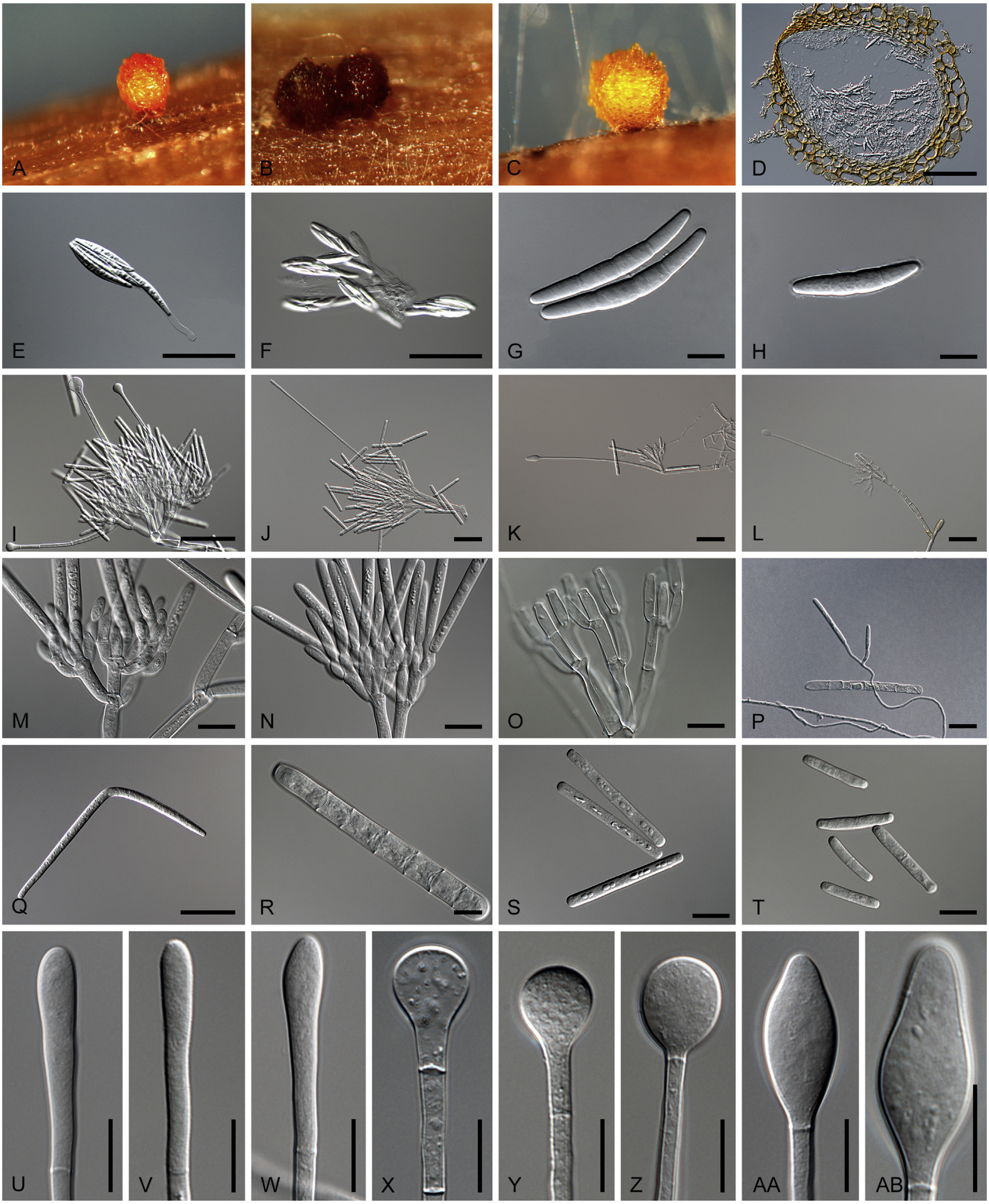


Fig. 9. *Calonectria* spp. **A–H.** Sexual morphs. **A–D.** Perithecia. **A.** *Calonectria asiatica* (ex-type CBS 114073). **B.** *Calonectria braziliensis* (ex-type CBS 230.51 × CBS 114257). b *Calonectria fujianensis* (ex-type CBS 127201**)**. **D.** Section through perithecium of *Calonectria asiatica* (ex-type CBS 114073). **E–F.** Asci. **E.** *Calonectria crousiana* (ex-type CBS 127198). **F.** *Calonectria asiatica* (ex-type CBS 114073). **G–H.** Ascospores. **G.** *Calonectria fujianensis* (ex-type CBS 127201**)**. **H.** *Calonectria acicola* (ex-type CBS 114813). **I–AB.** Asexual morphs. **I–L.** Macroconidiophores. **I.** *Calonectria malesiana* (ex-type CBS 112752). **J.** *Calonectria macroconidialis* (ex-type CBS 114880). **K.** *Calonectria spathulata* (ex-type CBS 555.92). **L.** *Calonectria ovata* (CBS 111307). **M–O.** Conidiogenous apparatus. **M.** *Calonectria brachiatica* (ex-type CBS 123700). **N.** *Calonectria ecuadoriae* (ex-type CBS 111406). **O.** *Calonectria hurae* (CBS 114551). **P.** Microconidiophore of *Calonectria reteaudii* (ex-type CBS 112144). **Q.** Megaconidia of *Calonectria hurae* (CBS 114551). **R, S.** Macroconidia. **R.** *Calonectria angustata* (ex-type CBS 109065). **S.** *Calonectria chinensis* (ex-type CBS 114827). **T.** Microconidia of *Calonectria pteridis* (ex-type CBS 111793). **U–AB.** Terminal vesicles of stipe extensions. **U.** *Calonectria brassicae* (ex-type CBS 111869). **V.** *Calonectria rumohrae* (CBS 109062). **W.** *Calonectria cylindrospora* (CBS 119670). **X.** *Calonectria hongkongensis* (ex-type CBS 114828). **Y.** *Calonectria chinensis* (ex-type CBS 114827). **Z.** *Calonectria humicola* (ex-type CBS 125251). **AA.** *Calonectria mexicana* (ex-type CBS 110918). **AB.** *Calonectria spathulata* (ex-type CBS 555.92). Scale bars: A–C = 500 µm; D–F = 100 µm; G, H, M–P, R–AB = 10 µm; I–L, Q = 20 µm.

Fig. 10. Disease symptoms associated with *Calonectria* spp. **A–B.** Root and collar rot of *Pinus* spp. **C.** Cutting rot of *Eucalyptus* sp. **D.** Calonectria leaf blight of *Eucalyptus* sp. **E.** Calonectria leaf blight of *Metrosideros thomasii*. **F.** Calonectria leaf blight of *Myrtus communis*. **G.** Seedling blight of *Drosera* sp. **H.** Buxus blight. **I.** Root rot of *Persea americana*. **J.** Potato tuber rot. **K–L**. Calonectria black rot of *Arachis hypogaea*.

Material examined: **Ecuador**, from soil, 20 Jun. 1997, M.J. Wingfield (**holotype** CBS H-23134, culture ex-type CBS 111706 = CPC 1636); *ibid*., culture CBS 114164 = CPC 1634.

Notes: *Calonectria ecuadorensis* can be distinguished from *Ca. ecuadoriae* (Crous *et al.* 2006a) by its fewer branches in the conidiogenous apparatus. Also, the conidia of *Ca. ecuadorensis* [(34–)35–39(–44) × (3–)3.5–4.5(–5) µm (av. 37 × 4 µm)] are smaller than those of *Ca. ecuadoriae* [(45–)48–55(–65) × (4–)4.5(–5) µm (av. 51 × 4.5 µm); Crous *et al.* 2006a].

Calonectria longiramosa L. Lombard & Crous, **sp. nov.** MycoBank MB820843. Fig. 13.

Etymology: Name refers to the characteristic long fertile branches of the conidiogenous apparatus in this fungus.

Macroconidiophores consist of a stipe bearing a penicillate arrangement of fertile branches, and a stipe extension terminating in a vesicle; *stipe* septate, hyaline, smooth, 100–245 × 6–9 µm; *stipe extension* septate, straight to flexuous, 155–310 µm long, 4–6 µm wide at apical septum, terminating in a clavate vesicle, 5–8 µm diam. *Conidiogenous apparatus* 50–85 µm wide, and 60–140 µm long; *primary branches* aseptate to 1-septate, 22–42 × 4–6 µm; *secondary branches* aseptate, 15–35 × 3–6 µm; *tertiary branches* aseptate, 12–30 × 3–6 µm; *quaternary branches* aseptate, 11–19 × 3–6 µm each terminal branch producing 2–4 phialides; *phialides* elongate doliiform to allantoid, hyaline, aseptate, 8–16 × 2–4 µm, apex with minute periclinal thickening and inconspicuous collarette. *Macroconidia* cylindrical, rounded at both ends, straight to slightly curved, (57–)66–76(–84) × (3–)4.5–5.5(–6) µm (av. 71 × 5 µm), 1-septate, lacking a visible abscission scar, held in parallel cylindrical clusters by colourless slime. *Mega*- and *microconidia* not observed.

Culture characteristics: Colonies moderately fast growing (35–70 mm diam) on MEA after 1 wk at room temperature; surface amber with moderate white, woolly aerial mycelium and moderate sporulation on the aerial mycelium and colony surface; reverse amber with abundant chlamydospores throughout the medium, forming microsclerotia.

Material examined: **Brazil**, Amazon, from *Eucalyptus* sp., 1993, P.W. Crous & A.C. Alfenas (**holotype** CBS H-22759, culture ex-type CBS 116319 = CPC 3761); *ibid*., cultures CBS 116305 = CPC 3765.

Notes: *Calonectria longiramosa* is a new species in the *Ca. pteridis* complex. This species is characterised by the long fertile branches of the conidiogenous apparatus distinguishing it from the other species in this complex (Alfenas *et al.* 2015).

Calonectria nemoralis L. Lombard & Crous, **sp. nov.** MycoBank MB820850. Fig. 14.

Etymology: Name refers to the environment, a *Eucalyptus* plantation, from where this fungus was collected.

Macroconidiophores consist of a stipe bearing a penicillate arrangement of fertile branches, and a stipe extension terminating in a vesicle; *stipe* septate, hyaline, smooth, 40–165 × 6–8 µm; *stipe extension* septate, straight to flexuous, 140–210 µm long, 3–5 µm wide at the apical septum, terminating in a fusiform to ovoid vesicle, 7–9 µm diam. *Conidiogenous apparatus* 20–45 µm wide, and 40–55 µm long; *primary branches* aseptate, 18–24 × 3–6 µm; *secondary*

Table 3. DNA barcodes of accepted *Calonectria* spp.

Species	Isolates[1]	GenBank accession numbers[2]							References
		tub2	*cmdA*	*tef1*	*his3*	*rpb2*	ITS	LSU	
Calonectria acicola	CBS 114812^{T}	DQ190590	GQ267359	GQ267291	DQ190693	KY653352	GQ280547	GQ280669	Crous *et al.* (2006a), Lombard *et al.* (2010c), present study
Ca. aconidialis	CBS 136086^{T}	–	KJ463017	KJ462785	KJ463133	–	–	–	Lombard *et al.* (2015)
Ca. amazonica	CBS 116250^{T}	KX784612	KX784555	KX784682	–	KY653355	KY653241	KY653297	Lombard *et al.* (2016), present study
Ca. amazoniensis	CBS 115440^{T}	KX784615	KX784558	KX784685	–	KY653358	KY653244	KY653300	Lombard *et al.* (2016), present study
Ca. angustata	CBS 109065^{T}	AF207543	GQ267361	FJ918551	DQ190696	KY653359	GQ280548	GQ280671	Crous & Kang (2001), Crous *et al.* (2006a), Lombard *et al.* (2010c, d), present study
Ca. arbusta	CBS 136079^{T}	KJ462904	KJ463018	KJ462787	KJ463135	–	–	–	Lombard *et al.* (2015)
Ca. asiatica	CBS 114073^{T}	AY725616	AY725741	AY725705	AY725658	–	GQ280550	GQ280672	Crous *et al.* (2004c), Lombard *et al.* (2010c)
Ca. australiensis	CBS 112954^{T}	DQ190596	GQ267363	GQ267293	DQ190699	KY653361	GQ280552	GQ280674	Crous *et al.* (2006a), Lombard *et al.* (2010c), present study
Ca. blephiliae	CBS 136425^{T}	KF777246	–	KF777243	–	–	KF777141	KF777197	Crous *et al.* (2013b)
Ca. brachiatica	CBS 123700^{T}	FJ696388	GQ267366	GQ267296	FJ696396	–	GQ280555	GQ280677	Lombard *et al.* (2009, 2010c)
Ca. brasiliana	CBS 111484^{T}	KX784616	KX784559	KX784686	–	KY653362	KY653245	KY653301	Lombard *et al.* (2016), present study
Ca. brasiliensis	CBS 230.51^{T}	GQ267241	GQ267421	GQ267328	GQ267259	KY653364	GQ280624	GQ280746	Lombard *et al.* (2010c), present study
Ca. brassiana	CBS 134855^{T}	KM395969	KM396056	KM395882	KM396139	–	–	–	Alfenas *et al.* (2015)
Ca. brassicae	CBS 111869^{T}	AF232857	GQ267382	FJ918567	DQ190720	KM232308	GQ280576	GQ280698	Crous *et al.* (1999, 2006a, b), Lombard *et al.* (2009, 2010c), present study
Ca. brassicicola	CBS 112841^{T}	KX784619	KX784561	KX784689	–	–	–	–	Lombard *et al.* (2016)
Ca. brevistipitata	CBS 115671^{T}	KX784623	KX784565	KX784693	–	KY653368	KY653248	KY653304	Lombard *et al.* (2016), present study
Ca. canadania	CBS 110817^{T}	AF348212	AY725743	GQ267297	AF348228	KY653369	GQ280556	GQ280678	Kang *et al.* (2001), Crous *et al.* (2004c), Lombard *et al.* (2010c), present study
Ca. candelabrum	CPC 1675	FJ972426	GQ267367	FJ972525	FJ972476	–	GQ280557	GQ280679	Lombard *et al.* (2010b, c)
Ca. cerciana	CBS 123693^{T}	FJ918510	GQ267369	FJ918559	FJ918528	–	GQ280559	GQ280681	Lombard *et al.* (2009, 2010c)
Ca. chinensis	CBS 114827^{T}	AY725619	AY725747	AY725710	AY725661	KY653371	GQ280561	GQ280683	Crous *et al.* (2004c), Lombard *et al.* (2010c), present study
Ca. clavata	CBS 114557^{T}	AF333396	GQ267377	GQ267305	DQ190623	KY653372	GQ280571	GQ280693	Schoch *et al.* (2001), Lombard *et al.* (2010c), present study
Ca. cliffordicola	CBS 111812^{T}	KX784624	KX784566	KX784694	–	KY653374	KY653249	KY653305	Lombard *et al.* (2016), present study
Ca. colhounii	CBS 293.79^{T}	DQ190564	GQ267373	GQ267301	DQ190639	KY653376	GQ280565	GQ280687	Crous *et al.* (2006a), Lombard *et al.* (2010c), present study
Ca. colombiana	CBS 115127^{T}	FJ972423	GQ267455	FJ972492	FJ972442	–	GQ280660	GQ280782	Lombard *et al.* (2010b, c)
Ca. colombiensis	CBS 112220^{T}	GQ267207	AY725748	AY725711	AY725662	–	GQ280566	GQ280688	Crous *et al.* (2004c), Lombard *et al.* (2010c)
Ca. crousiana	CBS 127198^{T}	HQ285794	–	HQ285822	HQ285808	–	–	–	Chen *et al.* (2011)
Ca. cylindrospora	CBS 110666	FJ918509	GQ267423	FJ918557	FJ918527	KY653378	GQ280626	GQ280748	Crous *et al.* (2006a), Lombard *et al.* (2010c), present study
Ca. densa	CBS 125261^{T}	GQ267232	GQ267444	GQ267352	GQ267281	–	GQ280647	GQ280769	Lombard *et al.* (2010c)
Ca. duoramosa	CBS 134656^{T}	KM395940	KM396027	KM395853	–	–	–	–	Alfenas *et al.* (2015)
Ca. ecuadoriae	CBS 111406^{T}	DQ190600	GQ267375	GQ267303	DQ190705	KY653381	GQ280569	GQ280691	Crous *et al.* (2006a), Lombard *et al.* (2010c), present study

(*continued on next page*)

Table 3. (Continued).

Species	Isolates[1]	GenBank accession numbers[2]							References
		tub2	*cmdA*	*tef1*	*his3*	*rpb2*	ITS	LSU	
Ca. ecuadorensis	CBS 111706^{T}	KX784674	KX784604	KX784747	–	KY653382	KY653252	KY653308	Lombard *et al.* (2016), present study
	CBS 114164	KX784677	KX784607	KX784750	–	KY653383	KY653253	KY653309	
Ca. ericae	CBS 114458^{T}	KX784629	KX784571	KX784699	–	KY653385	KY653255	KY653311	Lombard *et al.* (2016), present study
Ca. eucalypti	CBS 125275^{T}	GQ267218	GQ267430	GQ267338	GQ267267	–	GQ280633	GQ280755	Lombard *et al.* (2010c)
Ca. eucalypticola	CBS 134847^{T}	KM395964	KM396051	KM395877	KM396134	–	–	–	Alfenas *et al.* (2015)
Ca. expansa	CBS 136247^{T}	KJ462914	KJ463029	KJ462798	KJ463146	–	–	–	Lombard *et al.* (2015)
Ca. floridana	CBS 114692^{T}	KX784651	KX784588	KX784722	–	–	–	–	Lombard *et al.* (2016)
Ca. foliicola	CBS 136641^{T}	KJ462916	KJ463031	KJ462800	KJ463148	–	–	–	Lombard *et al.* (2015)
Ca. fujianensis	CBS 127201^{T}	HQ285792	–	HQ285820	HQ285806	–	–	–	Chen *et al.* (2011)
Ca. glaeboicola	CBS 134852^{T}	KM395966	KM396053	KM395879	KM396136	–	–	–	Alfenas *et al.* (2015)
Ca. gordoniae	CBS 112142^{T}	AF449449	GQ267381	GQ267309	DQ190708	KY653386	GQ280575	GQ280697	Crous *et al.* (2004c), Lombard *et al.* (2010c), present study
Ca. gracilipes	CBS 111141^{T}	DQ190566	GQ267385	GQ267311	DQ190644	KY653387	GQ280579	GQ280701	Crous *et al.* (2004c), Lombard *et al.* (2010c), present study
Ca. gracilis	CBS 111807^{T}	AF232858	GQ267407	GQ267323	DQ190646	KY653390	GQ280610	GQ280734	Crous *et al.* (2004c), Lombard *et al.* (2010c), present study
Ca. guangxiensis	CBS 136092^{T}	KJ462919	KJ463034	KJ462803	KJ463151	–	–	–	Lombard *et al.* (2015)
Ca. hainanensis	CBS 136248^{T}	–	KJ463036	KJ462805	KJ463152	–	–	–	Lombard *et al.* (2015)
Ca. hawksworthii	CBS 111870^{T}	AF333407	GQ267386	FJ918558	DQ190649	KY653391	GQ280580	GQ280702	Schoch *et al.* (2001), Lombard *et al.* (2010c), present study
Ca. henricotiae	CBS 138102^{T}	JX535308	KF815157	–	KF815185	–	JX535322	–	Gehesquière *et al.* (2016)
Ca. hodgesii	CBS 133609^{T}	KC491228	KC491222	KC491225	–	–	–	–	Alfenas *et al.* (2015)
Ca. hongkongensis	CBS 114828^{T}	AY725622	AY725755	AY725717	AY725667	–	GQ280581	GQ280703	Crous *et al.* (2004c), Lombard *et al.* (2010c)
Ca. humicola	CBS 125251^{T}	GQ267233	GQ267445	GQ267353	GQ267282	–	GQ280648	GQ280770	Lombard *et al.* (2010c)
Ca. hurae	CBS 114551	AF333408	GQ267387	FJ918548	DQ190728	–	GQ280583	GQ280705	Schoch *et al.* (2001), Lombard *et al.* (2010c, d)
Ca. ilicicola	CBS 190.50^{T}	AY725631	AY725764	AY725726	AY725676	KM232307	GQ280605	GQ280727	Crous *et al.* (2004c), Lombard *et al.* (2010c)
Ca. indonesiae	CBS 112823^{T}	AY725623	AY725756	AY725718	AY725668	KY653394	GQ280585	GQ280707	Crous *et al.* (2004c), Lombard *et al.* (2010c), present study
Ca. indonesiana	CBS 112936^{T}	KX784631	KX784573	KX784701	–	–	–	–	Lombard *et al.* (2016)
Ca. indusiata	CBS 144.36^{T}	GQ267239	GQ267453	GQ267332	GQ267262	KY653396	GQ280658	GQ280780	Lombard *et al.* (2010c), present study
Ca. insularis	CBS 114558^{T}	AF210861	GQ267389	FJ918556	FJ918526	KY653398	GQ280587	GQ280709	Schoch *et al.* (1999), Lombard *et al.* (2010b, c), present study
Ca. kyotensis	CBS 114525^{T}	AF348215	AY725750	AY725713	–	–	AF261741	–	Crous *et al.* (2004c)
Ca. lageniformis	CBS 111324^{T}	KX784632	KX784574	KX784702	–	KY653400	KY653256	KY653312	Lombard *et al.* (2016), present study
Ca. lateralis	CBS 136629^{T}	KJ462955	KJ463070	KJ462840	KJ463186	KY653402	KY653258	KY653314	Lombard *et al.* (2015), present study
Ca. lauri	CBS 749.70^{T}	GQ267210	GQ267388	GQ267312	GQ267250	KY653403	GQ280584	GQ280706	Lombard *et al.* (2010c), present study
Ca. leguminum	CBS 728.68^{T}	AF389837	GQ267391	FJ918547	DQ190654	–	GQ280589	GQ280711	Crous *et al.* (2004c), Lombard *et al.* (2010c)
Ca. leucothoes	CBS 109166^{T}	FJ918508	GQ267392	FJ918553	FJ918523	KY653404	GQ280590	GQ280712	Lombard *et al.* (2010b,c), present study

Ca. longiramosa	CBS 116319^{T}	KX784635	KX784577	KX784705	–	KY653406	KY653260	KY653316	Lombard *et al.* (2016), present study
Ca. machaerinae	CBS 123183^{T}	KX784636	–	KX784706	–	KY653407	KY653261	KY653317	Lombard *et al.* (2016), present study
Ca. madagascariensis	CBS 114572^{T}	DQ190572	GQ267394	GQ267314	DQ190658	KY653409	GQ280592	GQ280714	Crous *et al.* (2006a), Lombard *et al.* (2010c), present study
Ca. macroconidialis	CBS 114880^{T}	AF232855	GQ267393	GQ267313	DQ190655	KY653410	GQ280591	GQ280713	Crous et al. (1999, 2006a), Lombard et al. (2010c), present study
Ca. magnispora	CBS 136249^{T}	KJ462956	KJ463071	KJ462841	KJ463187	–	–	–	Lombard *et al.* (2015)
Ca. malesiana	CBS 112752^{T}	AY725627	AY725760	AY725722	AY725672	–	GQ280594	GQ280716	Crous *et al.* (2004c), Lombard *et al.* (2010c)
Ca. maranhensis	CBS 134811^{T}	KM395948	KM396035	KM395861	KM396118	–	–	–	Alfenas *et al.* (2015)
Ca. metrosideri	CBS 133603^{T}	KC294313	KC294304	KC294310	KC294308	–	–	–	Alfenas *et al.* (2013)
Ca. mexicana	CBS 110918^{T}	AF210863	GQ267396	FJ972526	FJ972460	KY653412	GQ280596	GQ280718	Schoch *et al.* (1999), Lombard *et al.* (2010b, c), present study
Ca. microconidialis	CBS 136638^{T}	KJ462960	KJ463075	KJ462845	KJ463191	KY653411	KY653262	KY653318	Lombard *et al.* (2015), present study
Ca. monticola	CBS 140645^{T}	KT964769	KT964771	KT964773	–	–	KT964775	KT983443	Crous *et al.* (2015e)
Ca. mossambicensis	CBS 137243^{T}	–	JX570722	JX570718	JX570726	–	JX570730	–	Crous *et al.* (2013b)
Ca. multilateralis	CBS 110932^{T}	KX784642	KX784580	KX784712	–	KY653413	KY653263	KY653319	Lombard *et al.* (2016), present study
Ca. multinaviculata	CBS 134858^{T}	KM395985	KM396072	KM395898	KM396155	–	–	–	Alfenas *et al.* (2015)
Ca. multiphialidica	CBS 112678^{T}	AY725628	AY725761	AY725723	AY725673	KY653415	GQ280597	GQ280719	Crous *et al.* (2004c), Lombard *et al.* (2010c), present study
Ca. multiseptata	CBS 112682^{T}	DQ190573	GQ267397	FJ918535	DQ190659	KY653416	GQ280598	GQ280720	Crous *et al.* (2006a), Lombard *et al.* (2010c, d), present study
Ca. naviculata	CBS 101121^{T}	GQ267211	GQ267399	GQ267317	GQ267252	KM232309	GQ280600	GQ280722	Lombard *et al.* (2010c, 2015)
Ca. nemicola	CBS 134837^{T}	KM395979	KM396066	KM395892	KM396149	–	–	–	Alfenas *et al.* (2015)
Ca. nemoralis	CBS 116249^{T}	KX784679	KX784609	KX784752	–	–	–	–	Lombard *et al.* (2016)
Ca. nymphaeae	CBS 131802^{T}	JN984864	–	KC555273	–	–	–	–	Xu *et al.* (2012)
Ca. octoramosa	CBS 111423^{T}	KX784674	KX784603	KX784746	–	KY653418	KY653265	KY653321	Lombard *et al.* (2016), present study
Ca. orientalis	CBS 125260^{T}	GQ267236	GQ267448	GQ267356	GQ267285	–	GQ267651	GQ280773	Lombard *et al.* (2010c)
Ca. ovata	CBS 111299^{T}	GQ267212	GQ267400	GQ267318	GQ267253	KY653419	GQ280601	GQ280723	Lombard *et al.* (2010c), present study
Ca. pacifica	CBS 109063^{T}	GQ267213	AY725762	AY725724	GQ267255	–	GQ280603	GQ280725	Crous *et al.* (2004c), Lombard *et al.* (2010c)
Ca. papillata	CBS 136097^{T}	KJ462964	KJ463079	KJ462849	KJ463195	KY653422	KY653267	KY653323	Lombard *et al.* (2015), present study
Ca. paracolhounii	CBS 114679^{T}	KX784644	KX784582	KX784714	–	KY653423	KY653268	KY653324	Lombard *et al.* (2016), present study
Ca. paraensis	CBS 134669^{T}	KM395924	KM396011	KM395837	KM396094	–	–	–	Alfenas *et al.* (2015)
Ca. parakyotensis	CBS 136085^{T}	–	KJ463081	KJ462851	KJ463197	–	–	–	Lombard *et al.* (2015)
Ca. parva	CBS 110798^{T}	KX784646	KX784583	KX784716	–	KY653425	KY653270	KY653326	Lombard *et al.* (2016), present study
Ca. parvispora	CBS 111465^{T}	DQ190607	KX784584	KX784717	–	–	–	–	Crous *et al.* (2006a), Lombard *et al.* (2016)
Ca. pauciramosa	CBS 138824^{T}	FJ918514	GQ267405	FJ918565	FJ918531	KY653426	GQ280608	GQ280730	Lombard *et al.* (2010b, c), present study
Ca. penicilloides	CBS 174.55^{T}	AF333414	GQ267406	GQ267322	GQ267257	KY653427	GQ280609	GQ280731	Schoch *et al.* (2001), Lombard *et al.* (2010c), present study
Ca. pentaseptata	CBS 133349^{T}	JX855942	–	JX855958	JX855946	–	JX855950	JX855954	Crous *et al.* (2012a)
Ca. piauiensis	CBS 134850^{T}	KM395973	KM396060	KM395886	KM396143	–	–	–	Alfenas *et al.* (2015)

(*continued on next page*)

Table 3. (Continued).

Species	Isolates[1]	GenBank accession numbers[2]							References
		tub2	*cmdA*	*tef1*	*his3*	*rpb2*	ITS	LSU	
Ca. pini	CBS 123698^{T}	GQ267224	GQ267436	GQ267344	GQ267273	–	GQ280639	GQ280761	Lombard *et al.* (2015)
Ca. polizzii	CBS 123402^{T}	FJ972419	–	FJ972488	FJ972438	–	–	–	Lombard *et al.* (2010b, c)
Ca. plurilateralis	CBS 111401^{T}	KX784648	KX784586	KX784719	–	KY653430	KY653271	KY653327	Lombard *et al.* (2016), present study
Ca. pluriramosa	CBS 136976^{T}	KJ462995	KJ463112	KJ462882	KJ463228	KY653431	KY653272	KY653328	Lombard *et al.* (2015), present study
Ca. propaginicola	CBS 134815^{T}	KM395953	KM396040	KM395866	KM396123	–	–	–	Alfenas *et al.* (2015)
Ca. pseudobrassicae	CBS 134662^{T}	KM395936	KM396023	KM395849	KM396106	–	–	–	Alfenas *et al.* (2015)
Ca. pseudocerciana	CBS 134824^{T}	KM395962	KM396049	KM395875	KM396132	–	–	–	Alfenas *et al.* (2015)
Ca. pseudocolhounii	CBS 127195^{T}	HQ285788	–	HQ285816	HQ285802	–	–	–	Chen *et al.* (2011)
Ca. pseudoecuadoriae	CBS 111402^{T}	KX784652	KX784589	KX784723	–	KY653432	KY653273	KY653329	Lombard *et al.* (2016), present study
Ca. pseudohodgesii	CBS 134818^{T}	KM395905	KM395991	KM395817	KM396079	–	–	–	Alfenas *et al.* (2015)
Ca. pseudokyotensis	CBS 137332^{T}	KJ462994	KJ463111	KJ462881	KJ463227	–	–	–	Lombard *et al.* (2015)
Ca. pseudometrosideri	CBS 134845^{T}	KM395909	KM395995	KM395821	KM396083	–	–	–	Alfenas *et al.* (2015)
Ca. pseudomexicana	CBS 130354^{T}	JN607281	–	JN607496	JN607266	–	–	–	Lombard *et al.* (2011)
Ca. pseudouxmalensis	CBS 110924^{T}	KX784654	–	KX784726	–	KY653437	KY653276	KY653332	Lombard *et al.* (2016), present study
Ca. pseudonaviculata	CBS 114417^{T}	GQ267214	GQ267409	GQ267325	GQ267258	KY653434	GQ280612	GQ280734	Lombard *et al.* (2010c), present study
Ca. pseudopteridis	CBS 163.28^{T}	–	KM396076	KM395902	–	–	–	–	Alfenas *et al.* (2015)
Ca. pseudoreteaudii	CBS 123694^{T}	FJ918504	GQ267411	FJ918541	FJ918519	–	GQ280614	GQ280736	Lombard *et al.* (2010c, d)
Ca. pseudoscoparia	CBS 125257^{T}	GQ267229	GQ267441	GQ267349	GQ267278	–	GQ280644	GQ280766	Lombard *et al.* (2010c)
Ca. pseudospathiphylli	CBS 109165^{T}	FJ918513	GQ267412	FJ918562	AF348241	KY653435	GQ280615	GQ280737	Kang *et al.* (2001), Lombard *et al.* (2010c, d), present study
Ca. pseudospathulata	CBS 134841^{T}	KM395983	KM396070	KM395896	KM396153	–	–	–	Alfenas *et al.* (2015)
Ca. pseudovata	CBS 134675^{T}	KM395946	KM396033	KM395859	KM396116	–	–	–	Alfenas *et al.* (2015)
Ca. pteridis	CBS 111793^{T}	DQ190578	GQ267413	FJ918563	DQ190679	KY653438	GQ280616	GQ280738	Crous *et al.* (2006a), Lombard *et al.* (2010c, d), present study
Ca. putriramosa	CBS 111449^{T}	KX784656	KX784591	KX784728	–	KY653440	KY653277	KY653333	Lombard *et al.* (2016), present study
Ca. queenslandica	CBS 112146^{T}	AF389835	GQ267415	FJ918543	FJ918521	–	GQ280618	GQ280740	Kang *et al.* (2001), Lombard *et al.* (2010c, d)
Ca. quinqueramosa	CBS 134654^{T}	KM395942	KM396029	KM395855	KM396112	–	–	–	Alfenas *et al.* (2015)
Ca. reteaudii	CBS 112144^{T}	AF389833	GQ267417	FJ918537	DQ190661	KY653443	GQ280620	GQ280742	Kang *et al.* (2001), Lombard *et al.* (2010c, d), present study
Ca. robigophila	CBS 134652^{T}	KM395937	KM396024	KM395850	KM396107	–	–	–	Alfenas *et al.* (2015)
Ca. rumohrae	CBS 111431^{T}	AF232871	GQ267419	FJ918549	DQ190675	KY653445	GQ280622	GQ280744	Crous *et al.* (1999), Lombard *et al.* (2010c), present study
Ca. seminaria	CBS 136632^{T}	KJ462998	KJ463115	KJ462885	KJ463231	KY653446	KY653279	KY653335	Lombard *et al.* (2015), present study
Ca. silvicola	CBS 135237^{T}	KM395978	KM396065	KM395891	KM396148	–	–	–	Alfenas *et al.* (2015)
Ca. spathulata	CBS 555.92^{T}	GQ267215	GQ267426	FJ918554	GQ267261	KY653449	GQ280630	GQ280752	Lombard *et al.* (2010c, d), present study
Ca. spathiphylli	CBS 114540	AF348214	GQ267424	GQ267330	AF348230	KY653447	GQ280627	GQ280749	Kang *et al.* (2001), Lombard *et al.* (2010c), present study

Ca. sphaeropendunculata	CBS 136081^T	KJ463003	KJ463120	KJ462890	KJ463236	–	–	–	Lombard *et al.* (2015)
Ca. stipitata	CBS 112513^T	KX784661	KX784596	KX784734	–	KY653450	KY653280	KY653336	Lombard *et al.* (2016), present study
Ca. sulawesiensis	CBS 125277^T	GQ267222	GQ267434	GQ267342	GQ267271	–	GQ280637	GQ280759	Lombard *et al.* (2010c)
Ca. sumatrensis	CBS 112829^T	AY725649	AY725771	AY725733	AY725696	–	GQ280654	GQ280776	Crous *et al.* (2004c), Lombard *et al.* (2010c)
Ca. syzygiicola	CBS 112831^T	KX784663	–	KX784736	–	–	–	–	Lombard *et al.* (2016)
Ca. telluricola	CBS 134664^T	KM395930	KM396017	KM395843	KM396100	–	–	–	Alfenas *et al.* (2015)
Ca. tereticornis	CBS 111301^T	KX784664	–	KX784737	–	–	–	–	Lombard *et al.* (2016)
Ca. terrae-reginae	CBS 112151^T	FJ918506	GQ267451	FJ918545	FJ918522	–	GQ280656	GQ280778	Kang *et al.* (2001), Lombard *et al.* (2010c, d)
Ca. terrestris	CBS 136642^T	KJ463004	KJ463121	KJ462891	KJ463237	–	–	–	Lombard *et al.* (2015)
Ca. terricola	CBS 116247^T	KX784665	–	KX784738	–	–	–	–	Lombard *et al.* (2016)
Ca. tetraramosa	CBS 136635^T	KJ463011	KJ463128	KJ462898	KJ463244	KY653453	KY653282	KY653338	Lombard *et al.* (2015), present study
Ca. trifurcata	CBS 112753^T	KX784667	KX784598	KX784740	–	KY653464	KY653292	KY653348	Lombard *et al.* (2016), present study
Ca. tropicalis	CBS 116271^T	KX784669	KX784599	KX784742	–	KY653455	KY653284	KY653340	Lombard *et al.* (2016), present study
Ca. turangicola	CBS 136077^T	KJ463013	–	KJ462900	KJ463246	–	KY653287	KY653343	Lombard *et al.* (2015)
Ca. tucuruiensis	CBS 114755^T	KX784670	KX784600	KX784743	–	KY653456	KY653285	KY653341	Lombard *et al.* (2016), present study
	CBS 116265	KX784680	KX784610	KX784753	–	KY653457	KY653286	KY653342	Lombard *et al.* (2016), present study
Ca. tunisiana	CBS 130357^T	JN607276	–	JN607291	JN607261	–	–	–	Lombard *et al.* (2011)
Ca. uniseptata	CBS 413.67^T	GQ267208	GQ267379	GQ267307	GQ267248	–	GQ280573	GQ280695	Lombard *et al.* (2010c)
Ca. uxmalensis	CBS 110925^T	KX784638	–	KX784708	–	KY653461	KY653288	KY653350	Lombard *et al.* (2016), present study
Ca. variabilis	CBS 112691	GQ267240	GQ267458	GQ267335	GQ267264	KY653459	GQ280663	GQ280785	Lombard *et al.* (2010c), present study
Ca. venezuelana	CBS 111052^T	KX784671	KX784601	KX784744	–	–	–	–	Lombard *et al.* (2016)
Ca. vietnamensis	CBS 112152^T	KX784672	KX784602	KX784745		KY653463	KY653291	KY653347	Lombard *et al.* (2016), present study
Ca. zuluensis	CBS 125268	FJ972414	GQ267459	FJ972483	FJ972433	–	GQ280664	GQ280786	Lombard *et al.* (2010b, c)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CPC: Culture collection of Pedro Crous, housed at Westerdijk Fungal Biodiversity Institute. $^{\mathbf{T}}$ indicates ex-type strains.

[2] *tub2*: partial β-tubulin gene; *cmdA*: partial calmodulin gene; *tef1*: partial translation elongation factor 1-alpha gene; *his3*: partial histone H3 gene; *rpb2*: RNA polymerase II second largest subunit; ITS: internal transcribed spacers and intervening 5.8S nrDNA; LSU: 28S large subunit RNA gene.

branches aseptate, 11–19 × 3–5 µm, each terminal branch producing 2–4 phialides; *phialides* elongate doliiform to reniform, hyaline, aseptate, 6–14 × 2–4 µm, apex with minute periclinal thickening and inconspicuous collarette. *Macroconidia* cylindrical, rounded at both ends, straight, (44–)47–59(–71) × (3–)3.5–4.5(–6) µm (av. 53 × 4 µm), 1-septate, lacking a visible abscission scar, held in parallel cylindrical clusters by colourless slime. *Mega-* and *microconidia* not observed.

Culture characteristics: Colonies moderately fast growing (35–55 mm diam) on MEA after 1 wk at room temperature; surface sienna with sparse buff to white, woolly aerial mycelium with moderate sporulation on the aerial mycelium and colony surface; reverse sienna with abundant chlamydospores throughout the medium, forming microsclerotia.

Material examined: **Brazil**, from soil in *Eucalyptus* plantation, 1996, P.W. Crous (**holotype** CBS H-23135, culture ex-type CBS 116249 = CPC 3533).

Notes: *Calonectria nemoralis* is closely related to *Ca. pseudovata*. The macroconidia of *Ca. nemoralis* [(44–)47–59(–71) × (3–)3.5–4.5(–6) µm (av. 53 × 4 µm)] are smaller than those of *Ca. pseudovata* [(55–)67–70(–80) × (4–)5(–7) µm (av. 69 × 5 µm); Alfenas *et al.* 2015]. Furthermore, no microconidiophores and microconidia were observed in *Ca. nemoralis*, although they are readily produced by *Ca. pseudovata* (Alfenas *et al.* 2015).

Calonectria octoramosa L. Lombard & Crous, **sp. nov.** MycoBank MB820851. Fig. 15.

Etymology: Name refers to the eight levels of branching of the conidiogenous apparatus.

Macroconidiophores consist of a stipe bearing a penicillate arrangement of fertile branches, and a stipe extension terminating in a vesicle; *stipe* septate, hyaline, smooth, 34–170 × 6–10 µm; *stipe extension* septate, straight to flexuous, 118–262 µm long, 3–8 µm wide at the apical septum, terminating in a clavate vesicle, 4–8 µm diam. *Conidiogenous apparatus* 58–128 µm wide, and 50–90 µm long; *primary branches* aseptate, 14–31 × 5–8 µm; *secondary branches* aseptate, 10–23 × 4–6 µm; *tertiary branches* aseptate, 7–19 × 3–5 µm; *quaternary branches and additional branches* (–8) aseptate, 8–14 × 3–5 µm, each terminal branch producing 2–6 phialides; *phialides* doliiform to reniform, hyaline, aseptate, 6–12 × 3–5 µm, apex with minute periclinal thickening and inconspicuous collarette. *Macroconidia* cylindrical, rounded at both ends, straight, (32–)34–38(–39) × 4–5 µm (av. 36 × 4 µm), 1(–3)-septate, lacking a visible abscission scar, held in parallel cylindrical clusters by colourless slime. *Mega-* and *microconidia* not observed.

Culture characteristics: Colonies fast growing (60–75 mm diam) on MEA after 1 wk at room temperature; surface cinnamon to brick with abundant white woolly aerial mycelium and abundant sporulation on the aerial mycelium and colony surface; reverse brick to sepia with abundant chlamydospores throughout the medium, forming microsclerotia.

Material examined: **Ecuador**, from soil, 20 Jun. 1997, M.J. Wingfield (**holotype** CBS H-23136, culture ex-type CBS 111423 = CPC 1650).

Notes: *Calonectria octoramosa* is a new species in the *Ca. brassicae* complex. It can be distinguished from other species in this complex by having eight levels of branching in its conidiogenous apparatus.

Calonectria parvispora L. Lombard & Crous, **sp. nov.** MycoBank MB820844. Fig. 16.

Etymology: Name refers to the small macroconidia of this fungus.

Macroconidiophores consist of a stipe bearing a penicillate arrangement of fertile branches, and a stipe extension terminating in a vesicle; *stipe* septate, hyaline, smooth, 36–152 × 7–9 µm; *stipe extension* septate, straight to flexuous, 137–277 µm long, 3–6 µm wide at the apical septum, terminating in a clavate vesicle, 4–8 µm diam. *Conidiogenous apparatus* 56–92 µm wide, and 50–70 µm long; *primary branches* aseptate, 16–34 × 4–7 µm; *secondary branches* aseptate, 11–20 × 4–6 µm; *tertiary branches* aseptate, 7–15 × 3–5 µm; *quaternary branches and additional branches* (–6) aseptate, 8–16 × 3–5 µm, each terminal branch producing 2–6 phialides; *phialides* doliiform to reniform, hyaline, aseptate, 7–12 × 3–5 µm, apex with minute periclinal thickening and inconspicuous collarette. *Macroconidia* cylindrical, rounded at both ends, straight, (24–)26–32(–36) × (3–)3.5–4.5(–5) µm (av. 29 × 4 µm), 1-septate, lacking a visible abscission scar, held in parallel cylindrical clusters by colourless slime. *Mega-* and *microconidia* not observed.

Culture characteristics. Colonies fast growing (50–75 mm diam) on MEA after 1 wk at room temperature; surface umber to sepia with abundant buff to white, woolly aerial mycelium and abundant sporulation on the aerial mycelium and colony surface; reverse amber to sepia with abundant chlamydospores throughout the medium, forming microsclerotia.

Material examined: **Brazil**, from soil, Jun. 1998, A.C. Alfenas (**holotype** CBS H-22765, culture ex-type CBS 111465 = CPC 1902). **Colombia**, La Paz, Rodal Seuiller, from soil, Jan. 1994, P.W. Crous, CBS 116108 = CPC 726.

Notes: *Calonectria parvispora* is a new species in the *Ca. brassicae* complex (Lombard *et al.* 2009, Alfenas *et al.* 2015). The macroconidia of *Ca. parvispora* [(24–)26–32(–36) × (3–)3.5–4.5(–5) µm (av. 29 × 4 µm)] are smaller than those of *Ca. clavata* [(44–)50–70(–80) × (4–)5–6 µm (av. 65 × 5 µm); Crous 2002], *Ca. brachiatica* [(37–)40–48(–50) × 4–6 µm (av. 44 × 5 µm); Lombard *et al.* 2009], *Ca. brassicae* [(38–)40–55(–65) × (3.5–)4–5(–6) µm (av. 53 × 4.5 µm); Crous 2002], *Ca. ecuadoriae* [(45–)48–55(–65) × (4–)4.5(–5) µm (av. 51 × 4.5 µm); Crous *et al.* 2006a], *Ca. gracilipes* [(35–)40–48(–60) × 4–5(–6) µm (av. 45 × 4.5 µm); Crous 2002] and *Ca. gracilis* [(40–)53–58(–65) × (3.5–)4–5 µm (av. 56 × 4.5 µm); Crous 2002].

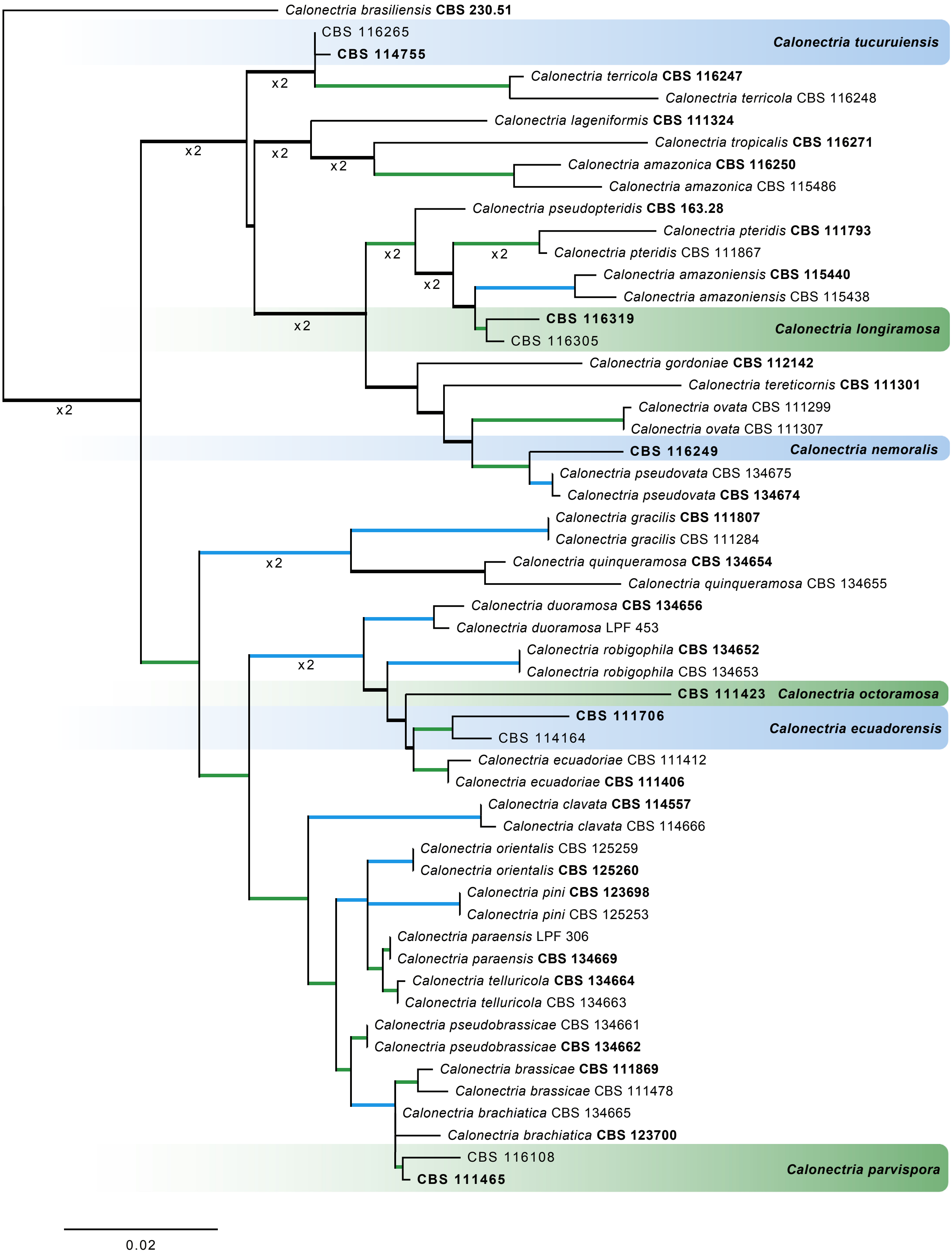


Fig. 11. The Maximum Likelihood (ML) consensus tree inferred from the combined *cmdA*, *tef1* and *tub2* sequence alignments. Thickened lines indicate branches present in the ML, Maximum parsimony (MP) and Bayesian consensus trees. Branches with ML-bootstrap (BS) & MP-BS = 100 % and posterior probabilities (PP) = 1.00 are in blue. Branches with ML-BS & MP-BS ≥ 75 % and PP ≥ 0.95 are in green. The scale bar indicates 0.02 expected changes per site. The tree is rooted to *Calonectria braziliensis* (CBS 230.51). Ex-type strains are indicated in bold. GenBank accession numbers are indicated in Lombard *et al.* (2010a, 2015, 2016) and Alfenas *et al.* (2015). TreeBASE: S20877.

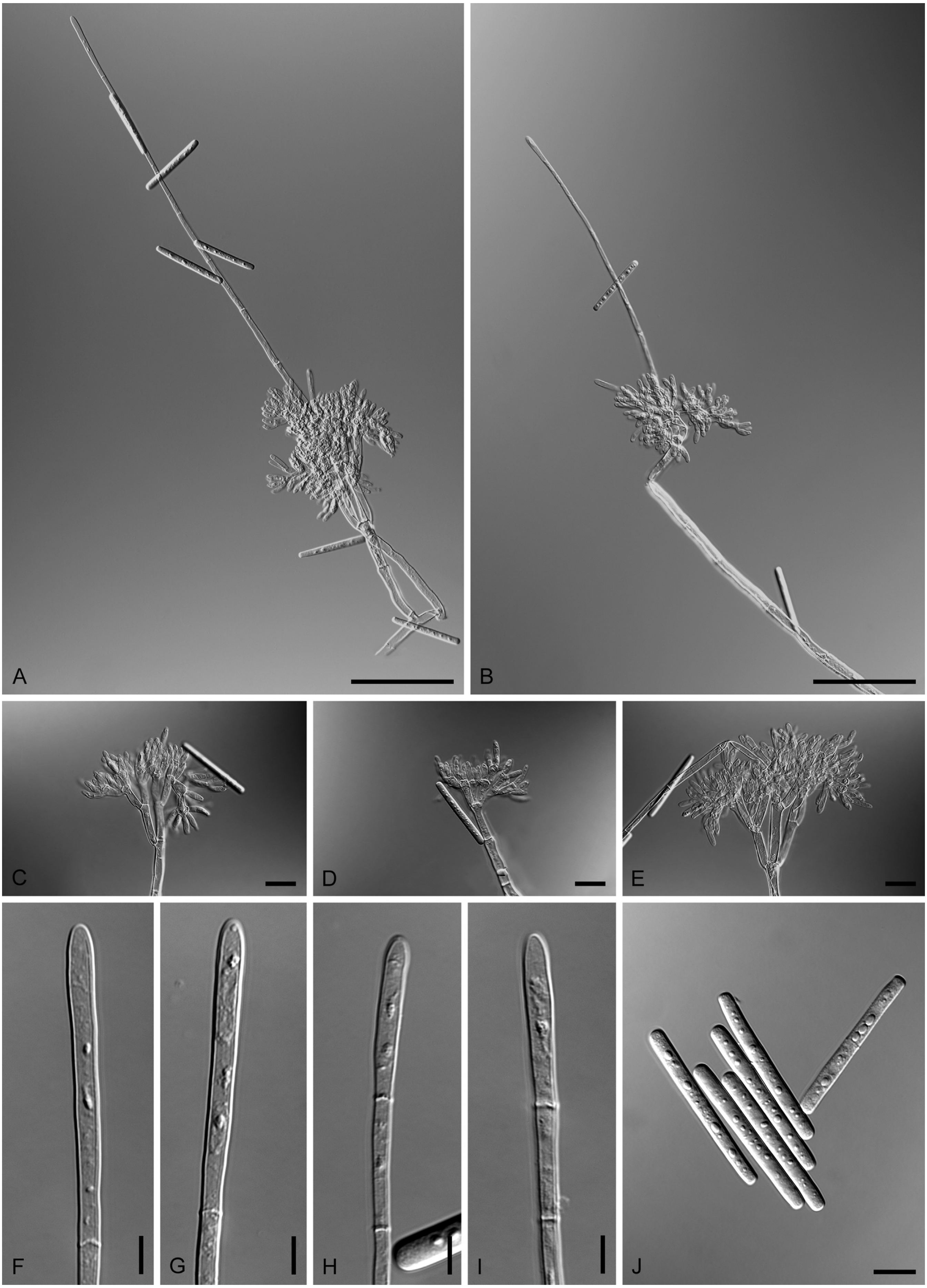


Fig. 12. *Calonectria ecuadorensis* (ex-type CBS 111706). **A, B.** Macroconidiophores. **C−E.** Conidiogenous apparatus with conidiophore branches and doliiform to reniform phialides. **F−I.** Clavate vesicles. **J.** Macroconidia. Scale bars: A, B = 50 µm; C−J = 10 µm.

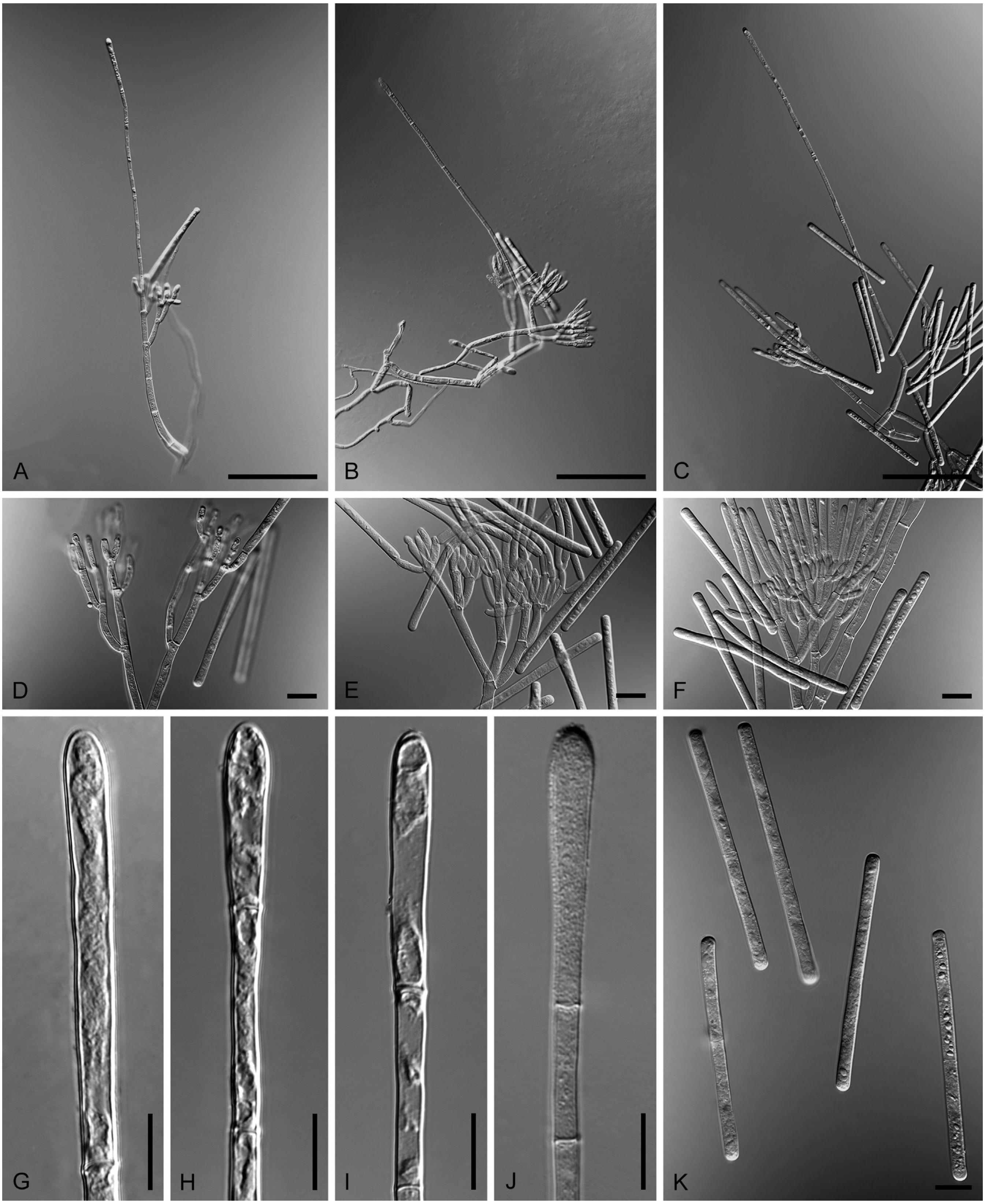


Fig. 13. *Calonectria longiramosa* (ex-type CBS 116319). **A–C.** Macroconidiophores. **D–F.** Conidiogenous apparatus with conidiophore branches and elongate doliiform to allantoid phialides. **G–J.** Clavate vesicles. **K.** Macroconidia. Scale bars: A–C = 50 µm; D–K = 10 µm.

Calonectria tucuruiensis L. Lombard & Crous, **sp. nov.** MycoBank MB820845. Fig. 17.

Etymology: Name refers to Tucuruí, the region in Brazil from which this fungus was collected.

Macroconidiophores consist of a stipe bearing a penicillate arrangement of fertile branches, and a stipe extension terminating in a vesicle; *stipe* septate, hyaline, smooth, 35–105 × 6–9 µm; *stipe extension* septate, straight to flexuous, 165–290 µm long, 4–6 µm wide at the apical septum,

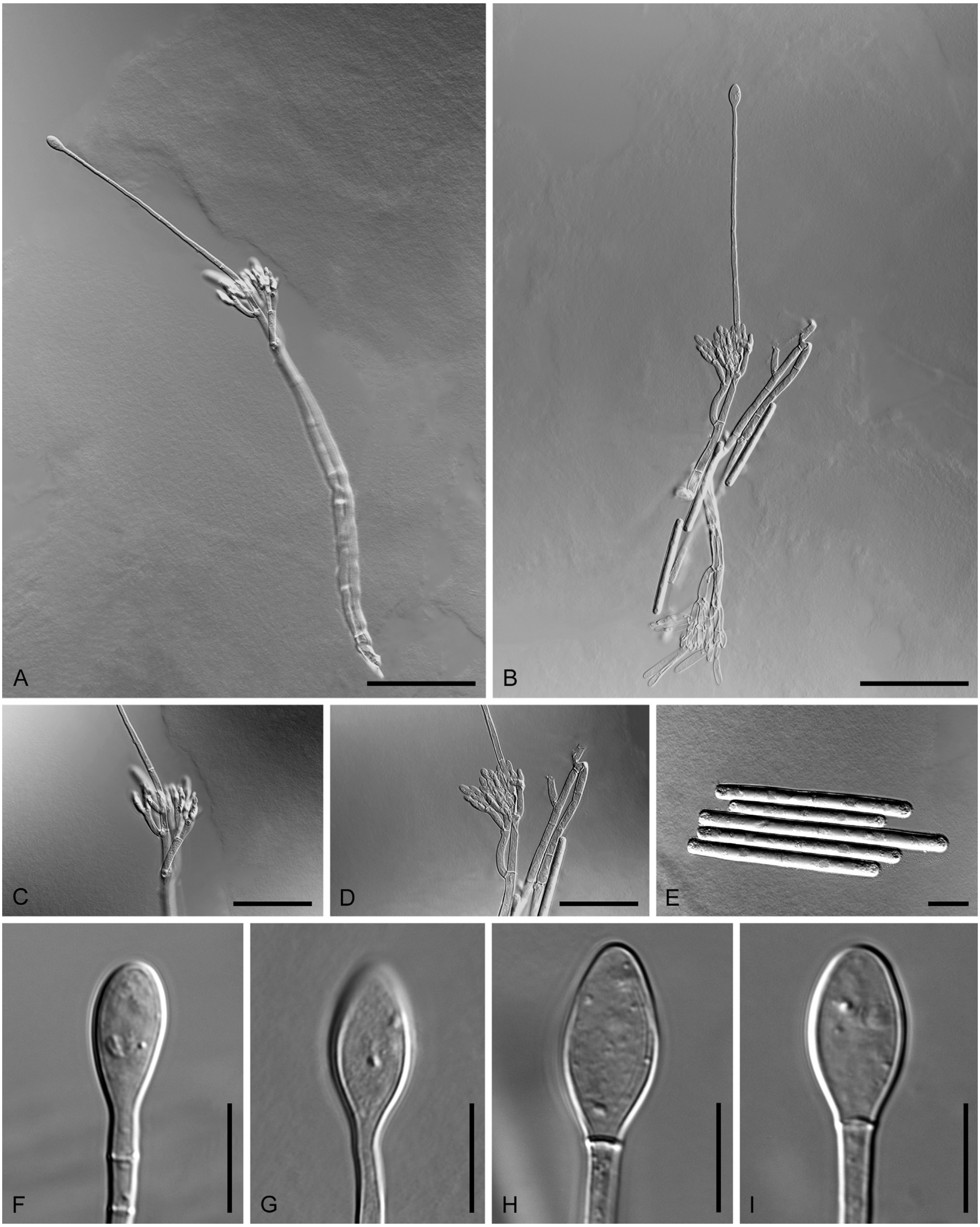


Fig. 14. *Calonectria nemoralis* (ex-type CBS 116319). **A, B.** Macroconidiophores. **C–D.** Conidiogenous apparatus with conidiophore branches and doliiform to reniform phialides. **E.** Macroconidia. **F–I.** Fusiform to ovoid vesicles. Scale bars: A, B = 50 µm; C–I = 10 µm.

terminating in a fusiform to ovoid to ellipsoid vesicle, 9–12 µm diam. *Conidiogenous apparatus* 40–95 µm wide, and 40–90 µm long; *primary branches* aseptate, 19–32 × 4–7 µm; *secondary branches* aseptate, 10–28 × 3–5 µm; *tertiary branches* aseptate, 11–16 × 3–6 µm; *quaternary branches* aseptate, 8–14 × 3–4 µm each terminal branch producing 2–4 phialides; *phialides* elongate doliiform to reniform, hyaline, aseptate, 8–17 × 3–5 µm, apex with minute periclinal thickening and inconspicuous collarette. *Macroconidia*

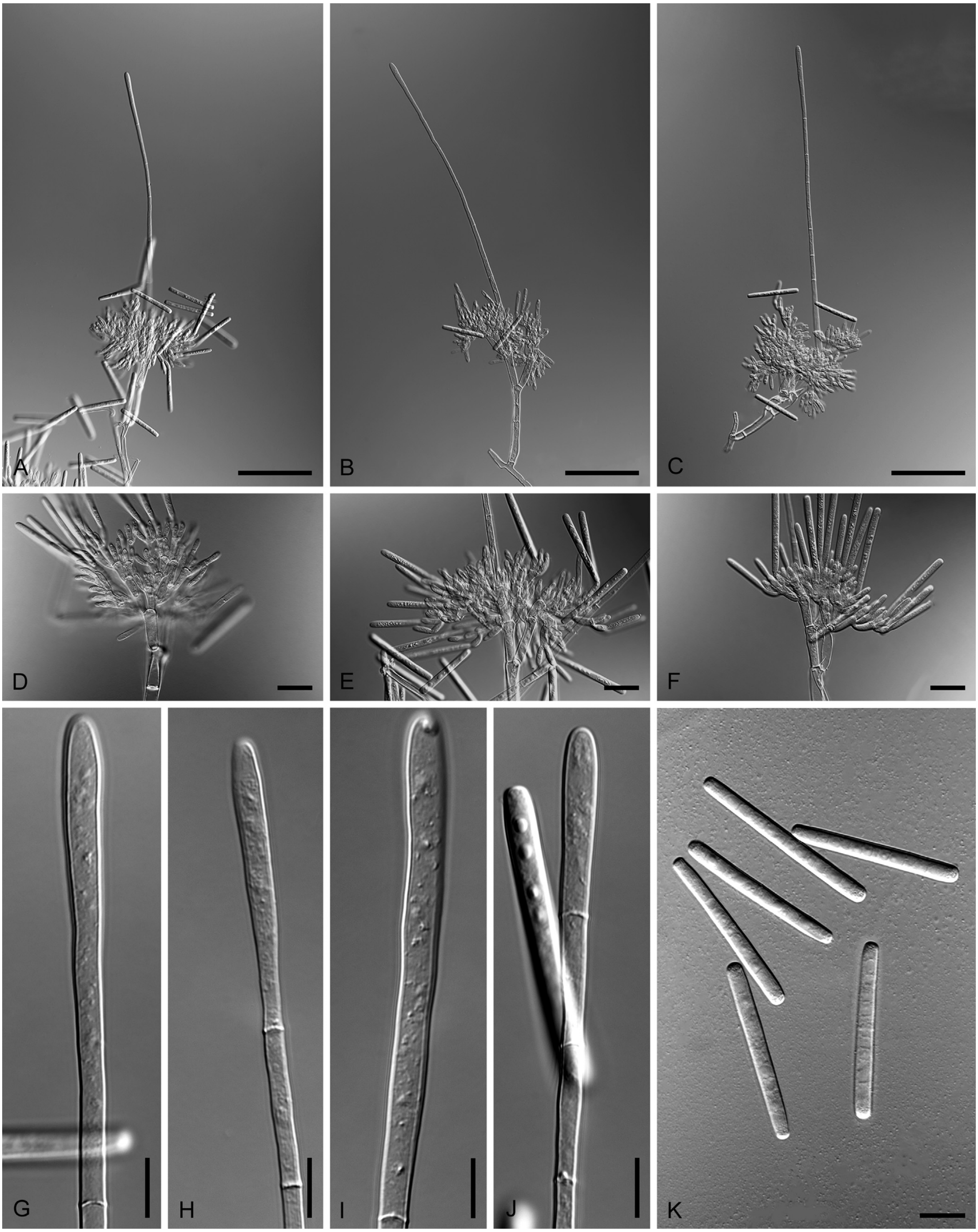


Fig. 15. *Calonectria octoramosa* (ex-type CBS 111423). **A–C.** Macroconidiophores. **D–F.** Conidiogenous apparatus with conidiophore branches and doliiform to reniform phialides. **G–J.** Clavate vesicles. **K.** Macroconidia. Scale bars: A–C = 20 μm; D–K = 10 μm.

cylindrical, rounded at both ends, straight, (51–)57–69(–71) × (4–)4.5–5.5(–6) μm (av. 63 × 5 μm), 1-septate, lacking a visible abscission scar, held in parallel cylindrical clusters by colourless slime. *Mega-* and *microconidia* not observed.

Culture characteristics. Colonies fast growing (55–75 mm diam) on MEA after 1 wk at room temperature; surface cinnamon to amber with sparse, buff to white, woolly aerial mycelium and abundant sporulation on the aerial mycelium and colony surface;

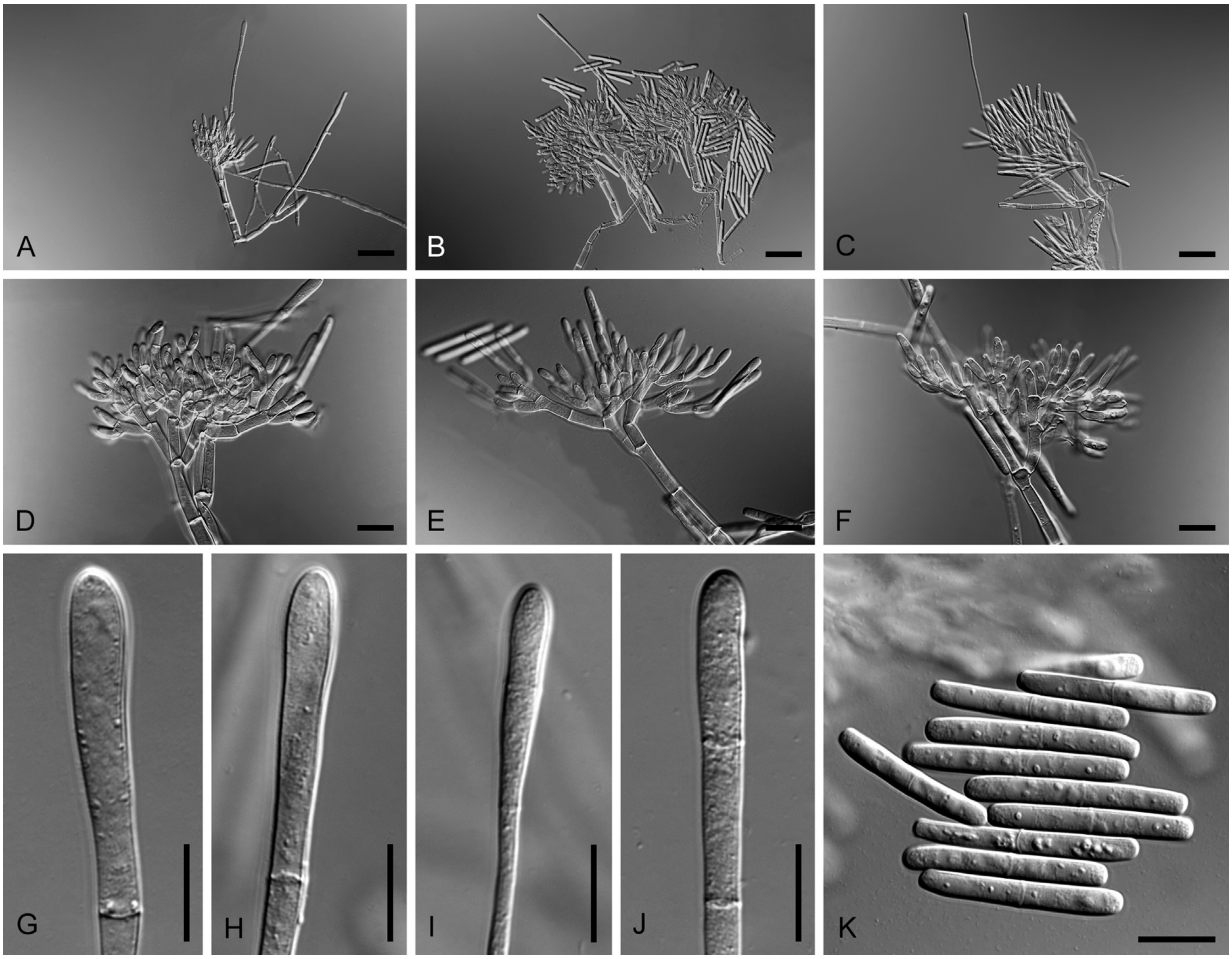


Fig. 16. *Calonectria parvispora* (ex-type CBS 111465). **A–C.** Macroconidiophores. **D–F.** Conidiogenous apparatus with conidiophore branches and doliiform to reniform phialides. **G–J.** Clavate vesicles. **K.** Macroconidia. Scale bars: A–C = 20 µm; D–K = 10 µm.

reverse sienna to amber with abundant chlamydospores throughout the medium, forming microsclerotia.

Material examined: **Brazil**, Tucuruí, from leaves of *Eucalyptus tereticornis*, 8 Aug. 1996, P.W. Crous (**holotype** CBS H-22777, culture ex-type CBS 114755 = CPC 1403); *ibid*., CBS 116265 = CPC 3552.

Notes: *Calonectria tucuruiensis* is closely related to *Ca. terricola* (Fig. 11). The macroconidia of *Ca. tucuruiensis* [(51–)57–69(–71) × (4–)4.5–5.5(–6) µm (av. 63 × 5 µm)] are larger than those of *Ca. terricola* [(40–)43–49(–53) × (3–)4–5(–6) µm (av. 46 × 4.5 µm); Lombard *et al.* (2016)].

Authors: L. Lombard & P.W. Crous

Ceratocystis Ellis & Halst., New Jersey Agric. Coll. Exp. Sta. Bull. 76: 14. 1890. Fig. 18.
Synonym: *Rostrella* Zimm., Meded. Lands Plantentuin 37: 24, 41. 1900.

Classification: *Sordariomycetes*, *Hypocreomycetidae*, *Microascales*, *Ceratocystidaceae.*

Type species: *Ceratocystis fimbriata* Ellis & Halst. Neotype: BPI 595863.

DNA barcodes (genus): 60S, LSU, *mcm7*.

DNA barcodes (species): ITS, *bt1*, *tef1*, *rpb2*, *ms204*. Table 4.

Ascomata perithecial, scattered or gregarious, immersed, partially embedded or superficial on the substrate; *bases* subglobose to globose or obpyriform, brown to black, covered with undifferentiated hyphae; *ostiolar necks* central, long, tapering towards apex; *ascomatal apex* straight or undulate, unbranched or branched, brown to black and becoming paler; *ostiolar hyphae* divergent or convergent, non-septate, straight, tapering towards apex, hyaline to light brown. *Asci* evanescent. *Ascospores* hyaline, 1-celled, ellipsoidal with gelatinous sheath which gives hat-shaped impression, accumulating in white, creamy to yellow masses at tips of necks. *Conidiophores* branched, straight or flexuous, hyaline to pale brown. *Conidiogenous cells* endophialidic, flask-shaped (lageniform) producing various shapes of cylindrical conidia or tubular-form producing barrel-shaped (doliiform) conidia, either lageniform alone or both forms present. *Conidia* hyaline, 1-celled, doliiform to cylindrical.

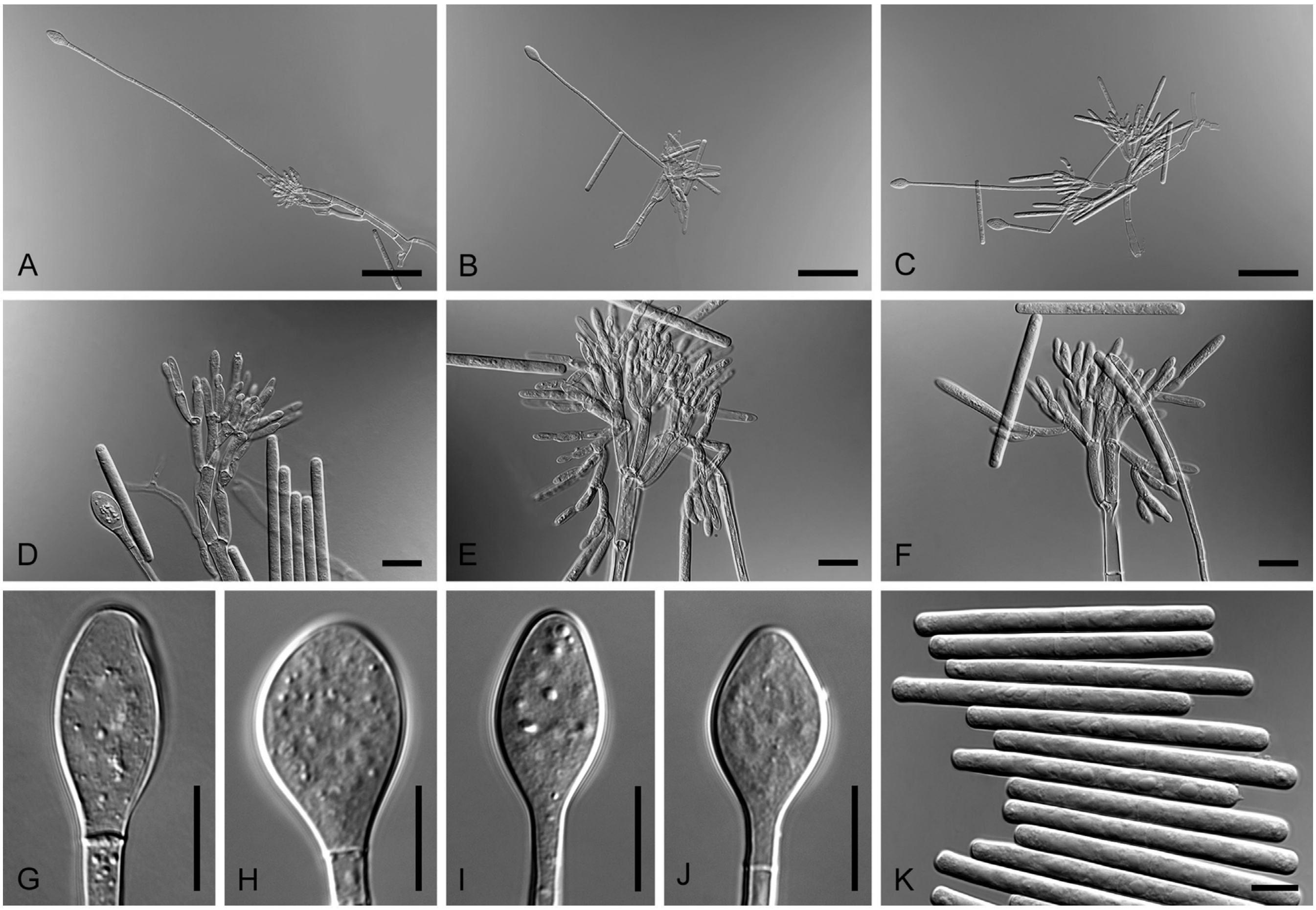


Fig. 17. *Calonectria tucuruiensis* (ex-type CBS 114755). **A–C.** Macroconidiophores. **D–F.** Conidiogenous apparatus with conidiophore branches and elongate doliiform to reniform phialides. **G–J.** Fusiform to ovoid to ellipsoid vesicles. **K.** Macroconidia. Scale bars: A–C = 50 μm; D–K = 10 μm.

Aleurioconidia (in some literature as *chlamydospores*) absent or present, pale brown to dark brown, pyriform, ellipsoidal to globose, singly or in chains.

Culture characteristics: Colonies showing circular growth with undulate margins, mycelium submerged to aerial, colour ranging from moderate yellowish brown to greyish or brownish olive when mature, releasing sweet fruity aroma. No growth on cycloheximide.

Optimal media and cultivation conditions: 2 % MEA incubated at 25 °C. Addition of thiamin stimulates the development of sexual morph.

Distribution: Worldwide.

Hosts: Herbaceous root crops, *Ipomea batatas* (sweet potato), wounds or larval tunnels of woody angiosperms, *Acacia*, *Annona*, *Carya*, *Citrus*, *Coffea*, *Colocacia*, *Colophospermum*, *Combretum*, *Corymbia*, *Cunninghamia*, *Dalbergia*, *Eucalyptus*, *Coffea*, *Mangifera*, *Platanus*, *Populus*, *Prosopis*, *Punica*, *Quercus*, *Rapanea*, *Saccharum*, *Schizolobium*, *Schotia*, *Styrax*, *Syzygium*, *Terminalia*, *Theobroma.* Some known to be vectored by flies (*Diptera*), non-specific ambrosia beetles (*Scolytinae*), or nitidulid beetles (*Nitidulidae*), but without specific insect associates.

Disease symptoms: Root rot, cankers and vascular stain.

Notes: *Ceratocystis sensu lato* included a heterogeneous group of fungi classified under this generic name due to similar morphology resulting from convergent evolution, despite their diverse ecological and biological features (Upadhyay 1981). The group has recently been divided into seven more narrowly defined homogeneous genera, supported by multigene phylogenies, morphological similarities and ecological commonality (Wingfield *et al.* 2013a, De Beer *et al.* 2014). The family *Ceratocystidaceae* includes nine genera, namely *Ambrosiella*, *Ceratocystis*, *Chalaropsis*, *Davidsoniella*, *Endoconidiophora*, *Huntiella*, *Thielaviopsis*, *Meredithiella* and *Phialophoropsis* (De Beer *et al.* 2014, Mayers *et al.* 2015). *Ceratocystis sensu stricto* is now restricted to those species producing ascomata with smooth bases, ascospores with hat-shaped sheaths, and thielaviopsis-like asexual morphs, which differentiate them from other genera (De Beer *et al.* 2014). Within *Ceratocystis*, morphological differences between species are insignificant and phylogenies based on multiple gene regions are used to distinguish them from each other (Fourie *et al.* 2015). The ITS region has been widely used for delimiting species of *Ceratocystis* (Schoch *et al.* 2012). However, discovery of multiple ITS types within single species in the genus (Al Adawi *et al.* 2013, Naidoo *et al.* 2013, Harrington *et al.* 2014) raised an awareness that the ITS region alone should not be applied to delimit species in *Ceratocystis*, and that additional gene regions should also be considered. Loci such as *bt1* and *tef1* do not provide good species resolution on their own, but provide strong support in combination with ITS (Fourie *et al.* 2015).

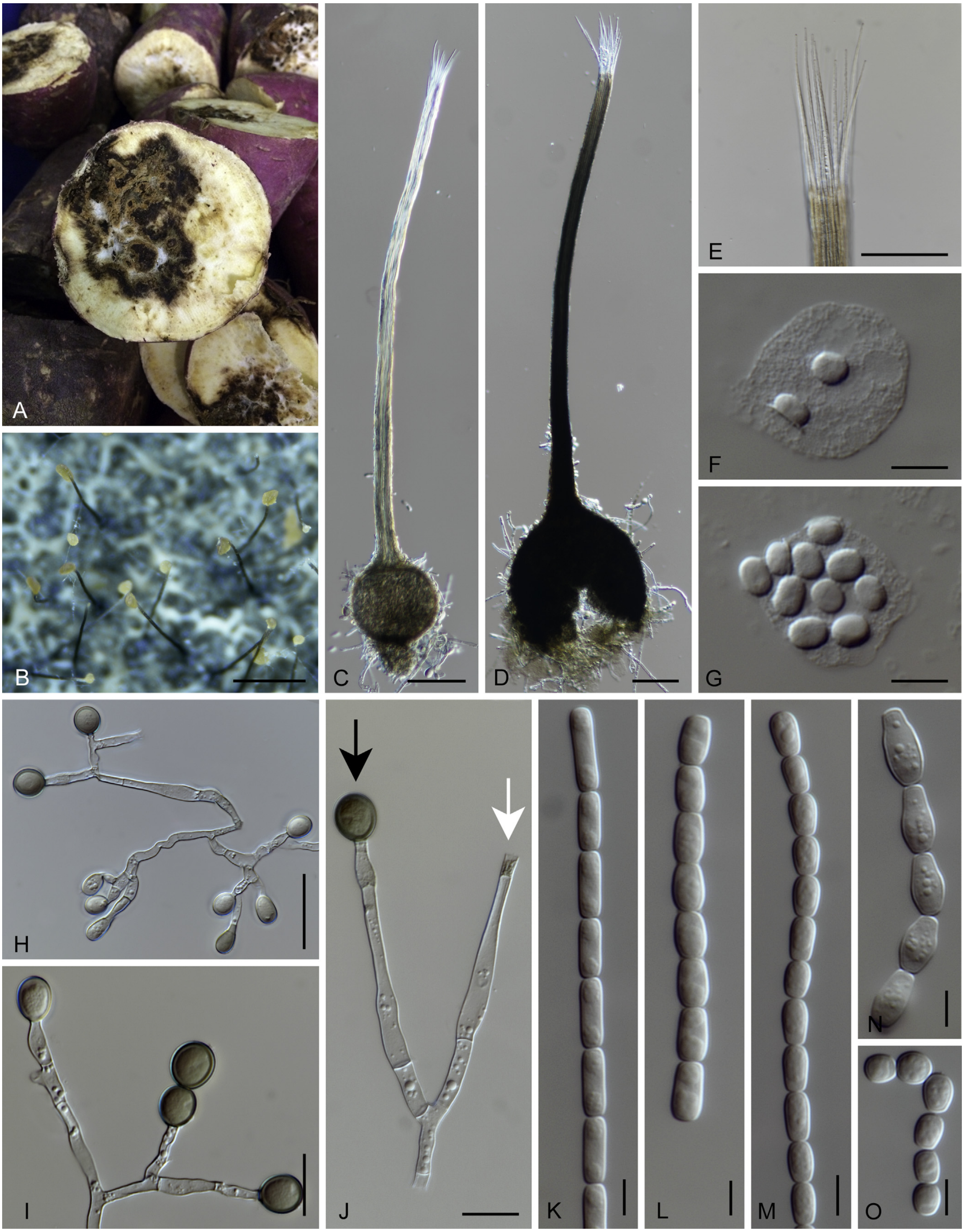


Fig. 18. **A.** Sweet potatoes (*Ipomea batatas*) infected with *Ceratocystis fimbriata*. **B−O.** Microscopic features of *Ceratocystis fimbriata* (CBS 114723 = CMW 14799) on 2 % MEA. **B.** Ascomata with yellowish droplets of ascospores at tips of necks, with asexual state (white background). **C.** Young ascoma. **D.** Mature ascoma. **E.** Ostiolar hyphae. **F, G.** Ascospores. **H, I.** Aleurioconidia. **J.** Conidiogenous cells producing aleurioconidia (black arrow) and cylindrical-shape conidia (white arrow). **K−O.** Conidia of various shapes in chains. Scale bars: B = 500 µm; C, D = 100 µm; E = 50 µm; F, G, K−O = 10 µm; H = 50 µm; I, J = 25 µm.

Table 4. DNA barcodes of accepted *Ceratocystis* spp.

Species	**Isolates**[1]	**GenBank accession numbers**[2]					**References**
		ITS	***bt1***	***tef1***	***ms204***	***rpb2***	
Ceratocystis adelpha	CBS 115169^{T}	DQ520637	KJ601509	KJ601516	–	–	Van Wyk *et al.* (2006), Fourie *et al.* (2015)
Ce. albifundus	CBS 128992	DQ520638	EF070429	EF070400	–	–	Van Wyk *et al.* (2006, 2007)
Ce. atrox	CBS 120518^{T}	NR_136981; EF070415	EF070431	EF070403	–	–	Van Wyk *et al.* (2007)
Ce. cacaofunesta	CBS 115172^{T}	AY157953	KJ601512	KJ601519	–	–	Baker *et al.* (2003), Fourie *et al.* (2015)
Ce. caryae	CBS 114716^{T}	NR_119530; AY907035; EF070424	EF070439	EF070412	–	–	Johnson *et al.* (2005), Van Wyk *et al.* (2007)
Ce. cercfabiensis	CBS 139654^{T}	KP727592; KP727593; KP727594*	KP727618	KP727643	–	–	Liu *et al.* (2015a)
Ce. collisensis	CBS 139679^{T}	KP727578	KP727614	KP727639	–	–	Liu *et al.* (2015a)
Ce. colombiana	CBS 121792^{T}	NR_119483; AY177233	AY177225	EU241493	KJ601567	KJ601603	Marin *et al.* (2003), Van Wyk *et al.* (2010), Fourie *et al.* (2015)
Ce. corymbiicola	CBS 127215^{T}	NR_119830; HM071902	HM071914	HQ236453	–	–	Kamgan Nkuekam *et al.* (2012)
Ce. curvata	CBS 122603^{T}	NR_137018; FJ151436	FJ151448	FJ151470	KJ601570	KJ601606	Van Wyk *et al.* (2011b), Fourie *et al.* (2015)
Ce. diversiconidia	CBS 123013^{T}	FJ151440	FJ151452	FJ151474	KJ601571	KJ601607	Van Wyk *et al.* (2011b), Fourie *et al.* (2015)
Ce. ecuadoriana	CBS 124020^{T}	FJ151432	FJ151444	FJ151466	KJ601573	KJ601609	Van Wyk *et al.* (2011b), Fourie *et al.* (2015)
Ce. eucalypticola	CBS 124016^{T}	FJ236723	FJ236783	FJ236753	KJ601576	KJ601612	Van Wyk *et al.* (2012), Fourie *et al.* (2015)
Ce. ficicola	MAFF 625119^{T}	NR_119410	KY685077	KY316544	KY685080	KY685082	Kajitani & Masuya (2011)
Ce. fimbriata	CBS 114723	KC493160	KF302689	KJ631109	KJ601578	KJ601614	Luchi *et al.* (2013), Fourie *et al.* (2015)
Ce. fimbriatomima	CBS 121786^{T}	EF190963	EF190951	EF190957	KJ601579	KJ601615	Van Wyk *et al.* (2009b), Fourie *et al.* (2015)
Ce. harringtonii	CBS 119.78	EF070418	EF070434	EF070406	–	–	Van Wyk *et al.* (2007)
Ce. larium	CBS 122512^{T}	NR_137016; EU881906	EU881894	EU881900	–	–	Van Wyk *et al.* (2009a)
Ce. mangicola	CBS 114721^{T}	AY953382	EF433307	EF433316	KJ601582	KJ601618	Van Wyk *et al.* (2005), Van Wyk *et al.* (2011a), Fourie *et al.* (2015)
Ce. manginecans	CBS 121659^{T}	NR_119532; AY953383*	EF433308	EF433317	KJ601584	KJ601620	Van Wyk *et al.* (2005, 2007), Fourie *et al.* (2015)
Ce. mangivora	CBS 128340^{T}	FJ200262	FJ200275	FJ200288	KJ601587	KJ601623	Van Wyk *et al.* (2011a), Fourie *et al.* (2015)
Ce. neglecta	CBS 121789^{T}	NR_137552; EF127990	EU881898	EU881904	KJ601588	KJ601624	Rodas *et al.* (2008), Van Wyk *et al.* (2009a), Fourie *et al.* (2015)
Ce. obpyriformis	CBS 122511^{T}	EU245003	EU244975	EU244935	–	–	Heath *et al.* (2009)
Ce. papillata	CBS 121793^{T}	NR_119486; AY233867	AY233874	EU241484	KJ601590	KJ601626	Van Wyk *et al.* (2010), Fourie *et al.* (2015)
Ce. pirilliformis	CBS 118128^{T}	NR_119452; AF427105	DQ371653	AY528983	KJ601594	KJ601630	Barnes *et al.* (2003), Van Wyk *et al.* (2004, 2006), Fourie *et al.* (2015)
Ce. platani	CBS 115162^{PT}	DQ520630	EF070425	EF070396	KJ601592	KJ601628	Van Wyk *et al.* (2006, 2007), Fourie *et al.* (2015)
Ce. polychroma	CBS 115778^{T}	AY528970	AY528966	AY528978	–	–	Van Wyk *et al.* (2004)
Ce. polyconidia	CBS 122289^{T}	EU245006	EU244978	EU244938	–	–	Heath *et al.* (2009)
Ce. smalleyi	CBS 114724^{T}	NR_119529; AY907030; EF070420	EF070436	EF070408	–	–	Johnson *et al.* (2005), Van Wyk *et al.* (2007)

Ce. tanganyicensis	CBS 122293^{T}	NR_137555; EU244999	EU244971	EU244931	–	–	Heath *et al.* (2009)
Ce. thulamelensis	CBS 131284^{T}	KC691456	KC691480	KC691504	–	–	Mbenoun *et al.* (2014)
Ce. tsitsikammensis	CBS 121018^{T}	NR_119633; EF408555	EF408569	EF408576	–	–	Kamgan *et al.* (2008)
Ce. variospora	CBS 114715^{PT}	AY907037; EF070421	EF070437	EF070409			Johnson *et al.* (2005), Van Wyk *et al.* (2007)
Ce. zambeziensis	CBS 131280^{T}	KC691458	KC691482	KC691506	–	–	Mbenoun *et al.* (2014)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; MAFF: Ministry of Agriculture, Forestry and Fisheries, Tsukuba, Ibaraki, Japan. ^{T} and ^{PT} indicate ex-type and ex-paratype, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *bt1*: partial β-tubulin gene; *tef1*: partial translation elongation factor 1-alpha gene; *ms204*: partial guanine nucleotide-binding protein subunit beta-like protein gene; *rpb2*: partial RNA polymerase II second largest subunit gene. *Multiple ITS types reported.

The loci *rpb2* and *ms204* give stronger resolution than *tef1* and *bt1*, but also need to be used in combination with ITS (Fourie *et al.* 2015).

References: Hunt 1956, Upadhyay 1981 (morphology); Nag Raj & Kendrick 1975, Paulin-Mahady *et al.* 2002 (asexual morphs and species); Kile 1993, Van Wyk *et al.* 2013 (pathogenicity); De Beer *et al.* 2013a (higher classification); De Beer *et al.* 2013b (nomenclator); Wilken *et al.* 2013, Van der Nest *et al.* 2014a, b, Wingfield *et al.* 2015, 2016a, b (genomes); Wingfield *et al.* 2013a, De Beer *et al.* 2014 (generic definitions and phylogenetic relationships); Wingfield *et al.* 2013b (international spread).

Authors: I. Barnes, S. Marincowitz, Z.W. de Beer, & M.J. Wingfield

Cladosporium Link, Mag. Gesell. naturf. Freunde, Berlin 7: 37. 1816 (1815). Fig. 19.
For synonyms see Bensch *et al.* (2012).

Classification: *Dothideomycetes*, *Dothideomycetidae*, *Capnodiales*, *Cladosporiaceae.*

Type species: *Cladosporium herbarum* (Pers. : Fr.) Link. Lectotype: L 910.225-733. Epitype and ex-epitype culture: CBS H-19853, CPC 12100 = CBS 121621.

DNA barcodes (genus): LSU.

DNA barcodes (species): *act* and *tef1*; in a few cases *tub2.* Table 5. Fig. 20.

Ascomata pseudothecial, black to red-brown, globose, inconspicuous and immersed beneath stomata to superficial, situated on a reduced stroma, with 1(–3) short, periphysate ostiolar necks; *periphysoids* frequently growing down into cavity; *ascomatal wall* consisting of 3–6 layers of *textura angularis*. *Pseudoparaphyses* frequently present in mature ascomata, hyaline, septate, subcylindrical. *Asci* fasciculate, short-stalked or not, subsessile, bitunicate, obovoid to broad ellipsoid or subcylindrical, straight to slightly curved, 8-spored. *Ascospores* bi- to multiseriate, hyaline, obovoid to ellipsoid-fusiform, with irregular luminar inclusions, mostly thick-walled, straight to slightly curved, frequently becoming brown and verruculose in asci, at times covered in mucoid sheath. *Dematiaceous hyphomycetes*. *In vivo*: *Mycelium* internal or external, superficial; *hyphae* branched, septate, subhyaline to usually pigmented, smooth, sometimes slightly rough-walled to verruculose. *Stromata* absent to sometimes well-developed. *Conidiophores* mononematous, usually macronematous, solitary, fasciculate, in small to large fascicles, loosely to densely caespitose, usually erect, occasionally subdecumbent, decumbent or repent, straight to flexuous, unbranched or branched, continuous to septate, subhyaline to usually distinctly pigmented, smooth to verruculose, proliferation holoblastic, occasionally enteroblastic (after a period when growth has stopped and then resumed), usually sympodial, rarely monopodial (sometimes leaving coarse annellations from repeated enteroblastic proliferation). *Conidiogenous cells* integrated, terminal or intercalary, monoblastic or usually polyblastic, mostly sympodially proliferating, more or less cylindrical, geniculate-sinuous

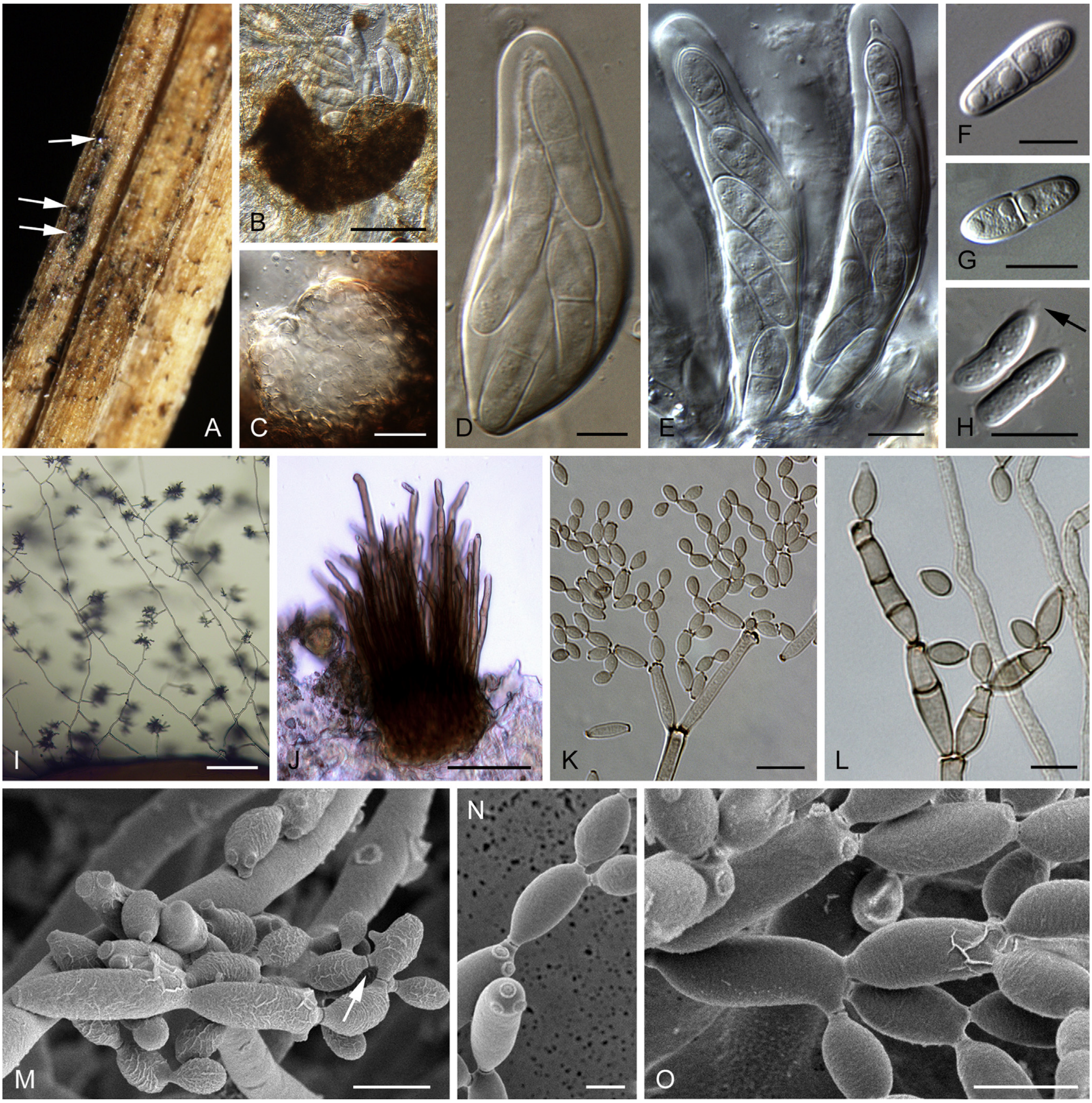


Fig. 19. *Cladosporium* spp. **A–H.** Sexual morphs. **A.** Ascomata on host tissue (arrows) of *Cladosporium silenes* (holotype CBS H-19874). **B.** Ascoma and asci of *Cladosporium herbarum* (CPC 11600). **C.** Ostiole of *Cladosporium macrocarpum* (CBS 299.67). **D, E.** Asci of *Cladosporium herbarum* (CPC 11600). **F, G.** Ascospores of *Cladosporium herbarum* (CPC 11600). **H.** Ascospores (arrow denotes mucoid appendage) of *Cladosporium silenes* (holotype CBS H-19874). **I–O.** Asexual morphs. **I.** Conidiophores of *Cladosporium halotolerans* (ex-type CBS 119416). **J.** Fascicle of conidiophores of *Cladosporium soldanellae* (BPI 427476). **K.** Macronematous conidiophores and conidial chains of *Cladosporium cladosporioides* (ex-neotype CBS 112388). **L.** Conidial chains, septa of secondary ramoconidia distinctly darkened of *Cladosporium paracladosporioides* (ex-type CBS 171.54). **M.** CryoSEM of different types of conidia on aerial structures of *Cladosporium exile* (ex-type CBS 125987). Note a remarkable pattern of blastoconidium formation (backwards) (arrow). **N.** Secondary ramoconidia, conidia and scars of *Cladosporium perangustum* (ex-type CBS 125996). **O.** Whorls of secondary ramoconidia and conidia of *Cladosporium scabrellum* (ex-type CBS 126358). Scale bars: B, C, M, O = 5 µm; D–H, K, L = 10 µm; I = 100 µm; J = 50 µm; N = 2 µm. Pictures taken from Bensch *et al.* (2012).

or nodulose, sometimes with unilateral swellings; *conidiogenous loci* usually conspicuous, protuberant, composed of a central convex dome surrounded by a more or less raised periclinal rim (coronate), thickened, refractive or barely to distinctly darkened; *conidial formation* holoblastic. *Conidia* solitary or catenate, in unbranched or branched acropetal chains, amero- to phragmosporous, shape and septation variable, usually subglobose, ovoid, obovoid, ellipsoid, fusiform, limoniform to cylindrical, aseptate or with several transverse eusepta, rarely with a single longitudinal septum, subhyaline to usually pigmented, smooth, verruculose, verrucose, echinulate, cristate; *hila* protuberant, coronate, with a central convex dome and raised periclinal rim, thickened, refractive to darkened; *microcyclic conidiogenesis* often occurring. *In vitro*: *Stromata* usually lacking. *Conidiophores* usually solitary, arising terminally or laterally from plagiotropous or ascending hyphae, often longer than *in vivo*. *Micronematous conidiophores*, lacking *in vivo*, are often formed in culture. *Conidial chains* often longer than *in vivo* (species with solitary conidia are often capable of forming conidial chains in culture).

Table 5. DNA barcodes of accepted *Cladosporium* spp.

Species	**Isolates**[1]	**GenBank accession numbers**[2]			**References**
		ITS	***act***	***tef1***	
Cladosporium acalyphae	CBS 125982^{T}	HM147994	HM148481	HM148235	Bensch *et al.* (2010)
Cl. aciculare	CBS 140488^{T}	KT600411	KT600607	KT600509	Bensch *et al.* (2015)
Cl. aggregatocicatricatum	CBS 140493^{T}	KT600448	KT600645	KT600547	Bensch *et al.* (2015)
Cl. alboflavescens	CBS 140690^{T}	LN834420	LN834604	LN834516	Sandoval-Denis *et al.* (2016)
Cl. allicinum	CBS 121624^{NT}	EF679350	EF679502	EF679425	Schubert *et al.* (2007)
Cl. allii	CBS 101.81^{RS}	JN906977	JN906996	JN906983	Bensch *et al.* (2012)
Cl. angulosum	CBS 140692^{T}	LN834425	LN834609	LN834521	Sandoval-Denis *et al.* (2016)
Cl. angustiherbarum	CBS 140479^{T}	KT600378	KT600574	KT600475	Bensch *et al.* (2015)
Cl. angustisporum	CBS 125983^{T}	HM147995	HM148482	HM148236	Bensch *et al.* (2010)
Cl. angustiterminale	CBS 140480^{T}	KT600379	KT600575	KT600476	Bensch *et al.* (2015)
Cl. antarcticum	CBS 690.92^{T}	EF679334	EF679484	EF679405	Schubert *et al.* (2007)
Cl. antropophilum	CBS 140685^{T}	LN834437	LN834621	LN834533	Sandoval-Denis *et al.* (2016)
Cl. aphidis	CBS 132182^{ET}	JN906978	JN906998	JN906985	Bensch *et al.* (2012)
Cl. arthropodii	CBS 124043^{ET}	JN906979	JN906998	JN906985	Bensch *et al.* (2012)
Cl. asperulatum	CBS 126340^{T}	HM147998	HM148485	HM148239	Bensch *et al.* (2010)
Cl. australiense	CBS 125984^{T}	HM147999	HM148486	HM148240	Bensch *et al.* (2010)
Cl. austroafricanum	CBS 140481^{T}	KT600381	KT600577	KT600478	Bensch *et al.* (2015)
Cl. austrohemisphaericum	CBS 140482^{T}	KT600382	KT600578	KT600479	Bensch *et al.* (2015)
Cl. basiinflatum	CBS 822.84^{T}	HM148000	HM148487	HM148241	Bensch *et al.* (2010)
Cl. chalastosporoides	CBS 125985^{T}	HM148001	HM148488	HM148242	Bensch *et al.* (2010)
Cl. chasmanthicola	CBS 142612^{T}	KY646221	KY646224	KY646227	Present study
Cl. chubutense	CBS 124457^{T}	FJ936158	FJ936165	FJ936161	Schubert *et al.* (2009)
Cl. cladosporioides	CBS 112388^{NT}	HM148003	HM148490	HM148244	Bensch *et al.* (2010)
Cl. colocasiae	CBS 386.64^{T}	HM148067	HM148555	HM148310	Bensch *et al.* (2010)
Cl. colombiae	CBS 274.80B^{T}	FJ936159	FJ936166	FJ936163	Schubert *et al.* (2009)
Cl. crousii	CBS 140686^{T}	LN834431	LN834615	LN834527	Sandoval-Denis *et al.* (2016)
Cl. cucumerinum	CBS 171.52^{ET}	HM148072	HM148561	HM148316	Bensch *et al.* (2010)
Cl. cycadicola	CPC 17251^{T}	KJ869122	KJ869227	KJ869236	Crous *et al.* (2014b)
Cl. delicatulum	CBS 126344^{RS}	HM148081	HM148570	HM148325	Bensch *et al.* (2010)
Cl. dominicanum	CBS 119415^{T}	DQ780353	EF101368	JN906986	Zalar *et al.* (2007), Bensch *et al.* (2012)
Cl. echinulatum	CBS 123191^{RS}	JN906980	JN906999	JN906987	Bensch *et al.* (2012)
Cl. exasperatum	CBS 125986^{T}	HM148090	HM148579	HM148334	Bensch *et al.* (2010)
Cl. exile	CBS 125987^{T}	HM148091	HM148580	HM148335	Bensch *et al.* (2010)
Cl. flabelliforme	CBS 126345^{T}	HM148092	HM148581	HM148336	Bensch *et al.* (2010)
Cl. flavovirens	CBS 140462^{T}	LN834440	LN834624	LN834536	Sandoval-Denis *et al.* (2016)
Cl. floccosum	CBS 140463^{T}	LN834416	LN834600	LN834512	Sandoval-Denis *et al.* (2016)
Cl. funiculosum	CBS 122129^{T}	HM148094	HM148583	HM148338	Bensch *et al.* (2010)
Cl. fusiforme	CBS 119414^{T}	DQ780388	EF101372	JN906988	Zalar *et al.* (2007), Bensch *et al.* (2012)
Cl. gamsianum	CBS 125989^{T}	HM148095	HM148584	HM148339	Bensch *et al.* (2010)
Cl. globisporum	CBS 812.96^{T}	HM148096	HM148585	HM148340	Bensch *et al.* (2010)
Cl. grevilleae	CBS 114271^{T}	JF770450	JF770473	JF770472	Crous *et al.* (2011b)
Cl. halotolerans	CBS 119416^{T}	DQ780364	EF101397	JN906989	Zalar *et al.* (2007), Bensch *et al.* (2012)
Cl. herbaroides	CBS 121626^{T}	EF679357	EF679509	EF679432	Schubert *et al.* (2007)
Cl. herbarum	CBS 121621^{ET}	EF679363	EF679516	EF679440	Schubert *et al.* (2007)
Cl. hillianum	CBS 125988^{T}	HM148097	HM148586	HM148341	Bensch *et al.* (2010)
Cl. inversicolor	CBS 401.80^{T}	HM148101	HM148590	HM148345	Bensch *et al.* (2010)
Cl. ipereniae	CBS 140483^{T}	KT600394	KT600589	KT600491	Bensch *et al.* (2015)
Cl. iranicum	CBS 126346^{T}	HM148110	HM148599	HM148354	Bensch *et al.* (2010)

Table 5. (Continued).

Species	Isolates[1]	GenBank accession numbers[2]			References
		ITS	*act*	*tef1*	
Cl. iridis	CBS 138.40^{ET}	EF679370	EF679523	EF679447	Schubert *et al.* (2007)
Cl. kenpeggii	CBS 142613^{T}	KY646222	KY646225	KY646228	Present study
Cl. langeronii	CBS 189.54^{NT}	DQ780379	EF101357	JN906990	Zalar *et al.* (2007), Bensch *et al.* (2012)
Cl. licheniphilum	CBS 125990^{ET}	HM148111	HM148600	HM148355	Bensch *et al.* (2010)
Cl. limoniforme	CBS 140484^{T}	KT600397	KT600592	KT600494	Bensch *et al.* (2015)
Cl. longicatenatum	CBS 140485^{T}	KT600403	KT600598	KT600500	Bensch *et al.* (2015)
Cl. longissimum	CBS 140485^{T}	DQ780352	EF101385	EU570259	Zalar *et al.* (2007), Dugan *et al.* (2008)
Cl. lycoperdinum	CBS 574.78C^{RS}	HM148115	HM148604	HM148359	Bensch *et al.* (2010)
Cl. macrocarpum	CBS 121623^{NT}	EF679375	EF679529	EF679453	Schubert *et al.* (2007)
Cl. montecillanum	CBS 140486^{T}	KT600406	KT600602	KT600504	Bensch *et al.* (2015)
Cl. myrtacearum	CBS 126350^{ET}	HM148117	HM148606	HM148361	Bensch *et al.* (2010)
Cl. ossifragi	CBS 842.91^{ET}	EF679381	EF679535	EF679459	Schubert *et al.* (2007)
Cl. oxysporum	CBS 125991^{RS}	HM148118	HM148607	HM148362	Bensch *et al.* (2010)
Cl. paracladosporioides	CBS 171.54^{T}	HM148120	HM148609	HM148364	Bensch *et al.* (2010)
Cl. parapenidielloides	CBS 140487^{T}	KT600410	KT600606	KT600508	Bensch *et al.* (2015)
Cl. penidielloides	CBS 140489^{T}	KT600412	KT600608	KT600510	Bensch *et al.* (2015)
Cl. perangustum	CBS 125996^{T}	HM148121	HM148610	HM148365	Bensch *et al.* (2010)
Cl. phaenocomae	CBS 128769^{T}	JF499837	JF499881	JF499875	Crous & Groenewald (2011)
Cl. phlei	CBS 358.69^{ET}	JN906981	JN907000	JN906991	Bensch *et al.* (2012)
Cl. phyllactiniicola	CBS 126352^{T}	HM148150	HM148639	HM148394	Bensch *et al.* (2010)
Cl. phyllophilum	CBS 125992^{ET}	HM148154	HM148643	HM148398	Bensch *et al.* (2010)
Cl. pini-ponderosae	CBS 124456^{T}	FJ936160	FJ936167	FJ936164	Schubert *et al.* (2009)
Cl. pseudiridis	CBS 116463^{T}	EF679383	EF679537	EF679461	Schubert *et al.* (2007)
Cl. pseudochalastosporioides	CBS 140490^{T}	KT600415	KT600611	KT600513	Bensch *et al.* (2015)
Cl. pseudocladosporioides	CBS 125993^{T}	HM148158	HM148647	HM148402	Bensch *et al.* (2010)
Cl. psychrotolerans	CBS 119412^{T}	DQ780386	EF101365	JN906992	Zalar *et al.* (2007), Bensch *et al.* (2012)
Cl. puyae	CBS 274.80A^{T}	KT600418	KT600614	KT600516	Bensch *et al.* (2015)
Cl. ramotenellum	CBS 121628^{T}	EF679384	EF679538	EF679462	Schubert *et al.* (2007)
Cl. rectoides	CBS 125994^{T}	HM148193	HM148683	HM148438	Bensch *et al.* (2010)
Cl. rhusicola	CBS 140492^{T}	KT600440	KT600637	KT600539	Bensch *et al.* (2015)
Cl. ruguloflabelliforme	CBS 140494^{T}	KT600458	KT600655	KT600557	Bensch *et al.* (2015)
Cl. rugulovarians	CBS 140495^{T}	KT600459	KT600656	KT600558	Bensch *et al.* (2015)
Cl. salinae	CBS 119413^{T}	DQ780374	EF101390	JN906993	Zalar *et al.* (2007), Bensch *et al.* (2012)
Cl. scabrellum	CBS 126358^{T}	HM148195	HM148685	HM148440	Bensch *et al.* (2010)
Cl. silenes	CBS 109082^{T}	EF679354	EF679506	EF679429	Schubert *et al.* (2007)
Cl. sinuosum	CBS 121629^{T}	EF679386	EF679540	EF679464	Schubert *et al.* (2007)
Cl. soldanellae	CBS 132186^{NT}	JN906982	JN907001	JN906994	Bensch *et al.* (2012)
Cl. sphaerospermum	CBS 193.54^{NT}	DQ780343	EF101380	EU570261	Zalar *et al.* (2007), Dugan *et al.* (2008)
Cl. spinulosum	CBS 119907^{T}	EF679388	EF679542	EF679466	Schubert *et al.* (2007)
Cl. subcinereum	CBS 140465^{T}	LN834433	LN834529	LN834617	Sandoval-Denis *et al.* (2016)
Cl. subinflatum	CBS 121630^{T}	EF679389	EF679543	EF679467	Schubert *et al.* (2007)
Cl. subtilissimum	CBS 113754^{T}	EF679397	EF679551	EF679475	Schubert *et al.* (2007)
Cl. subuliforme	CBS 126500^{T}	HM148196	HM148686	HM148441	Bensch *et al.* (2010)
Cl. succulentum	CBS 140466^{T}	LN834434	LN834618	LN834530	Sandoval-Denis *et al.* (2016)
Cl. tenellum	CBS 121634^{T}	EF679401	EF679555	EF679479	Schubert *et al.* (2007)
Cl. tenuissimum	CBS 125995^{ET}	HM148197	HM148687	HM148442	Bensch *et al.* (2010)
Cl. tuberosum	CBS 140693^{T}	LN834417	LN834601	LN834513	Sandoval-Denis *et al.* (2016)
Cl. uredinicola	ATCC 46649	AY251071	HM148712	HM148467	Braun *et al.* (2003), Bensch *et al.* (2010)
Cl. variabile	CBS 121635^{ET}	EF679402	EF679556	EF679480	Schubert *et al.* (2007)

(*continued on next page*)

Table 5. (Continued).

Species	**Isolates**[1]	**GenBank accession numbers**[2]			**References**
		ITS	***act***	***tef1***	
Cl. varians	CBS 126362^T	HM148224	HM148715	HM148470	Bensch *et al.* (2010)
Cl. velox	CBS 119417^T	DQ780361	EF101388	JN906995	Zalar *et al.* (2007), Bensch *et al.* (2012)
Cl. verrucocladosporioides	CBS 126363^T	HM148226	HM148717	HM148472	Bensch *et al.* (2010)
Cl. versiforme	CBS 140491^T	KT600417	KT600613	KT600515	Bensch *et al.* (2015)
Cl. welwitschiicola	CBS 142614^T	KY646223	KY646226	KY646229	Present study
Cl. xanthochromaticum	CBS 140691^T	LN834415	LN834599	LN834511	Sandoval-Denis *et al.* (2016)
Cl. xylophilum	CBS 125997^T	HM148230	HM148721	HM148476	Bensch *et al.* (2010)

[1] ATCC: American Type Culture Collection, Virginia, USA; CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CPC: Culture collection of Pedro Crous, housed at Westerdijk Fungal Biodiversity Institute. $^{T, ET, NT}$ and ^{RS} indicate ex-type, ex-epitype, ex-neotype and reference strains, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *act*: partial actin gene; *tef1*: partial translation elongation factor 1-alpha gene.

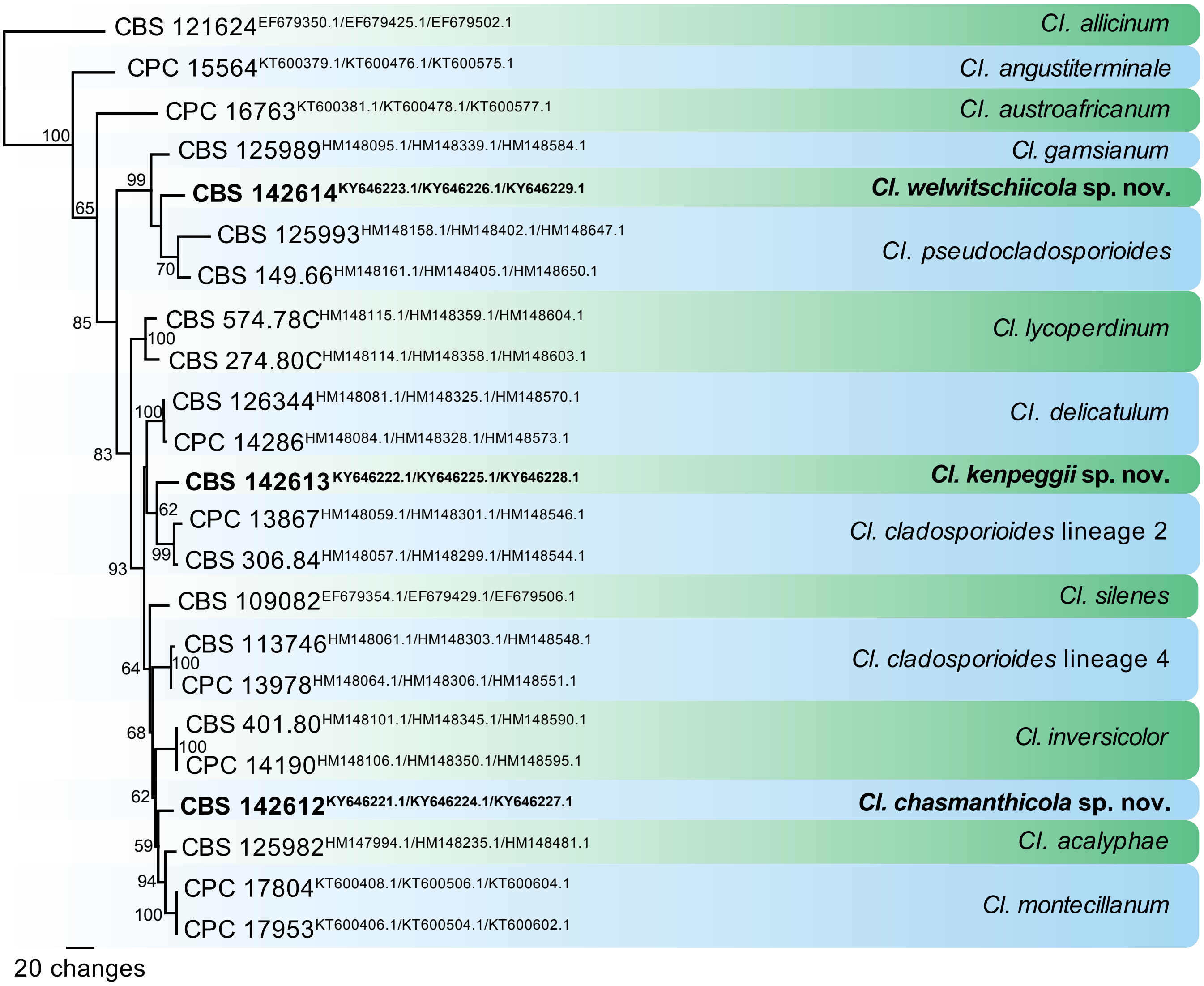


Fig. 20. The first of two equally most parsimonious trees obtained from a heuristic search of the combined ITS/*tef1*/*actA* alignment. The tree was rooted to *Cladosporium allicinum* CBS 121624 and the novel species described in this study are shown in **bold**. Bootstrap support values from 1000 replicates are shown at the nodes and the scale bar represents the number of changes. GenBank accession numbers are indicated in superscript (ITS/*tef1*/*actA*). TreeBASE: S20877.

Culture characteristics: Colonies on SNA often grey olivaceous or olivaceous grey, reverse leaden-grey or black, flat, velvety with fluffy or cottony patches, margin irregular or undulate, aerial mycelium loose diffuse or more abundantly formed, often with abundant submerged mycelium.

Optimal media and cultivation conditions: For morphological examinations SNA incubated under continuous near-ultraviolet light at 25 °C proved to be best suited to promote sporulation. The sexual morph can be induced by inoculating plates of 2 % WA onto which autoclaved stem pieces of *Urtica dioica*

(European stinging nettle) are placed. Inoculated plates have to be incubated on the laboratory bench for 1 wk, after that period they have to be further incubated at 10 °C in the dark for 1–2 mo to stimulate sexual morph development.

Distribution: Worldwide.

Hosts: *Asparagaceae*, *Asteraceae*, *Fabaceae*, *Myrtaceae*, *Orchidaceae*, *Poaceae* and many other hosts, including fungi and insects.

Disease symptoms: Leaf spots, leaf blight, discolourations, necrosis, or shot-hole symptoms, on stems and fruits, but also saprobic, endophytic or isolated from numerous substrates and environments, e.g. indoor environments, salterns and human and animal infections.

Notes: The monophyletic genus *Cladosporium* is well characterised by the coronate structure of its conidiogenous loci and conidial hila, consisting of a central convex dome surrounded by a raised periclinal rim (David 1997, Braun *et al.* 2003). At the moment it comprises about 200 species. *Cladosporium* was previously extremely heterogeneous and encompassed 772 names assigned to this genus (Dugan *et al.* 2004). Heuchert *et al.* (2005) examined *Cladosporium* spp. dwelling on other fungi, and Schubert (2005) provided a comprehensive treatment of foliicolous species. Crous *et al.* (2007a) encompassed a series of papers dealing with a reassessment and new circumscription of *Cladosporium s. str.* and treatments of several cladosporioid genera. Bensch *et al.* (2012) published a taxonomic monograph of the genus *Cladosporium* which can be consulted for further information on the history and many other aspects of this genus.

Species delimitation in *Cladosporium* based on morphology alone is limited since many species have overlapping characters. Some key differential features have been identified and detailed in a series of monographic papers (Schubert *et al.* 2007, Zalar *et al.* 2007, Bensch *et al.* 2010, 2012). The most relevant differential morphological traits are the shape, width and complexity of conidiophores, the presence of ramoconidia, and the formation and ornamentation of conidia. However, given the overlapping of these features, and the need for standardisation using special culture media and scanning electron microscopy procedures, the use of a molecular approach should be mandatory for correct identification of the species in this complex fungal group (Sandoval-Denis *et al.* 2016).

Three different species complexes are recognised within the genus, mainly based on morphology, and used for practical purposes. The *Cl. cladosporioides* species complex is characterised by mainly narrowly cylindrical or cylindrical-oblong, non-nodulose, mostly non-geniculate conidiophores and conidia with a quite variable surface ornamentation ranging from smooth to irregularly verrucose-rugose or rough-walled (reticulate or embossed stripes under SEM); the *Cl. herbarum* species complex includes species mainly having nodulose conidiophores, with conidiogenesis confined to swellings, and verruculose, verrucose or echinulate conidia; and the *Cl. sphaerospermum* complex is most remarkable due to forming numerous globose or subglobose terminal and intercalary conidia with variable surface ornamentation and often poorly differentiated conidiophores in most of the species (Bensch *et al.* 2012, 2015). Morphologically similar genera have been treated in Crous *et al.* (2007b).

Members of *Cladosporiaceae*: *Cladosporium*, *Graphiopsis*, *Neocladosporium*, *Rachicladosporium*, *Toxicocladosporium*, *Verrucocladosporium.*

References: Braun *et al.* 2003 (sexual morph); Crous *et al.* 2007a, b (cladosporium-like genera); Schubert *et al.* 2007 (morphology, phylogeny *Cl. herbarum* complex); Zalar *et al.* 2007 (morphology, phylogeny *Cl. sphaerospermum* complex); Bensch *et al.* 2010 (morphology, phylogeny *Cl. cladosporioides* complex); Bensch *et al.* 2012 (morphology, phylogeny and key of all *Cladosporium* species); Bensch *et al.* 2015 (morphology, additions to the three species complexes); Sandoval-Denis *et al.* 2016 (morphology, phylogeny of clinical samples).

Cladosporium chasmanthicola Bensch, U. Braun & Crous, **sp. nov.** MycoBank MB819978. Fig. 21.

Etymology: Epithet composed of the name of the host genus, *Chasmanthe*, and -cola, dweller.

Leaf spots solitary, distributed over leaf surface, amphigenous, ellipsoid, 1–2 mm diam, pale brown with dark red-brown margin, some spots also associated with uredinia of *Uromyces kentaniensis*. On SNA: *Mycelium* loosely branched, filiform, narrowly cylindrical-oblong or irregular in outline due to swellings and constrictions, 0.5–4 µm wide, septate, subhyaline or pale olivaceous or olivaceous brown, almost smooth, verruculose, distinctly verrucose or irregularly rough-walled. *Conidiophores* solitary, formed terminally or laterally from hyphae, straight or somewhat flexuous, macro- and micronematous; *macronematous conidiophores* cylindrical, sometimes geniculate, often irregular in outline due to lateral outgrowths, swellings and constrictions (not connected with conidiogenesis), mostly unbranched, 20–100(–140) × 3.5–5(–6) µm, up to 6 µm wide at the base, 1–6-septate, septa sometimes in short succession, not constricted at septa, pale olivaceous or pale to medium olivaceous brown, smooth, walls slightly thickened; *micronematous conidiophores* shorter, narrower and paler than macronematous ones, 15–30(–80) × 2–3 µm, 0–2-septate, subhyaline or pale olivaceous. *Conidiogenous cells* integrated, terminal and intercalary, 8–24 µm long, short cylindrical or often irregular in outline due to lateral prolongations and shoulders and numerous conidiogenous loci often crowded at or towards the apex, up to eight loci in terminal cells, 1–3 loci in intercalary cells, loci conspicuous, subdenticulate, 1–2 µm diam. *Ramoconidia* commonly formed, subcylindrical or irregular due to numerous loci at the distal end, 15–33 × 3–4.5 µm, 0–1(–3)-septate, base broadly truncate, 2.5(–3.5) µm wide. *Conidia* numerously formed, especially small terminal and intercalary conidia, in branched chains, branching in all directions with 1–3 conidia in the terminal unbranched part of the chain; *terminal conidia* very small, ovoid or obovoid, very pale, subhyaline or pale olivaceous brown, 2.5–4.5 × 2–2.5(–3) µm (av. ± SD: 3.4 ± 0.6 × 2.2 ± 0.3), apex rounded; *intercalary conidia* ovoid, limoniform, ellipsoid or irregular due to lateral outgrowths, 4–10.5 × (2–)3–3.5(–4) µm (av. ± SD: 7.2 ± 2.0 × 3.1 ± 0.5), aseptate, with 1–4 distal hila; *secondary ramoconidia* ellipsoid, subcylindrical or irregular in

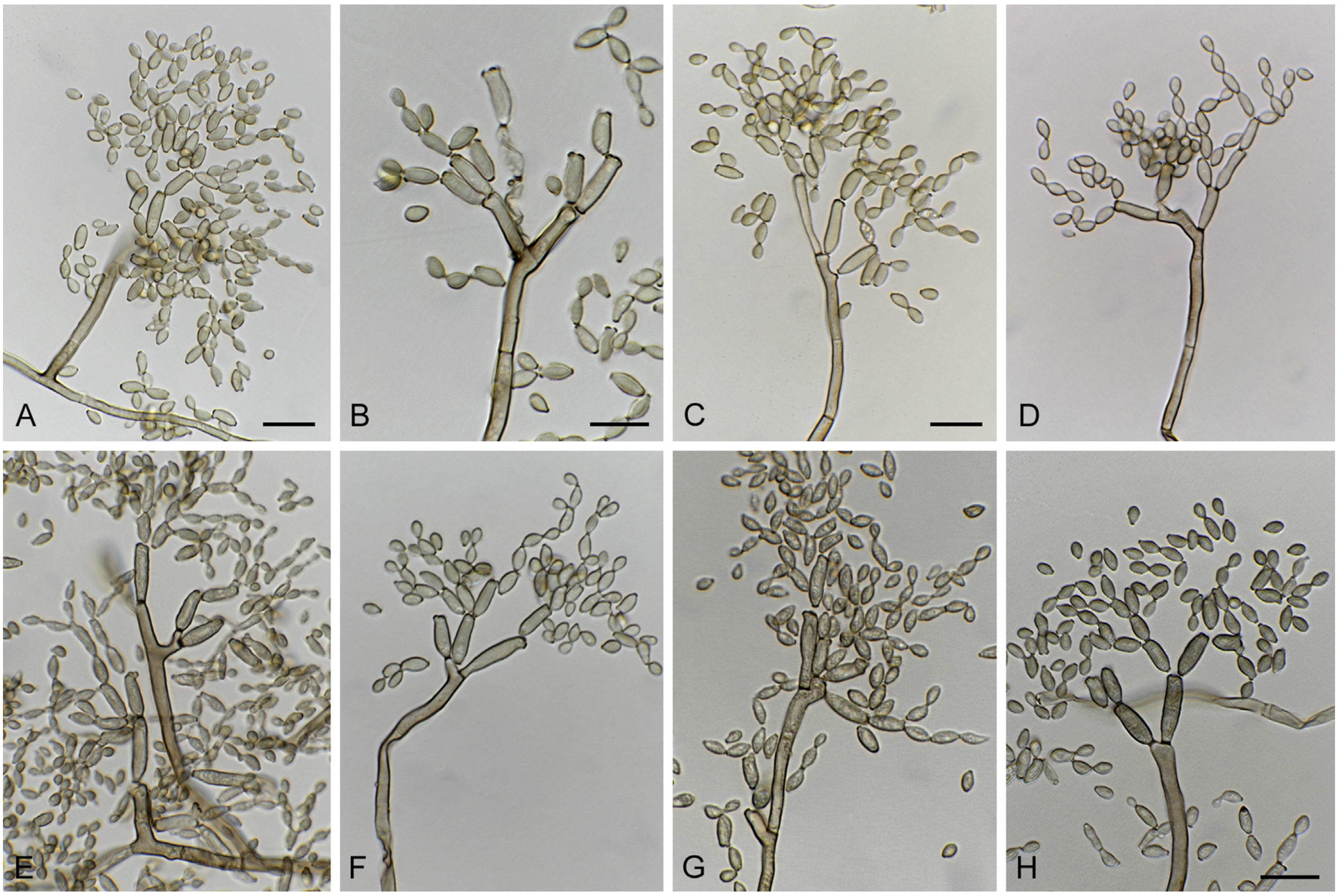


Fig. 21. *Cladosporium chasmanthicola* (ex-type CBS 142612). **A–H.** Conidiophores and conidial chains. Scale bars = 10 µm; C applies to C–G.

outline due to numerous hila crowded at or towards the distal end, sometimes located on lateral shoulders or lateral prolongations, those formed on micronematous conidiophores shorter and narrower, (5–)8–23 × (2.5–)3–4.5 µm (av. ± SD: 13.3 ± 5.4 × 3.5 ± 0.6), 0–1(–3)-septate, very pale olivaceous or pale olivaceous brown, smooth, walls unthickened, with (2–)3–6(–7) distal scars; *hila* conspicuous, 0.5–2 µm diam, darkened-refractive and somewhat thickened; *conidia* sometimes germinating.

Culture characteristics: Colonies on PDA reaching 28–35 mm diam after 2 wk, olivaceous grey, grey olivaceous with several smoke-grey patches of dense, felty aerial mycelium, reverse leaden-grey to olivaceous grey, powdery, margin white, broad, glabrous, colony centre somewhat folded and wrinkled, growth flat. Colonies on MEA attaining 29–35 mm diam, whitish, smoke-grey to pale olivaceous grey, reverse greyish sepia or olivaceous grey, velvety; margin glabrous, to somewhat feathery, radially furrowed, colony centre elevated, wrinkled and folded; aerial mycelium abundant, covering large parts of the colony surface, dense, fluffy. Colonies on OA reaching 20–28 mm diam, olivaceous grey with patches of smoke-grey, grey olivaceous or glaucous-grey towards margins, reverse leaden-grey to iron-grey, fluffy-felty; margin glabrous, undulate, colony centre somewhat elevated; aerial mycelium loose, diffuse to dense and fluffy in a few spots. On all media without prominent exudates, sporulation profuse.

Material examined: **South Africa**, Western Cape Province, Cape Town, Brackenfell, Bracken Nature Reserve, isol. from leaf spots on *Chasmanthe aethiopica*, 25 Sep. 2012, A.R. Wood (**holotype** CBS H-23117, culture ex-type CBS 142612 = CPC 21300).

Note: *Cladosporium chasmanthicola* is closely related to *Cl. acalyphae*, but the latter species has much longer and narrower conidiophores (150–430 × 3–4 µm) and smooth to loosely verruculose, irregularly verruculose-rugose or rough-walled conidia (Bensch *et al.* 2010).

Cladosporium kenpeggii Bensch, U. Braun & Crous, **sp. nov.** MycoBank MB819979. Fig. 22.

Etymology: Named after Dr Ken Pegg (Agri-Science and Biosecurity Queensland, Australia), the collector of the species, who celebrates his 80th birthday this year.

On SNA: *Superficial mycelium* sparingly formed, unbranched, occasionally branched, 2.5–3.5 µm wide, septate, without swellings and constrictions, pale olivaceous brown, almost smooth to verruculose. *Conidiophores* macronematous, solitary, arising mostly terminally, rarely laterally from hyphae, narrowly cylindrical-oblong, usually unbranched, non-nodulose, sometimes slightly geniculate towards the apex, 15–100(–150) × 2.5–4 µm, 0–2(–5)-septate, pale to medium olivaceous brown, smooth or minutely verruculose, walls unthickened or slightly thickened. *Conidiogenous cells* integrated, mainly terminally, narrowly cylindrical-oblong, 16–60 µm long, with (1–)2–3(–4) distal conidiogenous loci, crowded at or towards the apex, sometimes slightly geniculate due to sympodial proliferation, conidiogenous loci conspicuous, 1–2 µm diam,

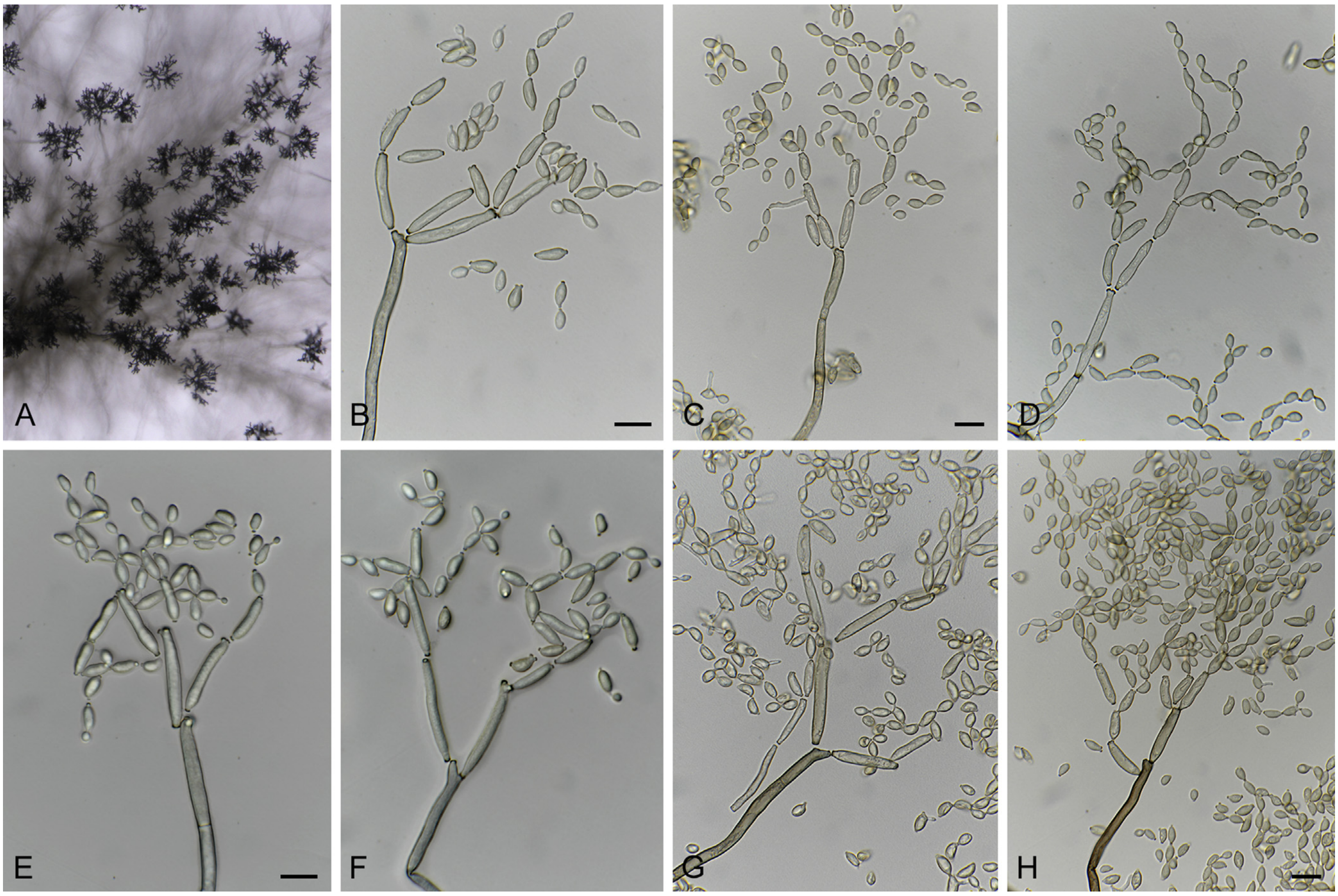


Fig. 22. *Cladosporium kenpeggii* (ex-type CBS 142613). **A.** Part of the colony on SNA. **B–H.** Conidiophores and conidial chains. Note the microcyclic conidiogenesis in C, forming a secondary conidiophore at a still attached conidium with giving rise to secondary conidia and the germinating conidia in C and G. Scale bars = 10 µm; C applies to C, D; E applies to E–G.

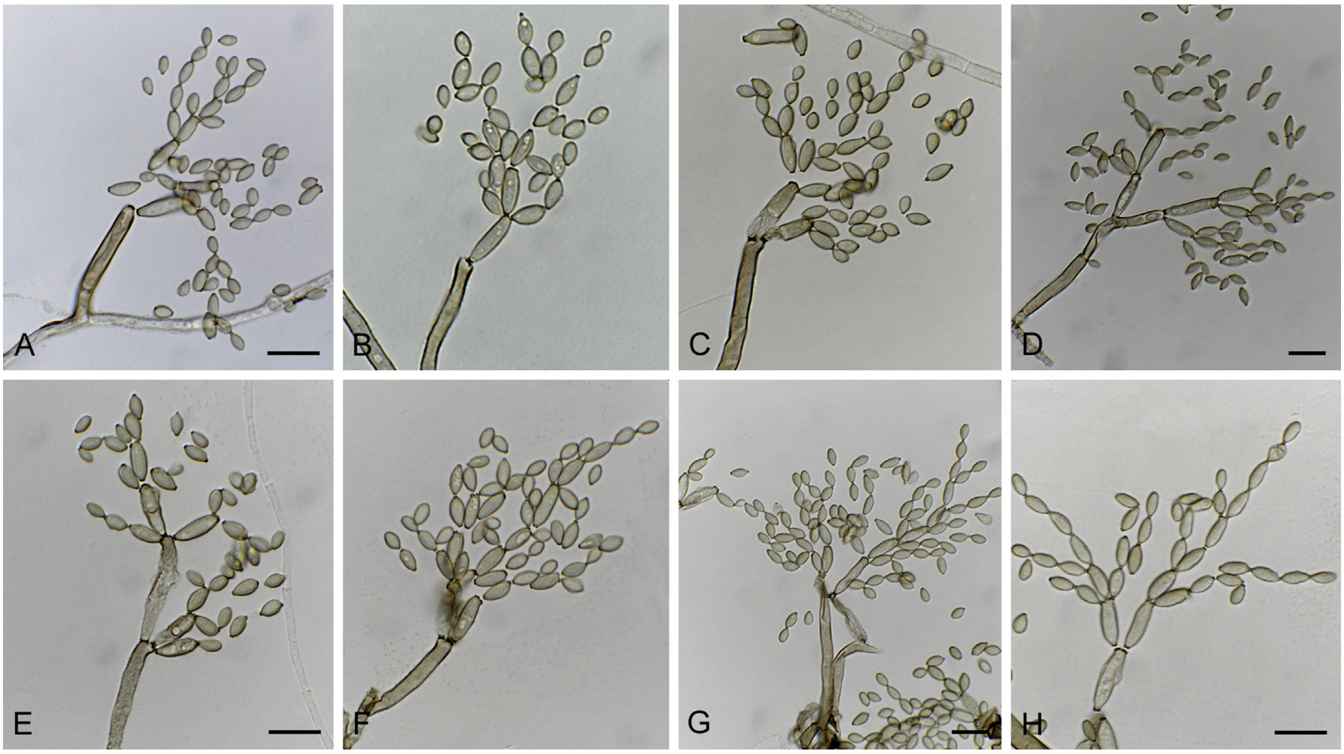
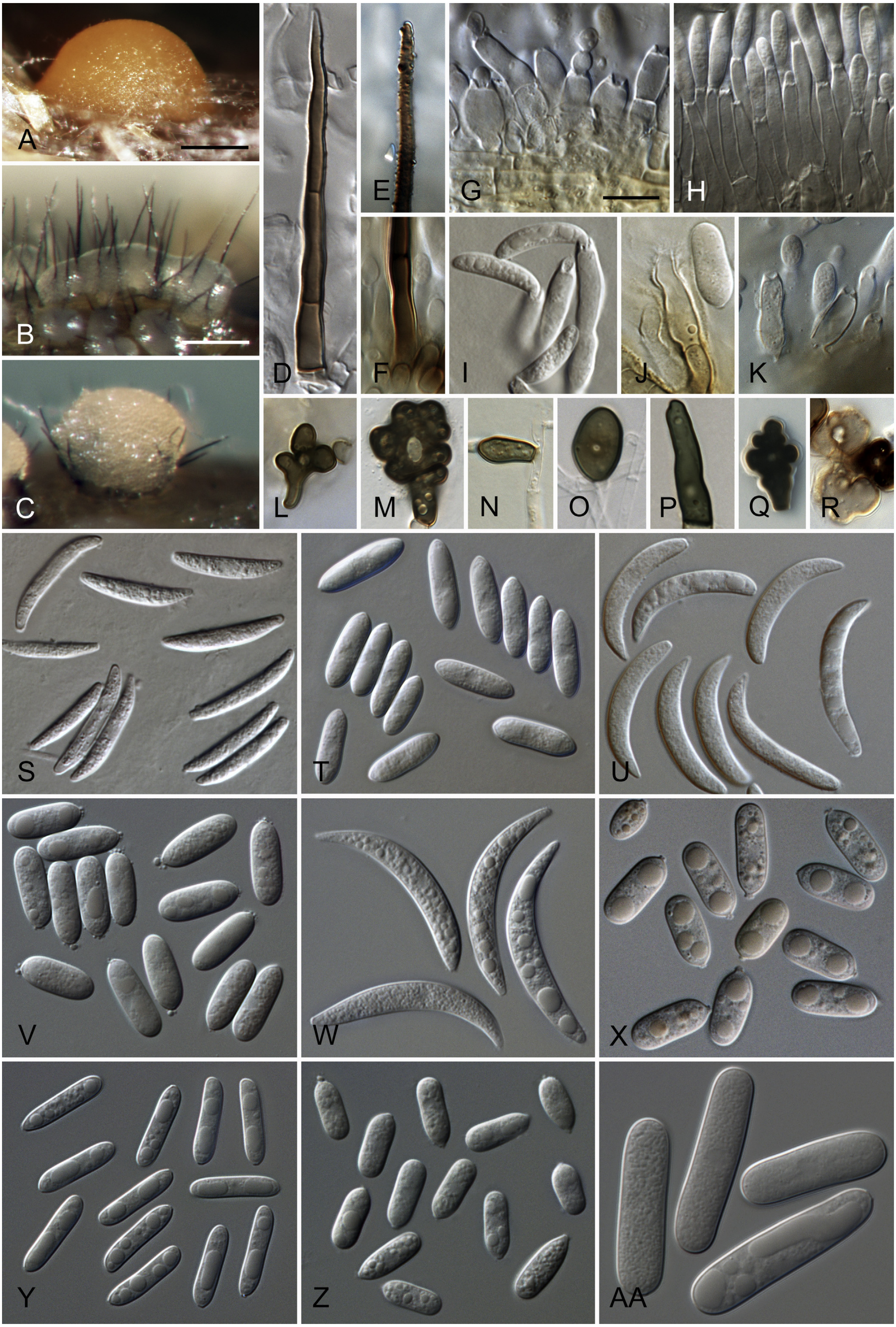


Fig. 23. *Cladosporium welwitschiicola* (ex-type CBS 142614). **A–G.** Conidiophores and conidial chains. **H.** Conidial chain. Scale bars = 10 µm; A applies to A–C; E applies to E, F.


A
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thickened and darkened-refractive, sometimes cells germinating. *Ramoconidia* frequently formed, (17–)25–55 × 3–4(–5) µm, 0–1(–2)-septate, base broadly truncate, 2–4 µm wide, unthickened, somewhat darkened-refractive. *Conidia* numerous, formed in branched chains, branching in all directions, up to eight conidia in the terminal unbranched part of the chain; *small terminal conidia* obovoid or ellipsoid, 4.5–6 × (2–)2.5–3(–3.5) µm (av. ± SD: 5.0 ± 0.5 × 2.7 ± 0.5), apex rounded; *intercalary conidia* ovoid or ellipsoid, 5.5–15 × (2–)2.5–3.5 µm (av. ± SD: 8.9 ± 3.2 × 3.0 ± 0.4), aseptate, with 1–2 distal hila, attenuated towards apex and base; *secondary ramoconidia* subcylindrical or cylindrical, 14.5–35 × 3–4(–5) µm (av. ± SD: 22.4 ± 5.8 × 3.8 ± 0.6), 0–1(–2)-septate, with 2–3 distal hila, pale olivaceous or pale olivaceous brown, smooth, walls slightly thickened; *hila* conspicuous, subdenticulate, 1–2 µm diam, somewhat thickened and darkened-refractive; *microcyclic conidiogenesis* occurring, conidia often germinating, often with more than one germination tube, tubes sometimes even branched, filiform or irregular in outline.

Culture characteristics: Colonies on PDA attaining 35–47 mm diam after 2 wk, olivaceous to olivaceous grey, dull green towards margins, reverse iron-grey, greyish blue towards margins, powdery to fluffy, margin feathery, growth flat, aerial mycelium loose, diffuse, dense, fluffy and high in a few spots, pale olivaceous grey, sporulation profuse, without prominent exudates. Colonies in MEA reaching 39–48 mm diam, grey olivaceous, reverse iron-grey, velvety, margin white, broad, feathery, colony centre elevated, wrinkled and folded, radially furrowed, aerial mycelium loose, diffuse to denser and fluffy, several small but prominent exudates formed, sporulation profuse. Colonies on OA grey olivaceous when sporulating profusely, whitish or smoke-grey due to aerial mycelium, reverse lead-grey or iron-grey, some parts with a cinnamon margin (both on top and reverse), powdery to fluffy-felty, aerial mycelium forming high strains, growth flat, without exudates.

Material examined: **Australia**, New South Wales, Upper Dungay, 28°15′ S 153°21′ E, isol. from leaves of *Passiflora edulis*, 20 Oct. 1999, K.G. Pegg & J. Dawes, FP 24737 (**holotype** BRIP 26701a, isotype CBS H-23118, culture ex-type CBS 142613 = CPC 19248 = BRIP 26701a).

Notes: The smooth conidia formed in long branched chains and the frequently formed ramoconidia remind one of *Cl. cladosporioides* and *Cl. iranicum*. However, compared with *Cl. cladosporioides*, *Cl. kenpeggii* possesses much shorter macronematous conidiophores, micronematous conidiophores are not formed and the conidia are very often germinating and forming secondary conidiophores. In *Cl. iranicum* the conidia also germinate quite often, but the conidiophores are longer, ramoconidia are shorter and somewhat wider with a narrower base and intercalary conidia are shorter and narrower (Bensch *et al.* 2012).

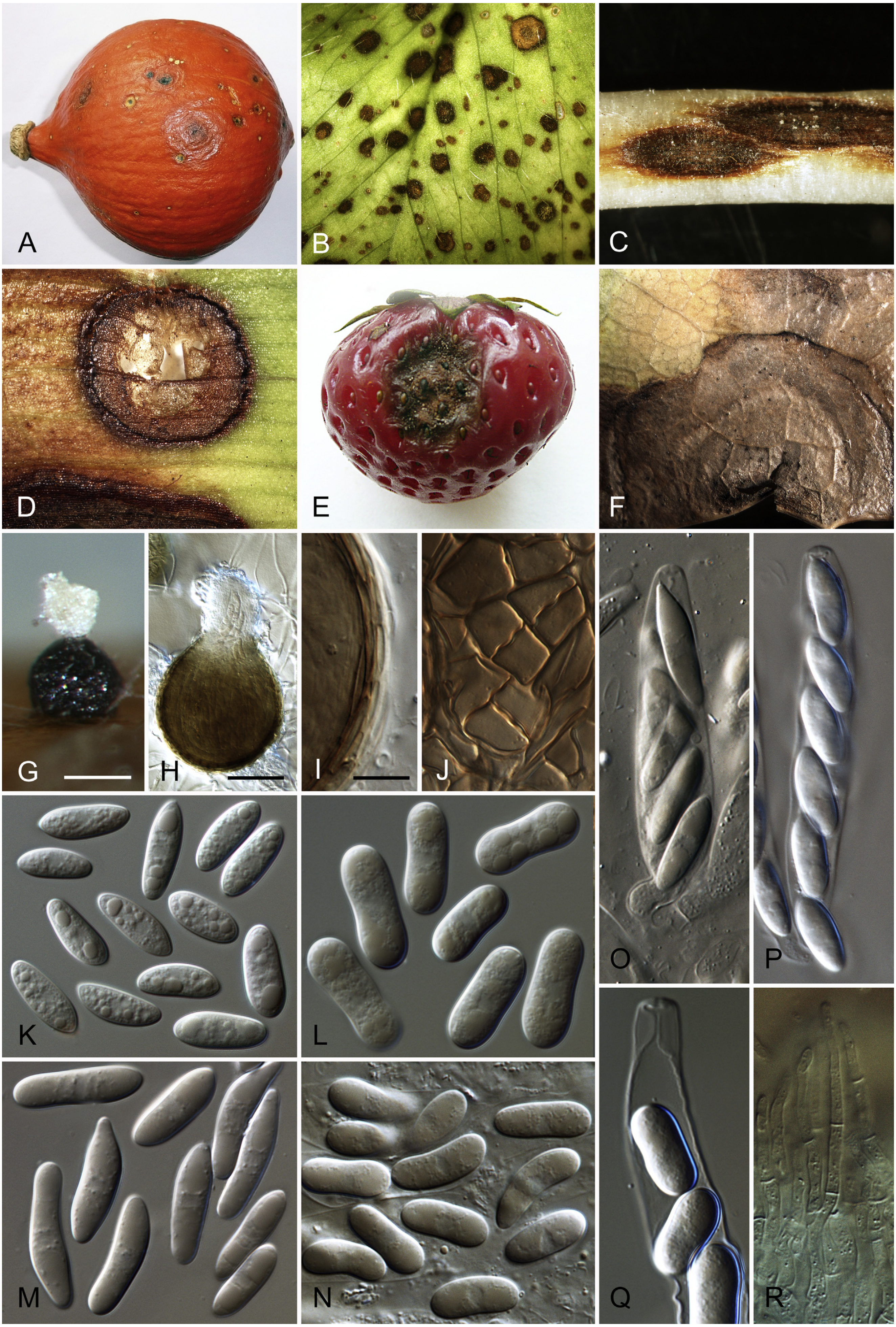
Cladosporium maracuja, described from *Passiflora* in Brazil in 1935, is morphologically quite similar in having smooth, catenate, 0–1-septate conidia and short conidiophores but since it is only known from the type specimen it is kept separate. The conidia of this species are shorter and wider and the conidiophores wider *in vivo*.

Cladosporium welwitschiicola Bensch, U. Braun & Crous, **sp. nov.** MycoBank MB819980. Fig. 23.

Etymology: Epithet composed of the name of the host genus, *Welwitschia*, and -cola, dweller.

On SNA: *Superficial mycelium* abundantly formed, filiform to cylindrical-oblong, unbranched or loosely branched, (0.5–)1–4 µm wide, sometimes slightly swollen or constricted, septate, subhyaline, pale olivaceous or pale olivaceous brown, surface ornamentation variable, smooth or almost so, asperulate, verruculose or sometimes even verrucose, walls unthickened, sometimes forming ropes of several hyphae. *Conidiophores* macronematous, solitary, erect, straight or slightly flexuous, terminally or laterally formed from hyphae, narrowly cylindrical-oblong, non-nodulose, occasionally once geniculate towards the apex due to sympodial proliferation, 25–90 × (2.5–)3–4.5(–5.5) µm, 0–3(–4)-septate, not constricted at septa, pale to medium olivaceous brown, smooth, sometimes verruculose or irregularly rough-walled towards the base, walls thickened. *Conidiogenous cells* integrated, usually terminal, cylindrical, 12.5–42 µm long, with 2–4 conidiogenous loci crowded at the apex, conspicuous, subdenticulate, 1–2 µm diam, somewhat thickened and darkened-refractive. *Ramoconidia* not observed. *Conidia* catenate, in branched chains, branching in all directions, (1–)2–5(–6) conidia in the terminal unbranched part of the chain; *small terminal conidia* obovoid, ellipsoid, 4–5 × 2.5–3.5 µm (av. ± SD: 4.6 ± 0.6 × 3.0 ± 0.4), rugulose, broadly rounded at the apex; *intercalary conidia* ellipsoid, limoniform or fusiform, sometimes irregular in outline due to surface ornamentation, slightly to distinctly attenuated towards apex and base, 5–11 × (2.5–)3–3.5(–4) µm (av. ± SD: 7.4 ± 1.9 × 3.2 ± 0.4), 0–1-septate, with 1–3 distal hila, rugulose to distinctly rugose; *secondary ramoconidia* ellipsoid or subcylindrical, often 3–4 formed at the apex of conidiophores, 8.5–21 × 3–4(–4.5) µm (av. ± SD: 14.6 ± 3.6 × 3.5 ± 0.4), 0–2(–3)-septate, mostly 1-septate, septum median or somewhat in the lower half, pale to medium olivaceous brown or dingy brown, smooth or almost so to rugulose, walls somewhat thickened; *hila* conspicuous, 0.5–2 µm diam; *microcyclic conidiogenesis* not occurring.

Fig. 24. *Colletotrichum* spp. **A–AA.** Asexual morphs. **A–C.** Conidiomata. **A.** *Colletotrichum acutatum* (ex-type CBS 112996). **B.** *Colletotrichum destructivum* (ex-type CBS 136228). **C.** *Colletotrichum cymbidiicola* (ex-type IMI 347923). **D.** Seta of *Colletotrichum torulosum* (ex-type CBS 128544). **E.** Tip of a seta of *Colletotrichum gloeosporioides* (ex-type CBS 112999). **F.** Basis of a seta of *Colletotrichum gloeosporioides* (ex-type CBS 112999). **G–K.** Conidiogenous cells. G. *Colletotrichum brasiliense* (ex-type CBS 128501). **H.** *Colletotrichum scovillei* (ex-type CBS 126529). **I.** *Colletotrichum tofieldiae* (CBS 495.85). **J.** *Colletotrichum petchii* (ex-type CBS 378.94). **K.** *Colletotrichum gloeosporioides* (ex-type CBS 112999). **L–R.** Appressoria. **L.** *Colletotrichum americae-borealis* (CBS 136855). **M.** *Colletotrichum graminicola* (ex-epitype CBS 130836). **N.** *Colletotrichum gloeosporioides* (ex-type CBS 112999). **O.** *Colletotrichum laticiphilum* (ex-type CBS 112989). **P.** *Colletotrichum phormii* (ex-type CBS 118194). **Q.** *Colletotrichum liriopes* (ex-type CBS 119444). **R.** *Colletotrichum truncatum* (ex-type CBS 151.35). **S–AA.** Conidia of the ex-type strains of the name-giving species of nine *Colletotrichum* species complexes. **S.** *Colletotrichum dematium* (ex-type CBS 125.25). **T.** *Colletotrichum acutatum* (ex-type CBS 112996). **U.** *Colletotrichum truncatum* (ex-type CBS 151.35). **V.** *Colletotrichum gloeosporioides* (ex-type CBS 112999). **W.** *Colletotrichum graminicola* (ex-epitype CBS 130836). **X.** *Colletotrichum boninense* (ex-type CBS 123755). **Y.** *Colletotrichum destructivum* (ex-type CBS 136228). **Z.** *Colletotrichum orbiculare* (ex-type CBS 570.97). **AA.** *Colletotrichum gigasporum* (ex-type CBS 133266). A–C, E–H, K. from *Anthriscus* stem. D, I, J, L–AA. from SNA. Scale bars: A = 200 µm; B applies to B, C = 100 µm; G applies to D–AA = 10 µm. A–AA Pictures taken by U. Damm; A, H, O–P, T from Damm *et al.* (2012b); B, L, Y from Damm *et al.* (2014); C, D, G, J, X from Damm *et al.* (2012a); I, Q–S, U from Damm *et al.* (2009); Z from Damm *et al.* (2013).


A
B
C
D
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Culture characteristics: Colonies on PDA reaching up to 78 mm diam after 2 wk, olivaceous grey, fawn at margins, reverse mouse-grey, vinaceous-buff at margins, fluffy; margins feathery, growth low convex. Colonies on MEA reaching up to 80 mm diam, smoke-grey, pale olivaceous grey to olivaceous grey, reverse iron-grey, fluffy; margin feathery. Colonies on OA reaching up to 72 mm diam, smoke-grey and pale olivaceous grey, reverse iron-grey, fluffy. On all three media aerial mycelium abundantly formed covering large parts of the colony, loose to dense, high, fluffy; without prominent exudates, sporulation profuse.

Material examined: **Namibia**, isol. from dead leaf of *Welwitschia mirabilis*, 1 Oct. 2010, M.J. Wingfield (**holotype** CBS H-23119, culture ex-type CBS 142614 = CPC 18648).

Notes: With its rugulose or distinctly rugose conidia and relatively short conidiophores, *Cl. welwitschiicola* reminds one of *Cl. exasperatum* and *Cl. verrucocladosporioides*, but the latter two species differ in forming ramoconidia and in having longer and slightly wider small, intercalary and secondary ramoconidia. Phylogenetically, it is closest to *Cl. gamsianum* and *Cl. pseudocladosporioides*, but these species are easily distinguishable in having smooth and narrower conidia (Bensch *et al.* 2012).

Authors: K. Bensch, U. Braun, J.Z. Groenewald & P.W. Crous

Colletotrichum Corda, in Sturm, Deutschl. Fl., 3 Abt. (Pilze Deutschl.) 3: 41, tab. 21. 1831. Figs 24, 25.
Synonyms: *Glomerella* Spauld. & H. Schrenk, Science, N.Y. 17: 751. 1903.
For additional synonyms see Sutton (1980).

Classification: *Sordariomycetes*, *Hypocreomycetidae*, *Glomerellales*, *Glomerellaceae.*

Type species: *Colletotrichum lineola* Corda. Holotype: PRM 155463. Epitype and ex-epitype culture: CBS H-20362, CBS 125337.

DNA barcodes (genus): ITS.

DNA barcodes (species): *act*, *ApMat*, *apn2*, *cal*, *chs-1*, *gapdh*, *gs*, *his3*, *sod2*, *tub2*. Tables 6, 7. Fig. 26.

Ascomata solitary or gregarious, globose to subglobose, dark brown to black, ostiole periphysate; *ascomatal wall* composed of pale to medium brown flattened cells of *textura angularis*. *Hamathecium* composed of hyaline, septate paraphyses, branched at the bases, rounded at the tips. *Asci* 8-spored, unitunicate, cylindrical to subfusoid, short pedicellate, with an inamyloid, refractive ring at the apex. *Ascospores* uni- to biseriate, aseptate, hyaline, smooth-walled, cylindrical, oval, fusiform or rhomboid, straight or curved, one end ± acute and one end rounded or both ends rounded. *Conidiomata* acervular, conidiophores and setae formed on cushions of pale to medium brown, roundish to angular cells, but very variable in culture, ranging from sporodochia-like aggregations of conidiophores directly on hyphae to closed conidiomata that open by rupture. *Setae* may or may not be present, straight, pale to dark brown, sometimes hyaline towards the tip, smooth-walled, verruculose to verrucose, 1–8-septate, base cylindrical, conical or slightly inflated, tip ± rounded to ± acute. *Conidiophores* hyaline to pale brown, simple or septate, branched or unbranched, smooth-walled, sometimes verruculose. *Conidiogenous cells* enteroblastic, hyaline to pale brown, smooth-walled, discrete, cylindrical, ellipsoidal, doliiform or ampulliform, collarette usually distinct, periclinal thickening visible to conspicuous, sometimes extending to form new conidiogenous loci (percurrent) or surrounded by a gelatinous coating. *Conidia* hyaline, smooth-walled, aseptate, cylindrical, clavate, fusiform, sometimes ellipsoidal to ovoid, straight or curved, apex rounded to acute, sometimes with a filiform appendage, base rounded to truncate, sometimes with a prominent hilum. *Appressoria* single or in small groups, pale to dark brown, with a globose, elliptical, clavate, navicular or irregular outline and an entire, undulate or lobate edge.

Culture characteristics: Colonies on PDA flat, with an entire to irregular margin, grey to dark in centre, aerial mycelium, if present, sparse to cottony, white, buff or pale olivaceous green in colour. Reverse first white, with age turning grey to black, olivaceous green or smoke-grey, concentric rings can be observed. Conidia in mass orange, salmon, pink, white or pale grey. Colonies on SNA flat, with an entire, erose, dentate or undulate margin, aerial mycelium, if present, hyaline, white, honey colour, iron-grey, greenish black or dark olivaceous. Reverse hyaline, honey, pale olivaceous grey to iron-grey. Colonies on OA flat, with an entire to umbonate margin, aerial mycelium, if present, white, buff, rosy-buff, very pale glaucous, hyaline or honey coloured. Reverse buff, rosy-buff, flesh, pale luteous, honey coloured, smoke-grey or olivaceous grey. Conidia in mass salmon, saffron, orange, white or rosy-buff.

Optimal media and cultivation conditions: For morphological examinations of the asexual morphs SNA amended with double autoclaved stems of *Anthriscus sylvestris* (wild chervil) and autoclaved filter paper placed onto the agar surface and incubated under near-ultraviolet light with a 12 h photoperiod at 20 °C for 10 d proved to be best suited to promote sporulation of most of the species, while for other species, culturing on OA or PDA incubated under the same conditions is more suitable.

Fig. 25. A–F. Disease symptoms caused by *Colletotrichum* spp. **A.** Anthracnose on fruit of *Cucurbita maxima* cv. Red Hokkaido caused by *Colletotrichum coccodes*. **B.** Leaf spot of red clover caused by *Colletotrichum utrechtense*. **C.** Anthracnose on bean hypocotyl caused by *Colletotrichum lindemuthianum*. **D.** Leaf spot of *Paphiopedilum* sp. caused by *Colletotrichum arxii*. **E.** Anthracnose on strawberry fruit caused by *Colletotrichum nymphaeae*. **F.** Leaf spot of *Mahonia aquifolium* caused by *Colletotrichum godetiae*. **G–R.** Sexual morphs of *Colletotrichum* spp. G, H. Ascomata. G. *Colletotrichum petchii* (ex-type CBS 378.94). **H.** *Colletotrichum karstii* (CBS 127597). I. Peridium in cross section of *Colletotrichum karstii* (CBS 127597). **J.** Outer surface of peridium of *Colletotrichum constrictum* (ex-type CBS 128504). **K–N.** Ascospores. **K.** *Colletotrichum salicis* (ex-type CBS 607.94). **L.** *Colletotrichum constrictum* (ex-type CBS 128504). **M.** *Colletotrichum cymbidiicola* (ex-type IMI 347923). **N.** *Colletotrichum parsonsiae* (ex-type CBS 128525). **O–Q.** Asci. **O.** *Colletotrichum cymbidiicola* (ex-type IMI 347923). **P.** *Colletotrichum salicis* (ex-type CBS 607.94). **Q.** *Colletotrichum constrictum* (ex-type CBS 128504). **R.** Paraphyses of *Colletotrichum salicis* (ex-type CBS 607.94). G, K, M, O–R. from *Anthriscus* stem. H–J, L, N. from SNA. Scale bars: G = 100 µm; H = 50 µm; I applies to I–R = 10 µm. A–R Pictures taken by U. Damm; E from Cannon *et al.* (2012); G–J, L–O, Q from Damm *et al.* (2012a); K, P, R from Damm *et al.* (2012b).

Table 6. DNA barcodes of accepted *Colletotrichum* spp. except for species in the *Col. graminicola* and *caudatum* complexes.

Species	**Isolates**[1]	**GenBank accession numbers**[2]										**References**
		ITS	***gapdh***	***chs-1***	***his3***	***act***	***tub2***	***cal***	***gs***	***sod2***	***ApMat***	
Colletotrichum abscissum	COAD 1877^{T}	KP843126	KP843129	KP843132	KP843138	KP843141	KP843135	–	–	–	–	Crous *et al.* (2015d)
Col. acerbum	CBS 128530^{T}	JQ948459	JQ948790	JQ949120	JQ949450	JQ949780	JQ950110	–	–	–	–	Damm *et al.* (2012b)
Col. acutatum	CBS 112996^{T}	JQ005776	JQ948677	JQ005797	JQ005818	JQ005839	JQ005860	–	–	–	–	Damm *et al.* (2012b)
Col. aenigma	ICMP 18608^{T}	JX010244	JX010044	JX009774	–	JX009443	JX010389	JX009683	JX010078	JX010311	KM360143	Weir *et al.* (2012)
Col. aeschynomenes	ICMP 17673^{T}	JX010176	JX009930	JX009799	–	JX009483	JX010392	JX009721	JX010081	JX010314	–	Weir *et al.* (2012)
Col. agaves	CBS 118190	DQ286221	–	–	–	–	–	–	–	–	–	Farr *et al.* (2006)
Col. alatae	ICMP 17919^{T}	JX010190	JX009990	JX009837	–	JX009471	JX010383	JX009738	JX010065	JX010305	KC888932	Weir *et al.* (2012)
Col. alienum	ICMP 12071^{T}	JX010251	JX010028	JX009882	–	JX009572	JX010411	JX009654	JX010101	JX010333	KM360144	Weir *et al.* (2012)
Col. americae-borealis	CBS 136232^{T}	KM105224	KM105579	KM105294	KM105364	KM105434	KM105504	–	–	–	–	Damm *et al.* (2014)
Col. annellatum	CBS 129826^{T}	JQ005222	JQ005309	JQ005396	JQ005483	JQ005570	JQ005656	JQ005743	–	–	–	Damm *et al.* (2012a)
Col. anthrisci	CBS 125334^{T}	GU227845	GU228237	GU228335	GU228041	GU227943	GU228139	–	–	–	–	Damm *et al.* (2009)
Col. antirrhinicola	CBS 102189^{T}	KM105180	KM105531	KM105250	KM105320	KM105390	KM105460	–	–	–	–	Damm *et al.* (2014)
Col. aotearoa	ICMP 18537^{T}	JX010205	JX010005	JX009853	–	JX009564	JX010420	JX009611	JX010113	JX010345	KC888930	Weir *et al.* (2012), Sharma *et al.* (2015)
Col. aracearum	CGMCC 3.14983 ^{T}	KX853167	KX893586			KX893578	KX893582					Hou *et al.* (2016)
Col. arxii	CBS 132511^{T}	KF687716	KF687843	KF687780	KF687858	KF687802	KF687881	KF687819	KF687756	–	–	Liu *et al.* (2014)
Col. asianum	ICMP 18580^{T}	FJ972612	JX010053	JX009867	–	JX009584	JX010406	FJ917506	JX010096	JX010328	FR718814	Prihastuti *et al.* (2009), Silva *et al.* (2012), Weir *et al.* (2012)
Col. australe	CBS 116478^{T}	JQ948455	JQ948786	JQ949116	JQ949446	JQ949776	JQ950106	–	–	–	–	Damm *et al.* (2012b)
Col. beeveri	CBS 128527^{T}	JQ005171	JQ005258	JQ005345	JQ005432	JQ005519	JQ005605	JQ005692	–	–	–	Damm *et al.* (2012a)
Col. bidentis	COAD 1020^{T}	KF178481	KF178506	KF178530	KF178554	KF178578	KF178602	–	KF178627	–	–	Damm *et al.* (2013)
Col. bletillum	CGMCC 3.15117^{T}	JX625178	KC843506	–	–	KC843542	JX625207	–	–	–	–	Tao *et al.* (2013)
Col. boninense	CBS 123755^{T}	JQ005153	JQ005240	JQ005327	JQ005414	JQ005501	JQ005588	JQ005674	–	–	–	Damm *et al.* (2012a)
Col. brasiliense	CBS 128501^{T}	JQ005235	JQ005322	JQ005409	JQ005496	JQ005583	JQ005669	JQ005756	–	–	–	Damm *et al.* (2012a)
Col. brassicola	CBS 101059^{T}	JQ005172	JQ005259	JQ005346	JQ005433	JQ005520	JQ005606	JQ005693	–	–	–	Damm *et al.* (2012a)
Col. brevisporum	BCC 38876^{T}	JN050238	JN050227	KF687760	–	JN050216	JN050244	–	–	–	–	Noireung *et al.* (2012)
Col. brisbanense	CBS 292.67^{T}	JQ948291	JQ948621	JQ948952	JQ949282	JQ949612	JQ949942	–	–	–	–	Damm *et al.* (2012b)
Col. bryoniicola	CBS 109849^{T}	KM105181	KM105532	KM105251	KM105321	KM105391	KM105461	–	–	–	–	Damm *et al.* (2014)
Col. cairnsense	BRIP 63642^{T}	KU923672	KU923704	KU923710	KU923722	KU923716	KU923688	–	–	–	–	De Silva *et al.* (2017)
Col. camelliae	CGMCC 3.14925^{T}	KJ955081	KJ954782	–	–	KJ954363	KJ955230	KJ954634	KJ954932	–	KJ954497	Liu *et al.* (2015b)
Col. camelliae-japonicae	CGMCC3.18118^{T}	KX853165	KX893584			KX893576	KX893580					Hou *et al.* (2016)
Col. carthami	SAPA100011^{T}	AB696998	–	–	–	–	AB696992	–	–	–	–	Damm *et al.* (2012b), Uematsu *et al.* (2012)

Col. changpingense	MFLUCC 15-0022	KP683152	KP852469	KP852449	–	KP683093	KP852490	–	–	–	–	Jayawardena *et al.* (2016a)
Col. chlorophyti	IMI 103806^{T}	GU227894	GU228286	GU228384	GU228090	GU227992	GU228188	–	–	–	–	Damm *et al.* (2009)
Col. chrysanthemi	SAPA100010	AB696999					AB696993	–	–	–	–	Uematsu *et al.* (2012), Damm *et al.* (2012b)
Col. circinans	CBS 221.81^{T}	GU227855	GU228247	GU228345	GU228051	GU227953	GU228149	–	–	–	–	Damm *et al.* (2009)
Col. citri	CBS 134233^{T}	KC293581	KC293741	–	–	KC293621	KC293661	KC293701	KC293781	–	–	Huang *et al.* (2013)
Col. citricola	CBS 134228^{T}	KC293576	KC293736	KC293792	–	KC293616	KC293656	KC293696	KC293776	–	–	Huang *et al.* (2013)
Col. clidemiae	ICMP 18658^{T}	JX010265	JX009989	JX009877	–	JX009537	JX010438	JX009645	JX010129	JX010356	KC888929	Weir *et al.* (2012)
Col. cliviae	CBS 125375^{T}	GQ485607	GQ856756	GQ856722	JX560963	GQ856777	GQ849440	–	–	–	–	Yang *et al.* (2009), Cannon *et al.* (2012)
Col. coccodes	CBS 369.75^{T}	HM171679	HM171673	JX546681	JX546779	HM171667	JX546873	–	–	–	–	Liu *et al.* (2011, 2013a)
Col. colombiense	CBS 129818^{T}	JQ005174	JQ005261	JQ005348	JQ005435	JQ005522	JQ005608	JQ005695	–	–	–	Damm *et al.* (2012a)
Col. conoides	CGMCC 3.17615^{T}	KP890168	KP890162	KP890156		KP890144	KP890174	KP890150				Diao *et al.* (2017)
Col. constrictum	CBS 128504^{T}	JQ005238	JQ005325	JQ005412	JQ005499	JQ005586	JQ005672	JQ005759	–	–	–	Damm *et al.* (2012a)
Col. cordylinicola	ICMP 18579^{T}	JX010226	JX009975	JX009864	–	HM470235	JX010440	HM470238	JX010122	JX010361	JQ899274	Weir *et al.* (2012)
Col. cosmi	CBS 853.73^{T}	JQ948274	JQ948604	JQ948935	JQ949265	JQ949595	JQ949925	–	–	–	–	Damm *et al.* (2012b)
Col. costaricense	CBS 330.75^{T}	JQ948180	JQ948510	JQ948841	JQ949171	JQ949501	JQ949831	–	–	–	–	Damm *et al.* (2012b)
Col. curcumae	IMI 288937^{T}	GU227893	GU228285	GU228383	GU228089	GU227991	GU228187	–	–	–	–	Damm *et al.* (2009)
Col. cuscutae	IMI 304802^{T}	JQ948195	JQ948525	JQ948856	JQ949186	JQ949516	JQ949846	–	–	–	–	Damm *et al.* (2012b)
Col. cymbidiicola	IMI 347923^{T}	JQ005166	JQ005253	JQ005340	JQ005427	JQ005514	JQ005600	JQ005687	–	–	–	Damm *et al.* (2012a)
Col. dacrycarpi	CBS 130241^{T}	JQ005236	JQ005323	JQ005410	JQ005497	JQ005584	JQ005670	JQ005757	–	–	–	Damm *et al.* (2012a)
Col. dematium	CBS 125.25^{T}	GU227819	GU228211	GU228309	GU228015	GU227917	GU228113	–	–	–	–	Damm *et al.* (2009)
Col. destructivum	CBS 136228^{T}	KM105207	KM105561	KM105277	KM105347	KM105417	KM105487	–	–	–	–	Damm *et al.* (2014)
Col. dracaenophilum	CBS 118199^{T}	DQ286209, JX519222	JX546707	JX519230	JX546756	JX519238	JX519247	–	–	–	–	Cannon *et al.* (2012), Farr *et al.* (2006)
Col. endophytica	MFLUCC 13–0418^{T}	KC633854	KC832854	–	–	KF306258	–	KC810018	–	–	–	Manamgoda *et al.* (2013)
Col. euphorbiae	CBS 134725^{T}	KF777146	KF777131	KF777128	KF777134	KF777125	KF777247	–	–	–	–	Crous *et al.* (2013b)
Col. excelsum-altitudum	CGMCC 3.15130^{T}	HM751815	KC843502	–	–	KC843548	JX625211	–	–	–	–	Tao *et al.* (2013)
Col. fioriniae	CBS 128517^{T}	JQ948292	JQ948622	JQ948953	JQ949283	JQ949613	JQ949943	–	–	–	–	Damm *et al.* (2012b)
Col. fructi	CBS 346.37^{T}	GU227844	GU228236	GU228334	GU228040	GU227942	GU228138	–	–	–	–	Damm *et al.* (2009)
Col. fructicola	ICMP 18581^{T}	JX010165	JX010033	JX009866	–	FJ907426	JX010405	FJ917508	JX010095	JX010327	JQ807838	Weir *et al.* (2012)
Col. fructivorum	CBS 133125^{T}	JX145145	–	–	–	–	JX145196	–	–	–	JX145300	Doyle *et al.* (2013)
Col. fuscum	CBS 133701^{T}	KM105174	KM105524	KM105244	KM105314	KM105384	KM105454	–	–	–	–	Damm *et al.* (2014)
Col. fusiforme	MFLUCC 12–0437^{T}	KT290266	KT290255	KT290253	–	KT290251	KT290256	–	–	–	–	Ariyawansa *et al.* (2015a)
Col. gigasporum	CBS 133266^{T}	AM982797, KF687715	KF687822	KF687761	KF687844	–	FN557442, KF687866	–	–	–	–	Rakotoniriana *et al.* (2013), Liu *et al.* (2014)

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Table 6. (Continued).

Species	Isolates[1]	GenBank accession numbers[2]										References
		ITS	*gapdh*	*chs-1*	*his3*	*act*	*tub2*	*cal*	*gs*	*sod2*	*ApMat*	
Col. gloeosporioides	CBS 112999^{T}	JQ005152	JQ005239	JQ005326	JQ005413	JQ005500	JQ005587	JQ005673	JX010085	JX010365	JQ807843	Weir *et al.* (2012)
Col. godetiae	CBS 133.44^{T}	JQ948402	JQ948733	JQ949063	JQ949393	JQ949723	JQ950053	–	–	–	–	Damm *et al.* (2012b)
Col. grevilleae	CBS 132879^{T}	KC297078	KC297010	KC296987	KC297056	KC296941	KC297102	KC296963	KC297033	–	–	Liu *et al.* (2013b)
Col. grossum	CGMCC3.17614^{T}	KP890165	KP890159	KP890153		KP890141	KP890171	KP890147				Diao *et al.* (2017)
Col. guajavae	IMI 350839^{T}	JQ948270	JQ948600	JQ948931	JQ949261	JQ949591	JQ949921	–	–	–	–	Damm *et al.* (2012b)
Col. guizhouensis	CGMCC 3.15112^{T}	JX625158	KC843507	–	–	KC843536	JX625185	–	–	–	–	Tao *et al.* (2013)
Col. hebeiense	MFLUCC13–0726^{T}	KF156863	KF377495	KF289008	–	KF377532	KF288975	–	–	–	–	Yan *et al.* (2015)
Col. hemerocallidis	CBS 130642^{T}	JQ400005	JQ400012	JQ399998	–	JQ399991	JQ400019	KJ781319	–	–	–	Yang *et al.* (2012)
Col. henanense	CGMCC 3.17354^{T}	KJ955109	KJ954810	–	–	KM023257	KJ955257	KJ954662	KJ954960	–	KJ954524	Liu *et al.* (2015b)
Col. higginsianum	IMI 349061^{T}	KM105184	KM105535	KM105254	KM105324	KM105394	KM105464	–	–	–	–	Damm *et al.* (2014)
Col. hippeastri	CBS 125376^{T}	JQ005231	JQ005318	JQ005405	JQ005492	JQ005579	JQ005665	JQ005752	–	–	–	Damm *et al.* (2012a)
Col. horii	ICMP 10492^{T}	GQ329690	GQ329681	JX009752	–	JX009438	JX010450	JX009604	JX010137	JX010370	JQ807840	Weir *et al.* (2012)
Col. hsienjenchang	MAFF 243051	AB738855	–	AB738846	AB738847	AB738845	–	–	–	–	–	Sato *et al.* (2012)
Col. hymenocallidicola	MFLUCC 12–0531^{T}	KT290264	KT290263	KT290262	–	KT290260	KT290261	–	–	–	–	Ariyawansa *et al.* (2015a)
Col. incanum	ATCC 64682^{T}	KC110789	KC110807	–	KC110798	KC110825	KC110816	–	–	–	–	Yang *et al.* (2014)
Col. indonesiense	CBS 127551^{T}	JQ948288	JQ948618	JQ948949	JQ949279	JQ949609	JQ949939	–	–	–	–	Damm *et al.* (2012b)
Col. insertae	MFLU 15–1895^{T}	KX618686	KX618684	KX618683		KX618682	KX618685					Hyde *et al.* (2016)
Col. jiangxiense	CGMCC 3.17363^{T}	KJ955201	KJ954902	–	–	KJ954471	KJ955348	KJ954752	KJ955051	–	KJ954607	Liu *et al.* (2015b)
Col. johnstonii	CBS 128532^{T}	JQ948444	JQ948775	JQ949105	JQ949435	JQ949765	JQ950095	–	–	–	–	Damm *et al.* (2012b)
Col. kahawae subsp. *kahawae*	ICMP 17816^{T}	JX010231	JX010012	JX009813	–	JX009452	JX010444	JX009642	JX010130	JX010350	JQ894579	Weir *et al.* (2012)
Col. kahawae subsp. *ciggaro*	ICMP 18539^{T}	JX010230	JX009966	JX009800		JX009523	JX010434	JX009635	JX010132	JX010346		Weir *et al.* (2012)
Col. karstii	CBS 132134^{T}	HM585409	HM585391	HM582023		HM581995	HM585428	HM582013	–	–	–	Yang *et al.* (2009)
Col. kinghornii	CBS 198.35^{T}	JQ948454	JQ948785	JQ949115	JQ949445	JQ949775	JQ950105	–	–	–	–	Damm *et al.* (2012b)
Col. lacticiphilum	CBS 112989^{T}	JQ948289	JQ948619	JQ948950	JQ949280	JQ949610	JQ949940	–	–	–	–	Damm *et al.* (2012b)
Col. ledebouriae	CBS 141284^{T}	KX228254	–	–	KX228365	KX228357	–	–	–	–	–	Crous *et al.* (2016c)
Col. lentis	CBS 127604^{T}	JQ005766	KM105597	JQ005787	JQ005808	JQ005829	JQ005850	–	–	–	–	Damm *et al.* (2014)
Col. liaoningense	CGMCC3.17616^{T}	KP890104	KP890135	KP890127		KP890097	KP890111	KP890119				Diao *et al.* (2017)
Col. lilii	CBS 109214	GU227810	GU228202	GU228300	GU228006	GU227908	GU228104	–	–	–	–	Damm *et al.* (2009)
Col. limetticola	CBS 114.14^{T}	JQ948193	JQ948523	JQ948854	JQ949184	JQ949514	JQ949844	–	–	–	–	Damm *et al.* (2012b)
Col. lindemuthianum	CBS 144.31^{T}	JQ005779	JX546712	JQ005800	JQ005821	JQ005842	JQ005863	–	KF178643	–	–	Damm *et al.* (2013), Liu *et al.* (2013a)
Col. lineola	CBS 125337^{T}	GU227829	GU228221	GU228319	GU228025	GU227927	GU228123	–	–	–	–	Damm *et al.* (2009)

Col. lini	CBS 172.51^{T}	JQ005765	KM105581	JQ005786	JQ005807	JQ005828	JQ005849	–	–	–	–	Damm *et al.* (2014)
Col. liriopes	CBS 119444^{T}	GU227804	GU228196	GU228294	GU228000	GU227902	GU228098	–	–	–	–	Damm *et al.* (2009)
Col. lupini	CBS 109225^{T}	JQ948155	JQ948485	JQ948816	JQ949146	JQ949476	JQ949806	–	–	–	–	Damm *et al.* (2012b)
Col. magnisporum	CBS 398.84^{T}	KF687718	KF687842	KF687782	KF687865	KF687803	KF687882	–	KF687742	–	–	Liu *et al.* (2014)
Col. malvarum	CBS 521.97^{T}	KF178480	KF178504	KF178529	KF178553	KF178577	KF178601	–	KF178626	–	–	Damm *et al.* (2013)
Col. melonis	CBS 159.84^{T}	JQ948194	JQ948524	JQ948855	JQ949185	JQ949515	JQ949845	–	–	–	–	Damm *et al.* (2012b)
Col. menispermi	MFLU 14–0625^{HT}	KU242357	KU242356	KU242355	–	KU242353	KU242354	–	–	–	–	Li *et al.* (2016)
Col. metake	MAFF 244029	AB738859	(Sequences available at http://www.gene.affrc.go.jp/databases-micro_search_en.php)									Sato *et al.* (2012)
Col. musae	ICMP 19119^{T}	JX010146	JX010050	JX009896	–	JX009433	HQ596280	JX009742	JX010103	JX010335	KC888926	Weir *et al.* (2012)
Col. neosansevieriae	CBS 139918^{T}	KR476747	KR476791	–	KR476792	KR476790	KR476797	–	–	–	–	Crous *et al.* (2015d)
Col. nigrum	CBS 169.49^{T}	JX546838	JX546742	JX546693	JX546791	JX546646	JX546885	–	–	–	–	Liu *et al.* (2013a)
Col. novae-zelandiae	CBS 128505^{T}	JQ005228	JQ005315	JQ005402	JQ005489	JQ005576	JQ005662	JQ005749	–	–	–	Damm *et al.* (2012a)
Col. nupharicola	ICMP 18187^{T}	JX010187	JX009972	JX009835	–	JX009437	JX010398	JX009663	JX010088	JX010320	JX145319	Weir *et al.* (2012), Doyle *et al.* (2013)
Col. nymphaeae	CBS 515.78^{T}	JQ948197	JQ948527	JQ948858	JQ949188	JQ949518	JQ949848	–	–	–	–	Damm *et al.* (2012b)
Col. ocimi	CBS 298.94^{T}	KM105222	KM105577	KM105292	KM105362	KM105432	KM105502	–	–	–	–	Damm *et al.* (2014)
Col. oncidii	CBS 129828^{T}	JQ005169	JQ005256	JQ005343	JQ005430	JQ005517	JQ005603	JQ005690	–	–	–	Damm *et al.* (2012a)
Col. orbiculare	CBS 570.97^{T}	KF178466	KF178490	KF178515	KF178539	KF178563	KF178587	–	KF178611	–	–	Damm *et al.* (2013)
Col. orchidophilum	CBS 632.80^{T}	JQ948151	JQ948481	JQ948812	JQ949142	JQ949472	JQ949802	–	–	–	–	Damm *et al.* (2012b)
Col. panacicola	C08048	GU935867	GU935847	–	–	GU944757	–	–	GU935807	–	–	Choi *et al.* (2011)
Col. paranaense	CBS 134729^{T}	KC204992	KC205026	KC205043	KC205004	KC205077	KC205060	–	–	–	–	Bragança *et al.* (2016)
Col. parsonsiae	CBS 128525^{T}	JQ005233	JQ005320	JQ005407	JQ005494	JQ005581	JQ005667	JQ005754	–	–	–	Damm *et al.* (2012a)
Col. paxtonii	IMI 165753^{T}	JQ948285	JQ948615	JQ948946	JQ949276	JQ949606	JQ949936	–	–	–	–	Damm *et al.* (2012b)
Col. petchii	CBS 378.94^{T}	JQ005223	JQ005310	JQ005397	JQ005484	JQ005571	JQ005657	JQ005744	–	–	–	Damm *et al.* (2012a)
Col. phormii	CBS 118194^{T}	JQ948446	JQ948777	JQ949107	JQ949437	JQ949767	JQ950097	–	–	–	–	Damm *et al.* (2012b)
Col. phyllanthi	CBS 175.67^{T}	JQ005221	JQ005308	JQ005395	JQ005482	JQ005569	JQ005655	JQ005742	–	–	–	Damm *et al.* (2012a)
Col. pisicola	CBS 724.97^{T}	KM105172	KM105522	KM105242	KM105312	KM105382	KM105452	–	–	–	–	Damm *et al.* (2014)
Col. proteae	CBS 132882^{T}	KC297079	KC297009	KC296986	KC297045	KC296940	KC297101	KC296960	–	KC297032	–	Liu *et al.* (2013b)
Col. pseudoacutatum	CBS 436.77^{T}	JQ948480	JQ948811	JQ949141	JQ949471	JQ949801	JQ950131	–	–	–	–	Damm *et al.* (2012b)
Col. pseudomajus	CBS 571.88^{T}	KF687722	KF687826	KF687779	KF687864	KF687801	KF687883	KF687807	KF687744	–	–	Liu *et al.* (2014)
Col. psidii	ICMP 19120	JX010219	JX009967	JX009901	–	JX009515	JX010443	JX009743	JX010133	JX010366	KC888931	Weir *et al.* (2012)
Col. pyricola	CBS 128531^{T}	JQ948445	JQ948776	JQ949106	JQ949436	JQ949766	JQ950096	–	–	–	–	Damm *et al.* (2012b)
Col. queenslandicum	ICMP 1778^{T}	JX010276	JX009934	JX009899	–	JX009447	JX010414	JX009691	JX010104	JX010336	KC888928	Weir *et al.* (2012)
Col. quinquefoliae	MFLU 14–0626^{HT}	KU236391	KU236390	–	–	KU236389	KU236392	–	–	–	–	Li *et al.* (2016)
Col. radicis	CBS 529.93^{T}	KF687719	KF687825	KF687762	KF687847	KF687785	KF687869	KF687806	KF687743	–	–	Liu *et al.* (2014)

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Table 6. (Continued).

Species	Isolates[1]	GenBank accession numbers[2]										References
		ITS	*gapdh*	*chs-1*	*his3*	*act*	*tub2*	*cal*	*gs*	*sod2*	*ApMat*	
Col. rhexiae	CBS 133134^{T}	JX145128	–	–	–		JX145179	–	–	–	JX145290	Doyle *et al.* (2013)
Col. rhombiforme	CBS 129953^{T}	JQ948457	JQ948788	JQ949118	JQ949448	JQ949778	JQ950108	–	–	–	–	Damm *et al.* (2012b)
Col. riograndense	ICMP 20083^{T}	KM655299	KM655298	KM655297	–	KM655295	KM655300	KM655296	–	–	–	Macedo *et al.* (2016)
Col. rusci	CBS 119206^{T}	GU227818	GU228210	GU228308	GU228014	GU227916	GU228112	–	–	–	–	Damm *et al.* (2009)
Col. salicis	CBS 607.94^{T}	JQ948460	JQ948791	JQ949121	JQ949451	JQ949781	JQ950111	–	–	–	–	Damm *et al.* (2012b)
Col. salsolae	ICMP 19051^{T}	JX010242	JX009916	JX009863	–	JX009562	JX010403	JX009696	JX010093	JX010325	KC888925	Weir *et al.* (2012)
Col. sansevieriae	MAFF 239721^{T}	AB212991	(Sequences available at http://www.gene.affrc.go.jp/databases-micro_search_en.php)									Nakamura *et al.* (2006)
Col. scovillei	CBS 126529^{T}	JQ948267	JQ948597	JQ948928	JQ949258	JQ949588	JQ949918	–	–	–	–	Damm *et al.* (2012b)
Col. sedi	MFLUCC 14–1002^{T}	KM974758;	KM974755	KM974754	–	KM974756	KM974757	–	–	–	–	Liu *et al.* (2015c)
Col. siamense	ICMP 18578^{T}	JX010171	JX009924	JX009865	–	FJ907423	JX010404	FJ917505	JX010094	JX010326	JQ899289	Phoulivong *et al.* (2009), Weir *et al.* (2012)
Col. sidae	CBS 504.97^{T}	KF178472	KF178497	KF178521	KF178545	KF178569	KF178593	–	KF178618	–	–	Damm *et al.* (2013)
Col. simmondsii	CBS 122122^{T}	JQ948276	JQ948606	JQ948937	JQ949267	JQ949597	JQ949927	FJ917510	FJ972591	–	–	Damm *et al.* (2012b), Prihastuti *et al.* (2009)
Col. sloanei	IMI 364297^{T}	JQ948287	JQ948617	JQ948948	JQ949278	JQ949608	JQ949938	–	–	–	–	Damm *et al.* (2012b)
Col. spaethianum	CBS 167.49^{T}	GU227807	GU228199	GU228297	GU228003	GU227905	GU228101	–	–	–	–	Damm *et al.* (2009)
Col. spinaceae	CBS 128.57	GU227847	GU228239	GU228337	GU228043	GU227945	GU228141	–	–	–	–	Damm *et al.* (2009)
Col. spinosum	CBS 515.97^{T}	KF178474	KF178498	KF178523	KF178547	KF178571	KF178595	–	KF178620	–	–	Damm *et al.* (2013)
Col. sydowii	CBS 135819 ^{T}	KY263783	KY263785	KY263787	KY263789	KY263791	KY263793					Present study
Col. syzygicola	MFLUCC 10–0624^{T}	KF242094	KF242156	–	–	KF157801	KF254880	KF254859	KF242125	–	–	Udayanga *et al.* (2013)
Col. tabacum	CPC 18945^{T}	KM105204	KM105557	KM105274	KM105344	KM105414	KM105484	–	–	–	–	Damm *et al.* (2014)
Col. tamarilloi	CBS 129814^{T}	JQ948184	JQ948514	JQ948845	JQ949175	JQ949505	JQ949835	–	–	–	–	Damm *et al.* (2012b)
Col. tanaceti	CBS 132693^{T}	JX218228	JX218243	JX259268	–	JX218238	JX218233	–	–	–	–	Barimani *et al.* (2013), Damm *et al.* (2014)
Col. tebeestii	CBS 522.97^{T}	KF178473	KF178505	KF178522	KF178546	KF178570	KF178594	–	KF178619	–	–	Damm *et al.* (2013)
Col. temperatum	CBS 133122^{T}	JX145159	–	–	–	–	JX145211	–	–	–	JX145298	Doyle *et al.* (2013)
Col. theobromicola	ICMP 18649^{T}	JX010294	JX010006	JX009869	–	JX009444	JX010447	JX009591	JX010139	JX010372	KC790726	Weir *et al.* (2012)
Col. ti	ICMP 4832^{T}	JX010269	JX009952	JX009898	–	JX009520	JX010442	JX009649	JX010123	JX010362	KM360146	Weir *et al.* (2012), Liu *et al.* (2015b)
Col. tofieldiae	CBS 495.85	GU227801	GU228193	GU228291	GU227997	GU227899	GU228095	–	–	–	–	Damm *et al.* (2009)
Col. torulosum	CBS 128544^{T}	JQ005164	JQ005251	JQ005338	JQ005425	JQ005512	JQ005512	JQ005512	–	–	–	Damm *et al.* (2012a)
Col. trichellum	CBS 217.64	GU227812	GU228204	GU228302	GU228009	GU227910	GU228106	–	–	–	–	Damm *et al.* (2009)

Col. trifolii	CBS 158.83^{T}	KF178478	KF178502	KF178527	KF178551	KF178575	KF178599	–	KF178624	–	–	Damm *et al.* (2014)
Col. tropicale	ICMP 18653^{T}	JX010264	JX010007	JX009870	–	JX009489	JX010407	JX009719	JX010097	JX010329	KC790728	Rojas *et al.* (2010), Weir *et al.* (2012)
Col. tropicicola	BCC 38877^{T}	JN050240	JN050229	–	–	JN050218	JN050246	–	–	–	–	Noireung *et al.* (2012)
Col. truncatum	CBS 151.35^{T}	GU227862	GU228254	GU228352	GU228058	GU227960	GU228156	–	–	–	–	Damm *et al.* (2009)
Col. utrechtense	CBS 130243^{T}	KM105201	KM105554	KM105271	KM105341	KM105411	KM105481	–	–	–	–	Damm *et al.* (2014)
Col. verruculosum	IMI 45525^{T}	GU227806	GU228198	GU228296	GU228002	GU227904	GU228100	–	–	–	–	Damm *et al.* (2009)
Col. vietnamense	CBS 125478^{T}	KF687721	KF687832	KF687769	KF687855	KF687792	KF687877	KF687816	KF687753	–	–	Liu *et al.* (2014)
Col. vignae	CBS 501.97^{T}	KM105183	KM105534	KM105253	KM105323	KM105393	KM105463	–	–	–	–	Damm *et al.* (2014)
Col. viniferum	GZAAS 5.08601^{T}	JN412804	JN412798	–	–	JN412795	JN412813	JQ309639	JN412787	–	–	Peng *et al.* (2013), Hyde *et al.* (2014)
Col. walleri	CBS 125472^{T}	JQ948275	JQ948605	JQ948936	JQ949266	JQ949596	JQ949926	–	–	–	–	Damm *et al.* (2012b)
Col. wuxiense	CGMCC 3.17894^{T}	KU251591	KU252045	KU251939	–	KU251672	KU252200	KU251833	KU252101	–	KU251722	Wang *et al.* (2016)
Col. xanthorrhoeae	ICMP 17903^{T}	JX010261	JX009927	JX009823	–	JX009478	JX010448	JX009653	JX010138	JX010369	KC790689	Shivas *et al.* (1998), Weir *et al.* (2012)
Col. yunnanense	CBS 132135^{T}	EF369490, JX546804	JX546706	JX519231	JX546755	JX519239	JX519248	–	–	–	–	Liu *et al.* (2007), Cannon *et al.* (2012)

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[1] ATCC: American Type Culture Collection, Virginia, USA; BCC: BIOTEC Culture Collection, National Center for Genetic Engineering and Biotechnology (BIOTEC), Khlong Luang, Pathumthani, Thailand; BRIP: Queensland Plant Pathology Herbarium, Brisbane, Australia; CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CGMCC: Chinese General Microbiological Culture Collection Center, Beijing, China; COAD: Coleção Octávio Almeida Drummond, Universidade Ferderal de Viçosa, Viçosa, Brazil; CPC: Culture collection of Pedro Crous, housed at Westerdijk Fungal Biodiversity Institute; GZAAS: Guizhou Academy of Agricultural Sciences, Guizhou Province, China. ICMP: International Collection of Micro-organisms from Plants, Landcare Research, Private Bag 92170, Auckland, New Zealand; IMI: International Mycological Institute, Kew, UK; MAFF: Ministry of Agriculture, Forestry and Fisheries, Tsukuba, Ibaraki, Japan; MFLU: Herbarium of Mae Fah Luang University, Chiang Rai, Thailand; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Ria, Thailand. ^{HT} and ^{T} indicate holotype specimens and ex-type strains, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *gapdh*: partial glyceraldehyde-3-phosphate dehydrogenase gene; *chs-1*: partial chitin synthase-1 gene; *his*: partial histone H3 gene; *act*: partial actin gene; *tub2*: partial beta-tubulin gene; *cal*: partial calmodulin gene; *gs*: partial glutamine synthetase gene; *sod2*: partial manganese superoxide dismutase gene; *ApMat*: partial Apn2-Mat1-2 intergenic spacer and partial mating type (Mat1-2) gene.

Table 7. DNA barcodes of accepted *Colletotrichum* spp. in the *Col. graminicola* and *caudatum* complexes.

Species	**Isolates**[1]	**GenBank accession numbers**[2]									**References**
		ITS	***gapdh***	***chs-1***	***his3***	***act***	***tub2***	***apn2***	***ApMat***	***sod2***	
Colletotrichum alcorni	IMI 176619^{T}	EU554079, JX076858	–	–	–	–	–	EU364987	FJ377901	EU554187	Crouch *et al.* (2009c), Crouch (2014)
Col. baltimorense	BPI 892771^{T}	JX076866	–	–	–	–	–	JX076927	JX076905	JX076886	Crouch (2014)
Col. caudasporum	CGMCC 3.15106^{T}	JX625162	KC843512	–	–	KC843526	JX625190	–	–	–	Tao *et al.* (2013)
Col. caudatum	BPI 423339^{LT}	JX076915	–	–	–	–	–	–	–	JX076878	Crouch (2014)
	CBS 131602^{ET}	JX076860	–	–	–	–	–	JX076932	JX076893	JX076878	Crouch (2014)
Col. cereale	CBS 129663	DQ126177, JQ005774	–	JQ005795	JQ005816	JQ005837	JQ005858	–	–	DQ133277	Crouch *et al.* (2006), O'Connell *et al.* (2012)
Col. duyunensis	CGMCC 3.15105^{T}	JX625160	KC843515	–	–	KC843530	JX625187	–	–	–	Tao *et al.* (2013)
Col. echinochloae	MAFF 511473^{T}	AB439811	–	–	–	–	–	–	–	AB440153	Moriwaki & Tsukiboshi (2009),
Col. eleusines	MAFF 511155^{T}	EU554131, JX519218	–	JX519226	–	JX519234	JX519243	EU365038	–	EU554234	Cannon *et al.* (2012), Crouch *et al.* (2009b, c),
Col. endophytum	CGMCC 3.15108^{T}	JX625177	KC843521	–	–	KC843533	JX625206	–	–	–	Tao *et al.* (2013)
Col. eremochloae	CBS 129661^{T}	JQ478447, JX519220	–	JX519228	–	JX519236	JX519245	JQ478476	JQ478462	JQ478449	Cannon *et al.* (2012), Crouch & Tomaso-Peterson (2012)
Col. falcatum	CBS 147945^{T}	HM171877, JQ005772		HM171677, JQ005793	JQ005814	JQ005835	JQ005856	HM569770	HM569769	–	Prihastuti *et al.* (2010), O'Connell *et al.* (2012)
Col. graminicola	CBS 130836^{T}	DQ003110, JQ005767	–	JQ005788	HQ005809	JQ005830	JQ005851	–	FJ377994	–	Crouch *et al.* (2009a, c), Du *et al.* (2005), O'Connell *et al.* (2012)
Col. hanaui	MAFF 3054042^{T}	EU554101, JX519217	–	JX519225	–	–	JX519242	EU365008	FJ377922	EU554205	Crouch *et al.* (2009b, c), Cannon *et al.* (2012)
Col. jacksonii	MAFF 305460^{T}	EU554108, JX519216	–	JX519224	–	JX519233	JX519241	–	–	EU554212	Crouch *et al.* (2009b, c), Cannon *et al.* (2012)
Col. miscanthi	MAFF 510857^{T}	EU554121, JX519221	–	JX519229	–	JX519237	JX519246	EU365028	–	EU554224	Crouch *et al.* (2009b, c), Cannon *et al.* (2012)
Col. navitas	CBS 125086^{T}	GQ919067, JQ005769	–	JQ005790	JQ005811	JQ005832	JQ005853	GQ919069	GQ919071	GQ919073	Crouch *et al.* (2009a), O'Connell *et al.* (2012)
Col. nicholsonii	MAFF 511115^{T}	EU554126, JQ005770	–	JQ005791	JQ005812	JQ005833	JQ005854	EU365033	FJ377946	EU554229	Crouch *et al.* (2009b, c), O'Connell *et al.* (2012)
Col. ochracea	CGMCC 3.15104^{T}	JX625168	KC843513	–	–	KC843527	JX625183	–	–	–	Tao *et al.* (2013)
Col. paspali	MAFF 305403^{T}	EU554100, JX519219	–	JX519227	–	JX519235	JX519244	EU365007	FJ377921	EU554204	Crouch *et al.* (2009b, c), Cannon *et al.* (2012)
Col. somersetense	CBS 131599^{T}	JX076862	–	–	–	–	–	JX076918	JX076895	JX076880	Crouch (2014)
Col. sublineola	CBS 131301^{T}	DQ003114, JQ005771	–	JQ005792	JQ005813	JQ005834	JQ005855	EU365121	FJ378029	DO132051	Crouch *et al.* (2006), Crouch & Tomaso-Peterson (2012), O'Connell *et al.* (2012)
Col. zoysia	MAFF 238573^{T}	JX076871	–	–	–	–	–	JX076922	JX076899	–	Crouch (2014)

[1] BPI: US National Fungus Collections, Beltsville, Maryland, USA; CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CGMCC: Chinese General Microbiological Culture Collection Center, Beijing, China; IMI: International Mycological Institute, Kew, UK; MAFF: Ministry of Agriculture, Forestry and Fisheries, Tsukuba, Ibaraki, Japan. ^{LT,} ^{ET} and ^{T} indicate lectotype specimen and ex-epitype and ex- type strains, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *gapdh*: partial glyceraldehyde-3-phosphate dehydrogenase gene; *chs-1*: partial chitin synthase-1 gene; *his*: partial histone H3 gene; *act*: partial actin gene; *tub2*: partial beta-tubulin gene; *apn2*: partial DNA lyase gene; *ApMat*: partial Apn2-Mat1-2 intergenic spacer and partial mating type (Mat1-2) gene; *sod2*: partial manganese superoxide dismutase gene.

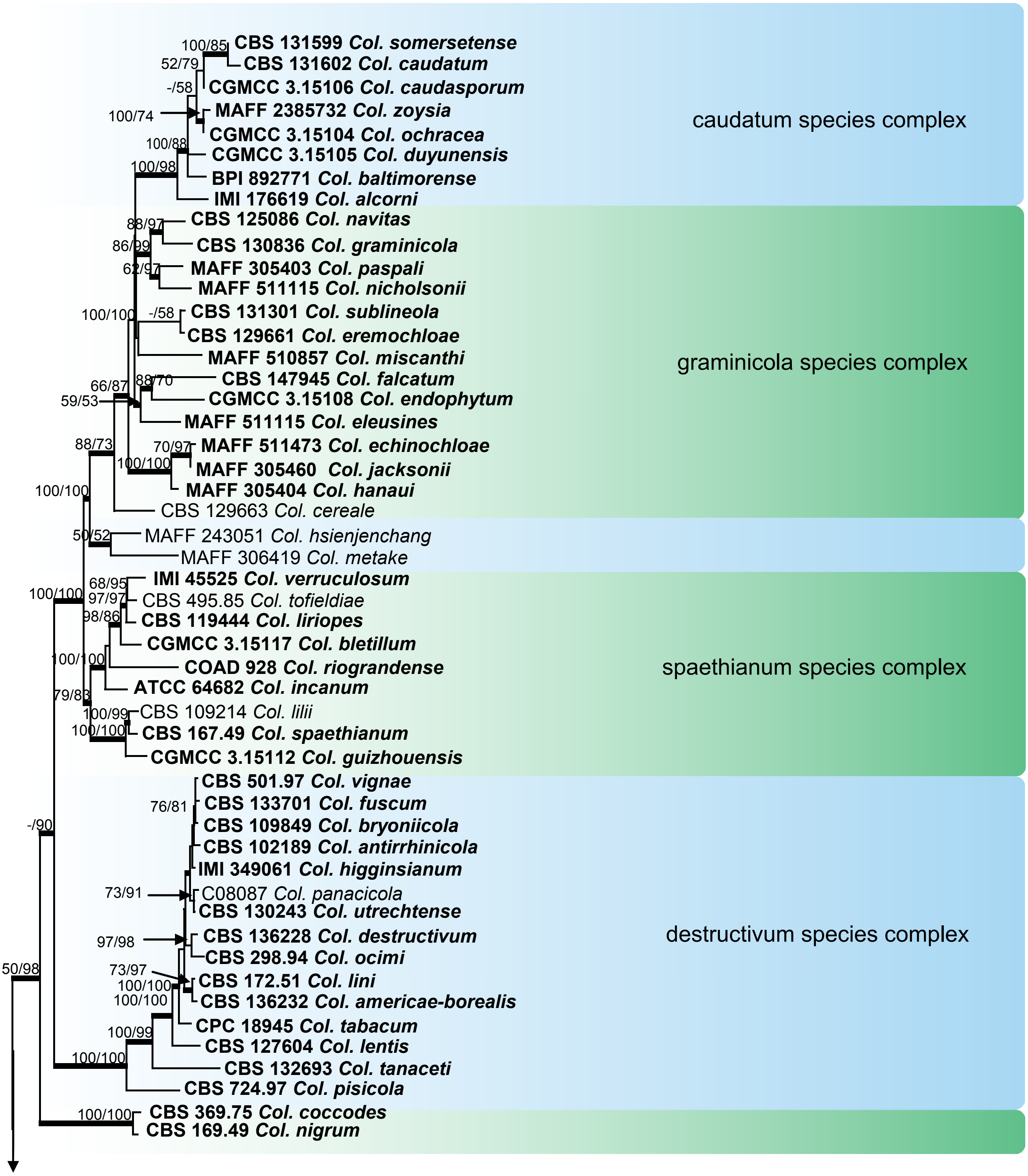


Fig. 26. One of the 100 equally most parsimonious trees obtained from a heuristic search of the combined ITS, *gapdh*, *chs-1*, *act* and *tub2* sequence data of the currently accepted species of *Colletotrichum*. Parsimony and likelihood bootstrap support values ≥ 50 % are indicated at the nodes and branches with Bayesian posterior probabilities above 0.80 given in bold. The tree is rooted with *Monilochaetes infuscans* CBS 869.96. GenBank accession numbers are listed in Tables 6 and 7. The ex-type strains are in bold. TreeBASE: S21045.

Plates sometimes need to be incubated for 1–2 mo to allow development of the sexual morph.

Distribution: Worldwide.

Hosts: Occurs on a wide range of plant families.

Disease symptoms: Anthracnose disease symptoms include defined, often sunken necrotic spots on leaves, stems, flowers or fruits. Additionally, crown and stem rots, ripe rot, seedling blights and brown blotch are caused by species of this genus.

Notes: Due to the overlapping morphological characters, species delimitation based on morphology alone is hardly possible in *Colletotrichum*. Multilocus sequence analyses combined with a polyphasic approach, including the analysis of geographical, ecological and morphological data, is generally suggested for

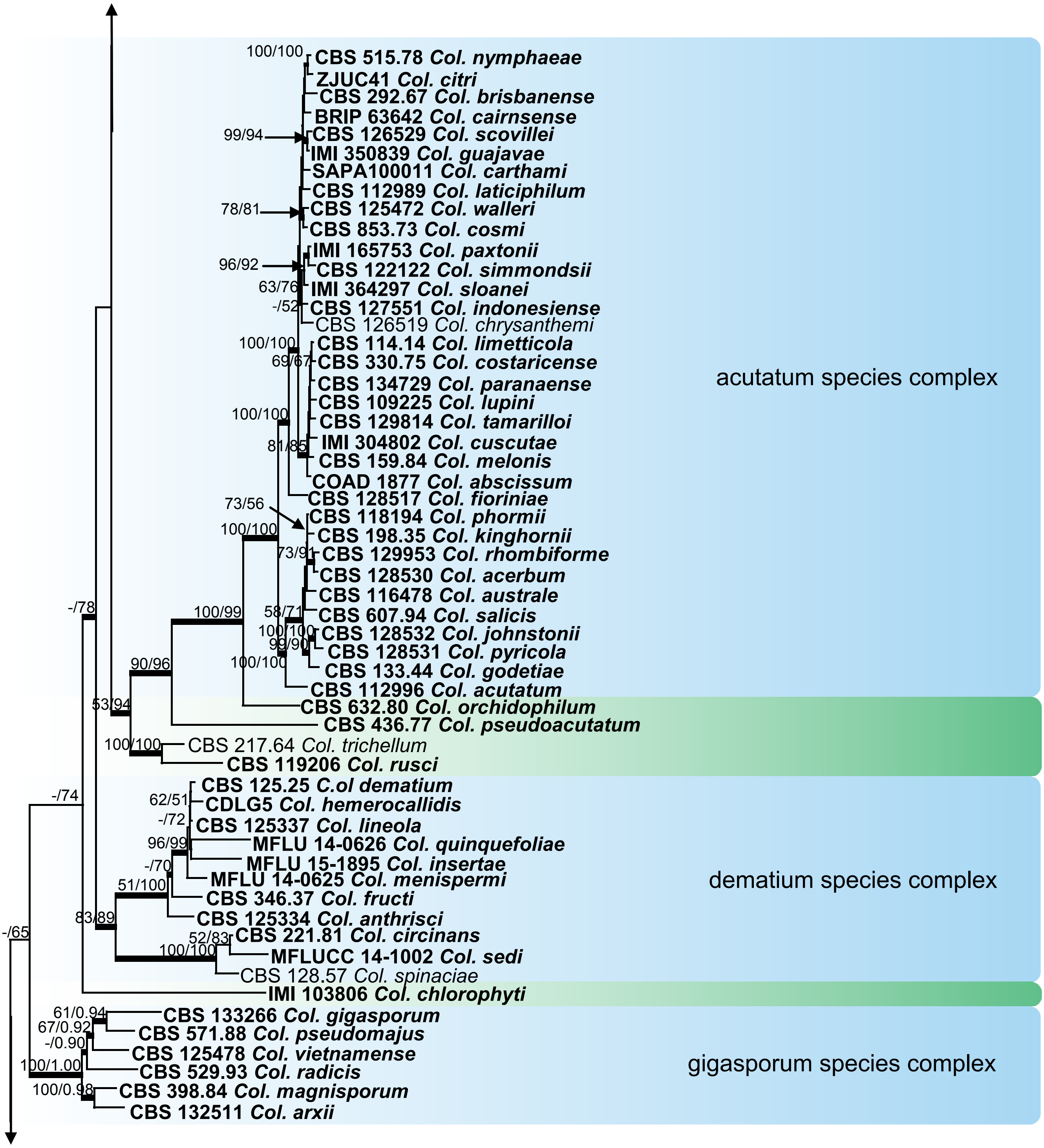


Fig. 26. (*continued*).

species differentiation within the genus *Colletotrichum* (Cai *et al.* 2009). This approach resulted in the differentiation of almost 200 species, most of them belonging to species complexes. Due to simultaneous studies in the genus by different researchers, the sets of loci used for differentiating species vary among the different species complexes. ITS, *gapdh*, *chs-1*, *act*, *his3* and *tub2* (with some also *gs* or *cal*) gene regions have been used for studying species within the *Col. acutatum*, *boninense*, *dematium*, *destructivum*, *gigasporum*, *orbiculare*, *spaethianum* and *truncatum* species complexes (Cannon *et al.* 2012, Damm *et al.* 2012a, b, 2013, 2014, Liu *et al.* 2014, Jayawardena *et al.* 2016b), while *gs*, *cal* and *sod2* were additionally applied for the species differentiation within the *Col. gloeosporioides* species complex (Weir *et al.* 2012) (Table 6). In contrast, Crouch *et al.* (2009b) and Crouch (2014) applied ITS, *sod2*, *apn2* and *Mat1/apn2* (= *ApMat*), to study the *Col. graminicola* and *Col. caudatum* species complexes (Table 7). Silva *et al.* (2012) and Sharma *et al.* (2015) emphasised the use of *ApMat* in *Colletotrichum* species delimitation because of its high resolution within the *Col. gloeosporioides* species complex compared to previously used loci. Liu *et al.* (2015b, 2016) applied different sets of loci and different phylogenetic methods on a large set of closely related *Colletotrichum* strains/species belonging to this complex and revealed that *ApMat* should be combined with other loci to achieve

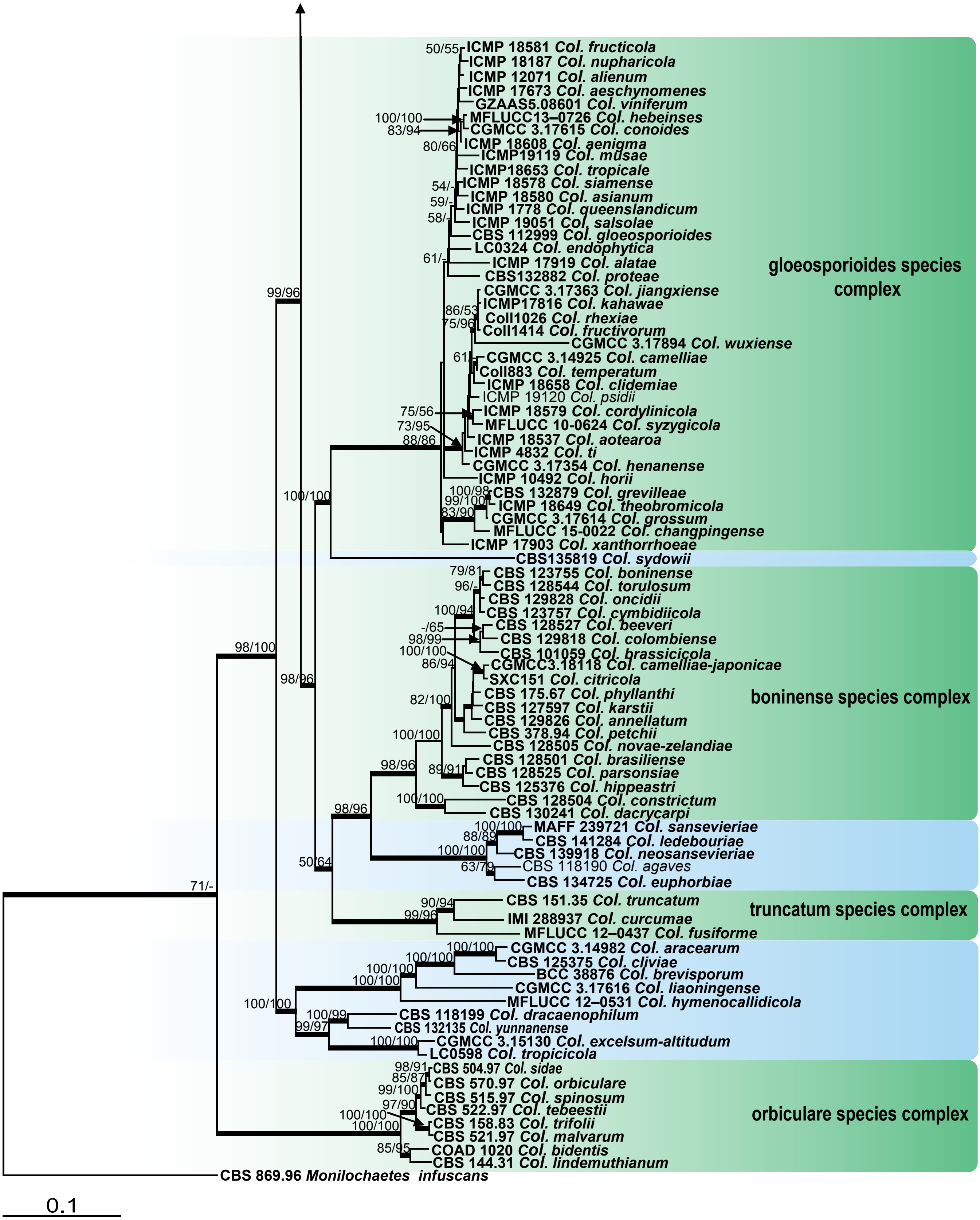


Fig. 26. (*continued*).

satisfactory species delimitation in the *Col. gloeosporioides* complex.

Because different sets of loci are used in different species complexes and the resolution of species differs depending on both locus and species, there is no agreement among the mycologists on the locus or loci to use for species identification/ barcoding. For example, most species in the *Col. acutatum* complex can be separated by *tub2* sequences (Damm *et al.* 2012b), while species in the *Col. gloeosporioides* complex can be identified with a combination of *ApMat* and *gs* sequences (Liu *et al.* 2015b). Research to select better genetic markers and the best secondary barcoding gene(s) is still ongoing.

References: Cannon *et al.* 2012 (species complexes); Crouch *et al.* 2009b, Crouch 2014 (phylogeny); Damm *et al.* 2009, 2012a, b, 2013, 2014, Weir *et al.* 2012, Liu *et al.* 2014 (morphology, phylogeny).

Colletotrichum sydowii Damm, **sp. nov.** MycoBank MB820688. Fig. 27.

Etymology: The species epithet is derived from Hans Sydow (1879–1946), a German mycologist who described several *Colletotrichum* species including one on *Sambucus*, host from which this fungus was isolated.

Sexual morph not observed. *Asexual morph on SNA: Vegetative hyphae* 1.5–9.5 µm diam, hyaline to pale brown, smooth-walled, septate, branched. *Chlamydospores* not observed. *Conidiomata* absent, conidiophores and setae formed directly on hyphae. *Setae* medium brown, smooth-walled, upper part verrucose, 60–115 µm long, 2–4-septate, base cylindrical, 4–6 µm diam, tip ± acute to ± rounded. *Conidiophores* hyaline to pale brown, smooth-walled to verrucose, septate, branched, to 50 µm long. *Conidiogenous cells* hyaline to pale brown, smooth-walled to verrucose, cylindrical to clavate, 13–28 × 4–5 µm, with a gelatinous coating, opening 1–2 µm diam, collarette $\leq$ 0.5 µm long, periclinal thickening visible. *Conidia* hyaline, smooth-walled, aseptate, straight, slightly clavate to cylindrical, with one end round and the other truncate, (17–)17.5–19.5(–21) × 5–5.5 µm, mean ± SD = 18.3 ± 0.9 × 5.2 ± 0.2 µm, L/W ratio = 3.5. *Appressoria* single, medium brown, smooth-walled, subglobose, elliptical or irregular in outline, with a strongly lobate margin, (7.5–)9–14(–17.5) × (5.5–)7–10.5(–12) µm, mean ± SD = 11.4 ± 2.4 × 8.6 ± 1.8 µm, L/W ratio = 1.3, appressoria of strain CBS 132889 shorter, measuring (7.5–)8.5–12.5(–14) × (6.5–)7.5–11(–13) µm, mean ± SD = 10.6 ± 1.9 × 9.1 ± 1.8 µm, L/W ratio = 1.2. *Asexual morph on* Anthriscus *stem*: *Conidiomata*, conidiophores and setae formed on pale brown, angular cells, 3.5–8 µm diam. *Setae* medium brown, verruculose to verrucose, 30–80 µm long, (1–)2–3-septate, base conical to ± inflated, 4.5–7.5 µm diam, tip ± acute to ± rounded. *Conidiophores* pale brown, smooth-walled, septate, branched, to 20 µm long. *Conidiogenous cells* pale brown, smooth-walled, cylindrical to doliiform, 6.5–18 × 5–6.5 µm, opening 1.5–2 µm diam, collarette 0.5–1 µm long, periclinal thickening distinct. *Conidia* hyaline, smooth-walled, aseptate, straight, cylindrical, with one end round and the other truncate, (14–)15.5–18.5(–20.5) × 5–6 µm, mean ± SD = 17.0 ± 1.6 × 5.5 ± 0.3 µm, L/W ratio = 3.1, conidia of strain CBS 132889 larger, measuring (15.5–)17–20(–20.5) × (4.5–)5–5.5(–6) µm, mean ± SD = 18.6 ± 1.4 × 5.4 ± 0.3 µm, L/W ratio = 3.5.

Culture characteristics: Colonies on SNA flat with entire margin, hyaline to honey, filter paper and *Anthriscus* stem partly pale to dark grey, agar medium partly covered with short felty whitish aerial mycelium, reverse similar; growth 27.5–29.5 mm diam in 1 wk ($\geq$ 40 mm diam in 10 d). Colonies on OA flat with entire margin; olivaceous buff to greenish olivaceous, partly covered with short felty whitish aerial mycelium and grey conidiomata, saffron to salmon conidial masses in the centre, reverse primrose, rosy-buff to grey olivaceous, growth 26–28 mm diam in 1 wk ($\geq$ 40 mm in 10 d). Conidia in mass saffron to salmon.

Material examined: **Taiwan**, from leaves of *Sambucus* sp., 18 Dec. 2011, P.W. Crous (**holotype** CBS H-21509, culture ex-type CBS 135819 = CPC 20071); *ibid.*, CBS 132889 = CPC 20070.

Notes: *Colletotrichum sydowii* is to date only known from *Sambucus* leaves in Taiwan. The conidia of this species resemble those of several species, e.g. *Col. clidemiae*, *Col. australe* and *Col. parsonsiae* belonging to the *Col. gloeosporioides*, *acutatum* and *boninense* species complexes (Damm *et al.* 2012a, b, Weir *et al.* 2012). Based on DNA sequences, *Col. sydowii* does not belong to any known *Colletotrichum* species complex; the closest matches in blastn searches of the ex-holotype strain in GenBank with sequences of the different loci resulted in sequences of strains from different species complexes. The ITS sequence is 99 % (1–2 nucleotide difference) identical to those of “*Col. gloeosporioides*” strain EECC-453 from *Ensete ventricosum* (GenBank KP942898, from an unpublished study in Ethiopia by Y. Mulugeta *et al.*) and “Fungal sp.” strain TCPR 106 from a photosynthetic root of *Tinospora cordifolia* in India (GenBank JX951175, R.N. Kharwar *et al.*, unpubl. data), as well as 93–94 % identical to the ITS sequences of several species of the *Col. gigasporum* and *gloeosporioides* complexes and *Col. coccodes*. The *tub2* sequence is 83 % (> 130 nucleotides difference) identical to those of *Col. vietnamense* strain CBS 125477 (GenBank KF687876), *Col. gigasporum* strain CBS 109355 (GenBank KF687870), both belonging to the *Col. gigasporum* complex (Liu *et al.* 2014), and *Col. dracaenophilum* isolate DMM 170 (GenBank KJ653227, Macedo & Barreto 2016). The *his3* sequence is 90–91 % identical with species from different complexes, including *Col. constrictum* strain CBS 128503 (GenBank JQ005498, *Col. boninense* complex, Damm *et al.* 2012a) and *Col. vietnamense* strain CBS 125477 (GenBank KF687854, *Col. gigasporum* complex, Liu *et al.* 2014) as well as *Col. yunnanense* strain CBS 132135 (GenBank JX546755, Liu *et al.* 2014). The *chs-1* sequence is 89–91 % identical with e.g. *Col. dacrycarpi* strain CBS 130241 (GenBank JQ005410, *Col. boninense* complex, Damm *et al.* 2012a) and *Col. grevilleae* strain CBS 132879 (GenBank KC296987, *Col. gloeosporioides* complex, Liu *et al.* 2013b). Closest match with the *act* sequence is *Col. magnisporum* strain CBS 398.84 with 82 % identity (GenBank KF687803, *Col. gigasporum* complex, Liu *et al.* 2014). There is no species with more than 52 % query cover to the *gapdh* of *Col. sydowii*.

There is one *Colletotrichum* species that was previously described from *Sambucus*, *Col. sambuci* Syd. 1942, that caused fruit anthracnose of *Sa. nigra* in Germany. Sydow (1942) regarded *Gloeosporium fructigenum* f. *sambuci* Müll.-Thurg. 1922, described from *Sa. nigra* in Switzerland, as a synonym of *Col. sambuci*. Conidia of *Col. sambuci* are cylindrical, elongate ellipsoidal to clavate with one end rounded tapering to the other slightly acute end, measuring 13–20 × 4.5–6 µm. They have similar dimensions as those of *Col. sydowii*, however it is unlikely that the fungus collected from *Sambucus* leaves in Taiwan is identical with the fruit anthracnose pathogen of black elderberry in Europe, as the morphological characters apply to many *Colletotrichum* species and all molecular data suggest a species in the

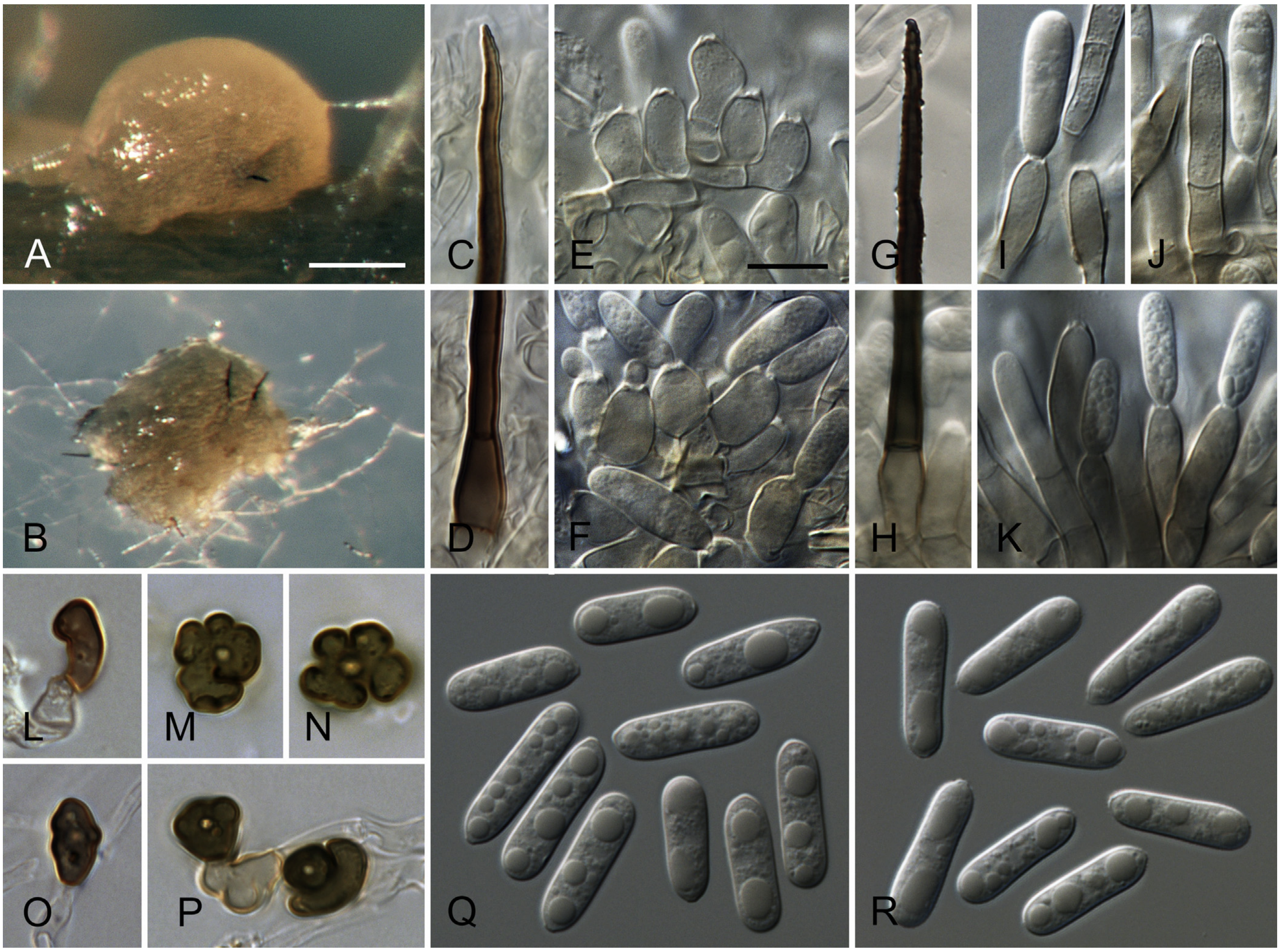


Fig. 27. *Colletotrichum sydowii* (holotype CBS 135819). **A–B**. Conidiomata. **C.** Tip of seta. **D.** Base of seta. **E–F.** Conidiophores. **G.** Tip of seta. **H.** Base of seta. **I–K.** Conidiophores. **L–P.** Appressoria. **Q–R.** Conidia. A, C–F, Q. from *Anthriscus* stem. B, G–P, R. from SNA. A–B. DM; C–R. DIC. Scale bars: A applies to A, B = 100 µm; E applies to C–R = 10 µm.

Col. acutatum species complex. Based on ITS sequences, Benduhn *et al.* (2011) and Michel *et al.* (2013) identified *Col. acutatum* (*s. lat.*) as causal agent of the fruit anthracnose of *Sa. nigra* in Germany and Switzerland, respectively. As part of the multilocus alignment of the *Col. acutatum* complex, *Col. godetiae* was identified from fruits of *Sa. nigra* in the Netherlands (Damm *et al.* 2012b). The ITS sequences of "*Col.* cf. *gloeosporioides*" strain BBA 67435 (GenBank AJ301931) from *Sa. nigra* in Germany and of strain BBA 71332 (GenBank AJ301972) also from *Sambucus* (Nirenberg *et al.* 2002) are identical with that of strain CBS 862.70; these isolates are probably also *Col. godetiae*. Conidia of the *Col. godetiae* strain from the Netherlands (CBS 862.70) measure (8–)14–19(–24) × (4–)4.5–5(–5.5) µm on SNA. The shape of this species can be either fusiform or clavate with only one acute end, depending on the strain (Damm *et al.* 2012b) and there were no setae observed. Strain BBA 67435 also had conidia pointed only at one end (Nirenberg *et al.* 2002), which agrees with the shape of *Col. sambuci*. It is possible that *Col. sambuci* is an older name of *Col. godetiae*, however, we cannot confirm this here as we could not locate the type material.

Another species was described from *Sambucus* in Canada, *Vermicularia sambucina* (Ellis & Dearness 1897), which however has curved conidia with different dimensions (24 × 3–3.5 µm, Saccardo & Sydow 1899). In contrast, *Col. fructicola*, a species with considerably shorter conidia belonging to the *Col. gloeosporioides* complex, was isolated from leaves with anthracnose leaf spot symptoms on *Sa. ebulus* in Iran (Arzanlou *et al.* 2015).

Authors: U. Damm, R.S. Jayawardena, L. Cai

Coniella Höhn. Ber. Deutsch. Bot. Ges. 36: 316. 1918. Fig. 28.
Synonyms: *Schizoparme* Shear, Mycologia 15: 120. 1923.
Baeumleria Petr. & Syd., Repert. Spec. Nov. Regni Veg. Beih. 42: 268. 1927.
Pilidiella Petr. & Syd., Repert. Spec. Nov. Regni Veg. Beih. 42: 462. 1927.
Anthasthoopa Subram. & K. Ramakr., Proc. Indian Acad. Sci., Sect. B 43: 173. 1956.
Cyclodomella Mathur *et al.*, Sydowia 13: 144. 1959.
Embolidium Bat., Brotéria, N.S. 33(3–4): 194. 1964 non Sacc. 1978.

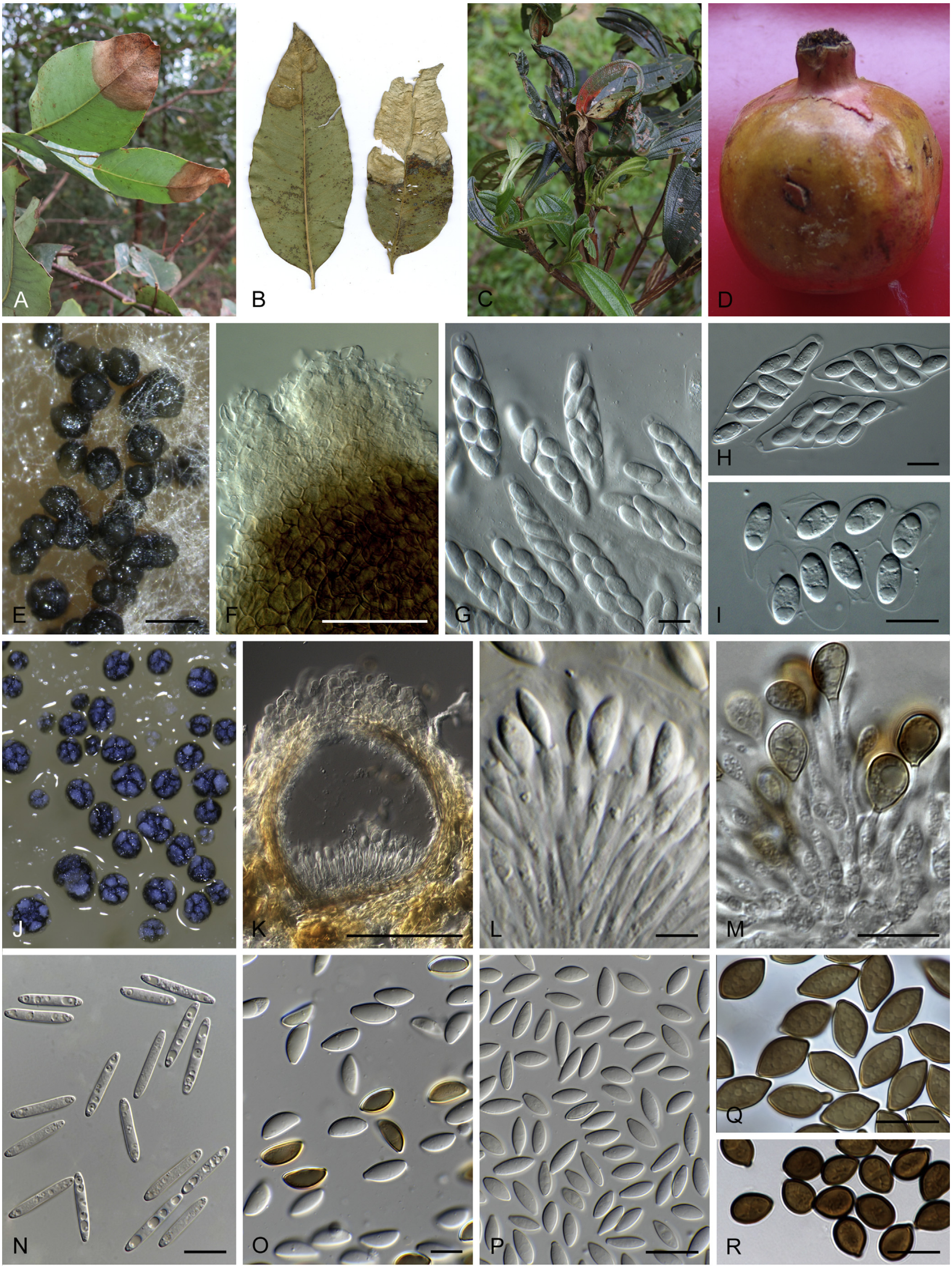


Fig. 28. *Coniella* spp. **A–D.** Disease symptoms. **A, B.** *Coniella eucalyptorum* on *Eucalyptus* sp. **C.** *Coniella tibouchinae* on *Tibouchina granulosa*. **D.** *Coniella granati* on *Punica granatum* (pictures taken by M. Mirabolfathy). **E–I.** Sexual morph of *Coniella eucalyptigena* (ex-type CBS 139893). **E.** Ascomata forming on OA. **F.** Ostiolar área. **G, H.** Asci. **I.** Ascospores. **J–R.** Asexual morphs. **J.** Conidiomata forming on OA of *Coniella diplodiella* (ex-epitype CBS 111858). **K.** Transverse section through a conidioma of *Coniella eucalyptorum* (ex-type CBS 112640). **L, M.** Conidiogenous cells giving rise to conidia. **L.** *Coniella diplodiopsis* (ex-type CBS 590.84). **M.** *Coniella obovata* (CBS 111025). **N–R.** Conidia. **N.** *Coniella africana* (ex-type CBS 114133). **O.** *Coniella diplodiella* (ex-epitype CBS 111858). **P.** *Coniella fusiformis* (ex-type CBS 141596). **Q.** *Coniella limoniformis* (ex-type CBS 111021). **R.** *Coniella obovata* (CBS 111025). Scale bars: E = 250 μm, others = 10 μm. Pictures taken from Alvarez *et al.* (2016).

Classification: *Sordariomycetes*, *Sordariomycetidae*, *Diaporthales*, *Schizoparmaceae.*

Type species: *Coniella fragariae* (Oudem.) B. Sutton (syn. *Coniella pulchella* Höhn.). Neotype and ex-neotype culture: CBS H-10697, CBS 172.49 = CPC 3930.

DNA barcodes (genus): LSU, *rpb2*.

DNA barcodes (species): ITS, *rpb2*, *tef1*. Table 8.

Ascomata brown to black, collapsed collabent, erumpent, becoming superficial, globose, papillate, with central periphysate ostiole. *Paraphyses* lacking. *Asci* clavate to subcylindrical, with distinct apical ring, free at maturity. *Ascospores* ellipsoid, aseptate, hyaline, at times becoming pale brown at maturity, smooth, with or without mucoid caps. *Conidiomata* pycnidial, immersed to semi-immersed, unilocular, glabrous, ostiolate; *ostiole* central, circular or oval, often situated in a conical or rostrate neck; *conidiomatal wall* brown to dark brown or black, composed of thin, pale brown *textura angularis* on exterior, and hyaline, thin-walled, *textura prismatica* in the inner layers except at base, which has a convex, pulvinate tissue of hyaline *textura angularis* giving rise to conidiophores or conidiogenous cells. *Conidiophores* mostly reduced to conidiogenous cells, occasionally septate and branched at base, invested in mucus. *Conidiogenous cells* discrete, cylindrical, subcylindrical, obclavate or lageniform, hyaline, smooth-walled, proliferating percurrently, with visible periclinal thickening. *Conidia* ellipsoid, fusiform, globose, napiform or naviculate with a truncate base and an obtuse to apiculate apex, unicellular, thin- or thick-walled, smooth, hyaline, pale yellowish, pale yellowish brown, or olivaceous brown to brown, sometimes with a longitudinal germ-slit, with or without a mucoid appendage extending from apex to base on one side; *basal hila* with or without a short tubular basal appendage. *Spermatophores* formed in same conidioma, hyaline, smooth, 1-septate with several apical conidiogenous cells, or reduced to conidiogenous cells. *Spermatogenous cells* hyaline, smooth, lageniform to subcylindrical, with visible periclinal thickening. *Spermatia* hyaline, smooth, rod-shaped with rounded ends (adapted from Crous *et al.* 2014a).

Culture characteristics: On PDA produces white aerial mycelium with or without black conidiomata. On OA frequently produces white aerial mycelium with black conidiomata, but sometimes with luteous to orange zones.

Optimal media and cultivation conditions: On 2 % MEA, PDA and OA, at 25 °C under continuous near-ultraviolet light to promote sporulation.

Distribution: Worldwide.

Hosts: Wide variety of hosts, e.g. *Eucalyptus* (*Myrtaceae*), *Fragaria* (*Rosaceae*), *Hibiscus* (*Malvaceae*), *Psidium* (*Myrtaceae*), *Punica* (*Lythraceae*), *Terminalia* (*Combretaceae*) and *Vitis* (*Vitaceae*).

Disease symptoms: Foliar, fruit, stem and root lesions, white rot and crown rot.

Notes: In the most recent revision of the members of *Schizoparmaceae*, *Pilidiella* and its sexual morph *Schizoparme* were synonymised under *Coniella* because the type species of the three genera clustered in a single well-supported clade in a phylogenetic analysis based on four different loci (LSU, ITS, *rpb2* and *tef1*) (Alvarez *et al.* 2016). *Coniella* and *Pilidiella* were initially distinguished by von Arx (1981) based on their conidial pigmentation, being hyaline to pale brown in *Pilidiella* and dark brown in *Coniella*. However, Alvarez *et al.* (2016) demonstrated that conidial colour evolved multiple times throughout the clade representing *Coniella*, and therefore rejected it as a character for generic delimitation in *Schizoparmaceae*. Sutton (1980) and Nag Raj (1993) also considered *Coniella* and *Pilidiella* synonymous since both genera presented identical conidiomata, conidiogenesis and orientation of conidiophores. However, Castlebury *et al.* (2002) demonstrated a separation of both genera in a phylogenetic study based on LSU sequences. This was further supported by van Niekerk *et al.* (2004b) based on their LSU, ITS and *tef1* sequence data. Based on these molecular studies, together with the difference in conidial pigmentation reported by von Arx (1981), Wijayawardene *et al.* (2016) regarded *Coniella* and *Pilidiella* as two separate genera in a recent study of dematiaceous coelomycetes. By adding more loci and expanding the number of isolates studied, Alvarez *et al.* (2016) resolved the conflict that lasted a few decades regarding the classification of these genera.

References: Van Niekerk *et al.* 2004b, Crous *et al.* 2014a, Alvarez *et al.* 2016 (morphology and phylogeny).

Coniella duckerae H.Y. Yip, Trans. Brit. Mycol. Soc. 89: 587. 1987. Fig. 29.

Description and illustration: Yip (1987).

Material examined: **Australia**, Victoria, Wilson's Promontory, Five Mile Road, on rhizosphere of *Lepidospermum concavum*, unknown collector and date (**holotype** DAR 55703, **isotype** VPRI 13689, culture ex-type VPRI 13689 = CBS 142045).

Notes: *Coniella duckerae* was excluded from the study of Alvarez *et al.* (2016), as no ex-type culture was available. However, the original culture was recently revived, and DNA barcodes could thus be generated for inclusion in this study.

Coniella hibisci (B. Sutton) Crous, **comb. nov.** MycoBank MB820811. Fig. 30.
Basionym: *Coniella musaiaensis* var. *hibisci* B. Sutton, The Coelomycetes (Kew): 420. 1980.

Plant pathogenic. *Conidiomata* separate, immersed or superficial, globose to depressed, initially appearing hyaline, becoming olivaceous to black with age, with plate-like structures, up to 350 µm diam; *ostiole* central, 40–80 µm diam; *conidiomatal wall* consisting of 2–4 layers of medium brown *textura angularis*. *Conidiophores* densely aggregated, slightly thicker, subulate, simple, frequently branched above, reduced to conidiogenous cells, or with 1–2 supporting cells, 25–35 × 3–5 µm. *Conidiogenous cells* simple, hyaline, smooth, tapering, 8–15 × 2.5–3 µm, 1.5–2 µm wide at apex, surrounded by a gelatinous coating, with visible periclinal thickening. *Conidia* hyaline to pale yellowish brown with age, fusoid to ellipsoidal, inequilateral, apex acutely rounded, widest at middle tapering to

Table 8. DNA barcodes of accepted *Coniella* spp.

Species	Isolates[1]	GenBank accession numbers[2]			References
		ITS	*rpb2*	*tef1*	
Coniella africana	CBS 114133^{T}	AY339344	KX833421	KX833600	Van Niekerk *et al.* (2004b), Alvarez *et al.* (2016)
Con. crousii	NFCCI 2213	HQ264189	–	–	Rajeshkumar *et al.* (2011)
Con. diplodiella	CBS 111858^{ET}	AY339323	KX833423	KX833603	Van Niekerk *et al.* (2004b), Alvarez *et al.* (2016)
Con. diplodiopsis	CBS 590.84^{T}	AY339334	–	–	Van Niekerk *et al.* (2004b)
Con. diplodiopsis	CBS 109.23	AY339332	KX833440	KX833624	Van Niekerk *et al.* (2004b), Alvarez *et al.* (2016)
Con. duckerae	VPRI 13689 = CBS 142045^{T}	KY924929	–	–	Present study
Con. erumpens	CBS 523.78^{T}	KX833535	KX833446	KX833630	Alvarez *et al.* (2016)
Con. eucalyptigena	CBS 139893^{T}	KR476725	–	–	Crous *et al.* (2015d)
Con. eucalyptorum	CBS 112640^{T}	AY339338	KX833452	KX833637	Van Niekerk *et al.* (2004b), Alvarez *et al.* (2016)
Con. fragariae	CBS 172.49^{NT}	AY339317	KX833472	KX833663	Van Niekerk *et al.* (2004b), Alvarez *et al.* (2016)
Con. fusiformis	CBS 141596^{T}	KX833576	KX833481	KX833674	Alvarez *et al.* (2016)
Con. granati	CBS 252.38	KX833581	KX833488	KX833681	Alvarez *et al.* (2016)
Con. hibisci	CBS 109757^{ET}	KX833589	–	KX833689	Present study
Con. javanica	CBS 455.68^{T}	KX833583	KX833489	KX833683	Alvarez *et al.* (2016)
Con. koreana	CBS 143.97^{T}	KX833584	KX833490	KX833684	Alvarez *et al.* (2016)
Con. lanneae	CBS 141597^{T}	KX833585	KX833491	KX833685	Alvarez *et al.* (2016)
Con. limoniformis	CBS 111021^{T}	KX833586	KX833492	KX833686	Alvarez *et al.* (2016)
Con. macrospora	CBS 524.73^{T}	KX833587	KX833493	KX833687	Alvarez *et al.* (2016)
Con. malaysiana	CBS 141598^{T}	KX833588	KX833494	KX833688	Alvarez *et al.* (2016)
Con. nicotianae	CBS 875.72^{T}	KX833590	KX833495	KX833690	Alvarez *et al.* (2016)
Con. nigra	CBS 165.60^{T}	AY339319	KX833496	KX833691	Van Niekerk *et al.* (2004b), Alvarez *et al.* (2016)
Con. obovata	CBS 111025	AY339313	KX833497	KX833692	Van Niekerk *et al.* (2004b), Alvarez *et al.* (2016)
Con. paracastaneicola	CBS 141292^{T}	KX833591	KX833498	KX833693	Alvarez *et al.* (2016)
Con. peruensis	CBS 110394^{T}	KJ710463	KX833499	KX833695	Crous *et al.* (2015c), Alvarez *et al.* (2016)
Con. pseudogranati	CBS 137980^{T}	KJ869132	–	–	Crous *et al.* (2014b)
Con. pseudostraminea	CBS 112624^{T}	KX833593	KX833500	KX833696	Alvarez *et al.* (2016)
Con. quercicola	CBS 904.69^{NT}	KX833595	KX833502	KX833698	Alvarez *et al.* (2016)
Con. solicola	CBS 766.71^{T}	KX833597	KX833505	KX833701	Alvarez *et al.* (2016)
Con. straminea	CBS 149.22	AY339348	KX833506	KX833704	Van Niekerk *et al.* (2004b), Alvarez *et al.* (2016)
Con. tibouchinae	CBS 131594^{T}	JQ281774	KX833507	JQ281778	Miranda *et al.* (2012), Alvarez *et al.* (2016)
Con. wangiensis	CBS 132530^{T}	JX069873	KX833509	KX833705	Crous *et al.* (2012b), Alvarez *et al.* (2016)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; NFCCI: National Fungal Culture Collection of India, Agharkar Research Institute, Pune, India; VPRI: Victorian Plant Pathogen Herbarium, Bundoora, Australia. ^{T,} ^{ET} and ^{NT} indicate ex-type, ex-epitype and ex-neotype strains, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *rpb2*: partial RNA polymerase II second largest subunit gene; *tef1*: partial translation elongation factor 1-alpha gene.

slightly truncate base, smooth-walled, mono- to multiguttulate, germ slits absent, (10–)11–13(–15) × (3–)3.5–4(–5) μm (L/W = 3.4), with a mucoid appendage alongside conidium.

Culture characteristics: Colonies on MEA surface dirty white, with prolific black conidial masses spreading from centre. On OA and PDA surface dirty white with profuse black conidiomata and sparse aerial mycelium.

Material examined: **Africa**, from *Hibiscus* sp., unknown date, A.R. Rossman (**epitype designated here** BPI 748426, MBT376042, culture ex-epitype CBS 109757 = ARS 3534). **Nigeria**, on leaves of *Hibiscus esculentus*, 25 Jul. 1967, Arny (**holotype** IMI 129200).

Notes: The morphology of the present African ex-epitype strain from *Hibiscus* sp. (CBS 109757 = ARS 3534) compares well with that of the holotype of *Coniella musaiaensis* var. *hibisci*, which was described from *Hibiscus esculentus* collected in Nigeria. A new combination is therefore proposed, elevating it to species rank. Presently there are still no cultures available of *Con. musaiaensis*, and further collections from *Bauhinia reticulata* (Sierra Leone) need to be made to resolve its phylogeny. *Coniella hibisci* is also morphologically similar to *Con. javanica* (on *Hibiscus sabdariffa*, Indonesia), although they are phylogenetically divergent (Alvarez *et al.* 2016).

Authors: Y. Marin-Felix, J. Edwards, A.Y. Rossman & P.W. Crous

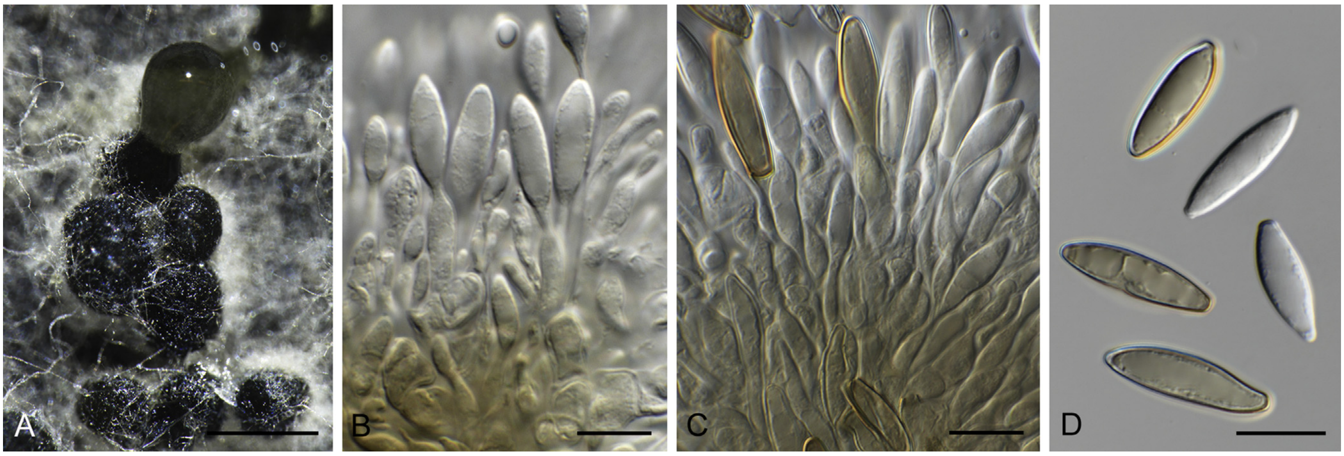


Fig. 29. *Coniella duckerae* (ex-type CBS 142045). **A.** Conidiomata forming on OA. **B, C.** Conidiogenous cells giving rise to conidia. **D.** Conidia. Scale bars: A = 350 μm, others = 10 μm.

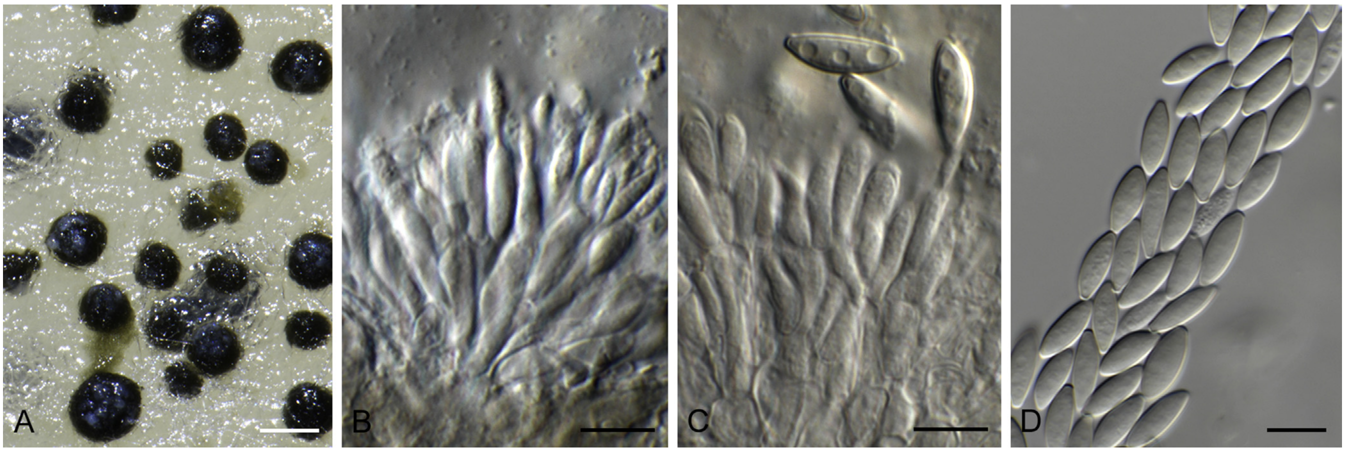


Fig. 30. *Coniella hibisci* (ex-epitype CBS 109757). **A.** Conidiomata forming on OA. **B, C.** Conidiogenous cells giving rise to conidia. **D.** Conidia. Scale bars: A = 350 μm, others = 10 μm.

Curvularia Boedijn, Bull. Jard. Bot. Buitenzorg, 3 Sér. 13: 123. 1933. Fig. 31.
Synonyms: *Malustela* Bat. & J.A. Lima, Publ. Inst. Micol. Recife 263: 5. 1960.
Curvusporium Corbetta as "Curvosporium", Riso 12: 28, 30. 1963.
Pseudocochliobolus Tsuda, *et al.*, Mycologia 69: 1117. 1978.

Classification: *Dothideomycetes*, *Pleosporomycetidae*, *Pleosporales*, *Pleosporaceae.*

Type species: *Curvularia lunata* (Wakker) Boedijn. Ex-neotype culture: CBS 730.96.

DNA barcodes (genus): LSU, ITS.

DNA barcodes (species): ITS, *gapdh*, *tef1*. Table 9. Fig. 32.

Ascomata pseudothecial, mostly globose to ellipsoidal, sometimes flask-shaped or flattened on hard substrata, brown or black, immersed, erumpent, partially embedded or superficial, free or developing on a basal columnar or flat stroma, smooth or covered with vegetative filaments; *ostiole* central, papillate or with a sub-conical, conical, paraboloid or cylindrical neck; *ascomatal wall* comprising pseudoparenchymatous cells of equal thickness or slightly thickened at apex of the ascoma. *Hamathecium* comprising septate, filiform, branched pseudoparaphyses. *Asci* bitunicate, clavate, cylindrical-clavate or broadly fusoid, straight or slightly curved, thin-walled, fissitunicate, often becoming more or less distended prior to dehiscence, short pedicellate, rounded at the apex. *Ascospores* multiseriate, filiform or flagelliform, hyaline or sometimes pale yellow or pale brown at maturity, septate, helically coiled within ascus, degree of ascospore coiling moderate to very strongly coiled, often with a mucilaginous sheath. *Conidiophores* straight to flexuous, often geniculate, multiseptate, usually simple, sometimes branched, smooth to verruculose, macronematous, mononematous, sometimes nodose, cylindrical. *Conidiogenous nodes* cylindrical, integrated, terminal and intercalary, proliferating sympodially, cicatrised. *Conidia* solitary, often curved, acropleurogenous, broadly fusoid, elliptical, obovoid or obpyriform, mostly smooth, sometimes verruculose, echinulate or tuberculate, 3 or more distoseptate, with or without an unequally swollen cell which is more pigmented than the other cells, septa sometimes accentuated with a dark band in some or all the cells, germinating mainly from one or both polar cells with the basal germ tube

Fig. 31. *Curvularia* spp. **A–F.** Conidiophores and conidia. **A.** *Curvularia geniculata*. **B.** *Curvularia neergaardii* (CBS 277.91). **C.** *Curvularia portulacea* (ex-isotype BRIP 14541). **D.** *Curvularia tropicalis* (ex-isotype BRIP 14834). **E.** *Curvularia hominis* (ex-type CBS 136985). **F.** *Curvularia muehlenbeckiae* (ex-type CBS 144.63). **G–I.** Conidia. **G.** *Curvularia crustacea* (ex-epitype BRIP 13524). **H.** *Curvularia nicotiae* (ex-isotype BRIP 11983). **I.** *Curvularia pseudolunata* (ex-type CBS 136987). **J.** Germinating conidium of *Curvularia neergaardii* (CBS 277.91). **K, L.** Microconidiation. **K.** *Curvularia americana* (ex-type CBS 136983). **L.** *Curvularia chlamydospora* (ex-type CBS 136984). **M.** Chlamydospores of *Curvularia pseudolunata* (ex-type CBS 136987). Scale bars: A = 50 µm; the others = 10 µm. Picture A taken from Samson *et al.* (2010); C, D, G, H from Tan *et al.* (2014); E, F, I, K–M from Madrid *et al.* (2014).

growing semiaxially, hilum in a slightly protruding truncate basal section of the conidial wall and often visible as two dark lenticular spots in optical section arranged close together with a small obscure narrow separating canal between them or distinctly protuberant, first conidial septum median or submedian, second septum often delimiting the basal cell of the mature conidium, third septum then distal. *Microconidiation* not common, producing conidia 1–2-celled, pale brown, globose to subglobose (adapted from Sivanesan 1987).

Culture characteristics: Colonies on PDA white or pale grey when young, orange to brown or different shades of grey (mainly dark olivaceous grey) when mature, fluffy, cottony, raised or convex with papillate surface, margin lobate, undulate, entire or sometimes rhizoid.

Optimal media and cultivation conditions: Sterilised *Zea mays* leaves placed on 1.5 % WA or slide cultures of half-strength PDA under near-ultraviolet light (12 h light, 12 h dark) to induce sporulation of the asexual morph, while for the sexual morph Sach's agar with sterilised rice or wheat straw at 25 °C is used.

Distribution: Worldwide.

Hosts: Wide host range, occurring as pathogens or saprobes. Mainly found on members of the *Poaceae*, being pathogens of

Table 9. DNA barcodes of accepted *Curvularia* spp.

Species	**Isolates**[1]	**GenBank accession numbers**[2]			**References**
		ITS	***gapdh***	***tef1***	
Curvularia aeria	CBS 294.61^{T}	HE861850	HF565450	–	da Cunha *et al.* (2013)
Cu. affinis	CBS 154.34^{SynT}	KJ909780	KM230401	KM196566	Manamgoda *et al.* (2015)
Cu. akaii	CBS 317.86	KJ909782	KM230402	KM196569	Manamgoda *et al.* (2015)
Cu. akaiiensis	BRIP 16080^{IsoT}	KJ415539	KJ415407	KJ415453	Tan *et al.* (2014)
Cu. alcornii	MFLUCC 10-0703^{T}	JX256420	JX276433	JX266589	Manamgoda *et al.* (2012a)
Cu. americana	UTHSC 08-3414^{T}	HE861833	HF565488	–	Madrid *et al.* (2014)
Cu. asiatica	MFLUCC 10-0711^{T}	JX256424	JX276436	JX266593	Manamgoda *et al.* (2012a)
Cu. australiensis	BRIP 12044^{T}	KJ415540	KJ415406	KJ415452	Tan *et al.* (2014)
Cu. australis	BRIP 12521^{T}	KJ415541	KJ415405	KJ415451	Tan *et al.* (2014)
Cu. bannonii	BRIP 16732^{IsoT}	KJ415542	KJ415404	KJ415450	Tan *et al.* (2014)
Cu. borreriae	CBS 859.73	HE861848	HF565455	–	da Cunha *et al.* (2013)
Cu. bothriochloae	BRIP 12522^{T}	KJ415543	KJ415403	KJ415449	Tan *et al.* (2014)
Cu. brachyspora	CBS 186.50	KJ922372	KM061784	KM230405	Manamgoda *et al.* (2014)
Cu. buchloës	CBS 246.49^{T}	KJ909765	KM061789	KM196588	Manamgoda *et al.* (2014)
Cu. carica-papayae	CBS 135941^{T}	HG778984	HG779146	–	Madrid *et al.* (2014)
Cu. chlamydospora	UTHSC 07-2764^{T}	HG779021	HG779151	–	Madrid *et al.* (2014)
Cu. clavata	BRIP 61680b	KU552205	KU552167	KU552159	Khemmuk *et al.* (2016)
Cu. coicis	CBS 192.29^{SynT}	JN192373	JN600962	JN601006	Manamgoda *et al.* (2015)
Cu. crustacea	BRIP 13524^{ET}	KJ415544	KJ415402	KJ415448	Tan *et al.* (2014)
Cu. cymbopogonis	CBS 419.78	HG778985	HG779129	HG779163	Madrid *et al.* (2014)
Cu. dactyloctenii	BRIP 12846^{T}	KJ415545	KJ415401	KJ415447	Tan *et al.* (2014)
Cu. ellisii	CBS 193.62^{T}	JN192375	JN600963	JN601007	Manamgoda *et al.* (2011)
Cu. eragrostidis	CBS 189.48	HG778986	HG779154	HG779164	Madrid *et al.* (2014)
Cu. geniculata	CBS 187.50	KJ909781	KM083609	KM230410	Manamgoda *et al.* (2015)
Cu. gladioli	CBS 210.79	HG778987	HG779123	–	Madrid *et al.* (2014)
Cu. graminicola	BRIP 23186^{T}	JN192376	JN600964	JN601008	Manamgoda *et al.* (2012b)
Cu. gudauskasii	DAOM 165085	AF071338	–	–	Berbee *et al.* (1999)
Cu. harveyi	BRIP 57412^{IsoT}	KJ415546	KJ415400	KJ415446	Tan *et al.* (2014)
Cu. hawaiiensis	BRIP 11987^{IsoLT}	KJ415547	KJ415399	KJ415445	Tan *et al.* (2014)
Cu. heteropogonicola	BRIP 14579^{IsoT}	KJ415548	KJ415398	KJ415444	Tan *et al.* (2014)
Cu. heteropogonis	CBS 284.91^{T}	JN192379	JN600969	JN601013	Manamgoda *et al.* (2012b)
Cu. hominis	CBS 136985^{T}	HG779011	HG779106	–	Madrid *et al.* (2014)
Cu. homomorpha	CBS 156.60^{T}	JN192380	JN600970	JN601014	Manamgoda *et al.* (2014)
Cu. inaequalis	CBS 102.42^{T}	KJ922375	KM061787	KM196574	Manamgoda *et al.* (2014)
Cu. intermedia	CBS 334.64	HG778991	HG779155	HG779169	Madrid *et al.* (2014)
Cu. ischaemi	CBS 630.82^{T}	JX256428	JX276440	–	Manamgoda *et al.* (2012b)
Cu. kusanoi	CBS 137.29	JN192381	–	JN601016	Manamgoda *et al.* (2015)
Cu. lunata	CBS 730.96^{NT}	JX256429	JX276441	JX266596	Manamgoda *et al.* (2012b)
Cu. malina	CBS 131274^{T}	JF812154	KP153179	KR493095	Tomaso-Peterson *et al.* (2016)
Cu. miyakei	CBS 197.29^{SynT}	KJ909770	KM083611	KM196568	Manamgoda *et al.* (2014)
Cu. muehlenbeckiae	CBS 144.63^{T}	HG779002	HG779108	–	Madrid *et al.* (2014)
Cu. neergaardii	BRIP 12919^{IsoT}	KJ415550	KJ415397	KJ415443	Tan *et al.* (2014)
Cu. neoindica	BRIP 17439	AF081449	AF081406	–	Berbee *et al.* (1999)
Cu. nicotiae	CBS 655.74^{IsoT} = BRIP 11983	KJ415551	KJ415396	KJ415442	Tan *et al.* (2014)
Cu. nodulosa	CBS 160.58	JN601033	JN600975	JN601019	Manamgoda *et al.* (2015)
Cu. oryzae	CBS 169.53^{IsoT}	KP400650	KP645344	KM196590	Manamgoda *et al.* (2015)
Cu. ovariicola	CBS 470.90^{T}	JN192384	JN600976	JN601020	Manamgoda *et al.* (2012b)
Cu. papendorfii	CBS 308.67^{T}	KJ909774	KM083617	KM196594	Manamgoda *et al.* (2014)

(*continued on next page*)

Table 9. (Continued).

Species	Isolates[1]	GenBank accession numbers[2]			References
		ITS	*gapdh*	*tef1*	
Cu. pallescens	CBS 156.35^{T}	KJ922380	KM083606	KM196570	Manamgoda *et al.* (2015)
Cu. perotidis	CBS 350.90^{T}	JN192385	KJ415394	JN601021	Manamgoda *et al.* (2015)
Cu. pisi	CBS 190.48^{T}	KY905678	KY905690	KY905697	Present study
Cu. portulacae	CBS 239.48^{IsoT} = BRIP 14541	KJ415553	KJ415393	KJ415440	Tan *et al.* (2014)
Cu. prasadii	CBS 143.64^{T}	KJ922373	KM061785	KM230408	Manamgoda *et al.* (2014)
Cu. protuberata	CBS 376.65^{IsoT}	KJ922376	KM083605	KM196576	Manamgoda *et al.* (2014)
Cu. pseudolunata	UTHSC 09-2092^{T}	HE861842	HF565459	–	da Cunha *et al.* (2013)
Cu. pseudorobusta	UTHSC 08-3458	HE861838	HF565476	–	da Cunha *et al.* (2013)
Cu. ravenelii	BRIP 13165^{T}	JN192386	JN600978	JN601024	Manamgoda *et al.* (2012b)
Cu. richardiae	BRIP 4371^{IsoLT}	KJ415555	KJ415391	KJ415438	Tan *et al.* (2014)
Cu. robusta	CBS 624.68^{IsoT}	KJ909783	KM083613	KM196577	Manamgoda *et al.* (2014)
Cu. ryleyi	BRIP 12554^{T}	KJ415556	KJ415390	KJ415437	Tan *et al.* (2014)
Cu. senegalensis	CBS 149.71	HG779001	HG779128	–	Madrid *et al.* (2014)
Cu. sesuvi	Bp-Zj 01	EF175940	–	–	Zhang & Li (2009)
Cu. soli	CBS 222.96^{T}	KY905679	KY905691	KY905698	Present study
Cu. sorghina	BRIP 15900^{IsoT}	KJ415558	KJ415388	KJ415435	Tan *et al.* (2014)
Cu. spicifera	CBS 274.52	JN192387	JN600979	JN601023	Manamgoda *et al.* (2012b)
Cu. subpapendorfii	CBS 656.74^{T}	KJ909777	KM061791	KM196585	Manamgoda *et al.* (2015)
Cu. trifolii	CBS 173.55	HG779023	HG779124	–	Madrid *et al.* (2014)
Cu. tripogonis	BRIP 12375^{T}	JN192388	JN600980	JN601025	Manamgoda *et al.* (2011)
Cu. tropicalis	BRIP 14834^{IsoT}	KJ415559	KJ415387	KJ415434	Tan *et al.* (2014)
Cu. tsudae	ATCC 44764^{PT}	KC424596	KC747745	KC503940	Deng *et al.* (2014)
Cu. tuberculata	CBS 146.63^{IsoT}	JX256433	JX276445	JX266599	Manamgoda *et al.* (2012b)
Cu. uncinata	CBS 221.52^{T}	HG779024	HG779134	–	Madrid *et al.* (2014)
Cu. verruciformis	CBS 537.75	HG779026	HG779133	HG779211	Madrid *et al.* (2014)
Cu. verruculosa	CBS 150.63	KP400652	KP645346	KP735695	Manamgoda *et al.* (2015)

[1] ATCC: American Type Culture Collection, Virginia, USA; BRIP: Queensland Plant Pathology Herbarium, Brisbane, Australia; Bp-Zj: Isolate housed in Biotechnology Institute, Zhejiang University, Hangzhou, China; CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; DAOM: Plant Research Institute, Department of Agriculture (Mycology), Ottawa, Canada; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Ria, Thailand, UTHSC: Fungus Testing Laboratory, Department of Pathology at the University of Texas Health Science Center, San Antonio, Texas, USA. $^{ET,\ IsoT,\ IsoLT,\ PT,\ SynT}$ and ^{T} indicate ex-epitype, ex-isotype, ex-isolectotype, ex-paratype, ex-syntype and ex-type strains, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *gapdh*: partial glyceraldehyde-3-phosphate dehydrogenase gene; *tef1*: partial translation elongation factor 1-alpha gene.

grass and staple crops, including rice, maize, wheat and sorghum. This genus also occurs on genera belonging to *Actinidiaceae*, *Aizoaceae*, *Caricaceae*, *Convolvulaceae*, *Fabaceae*, *Iridaceae*, *Lamiaceae*, *Lythraceae*, *Oleaceae*, *Polygonaceae* and *Rubiaceae.*

Disease symptoms: Leaf spots, leaf blight, melting out, root rot, foot rot, among others.

Notes: Species delimitation in *Curvularia* based on morphology only is difficult due to the morphological complexity within this genus, as also observed in *Bipolaris*. Furthermore, the differentiation of both genera based on morphology alone is sometimes complicated (see *Bipolaris* notes for morphological differences between *Bipolaris* and *Curvularia*). Therefore, molecular data are essential for an accurate identification of species within these genera, ITS, *gapdh* and *tef1* being the loci selected for this purpose (Manamgoda *et al.* 2014, 2015).

Curvularia is a rich genus in host range and geographic distribution compared to *Bipolaris*. Apart from phytopathogenic species, this genus comprises species that are pathogens of humans and other animals, causing respiratory tract, cutaneous, cerebral and corneal infections, mainly in immunocompromised patients (Carter & Boudreaux 2004). Some species can be found in association with both humans and plants, such as *Cu. hawaiiensis*, *Cu. lunata* and *Cu. spicifera* (Manamgoda *et al.* 2015).

References: Sivanesan 1987 (morphology and pathogenicity); Manamgoda *et al.* 2011 (pathogenicity), Manamgoda *et al.* 2015 (morphology, pathogenicity and phylogeny).

Curvularia pisi Y. Marín & Crous, **sp. nov.** MycoBank MB820814. Fig. 33.

Etymology: Name refers to the host genus from which it was isolated, *Pisum*.

Hyphae hyaline to pale brown, branched, septate, thin-walled, 1.5–5 µm. *Conidiophores* arising in groups, septate, straight or flexuous, geniculate at upper part, verruculose, tapering towards apex, sometimes branched, cells walls thicker than those of vegetative hyphae, mononematous, semi- to macronematous, pale brown to brown, paler towards apex, not swollen at the base, (35–)50–210 × 2.5–5 µm. *Conidiogenous cells* verruculose, terminal or intercalary, proliferating sympodially, pale brown to brown, subcylindrical to swollen, (2.5–)5–15.5 × 3–7.5 µm. *Conidia* verruculose, curved, rarely straight, middle cells unequally enlarged, reniform, rarely ellipsoidal, brown, with apical and basal cells paler than middle cells being subhyaline to pale brown, (2–)3-distoseptate, 16–35 × 9–15.5 µm; *hila* slightly protuberant, flat, darkened, slightly thickened, 1.5–4 µm. *Chlamydospores*, *microconidiation* and *sexual morph* not observed.

Culture characteristics: Colonies on PDA reaching 90 mm diam within 1 wk, with sparse to moderate aerial mycelium giving a slightly cottony appearance, margin lobate; surface apricot to chestnut; reverse umber to chestnut.

Material examined: **Canada**, Ontario, Renfrew, on *Pisum sativum* seeds, 15 Feb. 1943, J.W. Groves (**holotype** CBS H-11405, culture ex-type CBS 190.48).

Notes: *Curvularia pisi* is closely related to *Cu. muehlenbeckiae* and *Cu. hominis*. Morphologically, these species are similar but *Cu. pisi* produces shorter conidiophores. Moreover, *Cu. muehlenbeckiae* produces smaller conidia than *Cu. pisi*, and *Cu. hominis* is characterised by 3–4-distoseptate conidia while the conidia in the other two species are 3-distoseptate.

Curvularia pisi is known to occur on *Pisum sativum*, which is also host to two other species of *Curvularia*, *Cu. inaequalis* and *Cu. spicifera*. *Curvularia spicifera* produces a sexual morph, while no sexual morph has been observed in the other two species. Moreover, *Cu. spicifera* differs from *Cu. pisi* in having smooth-walled conidia. *Curvularia inaequalis* can be distinguished from *Cu. pisi* by its longer conidia, which are predominantly 4-distoseptate.

Curvularia soli Y. Marín & Crous, **sp. nov.** MycoBank MB820816. Fig. 34.

Etymology: Named after its ecology, occurring in soil, "*soli*".

Hyphae subhyaline to pale brown, branched, septate, thin-walled, 2.5–5.5 µm. *Conidiophores* arising in groups, septate, straight or flexuous, geniculate at upper part, smooth to verruculose, unbranched, cells walls thicker than those of vegetative hyphae, mononematous, semi- to macronematous, pale brown to brown, slightly paler towards apex, not swollen at the base, (65–)90–270(–390) × 2.5–5(–6) µm. *Conidiogenous cells* smooth-walled to finely verruculose, terminal or intercalary, proliferating sympodially, pale brown to brown, subcylindrical to swollen, 4–13 × 2.5–5 µm. *Conidia* verruculose, curved, rarely straight, middle cells unequally enlarged, reniform, rarely ellipsoidal, pale brown to brown, apical and basal cells paler than middle cells being subhyaline to pale brown, 3–4(–5)-distoseptate, (13.5–)18–28 × 7.5–11 µm; *hila* protuberant, flat, darkened, thickened, 1.3–3.5 µm. *Chlamydospores*, *microconidiation* and *sexual morph* not observed.

Culture characteristics: Colonies on PDA reaching 75–79 mm diam after 1 wk, velvety to slightly powdery; surface and reverse grey olivaceous to olivaceous black.

Material examined: **Papua New Guinea**, Madang, Jais Aben, isolated from soil along coral reef coast, Nov. 1995, collected by A. Aptroot, isol. by A. van Iperen (**holotype** CBS H-23116, culture ex-type CBS 222.96).

Notes: *Curvularia soli* is closely related to *Cu. asianensis*, *Cu. geniculata* and *Cu. senegalensis*. All three species are characterised by conidia that are predominantly 4-distoseptate. *Curvularia geniculata* is the only species that produces a sexual morph and has the longest conidia among these taxa (26–48 µm). *Curvularia asiatica* can be distinguished from *Cu. soli* by its much longer conidiophores [(75–)100–700(–708) µm] and shorter conidia [(11–)15–23(–23.5) µm]. *Curvularia senegalensis* is characterised by having shorter conidiophores (up to 150 µm) and wider conidia (10–14 µm) than *Cu. soli*.

Authors: Y. Marin-Felix, P.W. Crous & Y.P. Tan

Monilinia Honey, Mycologia 20: 153. 1928. Fig. 35.
Synonym: *Monilia* Bonord., Handb. Mykol.: 7. 1851.

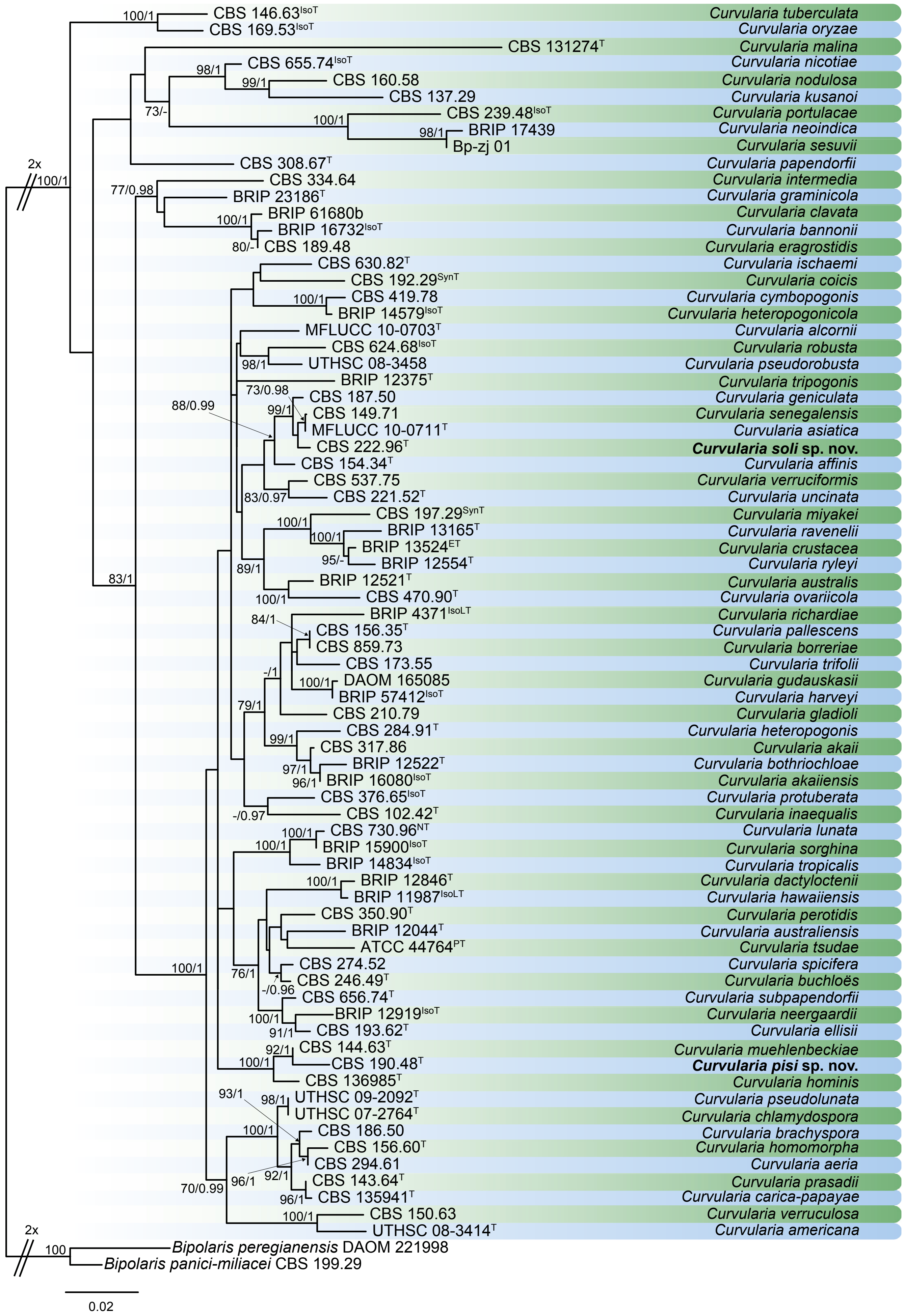
Classification: *Leotiomycetes*, *Leotiomycetidae*, *Helotiales*, *Sclerotiniaceae.*

Type species: *Monilinia fructicola* (G. Winter) Honey. Holotype: BPI 1109031.

DNA barcode (genus): ITS.

DNA barcode (species): *tef1.* Table 10. Fig. 36.

Ascomata apothecial, cup- or funnel-shaped, long stipitate, pale brown, formed solitary or in groups from pseudosclerotia in aborted or mummified fruits and debris partially or completely buried in soil; *stipe* cylindrical, flexuous, pale brown, often darker near the base; *hymenium* comprising filiform, septate, unbranched and hyaline paraphyses. *Asci* unitunicate, inoperculate, with amyloid apical apparatus, cylindrical to clavate, flattened or rounded at the apex, thin-walled, 8-spored. *Ascospores* ellipsoid, often with tapered ends, 1-celled, hyaline, sometimes covered with a gelatinous sheet. *Conidiophores* single or aggregated forming sporodochia, straight or flexuous, hyaline to subhyaline, branched, thin-walled, septate. *Macroconidia* blastic-acropetal, oval, lemon-shaped or broadly ellipsoidal, rarely doliiform, hyaline to subhyaline, thin-and smooth-walled, 1-celled, sometimes presenting distinct axial connections (disjunctors), formed in chains, simple or dichotomously branched; *microconidia* (spermatia) sometimes present in old cultures, globose to pyriform, hyaline, smooth- and thin-walled, borne on lageniform, often asymmetric phialides. *Arthric conidia* occasionally formed, ovoid to ellipsoid, smooth- and thin-walled.


100/1
CBS 146.63^{IsoT} Curvularia tuberculata
CBS 169.53^{IsoT} Curvularia oryzae
CBS 131274^{T} Curvularia malina
98/1
CBS 655.74^{IsoT} Curvularia nicotiae
99/1
CBS 160.58 Curvularia nodulosa
CBS 137.29 Curvularia kusanoi
73/-
100/1
CBS 239.48^{IsoT} Curvularia portulacae
98/1
BRIP 17439 Curvularia neoindica
Bp-zj 01 Curvularia sesuvii
2x
100/1
CBS 308.67^{T} Curvularia papendorfii
77/0.98
CBS 334.64 Curvularia intermedia
BRIP 23186^{T} Curvularia graminicola
100/1
BRIP 61680b Curvularia clavata
BRIP 16732^{IsoT} Curvularia bannonii
80/-
CBS 189.48 Curvularia eragrostidis
CBS 630.82^{T} Curvularia ischaemi
CBS 192.29^{SynT} Curvularia coicis
100/1
CBS 419.78 Curvularia cymbopogonis
BRIP 14579^{IsoT} Curvularia heteropogonicola
MFLUCC 10-0703^{T} Curvularia alcornii
CBS 624.68^{IsoT} Curvularia robusta
98/1
UTHSC 08-3458 Curvularia pseudorobusta
BRIP 12375^{T} Curvularia tripogonis
73/0.98
CBS 187.50 Curvularia geniculata
88/0.99
99/1
CBS 149.71 Curvularia senegalensis
MFLUCC 10-0711^{T} Curvularia asiatica
CBS 222.96^{T} **Curvularia soli sp. nov.**
CBS 154.34^{T} Curvularia affinis
CBS 537.75 Curvularia verruciformis
83/0.97
CBS 221.52^{T} Curvularia uncinata
100/1
CBS 197.29^{SynT} Curvularia miyakei
100/1
BRIP 13165^{T} Curvularia ravenelii
BRIP 13524^{ET} Curvularia crustacea
95/-
BRIP 12554^{T} Curvularia ryleyi
89/1
BRIP 12521^{T} Curvularia australis
83/1
100/1
CBS 470.90^{T} Curvularia ovariicola
84/1
BRIP 4371^{IsoLT} Curvularia richardiae
CBS 156.35^{T} Curvularia pallescens
CBS 859.73 Curvularia borreriae
CBS 173.55 Curvularia trifolii
-/1
100/1
DAOM 165085 Curvularia gudauskasii
BRIP 57412^{IsoT} Curvularia harveyi
79/1
CBS 210.79 Curvularia gladioli
99/1
CBS 284.91^{T} Curvularia heteropogonis
CBS 317.86 Curvularia akaii
97/1
BRIP 12522^{T} Curvularia bothriochloae
96/1
BRIP 16080^{IsoT} Curvularia akaiiensis
CBS 376.65^{IsoT} Curvularia protuberata
-/0.97
CBS 102.42^{T} Curvularia inaequalis
100/1
CBS 730.96^{NT} Curvularia lunata
100/1
BRIP 15900^{IsoT} Curvularia sorghina
BRIP 14834^{IsoT} Curvularia tropicalis
100/1
BRIP 12846^{T} Curvularia dactyloctenii
BRIP 11987^{IsoLT} Curvularia hawaiiensis
CBS 350.90^{T} Curvularia perotidis
BRIP 12044^{T} Curvularia australiensis
ATCC 44764^{PT} Curvularia tsudae
CBS 274.52 Curvularia spicifera
100/1
76/1
CBS 246.49^{T} Curvularia buchloës
-/0.96
CBS 656.74^{T} Curvularia subpapendorfii
BRIP 12919^{IsoT} Curvularia neergaardii
100/1
91/1
CBS 193.62^{T} Curvularia ellisii
92/1
CBS 144.63^{T} Curvularia muehlenbeckiae
100/1
CBS 190.48^{T} **Curvularia pisi sp. nov.**
CBS 136985^{T} Curvularia hominis
93/1
98/1
UTHSC 09-2092^{T} Curvularia pseudolunata
UTHSC 07-2764^{T} Curvularia chlamydospora
100/1
CBS 186.50 Curvularia brachyspora
CBS 156.60^{T} Curvularia homomorpha
CBS 294.61 Curvularia aeria
92/1
96/1
CBS 143.64^{T} Curvularia prasadii
70/0.99
96/1
CBS 135941^{T} Curvularia carica-papayae
100/1
CBS 150.63 Curvularia verruculosa
UTHSC 08-3414^{T} Curvularia americana
2x
100
Bipolaris peregianensis DAOM 221998
Bipolaris panici-miliacei CBS 199.29
0.02

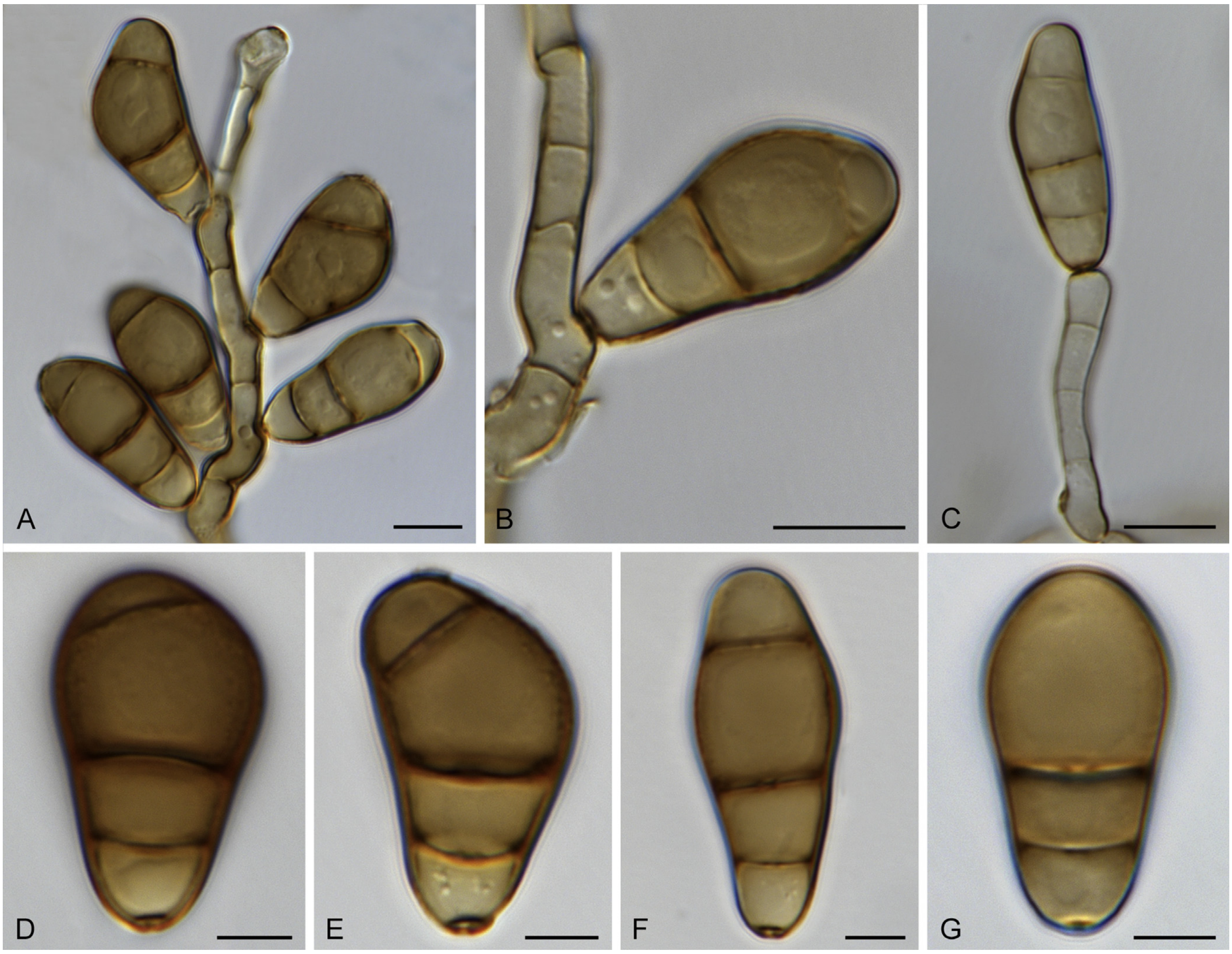


Fig. 33. *Curvularia pisi* (ex-type CBS 190.48). **A, B.** Conidiophores and conidia. **C–G.** Conidia. Scale bars: A–C = 10 μm; D–G = 5 μm.

Culture characteristics: Colonies on PDA white, yellow-grey, brown-grey or olive-grey, often zonate or forming concentric rings, felty to velvety, flat or concave, margin entire or lobed giving a rosette-like appearance, brown to black stromata can be present in old cultures.

Optimal media and cultivation conditions: PDA and WA, incubated under near-ultraviolet light (12 h light, 12 h dark) at 22–25 °C to determine growth rates, colour and shape of the colony, and induce sporulation of the asexual morph. The sexual morph is not formed under *in vitro* culture conditions but can be induced by inoculation on natural substrata and incubated several months partially buried in sterilised soil.

Distribution: Worldwide.

Hosts: Mostly found as crop pathogens or causing post-harvest losses on stone fruits, most commonly on members of *Rosaceae*, predominantly on *Cydonia* spp., *Malus* spp., *Prunus* spp. and *Pyrus* spp., but have been reported in at least 11 other genera on this family, linked to some kind of host specialisation. Other known hosts include members of *Actinidiaceae*, *Berberidaceae*, *Betulaceae*, *Ebernaceae*, *Ericaceae*, *Euphorbiaceae*, *Moraceae*, *Myricaceae*, *Myrtaceae*, *Solanaceae* and *Vitaceae.*

Disease symptoms: Leaf spots, blossom and twig blight, twig and stem canker, fruit rot.

Notes: Generic identification *in vivo* or *in vitro* is easy considering the characteristic monilioid hyphae and sexual-morphs. *Monilinia* is morphologically similar and closely related to the genus *Sclerotinia*, from which it can be differentiated by the absence of asexual reproduction and formation of true sclerotia in *Sclerotinia*. However, species identification in *Monilinia* is rather difficult by means of morphology alone. A combination of cultural features, physiology and host range is often necessary, including macro and micromorphology, growth rates, conidial dimension and characteristics of the germ tube during sporulation. Other employed techniques include AFLP and RFLP (Gril *et al.* 2010, Vasić *et al.* 2016), specific PCR amplification for the three major brown rot pathogens

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Fig. 32. RAxML phylogram obtained from the combined ITS (504 bp), *gapdh* (461 bp) and *tef1* (893 bp), sequences of all the accepted species of *Curvularia*. The tree was rooted to *Bipolaris panici-miliacei* CBS 199.29 and *Bipolaris peregianensis* DAOM 221998. The novel species described in this study are shown in **bold**. RAxML bootstrap support (BS) values above 70 % and Bayesian posterior probability scores $\geq$ 0.95 are shown at the nodes. GenBank accession numbers are indicated in Table 9. $^{\text{ET, IsoT, IsoLT, PT, SynT}}$ and $^{\text{T}}$ indicate ex-epitype, ex-isotype, ex-isolectotype, ex-paratype, ex-syntype and ex-type strains, respectively. TreeBASE: S20877.

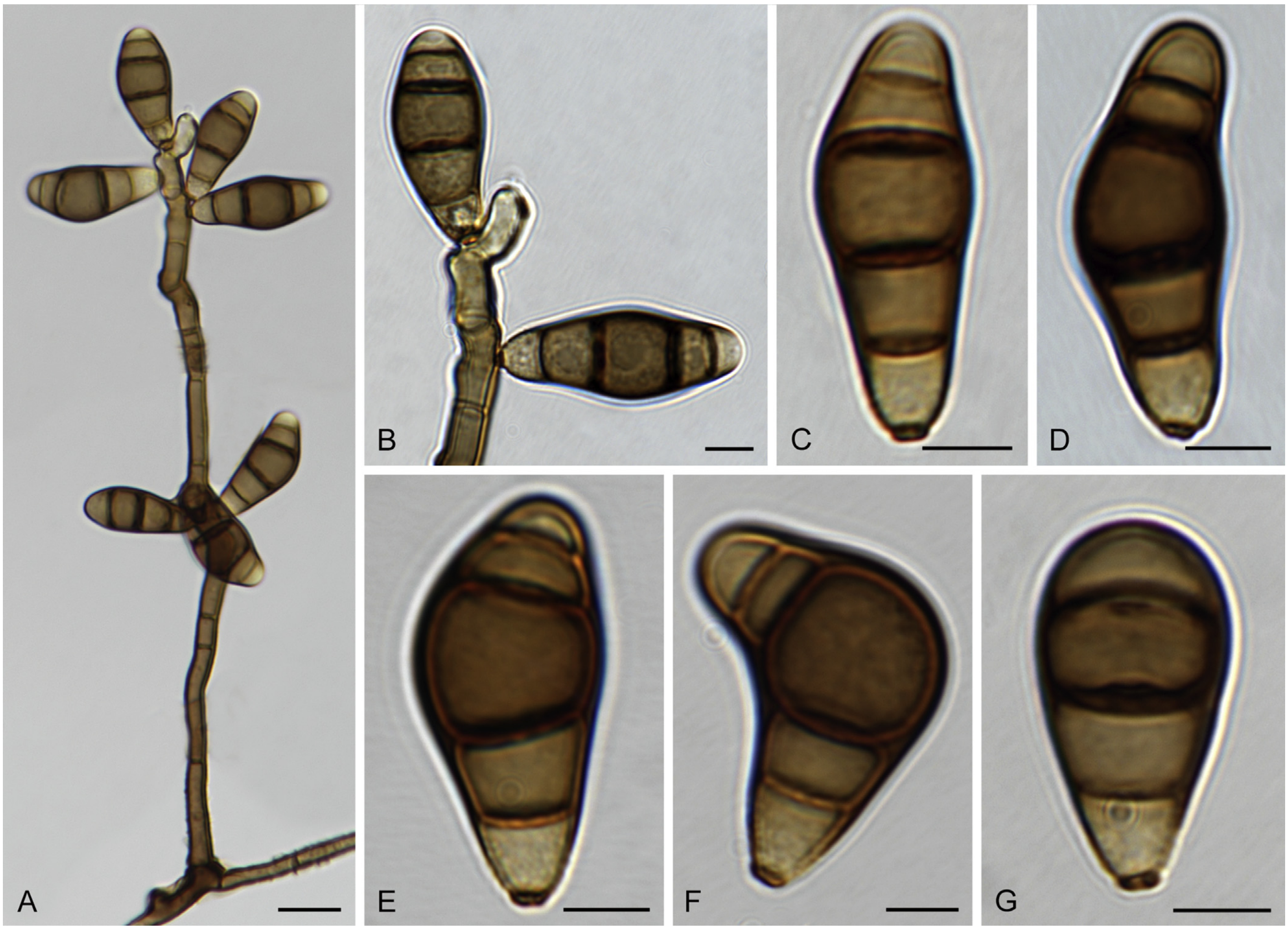


Fig. 34. *Curvularia soli* (ex-type CBS 222.96). **A–C.** Conidiophores and conidia. **D–G.** Conidia. Scale bars: A = 10 µm; others = 5 µm.

M. fructigena, *M. fructicola* and *M. laxa* (Cote *et al.* 2004, Gell *et al.* 2007) and amplification of specific introns for rapid identification of *M. fructicola* (Fulton & Brown 1997). A species delimitation based on molecular phylogeny is currently lacking and no ex-type material is known to exist for most taxa. However, several reference ITS and *tef1* sequences are available from a set of curated isolates in Q-bank (http://www.q-bank.eu/Fungi/).

A proposal to protect the generic name *Monilinia* over *Monilia* has been recently published based on the complex and often conflicting taxonomic history of the latter name (Johnston *et al.* 2014). Following this proposal, two new combinations are proposed below.

References: Batra 1988, 1991, Honey 1928, 1936, van Leeuwen *et al.* 2002 (morphology and pathogenicity); van Leeuwen 2000 (morphology, pathogenicity and epidemiology); OEPP/EPPO 2009, Martini & Mari 2014 (morphology, pathogenicity and biology).

Monilinia mumeicola (Y. Harada *et al.*) Sandoval-Denis & Crous, **comb. nov.** MycoBank MB819176.
Basionym: *Monilia mumeicola* [as 'mumecola'] Y. Harada *et al.*, J. Gen. Plant Pathol. 70: 305. 2004.

Notes: This species is only known from its asexual morph. It was described as a pathogen on Japanese apricot (*Prunus mume*) in Japan (Harada *et al.* 2004), and later reported causing brown rot of *Prunus armeniaca* (Yin *et al.* 2014) and *Prunus salicina* (Yin *et al.* 2015) in China. Our phylogeny (Fig. 36) included sequences of two authentic isolates of *Monilia numeicola* and supported its location in the genus *Monilinia*, being closely related to the common agents of brown rot *M. fructicola*, *M. fructigena* and *M. laxa*.

Monilinia yunnanensis (M.J. Hu & C.X. Luo) Sandoval-Denis & Crous, **comb. nov.** MycoBank MB819177.
Basionym: *Monilia yunnanensis* M.J. Hu & C.X. Luo, PloS ONE 6: 11. 2011.

Notes: This taxon was described as a pathogen of peach (*Prunus persica*) in China and has subsequently been isolated as the most prevalent pathogen of apple and pear in the southern, northern and western regions of that country (Zhu *et al.* 2016). Its phylogenetic placement in *Monilinia* was supported in our phylogeny (Fig. 36) based on sequences from two authentic isolates, showing that it forms a clade basal to the main cluster grouping the most economically relevant species of the genus.

Authors: M. Sandoval-Denis & P.W. Crous

Neofabraea H.S. Jacks., Rep. Oregon Exp. Sta. 1911–1912: 187. 1913. Fig. 37.

Classification: *Leotiomycetes*, *Leotiomycetidae*, *Helotiales*, *Dermateaceae.*

Type species: *Neofabraea malicorticis* H.S. Jacks. Neotype and ex-neotype culture: CBS H-22219, CBS 122030 = OSC 100036.

DNA barcodes (genus): LSU.

DNA barcodes (species): ITS, *tub2*, *rpb2.* Table 11. Fig. 38.

Ascomata apothecial, erumpent from bark, sessile to short-stalked, solitary or in clusters on a basal stroma; *disc* often not well-delimited, circular, elliptical, or irregular and merged, greyish, flesh-coloured to pale reddish or brownish, drying darker, 0.5–2.0 mm diam. *Paraphyses* numerous, filiform, septate, obtuse, simple or branched, hyaline, smooth-walled, apical cells mostly slightly swollen. *Asci* inoperculate, cylindrical-clavate, apex rounded or truncate-rounded, attenuated into a stalk of variable length, crozier present, 8-spored; apical apparatus with a well-developed apical thickening, Lugol's + or −, blue in herbarium material, Melzer's + or −. *Ascospores* inequilateral, elongated ellipsoid, ends rounded, straight or curved, aseptate, thin-walled, smooth, hyaline, with granular contents or small oil droplets; later septate, sometimes germinating or forming conidia from minute openings or phialides. *Conidiomata* erumpent from bark, stromatic, acervular, plane to pulvinate. *Conidiophores* simple or branched, smooth, hyaline, acrogenous or acropleurogenous. *Conidiogenous cells* discrete or integrated, determinate, phialidic, cylindrical to narrowly ampulliform, giving rise to macro- and/or microconidia. *Macroconidia* cylindrical-fusiform, allantoid to ellipsoid, straight or curved, rounded or somewhat pointed at apex, rounded or attenuated and with an indistinct, barely or non-protruding scar at base, smooth, aseptate, hyaline, and thin-walled when liberated, mostly filled with numerous oil droplets; later becoming septate and brown. *Microconidia* present or absent, cylindrical, rounded at apex, narrowly truncate at base, aseptate, hyaline, thin- and smooth-walled, with minute granular contents (adapted from Chen *et al.* 2016).

Culture characteristics: Colonies on OA white, cottony. Colonies on PDA orange or red, slimy.

Optimal media and cultivation conditions: OA at 25 °C under near-ultraviolet light (12 h light, 12 h dark); OA supplemented with sterile nettle stems (*Anthriscus sylvestris*) or direct inoculation into apple fruit (*Malus domestica*) can be used to induce sporulation.

Distribution: Worldwide.

Hosts: Pathogens or harmless saprobes of apples and pears, but also of several other hosts such as species of *Prunus* and *Populus*.

Disease symptoms: Anthracnose canker, perennial canker and bull's-eye rot.

Notes: *Neofabraea* was introduced by Jackson (1913) to accommodate the sexual morph *Gloeosporium malicorticis*. Subsequently, Nannfeldt (1932) synonymised this genus with *Pezicula*. However, Verkley (1999) revalidated it and observed that species of *Neofabraea* are more explicitly pathogenic than those of *Pezicula*. *Neofabraea* further differs from *Pezicula* in that *Neofabraea* produces ascomata with excipular tissues less differentiated and macroconidia more strongly curved with the basal scar less distinct than in *Pezicula*. Moreover, *Pezicula* comprises species that have two types of conidiogenesis: conidiogenous cells are determinate and phialidic, or indeterminate and proliferating percurrently, while *Neofabraea* spp. only produces phialidic conidiogenous cells (Chen *et al.* 2016). Recently, Chen *et al.* (2016) carried out a revision of the genus by performing a phylogenetic study based on LSU, ITS, *tub2* and *rpb2* sequences of *Neofabraea*, *Pezicula* and related genera. Consequently, the genus *Phlyctema* was re-established to accommodate *Neofabraea alba*, which is the main pathogen causing bull's eye rot in continental Europe. Moreover, the new genera *Parafabraea* and *Pseudofabraea* were introduced in order to accommodate *Neofabraea eucalypti* and *Neofabraea citricarpa*, respectively (Chen *et al.* 2016).

References: Verkley 1999 (morphology and pathogenicity), Wang *et al.* 2015 (morphology and key of *Neofabraea* spp.), Chen *et al.* 2016 (phylogeny).

Verkleyomyces Y. Marín & Crous, **gen. nov.** MycoBank MB820818.

Etymology: Named after Gerard J.M. Verkley, in recognition for his contributions to the understanding of *Neofabraea* and related genera.

Mycelium hyaline to pale brown, branched, septate. *Ascomata* apothecial, partly immersed, erumpent, sessile, solitary, sometimes gregarious; *medullary excipulum* weakly developed, composed of hyaline *textura prismatica*; *ectal excipulum* composed of brown to olivaceous brown *textura prismatica* at the base, and pale brown *textura intricata* towards the margin; *subhymenium* hyaline, composed of interwoven hyphae. *Paraphyses* cylindrical, slender, septate, apex rounded, hyaline, flexuous, numerous. *Asci* unitunicate, clavate to cylindrical-clavate, base truncate, short pedicellate, with an apical apparatus stained blue or purplish blue in Melzer's reagent, 8-spored, ascospores discharging through apical pore. *Ascospores* fusoid to ellipsoid, hyaline, ends rounded or somewhat pointed, straight or slightly curved, thin-walled, guttulate or eguttulate, initially aseptate, or later becoming 1-septate. *Conidiomata* acervular or cupulate, semi-immersed, dark, separate, formed of olivaceous brown *textura intricata*, dehiscence by irregular fissures, sometimes by a central ostiole. *Conidiophores* simple, hyaline, smooth, thin-walled, septate at the base, unbranched, discrete, or rarely integrated beneath the aged conidiogenous cell. *Conidiogenous cells* enteroblastic, phialidic, cylindrical, hyaline, smooth, thin-walled, sometimes with proliferation, periclinal thickening present. *Conidia* cylindrical, straight, apex obtuse, base abruptly tapered to a distinct scar, hyaline, smooth, thin-walled, aseptate, eguttulate to biguttulate.

Culture characteristics: Colonies on PDA glaucous to sky-grey, with irregular white margin; reverse olivaceous black.

Type species: *Verkleyomyces illicii* (X. Sun *et al.*) Y. Marín & Crous. Holotype and ex-type culture: HMAS244704, ASH-3-6-2-5b.

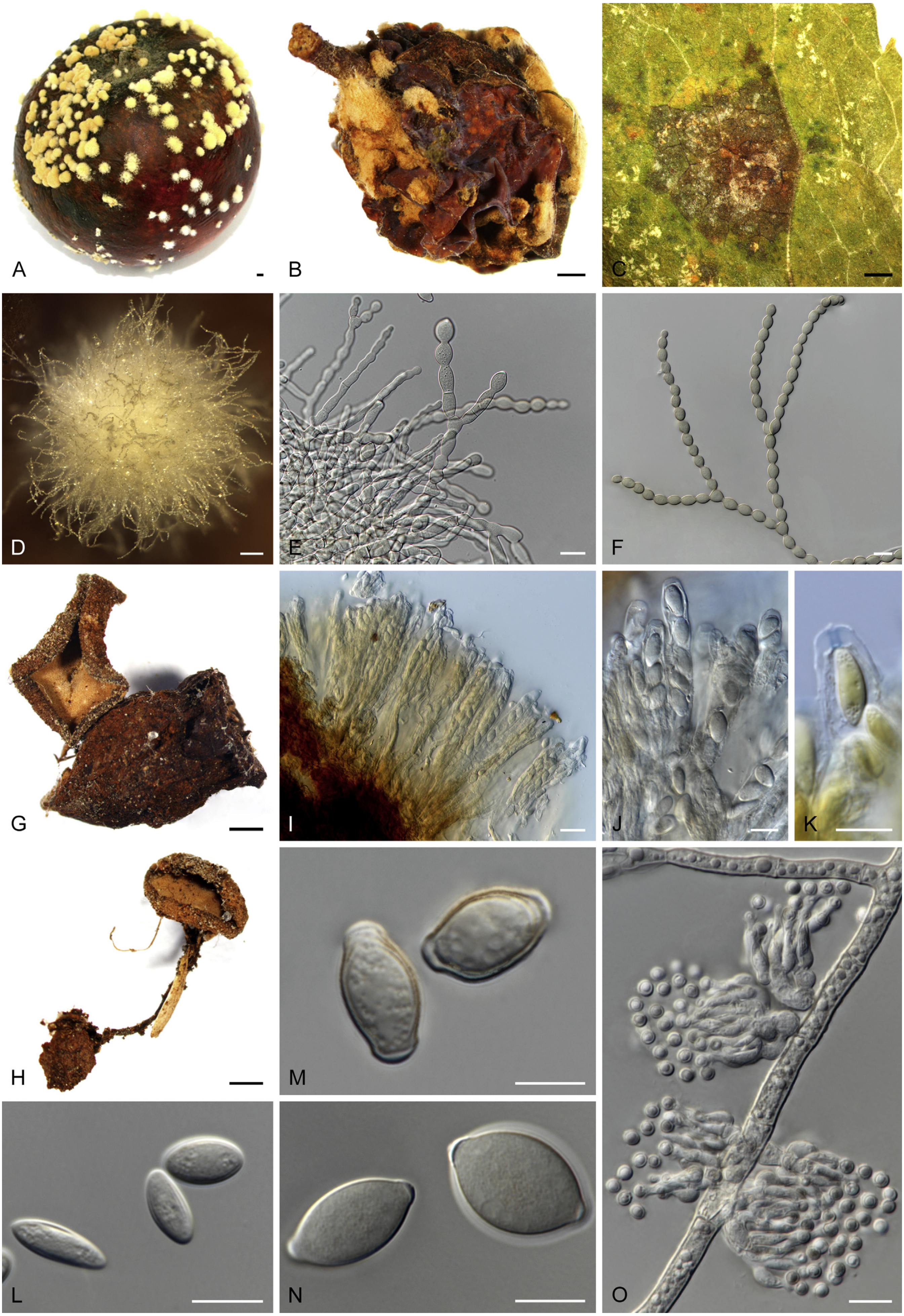

A
B
C
D
E
F
G
I
J
K
H
M
O
L
N

Table 10. DNA barcodes of accepted *Monilinia* spp.

Species	Isolates[1]	Genbank accession number[2]		References
		ITS	*tef1*	
Monilinia amelanchieris	ATCC 58538	Z73769	–	Holst-Jensen *et al.* (1997)
M. aucupariae	ARO 885.2	Z73771	–	Holst-Jensen *et al.* (1997)
M. azaleae	ATCC 58539	AB182266	–	Takahashi *et al.* (2005)
M. baccarum	CBS 388.93	KX982694	LT632532	Present study
M. cassiopes	ARO 1459.S	Z73776	–	Holst-Jensen *et al.* (1997)
M. fructicola	CBS 329.35	KX982695	LT632533	Present study
M. fructigena	CBS 348.72	KX982697	LT632535	Present study
M. gaylussaciae	ATCC 64508	Z73782	–	Holst-Jensen *et al.* (1997)
M. jezoensis	4222^{T} *	AB182265	–	Takahashi *et al.* (2005)
M. johnsonii	ATCC 58542	Z73783	–	Holst-Jensen *et al.* (1997)
M. kusanoi	NBRC 9725	00972502^{A}		Harada *et al.* (2004)
M. laxa	CBS 132.21	KX982699	LT632537	Present study
M. linhartiana	CBS 150.22	KX982701	LT632539	Present study
M. megalospora	ARO 619.2	Z73788	–	Holst-Jensen *et al.* (1997)
M. mali	2769*	AB125619	–	Harada *et al.* (2004)
M. mespili	CBS 139.23	KX982702	LT632540	Present study
M. mumeicola	3231 01-01*	AB125613	–	Harada *et al.* (2004)
M. oxycocci	ARO 1087.P	Z73789	–	Holst-Jensen *et al.* (1997)
M. padi	ARO 923.K	Z73791	–	Holst-Jensen *et al.* (1997)
M. polycodii	ATCC 58546	Z73792	–	Holst-Jensen *et al.* (1997)
M. polystroma	CBS102688^{T}	KX982704	LT632542	Present study
M. seaveri	CBS 170.24	KX982705	–	Present study
M. ssiori	HHUF 19771^{T}	AB220062	–	Harada *et al.* (2005)
M. urnula	ARO 476.1	Z73794	–	Holst-Jensen *et al.* (1997)
M. vaccinii-corymbosi	CBS 172.24	KX982706	LT632543	Present study
M. yunnanensis	KY-1	HQ908788	–	Hu *et al.* (2011)

[1] ARO: Ascomycete Systematics Research Group, University of Oslo, Norway; ATCC: American Type Culture Collection, Virginia, USA; CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; HHUF: Hirosaki University, Japan; KY: Strain code as stated in GenBank, * Hirosaki University Culture Collection, Japan. ^{T} indicates ex-type strain. ^{A} Accession number corresponding to the NITE Biological Resource Center, Japan.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *tef1*: partial translation elongation factor 1-alpha gene.

Notes: *Verkleyomyces* is introduced to accommodate *Neofabraea illicii*, the most recently published species of *Neofabraea* (Wang *et al.* 2015). In the phylogenetic analysis based on ITS sequences (Fig. 38), this species was located in a clade separate from the rest of the species belonging to *Neofabraea*. *Verkleyomyces* is mainly differentiated by its endophytic habit. Morphologically both genera are comparable, but *Verkleyomyces* produces 1-septate ascospores and aseptate conidia, while *Neofabraea* is characterised by aseptate ascospores and predominately septate conidia. *Parafabraea*, which is more closely related, also produces aseptate conidia, but this can be differentiated from *Verkleyomyces* by the production of aseptate ascospores. Other similar genera are *Pezicula* and *Dermea*, but these can easily be distinguished by the production of ascospores that are initially hyaline, and then become coloured or contain coloured oil droplets.

Verkleyomyces illicii (X. Sun *et al.*) Y. Marín & Crous, **comb. nov.** MycoBank MB820819.
Basionym: *Neofabraea illicii* X. Sun *et al.*, Mycoscience 56: 334. 2015.

Description and illustration: Wang *et al.* (2015).

Note: *Verkleyomyces illicii* is an endophytic fungus isolated from *Illicium verum*, cultivated in a plantation in southern China.

Authors: Y. Marin-Felix & P.W. Crous

Neofusicoccum Crous *et al.*, Stud. Mycol. 55: 247. 2006. Fig. 39.

Fig. 35. *Monilinia* spp. **A–C.** Disease symptoms. **A, B.** *Monilinia fructigena* on *Malus* sp. (A, CBS 348.72) and on *Sorbus aucuperiae* mummified fruit (B, CBS H-14553). **C.** *Monilinia laxa* (CBS H-14556) leaf spot on *Prunus padus*. **D.** Sporodochia *in vivo* of *Monilinia fructigena* (CBS 348.72). E, F. Conidiophores. **E.** *Monilinia fructigena* (CBS 348.72). **F.** *Monilinia fructicola* (CBS 101512). **G, H.** Apothecia. **G.** *Monilinia johnsonii* (CBS H-005908) on *Crategus* sp. mummified fruit. *H. Monilinia johnsonii* (CBS H-005908) stipitate apothecia. **I–K.** Asci of *Monilinia johnsonii* (CBS H-14554). **K.** Tip of an ascus showing a blue reaction with Meltzer's solution. **L.** Ascospores of *Monilinia johnsonii* (CBS H-14554). **M, N.** Macroconidia. **M.** *Monilinia fructicola* (CBS 101512). **N.** *Monilinia fructigena* (CBS 348.72). **O.** Microconidia of *Monilinia fructicola* (CBS 101512). Scale bars: A–C, G, H = 1 mm; D = 100 μm; E, F, I = 20 μm; J–O = 10 μm.

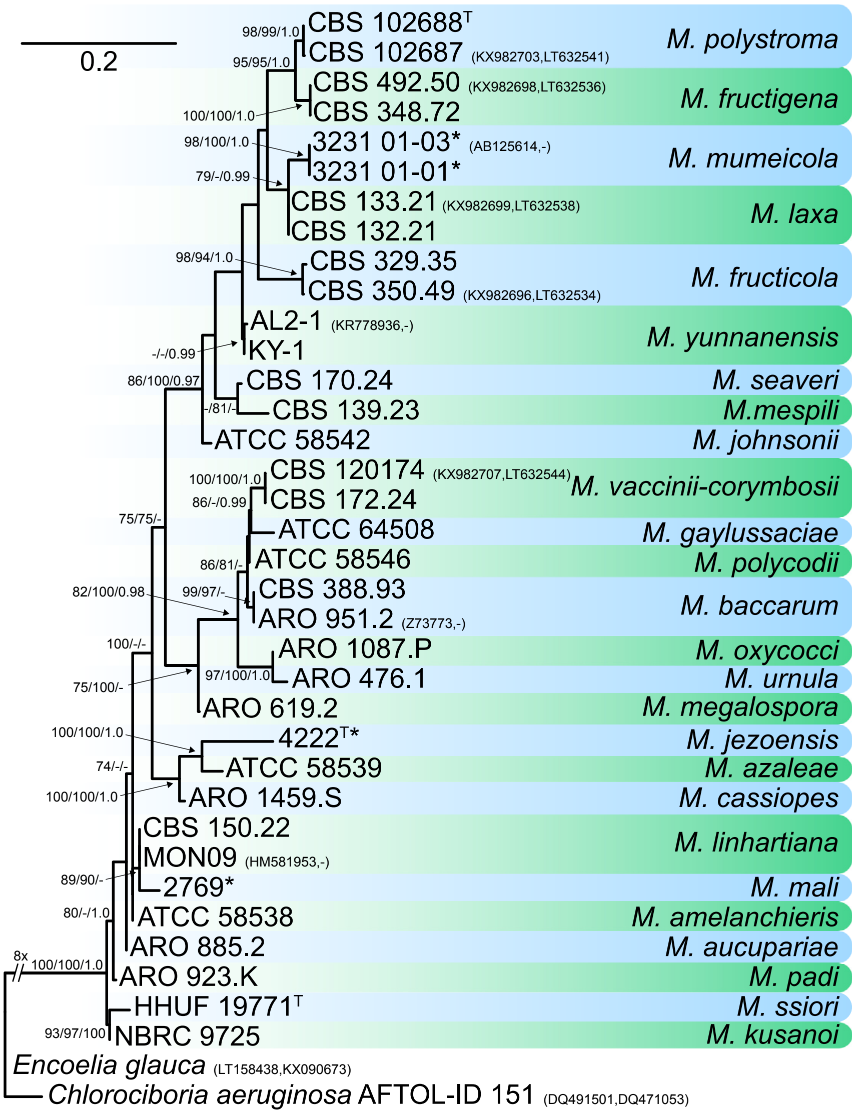


Fig. 36. RaxML phylogram obtained from the combined ITS (428 bp) and *tef1* (420 bp) sequences of *Monilinia* spp. currently known by DNA data. Maximum parsimony and RaxML bootstrap support (BS) values above 70 % are shown at the nodes. Numbers between parentheses correspond to GenBank accession numbers for ITS and *tef1* sequences, respectively. ^{T} indicates ex-type strain. TreeBASE: S20877.

Classification: *Dothideomycetes*, *Incertae sedis, Botryosphaeriales*, *Botryosphaeriaceae.*

Type species: *Neofusicoccum parvum* (Pennycook & Samuels) Crous *et al.* Holotype and ex-type culture: PDD 45438 (Herbarium of Plant Diseases Division), ATCC 58191 = CBS 138823 = PDDCC 8003 = ICMP 8003 = CMW 9081.

DNA barcodes (genus): LSU, *rpb2.*

DNA barcodes (species): ITS, *tef1*, *tub2*, *rpb2.* Table 12. Fig. 40.

Ascomata forming botryose clusters, each comprising many ascomata, erumpent through the bark, globose, with a short, conical papilla, dark brown to black, smooth, thick-walled; *ascomatal wall* composed of dark brown thick-walled cells of *textura angularis*, lined with thin-walled hyaline cells of *textura angularis*. *Asci* clavate, 8-spored, bitunicate. *Ascospores* broadly ellipsoidal to fusoid, hyaline, smooth, aseptate, occasionally becoming 1-septate. *Conidiomata* globose and non-papillate, entire locule lined with conidiogenous cells. *Conidiogenous cells* holoblastic, hyaline, subcylindrical, proliferating percurrently to form 1–2 annellations, or proliferating at the same level to form periclinal thickenings. *Conidia* ellipsoidal with apex round and base flat, unicellular, hyaline, old conidia becoming 1–2-septate hyaline, or light brown with the middle cell darker than the terminal cells. *Dichomera synasexual morph*: *Conidia* subglobose to obpyriform, brown, apex obtuse, base truncate, 1–3 transverse septa, 1–2 longitudinal septa, and 1–2 oblique septa.

Culture characteristics: Colonies initially white to buff turning olivaceous grey becoming black with age, moderately dense, appressed mycelial mat with irregular very dense aerial aggregations, some conidioma covered by mycelium, immersed-erumpent, conidia and spermatia present. Reverse white to olivaceous black. Reaching 90 mm diam on half strength MEA in 3–4 d.

Optimal media and cultivation conditions: Half strength MEA at 25–30 °C.

Distribution: Worldwide.

Hosts: Plurivorous, mainly pathogenic on *Anacardiaceae*, *Cupressaceae*, *Ebenaceae*, *Fagaceae*, *Juglandaceae*, *Lauraceae*, *Moraceae*, *Myrtaceae*, *Oleaceae*, *Pinaceae*, *Proteaceae*,

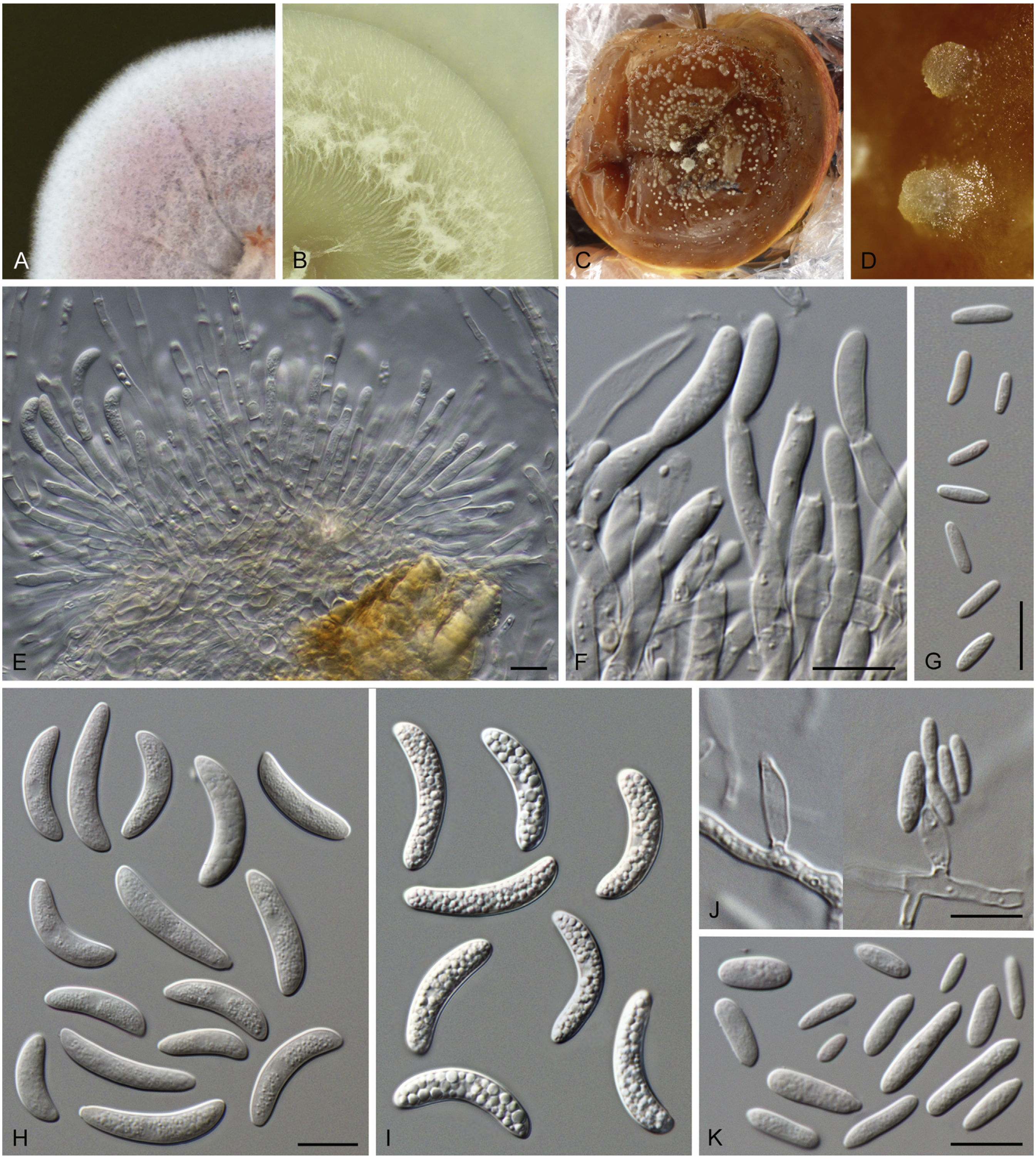


Fig. 37. *Neofabraea malicorticis* (ex-neotype CBS 122030). **A.** Colony on MEA. **B.** Colony on OA. **C.** Conidiomata on inoculated apple. **D.** Conidial mass on apple peel. **E.** Conidiogenous cells from sporodochium on OA. **F.** Conidiogenous cells giving rise to macroconidia. **G.** Microconidia on OA. **H.** Macroconidia from OA. **I.** Macroconidia from inoculated apple. **J, K.** Intermediate conidia between macro- and microconidia. Scale bars: 10 µm, I applies to H, I. Pictures taken from Chen *et al.* (2016).

Rosaceae, *Rutaceae*, *Vitaceae*, families belonging to *Lamiales* and various other host plants.

Disease symptoms: Fruit rot, wood canker, leaf spots.

Notes: *Neofusicoccum* was introduced by Crous *et al.* (2006b) to accommodate species morphologically similar to, but phylogenetically divergent from *Botryosphaeria* (= *Fusicoccum*). To separate *Neofusicoccum* from *Botryosphaeria* based solely on morphology can be difficult due to similar morphological characteristics. Therefore, molecular data are required to achieve accurate identification. One morphological difference between both genera is the presence of a *Dichomera* synasexual morph in *Neofusicoccum*. However, this synasexual morph is not produced by all *Neofusicoccum* species, nor even all isolates of any given species. Moreover, dichomera-like conidia

Table 11. DNA barcodes of accepted *Neofabraea* spp.

Species	Isolates[1]	GenBank accession numbers[2]			References
		ITS	*rpb2*	*tub2*	
Neofabraea actinidiae	CBS 121403^T	KR859079	KR859319	KR859285	Chen *et al.* (2016)
Na. brasiliensis	CNPUV499^T	KR107002	–	KR107011	Crous *et al.* (2015e)
Na. inaequalis	CBS 326.75^T	KR859081	KR859321	KR859287	Chen *et al.* (2016)
Na. kienholzii	CBS 126461^T	KR859082	KR859322	KR859288	Chen *et al.* (2016)
Na. krawtzewii	CBS 102867	KR859084	KR859324	AF281459	de Jong *et al.* (2001), Chen *et al.* (2016)
Na. malicorticis	CBS 122030^{NT}	KR859086	KR859326	KR859291	Chen *et al.* (2016)
Na. perennans	CBS 102869	KR859087	KR859327	AF281473	de Jong *et al.* (2001), Chen *et al.* (2016)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CNPUV: Centro Nacional de Pesquisa de Uva e Vinho, Bento Gonçalves, RS, Brazil. ^{T} and ^{NT} indicate ex-type and ex-neotype strains, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *rpb2*: partial RNA polymerase II second largest subunit gene; *tub2*: partial β-tubulin gene.

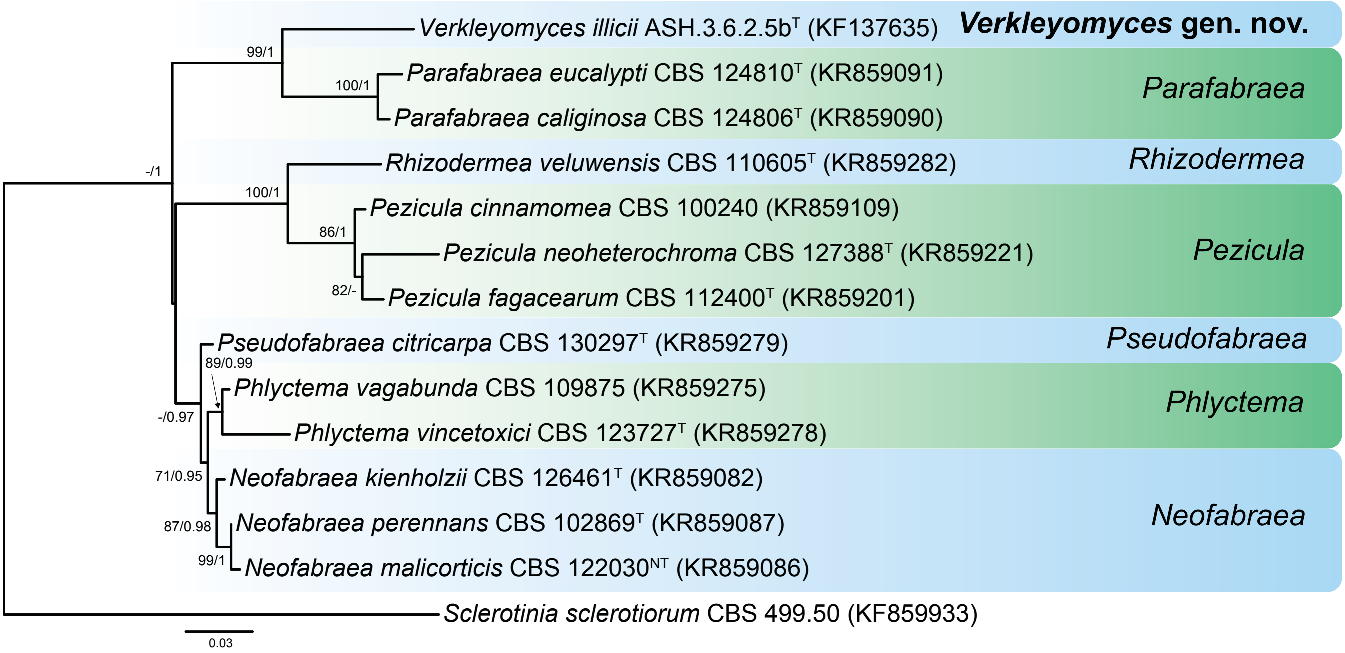


Fig. 38. RAxML phylogram obtained from the ITS (564 bp) sequences of *Neofabraea* spp. and related genera. Maximum parsimony and RAxML bootstrap support (BS) values above 70 % are shown in the nodes. The new genus introduced in this study is shown in **bold**. The tree was rooted to *Sclerotinia sclerotiorum* CBS 499.50. Numbers between parentheses correspond to GenBank accession numbers. ^{T} indicates ex-type strain. TreeBASE: S20877.

were reported in some isolates of *Bot. dothidea* (Barber *et al.* 2005, Phillips *et al.* 2005). Other morphological differences are the absence of paraphyses in the conidiomata of *Neofusicoccum* spp., while these have been seen in most of the currently accepted *Botryosphaeria* species, and the conidial L/W ratios being less than 4 in *Neofusicoccum*. Furthermore, the conidia of *Neofusicoccum* are more ellipsoidal than the fusiform ones of *Fusicoccum s. str.*

Species in *Neofusicoccum* are morphologically similar and hard to differentiate from one another. *Neofusicoccum* species are currently defined on the basis of conidial dimensions and pigmentation, pigment production in culture media and ITS sequence data. Taxa in some of the species complexes are defined exclusively on DNA sequence data (ITS, often together with *tef1*, *tub2* and *rpb2*. In some cases, multigene sequence data are essential for species identification.

References: Crous *et al.* 2006b, Berraf-Tebbal *et al.* 2014, Yang *et al.* 2017 (morphology and phylogeny); Pavlic *et al.* 2009a (phylogeny); Pavlic *et al.* 2009b (morphology, pathogenicity and phylogeny), Phillips *et al.* 2013 (morphology, phylogeny and dichotomous key).

Neofusicoccum italicum Dissanayake & K.D. Hyde, **sp. nov.** MycoBank MB820799, *Facesoffungi* number FOF02963. Fig. 41.

Etymology: Based on the country where the type specimen was collected, Italy.

Sexual morph not observed. *Conidiomata* 0.5–1.5 × 1.5–2 mm, black, scattered, uniloculate, globose; *conidiomatal wall* composed of dark brown *textura angularis*, becoming hyaline towards conidiogenous region. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 9–16.5 × 2.5–3.5 µm, lining inner wall of pycnidium, holoblastic, cylindrical to subobpyriform, hyaline, discrete, determinate, occasionally indeterminate and proliferating percurrently with indistinct annellations. *Conidia* 13–18.5 × 3.5–6 µm, obovoid, fusiform, base truncate, apex obtuse to subobtuse, hyaline, guttulate, non-septate, older conidia may become brownish and septate before germination. *Dichomera synasexual morph* not reported.

Culture characteristics: Colonies white with abundant aerial mycelium reaching 90 mm diam within 1 wk on PDA at 28 °C. Aerial mycelium becoming smoke-grey to olivaceous grey at the surface and dull green to brown-vinaceous at the reverse after 2 wk in the dark at 28 °C.

Materials examined: **Italy**, on a dead branch of *Vitis vinifera*, 22 Nov. 2014, E. Camporesi (**holotype** MFLU 16-2872, culture ex-type MFLUCC 15-0900). **New Zealand**, on *Malus* × *domestica*, unknown date, H.J. Boesewinkel, CBS 719.85.

Notes: According to the phylogenetic analysis *Neofusicoccum italicum* clustered close to *Nm. algeriense*, which has larger conidia (17.6 × 5.6 μm) than those of *Nm. italicum* (15.8 × 5.2 μm). Both species are pathogens of *Vitis vinifera*, but *Nm. algeriense* is restricted to this host while *Nm. italicum* was also isolated from *Malus* × *domestica*. Other species of *Neofusicoccum* associated with *Vitis vinifera* are *Nm. australe*, *Nm. luteum*, *Nm. mediterraneum*, *Nm. parvum*, *Nm. stellenboschiana*, *Nm. viticlavatum* and *Nm. vitifusiforme* (Van Niekerk *et al.* 2004a, Phillips *et al.* 2013, Yang *et al.* 2017). *Neofusicoccum* and other related genera belonging to *Botryosphaeriaceae* are widely distributed pathogens of grapevines that cause bud mortality, dieback, brown streaking inside the wood, internal necrotic lesions and in some cases bunch rot (Phillips *et al.* 2013).

Neofusicoccum pistaciicola Crous, **sp. nov.** MycoBank MB820820. Fig. 42.

Etymology: Named after the host genus from which it was collected, *Pistacia*.

Sexual morph not observed. *Conidiomata* stromatic, solitary, globose, up to 300 μm diam; *conidiomatal wall* 6–8 cell layers thick, of brown *textura angularis*, becoming hyaline toward inner region. *Conidiophores* 0–2-septate, branched, hyaline, smooth, subcylindrical, 15–25 × 4–5 μm. *Conidiogenous cells* holoblastic, hyaline, smooth, subcylindrical, proliferating percurrently, 12–17 × 2.5–3.5 μm. *Conidia* hyaline, smooth, thin-walled, granular, aseptate, subcylindrical to fusoid-ellipsoid, apex subobtuse, base truncate, 1.5–2.5 μm, straight to irregularly curved, (15–)18–24(–27) × (4–)4.5(–5) μm. *Spermatia or Dichomera synasexual morph* not observed.

Culture characteristics: Colonies on MEA reaching 90 mm diam within 1 wk, with fluffy moderate aerial mycelium; surface pale mouse-grey, reverse mouse-grey to dark mouse-grey.

Material examined: **USA**, California, Glenn County, on *Pistacia vera*, 12 Apr. 2002, T.J. Michailides (**holotype** CBS H-23108, culture ex-type CBS 113089).

Notes: *Neofusicoccum pistaciicola* is morphologically similar to *Nm. hellenicum*, which Chen *et al.* (2015b) recently described from *Pistacia vera* in the USA. However, compared with *Nm. hellenicum*, *Nm. pistaciicola* possesses smaller conidiomata and narrower conidia. The same features are used to distinguish it from *Nm. pistaciarum*, which is the closest phylogenetic species, and also a pathogen of *Pistacia vera*. Other species of *Neofusicoccum* associated to this host are *Nm. australe*, *Nm. mediterraneum*, *Nm. nonquaesitum*, *Nm. parvum* and *Nm. pistaciae* (Inderbitzin *et al.* 2010, Phillips *et al.* 2013, Yang *et al.* 2017).

Neofusicoccum pruni Crous, **sp. nov.** MycoBank MB820821. Fig. 43.

Etymology: Named after the host genus from which it was collected, *Prunus*.

Sexual morph not observed. *Conidiomata* stromatic, solitary, globose to obpyriform, up to 300 μm diam; *conidiomata wall* 6–10 cell layers thick, of brown *textura angularis*, becoming hyaline toward inner region. *Conidiophores* 0–1-septate, hyaline, subcylindrical, 10–20 × 2.5–4 μm. *Conidiogenous cells* holoblastic, hyaline, subcylindrical, 10–15 × 2.5–3.5 μm, proliferating percurrently with numerous proliferations, or proliferating at the same level (phialidic) with minute periclinal thickening. *Conidia* hyaline, granular, aseptate, fusoid to ellipsoid, widest in the middle or upper third with an obtuse apex and flattened, subtruncate base, (18–)20–23(–25) × (6.5–)7–7.5(–8.5) μm. *Spermatia or Dichomera synasexual morph* not observed.

Culture characteristics: Colonies on MEA reaching 90 mm diam within 1 wk, with fluffy moderate aerial mycelium; surface and reverse greenish black.

Material examined: **South Africa**, Limpopo, Mookgopong, from branches of *Prunus salicina*, Aug. 2004, U. Damm (**holotype** CBS H-23109, culture ex-type CBS 121112 = CPC 5912).

Notes: *Neofusicoccum vitifusiforme* was initially described from *Vitis vinifera* in South Africa by van Niekerk *et al.* (2004a). Damm *et al.* (2007) was the first to report this fungus as a pathogen from *Prunus salicina* in South Africa, although their phylogenetic tree showed this isolate (CBS 121112) to cluster basal to the grapevine strains based on ITS and *tef1* sequence data. A recent study by Yang *et al.* (2017), which incorporated all *Neofusicoccum* isolates available in the CBS culture collection, as well as additional genes (*rpb2* and *tub2*) showed the *Prunus* isolate to represent a distinct species. This isolate (formerly sterile) has subsequently been induced to sporulate, and is therefore named in the present study.

Authors: Y. Marin-Felix, E. Camporesi, A. Dissanayake, K.D. Hyde & P.W. Crous

Pilidium Kunze, Mykol. Hefte 2: 92. 1823. Fig. 44.
Synonyms: *Sclerotiopsis* Speg., Anal. Soc. Cient. Argent. 13: 14. 1882.
Hainesia Ellis & Sacc., in Saccardo, Syll. fung. (Abellini) 3: 698. 1884.
Discohainesia Nannf., Nova Acta Regiae Soc. Sci. Upsal., Ser. 4 8: 88. 1932.

Fig. 39. *Neofusicoccum* spp. **A–D.** Disease symptoms. **A.** Leaf blight on *Protea* sp. **B.** Canker on *Vitis vinifera*. **C, D.** Cankers on *Eucalyptus* sp. **E–J.** Sexual morphs. **E, F.** Ascomata. **E.** *Neofusicoccum parvum* (ex-type ATCC 58191). **F.** *Neofusicoccum luteum* (ex-type ATCC 58193). **G, H.** Asci. **G.** *Neofusicoccum luteum* (ex-type ATCC 58193). **H.** *Neofusicoccum australe* (ex-type CMW 6837). **I.** Detail of ascus apex of *Neofusicoccum parvum* (ex-type ATCC 58191). **J.** Ascospores of *Neofusicoccum parvum* (ex-type

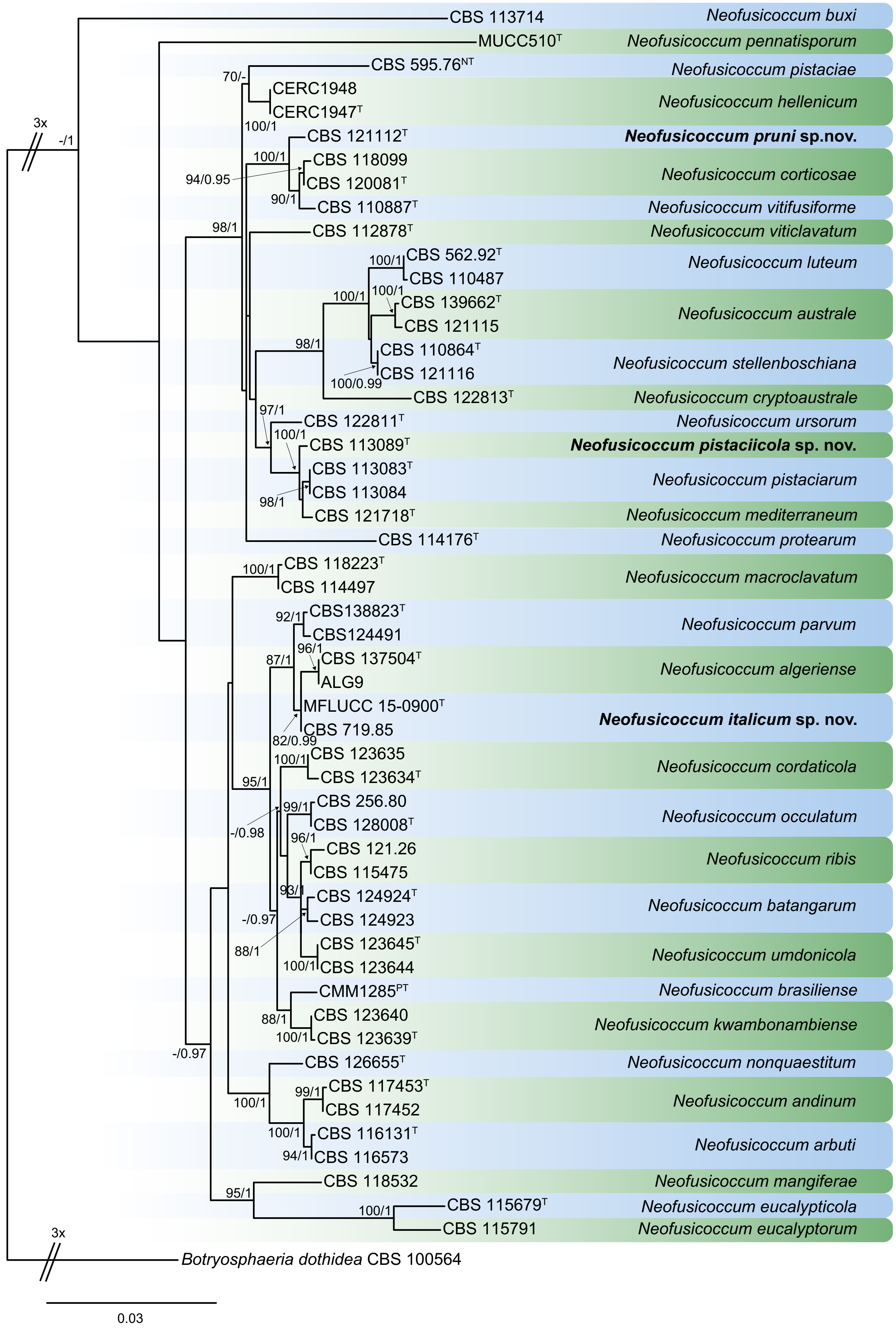
Table 12. DNA barcodes of accepted *Neofusicoccum* spp.

Species	**Isolates**[1]	**GenBank accession numbers**[2]				**References**
		ITS	***rpb2***	***tef1***	***tub2***	
Neofusicoccum algeriense	CBS 137504^{T}	KJ657702	–	KJ657715	–	Berraf-Tebbal *et al.* (2014)
Nm. andinum	CBS 117453^{T}	AY693976	KX464002	AY693977	KX464923	Mohali *et al.* (2006), Yang *et al.* (2017)
Nm. arbuti	CBS 116131^{T}	AY819720	KX464003	KF531792	KF531793	Farr *et al.* (2005), Phillips *et al.* (2013), Yang *et al.* (2017)
Nm. australe	CMW 6837^{T}	AY339262	EU339573	AY339270	AY339254	Slippers *et al.* (2004b), Burgess & Sakalidis (unpubl. data)
Nm. batangarum	CBS 124924^{T}	FJ900607	FJ900615	FJ900653	FJ900634	Begoude *et al.* (2010)
Nm. brasiliense	CMM 1285^{PT}	JX513628	–	JX513608	KC794030	Marques *et al.* (2013)
Nm. buxi	CBS 116.75^{T}	KX464165	KX464010	KX464678	–	Yang *et al.* (2017)
Nm. cordaticola	CBS 123634^{T}	EU821898	EU821928	EU821868	EU821838	Pavlic *et al.* (2009a)
Nm. corticosae	CBS 120081^{T}	DQ923533	KX464013	KX464682	KX464958	Summerell *et al.* (2006), Yang *et al.* (2017)
Nm. cryptoaustrale	CMW 23785^{T}	FJ752742	KX464014	FJ752713	FJ752756	Crous *et al.* (2013b), Yang *et al.* (2017)
Nm. eucalypticola	CBS 115679^{T}	AY615141	–	AY615133	AY615125	Slippers *et al.* (2004c)
Nm. eucalyptorum	CBS 115791	AF283686	–	AY236891	AY236920	Smith *et al.* (2001), Slippers *et al.* (2004a)
Nm. grevilleae	CBS 129518	JF951137	–	–	–	Crous *et al.* (2011a)
Nm. hellenicum	CERC1947^{T}	KP217053	–	KP217061	KP217069	Chen *et al.* (2015b)
Nm. italicum	MFLUCC 15-0900^{T}	KY856755	–	KY856754	–	Present study
Nm. kwambonambiense	CBS 123639^{T}	EU821900	EU821930	EU821870	EU821840	Pavlic *et al.* (2009a)
Nm. luteum	CBS 562.92^{T}	KX464170	KX464020	KX464690	KX464968	Yang *et al.* (2017)
Nm. macroclavatum	CBS 118223^{T}	DQ093196	KX464022	DQ093217	DQ093206	Burgess *et al.* (2005), Yang *et al.* (2017)
Nm. mangiferae	CBS 118532	AY615186	KX464023	DQ093220	AY615173	Slippers *et al.* (2005), Burgess *et al.* (2005), Yang *et al.* (2017)
Nm. mediterraneum	CBS 121718^{T}	EU040221	KX464024	–	–	Crous *et al.* (2007c), Yang *et al.* (2017)
Nm. nonquaesitum	CBS 126655^{T}	GU251163	KX464025	GU251295	GU251823	Inderbitzin *et al.* (2010), Yang *et al.* (2017)
Nm. occulatum	CBS 128008^{T}	EU301030	EU339558	EU339509	EU339472	Sakalidis *et al.* (2011)
Nm. parvum	CBS 138823^{T}	AY236943	EU821963	AY236888	AY236917	Pavlic *et al.* (2009a), Slippers *et al.* (2004a),
Nm. pennatisporum	MUCC 510^{T}	EF591925	–	EF591976	EF591959	Taylor *et al.* (2009)
Nm. pistaciae	CBS 595.76^{IsoT}	KX464163	KX464008	KX464676	KX464953	Yang *et al.* (2017)
Nm. pistaciarum	CBS 113083^{T}	KX464186	KX464027	KX464712	KX464998	Yang *et al.* (2017)
Nm. pistaciicola	CBS 113089^{T}	KX464199	KX464033	KX464727	KX465014	Yang *et al.* (2017)
Nm. protearum	CBS 114176^{T}	AF452539	KX464029	KX464720	KX465006	Denman *et al.* (2003), Yang *et al.* (2017)
Nm. pruni	CBS 121112^{T}	EF445349	KX464034	EF445391	KX465016	Damm *et al.* (2007), Yang *et al.* (2017)
Nm. ribis	CBS 115475	AY236935	EU339554	AY236877	AY236906	Slippers *et al.* (2004a), Sakalidis *et al.* (2011)
Nm. stellenboschiana	CBS 110864^{T}	AY343407	KX464042	AY343348	KX465047	van Niekerk *et al.* (2004a), Yang *et al.* (2017)
Nm. umdonicola	CBS 123645^{T}	EU821904	EU821934	EU821874	EU821844	Pavlic *et al.* (2009a)
Nm. ursorum	CMW 24480^{T}	FJ752746	KX464047	FJ752709	KX465056	Crous *et al.* (2013b), Yang *et al.* (2017)
Nm. viticlavatum	CBS 112878^{T}	AY343381	KX464048	AY343342	KX465058	van Niekerk *et al.* (2004a), Yang *et al.* (2017)
Nm. vitifusiforme	CBS 110887^{T}	AY343383	KX464049	AY343343	KX465061	van Niekerk *et al.* (2004a), Yang *et al.* (2017)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CERC: China Eucalypt Research Centre (CERC), Chinese Academy of Forestry (CAF), China; CMM: Culture collection of Phytopathogenic Fungi “Prof. Maria Menezes”, Universidade Federal Rural de Pernambuco, Recife, Brazil; CMW: Tree Pathology Co-operative Program, Forestry and Agricultural Biotechnology Institute, University of Pretoria, South Africa; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Ria, Thailand; MUCC: Murdoch University, Perth, Western Australia. ^{T,} ^{IsoT} and ^{PT} indicate ex-type, ex-isotype and ex-paratype strains, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *rpb2*: partial RNA polymerase II second largest subunit gene; *tef1*: partial translation elongation factor 1-alpha gene; *tub2*: partial β-tubulin gene.

ATCC 58191). **K–S.** Asexual morph. **K.** Conidiomata on pine needles in culture of *Neofusicoccum australe* (CMW 6837). **L, M.** Conidiogenous cells. **L.** *Neofusicoccum mediterraneum* (ex-type CBS 121718). **M.** *Neofusicoccum parvum* (ex-type ATCC 58191). N–P. Conidia. **N.** *Neofusicoccum arbuti* (ex-type CBS 116131). **O.** *Neofusicoccum australe* (ex-type CMW 6837). **P.** *Neofusicoccum vitifusiforme* (ex-type CBS 110887). **Q.** Coloured, 1- and 2-septate conidia of *Neofusicoccum parvum* (ex-type ATCC 58191). **R.** Spermatogenous cells of *Neofusicoccum mediterraneum* (ex-type CBS 121718). **S.** Spermatia of *Neofusicoccum mediterraneum* (ex-type CBS 121718). Scale bar: E–G = 50 μm; H, J, L–P, R = 10 μm; I, Q, S = 5 μm; K = 1 mm. Pictures taken from Phillips *et al.* (2013).


CBS 113714 Neofusicoccum buxi
MUCC510^{T} Neofusicoccum pennatisporum
70/-
CBS 595.76^{NT} Neofusicoccum pistaciae
CERC1948
CERC1947^{T} Neofusicoccum hellenicum
3x
-/1
100/1
CBS 121112^{T} **Neofusicoccum pruni sp.nov.**
100/1
94/0.95
CBS 118099
CBS 120081^{T} Neofusicoccum corticosae
90/1
CBS 110887^{T} Neofusicoccum vitifusiforme
98/1
CBS 112878^{T} Neofusicoccum viticlavatum
100/1
CBS 562.92^{T}
CBS 110487 Neofusicoccum luteum
100/1
100/1
CBS 139662^{T}
CBS 121115 Neofusicoccum australe
98/1
CBS 110864^{T}
CBS 121116 Neofusicoccum stellenboschiana
100/0.99
CBS 122813^{T} Neofusicoccum cryptoaustrale
97/1
CBS 122811^{T} Neofusicoccum ursorum
100/1
CBS 113089^{T} **Neofusicoccum pistaciicola sp. nov.**
CBS 113083^{T}
CBS 113084 Neofusicoccum pistaciarum
98/1
CBS 121718^{T} Neofusicoccum mediterraneum
CBS 114176^{T} Neofusicoccum protearum
100/1
CBS 118223^{T}
CBS 114497 Neofusicoccum macroclavatum
92/1
CBS138823^{T}
CBS124491 Neofusicoccum parvum
96/1
87/1
CBS 137504^{T}
ALG9 Neofusicoccum algeriense
MFLUCC 15-0900^{T}
CBS 719.85 **Neofusicoccum italicum sp. nov.**
82/0.99
100/1
CBS 123635
CBS 123634^{T} Neofusicoccum cordaticola
95/1
99/1
CBS 256.80
CBS 128008^{T} Neofusicoccum occulatum
-/0.98
96/1
CBS 121.26
CBS 115475 Neofusicoccum ribis
93/1
CBS 124924^{T}
CBS 124923 Neofusicoccum batangarum
-/0.97
88/1
CBS 123645^{T}
100/1
CBS 123644 Neofusicoccum umdonicola
CMM1285^{PT} Neofusicoccum brasiliense
88/1
CBS 123640
100/1
CBS 123639^{T} Neofusicoccum kwambonambiense
-/0.97
CBS 126655^{T} Neofusicoccum nonquaestitum
99/1
CBS 117453^{T}
100/1
CBS 117452 Neofusicoccum andinum
100/1
CBS 116131^{T}
94/1
CBS 116573 Neofusicoccum arbuti
95/1
CBS 118532 Neofusicoccum mangiferae
100/1
CBS 115679^{T} Neofusicoccum eucalypticola
CBS 115791 Neofusicoccum eucalyptorum
3x
Botryosphaeria dothidea CBS 100564
0.03

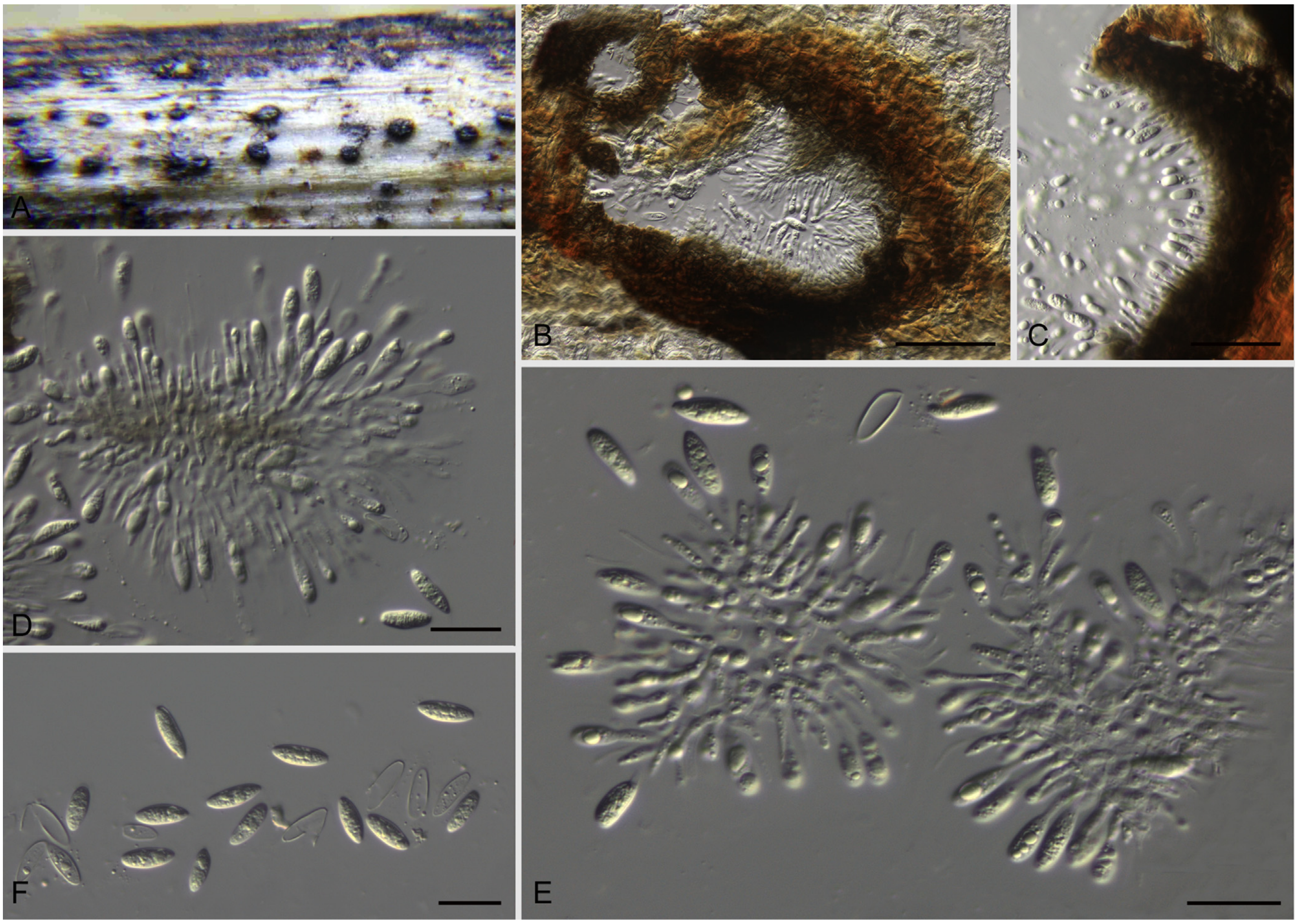


Fig. 41. *Neofusicoccum italicum* (ex-type MFLUCC 15-0900). **A**. Conidiomata on host substrate. **B, C**. Cross section of conidiomata. **D, E**. Immature and mature conidia attached to conidiogenous cells. **F**. Mature conidia. Scale bars: B, C = 100 μm. D–F = 20 μm.

Classification: *Leotiomycetes*, *Leotiomycetidae*, *Helotiales*, *Chaetomellaceae.*

Type species: *Pilidium acerinum* (Alb. & Schwein.) Kunze. Iconotype in Kunze & Schmidt (1817), table 2, fig. 5. Epitype and ex-epitype culture: BPI 843555, CBS 736.68.

DNA barcode (genus): LSU.

DNA barcode (species): ITS. Table 13. Fig. 45.

Ascomata apothecial, flat to funnel-shaped, short stipitate, white, pale brown to amber in the basal portion, wall pseudoparenchymatous (plectenchymatous). *Paraphyses* narrow, simple or branched, aseptate. *Asci* unitunicate, cylindrical, clavate, rounded or truncate at the apex, deliquescent. *Ascospores* ellipsoidal, somewhat enlarged at one side, straight to slightly curved, aseptate, smooth-walled. *Conidiomata* pycnidial or sporodochial; *pycnidia* globose, subglobose, obpyriform or oblong, sessile, pale brown when young, dark brown to black at maturity, superficial, solitary or gregarious, uniloculate, smooth; *conidiomatal wall* with two regions: outer region dark brown, inner region hyaline; opening by a stellate slit, rupturing irregularly, or lacking. *Conidiophores* hyaline, smooth, branched, cylindrical or filiform. *Conidiogenous cells* enteroblastic, phialidic, acropleurogenous, hyaline, smooth. *Conidia* mostly non-septate, hyaline, smooth, fusiform to falcate or cymbiform, with ends slightly pointed, straight to curved. *Sporodochia* globose becoming cupulate, discoid, with irregularly wavy margin, slimy, pale luteous, superficial, solitary, stalk pale brown near base, becoming dark brown at apex. *Conidiophores* hyaline, smooth, branched, cylindrical or filiform. *Conidiogenous cells* enteroblastic, phialidic, acropleurogenous, determinate, integrated, filiform or subcylindrical, hyaline, smooth, with minute collarette. *Conidia* aseptate, hyaline, smooth, fusiform to falcate or cymbiform to allantoid, with acute ends, straight to curved.

Culture characteristics: Colonies on PDA surface and reverse white to cinnamon, buff, honey, sepia or isabelline, slimy with aerial mycelium absent or sparse, flat, granulose due to production of fruiting bodies; margin smooth and lobate.

Optimal media and cultivation conditions: PDA, OA and MEA incubated at 25 °C for 1 wk at 25 °C under alternating fluorescent (12 h) and near ultraviolet (12 h) light are suitable to determine cultural characteristics and induce sporulation of the

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Fig. 40. RAxML phylogram obtained from the combined ITS (541 bp), *tef1* (302 bp), *rpb2* (594 bp) and *tub2* (463 bp) sequences of *Neofusicoccum* spp. The tree was rooted to *Botryosphaeria dothidea* CBS 100564. The novel species described in this study are shown in **bold**. RAxML bootstrap support (BS) values above 70 % and Bayesian posterior probability scores $\geq$ 0.95 are shown at the nodes. GenBank accession numbers were listed in Berraf-Tebbal *et al.* (2014), Chen *et al.* (2015b), and Yang *et al.* (2017). ^{T} and ^{NT} indicate ex-type and ex-neotype strains, respectively. TreeBASE: S20877.

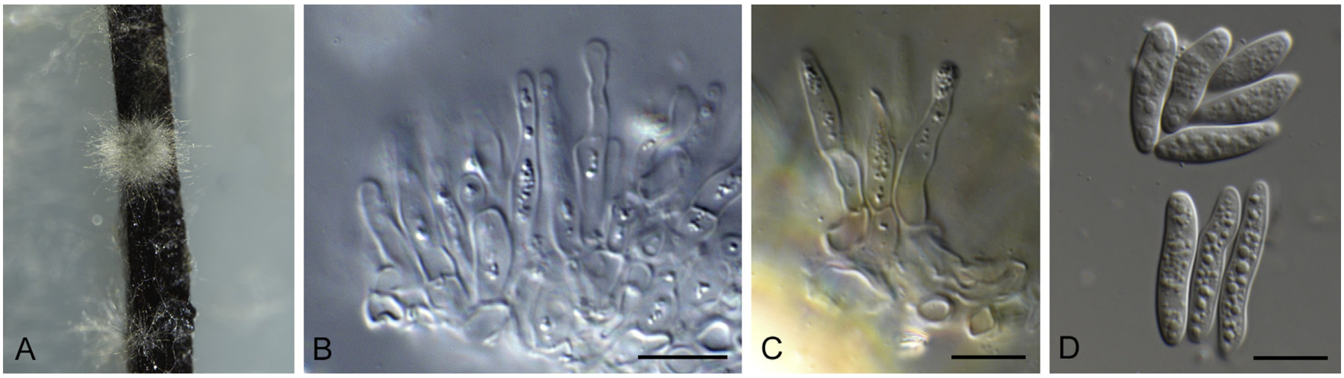

Fig. 42. *Neofusicoccum pistaciicola* (ex-type CBS 113089). **A.** Conidiomata forming on PNA. **B, C.** Conidiomata cells giving rise to conidia. **D.** Conidia. Scale bars: 10 µm.

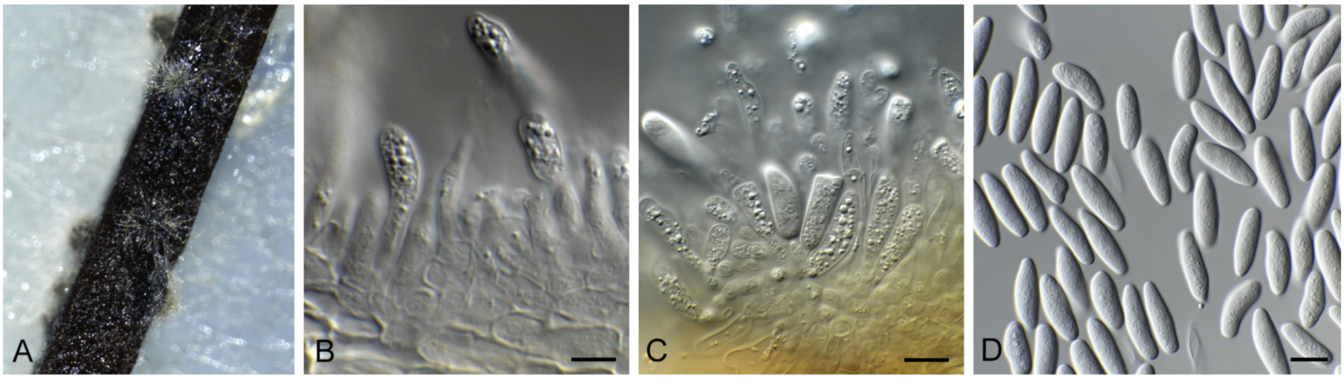

Fig. 43. *Neofusicoccum prunii* (ex-type CBS 121112). **A.** Conidiomata forming on PNA. **B, C.** Conidiomata cells giving rise to conidia. **D.** Conidia. Scale bars: 10 µm.

asexual morph. The sexual morph is not formed *in vitro*, and is relatively uncommon and inconspicuous.

Distribution: Worldwide.

Hosts: Species of this genus are mainly found on different hosts of *Anacardiaceae*, *Hippocastanaceae*, *Myrtaceae* and *Rosaceae*, and also in several other families such as *Betulaceae*, *Ebenaceae*, *Fabaceae*, *Geraniaceae*, *Oleaceae*, *Paeoniaceae*, *Pinaceae*, *Polygonaceae*, *Salicaceae*, *Sapindaceae*, *Saxifragaceae* and *Vitaceae.*

Disease symptoms: Leaf spots, root lesions and tan-brown rot of fruits.

Notes: Species of *Pilidium* are commonly found as plant-associated fungi or isolated from soil (Sutton 1980), and they are known to produce two kinds of conidiomata. *Pilidium lythri* (formerly known as *Pi. concavum*) and *Pi. pseudoconcavum* form sporodochia in culture. Although, the former species also produces the pycnidial morph, both species can be distinguished based on conidial shape (fusiform *vs.* cymbiform), sporodochial size (300–1000 µm diam *vs.* up to 300 µm diam) and DNA sequences (Crous *et al.* 2013b). Both *Pi. acerinum* and *Pi. eucalyptorum* produce brown pycnidia *in vitro* and they are closely related (Fig. 45). However, they differ in pycnidial size (200–1000 µm diam *vs.* up to 300 µm diam), conidiophore shape (cylindrical *vs.* filiform) and in the production of guttulate conidia, which are absent in *Pi. acerinum* and present in *Pi. eucalyptorum* (Rossman *et al.* 2004, Crous *et al.* 2015e).

Discohainesia oenotherae and *Hainesia lythri* were considered the sexual and synasexual morphs of *Pi. lythri* (Rossman *et al.* 2004). However, after the one fungus = one name initiative the generic name *Pilidium* was proposed for conservation over *Hainesia* and *Discohainesia* (Johnston *et al.* 2014).

References: Sutton 1980, Shear & Dodge 1921, Palm 1991 (morphology); Sutton & Gibson 1977 (morphology and pathogenicity); Rossman *et al.* 2004 (morphology, pathogenicity and ecology).

Pilidium septatum Giraldo & Crous, **sp. nov.** MycoBank MB820871. Fig. 46

Etymology: Refers to the presence of septate conidia.

Conidiomata pycnidial, superficial, solitary or gregarious, brown to black, smooth, uniloculate, subglobose to obpyriform, 97–260 × 127–230 µm; *outer conidiomatal wall* 11–27 µm thick, with *textura angularis*, formed by thick-walled, brown cells; *inner conidiomatal wall* 13–20 µm thick, with *textura angularis* or *globulosa*, formed by 4–5 layers of thick-walled, hyaline cells. *Conidiophores* branched, cylindrical, septate, hyaline, smooth, up to 24 µm long, 1.5–2 µm diam. *Conidiogenous cells* acropleurogenous, monophialidic, cylindrical, slightly curved, smooth, hyaline, delineating the inner part from the pycnidium, 7–11 × 1.5–2 µm. *Conidia* 1-septate, hyaline, falcate with ends slightly pointed, thin- and smooth-walled, (8.1–)9–11(–12.5) × (1–)1.5(–2) µm.

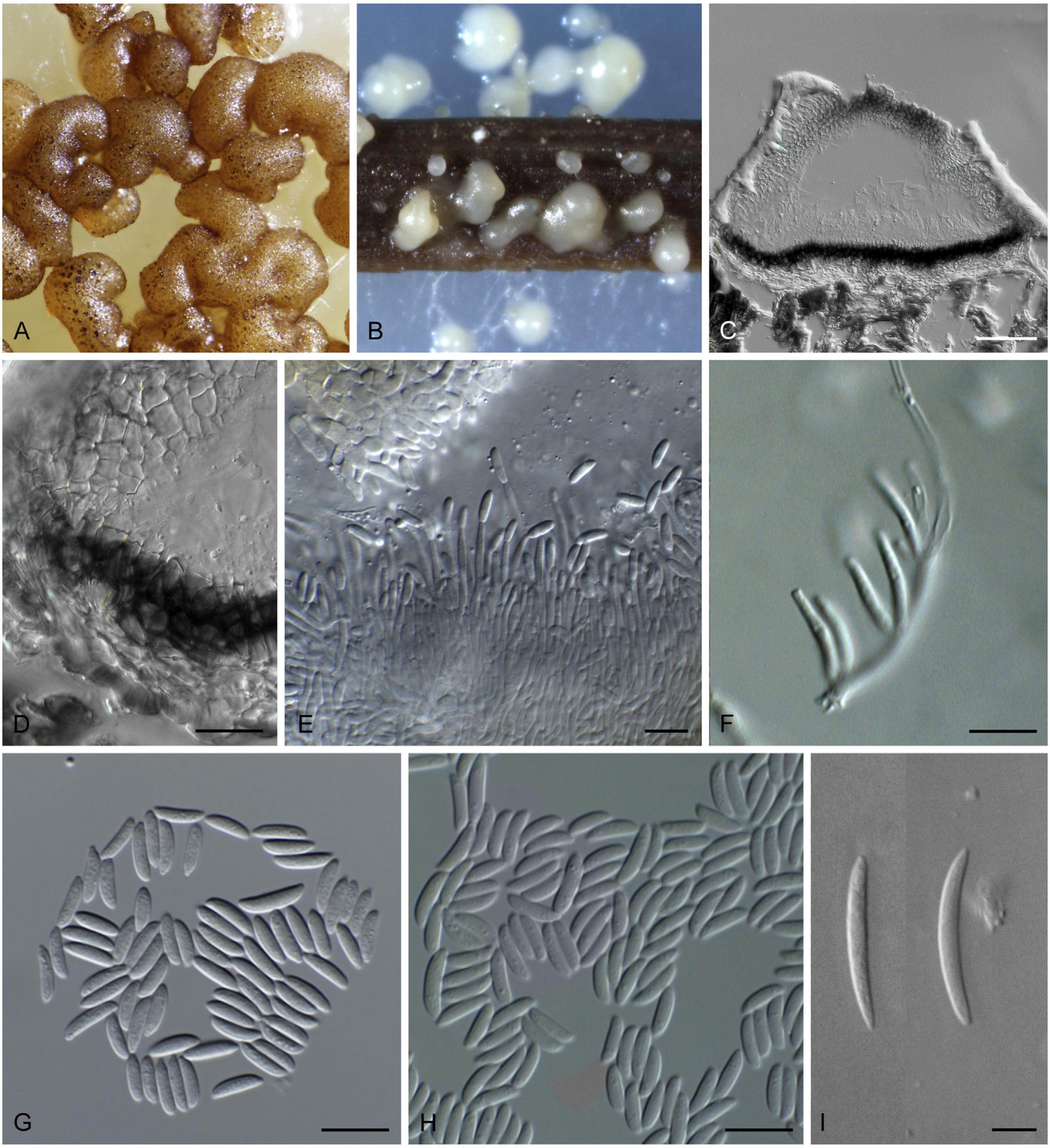

Fig. 44. *Pilidium* species. **A, E, G.** *Pilidium eucalyptorum* (CBS 140662). **B, F, H.** *Pilidium pseudoconcavum* (CBS 136433). **C, D, I.** *Pilidium leucospermi* (holotype PREM 59602). **A, B.** Conidiomata on OA and SNA, respectively. **C.** Vertical section of conidioma. **D.** Peridium. **E, F.** Conidiogenous cells. **G–I.** Conidia. Scale bars: C = 50 µm; D–I = 10 µm. Pictures C, D, I modified from Marincowitz *et al.* (2008a).

Culture characteristics: Colonies on OA and PDA reaching 30–40 mm in 2 wk. Colonies flat, granulose due to production of pycnidia, with scarce aerial mycelium, surface honey to isabelline.

Materials examined: **Thailand**, Nakhon Nayok province, Mueang Nakhon Nayok district, Wang Takhrai waterfall, N14.330023° E101.307168°, 64 m above sea level, from soil, 22 Jul. 2015, A. Giraldo (**holotype** metabolically inactive, culture ex-type BCC 79016); Nan province, Bo Kluea district, N19.14833333° E101.1566667, from soil, 8 Aug. 2015, A. Giraldo (BCC 79037).

Notes: Presently the genus includes only species with aseptate conidia, and thus *Pi. septatum*, with septate conidia, expands the generic concept of *Pilidium*. In addition to the phylogenetic relationship revealed through the analysis of LSU and ITS regions (Fig. 45), morphological characteristics such as the

Table 13. DNA barcodes of accepted *Pilidium* spp.

Species	Isolates[1]	GenBank accession numbers[2]		References
		ITS	LSU	
Pilidium acerinum	CBS 736.68^{ET}	AY487091	AY487092	Rossman *et al.* (2004)
Pi. lythri	CBS 114293	AY487094	AY487095	Rossman *et al.* (2004)
Pi. eucalyptorum	CBS 140662^{T}	KT950854	KT950868	Crous *et al.* (2015e)
Pi. pseudoconcavum	CBS 136433^{T}	KF777184	KF777236	Crous *et al.* (2013b)
Pi. septatum	BCC 79016^{T}	KY922832	KY922833	Present study

[1] BCC: BIOTEC Culture Collection, National Center for Genetic Engineering and Biotechnology (BIOTEC), Khlong Luang, Pathumthani, Thailand; CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands. ^{T} and ^{ET} indicate ex-type and ex-epitype strains, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; LSU: partial 28S large subunit RNA gene.

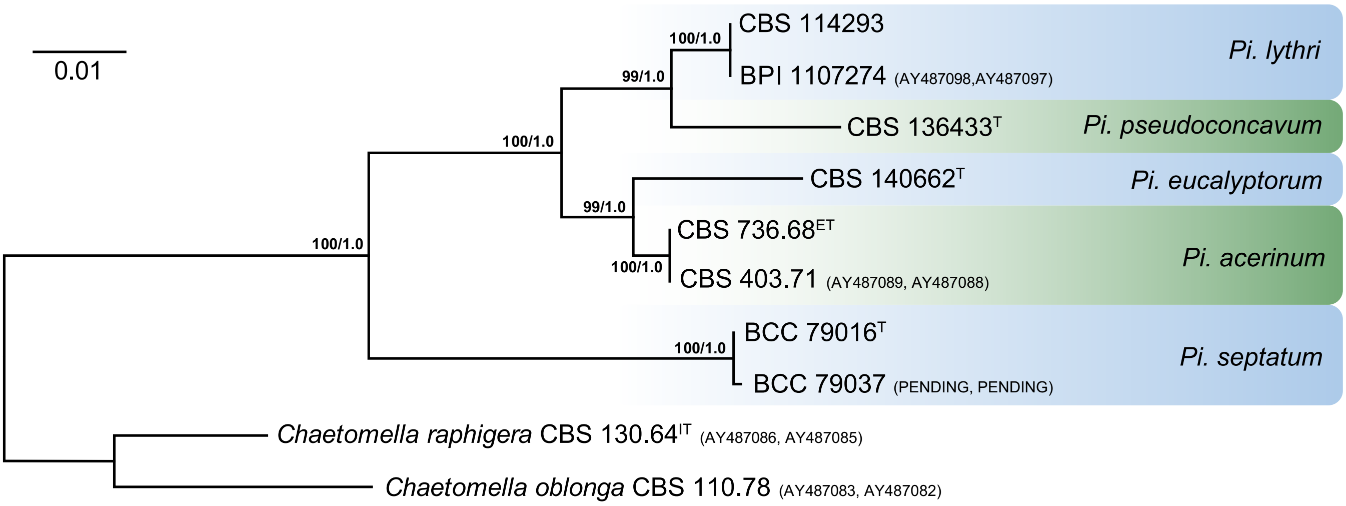

Fig. 45. Maximum likelihood (ML) tree based on partial sequences of LSU (792 bp) and ITS (477 bp) regions from reference and ex-type strains of *Pilidium* species. Bootstrap support values and posterior probabilities above 70 % and 0.95, respectively are shown at the nodes. *Chaetomella raphigera* and *Chaetomella oblonga* (*Chaetomellaceae*, *Helotiales*) were used as outgroup taxa. Numbers within parentheses correspond to GenBank accession numbers of LSU and ITS sequences, respectively.^{T} and ^{ET} indicate ex-type and ex-epitype strains, respectively. TreeBASE: S20877.

morphology of the pycnidia, the production of acropleurogenous conidiogenous cells and conidial shape, support the inclusion of this species within the genus.

Authors: A. Giraldo, J. Luangsa-ard & P.W. Crous

Pleiochaeta (Sacc.) S. Hughes, Mycol. Pap. 36: 39. 1951. Figs 47, 48.
Synonym: *Ceratophorum* subgen. *Pleiochaeta* Sacc., Syll. fung. (Abellini) 11: 622. 1895.

Classification: *Dothideomycetes*, *Pleosporomycetidae*, *Pleosporales*, *Dothidotthiaceae.*

Type species: *Pleiochaeta setosa* (Kirchner) S. Hughes. Epitype and ex-epitype culture designated here: CBS H-23058, CBS 496.63 = MUCL 8091).

DNA barcode (genus): LSU.

DNA barcode (species): ITS. Table 14. Figs 49, 50.

Sexual morph unknown. *Conidiophores* macronematous, mononematous or grouped in fascicles, simple, erect, straight to flexuous, or geniculate, hyaline to pale olivaceous, smooth. *Conidiogenous cells* mono- and polyblastic, integrated, terminal and intercalary, cylindrical. *Conidia* solitary, dry, subcylindrical to fusoid, mostly curved, narrowed to obtuse at the apex, truncate at the base, pale to dark brown, smooth, multiseptate; *apical cell* bears several long, hyaline, subulate appendages which are sometimes branched. *Chlamydospores* present or absent, brown to dark brown in chains or in groups.

Culture characteristics: Colonies on PDA grey to olivaceous black with aerial mycelium white, cottony, margin fimbriate, effuse; reverse black.

Optimal media and cultivation conditions: MEA, OA, PDA or SNA with sterilised twigs, incubated at 25 °C. Not all strains sporulate well in culture.

Distribution: Worldwide.

Hosts: Mainly pathogens of legumes, with one species reported from carrots.

Disease symptoms: Brown leaf spots, lesions are circular and zonate. It also can attack stems, pods and roots, and destroy whole plants.

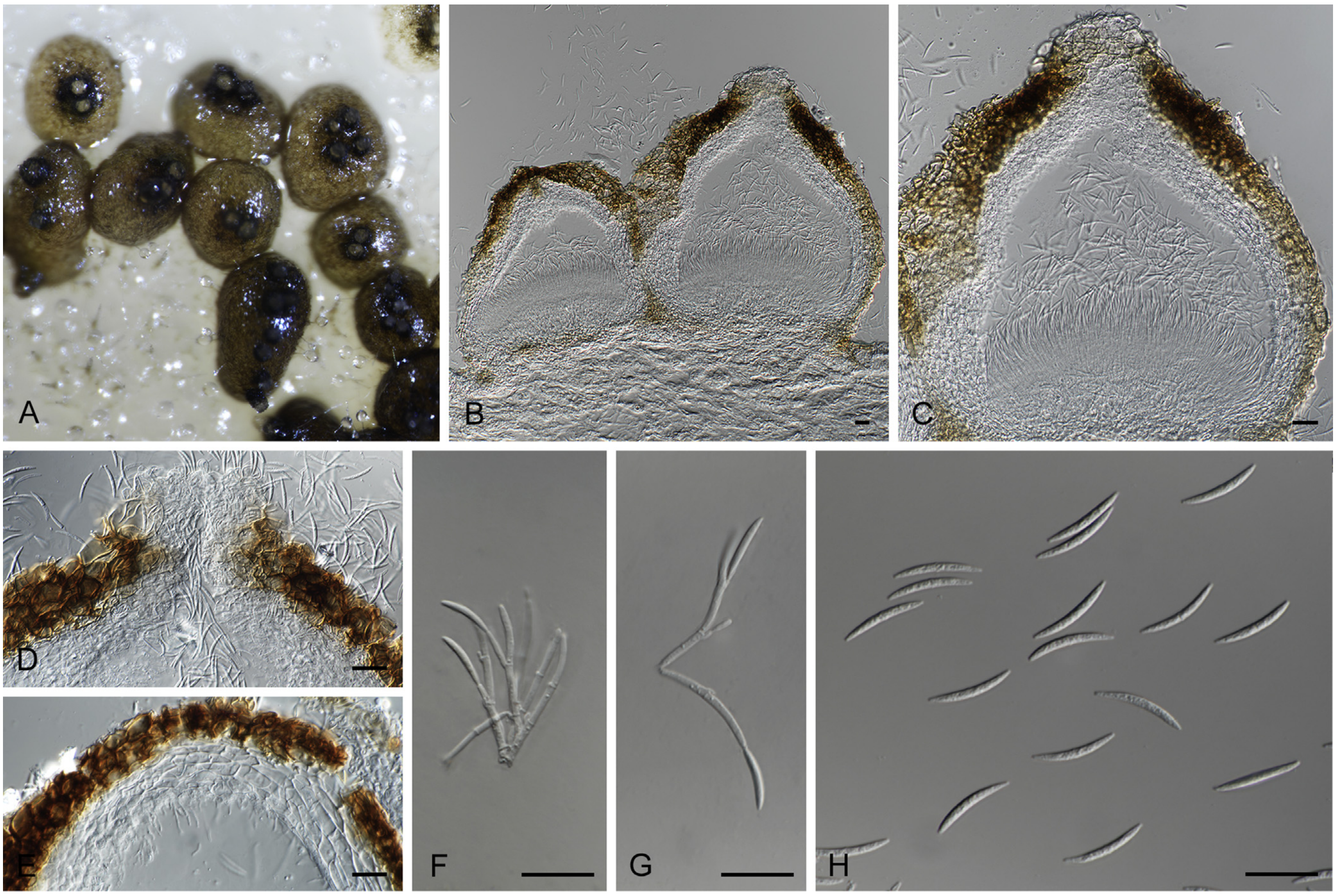

Fig. 46. *Pilidium septatum* (ex-type BCC 79016). **A.** Conidiomata on OA. **B, C.** Longitudinal sections of pycnidia. **D.** Details of ostiolar region. **E.** Details of the outer and inner pycnidial walls. **F, G.** Conidiophores and conidiogenous cells. **H.** Conidia. Scale bars: B–H = 10 µm.

Notes: *Pleiochaeta* was established by Hughes (1951) to accommodate two species previously included in *Ceratophorum*, namely *Plei. setosa* and *Plei. albizziae*. Currently this genus comprises six species, including pathogens and saprobes. *Pleiochaeta setosa*, the generic type, is the most important species from a phytopathogenic point of view, causing serious damage in *Lupinus* spp. and other legumes members of *Fabaceae*. Sequences available to date for the genus are scant. After the analysis of LSU and ITS sequences of the isolates studied with members of *Pleosporales* (*Dothideomycetes*), we support the phylogenetic position of *Plei. setosa* and *Plei. ghindensis* in the *Dothidotthiaceae*. Furthermore, our results allow us to describe a new species from South Africa, *Plei. carotae*, causing a disease on carrot leaves. Cultures of *Plei. albiziae*, *Plei. amazonensis*, *Plei. cassiae* and *Plei. stellaris* were not available for this study, and their phylogenetic position remains unknown. Further studies with additional molecular data of isolates from different origins and substrates, as well as pathogenicity tests, need to be conducted.

References: Hughes 1951 (taxonomy and morphology); Pirozynski 1974 (morphology and distribution); Bateman 1997 (pathogenicity); Yang & Sweetingham 2002 (morphology and pathogenicity).

Pleiochaeta carotae Hern.-Restr., van der Linde & Crous, **sp. nov.** MycoBank MB820795. Fig. 47.

Etymology: Named after the host genus from which it was isolated, *Daucus carota*.

Mycelium partly immersed, partly superficial, composed of branched, septate, hyaline to dark brown, smooth, 3–9 µm wide, hyphae. *Conidiophores* macronematous, mononematous, usually unbranched, flexuous, frequently geniculate, hyaline or pale olivaceous, smooth. *Conidiogenous cells* mono- and polyblastic, integrated, terminal and intercalary, sympodial, cylindrical to geniculate. *Conidia* solitary, dry, subcylindrical ellipsoid to fusoid, mostly curved, narrowed at apex, truncate at the base, at first colourless becoming orange-brown to olivaceous brown, smooth, 92–137 × 16–22 µm, 6–10-septate, usually constricted at the septa; *basal cell* conical, truncate, subhyaline to pale brown, 8–11 µm wide; *apical cell* obtuse, arising 2–3 hyaline appendages, with one appendage arising apically which are usually branched 2–4 times, and another two laterally on the sides which are usually branched 1–2(–3) times, appendages 70–114 µm long, 4.5–7 µm wide at the point of origin and pointed at their apices. *Chlamydospores* not observed.

Culture characteristics: Colonies reaching 40–55 mm diam after 1 wk at 25 °C on OA, PDA and MEA olivaceous black, cottony, with white aerial mycelium in the centre, exudate hyaline, margin fimbriate, effuse, colourless; reverse black.

Material examined: **South Africa**, Gauteng, Pretoria, on carrot leaf, Mar. 2015, M. Truter (**holotype** CBS H-23057, culture ex-type CPC 27452 = CBS 142644).

Notes: This is the first species of *Pleiochaeta* described from carrots, a non-legume host plant. Conidia of this species resemble those of *Plei. ghindensis*, having branched apical

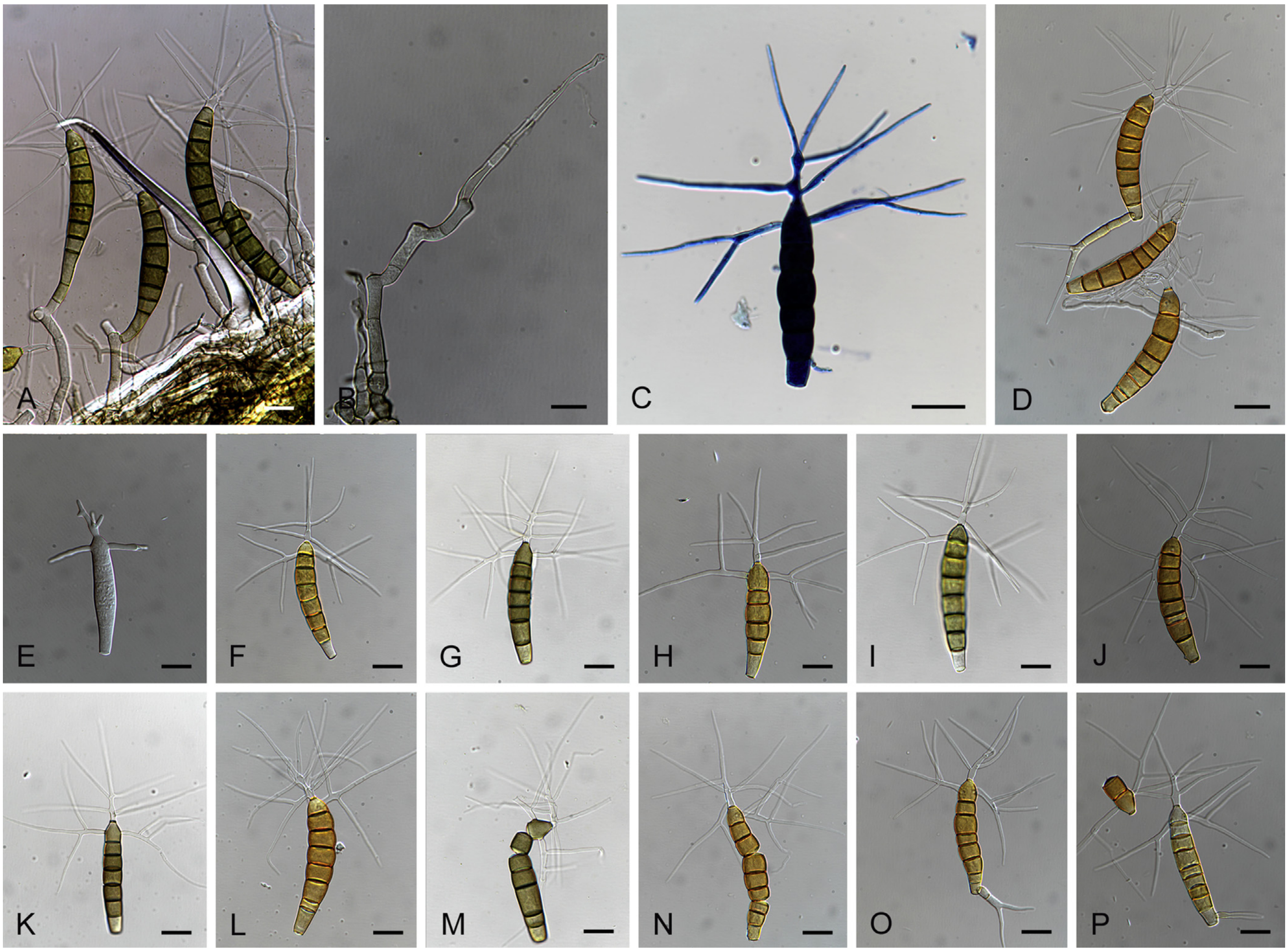

Fig. 47. *Pleiochaeta carotae* (ex-type CBS 142644) **A.** Conidiophores with conidia. **B.** Conidiophores and conidiogenous cells. **C–P.** Conidia. Scale bars: 10 µm

appendages, usually more than twice branched. In *Plei. ghindensis* conidiogenous cells are monoblastic, terminal and cylindrical with percurrent proliferations. However, in *Plei. carotae*, conidiogenous cells are mono- and polyblastic, terminal and intercalary and geniculate with sympodial proliferations. Furthermore, conidia in *Plei. carotae* are larger (92–137 µm *vs.* 85–115 µm in *Plei. ghindensis*) and with a larger number of septa (6–10 *vs.* 6–7 in *Plei. ghindensis*). Finally, the basal conidial cells are usually paler than the other cells (in *Plei. ghindensis* conidia are concolourous).

Pleiochaeta setosa (Kirchn.) S. Hughes. Mycol. Pap. 36: 34. 1951. Figs 48, 51.
Basionym: *Ceratophorum setosum* Kirchn. Z. Pflanzenkrankh. Pflanzenschutz 2: 324. 1892.
Synonyms: *Pestalotia lupini* Sorauer, Z. Pflanzenkrankh. Pflanzenschutz 8: 269. 1898.
Mastigosporium lupini (Sorauer) Cavara, Riv. Patol. Veg. 14: 13. 1924.

Mycelium partly immersed, partly superficial, composed of branched, septate, hyaline to brown, smooth, 4–7.5 µm wide, hyphae. *Conidiophores* macronematous, mononematous, usually unbranched, flexuous, frequently geniculate, hyaline or pale olivaceous, smooth, 34–138 × 5–11 µm. *Conidiogenous cells* mono-, usually polyblastic, integrated, terminal and intercalary, sympodial, cylindrical, geniculate, hyaline to pale olivaceous, 25–68 × 8–11.5 µm. *Conidia* solitary, dry, subcylindrical to fusoid, mostly curved, narrowed at the apex, truncate at the base, colourless or with the cell at each end hyaline or subhyaline and intermediate cells straw-coloured to golden brown, smooth, 68–88.5 × 11–25 µm, 8.5–11 µm wide at the base, 4–7-septate; *apical cell* bears 3–4 hyaline, subulate appendages, 89–150 × 2.5–5.5 µm, apical appendage at first simple later becoming branched, lateral appendages simple. *Chlamydospores* pale brown to dark brown, terminal and intercalary, in chains or in groups (observed in CBS 142.51 and 502.80, but not in the epitype).

Culture characteristics: Colonies reaching 25–50 mm diam after 1 wk at 25 °C on OA, PDA and MEA, cottony to glabrous, smoke-grey to olivaceous black, with aerial mycelium in the centre white, margin effuse, fimbriate; reverse black. On OA sometimes with hyaline exudate and apricot diffusible pigment.

Material examined: **Lectotype designated here**: figs 1–6 in Kirchner O. 1892. Über das Absterben junger Cytisus-Pflanzen. Z. Pflanzenkrankh. Pflanzenschutz 2: 324–327, MBT376013.

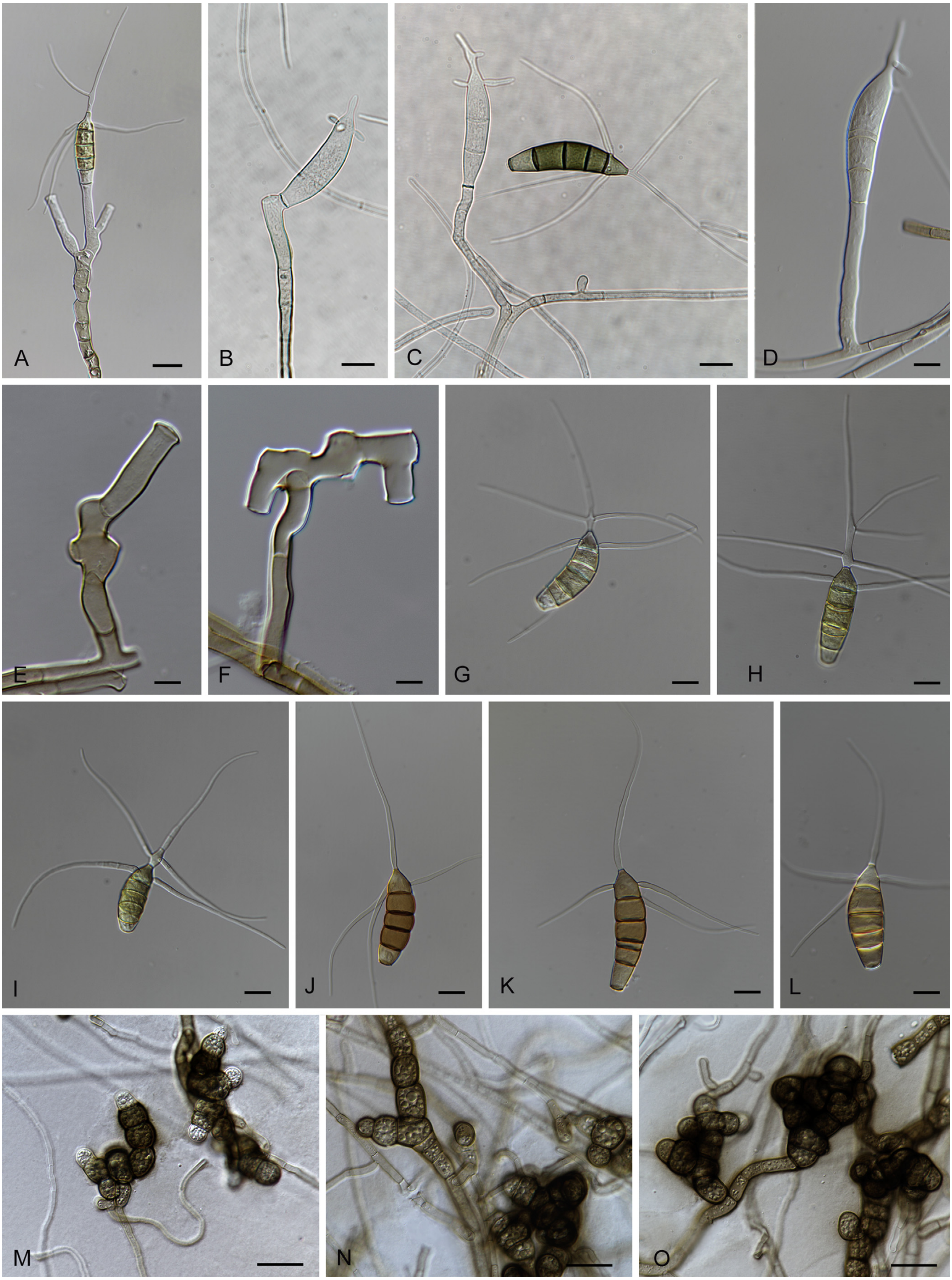

Fig. 48. *Pleiochaeta setosa* (ex-epitype CBS 496.63, CBS 502.80). **A–D.** Conidiophores with conidia (ex-epitype CBS 496.63). **E, F.** Conidiogenous cells (ex-epitype CBS 496.63). **G–L.** Conidia (ex-epitype CBS 496.63). **M–O.** Chlamydospores (CBS 502.80). Scale bars: 10 µm.

Table 14. DNA barcodes of accepted *Pleiochaeta* spp.

Species	Isolates[1]	GenBank accession numbers[2]		References
		ITS	LSU	
Pleiochaeta carotae	CBS 142644^{T}	KY905669	KY905663	Present study
Plei. ghindensis	CBS 552.92	EU167561	EU167561	Simon *et al.* (2009)
Plei. setosa	CBS 496.63^{ET}	EU167563	EU167563	Simon *et al.* (2009)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands. ^{T} and ^{ET} indicate ex-type and ex-epitype strains, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; LSU: partial 28S large subunit RNA gene.

Austria, Wallersberg, near Völkermarkt, on living stem and leaf of *Genista sagittale*, Aug. 1980, W. Gams, CBS 502.80. **Germany,** Berlin, on leaf of *Cytisus racemosus*, unknown date, R. Schneider (**epitype designated here** CBS H-23058, MBT376012, culture ex-epitype = CBS 496.63 = MUCL 8091). **The Netherlands**, Boskoop, on spot on stem of *Cytisus* sp., unknown date, I. de Boer, CBS 142.51. **Unknown country**, on leaf of *Laburnum* sp., unknown date, dep. C.M. Doyer, CBS 118.25.

Notes: *Pleiochaeta setosa* was introduced by Kirchner (1892) as *Ceratophorum setosum* for a fungus that infects *Cytisus* in Germany and later was transferred to *Pleiochaeta* by Hughes (1951). Since type material for *Plei. setosa* is inexistent, the illustrations included in the protologue reproduced here (Fig. 51) serve as lectotype. In addition, to fix the use of the name the strain CBS 496.63 is designated here as ex-epitype. This isolate was collected, from the same locality and host genus where it was found the first time (Kirchner 1892) and fits well with the description of the protologue. This species has a worldwide distribution and it is frequently reported as pathogen of *Lupinus* (Hughes 1951, Pirozynski 1974). Nevertheless, *Crotalaria*, *Genista*, *Laburnum* and *Ornithopus* can also be hosts of this species (Pirozynski 1974, Yang & Sweetingham 2002). Unfortunately, host specificity studies are not available for this species, even though Yang & Sweetingham (2002) reported morphological and pathogenicity differences among isolates from *Lupinus* spp. and *Ornithopus* spp.

Authors: M. Hernández-Restrepo, E.J. van der Linde & P.W. Crous

Plenodomus Preuss, Linnaea 24: 145. 1851. Fig. 52.
Synonyms: *Phoma* sect. *Plenodomus* (Preuss) Boerema, Kesteren & Loer., Trans. Brit. Mycol. Soc. 77: 61. 1981.
Diploplenodomus Diedicke, Ann. Mycol. 10: 140. 1912.
Plectophomella Moesz, Magyar Bot. Lapok 21: 13. 1922.
Apocytospora Höhn., Mitt. Bot. Lab. TH Wien 1: 43. 1924.
Deuterophoma Petri, Boll. R. Staz. Patalog. Veget. Roma 9: 396. 1929.
For Additional synonyms of the asexual morph and sexual morph genera listed below see Boerema *et al.* (1994) and Khashnobish *et al.* (1995), respectively.

Classification: *Dothideomycetes*, *Pleosporomycetidae*, *Pleosporales*, *Leptosphaeriaceae.*

Type species: *Plenodomus lingam* (Tode: Fr.) Höhn. Representative strains: CBS 532.66 and CBS 475.81.

DNA barcodes (genus): LSU, ITS.

DNA barcodes (species): *tub2*, *rpb2.* Table 15. Fig. 53.

Ascomata solitary, scattered or in small groups, erumpent to superficial, subglobose, broadly or narrowly conical, small- to medium sized, dark brown to black, smooth, ostiolate; *ostiole* apex with a conical, well developed papilla; *ascomatal wall* composed of two to several layers of scleroplectenchymatous cells. *Hamathecium* comprising long, septate, pseudoparaphyses. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical, rounded at the apex, with an ocular chamber, short pedicel. *Ascospores* cylindrical to ellipsoidal, yellowish brown, septate, not or slightly constricted at septa, guttulate and lacking a mucilaginous sheath, cell above central septum slightly wider. *Conidiomata*. Type 1: solitary, scattered or in small groups, erumpent to superficial, subglobose or flask shaped with a broad base, mostly black, ostiolate; *ostiole* with a long neck and well developed poroid papilla in the apex. Type 2: solitary, scattered or in small groups, erumpent to superficial, mostly subglobose, ostiolate; *ostiole* slightly papillate with a narrow pore or opening via a rupture. *Conidiomatal wall* composed of several layers with thick-walled cells of *textura angularis*, surface heavily pigmented. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* phialidic, hyaline, smooth, ampulliform. *Conidia* hyaline, aseptate, ellipsoidal to subcylindrical (adapted from Ariyawansa *et al.* 2015b).

Culture characteristics: Colonies on OA yellow/green to olivaceous grey, dull green, or translucent, aerial mycelium tenuous, margin irregular and whitish, compact, floccose.

Optimal media and cultivation conditions: OA or PNA near-ultraviolet light (12 h light, 12 h dark) to promote sporulation at 25 °C.

Distribution: Worldwide.

Hosts: As pathogens of herbaceous plants in different families, most records refer to *Asteraceae*, and on leaves, branches, bark, wood and dead stems of various trees and shrubs of *Brassicaceae*, *Lamiaceae*, *Rutaceae*, *Salicaceae* and *Vitaceae*. In addition, some *Plenodomus* species are found as opportunistic or pathogenic fungi on *Apiaceae*, *Bignoniaceae*, *Caprifoliaceae*, *Fabaceae*, *Rosaceae*, *Ulmaceae* and *Umbelliferae*.

Disease symptoms: Leaf spots, stem lesions, slow wilt, bark canker, root rot, shoot dieback.

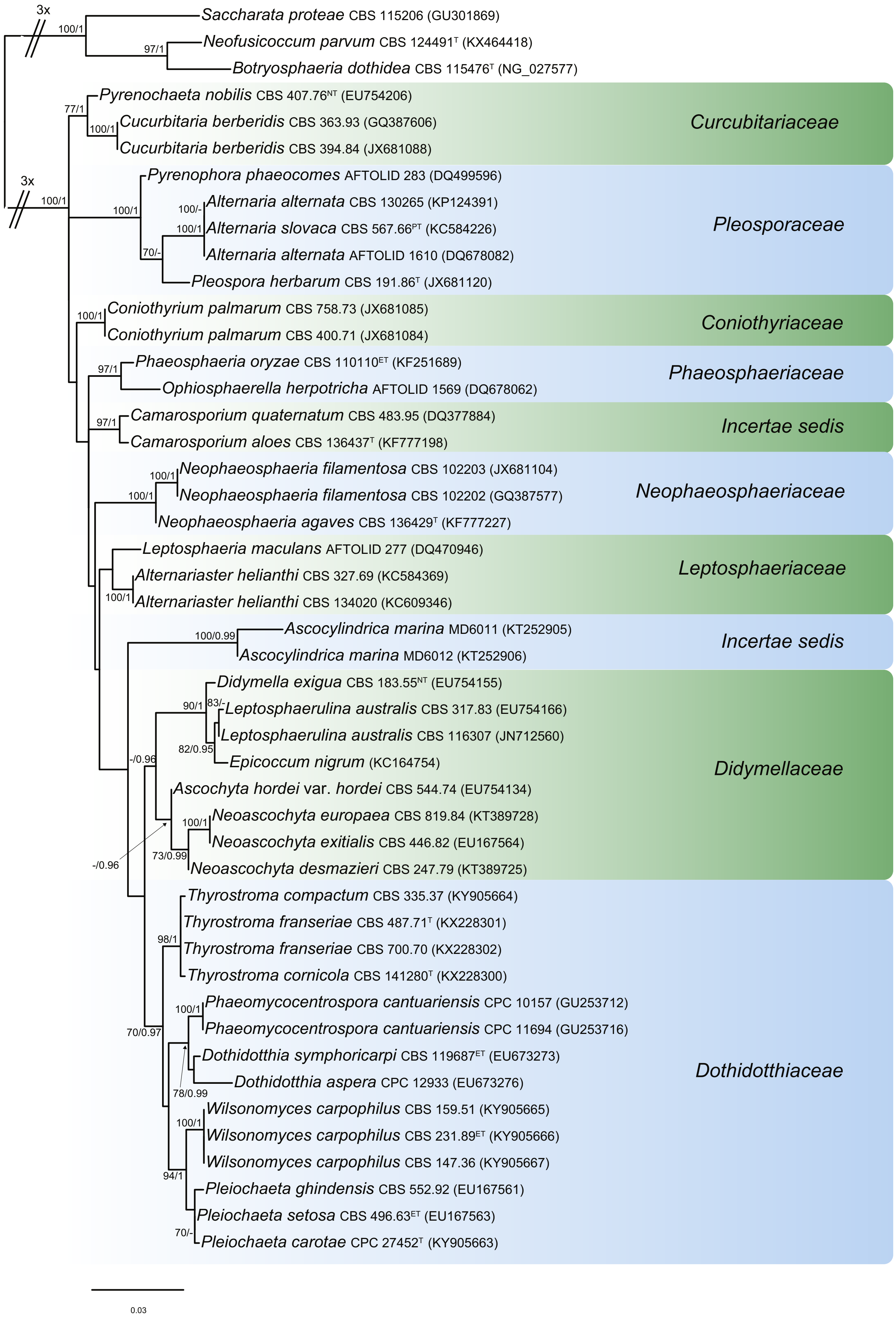

Fig. 49. RAxML phylogram obtained from LSU (883 bp) sequences of *Dothideomycetes*. RAxML bootstrap support (BS) values above 70 % and Bayesian posterior probability scores $\geq$ 0.95 are shown at the nodes. The tree was rooted to *Botryosphaeria dothidea* CBS 115476, *Neofusicoccum parvum* CBS 124491 and *Saccharata proteae* CBS 115206. Numbers between parentheses correspond to GenBank accession numbers. $^{T, ET, NT}$ and ^{PT} indicate ex-type, ex-epitype, ex-neotype and ex-paratype, respectively. TreeBASE: S20877.

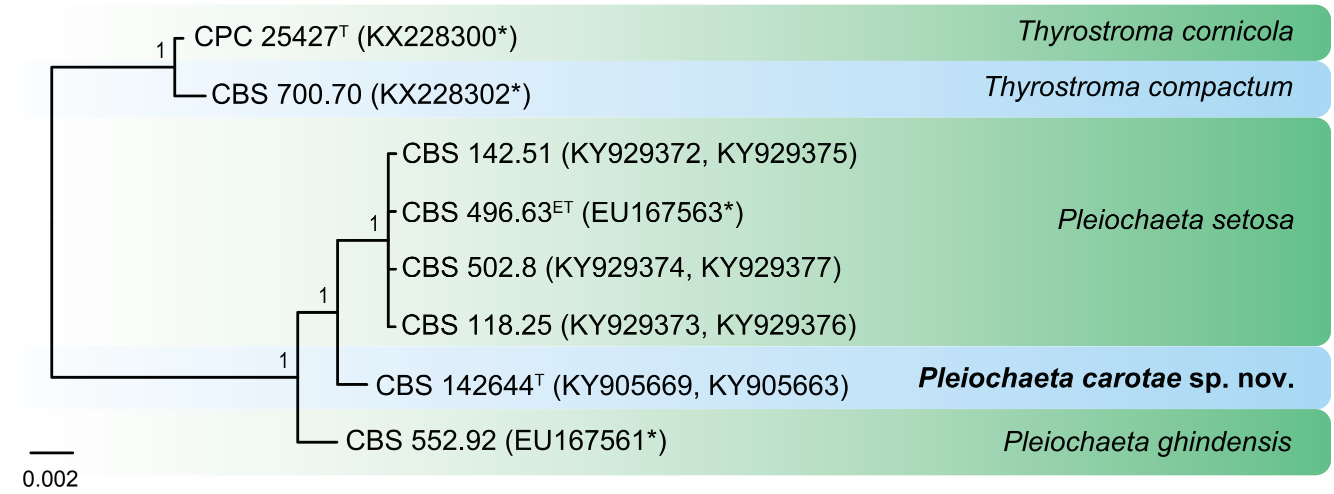

Fig. 50. Phylogenetic tree resulting from a Bayesian analysis of the combined LSU and ITS sequences alignment of *Pleiochaeta* species. Bayesian posterior probabilities >0.95 are indicated at the nodes. The tree was rooted to *Thyrostroma compactum* and *Thyrostroma cornicola*. Numbers between parentheses correspond to GenBank accession numbers of ITS and LSU, respectively. ^{T} and ^{ET} indicate ex-type and ex-epitype strains, respectively. *, ITS and LSU sequences. TreeBASE: S20877.

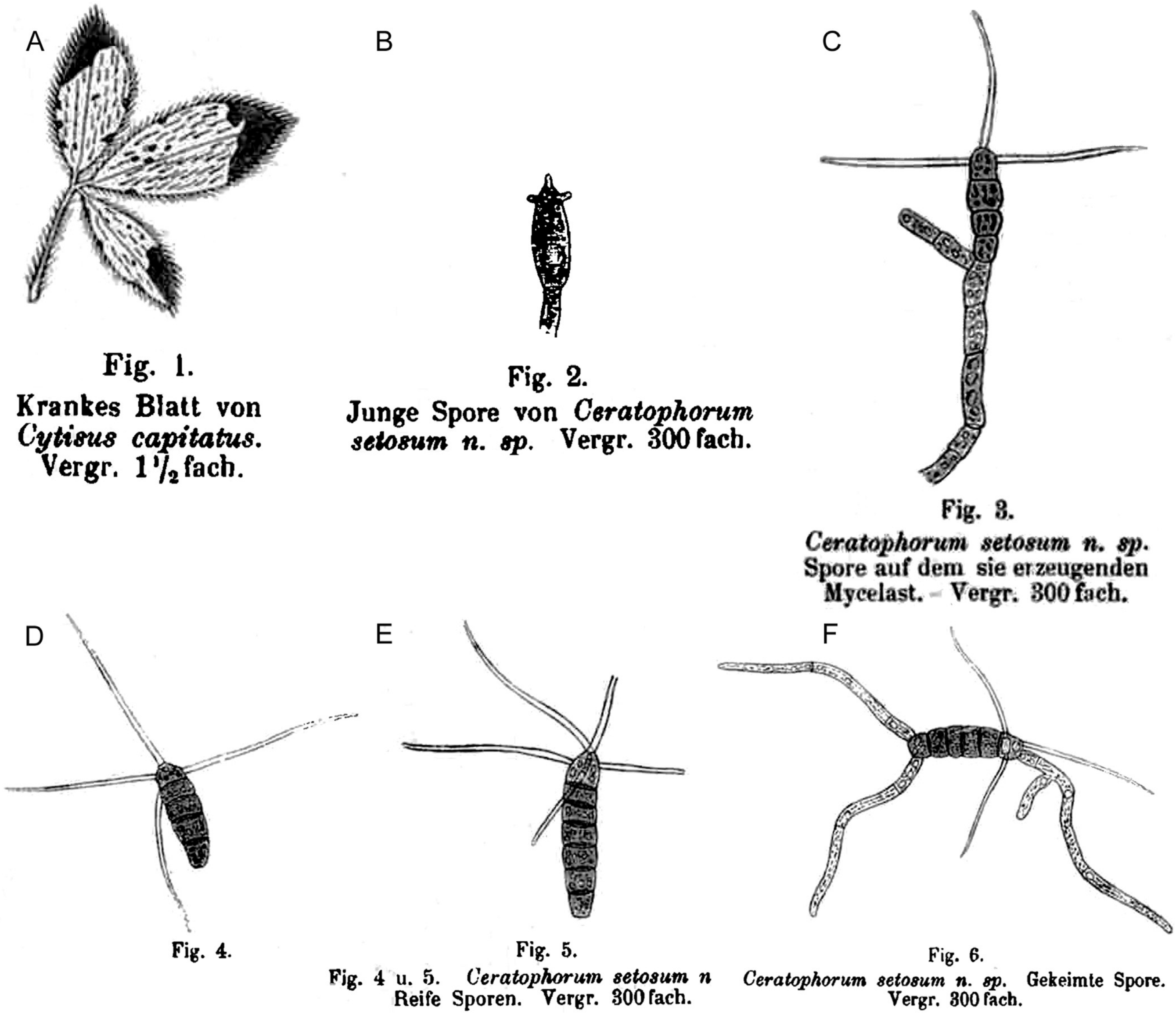

Fig. 51. Reproduction of the original drawings by Kirchner (1892) illustrating *Ceratophorum setosum* (original numbers are maintained to indicate the different structures). **A.** fig. 1. Symptoms in *Cytisus capitatus*. **B.** fig. 2. Young conidia. **C.** fig. 3. Conidiophores and conidia. **D, E.** figs 4, 5. Conidia. **F.** fig. 6. Germinating conidia.

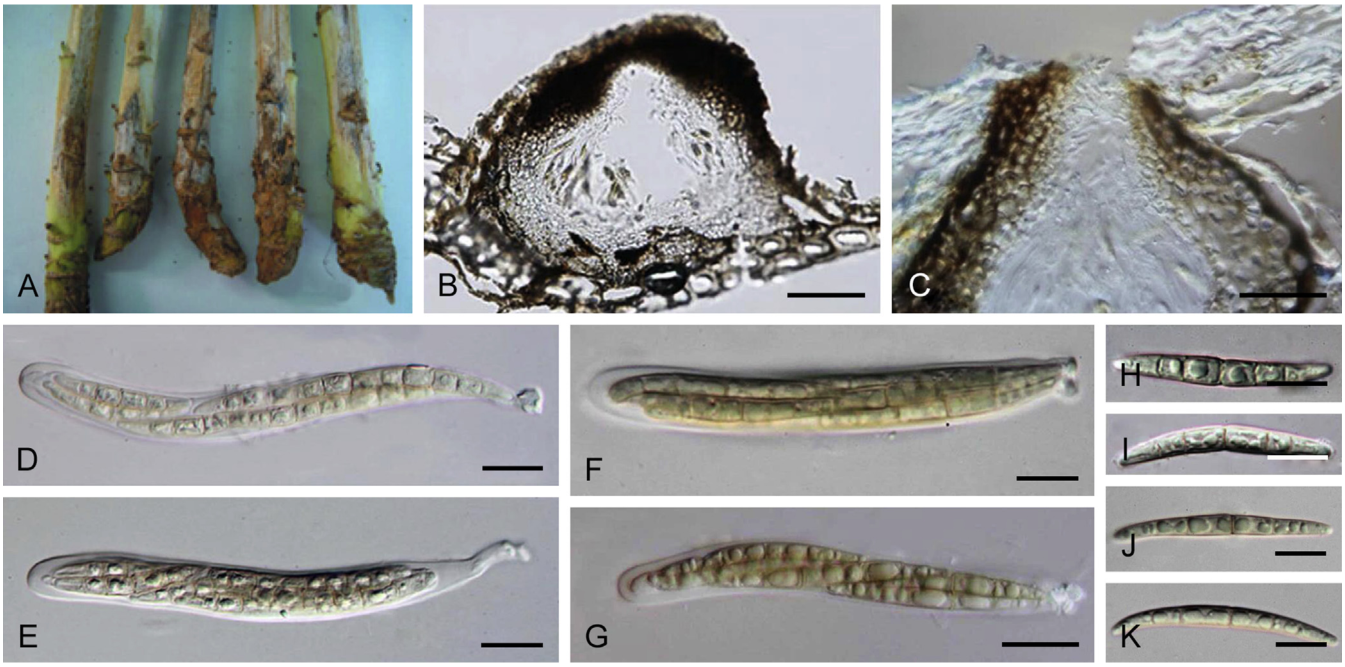

Fig. 52. *Plenodomus* spp. **A.** Symptoms of stem canker of *Plenodomus biglobosa*. **B, C.** Section through ascomata. B. *Plenodomus guttulatus* (holotype MFLU 15-1876). **C.** *Plenodomus salviae* (holotype MFLU 15-0515). **D–G.** Asci. **D, E.** *Plenodomus guttulatus* (holotype MFLU 15-1876); **F, G.** *Plenodomus salviae* (holotype MFLU 15-0515). **H–K.** Ascospores. **H, I.** *Plenodomus guttulatus* (holotype MFLU 15-1876). **J, K.** *Plenodomus salviae* (holotype MFLU 15-0515). Scale bars: B = 75 µm; C = 25 µm; D–G, J, K = 10 µm; H, I = 5 µm. Picture A taken from Fitt *et al.* (2008); B–K from Ariyawansa *et al.* (2015b).

Notes: The genus *Plenodomus* was first established by Preuss (1851), and recently re-introduced and placed in the family *Leptosphaeriaceae* by de Gruyter *et al.* (2013). The genus mainly consists of species that formerly belonged to *Phoma* section *Plenodomus* and the sexual morph *Leptosphaeria*. *Plenodomus* includes several well-known important plant pathogens, such as *Plen. biglobosus*, *Plen. lindquistii*, *Plen. tracheiphilus*, and *Plen. wasabiae*.

References: Boerema *et al.* 2004 (morphology and pathogenicity); de Gruyter *et al.* 2013, Ariyawansa *et al.* 2015b (morphology and phylogeny).

Plenodomus deqinensis Q. Chen & L. Cai, **sp. nov.** MycoBank MB818821. Fig. 54.

Etymology: Named after the location where the holotype was collected, Deqin, Yunnan Province in China.

Conidiomata pycnidial, solitary, globose to subglobose, glabrous, superficial, (150–)165–355 × (105–)125–305 µm; *ostiole* single, slightly papillate with a narrow pore or opening via a rupture; *conidiomatal wall* pseudoparenchymatous, 3–6-layered, 16–28 µm thick, composed of isodiametric to oblong cells, outer layer brown. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* phialidic, hyaline, smooth, ampulliform, 5–7 × 4–6.5 µm. *Conidia* ellipsoidal-cylindrical, smooth- and thin-walled, aseptate, 3.5–5.5 × 1.5–2.5 µm, with 2 minute polar guttules. *Conidial exudates* not recorded. *Sexual morph* not observed.

Culture characteristics: Colonies on OA 35 mm diam after 1 wk, margin regular, floccose, white, pale grey near the centre; reverse white to slightly pale olivaceous. Colonies on MEA 17–23 mm diam after 1 wk, margin irregular, aerial mycelia sparse, pale green; reverse concolourous. Colonies on PDA 25–27 mm diam after 1 wk, margin regular, floccose, white, greyish brown near the centre; reverse buff to amber. NaOH test negative.

Material examined: **China**, Yunnan, Dequin, isolated from soil, Apr. 2011, M.M. Wang (**holotype** HMAS 247058, culture ex-type CGMCC 3.18221 = LC 5189).

Notes: *Plenodomus deqinensis* was collected from soil on a snow mountain in China, and proved able to grow at a low temperature (15 °C). This species clustered with *Plen. agnitus*, *Plen. fallaciosus* and *Plen. lupini* in the phylogenetic tree (Fig. 53). The NaOH test of *Plen. deqinensis* proved negative, while in *Plen. agnitus* it was positive (Boerema *et al.* 1994). Morphologically, *Plen. deqinensis* differs from *Plen. lupini* in the slightly wider conidiogenous cells (5–7 × 4–6.5 µm *vs.* 3–8 × 3–6 µm), and being conspicuously biguttulate (de Gruyter *et al.* 1993). *Plenodomus fallaciosus* has hitherto only been observed as a sexual morph.

Authors: Q. Chen & L. Cai

Protostegia Cooke, Grevillea 9: 19. 1880. Fig. 55.

Classification: *Dothideomycetes*, *Dothideomycetidae*, *Capnodiales*, *Mycosphaerellaceae.*

Type species: *Protostegia eucleae* Kalchbr. & Cooke. Slide holotype: IMI 230771. Epitype and ex-epitype cultures: PREM 60879, CPC 23549 = CBS 137232.

DNA barcode (genus): LSU.

DNA barcode (species): ITS. Table 16.

Sexual morph unknown. *Conidiomata* pycnidial, immersed, becoming somewhat erumpent, solitary, exuding a mucoid

Table 15. DNA barcodes of accepted *Plenodomus* spp.

Species	Isolates[1]	GenBank accession numbers[2]			References
		ITS	*rpb2*	*tub2*	
Plenodomus agnitus	CBS 121.89	JF740194	KY064036	KY064053	de Gruyter *et al.* (2013), present study
Plen. biglobosus	CBS 119951	JF740198	KY064037	KY064054	de Gruyter *et al.* (2013), present study
Plen. chrysanthemi	CBS 539.63^T	JF740253	KY064038	KY064055	de Gruyter *et al.* (2013), present study
Plen. collinsoniae	CBS 120227	JF740200	KY064039	KY064056	de Gruyter *et al.* (2013), present study
Plen. confertus	CBS 375.64	AF439459	KY064040	KY064057	Câmara *et al.* (2002), present study
Plen. congestus	CBS 244.64	AF439460	KY064041	KY064058	Câmara *et al.* (2002), present study
Plen. deqinensis	CGMCC 3.18221	KY064027	KY064034	KY064052	Present study
Plen. enteroleucus	CBS 142.84^{ET}	JF740214	KY064042	KT266266	de Gruyter *et al.* (2013), present study
Plen. fallaciosus	CBS 414.62	JF740222	KY064043	KT266271	de Gruyter *et al.* (2013), present study
Plen. guttulatus	MFLUCC 151876	KT454721	–	–	Ariyawansa *et al.* (2015b)
Plen. hendersoniae	CBS 113702	JF740225	KY064044	KT266271	de Gruyter *et al.* (2013), present study
Plen. influorescens	CBS 143.84^T	JF740228	KY064045	KT266267	de Gruyter *et al.* (2013), present study
Plen. libanotidis	CBS 113795	JF740231	KY064046	KY064059	de Gruyter *et al.* (2013), present study
Plen. lindquistii	CBS 381.67	JF740233	–	AY749028	Voigt *et al.* (2005), de Gruyter *et al.* (2013)
Plen. lingam	CBS 260.94	JF740235	KY064047	KY064060	de Gruyter *et al.* (2013), present study
Plen. lupini	CBS 248.92	JF740236	KY064048	KY064061	de Gruyter *et al.* (2013), present study
Plen. pimpinellae	CBS 101637^T	JF740240	–	KY064062	de Gruyter *et al.* (2013), present study
Plen. salviae	MFLUCC 130219	KT454725	–	–	Ariyawansa *et al.* (2015b)
Plen. tracheiphilus	CBS 551.93	JF740249	KY064049	KT266269	de Gruyter *et al.* (2013), present study
Plen. visci	CBS 122783^{ET}	JF740256	KY064050	KY064063	de Gruyter *et al.* (2013), present study
Plen. wasabiae	CBS 120119	JF740257	–	KT266272	de Gruyter *et al.* (2013), present study

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CGMCC: Chinese General Microbiological Culture Collection Center, Beijing, China; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Ria, Thailand. ^{T} and ^{ET} indicate ex-type and ex-epitype strains, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *rpb2*: partial RNA polymerase II second largest subunit gene; *tub2*: partial β-tubulin gene.

conidial cirrhus, pale brown, splitting the leaf surface, with central ostiole; *conidiomatal wall* brown, *textura intricata*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, smooth, lining the inner cavity, lageniform to subcylindrical, proliferating percurrently at apex. *Conidia* hyaline, smooth, scolecosporous, euseptate (adapted from Crous *et al.* 2015a).

Culture characteristics: Colonies erumpent, slow growing, with uneven or lobate, feathery margins and sparse to moderate aerial mycelium. On MEA surface and reverse greyish sepia or surface pale olivaceous grey and reverse olivaceous grey; on OA surface mouse-grey or pale olivaceous grey, reverse olivaceous grey; on PDA surface greyish sepia or pale olivaceous grey, reverse mouse-grey or olivaceous grey.

Optimal media and cultivation conditions: PNA incubated at 25 °C under continuous near-ultraviolet light to promote sporulation.

Distribution: South Africa.

Hosts: *Euclea divinorum*, *E. lanceolata*, *E. natalensis*, *E. racemosa* and *E. undulata*.

Disease symptoms: Leaf spots.

Notes: The genus *Protostegia* is thus far only known from South Africa, where it has been reported from leaves of various *Euclea* spp. However, *Euclea* is widespread throughout Africa, and therefore *Protostegia* may be more widespread than currently known. *Protostegia* was introduced by Kalchbrenner & Cooke (1880) in order to accommodate *Stegia magnoliae* and the new species *Pr. eucleae*, and then four more species were allocated in this genus. However, Dyko *et al.* (1979) transferred three of these species to other genera and another two species were rejected as doubtful. Therefore, only the type species *Pr. eucleae* was retained and until now this genus has remained monotypic. *Protostegia* is characterised by immersed conidiomata with walls of *textura intricata*, splitting the epidermis and appearing acervular, but having a well-developed ostiole (Dyko *et al.* 1979). Recently *Pr. eucleae* was placed in the *Mycosphaerellaceae* together with *Cytostagonospora martiniana* and *Phaeophleospora* spp. on the basis of phylogenetic analysis of ITS and LSU sequences (Crous *et al.* 2015a). *Cytostagonospora martiniana* can be distinguished from *Protostegia* by having percurrent and polyphialidic conidiogenous cells, and solitary to aggregated conidiomata embedded in stromatic tissue (Quaedvlieg *et al.* 2013). *Phaeophleospora* differs by the production of pigmented conidiogenous cells and conidia (Crous *et al.* 2009b).

References: Dyko *et al.* 1979 (morphology); Crous *et al.* 2015a (morphology and phylogeny).

Protostegia eucleicola Crous, **sp. nov.** MycoBank MB820822. Fig. 55.

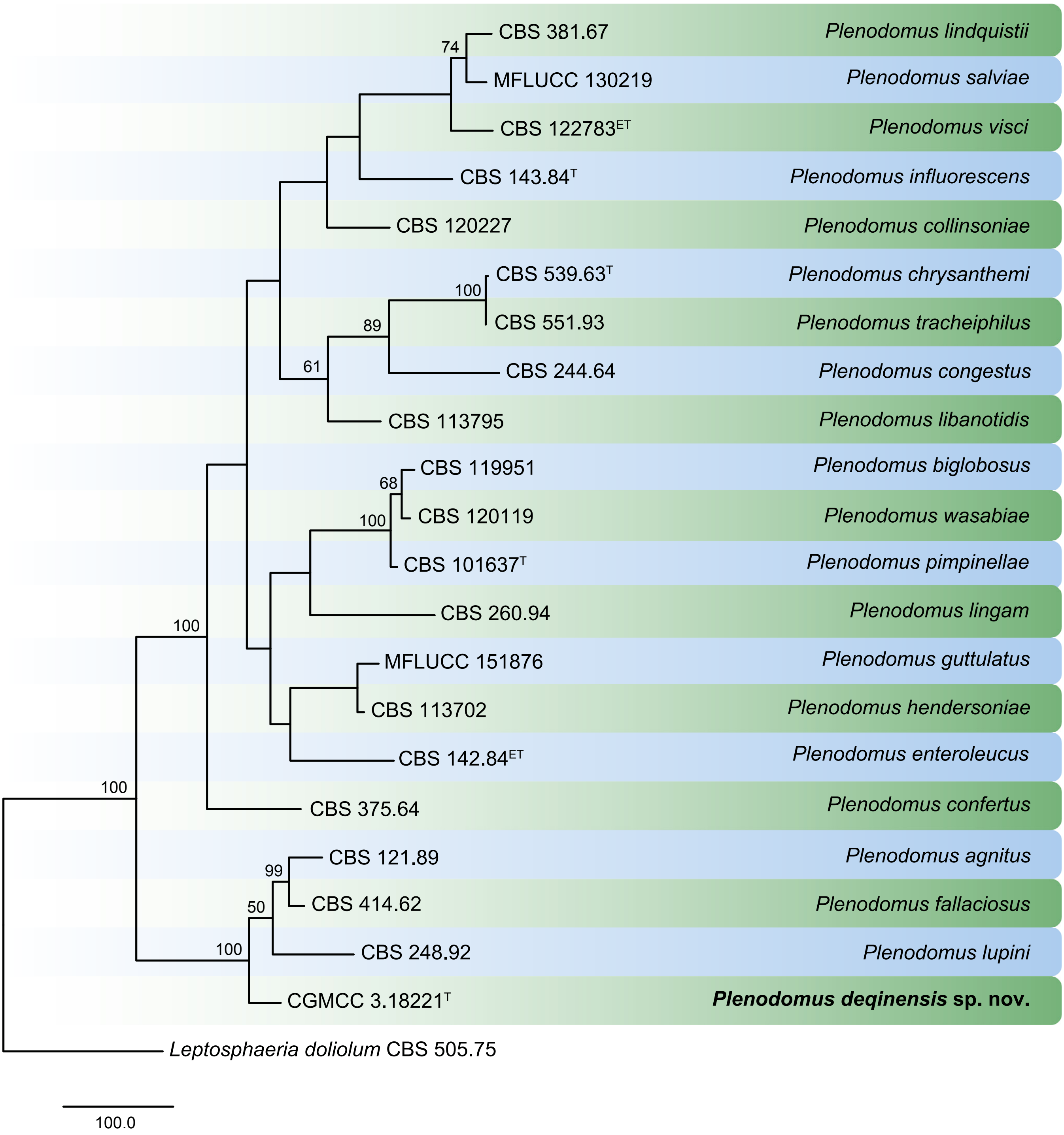

Fig. 53. Phylogenetic tree generated from a maximum parsimony analysis based on the combined LSU, ITS, *tub2* and *rpb2* sequences. Values above the branches represent parsimony bootstrap support values (> 50 %). Novel species are shown in **bold**. The tree is rooted with *Leptosphaeria doliolum* CBS 505.75. GenBank accession numbers are listed in Table 15. ^{T} and ^{ET} indicate ex-type and ex-epitype strains, respectively. TreeBASE: S21048.

Etymology: Name refers to the host genus it was isolated from, *Euclea.*

Conidiomata epiphyllous on living leaves, erumpent, solitary, not associated with leaf spots, exuding a mucoid conidial cirrhus that dries to a hard, dark brown crystalline droplet on the leaf surface, up to 250 µm diam, immersed, pale brown, splitting the leaf surface, with central ostiole, 10–30 µm diam; *conidiomatal wall* brown, *textura intricata*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, smooth, lining the inner cavity, lageniform to subcylindrical, 8–10 × 4–5 µm, proliferating percurrently at apex. *Conidia* hyaline, smooth, curved, guttulate, apices subacutely rounded, basal cell tapering to a truncate hilum, 1.5–2 µm diam, 3–7-septate, (40–)50–70(–75) × (2.5–)3–4 µm.

Culture characteristics: Colonies erumpent, slow growing, with lobate, feathery margins and sparse aerial mycelium; on MEA surface and reverse greyish sepia; on OA surface mouse-grey; on PDA surface greyish sepia, reverse mouse-grey.

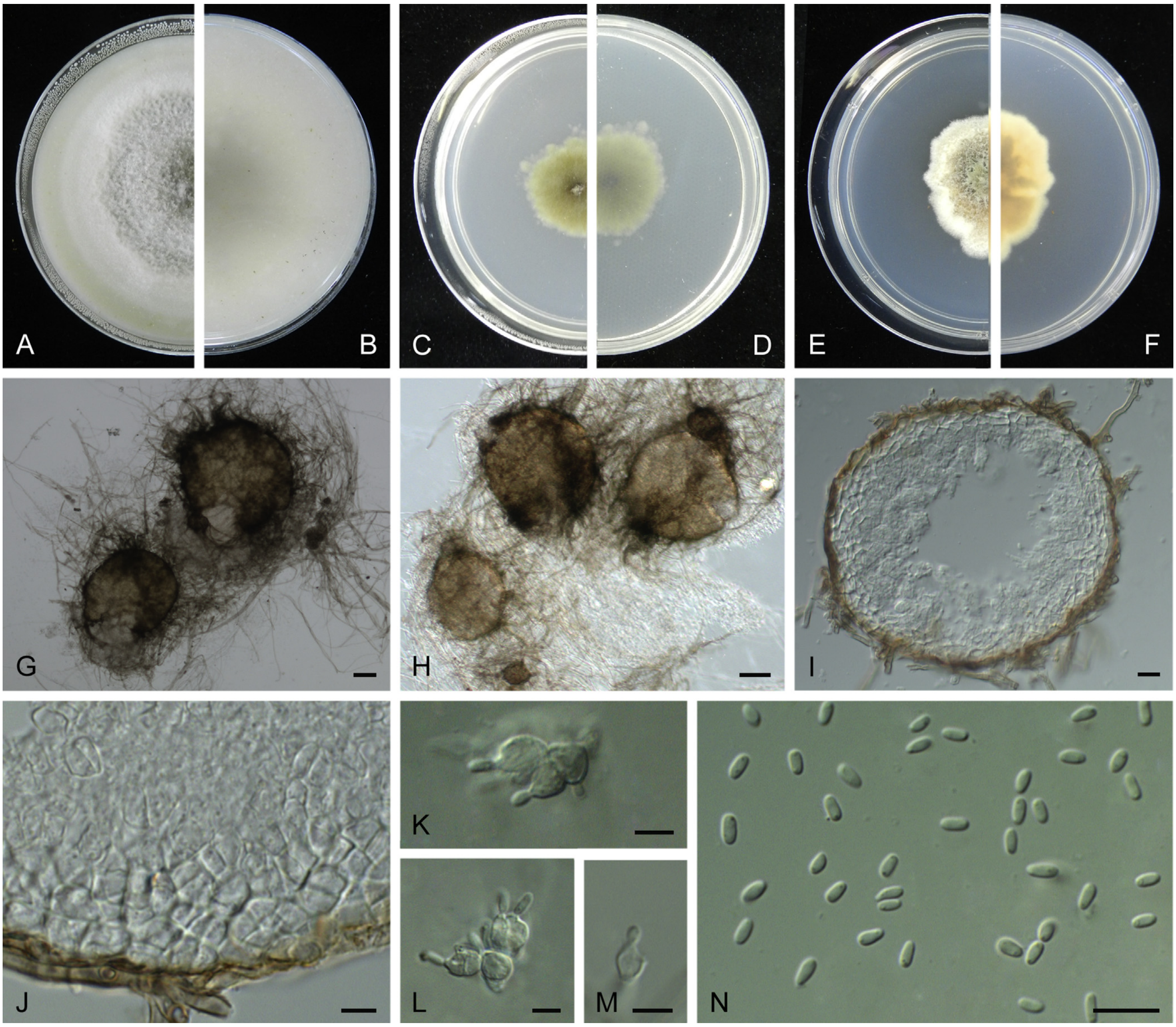

Fig. 54. *Plenodomus deqinensis* (ex-type CGMCC 3.18221). **A, B.** Colony on OA (front and reverse). **C, D.** Colony on MEA (front and reverse). **E, F.** Colony on PDA (front and reverse). **G, H.** Pycnidia. **I.** Section of pycnidium. **J.** Section of pycnidial wall. **K–M.** Conidiogenous cells. **N.** Conidia. Scale bars: G, H = 50 µm; I = 10 µm; J–M = 5 µm; N = 10 µm.

Material examined: **South Africa**, Western Cape Province, Porcupine Hills wine farm, between Botrivier and Villiersdorp, on *Euclea racemosa*, 29 Dec. 2014, A.R. Wood (**holotype** CBS H-23110, culture ex-type CPC 27224 = CBS 142615).

Notes: With the description of *Pr. eucleicola*, the genus is presently known from only two species. *Protostegia eucleae* [conidia (40–)50–75(–80) × (2–)2.5–3 µm] is morphologically similar to *Pr. eucleicola* [conidia (40–)50–70(–75) × (2.5–)3–4 µm], although the conidia are slightly wider in the latter. The two species are best distinguished based on their DNA data. It is possible that many collections originally reported as *Pr. eucleae*, actually represent *Pr. eucleicola.*

Authors: Y. Marin-Felix, A.R. Wood & P.W. Crous

Pseudopyricularia Klaubauf *et al.*, Stud. Mycol. 79: 109. 2014. Fig. 56.

Classification: *Sordariomycetes*, *Sordariomycetidae*, *Magnaporthales*, *Pyriculariaceae.*

Type species: *Pseudopyricularia kyllingae* Klaubauf *et al.* Holotype and ex-type culture: CBS H-21841, CBS 133597.

DNA barcodes (genus): LSU, *rpb1*.

DNA barcodes (species): ITS, *rpb1*, *act*, *cal.* Table 17. Fig. 57.

Sexual morph unknown. *Conidiophores* solitary, erect, straight or curved, branched or not, medium brown, smooth or finely roughened, septate. *Conidiogenous cells* integrated, terminal, rarely intercalary, medium brown, smooth or finely roughened, forming a rachis with several protruding denticles usually flat-tipped. *Conidia* solitary, obclavate, pale to medium brown, smooth or/to finely roughened, guttulate, 1–2-septate; *hila* truncate, slightly protruding, unthickened, not darkened (adapted from Klaubauf *et al.* 2014).

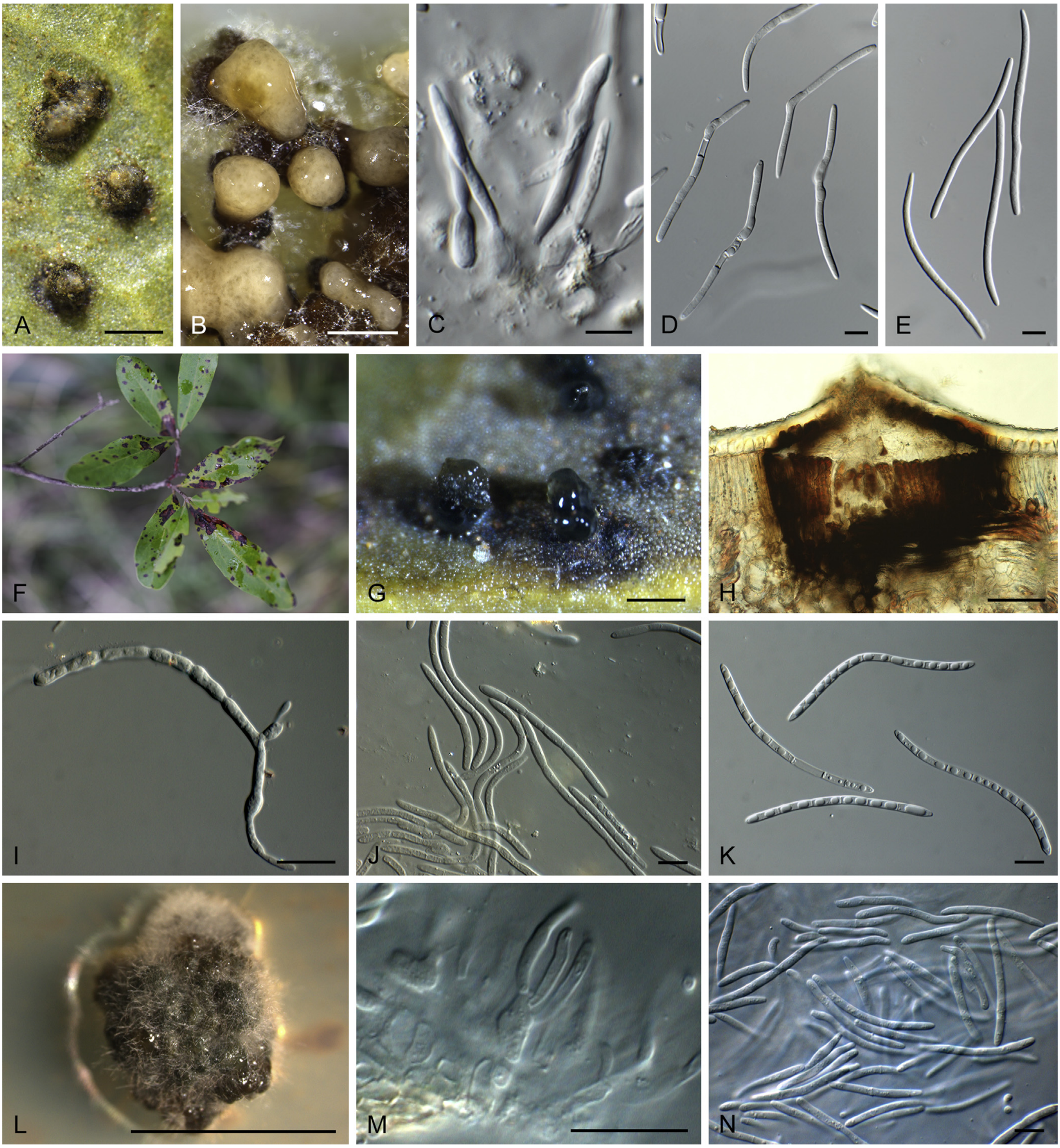

Fig. 55. **A–E.** *Protostegia eucleadicola* (ex-type CBS 142615). **A, B.** Conidiomata on leaf and OA, respectively. **C.** Conidiogenous cells. **D, E.** Conidia. **F–N.** *Protostegia eucleae* (ex-epitype CBS 137232). **F.** Leaf symptoms. **G.** Close-up of conidiomata *in vivo*. **H.** Vertical section through conidioma. **I–K.** Conidia. **L.** Colony on MEA. **M.** Conidiogenous cells. **N.** Conidia *in vitro*. Scale bars: A, B, G = 250 µm, H = 60 µm, L = 5 mm, all others = 10 µm. Pictures G–N taken from Crous *et al.* (2015a).

Culture characteristics: Colonies smooth with sparse to moderate aerial mycelium. On MEA transparent, buff, honey to isabelline or white with patches of greyish sepia. On OA transparent sometimes with patches of olivaceous grey or greyish sepia. On PDA transparent, white, greyish sepia or olivaceous black.

Optimal media and cultivation conditions: Sterile barley seed on SNA at 25 °C under continuous near-ultraviolet light to promote sporulation.

Distribution: Mainly found in Asia, but also in North America, Africa and New Zealand.

Hosts: Pathogens of *Cyperaceae*, but also found on *Bothriochloa bladhii* (*Poaceae*) and *Typha orientalis* (*Typhaceae*).

Disease symptoms: Leaf spots.

Notes: *Pseudopyricularia* was one of the genera introduced recently in order to resolve the polyphyletic nature of

Table 16. DNA barcodes of accepted *Protostegia* spp.

Species	Isolates[1]	GenBank accession numbers[2]		References
		ITS	LSU	
Protostegia eucleae	CBS 137232^{ET}	KR873252	KR873280	Crous *et al.* (2015a)
Pr. eucleicola	CBS 142615^{T}	KY905668	KY905662	Present study

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands. ^{T} and ^{ET} indicate ex-type and ex-epitype strains, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; LSU: partial 28S large subunit RNA gene.

Pyricularia (Klaubauf *et al.* 2014). *Pseudopyricularia* is mainly distinguished from *Pyricularia* by having short, determinate, brown conidiophores with an apical rachis with flat-tipped denticles.

Reference: Klaubauf *et al.* 2014 (morphology and phylogeny).

Pseudopyricularia bothriochloae (Crous & Cheew.) Y. Marín & Crous, **comb. nov.** MycoBank MB819002.
Basionym: *Pyricularia bothriochloae* Crous & Cheew., Persoonia 31: 229. 2013.

Notes: This fungus was initially described as a new species of *Pyricularia* (Crous *et al.* 2013b) before Klaubauf *et al.* (2014) introduced the new genus *Pseudopyricularia*. In the latter study, this species was incorporated in the phylogenetic analysis based on LSU sequence data, but not in the combined analysis, since only ITS and LSU sequences were available. Although the ex-type strain of *Py. bothriochloae* grouped in the *Pseudopyricularia* clade, a new combination was not proposed, as it could not be incorporated in the combined analysis. However, in the phylogenetic tree based on ITS and LSU sequences (Fig. 57), *Py. bothriochloae* was located in the *Pseudopyricularia* clade (100 % bootstrap support / 1 Posterior Probability) and accordingly the new combination, *Py. bothriochloae*, is made here. This species produces conidiophores with apical rachis with flat-tipped denticles with periclinal thickening, which characterises *Pseudopyricularia* spp.

Pseudopyricularia spp. are mainly pathogens of *Cyperaceae*. However, this species was found on *Bothriochloa bladhii* (*Poaceae*), producing angular leaf spots. Morphologically, *Py. bothriochloae* can be easily distinguished by the 1-septate conidia (2-septate in all the other species).

Authors: Y. Marin-Felix & P.W. Crous

Puccinia Pers., Neues Mag. Bot. 1: 118. 1794. Fig. 58.
For synonyms see Cunningham (1931).

Classification: *Basidiomycota*, *Pucciniomycotina*, *Pucciniomycetes*, *Pucciniales*, *Pucciniaceae.*

Type species: *Puccinia graminis* Pers. Designated as type species of *Puccinia* by Cunningham (1931) on cultivated *Triticum*; lectotypified by Jørstad (1958).

DNA barcodes (genus): ITS, LSU.

DNA barcode (species): ITS (evidence for intraspecific and intra-isolate diversity), LSU. Table 18. Fig. 59.

Spermogonia dark brown to black, often on adaxial leaf surface, subepidermal, concave hymenia with well-developed periphyses at ostiole [Group V, type 4 *sensu* Hiratsuka & Hiratsuka (1980)]. *Spermatia* exuded in droplets, small, aseptate, hyaline. *Aecia* erumpent, usually abaxial, cup-shaped, with well-developed peridium; *peridial cells* irregular and verrucose. *Aeciospores* catenulate, globose to subglobose, verruculose. *Uredinia* subepidermal or erumpent, on both leaf surfaces and stems, without peridium, pale yellow to brown. *Paraphyses* either absent, peripheral or within the sorus. *Urediniospores* borne singly on pedicels, mostly echinulate, usually globose, subglobose, ellipsoid to obovoid, germ pores absent or conspicuous. *Telia* subepidermal or erumpent, mostly dark brown to black, on both leaf surfaces and stems. *Teliospores* typically 2-celled by transverse or oblique septa (but may have variations of 1–4 cells in some species), borne singly on pedicels, mostly pale to dark brown, cell walls smooth or ornamented. *Basidia* transversely septate (phragmobasidia), 2–4 celled, external. *Basidiospores* formed singly from each basidial cell on a sterigma, sometimes ballistosporic.

Distribution: Worldwide.

Hosts: Species of *Puccinia* are obligate plant pathogens that occur on host species in many families, especially *Asteraceae*, *Cyperaceae*, *Fabaceae*, *Lamiaceae*, *Liliaceae s. lat.*, *Malvaceae* and *Poaceae*. Heteroecious species of *Puccinia*, e.g. *Pu. graminis*, require two host plant species to complete their life cycle. The spermogonia and aecia of heteroecious species occur on one host species, while the uredinia and telia occur on another, often unrelated, host species. Autoecious species complete their life cycle on one host species. There are many variations in the life cycles of species of *Puccinia*. For example, some species, e.g. *Pu. lagenophorae*, do not form spermogonia or uredinia. Other species are known only from their telia, or telia and spermogonia, e.g. *Pu. malvacearum* and *Pu. grevilleae*. Frequent host jumps in the evolution of *Puccinia* and related genera have resulted in closely related species of *Puccinia* across wide host ranges, as well as distantly related species that occur on the same host plant species (Maier *et al.* 2007, van der Merwe *et al.* 2008, Dixon *et al.* 2010, McTaggart *et al.* 2016a).

Disease symptoms: Spermogonia, aecia (Fig. 58A, B), uredinia (Fig. 58C, G) and telia (Fig. 58H, I) occur on leaves and stems, often associated with chlorotic lesions, sometimes on bullate swellings, solitary or scattered or aggregated in groups, arranged linearly or concentrically or irregularly, often erumpent, in cases of severe infection leaves prematurely wilt and senesce.

Notes: The starting publication for names of all rust fungi for purposes of priority as provided by Art. 13 of the *International Code of Nomenclature for algae, fungi, and plants* (ICN) (McNeill *et al.* 2012) is the *Synopsis Methodica Fungorum* by Persoon (1801), who listed 11 species of *Puccinia*, 19 species of *Aecidium* and 30 species of *Uredo*. The genera *Aecidium*, *Uredo* and *Puccinia* were established for rust fungi with aecia, uredinia and telia, respectively. Many species described in these three genera are conspecific, e.g. the lectotype of *Aecidium berberidis* designated by Clements & Shear (1931) is the aecial

Table 17. DNA barcodes of accepted *Pseudopyricularia* spp.

Species	Isolates[1]	GenBank accession numbers[2]				References
		ITS	*rpb1*	*act*	*cal*	
Pseudopyricularia bothriochloae	CBS 136427^T	KF777186	KY905701	KY905700	–	Crous *et al.* (2013b), present study
Py. cyperi	CBS 133595^T	KM484872	AB818013	AB274453	AB274485	Klaubauf *et al.* (2014), Murata *et al.* (2014), Hirata *et al.* (2014)
Py. hagahagae	CPC 25635^T	KT950851	KT950877	KT950873	–	Crous *et al.* (2015e)
Py. higginsii	CBS 121934	KM484875	KM485095	KM485180	KM485250	Klaubauf *et al.* (2014)
Py. kyllingae	CBS 133597^T	KM484876	KM485096	AB274451	AB274484	Klaubauf *et al.* (2014), Hirata *et al.* (2014)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CPC: Culture collection of Pedro Crous, housed at Westerdijk Fungal Biodiversity Institute. ^{T} indicates ex-type strains.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *rpb1*: partial RNA polymerase II largest subunit gene; *act*: partial actin gene; *cal*: partial calmodulin gene.

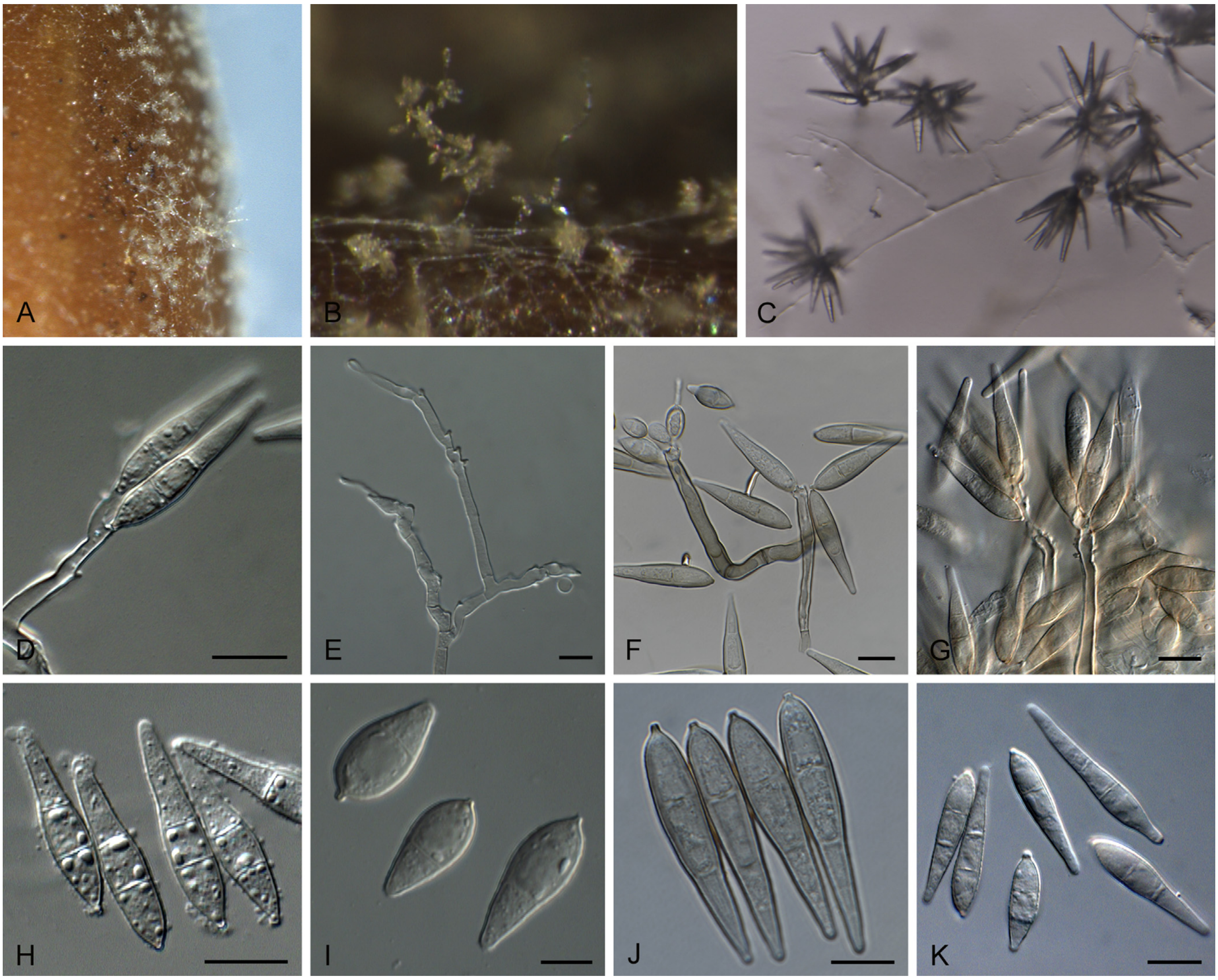

Fig. 56. *Pseudopyricularia* spp. **A.** Sporulation of *Pseudopyricularia kyllingae* (ex-type CBS 133597) on sterile barley seed on SNA. **B.** Sporulation of *Pseudopyricularia bothriochloae* (ex-type CBS 136427) on PNA. **C–G.** Conidiophores. **C.** *Pseudopyricularia hagahagae* (ex-type CPC 25635). **D.** *Pseudopyricularia cyperi* (ex-type CBS 133595). **E.** *Pseudopyricularia bothriochloae* (ex-type CBS 136427). **F.** *Pseudopyricularia hagahagae* (ex-type CPC 25635). **G.** *Pseudopyricularia kyllingae* (ex-type CBS 133597). **H–K.** Conidia. **H.** *Pseudopyricularia cyperi* (ex-type CBS 133595). **I.** *Pseudopyricularia bothriochloae* (ex-type CBS 136427). **J.** *Pseudopyricularia hagahagae* (ex-type CPC 25635). **K.** *Pseudopyricularia kyllingae* (ex-type CBS 133597). Scale bars = 10 μm. Pictures A, D, G, H, K taken from Klaubauf *et al.* (2014); B, E, I taken from Crous *et al.* (2013b), C, F, J taken from Crous *et al.* (2015e).

stage of *Pu. graminis*. There is little possibility that *Aecidium* and *Uredo* (asexual genera) will displace *Puccinia* (sexual genus) under Art. 57.2 of the ICN (McNeill *et al.* 2012). Whether *Uredo* is a synonym of *Puccinia* depends on the phylogenetic placement of *Uromyces beticola*, the lectotype of *Uredo* (Laundon 1970). A taxonomic working group on the *Basidiomycota* in 2011 recommended the use of *Uredo* for uredinial species that could not be assigned to a monophyletic sexual

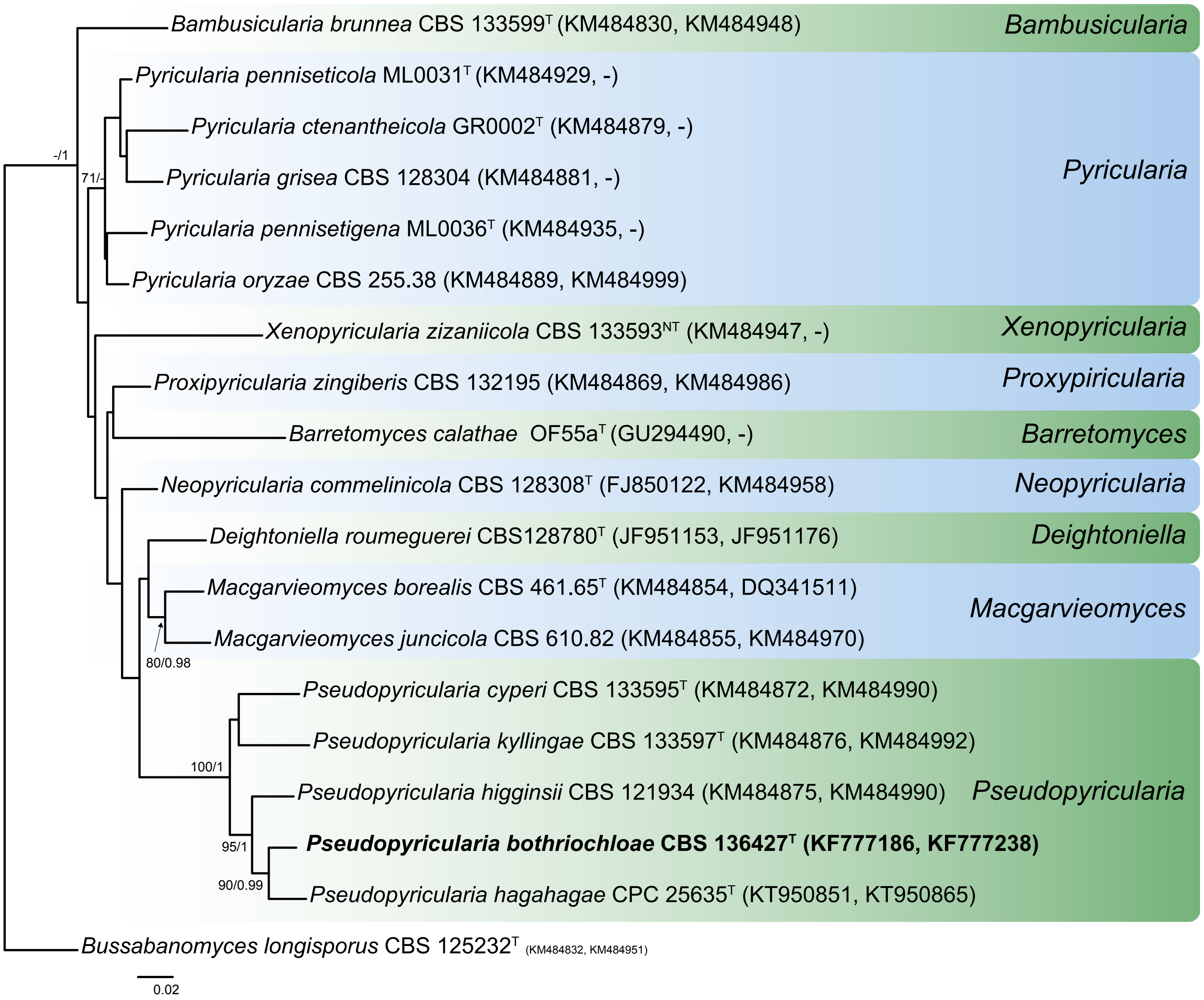

Fig. 57. RAxML phylogram obtained from the combined ITS (546 bp) and LSU (750 bp) sequences of members of *Pyriculariaceae*. The tree was rooted to *Bussabanomyces longisporus* CBS 125232. The new combination proposed is indicated in **bold**. RAxML bootstrap support (BS) values above 70 % and Bayesian posterior probability scores ≥ 0.95 are shown at the nodes. Numbers between parentheses correspond to GenBank accession numbers of ITS and LSU sequences, respectively. ^{T} and ^{NT} indicate ex-type and ex-neotype strains, respectively. TreeBASE: S20877.

genus (available at: http://www.imafungus.org/Issue/31/05.pdf). Many species of *Aecidium* and *Uredo* will need to be transferred to *Puccinia*, or other monophyletic genera, in order to preserve the one name equals one fungus principle (Hawksworth *et al.* 2011).

There are about 4 000 described species of *Puccinia* (Kirk *et al.* 2008), which have mostly been delimited by host taxon. Many of these species have diversified in the last 50 million years as a result of host jumps (McTaggart *et al.* 2016b), with the aecial host serving as a pathway for further speciation (van der Merwe *et al.* 2008). The morphology of teliospores and urediniospores is often sufficient to distinguish species of *Puccinia* that occur on the same host. Molecular approaches have uncovered cryptic diversity in some species of *Puccinia* (Liu & Hambleton 2013) as well as linking aecial to telial morphs in the life cycles of heteroecious rusts (Jin *et al.* 2010). Other studies have shown there is less species biodiversity in some rusts than previously thought, e.g. *Pu. lagenophorae* and closely related species (Scholler *et al.* 2011, McTaggart *et al.* 2014). Intraspecific and intra-isolate diversity of the ITS region was found in *Pu. horiana* and *Pu. kuehnii* (Virtudazo *et al.* 2001, Alaei *et al.* 2009). Multiple haplotypes and paralogous copies of the ITS region within species of rust must be considered for phylogenetic and molecular barcode studies.

Phylogenetic studies have identified several sexual genera as potentially congeneric with *Puccinia*. *Puccinia* is either paraphyletic or polyphyletic with respect to *Ceratocoma* (McTaggart *et al.* 2016b), *Cumminsiella* (Maier *et al.* 2003), *Dietelia* (Wingfield *et al.* 2004), *Diorchidium* (Beenken & Wood 2015), *Endophyllum* (Maier *et al.* 2003), *Macruropyxis* (Beenken & Wood 2015), *Miyagia* (Wingfield *et al.* 2004), *Sphenospora* (Aime 2006) and *Uromyces* (Maier *et al.* 2003). Three major clades that contained *Puccinia* and related genera were identified in molecular phylogenetic studies (van der Merwe *et al.* 2008, Dixon *et al.* 2010). One clade diversified on *Cyperaceae*, *Juncaceae* and orders of plants in the asterids and rosids (The Angiosperm Phylogeny 2016), and the another on *Poaceae* and *Ranunculaceae* (van der Merwe *et al.* 2008). A third clade included species of *Puccinia* on *Poaceae* (Dixon *et al.* 2010). The

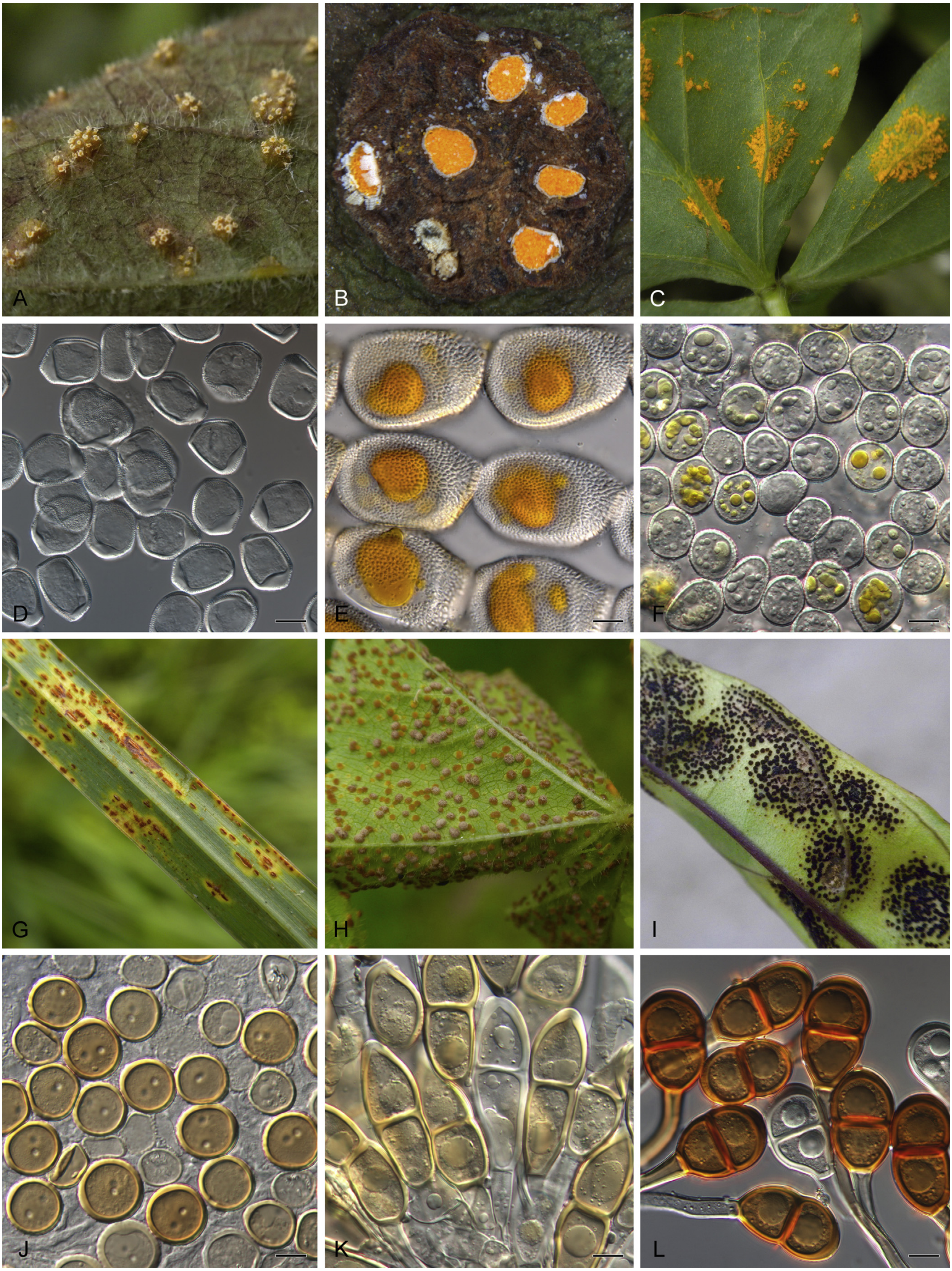

Fig 58. *Puccinia* spp. **A, D.** Aecia and aeciospores of *Puccinia paederiae* (BRIP 58338). **B, E.** Aecia and aeciospores of *Puccinia loranthicola* (BRIP 59685). **C, F.** Uredinia and urediniospores of *Puccinia oxalidis* (BRIP 58379). **G, J.** Uredinia and urediniospores of *Puccinia philippinensis* (BRIP 57418). **H, K.** Telia and teliospores of *Puccinia malvacearum* (BRIP 60128). **I, L.** Telia and teliospores of *Puccinia thwaitesii* (BRIP 58354). Scale bars = 10 µm.

Table 18. DNA barcodes of accepted *Puccinia* spp.

Species	Isolates[1]	GenBank accession numbers[2]		References
		ITS	LSU	
Puccinia abrupta var. *partheniicola*	BRIP 59295	–	KX999864	Present study
Pu. acroptili	BPI 863523	JN204187	JN204187	Bruckart *et al.* (2012)
Pu. arthrocnemi	BRIP 57772	–	KX999865	Present study
Pu. aucta	BRIP 60028	–	KX999866	Present study
Pu. bassiae	BRIP 57788	–	KX999867	Present study
Pu. brachypodii	BRIP 59466	–	KX999868	Present study
Pu. caricina	BRIP 57951	–	KX999870	Present study
Pu. carissae	BRIP 53242	–	KX999871	Present study
Pu. chrysanthemi	NA	EU816926	EU816926	Pedley (2009)
Pu. convolvuli	BPI 871465	–	DQ354512	Aime (2006)
Pu. coronata var. *avenae* f. sp. *avenae*	PUR 22125^{LT}	HM131256	–	Liu & Hambleton (2013)
Pu. coronata var. *avenae* f. sp. *graminicola*	PRM 155608	HM131309	–	Liu & Hambleton (2013)
Pu. coronati-agrostis	PUR N114^{T}	HM131319	–	Liu & Hambleton (2013)
Pu. coronati-brevispora	PUR N652^{T}	HM131235	–	Liu & Hambleton (2013)
Pu. coronati-calamagrostidis	PUR 22155^{LT}	HM131304	–	Liu & Hambleton (2013)
Pu. coronati-hordei	PUR 89857^{T}	HM131225	–	Liu & Hambleton (2013)
Pu. coronati-japonica	PUR F16131^{T}	HM131317	–	Liu & Hambleton (2013)
Pu. coronati-longispora	PRC 196^{T}	HM131232	–	Liu & Hambleton (2013)
Pu. cygnorum	NA	EF490601	–	Langrell *et al.* (2008)
Pu. cynodontis	BRIP 57556	–	KX999873	Present study
Pu. dianellae	BRIP 57433	–	KM249859$^{\#}$	McTaggart *et al.* (2016a)
Pu. dichondrae	BRIP 60027	–	KX999874	Present study
Pu. dioicae	BPI 879279	–	GU058019$^{\#}$	Dixon *et al.* (2010)
Pu. duthiei	BRIP 61025	–	KX999875	Present study
Pu. flavenscentis	BRIP 57992	–	KX999876	Present study
Pu. gastrolobii	BRIP 57735	–	KX999877	Present study
Pu. geitonoplesii	BRIP 55679	KM249860	KM249860	McTaggart *et al.* (2016a)
Pu. gilgiana	BRIP 57723	KF690673	KF690690	McTaggart *et al.* (2014)
Pu. graminis f. sp. *tritici*	CDL 75-36-700-3	NW_003526581.1*		Duplessis *et al.* (2011)
Pu. grevilleae	BRIP 55600	–	KX999878	Present study
Pu. haemodori	BRIP 57777	KF690676	KF690694	McTaggart *et al.* (2014)
Pu. hemerocallidis	BRIP 53476	KM249855	KM249855	McTaggart *et al.* (2016a)
Pu. horiana	NA	HQ201326	HQ201326	Alaei *et al.* (2009)
Pu. hypochoeridis	BRIP 57771	–	KX999879	Present study
Pu. kuehnii	BPI 879137	GQ283007	–	Flores *et al.* (2009)
Pu. lagenophorae	BRIP 57563	KF690677	KF690696	McTaggart *et al.* (2014)
Pu. levis var. *tricholaenae*	BRIP 56867	–	KX999880	Present study
Pu. liberta	BRIP 59686	–	KX999881	Present study
Pu. loranthicola	BRIP 59685	–	KX999882	Present study
Pu. ludwigii	BRIP 60129	–	KX999883	Present study
Pu. magnusiana	BPI 879281	–	GU058000$^{\#}$	Dixon *et al.* (2010)
Pu. malvacearum	PBM 2572	–	EF561641$^{\#}$	Matheny & Hibbett (unpubl. data)
Pu. melanocephala	BPI 878929	–	GU058001$^{\#}$	Dixon *et al.* (2010)
Pu. menthae	BPI 871110	–	DQ354513$^{\#}$	Aime (2006)
Pu. mixta	BRIP 61576	KU296893	KU296893	McTaggart *et al.* (2016a)
Pu. muehlenbeckiae	BRIP 57718	–	KX999884	Present study
Pu. myrsiphylli	BRIP 57782	–	KM249854$^{\#}$	McTaggart *et al.* (2016a)
Pu. nakanishikii	BPI 879283	–	GU058002$^{\#}$	Dixon *et al.* (2010)
Pu. merrilliana	BRIP 56913	–	KX999885	Present study

Table 18. (Continued).

Species	Isolates[1]	GenBank accession numbers[2]		References
		ITS	LSU	
Pu. paullula	BRIP 60018	–	KX999886	Present study
Pu. pelargonii-zonalis	BRIP 57414	–	KX999887	Present study
Pu. polysora	HSZ1879	HQ189433	HQ189433	Crouch & Szabo (2011)
Pu. porri	BRIP 61579	KU296902	KU296902	McTaggart *et al.* (2016a)
Pu. pritzeliana	BRIP 57798	–	KX999888	Present study
Pu. purpurea	BRIP 57994	–	KX999889	Present study
Pu. rhagodiae	BRIP 60078	–	KX999890	Present study
Pu. rhaphidophorae	BRIP 56840	–	KX999891	Present study
Pu. scirpi	BRIP 61027	–	KX999892$^{\#}$	Present study
Pu. scleriae	BRIP 56911	–	KX999893	Present study
Pu. smilacis	BPI 871784	DQ354533	DQ354533	Aime (2006)
Pu. sparganioidis	BPI 879285A	–	GU058027$^{\#}$	Dixon *et al.* (2010)
Pu. striiformis	HSZ1834	GQ457306	GQ457306	Jin *et al.* (2010)
Pu. stylidii	BRIP 60107	KJ622216	KJ622215	McTaggart *et al.* (2014)
Pu. tetragoniae	BRIP 59703	–	KX999894	Present study
Pu. triticina	NA	ADAS02000001.1*		Kiran *et al.* (2016)
Pu. unica	BRIP 56930	–	KX999895	Present study
Pu. ursiniae	BRIP 57993	KF690684	KF690705	McTaggart *et al.* (2014)
Pu. xanthii	BRIP 56946	–	KX999896	Present study

[1] CDL: US Department of Agriculture, Agricultural Research Service, Cereal Disease Laboratory; BPI: US National Fungus Collections, Beltsville, Maryland, USA; BRIP: Queensland Plant Pathology Herbarium, Brisbane, Australia; HSZ: Cereal Disease Laboratory collection, St. Paul, Minnesota, USA; PBM: P. Brandon Matheny (personal collection); PRC: Charles University in Prague, Prague, Czech Republic; PRM: National Museum, Prague, Czech Republic; PUR: Purdue University, west Lafayette, Indiana, USA. $^{\text{T}}$ and $^{\text{LT}}$ indicate ex-type and ex-lectotype, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; LSU: partial 28S large subunit RNA gene. *Whole genome sequence. $^{\#}$ITS2–LSU sequence.

relationships between the major clades in *Puccinia* can be observed in our phylogenetic analysis (Fig. 59).

Uromyces requires particular consideration as it has long been thought an aseptate variant of *Puccinia* (Sydow & Sydow 1904, Savile 1978). Morphology alone does not reliably separate *Puccinia* and *Uromyces*, because puccinioid (2-celled) and 1-celled spores and characteristics of the pedicel are homoplasious in the *Pucciniales* (Maier *et al.* 2007, Minnis *et al.* 2012, Beenken & Wood 2015). Several studies have shown that *Puccinia* and *Uromyces* are polyphyletic, and furthermore that *Puccinia* is paraphyletic with respect to the type of *Uromyces* (*U. appendiculatus*) and other species of *Uromyces* on *Fabaceae* (Maier *et al.* 2007, van der Merwe *et al.* 2008). Consequently, either a taxonomy that accepts *Puccinia* as a paraphyletic group must be adopted or *Uromyces* must be synonymised under *Puccinia.* In the latter case, many important species of *Uromyces* will require name changes. The traditional use of *Uromyces* for species with aseptate teliospores has been replaced by a phylogenetic approach; for example, Demers *et al.* (2017) used a phylogenetic approach to describe two species of *Puccinia* with aseptate teliospores, which would have been described as *Uromyces* based on morphology.

The future of *Puccinia* depends on whether it can be divided into monophyletic genera or sub-genera that reflect synapomorphies or ecological relationships on which a natural classification can be based. A broad concept of *Puccinia* that accepts species with puccinioid spores that are recovered in closely related clades as defined by van der Merwe *et al.* (2008) and Dixon *et al.* (2010) is adopted here. Based on this molecular phylogenetic taxonomic concept, we have transferred four species of *Uredo* from the Australasian region to *Puccinia*. Further examples of taxa recovered in *Puccinia*, include *Aecidium kalanchoe* (Hernádez *et al.* 2004) and *Uredo guerichiani* (Maier *et al.* 2007). We have chosen not to make new combinations of these species without examination of a specimen. Molecular phylogenetic support must be an essential requirement for the description of new species or new combinations in *Puccinia* because several species known from an anamorphic stage have an affinity with other genera of rust fungi, e.g. *Uredo rolliniae* (now *Phakopsora rolliniae*) (Beenken 2014).

ITS and LSU sequences are available for approximately 200 species of Puccinia on GenBank (accessed 5 Sep. 2016). These two gene regions are generally reliable as a molecular barcode for identification of species of Puccinia. GenBank numbers for some of the most important species of Puccinia that are associated with a herbarium specimen, reference genome sequence, or peer reviewed study, are provided in Table 18.

References: Sydow & Sydow 1904 (morphology); Cummins & Hiratsuka 2003 (biology, morphology and taxonomy).

Puccinia dianellae (Dietel) McTaggart & R.G. Shivas, **comb. nov.** MycoBank MB819750.
Basionym: *Uredo dianellae* Dietel, Hedwigia 37: 213. 1898.

Material examined: **Philippines**, Benguet, Tuba, Mount Santo Tomas, on *Dianella javanica*, 26 Jun. 2012, K.L. Lancetta, V.A.

Felices, T.U. Dalisay, A.I. Llano, A.R. McTaggart, R.G. Shivas & M.D.E. Shivas (BRIP 57433).

Notes: *Puccinia dianellae* was recovered in a monophyletic group with species of *Puccinia* on *Hemerocallidaceae* (McTaggart *et al.* 2016a). Telia have not been reported.

Puccinia geitonoplesii (McAlpine) McTaggart & R.G. Shivas, **comb. nov.** MycoBank MB819751.
Basionym: *Uredo geitonoplesii* McAlpine, The Rusts of Australia, their Structure, Nature and Classification: 203. 1906.

Material examined: **Australia**, Queensland, Coochiemudlo Island, Victoria Parade, on leaf of *Geitonoplesium cymosum*, 25 Aug. 2012, C. Doungsa-ard & A.R. McTaggart (BRIP 57603).

Notes: *Puccinia geitonoplesii* was recovered in a monophyletic group with species of *Puccinia* on *Hemerocallidaceae* (McTaggart *et al.* 2016a). Telia have not been reported. Morphological identification of *P. geitonoplesii* can be assisted by the *Rust Fungi of Australia Lucid Key* (Shivas *et al.* 2014) (http://collections.daff.qld.gov.au/web/key/rustfungi/).

Puccinia merrilliana (Syd. & P. Syd.) McTaggart & R.G. Shivas, **nom. nov.** MycoBank MB819752.
Basionym: *Uredo operculinae* Syd. & P. Syd., Philipp. J. Sci., C, Bot. 8: 476. 1913.

Material examined: **Australia**, Western Australia, Kununurra, Ivanhoe Crossing turnoff, on leaf of *Operculina aequisepala*, 16 Apr. 2012, M. Butt, C. Doungsa-ard, A.R. McTaggart, R. Berndt, V. Faust-Berndt, M.D.E. Shivas & R.G. Shivas (BRIP 56913).

Notes: *Uredo operculinae* was first described on *Operculina turpethum* from the Philippines (Sydow & Sydow 1913). The transfer of *U. operculinae* to *Puccinia* requires a new name, *Pu. merrilliana*, as *Pu. operculiniae* is already occupied for a rust on *O. turpethum* in the Malabar region in southern India (Ramakrishnan & Sundaram 1953). The new name honours Elmer Drew Merrill (1876–1956), an American botanist, who collected this fungus while living in the Philippines, where he became an expert on the flora of the Asia-Pacific region. *Puccinia merrilliana* has fewer (1–2) germ pores than *Pu. operculinae*, which has 3–4 germ pores. Telia have not been reported for *Pu. merrilliana*. The specimens examined from Australia are morphologically identical to the type description by Sydow & Sydow (p. 425, 1924). Morphological identification of *Pu. merrilliana* can be assisted by the *Rust Fungi of Australia Lucid Key* (Shivas *et al.* 2014) (http://collections.daff.qld.gov.au/web/key/rustfungi/). *Puccinia merrilliana* was recovered in *Puccinia* in Group I *sensu* van der Merwe *et al.* (2008).

Puccinia rhagodiae (Cooke & Massee) McTaggart & R.G. Shivas, **comb. nov.** MycoBank MB819756.
Basionym: *Uredo rhagodiae* Cooke & Massee, Grevillea 15 (no. 76): 99. 1887.

Material examined: **Australia**, Tasmania, Lilico Beach, on leaf of *Chenopodium candolleanum*, 15 Dec. 2013, A.R. McTaggart, L.S. Shuey, M.D.E. Shivas & R.G. Shivas (BRIP 60078).

Notes: *Puccinia rhagodiae* was recovered in *Puccinia* group I *sensu* van der Merwe *et al.* (2008). Telia have not been reported. Several other species of *Puccinia* on *Amaranthaceae* were shown to be closely related, including *Pu. arthrocnemi*, *Pu. bassiae* and *Pu. tetragoniae*, although they did not form a monophyletic group. Morphological identification of *Pu. rhagodiae* can be assisted by the *Rust Fungi of Australia Lucid Key* (Shivas *et al.* 2014) (http://collections.daff.qld.gov.au/web/key/rustfungi/).

Authors: A.R. McTaggart & R.G. Shivas

Saccharata Denman & Crous, CBS Biodiversity Ser. (Utrecht) 2: 104. 2004. Fig. 60.

Classification: *Dothideomycetes*, *Incertae sedis*, *Botryosphaeriales*, *Saccharataceae.*

Type species: *Saccharata proteae* (Wakef.) Denman & Crous. Holotype and ex-type culture: PREM 32915, STE-U 1694.

DNA barcode (genus): LSU.

DNA barcodes (species): ITS, *rpb2*, *tef1*, *tub2*. Table 19.

Ascomata epiphyllous, separate, becoming aggregated, unilocular, immersed, substomatal, with a central, flattened ostiole, surrounded by a continuous, clypeus-like apical thickening of the wall, obovoid, slightly depressed; *ascomata wall* consisting of 8–11 layers of brown pseudoparenchymatous *textura angularis*. *Pseudoparaphyses* hyaline, septate, branched, frequently attached to the top and base of the pseudothecial cavity. *Asci* clavate to cylindrical, stipitate, bitunicate, fissitunicate; *apical chamber* visible as a notch-like indentation at the apex. *Ascospores* uni- to biseriate, hyaline, guttulate, smooth, ellipsoidal, clavate to fusiform, frequently widest in the upper third of the ascospore, tapering to obtuse ends. *Conidiomata* pycnidial, black, opening by a single, central ostiole, infrequently embedded in stromatic tissue with thickened, darkened upper layer; *conidiomatal wall* consisting of 2–3 layers of brown *textura angularis*. *Conidiophores* hyaline, smooth, subcylindrical, branched, or reduced to conidiogenous cells, lining the inner layer of the cavity, 1–3-septate. *Paraphyses* intermingled among conidiophores, hyaline, smooth, subcylindrical, unbranched or branched above, with obtuse ends, 0–3-septate, extending above conidiophores or slightly above the conidia. *Conidiogenous cells* hyaline, smooth, phialidic, proliferating via periclinal thickening or percurrent proliferation, with or without collarettes. *Conidia* hyaline, smooth, thin-walled, aseptate, granular, fusiform to narrowly ellipsoid or fusoid-ellipsoid, apex subobtuse, base subtruncate or truncate with minute marginal frill, widest in the middle of the conidium. *Synasexual morph* formed in separate conidiomata, or in same conidiomata with asexual morph. *Synasexual conidia* pigmented, thick-walled, finely verruculose, ellipsoid or oval, aseptate. *Spermatogonia* similar to conidiomata in anatomy. *Spermatogenous cells* ampulliform to lageniform or subcylindrical, hyaline smooth, phialidic. *Spermatia* developing in conidiomata or spermatogonia, hyaline, smooth, granular, subcylindrical or dumbbell-shaped, with rounded ends (adapted from Crous *et al.* 2004a and Slippers *et al.* 2013).

Culture characteristics: Colonies on PDA, OA and MEA spreading, with moderate aerial mycelium, usually erumpent, less frequent flat, margins irregular; surface and reverse show different shades of grey.

Optimal media and cultivation conditions: On OA or PNA at 25 °C under continuous near-ultraviolet light to promote sporulation.

Distribution: Commonly found in South Africa, but also Australia, North America (incl. Hawaii) and Europe.

Hosts: Members of *Proteaceae*, especially in species of *Banksia*, *Hakea*, *Isopogon*, *Lambertia*, *Leucospermum*, *Petrophile* and *Protea.* Also found on *Daviesia* (*Fabaceae*), *Encephalartos* (*Zamiaceae*), and *Eucalyptus* (*Myrtaceae*) (see Crous *et al.* 2016b).

Disease symptoms: Leaf tip die-back and leaf spots.

Notes: *Saccharata* is the only genus located in the family *Saccharataceae*, which was recently introduced by Slippers *et al.* (2013). This genus was described by Crous *et al.* (2004a) in order to accommodate "*Botryosphaeria*" *proteae*, and subsequently several additional species were added to the genus from South Africa. All the species were found on *Proteaceae* expect *Saccharata kirstenboschensis*, which was isolated from *Encephalartos princeps* (Crous *et al.* 2008). South African *Saccharata* spp. that occur on *Proteaceae* can be distinguished from other members of *Botryosphaeriales* by their asexual morphology, which includes a hyaline, fusicoccum-like and a pigmented diplodia-like asexual morph (Crous *et al.* 2013a). However, Crous *et al.* (2016b) introduced eight species from a range of hosts (*Myrtaceae* and *Proteaceae*) in Australia, and also widened the generic concept to include the genus *Neoseptorioides* (3-septate, cylindrical conidia; Crous *et al.* 2015e). In spite of the range of variation observed in the asexual morphs, morphology of the sexual morphs of Australian and South African species appear remarkably conserved.

References: Crous *et al.* 2008, 2013a, 2016b (morphology and phylogeny).

Saccharata leucospermi Crous, **sp. nov.** MycoBank MB820823. Fig. 61.

Etymology: Named for the host genus from which it was collected, *Leucospermum.*

Conidiomata on PDA pycnidial, black, up to 300 µm diam, with a single, central ostiole; *conidiomatal wall* consisting of 2–3 layers of brown *textura angularis*. *Conidiophores* subcylindrical, hyaline, smooth, frequently reduced to conidiogenous cells or branched in apical part, 1–2-septate, 7–20 × 2–3.5 µm. *Paraphyses* rarely observed, intermingled among conidiophores, unbranched hyaline, smooth, 0–1-septate, 2–3 µm wide, extending above conidiophores. *Conidiogenous cells* terminal, subcylindrical, hyaline, 7–10 × 2–3 µm, with periclinal thickening, rarely with percurrent proliferations. *Conidia* hyaline, smooth, fusiform to narrowly ellipsoid, apex subobtuse, base truncate with minute marginal frill, minutely guttulate, thin-walled, (13–)14–16(–19) × (4–)4.5(–5) µm.

Culture characteristics: Colonies on MEA at 25 °C in the dark after 1 wk: spreading, erumpent, surface crumpled, irregular, with uneven, feathery margin and moderate aerial mycelium; surface pale mouse-grey, reverse mouse-grey.

Material examined: **South Africa**, Western Cape Province, Kogelberg Nature Reserve, on leaf litter of *Leucospermum conocarpodendron* subsp. *viridum*, 11 Jul. 2000, S. Marincowitz (**holotype** CBS H-20078, culture ex-type CBS 122694 = CPC 13698 = CMW 22197).

Notes: In the treatment of microfungi occurring on leaf litter of *Proteceae*, Marincowitz *et al.* (2008a) listed CBS 122694 as a *Saccharata* sp., acknowledging the fact that it appeared to be different. Three other species are known from *Protea* leaves in South Africa, namely *S. proteae* (conidia 20–30 × 4.5–6 µm; Denman *et al.* 1999), *S. intermedia* [conidia (17–)18–20(–22) × (3.5–)5–6 µm; Crous *et al.* 2009a], and *S. hawaiiensis* [conidia (17–)24–30(–38) × (4–)5–7(–8) µm; Yang *et al.* 2017]. *Saccharata leucospermi* can readily be distinguished from these three species by having smaller conidia.

Saccharata protearum Crous, **sp. nov.** MycoBank MB820824. Fig. 62.

Etymology: Named after the host genus from which it was collected, *Protea.*

Conidiomata pycnidial, eustromatic, to 400 µm diam, immersed, subepidermal, erumpent in culture, separate, or aggregated, linked by a stroma, dark brown, uni- to multi-locular, walls consisting of dark brown *textura angularis*, ostiolate. *Fusicoccum-like asexual morph*: *Conidiophores* hyaline, smooth, branched, subcylindrical, 1–3-septate, formed from the inner layer of the locule, 10–30 × 2.5–3.5 µm, intermingled with hyaline, septate paraphyses. *Conidiogenous cells* phialidic, discrete or integrated, hyaline, smooth, cylindrical, enteroblastic, proliferating percurrently with 1–2 annellations, 9–15 × 2.5–3.5 µm. *Conidia* hyaline, thin-walled, aseptate, smooth, fusoid, widest in the middle or upper third of the conidium, with a subobtuse apex, and a truncate base, (17–)20–25(–27) × (4–)4.5–5(–6) µm. *Microconidial morph* occurring in separate or the same conidiomata as the fusicoccum-like asexual morph. *Microconidiophores* hyaline, smooth, branched, cylindrical, 1–3-septate, formed from the inner layers of the locule, 20–30 × 2.5–3 µm. *Microconidiogenous cells* phialidic, discrete or integrated, hyaline, smooth, cylindrical, determinate, with prominent periclinal thickening, 5–11 × 2–2.5 µm. *Microconidia* medium brown, thin-walled, finely verruculose, guttulate, aseptate, subcylindrical to narrowly ellipsoid with rounded ends, (7–)10–15(–17) × (2.5–)3(–4) µm.

Culture characteristics: Colonies on MEA at 25 °C in the dark after 1 wk: flat, spreading, with moderate aerial mycelium; surface pale mouse-grey with patches of dirty white, reverse mouse-grey.

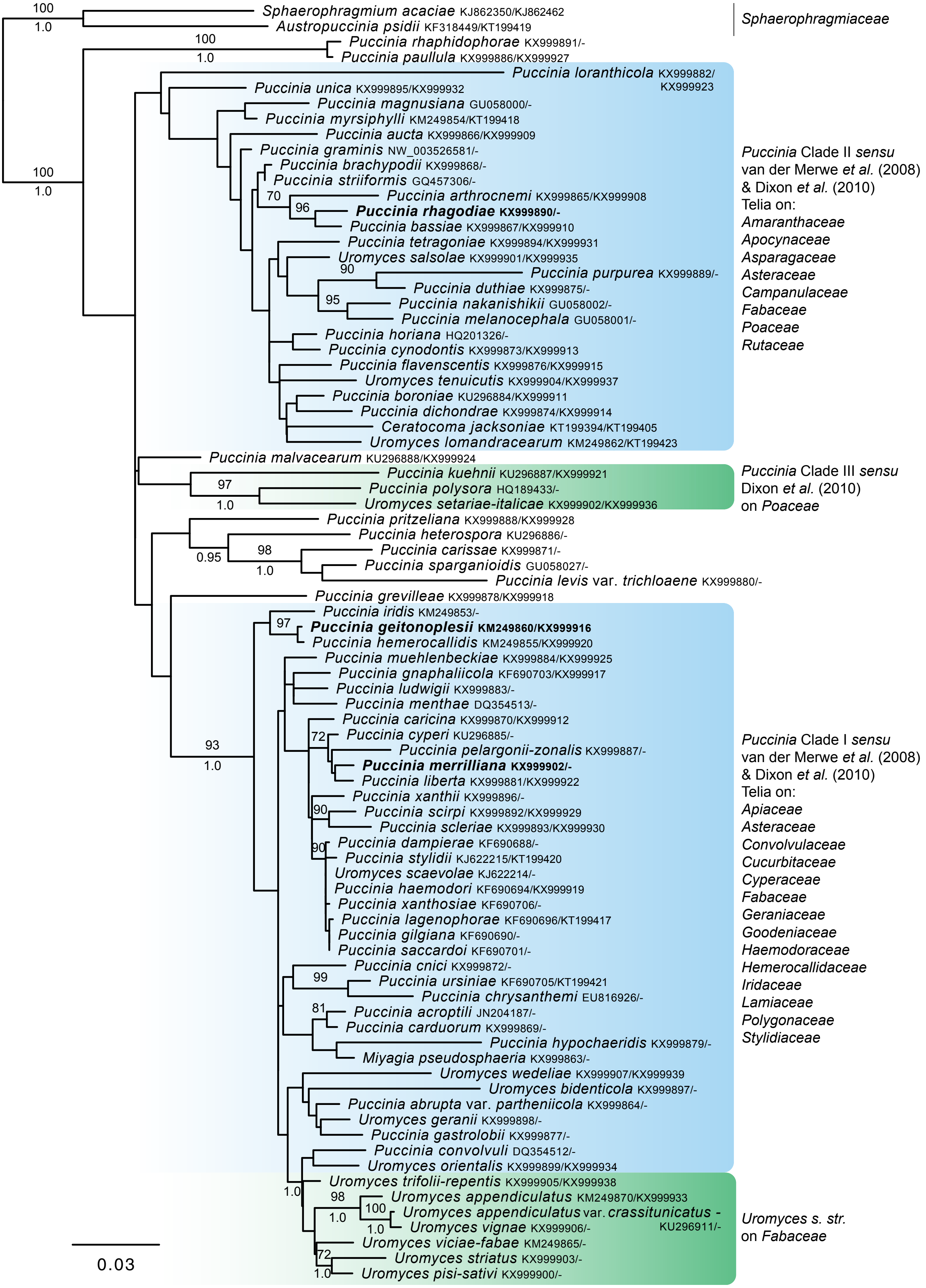

Fig 59. Phylogram obtained from a maximum likelihood search of LSU and cytochrome c oxidase subunit 3 of mitochondrial DNA (*co3*), partitioned as two separate genes in RAxML. Bootstrap values (≥ 70 %) from 1 000 replicates in a maximum likelihood search shown above nodes. Posterior probabilities (≥0.95) summarised from 30 000 trees obtained by Bayesian inference in MrBayes are shown below nodes. General time-reversible (GTR) with GAMMA distribution was used as a model of evolution for both

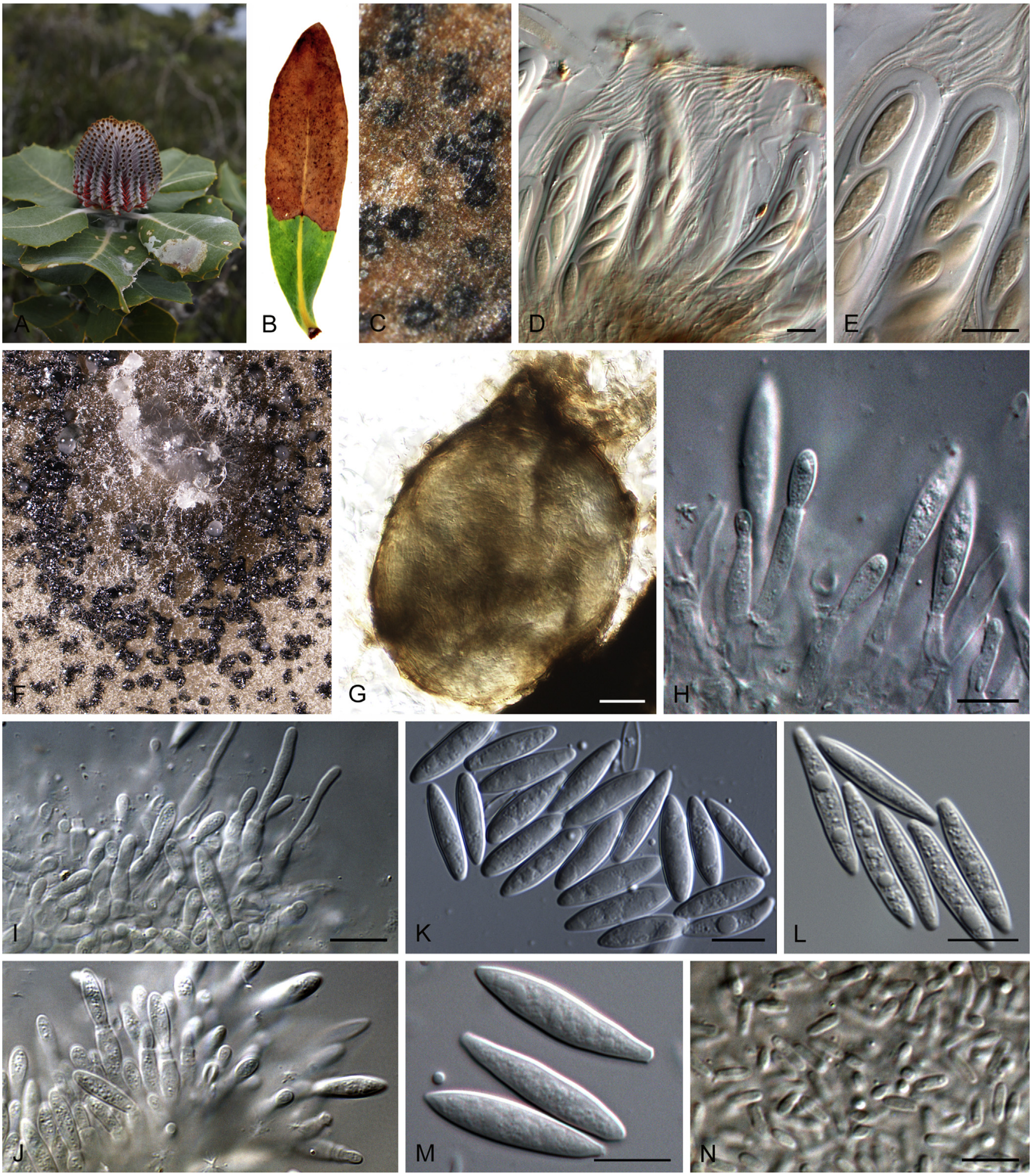

Fig. 60. *Saccharata* spp. **A.** On *Banksia* sp. **B.** Symptomatic leaves of *Saccharata proteae* (CBS 121406). **C.** Close-up of subepidermal conidiomata of *Saccharata proteae*. **D–E.** Sexual morph of *Saccharata proteae* (CBS 121406). **D, E.** Asci, paraphyses and ascospores. **F–N.** Asexual morphs. **F.** Colony sporulating on OA of *Saccharata capensis* (ex-type CBS 122693). **G.** Pycnidial conidioma of *Saccharata capensis* (ex-type CBS 122693). **H–J.** Conidiogenous cells and conidia. H. *Saccharata proteae* (CBS 121406). **I, J.** *Saccharata capensis* (ex-type CBS 122693). **K–M.** Conidia. K. *Saccharata intermedia* (ex-type CBS 125546). **L.** *Saccharata kirstenboschensis* (ex-type CBS 123537). **M.** *Saccharata proteae* (CBS 121406). **N.** Spermatia of *Saccharata capensis* (ex-type CBS 122693). Scale bars: G = 100 µm, others = 10 µm; I applies to I, J. Pictures B–K, J–N taken from Crous *et al.* (2013a); L from Crous *et al.* (2008).

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phylogenetic criteria. Major clades of *Puccinia* obtained in previous studies are shaded. New combinations made in the present study are in **bold**. Two species of *Sphaerophragmiaceae* were selected as outgroup to the *Pucciniaceae*. Numbers between parentheses correspond to GenBank accession numbers for LSU and *co3* sequences, respectively. The locus *co3* was used as a second, independent gene in the phylogenetic analyses; however it is not regarded as a molecular barcode for species of *Puccinia* as there are limited nucleotide differences between closely related species. TreeBASE: S21061.

Table 19. DNA barcodes of accepted *Saccharata* spp.

Species	Isolates[1]	GenBank accession numbers[2]				References
		ITS	***rpb2***	***tef1***	***tub2***	
Saccharata banksiae	CBS 142137^{T}	KY173449	KY173588	KY173596	–	Crous *et al.* (2016b)
S. capensis	CBS 122693^{T}	EU552130	KX464061	EU552095	KX465073	Marincowitz *et al.* (2008a), Yang *et al.* (2017)
S. daviesiae	CBS 142120^{T}	KY173450	KY173589	–	–	Crous *et al.* (2016b)
S. eucalypti	CBS 140665^{T}	KT950857	–	KT950882	–	Crous *et al.* (2015e)
S. eucalyptorum	CBS 142122^{T}	KY173451	–	–	–	Crous *et al.* (2016b)
S. hakeae	CBS 142121^{T}	KY173454	–	–	–	Crous *et al.* (2016b)
S. hakeicola	CBS 142124^{T}	KY173458	–	–	–	Crous *et al.* (2016b)
S. hawaiiensis	CBS 111787^{T}	KX464233	KX464062	KX464767	KX465074	Yang *et al.* (2017)
S. intermedia	CBS 125546^{T}	GU229888	KX464064	KX464769	KX465076	Crous *et al.* (2009a), Yang *et al.* (2017)
S. kirstenboschensis	CBS 123537^{T}	FJ372392	KX464065	KX464770	KX465077	Crous *et al.* (2008), Yang *et al.* (2017)
S. lambertiae	CBS 142123^{T}	KY173459	KY173590	KY173597	–	Crous *et al.* (2016b)
S. leucospermi	CBS 122694^{T}	EU552129	KX464073	EU552094	–	Marincowitz *et al.* (2008a), Yang *et al.* (2017)
S. petrophiles	CBS 142138^{T}	KY173463	–	–	–	Crous *et al.* (2016b)
S. petrophilicola	CBS 142125^{T}	KY173462	–	–	–	Crous *et al.* (2016b)
S. proteae	CBS 115206	KF766226	GU357753	KF766438	KF531790	Schoch *et al.* (2009), Phillips *et al.* (2013), Slippers *et al.* (2013)
S. protearum	CBS 114569^{T}	FJ150706	KX464072	FJ150712	–	Marincowitz *et al.* (2008b), Yang *et al.* (2017)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands. ^{T} indicates ex-type strain.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *rpb2*: partial RNA polymerase II second largest subunit gene; *tef1*: partial translation elongation factor 1-alpha gene; *tub2*: partial β-tubulin gene.

Material examined: **USA**, Hawaii, Maui, on leaf of *Protea* sp., 16 Dec. 1998, P.W. Crous & M.E. Palm, (**holotype** CBS H-23111, culture ex-type CPC 2169 = CBS 114569).

Notes: In the reassessment of *Botryosphaeriaceae* and allied taxa published by Marincowitz *et al.* (2008b), the ITS DNA data could not distinguish CBS 114569 from isolates of *S. proteae*. However, in the recent study of Yang *et al.* (2017), the combined sequence dataset (ITS, *rpb2* and *tef1*), showed CBS 114569 to cluster basal to *S. hawaiiensis*. Morphologically, conidia of isolates of CBS 114569 [(17–)20–25(–27) × (4–)4.5–5(–6) μm] are also smaller than those of *S. hawaiiensis* [(17–)24–30(–38) × (4–)5–7(–8) μm; Yang *et al.* 2017], and thus this isolate is herewith introduced as a new species, *S. protearum.*

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Thyrostroma Höhn., Sitzungsber. Kaiserl. Akad. Wiss., Math.-Naturwiss. Cl., Abt. 1 120: 472 (94 repr.). 1911. Fig. 63.

Classification: *Dothideomycetes*, *Pleosporomycetidae*, *Pleosporales*, *Dothidotthiaceae.*

Type species: *Thyrostroma compactum* (Sacc.) Höhn. Holotype could not be located, and a neotype from Europe is required.

DNA barcode (genus): LSU.

DNA barcodes (species): ITS, *tef1.* Table 20. Fig. 64.

Sexual morph unknown. *Conidiomata* sporodochial, punctiform, dark brown or black. *Stroma* immersed to superficial, brown. *Conidiophores* brown, finely roughened, cylindrical to subcylindrical, 1–3-septate. *Conidiogenous cells* brown, subcylindrical, finely roughened, proliferating percurrently at apex. *Conidia* cylindrical, clavate, or ellipsoid to fusoid, pale to medium brown, smooth-walled, with (1–)4 transverse septa, and 0–3 oblique or longitudinal septa, rounded at the apex, base truncate.

Culture characteristics: Colonies reaching 90 mm diam after 2 wk, with sparse or fluffy aerial mycelium. Colonies on MEA, PDA and OA showing different shades of grey or chestnut to umber.

Optimal media and cultivation conditions: MEA, PDA and OA at 25 °C.

Distribution: Asia, Europe and North America.

Hosts: Pathogens of *Ulmus* spp., *Sambucus caerulea*, *Styphnolobium japonicum*, *Tilia* spp., and *Cornus officinalis*.

Disease symptoms: Thyrostroma canker, dieback and leaf spots.

Notes: *Thyrostroma* was introduced in 1911 in order to accommodate *T. compactum* (von Höhnel 1911). Despite being described more than 100 years ago, the phylogenetic position of *Thyrostroma* remains unresolved. *Thyrostroma* was considered the asexual morph of *Dothidotthia* by Phillips *et al.* (2008). Subsequently, Slippers *et al.* (2013) placed *Thyrostroma* in the *Botryosphaeriaceae* based on morphology, since molecular data of *Thyrostroma* spp. were lacking. In the phylogenetic trees based on LSU sequences (Fig. 49), the type species of *Thyrostroma*, *T. compactum*, does not cluster with *Dothidotthia* (*Dothidotthiaceae*), demonstrating that these genera are not

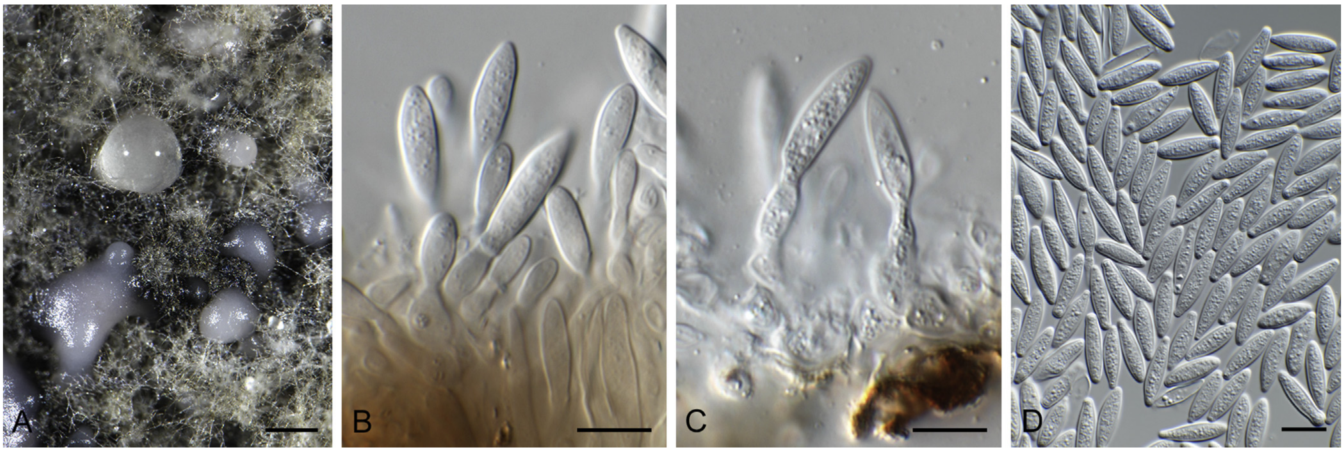

Fig. 61. *Saccharata leucospermi* (ex-type CBS 122694). **A.** Conidiomata forming on OA. **B, C.** Conidiogenous cells giving rise to conidia. **D.** Conidia. Scale bars: A = 300 µm, others = 10 µm.

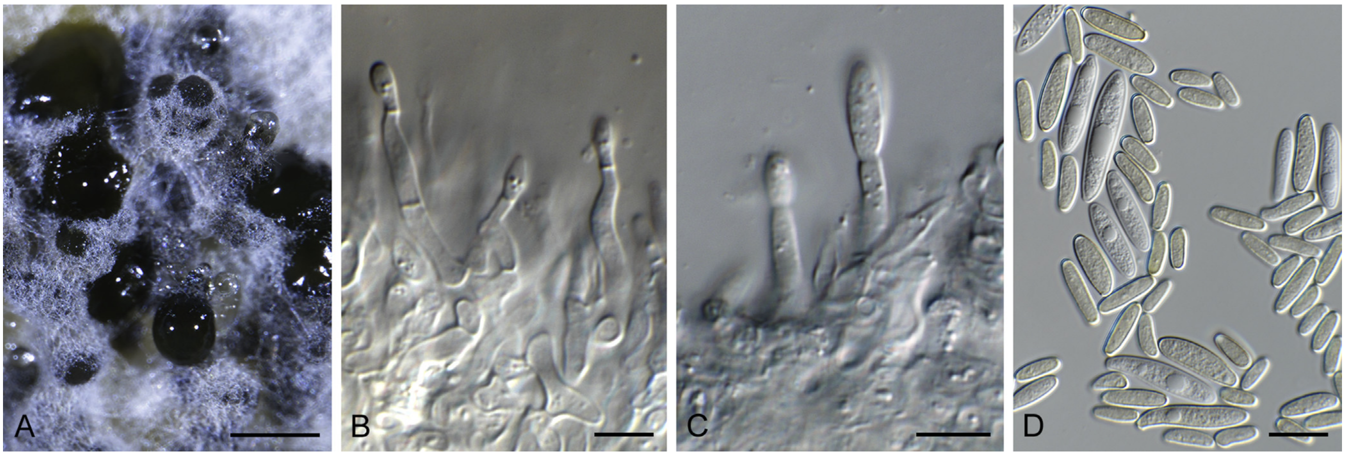

Fig. 62. *Saccharata protearum* (ex-type CBS 114569). **A.** Conidiomata forming on OA. **B, C.** Conidiogenous cells giving rise to conidia. **D.** Conidia. Scale bars: A = 400 µm, others = 10 µm.

congeneric, as was recently mentioned by Crous *et al.* (2016c). However, *Thyrostroma* did cluster in the *Dothidotthiaceae* clade, as originally proposed by Phillips *et al.* (2008).

References: Ellis 1959, 1971, Crous *et al.* 2016c (morphology).

Thyrostroma franseriae Crous, **sp. nov.** MycoBank MB820825. Fig. 63.

Etymology: Named after the host genus from which it was collected, *Franseria.*

Sporodochia dark brown, punctiform, up to 250 µm diam. *Stromata* brown, superficial, 100–150 µm diam. *Conidiophores* brown, finely roughened, subcylindrical, 0–1-septate, 10–18 × 6–11 µm. *Conidiogenous cells* brown, subcylindrical, finely roughened, proliferating percurrently at apex, 5–10 × 6–11 µm. *Conidia* brown, ellipsoid to fusoid, with 2–4 oblique or longitudinal septa, 1–3 transverse septa, apex broadly obtuse, base truncate, 8–9 µm diam, (25–)28–33(–35) × (18–)20–25 µm.

Culture characteristics: Colonies flat, spreading, with sparse aerial mycelium and feathery margins, reaching 60 mm diam after 2 wk on MEA, PDA and OA; surface and reverse iron-grey.

Material examined: **USA**, Nevada, Death Valley, on dead leaf of *Franseria* sp., 7 Jul. 1970, F.W. Went (**holotype** CBS H-23112, culture ex-type CBS 487.71); Nevada, north end of Death Valley, on green, living leaf of *Franseria* sp., Jul. 1970, F.W. Went, CBS H-18568, culture CBS 700.70.

Notes: *Thyrostroma franseriae* is known from two isolates, both of which were collected from leaves of *Franseria* sp. in Death Valley, Nevada (USA) in 1970. Morphologically, isolate CBS 700.70 differs from CBS 487.71 in having larger conidia that are more cylindrical, clavate to ellipsoid, with 2–4 transverse septa, 2–8 oblique or longitudinal septa, 40–65 × 18–25 µm. However, the two isolates are phylogenetically indistinguishable (Fig. 64).

Thyrostroma compactum is a European species originally described from *Ulmus* in Italy. One such isolate was available for study, namely CBS 335.37, collected by J.C. Carter (a US-based researcher), but the origin of this strain remains unknown, and it proved to be sterile in culture. Phylogenetically, however, CBS 335.37 is distinct from *T. franseriae* (Fig. 64), although we could not confirm that CBS 335.37 is authentic for the name it was deposited under by J.C. Carter.

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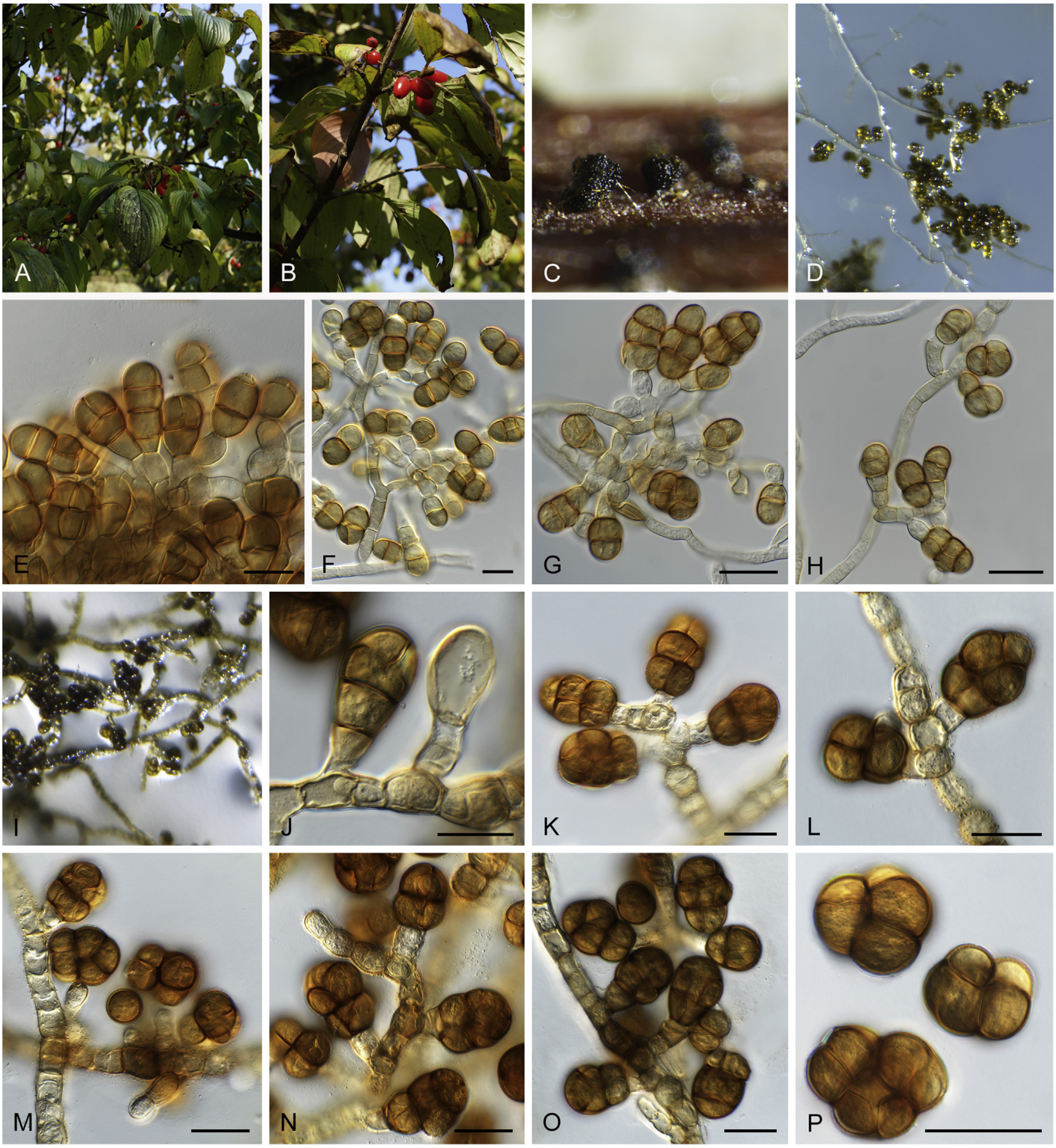

Fig. 63. A–H. *Thyrostroma cornicola* (ex-type CBS 141280). **A, B.** Symptomatic leaves of *Cornus officinalis*. **C.** Sporodochia on PNA. **D.** Sporulation on PNA. **E–H.** Conidiogenous cells giving rise to conidia. **I–O.** *Thyrostroma franseriae* (ex-type CBS 487.71). **I.** Sporulation on PNA. **J–O.** Conidiogenous cells giving rise to conidia. **P.** Conidia. Scale bars: 20 µm. Pictures B–F, H taken from Crous *et al.* (2016c).

Venturia Sacc., Syll. fung. (Abellini) 1: 586. 1882. Fig. 65.
Synonyms: *Fusicladium* Bonord., Handb. Mykol.: 80. 1851.
Apiosporina Höhn., Sitzungsber. Kaiserl. Akad. Wiss., Math.-Naturw. Cl., Abt. 1, 119: 439. 1910.
Metacoleroa Petr., Ann. Mycol. 25: 332. 1927.
Caproventuria U. Braun, A Monograph of Cercosporella, Ramularia and Allied Genera (Phytopathogenic Hyphomycetes) 2: 396. 1998.
Pseudocladosporium U. Braun, A Monograph of Cercosporella, Ramularia and Allied Genera (Phytopathogenic Hyphomycetes) 2: 392. 1998.

Classification: *Dothideomycetes*, *Pleosporomycetidae*, *Venturiales*, *Venturiaceae*.

Type species: *Venturia inaequalis* (Cooke) G. Winter. Type material in Kew: IMI 47413.

DNA barcode (genus): LSU.

DNA barcodes (species): ITS, *tef1*, *tub2*. Table 21. Fig. 66.

Ascomata pseudothecial, globose, subglobose, black, initially immersed, becoming erumpent, solitary, scattered or gregarious,

Table 20. DNA barcodes of accepted *Thyrostroma* spp.

Species	Isolates[1]	GenBank accession numbers[2]		References
		ITS	*tef1*	
Thyrostroma compactum	CBS 335.37	KY905670	KY905681	Present study
T. cornicola	CBS 141280^{T}	KX228248	KX228372	Crous *et al.* (2016c)
T. franseriae	CBS 487.71^{T}	KX228249	KY905680	Crous *et al.* (2016c), present study
	CBS 700.70	KX228250	KY905682	Crous *et al.* (2016c), present study

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands. ^{T} indicates ex-type strains.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *tef1*: partial translation elongation factor 1-alpha gene.

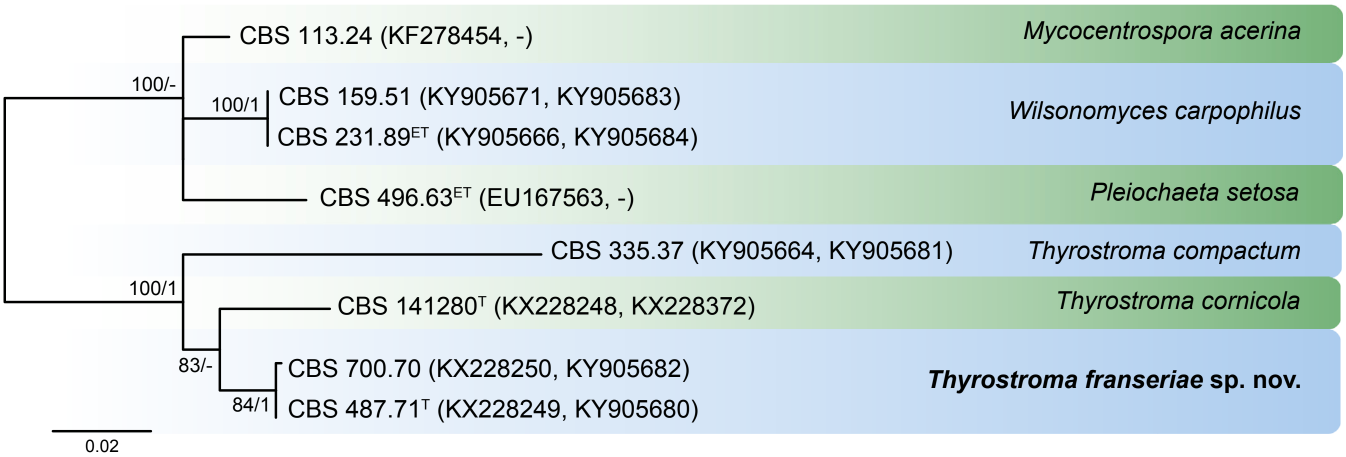

Fig. 64. RAxML phylogram obtained from the combined ITS (531 bp) and *tef1* (389 bp) sequences of members of *Dothidotthiaceae*. The new species proposed is indicated in **bold**. RAxML bootstrap support (BS) values above 70 % and Bayesian posterior probability scores ≥ 0.95 are shown in the nodes. Numbers between parentheses correspond to GenBank accession numbers of ITS and *tef1* sequences, respectively. ^{T} and ^{ET} indicate ex-type and ex-epitype strains, respectively. TreeBASE: S20877.

covered with setae; *ostiole* central, papillate; *ascomatal wall* composed of a few layers of pigmented cells of *textura angularis*, which is of equal thickness or slightly thickened at apex. *Hamathecium* comprising septate, filiform pseudoparaphyses, evanescent in mature ascomata. *Asci* bitunicate, oblong to obclavate, fissitunicate dehiscence unknown, with or without a short, thick pedicel, rounded at the apex with an inconspicuous ocular chamber. *Ascospores* obliquely uniseriate, partially overlapping to biseriate, especially at the base, ellipsoidal, with broadly rounded ends, pale brown, 1-septate, slightly constricted at the septum, the upper cell shorter than the lower one, smooth-walled. *Conidiophores* single, sometimes arranged in small groups, straight to flexuous, pale olivaceous to dark brown, unbranched or occasionally branched, thin- to slightly thick-walled, conidiophores often reduced to conidiogenous cells or composed of several cells. *Conidiogenous nodes* smooth to verruculose. *Conidia* in simple or branched acropetal chains, ellipsoid-ovoid, obovoid, fusoid, obclavate-subcylindrical, canoe-shaped, straight to curved, subhyaline to medium brown, but mostly olivaceous, thin- to thick-walled, smooth to verruculose, 0–3(–4)-euseptate, germinating by production of germination tubes from middle or polar cells; *hila* often denticle-like, somewhat protuberant, unthickened or almost so, occasionally somewhat darkened-refractive; *septum ontogeny*: first septum median to sub-median.

Culture characteristics: Colonies on PDA fuscous black, and reverse dark fuscous-black, with moderate aerial mycelium and regular, but feathery margins. Colonies normally reaching not more than 15 mm diam after 1 mo on PDA at 25 °C in the dark.

Optimal media and cultivation conditions: PDA, MEA and CMA. Optimal growing temperature is 24–28 °C. Sometimes grows faster after cold-shock under 10 °C for 1 wk.

Distribution: Worldwide.

Hosts: Mainly on woody dicotyledonous plants. Twenty-four families of plants have been reported hosting venturiaceous fungi, i.e. *Aceraceae*, *Amaryllidaceae*, *Asteraceae*, *Betulaceae*, *Caprifoliaceae*, *Cornaceae*, *Dipsacaceae*, *Ericaceae*, *Fagaceae*, *Gentianaceae*, *Geraniaceae*, *Iridaceae*, *Juncaginaceae*, *Liliaceae*, *Onagraceae*, *Oleaceae*, *Polygonaceae*, *Ranunculaceae*, *Rhamnaceae*, *Rosaceae*, *Rubiaceae*, *Salicaceae*, *Sapindaceae* and *Ulmaceae* (Barr 1968, 1989, Sivanesan 1977). After studying a large number of type materials of *Venturia* species, many have been found to be representative of other genera (Shen *et al.* in prep.).

Disease symptoms: Leaf spots, flower and fruit canker.

Notes: Species of *Venturia* are widely distributed in the northern temperate region of the world, and are saprobic or parasitic on a large variety of dicotyledonous plants. *Venturia* comprises 198 species according to Index Fungorum. Based on the morphology of type specimens studied, the diagnostic characteristics of

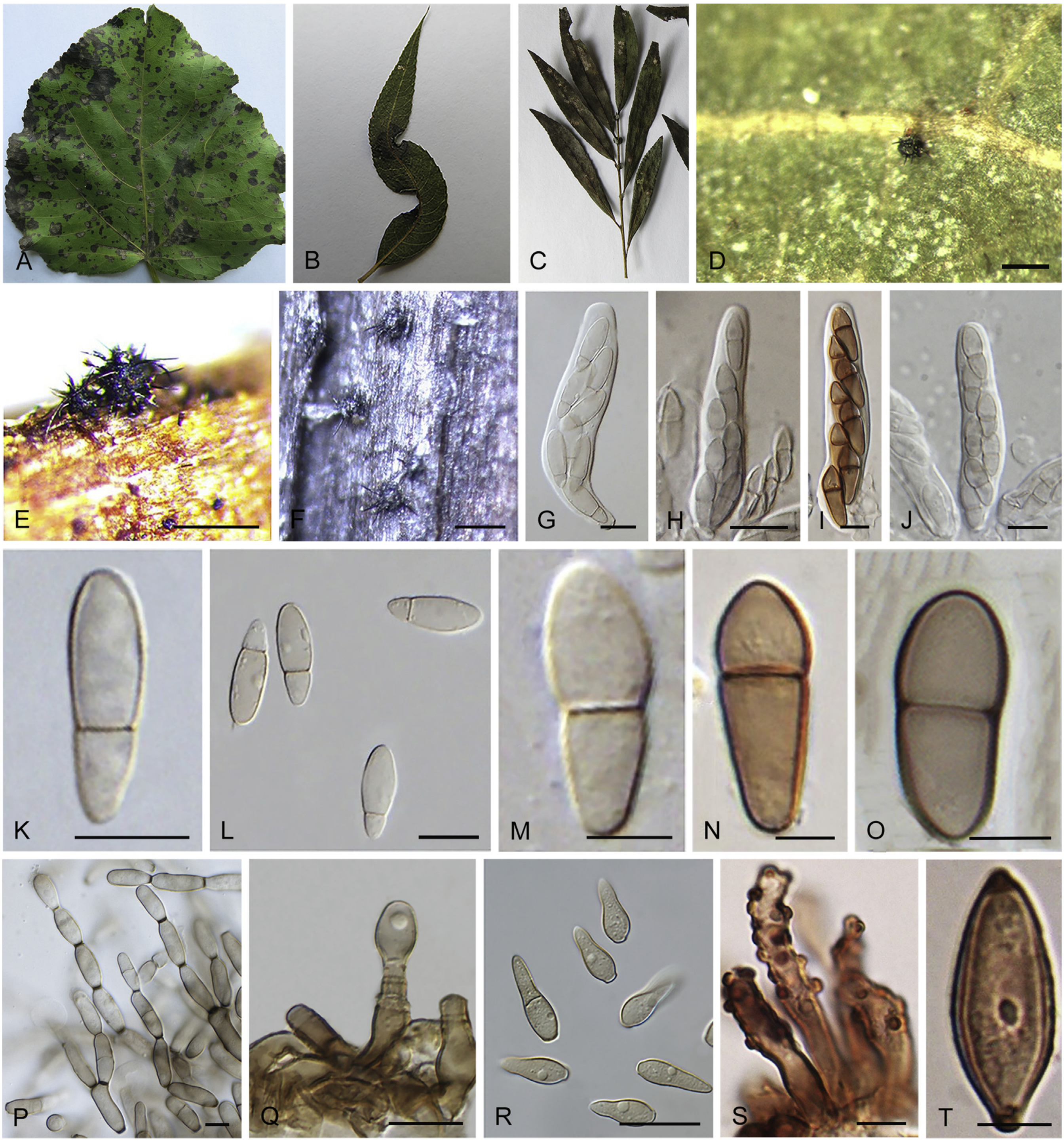

Fig. 65. *Venturia* spp. **A–C.** Disease symptoms. **A.** Symptoms caused by *Venturia martianoffiana* (HMAS 247008). **B.** Symptoms caused by *Venturia catenospora* (HMAS 247006). **C.** Symptoms caused by *Venturia fuliginosa* (HMAS 247007). **D–O.** Sexual morphs. **D–F.** Ascomata on the host. **D.** *Venturia chinensis* (HMAS 246485). **E.** *Venturia canadensis* (NY 00914436). **F.** *Venturia atriseda* (K 189232). **G–J.** Asci. **G.** *Venturia cephalariae* (K 189236). **H.** *Venturia chinensis* (HMAS 246485). **I.** *Venturia inaequalis* (NY 00914442). **J.** *Venturia asperata* (PDD 31846). **K–O.** Ascospores. **K.** *Venturia atriseda* (K 189232). **L.** *Venturia cephalariae* (K 189236). **M.** *Venturia carpophila* (K 189234). **N.** *Venturia inaequalis* (NY 00914442). **O.** *Venturia helvética* (ZT 49111). **P–T.** Asexual morphs. **P.** Conidial chains of *Venturia phaeosepta* (ex-type CGMCC 3.18368). **Q.** Conidiophores sporulation of *Venturia inaequalis* (CGMCC 3.18372). **R.** Conidia of *Venturia inaequalis* (CGMCC 3.18372). **S.** Fasciculate conidiophores of *Venturia pyrina* (HMAS 03923). **T.** Conidium of *Venturia pyrina* (HMAS 03923). Scale bars: D = 300 µm; E, F = 0.2 mm; G, H, J–M, Q, T = 10 µm; I, N, O, S = 5 µm; P, R = 20 µm.

Venturia are as follows: Ascomata immersed, semi-immersed or superficial, scattered or gregarious, often papillate and ostiolate with setae. Hamathecium narrowly cellular, hyaline, evanescent in mature ascomata. Asci 8-spored, bitunicate, fissitunicate, broadly cylindrical to obclavate, usually lacking a pedicel. Ascospores pale olivaceous to brown, 1-septate, usually asymmetrical. Morphological discrimination of the sexual morph is limited, and the asexual morph is more informative (Sivanesan 1977). The genus is morphologically comparable to the *Mycosphaerella* morph of *Ramularia* in having bitunicate, oblong to obclavate asci with a short, thick pedicel or pedicel lacking, ellipsoidal, 1-septate ascospores which are slightly constricted at the septum. However, *Venturia* can be distinguished from the sexual morph of *Ramularia* by its setose ascomata, pale olivaceous to brown and asymmetrical ascospores. In addition, pseudoparaphyses are lacking in the sexual morph of *Ramularia*.

Table 21. DNA barcodes of accepted *Venturia* spp.

Species	**Isolates**[1]	**GenBank accession numbers**[2]			**References**
		ITS	***tef1***	***tub2***	
Venturia anemones	CBS 370.55	EU035447	KF853965	KF808264	Crous *et al.* (2007d), Hamelin *et al.* (unpubl. data)
V. aucupariae	CBS 365.35	EU035450	–	–	Crous *et al.* (2007d)
V. catenospora	CBS 447.91^{T}	EU035427	KF853957	KF808256	Crous *et al.* (2007d), Hamelin *et al.* (unpubl. data)
V. chinensis	CGMCC 3.17685^{T}	KP689596	–	–	Zhang *et al.* (2016)
V. fraxini	CBS 140930	KT823548	KT823582	KT823514	Ibrahim *et al.* (2016)
V. fuliginosa	CGMCC 3.18370^{T}	KU220965	–	–	Shen *et al.* (2017)
V. helvetica	CBS 474.61	EU035458	KF853974	KF808274	Crous *et al.* (2007d), Hamelin *et al.* (unpubl. data)
V. hystrioides	CBS 117727	EU035459	KF853975		Crous *et al.* (2007d)
V. inaequalis	CBS 476.61	EU282478	GU456288	–	Sanchez-Torres *et al.* (2009), Zhang *et al.* (2011)
V. inopina	MYA 2852^{T}	AY177406	–	–	Newcombe (2003)
V. macularis	CBS 477.61	EU035462	KF853977	KF808277	Crous *et al.* (2007d), Hamelin *et al.* (unpubl. data)
V. martianoffiana	CGMCC 3.18376	KU985131	–	–	Present study
V. nashicola	OYO-1	HQ434393	HQ434349	HQ434437	Zhao *et al.* (2012)
V. orni	CBS 140924^{T}	KT823564	KT823598	KT823530	Ibrahim *et al.* (2016)
V. phaeosepta	CGMCC 3.18368^{T}	KU985133	–	–	Present study
V. polygoni-vivipari	CBS 114207	EU035466	KF853984	KF808284	Crous *et al.* (2007d)
V. pyrina	38995	HQ434425	HQ434381	HQ434469	Zhao *et al.* (2012)
V. saliciperda	CBS 480.61	EU035471	–	–	Crous *et al.* (2007d)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CGMCC: Chinese General Microbiological Culture Collection Center, Beijing, China; MYA: the American Type Culture Collection; OYO: Private collection. ^{T} indicates ex-type strain.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *tef1*: partial translation elongation factor 1-alpha gene; *tub2*: partial beta-tubulin gene.

Although several studies have been conducted on the phylogeny of *Venturia*, they mostly relied on rDNA sequences of the ITS and LSU, which proved insufficient in distinguishing some species (Crous *et al.* 2007d, Zhang *et al.* 2011). More genes, especially protein coding genes are required to provide a better resolution at the species level.

References: Menon 1956, Nüesch 1960, Barr 1968, Sivanesan 1977 (morphology); Schubert *et al.* 2003 (morphology of asexual stage); Crous *et al.* 2007d, Zhang *et al.* 2011, 2016 (morphology and phylogeny).

Venturia martianoffiana (Thüm.) Y. Zhang ter & J.Q. Zhang, **comb. nov.** Mycobank MB821418.
Basionym: *Cladosporium martianoffianum* Thüm., Byull. Moskovsk. Obshch. Isp. Prir., Otd. Biol. 55: 74. 1880.

Venturia phaeosepta Y. Zhang ter & J.Q. Zhang, **sp. nov.** MycoBank MB817355. Fig. 67.

Etymology: Latin “phaeo-”, in reference to “dark” septum.

On *Populus*: *Leaf spots* amphigenous, subcircular to angular, 1.5–13 mm wide, often confluent, diffuse, mostly spread along leaf veins, dark brown to black, with an irregular margin. *Colonies* amphigenous, caespitose, greenish brown to blackish. *Mycelium* mainly subcuticular. *Stromata* variable in size, composed of pale olivaceous to brown, angular to rounded, thick-walled, pseudoparenchymatous cells, 4–8 μm diam. *Conidiophores* solitary or loosely fasciculate, arising mostly from stromata or from hyphae, erect, straight, sometimes flexuous at the apex, unbranched or apically branched, 12–29 × 5–8 μm, 0–1-septate, pale to medium brown, smooth, with somewhat thickened walls, sometimes conidiophores reduced to conidiogenous cells. *Conidiogenous cells* integrated, terminal, 15–27 × 5–8 μm, with a 1–2(–3) denticle-like conidiogenous loci, proliferation sympodial, loci unthickened, not or only somewhat darkened-refractive, 2–3 μm wide. *Conidia* in simple or branched chains, clavate, subcylindrical, ellipsoid or rarely fusiform, (12–)16–29 × 4–7 μm, pale olivaceous brown, 0–1(–3)-septate, smooth, tapering towards both ends, apex mostly truncate, occasionally rounded or pointed, base truncate; *hila* often somewhat thickened and darkened-refractive, 1.5–3 μm wide. *Sexual morph* not observed. On MEA: *Mycelium* consisting of pale olivaceous, smooth, branched, 1.5–3 μm wide hyphae. *Conidiophores* integrated, produced in the middle of the mycelium, 3–6-septate, visible as small, protruding, denticle-like loci, up to 92 μm long, 5–6 μm wide. *Conidiogenous cells* subcylindrical, 15–25 × 5–7 μm, pale to medium olivaceous, smooth, tapering to 1–2 apical truncate loci, 2–4 μm wide. *Conidia* pale olivaceous, smooth, subcylindrical to narrowly ellipsoid, occurring in simple or branched chains, 0–1(–2)-septate, tapering towards subtruncate ends, ends 2–4 μm wide, aseptate conidia 12–21.5 × 5–7 μm, septate conidia up to 28 μm long and 5–7 μm wide; *basal hila* usually thickened and darkened-refractive; *microcyclic conidiation* common in older cultures. *Sexual morph* not observed.

Culture characteristics: Colonies reaching 43 mm diam after 1 mo on PDA at 25 °C in the dark. Colonies sporulated, erumpent, spreading, with abundant aerial mycelium and feathery to

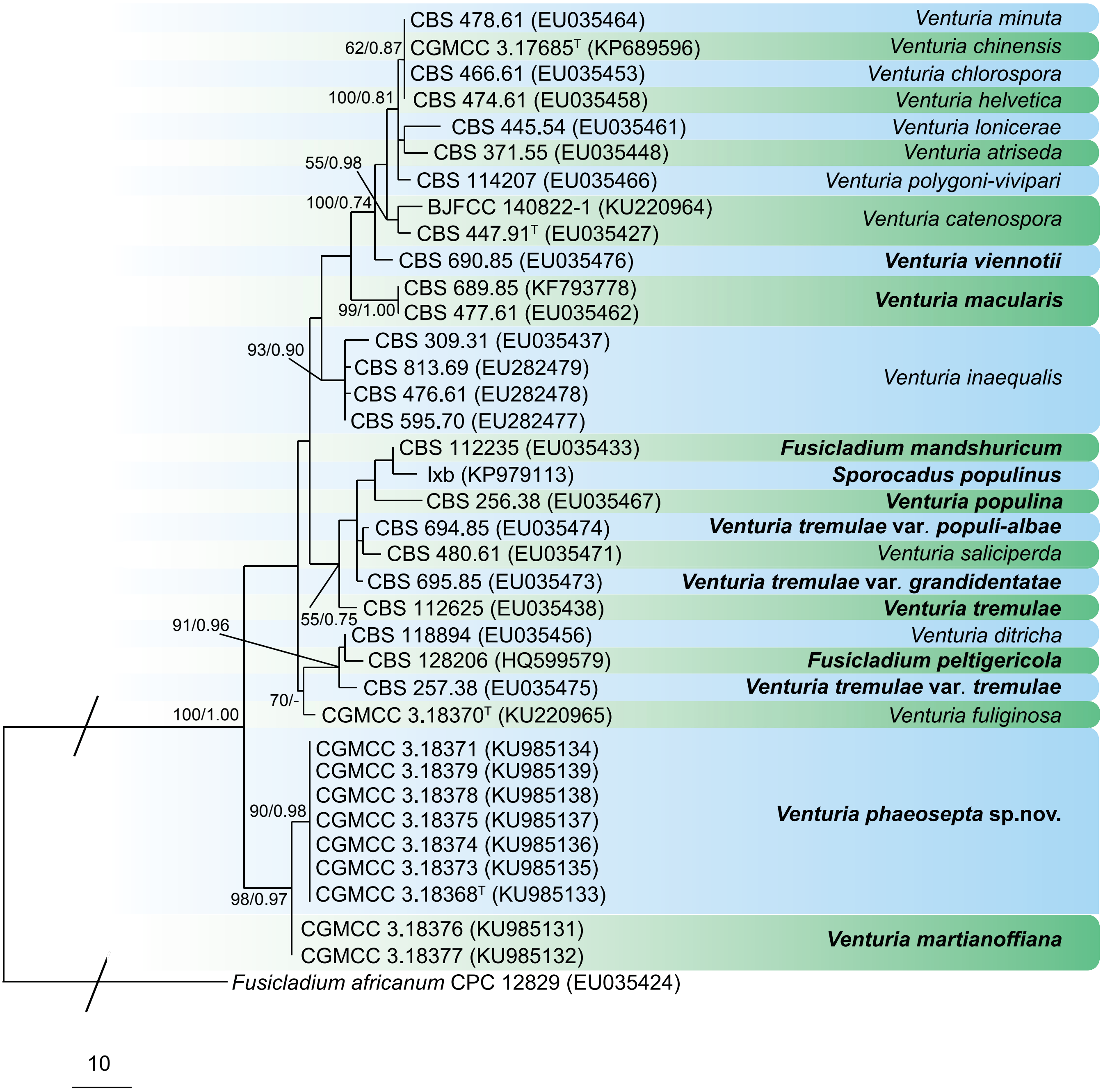

Fig. 66. Maximum likelihood tree generated from a sequence analysis of the ITS rDNA dataset. The outgroup is *Fusicladium africanum* CPC 12829. Maximum likelihood bootstrap support values above 50 % are shown at the nodes and based on 1 000 replicates. Bayesian posterior probability values above 0.70 are shown at the nodes. The species from poplar are in **bold**. Numbers between parentheses correspond to GenBank accession numbers. ^{T} indicates ex-type strain. TreeBASE: S21068.

smooth margins; grey olivaceous (surface), reverse dark olivaceous.

Habitat and distribution: China (Henan, Shannxi), on leaves of *Populus* spp.

Material examined: **China**, Henan, Puyang City Academy Experimental Farm, on leaves of *Populus* × *euramericana* cv. 74/76 (sect. *Aigeiros*), 20 May 2015, W. He (**holotype**, HMAS 246998, culture ex-type CGMCC3.18368); on leaves of *Populus* × *euramericana* cv. 74/76 (sects. *Aigeiros*), Y.F. Zhang, 20 Jun. 2015 (**paratype**, HMAS 246999, CGMCC3.18371); 6 August 2015 (**paratype**, HMAS 247000, CGMCC3.18373); 7 Aug. 2015 (**paratype**, HMAS 247002, CGMCC3.18374); 8 Aug. 2015 (**paratype**, HMAS 247001, CGMCC3.18375); Shanxi, Yangling, on leaves of *Populus* sp. (sects. *Aigeiros*), 4 Sep. 2015, Y.F. Zhang (**paratype**, HMAS 247004, CGMCC3.18378); *ibid*. (**paratype**, HMAS 247005, CGMCC3.18379).

Notes: Among the reported venturiaceous species occurring on *Populus*, the asexual morph of *Venturia phaeosepta* is more comparable with *Venturia martianoffiana* and *F. romellianum* in the morphology of the conidiophore and mode of conidia production (Schubert *et al.* 2003). *Venturia phaeosepta*, however, can readily be distinguished from *V. martianoffiana* by its 1–2(–3) apical denticle-like conidiogenous loci (*vs.* a single or several (>3) conidiogenous loci of *V. martianoffiana*). *Venturia phaeosepta* differs from *F. romellianum* by its septate (*vs.* chiefly aseptate) conidia (Schubert *et al.* 2003).

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Wilsonomyces Adask. *et al.*, Mycotaxon 37: 283. 1990. Fig. 68.

Classification: *Dothideomycetes*, *Pleosporomycetidae*, *Pleosporales*, *Dothidotthiaceae.*

Type species: *Wilsonomyces carpophilus* (Lév.) Adask. *et al.* Lectotype: plate 7, fig. 5 in Léveillé JH. 1843. Ann. Sci. Nat., Bot., sér. 2 19: 215. Epitype and ex-epitype culture designated here: CBS H-23113, CBS 231.89.

DNA barcode (genus): LSU.

DNA barcodes (species): ITS, *tef1.* Table 22. Fig. 64.

Sexual morph unknown. *Conidiomata* sporodochial, usually punctiform, tan to olivaceous brown, finally becoming black. *Stroma* present in host tissue, compact, immersed, erumpent, discoid on leaves, fusoid on twigs. *Conidiophores* macronematous, mononematous, densely compacted, straight or flexuous, branched or not, subcylindrical, geniculate, smooth, subhyaline to pale brown, cicatrised, 1–4-septate*. Conidiogenous cells* terminal and intercalary, subcylindrical, subhyaline, smooth, proliferating sympodially at apex, scars unthickened. *Conidia* holoblastic, solitary, dry, acrogenous, simple, thick-walled, cylindrical, clavate, ellipsoidal or fusiform, occasionally forked, rounded to acute at the apex, truncate at the base, generally (2–)3–5(–10) transverse with occasionally 1–2 oblique septa, rarely with 1 longitudinal septum, subhyaline, becoming medium brown to golden-brown, dark olivaceous to black in mass, conidia *in vivo* are larger (adapted from Adaskaveg *et al.* 1990).

Culture characteristics: Growth moderate, PDA plates covered in 4 wk, mostly consisting of submerged hyphae with sparse aerial mycelium. In cultures grown in the dark, aerial mycelium subfelty to felty, initially white becoming pale olive-grey to greyish olive, occasionally olive-ochre. In cultures grown exposed to light, submerged light brownish olive to olive-brown hyphae radiate outward from mycelial mat; aerial hyphae buffy-brown; olivaceous black to black conidia produced in mass (more details in Adaskaveg *et al.* 1990).

Optimal media and cultivation conditions: PDA at 20 °C on the laboratory bench.

Distribution: Worldwide.

Hosts: Pathogens mainly of *Prunus* spp., particularly peaches and apricots, but also of other members of the family *Rosaceae*, i.e. *Pyrus communis*, *Malus domestica*, *Sorbus aucuparia* and *Cydonia oblonga.* Also reported in *Cleome* sp. (*Cleomaceae*) and *Quercus ilex* (*Fagaceae*).

Disease symptoms: *Wilsonomyces* causes a disease known as shot-hole disease because of the symptoms on the host leaves: small circular purple lesions with pale centres that gradually enlarge and become necrotic in the centre until the centre falls out. This genus also produces necrotic spots on the twigs and necrotic lesions on fruit.

Notes: *Wilsonomyces* is a monotypic genus. *Wilsonomyces carpophilus* was initially described as a new species of *Helminthosporium*, and was subsequently transferred to different genera until Adaskaveg *et al.* (1990) introduced *Wilsonomyces* to accommodate it. The taxonomy of the genus was controversial, and Sutton (1997) regarded it as synonym of *Thyrostroma*. However, all the strains of *Wilsonomyces carpophilus* included in the phylogenetic analysis based on LSU, ITS and *tef1* (Figs 49, 64) sequences were located in a clade separate from the rest of the taxa incorporated in the tree including the type species of *Thyrostroma*, *T. compactum*. Therefore, it is herewith supported that *Wilsonomyces* represents a distinct genus. Finally, its location in the *Dothidotthiaceae* is also supported.

References: Ellis 1959, Adaskaveg *et al.* 1990 (morphology); Ahmadpour *et al.* 2012a (morphology and pathogenicity).

Wilsonomyces carpophilus (Lév.) Adask. *et al.*, Mycotaxon 37: 283. 1990. Fig. 68.
Basionym: *Helminthosporium carpophilum* Lév., Annls Sci. Nat., Bot., sér. 2 19: 215. 1843.
Synonyms: *Clasterosporium carpophilum* (Lév.) Aderh., Landw. Jahrb. 30: 815. 1901.
Coryneum carpophilum (Lév.) Jauch, Int. Bull. Pl. Protect. 14: 99. 1940.
Stigmina carpophila (Lév.) M.B. Ellis, Mycol. Pap. 72: 56. 1959.
Sciniatosporium carpophilum (Lév.) Morgan-Jones, Canad. J. Bot. 49: 995. 1971.
Sporocadus carpophilus (Lév.) Arx, Gen. Fungi Sporul. Cult., Edn 3 (Vaduz): 224. 1981.
Thyrostroma carpophilum (Lév.) B. Sutton, Arnoldia 14: 34. 1997.
For additional synonyms see Adaskaveg *et al.* (1990).

Conidiomata sporodochial, brown, with immersed to erumpent stromata, 30–200 µm diam. *Conidiophores* subcylindrical, branched or not, geniculate, 10–70 × 5–7 µm, subhyaline to pale brown, smooth, 1–4-septate. *Conidiogenous cells* terminal and intercalary, subcylindrical, subhyaline, smooth, 10–30 × 5–7 µm, proliferating sympodially, scars unthickened, 3.5–5 µm diam. *Conidia* narrowly ellipsoid to subcylindrical or fusoid, subhyaline, becoming medium brown to golden-brown, smooth, with (2–)3–7(–11) dark, transverse septa, rarely with any oblique septum, (27–)32–45(–55) × (12–)13–14(–16) µm, base truncate, 4–6 µm diam *in vitro*. *Conidia in vivo* are larger, namely 20–90 × 7–16 µm (adapted from Adaskaveg *et al.* 1990).

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium, and feathery margins, reaching 40 mm diam after 2 wk. On MEA, PDA and OA surface umber, reverse isabelline.

Material examined: **Lectotype**: plate 7, fig. 5 in Léveillé JH. 1843. Ann. Sci. Nat., Bot., sér. 2 19: 215. **Unknown country**, on petiole of *Prunus subhirtella*, 1989, J.W. Veenbaas-Rijks (**epitype designated here** CBS H-23113, MBT376057, culture ex-epitype CBS 231.89).

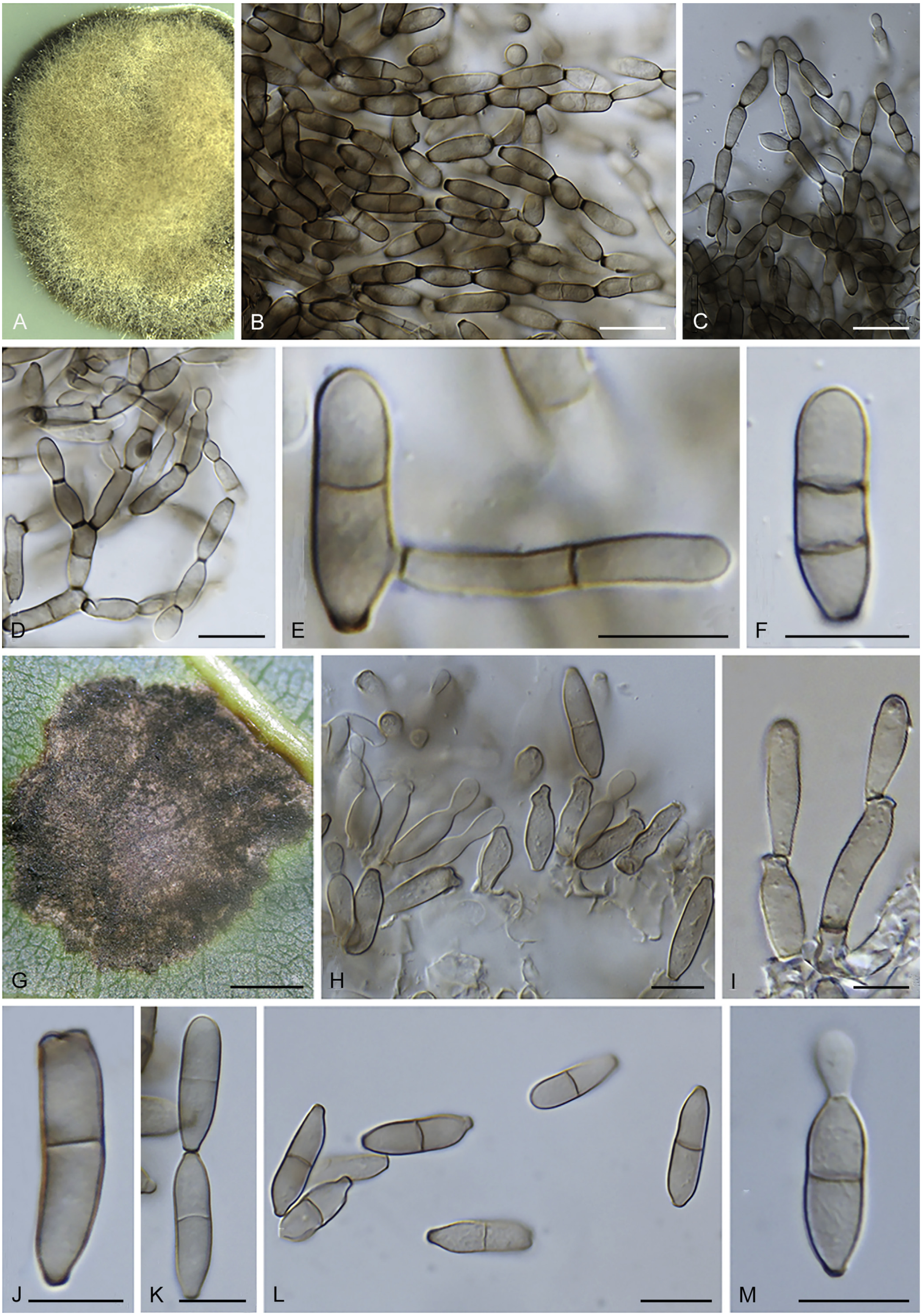

Fig. 67. *Venturia phaeosepta* (ex-type CGMCC3.18368). **A–F.** On MEA. **A.** Colony on MEA. **B.** Conidial chains. **C–D.** Ramoconidia and conidia. **E.** Germinating conidium. **F.** Conidium. **G–M.** On leaves. **G.** Leaves infected by *Venturia phaeosepta*. **H.** Conidiophores and conidia. **I.** Conidiogenous cells giving rise conidia. **J.** Conidiogenous cell. **K.** Conidial chains. **L.** Conidia. **M.** Germinating conidium. Scale bars: B–D = 20 μm; E, F = 10 μm; G = 0.5 cm; H–M = 10 μm.

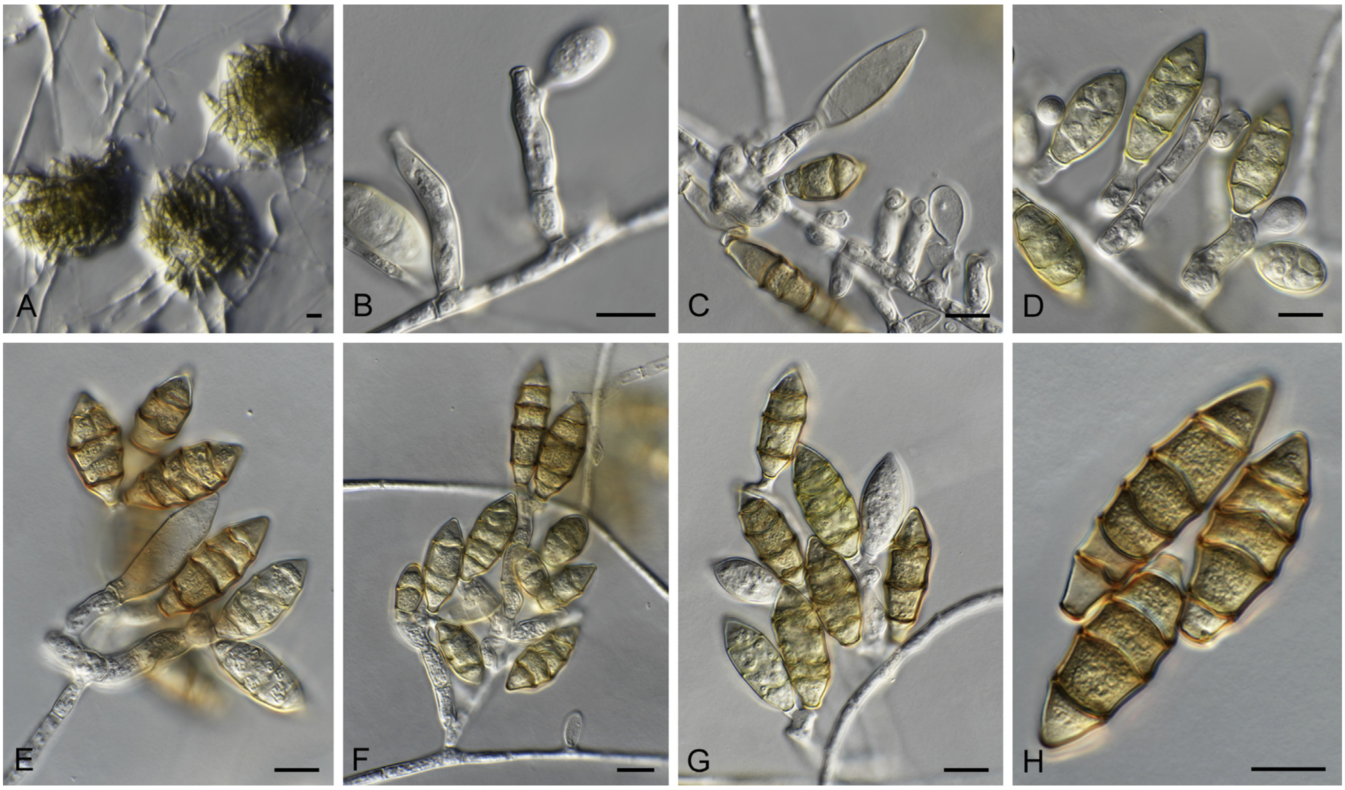

Fig. 68. *Wilsonomyces carpophilus* (ex-epitype CBS 231.89). **A.** Conidiomata. **B–G.** Conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars: 10 µm.

Table 22. DNA barcodes of accepted *Wilsonomyces* sp.

Species	Isolates[1]	GenBank accession numbers[2]		References
		ITS	*tef1*	
Wilsonomyces carpophilus	CBS 231.89^{ET}	KY905672	KY905684	Present study

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands. ^{ET} indicates ex-epitype strain.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *tef1*: partial translation elongation factor 1-alpha gene.

Notes: The holotype of *W. carpophilus* was not located by Adaskaveg *et al.* (1990) when they introduced the genus *Wilsonomyces* to accommodate *Helminthosporium carpophilum*, although they searched in several herbaria in Europe. The holotype was probably lost when Léveillé's collection was destroyed in the Franco-Prussian War in 1870–1871. Therefore, Adaskaveg *et al.* (1990) selected the drawings of Léveillé present in the original description of this taxon as lectotype (Ann. Sci. Nat., Bot., sér. 2 19: 215, plate 7, fig. 5). To fix the application of the generic name, an epitype for this species is therefore designated here.

Authors: Y. Marin-Felix & P.W. Crous

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