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Genera of phytopathogenic fungi: GOPHY 2

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Abstract: This paper represents the second contribution in the Genera of Phytopathogenic Fungi (GOPHY) series. The series provides morphological descriptions and information regarding the pathology, distribution, hosts and disease symptoms for the treated genera. In addition, primary and secondary DNA barcodes for the currently accepted species are included. This second paper in the GOPHY series treats 20 genera of phytopathogenic fungi and their relatives including: *Allantophomopsiella, Apoharknessia, Cylindrocladiella, Diaporthe, Dichotomophthora, Gaeumannomyces, Harknessia, Huntiella, Macgarvieomyces, Metulocladosporiella, Microdochium, Oculimacula, Paraphoma, Phaeoacremonium, Phyllosticta, Proxypiricularia, Pyricularia, Stenocarpella*, *Utrechtiana* and *Wojnowiciella*. This study includes the new genus *Pyriculariomyces*, 20 new species, five new combinations, and six typifications for older names.

Key words: DNA barcodes, Fungal systematics, 26 new taxa, Six new typifications.

Taxonomic novelties: New genera: *Pyriculariomyces* Y. Marín, M.J. Wingf. & Crous; **New species:** *Apoharknessia eucalypti* Crous & M.J. Wingf., *Cylindrocladiella addiensis* L. Lombard & Crous, *Cylindrocladiella nauliensis* L. Lombard & Crous, *Diaporthe heterophyllae* Guarnaccia & Crous, *Diaporthe racemosae* A.R. Wood, Guarnaccia & Crous, *Dichotomophthora basellae* Hern.-Restr., Cheew. & Crous, *Dichotomophthora brunnea* Hern.-Restr. & Crous, *Harknessia bourbonica* Crous & M.J. Wingf., *Harknessia corymbiae* Crous & A.J. Carnegie, *Harknessia cupressi* Crous & R.K. Schumach., *Harknessia pilularis* Crous & A.J. Carnegie, *Huntiella abstrusa* A.M. Wilson, Marinc., M.J. Wingf., *Metulocladosporiella chiangmaiensis* Y. Marín, Cheew. & Crous, *Metulocladosporiella malaysiana* Y. Marín & Crous, *Metulocladosporiella musigena* Y. Marín, Cheew. & Crous, *Metulocladosporiella samutensis* Y. Marín, Luangsa-ard & Crous, *Microdochium novae-zelandiae* Hern.-Restr., Thangavel & Crous, *Phaeoacremonium pravum* C.F.J. Spies, L. Mostert & Halleen, *Phyllosticta iridigena* Y. Marín & Crous, *Phyllosticta persooniae* Y. Marín & Crous; **New combinations:** *Macgarvieomyces luzulae* (Ondřej) Y. Marín, Akulov & Crous, *Pyriculariomyces asari* (Crous & M.J. Wingf.) Y. Marín, M.J. Wingf. & Crous, *Utrechtiana arundinacea* (Corda) Crous, Quaedvl. & Y. Marín, *Utrechtiana constantinescui* (Melnik & Shabunin) Crous & Y. Marín; **New status and combination:** *Oculimacula acuformis* (Nirenberg) Y. Marín & Crous; **Typification: Epitypification:** *Helminthosporium arundinaceum* Corda, *Phomopsis pseudotsugae* M. Wilson, *Pyricularia luzulae* Ondřej, *Pyricularia zingiberis* Y. Nishik; **Lectotypification:** *Phomopsis pseudotsugae* M. Wilson, *Pyricularia zingiberis* Y. Nishik.

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INTRODUCTION

The series, Genera of Phytopathogenic Fungi (GOPHY), was launched by Marin-Felix *et al.* (2017) to provide a stable platform for the taxonomy of phytopathogenic fungi. The common denominator of the genera included in this series is their association with plant diseases. The authors recognise that many species treated are not well-known plant pathogens or where Koch's postulates have not been proven for them. The focus of the series is mainly to resolve generic and species concepts of the fungi studied. This is particulary important because many taxa have been shown to represent species complexes, or to be accommodated in genera that are poly- or paraphyletic (Crous *et al.* 2015b). The series links to a larger initiative known as the "The Genera of Fungi project" (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). Some of the main problems are that for many genera and species type material has not been designated or/and that the vast majority of these taxa were described before the DNA phylogenetic era (Hibbett *et al.* 2011) and thus lack DNA barcodes (Schoch *et al.* 2012). Another important aim of this project is to secure the application of names by generating DNA barcodes of type species of genera and type specimens of species. In those cases where no type material has been preserved, taxa need to be recollected, epi- or neotypes designated,

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and registered in MycoBank to ensure traceability of the nomenclatural act (Robert *et al.* 2013). The ultimate objective is to move to a single scientific name for fungi (Crous *et al.* 2015b) for which sexual-asexual links have been resolved.

For each paper in the GOPHY series, morphological descriptions and information regarding the pathology, distribution, hosts and disease symptoms are provided for the treated genera. In addition, this information is linked to primary and secondary DNA barcodes of the currently accepted species in each genus. These DNA barcodes are critically important because of problems relating to generic delimitation and species identification based solely on morphology. A clear example is the delimitation of the genera *Bipolaris* and *Curvularia*, treated in the first paper of the GOPHY series (Marin-Felix *et al.* 2017). These two genera share many morphological similarities, and intermediate conidial characters (Manamgoda *et al.* 2012). Species delimitation in both genera based on morphology alone is of limited value because many species have overlapping characters (Sivanesan 1987, Madrid *et al.* 2014, Manamgoda *et al.* 2014). Some genera include species that do not produce reproductive structures and their identification must rely on DNA data. For some phytopathogenic genera, the DNA barcodes for species delimitation have been established in previous studies, but for the vast majority, these data remain unavailable.

Mycologists wishing to contribute to future issues in the GOPHY series are encouraged to contact Pedro Crous (p.crous@westerdijkinstitute.nl) before submitting their contributions. This will ensure there is no overlap with activities arising from other research groups. Preference will be given to genera that include novel DNA data and/or novel species, combinations or typifications. The generic contributions, apart from being published in this series of papers, will also be placed in the database displayed on www.plantpathogen.org.

MATERIAL AND METHODS

Isolates and morphological analysis

Descriptions of the new taxa and typifications are based on cultures obtained from the collection at the Westerdijk Fungal Biodiversity Institute in Utrecht, The Netherlands (CBS), the working collection of P.W. Crous (CPC), housed at the Westerdijk Fungal Biodiversity Institute, and the culture collection (CMW) of the Forestry and Agricultual Biotechnology Institute (FABI), at the University of Pretoria, South Africa. For fresh collections, we followed the procedures previously described in Crous *et al.* (1991a). Colonies were transferred to different media, i.e. cherry decoction agar (CHA), 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.* 2009), autoclaved pieces of grapevine canes placed on water agar (grapevine water agar; GWA), pine needle agar (PNA; Smith *et al.* 1996), or malt extract peptone agar (MPA; Speakman 1984), and incubated at different conditions depending on the taxon to induce sporulation. Requirements of media and conditions of incubations are specified in each genus. Reference strains and specimens are maintained at the CBS, CMW and CPC.

Vegetative and reproductive structures were mounted in 100 % lactic acid either directly from specimens or from colonies sporulating on MEA, PDA, PNA, OA or SNA. 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). Taxonomic novelties were deposited in MycoBank (www.MycoBank.org; Crous *et al.* 2004a).

DNA isolation, amplification and analyses

Fungal DNA was extracted and purified directly from the colonies or host material as specified for each genus. Primers and protocols for the amplification and sequencing of gene loci, and software used for phylogenetic analyses can be found in the bibliography related to the phylogeny presented for each respective genus. Phylogenetic analyses consisted of Maximum-Likelihood (ML), Bayesian Inference (BI), and Maximum Parsimony (MP). The ML and the BI were carried out using methods described by Hernández-Restrepo *et al.* (2016b), and the MP using those described by Crous *et al.* (2006b). Sequence data generated in this study were deposited in GenBank and the alignments and trees in TreeBASE (http://www.treebase.org).

RESULTS

Allantophomopsiella Crous, IMA Fungus 5: 180. 2014. Fig. 1.

Classification: *Leotiomycetes, Leotiomycetidae, Phacidiales, Phacidiaceae.*

Type species: *Allantophomopsiella pseudotsugae* (M. Wilson) Crous., basionym: *Phomopsis pseudotsugae* M. Wilson. Lectotype designated here: material deposited in Royal Botanic Garden Edinburgh, E00414771. Epitype and ex-epitype strain designated here: CBS H-23354, CBS 320.53.

DNA barcodes (genus): ITS, LSU.

DNA barcodes (species): ITS, *rpb2*. Table 1.

Conidiomata up to 600 µm diam, pycnidial, immersed, becoming erumpent, irregularly multilocular, dark brown, ostiolate; *conidiomatal wall* composed of 3–4 layers of dark brown cells, *textura angularis*. *Conidiophores* arising from inner layer of conidioma, branched, septate, at times reduced to conidiogenous cells. *Conidiogenous cells* integrated or discrete, ampulliform to subcylindrical or lageniform, hyaline, smooth with minute periclinal thickening at apex. *Conidia* inequilaterally fusiform or naviculate, hyaline, smooth, aseptate, guttulate, bearing mucoid apical appendages, flabelliform to irregular in shape. *Sexual morph* unknown (adapted from Crous *et al.* 2014b).

Culture characteristics: Colonies spreading, flat with sparse aerial mycelium and feathery margins. On PDA surface olivaceous grey, reverse iron-grey. On OA surface olivaceous grey with patches of iron-grey.

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

Distribution: North America and Europe.

Hosts: Conifers (*Pinaceae*).

Disease symptoms: Canker and dieback.

Notes: This genus was recently introduced by Crous *et al.* (2014b) to accommodate *A. pseudotsugae*, a pathogen of conifers that was found to be very damaging, especially after

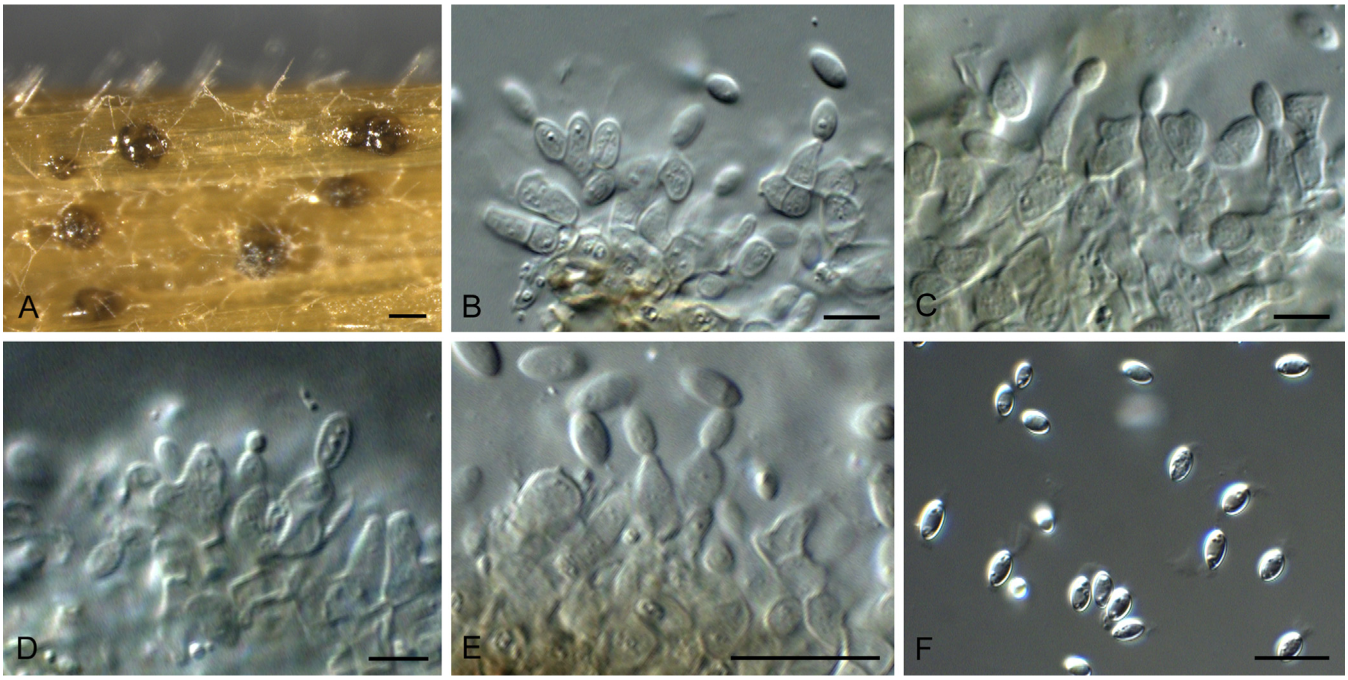


Fig. 1. *Allantophomopsiella pseudotsugae* (CBS 841.91). **A.** Conidiomata forming on autoclaved barley leaves. **B–E.** Conidiogenous cells giving rise to conidia. **F.** Conidia. Scale bars: A = 300 μm; others = 10 μm. Pictures taken from Crous *et al.* (2014b).

Table 1. DNA barcodes of accepted *Allantophomopsiella* sp.

Species	Isolate[1]	GenBank accession numbers[2]		Reference
		ITS	*rpb2*	
Allantophomopsiella pseudotsugae	CBS 320.53^{ET}	KJ663825	KJ663905	Crous *et al.* (2014b)

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

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

wounding during tree dormancy (Roll Hansen 1992). In a study considering the pathogenicity of this fungus on *Pinus sylvestris* associated with pruning wounds, it was observed that *Allantophomopsis pseudotsugae* occurred commonly in slash of pine trees wounded during the autumn (Uotila 1990).

Allantophomopsiella is morphologically related to the phytopathogenic genera *Apostrasseria* and *Allantophomopsis*. However, it can be easily differentiated from both genera by the lack of percurrent proliferation on its conidiogenous cells, and by the production of inequilaterally fusiform or naviculate conidia.

References: Uotila 1990 (pathogenicity); Crous *et al.* 2014b (morphology and phylogeny).

Allantophomopsiella pseudotsugae (M. Wilson) Crous, IMA Fungus 5: 180. 2014. Fig. 1.
Basionym: *Phomopsis pseudotsugae* M. Wilson, Transactions of the Royal Scottish Arboricultural Society 34: 147. 1920.
Synonyms: *Phacidiella coniferarum* G.G. Hahn, Mycologia 49: 227. 1957.
Phacidium coniferarum (G.G. Hahn) DiCosmo, *et al.*, Canad. J. Bot. 61: 37. 1983.
Allantophomopsis pseudotsugae (M. Wilson) Nag Raj, Coelomycetous anamorphs with appendage-bearing conidia: 116. 1993.
Additional synonyms are provided in Nag Raj (1993).

Materials examined: **UK**, Scotland, Murthly, on *Pseudotsuga menziesii* (*Pinaceae*), Apr. 1920, M. Wilson (**lectotype of *Phomopsis pseudotsugae* designated here**: MBT379803, material deposited in Royal Botanic Garden Edinburgh, E00414771). **Norway**, Førde in Sunnfjord, shoot of *Pseudotsuga menziesii* (*Pinaceae*), Apr. 1948, H. Robak (**epitype of *Phomopsis pseudotsugae* designated here** CBS H-23354, MBT379804, culture ex-epitype CBS 320.53).

Notes: *Allantophomopsis pseudotsugae* was introduced by Wilson (1920) as *Phomopsis pseudotsugae* to accommodate a fungus that infects *Pseudotsuga menziesii* in Scotland. Type material was not specified when it was described, but the author deposited original material used for the Royal Botanic Garden Edinburgh. This material with the barcode number E00414771, which appears to be syntype material of the species, is selected here as lectotype. To fix the use of the name, the strain CBS 320.53 is designated here as ex-epitype. This strain was collected in Norway, occurring on the type host (Wilson 1920), and fits well with the description of the species recently provided by Crous *et al.* (2014b).

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

Apoharknessia Crous & S.J. Lee, Stud. Mycol. 50: 239. 2004. Fig. 2.

Classification: *Sordariomycetes*, *Diaporthomycetidae*, *Diaporthales*, *Apoharknessiaceae*.

Type species: *Apoharknessia insueta* (B. Sutton) Crous & S.J. Lee, basionym: *Harknessia insueta* B. Sutton. Holotype of *H. insueta*: IMI 22697. Epitype and ex-epitype strain designated by Lee *et al.* (2004): CBS H-9913, CBS 111377 = STE-U 1451.

DNA barcodes (genus): ITS, LSU.

DNA barcodes (species): ITS, *cal*, *tub2*. Table 2.

Conidiomata pycnidial, separate to gregarious, subepidermal, becoming erumpent, stromatic, amphigenous, depressed

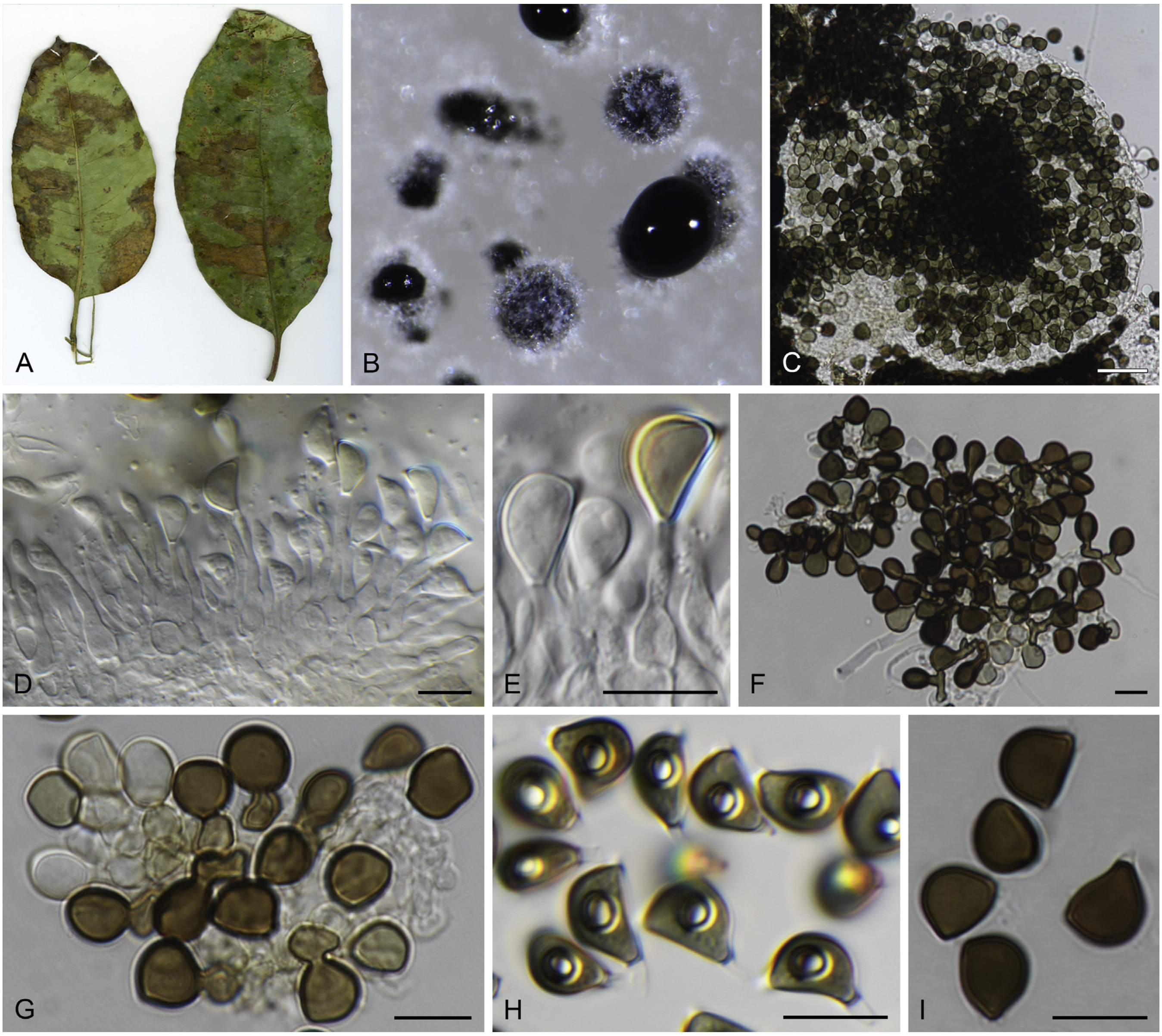


Fig. 2. *Apoharknessia* spp. **A.** Disease symptoms of *Apoharknessia eucalyptorum* on *Eucalyptus pellita*. **B, C.** Conidiomata. **B.** *Apoharknessia eucalyptorum* (ex-type CBS 142519). **C.** *Apoharknessia insueta* (ex-type CBS 111377). **D–G.** Conidiogenous cells and conidia. **D, E.** *Apoharknessia eucalyptorum* (ex-type CBS 142519). **F, G.** *Apoharknessia insueta* (ex-type CBS 111377). **H, I.** Conidia. **H.** *Apoharknessia eucalyptorum* (ex-type CBS 142519). **I.** *Apoharknessia insueta* (ex-type CBS 111377). Scale bars: C = 25 μm; others = 10 μm. Picture B taken from Crous *et al.* (2017a).

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

Species	**Isolates**[1]	**GenBank accession numbers**[2]			**References**
		ITS	***cal***	***tub2***	
Apoharknessia eucalypti	CBS 142518^{T}	MG934432	MG934510	MG934505	Present study
Ap. eucalyptorum	CBS 142519^{T}	KY979752	KY979867	KY979919	Crous *et al.* (2017a)
Ap. insueta	CBS 111377^{ET}	JQ706083	MG934511	MG934506	Crous *et al.* (2012c), present study

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

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *cal*: partial calmodulin gene; *tub2*: partial β-tubulin gene.

globose or subglobose to irregular, unilocular, glabrous; *opening* irregularly, with yellowish, furfuraceous cells, lacking a definite ostiole; *conidiomatal wall* of *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining cavity. *Conidiogenous cells* lageniform to ampulliform or ampulliform to subcylindrical, hyaline, smooth, in mucilage, percurrently proliferating once or twice near apex. *Conidia* broadly ellipsoidal to obovoid or obliquely gibbose, apex obtusely rounded, aseptate, non-apiculate, medium brown or brown, with or without a longitudinal hyaline band on flat surface, thick-walled, smooth, with or without striations along length of conidia, with prominent central guttule; *basal appendage* absent or hyaline, tubular, smooth, thin-walled, devoid of cytoplasm; *apical appendage* absent or hyaline, conical or tubular, short, smooth, thin-walled, devoid of cytoplasm. *Sexual morph* unknown.

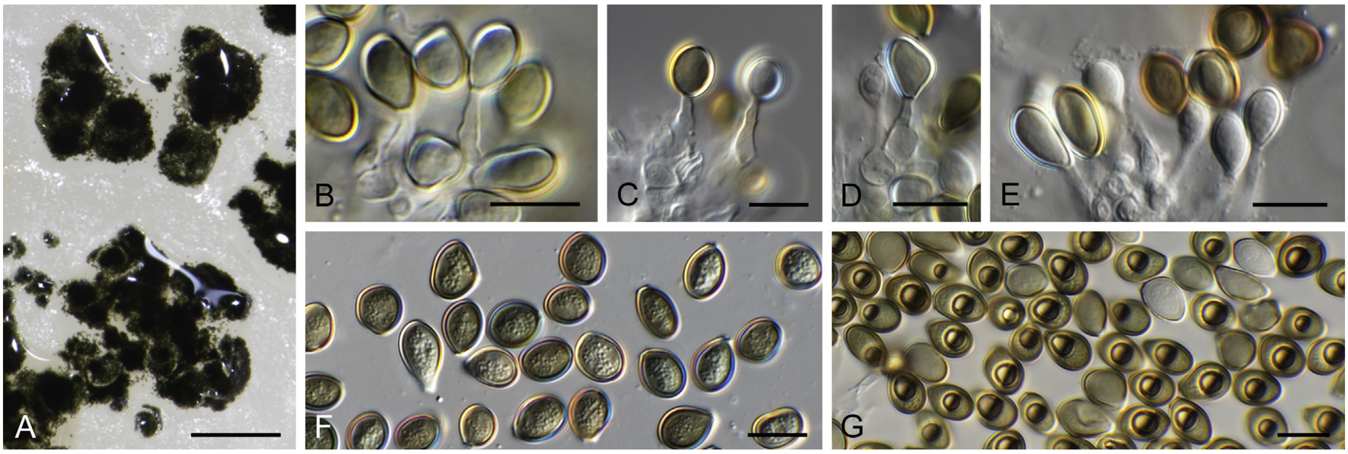


Fig. 3. *Apoharknessia eucalypti* (ex-type CBS 142518). **A.** Conidiomata sporulating on SNA. **B–E.** Conidiogenous cells and conidia. **F, G.** Conidia. Scale bars: A = 250 µm, B–G = 10 µm.

Culture characteristics: Colonies flat on MEA, PDA and OA, with sparse or moderate aerial mycelium, smooth, lobate margins, fast sporulating. On MEA surface greenish black or olivaceous black in centre, dirty white in outer region; reverse olivaceous grey in centre, dirty white in outer region.

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

Distribution: Brazil, Colombia, Cuba, Malaysia and Mauritius.

Hosts: *Eucalyptus* (*Myrtaceae*).

Disease symptoms: Leaf spots.

Notes: The genus *Apoharknessia* was established by Lee *et al.* (2004) for *Ap. insueta*, a presumed foliar pathogen of eucalypts in Brazil, Colombia, Cuba and Mauritius. The genus included two species following the description of *Ap. eucalyptorum* to accommodate a presumed endophyte of *Eucalyptus pellita* isolated from collections made in Malaysia (Crous *et al.* 2017a).

Apoharknessia is distinguished from *Harknessia* by having an apical appendage on its conidia, and cultures that lack fluffy aerial mycelium and sporulate abundantly on the aerial hyphae. Cultures of *Harknessia s. str.* are slow to sporulate, and tend to form abundant pycnidial conidiomata in culture (Lee *et al.* 2004).

Recently, the family *Apoharknessiaceae* was introduced based on a phylogenetic study of the members of the *Diaporthales*, in order to accommodate *Apoharknessia*, designated as the type genus of the family, together with *Lasmenia*, which is also a genus associated with plant disease (Senanayake *et al.* 2017).

References: Lee *et al.* 2004 (morphology and phylogeny); Crous *et al.* 2012c, 2017a, Senanayake *et al.* 2017 (phylogeny).

Apoharknessia eucalypti Crous & M.J. Wingf., **sp. nov.** MycoBank MB820945. Fig. 3.

Etymology: Name refers to *Eucalyptus*, the host genus from which this fungus was collected.

Foliicolous, isolated from leaves incubated in moist chambers (presumed endophytic). *Conidiomata* up to 250 µm diam, pycnidial, solitary to gregarious, subepidermal, becoming erumpent, stromatic, amphigenous, depressed globose; *opening* irregularly, with yellowish, furfuraceous cells; *conidiomatal wall* of *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining cavity. *Conidiogenous cells* 8–12 × 3–5 µm, ampulliform to subcylindrical, hyaline, smooth, in mucilage, percurrently proliferating once or twice near apex. *Conidia* (7–)8–10(–11) × (5–)6(–7) µm, broadly ellipsoid to obovoid, apex obtusely rounded, aseptate, non-apiculate, medium brown, thick-walled, smooth, striations along length of conidium body, with prominent central guttule. *Basal appendage* absent or 0–2 µm long, 2 µm diam, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm.

Culture characteristics: Colonies on MEA, PDA and OA, with moderate aerial mycelium and smooth, lobate margins, reaching 60 mm diam after 2 wk at 25 °C. On MEA surface greenish black in middle, dirty white in outer region; reverse olivaceous grey in centre, dirty white in outer region. On PDA surface and reverse olivaceous grey in centre, dirty white in outer region. On OA surface greenish black in middle, outer region dirty white.

Material examined: **Malaysia**, Sabah, isolated from leaves of *Eucalyptus pellita* (*Myrtaceae*), May 2015, M.J. Wingfield (**holotype** CBS H-23081, culture ex-type CPC 27550 = CBS 142518).

Notes: *Apoharknessia eucalypti* is an odd member of the genus in that its conidia generally lack an apical appendage. The latter was observed on one or two conidia, irrespective of the media used for cultivation. The ITS sequence of *Ap. eucalypti* is only 92 % similar to that of *Ap. insueta* [GenBank JQ706083; Identities = 569/618 (92 %), 33 gaps (5 %)] and 97 % similar to that of *Ap. eucalyptorum* [GenBank KY979752; Identities = 604/621 (97 %), 5 gaps (0 %)].

Authors: P.W. Crous, Y. Marin-Felix, J.Z. Groenewald & M.J. Wingfield

Cylindrocladiella Boesew., Canad. J. Bot. 60: 2289. 1982. Fig. 4.

Synonym: *Nectricladiella* Crous & C.L. Schoch, Stud. Mycol. 45: 54. 2000.

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

Type species: *Cylindrocladiella parva* (P.J. Anderson) Boesew., basionym: *Cylindrocladium parvum* P.J. Anderson. Representative strain: CBS 114524 = ATCC 28272.

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

DNA barcodes (*species*): *his3*, *tef1*, *tub2*. Table 3. Fig. 5.

Ascomata perithecial, superficial, solitary, basal stroma absent, globose to obpyriform, collapsing laterally when dry, smooth, with

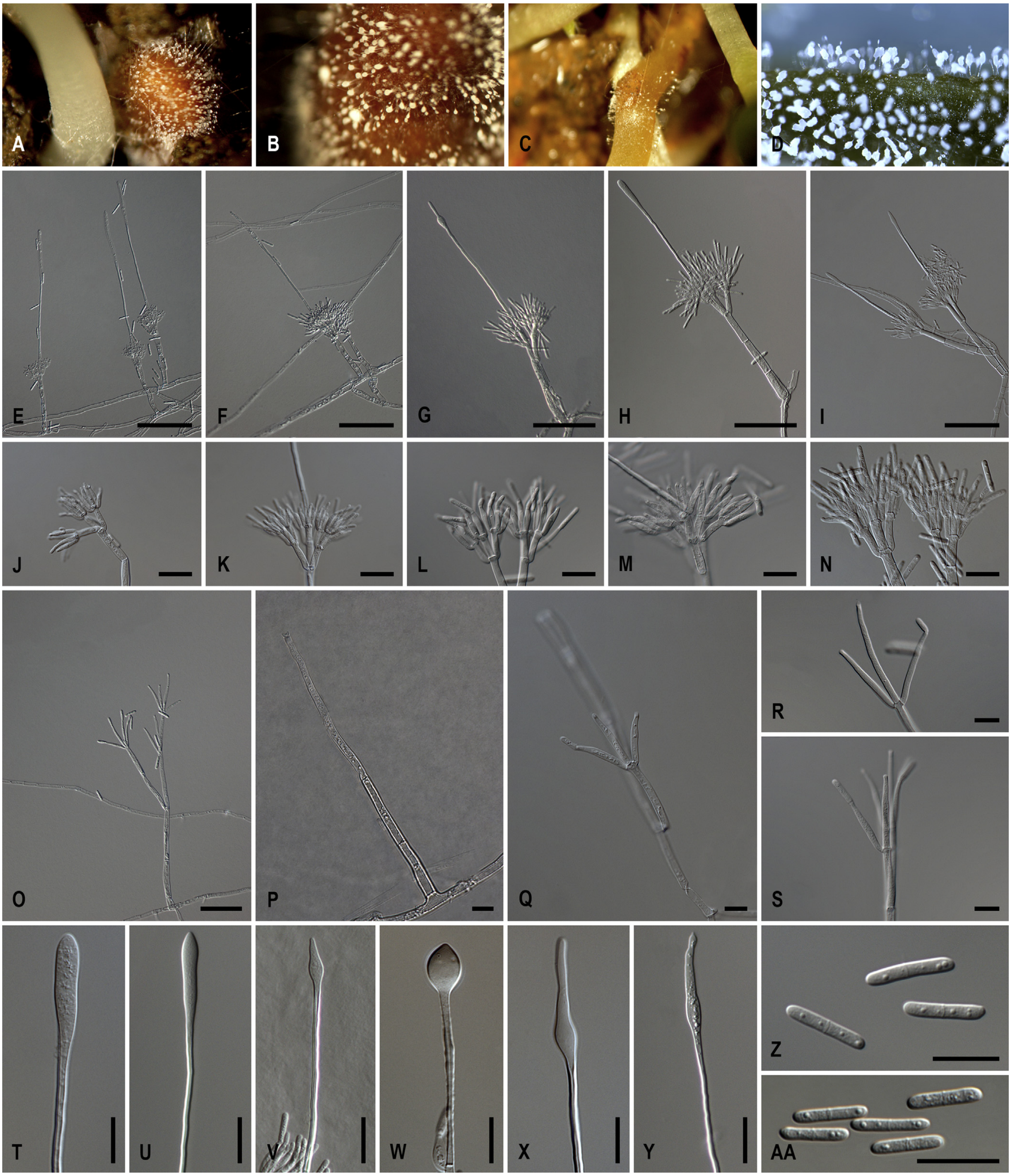


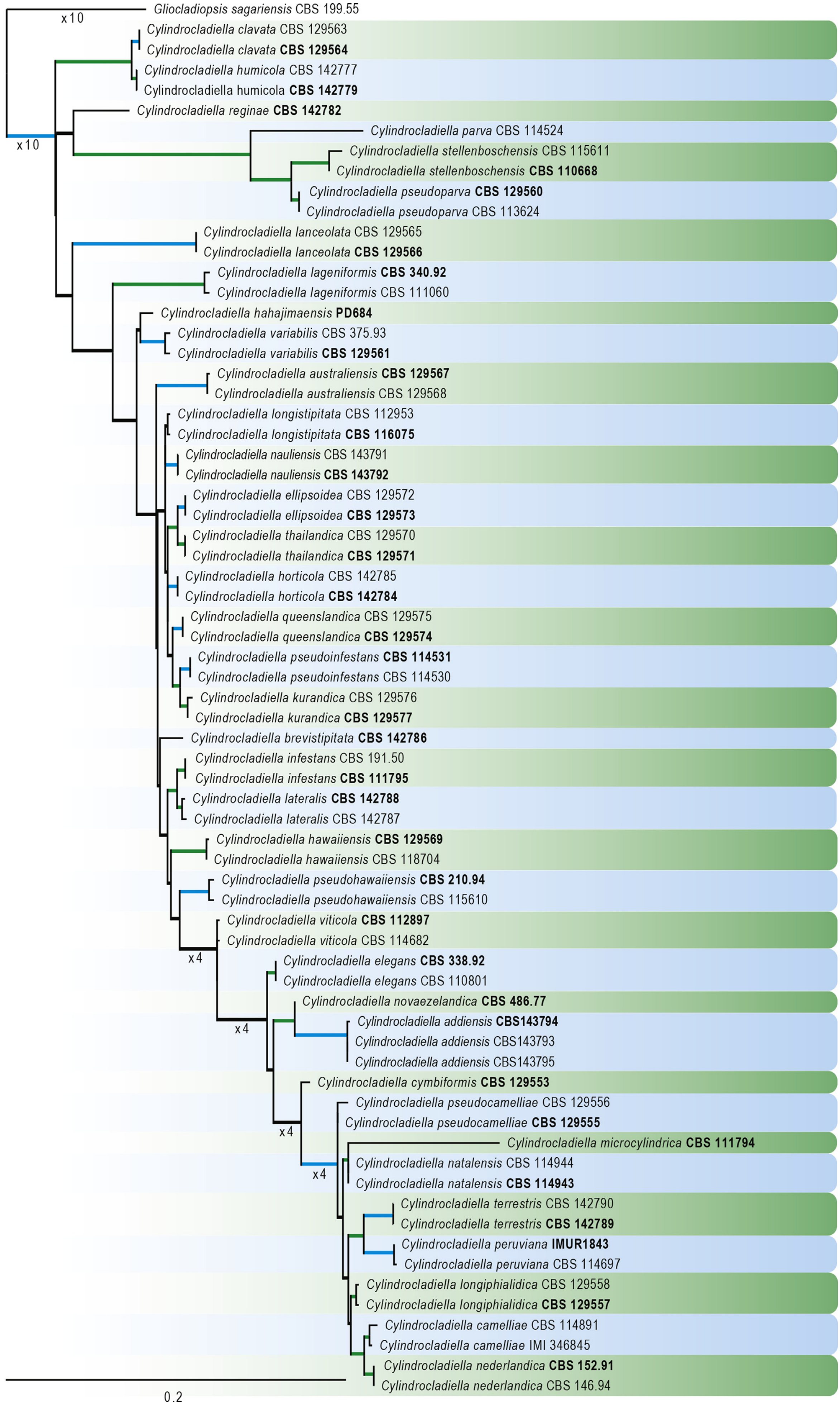
Fig. 4. *Cylindrocladiella* spp. **A–D.** Conidiophores of *Cylindrocladiella* spp. on infected alfalfa seeds **A–B.** *Cylindrocladiella* spp. sporulating on the seed coat of *Medicago sativa*. **C.** Root rot of *M. sativa* seedling. **D.** *Cylindrocladiella* spp. on carnation leaf. **E–AA.** Asexual morph. **E–I.** Penicillate conidiophores. **E.** *Cylindrocladiella longistipitata* (ex-type CBS 116075). **F.** *Cylindrocladiella kurandica* (ex-type CBS 129577). **G.** *Cylindrocladiella lanceolata* (ex-type CBS 129566). **H.** *Cylindrocladiella pseudoparva* (ex-type CBS 129560). **I.** *Cylindrocladiella nederlandica* (ex-type CBS 152.91). **J–N.** Penicillate conidiogenous apparatus. **J.** *Cylindrocladiella hawaiiensis* (ex-type CBS 129569). **K.** *Cylindrocladiella australiensis* (ex-type CBS 129567). **L.** *Cylindrocladiella natalensis* (ex-type CBS 114943). **M.** *Cylindrocladiella cymbiformis* (ex-type CBS 129553). **N.** *Cylindrocladiella ellipsoidea* (ex-type CBS 129573). **O–S.** Subverticillate conidiophores. **O.** *Cylindrocladiella australiensis* (ex-type CBS 129567). **P.** *Cylindrocladiella longiphialidica* (ex-type CBS 129557). **Q.** *Cylindrocladiella pseudohawaiiensis* (ex-type CBS 210.94). **R, S.** *Cylindrocladiella natalensis* (ex-type CBS 114943). **T–Y.** Terminal vesicles of stipe extensions. **T.** *Cylindrocladiella hawaiiensis* (ex-type CBS 129569). **U.** *Cylindrocladiella stellenboschensis* (ex-type CBS 110668). **V.** *Cylindrocladiella cymbiformis* (ex-type CBS 129553). **W.** *Cylindrocladiella variabilis* (ex-type CBS 129561). **X.** *Cylindrocladiella lanceolata* (ex-type CBS 129566). **Y.** *Cylindrocladiella kurandica* (ex-type CBS 129577). **Z, AA.** Conidia. **Z.** *Cylindrocladiella natalensis* (ex-type CBS 114943). **AA.** *Cylindrocladiella brevistipitata* (ex-type CBS 142783). Scale bars: E–I, O = 50 µm; J–N, P–AA = 10 µm.

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

Species	**Isolates**[1]	**GenBank accession numbers**[2]					**References**
		ITS	**LSU**	***his3***	***tef1***	***tub2***	
Cylindrocladiella addiensis	CBS 143794^{T}	MH111383	–	–	MH111393	MH111388	Present study
	CBS 143793	MH111385	–	–	MH111395	MH111390	Present study
	CBS 143795	MH111384	–	–	MH111394	MH111389	Present study
C. australiensis	CBS 129567^{T}	JN100624	JN099222	JN098932	JN099060	JN098747	Lombard *et al.* (2012)
C. brevistipitata	CBS 142786^{T}	–	–	–	MF444940	MF444926	Lombard *et al.* (2017)
C. camelliae	IMI 346845	AF220952	JN099249	AY793509	JN099087	AY793471	Van Coller *et al.* (2005), Lombard *et al.* (2012)
C. clavata	CBS 129564^{T}	JN099095	JN099135	JN098858	JN098974	JN098752	Lombard *et al.* (2012)
C. cymbiformis	CBS 129553^{T}	JN099103	JN099143	JN098866	JN098988	JN098753	Lombard *et al.* (2012)
C. elegans	CBS 338.92^{T}	AY793444	JN099201	AY793512	JN099039	AY793474	van Coller *et al.* (2005), Lombard *et al.* (2012)
C. ellipsoidea	CBS 129573^{T}	JN099094	JN099134	JN098857	JN098973	JN098757	Lombard *et al.* (2012)
C. hahajimaensis	MAFF 238172^{T}	JN687561	–	–	JN687562	–	Inderbitzin *et al.* (2012)
C. hawaiiensis	CBS 129569^{T}	JN100621	JN099219	JN098929	JN099057	JN098761	Lombard *et al.* (2012)
C. horticola	CBS 142784^{T}	MF444911	–	–	MF444938	MF444924	Lombard *et al.* (2017)
C. humicola	CBS 142779^{T}	MF444906	–	–	MF444933	MF444919	Lombard *et al.* (2017)
C. infestans	CBS 111795^{T}	AF220955	JN099199	AY793513	JN099037	AF320190	Schoch *et al.* (2000), Crous *et al.* (2001), van Coller *et al.* (2005), Lombard *et al.* (2012)
C. kurandica	CBS 129577^{T}	JN100646	JN099245	JN098953	JN099083	JN098765	Lombard *et al.* (2012)
C. lageniformis	CBS 340.92^{T}	AF220959	JN099165	AY793520	JN099003	AY793481	Schoch *et al.* (2000), van Coller *et al.* (2005), Lombard *et al.* (2012)
C. lanceolata	CBS 129566^{T}	JN099099	JN099139	JN098862	JN098978	JN098789	Lombard *et al.* (2012)
C. lateralis	CBS 142788^{T}	MF444914	–	–	MF444942	MF444928	Lombard *et al.* (2017)
C. longiphialidica	CBS 129557^{T}	JN100585	JN099264	JN098851	JN098966	JN098790	Lombard *et al.* (2012)
C. longistipitata	CBS 116075^{T}	AF220958	JN099155	AY793546	JN098993	AY793506	Schoch *et al.* (2000), van Coller *et al.* (2005), Lombard *et al.* (2012)
C. microcylindrica	CBS 111794^{T}	AY793452	JN099203	AY793523	JN099041	AY793483	van Coller *et al.* (2005), Lombard *et al.* (2012)
C. natalensis	CBS 114943^{T}	JN100588	JN099178	JN098895	JN099016	JN098794	Lombard *et al.* (2012)
C. nederlandica	CBS 152.91^{T}	JN100603	JN099195	JN098910	JN099033	JN098800	Lombard *et al.* (2012)
C. novazelandica	CBS 486.77^{T}	AF220963	JN099212	AY793525	JN099050	AY793485	Schoch *et al.* (2000), van Coller *et al.* (2005), Lombard *et al.* (2012)
C. nauliensis	CBS 143792^{T}	MH111387	–	–	MH111397	MH111392	Present study
	CBS 143791	MH111386	–	–	MH111396	MH111391	Present study
C. parva	CBS 114524	AF220964	JN099171	AY793526	JN099009	AY793486	Schoch *et al.* (2000), van Coller *et al.* (2005), Lombard *et al.* (2012)
C. peruviana	IMUR 1843^{T}	AF220966	JN099266	AY793540	JN098968	AY793500	Schoch *et al.* (2000), van Coller *et al.* (2005), Lombard *et al.* (2012)
C. pseudocamelliae	CBS 129555^{T}	JN100577	JN099256	JN098843	JN098958	JN098814	Lombard *et al.* (2012)
C. pseudohawaiiensis	CBS 210.94^{T}	JN099128	JN099174	JN098890	JN099012	JN098819	Lombard *et al.* (2012)
C. pseudoinfestans	CBS 114531^{T}	AF220957	JN099166	AY793548	JN099004	AY793508	Schoch *et al.* (2000), van Coller *et al.* (2005), Lombard *et al.* (2012)
C. pseudoparva	CBS129560^{T}	JN100620	JN099218	JN098927	JN099056	JN098824	Lombard *et al.* (2012)
C. queenslandica	CBS 129574^{T}	JN099098	JN099098	JN098861	JN098977	JN098826	Lombard *et al.* (2012)
C. reginae	CBS 142782^{T}	MF444909	–	–	MF444936	MF444922	Lombard *et al.* (2017)
C. stellenboschensis	CBS 110668^{T}	JN100615	JN099213	JN098922	JN099051	JN098829	Lombard *et al.* (2012)
C. terrestris	CBS 142789^{T}	MF444915	–	–	MF444943	MF444929	Lombard *et al.* (2017)
C. thailandica	CBS 129571^{T}	JN100582	JN099261	JN098848	JN098963	JN098834	Lombard *et al.* (2012)
C. variabilis	CBS 129561^{T}	JN100643	JN099242	JN098950	JN099080	JN098719	Lombard *et al.* (2012)
C. viticola	CBS 112897^{T}	AY793468	JN099226	AY793544	JN099064	AY793504	van Coller *et al.* (2005), Lombard *et al.* (2012)
C. vitis	CBS 142517^{T}	KY979751	KY979806	–	KY979891	KY979918	Crous *et al.* (2017a)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; IMI: International Mycological Institute, CABI-Bioscience, Egham, Bakeham Lane, U.K; IMUR: Institute of Mycology, University of Recife, Recife, Brazil; MAFF: Genetic Resources Centre, National Agriculture and Food Research Organization (NARO), NARO Genebank, Ibaraki, Japan. ^{T} indicates ex-type strains.

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


Gliocladiopsis sagariensis CBS 199.55
x10
Cylindrocladiella clavata CBS 129563
Cylindrocladiella clavata **CBS 129564**
Cylindrocladiella humicola CBS 142777
Cylindrocladiella humicola **CBS 142779**
Cylindrocladiella reginae **CBS 142782**
x10
Cylindrocladiella parva CBS 114524
Cylindrocladiella stellenboschensis CBS 115611
Cylindrocladiella stellenboschensis **CBS 110668**
Cylindrocladiella pseudoparva **CBS 129560**
Cylindrocladiella pseudoparva CBS 113624
Cylindrocladiella lanceolata CBS 129565
Cylindrocladiella lanceolata **CBS 129566**
Cylindrocladiella lageniformis **CBS 340.92**
Cylindrocladiella lageniformis CBS 111060
Cylindrocladiella hahajimaensis **PD684**
Cylindrocladiella variabilis CBS 375.93
Cylindrocladiella variabilis **CBS 129561**
Cylindrocladiella australiensis **CBS 129567**
Cylindrocladiella australiensis CBS 129568
Cylindrocladiella longistipitata CBS 112953
Cylindrocladiella longistipitata **CBS 116075**
Cylindrocladiella nauliensis CBS 143791
Cylindrocladiella nauliensis **CBS 143792**
Cylindrocladiella ellipsoidea CBS 129572
Cylindrocladiella ellipsoidea **CBS 129573**
Cylindrocladiella thailandica CBS 129570
Cylindrocladiella thailandica **CBS 129571**
Cylindrocladiella horticola CBS 142785
Cylindrocladiella horticola **CBS 142784**
Cylindrocladiella queenslandica CBS 129575
Cylindrocladiella queenslandica **CBS 129574**
Cylindrocladiella pseudoinfestans **CBS 114531**
Cylindrocladiella pseudoinfestans CBS 114530
Cylindrocladiella kurandica CBS 129576
Cylindrocladiella kurandica **CBS 129577**
Cylindrocladiella brevistipitata **CBS 142786**
Cylindrocladiella infestans CBS 191.50
Cylindrocladiella infestans **CBS 111795**
Cylindrocladiella lateralis **CBS 142788**
Cylindrocladiella lateralis CBS 142787
Cylindrocladiella hawaiiensis **CBS 129569**
Cylindrocladiella hawaiiensis CBS 118704
Cylindrocladiella pseudohawaiiensis **CBS 210.94**
Cylindrocladiella pseudohawaiiensis CBS 115610
Cylindrocladiella viticola **CBS 112897**
Cylindrocladiella viticola CBS 114682
x4
Cylindrocladiella elegans **CBS 338.92**
Cylindrocladiella elegans CBS 110801
Cylindrocladiella novaezelandica **CBS 486.77**
x4
Cylindrocladiella addiensis **CBS143794**
Cylindrocladiella addiensis CBS143793
Cylindrocladiella addiensis CBS143795
Cylindrocladiella cymbiformis **CBS 129553**
Cylindrocladiella pseudocamelliae CBS 129556
Cylindrocladiella pseudocamelliae **CBS 129555**
x4
Cylindrocladiella microcylindrica **CBS 111794**
x4
Cylindrocladiella natalensis CBS 114944
Cylindrocladiella natalensis **CBS 114943**
Cylindrocladiella terrestris CBS 142790
Cylindrocladiella terrestris **CBS 142789**
Cylindrocladiella peruviana **IMUR1843**
Cylindrocladiella peruviana CBS 114697
Cylindrocladiella longiphialidica CBS 129558
Cylindrocladiella longiphialidica **CBS 129557**
Cylindrocladiella camelliae CBS 114891
Cylindrocladiella camelliae IMI 346845
Cylindrocladiella nederlandica **CBS 152.91**
Cylindrocladiella nederlandica CBS 146.94
0.2

minute, brown setae arising from ascomatal wall surface, red, changing colour in KOH, ostiole consisting of clavate cells, lined with inconspicuous periphyses. *Asci* unitunicate, 8-spored, cylindrical, sessile, thin-walled, with a flattened apex, and a refractive apical apparatus. *Ascospores* uniseriate, overlapping, hyaline, ellipsoid to fusoid with obtuse ends, smooth, 1-septate. *Conidiophores* monomorphic, penicillate, or dimorphic (penicillate and subverticillate), mononematous, hyaline. *Penicillate conidiophores* consist of a stipe, a penicillate arrangement of fertile branches, a stipe extension, and a terminal vesicle. *Subverticillate conidiophores* consist of a stipe, and one or two series of phialides. *Stipe* septate, hyaline, smooth. *Stipe extensions* aseptate, straight, thick-walled, with one basal septum, terminating in a thin-walled vesicle of characteristic shape. *Conidiogenous apparatus* with primary branches 0–1-septate, secondary branches aseptate, terminating in 2–4 phialides. *Phialides* cylindrical, straight or doliiform to reniform to cymbiform, hyaline, aseptate, apex with minute periclinal thickening and collarette. *Conidia* cylindrical, rounded at both ends, straight, (0–)1(–3)-septate, frequently slightly flattened at base, held in asymmetrical clusters by hyaline slime. *Chlamydospores* brown, thick-walled, more frequently arranged in chains than clusters (adapted from Boesewinkel 1982 and Lombard *et al.* 2012).

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.

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, weak pathogen of forestry, agricultural and horticultural crops (Crous 2002, Lombard *et al.* 2012).

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

Notes: Boesewinkel (1982) established the asexual genus *Cylindrocladiella*, based on *C. parva*, to accommodate several cylindrocladium-like species characterised by small (<20 µm long), 1-septate, cylindrical conidia and aseptate stipe extensions. Initially, *Cylindrocladiella* spp. were linked to the sexual genus *Nectricladiella* (Crous & Wingfield 1993, Schoch *et al.* 2000). Following the implementation of the International Code of Nomenclature for algae, fungi and plants (ICN; McNeill *et al.* 2012), Rossman *et al.* (2013) proposed that the generic name *Cylindrocladiella* be retained over *Nectricladiella*. Recently, Lombard *et al.* (2015) showed that the genus *Cylindrocladiella* formed a monophyletic group in the *Nectriaceae*, closely related to the genera *Aquanectria* and *Gliocladiopsis*. To date, 36 species of *Cylindrocladiella* have been recognised (Crous & Wingfield 1993, van Coller *et al.* 2005, Inderbitzin *et al.* 2012, Lombard *et al.* 2012, 2015, 2017; Crous *et al.* 2017a), of which two are linked to nectricladiella-like sexual morphs (Schoch *et al.* 2000, Crous 2002, Lombard *et al.* 2012, 2015). These fungi are generally soil-borne and regarded as saprobes or weak pathogens of numerous plant hosts (Crous 2002, van Coller *et al.* 2005, Scattolin & Montecchio 2007, Lombard *et al.* 2012). Disease symptoms associated with *Cylindrocladiella* infection include leaf spots and root, stem and cutting rots (Crous *et al.* 1991b, Peerally 1991, Crous & Wingfield 1993, Crous 2002, van Coller *et al.* 2005, Scattolin & Montecchio 2007, Lombard *et al.* 2012).

References: Boesewinkel 1982 (morphology and pathogenicity); Crous & Wingfield 1993 (morphology); Schoch *et al.* 2000, Lombard *et al.* 2012, 2017 (morphology and phylogeny); Crous 2002 (morphology, pathogenicity and monograph); van Coller *et al.* 2005 (morphology, pathogenicity and phylogeny).

Cylindrocladiella addiensis L. Lombard & Crous, **sp. nov.** MycoBank MB824497.

Etymology: Name refers to Addis Ababa, Ethiopia, from where this fungus was collected.

Cultures sterile. *Cylindrocladiella addiensis* differs from its closest phylogenetic neighbours, *C. elegans* and *C. noveazelandica*, by unique fixed alleles in three loci based on the alignments deposited in TreeBASE (S22340): ITS position 92(T); *tef1* positions 32(T), 80(C), 84(C), 154(indel), 155(A), 156(G), 157(indel), 199(A), 244(G), 261(G), 368(T), 398(T), 458(G/C), 466(G), 467(C), 475(T), 478(C), 483(T), 485(T), 487(T), 490(T) and 492(G); *tub2* position 174(indel).

Culture characteristics: Colonies convex, cottony, with smooth margins, cream; reverse pale luteous; chlamydospores not seen; reaching 45–65 mm after 1 wk on MEA at 24 °C in ambient light.

Materials examined: **Ethiopia**, Addis Ababa, from soil, 2010, coll. P.W. Crous, isol. L. Lombard [**holotype** CBS 143794 (maintained as metabolically inactive culture), isotype cultures CBS 143793, CBS 143795 (also maintained as metabolically inactive cultures).

Note: None of the three isolates of *C. addiensis* could be induced to sporulate on MEA, PDA, OA, SNA or SNA amended with carnation leaf pieces.

Cylindrocladiella nauliensis L. Lombard & Crous, **sp. nov.** MycoBank MB824500. Fig. 6.

Etymology: Name refers to the area Aek Nauli, Indonesia, from where this fungus was collected.

Conidiophores 35–55 × 3–6 µm, dimorphic, penicillate and subverticillate, mononematous and hyaline, comprising a stipe, a penicillate arrangement of fertile branches, a stipe extension and a terminal vesicle; *stipe* septate, hyaline, smooth; *stipe extension* 100–135 µm long, 4–5 µm wide, aseptate, straight, thick-walled with one basal septum, terminating in thin-walled, broadly clavate to ellipsoidal vesicles sometimes with papillate apex. *Penicillate conidiogenous apparatus* 10–22 × 2–4 µm, with primary branches aseptate, secondary branches 8–15 × 2–4 µm, aseptate, each terminal branch producing 2–4 phialides; *phialides* 8–13 × 2–3 µm, elongate doliiform to reniform to cymbiform, hyaline, aseptate, apex with minute periclinal thickening and collarette. *Subverticillate conidiophores* abundant, comprised of a

Fig. 5. The Maximum Likelihood (ML) consensus tree of *Cylindrocladiella* spp. inferred from the combined ITS (547 bp), *tef1* (527 bp) and *tub2* (502 bp) sequence alignment. 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 *Gliocladiopsis sagariensis* CBS 199.55. Ex-type strains are indicated in **bold**. GenBank accession numbers are indicated in Table 3 and in Lombard *et al.* (2012, 2017). TreeBASE: S22340.

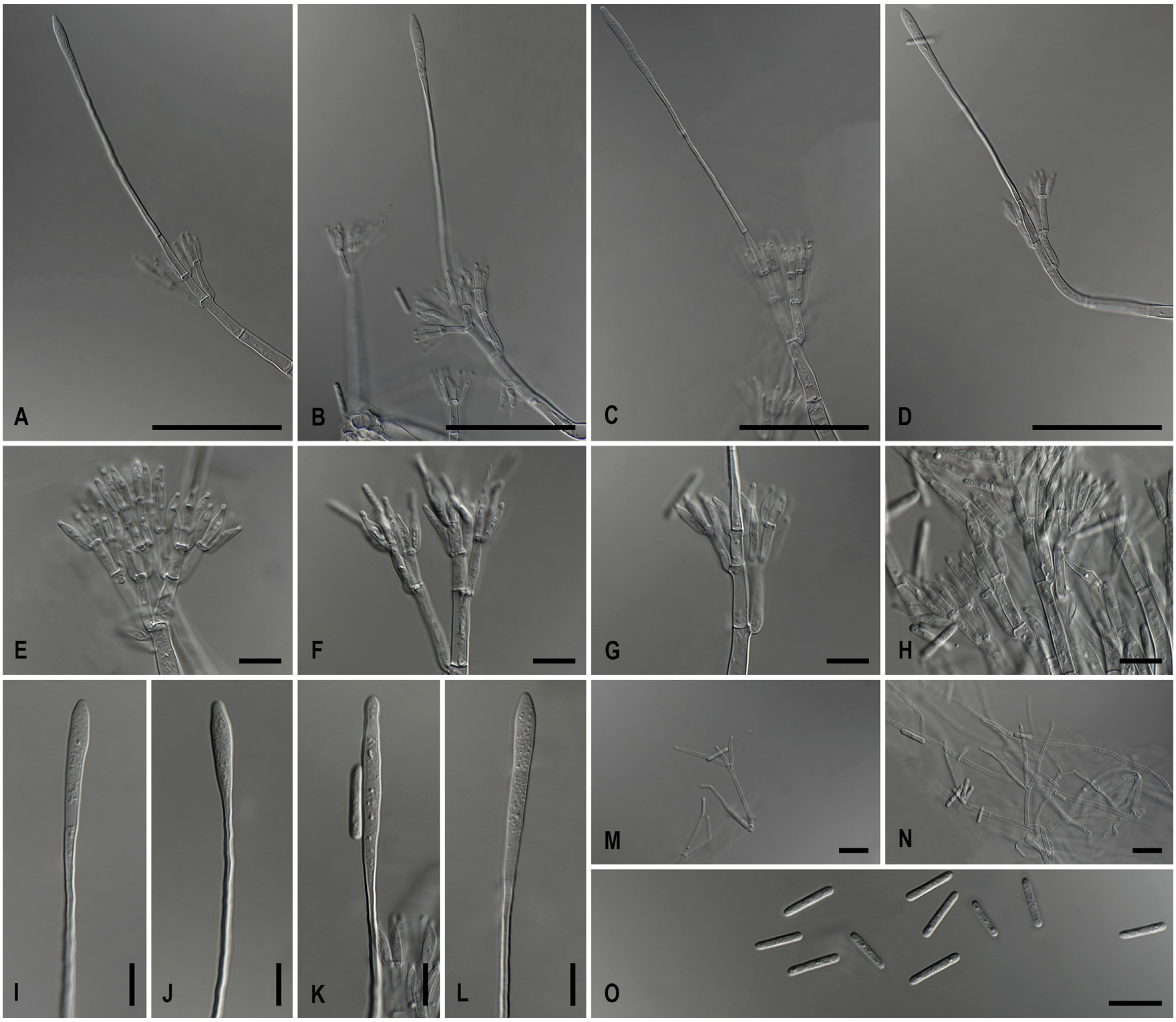


Fig. 6. *Cylindrocladiella nauliensis* (ex-type CBS 143792). **A–D.** Penicillate conidiophores. **E–H.** Penicillate conidiogenous apparatus. **I–L.** Terminal vesicles of stipe extensions. **M, N.** Subverticillate conidiophores. **O.** Conidia. Scale bars: A–D = 50 µm; E–O = 10 µm.

septate stipe and rarely primary branches terminating in 2–4 phialides; *primary branches* 25–45 × 2–4 µm, straight, hyaline, 0–1-septate; *phialides* 12–32 × 2–3 µm, cymbiform to cylindrical, hyaline, aseptate, apex with minute periclinal thickening and collarette. *Conidia* (10–)11–13(–14) × 2–3 µm (av. = 12 × 2 µm), cylindrical, rounded at both ends, straight, 1-septate, frequently slightly flattened at base, held in asymmetrical clusters by hyaline slime. *Sexual morph* unknown.

Culture characteristics: Colonies convex, cottony, with smooth margins, cream with pale luteous to brick centre; reverse pale luteous to honey with sepia centre; chlamydospores moderate throughout medium arranged in chains; reaching 60–70 mm after 1 wk on MEA at 24 °C in ambient light.

Materials examined: **Indonesia**, Sumatra Utara, Aek Nauli, from soil, May 2005, coll. M.J. Wingfield, isol. L. Lombard (**holotype** CBS H-23400, culture ex-type CBS 143792), isotype culture CBS 143791 (metabolically inactive).

Notes: *Cylindrocladiella nauliensis* is closely related to *C. longistipitata*. The stipe extensions of *C. nauliensis* (up to 135 µm long) are shorter than those of *C. longistipitata* (up to 216 µm long; Lombard *et al.* 2012). Additionally, the conidia of *C. nauliensis* are smaller [(10–)11–13(–14) × 2–3 µm (av. = 12 × 2 µm)] than those of *C. longistipitata* [(12–)14–16(–17) × 2–4 µm (av. = 15 × 3 µm); Lombard *et al.* 2012].

Authors: L. Lombard & P.W. Crous

Diaporthe Nitschke, Pyrenomyc. Germ. 2: 240. 1870. Figs 7, 8.
Synonym: *Phomopsis*, Sacc., Syll. fung. (Abellini) 2: 484. 1883.

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

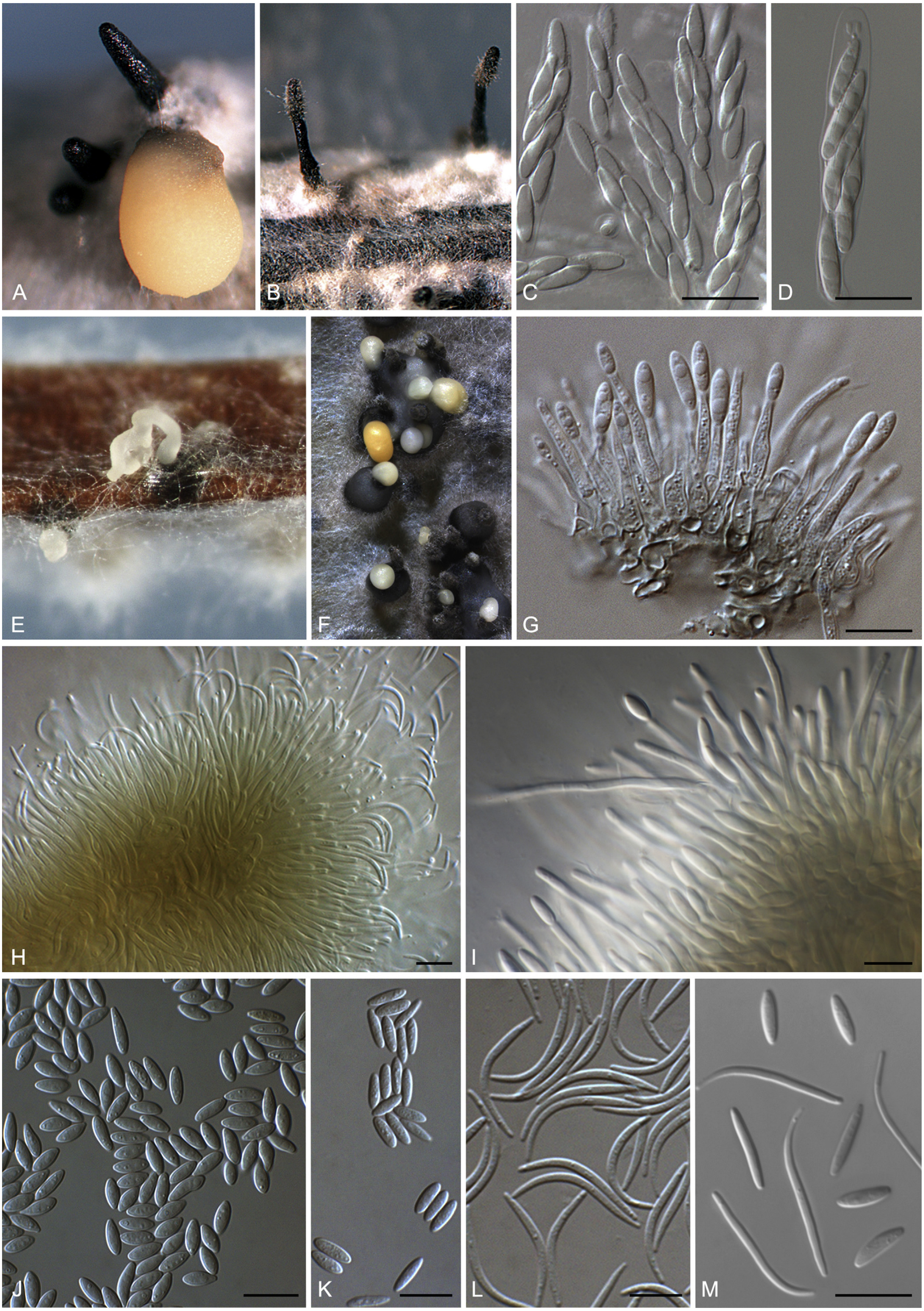
Type species: *Diaporthe eres* Nitschke. Lectotype designated by Udayanga *et al.* (2014a): B 70 0009145. Epitype and ex-epitype strain designated by Udayanga *et al.* (2014a): BPI 892912, AR5193 = CBS 138594.

DNA barcodes (*genus*): ITS.

DNA barcodes (*species*): *cal*, *his3*, *tef1*, *tub2*. Table 4. Fig. 9.

Ascomata immersed in substrate, subglobose or irregular, solitary or clustered in groups, often erumpent through a pseudostroma mostly surrounding ascomata with more or less elongated ascomatal necks. *Pseudostroma* distinct, often delimited with dark lines. *Asci* unitunicate, 8-spored, sessile, elongate to clavate or cylindrical, loosening from ascogenous cells at an

Fig. 7. Disease symptoms associated with *Diaporthe* spp. **A, B.** *Helianthus annuus* plants affected by *Diaporthe gulyae* (courtesy Susan Thompson). **C, D.** Branch canker of *Persea americana* with associated *Diaporthe foeniculina* and *Diaporthe sterilis*. **E, F.** Phomopsis cane (courtesy Alessandro Vitale) and cane bleaching on shoot of *Vitis vinifera* caused by *Diaporthe* spp. (courtesy José Luis Ramos Sáez de Ojer). **G, H.** Decay of *Vaccinium corymbosum* caused by *Diaporthe baccae* and *Diaporthe sterilis* and artificial infection caused by inoculation of *Diaporthe sterilis*. **I.** Trunk canker with gummosis of *Citrus limon* caused by *Diaporthe limonicola* and *Diaporthe melitensis*. Pictures C, D taken from Guarnaccia *et al.* (2016); I from Guarnaccia & Crous (2017).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early stage and floating free in ascomata. *Ascospores* biseriate to uniseriate in ascus, fusoid, ellipsoid to cylindrical, straight, inequilateral or curved, septate, hyaline, sometimes with appendages. *Conidiomata* pycnidial, deeply embedded in culture on several media, globose to conical, eustromatic, multilocular, occasionally with ostiolate necks, scattered or aggregated, brown to black, surface covered with hyphae, cream to pale luteous or yellowish, conidial droplets or cirrus exuding from central ostioles; *conidiomatal wall* consisting of pale brown, thick walled, *textura angularis*. *Conidiophores* cylindrical to clavate, straight to sinuous, densely aggregated, branched, 0–6-septate, smooth, hyaline in upper region, pale brown at base. *Conidiogenous cells* phialidic, hyaline, cylindrical, terminal and lateral, tapering slightly towards apex. *Paraphyses* occasionally produced, intermingled among conidiophores, hyaline, smooth, 1–3-septate. *Alpha conidia* aseptate, generally hyaline, smooth, fusiform to ellipsoidal, with obtuse or acute to rounded ends, non- to multi-guttulate, but often bi-guttulate. *Beta conidia* aseptate, hyaline, filiform, smooth, straight or more often hooked, eguttulate, tapering or truncated towards ends. *Gamma conidia* rarely produced, hyaline, smooth, non- to multi-guttulate, fusiform to subcylindrical with acute or rounded apex (adapted from Gomes *et al.* 2013, Udayanga *et al.* 2014a).

Culture characteristics: Colonies on MEA, PDA and OA producing abundant compact, flattened, aerial mycelium, sometimes in rings, with an entire to irregular margin, white, cream to yellowish or pale olivaceous grey, smoke grey to grey, cottony; reverse pale brown to grey, dark green, producing brownish dots with age, with solitary or aggregated conidiomata at maturity.

Optimal media and cultivation conditions: On MEA, PDA and OA at 25 °C, or sterile pine needles placed on SNA at 25 °C under near-ultraviolet light (12 h light, 12 h dark) to induce sporulation of the asexual morph.

Distribution: Worldwide.

Hosts: On a wide range of plant families.

Disease symptoms: Root and fruit rots, dieback, stem cankers, leaf spots, leaf and pod blights, and seed decay.

Notes: The genus *Diaporthe* presently includes 213 species supported by ex-type cultures and supplementary DNA barcodes, which include endophytes, saprobes and important plant pathogenic species. Recent phylogenetic analyses of the genus *Diaporthe* grouped some of those species into complexes, such as *D. arecae*, *D. eres* and *D. sojae* (Huang *et al.* 2013, Udayanga *et al.* 2014a, 2015). Several pathology studies confirmed *Diaporthe* species to be associated with diverse suites of diseases (Fig. 7) on a broad range of economically important agricultural crops (Udayanga *et al.* 2011). More than one *Diaporthe* species is frequently reported as causative agents of the same disease (Thompson *et al.* 2011, Guarnaccia *et al.* 2016).

Although *Diaporthe* was historically considered monophyletic based on the typical phomopsis-like asexual morph, the paraphyletic nature of this genus was recently revealed (Gao *et al.* 2017, Senanayake *et al.* 2017). Most of the known species in early literature were described in relation to their host association and morphological characters. However, a single species of *Diaporthe* can be found on diverse hosts, and can co-occur on the same host or lesion in different life modes. Phylogenetic studies demonstrated that morphological characters are not always reliable for species level identification due to their variability under changing environmental conditions (Gomes *et al.* 2013). As a consequence, identification and description of species based on host association alone is no longer tenable. For accurate species delimitation, phylogenetic inference of the ITS, *cal*, *his3*, *tef1* and *tub2* or combinations of these is required.

References: Mostert *et al.* 2001, Van Niekerk *et al.* 2005, Thompson *et al.* 2011, Guarnaccia *et al.* 2016, 2018 (morphology, pathogenicity and phylogeny); Udayanga *et al.* 2011, 2014a, 2015, Gomes *et al.* 2013 (morphology and phylogeny); Dissanayake *et al.* 2017b, c, Gao *et al.* 2017 (phylogeny).

Diaporthe heterophyllae Guarnaccia & Crous, **sp. nov.** MycoBank MB823830. Fig. 10.

Etymology: Name refers to *Acacia heterophylla*, the host from which this fungus was collected.

On PNA: *Conidiomata* 250–350 µm diam, pycnidial, globose or irregular, solitary, deeply embedded in media, erumpent, dark brown to black, whitish translucent to yellow conidial drops and/or cirrus exuded from ostioles; *conidiomatal wall* consisting of 3–4 layers of medium brown *textura angularis*. *Conidiophores* 7–22 × 1.5–4 µm, hyaline, smooth, 0–1-septate, densely aggregated, cylindrical, straight. *Conidiogenous cells* 6–9 × 1–2 µm, phialidic, hyaline, terminal, cylindrical, tapered towards apex. *Paraphyses* not observed. *Alpha conidia* 6–10.5 × 2.5–4.5 µm, mean ± SD = 8.4 ± 1.1 × 3.2 ± 0.4 µm, L/W ratio = 2.6, aseptate, ovate to ellipsoidal, hyaline, multi-guttulate and acute or rounded at both ends. *Beta conidia* 17–24 × 1–2 µm, mean ± SD = 21.7 ± 1.8 × 1.5 ± 0.3 µm, L/W ratio = 14.5, hyaline, aseptate, eguttulate, filiform, curved, tapering towards both ends. *Gamma conidia* not observed.

Culture characteristics: Colonies covering medium within 10 d at 21 °C, with surface mycelium flattened, dense and felty. Colony on MEA, PDA and OA at first white, becoming cream to yellowish, flat on MEA and OA, dense, felted on PDA; reverse grey with brownish dots with age, with visible solitary conidiomata at maturity on all media.

Material examined: **France**, La Rèunion, on *Acacia heterophylla* (*Fabaceae*), 8 Mar. 2015, P.W. Crous (**holotype** CBS H-23376, culture ex-type CBS 143769 = CPC 26215).

Notes: *Diaporthe heterophyllae* is phylogenetically close but clearly differentiated from *D. eres* based on ITS, *tef1*, *tub2*, *his3* and *cal* sequence similarity (98 %, 88 %, 97 %, 95 %, and 97 %, respectively). Morphologically, *D. heterophyllae* differs from *D. eres* in its

Fig. 8. *Diaporthe* spp. **A–D.** Sexual morph. **A, B.** Ascomata. **A.** *Diaporthe ambigua* (ex-type CBS 114015). **B.** *Diaporthe aspalathi* (ex-type CBS 117169). **C, D.** Asci with ascospores. **C.** *Diaporthe ambigua* (ex-type CBS 114015). **D.** *Diaporthe aspalathi* (ex-type CBS 117169). **E–M.** Asexual morph. **E, F.** Conidiomata sporulating. **E.** *Diaporthe limonicola* (ex-type CBS 142549). **F.** *Diaporthe pseudomangiferae* (ex-type CBS 101339). **G–I.** Conidiogenous cells and conidia. **G.** *Diaporthe raonikayaporum* (ex-type CBS 133182). **H.** *Diaporthe tecomae* (CBS 100547). **I.** *Diaporthe limonicola* (ex-type CBS 142549). **J, K.** Alpha conidia. **J.** *Diaporthe cinerascens* (CBS 719.96). **K.** *Diaporthe pseudomangiferae* (ex-type CBS 101339). **L.** Beta conidia of *Diaporthe eleagni* (CBS 504.72). **M.** Alpha, beta and gamma conidia of *Diaporthe limonicola* (ex-type CBS 142549). Scale bars = 10 µm. Pictures A–D taken from Van Rensburg *et al.* (2006); F–H, J–L from Gomes *et al.* (2013); E, I, M from Guarnaccia & Crous (2017).

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

Species	**Isolates**[1]	**GenBank accession numbers**[2]					**References**
		ITS	***tub2***	***his3***	***tef1***	***cal***	
Diaporthe acaciarum	CBS 138862^{T}	KP004460	KP004509	KP004504	–	–	Crous *et al.* (2014b)
D. acaciigena	CBS 129521^{T}	KC343005	KC343973	KC343489	KC343731	KC343247	Gomes *et al.* (2013)
D. acericola	MFLUCC 17-0956^{T}	KY964224	KY964074	–	KY964180	KY964137	Dissanayake *et al.* (2017a)
D. acerina	CBS 137.27	KC343006	KC343974	KC343490	KC343732	KC343248	Gomes *et al.* (2013)
D. acutispora	CGMCC 3.18285^{T}	KX986764	KX999195	KX999235	KX999155	KX999274	Gao *et al.* (2017)
D. alleghaniensis	CBS 495.72^{T}	FJ889444	KC843228	KC343491	GQ250298	KC343249	Gomes *et al.* (2013)
D. alnea	CBS 146.46^{T}	KC343008	KC343976	KC343492	KC343734	KC343250	Gomes *et al.* (2013)
D. ambigua	CBS 114015^{T}	KC343010	KC343978	KC343494	KC343736	KC343252	Gomes *et al.* (2013)
D. ampelina	CBS 114016^{T}	AF230751	JX275452	–	GQ250351	JX197443	Gomes *et al.* (2013)
D. amygdali	CBS 126679^{T}	KC343022	KC343990	KC343506	KC343748	KC343264	Gomes *et al.* (2013)
D. anacardii	CBS 720.97^{T}	KC343024	KC343992	KC343508	KC343750	KC343266	Gomes *et al.* (2013)
D. angelicae	CBS 111592^{T}	KC343026	KC343994	KC343511	KC343752	KC343268	Gomes *et al.* (2013)
D. apiculatum	LC 3418^{T}	KP267896	KP293476	KP293550	KP267970	–	Gao *et al.* (2016)
D. aquatica	IFRDCC 3051^{T}	JQ797437	–	–	–	–	Hu *et al.* (2012)
D. arctii	CBS 136.25	KC343031	KC343999	KC343515	KC343757	KC343273	Gomes *et al.* (2013)
D. arecae	CBS 161.64^{T}	KC343032	KC344000	KC343516	KC343758	KC343274	Gomes *et al.* (2013)
D. arengae	CBS 114979^{T}	KC343034	KC344002	KC343518	KC343760	KC343276	Gomes *et al.* (2013)
D. aseana	MFLUCC 12-0299a^{T}	KT459414	KT459432	–	KT459448	KT459464	Hyde *et al.* (2016)
D. asheicola	CBS 136967^{T}	KJ160562	KJ160518	–	KJ160594	KJ160542	Lombard *et al.* (2014)
D. aspalathi	CBS 117169^{T}	KC343036	KC344004	KC343520	KC343762	KC343278	Van Rensburg *et al.* (2006)
D. australafricana	CBS 111886^{T}	KC343038	KC344006	KC343522	KC343764	KC343280	Gomes *et al.* (2013)
D. baccae	CBS 136972^{T}	KJ160565	MF418509	MF418264	KJ160597	–	Lombard *et al.* (2014)
D. batatas	CBS 122.21	KC343040	KC344008	KC343524	KC343766	KC343282	Gomes *et al.* (2013)
D. beckhausii	CBS 138.27	KC343041	KC344009	KC343525	KC343767	KC343283	Gomes *et al.* (2013)
D. beilharziae	BRIP 54792^{T}	JX862529	KF170921	–	JX862535	–	Thompson *et al.* (2015)
D. benedicti	CFCC 50062^{T}	KP208847	KP208855	KP208851	KP208853	KP208849	Fan *et al.* (2015)
D. betulae	CFCC 50469^{T}	KT732950	KT733020	KT732999	KT733016	KT732997	Du *et al.* (2016)
D. betulicola	CFCC 51128^{T}	KX024653	KX024657	KX024661	KX024655	KX024659	Du *et al.* (2016)
D. bicincta	CBS 121004^{T}	KC343134	KC344102	KC343618	KC343860	KC343376	Gomes *et al.* (2013)
D. biconispora	CGMCC 3.17252^{T}	KJ490597	KJ490418	KJ490539	KJ490476	–	Huang *et al.* (2015)
D. biguttulata	ICMP20657^{T}	KJ490582	KJ490403	KJ490524	KJ490461	–	Huang *et al.* (2015)
D. biguttusis	CGMCC 3.17081^{T}	KF576282	KF576306	–	KF576257	–	Gao *et al.* (2015)
D. bohemiae	CBS 143347^{T}	MG281015	MG281188	MG281361	MG281536	MG281710	Guarnaccia *et al.* (2018)
D. brasiliensis	CBS 133183^{T}	KC343042	KC344010	KC343526	KC343768	KC343284	Gomes *et al.* (2013)
D. caatingaensis	CBS 141542^{T}	KY085927	KY115600	KY115605	KY115603	KY115597	Crous *et al.* (2016a)
D. camptothecicola	CFCC 51632^{T}	KY203726	KY228893	KY228881	KY228887	KY228877	Yang *et al.* (2017c)
D. canthii	CBS 132533^{T}	JX069864	KC843230	–	KC843120	KC843174	Crous *et al.* (2012b)
D. carpini	CBS 114437	KC343044	KC344012	KC343528	KC343770	KC343286	Gomes *et al.* (2013)
D. cassines	CBS 136440^{T}	KF777155	–	–	KF777244	–	Crous *et al.* (2013)
D. caulivora	CBS 127268^{T}	KC343045	KC344013	KC343529	KC343771	KC343287	Gomes *et al.* (2013)
D. celastrina	CBS 139.27^{T}	KC343047	KC344015	KC343531	KC343773	KC343289	Gomes *et al.* (2013)
D. celeris	CBS 143349^{T}	MG281017	MG281190	MG281363	MG281538	MG281712	Guarnaccia *et al.* (2018)
D. ceratozamiae	CBS 131306^{T}	JQ044420	–	–	–	–	Crous *et al.* (2011b)
D. cf. *heveae* 1	CBS 852.97	KC343116	KC344084	KC343600	KC343842	KC343358	Gomes *et al.* (2013)
D. cf. *heveae* 2	CBS 681.84	KC343117	KC344085	KC343601	KC343843	KC343359	Gomes *et al.* (2013)
D. chamaeropis	CBS 454.81	KC343048	KC344016	KC343532	KC343774	KC343290	Gomes *et al.* (2013)
D. charlesworthii	BRIP 54884m^{T}	KJ197288	KJ197268	–	KJ197250	–	Thompson *et al.* (2015)
D. cichorii	MFLUCC 17-1023^{T}	KY964220	KY964104	–	KY964176	KY964133	Dissanayake *et al.* (2017a)
D. cinerascens	CBS 719.96	KC343050	KC344018	KC343534	KC343776	KC343292	Gomes *et al.* (2013)

Table 4. (Continued).

Species	Isolates[1]	GenBank accession numbers[2]					References
		ITS	*tub2*	*his3*	*tef1*	*cal*	
D. cissampeli	CBS 141331^T	KX228273	KX228384	KX228366	–	–	Crous *et al.* (2016b)
D. citri	CBS 135422^T	KC843311	KC843187	MF418281	KC843071	KC843157	Udayanga *et al.* (2014b)
D. citriasiana	CBS 134240^T	JQ954645	KC357459	MF418282	JQ954663	KC357491	Huang *et al.* (2013)
D. citrichinensis	CBS 134242^T	JQ954648	MF418524	KJ420880	JQ954666	KC357494	Huang *et al.* (2013)
D. compacta	LC3083^T	KP267854	KP293434	KP293508	KP267928	–	Gao *et al.* (2016)
D. convolvuli	CBS 124654	KC343054	KC344022	KC343538	KC343780	KC343296	Gomes *et al.* (2013)
D. crataegi	CBS 114435	KC343055	KC344023	KC343539	KC343781	KC343297	Gomes *et al.* (2013)
D. crotalariae	CBS 162.33^T	KC343056	KC344024	KC343540	KC343782	KC343298	Gomes *et al.* (2013)
D. cucurbitae	DAOM 42078^T	KM453210	KP118848	KM453212	KM453211	–	Udayanga *et al.* (2015)
D. cuppatea	CBS 117499^T	AY339322	JX275420	KC343541	AY339354	JX197414	Van Rensburg *et al.* (2006)
D. cynaroidis	CBS 122676	KC343058	KC344026	KC343542	KC343784	KC343300	Gomes *et al.* (2013)
D. cytosporella	CBS 137020^T	KC843307	KC843221	*MF418283*	KC843116	KC843141	Udayanga *et al.* (2014b)
D. decedens	CBS 109772	KC343059	KC344027	KC343543	KC343785	KC343301	Gomes *et al.* (2013)
D. detrusa	CBS 109770	KC343061	KC344029	KC343545	KC343787	KC343303	Gomes *et al.* (2013)
D. diospyricola	CBS 136552^T	KF777156	–	–	–	–	Crous *et al.* (2013)
D. discoidispora	ICMP20662^T	KJ490624	KJ490445	KJ490566	KJ490503	–	Huang *et al.* (2015)
D. dorycnii	MFLUCC 17-1015^T	KY964215	KY964099	–	KY964171	–	Dissanayake *et al.* (2017a)
D. elaeagni-glabrae	CGMCC 3.18287^T	KX986779	KX999212	KX999251	KX999171	KX999281	Gao *et al.* (2017)
D. eleagni	CBS 504.72	KC343064	KC344032	KC343548	KC343790	KC343306	Gomes *et al.* (2013)
D. ellipicola	CGMCC 3.17084^T	KF576270	KF576291	–	KF576245	–	Gao *et al.* (2015)
D. endophytica	CBS 133811^T	KC343065	KC344033	KC343549	KC343791	KC343307	Gomes *et al.* (2013)
D. eres	CBS 138594^T	KJ210529	KJ420799	KJ420850	KJ210550	KJ434999	Udayanga *et al.* (2014a)
D. eucalyptorum	CBS 132525^T	JX069862	–	–	–	–	Crous *et al.* (2012b)
D. eugeniae	CBS 444.82	KC343098	KC344066	KC343582	KC343824	KC343340	Gomes *et al.* (2013)
D. fibrosa	CBS 109751	KC343099	KC344067	KC343583	KC343825	KC343341	Gomes *et al.* (2013)
D. foeniculina	CBS 111553^T	KC343101	KC344069	KC343585	KC343827	KC343343	Gomes *et al.* (2013)
D. fraxini-angustifoliae	BRIP 54781^T	JX862528	KF170920	–	JX852534	–	Tan *et al.* (2013)
D. fusicola	CGMCC 3.17087^T	KF576281	KF576305	–	KF576256	KF576233	Gao *et al.* (2015)
D. ganjae	CBS 180.91^T	KC343112	KC344080	KC343596	KC343838	KC343354	Gomes *et al.* (2013)
D. gardeniae	CBS 288.56	KC343113	KC344081	KC343597	KC343839	KC343355	Gomes *et al.* (2013)
D. garethjonesii	MFLUCC 12-0542a^T	KT459423	KT459441	–	KT459457	KT459470	Hyde *et al.* (2016)
D. goulteri	BRIP 55657a^T	KJ197290	KJ197270	–	KJ197252	–	Thompson *et al.* (2015)
D. gulyae	BRIP 54025^T	JF431299	KJ197271	–	JN645803	–	Thompson *et al.* (2015)
D. helianthi	CBS 592.81^T	KC343115	KC344083	KC343599	KC343841	JX197454	Gomes *et al.* (2013)
D. helicis	CBS 138596^T	KJ210538	KJ420828	KJ420875	KJ210559	KJ435043	Udayanga *et al.* (2014a)
D. heterophyllae	CBS 143769^T	MG600222	MG600226	MG600220	MG600224	MG600218	Present study
D. hickoriae	CBS 145.26^T	KC343118	KC344086	KC343602	KC343844	KC343360	Gomes *et al.* (2013)
D. hispaniae	CBS 143351^T	MG281123	MG281296	MG281471	MG281644	MG281820	Guarnaccia *et al.* (2018)
D. hongkongensis	CBS 115448^T	KC343119	KC344087	KC343603	KC343845	KC343361	Gomes *et al.* (2013)
D. hordei	CBS 481.92	KC343120	KC344088	KC343604	KC343846	KC343362	Gomes *et al.* (2013)
D. hungariae	CBS 143353^T	MG281126	MG281299	MG281474	MG281647	MG281823	Guarnaccia *et al.* (2018)
D. impulsa	CBS 114434	KC343121	KC344089	KC343605	KC343847	KC343363	Gomes *et al.* (2013)
D. incompleta	CGMCC 3.18288^T	KX986794	KX999226	KX999265	KX999186	KX999289	Gao *et al.* (2017)
D. inconspicua	CBS 133813^T	KC343123	KC344091	KC343607	KC343849	KC343365	Gomes *et al.* (2013)
D. infecunda	CBS 133812^T	KC343126	KC344094	KC343610	KC343852	KC343368	Gomes *et al.* (2013)
D. infertilis	CBS 230.52^T	KC343052	KC344020	KC343536	KC343778	KC343294	Guarnaccia & Crous (2017)
D. isoberliniae	CBS 137981^T	KJ869133	KJ869245	–	–	–	Crous *et al.* (2014c)
D. juglandicola	CFCC 51134^T	KU985101	KX024634	–	KX024628	KX024616	Yang *et al.* (2017a)

(*continued on next page*)

Table 4. (Continued).

Species	**Isolates**[1]	**GenBank accession numbers**[2]					**References**
		ITS	***tub2***	***his3***	***tef1***	***cal***	
D. kochmanii	BRIP 54033^{T}	JF431295	–	–	JN645809	–	Thompson *et al.* (2011)
D. kongii	BRIP 54031^{T}	JF431301	KJ197272	–	JN645797	–	Thompson *et al.* (2011)
D. leucospermi	CBS 111980^{T}	JN712460	KY435673	KY435653	KY435632	KY435663	Crous *et al.* (2011c)
D. limonicola	CBS 142549^{T}	MF418422	MF418582	MF418342	MF418501	MF418256	Guarnaccia & Crous (2017)
D. litchicola	BRIP 54900^{T}	JX862533	KF170925	–	JX862539	–	Tan *et al.* (2013)
D. lithocarpus	CGMCC 3.15175^{T}	KC153104	KF576311	–	KC153095	–	Gao *et al.* (2014)
D. litoricola	MFLUCC 16-1195^{T}	MF190139	–	–	–	–	Senanayake *et al.* (2017)
D. longicicola	CGMCC 3.17089^{T}	KF576267	KF576291	–	KF576242	–	Gao *et al.* (2015)
D. longicolla	FAU 599^{T}	KJ590728	KJ610883	KJ659188	KJ590767	KJ612124	Udayanga *et al.* (2015)
D. longispora	CBS 194.36^{T}	KC343135	KC344103	KC343619	KC343861	KC343377	Gomes *et al.* (2013)
D. lonicerae	MFLUCC 17-0963^{T}	KY964190	KY964073	–	KY964146	KY964116	Dissanayake *et al.* (2017a)
D. lusitanicae	CBS 123212^{T}	KC343136	KC344104	KC343620	KC343862	KC343378	Gomes *et al.* (2013)
D. macintoshii	BRIP 55064a^{T}	KJ197289	KJ197269	–	KJ197251	–	Thompson *et al.* (2015)
D. mahothocarpus	CGMCC 3.15181	KC153096	–	–	KC153087	–	Gao *et al.* (2014)
D. malorum	CBS142383^{T}	KY435638	KY435668	KY435648	KY435627	KY435658	Santos *et al.* (2017)
D. manihotia	CBS 505.76	KC343138	KC344106	KC343622	KC343864	KC343380	Gomes *et al.* (2013)
D. maritima	DAOMC 250563^{T}	KU552025	KU574615	–	KU552023	–	Tanney *et al.* (2016)
D. masirevicii	BRIP 57892a^{T}	KJ197277	KJ197257	–	KJ197239	–	Thompson *et al.* (2015)
D. mayteni	CBS 133185^{T}	KC343139	KC344107	KC343623	KC343865	KC343381	Gomes *et al.* (2013)
D. maytenicola	CBS 136441^{T}	KF777157	KF777250	–	–	–	Crous *et al.* (2013)
D. megalospora	CBS 143.27	KC343140	KC344108	KC343624	KC343866	KC343382	Gomes *et al.* (2013)
D. melitensis	CBS 142551^{T}	MF418424	MF418584	MF418344	MF418503	MF418258	Guarnaccia & Crous (2017)
D. melonis	CBS 507.78^{T}	KC343142	KC344110	KC343626	KC343868	KC343384	Gomes *et al.* (2013)
D. middletonii	BRIP 54884e^{T}	KJ197286	KJ197266	–	KJ197248	–	Thompson *et al.* (2015)
D. miriciae	BRIP 54736j^{T}	KJ197283	KJ197263	–	KJ197245	–	Thompson *et al.* (2015)
D. momicola	MFLUCC 16-0113^{T}	KU557563	KU557587	–	KU557631	KU557611	Dissanayake *et al.* (2017c)
D. multigutullata	ICMP20656^{T}	KJ490633	KJ490454	KJ490575	KJ490512	–	Huang *et al.* (2015)
D. musigena	CBS 129519^{T}	KC343143	KC344111	KC343627	KC343869	KC343385	Gomes *et al.* (2013)
D. neilliae	CBS 144.27^{T}	KC343144	KC344112	KC343628	KC343870	KC343386	Gomes *et al.* (2013)
D. neoarctii	CBS 109490	KC343145	KC344113	KC343629	KC343871	KC343387	Gomes *et al.* (2013)
D. neoraonikayaporum	MFLUCC 14-1136^{T}	KU712449	KU743988	–	KU749369	KU749356	Doilom *et al.* (2017)
D. nomurai	CBS 157.29	KC343154	KC344122	KC343638	KC343880	KC343396	Gomes *et al.* (2013)
D. nothofagi	BRIP 54801^{T}	JX862530	KF170922	–	JX862536	–	Tan *et al.* (2013)
D. novem	CBS 127271^{T}	KC343157	KC344125	KC343641	KC343883	KC343399	Gomes *et al.* (2013)
D. obtusifoliae	CBS 143449^{T}	MG386072	–	MG386137	–	–	Crous *et al.* (2017b)
D. ocoteae	CBS 141330^{T}	KX228293	KX228388	–	–	–	Crous *et al.* (2016b)
D. oncostoma	CBS 589.78	KC343162	KC344130	KC343646	KC343888	KC343404	Gomes *et al.* (2013)
D. oraccinii	LC 3166^{T}	KP267863	KP293443	KP293517	KP267937	–	Gao *et al.* (2016)
D. ovalispora	ICMP20659^{T}	KJ490628	KJ490449	KJ490570	KJ490507	–	Huang *et al.* (2015)
D. ovoicicola	CGMCC 3.17092^{T}	KF576264	KF576288	–	KF576239	KF576222	Gao *et al.* (2015)
D. oxe	CBS 133186^{T}	KC343164	KC344132	KC343648	KC343890	KC343406	Gomes *et al.* (2013)
D. padi var. *padi*	CBS 114200	KC343169	KC344137	KC343653	KC343895	KC343411	Gomes *et al.* (2013)
D. paranensis	CBS 133184	KC343171	KC344139	KC343655	KC343897	KC343413	Gomes *et al.* (2013)
D. parapterocarpi	CBS 137986^{T}	KJ869138	KJ869248	–	–	–	Crous *et al.* (2014c)
D. pascoei	BRIP 54847^{T}	JX862532	KF170924	–	JX862538	–	Tan *et al.* (2013)
D. passiflorae	CBS 132527^{T}	JX069860	KY435674	KY435654	KY435633	KY435664	Crous *et al.* (2012b)
D. passifloricola	CBS 141329^{T}	KX228292	KX228387	KX228367	–	–	Crous *et al.* (2016b)
D. penetriteum	LC 3353	KP714505	KP714529	KP714493	KP714517	–	Gao *et al.* (2016)
D. perjuncta	CBS 109745^{T}	KC343172	KC344140	KC343656	KC343898	KC343414	Gomes *et al.* (2013)

Table 4. (Continued).

Species	**Isolates**[1]	**GenBank accession numbers**[2]					**References**
		ITS	***tub2***	***his3***	***tef1***	***cal***	
D. perniciosa	CBS 124030	KC343149	KC344117	KC343633	KC343875	KC343391	Gomes *et al.* (2013)
D. perseae	CBS 151.73	KC343173	KC344141	KC343657	KC343899	KC343415	Gomes *et al.* (2013)
D. pescicola	MFLUCC 16-0105^{T}	KU557555	KU557579	–	KU557623	KU557603	Dissanayake *et al.* (2017c)
D. phaseolorum	CBS 113425	KC343174	KC344142	KC343658	KC343900	KC343416	Gomes *et al.* (2013)
D. phragmitis	CBS 138897^{T}	KP004445	KP004507	KP004503	–	–	Crous *et al.* (2014b)
D. podocarpi-macrophylli	CGMCC3.18281^{T}	KX986774	KX999207	KX999246	KX999167	KX999278	Gao *et al.* (2017)
D. pseudomangiferae	CBS 101339^{T}	KC343181	KC344149	KC343665	KC343907	KC343423	Gomes *et al.* (2013)
D. pseudophoenicicola	CBS 462.69^{T}	KC343184	KC344152	KC343668	KC343910	KC343426	Gomes *et al.* (2013)
D. pseudotsugae	MFLU 15-3228	KY964225	KY964108	–	KY964181	KY964138	Dissanayake *et al.* (2017a)
D. psoraleae	CBS 136412^{T}	KF777158	KF777251	–	KF777245	–	Crous *et al.* (2013)
D. psoraleae-pinnatae	CBS 136413^{T}	KF777159	KF777252	–	–	–	Crous *et al.* (2013)
D. pterocarpi	MFLUCC 10-0571	JQ619899	JX275460	–	JX275416	JX197451	Udayanga *et al.* (2012)
D. pterocarpicola	MFLUCC 10-0580a	JQ619887	JX275441	–	JX275403	JX197433	Udayanga *et al.* (2012)
D. pulla	CBS 338.89^{T}	KC343152	KC344120	KC343636	KC343878	KC343394	Gomes *et al.* (2013)
D. pustulata	CBS 109742	KC343185	KC344153	KC343669	KC343911	KC343427	Gomes *et al.* (2013)
D. pyracanthae	CBS142384^{T}	KY435635	KY435666	KY435645	KY435625	KY435656	Santos *et al.* (2017)
D. racemosae	CBS 143770^{T}	MG600223	MG600227	MG600221	MG600225	MG600219	Present study
D. raonikayaporum	CBS 133182^{T}	KC343188	KC344156	KC343672	KC343914	KC343430	Gomes *et al.* (2013)
D. ravennica	MFLUCC 15-0479^{T}	KU900335	KX432254	–	KX365197	–	Dissanayake *et al.* (2017a)
D. rhoina	CBS 146.27	KC343189	KC344157	KC343673	KC343915	KC343431	Gomes *et al.* (2013)
D. rostrata	CFCC 50062^{T}	KP208847	KP208855	KP208851	KP208853	KP208849	Fan *et al.* (2015)
D. rudis	CBS 113201	KC343234	KC344202	KC343718	KC343960	KC343476	Udayanga *et al.* (2014b)
D. saccarata	CBS 116311^{T}	KC343190	KC344158	KC343674	KC343916	KC343432	Gomes *et al.* (2013)
D. sackstonii	BRIP 54669b^{T}	KJ197287	KJ197267	–	KJ197249	–	Thompson *et al.* (2015)
D. salicicola	BRIP 54825^{T}	JX862531	KF170923	–	JX862537	–	Tan *et al.* (2013)
D. sambucusii	CFCC 51986^{T}	KY852495	KY852511	KY852503	KY852507	KY852499	Yang *et al.* (2018)
D. schini	CBS 133181^{T}	KC343191	KC344159	KC343675	KC343917	KC343433	Gomes *et al.* (2013)
D. schisandrae	CFCC 51988^{T}	KY852497	KY852513	KY852505	KY852509	KY852501	Yang *et al.* (2018)
D. schoeni	MFLU 15-1279^{T}	KY964226	KY964109	–	KY964182	KY964139	Dissanayake *et al.* (2017a)
D. sclerotioides	CBS 296.67^{T}	KC343193	KC344161	KC343677	KC343919	KC343435	Gomes *et al.* (2013)
D. scobina	CBS 251.38	KC343195	KC344163	KC343679	KC343921	KC343437	Gomes *et al.* (2013)
D. sennae	CFCC 51636^{T}	KY203724	KY228891	–	KY228885	KY228875	Yang *et al.* (2017b)
D. sennicola	CFCC 51634^{T}	KY203722	KY228889	–	KY228883	KY228873	Yang *et al.* (2017b)
D. serafiniae	BRIP 55665a^{T}	KJ197274	KJ197254	–	KJ197236	–	Thompson *et al.* (2015)
D. siamensis	MFLUCC 10-0573a	JQ619879	JX275429	–	JX275393	–	Udayanga *et al.* (2012)
D. sojae	CBS 139282^{T}	KJ590719	KJ610875	KJ659208	KJ590762	KJ612116	Udayanga *et al.* (2015)
D. spartinicola	CBS 140003^{T}	KR611879	KR857695	KR857696	–	–	Crous *et al.* (2015c)
D. sterilis	CBS 136969^{T}	KJ160579	KJ160528	MF418350	KJ160611	KJ160548	Lombard *et al.* (2014)
D. stewartii	CBS 193.36	FJ889448	–	–	GQ250324	–	Santos *et al.* (2010)
D. sticticа	CBS 370.54	KC343212	KC344180	KC343696	KC343938	KC343454	Gomes *et al.* (2013)
D. subclavata	ICMP20663^{T}	KJ490630	KJ490451	KJ490572	KJ490509	–	Huang *et al.* (2015)
D. subordinaria	CBS 101711	KC343213	KC344181	KC343697	KC343939	KC343455	Gomes *et al.* (2013)
D. taoicola	MFLUCC 16-0117^{T}	KU557567	KU557591	–	KU557635	–	Dissanayake *et al.* (2017c)
D. tecomae	CBS 100547	KC343215	KC344183	KC343699	KC343941	KC343457	Gomes *et al.* (2013)
D. tectonae	MFLUCC 12-0777^{T}	KU712430	KU743977	–	KU749359	KU749345	Doilom *et al.* (2017)
D. tectonendophytica	MFLUCC 13-0471^{T}	KU712439	KU743986	–	KU749367	KU749354	Doilom *et al.* (2017)
D. tectonigena	MFLUCC 12-0767^{T}	KU712429	KU743976	–	KU749371	KU749358	Doilom *et al.* (2017)
D. terebinthifolii	CBS 133180^{T}	KC343216	KC344184	KC343700	KC343942	KC343458	Gomes *et al.* (2013)

(*continued on next page*)

Table 4. (Continued).

Species	Isolates[1]	GenBank accession numbers[2]					References
		ITS	*tub2*	*his3*	*tef1*	*cal*	
D. ternstroemia	CGMCC 3.15183^T	KC153098	–	–	KC153089	–	Gao *et al.* (2014)
D. thunbergii	MFLUCC 10-0756a	JQ619893	JX275449	–	JX275409	JX197440	Udayanga *et al.* (2012)
D. torilicola	MFLUCC 17-1051^T	KY964212	KY964096	–	KY964168	KY964127	Dissanayake *et al.* (2017a)
D. toxica	CBS 534.93^T	KC343220	KC344188	KC343704	KC343946	KC343462	Gomes *et al.* (2013)
D. toxicodendri	FFPRI420987	LC275192	LC275224	LC275216	LC275216	LC275200	Ando *et al.* (2017)
D. tulliensis	BRIP 62248a	KR936130	KR936132	–	KR936133	–	Crous *et al.* (2015e)
D. ueckerae	FAU 656	KJ590726	KJ610881	KJ659215	KJ590747	KJ612122	Huang *et al.* (2015)
D. undulata	CGMCC 3.18293^T	KX986798	KX999230	KX999269	KX999190	–	Gao *et al.* (2017)
D. unshiuensis	CGMCC3.17569^T	KJ490587	KJ490408	KJ490529	KJ490466	–	Huang *et al.* (2015)
D. vaccinii	CBS 160.32^T	AF317578	KC344196	KC343712	GQ250326	KC343470	Gomes *et al.* (2013)
D. vangueriae	CBS 137985^T	KJ869137	KJ869247	–	–	–	Crous *et al.* (2014c)
D. vawdreyi	BRIP 57887a	KR936126	KR936128		KR936129	–	Crous *et al.* (2015e)
D. velutina	CGMCC 3.18286^T	KX986790	KX999223	KX999261	KX999182	–	Gao *et al.* (2017)
D. vexans	CBS 127.14	KC343229	KC344197	KC343713	KC343955	KC343471	Gomes *et al.* (2013)
D. virgiliae	CBS 138788^T	KP247573	KP247582	–	–	–	Machingambi *et al.* (2015)
D. woodii	CBS 558.93	KC343244	KC344212	KC343728	KC343970	KC343486	Gomes *et al.* (2013)
D. woolworthii	CBS 148.27	KC343245	KC344213	KC343729	KC343971	KC343487	Gomes *et al.* (2013)
D. xishuangbanica	CGMCC 3.18282^T	KX986783	KX999216	KX999255	KX999175	–	Gao *et al.* (2017)
D. yunnanensis	CGMCC 3.18289^T	KX986796	KX999228	KX999267	KX999188	KX999290	Gao *et al.* (2017)

[1] BRIP: Queensland Plant Pathology Herbarium, Brisbane, Australia; CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CFCC: China Forestry Culture Collection Center, Beijing, China; CGMCC: Chinese General Microbiological Culture Collection Center, Beijing, China; DAOM: Plant Research Institute, Department of Agriculture (Mycology), Ottawa, Canada; DAOMC: Canadian Collection of Fungal Cultures, Ottawa, Canada; FAU: Isolates in culture collection of Systematic Mycology and Microbiology Laboratory; FFPRI: Forestry and Forest Products Research Institute, Japan; ICMP: International Collection of Micro-organisms from Plants, Landcare Research, Private Bag 92170, Auckland, New Zealand; IFRDCC: International Fungal Research and Development Culture Collection; MFLU: Mae Fah Luang University herbarium, Thailand; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Rai, Thailand; LC: Working collection of Lei Cai, housed at Institute of Microbiology, Chinese Academy of Sciences, Beijing, China. ^{T} indicates ex-type strains.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *tub2*: partial β-tubulin gene; *his3*: partial histone H3 gene; *tef1*: partial elongation factor 1-alpha gene; *cal*: partial calmodulin gene.

longer alpha conidia (6.5–10.5 *vs.* 6–8.5 μm) and in its shorter beta conidia (17–24 *vs.* 22–28 μm) (Udayanga *et al.* 2014a).

Diaporthe racemosae A.R. Wood, Guarnaccia & Crous, **sp. nov.** MycoBank MB823831. Fig. 11.

Etymology: Name refers to *Euclea racemosa*, the host from which this fungus was collected.

On PNA: *Conidiomata* 350–600 μm diam, pycnidial, globose or irregular, solitary, deeply embedded in media, erumpent, dark brown to black, yellowish translucent to pale brown conidial drops and/or cirrus exuded from ostioles; *conidiomatal wall* consisting of 3–4 layers of pale brown *textura angularis*. *Conidiophores* 7–17 × 2–4 μm, hyaline, smooth, 0–1-septate, densely aggregated, cylindrical, straight. *Conidiogenous cells* 5.5–8 × 1–2 μm, phialidic, hyaline, terminal, subcylindrical, tapered towards apex. *Paraphyses* not observed. *Alpha conidia* 4–6.5 × 2–3 μm, mean ± SD = 5.7 ± 0.6 × 2.3 ± 0.3 μm, L/W ratio = 2.5, aseptate, ellipsoidal to subcylindrical, hyaline, non- to multi-guttulate and acute or rounded at both ends. *Beta* and *gamma conidia* not observed.

Culture characteristics: Colonies covering medium within 10 d at 21 °C, with surface mycelium flattened, dense and felty. Colony on MEA and OA at first white, becoming olivaceous to dark grey. On PDA at first white, becoming white to yellowish; reverse grey with brownish dots with age, with visible solitary conidiomata at maturity on all media.

Material examined: **South Africa**, Western Cape, Bot River, from *Euclea racemosa* (*Ebenaceae*), 29 Dec. 2014, A.R. Wood (**holotype** CBS H-23377, culture ex-type CBS 143770 = CPC 26646).

Notes: *Diaporthe racemosae* is phylogenetically close but clearly differentiated from *D. schini* based on ITS, *tef1*, *tub2*, *his3* and *cal* sequence similarity (98 %, 94 %, 98 %, 94 %, and 96 %, respectively). Moreover, *D. racemosa* produces only alpha conidia, while *D. schini* produces only beta conidia (Gomes *et al.* 2013).

Authors: V. Guarnaccia, A.R. Wood & P.W. Crous

Dichotomophthora Mehrl. & Fitzp. ex M.B. Ellis, Dematiaceous Hyphomycetes (Kew): 388. 1971. Fig. 12.
Synonyms: Dichotomophthora Mehrl. & Fitzp., Mycologia 27: 550. 1935. (nom. inval., Art. 39.1, Melbourne).
Dichotomophthora Mehrl. & Fitzp. ex P.N. Rao, Mycopath. Mycol. appl. 28: 139. 1966. (nom. inval., Art. 39.1, Melbourne).

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

Type species: *Dichotomophthora portulacae* Mehrl. & Fitzp. ex M.B. Ellis. Type specimen and ex-paratype strain: IMI 8742, CBS 174.35.

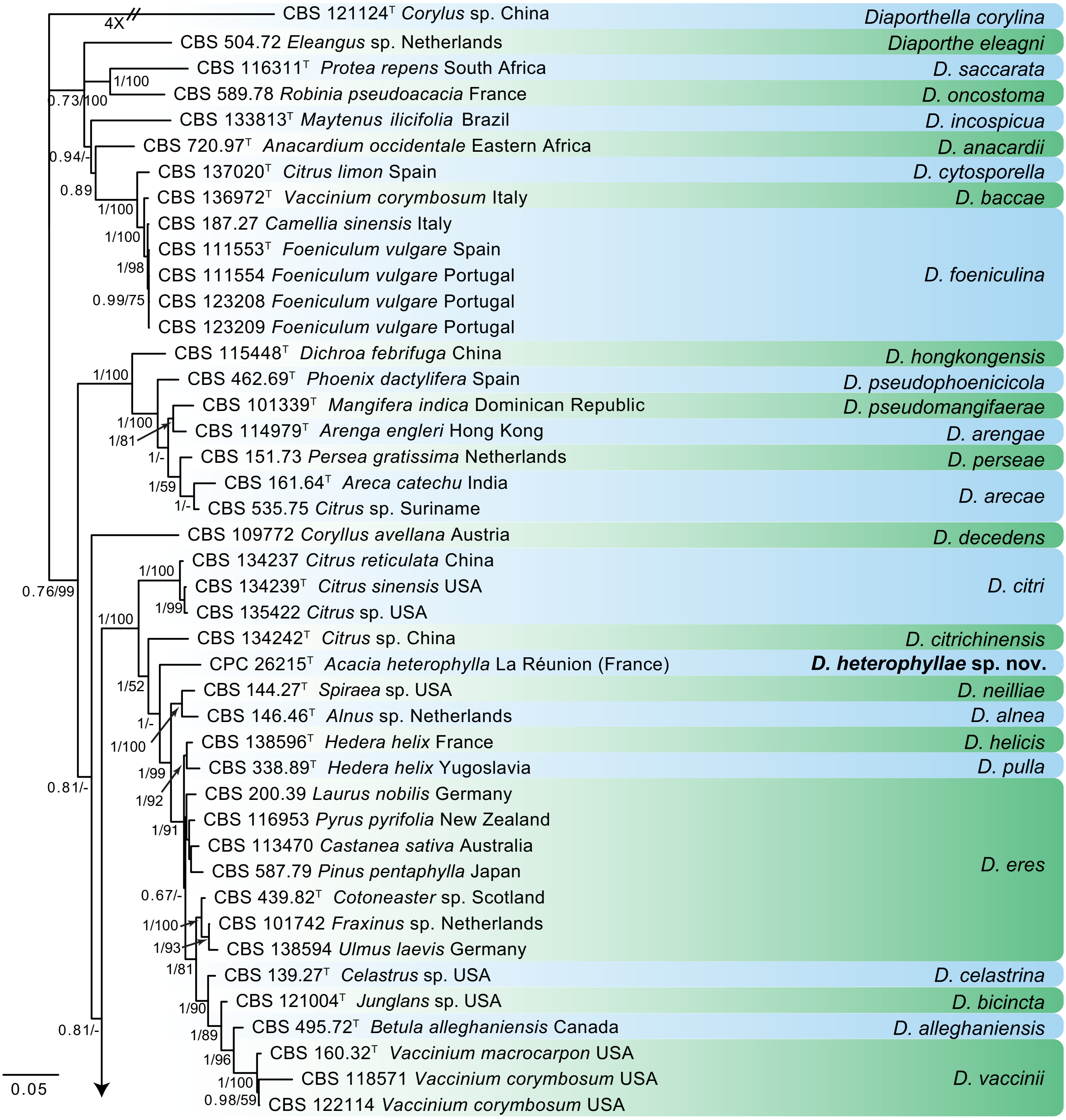

Fig. 9. Consensus phylogram of 2 052 trees resulting from a Bayesian analysis of the combined ITS (637 bp), *tub2* (833 bp), *his3* (592 bp), *tef1* (496 bp) and *cal* (817 bp) sequence alignment of *Diaporthe* spp. Bootstrap support values and Bayesian posterior probability values are indicated at the nodes. Substrate and country of origin are listed next to the strain numbers. The newly recognised species are showed in **bold**. The tree was rooted to *Diaporthella corylina* CBS 121124. ^{T} indicates ex-type strain. TreeBASE: S21865.

DNA barcodes (genus): ITS.

DNA barcodes (species): ITS, *rpb2, gpdh*. Table 5. Fig. 13.

Conidiophores macronematous, mononematous, unbranched or irregularly branched, sometimes swollen and repeatedly dichotomously or trichotomously branched or lobed at apex, forming a stipe and head; *stipe* hyaline to brown; *branches* usually short. *Conidiogenous cells* mono- or polytretic, integrated, terminal, lobed, cicatrized. *Conidia* solitary, dry, simple, ellipsoidal to cylindrical, rounded at ends, subhyaline to brown, multi-distoseptate. *Microconidia* ovoid, 0–2-distoseptate. *Sclerotia* often formed in culture resembling immature perithecia, semi- or immersed in agar, subglobose, ellipsoidal, ovoid, dark brown or black. *Sexual morph* unknown (adapted from Ellis 1971).

Culture characteristics: Colonies on PDA and OA white, hazel, orange, or dark grey to olivaceous, cottony, velvety, somewhat fluffy, or flat, margin irregular, effuse; reverse centre hazel, dark brown, periphery hazel, orange to luteous. Diffusible pigment luteous to orange (produced in some strains).

Optimal media and cultivation conditions: On PDA and OA at 25 °C under near-ultraviolet light (12 h light, 12 h dark). Some strains are sterile in culture.

Distribution: Worldwide.

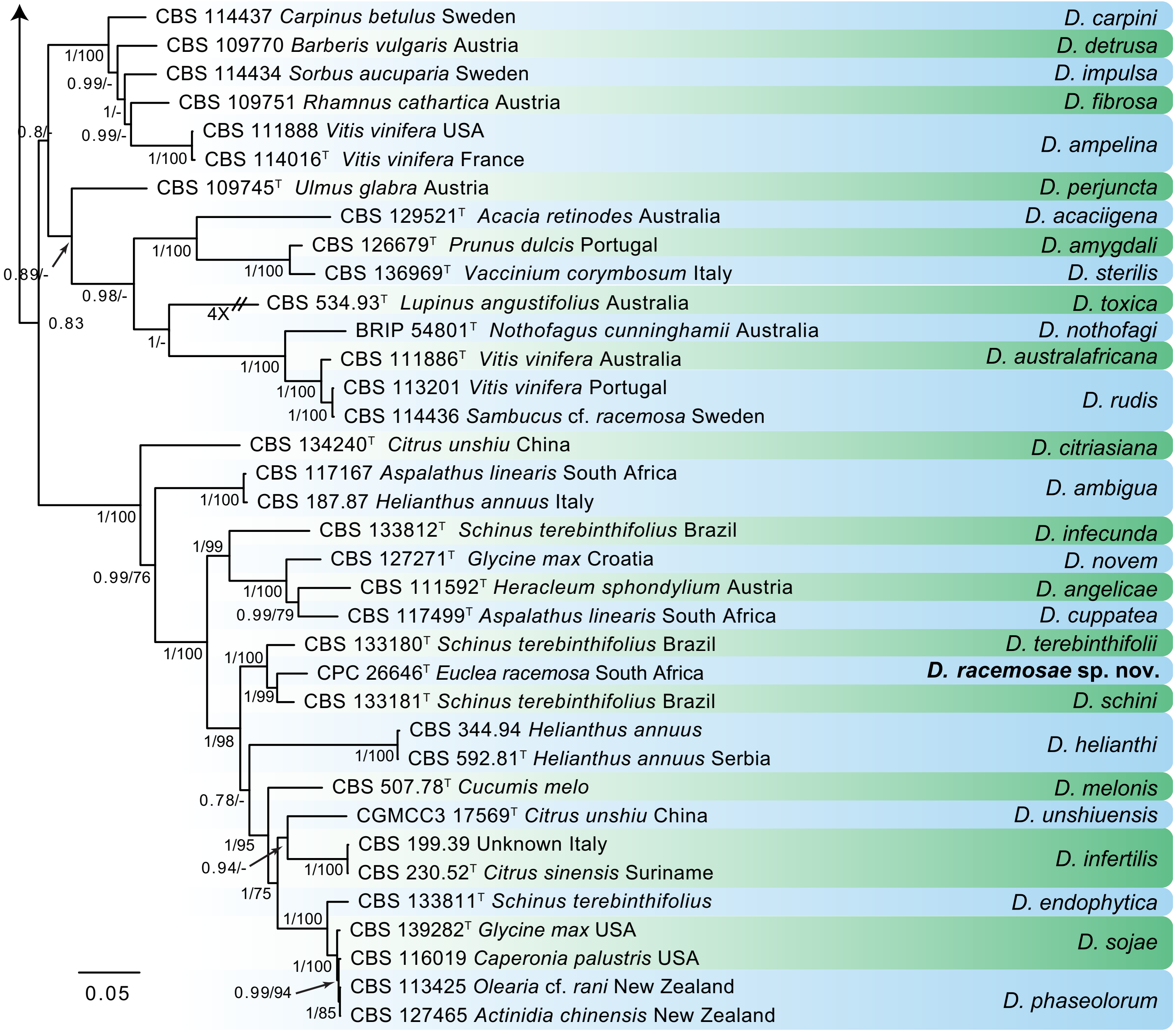

Fig. 9. (Continued).

Hosts: *Anredera* and *Basella* (*Basellaceae*), *Beta vulgaris* (*Chenopodiaceae*), *Gymnocalycium mihanovichii* var. *friedrichii* and *Myrtillocactus geometrizans* (*Cactaceae*), *Portulaca* (*Portulacaceae*), and soil.

Disease symptoms: Leaf spots, foliar abscission, stem blight, seed rot and damping-off.

Notes: *Dichotomophthora* was introduced as a monotypic genus with *Di. portulacae* isolated from *Portulaca oleracea* in Hawaii (Mehrlich & Fitzpatrick 1935). However, the publication lacked a Latin diagnosis of the fungus and the name was therefore invalid. Later, Rao (1966) provided a Latin description of *Di. portulacae* and introduced a new species, *Di. indica*, but the validation was misapplied and both names were regarded as invalid (de Hoog & van Oorschot 1983). Ellis (1971) validated the genus and the species based on the holotype specimen of *Di. portulacae* (IMI 8742). De Hoog & van Oorschot (1983) revised the taxonomy of *Dichotomophthora* and included *Di. portulacae* and *Di. lutea*. *Dichotomophthora portulacae* was restricted to species with dichotomously branched conidiophores, and conidia with 2–3 septa, 45–75 × 20–30 µm. *Dichotomophthora lutea* was introduced based on *Dactylaria lutea,* which is characterised by unbranched or irregularly branched conidiophores, and conidia with 1–5 septa, 30–115 × 10–20 µm.

Dichotomophthora species are mainly known as plant pathogens with a wide host range as well as soil-borne fungi or saprobes (Mehrlich & Fitzpatrick 1935, Routien 1957, Rao 1966, Ellis 1971, Klisiewicz 1985, Baudoin 1986, Pfeiffer *et al.* 1989, Eken 2003, Farr & Rossman 2017, Soares & Nechet 2017). However, a case of human keratitis caused by *Di. portulacae* was reported from subtropical Africa (de Hoog *et al.* 2000). Since many records of *Di. portulacae* may represent *Di. lutea* due to previous taxonomic confusion, host and distribution data need to be re-evaluated (de Hoog & van Oorschot 1983, Farr & Rossman 2017, Soares & Nechet 2017).

This is the first time that numerous isolates, including the ex-type strains of both species of *Dichotomophthora*, have been subjected to phylogenetic analyses. Our results suggest that *Dichotomophthora* belongs in the *Pleosporaceae* (*Pleosporales*), closely related to *Curvularia*. The phylogenetic analysis and subtle morphological evidence revealed two additional new species, introduced here as *Di. basellae* and *Di. brunnea*. For an

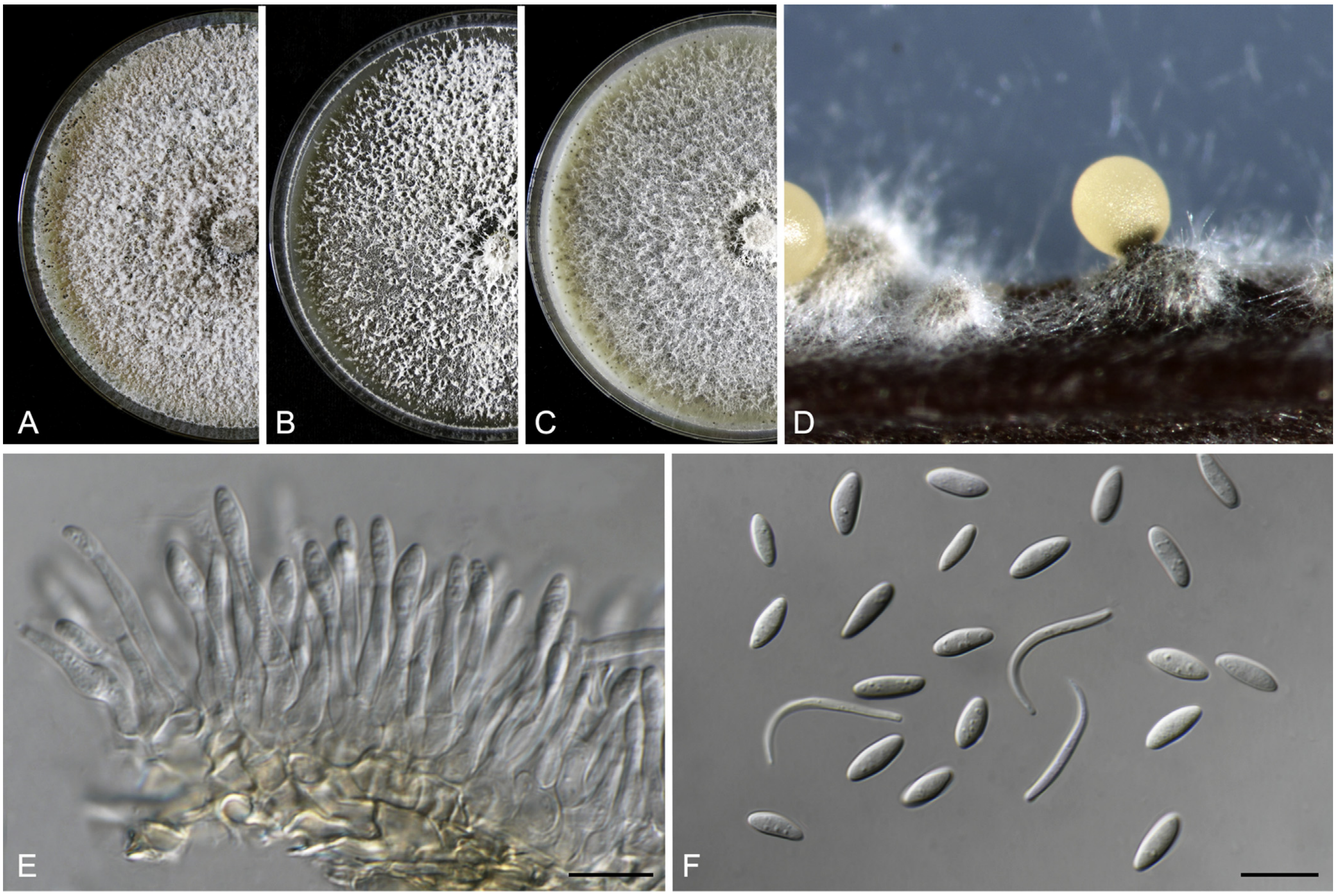

Fig. 10. *Diaporthe heterophyllae* (ex-type CBS 143769). **A–C.** Colonies on MEA, PDA and OA, respectively. **D.** Conidiomata sporulating on PNA. **E.** Conidiogenous cells and conidia. **F.** Alpha and beta conidia. Scale bars = 10 µm.

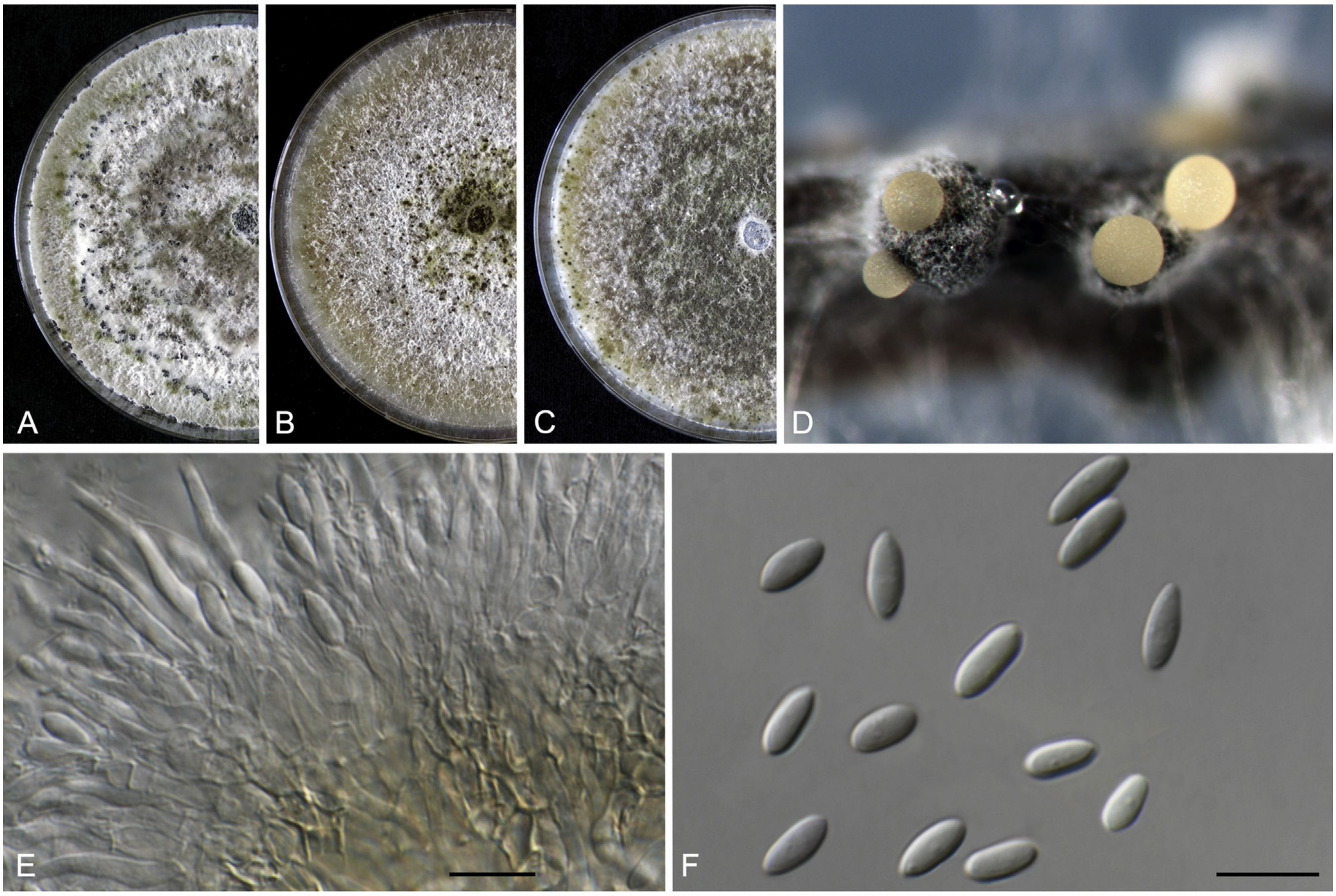

Fig. 11. *Diaporthe racemosae* (ex-type CBS 143770). **A–C.** Colonies on MEA, PDA and OA, respectively. **D.** Conidiomata sporulating on PNA. **E.** Conidiogenous cells and conidia. **F.** Alpha conidia. Scale bars = 10 µm.

Fig. 12. *Dichotomophthora lutea*. **A–E.** Colonies on PDA. **F–J.** Colonies on OA. **K.** Habit. **L–N.** Conidiophores and conidia. **O–Q.** Conidiogenous cells. **R, S.** Conidiogenous cells and conidia. **T, U.** Conidia and microconidia. **V–X.** Sclerotia. **Y.** Anastomosing conidia. (**A, F** = ex-type CBS 145.57; **B, G, K, O–T, V, Y** = CBS 584.71; **C, H** = CBS 585.71; **D, I, U** = CBS 132.81; **E, J, W, X** = CBS 518.78). Scale bars: V–X = 100 µm; L, P = 20 µm; others = 10 µm.

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

Species	Isolates[1]	GenBank accession numbers[2]			References
		ITS	*gapdh*	*rpb2*	
Dichotomophthora basellae	CPC 33016^{T}	LT990654	LT990670	LT990640	Present study
Di. brunnea	CBS 149.94^{T}	LT990653	LT990669	LT990639	Present study
Di. lutea	CBS 145.57^{T}	LT990647	LT990663	LT990634	Present study
	CBS 584.71	LT990648	LT990664	LT990635	Present study
	CBS 585.71	LT990649	LT990665	LT990636	Present study
	CBS 518.78	LT990650	LT990666	–	Present study
	CBS 132.81	LT990651	LT990667	LT990637	Present study
Di. portulacae	CBS 174.35^{PT}	LT990652	LT990668	LT990638	Present study

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

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *gapdh*: partial glyceraldehyde-3-phosphate dehydrogenase gene; *rpb2*: partial RNA polymerase II second largest subunit gene.

accurate identification at the species level, a DNA sequence analysis is recommended, since *Dichotomophthora* species are morphologically variable in culture and on natural substrates.

References: Mehrlich & Fitzpatrick 1935, Routien 1957, Rao 1966, Ellis 1971, de Hoog & van Oorschot 1983 (taxonomy and morphology); Klisiewicz 1985, Baudoin 1986, Pfeiffer *et al.* 1989, Eken 2003, Soares & Nechet 2017 (pathogenicity).

Dichotomophthora basellae Hern.-Restr., Cheew. & Crous, **sp. nov.** MycoBank MB824604. Fig. 14.

Etymology: Name reflects the substrate from which this fungus was isolated, *Basella alba*.

Hyphae 3–7.5 µm wide, hyaline to brown, septate, smooth to verruculose. *Conidiophores* macronematous, mononematous, unbranched or irregularly branched, sometimes swollen and repeatedly dichotomously or trichotomously branched or lobed at apex, forming a stipe and head; *stipe* 970–1370 × 10–12(–14) µm, pale brown, smooth; *branches* usually short; *head* 23–65 µm wide, pale brown to brown. *Conidiogenous cells* polytretic, integrated and terminal, lobed, cicatrized, individual lobes 6–14 × 6–9.5 µm. *Conidia* 32–86 × 10–18 µm, solitary, dry, ellipsoidal to cylindrical rounded at ends, subhyaline to yellow brown, 2–5-distoseptate. *Microconidia* 11–30 × 9–13(–15) µm, obovoid to ellipsoidal, 0–2-distoseptate. *Sclerotia* 295–444 × 234–409 µm, resembling immature perithecia, semi- or immersed in agar, globose, subglobose, ellipsoidal, ovoid, dark brown or black. *Sexual morph* unknown.

Culture characteristics: Colonies at 25 °C under near-ultraviolet light (12 h light, 12 h dark), on PDA and OA reaching 45–50 mm after 1 wk, centre black, periphery luteous, velvety, flat, margin regular, effuse; reverse centre olivaceous, dark brown, periphery pale luteous. Diffusible pigment luteous.

Material examined: **Thailand**, Chiang Mai, Chiang Mai university experimental farm, on leaves of *Basella alba* (*Basellaceae*), 2010, R. Cheewangkoon (**holotype** CBS H-23383, culture ex-type CPC 33016).

Notes: *Dichotomophthora basellae* is represented by one strain isolated from leaf spots on *Basella rubra* in Thailand. This species is morphologically similar to *Di. lutea* in having multi-lobed conidiogenous cells producing pale brown conidia, and colonies that produce a luteous to orange diffusible pigment in culture. In our study, *Di. basellae* produces larger conidia than *Di. lutea* (32–86 × 10–18 µm *vs*. 14–65.5 × 7.5–13 µm). However, de Hoog & van Oorschot (1983) described larger conidia in *Di. lutea* (30–115 × 10–20 µm). Additional studies with more isolates are thus required to compare these morphological differences and substrate preferences of both species.

Dichotomophthora brunnea Hern.-Restr. & Crous, **sp. nov.** MycoBank MB824605. Fig. 15.

Etymology: From the Latin *brunnea* meaning brown, because of the brown colour of the conidia.

Hyphae 2.5–7 µm wide, hyaline to dark brown, septate, slightly constricted at septa, smooth. *Conidiophores* macronematous, mononematous, repeatedly dichotomously or irregularly branched, lobed at apex, forming a stipe and head; *stipe* 42–536 × 4.5–7.5 µm, pale brown to brown, smooth; *branches* usually short; *head* 10–28 µm wide, brown to pale brown. *Conidiogenous cells* mono- or polytretic, integrated, terminal, lobed, cicatrized, individual lobes 6.5–17 × 4–9 µm. *Conidia* 29–56.5 × 6–10 µm, solitary, dry, ellipsoidal to cylindrical rounded at ends, brown to dark brown, 2–6(–8)-distoseptate, straight or slightly curved. *Microconidia* 13–19.5 × 7–9.5 µm, obovoid to ellipsoidal, 0–1-distoseptate. *Sclerotia* not observed. *Sexual morph* unknown.

Culture characteristics: Colonies on PDA and OA at 25 °C under near-ultraviolet light (12 h light, 12 h dark), after 1 wk, reaching 90 mm, dark olivaceous, velvety, margin irregular, rhizoid (PDA) or entire (OA); reverse black. Diffusible pigment not produced.

Material examined: **Unknown country**, unknown substrate, date and collector (**holotype** CBS H-23382, culture ex-type dep. A. Arambarri LPS 325 = CBS 149.94).

Notes: *Dichotomophthora brunnea* was previously maintained as *Di. portulacae* in the CBS collection. However, the phylogenetic analysis suggests that the strain CBS 149.94 is a distinct species. Morphologically, the new species differs from *Di. basellae* and *Di. lutea* in having dark brown conidia and conidiogenous cells with 1–3 lobes (*vs*. yellowish or pale brown conidia and conidiogenous cells with usually more than three lobes). Neither pigment nor sclerotia were observed on the media tested.

Dichotomophthora lutea (Routien) de Hoog & Oorschot, Proc. Kon. Ned. Akad. Wetensch., Sect. C 86: 56. 1983. Fig. 12.
Basionym: Dactylaria lutea Routien, Mycologia 49: 191. 1957.
Synonym: *Dichotomophthora indica* Rao, Mycopath. Mycol. Appl. 28: 139. 1966. (nom. inval., Art. 35.1, Melbourne).

Hyphae 3–7.5 µm wide, hyaline to brown, septate, smooth to verruculose. *Conidiophores* macronematous, mononematous,

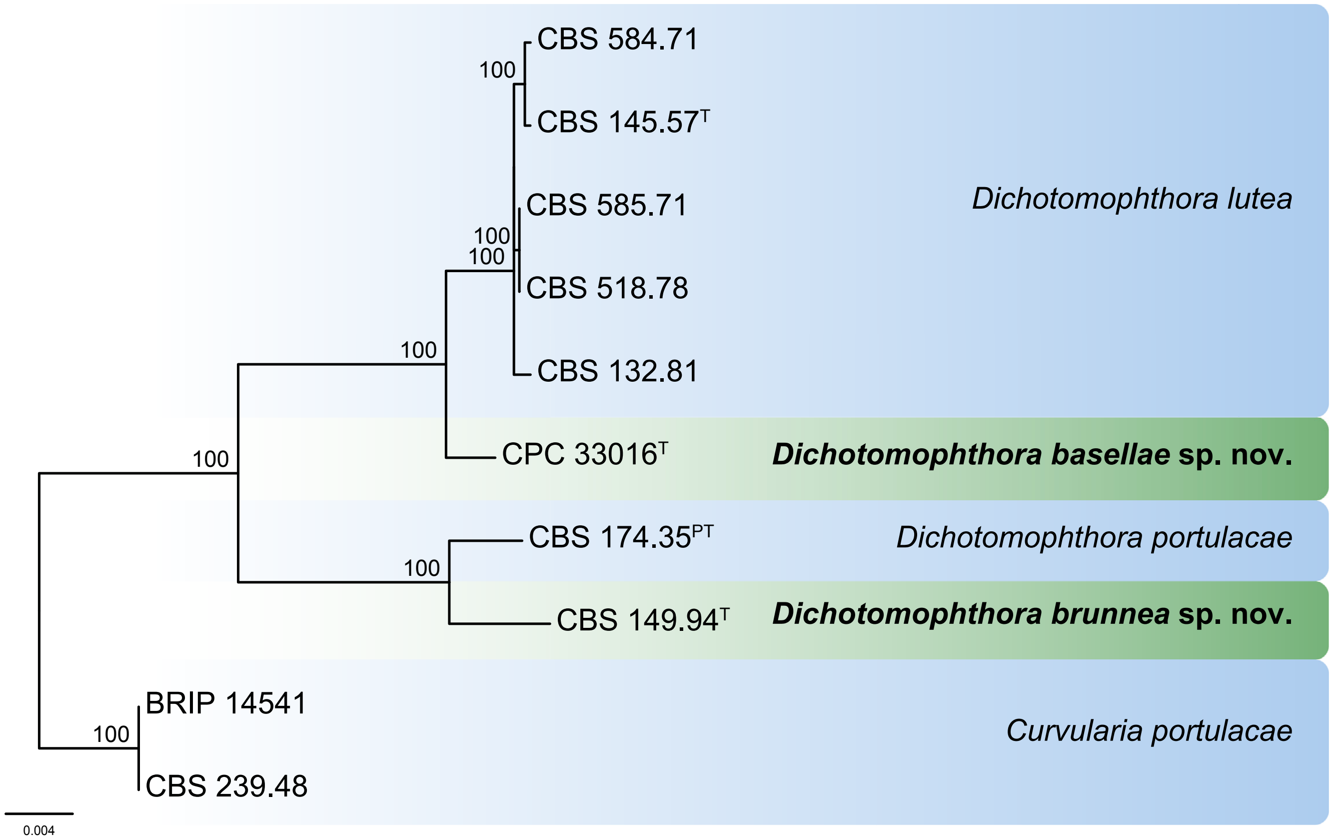

Fig. 13. RAxML phylogram obtained from the combined ITS (759 bp), LSU (880 bp), *gapdh* (594 bp) and *rpb2* (958 bp) sequence alignment of all the accepted species of *Dichotomophthora*. The tree was rooted to *Curvularia portulacae* CBS 239.48 and BRIP 14541. The novel species described in this study are shown in **bold**. RAxML bootstrap support (BS) values above 70 % are shown in the nodes. GenBank accession numbers are indicated in Table 5. ^{T} and ^{PT} indicate ex-type and ex-paratype strains, respectively. TreeBASE: S21899.

unbranched or irregularly branched, sometimes swollen and repeatedly dichotomously or trichotomously branched or lobed at apex, forming a stipe and head; *stipe* 7.5–10(–12) µm wide, hyaline to brown, smooth; *branches* usually short; *head* 16.5–62 µm wide, pale brown to brown. *Conidiogenous cells* polytretic, integrated and terminal, discrete, lobed, cicatrized, individual lobes 8–13 × 4–11 µm. *Conidia* 14–65.5 × 7.5–13 µm, solitary, dry, ellipsoidal to cylindrical rounded at ends, straight to slightly curved, subhyaline to yellow brown, 0–4-distoseptate, sometimes constricted at septa, sometimes anastomosing conidia observed. *Microconidia* 12–27 × 7–13 µm, obovoid, 0–2-distoseptate. *Sclerotia* 146–325 × 197–370 µm, present or absent, often formed in culture, resembling immature perithecia, semi- or immersed in agar, globose, subglobose, ellipsoidal or ovoid, dark brown or black. *Sexual morph* unknown.

Culture characteristics: Colonies on PDA and OA at 25 °C under near-ultraviolet light (12 h light, 12 h dark), reaching 20–80 mm after 1 wk, white, hazel, orange, or dark grey to olivaceous, cottony, velvety, somewhat fluffy, or flat, margin irregular, effuse; reverse centre hazel, dark brown, periphery hazel, orange to luteous. Diffusible pigment luteous to orange (produced in some strains).

Materials examined: **Argentina**, isolated from soil, unknown date, J.B. Routien, (culture ex-type of *Dactylaria lutea* CBS 145.57). **Cuba**, Santiago de las Vegas, on leaves of *Portulaca oleracea* (*Portulacaceae*), 9 Mar. 1980, G. Arnold, INIFAT A80/85 = CBS 132.81. **Italy**, isolated from seedbed of *Pinus radiata* (*Pinaceae*), unknown date, G. Magnani, CBS 584.71. **The Netherlands**, on leaves of *Portulaca oleracea* (*Portulacaceae*), unknown date and collector, CBS 585.71; The Hague, on leaves of *Portulaca oleracea* (*Portulacaceae*), Jul. 1978, G.H. Boerema, CBS 518.78.

Notes: In the phylogenetic tree (Fig. 13), *Di. lutea* is represented by five strains isolated from soil and leaves of *Po. oleraceae* from Argentina, Cuba, Italy and the Netherlands. This species shows morphological variation among strains, with different colour and aspect of the colonies, production or absence of diffusible pigment and sclerotia. The above description is based on CBS 584.71, CBS 585.71, CBS 518.78 and CBS 132.81. The conidia were smaller than those described by de Hoog & van Oorschot (1983) based on the ex-type strain CBS 145.57 (14–65.5 × 7.5–13 *vs.* 30–115 × 10–20 µm). Unfortunately, the ex-type strain was sterile under the culture media and conditions tested.

Dichotomophthora portulacae Mehrl. & Fitzp. ex M.B. Ellis, Dematiaceous Hyphomycetes (Kew): 388. 1971.
Synonyms: *Dichotomophthora portulacae* Mehrl. & Fitzp., Mycologia 27: 550. 1935. (nom. inval., Art. 39.1, Melbourne).
Dichotomophthora portulacae Mehrl. & Fitzp. ex P.N. Rao, Mycopath. Mycol. Appl. 28: 139. 1966. (nom. inval., Art. 38.5(a), Melbourne).

Hyphae 1.5–6 µm wide, subhyaline to pale brown, septate, slightly constricted at septa, smooth to verruculose. *Conidiophores* macronematous, mononematous, branched more or less dichotomously in apical region, forming a stipe and head; *stipe* 120–220 µm long, up to 14 µm wide at apex, reddish brown, smooth, verruculose near base, terminal branches up to 110 µm long, each ending in two slightly swollen, rounded or angular

Fig. 14. *Dichotomophthora basella* (ex-type CPC 33016). **A–C.** Disease symptoms caused by *Di. basella* in leaves of *Basella rubra*. **D.** Colony on PDA. **E.** Colony on OA. **F.** Colony overview with sclerotia and conidiophores. **G–I.** Conidiophores and conidia. **J, K.** Conidiogenous cells. **L.** Conidia. **M.** Microconidia. **N, O.** Sclerotia. Scale bars: N, O = 100 µm; H = 50 µm; others = 10 µm.

lobes. *Conidiogenous cells* mono- or polytretic, integrated and terminal, cicatrized. *Conidia* 45–75 × 20–30 µm, solitary, dry, ellipsoidal to cylindrical rounded at ends, dark reddish-brown, smooth, 2–3-distoseptate. *Sclerotia* 120–170 µm diam, often formed in culture, resembling perithecia, subglobose to globose or ovoid, dark reddish-brown. *Sexual morph* unknown (adapted from de Hoog & van Oorschot 1983).

Culture characteristics: Colonies at 25 °C under near-ultraviolet light (12 h light, 12 h dark) after 1 wk, on PDA reaching 60 mm, centre white, periphery olivaceous, cottony, margin irregular, effuse, white; reverse centre black, periphery olive. On OA reaching 45 mm, pale greenish grey, cottony, margin effuse, buff; reverse greenish olivaceous. Diffusible pigment not produced.

Material examined: **USA**, Hawaii, on *Portulaca oleracea* (*Portulacaceae*), unknown date and collector, isol. F.P. Mehrlich (ex-paratype culture CBS 174.35).

Notes: In this study *Di. portulacae* was represented only by the ex-paratype strain, which together with *Di. brunnea* (CBS 149.94) formed a subclade in *Dichotomophthora*. Both species have dark brown or reddish brown conidia and conidiogenous cells with 1–3 lobes. Nevertheless, *Di. portulacae* has shorter conidia with fewer septa, (45–75 × 20–30 µm, 2–3-distoseptate *vs.* 29–56.5 × 6–10 µm, 2–6-distoseptate).

Authors: M. Hernández-Restrepo, R. Cheewangkoon & P.W. Crous

Gaeumannomyces Arx & D.L. Olivier, Trans. Brit. Mycol. Soc. 35: 32. 1952. Fig. 16.

Fig. 15. *Dichotomophthora brunnea* (ex-type CBS 149.49). **A.** Colony on PDA. **B.** Colony on OA. **C.** Colony overview with conidiophores. **D–J.** Conidiophores, conidiogenous cells and conidia. **K.** Microconidia. **L–Q.** Conidia. Scale bars: D–G = 50 µm; H = 20 µm; others = 10 µm.

Synonyms: *Rhaphidospora* Fr., Summa veg. Scand. 2: 401. 1849.
Rhaphidophora Ces. & De Not., Sfer. Ital.: 79. 1863.

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

Type species: *Gaeumannomyces graminis* (Sacc.) Arx & D.L. Olivier, basionym: *Rhaphidophora graminis* Sacc. Representative strain: CPC 26020 = CBS 141384.

DNA barcode (genus): LSU.

DNA barcodes (species): ITS, *tef1*, *rpb1*. Table 6. Fig. 17.

Ascomata perithecial, superficial, submerged, globose, subglobose to elliptical, with a central, ostiolate, cylindrical neck, dark brown to black; *ascomatal wall* comprised of pseudoparenchymatous cells, light or brown. *Hamathecium* comprised of septate, often constricted at septa, hyaline paraphyses, widest at base and gradually narrow at apex, exceeding asci, dissolving at maturity. *Asci* numerous, unitunicate, cylindrical to elongated clavate, short stalked, with apical refractile ring, 8-spored. *Ascospores* cylindrical, slightly curved to sinuate, widest in middle, ends rounded, vacuolated, septate, septa often indistinct, hyaline to pale brown, faintly tinted yellowish in mass. *Conidiophores* branched, verticillate, indeterminate, brown, often reduced to conidiogenous cells, hyaline to brown. *Conidiogenous cells* phialidic, solitary or in dense clusters, lageniform, cylindrical, straight or slightly curved tapering to a short cylindrical to funnel-shaped or hardly visible collarette. *Conidia* dimorphic (A) according to Wong & Walker (1975) "germinating phialidic conidia": solitary, grouped in slimy heads, ovoid to cylindrical, straight or slightly curved, tapering to an often acute base, hyaline, and/or (B) according to Wong & Walker (1975) "non-germinating phialidic conidia": solitary, arranged in heads, hyaline, falcate to lunate, usually strongly curved in a semicircle with varying degrees of curvature. *Hyphopodia* when present hyaline becoming brown when mature, simple or lobed. *Sclerotia* present or absent (adapted from Hernández-Restrepo *et al.* 2016b).

Culture characteristics: Colonies on PDA mycelium mostly submerged, dark (grey olivaceous, greyish sepia, isabelline) aerial mycelium scarce, or sometimes cottony, white; margin effuse, irregular to rhizoid. On MEA elevated, cottony to funiculose, aerial mycelium white or pale i.e. pale greenish grey, smoke grey, submerged mycelium black, margin effuse to rhizoid. Cultures of *Gaeumannomyces* vary in colour, growth rate and amount of aerial mycelium, dark hyphal strands and black sclerotia.

Optimal media and cultivation conditions: MEA and PDA incubated at 15–30 °C depending of species. Other methods described for production of perithecia include PDA with wheat seedlings (Speakman 1982) and flooded cultures in MPA (Speakman 1984).

Distribution: Worldwide.

Hosts: Mainly pathogens on grasses (*Poaceae* on *Avena*, *Hordeum*, *Oryza* & *Leersia*, *Secale*, *Sorghum*, *Triticum*, x*Triticale*, *Zea*, turf grasses, buffalo grass and other grasses) and *Cyperaceae*, but some occur on non-grass hosts as saprobes or endophytes.

Disease symptoms: Take-all, crown black sheath rot, dieback, root decline, patches of white heads after flowering, stem- and root rot.

Notes: Gaeumannomyces comprises about 20 species (Hernández-Restrepo *et al.* 2016b) that are mainly pathogenic to grasses, but some species are also regarded as saprobic or endophytic. The generic type *Gaeumannomyces graminis* included four varieties based on ascospore size, hyphopodial morphology and host preferences i.e. *G. graminis* var. *graminis*, *G. graminis* var. *avenae, G. graminis* var. *tritici* and *G. graminis* var. *maydis* (Turner 1940, Dennis 1960, Walker 1972, Yao *et al.* 1992). After a wide range of isolates were subjected to DNA sequence analyses, it was demonstrated that these established varieties and cryptic species represent different, phylogenetically supported species (Ward & Bateman 1999, Ulrich *et al.* 2000, Freeman & Ward 2004, Hernández-Restrepo *et al.* 2016b). *Gaeumannomyces tritici* and *G. avenae*, the causal agents of take-all of wheat and oat respectively, are more aggressive pathogens than *G. graminis* and other species in the genus. Species of *Gaeumannomyces* are morphologically difficult to distinguish because of their simple morphology, overlapping morphological features and considerable intraspecific variation.

References: von Arx & Olivier 1952, Deacon 1973, 1974 (taxonomy); Walker 1972, 1975, 1980, 1981 (taxonomy, morphology, pathogenicity); Asher & Shipton 1981 (biology and control); Elliott 1991, Elliott *et al.* 1993 (pathogenicity); Bateman *et al.* 1992, Augustin *et al.* 1999, Ulrich *et al.* 2000, Rachdawong *et al.* 2002 (molecular data); Freeman & Ward 2004 (review); Hernández-Restrepo *et al.* 2016b (morphology and phylogeny).

Authors: M. Hernández-Restrepo & P.W. Crous

Harknessia Cooke, Grevillea 9: 85. 1881. Fig. 18.
Synonyms: *Caudosporella* Höhn., Sber. Akad. Wiss. Wien, Math.-naturw. Kl., Abt. 1 123: 135. 1914.
Mastigonetron Kleb., Mykol. Zentbl. 4: 17. 1914.
Cymbothyrium Petr., Sydowia 1: 148. 1947.

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

Type species: *Harknessia eucalypti* Cooke. Representative strain: CBS 342.97.

DNA barcode (genus): LSU.

DNA barcodes (species): ITS, *cal*, *tub2.* Table 7. Fig. 19.

Ascomata perithecial, single or aggregated, immersed, brown; *necks* emergent to depressed; *ascomatal wall* of 3–5 layers of brown cells of *textura angularis*. *Paraphyses* hyaline, septate, dispersed between asci. *Asci* 8-spored, unitunicate, cylindrical to clavate, short pedicellate, with J- apical ring. *Ascospores* uni- to biseriate, ellipsoid to fusoid, hyaline, aseptate, thick-walled, guttulate, smooth-walled. *Conidiomata* erumpent, scattered, pycnidial, unilocular, globose to subglobose, brown; *conidiomatal wall* comprising 3–4 layers of brown-walled cells of *textura angularis*. *Macroconidiophores* lining cavity or limited to a basal layer in some species; usually reduced to conidiogenous cells, rarely septate and branched; commonly invested in mucus. *Macroconidiogenesis cells* ampulliform, subcylindrical or cylindrical, hyaline, proliferating percurrently. *Macroconidia* consisting of a body with a basal appendage, delimited by a septum; *conidium body* unicellular, ellipsoid to fusoid, subcylindrical, globose, broadly ventricose, broadly ellipsoid or broadly fusoid, thick-walled, smooth, brown, with or without pale and dark coloured longitudinal bands, occasionally longitudinally striate, guttulate; *basal appendages* hyaline, tubular, smooth, thin-walled, often collapsing. *Microconidiophores* absent or present, in same conidioma, reduced to microconidiogenous cells. *Microconidiogenous cells* ampulliform or subcylindrical to lageniform, hyaline, smooth, with apical periclinal thickening. *Microconidia* hyaline, smooth, aseptate, oval to ellipsoid.

Culture characteristics: Colonies spreading, fluffy, with moderate to abundant aerial mycelium, covering plate in 1 mo. On MEA surface dirty white to cream or pale luteous; reverse cream; sometimes sporulating with black conidiomata, oozing black masses. These culture characteristics also apply to the new taxa described below.

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

Distribution: Worldwide.

Hosts: On diverse gymnosperm and dicotyledonous hosts, especially on *Eucalyptus* (*Myrtaceae*), which is host to 27 of the currently accepted 38 species.

Disease symptoms: Associated with leaf spots, leaf tip dieback or leaf scorch and stem cankers, but pathogenicity has not been established definitively (Crous *et al.* 2012c).


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Table 6. DNA barcodes of accepted *Gaeumannomyces* spp.

Species	**Isolates**[1]	**GenBank accession numbers**[2]			**References**
		ITS	***rpb1***	***tef1***	
Gaeumannomyces amomi	CBS 109354^{T}	AY265318	–	KX306679	Bussaban *et al.* (2005), Hernández-Restrepo *et al.* (2016b)
G. arxii	CBS 903.73^{T}	KM484837	KM485053	KX306681	Klaubauf *et al.* (2014), Hernández-Restrepo *et al.* (2016b)
G. australiensis	CBS 141387^{T}	KX306480	KX306619	KX306683	Hernández-Restrepo *et al.* (2016b)
G. avenae	CPC 26258^{ET}	KX306486	KX306622	KX306688	Hernández-Restrepo *et al.* (2016b)
G. californicus	CBS 141377^{T}	KX306490	KX306625	KX306691	Hernández-Restrepo *et al.* (2016b)
G. ellisiorum	CBS 387.81^{T}	KM484835	KM485051	KX306692	Klaubauf *et al.* (2014), Hernández-Restrepo *et al.* (2016b)
G. floridanus	CBS 141378^{T}	KX306491	KX306626	KX306693	Hernández-Restrepo *et al.* (2016b)
G. fusiformis	CBS 141379^{T}	KX306492	KX306627	KX306694	Hernández-Restrepo *et al.* (2016b)
G. glycinicola	CPC 26057^{T}	KX306493	KX306628	KX306695	Hernández-Restrepo *et al.* (2016b)
G. graminicola	CBS 352.93^{T}	KM484834	KM485050	KX306697	Klaubauf *et al.* (2014), Hernández-Restrepo *et al.* (2016b)
G. graminis	CPC 26020	KX306498	KX306633	KX306701	Hernández-Restrepo *et al.* (2016b)
G. hyphopodioides	CBS 350.77^{T}	KX306506	KM009192	KM009204	Hernández-Restrepo *et al.* (2016b), Luo *et al.* (2014)
G. oryzicola	CBS 141390^{T}	KX306516	KX306646	KX306717	Hernández-Restrepo *et al.* (2016b)
G. oryzinus	CBS 235.32	JX134669	KM485049	JX134695	Klaubauf *et al.* (2014), Luo & Zhang (2013)
G. radicicola	CBS 296.53^{T}	KM484845	KM485061	KM009206	Klaubauf *et al.* (2014)
G. setariicola	CBS 141394^{T}	KX306524	KX306654	KX306725	Hernández-Restrepo *et al.* (2016b)
G. tritici	CBS 905.73	KM484841	KM485057	KX306731	Klaubauf *et al.* (2014), Hernández-Restrepo *et al.* (2016b)
G. walkeri	CBS 141400^{T}	KX306543	KX306670	KX306746	Hernández-Restrepo *et al.* (2016b)
G. wongoonoo	BRIP 60376^{A}	KP162137	–	–	Wong (2002)

[1] BRIP: Queensland Plant Pathology Herbarium, Brisbane, Australia; CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CPC: Culture collection of Pedro Crous, housed at the Westerdijk Fungal Biodiversity Institute. $^{T,\ ET}$ and ^{A} indicate ex-type, ex-epitype and authentic strains, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *rpb1*: partial RNA polymerase II largest subunit gene; *tef1*: partial elongation factor gene.

Notes: *Harknessia* is characterised by having stromatic to pycnidial conidiomata, and dark brown conidia with tube-shaped basal appendages, longitudinal striations, and rhexolytic secession (Crous *et al.* 2012c). Sexual morphs were initially described in *Cryptosporella* (Nag Raj & DiCosmo 1981), which was rejected in favour of the older genus *Wuestneia* (Reid & Booth 1989). However, the type species of *Wuestneia*, *Wu. aurea* (= *Wuestneia xanthostroma*), was located in the *Cryphonectriaceae* and was associated with a coelomycete asexual morph having hyaline conidia. *Wuestneia* is therefore not considered as synonym of *Harknessia*, and only species placed in the *Harknessiaceae* and linked to *Harknessia* morphs were thus transferred to *Harknessia* (Crous *et al.* 2012c).

The family *Harknessiaceae* was introduced based on LSU sequences of taxa belonging to *Diaporthales* in order to accommodate *Harknessia* (Crous *et al.* 2012c).

References: Lee *et al.* 2004 (morphology and phylogeny); Crous *et al.* 2012c (morphology and phylogeny).

Harknessia bourbonica Crous & M.J. Wingf., **sp. nov.** MycoBank MB824016. Fig. 20.

Etymology: Name refers to Île Bourbon, the original name of La Réunion Island.

Caulicolous and *foliicolous*, isolated from leaves and twigs incubated in moist chambers (presumed endophyte). *Conidiomata* up to 300 μm diam, pycnidial, separate to gregarious, subepidermal, becoming erumpent, stromatic, amphigenous, depressed globose; with irregular opening and border of yellowish, furfuraceous cells; *conidiomatal wall* of *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining conidiomatal cavity. *Conidiogenous cells* 8–10 × 4–8 μm, ampulliform to subcylindrical, hyaline, smooth, invested in mucilage, percurrently proliferating once or twice near apex. *Conidia* (12–)13–14(–15) × (8–)9–10 μm *in vitro*, broadly ventricose to ellipsoid, apex subobtusely rounded, aseptate, nonapiculate, yellow-brown, thick-walled, striations in restricted areas, multi-guttulate. *Basal appendage* (5–)8–12 × 2–2.5 μm

Fig. 16. *Gaeumannomyces* spp. **A–F.** Sexual morph. **A.** Ascoma of *Gaeumannomyces oryzicola* (ex-type CBS 141390). **B.** Asci and paraphyses of *Gaeumannomyces oryzinus* (CPC 26065). **C–E.** Asci. **C, D.** *Gaeumannomyces oryzinus* (CPC 26043). **E.** *Gaeumannomyces oryzicola* (ex-type CBS 141390). **F.** Ascospores of *Gaeumannomyces oryzinus* (CBS 235.32). **G–AH.** Asexual morph. **G–P.** Conidiophores and conidiogenous cells. **G.** *Gaeumannomyces californicus* (ex-type CBS 141377). **H.** *Gaeumannomyces fusiformis* (ex-type CBS 141379). **I.** *Gaeumannomyces arxii* (CBS 903.73). **J, N.** *Gaeumannomyces walkeri* (ex-type CBS 141400). **K.** *Gaeumannomyces graminis* (CBS 141386). **L.** *Gaeumannomyces graminicola* (CBS 352.93). **M.** *Gaeumannomyces oryzicola* (ex-type CBS 141390). **O.** *Gaeumannomyces oryzinus* (CPC 26032). **P.** *Gaeumannomyces radicicola* (ex-type CBS 296.53). **Q–Y.** Conidia. **Q.** *Gaeumannomyces radicicola* (ex-type CBS 296.53). **R.** *Gaeumannomyces oryzicola* (ex-type CBS 141390). **S, T.** *Gaeumannomyces walkeri* (ex-type CBS 141400). **U.** *Gaeumannomyces oryzinus* (CPC 26067). **V.** *Gaeumannomyces ellisiorum* (ex-type CBS 387.81). **W.** *Gaeumannomyces floridanus* (ex-type CBS 141378). **X.** *Gaeumannomyces graminicola* (CPC 26036). **Y.** *Gaeumannomyces arxii* (CBS 903.73). **Z–AH.** Hyphopodia. **Z.** *Gaeumannomyces ellisiorum* (ex-type CBS 387.81). **AA, AC.** *Gaeumannomyces glycinicola* (CBS 141380). **AB.** *Gaeumannomyces floridanus* (ex-type CBS 141378). **AD.** *Gaeumannomyces graminicola* (CPC 26025). **AE.** *Gaeumannomyces californicus* (ex-type CBS 141377). **AG.** *Gaeumannomyces oryzinus* (CPC 26032). **AF.** *Gaeumannomyces hyphopodioides* (CPC 26267). **AH.** *Gaeumannomyces walkeri* (ex-type CBS 141400). Scale bars: A, B = 50 μm; C–F = 20 μm; others = 10 μm. Pictures taken from Hernández-Restrepo *et al.* (2016b).

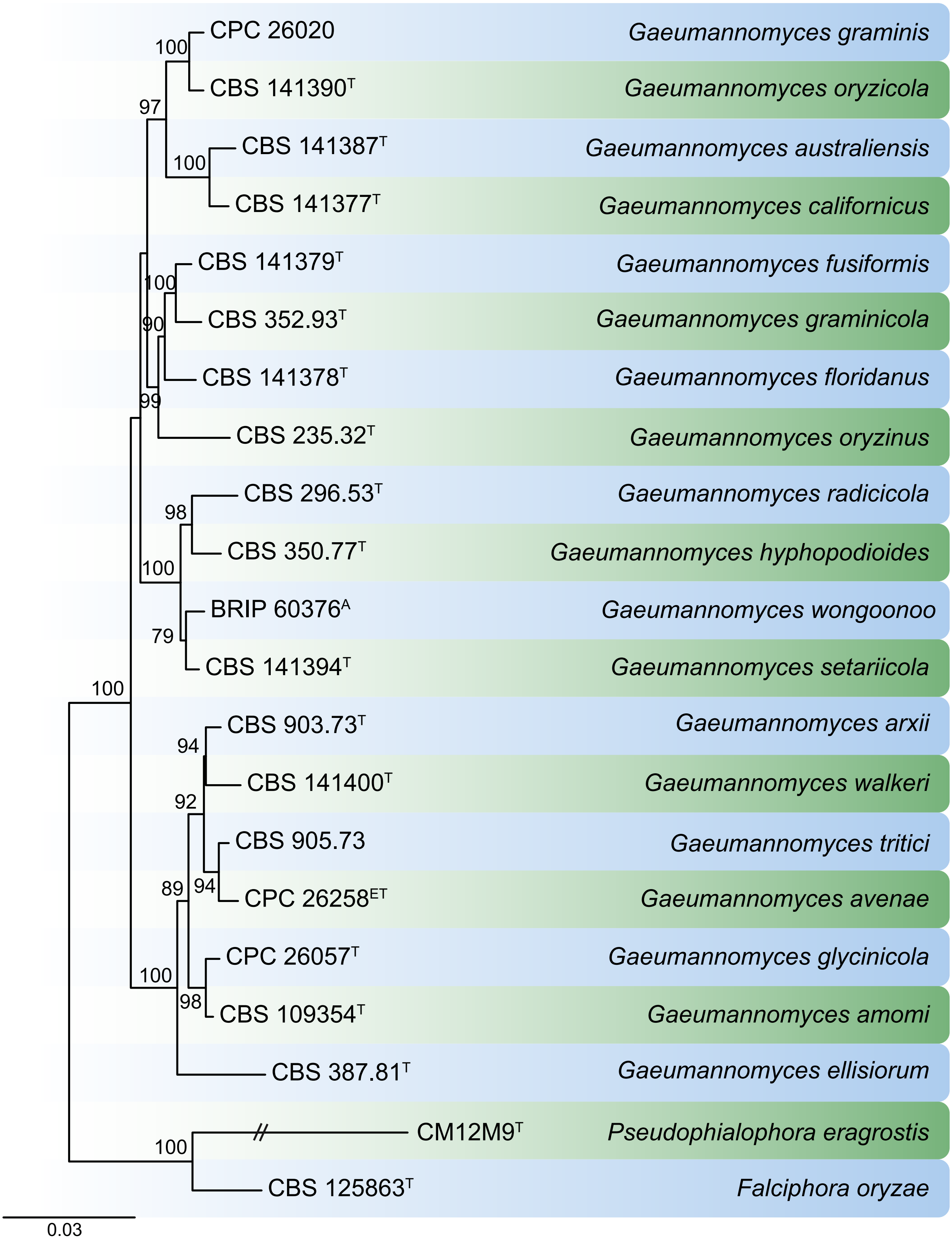

Fig. 17. RAxML phylogram obtained from the combined ITS (715 bp), LSU (881 bp), *rpb1* (617 bp) and *tef1* (427 bp) sequence alignment of all the accepted species of *Gaeumannomyces*. The tree was rooted to *Pseudophialophora eragrostis* CM12m9 and *Falciphora oryzae* CBS 125863. RAxML bootstrap support (BS) values above 70 % are shown in the nodes. GenBank accession numbers are indicated in Table 6. T, ET and A indicate ex-type, ex-epitype and authentic strains, respectively. TreeBASE: S21899.

in vitro, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm. *Microconidia* not seen.

Material examined: **France**, La Réunion, 21°15'5.4"S 55°36'3.3"E, on leaf litter of *Eucalyptus robusta* (*Myrtaceae*), 8 Mar. 2015, P.W. Crous & M.J. Wingfield (**holotype** CBS H-23387, culture ex-type CBS 143913 = CPC 26533).

Notes: *Harknessia bourbonica* is related to *Ha. ravenstreetina*, which was also isolated from *Eucalyptus* leaves. The two species are distinguished in that *Ha. ravenstreetina* has longer conidia (14–20 μm) that lack striations and has shorter basal appendages (1.5–5 × 2–2.5 μm).

Harknessia corymbiae Crous & A.J. Carnegie, **sp. nov.** MycoBank MB824017. Fig. 21.

Etymology: Name refers to the host genus, *Corymbia*.

Caulicolous and *foliicolous*, isolated from leaves and twigs incubated in moist chambers (presumed endophyte). *Conidiomata* up to 250 μm diam, pycnidial, separate to gregarious, subepidermal, becoming erumpent, stromatic, amphigenous, depressed globose; with irregular opening and border of yellowish, furfuraceous cells; *conidiomatal wall* of *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining conidiomatal cavity. *Conidiogenous cells* 6–10 × 4–5 μm, ampulliform to subcylindrical, hyaline, smooth, invested in mucilage, percurrently proliferating once or twice near apex. *Conidia* (23–)25–28(–30) × (8–)9 μm *in vitro*, subcylindrical, apex apiculate, aseptate, yellow-brown, thick-walled, lacking striations, granular; in lactic acid some conidia appear to have a central line of paler pigment. *Basal appendage* (50–)65–80(–100) × 3–4 μm *in vitro*, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm. *Microconidia* 3–4 × 1.5–2 μm, hyaline, smooth, guttulate, aseptate, subcylindrical with obtuse ends.

Material examined: **Australia**, New South Wales, Bom Bom State Forest, on leaf litter of *Corymbia maculata* (*Myrtaceae*), 13 Mar. 2017, A.J. Carnegie (**holotype** CBS H-23388, culture ex-type CPC 33289).

Notes: *Harknessia corymbiae* was located in a distinct clade distant from the other species of the genus. The only accepted species presently known from *Corymbia* is *Ha. rhabdosphaera*. Both species were collected from Australia, but *Ha. rhabdosphaera* has smaller, striated conidia [(13–)15–17 × (13–)14–15 μm] with short basal appendages (up to 5 μm long).

Harknessia cupressi Crous & R.K. Schumach., **sp. nov.** MycoBank MB824018. Fig. 22.

Etymology: Name refers to the host genus, *Cupressus*.

Caulicolous and *foliicolous*, isolated from needles incubated in moist chambers (presumed endophyte). *Conidiomata* up to 250 μm diam, pycnidial, separate to gregarious, subepidermal, becoming erumpent, stromatic, amphigenous, depressed globose; with irregular opening and border of yellowish, furfuraceous cells; *conidiomatal wall* of *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining conidiomatal cavity. *Conidiogenous cells* 5–10 × 3–5 μm, ampulliform to subcylindrical, hyaline, smooth, invested in mucilage, percurrently proliferating once or twice near apex. *Conidia* (20–)21–23(–25) × (8–)9–11(–13) μm *in vitro*, broadly ventricose, apex apiculate, aseptate, yellow-brown, thick-walled, striations in restricted areas, multi-guttulate. *Basal appendage* 2–5(–12) × 2–2.5 μm *in vitro*, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm. *Microconidia* 4–7 × 3–4 μm, hyaline, smooth, aseptate, broadly ellipsoid.

Materials examined: **Spain**, Zaragoza, Carretera El Frago, on needles of *Cupressus sempervirens* (*Cupressaceae*), 7 Jan. 2016, coll. R. Blasco, det. R.K. Schumacher (**holotype** CBS H-23389, culture ex-type CBS 143914 = CPC 30192); *ibid*., CPC 30174.

Notes: *Harknessia cupressi* was located in an independent clade distant from the other species of the genus. *Harknessia cupressi* is the only species known from *Cupressus sempervirens*.

Harknessia pilularis Crous & A.J. Carnegie, **sp. nov.** MycoBank MB824020. Fig. 23.

Etymology: Name refers to *Eucalyptus pilularis*, the host species from which this fungus was isolated.

Caulicolous and *foliicolous*, isolated from leaves and twigs incubated in moist chambers (presumed endophyte). *Conidiomata* up to 250 μm diam, pycnidial, separate to gregarious, subepidermal, becoming erumpent, stromatic, amphigenous, depressed globose; with irregular opening and border of yellowish, furfuraceous cells; *conidiomatal wall* of *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining conidiomatal cavity. *Conidiogenous cells* 4–7 × 2–5 μm, ampulliform to subcylindrical, hyaline, smooth, invested in mucilage, percurrently proliferating once or twice near apex. *Conidia* (13–)14–16(–20) × (8–)11–12(–13) μm *in vitro*, globose to rarely broadly ellipsoid, apex obtusely rounded, aseptate, non-apiculate, yellow-brown, thick-walled, striations covering entire conidial body, multi-guttulate. *Basal appendage* (2–)3–5 × 2–2.5 μm *in vitro*, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm. *Microconidia* not seen.

Materials examined: **Australia**, New South Wales, Pine Creek State Forest, 30.405423S 152.932698E, on leaves of *Eucalyptus pilularis* (*Myrtaceae*), 23 Jan. 2017, A.J. Carnegie (**holotype** CBS H-23391, culture ex-type CPC 33218); *ibid*., CPC 33356.

Notes: *Harknessia pilularis* is related to *Ha. rhabdosphaera*, but *Ha. rhabdosphaera* produces longer conidiogenous cells (7–15 × 4–6 μm), and wider conidia (13–15 μm).

Authors: Y. Marin-Felix, A.J. Carnegie, M.J. Wingfield, R.K. Schumacher & P.W. Crous

Huntiella Z.W. de Beer, *et al.*, Stud. Mycol. 79: 211. 2014. Fig. 24.

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

Type species: Huntiella moniliformis (Hedgc.) Z.W. de Beer, *et al.*, basionym: *Ceratostomella moniliformis* Hedgc. Holotype: BPI 595959.

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

DNA barcodes (species): ITS, *mcm7*, *tef1*, *tub2*. Table 8. Fig. 25.

Ascomata perithecial, ellipsoidal, subglobose, globose to obpyriform or ovoid; *bases* ornamented with dark brown to black conical spines or pale brown, unbranched hyphae; *necks* long, straight or slightly curved, tapering towards apex, dark brown to black at base, becoming paler towards apex, ostiolate, with a disciform base; *hyphae* on neck hyaline, not divergent, straight or convergent. *Asci* evanescent. *Ascospores* hyaline, aseptate, in face view subglobose, in side view ellipsoidal giving an impression of a hat, with hood-like gelatinous sheath. *Conidiophores* macronematous, rarely branched, septate, occasionally reduced to conidiogenous cells. *Conidiogenous cells* hyaline, enteroblastic, mostly of two types, lageniform, producing rectangular-shaped conidia and cylindrical, producing barrel-shaped conidia. *Conidia* aseptate, majority of species have two distinct shapes: bacilliform, hyaline, or barrel-shaped or oblong to ellipsoidal, hyaline or subhyaline. *Chlamydospores* absent.

Culture characteristics: On 2 % MEA aerial mycelium abundant, colonies white, yellow green to brown, smoke grey, dark olive to black. Some species produce aromas: *Hu. bhutanensis* produces an unpleasant rotten odour, *Hu. decipiens*, *Hu. moniliformis* and *Hu. salinaria* a pleasant banana-oil aroma, *Hu. moniliformopsis* little to no distinct odour, and *Hu. omanensis* fruity aroma that turns to a fermented odour with age.


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Table 7. DNA barcodes of accepted *Harknessia* spp.

Species	**Isolates**[1]	**GenBank accession number**[2]			**References**
		ITS	***cal***	***tub2***	
Harknessia arctostaphyli	CBS 137228^{ET}	KJ152781	–	KJ179923	Moreno-Rico *et al.* (2014)
Ha. australiensis	CBS 132119^{T}	JQ706085	JQ706171	JQ706130	Crous *et al.* (2012c)
Ha. banksiae	CBS 142539^{T}	KY979782	KY979872	KY979938	Crous *et al.* (2017a)
Ha. banksiae-repens	CBS 142541^{T}	KY979785	KY979875	KY979940	Crous *et al.* (2017a)
Ha. banksiigena	CBS 142540^{T}	KY979784	KY979874	–	Crous *et al.* (2017a)
Ha. bourbonica	CBS 143913^{T}	MG934433	MG934512	–	Present study
Ha. capensis	CBS 111829^{T}	AY720719	AY720782	AY720751	Lee *et al.* (2004)
Ha. communis	CBS 142538^{T}	KY979778	KY979868	–	Crous *et al.* (2017a)
Ha. corymbiae	CPC 33289^{T}	MG934434	MG934513	MG934507	Present study
Ha. cupressi	CBS 143914^{T} CPC 30174	MG934435 MG934436	MG934514 MG934515	– –	Present study Present study
Ha. ellipsoidea	CBS 132121^{T}	JQ706087	JQ706173	JQ706132	Crous *et al.* (2012c)
Ha. eucalypti	CBS 342.97	AY720745	AY720808	AY720777	Lee *et al.* (2004)
Ha. eucalyptorum	CBS 111115^{T}	AY720747	AY720810	AY720779	Lee *et al.* (2004)
Ha. fusiformis	CBS 110785^{T}	AY720721	AY720784	AY720753	Lee *et al.* (2004)
Ha. gibbosa	CBS 120033^{T}	EF110615	JQ706182	JQ706142	Crous *et al.* (2007), (2012c)
Ha. globispora	CBS 111578^{T}	AY720722	AY720785	AY720754	Lee *et al.* (2004)
Ha. hawaiiensis	CBS 114811	AY720723	AY720786	AY720755	Lee *et al.* (2004)
Ha. ipereniae	CBS 120030^{T}	EF110614	JQ706192	JQ706151	Crous *et al.* (2007), (2012c)
Ha. karwarrae	CBS 115648	AY720748	AY720811	AY720780	Lee *et al.* (2004)
Ha. kleinzeeina	CPC 16277^{T}	JQ706108	JQ706193	JQ706152	Crous *et al.* (2012c)
Ha. leucospermi	CBS 775.97^{T}	AY720727	AY720790	AY720759	Lee *et al.* (2004)
Ha. malayensis	CBS 142544^{T}	KY979789	KY979879	KY979941	Crous *et al.* (2017a)
Ha. molokaiensis	CBS 114877^{T}	AY720749	AY720812	AY579335	Lee *et al.* (2004), Mostert *et al.* (2005)
Ha. pellitae	CBS 142543^{T}	KY979788	KY979878	–	Crous *et al.* (2017a)
Ha. pilularis	CPC 33218^{T} CPC 33356	MG934438 MG934439	MG934517 MG934518	MG934508 MG934509	Present study Present study
Ha. platyphyllae	CBS 142542^{T}	KY979787	KY979877	–	Crous *et al.* (2017a)
Ha. proteae	CBS 136426^{T}	KF777162	–	–	Crous *et al.* (2013)
Ha. protearum	CBS 112618^{T}	AY720732	AY720795	AY720764	Lee *et al.* (2004)
Ha. pseudohawaiiensis	CBS 132124^{T}	JQ706111	JQ706196	JQ706155	Crous *et al.* (2012c)
Ha. ravenstreetina	CBS 132125^{T}	JQ706112	JQ706197	JQ706156	Crous *et al.* (2012c)
Ha. renispora	CBS 153.71^{IsoT}	AY720737	AY720800	AY720769	Lee *et al.* (2004)
Ha. rhabdosphaera	CBS 122373	JQ706118	JQ706201	JQ706161	Crous *et al.* (2012c)
Ha. spermatoidea	CBS 132127^{ET}	JQ706120	JQ706203	JQ706163	Crous *et al.* (2012c)
Ha. syzygii	CBS 111124^{T}	AY720738	AY720801	AY720770	Lee *et al.* (2004)
Ha. uromycoides	CBS 110729	AY720739	AY720802	AY720771	Lee *et al.* (2004)
Ha. viterboensis	CBS 115647^{T}	AY720740	AY720803	AY720772	Lee *et al.* (2004)
Ha. weresubiae	CBS 132128^{ET}	JQ706122	JQ706205	JQ706165	Crous *et al.* (2012c)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands; CPC: Culture collection of Pedro Crous, housed at the Westerdijk Fungal Biodiversity Institute. ^{T}, ^{ET} and ^{IsoT} indicate ex-type, ex-epitype and ex-isotype strains, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *cal*: partial calmodulin gene; *tub2*: partial β-tubulin gene.

Fig. 18. *Harknessia* spp. **A–E.** Disease symptoms on *Eucalyptus*. **A.** *Harknessia fusiformis* (CPC 13649). **B.** *Harknessia hawaiiensis* (CPC 15003). **C.** *Harknessia ravenstreetina* (ex-type CBS 132125). **D.** *Harknessia rhabdosphaera* (CPC 13593). **E.** *Harknessia globispora* (CPC 14924). **F–L.** Sexual morph of *Harknessia eucalyptorum* (CPC 12697). **F.** Ascoma with short neck, oozing ascospores. **G, H.** Paraphyses and asci. **I, J.** Asci. **K.** Paraphyses and ascal tip. **L.** Ascospores. **M–AA.** Asexual morphs. **M.** Sporulating colony on OA of *Harknessia ellipsoidea* (ex-type CBS 132121). **N–R.** Conidiogenous cells giving rise to conidia. **N, O.** *Harknessia gibbosa* (ex-type CBS 120033). **P.** *Harknessia pseudohawaiiensis* (CPC 17380). **Q.** *Harknessia ravenstreetina* (ex-type CBS 132125). **R.** *Harknessia renispora* (CPC 17163). **S–X.** Conidia. **S, T.** *Harknessia australiensis* (ex-type CBS 132119). **U.** *Harknessia kleinzeeina* (ex-type CPC 16277). **V.** *Harknessia eucalyptorum* (CPC 12697). **W.** *Harknessia ravenstreetina* (ex-type CBS 132125). **X.** *Harknessia renispora* (CPC 17163). **Y.** Microconidiogenous cells giving rise to microconidia of *Harknessia renispora* (CPC 17163). **Z, AA.** Microconidia. **Z.** *Harknessia renispora* (CPC 17163). **AA.** *Harknessia pseudohawaiiensis* (CPC 17380). Scale bars = 10 µm. Pictures taken from Crous *et al.* (2012c).

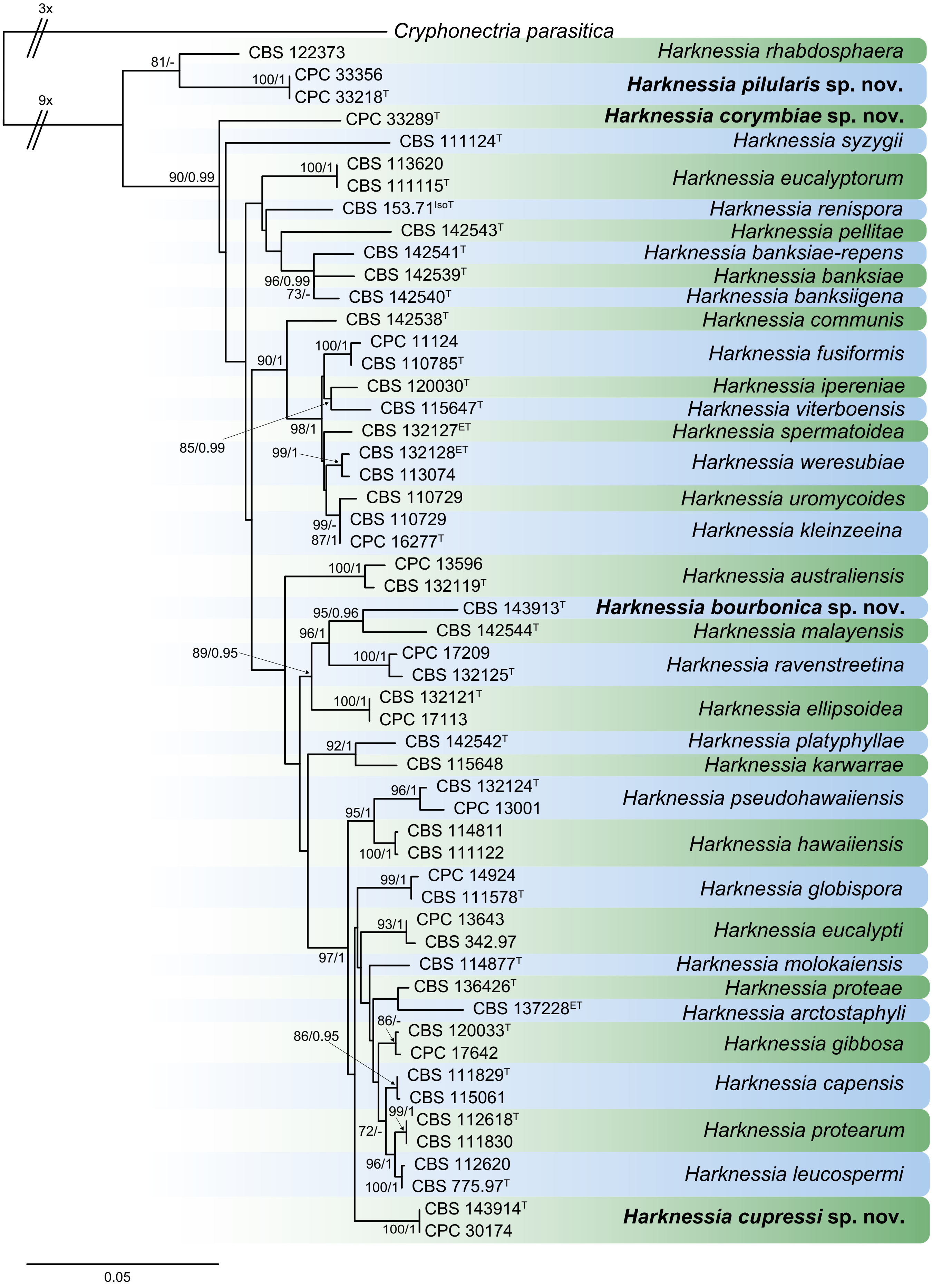

Fig. 19. RAxML phylogram obtained from the combined ITS (643 bp), *cal* (499 bp) and *tub2* (838 bp) sequence alignment of all accepted species of *Harknessia*. The tree was rooted to *Cryphonectria parasitica*. The novelties proposed in this study are indicated in **bold**. RAxML bootstrap support (BS) values above 70 % and Bayesian posterior probability scores above 0.95 are shown at the nodes. GenBank accession numbers were listed in Table 7 or in Crous *et al.* (2012c). $^{T,\ ET}$ and ^{IsoT} indicate ex-type, ex-epitype and ex-isotype strains, respectively. TreeBASE: S21899.

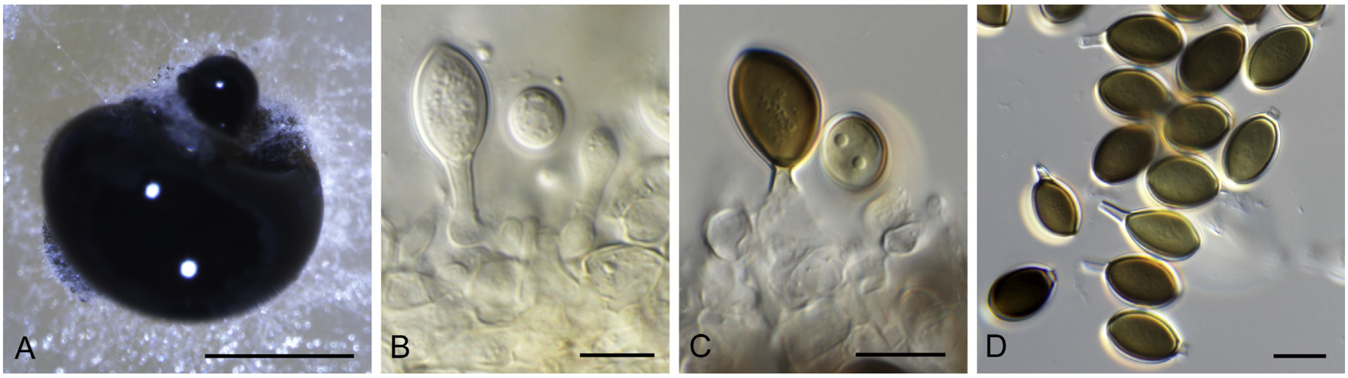

Fig. 20. *Harknessia bourbonica* (ex-type CBS 143913). **A.** Conidioma on OA. **B, C.** Conidiogenous cells giving rise to conidia. **D.** Conidia. Scale bars: A = 150 µm, B–D = 10 µm.

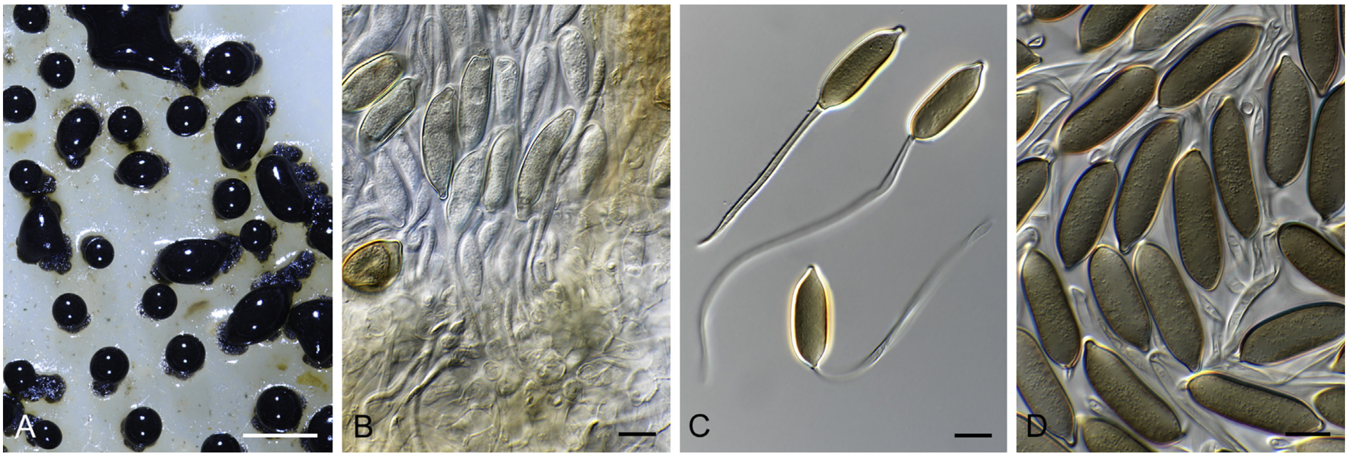

Fig. 21. *Harknessia corymbiae* (ex-type CPC 33289). **A.** Conidiomata on OA. **B.** Conidiogenous cells giving rise to conidia. **C, D.** Conidia. Scale bars: A = 250 µm, B–D = 10 µm.

Fig. 22. *Harknessia cupressi* (ex-type CBS 143914). **A.** Conidiomata on OA. **B, C.** Conidiogenous cells giving rise to conidia. **D, E.** Conidia. Scale bars: A = 250 µm, B–E = 10 µm.

Optimal media and cultivation conditions: On 2 % MEA in dark, optimum growth varies between species: *Hu. sublaevis* 20–30 °C; *Hu. bhutanensis, Hu. oblonga, Hu. ceramica* and *Hu. tribiliformis* 20–25 °C; *Hu. decipiens, Hu. chinaeucensis, Hu. inquinans, Hu. microbasis, Hu. salinaria* and *Hu. sumatrana* 25–30 °C; *Hu. cryptoformis, Hu. omanensis*, *Hu. savannae* and *H. tyalla* 30–35 °C.

Distribution: Australia, Bhutan, China, Ecuador, Indonesia, Malawi, Oman, South Africa and Tasmania.

Hosts: *Acacia* (*Fabaceae*), *Combretum* and *Terminalia* (*Combretaceae*), *Eucalyptus* (*Myrtaceae*), *Mangifera* (*Anacardiaceae*) associated with *Cryphalus scabricollis* (bark beetle, *Scolytinae*), *Picea* (*Pinaceae*) infested with *Ips schmutzenhoferi* (bark beetle, *Scolytinae*), *Pinus* (*Pinaceae*), *Ziziphus* (*Rhamnaceae*), and *Staphilinid* (rove beetle, *Staphylinidae*).

Disease symptoms: *Huntiella* species do not produce distinct disease symptoms on their hosts in nature. They usually infect freshly made wounds on trees and infections are often associated with nitidulid beetles (*Coleoptera*: *Nitidulidae*) and flies (*Diptera*). Pathogenicity tests using some of the species have given rise to lesions under controlled environments, but, based on the size of lesions and failure to re-isolate the fungus from

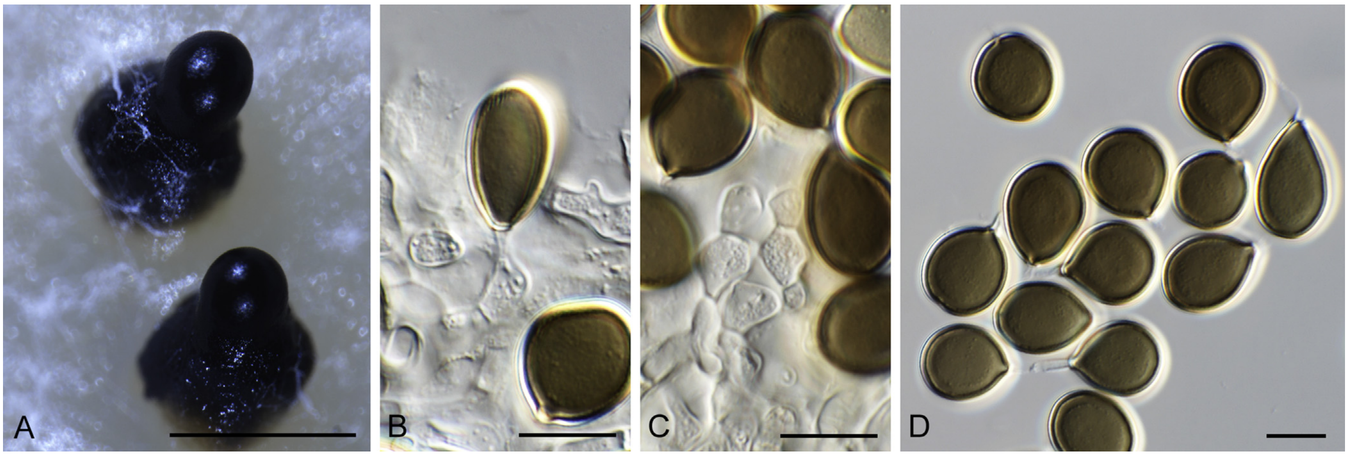

Fig. 23. *Harknessia pilularis* (ex-type CPC 33218). **A.** Conidiomata on OA. **B, C.** Conidiogenous cells giving rise to conidia. **D.** Conidia. Scale bars: A = 250 µm, B–D = 10 µm.

these lesions, they are generally considered not to be primary pathogens (Tarigan *et al.* 2010, van Wyk *et al.* 2011, de Beer *et al.* 2014).

Notes: *Huntiella* is one of nine genera in the recently erected family, *Ceratocystidaceae* (De Beer *et al.* 2014, Mayers *et al.* 2015, Nel *et al.* 2018). The genus was proposed to accommodate *Ceratocystis moniliformis* and related species that form a well-defined monophyletic lineage within the group previously treated as *Ceratocystis sensu lato* (Wingfield *et al.* 2013). *Huntiella* currently includes 17 species.

Species of *Huntiella* have several features in common, namely conical spines on their ascomatal bases, disk-like structures at the bases of the ascomatal necks, which break off easily, hat-shaped ascospores and one to two types of conidia (De Beer *et al.* 2014). Although morphological and culture characteristics overlap between the species, some species can be differentiated. These include *Hu. sublaevis* that has a limited number of spines on the ascomata (Van Wyk *et al.* 2011), and *Hu. chinaeucensis* and *Hu. microbasis* that have only rectangular-shaped conidia (Tarigan *et al.* 2010, Chen *et al.* 2013). With the exception of *Hu. ceramica* that is known only from the asexual morph, all other species have both sexual and asexual morphs. Different *Huntiella* species exhibit a variety of sexual strategies, with *Hu. omanensis* undergoing heterothallic mating while MAT2 isolates of *Hu. moniliformis* are able to reproduce unisexually (Wilson *et al.* 2015).

References: Kamgan *et al.* 2008, Heath *et al.* 2009, Tarigan *et al.* 2010, Kamgan Nkuekam *et al.* 2012, Chen *et al.* 2013, Kamgan Nkuekam *et al.* 2013 (pathogenicity); De Beer *et al.* 2013a (higher classification); De Beer *et al.* 2013b (nomenclature); Wingfield *et al.* 2013, De Beer *et al.* 2014 (generic definitions and phylogenetic relationships); Wilson *et al.* 2015 (mating strategies).

Huntiella abstrusa A.M. Wilson, Marinc., M.J. Wingf., **sp. nov.** MycoBank MB821072. Fig. 26.

Etymology: Name refers to the fact that this cryptic species was obscured by the name *Ceratocystis moniliformis* for more than a decade.

On MEA: *Ascomata* 145–315 × 130–275 µm, perithecial, embedded in media or superficial in mycelial mass, single or in groups, pale brown when young, becoming dark brown with age, ellipsoidal to subglobose; *ascomatal wall of textura epidermoidea* to *textura globulosa*, covered with short sterile hyphae, 30–105 µm long, hyaline becoming pale brown with age, mostly unbranched, flexuous, tapering towards apex, with conical spines; *necks* 595–1100 µm long, 21–71.5 µm wide near base, 11–18 µm wide near apex, dark brown, tapering towards apex, becoming easily detached from ascomatal base when pressed, with a disk-like structure near base; *hyphae* near apex 18.5–37 µm long, 1–2 µm wide near base, 0.5–1.5 µm wide, mostly straight, showing no distinct divergent nor convergent, aseptate, unbranched, hyaline, tapering towards apex. *Asci* not observed. *Ascospores* 4.5–5.5 × 3.5–6 µm (av. 5.2 × 4.6 µm) without sheath, 2–3.5 µm thick in side-view, hyaline, oblong to subglobose, clothed with gelatinous sheath, 0.5–1.5 µm thick, in side-view giving an impression of a hat. *Conidiophores* up to 80 µm long, septate, flexuous, sometimes branched, occasionally reduced to conidiogenous cells, often lightly sub-hyaline to pale brown near base. *Conidiogenous cells* hyaline, enteroblastic, in two shapes, originating from same or different hyphae; lageniform, 15.5–33 µm long, 2–4.5 µm wide at base, gradually tapering towards apex, 1–3 µm wide at apex, producing rectangular conidia; or cylindrical with wide-mouthed, 22–50 µm long, 3.5–6.5 µm wide at apex, 3–4 µm wide at base, producing barrel-shaped conidia. *Conidia* in chains, hyaline, aseptate, in two shapes, rectangular, 4–8.5 × 1.5–2.5 µm (av. 5.6 × 1.8 µm); or barrel-shaped, 5–14.5 × 4–7 µm (av. 8.1 × 5.9 µm). *Chlamydospores* absent.

Culture characteristics: On 2 % MEA optimum growth at 30 °C reaching 82.7 mm in dark in 3 d, followed by 25 °C reaching 77.3 mm, showing slow growth at 10, 15, 20, 35 °C. Cultures circular with smooth margins, aerial mycelium fluffy to velvety, moderately dense, above and below dark brown fading towards edge and with white margins.

Material examined: **Indonesia**, Riau province, Teso East, S 0°04'33.00", E 101°37'23.00", on the bark of *Eucalyptus* sp. (*Myrtaceae*), Oct. 2005, M. Tarigan (**holotype** PREM 61671, culture ex-type CBS 142243 = CMW 21092).

Notes: For more than a decade, *Hu. abstrusa* was thought to be *Ceratocystis moniliformis* (now *Hu. moniliformis*). Phylogenetic analyses of ITS, LSU, 60S, *mcm7* and *tub2* have shown that *Hu. abstrusa* is distinct from *Hu. moniliformis* and other *Huntiella* spp. It is most closely related to *Hu. inquinans*, *Hu. microbasis* and *Hu. sumatrana* from Indonesia, *Hu. chinaeucensis* from China and *Hu. bhutanensis* from Bhutan (De Beer *et al.* 2014, Van Wyk *et al.* 2004, Tarigan *et al.* 2010, Chen *et al.* 2013). Neither *Hu. abstrusa* nor any of the other *Huntiella* species are primary pathogens and

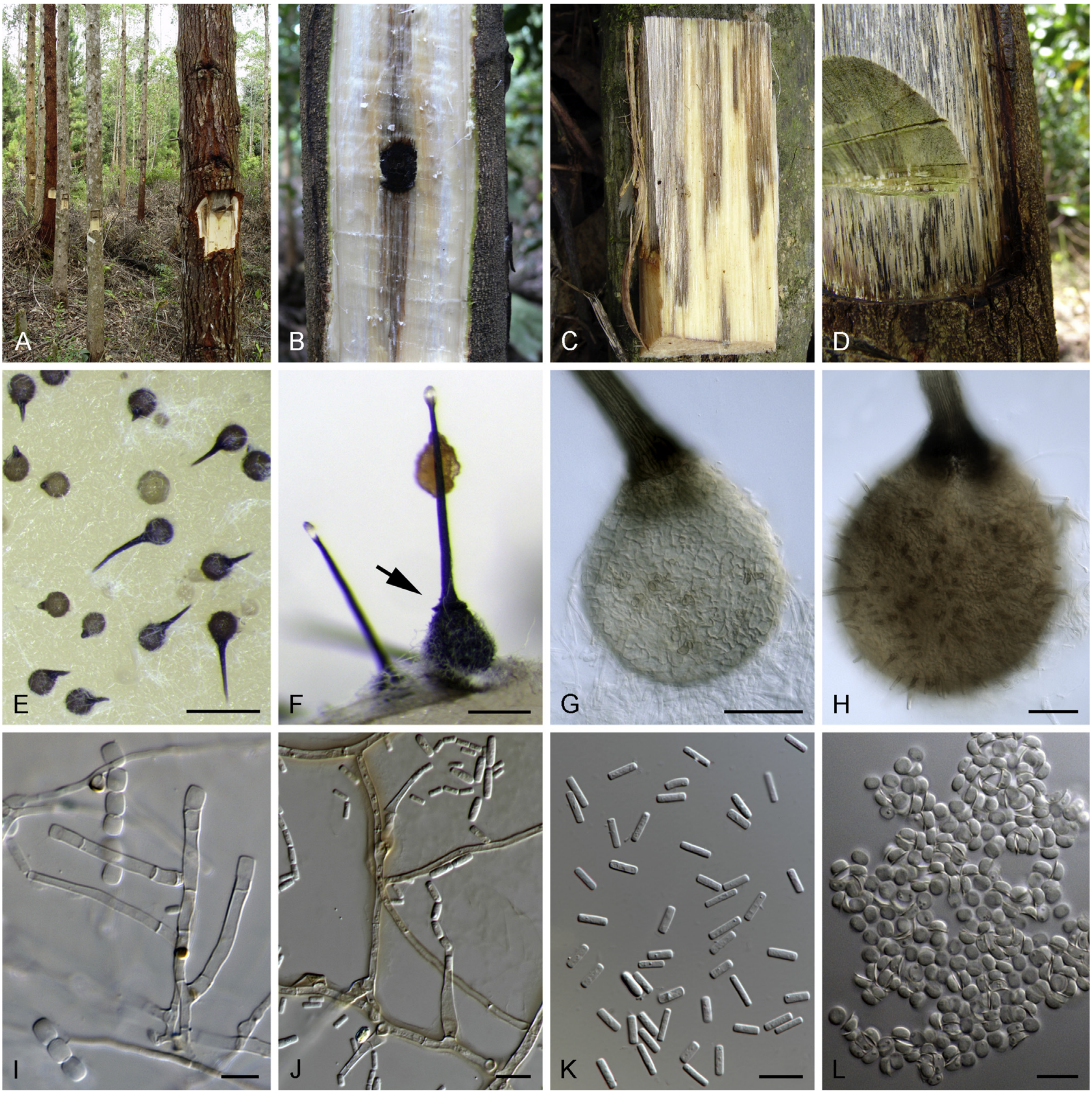

Fig. 24. *Huntiella* spp. **A–D.** Disease symptoms. **A.** *Eucalyptus* trees artificially wounded to trap *Huntiella* spp. **B.** Lesion associated with inoculation with *Huntiella sumatrana* on an *Acacia mangium* stem. **C.** Discolouration of wood associated with artificially induced wound on the stem of a *Eucalyptus* tree from which *Huntiella* spp. were isolated. **D.** Blue-stained *Eucalyptus* wood associated with *Huntiella* infection. **E–H, L.** Sexual morphs. **E.** Ascomata on 2 % MEA in various developmental stage from young (paler) to mature (darker). **F.** Mature ascomata with fresh ascospore droplets at the tip of necks and ostiolar neck with a disc-like base (arrow). **G, H.** Young ascoma showing developing of conical spines (G) and ascomatal hyphae (H). **L.** Ascospores. **I–K.** Asexual morphs. **I.** Tubular-form conidiogenous cell producing barrel-shaped conidia. **J.** Flask-shaped conidiogenous cells producing rectangular-shaped conidia. **K.** Rectangular-shaped conidia. **E, F, H, K.** *Huntiella omanensis* (CMW 11056). **G, L.** *Huntiella moniliformis* (CMW 36908). **I, J.** *Huntiella abstrusa* (CMW 21092). Scale bars: E = 500 µm; F = 250 µm; G, H = 50 µm; I–L = 10 µm.

typically infect freshly made wounds on trees. Despite only minor morphological differences between *Huntiella* species, *Hu. abstrusa* can be distinguished from the other species by its longer necks and the presence of barrel-shaped conidia. The *Hu. abstrusa* isolate examined is considered heterothallic.

Authors: A.M. Wilson, S. Marincowitz, M.J. Wingfield & B.D. Wingfield

Macgarvieomyces Klaubauf, *et al.*, Stud. Mycol. 79: 106. 2014. Fig. 27.

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

Type species: *Macgarvieomyces borealis* (de Hoog & Oorschot) Klaubauf, *et al.*, basionym: *Pyricularia borealis* de Hoog & Oorschot. Holotype and ex-type strain: IMI 105288, CBS 461.65.

DNA barcodes (genus): LSU, ITS.

DNA barcodes (species): ITS, *act, cal*, *rpb1*. Table 9. Fig. 28.

Mycelium consisting of smooth, hyaline, branched, septate hyphae. *Conidiophores* solitary, erect, straight or curved, mostly unbranched, medium to dark brown, smooth or finely verruculose, septate. *Conidiogenous cells* integrated, terminal, rarely intercalary, medium to dark brown, smooth or finely verruculose, forming a rachis with protruding denticles, appearing flat-tipped.

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

Species	Isolates[1]	GenBank accession numbers[2]				References
		ITS	*tub2*	*mcm7*	*tef1*	
Huntiella abstrusa	CBS 142243^{T}	KY913291	KY913290	KY913289	–	Present study
Hu. bhutanensis	CBS 114289^{T}	AY528952 NR119506	AY528962	KM495412	AY528962^{a}	Van Wyk *et al.* (2004), De Beer *et al.* (2014)
Hu. ceramica	CBS 122299^{T}	EU245022	EU244994	KM495485	EU244926^{b}	Heath *et al.* (2009), De Beer *et al* (2014)
Hu. chinaeucensis	CBS 127185^{T}	JQ862729	JQ862717	KM495416	JQ862741^{c}	Chen *et al.* (2013), De Beer *et al.* (2014)
Hu. cryptoformis	CBS 131279^{T}	KC691464	KC691488	–	KC691512^{c}	Mbenoun *et al.* (2014)
Hu. decipiens	CBS 129736^{T}	HQ203216	HQ203233	KM495422	HQ236435^{c}	Kamgan Nkuekam *et al.* (2013), De Beer *et al.* (2014)
Hu. inquinans	CBS 124388^{T}	EU588587	EU588666	KM495436	EU588674^{a}	Tarigan *et al.* (2010), De Beer *et al* (2014)
Hu. microbasis	CBS 124013^{T}	EU588593	EU588672	KM495442	EU588680^{a}	Tarigan *et al.* (2010); De Beer *et al.* (2014)
Hu. moniliformis	CBS 118127	FJ151422	FJ151456	KM495443	FJ151478^{a}	Van Wyk *et al.* (2011), De Beer *et al.* (2014)
Hu. moniliformopsis	CBS 109441^{T}	AY528998	AY528987	KM495444	AY529008^{a}	Yuan & Mohammed (2002), Van Wyk *et al.* (2004), De Beer *et al.* (2014)
Hu. oblonga	CBS 122291^{T}	EU245019	EU244991	KM495447	EU244951^{b}	Heath *et al.* (2009), De Beer *et al.* (2014)
Hu. omanensis	CBS 115787	DQ074742	DQ074732	KM495449	DQ074737^{a}	Al-Subhi *et al.* (2006)
Hu. salinaria	CBS 129733^{T}	HQ203213	HQ203230	KM495461	HQ236432^{c}	Kamgan Nkuekam *et al.* (2013), De Beer *et al.* (2014)
Hu. savannae	CBS 121151^{T}	EF408551	EF408565	KM495462	EF408572^{c}	Kamgan *et al.* (2008), De Beer *et al.* (2014)
Hu. sublaevis	CBS 122517	FJ151431	FJ151465	KM495464	FJ151486^{b}	Van Wyk *et al.* (2011), De Beer *et al.* (2014)
Hu. sumatrana	CBS 124011^{PT}	EU588589	EU588668	KM495465	EU588678^{a}	Tarigan *et al.* (2010), De Beer *et al.* (2014)
Hu. tribiliformis	CBS 115866^{T}	AY529003	AY529003	KM495468	AY529014^{a}	Van Wyk *et al.* (2006), De Beer *et al.* (2014)
Hu. tyalla	CBS 128703^{T}	HM071900	HM071913	KM495470	HQ236452^{c}	Kamgan Nkuekam *et al.* (2012), De Beer *et al.* (2014)

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

[2] ITS: internal transcribed spaces and intervening 5.8S nrDNA, *tub2*: partial β-tubulin gene, *mcm7*: mini-chromosome maintenance complex component 7, *tef1*: partial translation elongation factor 1-alpha gene. $^{a,\ b}$ and ^{c} in *tef1* column indicate the primers used in sequencing: a: Ef1-728f, ef1-986r, b: EF1f, EF1r, c:EF1f, EF2r.

Conidia solitary, narrowly obclavate to narrowly pyriform, hyaline, often becoming pale brown with age, smooth, granular, guttulate, medianly 1-septate, apex obtusely rounded; *hila* somewhat thickened, refractive or not, not or slightly darkened. *Chlamydospores* brown, ellipsoid, arranged in chains (adapted from Klaubauf *et al.* 2014).

Culture characteristics: Colonies on MEA buff to rosy buff, isabelline or pale luteous, with pale olivaceous grey central mycelium, with entire, lobate or round and hairy edge, umbonate to conical or flat to slightly raised colony with somewhat velvety or wool-like texture; reverse iron grey, ochreous and buff towards edge or pale luteous. On CMA and OA transparent, pale luteous to olivaceous or grey olivaceous, flat, smooth and velutinous surface, undulate margin. Colonies on PDA pale luteous, white with buff centre or whitish to buff with honey centre, round, flat, fringed margin; reverse white with buff centre or whitish to buff with honey centre.

Optimal media and cultivation conditions: On OA at 25 °C under dark, or autoclaved barley seeds placed on SNA at 25 °C under near-ultraviolet light (12 h light, 12 h dark).

Distribution: Europe and New Zealand.

Hosts: Primarily on *Juncus effusus* and *Luzula* spp. (*Juncaceae*), also reported on *Carex* sp. and *Kyllinga brevifolia* (*Cyperaceae*).

Disease symptoms: Leaf spots.

Notes: *Macgarvieomyces* was recently introduced to accommodate two species previously placed in *Pyricularia*. Phylogenetic analyses based on LSU, ITS, *act*, *cal* and *rpb1* demonstrated that these taxa are not congeneric with *Pyricularia s. str.* (Klaubauf *et al.* 2014). Species in this genus were isolated from *Juncaceae* in Europe and associated with leaf spots. Species have also been reported on *Cyperaceae* and New Zealand (Farr & Rossman 2017); however, these host and distribution data have not been corroborated based on DNA sequence analyses.

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

Macgarvieomyces luzulae (Ondřej) Y. Marín, Akulov & Crous, **comb. nov.** MycoBank MB823764. Fig. 29.
Basionym: *Pyricularia luzulae* Ondřej, Česká Mykol. 42: 81. 1988.

Leaf spots up to 17 mm long, ellipsoid to fusiform, grey to pale brown at middle, dark brown at margin. On SNA: *Mycelium* with hyaline, smooth, septate, branched, 2–3 μm diam hyphae. *Conidiophores* 60–120 × 4–7 μm, erect, dark brown, unbranched, subcylindrical, straight to flexuous, thick-walled, finely verruculose, 2–3-septate. *Conidiogenous cells* 30–50 × 4–6 μm, terminal and subcylindrical, finely verruculose, dark brown, tapering toward apex with numerous denticles pointing upwards, 1–4 × 1–1.5 μm; *scars* unthickened. *Conidia* (18–)20–22(–30) × (4–)5(–6) μm, solitary, narrowly pyriform, hyaline, becoming pale brown with age, guttulate, 1(–2)-septate, apex obtusely rounded, base truncate, 2 μm diam, slightly darkened, refractive.

Culture characteristics: Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, lobate margins, covering plate after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse pale luteous.

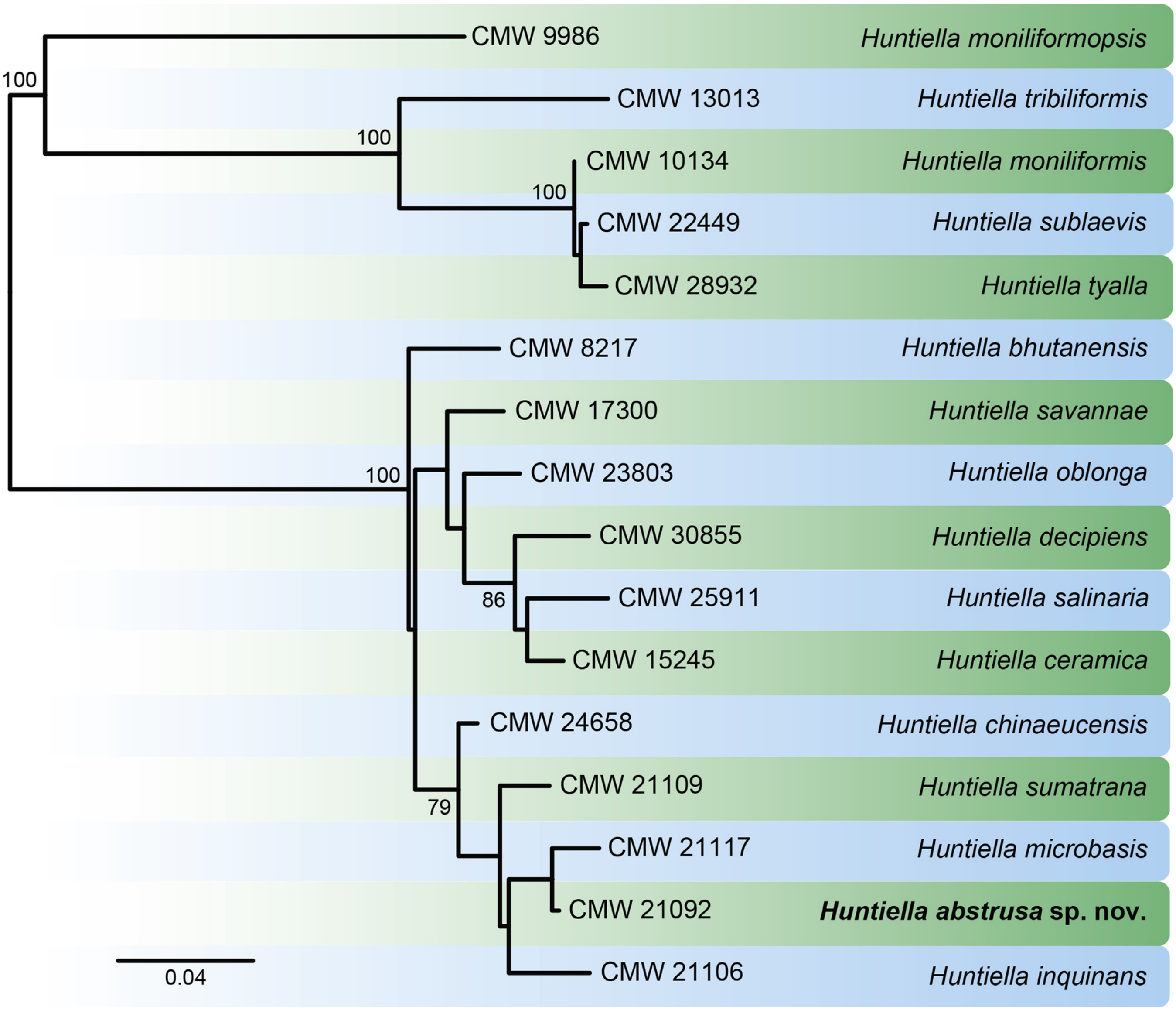

Fig. 25. A maximum likelihood (ML) phylogram constructed using the combined dataset of the 60S (370 bp), LSU (813 bp), ITS (393 bp), *mcm7* (589 bp) and *tub2* (433 bp) gene regions of *Huntiella* spp. ML analyses were performed using PhyML with Smart Model Selection Online, selecting the GTR substitution model. Bootstrap values of 70 % or more are indicated above the branches. The newly described species, *Hu. abstrusa*, is indicated in **bold**. TreeBASE: S20860.

Materials examined: **Slovakia**, on leaves of *Luzula sylvatica* (*Juncaceae*), Jul. 1984 (**holotype of *Pyricularia luzulae*** PRM 842743). **Ukraine**, on leaves of *Luzula* sp. (*Juncaceae*), 2016, A. Akulov (**epitype of *Pyricularia luzulae* designated here** MBT379806, CBS H-23355, culture ex-epitype CBS 143401 = CPC 32458); *ibid*., CWU (Myc) AS 5966 / 6437; Carpathian Biosphere reserve, on leaves of *Luzula sylvatica* (*Juncaceae*), Aug. 2016, A. Akulov, CPC 31555; *ibid*., CPC 31571.

Notes: *Pyricularia luzulae* was introduced for a fungus isolated on *Luzula sylvatica* from Slovakia (Ondřej 1988). In the original description PRM 842743 was designated as holotype, but no living culture was associated with this specimen. Therefore, a strain that closely fits the description of the protologue, and isolated from the same host in a close country to Slovakia, namely Ukraine, is designated here as epitype. The only difference observed was in the conidial size, since in the original description (*in vivo*) the conidia were larger and 1–2-septate (17.5–36 × 3.5–7.5 µm). However, the measurements of our isolate growing *in vivo* are 27.5–33 × 6.5–7.5 µm, and *in vitro* 18–30 × 4–6 µm, and conidia could become 2-septate with age.

The phylogenetic study of *Py. luzulae* revealed that it belongs to *Macgarvieomyces*. As noted above, the host of this genus is *Juncus effusus* in the same family as *Luzula* (*Juncaceae*).

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

Metulocladosporiella Crous, *et al.*, Mycol. Res. 110: 269. 2006. Fig. 30.

Classification: *Eurotiomycetes, Chaetothyriomycetidae, Chaetothyriales, Herpotrichiellaceae.*

Type species: *Metulocladosporiella musae* (E.W. Mason) Crous, *et al.*, basionym: *Cladosporium musae* E.W. Mason. Lectotype designated by Crous *et al.* (2006a): IMI 7521 (slide). Epitype and ex-epitype strain designated by Crous *et al.* (2006a): CBS H-14788, CBS 161.74 = ATCC 36973.

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

DNA barcodes (*species*): ITS, *tef1*. Table 10. Fig. 31.

Mycelium internal and external on substrate, hyphae branched, septate, hyaline, subhyaline to pale olivaceous, thin-walled. *Stromata* lacking. *Conidiophores* macronematous, mononematous, occasionally with intermixed micronematous conidiophores, solitary or in loose groups, arising from hyphae, erect, with a long, subcylindrical, simple stipe and a branched

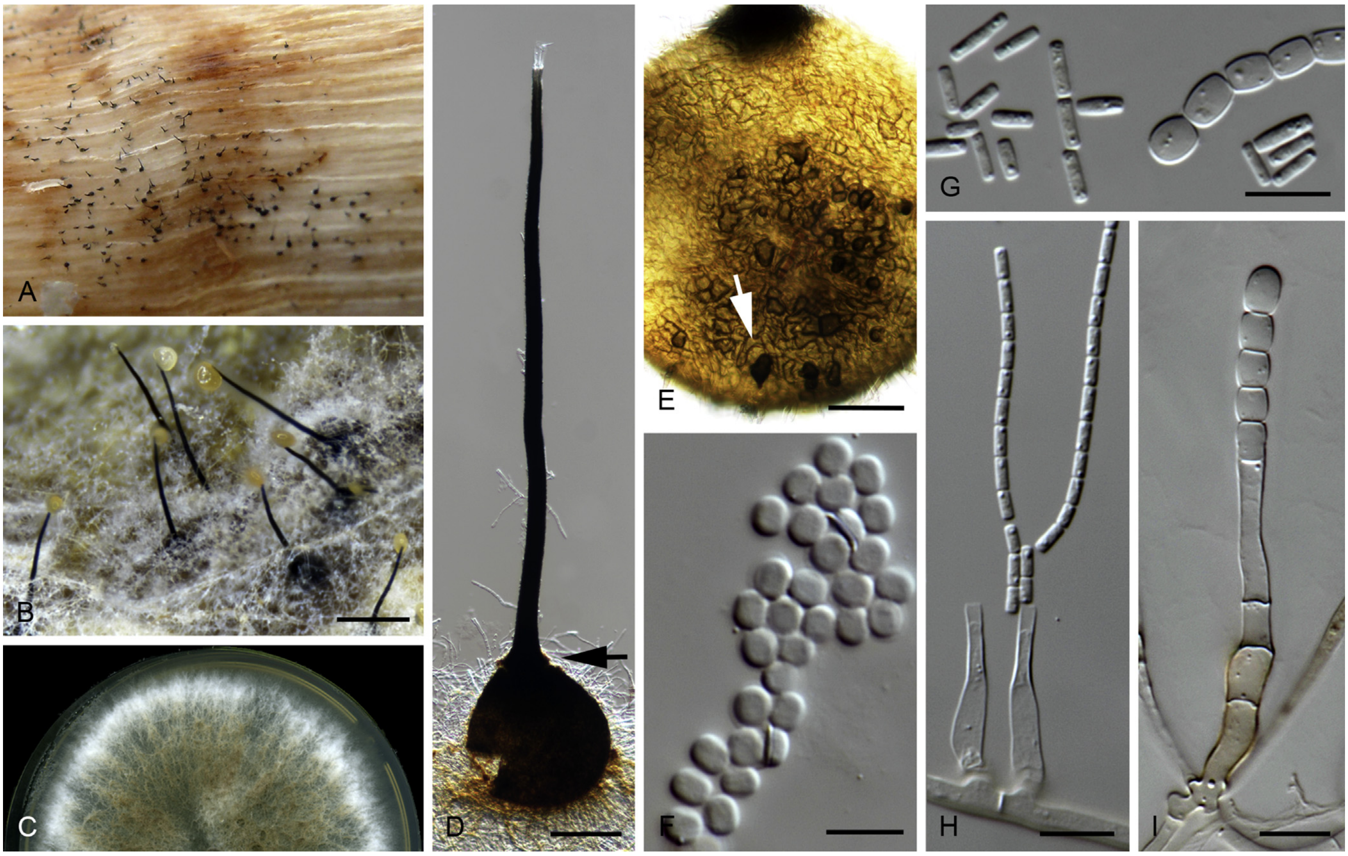

Fig. 26. *Huntiella abstrusa* (ex-type CBS 142243 = CMW 21092). **A.** Ascomata on host substrate. **B.** Ascospore droplets of cream to yellow-coloured at the tip of ascomatal neck and ascomata embedded in aerial hyphae producing asexual structures. **C.** Colony on 2 % MEA grown in the dark at 30 °C for 3 d. **D.** Mature ascoma with a disk-like base (arrow). **E.** Base of young ascoma (1 wk) with conical spines (arrow) (image taken in bright field). **F.** Ascospores. **G.** Two types of conidia: rectangular-shaped and barrel-shaped conidia. **H.** Flask-shaped conidiogenous cells and rectangular-shaped conidia. **I.** Tubular-shaped conidiogenous cell and barrel-shaped conidia. Scale bars: B = 500 µm; D = 100 µm; E = 50 µm; F–I = 10 µm.

terminal part; *stipe* septate, medium to brown, smooth or almost so, usually swollen at base; *branched part* loose to dense, metuloid, of short to long branchlets and ramoconidia, tips paler than stipes, subhyaline to pale olivaceous. *Conidiogenous cells* integrated, terminal, occasionally intercalary, polyblastic, sympodial; *conidiogenous loci* (conidial scars) subconspicuous to conspicuous, subdenticulate, truncate, unthickened to slightly thickened, and somewhat darkened-refractive. *Conidia* and *ramoconidia* in simple and branched chains, ellipsoid, ovoid, subcylindrical, or fusiform, 0–1-septate, subhyaline to pale olivaceous, thin-walled, smooth; *hila* truncate, unthickened to slightly thickened or slightly darkened-refractive; *secession* schizolytic. *Sexual morph* unknown (adapted from Crous *et al.* 2006a).

Culture characteristics: Colonies on PDA and OA under near-ultraviolet light with smooth, regular margins and sparse to moderate aerial mycelium. On PDA surface pale mouse grey to mouse grey or dirty white-grey, greyish sepia, smoke grey to grey olivaceous, or olivaceous; reverse greenish black, cinnamon to isabelline with centre fuscous black, or grey olivaceous to dark grey olivaceous or olivaceous black.

Optimal media and cultivation conditions: SNA under near-ultraviolet light at 25 °C to induce sporulation.

Distribution: Africa, America, Asia and Oceania.

Hosts: *Musa* spp. (*Musaceae*).

Disease symptoms: Leaf spots; Cladosporium speckle disease of banana.

Notes: *Metulocladosporiella* was introduced by Crous *et al.* (2006a) to accommodate two cladosporium-like species causing speckle disease on banana. *Metulocladosporiella* can be distinguished from *Cladosporium* and allied genera by the presence of apically branched, brown conidiophores with paler tips and chains of pale, smooth, often subhyaline conidia.

The phylogenetic analysis based on the ITS and LSU sequences demonstrated that *Metulocladosporiella* belongs in *Chaetothyriales*. Morphologically, the conidiogenous loci and conidial hila resemble those of *Cladophialophora*, which is another member of this order. However, *Cladophialophora* produces unbranched, micro- to semimacronematous conidiophores, and concolourous conidia. Moreover, *Cladophialophora* includes human pathogenic species (Crous *et al.* 2006a). In the present study, the recommended barcodes for species delimitation are ITS and *tef1*.

Hitherto, all species described in *Metulocladosporiella* are pathogens of banana and occur in countries where this crop is cultivated (Jones 2000, Crous *et al.* 2006a).

Reference: Crous *et al.* 2006a (morphology and phylogeny).

Metulocladosporiella chiangmaiensis Y. Marín, Cheew. & Crous, **sp. nov.** MycoBank MB824031. Fig. 32.

Etymology: Name from Chiang Mai, the province in Thailand where this fungus was collected.

Mycelium internal and external, superficial; *hyphae* 1.5–3.5 µm wide, branched, septate, occasionally slightly constricted at septa, with small swellings, hyaline, subhyaline to pale

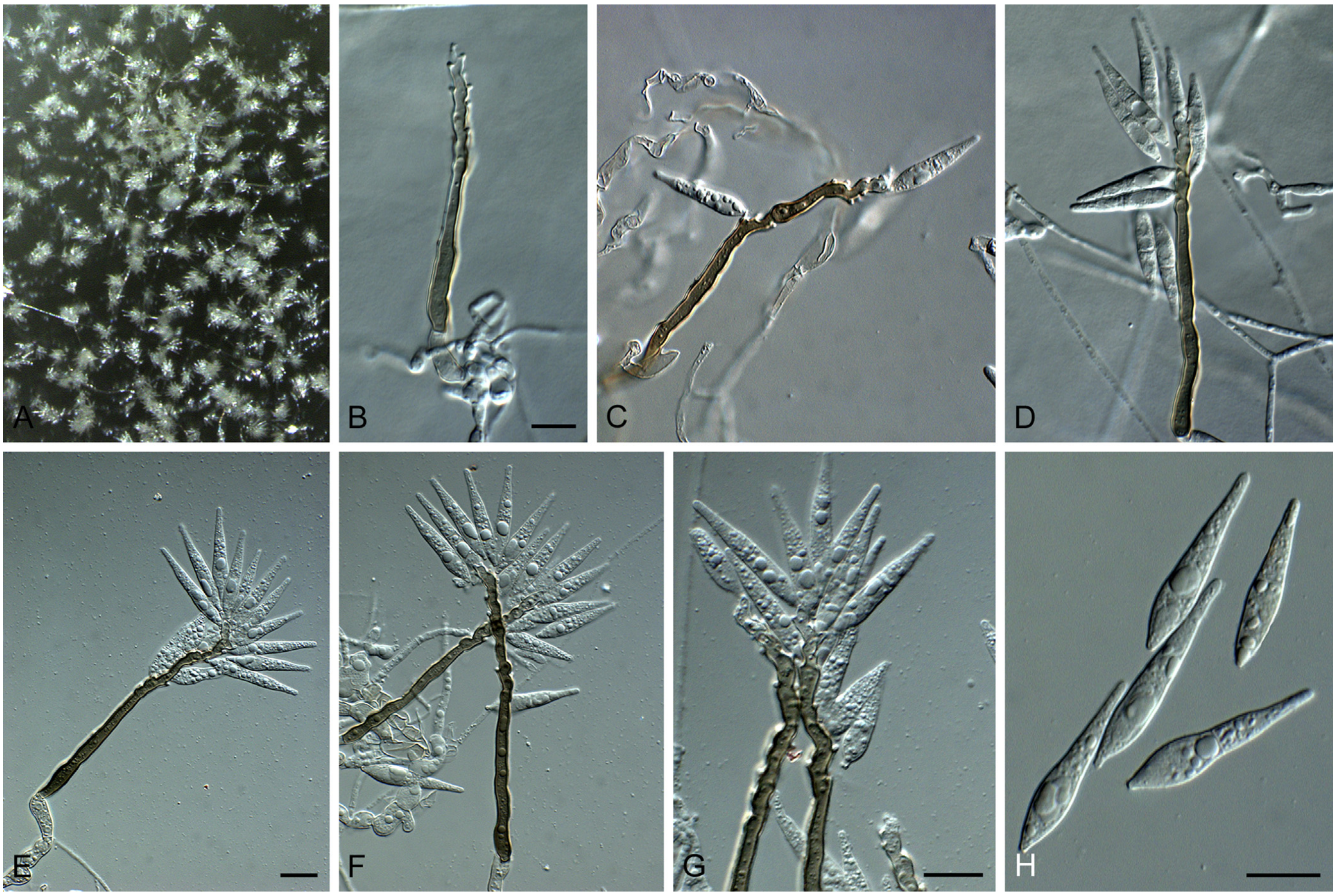

Fig. 27. **A–H.** *Macgarvieomyces juncicola* (CBS 610.82). **A.** Colony sporulating on OA. **B–G.** Conidiophores and conidia forming on SNA. **H.** Conidia. Scale bars = 10 µm. Pictures taken from Klaubauf *et al.* (2014).

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

Species	**Isolates**[1]	**GenBank accession numbers**[2]				**References**
		ITS	***act***	***cal***	***rpb1***	
Macgarvieomyces borealis	CBS 461.65^T	KM484854	KM485170	KM485239	KM485070	Klaubauf *et al.* (2014)
Ma. juncicola	CBS 610.82	KM484855	KM485171	KM485240	KM485071	Klaubauf *et al.* (2014)
Ma. luzulae	CBS 143401^{ET}	MG934440	MG934463	MG934519	MG934469	Present study
	CPC 31555	MG934441	MG934464	MG934520	MG934470	Present study
	CPC 31571	MG934442	MG934465	MG934521	MG934471	Present study

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

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

olivaceous, thin-walled, smooth, hyphae occasionally aggregated, forming ropes; with numerous intermixed *micronematous conidiophores*, erect from vegetative mycelium, intercalary, straight to flexuous, unbranched, subhyaline, usually with simple terminal conidial chains. *Macronematous conidiophores* 85–1050 µm long, arising from superficial hyphae, erect, solitary to loosely aggregated, composed of a subcylindrical stipe, 5.5–9.5(–10.5) µm wide, 3–18 septate, swollen or lobed at base, 8–17(–18.5) µm diam, with short, rhizoid, subhyaline to pale brown hyphae growing from base, medium to brown in lower half, paler towards apex, tips pale brown or even subhyaline, thick-walled below, thin-walled towards apex, smooth; *apex* persistently branched, branched part composed of usually fairly compact, closely arranged subcylindrical branchlets; *primary branches* (13–)17–45(–55) × 3–5.5 µm, 0(–1)-septate, giving rise to 1–3 secondary branches, or to conidiogenous cells; *secondary branches* 13–28 × 2.5–5(–5.5) µm, 0(–1)-septate, giving rise to 1–2(–3) conidiogenous cells; *conidiogenous cells* 9–17 × 3–5 µm, subcylindrical, terminal or occasionally intercalary, sympodial, polyblastic, conidiogenous loci 1–1.5(–2) µm wide, subconspicuous to conspicuous, subdenticulate, somewhat protuberant, truncate, wall unthickened to somewhat so, darkened-refractive. *Conidia* 5.5–10(–12.5) × 2.5–4 µm, in simple and branched acropetal chains, ellipsoid-ovoid, fusoid, subcylindrical, aseptate, subhyaline to pale brown, thin-walled, smooth, with 1–3(–4) hila, 1–1.5 µm diam, up to 2 µm diam at base of ramoconidia, truncate, unthickened or almost so, and somewhat darkened-refractive, secession schizolytic; *ramoconidia* 7–15(–17) × 3–4.5 µm.

Culture characteristics: Colonies on PDA reaching 25–28 mm diam after 2 wk at 25 °C, moderate aerial mycelium, velvety,

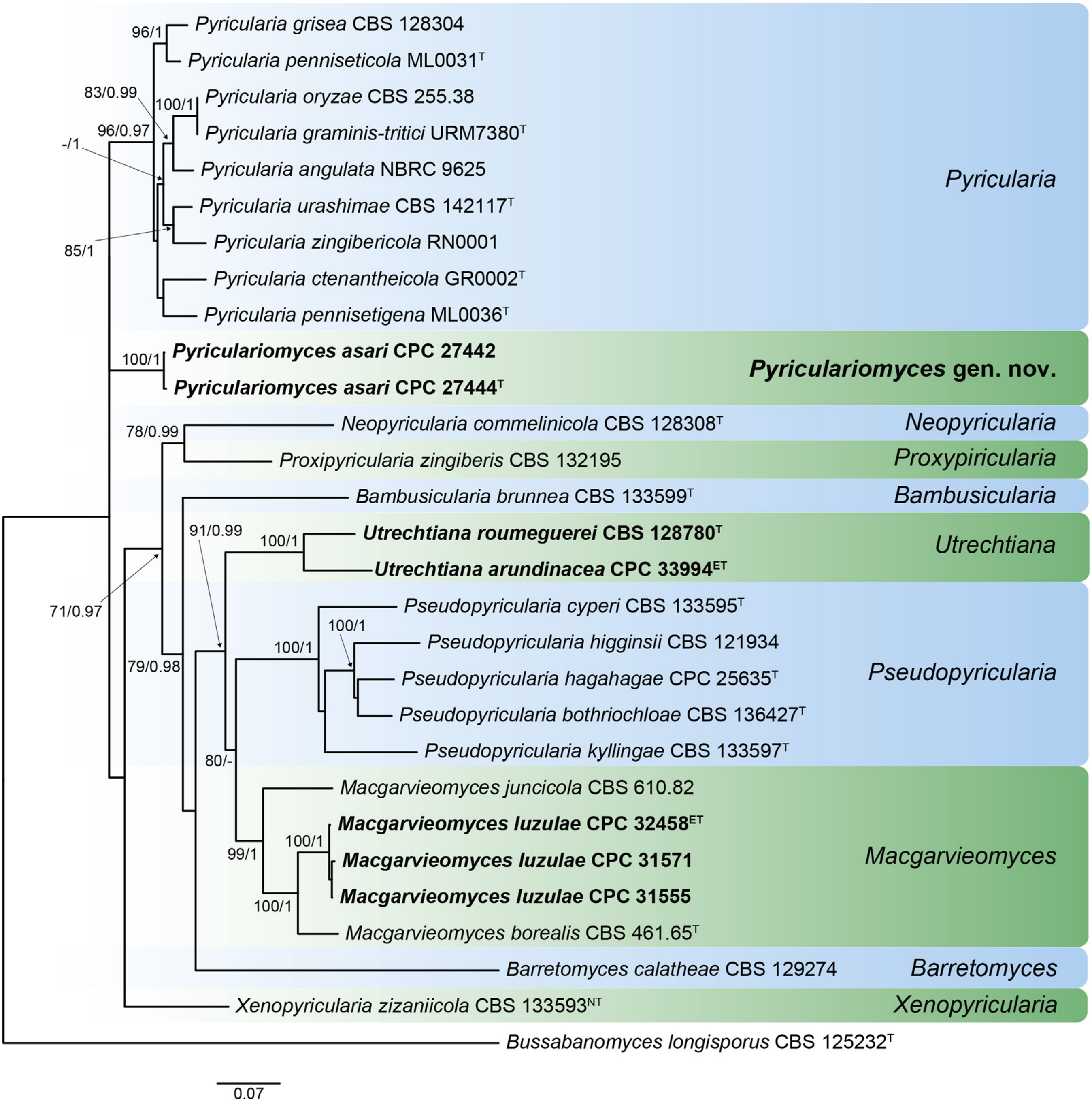

Fig. 28. RAxML phylogram obtained from the combined ITS (548 bp), *act* (375 bp), *cal* (579 bp) and *rpb1* (1011 bp) sequence alignment of members of *Pyriculariaceae*. The tree was rooted to *Bussabanomyces longisporus* CBS 125232. The novelties proposed in this study are indicated in **bold**. RAxML bootstrap support (BS) values above 70 % and Bayesian posterior probability scores above 0.95 are shown at the nodes. GenBank accession numbers were listed in Klaubauf *et al.* (2014). T, ET and NT indicate ex-type, ex-epitype and ex-neotype strains, respectively. TreeBASE: S21899.

umbonate; surface greyish sepia, halo surrounding centre vinaceous buff, and margins hazel; reverse cinnamon to isabelline, centre fuscous black. Colonies on OA reaching 32–35 mm diam after 2 wk at 25 °C, sparse aerial mycelium, flat except margins due to aerial mycelium; surface hazel, centre brown vinaceous, margins smoke grey; reverse livid vinaceous, centre brown vinaceous, margins pale brown vinaceous.

Material examined: **Thailand**, Chiang Mai Province, Mae Klang Luang, N 18° 32.465', E 98° 32.874', from leaves of *Musa* sp. (*Musaceae*), 6 Oct. 2008, P.W. Crous & R. Cheewangkoon (**holotype** CBS H-23393, culture ex-type CBS 143918= CPC 18646).

Notes: *Metulocladosporiella chiangmaiensis* is related to *M. musigena*. Both species are known from Thailand, and produce more micronematous conidiophores than any other species in the genus. However, *M. chiangmaiensis* produces longer macronematous conidiophores and shorter conidia than *M. musigena*, which produces conidiogenous cells directly from the apex of its macronematous conidiophores, which is not the case in *M. chiangmaiensis*.

Metulocladosporiella malaysiana Y. Marín & Crous, **sp. nov.** MycoBank MB824032. Fig. 33.

Etymology: Name refers to Malaysia, the country from where it was isolated.

Mycelium internal and external, superficial; *hyphae* 1–3.5 µm wide, branched, septate, occasionally constricted at septa, with

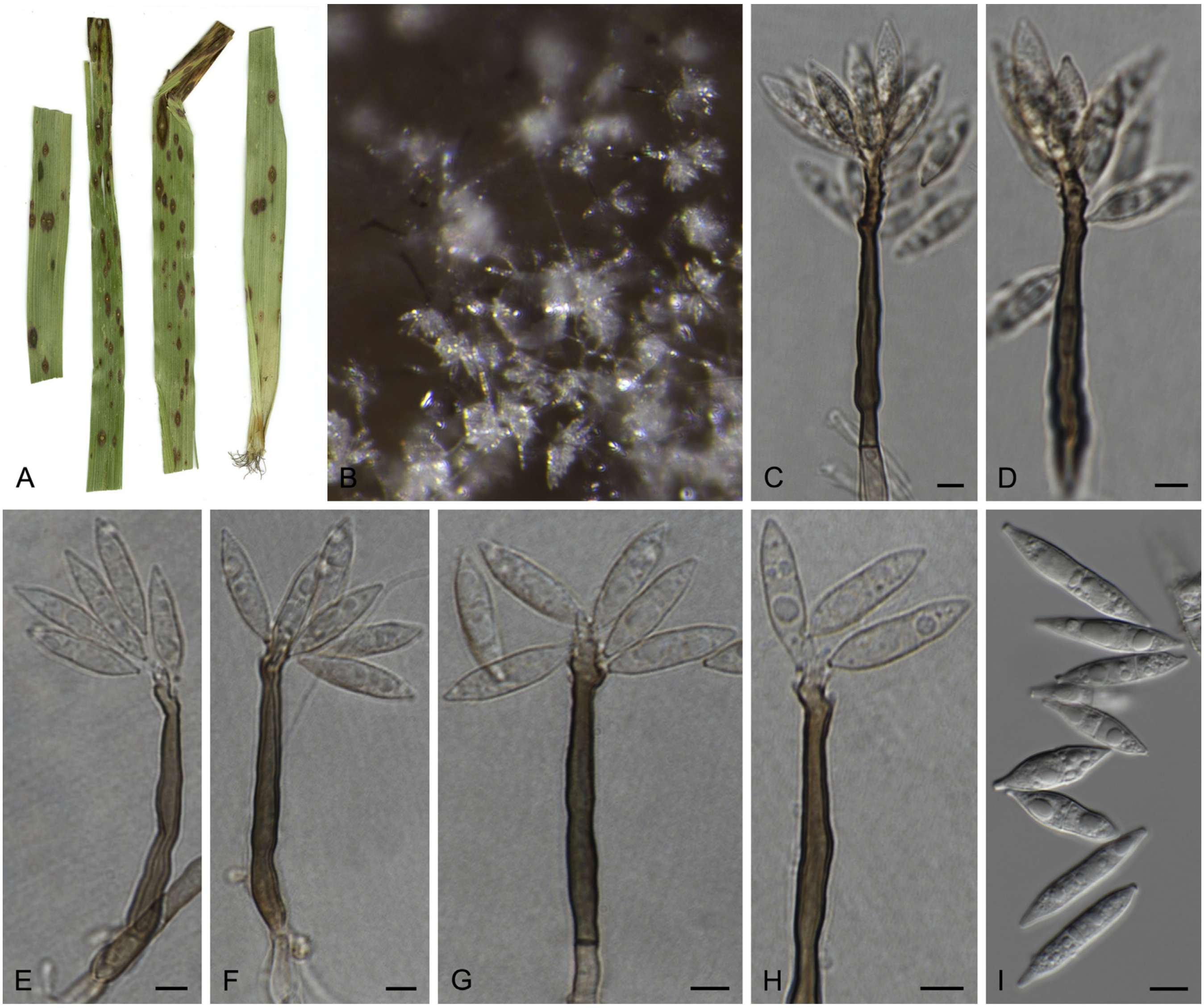

Fig. 29. A–I. *Macgarvieomyces luzulae* (ex-epitype CBS 143401). **A.** Disease symptoms on leaves of *Luzula sylvatica*. **B.** Colony sporulating on OA. **C–H.** Conidiophores and conidia forming on SNA. **I.** Conidia. Scale bars = 5 µm.

swellings, hyaline, subhyaline to pale brown, thin-walled, smooth, hyphae occasionally aggregated, forming ropes; occasionally with intermixed *micronematous conidiophores*, erect from vegetative mycelium, intercalary, straight to flexuous, unbranched, subhyaline, usually with simple terminal conidial chains. *Macronematous conidiophores* 57–565 µm long, arising from superficial hyphae, erect, solitary to loosely aggregated, composed of a subcylindrical stipe, 5–8 µm wide, (1–)2–11-septate, swollen or lobed at base, 7–15 µm diam, with short, rhizoid, subhyaline to pale brown hyphae growing from base, medium to brown in lower half, paler towards apex, tips pale brown or even subhyaline, thick-walled below, thin-walled towards apex, smooth; *apex* persistently branched, composed of fairly compact, closely arranged subcylindrical branchlets; *primary branches* (12–)16–44(–60) × 3.5–5.5 µm, 0–1(–2)-septate, giving rise to 1–2(–3) secondary branches, or to conidiogenous cells; *secondary branches* 11.5–26.5(–39) × 3–4.5 µm, 0(–1)-septate, giving rise to 1–2(–3) conidiogenous cells; *conidiogenous cells* 10–23 × 2.5–4.5 µm, subcylindrical, terminal or occasionally intercalary, sympodial, polyblastic, conidiogenous loci 1–2 µm wide, subconspicuous to conspicuous, subdenticulate, somewhat protuberant, truncate, wall not to slightly thickened, darkened-refractive. *Conidia* 5.5–13.5(–14.5) × (2.5–)3–4.5(–5) µm, in simple and branched acropetal chains, ellipsoid-ovoid, fusoid, subcylindrical, aseptate, subhyaline to pale brown, thin-walled, smooth, with 1–3 hila, 0.8–1.4 µm diam, up to 2 µm diam at base of ramoconidia, truncate, not to slightly thickened, and somewhat darkened-refractive, secession schizolytic; *ramoconidia* 7–13(–14) × 3–4.5(–5) µm.

Culture characteristics: Colonies on PDA reaching 23–27 mm diam after 2 wk at 25 °C, moderate aerial mycelium, giving cottony appearance, umbonate, margins fringed; surface olivaceous, mycelium smoke grey; reverse grey olivaceous to dark grey olivaceous. Colonies on OA reaching 30–34 mm diam after 2 wk at 25 °C, sparse aerial mycelium, umbonate, margins fringed; surface olivaceous, mycelium smoke grey to grey olivaceous; reverse dark grey olivaceous.

Material examined: **Malaysia**, from leaves of *Musa* sp. (*Musaceae*), 2010, M.H. Wong (**holotype** CBS H-23394, culture ex-type CBS 143919 = CPC 18131).

Notes: *Metulocladosporiella malaysiana* is related to *M. samutensis*. These can be easily distinguished based on the length of the macronematous conidiophores (57–565 in *M. malaysiana vs.* 200–1120 µm in *M. samutensis*), and the

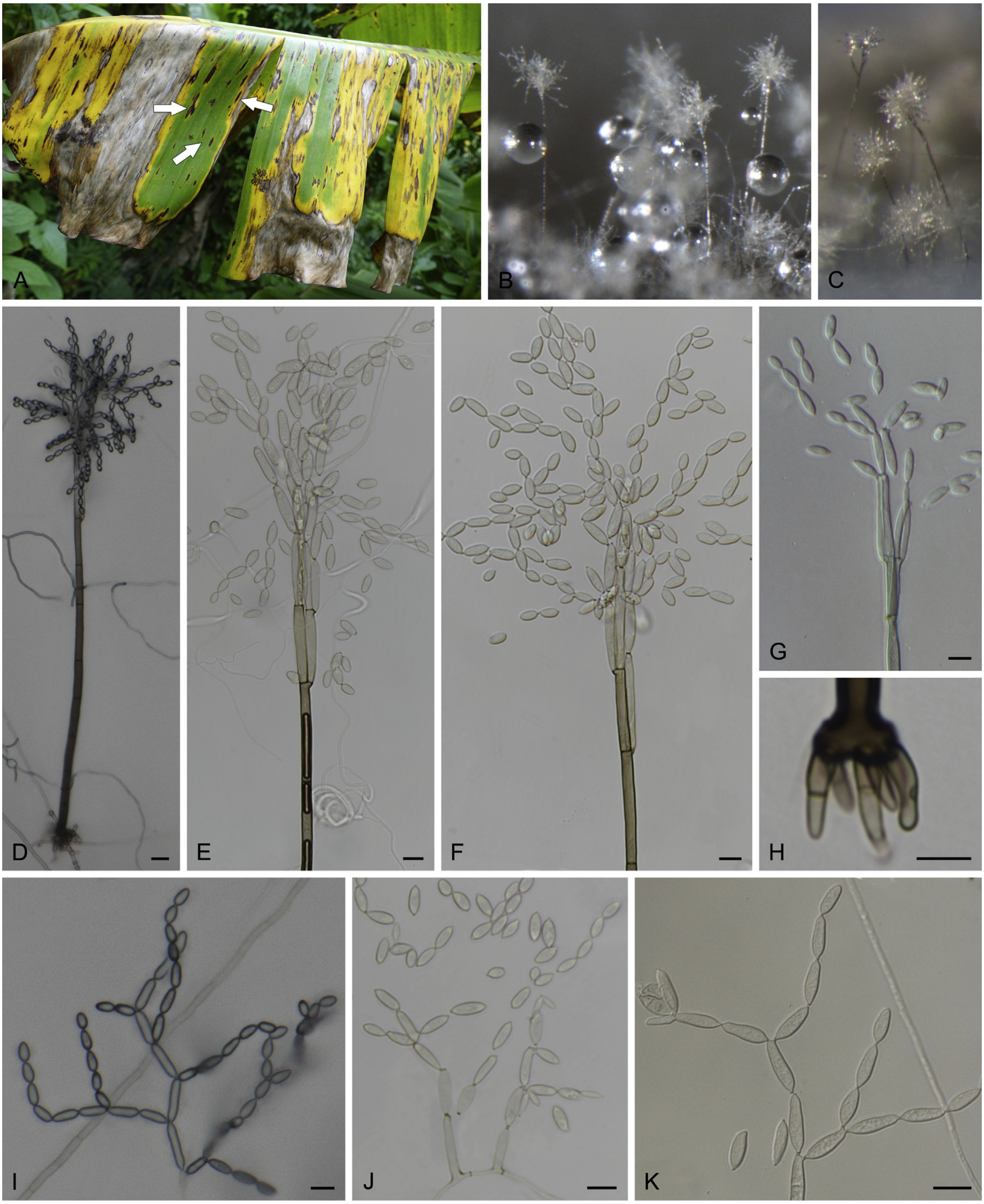

Fig. 30. *Metulocladosporiella* spp. **A.** Disease symptoms on *Musa* sp (indicated by the arrows). **B–K.** Asexual morph. **B–D.** Macronematous conidiophores. **B.** *Metulocladosporiella musicola* (CBS 121396). **C.** *Metulocladosporiella musicola* (ex-type CBS 110960). **D.** *Metulocladosporiella musae* (CPC 33937). **E–G.** Conidiogenous apparatus. **E, F.** *Metulocladosporiella musae* (CPC 33937). **G.** *Metulocladosporiella musicola* (ex-type CBS 110960). **H.** Lobed bases of macronematous conidiophore of *Metulocladosporiella musae* (CPC 33937). **I–K.** Micronematous conidiophores. **I, J.** *Metulocladosporiella musae* (CPC 33937). **K.** *Metulocladosporiella musicola* (CBS 121396). Scale bars = 10 µm.

almost total absence of secondary branches in *M. samutensis*. Moreover, *M. malaysiana* produces fewer micronematous conidiophores than the other species of *Metulocladosporiella*.

Metulocladosporiella musigena Y. Marín, Cheew. & Crous, **sp. nov.** MycoBank MB824033. Fig. 34.

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

Mycelium internal and external, superficial; *hyphae* 1–4 µm wide, branched, septate, occasionally slightly constricted at septa, with small swellings, hyaline, subhyaline to pale

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

Species	**Isolates**[1]	**GenBank accession numbers**[2]			**References**
		ITS	***cal***	***tef1***	
Metulocladosporiella chiangmaiensis	CBS 143918^{T}	MG934443	MG934522	MG934476	Present study
M. malaysiana	CBS 143919^{T}	MG934444	MG934523	MG934477	Present study
M. musae	CBS 161.74^{ET}	DQ008137	–	MG934478	Crous *et al.* (2006a), present study
	CBS 113863	DQ008138	MG934524	MG934479	Crous *et al.* (2006a), present study
	CPC 33937	MG934445	MG934525	MG934480	Present study
M. musicola	CBS 110960^{T}	DQ008127	MG934526	MG934481	Crous *et al.* (2006a), present study
	CBS 110962	MG934446	MG934527	MG934482	Crous *et al.* (2006a), present study
	CBS 110964	MG934447	MG934528	MG934483	Crous *et al.* (2006a), present study
	CBS 113860	DQ008130	MG934529	MG934484	Crous *et al.* (2006a), present study
	CBS 113861	DQ008131	MG934530	MG934485	Crous *et al.* (2006a), present study
	CBS 113862	DQ008132	MG934531	MG934486	Crous *et al.* (2006a), present study
	CBS 113864	DQ008133	MG934532	MG934487	Crous *et al.* (2006a), present study
	CBS 113865	DQ008134	MG934533	MG934488	Crous *et al.* (2006a), present study
	CBS 113873	DQ008135	MG934534	MG934489	Crous *et al.* (2006a), present study
	CPC 18124	MG934448	MG934535	MG934490	Present study
	CPC 32807	MG934449	MG934536	MG934491	Present study
	CPC 32849	MG934450	MG934537	MG934492	Present study
	CPC 32970	MG934451	MG934538	MG934493	Present study
M. musigena	CBS 143920^{T}	MG934452	MG934539	MG934494	Present study
M. samutensis	CBS 143921^{T}	MG934453	MG934540	MG934495	Present study

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

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

olivaceous, thin-walled, smooth, hyphae occasionally aggregated, forming ropes; with a great amount of intermixed *micronematous conidiophores*, erect from vegetative mycelium, intercalary, straight to flexuous, unbranched, subhyaline, usually with simple terminal conidial chains. *Macronematous conidiophores* (115–)170–780 µm long, arising from superficial hyphae, erect, solitary to loosely aggregated, composed of a subcylindrical stipe, 4.5–7.5 µm wide, 5–14 septate, swollen or lobed at base, 7.5–14.5(–18.5) µm diam, with short, rhizoid, subhyaline to pale brown hyphae growing from base, medium to brown in lower half, paler towards apex, tips brown, pale brown or subhyaline, thick-walled below, thinner-walled towards apex, smooth; *apex* usually persistently branched, branched part composed of usually fairly compact, closely arranged subcylindrical branchlets, or sometimes giving rise directly to conidiogenous cells; *primary branches* 19–32.5(–43.5) × 3–4.5 µm, 0(–1)-septate, giving rise to 1–3 secondary branches, or to conidiogenous cells; *secondary branches* 15.5–31(–38) × 3–4.5 µm, 0(–1)-septate, giving rise to 1–3 conidiogenous cells; *conidiogenous cells* 13.5–28(–39.5) × 2.5–5 µm, subcylindrical, terminal or occasionally intercalary, sympodial, polyblastic, conidiogenous loci 1–2 µm wide, subconspicuous to conspicuous, subdenticulate, somewhat protuberant, truncate, wall unthickened to somewhat so, darkened-refractive. *Conidia* 5–15.5(–19.5) × 2–3.5 µm, in simple and branched acropetal chains, ellipsoid-ovoid, fusoid, subcylindrical, aseptate, subhyaline to pale brown, thin-walled, smooth, with 1–3(–4) hila, 0.8–1.2 µm diam, up to 1.7 µm diam at base of ramoconidia, truncate, unthickened or almost so, and somewhat darkened-refractive, secession schizolytic; *ramoconidia* 8–20.5 × 2.5–4 µm.

Culture characteristics: Colonies on PDA reaching 21–24 mm diam after 2 wk at 25 °C, moderate aerial mycelium, powdery, umbonate; surface smoke grey to grey olivaceous; reverse grey olivaceous to olivaceous black. Colonies on OA reaching 31–34 mm diam after 2 wk at 25 °C, moderate aerial mycelium, powdery, umbonate, slightly lobate; surface dark olivaceous, mycelium smoke grey to grey olivaceous; reverse dark slate blue.

Material examined: **Thailand**, Chiang Mai Province, Mae Rim District, Queen Sirikit Botanic Garden, from *Musa* sp. (*Musaceae*), 19 Jul. 2008, P.W. Crous & R. Cheewangkoon (**holotype** CBS H-23395, culture ex-type CBS 143920 = CPC 31490).

Notes: *Metulocladosporiella musigena* produces macronematous conidiophores directly producing conidiogenous cells at the apex, or composed of fairly compact branches, which are not observed in the other species of the genus. Moreover, it is characterised by the production of an excessive number of micronematous conidiophores.

Metulocladosporiella samutensis Y. Marín, Luangsa-ard & Crous, **sp. nov.** MycoBank MB824034. Fig. 35.

Etymology: Name from Samut Songkhram, the province in Thailand from where it was isolated.

Mycelium internal and external, superficial; *hyphae* 1.5–4 µm wide, branched, septate, occasionally slightly constricted at septa, with small swellings, hyaline, subhyaline to pale brown, thin-walled, smooth, hyphae occasionally aggregated, forming ropes; with intermixed *micronematous conidiophores*, erect from vegetative mycelium, intercalary, straight to flexuous, unbranched, subhyaline to pale brown, usually with simple terminal conidial chains. *Macronematous conidiophores* (200–)425–1000(–1120) µm long, arising from superficial hyphae, erect, solitary to loosely aggregated, composed of a subcylindrical stipe, 5.5–7.5(–8) µm wide, (4–)8–21(–29)-septate, swollen or lobed at base, 7–14.5(–20.5) µm diam, with short rhizoid subhyaline to pale brown hyphae growing from base, medium to brown in lower half, paler towards apex, tips pale

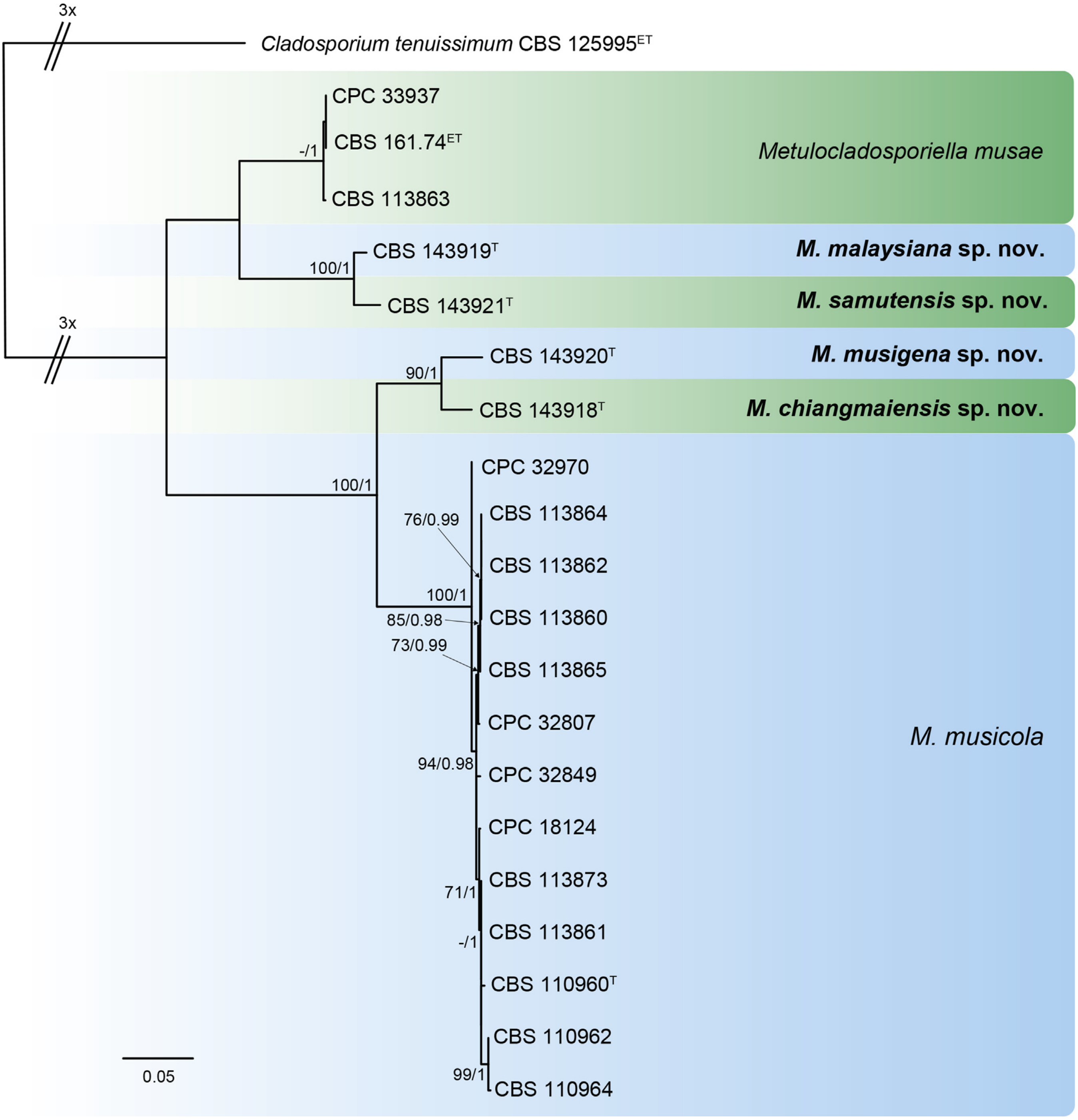

Fig. 31. RAxML phylogram obtained from the combined ITS (667 bp), *cal* (524 bp) and *tef1* (454 bp) sequence alignment of taxa belonging to *Metulocladosporiella*. The tree was rooted to *Cladosporium tenuissimum* CBS 125995^{ET}. The novelties proposed in this study are indicated in **bold**. RAxML bootstrap support (BS) values above 70 % and Bayesian posterior probability scores above 0.95 are shown at the nodes. GenBank accession numbers are indicated in Table 10. ^{T} and ^{ET} indicate ex-type and ex-epitype strains, respectively. TreeBASE: S21899.

brown or occasionally subhyaline, thick-walled below, thinner towards apex, smooth; *apex* giving rise directly to 1–2(–3) conidiogenous cells, or branched, branched part composed of loosely arranged subcylindrical branchlets; *primary branches* 24.5–39(–44) × 3–4(–5) µm, 0–1-septate, giving rise to 1–2(–3) conidiogenous cells, or rarely 1–2 secondary branches; *conidiogenous cells* (12–)14–25(–32) × 3.5–5 µm, subcylindrical, terminal or occasionally intercalary, sympodial, polyblastic, conidiogenous loci 1–2 µm wide, subconspicuous to conspicuous, subdenticulate, somewhat protuberant, truncate, wall unthickened to somewhat so, darkened-refractive. *Conidia* 4.5–12.5(–13.5) × 3–4 µm, in simple and branched acropetal chains, ellipsoid–ovoid, fusiform, subcylindrical, aseptate, subhyaline to pale brown, thin-walled, smooth, with 1–3 hila, 1–1.5(–2) µm diam, truncate, unthickened or almost so, and somewhat darkened-refractive, secession schizolytic; *ramoconidia* 8–13.5(–15.5) × 3–5 µm.

Culture characteristics: Colonies on PDA reaching a diameter of 34–36 mm after 2 wk at 25 °C, moderate aerial mycelium, powdery because of macroconidia, margins fringed; surface smoke grey to grey olivaceous, margins olivaceous; reverse olivaceous grey. Colonies on OA reaching a diameter of 39–40 mm after 2 wk at 25 °C, moderate aerial mycelium, powdery because of macroconidia, margins fringed; surface

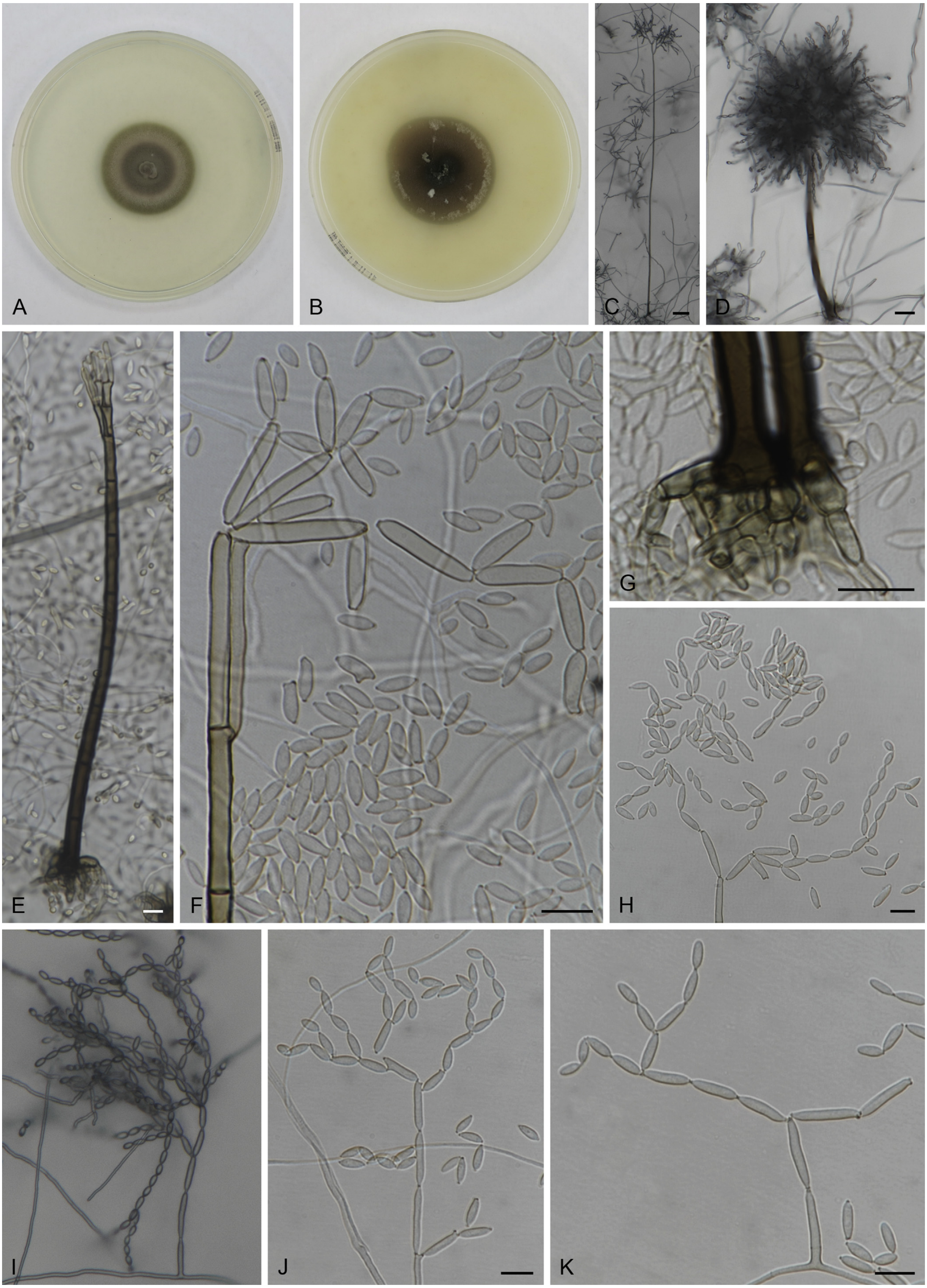

Fig. 32. *Metulocladosporiella chiangmaiensis* (ex-type CBS 143918). **A.** Colony on PDA. **B.** Colony on OA. **C–E.** Macronematous conidiophores. **F.** Conidiogenous apparatus. **G.** Lobed bases of macronematous conidiophore. **H–K.** Micronematous conidiophores. Scale bars: C = 50 µm; D = 20 µm; others = 10 µm.

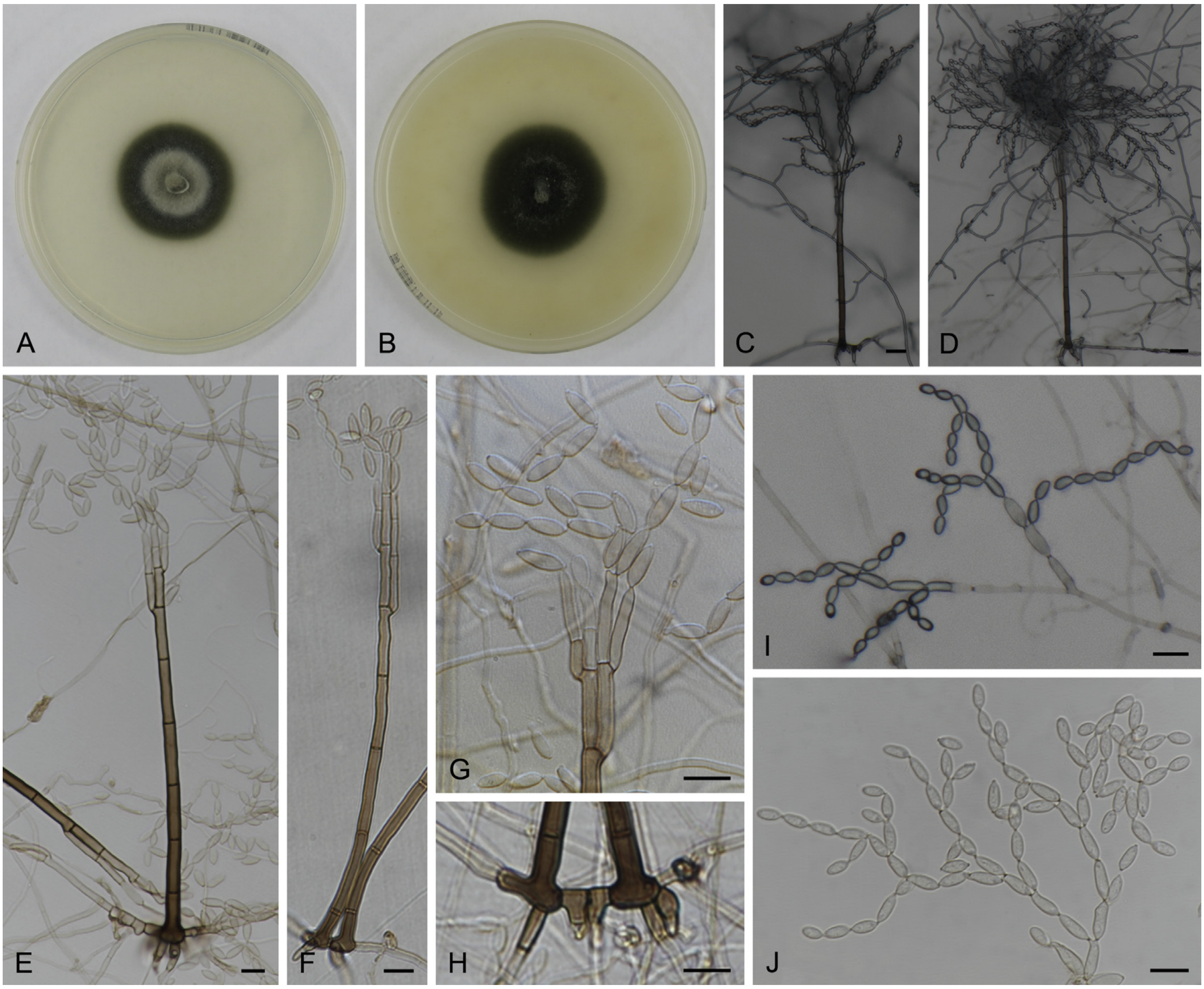

Fig. 33. *Metulocladosporiella malaysiana* (ex-type CBS 143919). **A.** Colony on PDA. **B.** Colony on OA. **C–F.** Macronematous conidiophores. **G.** Conidiogenous apparatus. **H.** Lobed bases of macronematous conidiophore. **I, J.** Micronematous conidiophores. Scale bars: C, D = 20 µm; others = 10 µm.

smoke grey to grey olivaceous, margins grey olivaceous; reverse olivaceous grey.

Material examined: **Thailand**, Samut Songkhram Province, from *Musa* sp. (*Musaceae*), 8 Jun. 2008, P.W. Crous (**holotype** CBS H-23396, culture ex-type CBS 143921 = CPC 33939).

Notes: *Metulocladosporiella samutensis* can easily be distinguished from other species of *Metulocladosporiella* by the production of conidiogenous cells directly from the apex, or loosely arranged primary branches, being almost totally absent of secondary branches.

Authors: Y. Marin-Felix, R. Cheewangkoon, J. Luangsa-ard & P.W. Crous

Microdochium Syd. & P. Syd., Ann. Mycol. 22: 267. 1924. Fig. 36.

Synonyms: *Monographella* Petr., Ann. Mycol. 22: 144. 1924.
Griphosphaerella Petr., Ann. Mycol. 25: 209. 1927.
Gloeocercospora D.C. Bain & Edgerton, Phytopathology 33: 225. 1943. (nom. inval., Art. 39.1, Melbourne).
Gloeocercospora D.C. Bain & Edgerton ex Deighton, Trans. Brit. Mycol. Soc. 57: 358. 1971.
Gerlachia W. Gams & E. Müll., Neth. J. Pl. Path. 86: 49. 1980.

Classification: *Sordariomycetes*, *Xylariomycetidae*, *Xylariales*, *Microdochiaceae*.

Type species: *Microdochium phragmitis* Syd. Holotype: K-IMI 193888. Epitype and ex-epitype strain designated by Hernández-Restrepo *et al.* (2016a): CBS H-22135, CBS 285.71.

DNA barcode (genus): LSU.

DNA barcodes (species): ITS, *rpb2*, *tub2*. Table 11. Fig. 37.

Ascomata perithecial, immersed, subepidermal, solitary or in groups, pale brown to black, globose, subglobose to oval; *ostiole* central, neck papillate and often acute, usually more distinctly pigmented than ascomatal body, filled with slightly clavate periphyses; *ascomatal wall* brown, thin-walled, thickened and darker around ostiole, in face view *textura angularis-epidermoidea*. *Hamathecium* comprising septate, filamentous, apically free, thin-walled paraphyses. *Asci* unitunicate, oblong to clavate, with 8 bi- to multiseriate ascospores, apex with an amyloid, refractive, flat, funnel-shaped ring. *Ascospores* clavate, fusoid or oblong, hyaline to brownish, straight or curved, smooth, septate. *Conidiomata* absent or present, sporodochial, epidermal or subepidermal, erumpent through stomata, or rupture of outer epidermal wall and cuticle, or by specialised egression hyphae

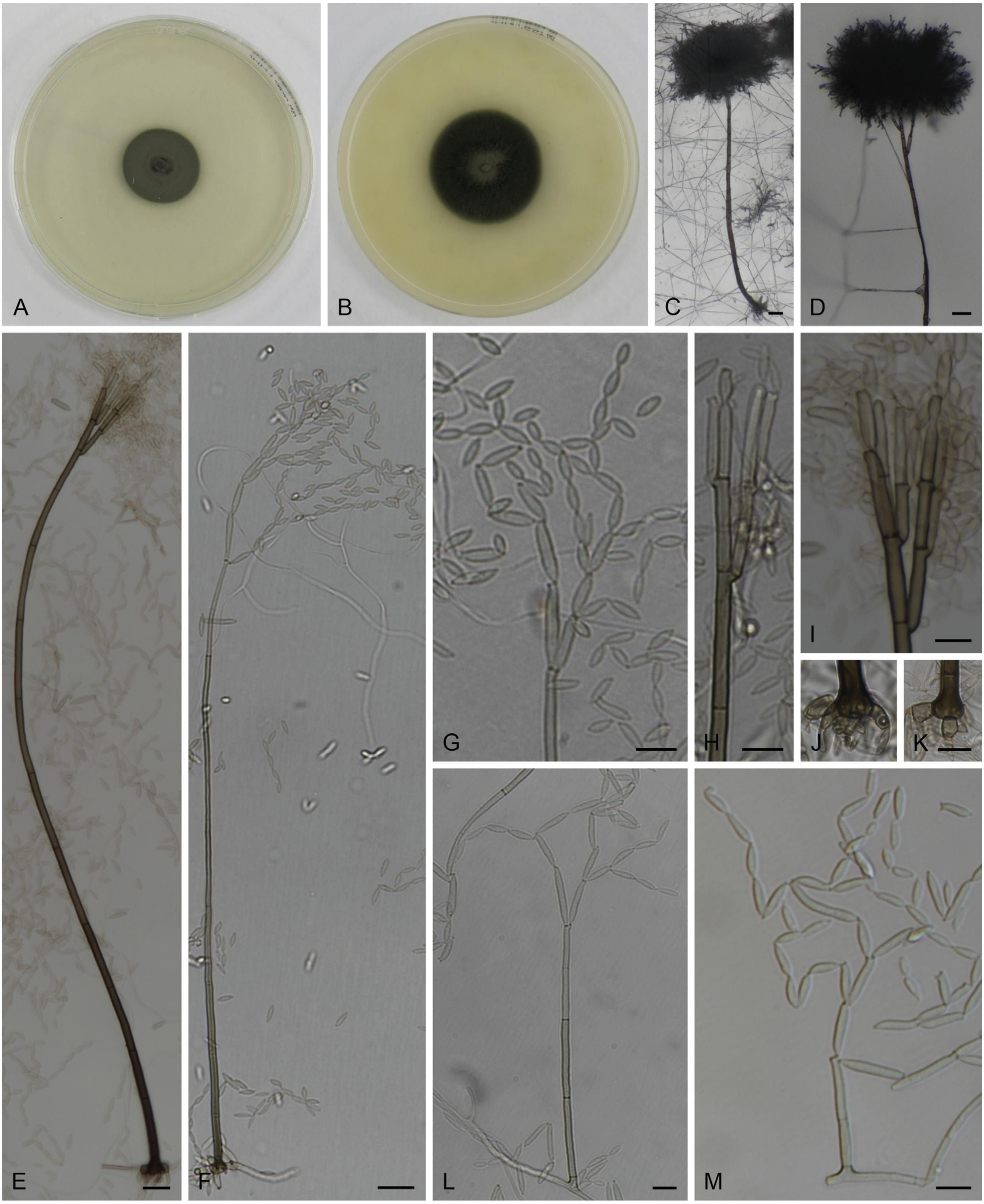

Fig. 34. *Metulocladosporiella musigena* (ex-type CBS 143920). **A.** Colony on PDA. **B.** Colony on OA. **C–F.** Macronematous conidiophores. **G–I.** Conidiogenous apparatus. **J, K.** Lobed bases of macronematous conidiophore. **L, M.** Micronematous conidiophores. Scale bars: C–F = 20 µm; G–M = 10 µm; K applies to J, K.

through outer epidermal wall, hyaline, pseudoparenchymatic, spreading after egress. *Conidiophores* more or less verticillate, often slightly differentiated, reduced to conidiogenous cells, hyaline, smooth. *Conidiogenous cells* holoblastic, discrete, hyaline, smooth, solitary or aggregated in small sporodochia. Two kinds: with sympodial proliferation, cylindrical or slightly tapering to clavate, denticulate with one or more apical denticles; or with percurrent proliferation (annellidic), subcylindrical, obpyriform, ampulliform to lageniform. *Conidia* dry or in slimy mass, unicellular or multiseptate, hyaline, smooth, lunate, falcate, fusiform, filiform, obovoid or subpyriform, straight or curved, apex rounded, base flattened. Sometimes conidia originate directly

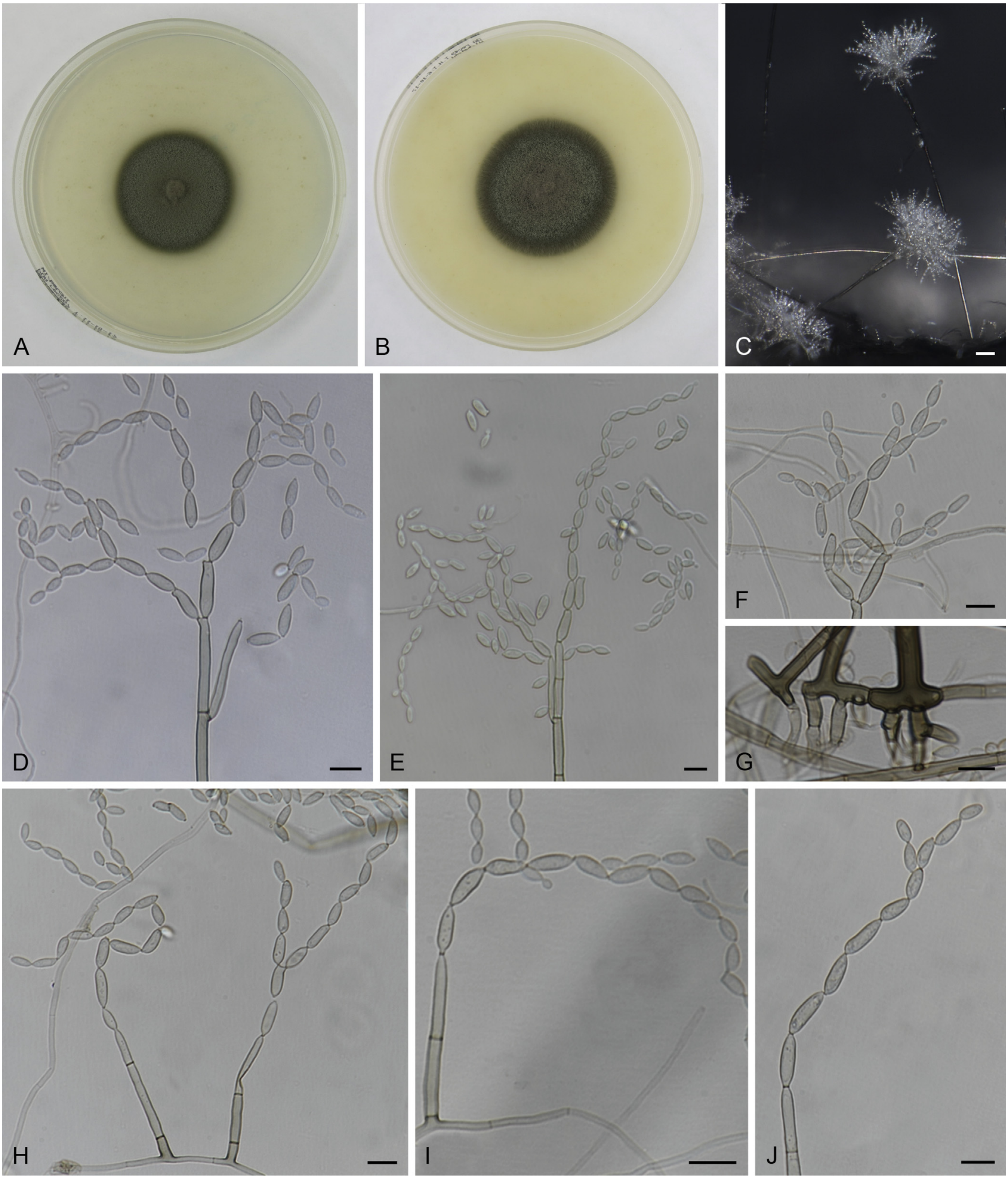

Fig. 35. *Metulocladosporiella samutensis* (ex-type CBS 143921). **A.** Colony on PDA. **B.** Colony on OA. **C.** Macronematous conidiophores. **D–F.** Conidiogenous apparatus. **G.** Lobed bases of macronematous conidiophore. **H–J.** Micronematous conidiophores. Scale bars: C = 20 μm; others = 10 μm.

from hyphae. *Chlamydospores* terminal or intercalary, solitary, in chains or grouped in clusters, brown (adapted from Hernández-Restrepo *et al.* 2016a).

Culture characteristics: Colonies on OA saffron, salmon, peach or white when young, some species grey or dark grey when mature, glabrous or with moderate amount of mycelium, cottony to floccose, margin effuse.

Optimal media and cultivation conditions: OA at 25 °C under dark conditions.

Distribution: Worldwide.

Hosts: Mainly pathogens of grasses and cereals, but some also occur on non-grass hosts as *Opuntia* (*Cactaceae*) and *Lycopodium* (*Lycopodiaceae*), may cause losses to crops including rice, maize, wheat, barley and sorghum. Other species can be found in harvested grains.

Disease symptoms: Microdochium patch or pink snow patch, leaf scald disease, tar spot disease, root necrosis and decay of grasses, leaf spots, among others.

Notes: *Microdochium* includes plant pathogenic as well as saprobic and soil fungi (Sydow 1924, de Hoog & Hermanides-Nijhof 1977, Parkinson *et al.* 1981, Jaklitsch & Voglmayr 2012, Zhang *et al.* 2015, Hernández-Restrepo *et al.* 2016a, Crous *et al.* 2018). For many years, species of *Microdochium* were recognised as fusarium-like fungi; however, morphological and molecular data separate these genera. Conidiogenesis in *Microdochium* is not phialidic as in true *Fusarium* species and the conidia have truncate basal cells rather than "foot-cells". The sexual morphs of *Microdochium* are monographella-like, and it belongs in the *Microdochiaceae* (*Xylariales*) phylogenetically distant from true *Fusarium* in *Nectriaceae* (*Hypocreales*).

For an accurate species identification of *Microdochium* species, DNA sequence analyses are required. Among the four loci studied (i.e. LSU, ITS, *rpb2* and *tub2*), LSU is useful only for generic placement. Phylogenies based on individual gene regions of ITS, *rpb2* and *tub2*, can be used to distinguish 14 species in *Microdochium*; those phylogenies generated from *tub2* show longer distances between species and higher support values. This is more informative than ITS and *rpb2* (Hernández-Restrepo *et al.* 2016a).

References: Parkinson *et al.* 1981, Müller & Samuels 1984, Zhang *et al.* 2015 (morphology and pathogenicity); von Arx 1981, 1984, Braun 1995 (taxonomy); Hong *et al.* 2008 (pathogenicity); Hernández-Restrepo *et al.* 2016a (morphology and phylogeny).

Microdochium novae-zelandiae Hern.-Restr., Thangavel & Crous, **sp. nov.** MycoBank MB824606. Fig. 38.

Etymology: Name is derived from New Zealand, the country where this fungus was collected.

Mycelium superficial and immersed, composed of septate, branched, hyaline, smooth, 1–2.5 wide hyphae. *Conidiomata* sporodochium-like, formed in aerial mycelium or on agar surface, hyaline to pink. *Conidiophores* often reduced to conidiogenous cells. *Conidiogenous cells* 4–10 × 2–3 µm, integrated, terminal, polyblastic, proliferation sympodial, cylindrical to lageniform, hyaline, smooth; sometimes conidia formed directly on mycelium. *Conidia* 5.5–10 × 2–2.5 µm, solitary, fusoid, allantoid, lunate or slightly sigmoid, straight or curved, hyaline, smooth, 0(–1)-septate, base truncate. *Chlamydospores* not observed.

Culture characteristics: Colonies on OA reaching 45 mm diam after 1 wk at 25 °C, centre flat and rosy buff, periphery cottony and white, margins effuse; reverse rosy buff in centre.

Materials examined: **New Zealand**, Christchurch, from turf leaves (*Poaceae*), 2015, R. Thangavel (**holotype** CBS H-23384, culture ex-type CBS 143847 = CPC 29376 = ICMP 21872 = MPI T15_05208H); *ibid.*, Richmond, Nelson, on spruce (*Pinaceae*), 2014, R. Thangavel (CPC 29693 = MPI T14_00277D).

Notes: *Microdochium novae-zelandiae* is known from two isolates, both of which were collected in New Zealand from different hosts belonging to the families *Pinaceae* and *Poaceae*. Based on a four-gene analysis, the new species was placed in a clade distinct from *M. bolleyi*, *M. colombiense*, *M. majus* and *M. nivale* (Fig. 37). Morphologically, *M. novae-zelandiae* has conidia similar in size to *M. bolleyi* and *M. colombiense*. However, subtle morphological differences exist in the conidial shapes of these taxa with *M. novae-zelandiae* having sigmoidal conidia. Compared with *M. phragmitis*, conidia of *M. novae-zelandiae* are smaller, mainly aseptate with variable shape [5.5–10 × 2–2.5 µm, 0(–1)-septate, fusiform, allantoid, lunate or slightly sigmoid in *M. novae-zelandiae vs.* 10–14.5 × 2–3 µm, 0–1-sepate, fusiform to navicular in *M. phragmitis*].

Authors: M. Hernández-Restrepo, R. Thangavel & P.W. Crous

Oculimacula Crous & W. Gams, Eur. J. Pl. Path. 109: 845. 2003. Fig. 39.

Synonym: *Helgardia* Crous & W. Gams, Eur. J. Pl. Path. 109: 845. 2003.

Classification: *Leotiomycetes*, *Leotiomycetidae*, *Helotiales*, *Incertae sedis*.

Type species: *Oculimacula yallundae* (Wallwork & Spooner) Crous & W. Gams = *Helgardia herpotrichoides* (Fron) Crous & W. Gams, basionym: *Cercosporella herpotrichoides* Fron. Holotype: K(M) 233697. Neotype and ex-neotype strain of *Helgardia herpotrichoides* designated by Crous *et al.* (2003): CBS H-23003, CBS 110665.

DNA barcode (genus): LSU.

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

Ascomata 0.5–2.5 mm diam, apothecial, sessile, gregarious, circular to lobate, on a subiculum of white to dark brown hyphae, attached to substrate via a superficial mat of pale brown, thin hyphae. *Disk* smooth, grey with a pale grey margin, becoming emarginate and flattened to convex at maturity. *Receptacle* pale brown to grey-brown, cup-shaped. *Medullary excipulum* of multiseptate, hyaline hyphae. *Ectal excipulum* of thin-walled, dark brown, angular cells, becoming more elongated towards margin. *Paraphyses* filiform with obtuse ends, similar in length to asci. *Asci* 8-spored, unitunicate, clavate to subcylindrical or fusoid, with a short stalk, and an apical pore staining blue in Melzer's reagent. *Ascospores* bi- to multiseriate, hyaline, smooth, aseptate, fusoid to subcylindrical or clavate with rounded ends, mostly straight. *Conidiophores* fasciculate or solitary on superficial mycelium, or arising from pale brown stromata, subcylindrical to geniculate-sinuous, rarely branching, hyaline to pale olivaceous, smooth, consisting of conidiogenous cells only, or slightly differentiated with up to 2 septa. *Conidiogenous cells* integrated, proliferating sympodially at apex, with inconspicuous, dense geniculations; *conidiogenous loci* unthickened, inconspicuous, not darkened. *Conidia* solitary, hyaline, smooth, arranged in slimy packets, acicular, filiform, straight to curved, one- to multiseptate, forming smaller, secondary conidia via microcyclic conidiation (adapted from Crous *et al.* 2003).

Culture characteristics: Colonies with moderate aerial mycelium giving a cottony appearance. On PDA surface grey to olive grey, brownish-grey, pinkish-grey or greenish; reverse grey to greenish-black, greenish, brownish or creamy pink.

Optimal media and cultivation conditions: SNA under continuous near-ultraviolet light at 25 °C.

Distribution: Africa, Australasia, Europe, New Zealand and North America.


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

Species	Isolates[1]	GenBank accession numbers[2]			References
		ITS	*rpb2*	*tub2*	
Microdochium albescens	CBS 290.79	KP859014	KP859123	KP859077	Hernández-Restrepo *et al.* (2016a)
Mi. bolleyi	CBS 540.92	KP859010	KP859119	KP859073	Hernández-Restrepo *et al.* (2016a)
	CPC 29378	LT990657	LT990643	LT990610	Present study
Mi. citrinidiscum	CBS 109067^{T}	KP859003	KP859112	KP859066	Hernández-Restrepo *et al.* (2016a)
Mi. colombiense	CBS 624.94^{T}	KP858999	KP859108	KP859062	Hernández-Restrepo *et al.* (2016a)
Mi. chrysanthemoides	CGMCC3.17929^{T}	KU746690	–	KU746781	Zhang *et al.* (2017)
Mi. fisheri	CBS 242.91^{T}	KP859015	KP859124	KP859078	Hernández-Restrepo *et al.* (2016a)
Mi. lycopodinum	CBS 122885^{T}	KP859016	KP859125	KP859079	Hernández-Restrepo *et al.* (2016a)
Mi. majus	CBS 741.79	KP859001	KP859110	KP859064	Hernández-Restrepo *et al.* (2016a)
Mi. neoqueenslandicum	CBS 108926^{T}	KP859002	KP859111	KP859065	Hernández-Restrepo *et al.* (2016a)
Mi. nivale	CBS 116205^{T}	KP859008	KP859117	KP859071	Hernández-Restrepo *et al.* (2016a)
Mi. novae-zelandiae	CBS 143847	LT990655	LT990641	LT990608	Present study
	CPC 29693	LT990656	LT990642	LT990609	Present study
Mi. phragmitis	CBS 285.71^{ET}	KP859013	KP859122	KP859076	Hernández-Restrepo *et al.* (2016a)
Mi. seminicola	CBS 139951^{T}	KP859038	KP859147	KP859101	Hernández-Restrepo *et al.* (2016a)
Mi. sorghi	CBS 691.96	KP859000	KP859109	KP859063	Hernández-Restrepo *et al.* (2016a)
Mi. tainanense	CBS 269.76^{T}	KP859009	KP859118	KP859072	Hernández-Restrepo *et al.* (2016a)
Mi. trichocladiopsis	CBS 623.77^{T}	KP858998	KP859107	KP859061	Hernández-Restrepo *et al.* (2016a)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CPC: Personal collection of Pedro Crous housed at the Westerdijk Fungal Biodiversity Institute; CGMCC: China General Microbiological Culture Collection Center. ^{T} and ^{ET} indicate ex-type and ex-epitype strains.

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

Hosts: *Poaceae*, including *Triticum* and *Hordeum*, among others.

Disease symptoms: Eyespot lesions that girdle the stem and soften the stem-base.

Notes: *Oculimacula* encompasses four species associated with eyespot disease symptoms of cereals in the temperate regions of the world. Eyespot is an important disease of stem bases in which the infection occurs at or near the soil line, attacking chiefly the basal leaf sheaths and internodal tissues of the culms (Sprague & Fellows 1934, Lucas *et al.* 2000). The fungus sporulates in the fall and spring producing the disease, and survives the winter on diseased stubble standing or lying in the field (Sprague & Fellows 1934). Disease control relies on the use of fungicides, delayed seeding in the fall and by planting resistant cultivars (Murray 1996, Douhan *et al.* 2002).

Oculimacula was introduced by Crous *et al.* (2003) to accommodate sexual morphs previously classified in *Tapesia*, while *Helgardia* was introduced for the asexual morphs linked to *Oculimacula*. Johnston *et al.* (2014) synonymised these generic names and conserved the name *Oculimacula* because it is most commonly used by plant pathologists for the eyespot diseases of wheat and barley.

References: Sprague & Fellows 1934 (morphology and pathogenicity); Sprague 1936, Lucas *et al.* 2000 (pathogenicity); Nirenberg 1981 (morphology and pathogenicity); Crous *et al.* 2003 (morphology and phylogeny).

Oculimacula acuformis (Nirenberg) Y. Marín & Crous, **comb. et stat. nov.** MycoBank MB824638.
Basionym: *Pseudocercosporella herpotrichoides* var. *acuformis* Nirenberg, Z. PflKrankh. PflSchutz 88: 244. 1981.
Synonyms: *Ramulispora herpotrichoides* var. *acuformis* (Nirenberg) Boerema, *et al.*, Netherlands Journal of Plant Pathology, Supplement 1 98: 22. 1992.
Tapesia yallundae var. *acuformis* Boerema, *et al.*, Netherlands J. of Pl. Path., Supplement 1 98: 22. 1992. (nom. inval., Art. 40.3, Melbourne).
Ramulispora acuformis (Nirenberg) Crous, S. Afr. J. Bot. 61: 46. 1995.
Tapesia acuformis (Boerema, *et al.*) Crous, S. Afr. J. Bot. 61: 46. 1995. (nom. inval., Art. 40.3, Melbourne).
Helgardia acuformis (Nirenberg) Crous & W. Gams, Eur. J. Pl. Path. 109: 846. 2003.
Oculimacula acuformis (Boerema, *et al.*) Crous & W. Gams, Eur. J. Pl. Path. 109: 846. 2003. (nom. inval., Art. 40.3, Melbourne).

Material examined: Germany, Tübingen, from *Secale cereale* (*Poaceae*) culm base, 1978, H. Nirenberg (culture ex-type CBS 495.80).

Notes: *Oculimacula acuformis* was introduced to accommodate *Tapesia yallundae* var. *acuformis* (Crous *et al.* 2003). However,

Fig. 36. *Microdochium* spp. **A–F.** Sexual morph of *Microdochium seminicola* (ex-type CBS 139951). **A.** Colony overview. **B.** Ascomata. **C–E.** Asci. **F.** Ascospores. **G–U.** Asexual morphs. **G, H.** Sporodochium. **G.** *Microdochium phragmites* (CBS 423.78). **H.** *Microdochium lycopodinum* (CBS 109399). **I–N.** Conidiophores and conidiogenous cells. **I.** *Microdochium neoqueenslandicum* (ex-type CBS 108926). **J.** *Microdochium citrinidiscum* (ex-type CBS 109067). **K.** *Microdochium seminicola* (ex-type CBS 139951). **L.** *Microdochium phragmites* (ex-epitype CBS 285.71). **M.** *Microdochium phragmites* (CBS 423.78). **N.** *Microdochium fisheri* (ex-type CBS 242.91). **O–U.** Conidia. **O.** *Microdochium seminicola* (ex-type CBS 139951). **P.** *Microdochium lycopodinum* (CBS 109399). **Q.** *Microdochium fisheri* (ex-type CBS 242.91). **R.** *Microdochium neoqueenslandicum* (ex-type CBS 108926). **S.** *Microdochium phragmites* (CBS 423.78). **T.** *Microdochium phragmites* (ex-epitype CBS 285.71). **U.** *Microdochium citrinidiscum* (ex-type CBS 109067). **V, W.** Chlamydospores. **V.** *Microdochium bolleyi* (CPC 29379). **W.** *Microdochium trichocladiopsis* (ex-type CBS 623.77). Scale bars: H = 100 μm; G = 50 μm; others = 10 μm.

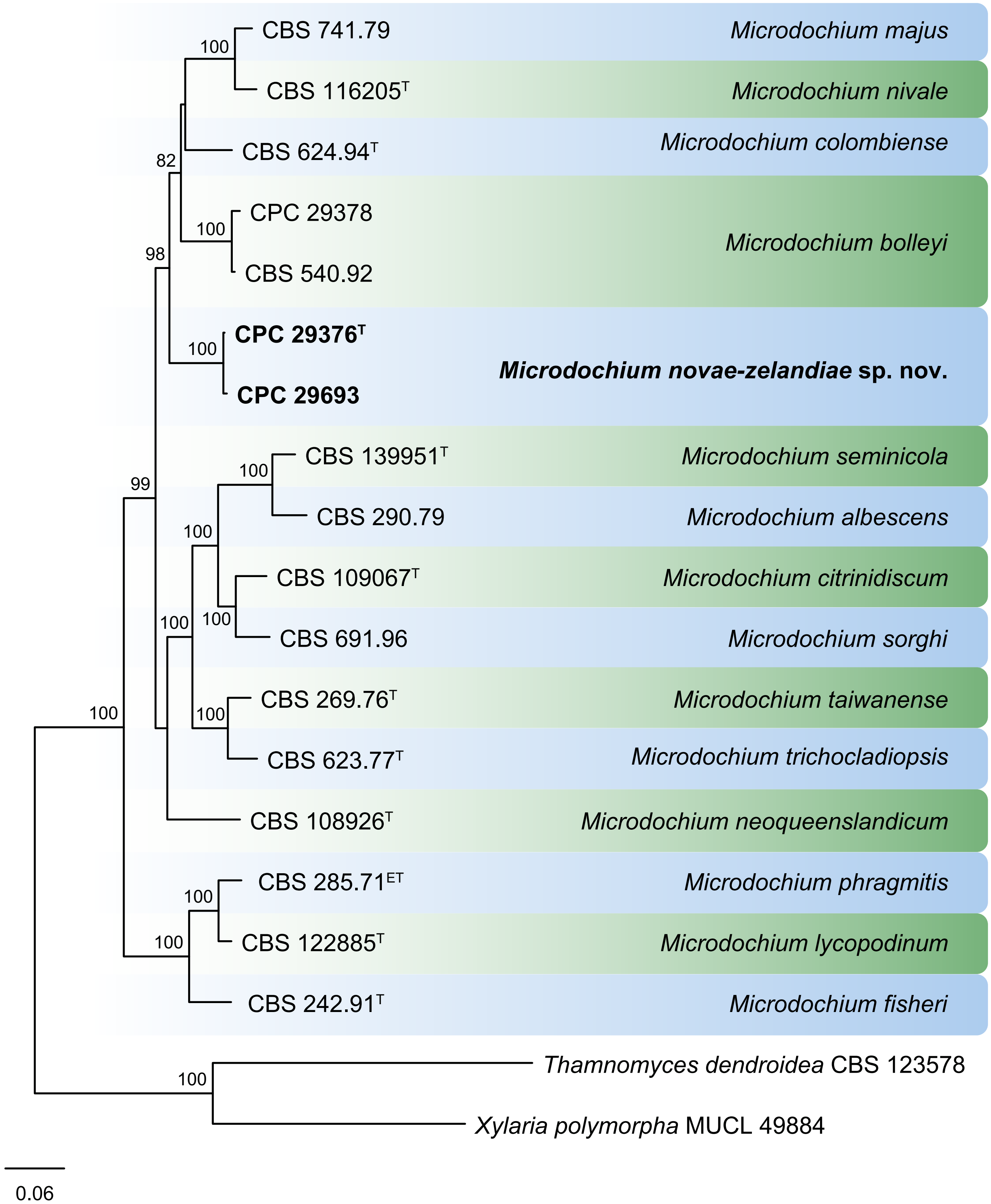


Fig. 37. RAxML phylogram obtained from the combined ITS (618 bp), LSU (838 bp), *tub2* (689 bp) and *rpb2* (858 bp) sequence alignment of all the accepted species of *Microdochium*. The tree was rooted to *Thamnomyces dendroidea* CBS 123578 and *Xylaria polymorpha* MUCL 49884. The novel species described in this study is shown in **bold**. RAxML bootstrap support (BS) values above 70 % are shown in the nodes. GenBank accession numbers are indicated in Table 11. T and ET indicate ex-type and ex-epitype strains, respectively. TreeBASE: S21899.

the combination is invalid because the basionym lacks details for the ex-type strain (Art 40.3). We have consequently proposed the new combination based on its asexual morph *Pseudocercosporella herpotrichoides* var. *acuformis*. This latter species was transferred to *Helgardia* in the same publication where *Oculimacula acuformis* was proposed and when both genera were first introduced (Crous *et al.* 2003). *Helgardia acuformis* is a synonym of *Oculimacula acuformis*.

Authors: Y. Marin-Felix, J.Z. Groenewald & P.W. Crous

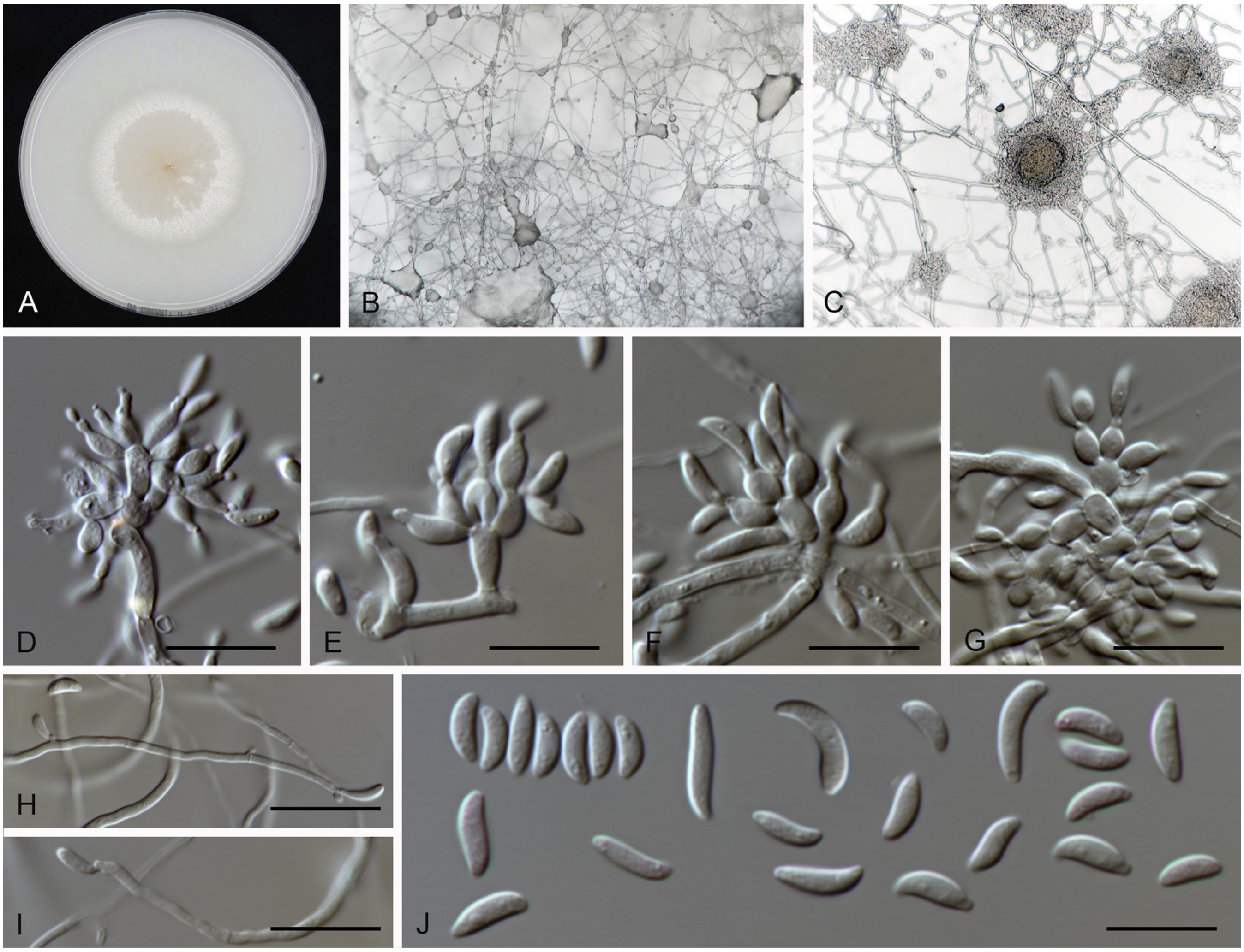


Fig. 38. *Microdochium novae-zelandiae* (ex-type CPC 29376). **A.** Colony overview. **B, C.** Sporodochium overview. **B.** From aerial mycelium. **C.** From agar surface. **D–G.** Conidiogenous cells and conidia. **H, I.** Hyphae and conidia. **J.** Conidia. Scale bars = 10 µm.

Paraphoma Morgan-Jones & J.F. White, Mycotaxon 18: 58. 1983. Fig. 41.
Synonym: *Phoma* section *Paraphoma* (Morgan-Jones & J.F. White) Boerema, Stud. Mycol. 32: 7. 1990.

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

Type species: *Paraphoma radicina* (McAlpine) Morgan-Jones & J.F. White, basionym: *Pyrenochaeta radicina* McAlpine. Holotype: in VPRI [Australia, Shepparton, Victoria, on roots of *Prunus cerasus* (*Rosaceae*), 21 Oct 1901, Piscott, 2064.3]. Epitype and ex-epitype strain designated by de Gruyter *et al.* (2010): CBS H-16560, CBS 111.79.

DNA barcodes (genus): LSU, SSU.

DNA barcodes (species): ITS, *rpb2*, *tef1*, *tub2*. Table 13. Fig. 42.

Conidiomata pycnidial, globose to subglobose, papillate, thick-walled, pseudoparenchymatous, ostiolate, uniloculate; *conidiomatal matrix* white or buff, cream, yellow, brown or hyaline; *setae* abundant, straight or flexuous, septate, pale brown to brown, short or relatively long, stiff or hyphal-like, scattered on surface of conidiomata, or abundant around ostioles. *Micropycnidia* fertile or sterile, produced abundantly in some species of *Paraphoma*, submerged in medium. *Conidiophores* ampulliform, hyaline, mostly reduced to phialidic conidiogenous cells. *Conidiogenous cells* lageniform, monophialidic, hyaline to subhyaline. *Conidia* ellipsoidal to subglobose, hyaline, guttulate, aseptate *in vivo* and *in vitro*. *Chlamydospores* absent or present, solitary, in short or long chains or aggregated, uni- or multicellular; *multicellular chlamydospores* alternarioid, pseudosclerotioid, epicoccoid and botryoid depending on species. *Sexual morph* unknown.

Culture characteristics: Colony colour, growth and pigmentation greatly dependant on media and incubation conditions. Colonies black, brown, olivaceous, yellow, red to pink, or grey and white; slow growing; aerial mycelium flat to effuse, aerial mycelium sparsely formed, floccose to tufted, felty, woolly or compact; margins regular, smooth and sharp, or irregular, crenate and lobate.

Optimal media and cultivation conditions: CHA for colony growth and pigmentation, MEA mostly for colony pigmentation and acidified OA for both colony pigmentation and morphological identification, incubated for 1 wk in dark and 1 wk under near-ultraviolet light (13 h light, 11 h dark) at 20–22 °C to simulate colony pigmentation and sporulation.

Distribution: Temperate areas of Australia, Eurasia and North America.

Hosts: Mostly foliar pathogens of herbaceous plants, chiefly soil-borne, with wide host range including monocotyledonous plants,

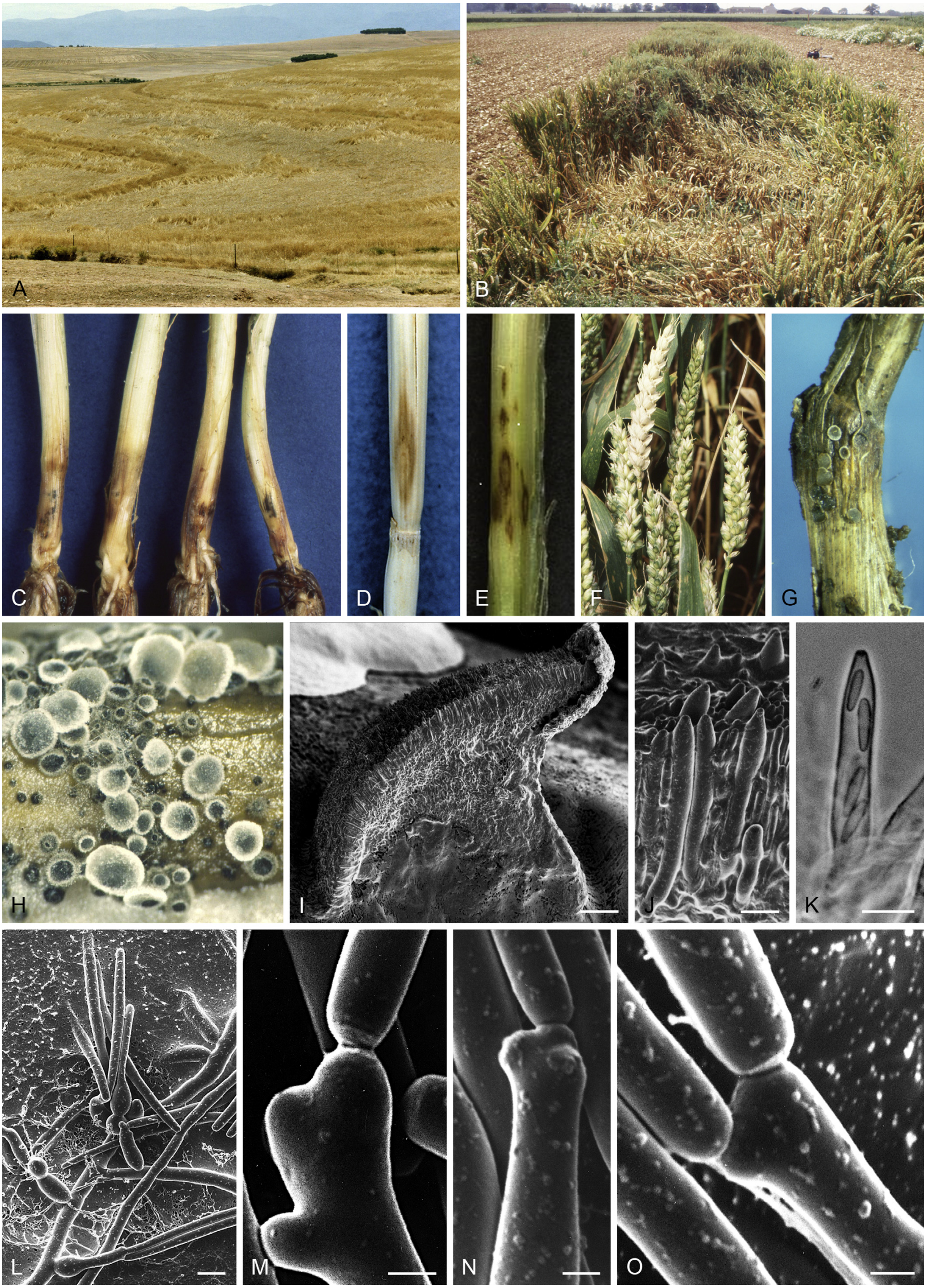


Fig. 39. *Oculimacula* spp. **A–G.** Disease symptoms. **A, B.** Eyespot lodging. **C–E.** Eyespots. **F.** Whiteheads of wheat. **G.** Apothecia of *Oculimacula gamsii* on wheat stubble. **H–K.** Sexual morphs of *Oculimacula yallundae*. **H, I.** Ascomata. **J.** Section through the ascoma showing ascal layer. **K.** Ascus and ascospores. **L–O.** Asexual morphs. **L.** Conidia and conidiogenous cells of *Oculimacula gamsii*. **M.** Conidial hila and conidiogenous cell of *Oculimacula yallundae*. **N.** Conidial hila and conidiogenous cell of *Oculimacula gamsii*. **O.** Conidial hila and conidiogenous cell of *Oculimacula anguoides*. Scale bars: I = 100 μm; J, K = 10 μm; L = 5 μm; M–O = 1 μm.

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

Species	Isolates[1]	GenBank accession numbers[2]		References
		ITS	*tef1*	
Oculimacula acuformis	CBS 495.80^T	MG934455	MG934497	Present study
O. aestiva	CBS 114730	MG934454	MG934496	Present study
O. anguioides	CBS 496.80^T	LT990662	LT990618	Present study
O. yallundae	CBS 110665^{NT}	MG934456	MG934498	Present study
	CBS 128.31	MG934457	MG934499	Present study
	CBS 494.80	JF412009	MG934500	Tsang (unpubl. data), present study

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

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

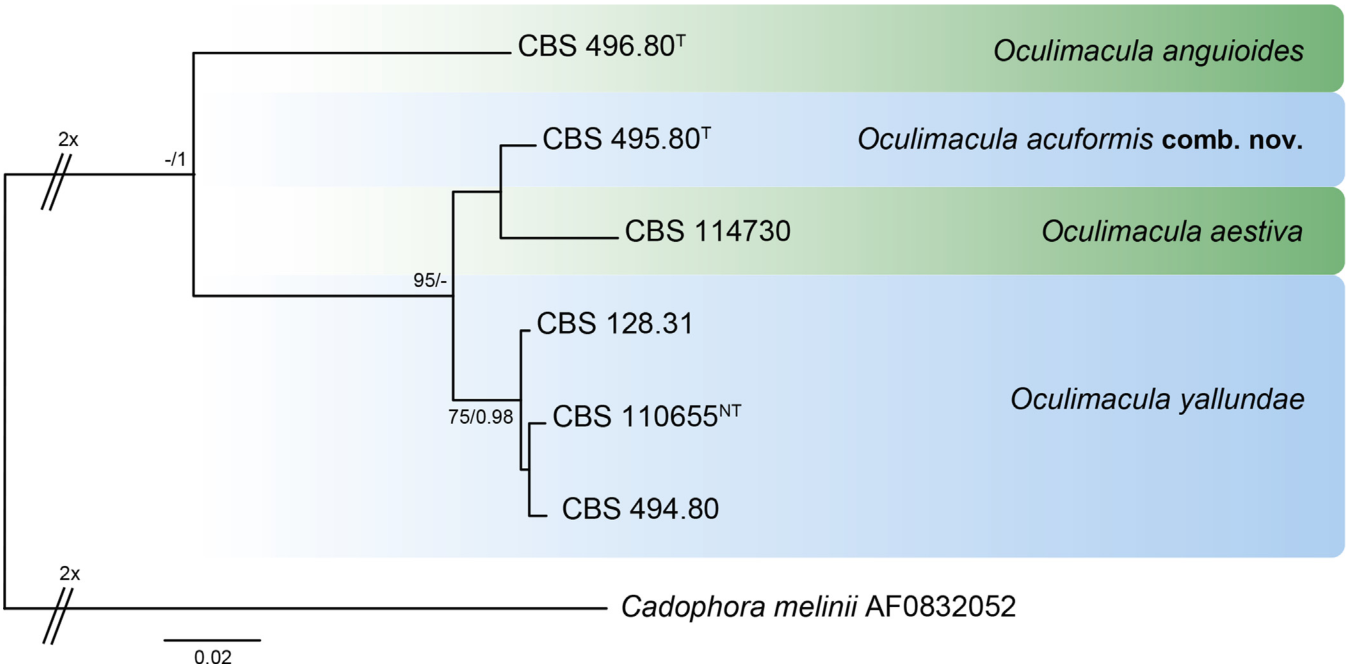


Fig. 40. RAxML phylogram obtained from the combined ITS (631 bp) and *tef1* (575 bp) sequence alignment of taxa belonging to *Oculimacula*. The tree was rooted to *Cadophora melinii*. The new combination proposed in this study is indicated in **bold**. RAxML bootstrap support (BS) values above 70 % and Bayesian posterior probability scores above 0.95 are shown at the nodes. GenBank accession numbers are indicated in Table 12. ^{T} and ^{NT} indicate ex-type and ex-neotype strains, respectively. TreeBASE: S21899.

Asteraceae, *Cupressaceae*, *Rosaceae* and *Solanaceae*, occasionally saprobic.

Disease symptoms: Crown discolouration, root rot and necrotic leaf spots.

Notes: The type species of *Paraphoma, Pa. radicina,* clustered in a separate group outside *Didymellaceae* and hence was excluded from *Phoma* (de Gruyter *et al.* 2013). In a phylogenetic analysis based on LSU and SSU, *Paraphoma radicina* clustered in the *Phaeosphaeriaceae*, although other species belonged to the *Cucurbitariaceae* and *Coniothyriaceae*. Setose pycnidial conidiomata and dictyochlamydospores, which are characteristics of species of *Paraphoma* and *Peyronellaea*, can be observed in species of other phoma-like genera, such as *Pyrenochaeta* and *Pleurophoma*. Therefore, these morphological characters are not specific to these genera. In order to delineate *Paraphoma*, phylogenetic studies based on ITS, LSU, *rpb2*, *tef1* and *tub2* have been performed (Aveskamp *et al.* 2010, Moslemi *et al.* 2016, 2018, Crous *et al.* 2017a). Using ITS and LSU in combination with protein coding genes *rpb2, tef1* and *tub2* for precise identification of species of *Paraphoma* is necessary, as LSU alone is too conservative.

References: de Gruyter & Boerema 2002, Zhang *et al.* 2009, 2012, de Gruyter *et al.* 2010, 2013 (pathogenicity, phylogeny and distribution); Boerema *et al.* 2004 (morphology, pathogenicity, media and incubation conditions); Aveskamp *et al.* 2009, 2010 (morphology, phylogeny and key of all *Paraphoma* spp.); Hay *et al.* 2015 (hosts).

Authors: A. Moslemi, P.W.J. Taylor & P.W. Crous

Phaeoacremonium W. Gams, *et al.*, Mycologia 88: 789. 1996. Fig. 43.
Synonym: *Togninia* Berl., Icon. fung. (Abellini) 3: 9. 1900.

Classification: *Sordariomycetes*, *Sordariomycetidae*, *Togniniales*, *Togniniaceae*.

Type species: *Phaeoacremonium parasiticum* (Ajello, *et al.*) W. Gams, *et al.*, basionym: *Phialophora parasitica* Ajello, *et al.* Holotype and ex-type strain: CBS H-17463, CBS 860.73.

DNA barcodes (genus): SSU, LSU.

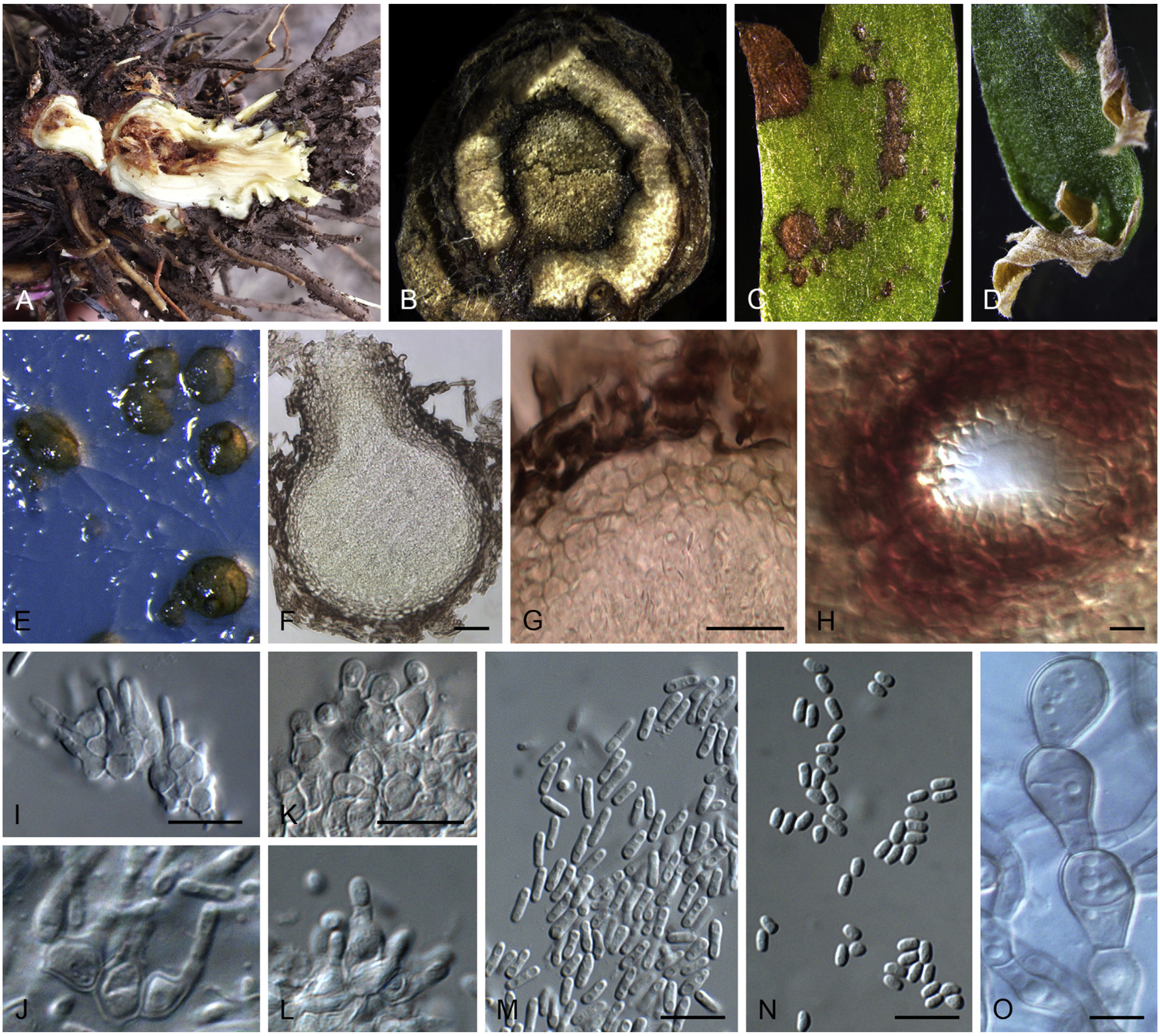


Fig. 41. *Paraphoma* spp. **A–E.** Disease symptoms. **A, B.** Crown discolouration caused by *Paraphoma vinacea* (ex-type BRIP 63684). **C.** Water-soaked and necrotic leaf lesions caused by *Paraphoma chlamydocopiosa* (ex-type BRIP 65168). **D.** Marginal leaf chlorosis caused by *Paraphoma pye* on pyrethrum leaf (ex-type BRIP 65169). **E–O.** Asexual morphs. **E.** Conidiomata on SNA of *Paraphoma fimeti* (ex-neotype CBS 170.70). **F.** Conidiomata of *Paraphoma vinacea* (ex-type BRIP 63684). **G.** Conidiomatal wall of *Paraphoma vinacea* (ex-type BRIP 63684). **H.** Ostiolar zone of *Paraphoma vinacea* (ex-type BRIP 63684). **I–L.** Condiogenous cells. **I, J.** *Paraphoma dioscoreae* (ex-type CBS 135100). **K, L.** *Paraphoma fimeti* (ex-neotype CBS 170.70). **M, N.** Conidia. **M.** *Paraphoma dioscoreae* (ex-type CBS 135100). **N.** *Paraphoma fimeti* (ex-neotype CBS 170.70). **O.** Chlamydospores of *Paraphoma vinacea* (ex-type BRIP 63684). Scale bars: F = 100 μm; G, H = 20 μm; I, K, M–O = 10 μm; I applies to I, J; K applies to K, L. Pictures B, F, G taken from Moslemi *et al.* (2016); C, D from Moslemi *et al.* (2018); I, J, M from Quaedvlieg *et al.* (2013).

DNA barcodes (species): *act*, *tub2*. Table 14. Fig. 44.

Ascomata perithecial, aggregated or solitary, superficial to immersed, non-stromatic, globose to subglobose, dark, opaque, long-necked; *necks* straight or flexuous; *ascomatal wall* fragile to leathery, comprising two layers of *textura angularis*: *outer layer* brown to dark brown, with cells smaller and more rounded than those of inner layer; *inner layer* hyaline to pale brown, cells flattened. *Paraphyses* abundant, broadly cellular, slightly constricted at septa, branching, hyaline, slightly tapering apically or thread-like towards apex. *Ascogenous hyphae* hyaline, sometimes branched in basal region, elongating during ascal formation with remnant tissue from which single asci arise. *Asci* arising in acropetal succession, appearing spicate when mature, unitunicate, 8-spored, ascal apex thickened with a nonamyloid apical ring, basally bluntly obtuse, sessile. *Ascospores* hyaline, aseptate, allantoid, reniform, cylindrical or oblong-ellipsoidal, mostly biseriate or in a single row. *Conidiophores* branched in basal region or unbranched, arising from aerial or submerged hyphae, erect, nearly cylindrical when unbranched, slightly tapering, straight or flexuous, variable in length, up to 7-septate, mostly pale brown, paler towards tip, percurrent rejuvenation observed, small warts or verruculose ornamentation mostly at base, usually with one integrated terminal phialide and one or two additional, discrete phialides at uppermost septum. *Conidiogenous cells* phialidic, discrete or integrated, terminal or lateral, mostly monophialidic, sometimes polyphialidic, sparsely warted, verruculose or smooth, pale brown to hyaline, with an inconspicuous funnel-shaped collarette. Three distinct classes of phialides (Types I–III) can be observed. *Conidia* aggregated into

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

Species	Isolates[1]	GenBank accession number[2]				References
		ITS	*tef1*	*tub2*	*rpb2*	
Paraphoma chlamydocopiosa	BRIP 65168^{T}	KU999072	KU999080	KU999084	–	Moslemi *et al.* (2018)
Pa. chrysanthemicola	CBS 522.66^{NT}	KF251166	KF253124	KF252661	KF252174	Quaedvlieg *et al.* (2013)
Pa. dioscoreae	CBS 135100^{T}	KF251167	KF253125	KF252662	KF252175	Quaedvlieg *et al.* (2013)
Pa. fimeti	CBS 170.70^{NT}	KF251170	KF253128	KF252665	KF252178	Quaedvlieg *et al.* (2013)
Pa. pye	BRIP 65169^{T}	KU999073	KU999081	KU999085	–	Moslemi *et al.* (2018)
Pa. radicina	CBS 111.79^{ET}	KF251172	KF253130	KF252667	KF252180	Quaedvlieg *et al.* (2013)
Pa. rhaphiolepidis	CBS 142524^{T}	KY979758	KY979896	KY979924	KY979851	Crous *et al.* (2017a)
Pa. vinacea	BRIP 63684^{T}	KU176884	KU176896	KU176892	–	Moslemi *et al.* (2016)

[1] BRIP: Queensland Plant Pathology Herbarium, Brisbane, Australia; CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands. $^{T,\ ET}$ and ^{NT} indicate ex-type, ex-epitype and ex-neotype strains, respectively.

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

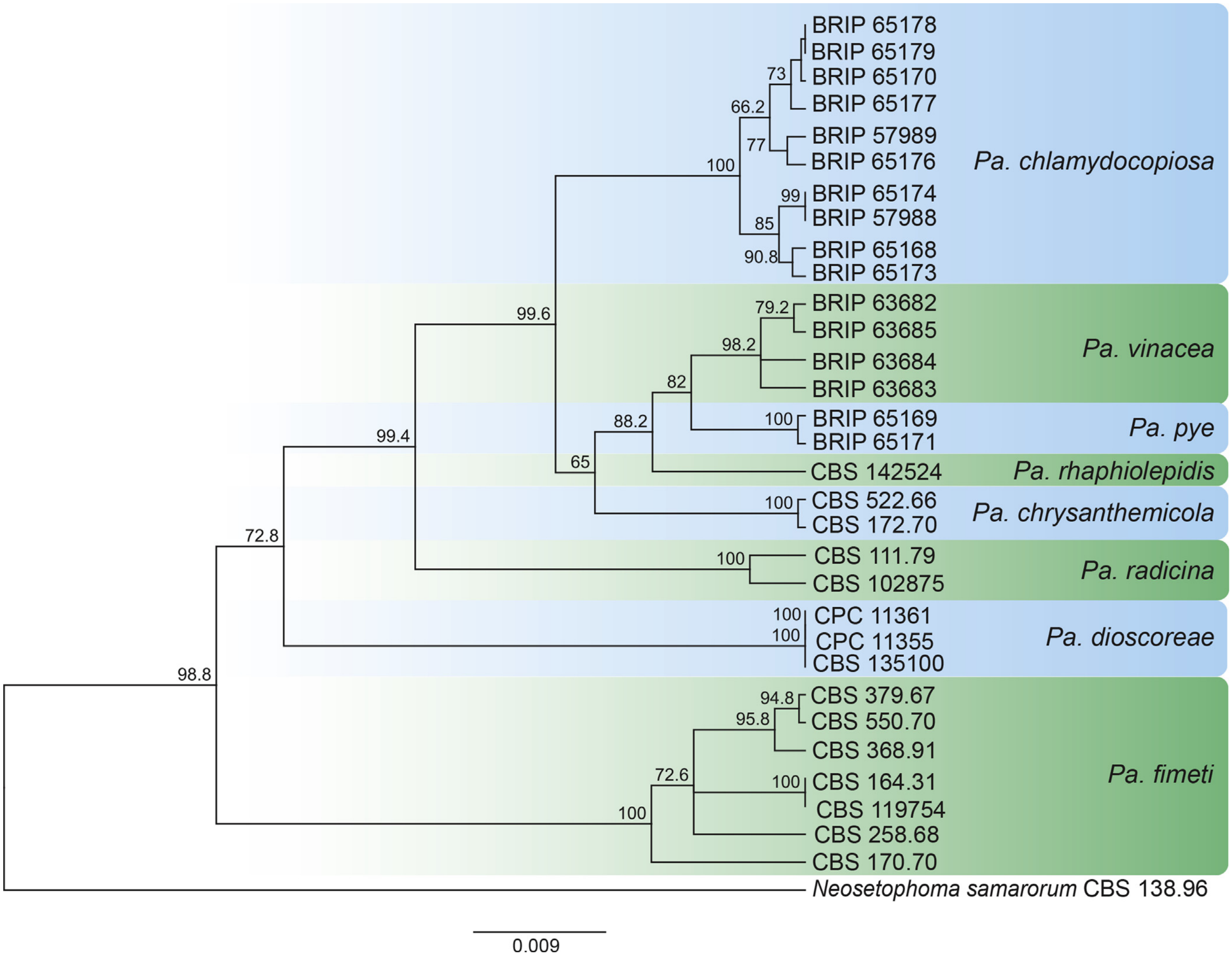


Fig. 42. Maximum likelihood PhyML combined phylogenetic tree of *Paraphoma* spp. inferred from ITS (680 bp), *tef1* (550 bp) and *tub2* (350 bp) using a GTR substitution model. Highest log likelihood -3812.4179. Bootstrap support values less than 65 % were removed. Scale bar indicated expected changes per site. The tree was rooted to *Neosetophoma samarorum* CBS 138.96. GenBank accession numbers are indicated in Table 13. TreeBASE: S22303.

round, slimy heads at apices of phialides, hyaline, aseptate, smooth-walled, oblong-ellipsoidal to obovate, cylindrical, allantoid or reniform, uncommonly fusiform-ellipsoidal or globose, becoming biguttulate with age.

Culture characteristics: Colonies on MEA flat with entire margins, mostly moderately dense, predominantly felty, and sometimes woolly; brown, olive-grey, pale yellow to beige or pink to dark pink.

Optimal media and cultivation conditions: 2 % MEA to induce sporulation of asexual morph. Cultural characters that are useful to distinguish *Phaeoacremonium* species include colour of colonies on MEA, and yellow pigment production on PDA and OA.

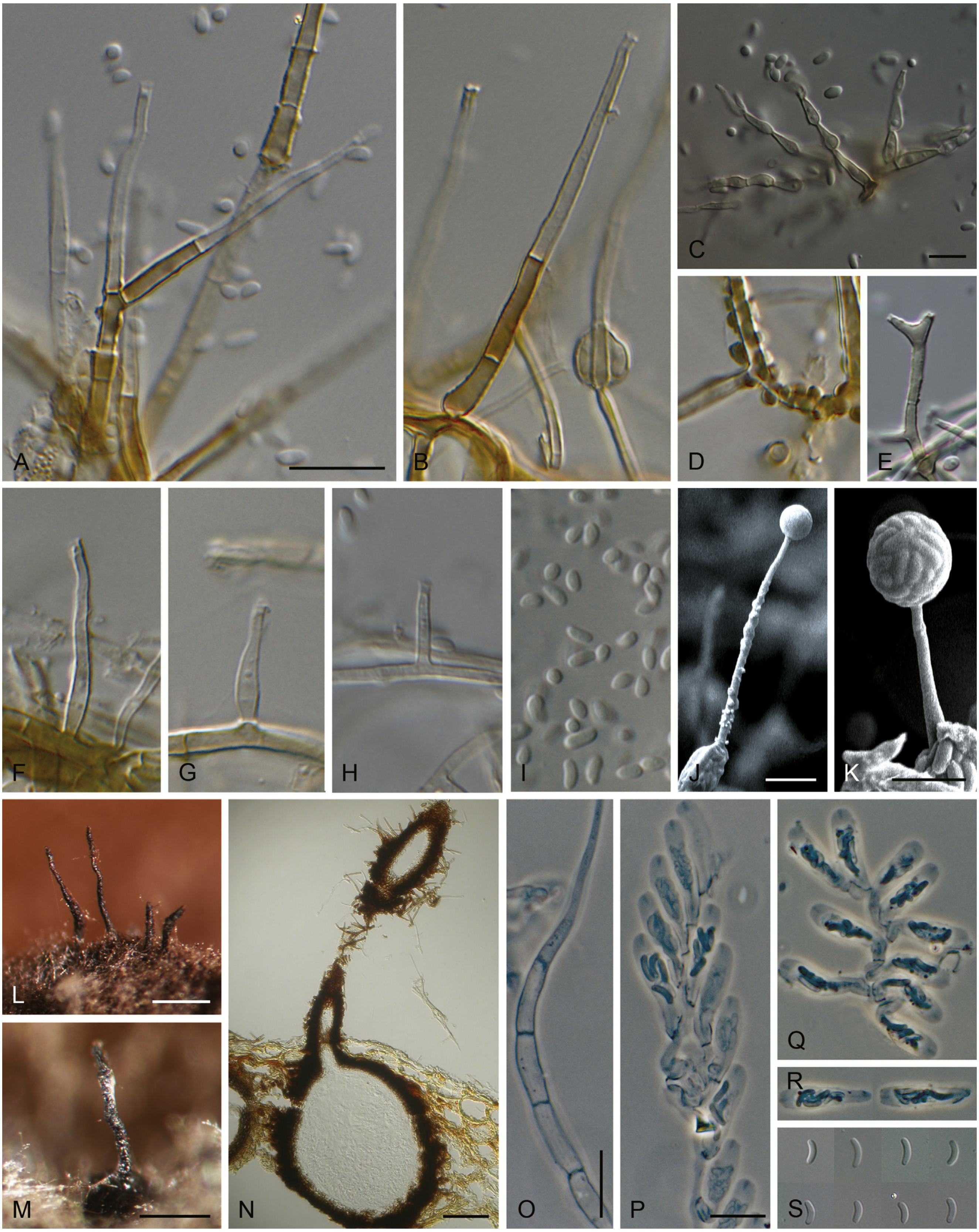


Fig. 43. Morphological structures of *Phaeoacremonium* spp. **A–K.** Asexual morphs. **A.** Conidiophores branched. **B.** Conidiophores unbranched. **C.** Percurrent rejuvenation of conidiophore. **D.** Mycelium showing prominent exudate droplets observed as warts. **E.** Conidiophore with polyphialides. **F.** Type III phialides. **G.** Type II phialide. **H.** Type I phialide. **I.** Conidia. **J.** Conidiophore. **K.** Type II phialide. **L–S.** Sexual morph. **L, M.** Ascomata on canes of *Vitis vinifera*. **N.** Longitudinal section through ascoma. **O.** One paraphyses. **P, Q.** Asci attached to ascogenous hyphae. **R.** Asci. **S.** Ascospores. **A, B, D, F, G, I.** *Phaeoacremonium parasiticum* (ex-type CBS 860.73). **C.** *Phaeoacremonium hispanicum* (ex-type CBS 123910). **E.** *Phaeoacremonium amygdalinum* (ex-type CBS 128570). **H.** *Phaeoacremonium minimum* (ex-type CBS 246.91). **L–S.** *Phaeoacremonium minimum* (holotype CBS 17463). Scale bars: A, C, J, K, O, P = 10 µm; L, M = 200 µm; N = 100 µm; A applies to A, B, D, F–I; C applies to C, E; P applies to P–S.

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

Species	**Isolates**[1]	**GenBank accession numbers**[2]		**References**
		act	***tub2***	
Phaeoacremonium africanum	CBS 120863^{T}	EU128142	EU128100	Damm *et al.* (2008)
Pha. album	CBS 142688^{T}	KY906884	KY906885	Spies *et al.* (2018)
Pha. alvesii	CBS 110034^{T}	AY579234	AY579301	Mostert *et al.* (2005)
Pha. amstelodamense	CBS 110627^{T}	AY579228	AY579295	Mostert *et al.* (2005)
Pha. amygdalinum	CBS 128570^{T}	JN191303	JN191307	Gramaje *et al.* (2012)
Pha. angustius	CBS 114992^{T}	DQ173127	DQ173104	Mostert *et al.* (2006)
Pha. aquaticum	IFRDCC 3035^{T}	n/a[3]	n/a[3]	Hu *et al.* (2012)
Pha. argentinense	CBS 777.83^{T}	DQ173135	DQ173108	Mostert *et al.* (2006)
Pha. armeniacum	ICMP 17421^{T}	EU595463	EU596526	Graham *et al.* (2009)
Pha. aureum	CBS 142691^{T}	KY906656	KY906657	Spies *et al.* (2018)
Pha. australiense	CBS 113589^{T}	AY579229	AY579296	Mostert *et al.* (2005)
Pha. austroafricanum	CBS 112949^{T}	DQ173122	DQ173099	Mostert *et al.* (2006)
Pha. bibendum	CBS 142694^{T}	KY906758	KY906759	Spies *et al.* (2018)
Pha. canadense	PARC 327^{T}	KF764499	KF764651	Úrbez-Torres *et al.* (2014)
Pha. cinereum	CBS 123909^{T}	FJ517153	FJ517161	Gramaje *et al.* (2009)
Pha. croatiense	CBS 123037^{T}	EU863514	EU863482	Essakhi *et al.* (2008)
Pha. fraxinopennsylvanicum	CBS 101585^{T}	DQ173137	AF246809	Groenewald *et al.* (2001)
Pha. fuscum	STE-U 5969^{T}	EU128141	EU128098	Damm *et al.* (2008)
Pha. gamsii	CBS 142712^{T}	KY906740	KY906741	Spies *et al.* (2018)
Pha. geminum	CBS 142713^{T}	KY906648	KY906649	Spies *et al.* (2018)
Pha. globosum	ICMP 16988^{T}	EU595466	EU596525	Graham *et al.* (2009)
Pha. griseo-olivaceum	STE-U 5966^{T}	EU128139	EU128097	Damm *et al.* (2008)
Pha. griseorubrum	CBS 111657^{T}	AY579227	AY579294	Mostert *et al.* (2005)
Pha. hispanicum	CBS 123910^{T}	FJ517156	FJ517164	Gramaje *et al.* (2009)
Pha. hungaricum	CBS 123036^{T}	EU863515	EU863483	Essakhi *et al.* (2008)
Pha. inflatipes	CBS 391.71^{T}	AY579259	AF246805	Mostert *et al.* (2006)
Pha. iranianum	CBS 101357^{T}	DQ173120	DQ173096	Mostert *et al.* (2006)
Pha. italicum	CBS 137763^{T}	KJ534046	KJ534074	Raimondo *et al.* (2014)
Pha. junior	CBS 142697^{T}	KY906708	KY906709	Spies *et al.* (2018)
Pha. krajdenii	CBS 109479^{T}	AY579267	AY579330	Mostert *et al.* (2005)
Pha. leptorrhynchum	CBS 110156*	DQ173139	DQ173110	Mostert *et al.* (2006)
Pha. longicollarum	CBS 142699^{T}	KY906688	KY906689	Spies *et al.* (2018)
Pha. luteum	CBS 137497^{T}	KF835406	KF823800	Gramaje *et al.* (2014)
Pha. meliae	CBS 142710^{T}	KY906824	KY906825	Spies *et al.* (2018)
Pha. minimum	CBS 246.91^{T}	AY735497	AF246811	Mostert *et al.* (2006)
Pha. nordesticola	CMM 4312^{T}	KY030803	KY030807	da Silva *et al.* (2017)
Pha. occidentale	ICMP 17037^{T}	EU595460	EU596524	Graham *et al.* (2009)
Pha. oleae	CBS 142704^{T}	KY906936	KY906937	Spies *et al.* (2018)
Pha. parasiticum	CBS 860.73^{T}	AY579253	AF246803	Mostert *et al.* (2006)
Pha. pallidum	STE-U 6104^{T}	EU128144	EU128103	Damm *et al.* (2008)
Pha. paululum	CBS 142705^{T}	KY906880	KY906881	Spies *et al.* (2018)
Pha. pravum	CBS 142686^{T}	KY084248	KY084246	Present study
Pha. proliferatum	CBS 142706^{T}	KY906902	KY906903	Spies *et al.* (2018)
Pha. prunicola	STE-U 5967^{T}	EU128137	EU128095	Damm *et al.* (2008)
Pha. pseudopanacis	CBS 142101^{T}	KY173569	KY173609	Crous *et al.* (2016a)
Pha. roseum	PARC 273^{T}	KF764506	KF764658	Úrbez-Torres *et al.* (2014)
Pha. rosicola	CBS 142708^{T}	KY906830	KY906831	Spies *et al.* (2018)
Pha. rubrigenum	CBS 498.94^{T}	AY579238	AF246802	Mostert *et al.* (2006)

(*continued on next page*)

Table 14. (Continued).

Species	Isolates[1]	GenBank accession numbers[2]		References
		act	***tub2***	
Pha. santali	CBS 137498^T	KF835403	KF823797	Gramaje *et al.* (2014)
Pha. scolyti	CBS 113597^T	AY579224	AF246800	Mostert *et al.* (2005)
Pha. sicilianum	CBS 123034^T	EU863520	EU863488	Essakhi *et al.* (2008)
Pha. spadicum	CBS 142711^T	KY906838	KY906839	Spies *et al.* (2018)
Pha. sphinctrophorum	CBS 337.90^T	DQ173142	DQ173113	Mostert *et al.* (2006)
Pha. subulatum	CBS 113584^T	AY579231	AY579298	Mostert *et al.* (2005)
Pha. tardicrescens	CBS 110573^T	AY579233	AY579300	Mostert *et al.* (2005)
Pha. tectonae	MFLUCC 13-0707^T	KT285563	KT285555	Ariyawansa *et al.* (2015)
Pha. theobromatis	CBS 111586^T	DQ173132	DQ173106	Mostert *et al.* (2006)
Pha. tuscanicum	CBS 123033^T	EU863490	EU863458	Essakhi *et al.* (2008)
Pha. venezuelense	CBS 651.85^T	AY579256	AY579320	Mostert *et al.* (2005)
Pha. vibratile	CBS 117115^T	DQ649063	DQ649064	Réblová & Mostert (2007)
Pha. viticola	CBS 101738^T	DQ173131	AF192391	Dupont *et al.* (2000)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands; IFRDCC: International Fungal Research and Development Center, Bailongsi, China; ICMP: International Collection of Microorganisms from Plants, Auckland, New Zealand; PARC: Pacific Agri-Food Research Centre in Summerland, British Columbia, Canada; CMM: Culture Collection of Phytopathogenic Fungi “Prof. Maria Menezes”, Universidade Federal Rural de Pernambuco, Recife, Brazil; STE-U: Department of Plant Pathology, Stellenbosch University, South Africa; MFLUCC: Mae Fah Luang Culture Collection, Chiang Rai, Thailand. ^{T} indicates ex-type strains. *Ex-type of *Pha. novae-zealandiae*, synonymised with *Pha. leptorrhynchum* by Réblová (2011).

[2] *act*: partial actin gene; *tub2*: partial β-tubulin gene.

[3] Not available. Only ITS sequence available: NR136032.

For the sexual morph 2 % WA is used with twice-autoclaved pieces of 3–4 cm of grapevine cane at 22 °C (GWA).

Distribution: Worldwide.

Hosts: Frequently isolated from both diseased woody plants with brown wood streaking, and humans with phaeohyphomycotic infections. Other hosts include larvae of bark beetles, arthropods, and soil. Because of the involvement of members of this genus in Petri disease and esca of grapevines (*Vitis* spp.), isolates from this host have been intensively studied (Mostert *et al.* 2006, Gramaje *et al.* 2015, Spies *et al.* 2018). Even though *Phaeoacremonium* species can infect a wide range of woody hosts (more than 40 host plants), recent publications have shown the importance of *Phaeoacremonium* species in causing brown wood streaking of *Olea europaea* (*Oleaceae*) and *Prunus* spp. (*Rosaceae*) (Damm *et al.* 2008, Carlucci *et al.* 2015).

Notes: Species delimitation based on morphology alone has little value since many species have overlapping characters. Moreover, the morphology of the sexual morph cannot be used because only 15 taxa are known. The two gene regions used most frequently for phylogenetic analyses are actin (*act*) and partial beta-tubulin (*tub2*) genes (Mostert *et al.* 2006). Phylogenetic analyses combining these two regions allow for the resolution of almost all currently known *Phaeoacremonium* species with good support ($\geq$0.97 PP, $\geq$96 % BS) (Fig. 44). The three exceptions to this are *Pha. griseorubrum* (paraphyletic), *Pha. roseum* (0.72 PP, 100 % BS) and *Pha. viticola* (0.87 PP, 62 % BS) (Fig. 44, also see Gramaje *et al.* 2015 and Spies *et al.* 2018). Other gene regions that have been used include the ITS, *tef1* and *cal* (Groenewald *et al.* 2001, Mostert *et al.* 2005, Úrbez-Torres *et al.* 2014). Úrbez-Torres *et al.* (2014) included ITS and *tef1* data along with *act* and *tub* in their phylogeny, which resolved all included species with more than 97 % or 96 % bootstrap support in maximum parsimony and neighbour joining analyses respectively. The ITS region is considered insufficiently variable to distinguish between several of the species and is not recommended as a barcode (Mostert *et al.* 2005); however, considering the resolution and support in the phylogeny of Úrbez-Torres *et al.* (2014), the *tef1* region is valuable in resolving issues with support and resolution in the *act-tub2* phylogeny. The *cal* region was sequenced for a limited number of species by Mostert *et al.* (2005) to resolve taxa related to *Pha. rubrigenum*. Unfortunately, sequence data for this region are available for a limited number of species and its usefulness in distinguishing between *Phaeoacremonium* species remains uncertain.

References: Crous *et al.* 1996 (taxonomy); Eskalen *et al.* 2005, Rooney-Latham *et al.* 2005 (sexual morph); Mostert *et al.* 2006, Gramaje *et al.* 2015 (taxonomy, distribution, host range, detection, identification, pathogenesis and epidemiology); Aroca & Raposo 2007, Pouzoulet *et al.* 2013, Úrbez-Torres *et al.* 2015 (detection and identification); Halleen *et al.* 2007, Damm *et al.* 2008; Aroca & Raposo 2009, Gramaje *et al.* 2010 (pathogenicity); Blanco-Ulate *et al.* 2013 (genome sequence); Moyo *et al.* 2014, Agustí-Brisach *et al.* 2015 (epidemiology); Réblová *et al.* 2015 (systematics).

Phaeoacremonium pravum C.F.J. Spies, L. Mostert & Halleen, **sp. nov.** MycoBank MB821019. Fig. 45.

Etymology: Latin, *pravum* meaning crooked, in reference to the crooked shape of some phialides.

Mycelium of branched, prominently septate, hyaline to pale brown, smooth to finely verruculose (1–)1.5–2.5 (av. 2) µm diam hyphae, forming bundles of up to 5 strands, individual strands in bundles often forming direct hyphal connections. *Conidiophores* (14.5–)16–61(–77) × 1.5–2.5 (av. 28.5 × 2) µm, smooth to finely verruculose, usually branched, hyaline, up to 9 septa. *Phialides* terminal or lateral, monophialidic, sometimes proliferating vegetatively behind collarette, types I and II dominant, collarettes funnel-shaped, 0.5–1.5 × 0.5–2 (av. 1 × 1.5) µm, smooth, hyaline; *type I* mainly subcylindrical, sometimes elongate ampulliform, (2–)2.5–10.5(–11) × 1–2 (av. 6 × 1.5) µm; *type II* subcylindrical with tapering apex to elongate ampulliform, sometimes curved or bent especially at apex, (8–)8.5–14(–14.5) × 1.5–2(–2.5) (av. 11.5 × 2) µm; *type III* subcylindrical with tapering apex to subulate, sometimes slender navicular, (14–)14.5–26.5(–31.5) × 1.5–2 (av. 19 × 1.5) µm. *Conidia* 3–4(–4.5) × 1.5(–2) (av. 3.5 × 1.5) µm, borne in slimy heads, oblong-ovoid to ellipsoidal to allantoid.

Culture characteristics: Colonies reaching a radius of 8–10 mm after 8 d at 25 °C. Minimum temperature for growth 10 °C, optimum 20 °C, maximum 35 °C. Colonies on MEA smooth, submerged with entire edge, after 16 d white to pale buff above and in reverse. Colonies on PDA smooth, submerged, with central folds, with entire margin, after 16 d white to pale buff above and in reverse. Colonies on OA felty, folded, with submerged margins, with entire edge, after 16 d white to pale smoke grey with darker margins.

Materials examined: **South Africa**, from wood of *Vitis berlandieri* × *V. rupestris* (rootstock cv. Richter 110) (*Vitaceae*), 18 Sep. 2014, A. Vermeulen (**holotype** CBS-H 23158, culture ex-type CBS 142686 = STE-U 8363 = CSN3); ibid., on *Vitis vinifera* cv. Early Sweet cordon (*Vitaceae*), 18 Sep. 2014, A. Vermeulen, CBS 142687 = STE-U 8364 = CSN11.

Notes: There are several differences between the ex-type strain (CBS 142686) and strain CBS 142687. Strain CBS 142687 had a higher optimum and maximum temperatures for growth (25 °C and 37 °C, respectively) than strain CBS 142686 and reached a radius of 11–12 mm after 8 d at 25 °C. After 16 d, colonies of strain CBS 142687 also had pronounced pigmentation on MEA i.e. rosy vinaceous with dark purple patches with central white tufts of aerial mycelium, and on PDA i.e. livid red to dark vinaceous with white to smoke grey woolly aerial mycelium, and on OA i.e. mouse grey to olivaceous grey with white margins. The *act* sequence of strain CBS 142687 differs from that of the ex-type (CBS 142686) at six positions over a length of 210 bases, resulting in paraphyly of this species in an *act*-only phylogeny (Spies *et al.* 2018). Considering the high similarity of *tub2* sequences (598/599 identical bases), strong support for the monophyly of *Pha. pravum* in the combined *act*-*tub2* phylogeny, and the fact that both strains produced curved phialides, CBS 142687 is regarded as *Pha. pravum* until additional strains and data become available to indicate differently.

Authors: D. Gramaje, L. Mostert, C.F.J. Spies & F. Halleen

Phyllosticta Pers., Traité sur les Champignons Comestibles (Paris): 55. 147. 1818. Fig. 46.
Synonym: Guignardia Viala & Ravaz, Bull. Soc. mycol. Fr. 8: 63. 1892.

Classification: *Dothideomycetes*, *Dothideomycetidae*, *Botryosphaeriales*, *Phyllostictaceae*.

Type species: *Phyllosticta convallariae* Pers., nom. inval. (= *Phyllosticta cruenta* (Fr.) J. Kickx f.). Reference strain: CBS 858.71.

DNA barcode (*genus*): LSU.

DNA barcodes (*species*): ITS, *act*, *gapdh*, *tef1*. Table 15. Fig. 47.

Ascomata pseudothecial, separate to gregarious, globose to subglobose, brown to black, unilocular with a central ostiole. *Pseudoparaphyses* mostly absent at maturity, filamentous, branched, septate when present. *Asci* bitunicate, fissitunicate, clavate to subcylindrical, 8-spored, fasciculate, stipitate, with an ocular chamber. *Ascospores* bi- to triseriate, hyaline, guttulate to granular, aseptate, ellipsoid, ellipsoid-fusoid to limoniform, smooth-walled, usually with mucilaginous caps at ends, or surrounded by a mucilaginous sheath. *Conidiomata* and *spermatogonia* pycnidial, immersed, subepidermal to erumpent, unilocular, rarely multilocular, glabrous, ostiolate, dark brown to black; *ostiole* circular to oval; *conidiomatal wall* thick-walled, dark brown, *textura angularis*, with inner layers of hyaline to pale brown, thin-walled, *textura prismatica* to *angularis*. *Conidiophores* lining cavity of conidioma, reduced to conidiogenous cells, invested in mucus. *Conidiogenous cells* discrete, producing macroconidia and spermatia, also produced in separate spermatogonia, ampulliform, lageniform, doliiform to subcylindrical, hyaline, smooth, proliferating percurrently near apex, invested in a mucoid layer. *Conidia* ellipsoid-fusoid to obovoid or ovoid, rarely subcylindrical, aseptate, broadly rounded at apex, often tapering strongly toward base, unicellular, hyaline, smooth-walled, guttulate to granular, often enclosed in a persistent mucilaginous sheath, and bearing an unbranched, tapering, straight to curved, mucoid apical appendage. *Spermatogenous cells* ampulliform to lageniform or subcylindrical, hyaline, smooth, phialidic. *Spermatia* hyaline, smooth, granular, subcylindrical or dumbbell-shaped, with rounded or blunt ends (adapted from Wikee *et al.* 2013b).

Culture characteristics: Colonies on MEA, OA and PDA after 2 wk in dark at 27 °C erumpent or flat, spreading with sparse or moderate aerial mycelium; on MEA, OA and PDA surface frequently iron-grey or olivaceous grey, less frequently greenish to dark green; reverse iron-grey, olivaceous grey or black.

Optimal media and cultivation conditions: PNA, OA, PDA and SNA under near-ultraviolet light at 27 °C to induce sporulation.

Distribution: Worldwide.

Hosts: Wide range of hosts from trees to ornamentals.

Disease symptoms: Leaf spots and various fruit diseases.

Notes: *Phyllosticta* was introduced by Persoon (1818), with *Phy. convallariae* designated as type species (Donk 1968). However, this species was invalid because it lacked a description. Therefore, *Phy. cruenta*, which is a synonym of *Phy. convallariae*, was designated as type of the genus (van der Aa & Vanev 2002). There is no available type material for this species, which was described from *Polygonatum multiflorum* collected in Germany. A strain deposited in CBS previously identified as *Guignardia reticulata*, which is the sexual morph of *Phy. cruenta*, was isolated from *Polygonatum odoratum* in the Czech Republic, being a potential neotype for *Phy. cruenta*. However, this strain is sterile and we have chosen to consider it as a reference strain since we could not confirm its identification based on morphology.

Phyllosticta includes plant pathogenic species that cause diseases of significant economic importance. For example, *Phy. citricarpa* is the responsible for citrus black spot, which is considered a quarantine pest in Europe and the USA (Baayen *et al.* 2002, Glienke *et al.* 2011, Guarnaccia *et al.* 2017). Other examples include the *Phy. ampelicida* species complex that causes black rot disease on grapevines (Wicht *et al.* 2012, Carstens *et al.* 2017), and the *Phy. musarum* species complex

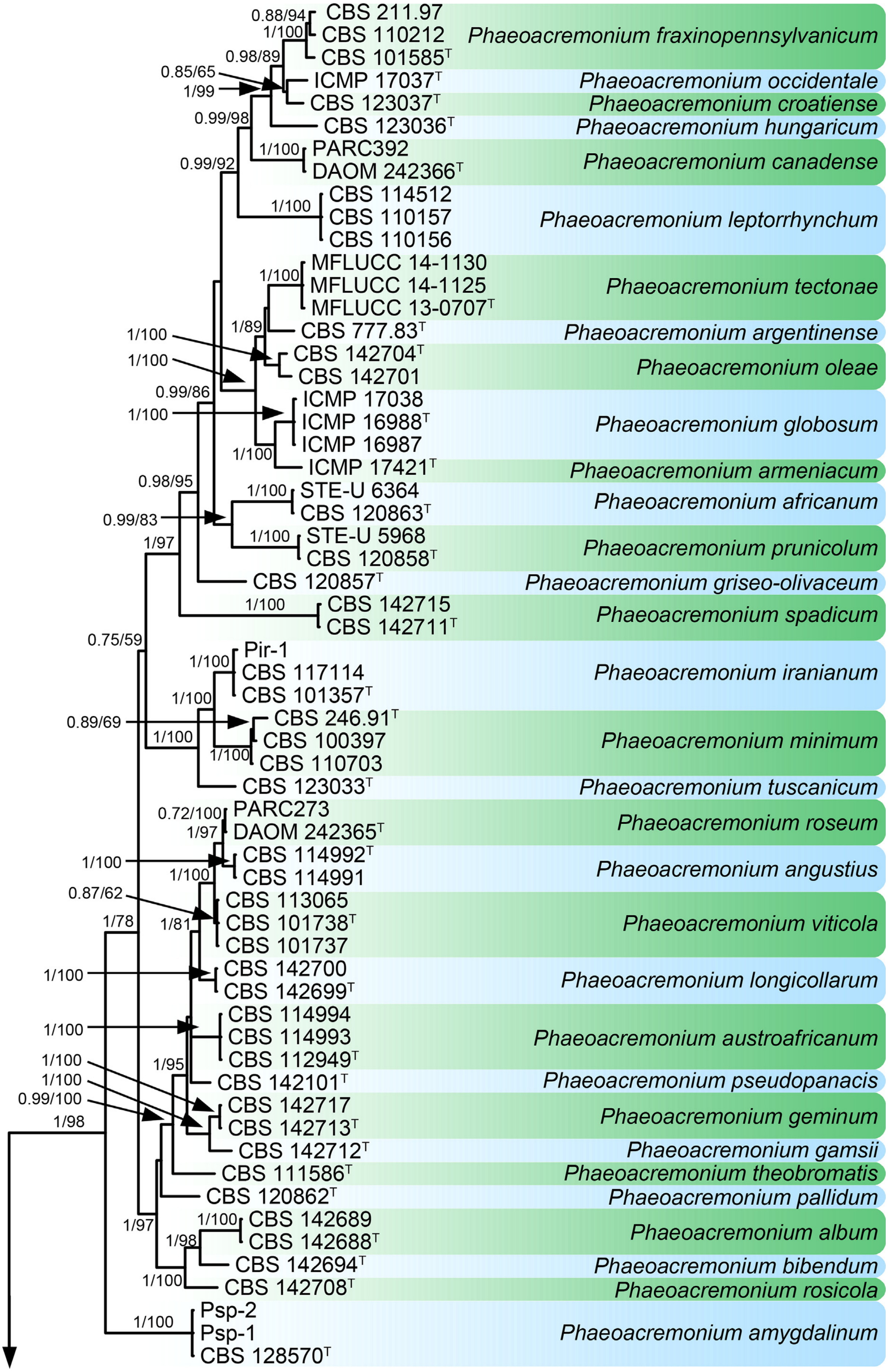


Fig. 44. Bayesian consensus tree of the genus *Phaeoacremonium* as estimated from the combined *act* (~260 bp) and *tub2* (~680 bp) regions. Bayesian posterior probability values and bootstrap support percentages are shown at the nodes. Support values of less than 0.7 posterior probability and 70 % bootstrap are not shown. *Jattaea algeriensis*, *Calosphearia africana* and *Pleurostoma richardsiae* were used as outgroups. GenBank accession numbers are listed in Spies *et al.* (2018). ^{T} indicates ex-type strains. TreeBASE: S22407.

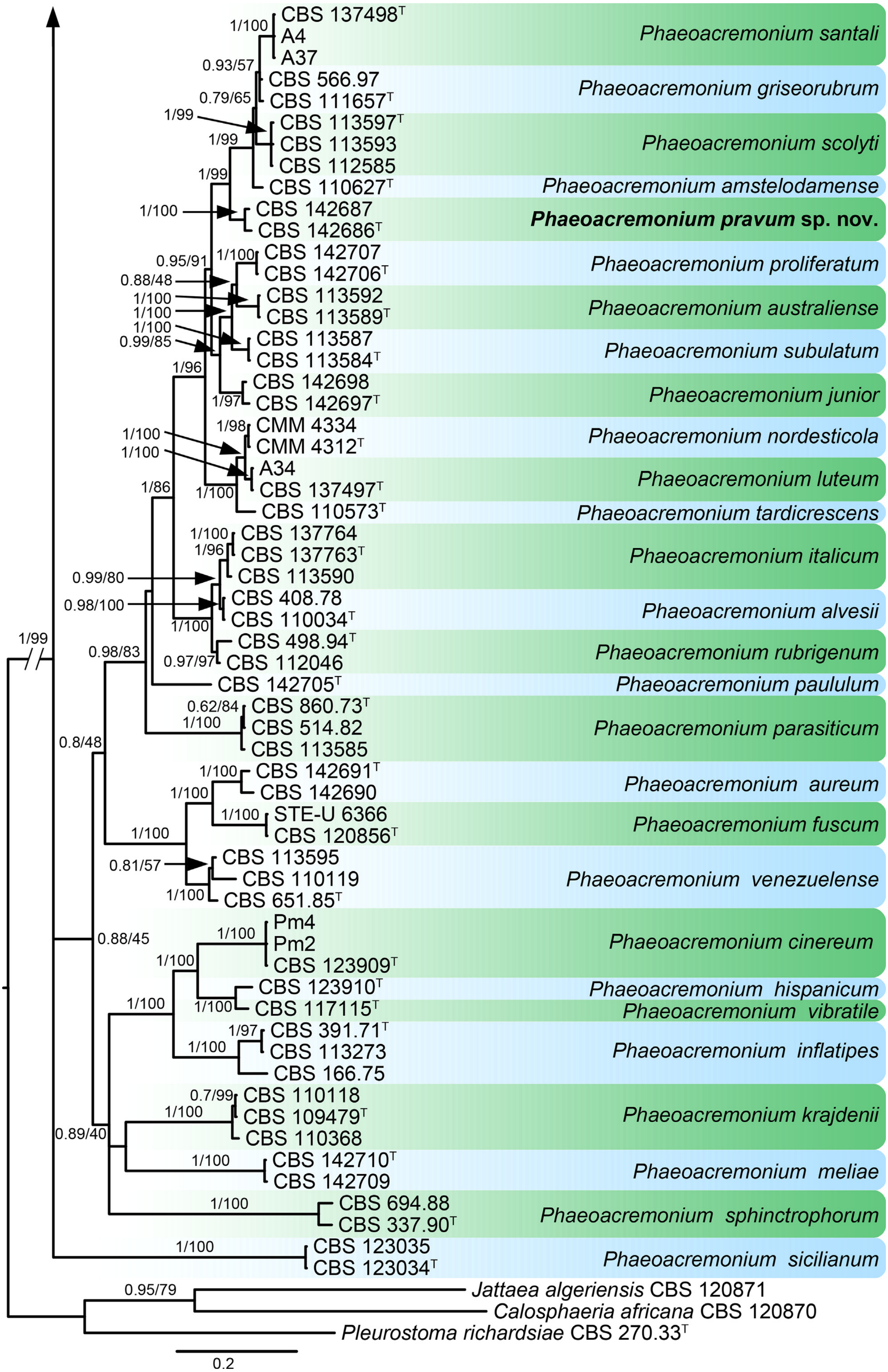


Fig. 44. (Continued).

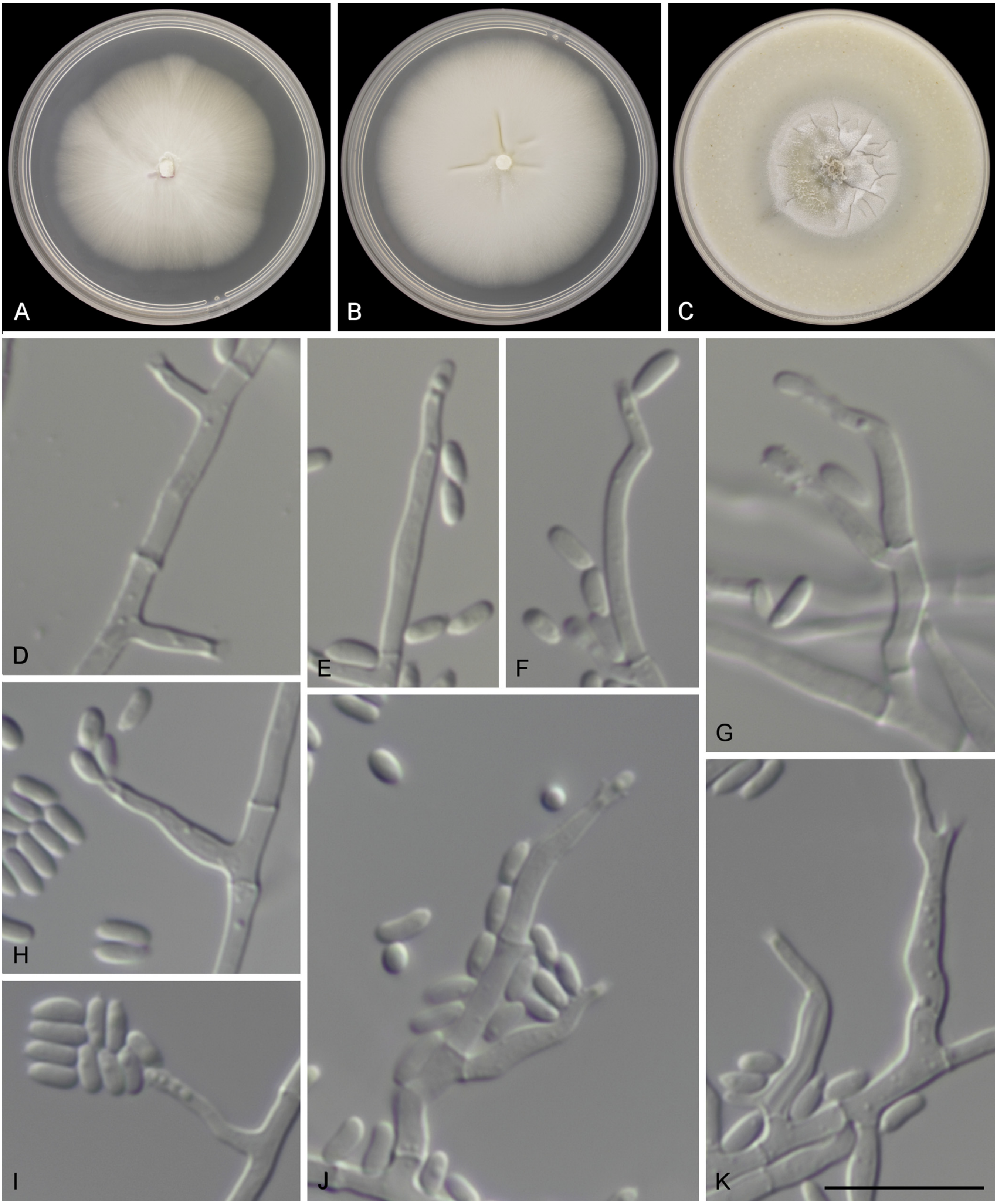


Fig. 45. *Phaeoacremonium pravum* (ex-type CBS 142686). **A–C.** Eight-d-old colonies on MEA (A), PDA (B) and OA (C). **D.** Subcylindrical type I phialides with funnel-shaped collarettes. **E, F.** Type III phialides. **G, J.** Branched conidiophores with crooked type II phialides. **H.** Elongate ampulliform type I phialide. **I.** Type I phialide with conidia borne in a slimy head. **K.** Crooked elongate ampulliform type I phialide with a funnel-shaped collarette showing lateral vegetative proliferation. Scale bar: K = 10 µm, K applies to D–K.

that is responsible for banana freckle disease (Pu *et al.* 2008, Wong *et al.* 2012).

Phoma and *Phyllosticta* have been difficult to distinguish since both genera were recognised as pycnidial fungi producing unicellular, hyaline conidia. Subsequent molecular data enabled the discrimination of both genera, as well as the fact that *Phyllosticta* was linked to its sexual morph, *Guignardia* (Glienke *et al.* 2011, Wikee *et al.* 2011, 2013b, Wong *et al.* 2012, Zhou *et al.* 2015, Guarnaccia *et al.* 2017).

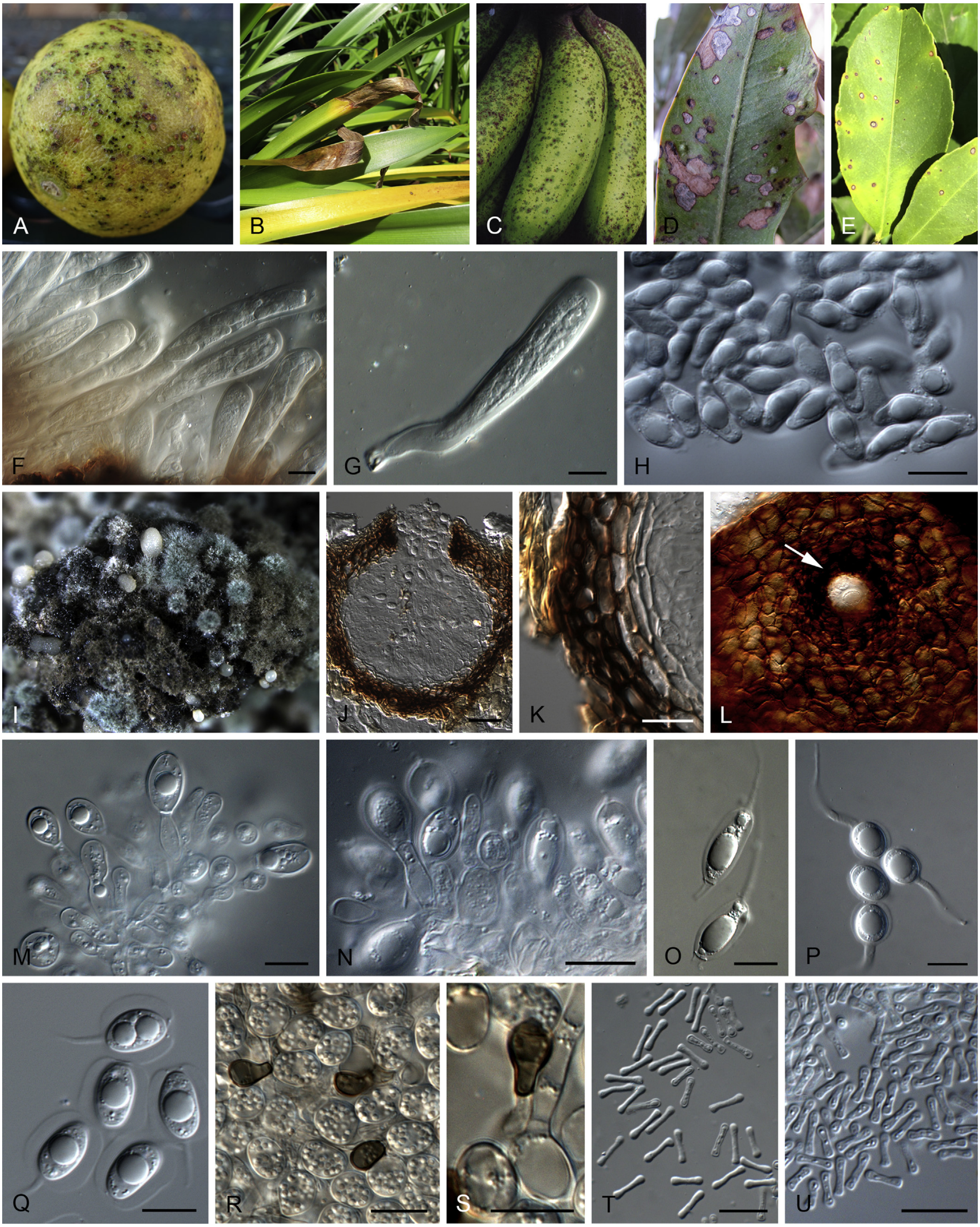


Fig. 46. *Phyllosticta* spp. **A–E.** Disease symptoms. **A.** Aloe with dead leaf tips that harbour *Phyllosticta aloeicola*. **B.** Symptoms on *Citrus maxima* caused by *Phyllosticta citrimaxima*. **C.** Water-soaked lesions on banana fruit associated with freckle disease on banana caused by *Phyllosticta* sp. **D.** Symptomatic leaf of *Cussonia* sp. caused by *Phyllosticta cussoniae*. **E.** Symptoms on lemon leaf caused by *Phyllosticta* sp. **F–H.** Sexual morphs. **F, G.** Asci and ascospores of *Phyllosticta abieticola* (ex-type CBS 112067). **H.** Ascospores of *Phyllosticta capitalensis* (ex-epitype CBS 128856). **I–U.** Asexual morphs. **I.** Conidiomata sporulating on OA of *Phyllosticta cussoniae* (ex-epitype CPC 14873). **J.** Vertical section through conidioma of *Phyllosticta rhaphiolepidis* (ex-type MUCC 432). **K.** Conidiomatal wall of *textura angularis* of *Phyllosticta rhaphiolepidis* (ex-type MUCC 432). **L.** Conidioma with ostiole (arrowed) of *Phyllosticta cordylinophila* (ex-neotype CPC 20261). **M, N.** Conidiogenous cells giving rise to conidia. **M.** *Phyllosticta foliorum* (ex-neotype CBS 447.68). **N.** *Phyllosticta capitalensis* (ex-epitype CBS 128856). **O–Q.** Conidia. **O.** *Phyllosticta aloeicola* (CPC 20677). **P.** *Phyllosticta podocarpicola* (ex-type CBS 728.79). **Q.** *Phyllosticta capitalensis* (ex-epitype CBS 128856). **R, S.** Appressoria of *Phyllosticta mangifera-indica* (ex-type CPC 20274). **T, U.** Spermatia. **T.** *Phyllosticta cussoniae* (ex-epitype CPC 14873). **U.** *Phyllosticta leucothoicola* (ex-type MUCC 553). Scale bars: I = 25 µm; others = 10 µm. Pictures A, B, D, F–M, O, P, R–U taken from Wikee *et al.* (2013b); C from Wong *et al.* (2012); N, Q from Glienke *et al.* (2011).

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

Species	Isolates[1]	GenBank accession number[2]				References
		ITS	*act*	*gapdh*	*tef1*	
Phyllosticta abieticola	CBS 112067^{T}	KF170306	KF289238	–	–	Wikee *et al.* (2013b)
Phy. alliacea	MUCC 0014^{T}	AB454263	AB704207	–	–	Motohashi *et al.* (2009), Ando *et al.* (2013)
Phy. aloeicola	CBS 136058^{T}	KF154280	KF289311	KF289124	KF289193	Wikee *et al.* (2013b)
Phy. ampelicida	ATCC 200578^{NT}	KC193586	KC193581	KC193584	–	Zhang *et al.* (2013b)
Phy. ardisiicola	MUCC 0031^{T}	AB454274	AB704216	–	–	Motohashi *et al.* (2009), Ando *et al.* (2013)
Phy. aristolochiicola	BRIP 53316a^{T}	JX486129	–	–	–	Crous *et al.* (2012a)
Phy. aspidistricola	MUCC 0010^{T}	AB454260	AB704204	–	–	Motohashi *et al.* (2009), Ando *et al.* (2013)
Phy. beaumarisii	CBS 535.87^{T}	AY042927	KF306232	KF289074	KF289170	Baayen *et al.* (2002), Wikee *et al.* (2013b)
Phy. bifrenariae	CBS 128855^{T}	JF343565	JF343649	JF343744	JF343586	Glienke *et al.* (2011)
Phy. brazillianiae	CBS 129060^{T}	JF343572	JF343656	JF343758	JF343593	Glienke *et al.* (2011)
Phy. capitalensis	CBS 128856^{ET}	JF261465	JF343647	JF343776	JF261507	Glienke *et al.* (2011)
Phy. carissicola	CPC 25665^{T}	KT950849	KT950872	KT950876	KT950879	Crous *et al.* (2015e)
Phy. carochlae	CGMCC 3.17317^{T}	KJ847422	KJ847430	KJ847438	KJ847444	Zhou *et al.* (2015)
Phy. catimbauensis	URM 7672^{T}	MF466160	MF466157	–	MF466155	Crous *et al.* (2017b)
Phy. cavendishii	BRIP 55420^{IsoT}	JQ743562	–	–	–	Wong *et al.* (2012)
Phy. citriasiana	CBS 120486^{T}	FJ538360	FJ538476	JF343686	FJ538418	Wulandari *et al.* (2009), Glienke *et al.* (2011)
Phy. citribraziliensis	CBS 100098^{T}	FJ538352	FJ538468	JF343691	FJ538410	Wulandari *et al.* (2009), Glienke *et al.* (2011)
Phy. citricarpa	CBS 127454^{ET}	JF343583	JF343667	JF343771	JF343604	Glienke *et al.* (2011)
Phy. citrichinaensis	CBS 130529^{T}	JN791597	JN791526	–	JN791452	Wang *et al.* (2011)
Phy. citrimaxima	CBS 136059^{T}	KF170304	KF289300	KF289157	KF289222	Wikee *et al.* (2013b)
Phy. concentrica	CBS 937.70^{ET}	FJ538350	KF289257	JF411745	FJ538408	Wulandari *et al.* (2009), Glienke *et al.* (2011), Wikee *et al.* (2013b)
Phy. cordylinophila	CBS 136244^{NT}	KF170287	KF289295	KF289076	KF289172	Wikee *et al.* (2013b)
Phy. cornicola	CBS 111639	KF170307	KF289234	–	–	Wikee *et al.* (2013b)
Phy. cruenta	CBS 858.71	MG934458	MG934465	MG934474	MG934501	Present study
Phy. cussonia	CBS 136060^{ET}	JF343578	JF343662	JF343764	JF343599	Glienke *et al.* (2011)
Phy. elongata	CBS 126.22^{T}	FJ538353	FJ538469	KF289164	FJ538411	Wulandari *et al.* (2009), Wikee *et al.* (2013b)
Phy. ericarum	CBS 132534^{T}	KF206170	KF289291	KF289162	KF289227	Wikee *et al.* (2013b)
Phy. eugeniae	CBS 445.82	AY042926	KF289246	KF289139	KF289208	Baayen *et al.* (2002), Wikee *et al.* (2013b)
Phy. fallopiae	MUCC 0113^{T}	AB454307	AB704228	–	–	Motohashi *et al.* (2009), Ando *et al.* (2013)
Phy. foliorum	CBS 447.68^{NT}	KF170309	KF289247	KF289132	KF289201	Wikee *et al.* (2013b)
Phy. gaultheriae	CBS 447.70^{T}	JN692543	KF289248	JN692508	JN692531	Su & Cai (2012)
Phy. hamamelidis	MUCC 149	KF170289	KF289309	–	–	Wikee *et al.* (2013b)
Phy. hostae	CGMCC 3.14355^{T}	JN692535	JN692511	JN692503	JN692523	Su & Cai (2012)
Phy. hubeiensis	CGMCC 3.14986^{T}	JX025037	JX025032	JX025027	JX025042	Zhang *et al.* (2013a)
Phy. hymenocallidicola	CBS 131309^{T}	JQ044423	KF289242	KF289142	KF289211	Crous *et al.* (2011b), Wikee *et al.* (2013b)
Phy. hypoglossi	CBS 434.92^{NT}	FJ538367	FJ538483	JF343695	FJ538425	Wulandari *et al.* (2009), Glienke *et al.* (2011), Wikee *et al.* (2013b)
Phy. ilicis-aquifolii	CGMCC 3.14358^{T}	JN692538	JN692514	–	JN692526	Su & Cai (2012)
Phy. iridigena	CBS 143410^{T}	MG934459	MG934466	–	MG934502	Present study
Phy. kerriae	MUCC 0017^{T}	AB454266	AB704209	–	KC342576	Motohashi *et al.* (2009), Ando *et al.* (2013), Wikee *et al.* (2013a)

Table 15. (Continued).

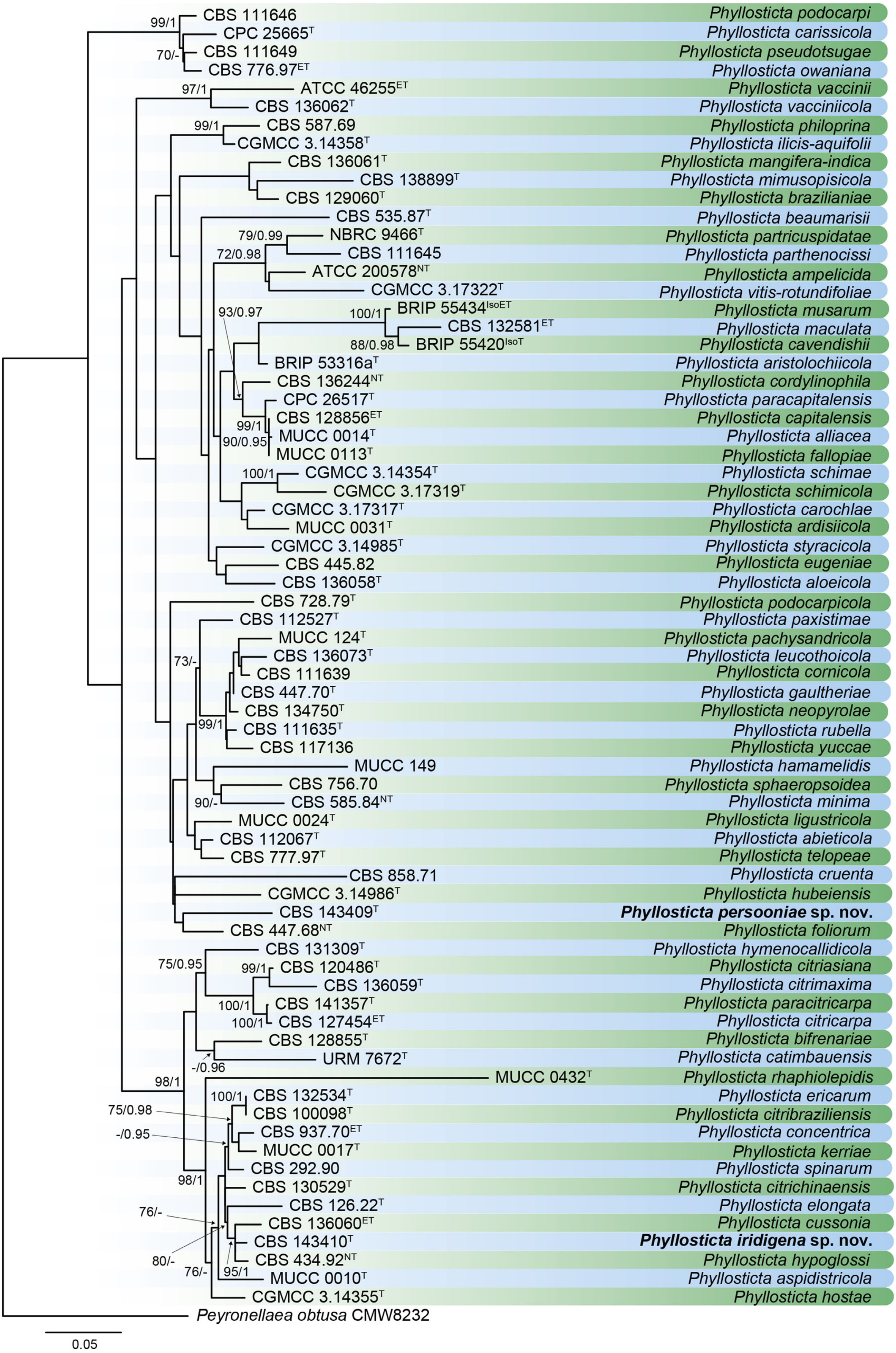
Species	Isolates[1]	GenBank accession number[2]				References
		ITS	*act*	*gapdh*	*tef1*	
Phy. leucothoicola	CBS 136073^{T}	AB454370	KF289310	–	–	Motohashi *et al.* (2009), Wikee *et al.* (2013b)
Phy. ligustricola	MUCC 0024^{T}	AB454269	AB704212	–	–	Motohashi *et al.* (2009), Ando *et al.* (2013)
Phy. maculata	CBS 132581^{ET}	JQ743570	–	–	–	Wong *et al.* (2012)
Phy. mangiferae-indicae	CBS 136061^{T}	KF170305	KF289296	KF289121	KF289190	Wikee *et al.* (2013b)
Phy. mimusopisicola	CBS 138899^{T}	KP004447	–	–	–	Crous *et al.* (2014d)
Phy. minima	CBS 585.84^{NT}	KF206176	KF289249	KF289135	KF289204	Wikee *et al.* (2013b)
Phy. musarum	BRIP 55434^{IsoET}	JQ743584	–	–	–	Wong *et al.* (2012)
Phy. neopyrolae	CBS 134750^{T}	AB454318	AB704233	–	–	Motohashi *et al.* (2009), Ando *et al.* (2013)
Phy. owaniana	CBS 776.97^{ET}	FJ538368	KF289254	JF343767	FJ538426	Wulandari *et al.* (2009), Glienke *et al.* (2011), Wikee *et al.* (2013b)
Phy. pachysandricola	MUCC 124^{T}	AB454317	AB704232	–	–	Motohashi *et al.* (2009), Ando *et al.* (2013)
Phy. paracapitalensis	CBS 141353^{T}	KY855622	KY855677	KY855735	KY855951	Guarnaccia *et al.* (2017)
Phy. paracitricarpa	CBS 141357^{T}	KY855635	KY855690	KY855748	KY855964	Guarnaccia *et al.* (2017)
Phy. parthenocisii	CBS 111645	JN692542	JN692518	–	JN692530	Su & Cai (2012)
Phy. partricuspidatae	NBRC 9466^{T}	KJ847424	KJ847432	KJ847440	KJ847446	Zhou *et al.* (2015)
Phy. paxistimae	CBS 112527^{T}	KF206172	KF289239	KF289140	KF289209	Wikee *et al.* (2013b)
Phy. persooniae	CBS 143409^{T}	MG934460	MG934467	MG934475	MG934503	Present study
Phy. philoprina	CBS 587.69	KF154278	KF289250	KF289137	KF289206	Wikee *et al.* (2013b)
Phy. podocarpi	CBS 111646	AF312013	KC357670	KF289169	KC357671	Wikee *et al.* (2013b), Carroll (unpubl. data), Wikee (unpubl. data)
Phy. podocarpicola	CBS 728.79^{T}	KF206173	KF289252	KF289134	KF289203	Wikee *et al.* (2013b)
Phy. pseudotsugae	CBS 111649	KF154277	KF289236	KF289167	KF289231	Wikee *et al.* (2013b)
Phy. rhaphiolepidis	MUCC 432^{T}	DQ632660	AB704242	–	DQ632724	Andjic *et al.* (2007), Ando *et al.* (2013)
Phy. rubella	CBS 111635^{T}	KF206171	KF289233	KF289129	KF289198	Wikee *et al.* (2013b)
Phy. schimae	CGMCC 3.14354^{T}	JN692534	JN692510	JN692506	JN692522	Su & Cai (2012)
Phy. schimicola	CGMCC 3.17319^{T}	KJ847426	KJ847434	KJ854895	KJ847448	Zhou *et al.* (2015)
Phy. sphaeropsoidea	CBS 756.70	AY042934	KF289253	KF289133	KF289202	Baayen *et al.* (2002), Wikee *et al.* (2013b)
Phy. spinarum	CBS 292.90	JF343585	JF343669	JF343773	JF343606	Glienke *et al.* (2011)
Phy. styracicola	CGMCC 3.14985^{T}	JX052040	JX025035	JX025030	JX025045	Zhang *et al.* (2013a)
Phy. telopeae	CBS 777.97^{T}	KF206205	KF289255	KF289141	KF289210	Wikee *et al.* (2013b)
Phy. vaccinii	ATCC 46255^{ET}	KC193585	KC193580	KC193583	KC193582	Zhang *et al.* (2013b)
Phy. vacciniicola	CBS 136062^{T}	KF170312	KF289287	KF289165	KF289229	Wikee *et al.* (2013b)
Phy. vitis-rotundifoliae	CGMCC 3.17322^{T}	KJ847428	KJ847436	KJ847442	KJ847450	Zhou *et al.* (2015)
Phy. yuccae	CBS 117136	JN692541	JN692517	JN692507	JN692529	Su & Cai (2012)

[1] ATCC: American Type Culture Collection, Virginia, USA; BRIP: Queensland Plant Pathology Herbarium, Brisbane, Australia; CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands; CGMCC: Chinese General Microbiological Culture Collection Center, Beijing, China; CPC: Culture collection of Pedro Crous, housed at Westerdijk Fungal Biodiversity Institute; MUCC: Murdoch University, Perth, Western Australia; NBRC: Biological Resource Center, NITE, Chiva, Japan; URM: Culture Collection Mycobank, Prof. Maria Auxiliadora Cavalcanti, Federal University of Pernambuco, Recife, Brazil. $^{T,\ ET,\ IsoT,\ IsoET}$ and ^{NT} indicate ex-type, ex-epitype, ex-isotype, ex-isoepitype and ex-neotype strains, respectively.

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

Phyllosticta was formerly placed in the *Botryosphaeriaceae,* together with *Botryosphaeria* (Schoch *et al.* 2006). However, Wikee *et al.* (2013b) showed that it represents a different phylogenetic lineage, for which the family name *Phyllostictaceae* (Fries 1849) was resurrected.

References: van der Aa 1973 (morphology and pathogenicity); van der Aa & Vanev 2002 (synonyms, collection information and notes); Glienke *et al.* 2011, Wong *et al.* 2012, Wikee *et al.* 2013b, Zhou *et al.* 2015, Guarnaccia *et al.* 2017 (ecology, morphology and phylogeny); Wikee *et al.* 2011 (pathogenicity and phylogeny).


99/1
CBS 111646 Phyllosticta podocarpi
CPC 25665T Phyllosticta carissicola
70/-
CBS 111649 Phyllosticta pseudotsugae
CBS 776.97ET Phyllosticta owaniana
97/1
ATCC 46255ET Phyllosticta vaccinii
CBS 136062T Phyllosticta vacciniicola
99/1
CBS 587.69 Phyllosticta philoprina
CGMCC 3.14358T Phyllosticta ilicis-aquifolii
CBS 136061T Phyllosticta mangifera-indica
CBS 138899T Phyllosticta mimusopisicola
CBS 129060T Phyllosticta brazilianiae
CBS 535.87T Phyllosticta beaumarisii
79/0.99
NBRC 9466T Phyllosticta partricuspidatae
72/0.98
CBS 111645 Phyllosticta parthenocissi
ATCC 200578NT Phyllosticta ampelicida
CGMCC 3.17322T Phyllosticta vitis-rotundifoliae
93/0.97
100/1
BRIP 55434IsoET Phyllosticta musarum
CBS 132581ET Phyllosticta maculata
88/0.98
BRIP 55420IsoT Phyllosticta cavendishii
BRIP 53316aT Phyllosticta aristolochiicola
CBS 136244NT Phyllosticta cordylinophila
CPC 26517T Phyllosticta paracapitalensis
CBS 128856ET Phyllosticta capitalensis
99/1
90/0.95
MUCC 0014T Phyllosticta alliacea
MUCC 0113T Phyllosticta fallopiae
100/1
CGMCC 3.14354T Phyllosticta schimae
CGMCC 3.17319T Phyllosticta schimicola
CGMCC 3.17317T Phyllosticta carochlae
MUCC 0031T Phyllosticta ardisiicola
CGMCC 3.14985T Phyllosticta styracicola
CBS 445.82 Phyllosticta eugeniae
CBS 136058T Phyllosticta aloeicola
CBS 728.79T Phyllosticta podocarpicola
CBS 112527T Phyllosticta paxistimae
MUCC 124T Phyllosticta pachysandricola
73/-
CBS 136073T Phyllosticta leucothoicola
CBS 111639 Phyllosticta cornicola
CBS 447.70T Phyllosticta gaultheriae
CBS 134750T Phyllosticta neopyrolae
99/1
CBS 111635T Phyllosticta rubella
CBS 117136 Phyllosticta yuccae
MUCC 149 Phyllosticta hamamelidis
CBS 756.70 Phyllosticta sphaeropsoidea
90/-
CBS 585.84NT Phyllosticta minima
MUCC 0024T Phyllosticta ligustricola
CBS 112067T Phyllosticta abieticola
CBS 777.97T Phyllosticta telopeae
CBS 858.71 Phyllosticta cruenta
CGMCC 3.14986T Phyllosticta hubeiensis
CBS 143409T **Phyllosticta persooniae sp. nov.**
CBS 447.68NT Phyllosticta foliorum
CBS 131309T Phyllosticta hymenocallidicola
75/0.95
99/1
CBS 120486T Phyllosticta citriasiana
CBS 136059T Phyllosticta citrimaxima
100/1
CBS 141357T Phyllosticta paracitricarpa
100/1
CBS 127454ET Phyllosticta citricarpa
CBS 128855T Phyllosticta bifrenariae
URM 7672T Phyllosticta catimbauensis
-/0.96
MUCC 0432T Phyllosticta rhaphiolepidis
98/1
100/1
CBS 132534T Phyllosticta ericarum
75/0.98
CBS 100098T Phyllosticta citribraziliensis
-/0.95
CBS 937.70ET Phyllosticta concentrica
MUCC 0017T Phyllosticta kerriae
CBS 292.90 Phyllosticta spinarum
98/1
CBS 130529T Phyllosticta citrichinaensis
CBS 126.22T Phyllosticta elongata
76/-
CBS 136060ET Phyllosticta cussonia
CBS 143410T **Phyllosticta iridigena sp. nov.**
80/-
CBS 434.92NT Phyllosticta hypoglossi
76/-
95/1
MUCC 0010T Phyllosticta aspidistricola
CGMCC 3.14355T Phyllosticta hostae
Peyronellaea obtusa CMW8232
0.05

Phyllosticta iridigena Y. Marín & Crous, **sp. nov.** MycoBank MB823971. Fig. 48.

Etymology: Name reflects the host it was isolated from, *Iris*.

Conidiomata 90−200 μm diam, pycnidial, solitary, globose, dark brown, with central ostiole; *conidiomatal wall* of 3−8 layers of brown *textura angularis. Conidiophores* lining cavity, reduced to conidiogenous cells. *Conidiogenous cells* 4−7 × 4−6 μm, doliiform, hyaline, smooth, proliferating percurrently at apex. *Conidia* (10−)12−13(−15) × (7−)8(−9) μm, solitary, ellipsoid to obovoid, aseptate, smooth, hyaline, guttulate, granular; conidia encased in a mucoid sheath 2−3 μm diam, and a single apical mucoid appendage, 7−15 × 2 μm, tapering to acutely rounded apex.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth, feathery margins, reaching 45 mm diam after 2 wk at 25 °C. On MEA surface pale olivaceous grey; reverse iron-grey. On PDA surface and reverse olivaceous grey. On OA surface pale olivaceous grey with diffuse yellow pigment in agar.

Material examined: **South Africa**, on *Iris* sp. (*Iridaceae*), 16 Jan. 2010, P.W. Crous (**holotype** CBS H-23385, culture ex-type CBS 143410 = CPC 32669).

Notes: This species clusters in a well-supported clade (95 % BS / 1 PP) with *Phy. hypoglossi* and *Phy. cussoniae*. *Phyllosticta hypoglossi* produces longer conidiogenous cells (10−15 μm) and wider conidia [(9−)10(−11) μm] than *Phy. iridigena*. Moreover, these three species are isolated from different hosts, i.e. *Phy. hypoglossi* from *Ruscus* (*Ruscaceae*), *Phy. cussoniae* from *Cussonia* (*Araliaceae*) and *Phy. iridigena* from *Iris* (*Iridaceae*). *Phyllosticta cussonia* and *Phy. iridigena* have been found in the same country, South Africa, while *Phy. hypoglossi* is an European species.

Phyllosticta persooniae Y. Marín & Crous, **sp. nov.** MycoBank MB823972. Fig. 49.

Etymology: Name reflects the host genus *Persoonia* from which it was isolated.

Conidiomata 200−300 μm diam, pycnidial, solitary, globose, dark brown, with central ostiole; *conidiomatal wall* of 3−8 layers of brown *textura angularis. Conidiophores* 10−18 × 6−7 μm, lining cavity, 0−1-septate, subcylindrical, hyaline, smooth, rarely branched. *Conidiogenous cells* 9−17 × 4−5 μm, terminal, subcylindrical, hyaline, smooth, proliferating percurrently at apex. *Conidia* (9−)10−11(−12) × (7−)8(−9) μm, solitary, ellipsoid to obovoid, aseptate, smooth, hyaline, guttulate, granular; conidia encased in a mucoid sheath that is inconspicuous and dissolves at maturity, but with a single apical mucoid appendage, 7−15 × 2−3 μm, tapering to acutely rounded apex.

Culture characteristics: Colonies flat to erumpent, spreading, with sparse to moderate aerial mycelium and feathery, lobate margins, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface smoke grey; reverse olivaceous grey. On PDA surface and reverse olivaceous grey. On OA surface pale mouse grey.

Material examined: **Australia**, New South Wales, South East Forests National Park, Nunnock Swamp, on *Persoonia* sp. (*Proteaceae*), 28 Nov. 2016, P.W. Crous (**holotype** CBS H-23386, culture ex-type CBS 143409 = CPC 32603).

Notes: *Phyllosticta persooniae* is phylogenetically distant from all other species of *Phyllosticta,* the most closely related species being *Phy. foliorum*. Morphologically, these can be distinguished by the size of their conidia. *Phyllostica foliorum* is characterised by its larger conidia i.e. (12−)13−14(−15) × (9−)10(−11) ìm *vs.* (9−)10−11(−12) × (7−)8(−9) μm in *Phy. persooniae*. Moreover, *Phy. foliorum* has never been found on *Persoonia* (*Proteaceae*) or in Australia, which is the host and distribution of *Phy. persooniae* (Farr & Rossman 2017). Most species of *Phyllosticta* are host-specific.

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

Proxipyricularia Klaubauf, *et al.*, Stud. Mycol. 79: 109. 2014. Fig. 50.

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

Type species: *Proxipyricularia zingiberis* (Y. Nisik.) Klaubauf, *et al.*, basionym: *Pyricularia zingiberis* Y. Nishik. Lectotype designated here: plate 4, fig. 3−8 in Nishikado Y. 1917. Ber. Ohara Inst. Landwirt. Forsch. 1: 222. Epitype and ex-epitype strain designated here: CBS H-23356, CBS 133594.

DNA barcodes (genus): LSU, ITS.

DNA barcodes (species): ITS, *act*, *cal*, *rpb1*. Table 16. Fig. 28.

Conidiophores solitary or in fascicles, subcylindrical, erect, olivaceous to medium brown, smooth, septate. *Conidiogenous cells* terminal and intercalary, pale brown, with denticulate conidiogenous loci and rhexolytic secession. *Conidia* solitary, formed sympodially, pyriform to obclavate, narrowed toward apex, rounded at base, 2-septate, subhyaline to pale brown, with a distinct protruding basal hilum, frequently with minute marginal frill (adapted from Klaubauf *et al.* 2014).

Culture characteristics: Colonies reaching 43−50 mm in 1 wk at 25 °C, without or with moderate aerial mycelium. On CMA surface and reverse transparent. On OA surface salmon to ochreous; reverse pale luteous to luteous. On PDA surface olivaceous to grey olivaceous with margins transparent; reverse olivaceous to grey olivaceous with margins buff.

Optimal media and cultivation conditions: On CMA and OA at 25 °C in dark, or autoclaved barley seeds placed on SNA at 25 °C under near-ultraviolet light (12 h light, 12 h dark).

Distribution: Japan.

Hosts: *Zingiber mioga* and *Z. officinale* (*Zingiberaceae*).

Disease symptoms: Leaf spots.

Notes: In a phylogenetic study of the genus *Pyricularia* based on LSU, ITS, *act*, *cal* and *rpb1*, *Pyricularia zingiberis* clustered in an independent clade distant from the type species of *Pyricularia* (Klaubauf *et al.* 2014). Therefore, the genus *Proxipyricularia* was

Fig. 47. RAxML phylogram obtained from the combined ITS (492 bp), *act* (291 bp), *gapdh* (629 bp) and *tef1* (341 bp) sequence alignment of all the accepted species of *Phyllosticta*. The tree was rooted to *Peyronellaea obtusa* CMW8232. The novelties proposed in this study are indicated in **bold**. RAxML bootstrap support (BS) values above 70 % and Bayesian posterior probability scores above 0.95 are shown at the nodes. GenBank accession numbers are indicated in Table 15. $^{\text{T, ET, IsoT, IsoET}}$ and $^{\text{NT}}$ indicate ex-type, ex-epitype, ex-isotype, ex-isoepitype and ex-neotype strains, respectively. TreeBASE: S21899.

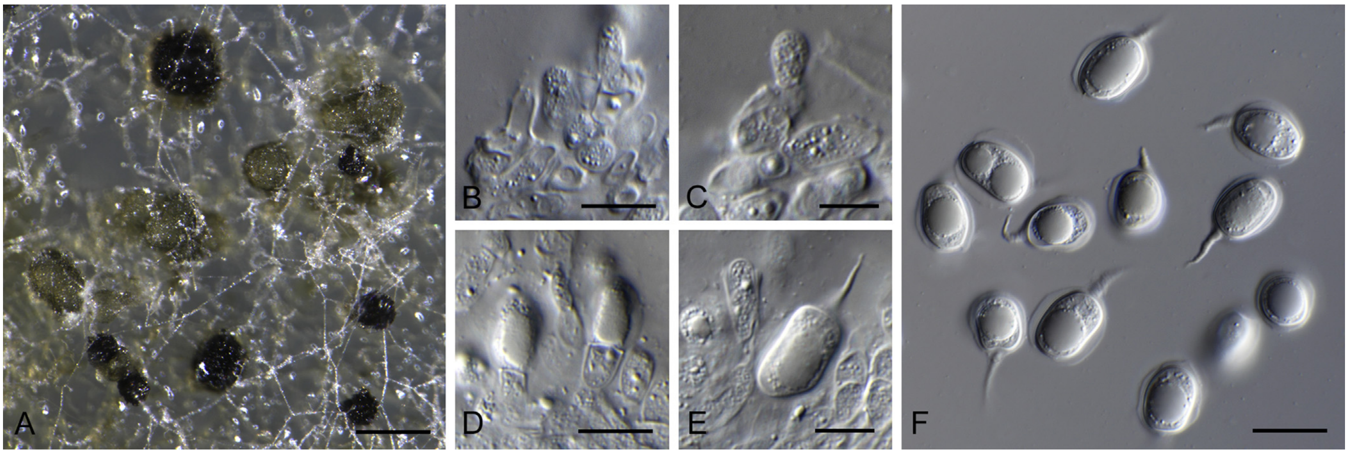


Fig. 48. *Phyllosticta iridigena* (ex-type CBS 143410). **A.** Conidiomata sporulating on SNA. **B–E.** Conidiogenous cells giving rise to conidia. **F.** Conidia. Scale bars: A = 200 µm, B–F = 10 µm.

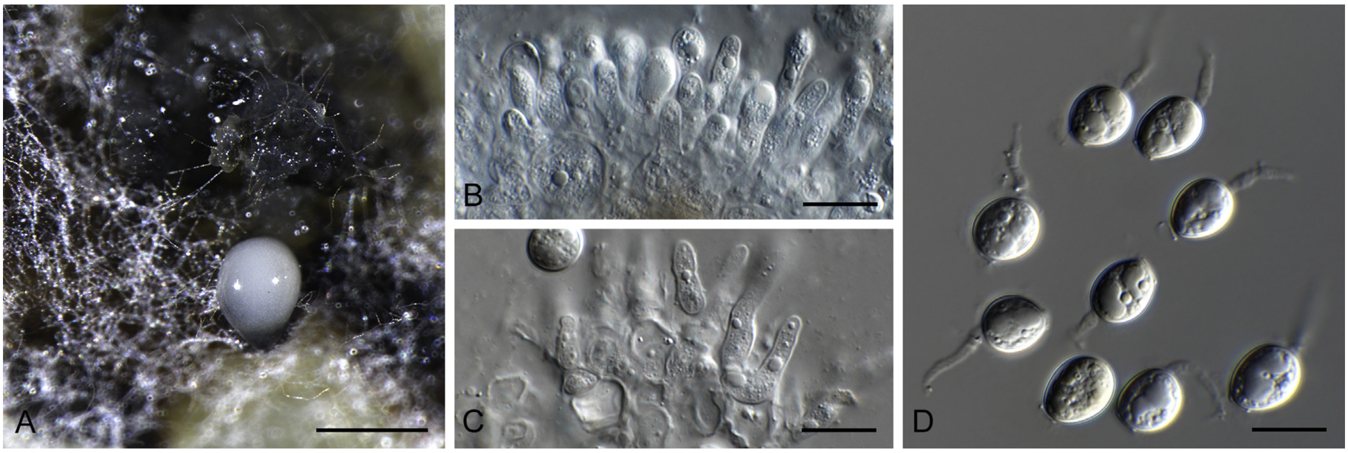


Fig. 49. *Phyllosticta persooniae* (ex-type CBS 143409). **A.** Conidiomata sporulating on OA. **B, C.** Conidiogenous cells giving rise to conidia. **D.** Conidia. Scale bars: A = 200 µm, B–D = 10 µm.

introduced to accommodate this species, which is pathogen of *Zingiber* in Japan. Morphologically, both genera are similar, being characterised by medium brown conidiophores and a terminal and intercalary denticulate rachis, and subhyaline, 2-septate, obclavate conidia (Klaubauf *et al.* 2014).

References: Nishikado 1917 (morphology and pathogenicity); Klaubauf *et al.* 2014 (morphology and phylogeny).

Proxipyricularia zingiberis (Y. Nisik.) Klaubauf, *et al.*, Stud. Mycol. 79: 109. 2014. Fig. 50.
Basionym: *Pyricularia zingiberis* Y. Nishik. (as "*Piricularia zingiberi*"), Ber. Ohara Inst. Landwirt. Forsch. 1: 216. 1917.

Description: Klaubauf *et al.* (2014).

Culture characteristics: Colonies on CMA reaching 43–50 mm after 1 wk at 25 °C, without aerial mycelium; surface and reverse transparent. On OA reaching 48–50 mm after 1 wk at 25 °C, with moderate aerial mycelium appearing slightly cottony, margins arachnoid; surface salmon to ochreous; reverse pale luteous to luteous. On PDA reaching 47–48 mm after 1 wk at 25 °C, with sparse aerial mycelium, margins fringed; surface olivaceous to grey olivaceous with margins transparent; reverse olivaceous to grey olivaceous with margins buff.

Materials examined: **Japan**, on leaves of *Zingiber officinale* (*Zingiberaceae*) (**lectotype of *Pyricularia zingiberis* designated here**, MBT379808, plate 4, fig. 3–8 in Nishikado Y. 1917. Ber. Ohara Inst. Landwirt. Forsch. 1: 222). **Japan**, Hyogo, on *Zingiber mioga* (*Zingiberaceae*), 2002, H. Kato [**epitype of *Pyricularia zingiberis* designated here** CBS H-23356, MBT379809, culture ex-epitype CBS 133594 = MAFF 240222 = HYZiM201-0-1(Z-2J)].

Notes: Type material was not designated when *Py. zingiberis* was introduced (Nishikado 1917). Therefore, we selected the drawings of Nishikado in the original description as lectotype (Ber. Ohara Inst. Landwirt. Forsch. 1: 222, plate 4, fig. 3–8). To fix the application of the generic name, an epitype for this species is designated here from the same country (Japan) and host (*Zingiber*) as that of the original specimen.

Pyriculariomyces Y. Marín, M.J. Wingf. & Crous, **gen. nov.** MycoBank MB823760. Fig. 51. Table 17.

Etymology: Named after the genus *Pyricularia*, which it resembles morphologically.

Ascomata separate, immersed, globose, brown, with central papillate neck and ostiole; *ascomatal wall* of 2–4 layers of brown cells of *textura angularis. Hamathecium* dissolving upon maturity, with some cells remaining among asci. *Asci* unitunicate, hyaline, smooth, 8-spored, subcylindrical, stipitate, apical mechanism refractive, but not staining in Meltzer's. *Ascospores* biseriate, fusoid-ellipsoid, widest in middle, tapering towards subobtusely rounded ends, slightly curved to straight, 3-septate, pale brown, guttulate. *Conidiophores* solitary, erect, straight to flexuous, unbranched, subcylindrical, brown, smooth, 1–8-septate.

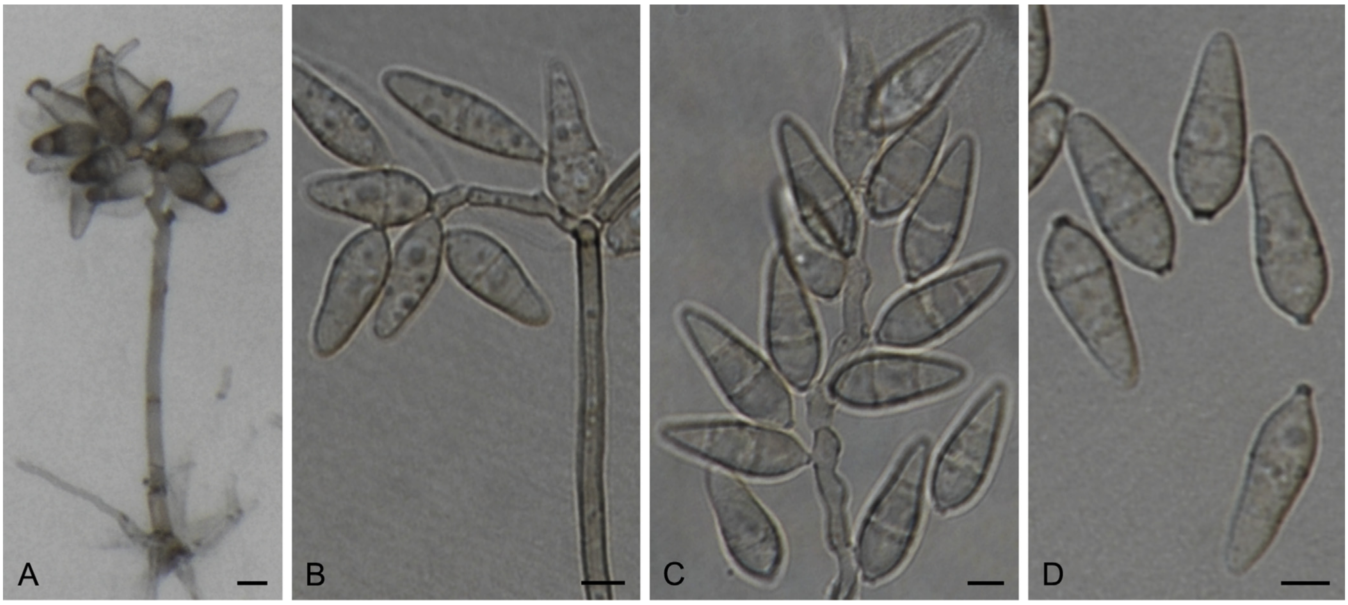


Fig. 50. *Proxipyricularia zingiberis* (ex-epitype CBS 133594). **A–C.** Conidiophores and conidia. **D.** Conidia. Scale bars = 5 μm.

Table 16. DNA barcodes of accepted *Proxipyricularia* sp.

Species	Isolates[1]	GenBank accession numbers[2]				References
		ITS	*act*	*cal*	*rpb1*	
Proxypiricularia zingiberis	CBS 133594^{ET}	AB274434	AB274446	KM485246	KM485091	Hirata *et al.* (2007), Klaubauf *et al.* (2014)

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

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

Conidiogenous cells integrated, terminal, apex somewhat swollen with numerous denticle-like loci, slightly thickened and darkened. *Conidia* solitary, pyriform, brown, finely verruculose, guttulate, granular, apex subobtusely rounded, with or without mucoid cap, base truncate, hilum darkened, thickened, 2-septate.

Culture characteristics: Colonies reaching 90 mm after 2 wk at 25 °C, with moderate aerial mycelium and smooth, even margins. On MEA surface pale mouse grey with patches of dirty white; reverse isabelline with patches of pale luteous. On OA surface honey with patches of pale mouse grey. On PDA surface honey; reverse isabelline to honey.

Type species: Pyriculariomyces asari (Crous & M.J. Wingf.) Y. Marín, M.J. Wingf. & Crous. Holotype and ex-type cultures: CBS H-22625, CBS 141328 = CPC 27444.

Notes: *Pyriculariomyces* is phylogenetically closely related to *Pyricularia*. However, *Pyriculariomyces* can easily be distinguished by production of integrated terminal conidiogenous cells, while *Pyricularia* produces terminal and intercalary conidiogenous cells. In *Pyriculariaceae*, the only genera characterised by only terminal conidiogenous cells are *Barretomyces* and *Utrechtiana*. However, these genera can easily be distinguished from *Pyriculariomyces* by the septation of the conidia i.e. 4(–5)-septate in *Barretomyces* and 1–2-septate in *Utrechtiana*. Moreover, *Utrechtiana* differs in the presence of conidiogenous cells that proliferate percurrently. Moreover, *Pyriculariomyces* can be distinguished from *Pyricularia* by the production of ascomata with papillate necks with ostioles, while *Pyricularia* is characterised by ascomata with long necks.

Pyriculariomyces asari (Crous & M.J. Wingf.) Y. Marín, M.J. Wingf. & Crous, **comb. nov.** MycoBank MB823761. Fig. 51.
Basionym: *Proxipyricularia asari* Crous & M.J. Wingf., Persoonia 36: 393. 2016.

Description: Crous *et al.* (2016b).

Materials examined: **Malaysia**, Sabah, on leaves and stems of *Asarum* sp. (*Aristolochiaceae*), May 2015, M.J. Wingfield (**holotype** CBS H-22625, culture ex-type CPC 27444 = CBS 141328); ibid., CPC 27442.

Notes: *Pyriculariomyces asari* was introduced as a species of *Proxypiricularia* to accommodate two specimens collected from *Asarum* (Crous *et al.* 2016b). However, the authors at the time suggested that this species could represent another genus in the *Pyricularia* complex. The phylogenetic analysis generated here based on four different loci (Fig. 28), support this hypothesis.

Authors: Y. Marin-Felix, M.J. Wingfield & P.W. Crous

Pyricularia Sacc. Michelia 2: 20. 1880. Fig. 52.

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

Type species: *Pyricularia grisea* Sacc. Lectotype designated by Rossman *et al.* (1990): BPI undistributed set. Epitype and ex-epitype strain designated by Crous *et al.* (2015a): CBS H-22280, CBS 138707.

DNA barcode (genus): LSU.

DNA barcodes (species): ITS, *act*, *cal*, *rpb1*. Table 18. Fig. 28.

Ascomata ostiolate, solitary to gregarious, subspherical, brown to black, base immersed in host tissue, with long neck protruding above plant tissue; *ascomatal wall* consisting of several layers of

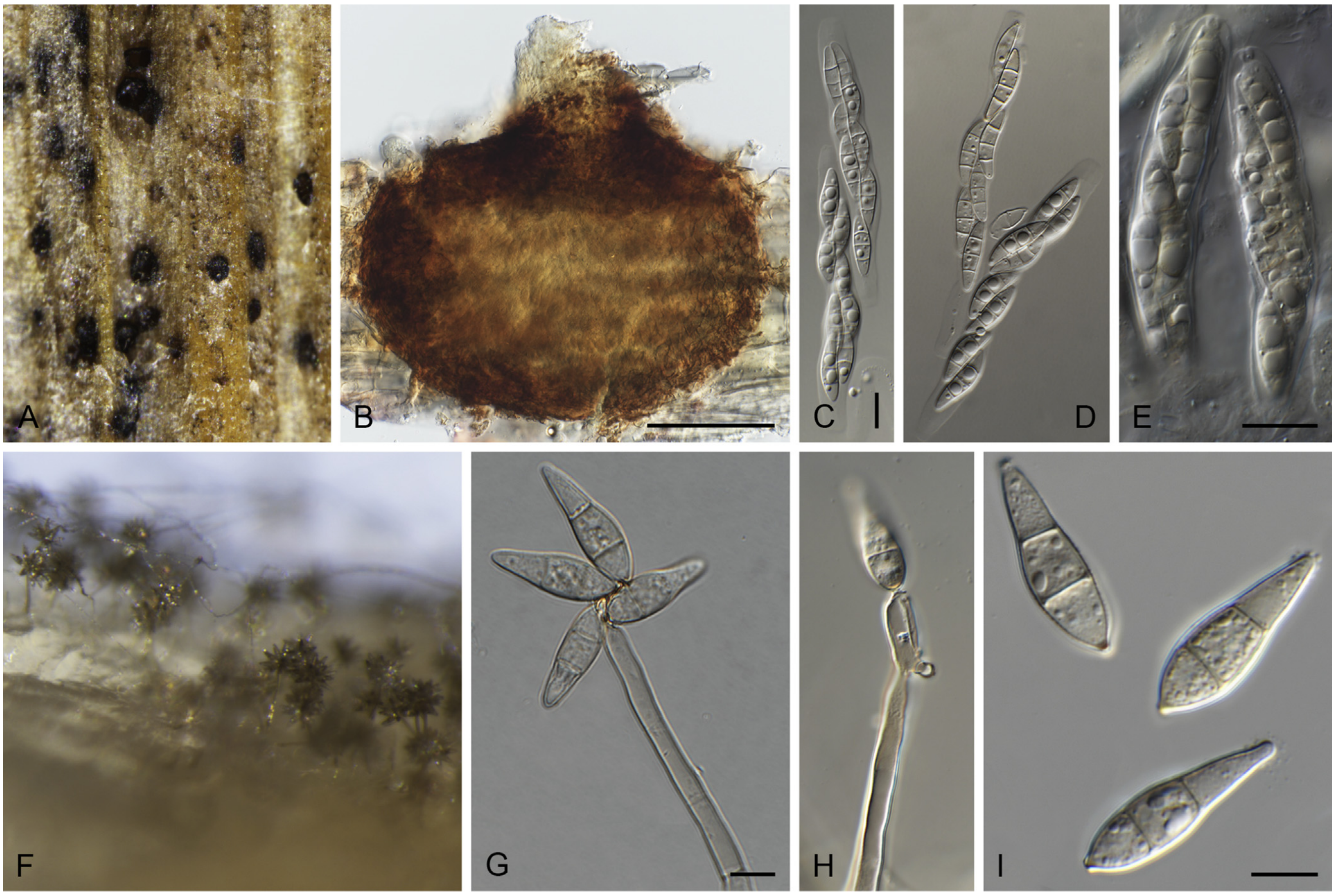


Fig. 51. *Pyriculariomyces asari* (ex-type CBS 141328). **A.** Ascomata on host tissue. **B.** Section of ascoma. **C–E.** Asci and ascospores. **F.** Conidiophores on SNA. **G, H.** Conidiophores and conidia. **I.** Conidia. Scale bars: B = 100 μm; others = 10 μm; C applies to C, D; G applies to G, I. Pictures A, B, D, E, G, H taken from Crous *et al.* (2016b).

Table 17. DNA barcodes of accepted *Pyriculariomyces* sp.

Species	Isolates[1]	GenBank accession numbers[2]				References
		ITS	*act*	*cal*	*rpb1*	
Pyriculariomyces asari	CBS 141328^{T}	KX228291	KX228361	MG934541	KX228368	Crous *et al.* (2016b), present study
	CPC 27442	KX228290	KX228360	–	MG934472	Crous *et al.* (2016b), present study

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

brown cells of *textura angularis*. *Paraphyses* intermingled among asci, unbranched, septate. *Asci* 8-spored, hyaline, subcylindrical to clavate, unitunicate, short-stipitate, with prominent apical ring. *Ascospores* bi- to multiseriate in asci, hyaline, guttulate, smooth-walled, fusiform, curved with rounded ends, transversely 3-septate, slightly constricted at septa. *Conidiophores* solitary or in fascicles, subcylindrical, erect, brown, smooth, rarely branched, with sympodial proliferation. *Conidiogenous cells* terminal and intercalary, pale brown, with denticulate conidiogenous loci and rhexolytic secession. *Conidia* solitary, pyriform to obclavate, narrowed toward tip, rounded at base, 2-septate, hyaline to pale brown, with a distinct basal hilum, sometimes with marginal frill (adapted from Klaubauf *et al.* 2014).

Culture characteristics: Colonies on MEA white to vinaceous, pale olivaceous grey, smoke grey, or grey, cottony. Colonies on OA iron grey, transparent with greenish olivaceous parts, fuscous black with grey centre or hazel with smokey grey tufts.

Optimal media and cultivation conditions: On OA at 25 °C in dark, or autoclaved barley seeds placed on SNA at 25 °C under near-ultraviolet light (12 h light, 12 h dark).

Distribution: Worldwide.

Hosts: Wide range of monocot plants, including important crops of the *Poaceae* such as rice, barley, millet, oat and wheat.

Disease symptoms: Leaf spot and blast diseases.

Notes: *Pyricularia* was recently re-evaluated in a phylogenetic study based on five loci (Klaubauf *et al.* 2014). In this study, the polyphyletic nature of the genus was resolved introducing eight new genera to accommodate the species of *Pyricularia* that were not grouped with the type species *Py. grisea* and *Py. oryzae* in *Pyricularia s. str.* Moreover, the family *Pyriculariaceae* was introduced to accommodate *Pyricularia*, which was previously considered a member of *Magnaporthaceae*. *Pyriculariaceae,* as well as *Magnaporthaceae*, accommodate mainly plant

Fig. 52. *Pyricularia* spp. **A–C.** Leaf spots of rice caused by *Pyricularia oryzae*. **D–H.** Sexual morph of *Pyricularia oryzae*. **D, E.** Crossing of different strains of *Pyricularia oryzae* to produce the sexual morph. **F.** Ascoma. **G.** Asci. **H.** Germinating ascospore. **I–U.** Asexual morph. **I, J.** Sporulation on sterile barley seed on SNA. **I.** *Pyricularia grisea* (BR0029). **J.** *Pyricularia graminis-tritici* (ex-type URM7380). **K–P.** Conidiophores and conidia. **K, L.** *Pyricularia ctenantheicola* (GR0002). **M, N.** *Pyricularia graminis-tritici* (ex-type URM7380). **O.** *Pyricularia oryzae* (URM7369). **P.** *Pyricularia oryzae* (BF0028). **Q–S.** Conidia. **Q.** *Pyricularia ctenantheicola* (GR0002). **R.** *Pyricularia oryzae* (URM7369). **S.** *Pyricularia graminis-tritici* (ex-type URM7380). **T.** Macroconidia of *Pyricularia grisea* (BR0029) (arrows indicate apical marginal frill, which is a remnant of the apical mucoid cap). **U.** Microconidia of *Pyricularia grisea* (BR0029). Scale bars: F = 50 µm; others = 10 µm. Pictures D, E, G taken by Dounia Saleh, CIRAD; F, H by Didier Tharreau, CIRAD; I, K, L, P, Q, T from Klaubauf *et al.* (2014); J, M–O, R, S from Castroagudín *et al.* (2016).

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

Species	Isolates[1]	GenBank accession numbers[2]				References
		ITS	*act*	*cal*	*rpb1*	
Pyricularia angulata	NBRC 9625	AY265322	–	–	–	Bussaban *et al.* (2005)
Py. ctenantheicola	CBS 138601^T	KM484879	KM485183	KM485253	KM485099	Klaubauf *et al.* (2014)
Py. graminis-tritici	URM7380^T	–	KU952138	KU952892	–	Castroagudín *et al.* (2016)
Py. grisea	CBS 128304	KM484881	KM485184	KM485255	KM485101	Klaubauf *et al.* (2014)
Py. oryzae	CBS 255.38	KM484889	KM485190	KM485261	KM485109	Klaubauf *et al.* (2014)
Py. penniseticola	CBS 138603^T	KM484929	KM485220	–	KM485148	Klaubauf *et al.* (2014)
Py. pennisetigena	CBS 138604^T	KM484935	KM485225	KM485294	KM485153	Klaubauf *et al.* (2014)
Py. urashimae	CBS 142117^T	KY173437	KY173571	–	KY173578	Crous *et al.* (2016a)
Py. zingibericola	CBS 138605^T	KM484941	KM485229	KM485297	KM485157	Klaubauf *et al.* (2014)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; NBRC: Biological Resource Center, NITE, Chiva, Japan; URM: Culture Collection Mycobank, Prof. Maria Auxiliadora Cavalcanti, Federal University of Pernambuco, Recife, Brazil. ^{T} indicates ex-type strains.

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

pathogenic species, some of which are of major importance in agriculture.

Pyricularia oryzae is the causal agent of rice blast disease, which can result in up to a 30 % yield loss worldwide (Skamnioti & Gurr 2009). In a phylogenetic study based on 10 loci and 128 isolates of this species, three major clades were identified (Castroagudín *et al.* 2016). The first clade grouped the isolates associated only with rice and corresponds to the previously described rice blast pathogen *Py. oryzae* pathotype *Oryza*. The second clade accommodated isolates associated almost exclusively with wheat and corresponds to the previously described wheat blast pathogen *Py. oryzae* pathotype *Triticum*. A third clade accommodated isolates obtained from wheat as well as other *Poaceae*. This clade was distinct from *Py. oryzae* and represented a new species, *Pyricularia graminis-tritici*. This new species could not be morphologically distinguished from *Py. oryzae*, but a distinctive pathogenicity spectrum was observed (Castroagudín *et al.* 2016). However, the "*oryzae"* clade consists of various populations specific to different grass hosts that appear to be in the process of speciation. Consequently, the species in the "*oryzae"* clade are not commonly accepted, and some authors refer to them as lineages of *Py. oryzae* (Castroagudín *et al.* 2017). Further research is needed to resolve speciation within what is presently circumscribed as *Py. oryzae*.

The sexual morph has been reported only in *Py. grisea* and *Py. oryzae*, both being heterothallic species. These are indistinguishable in conidium, perithecium and ascospore morphology. However, *Py. oryzae* was described as a new species distinct from *Py. grisea* based on DNA sequence differences in three different loci (*act, cal* and *tub*) and host range, since *Py. grisea* infects only crab grass (Couch & Kohn 2002).

References: Klaubauf *et al.* 2014 (morphology and phylogeny); Castroagudín *et al.* 2016, 2017 (morphology, pathogenicity and phylogeny); Reges *et al.* 2016 (pathogenicity and phylogeny).

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

Stenocarpella Syd. & P. Syd., Ann. Mycol. 15: 258. 1917. Fig. 53.

Synonyms: *Hendersoniopsis* Woron., Fungal and Bacterial Diseases of Agricultural Plants: 255. 1922.

Phaeostagonosporopsis Woron., La Defense des Plantes, Leningrad 2: 333. 1925.

Classification: *Sordariomycetes*, *Diaporthomycetidae*, *Diaporthales*, *Diaporthaceae*.

Type species: *Stenocarpella macrospora* (Earle) B. Sutton, basionym: *Diplodia macrospora* Earle. Isotype: IMI 12790. Ex-epitype strain designated by Crous *et al.* (2006b): CBS 117560 = MRC 8615.

DNA barcodes (genus): LSU, ITS.

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

Mycelium immersed, brown, branched, septate. *Conidiomata* pycnidial, solitary or sometimes confluent, globose or elongated, dark brown, subepidermal, unilocular; *conidiomatal wall* composed of dark brown, thick-walled cells of *textura angularis*; *neck* single, circular, papillate, protruding. *Conidiophores* usually reduced to conidiogenous cells. *Conidiogenous cells* enteroblastic, phialidic, determinate, discrete, rarely integrated on 1-septate conidiophores, cylindrical, collarette with minute channel, periclinal wall thickened, formed from inner cells of pycnidial wall. *Conidia* pale brown, 0−3-septate, continuous or constricted, cylindrical to fusiform, straight or curved, apex obtuse, base tapered and truncate, thick and smooth-walled, eguttulate. *Beta conidia* absent or present, hyaline, scolecosporous, curved. *Sexual morph* unknown (adapted from Sutton 1980).

Culture characteristics: Colonies flat, with abundant aerial mycelium giving a cottony appearance; under continuous near-ultraviolet light abundant sporulation in 1 wk. On OA surface white to rosy buff to vinaceous buff, centre isabelline; reverse vinaceous buff, centre isabelline.

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

Distribution: Africa, America, Asia and Europe.

Host: *Zea mays* (*Poaceae*).

Notes: The genus *Stenocarpella* was introduced by Sydow & Sydow (1917), with *S. zeae* designated as type species. Sutton (1977) synonymised *S. zeae* with *Diplodia macrospora*, transferring this latter species to *Stenocarpella,* recognising *S. macrospora* as the correct name for the type species. Two species are included in this genus i.e. *S. macrospora* and

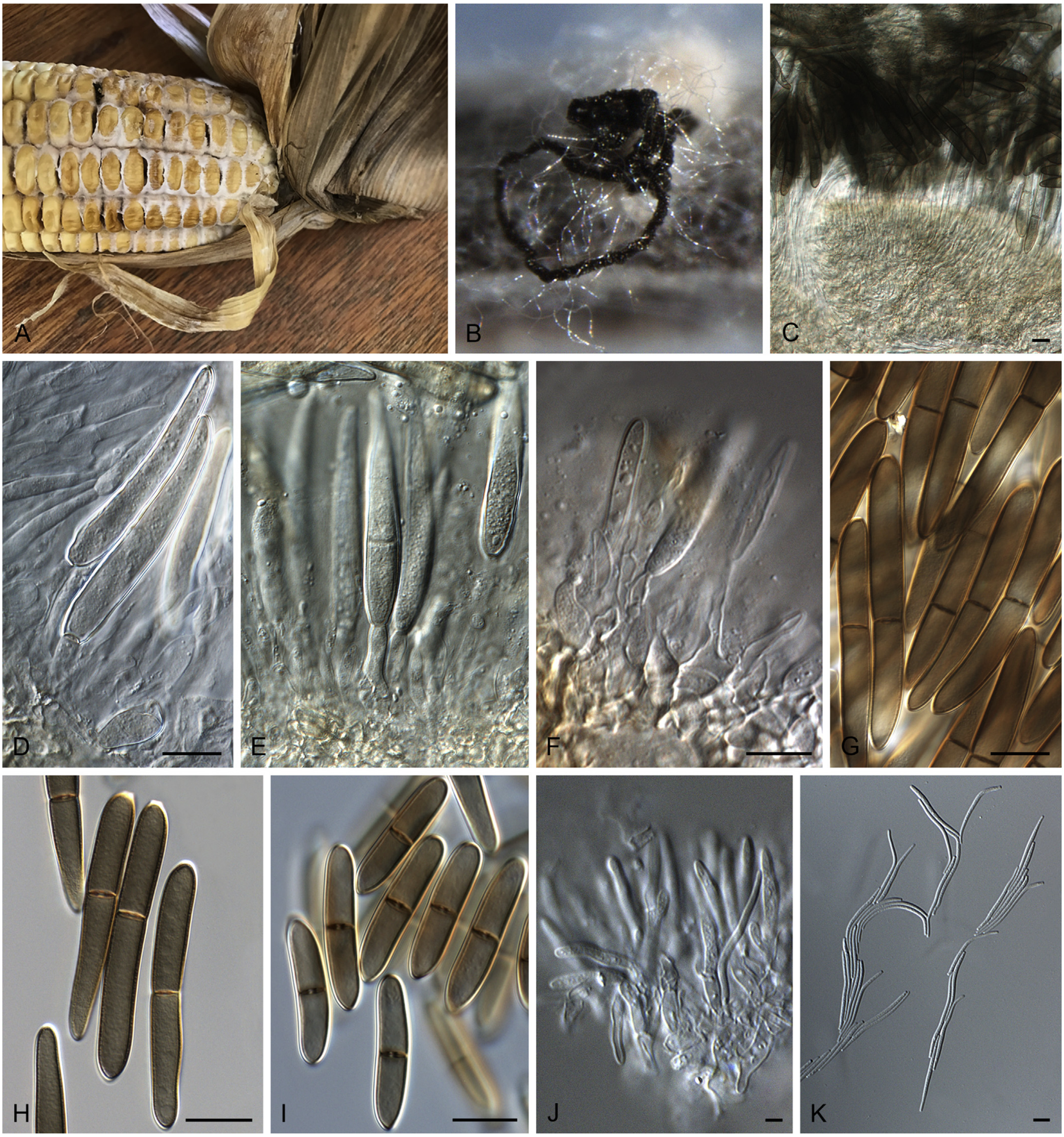


Fig. 53. *Stenocarpella* spp. **A.** *Zea mays* infected with *Stenocarpella maydis*. **B–K.** Asexual morphs. **B.** Conidiomata with exuding conidial mass on pine needle agar of *Stenocarpella maydis* (ex-epitype CBS 117559). **C.** Hyaline layer of conidiogenous cells giving rise to brown conidial mass of *Stenocarpella macrospora* (CPC 11863). **D–F.** Conidiogenous cells giving rise to conidia. **D, E.** *Stenocarpella macrospora* (CPC 11863). **F.** *Stenocarpella maydis* (ex-epitype CBS 117559). **G–I.** Conidia. **G, H.** *Stenocarpella macrospora* (CPC 11863). **I.** *Stenocarpella maydis* (ex-epitype CBS 117559). **J.** Conidiogenous cells giving rise to beta conidia of *Stenocarpella macrospora* (CPC 11863). **K.** Beta conidia of *Stenocarpella macrospora* (CPC 11863). Scale bars = 10 µm. All pictures except for A taken from Lamprecht *et al.* (2011).

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

Species	Isolates[1]	GenBank accession number[2]		References
		ITS	*tef1*	
Stenocarpella macrospora	CBS 117560^{ET}	FR748048	MG934504	Lamprecht *et al.* (2011), present study
S. maydis	CBS 117558^{ET}	FR748051	FR748080	Lamprecht *et al.* (2011)

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

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

S. maydis, which cause Diplodia ear rot of maize (Crous *et al.* 2006b).

Stenocarpella was initially placed in the *Botryosphaeriaceae* (*Botryosphaeriales*) because of the similarity with *Diplodia*. In a phylogenetic study based on LSU sequences, Crous *et al.* (2006b) showed that *Stenocarpella* belongs to the *Diaporthaceae* (*Diaporthales*). Subsequently, Lamprecht *et al.* (2011) confirmed this placement based on ITS and *tef1* sequences.

References: Sutton 1977, 1980 (morphology and pathogenicity); Crous *et al.* 2006b (morphology and phylogeny); Lamprecht *et al.* 2011 (morphology, pathogenicity and phylogeny).

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

Utrechtiana Crous & Quaedvl., Persoonia 26: 153. 2011. Fig. 54.

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

Type species: *Utrechtiana roumeguerei* (Cavara) Videira & Crous, basionym: *Scolicotrichum roumeguerei* Cavara = *Utrechtiana cibiessia* Crous & Quaedvlieg. Holotype and ex-type strain of *Utrechtiana cibiessia*: CBS H-20594, CBS 128780.

DNA barcodes (genus): LSU, ITS.

DNA barcodes (species): ITS, *act, cal*, *rpb1*. Table 20. Fig. 28.

Mycelium internal, consisting of septate, smooth, hyaline, branched hyphae. *Conidiophores* predominantly solitary, erect, straight to flexuous, unbranched, 1-septate, medium brown to dark brown, subcylindrical with swollen basal cell. *Conidiogenous cells* integrated, terminal, cylindrical or subcylindrical, smooth or finely verruculose, thick-walled with thin-walled, clavate, bluntly rounded apex, with truncate, flattened scar, holoblastic; conidiophores rejuvenating percurrently. *Conidia* solitary, obpyriform or ellipsoid, pale brown, guttulate to granular, finely verruculose, 1–2-septate, thin-walled, apex bluntly to acutely rounded, base obtusely rounded with a flattened, darkened and thickened hilum that has a central pore. *Synasexual morph* selenosporella-like present or absent. *Microconidiophores* arranged in rosettes, branched, septate, pale brown, smooth, subcylindrical. *Microconidiogenous cells* pale brown, smooth to finely roughened, phialidic, terminal and lateral, fusoid-ellipsoid to ampulliform. *Microconidia* hyaline, smooth, aseptate, subcylindrical, straight to curved, ends obtuse.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and even smooth margins. On MEA surface dirty white, sometimes turning grey olivaceous when fertile; reverse luteous or olivaceous grey in centre and luteous in outer region. On OA olivaceous grey to iron-grey or dirty white.

Optimal media and cultivation conditions: On OA at 25 °C under dark, or autoclaved barley seeds placed on SNA at 25 °C under near-ultraviolet light (12 h light, 12 h dark).

Distribution: America, Asia, Australia and Europe.

Hosts: *Phragmites* spp (*Poaceae*).

Disease symptoms: Leaf spot.

Notes: The genus *Utrechtiana* was described by Crous *et al.* (2011a) to accommodate the type species named *Utrecthiana cibiessia*, which is a foliar pathogen of *Phragmites*. However, this genus was considered synonymous with *Deightoniella* by Seifert *et al.* (2011) because of the morphology of the conidiophores (solitary, brown, with percurrent rejuvenation) and conidia (brown and septate). Moreover, *U. cibiessia* was demonstrated to be a synonym of *Deightoniella roumeguerei*, which Klaubauf *et al.* (2014) showed to belong to *Pyriculariaceae*, a family containing numerous cryptic fungal genera on *Poaceae*.

However, *Deightoniella* has been shown to represent a polyphyletic genus. For example, *Deightoniella torulosa*, which is a foliar pathogen of *Musa*, proved to be a species of *Corynespora* (Crous *et al.* 2013), while a similar fungus occurring on leaf spots of *Phragmites* in South Africa was placed in *Neodeightoniella* (Crous *et al.* 2013). In a recent study, Videira *et al.* (2017) considered *Utrechtiana* and *Deightoniella* based on the type species *Deightoniella africana* to be different genera based on morphological characteristics. *Utrechtiana* lacks torsive to flexuous conidiophores with prominent conidiophore swellings, and its conidia are also pale brown, smooth to finely roughened, with prominent thickened, darkened scars. In contrast, conidia in *Deightoniella* are medium brown, verruculose, and obpyriform with prominent apical taper. In order to clarify the phylogenetic relationships between both genera, fresh material of *Deightoniella africana* is needed.

References: Constantinescu 1983 (morphology and pathogenicity); Crous *et al.* 2011a, Klaubauf *et al.* 2014, Videira *et al.* 2017 (morphology and phylogeny); Mel'nik & Shabunin 2011 (morphology).

Utrechtiana arundinacea (Corda) Crous, Quaedvl. & Y. Marín, **comb. nov.** MycoBank MB824141. Fig. 54.
Basionym: *Helminthosporium arundinaceum* Corda, as "*Helmisporium*", Icon. fung. (Prague) 3: 10, tab. 2, fig. 25. 1839.
Synonyms: *Napicladium arundinaceum* (Corda) Sacc., Syll. fung. 4: 482. 1886.
Deightoniella arundinacea (Corda) S. Hughes, Mycol. Pap. 48: 29. 1952.

Causing blight-like amphigenous lesions along leaves of *Phragmites*, medium brown with red-purple margins and yellow halo, extending across breadth of leaf, up to 7 mm diam, and along length, up to 20 cm long. *Macroconidiophores* 30–50 × 9–12 µm, amphigenous, predominantly solitary, but at times in fascicles of up to three, straight to flexuous, unbranched, 1-septate, medium brown, smooth, subcylindrical with swollen basal cell, 10–15 µm diam. *Macroconidiogenous cells* 20–35 × 7–9 µm, integrated, terminal, cylindrical, thick-walled with thin-walled apex, holoblastic; conidiophores proliferate percurrently. *Macroconidia* (22–)37–42(–45) × (17–)19–20(–21) µm, solitary, obpyriform, pale brown, guttulate, finely verruculose, (1–)2-septate, with distinct dark brown hilum, 3–4 µm. A selenosporella-like *synasexual morph* develops in culture, with microconidiophores arranged in rosettes, 15–40 × 3–6 µm, branched, 3–6-septate, pale brown, smooth, subcylindrical. *Microconidiogenous cells* 5–14 × 3–4 µm, pale brown, smooth to finely roughened, phialidic, terminal and lateral, fusoid-ellipsoid to ampulliform. *Microconidia* 7–10 × 1.5–2 µm, hyaline, smooth, aseptate, subcylindrical, straight to curved, ends obtuse. *Macroconidiophores* in culture up to 6-septate, 100 µm tall. *Macroconidia* 23–50 × 11–15 µm, slender, pyriform, prominently verrucose, medium brown.

Fig. 54. **A–I.** *Utrechtiana arundinacea* (ex-epitype CPC 33994). **A.** Leaf spot on *Phragmites* sp. **B–E.** Macroconidiophores bearing macroconidia. **F–H.** Microconidiophores bearing microconidia. **I.** Microconidia. **J–S.** *Utrechtiana roumeguerei* (ex-type CBS 128780). **J.** Leaf spot on *Phragmites australis*. **K.** Close-up of conidiophores on leaf surface. **L–P.** Conidiophores bearing conidia. **Q.** Germinating conidium. **R, S.** Conidia. Scale bars = 10 µm. Pictures J–S taken from Klaubauf *et al.* (2014).

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

Species	Isolates[1]	GenBank accession numbers[2]				References
		ITS	*act*	*cal*	*rpb1*	
Utrechtiana arundinacea	CPC 33994^{ET}	MG934461	MG934468	MG934542	MG934473	Present study
U. roumeguerei	CBS 128780^{T}	JF951153	KM485163	KM485232	KM485047	Crous *et al.* (2011a), Klaubauf *et al.* (2014)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CPC: Personal collection of Pedro Crous housed at the Westerdijk Fungal Biodiversity Institute.
^{T} and ^{ET} indicate ex-type and ex-epitype strains, respectively.
[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *act*: partial actin gene; *cal*: partial calmodulin gene; *rpb1*: partial RNA polymerase II largest subunit gene.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and even smooth margins. On MEA surface dirty white; reverse olivaceous grey in centre, luteous in outer region. On OA olivaceous grey to iron-grey.

Materials examined: **Czech Republic**, Prague, on living leaves of *Phragmites* sp. (*Poaceae*), 1838 (**holotype** in PRM missing, but slide ex-holotype**,** DAOM 19793). **The Netherlands**, on leaves of *Phragmites* sp. (*Poaceae*), 2 Jun. 2017, A. Mulder (**epitype of *Helminthosporium arundinaceum* designated here** CBS H-23402, MBT380884, culture ex-epitype CPC 33994).

Notes: *Utrechtiana arundinacea* is a commonly encountered European taxon treated in *Deightoniella* in previous studies (Constantinescu 1983, Mel'nik & Shabunin 2011, Ghosta & Abrinbana 2016). Morphologically, *U. arundinacea* and *U. constantinescui* appear to be related.

Macroconidia of *U. arundinaceum* exhibit a strange phenomenon where a third septum develops 3–5 µm from the apex. The conidium body is prominently guttulate, except for this terminal chamber, which is smooth, pale brown, and lacks any guttules. This strange conidial apex is also visible in conidia of *U. constantinescui* (Mel'nik & Shabunin 2011), and apparently plays some role in infection/attachment, probably exuding a mucoid droplet, as is also seen in some genera in the *Pyriculariaceae* (Klaubauf *et al.* 2014). Furthermore, Mel'nik & Shabunin (2011) illustrate a selenosporella-like synasexual morph in both species, which has not been seen in *U. roumeguerei*, the type species of the genus.

Utrechtiana roumeguerei was considered conspecific with *U. arundinacea* (Ellis 1957) until Constantinescu (1983) demonstrated that they are distinct species based on morphology and pathogenicity. *Utrechtiana arundinacea* often produces percurrently proliferating conidiogenous cells and obclavate 2-septate conidia, while *U. roumeguerei* is characterised by rarely percurrent conidiogenous cells and ovate to broadly ellipsoidal, 1-septate conidia. Moreover, *U. arundinacea* produces systemic infection in the host issues, whereas *U. roumeguerei* induces a local infection with limited development. In the present study, the DNA data support the placement of both taxa in the same genus (Fig. 28).

The holotype specimen of *Helminthosporium arundinaceum* could not be located in PRM, and is presumed missing. However, a slide from the original material was preserved in DAOM. Due to the lack of living culture of that species, a specimen isolated from the same host and region is here designated as epitype.

Utrechtiana constantinescui (Melnik & Shabunin) Crous & Y. Marín**,** **comb. nov.** MycoBank MB824142.
Basionym: *Deightoniella constantinescui* Melnik & Shabunin, Mikol. Fitopatol. 45: 257. 2011.

Notes: The new combination *U. constantinescui* is designated here based on the morphology of its macro- and microconidial morphs. Fresh material should be recollected to verify this placement. As we mentioned above, this species is morphologically related to *U. arundinacea*. Both species can be distinguished based on the shape of their macroconidia (obpyriform in *U. arundinacea vs.* barrel-shaped in *U. constantinescui*) and the position of the conidial septa in *U. constantinescui*, 7–13 µm apart.

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

Wojnowiciella Crous, *et al.*, Persoonia 34: 201. 2015. Fig. 55.

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

Type species: *Wojnowiciella eucalypti* Crous, *et al.* Holotype and ex-type strain: CBS H-22233, CBS 139904.

DNA barcode (genus): LSU.

DNA barcodes (species): ITS, *rpb2, tef1*. Table 21. Fig. 56.

Conidiomata pycnidial, globose, brown, separate, non-papillate or papillate, with central ostiole; *conidiomatal wall* composed of 3–6 layers of brown cells, *textura angularis. Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining cavity, hyaline to pale brown, smooth, ampulliform to subcylindrical, appearing phialidic. *Macroconidia* subcylindrical, straight to slightly curved, apex subobtuse, base truncate, septate, at times with 1–2 oblique septa, thick-walled, verruculose, guttulate, golden brown. *Microconidia* in same or different conidiomata as macroconidia*. Microconidiophores* intermingled with macroconidiogenous cells, branched at base, septate, subcylindrical, hyaline, smooth. *Microconidiogenous cells* terminal and intercalary, hyaline, smooth, ampulliform to subcylindrical, phialidic with periclinal thickening. *Microconidia* solitary, hyaline, guttulate, smooth, subcylindrical to ellipsoid, apex obtuse to subobtuse, base truncate.

Culture characteristics: Colonies on MEA, cottony, isabelline, greenish olivaceous, mouse grey to greyish sepia, sometimes with luteous exudate; reverse greyish sepia, chestnut, fulvous. Colonies on PDA pale mouse grey, brown vinaceous or greenish olivaceous, sometimes with luteous diffusible pigment; reverse luteous and black, greyish sepia or brown vinaceous.

Optimal media and cultivation conditions: On autoclaved banana leaves placed on SNA at 25 °C under near-ultraviolet light (12 h light, 12 h dark).

Distribution: Australia, China, Colombia, Italy and South Africa.

Hosts: *Cissampelos capensis* (*Menispermaceae*), *Dactylis glomerata* (*Poaceae*), *Eucalyptus grandis* (*Myrtaceae*), *Leptocarpus* sp. (*Restionaceae*), *Lonicera* sp. and *Viburnum utile* (*Caprifoliaceae*), and *Spartium* sp. (*Fabaceae*).

Fig. 55. *Wojnowiciella* spp. **A–F.** Conidiomata overview. **A.** *Wojnowiciella leptocarpi* (ex-type CBS 116584). **B, E.** *Wojnowiciella dactylidis* (CPC 30353). **C.** *Wojnowiciella cissampeli* (ex-type CBS 141297). **D.** *Wojnowiciella eucalypti* (ex-type CBS 139904). **F.** *Wojnowiciella dactylidis* (CPC 32741). **G, H.** Hand section of the conidiomata with hyaline conidiogenous cells and dark brown conidia of *Wojnowiciella leptocarpi* (ex-type CBS 116584). **I–L.** Conidiogenous cells. **I, J.** *Wojnowiciella cissampeli* (ex-type CBS 141297). **K.** *Wojnowiciella eucalypti* (ex-type CBS 139904). **L.** *Wojnowiciella leptocarpi* (CBS 116585). **M–Q.** Macroconidia. **M, N.** *Wojnowiciella leptocarpi* (ex-type CBS 116584). **O.** *Wojnowiciella cissampeli* (ex-type CBS 141297). **P.** *Wojnowiciella dactylidis* (CPC 32741). **Q.** *Wojnowiciella dactylidis* (CPC 30353). **R.** Microconidia of *Wojnowiciella eucalypti* (ex-type CBS 139904). Scale bars: E–G = 50 µm; H = 20 µm; others = 10 µm. Pictures taken from Crous *et al.* (2015d, 2016b).

Disease symptoms: Leaf spots.

Notes: *Wojnowiciella* was established with *W. eucalypti* as type species, which differs from *Septoriella hirta* (syn. *Wojnowicia hirta*) by non-setous conidiomata, dark brown conidia and hyaline microconidia (Crous *et al.* 2015d). Although both genera belong to *Phaeosphaeriaceae*, *Wojnowicia* has been synonymised with *Septoriella* (Crous *et al.* 2015a). Currently *Wojnowiciella* comprises seven species isolated from leaf spots and twigs of different hosts (Table 21). Although they were associated with disease symptoms, their pathogenicity needs to be proven.

References: Wijayawardene *et al.* 2013 (morphology, as *Wojnowicia*); Crous *et al.* 2015d, 2016b (morphology); Li *et al.* 2015 (morphology and phylogeny, as *Wojnowicia*); Liu *et al.* 2015 (morphology and phylogeny, as *Wojnowicia*); Hernández-Restrepo *et al.* 2016c (morphology and phylogeny).

Authors: M. Hernández-Restrepo & P.W. Crous

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

Species	**Isolates**[1]	**GenBank accession numbers**[2]				**References**
		ITS	**LSU**	***rpb2***	***tef1***	
Wojnowiciella cissampeli	CBS 141297^{T}	KX228272	KX228323	–	LT990616	Crous *et al.* (2016b), present study
W. dactylidis	MFLUCC 13-0735^{T}	KP744470	KP684149	–	–	Liu *et al.* (2015)
	CPC 27468	LT990658	LT990630	LT990644	LT990611	Present study
	CPC 30353	LT990659	LT990631	–	LT990612	Present study
	CPC 32741	LT990660	LT990632	–	LT990613	Present study
	CPC 33929	LT990661	LT990633	LT990645	LT990614	Present study
W. eucalypti	CBS 139904^{T}	KR476741	KR476774	–	LT990617	Crous *et al.* (2015d), present study
W. leptocarpi	CBS 115684^{T}	KX306775	KX306800	LT990646	LT990615	Hernández-Restrepo *et al.* (2016c), present study
W. lonicerae	MFLUCC 13-0737^{T}	KP744471	KP684151	–	–	Liu *et al.* (2015)
W. spartii	MFLUCC 13-0402^{T}	KU058719	KU058729	–	–	Li *et al.* (2015)
W. viburni	MFLUCC 12-0733^{T}	KC594286	KC594287	–	–	Wijayawardene *et al.* (2013)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CPC: Personal collection of Pedro Crous housed at the Westerdijk Fungal Biodiversity Institute; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Rai, Thailand. ^{T} indicates ex-type strain.

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

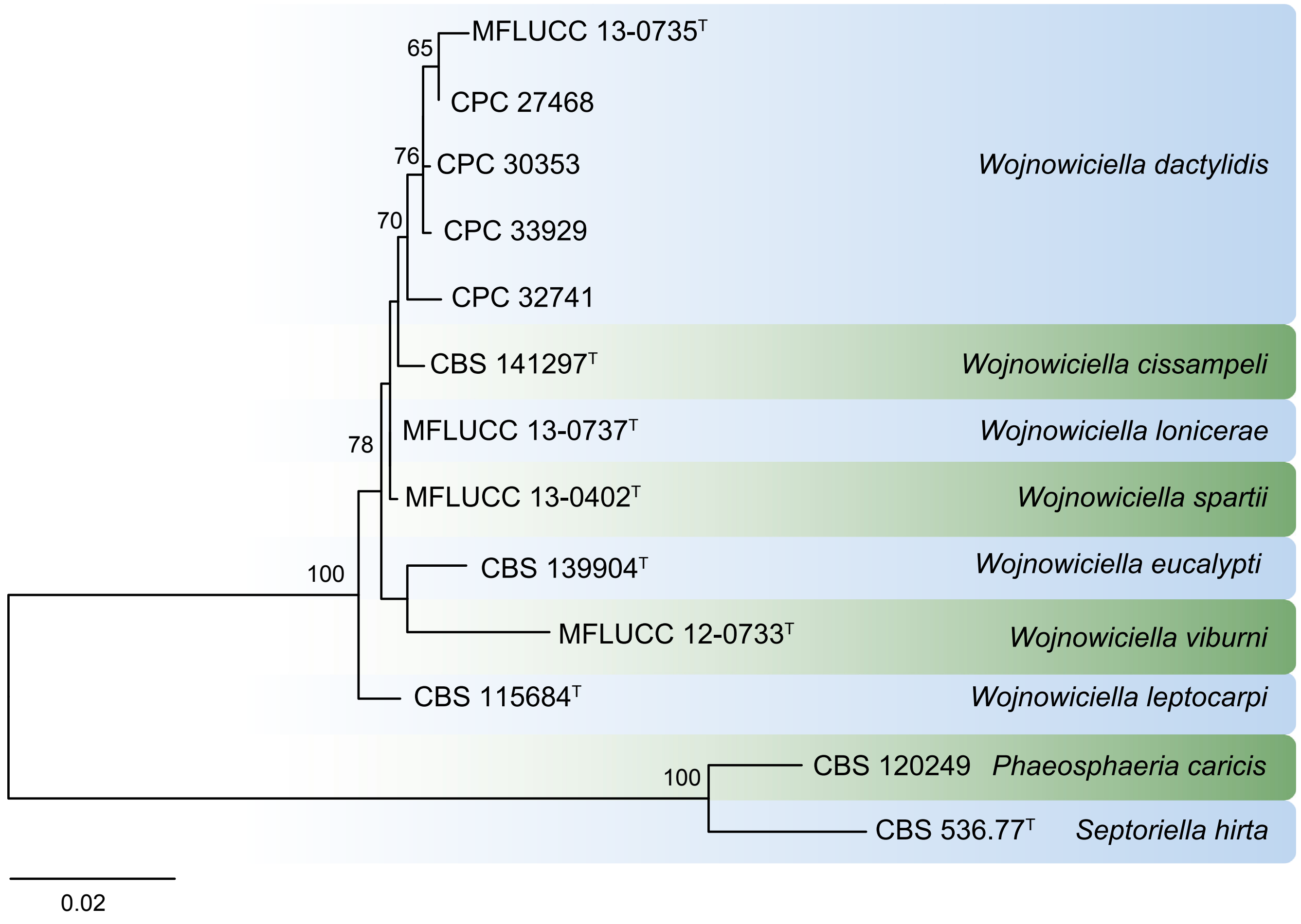


Fig. 56. RAxML phylogram obtained from the combined ITS (742 bp), LSU (885 bp), *rpb2* (1029 bp) and *tef1* (998 bp) sequence alignment of all the accepted species of *Wojnowiciella*. The tree was rooted to *Phaeosphaeria caricis* CBS 120249 and *Septoriella hirta* CBS 536.77. RAxML bootstrap support (BS) values above 70 % are shown in the nodes. GenBank accession numbers are indicated in Table 21. ^{T} indicates ex-type strains. TreeBASE: S21899.

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