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Genera of phytopathogenic fungi: GOPHY 3

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Abstract: This paper represents the third contribution in the Genera of Phytopathogenic Fungi (GOPHY) series. The series provides morphological descriptions, information about the pathology, distribution, hosts and disease symptoms for the treated genera, as well as primary and secondary DNA barcodes for the currently accepted species included in these. This third paper in the GOPHY series treats 21 genera of phytopathogenic fungi and their relatives including: *Allophoma*, *Alternaria*, *Brunneosphaerella*, *Elsinoe*, *Exserohilum*, *Neosetophoma*, *Neostagonospora*, *Nothophoma*, *Parastagonospora*, *Phaeosphaeriopsis*, *Pleiocarpon*, *Pyrenophora*, *Ramichloridium*, *Seifertia*, *Seiridium*, *Septoriella*, *Setophoma*, *Stagonosporopsis*, *Stemphylium*, *Tubakia* and *Zasmidium*. This study includes three new genera, 42 new species, 23 new combinations, four new names, and three typifications of older names.

Key words: DNA barcodes, Fungal systematics, New taxa.

Taxonomic novelties: New genera: *Arezzomyces* Y. Marín & Crous, *Globoramichloridium* Y. Marín & Crous, *Wingfieldomyces* Y. Marín & Crous; **New species:** *Allophoma pterospermicola* Q. Chen & L. Cai, *Alternaria aconidiophora* Iturrieta-González, Dania García & Gené, *Alternaria altcampina* Iturrieta-González, Dania García & Gené, *Alternaria chlamydosporifera* Iturrieta-González, Dania García & Gené, *Alternaria curvata* Iturrieta-González, Dania García & Gené, *Alternaria fimeti* Iturrieta-González, Dania García & Gené, *Alternaria inflata* Iturrieta-González, Dania García & Gené, *Alternaria lawrencei* Iturrieta-González, Dania García & Gené, *Alternaria montsantina* Iturrieta-González, Dania García & Gené, *Alternaria pobletensis* Iturrieta-González, Dania García & Gené, *Alternaria pseudoventricosa* Iturrieta-González, Dania García & Gené, *Brunneosphaerella roupeliae* Crous, *Elsinoe picconiae* Crous, *Elsinoe veronicae* Crous, Thangavel & Y. Marín, *Neosetophoma aseptata* Crous, R.K. Schumach. & Y. Marín, *Neosetophoma phragmitis* Crous, R.K. Schumach. & Y. Marín, *Neosetophoma sambuci* Crous, R.K. Schumach. & Y. Marín, *Neostagonospora sorghi* Crous & Y. Marín, *Parastagonospora novozelandica* Crous, Thangavel & Y. Marín, *Parastagonospora phragmitis* Crous & Y. Marín, *Phaeosphaeriopsis aloes* Crous & Y. Marín, *Phaeosphaeriopsis aloicola* Crous & Y. Marín, *Phaeosphaeriopsis grevilleae* Crous & Y. Marín, *Phaeosphaeriopsis pseudoagavacearum* Crous & Y. Marín, *Pleiocarpon livistonae* Crous & Quaedvl., *Pyrenophora avenicola* Y. Marín & Crous, *Pyrenophora cynosuri* Y. Marín & Crous, *Pyrenophora novozelandica* Y. Marín & Crous, *Pyrenophora pseudoerythrospila* Y. Marín & Crous, *Pyrenophora sieglingiae* Y. Marín & Crous, *Pyrenophora variabilis* Hern.-Restr. & Y. Marín, *Septoriella germanica* Crous, R.K. Schumach. & Y. Marín, *Septoriella hibernica* Crous, Quaedvl. & Y. Marín, *Septoriella hollandica* Crous, Quaedvl. & Y. Marín, *Septoriella pseudophragmitis* Crous, Quaedvl. & Y. Marín, *Setophoma brachypodii* Crous, R.K. Schumach. & Y. Marín, *Setophoma pseudosacchari* Crous & Y. Marín, *Stemphylium rombundicum* Moslemi, Y.P. Tan & P.W.J. Taylor, *Stemphylium truncatulae* Moslemi, Y.P. Tan & P.W.J. Taylor, *Stemphylium waikerieanum* Moslemi, Jacq. Edwards & P.W.J Taylor, *Vagicola arundinis* Phukhams., Camporesi & K.D. Hyde, *Zasmidium thailandicum* Crous; **New combinations:** *Arezzomyces cytisi* (Wanas. *et al.*) Y. Marín & Crous, *Globoramichloridium indicum* (Subram.) Y. Marín & Crous, *Phaeosphaeria phoenicicola* (Crous & Thangavel) Y. Marín & Crous, *Pyrenophora poae* (Baudyš) Y. Marín & Crous, *Pyrenophora wirreganensis* (Wallwork *et al.*) Y. Marín & Crous, *Seiridium cupressi* (Nattrass *et al.*) Bonthond, Sandoval-Denis & Crous, *Seiridium pezizoides* (de Not.) Crous, *Septoriella agrostina* (Mapook *et al.*) Y. Marín & Crous, *Septoriella artemisiae* (Wanas. *et al.*) Y. Marín & Crous, *Septoriella arundinicola* (Wanas. *et al.*) Y. Marín & Crous, *Septoriella arundinis* (W.J. Li *et al.*) Y. Marín & Crous, *Septoriella bromi* (Wijayaw. *et al.*) Y. Marín & Crous, *Septoriella dactylidis* (Wanas. *et al.*) Y. Marín & Crous, *Septoriella elongata* (Wehm.) Y. Marín & Crous, *Septoriella forlicesenica* (Thambug. *et al.*) Y. Marín & Crous, *Septoriella garethjonesii* (Thambug. *et al.*) Y. Marín & Crous, *Septoriella italica* (Thambug. *et al.*) Y. Marín & Crous, *Septoriella muriformis* (Ariyaw. *et al.*) Y. Marín & Crous, *Septoriella rosae* (Mapook *et al.*) Y. Marín & Crous, *Septoriella subcylindrospora* (W.J. Li *et al.*) Y. Marín & Crous, *Septoriella vagans* (Niessl) Y. Marín & Crous, *Wingfieldomyces cyperi* (Crous & M.J. Wingf.) Y. Marín & Crous, *Zasmidium ducassei* (R.G. Shivas *et al.*) Y. Marín & Crous; **New names:** *Pyrenophora nisikadoi* Y. Marín & Crous, *Septoriella dactylidicola* Y. Marín & Crous, *Septoriella neoarundinis* Y. Marín & Crous, *Septoriella neodactylidis* Y. Marín & Crous; **Typification: epitypification:** *Ascochyta chrysanthemi* F. Stevens, *Pestalotia unicornis* Cooke & Ellis, *Rhynchosphaeria cupressi* Nattrass *et al.*

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INTRODUCTION

Genera of Phytopathogenic Fungi (GOPHY) is a series of papers with the main focus to provide a stable platform for the taxonomy of phytopathogenic fungi. All genera included here are associated with plant disease, but note that many species treated are not well-known plant pathogens, or Koch's postulates remain to be completed for them. This 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). Specific aims were detailed by Marin-Felix *et al.* (2017), when this series was launched. One of the most important aims is to resolve generic and species concepts of the fungi studied, since many taxa have been shown to represent species complexes, or to comprise poly- or paraphyletic genera (Crous *et al.* 2015b). Other issues to resolve include the fact that type material for many genera and species has not been designated or is missing, and that the vast majority of these taxa were described before the DNA era (Hibbett *et al.* 2011) and thus lack DNA barcodes (Schoch *et al.* 2012). Therefore, another important aim is to generate DNA barcodes of type species and type specimens in order to fix the application of these names. Moreover, in cases where no type material has been preserved, taxa need to be recollected, epi- or neotypes designated, and registered in MycoBank to ensure traceability of the nomenclatural act (Robert *et al.* 2013). Finally, it is necessary to designate a single scientific name for fungi (Crous *et al.* 2015b) for which sexual-asexual links have been resolved.

Two issues of GOPHY have already been published, in which 41 genera were treated, including a total of two new genera, 46 new species, 15 new combinations and 10 typifications of older names (Marin-Felix *et al.* 2017, 2019). In this third contribution, a further 21 genera are treated, resulting in the clarification of their taxonomy and classification, and the introduction of three new genera, 42 new species, 23 new combinations, four new names and the typification of three older names.

For submissions to future issues in the GOPHY series, mycologists are encouraged to contact Pedro Crous (p.crous@wi.knaw.nl) to ensure there is no overlap with activities arising from other research groups. Preference will be given to genera that include novel species, combinations or typifications. Generic contributions published in each issue 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 American Type Culture Collection, Manassas, Virginia, USA (ATCC), the Queensland Plant Pathology Herbarium, Brisbane, Australia (BRIP), the Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands (CBS), the working collection of P.W. Crous (CPC), housed at the Westerdijk Fungal Biodiversity Institute (WI), the Chinese General Microbiological Culture Collection Center, Beijing, China (CGMCC), the Facultat de Medicina i Ciències de la Salut, University Rovira i Virgili, Reus, Spain (FMR), and the Victorian Plant Pathogen Herbarium, Bundoora, Australia (VPRI). For fresh collections, we followed the procedures previously described in Waksman (1922), Crous *et al.* (1991) and Calduch *et al.* (2004). Colonies were transferred to different media, *i.e.* cornmeal agar (CMA), 2 % malt extract agar (MEA), potato carrot agar (PCA), 2 % potato dextrose agar (PDA), synthetic nutrient-poor agar (SNA), oatmeal agar (OA), water agar (WA) (Crous *et al.* 2019b), pine needle agar (PNA; Smith *et al.* 1996), and incubated under different conditions to induce sporulation. Requirements of media and conditions of incubation are specified for each genus. Reference strains and specimens are maintained at ATCC, BRIP, CBS, CPC, CGMCC, FMR and VPRI.

Vegetative and reproductive structures were mounted in 100 % lactic acid or Shear's solution either directly from specimens or from colonies sporulating on CMA, MEA, OA, PCA, PDA, PNA, SNA or WA. For cultural characterisation, isolates were grown and incubated on different culture media and temperatures as indicated for each genus. Colour notations were rated according to the colour charts of Kornerup & Wanscher (1978) for *Alternaria*, and Rayner (1970) for all other genera. Taxonomic novelties were deposited in MycoBank (www.MycoBank.org; Crous *et al.* 2004).

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 bibliographies provided for each genus. Phylogenetic analyses consisted of Maximum-Likelihood (ML) and Bayesian Inference (BI). ML was inferred as described in Hernández-Restrepo *et al.* (2016b), or by using MEGA v. 6.0 (Tamura *et al.* 2013). BI was carried out as described by Hernández-Restrepo *et al.* (2016b), or by using MrBayes on XSEDE v. 3.2.6 on the CIPRES portal (www.phylo.org). Sequence data generated in this study were deposited in GenBank and the alignments and trees in TreeBASE (http://www.treebase.org).

RESULTS

Allophoma Q. Chen & L. Cai, Stud. Mycol. 82: 162. 2015. Fig. 1.

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

Type species: *Allophoma tropica* (R. Schneid. & Boerema) Q. Chen & L. Cai, basionym: *Phoma tropica* R. Schneid. & Boerema, Phytopathol. Z. 83: 361. 1975. Isotype and ex-isotype strain: CBS H-7629, CBS 436.75 = DSM 63365.

DNA barcodes (genus): LSU, ITS.

DNA barcodes (species): *rpb2*, *tub2*. Table 1. Fig. 2.

Conidiomata pycnidial, globose to flask-shaped, ovoid, superficial or (semi-)immersed, solitary or confluent, ostiolate, sometimes with an elongated neck; *conidiomatal wall* pseudoparenchymatous, multi-layered. *Conidiogenous cells* phialidic, hyaline, smooth-walled, ampulliform to doliiform, sometimes flask-shaped or isodiametric. *Conidia* hyaline, smooth- and thin-walled, aseptate or 1-septate, variable in shape

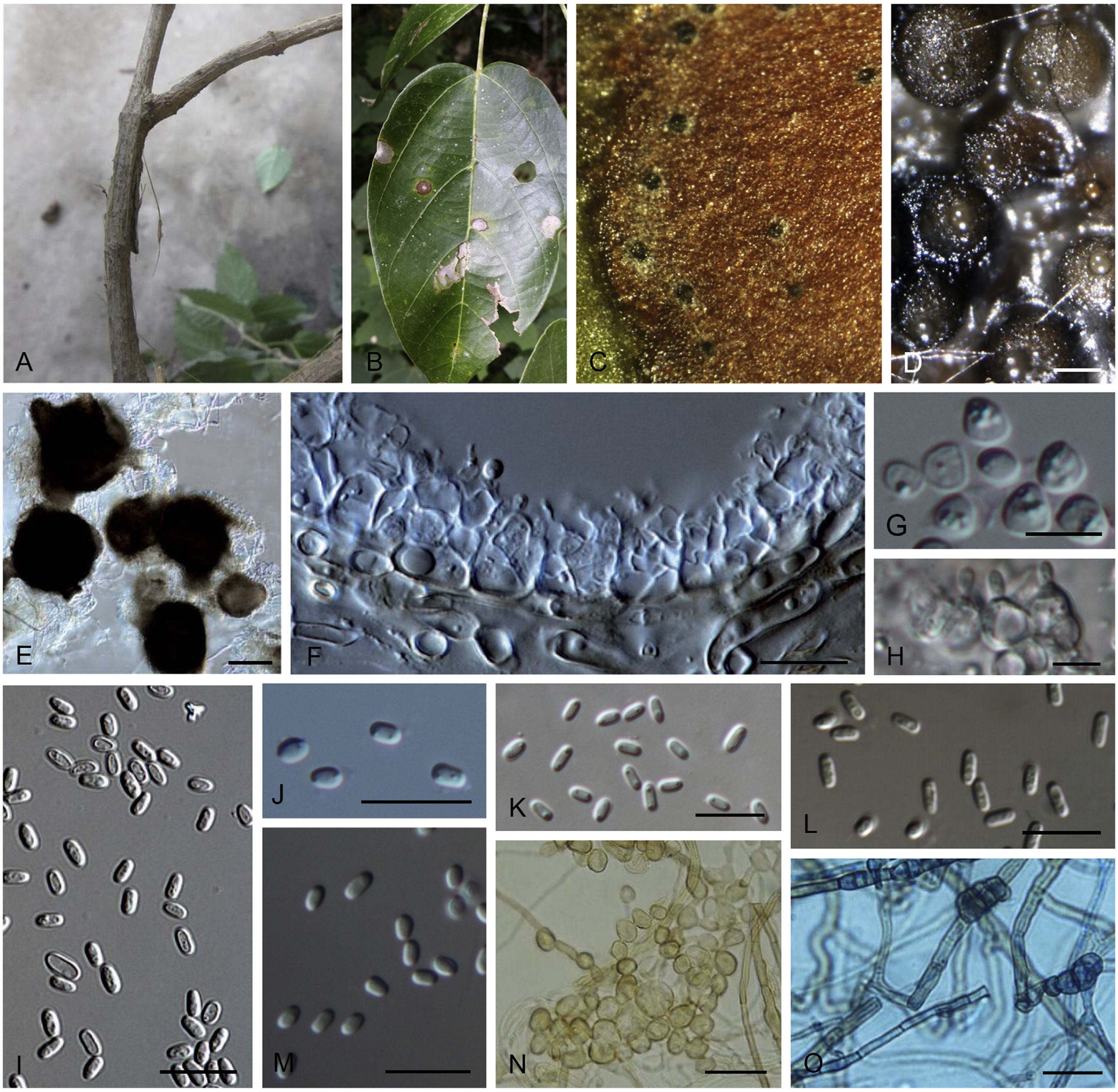

Fig. 1. *Allophoma* spp. **A, B.** Disease symptoms. **A.** Symptoms caused by *Allophoma hayatii* (ex-type CBS 142859) on *Lantana camara*. **B.** Symptoms caused by *Allophoma pterospermicola* (ex-type CGMCC 3.19245) on *Pterospermum xylocarpum*. **C–O.** Asexual morph. **C.** Conidiomata of *Allophoma pterospermicola* (LC12181) sporulating on *Maesa montana*. **D.** Conidiomata of *Allophoma oligotrophica* (ex-type CGMCC 3.18114) sporulating on OA. **E.** Conidiomata of *Allophoma minor* (ex-type CBS 325.82). **F.** Section of the conidiomatal wall of *Allophoma minor* (ex-type CBS 325.82). **G, H.** Conidiogenous cells. **G.** *Allophoma piperis* (ex-epitype CBS 268.93). **H.** *Allophoma oligotrophica* (ex-type CGMCC 3.18114). **I–M.** Conidia. **I.** *Allophoma minor* (ex-type CBS 325.82). **J.** *Allophoma piperis* (ex-epitype CBS 268.93). **K.** *Allophoma oligotrophica* (ex-type CGMCC 3.18114). **L.** *Allophoma cylindrispora* (ex-type CBS 142453). **M.** *Allophoma nicaraguensis* (ex-type CBS 506.91). **N.** Swollen cells of *Allophoma hayatii* (ex-type CBS 142859). **O.** Chlamydospores of *Allophoma hayatii* (ex-type CBS 142859). Scale bars: D, E = 100 µm; O = 50 µm; N = 20 µm; F, I–M = 10 µm; G, H = 5 µm. Pictures A, N–O taken from Babaahmadi *et al.* (2018); D, H, K, from Chen *et al.* (2017); E, F, I from Aveskamp *et al.* (2010); G, J, M from Chen *et al.* (2015); L from Valenzuela-Lopez *et al.* (2018).

and size, *i.e.* ovoid, oblong, ellipsoidal to cylindrical, or slightly allantoid, mostly guttulate. *Chlamydospores* uni- or multicellular (pseudosclerotioid and dictyosporous), solitary or in chains, intercalary or terminal, smooth-walled, brown, where multicellular variable in shape and size. *Swollen cells* (pseudo-chlamydospores) pale brown, terminal or intercalary, solitary or in clusters, variable in size and shape, commonly in aerial mycelia. *Sexual morph* unknown (adapted from Chen *et al.* 2015, Babaahmadi *et al.* 2018).

Culture characteristics: Colonies on OA white when young, grey to olivaceous or dull green, brown, floccose to woolly, sometimes with rosy-buff tinges near the colony margins or yellow pigment in the sterile sectors, margins regular.

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

Distribution: Worldwide.

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

Species	Isolates[1]	GenBank accession numbers[2]				References
		ITS	LSU	*rpb2*	*tub2*	
Allophoma cylindrispora	CBS 142453^{T}	LT592920	LN907376	LT593058	LT592989	Valenzuela-Lopez *et al.* (2018)
Al. hayatii	CBS 142859^{T}	KY684812	KY684814	MF095108	KY684816	Babaahmadi *et al.* (2018)
	CBS 142860	KY684813	KY684815	MF095109	KY684817	Babaahmadi *et al.* (2018)
Al. labilis	CBS 124.93	GU237765	GU238091	KT389552	GU237619	Aveskamp *et al.* (2010), Chen *et al.* (2015)
Al. minor	CBS 325.82^{T}	GU237831	GU238107	KT389553	GU237632	Aveskamp *et al.* (2010), Chen *et al.* (2015)
Al. nicaraguensis	CBS 506.91^{T}	GU237876	GU238058	KT389551	GU237596	Aveskamp *et al.* (2010), Chen *et al.* (2015)
Al. oligotrophica	CGMCC 3.18114^{T}	KY742040	KY742194	KY742128	KY742282	Chen *et al.* (2017)
	CGMCC 3.18115	KY742041	KY742195	KY742129	KY742283	Chen *et al.* (2017)
Al. piperis	CBS 268.93^{ET}	GU237816	GU238129	KT389554	GU237644	Aveskamp *et al.* (2010), Chen *et al.* (2015)
	CBS 108.93	GU237921	GU238130	KT389555	GU237645	Aveskamp *et al.* (2010), Chen *et al.* (2015)
Al. pterospermicola	CGMCC 3.19245^{T}	MK088573	MK088580	MK088587	MK088594	Present study
	LC12181	MK088569	MK088576	MK088583	MK088590	Present study
	LC12182	MK088570	MK088577	MK088584	MK088591	Present study
	LC12183	MK088571	MK088578	MK088585	MK088592	Present study
	LC12184	MK088572	MK088579	MK088586	MK088593	Present study
Al. tropica	CBS 436.75^{IsoT}	GU237864	GU238149	KT389556	GU237663	Aveskamp *et al.* (2010), Chen *et al.* (2015)
Al. zantedeschiae	CBS 131.93	FJ427084	GU238159	KT389557	FJ427188	Aveskamp *et al.* (2010), Chen *et al.* (2015)
	CBS 229.32	KT389473	KT389690	KT389558	KT389767	Aveskamp *et al.* (2010), Chen *et al.* (2015)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CGMCC: Chinese General Microbiological Culture Collection Center, Beijing, China; LC: Dr Lei Cai's personal culture collection, housed at CAS, China. $^{T,\ ET}$ and ^{IsoT} indicate ex-type,ex-epitype and ex-isotype strains, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; LSU: partial large subunit (28S) nrRNA gene; *rpb2*: partial DNA-directed RNA polymerase II second largest subunit gene; *tub2*: partial β-tubulin gene.

Hosts: Wide host range, occurring as pathogens or saprobes, on *Araceae*, *Fabaceae*, *Gesneriaceae*, *Myrtaceae*, *Papaveraceae*, *Piperaceae*, *Primulaceae*, *Rosaceae*, *Rubiaceae*, *Solanaceae*, *Sterculiaceae*, *Verbenaceae* and other hosts, including humans.

Disease symptoms: Dieback, tissue necrosis, leaf spots, stem rot, leaf blotch, but also saprobic or isolated from other substrates and environments, *e.g.* air from karst caves and human infections.

Notes: The genus *Allophoma* was introduced by Chen *et al.* (2015) to accommodate five previously described *Phoma* species, namely *Al. labilis* (syn. *Pho. labilis*), *Al. minor* (syn. *Pho. minor*), *Al. piperis* (syn. *Pho. piperis*), *Al. tropica* (syn. *Pho. tropica*) and *Al. zantedeschiae* (syn. *Pho. zantedeschiae*), and a new species *Al. nicaraguensis*. Another four species have been described in the subsequent years, *i.e. Al. cylindrispora* (Valenzuela-Lopez *et al.* 2018), *Al. hayatii* (Babaahmadi *et al.* 2018), *Al. oligotrophica* (Chen *et al.* 2017) and *Al. pterospermicola sp. nov.* in the present study. Differentiating *Allophoma* from related phoma-like genera based on morphology alone is sometimes complicated. Furthermore, *Allophoma* species are morphologically similar and hard to differentiate from one another. Therefore, molecular data are essential for accurate identification of species within this genus, with ITS, LSU, *tub2* and *rpb2* being the loci selected for this purpose (Chen *et al.* 2015, 2017, Valenzuela-Lopez *et al.* 2018). No sexual morph of this genus has been observed to date.

These fungi are generally found in soil, air and regarded as saprobes or as the causal organisms of various diseases of different herbaceous and woody plants, such as some ornamental plants, coffee, *etc.*, and even human eye lesions (Boerema *et al.* 2004, Aveskamp *et al.* 2010, Chen *et al.* 2015, 2017, Babaahmadi *et al.* 2018, Valenzuela-Lopez *et al.* 2018).

References: Boerema *et al.* 2004 (morphology and pathogenicity), Aveskamp *et al.* 2010, Chen *et al.* 2015, 2017, Babaahmadi *et al.* 2018, Valenzuela-Lopez *et al.* 2018 (morphology, phylogeny and pathogenicity).

Allophoma pterospermicola Q. Chen & L. Cai, ***sp. nov.*** MycoBank MB828313. Fig. 3.

Etymology: Name reflects *Pterospermum*, the host genus from which it was collected.

Conidiomata pycnidial, solitary or aggregated, globose to subglobose, brown, glabrous or with a few hyphal outgrowths, superficial, 60–330 × 67–280 μm, with 1–5 ostioles, sometimes elongated as a long neck, up to 150 μm long, papillate; *conidiomatal wall* pseudoparenchymatous, 3–5-layered, 12–20 μm thick, composed of isodiametric cells. *Conidiogenous cells* phialidic, hyaline, smooth-walled, ampulliform to doliiform, 6–10 × 3–6 μm. *Conidia* oval to oblong, occasionally bacilliform, smooth- and thin-walled, hyaline, aseptate, 3–5.5 × 1.5–2 μm, with 1–2 minute guttules. *Conidial matrix* cream.

Culture characteristics: Colonies on OA, 33–40 mm diam after 1 wk, margins regular, floccose to woolly, white, pale brownish grey, with a pale salmon concentric ring, pale salmon near the margins, black pycnidia visible; reverse concolourous. Colonies on MEA, 20–25 mm diam after 1 wk, margins regular, aerial mycelium sparse, olivaceous; reverse concolourous. Colonies on PDA, 20–30 mm diam after 1 wk, margins regular, floccose to woolly, olivaceous, white near the margins; reverse dull green,

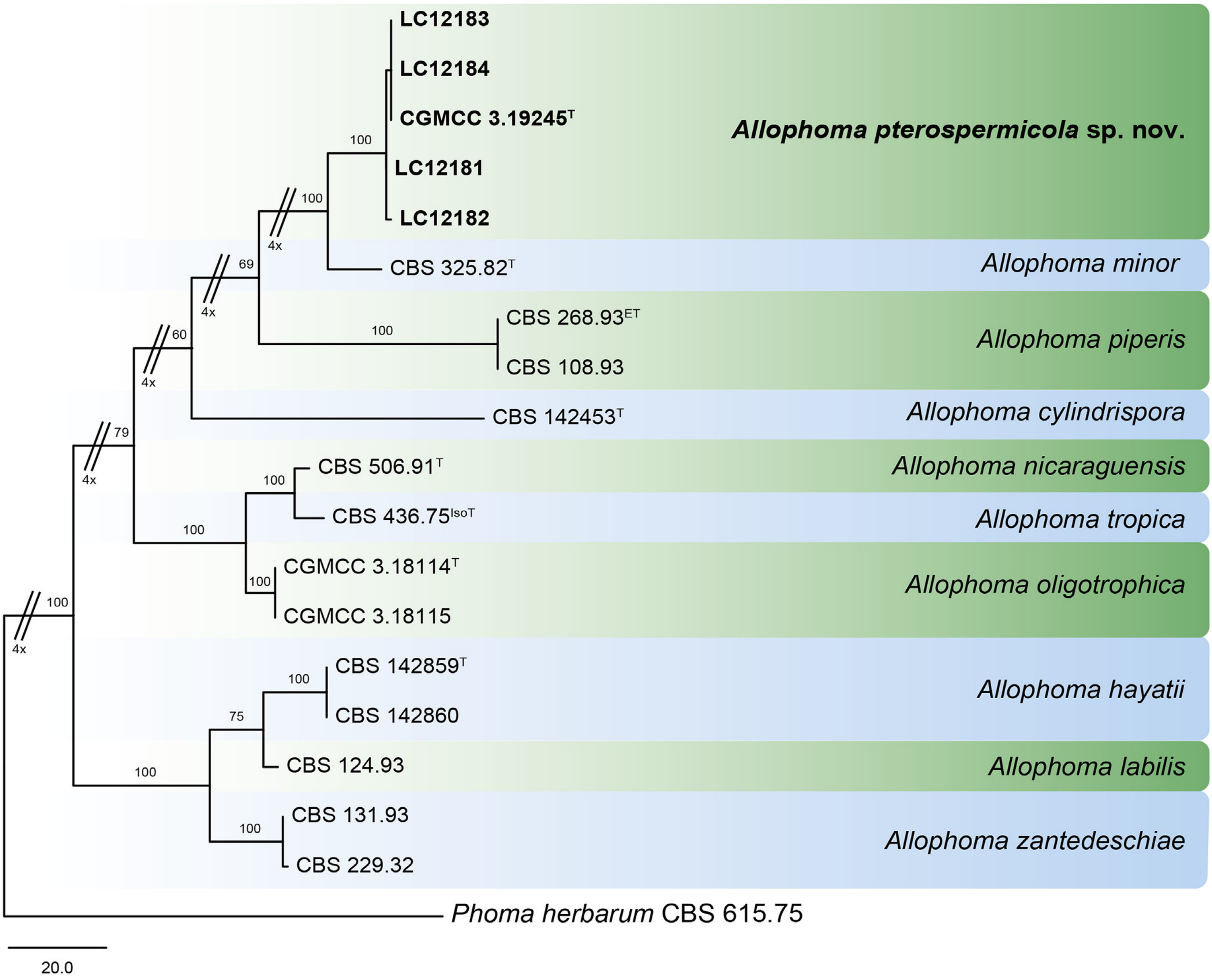

Fig. 2. Phylogenetic tree generated from a maximum parsimony analysis based on the combined LSU (860 bp), ITS (480 bp), *tub2* (333 bp) and *rpb2* (803 bp) sequences of all accepted species of *Allophoma*. The tree was rooted to *Phoma herbarum* CBS 615.75. Values above the branches represent parsimony bootstrap support values (> 50 %). Novel sequences and novel taxon are printed in **bold**. GenBank accession numbers are indicated in Table 1. $^{T,\ ET}$ and ^{IsoT} indicate ex-type, ex-epitype and ex-isotype strains, respectively. TreeBASE: S23493.

white near the margins. Application of NaOH results in a pale brownish olivaceous discolouration of the agar.

Typus: **China**, Guangxi, Nonggang National Nature Reserve, on diseased leaves of *Pterospermum xylocarpum* (*Sterculiaceae*), Jun. 2017, Z.Y. Ma (**holotype** HMAS 247983, culture ex-type CGMCC 3.19245 = LC 12185).

Additional materials examined: **China**, Guangxi, Nonggang National Nature Reserve, on diseased leaves of *Pterospermum xylocarpum* (*Sterculiaceae*), Jun. 2017, Z.Y. Ma, LC 12183; *ibid*., LC 12184; Guangxi, Jingxi, Gulongshan, on diseased leaves of *Maesa montana* (*Primulaceae*), Jun. 2017, Z.Y. Ma, LC 12181; *ibid*., LC 12182.

Notes: *Allophoma pterospermicola* represents the first report of a species in the family *Didymellaceae* on the two host genera *Pterospermum* (*Sterculiaceae*) and *Maesa* (*Primulaceae*). This species is closely related to *Al. minor*, but differs in producing longer conidiogenous cells [6–10 × 3–6 µm in *Al. pterospermicola vs.* 4–5.5(–6.2) × 3–4.5(–4.7) in *Al. minor*] and slightly narrower conidia [3–5.5 × 1.5–2 µm in *Al. pterospermicola vs.* (3–)3.5–4.5(–5) × 1.8–2.5(–3) µm in *Al. minor*]. In addition, *Al. pterospermicola* grows much slower on OA, MEA and PDA than *Al. minor*, and the latter species has only been recorded on *Syzygium aromaticum* (*Myrtaceae*) (Aveskamp *et al.* 2010).

Authors: Q. Chen & L. Cai

Alternaria Nees, Das System der Pilze und Schwämme: 72. 1816 (1816–1817). Fig. 4.
For synonyms see Woudenberg *et al.* (2013).

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

Type species: *Alternaria alternata* (Fries) Keissler, basionym: *Torula alternata* Fr., Syst. Mycol. (Lundae) 3: 500. 1832 (nom. sanct.); additional synonyms listed in Woudenberg *et al.* (2015). Neotype designated by Simmons (1967): E.G.S. 11.050. Ex-epitype strain designated by de Hoog & Horré (2002): CBS 916.96 = E.G.S. 34.016.

DNA barcodes (genus): LSU, ITS.

DNA barcodes (species): ITS, *ATPase*, *gapdh*, *rpb2*, *tef1*. Table 2. Figs 5–7.

Ascomata small, solitary to clustered, erumpent to almost superficial at maturity, dark brown, globose to ovoid, apically

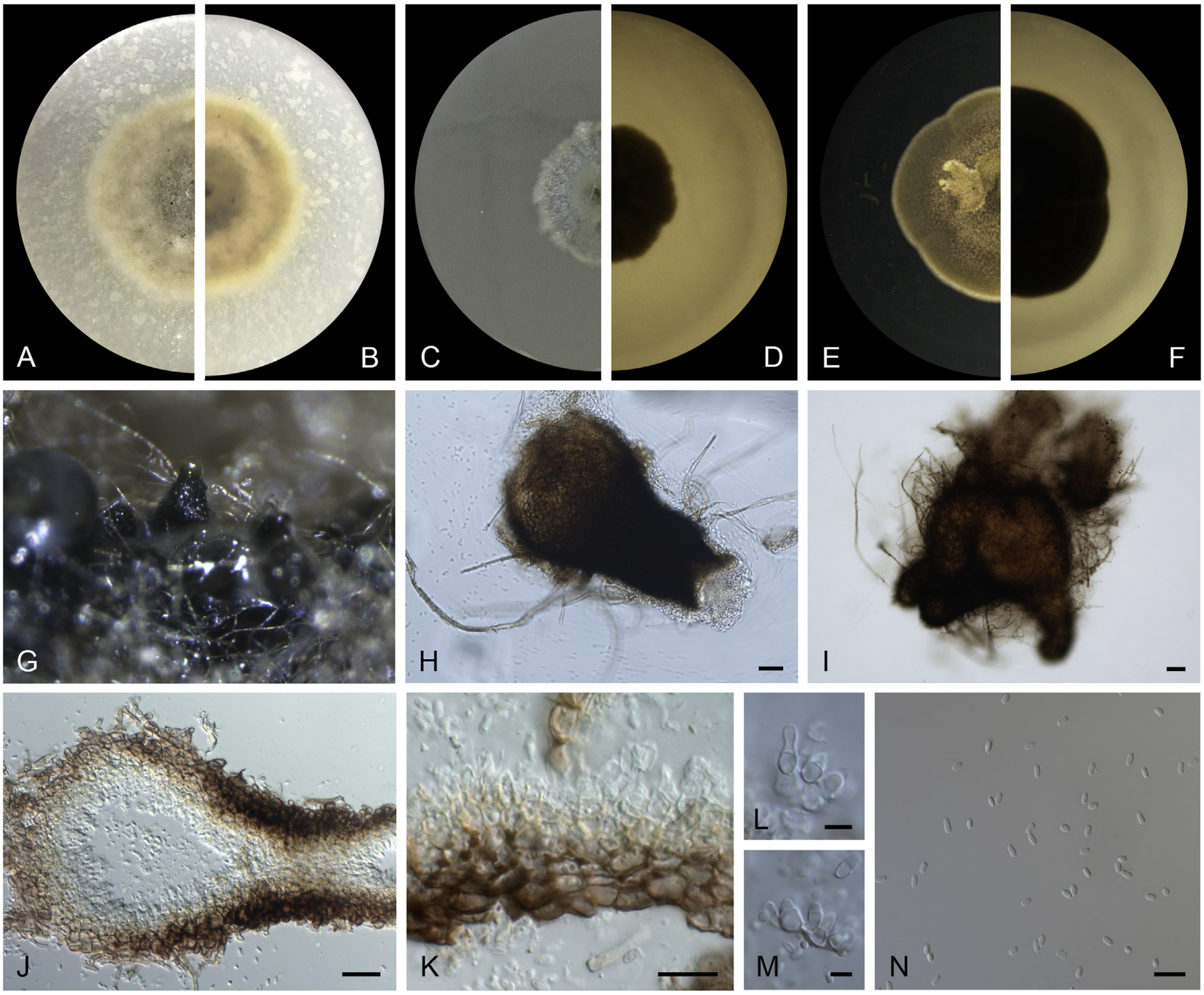

Fig. 3. *Allophoma pterospermicola* (ex-type CGMCC 3.19245). **A, B.** Colony on OA (front and reverse). **C, D.** Colony on MEA (front and reverse). **E, F.** Colony on PDA (front and reverse). **G.** Conidiomata sporulating on OA. **H, I.** Conidiomata. **J.** Section of conidioma. **K.** Section of conidiomatal wall. **L, M.** Conidiogenous cells. **N.** Conidia. Scale bars: H, J = 20 µm; I = 40 µm; K, N = 10 µm; L, M = 5 µm.

papillate, ostiolate, smooth or setose at maturity, with a thin ascomatal wall; *centrum* formed by a hamathecium with cellular pseudoparaphyses and asci in basal layer. *Asci* bitunicate, fissitunicate, uni- or biseriate, (4–6–)8-spored, cylindrical to cylindro-clavate, straight or somewhat curved, with a short furcate pedicel. *Ascospores* ellipsoid to fusoid, muriform, slightly constricted at septa, 3–7-transverse septa, 1–2 series of longitudinal septa through the two original central segments, end cells without septa, or with one longitudinal or oblique septum, or with a Y-shaped pair of septa, yellow-brown, smooth-walled, without guttules. *Conidiophores* macronematous or semi-macronematous, mononematous, simple or branched, pale brown or brown. *Conidiogenous cells* integrated, terminal becoming intercalary, mono- or polytretic and sympodial, cicatrised. *Conidia* solitary or in simple or branched chains, dry, ovoid, obovoid, cylindrical, narrowly ellipsoid or obclavate, beaked or non-beaked, pale or medium olivaceous brown to brown, smooth-walled or verrucose, with transverse and with or without oblique or longitudinal septa; *septa* can be thick, dark, an internal cell-like structure can be formed. Species with meristematic growth are known (adapted from Ellis 1976, Woudenberg *et al.* 2013, 2014, Grum-Grzhimaylo *et al.* 2016).

Culture characteristics: Colonies effuse, grey, olivaceous brown, dark blackish brown or black; mycelium immersed or partly superficial, composed of colourless, olivaceous brown or brown hyphae.

Optimal media and cultivation conditions: For morphological examinations the use of PCA and V-8 is recommended, incubated at moderate temperatures (*ca*. 22–25 ºC) under near-ultraviolet light (8 h light, 16 h dark), without humidity control, for 5–7 d or more if necessary (Simmons 2007). We also recommend microscopic examination of OA cultures due to the alterations observed on the conidial wall when grown on PCA.

Distribution: Worldwide.

Hosts: Mainly pathogens of a wide range of plant families, such as *Apiaceae*, *Asteraceae*, *Brassicaceae*, *Cyperaceae*, *Poaceae*, *Rosaceae*, *Rutaceae*, *Solanaceae*, among others (Thomma 2003, Lawrence *et al.* 2016). Some are implicated as human pathogens (de Hoog *et al.* 2011).

Disease symptoms: Most species are foliar pathogens, causing necrotic lesions as brown/black spots or "target spot" with the fungus residing in the central area, but also inducing leaf blight;

Fig. 4. *Alternaria* spp. **A–D.** Disease symptoms. **A.** *Alternaria dauci* on *Daucus carota*. **B.** *Alternaria linariae* on *Solanum lycopersicum*. **C.** *Alternaria neoipomoeae* on *Ipomoeae batatas* (Photo A.H. Thompson, ARC, South Africa). **D.** *Alternaria solani* on *Solanum tuberosum* (Photo J.E. van der Waals, University of Pretoria, South Africa). **E–V.** Asexual morph. **E–O.** Conidiophores. **E.** *Alternaria caricis*. **F.** *Alternaria chartarum*. **G.** *Alternaria cinerariae*. **H.** *Alternaria conjuncta*. **I.** *Alternaria elegans*. **J.** *Alternaria embellisia*. **K.** *Alternaria indefessa*. **L.** *Alternaria japonica*. **M.** *Alternaria penicillata*. **N.** *Alternaria proteae*. **O.** *Alternaria tenuissima*. **P–T.** Conidia. **P.** *Alternaria blumeae*. **Q.** *Alternaria calendulae*. **R.** *Alternaria perpunctulata*. **S.** *Alternaria carotiincultae*. **T.** *Alternaria triglochinicola*. **U, V.** Conidia producing secondary conidia. **U.** *Alternaria mimicola*. **V.** *Alternaria molesta*. Scale bars: 10 µm. Pictures A–D, P, Q taken from Woudenberg *et al.* (2014); E–O, R–V from Woudenberg *et al.* (2013).

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

Species	**Section**	**Isolates**[1]	**GenBank accession numbers**[2]					**References**
			ITS	***gapdh***	***rpb2***	***tef1***	***ATPase***	
Alternaria abundans	*Chalastospora*	CBS 534.83^{T}	JN383485	KC584154	KC584448	KC584707	JQ671802	Woudenberg *et al.* (2013), Deng *et al.* (2018)
A. acalyphicola	*Porri*	CBS 541.94^{T}	KJ718097	KJ717952	KJ718271	KJ718446	–	Woudenberg *et al.* (2014)
A. aconidiophora	*Infectoriae*	FMR 17111^{T}	LR133931	LR133965	LR133967	LR133968	LR133969	Present study
A. agerati	*Porri*	CBS 117221	KJ718098	KJ717953	KJ718272	KJ718447	–	Woudenberg *et al.* (2014)
A. agripestis	*Porri*	CBS 577.94^{T}	KJ718099	JQ646356	KJ718273	KJ718448	–	Woudenberg *et al.* (2014)
A. allii	*Porri*	CBS 107.28^{T}	KJ718100	KJ717954	KJ718274	KJ718449	–	Woudenberg *et al.* (2014)
A. alstroemeriae	*Alternaria*	CBS 118809^{T}	KP124297	KP124154	KP124765	KP125072	–	Woudenberg *et al.* (2015)
A. altcampina	*Pseudoalternaria*	FMR 16476^{T}	LR133895	LR133900	–	–	LR133906	Present study
A. alternantherae	*Althernantherae*	CBS 124392	KC584179	KC584096	KC584374	KC584633	–	Woudenberg *et al.* (2013)
A. alternariacida	*Porri*	CBS 105.51^{T}	KJ718105	KJ717959	KJ718279	KJ718454	–	Woudenberg *et al.* (2014)
A. alternariae	*Ulocladium*	CBS 126989^{T}	AF229485	AY278815	KC584470	KC584730	–	Woudenberg *et al.* (2013)
A. alternarina	*Infectoriae*	CBS 119396^{T}	JQ693648	JQ646289	JQ905199	LR134367	JQ671817	Poursafar *et al.* (2018), Geng *et al.* (unpubl. data), present study
A. alternata	*Alternaria*	CBS 916.96^{T}	AF347031	AY278808	KC584375	KC584634	–	Woudenberg *et al.* (2013)
A. anagallidis	*Porri*	CBS 117128	KJ718106	JQ646338	KJ718280	EU130544	–	Woudenberg *et al.* (2014)
A. anigozanthi	*Eureka*	CBS 121920^{T}	KC584180	KC584097	KC584376	KC584635	–	Woudenberg *et al.* (2013)
A. anodae	*Porri*	PPRI 12376	KJ718110	KJ717963	KJ718284	KJ718458	–	Woudenberg *et al.* (2014)
A. aragakii	*Porri*	CBS 594.93^{T}	KJ718111	KJ717964	KJ718285	KJ718459	–	Woudenberg *et al.* (2014)
A. arborescens	*Alternaria*	CBS 102605^{T}	AF347033	AY278810	KC584377	KC584636	–	Woudenberg *et al.* (2013)
A. arbusti	*Infectoriae*	CBS 596.93^{T}	JQ693644	JQ646365	LR134184	–	JQ671940	Poursafar *et al.* (2018), present study
A. argyranthemi		CBS 116530^{T}	KC584181	KC584098	KC584378	KC584637	–	Woudenberg *et al.* (2013)
A. argyroxiphii	*Porri*	CBS 117222^{T}	KJ718112	JQ646350	KJ718286	KJ718460	–	Woudenberg *et al.* (2014)
A. armoraciae	*Chalastospora*	CBS 118702^{T}	KC584182	KC584099	KC584379	KC584638	LR134098	Woudenberg *et al.* (2013), present study
A. arrhenatheri	*Pseudoalternaria*	LEP 140372^{T}	JQ693677	JQ693635	–	–	JQ693603	Poursafar *et al.* (2018)
A. aspera	*Pseudoulocladium*	CBS 115269^{T}	KC584242	KC584166	KC584474	KC584734	–	Woudenberg *et al.* (2013)
A. atra	*Ulocladioides*	CBS 195.67^{T}	AF229486	KC584167	KC584475	KC584735	–	Woudenberg *et al.* (2013)
A. avenicola	*Panax*	CBS 121459^{T}	KC584183	KC584100	KC584380	KC584639	–	Woudenberg *et al.* (2013)
A. axiaeriisporifera	*Gypsophilae*	CBS 118715^{T}	KC584184	KC584101	KC584381	KC584640	–	Woudenberg *et al.* (2013)
A. azadirachtae	*Porri*	CBS 116444^{T}	KJ718115	KJ717967	KJ718289	KJ718463	–	Woudenberg *et al.* (2014)
A. bataticola	*Porri*	CBS 531.63^{T}	KJ718117	JQ646349	KJ718291	KJ718465	–	Woudenberg *et al.* (2014)
A. betae-kenyensis	*Alternaria*	CBS 118810^{T}	KP124419	KP124270	KP124888	KP125197	–	Woudenberg *et al.* (2015)

Table 2. (Continued).

Species	Section	Isolates[1]	GenBank accession numbers[2]					References
			ITS	*gapdh*	*rpb2*	*tef1*	*ATPase*	
A. blumeae	*Porri*	CBS 117364^{T}	KJ718126	AY562405	KJ718300	KJ718474	–	Woudenberg *et al.* (2014)
A. bornmuelleri	*Undifilum*	DAOM 231361^{T}	FJ357317	FJ357305	KC584491	KC584751	–	Woudenberg *et al.* (2013)
A. botryospora	*Embellisioides*	CBS 478.90^{T}	AY278844	AY278831	KC584461	KC584720	–	Woudenberg *et al.* (2013)
A. botrytis	*Ulocladium*	CBS 197.67^{T}	KC584243	KC584168	KC584476	KC584736	–	Woudenberg *et al.* (2013)
A. brassicae		CBS 116528	KC584185	KC584102	KC584382	KC584641	–	Woudenberg *et al.* (2013)
A. brassicaepekinensis	*Ulocladioides*	CBS 121493^{T}	KC584244	KC584170	KC584478	KC584738	–	Woudenberg *et al.* (2013)
A. brassicicola	*Brassicicola*	CBS 118699	JX499031	KC584103	KC584383	KC584642	–	Woudenberg *et al.* (2013)
A. brassicifolii	*Pseudoalternaria*	CNU 111118^{T}	JQ317188	KM821537	–	–	KY412558	Deng *et al.* (2018)
A. breviramosa	*Chalastospora*	CBS 121331^{T}	FJ839608	KC584148	KC584442	KC584700	LR134099	Woudenberg *et al.* (2013), present study
A. broccoli-italicae	*Infectoriae*	CBS 118485^{T}	KM821536	KM821538	LR134194	LR134262	KY412557	Deng *et al.* (2018), present study
A. burnsii	*Alternaria*	CBS 107.38^{T}	KP124420	JQ646305	KP124889	KP125198	–	Woudenberg *et al.* (2015)
A. caespitosa	*Infectoriae*	CBS 177.80^{T}	KC584250	KC584178	KC584492	KC584752	LR134114	Woudenberg *et al.* (2013), present study
A. calendulae	*Porri*	CBS 224.76^{T}	KJ718127	KJ717977	KJ718301	KJ718475	–	Woudenberg *et al.* (2014)
A. californica	*Infectoriae*	CBS 119409^{T}	JQ693645	JQ646285	LR134181	LR134245	JQ671813	Poursafar *et al.* (2018), present study
A. calycipyricola	*Panax*	CBS 121545^{T}	KC584186	KC584104	KC584384	KC584643	–	Woudenberg *et al.* (2013)
A. cantlous	*Ulocladioides*	CBS 123007^{T}	KC584245	KC584171	KC584479	KC584739	–	Woudenberg *et al.* (2013)
A. capsici-annui	*Ulocladium*	CBS 504.74	KC584187	KC584105	KC584385	KC584644	–	Woudenberg *et al.* (2013)
A. caricis	*Nimbya*	CBS 480.90^{T}	AY278839	AY278826	KC584467	KC584726	JQ671780	Woudenberg *et al.* (2013), Deng *et al.* (2018)
A. carotiincultae	*Radicina*	CBS 109381^{T}	KC584188	KC584106	KC584386	KC584645	–	Woudenberg *et al.* (2013)
A. carthami	*Porri*	CBS 635.80	KJ718131	KJ717981	KJ718305	KJ718479	–	Woudenberg *et al.* (2014)
A. carthamicola	*Porri*	CBS 117092^{T}	KJ718134	KJ717984	KJ718308	KJ718482	–	Woudenberg *et al.* (2014)
A. cassiae	*Porri*	CBS 478.81	KJ718135	KJ717985	KJ718309	KJ718483	–	Woudenberg *et al.* (2014)
A. catananches	*Porri*	CBS 137456^{T}	KJ718139	KJ717989	KJ718313	KJ718487	–	Woudenberg *et al.* (2014)
A. centaureae	*Porri*	CBS 116446^{T}	KJ718140	KJ717990	KJ718314	KJ718488	–	Woudenberg *et al.* (2014)
A. cerasidanica	*Infectoriae*	CBS 121923^{T}	LR135744	LR135747	LR135746	LR135745	LR135748	Present study
A. cesenica	*Infectoriae*	MFLUCC 13-0450^{T}	KP711383	–	–	KP711386	–	Liu *et al.* (2015)
A. cetera	*Chalastospora*	CBS 121340^{T}	JN383482	AY562398	KC584441	KC584699	LR134101	Woudenberg *et al.* (2013), Deng *et al.* (2018)
A. chartarum	*Pseudoulocladium*	CBS 200.67^{T}	AF229488	KC584172	KC584481	KC584741	–	Woudenberg *et al.* (2013)
A. cheiranthi	*Cheiranthus*	CBS 109384	AF229457	KC584107	KC584387	KC584646	–	Woudenberg *et al.* (2013)
A. chlamydospora	*Phragmosporae*	CBS 491.72^{T}	KC584189	KC584108	KC584388	KC584647	–	Woudenberg *et al.* (2013)

(*continued on next page*)

Table 2. (Continued).

Species	**Section**	**Isolates**[1]	**GenBank accession numbers**[2]					**References**
			ITS	***gapdh***	***rpb2***	***tef1***	***ATPase***	
A. chlamydosporigena	*Embellisia*	CBS 341.71	KC584231	KC584156	KC584451	KC584710	–	Woudenberg *et al.* (2013)
A. chlamydosporifera	*Radicina*	FMR 17360^{T}	LR133924	LR133927	LR133926	LR133929	–	Present study
A. cichorii	*Porri*	CBS 102.33^{T}	KJ718141	KJ717991	KJ718315	KJ718489	–	Woudenberg *et al.* (2014)
A. cinerariae	*Sonchi*	CBS 116495	KC584190	KC584109	KC584389	KC584648	–	Woudenberg *et al.* (2013)
A. cirsinoxia	*Porri*	CBS 113261^{T}	KJ718143	KJ717993	KJ718317	KJ718491	–	Woudenberg *et al.* (2014)
A. citrullicola	*Porri*	CBS 103.32^{T}	KJ718144	KJ717994	KJ718318	KJ718492	–	Woudenberg *et al.* (2014)
A. concatenata	*Pseudoulocladium*	CBS 120006^{T}	KC584246	AY762950	KC584480	KC584740	–	Woudenberg *et al.* (2013)
A. conidiophora	*Porri*	CBS 137457^{T}	KJ718145	KJ717995	-	KJ718493	–	Woudenberg *et al.* (2014)
A. conjuncta	*Infectoriae*	CBS 196.86^{T}	FJ266475	AY562401	KC584390	KC584649	JQ671824	Woudenberg *et al.* (2013), Poursafar *et al.* (2018)
A. conoidea	*Brassicicola*	CBS 132.89	AF348226	FJ348227	KC584452	KC584711	–	Woudenberg *et al.* (2013)
A. consortialis	*Ulocladioides*	CBS 104.31^{T}	KC584247	KC584173	KC584482	KC584742	–	Woudenberg *et al.* (2013)
A. crassa	*Porri*	CBS 110.38^{T}	KJ718147	KJ717997	KJ718320	KJ718495	–	Woudenberg *et al.* (2014)
A. cyamopsidis	*Porri*	CBS 364.67	KJ718156	KJ718003	KJ718329	KJ718504	–	Woudenberg *et al.* (2014)
A. cumini	*Eureka*	CBS 121329^{T}	KC584191	KC584110	KC584391	KC584650	–	Woudenberg *et al.* (2013)
A. cucumerina	*Porri*	CBS 116114^{T}	KJ718153	KJ718000	KJ718326	KJ718501	–	Woudenberg *et al.* (2014)
A. cucurbitae	*Ulocladioides*	CBS 483.81	FJ266483	AY562418	KC584483	KC584743	–	Woudenberg *et al.* (2013)
A. curvata	*Infectoriae*	FMR 16901^{T}	LR133898	LR133899	LR133901	LR133902	LR133905	Present study
A. dactylidicola	*Infectoriae*	MFLUCC 15-0466^{T}	KY703616	–	KY750720	–	–	Thambugala *et al.* (2017)
A. dauci	*Porri*	CBS 111.38^{T}	KJ718158	KJ718005	KJ718331	KJ718506	–	Woudenberg *et al.* (2014)
A. daucicaulis	*Infectoriae*	CBS 119398^{T}	JQ693653	JQ646294	LR134177	LR134241	JQ671822	Poursafar *et al.* (2018), present study
A. dennisii		CBS 476.90^{T}	JN383488	JN383469	KC584454	KC584713	–	Woudenberg *et al.* (2013)
A. deserticola	*Porri*	CBS 110799^{T}	KJ718249	KJ718077	KJ718424	KJ718595	–	Woudenberg *et al.* (2014)
A. dianthicola	*Dianthicola*	CBS 116491	KC584194	KC584113	KC584394	KC584653	–	Woudenberg *et al.* (2013)
A. dichondrae	*Porri*	CBS 200.74^{T}	KJ718167	KJ718012	KJ718340	KJ718515	–	Woudenberg *et al.* (2014)
A. didymospora	*Phragmosporae*	CBS 766.79	FJ357312	FJ357300	KC584455	KC584714	JQ671796	Woudenberg *et al.* (2013), Deng *et al.* (2018)
A. doliconidium	*Alternaria*	KUMCC 17-0263^{T}	MG828864	–	–	–	–	Wanasinghe *et al.* (2018)
A. echinaceae	*Porri*	CBS 116117^{T}	KJ718170	KJ718015	KJ718343	KJ718518	–	Woudenberg *et al.* (2014)
A. eichhorniae	*Alternaria*	CBS 489.92^{T}	KC146356	KP124276	KP124895	KP125204	–	Woudenberg *et al.* (2015)
A. elegans	*Dianthicola*	CBS 109159^{T}	KC584195	KC584114	KC584395	KC584654	–	Woudenberg *et al.* (2013)
A. ellipsoidea	*Gypsophilae*	CBS 119674^{T}	KC584196	KC584115	KC584396	KC584655	–	Woudenberg *et al.* (2013)
A. embellisia	*Embellisia*	CBS 339.71	KC584230	KC584155	KC584449	KC584708	–	Woudenberg *et al.* (2013)

Table 2. (Continued).

Species	Section	Isolates[1]	GenBank accession numbers[2]					References
			ITS	*gapdh*	*rpb2*	*tef1*	*ATPase*	
A. eryngii	*Panax*	CBS 121339	JQ693661	AY562416	KC584397	KC584656	–	Woudenberg *et al.* (2013)
A. ethzedia	*Infectoriae*	CBS 197.86^{T}	AY278833	AY278795	KC584398	KC584657	JQ671805	Woudenberg *et al.* (2013), Poursafar *et al.* (2018)
A. euphorbiicola	*Euphorbiicola*	CBS 119410	KJ718173	KJ718018	KJ718346	KJ718521	–	Woudenberg *et al.* (2014)
A. eureka	*Eureka*	CBS 193.86^{T}	JN383490	JN383471	KC584456	KC584715	–	Woudenberg *et al.* (2013)
A. fimeti	*Infectoriae*	FMR 17110^{T}	LR133920	LR133921	LR133923	LR133922	LR133925	Present study
A. forlicesenensis	*Infectoriae*	MFLUCC 13-0456^{T}	KY769657	–	–	–	–	Thambugala *et al.* (2017)
A. frumenti	*Infectoriae*	CBS 119401^{T}	JQ693654	JQ646295	LR134172	LR134370	JQ671823	Poursafar *et al.* (2018), present study
A. gaisen	*Alternaria*	CBS 632.93	KC584197	KC584116	KC584399	KC584658	–	Woudenberg *et al.* (2013)
A. geniostomatis	*Eureka*	CBS 118701^{T}	KC584198	KC584117	KC584400	KC584659	–	Woudenberg *et al.* (2013)
A. gossypina	*Alternaria*	CBS 104.32^{T}	KP124430	JQ646312	KP124900	KP125209	–	Woudenberg *et al.* (2015)
A. graminicola	*Infectoriae*	CBS 119400^{T}	JQ693650	JQ646291	LR134180	LR134249	JQ671819	Poursafar *et al.* (2018), present study
A. grandis	*Porri*	CBS 109158^{T}	KJ718239	JQ646341	KJ718414	EU130547	–	Woudenberg *et al.* (2014)
A. gypsophilae	*Gypsophilae*	CBS 107.41^{T}	KC584199	KC584118	KC584401	KC584660	–	Woudenberg *et al.* (2013)
A. hampshirensis	*Infectoriae*	MFLUCC 17-0783^{T}	MG828866	–	MG829247	–	–	Wanasinghe *et al.* (2018)
A. helianthiinficiens		CBS 208.86^{T}	JX101649	KC584120	KC584403	EU130548	–	Woudenberg *et al.* (2013)
A. heterospora	*Ulocladioides*	CBS 123376^{T}	KC584248	KC584176	KC584488	KC584748	–	Woudenberg *et al.* (2013)
A. hordeiaustralica	*Infectoriae*	CBS 119402^{T}	JQ693641	JQ646283	LR134179	LR134243	JQ671811	Poursafar *et al.* (2018), present study
A. hordeicola	*Infectoriae*	CBS 121458^{T}	JQ693642	JQ646284	LR134175	LR134371	JQ671812	Poursafar *et al.* (2018), present study
A. humuli	*Infectoriae*	CBS 119404^{T}	JQ693652	JQ646293	LR134174	LR134199	JQ671821	Poursafar *et al.* (2018), present study
A. hyacinthi	*Embellisioides*	CBS 416.71^{T}	KC584233	KC584158	KC584457	KC584716	–	Woudenberg *et al.* (2013)
A. incomplexa	*Infectoriae*	CBS 121330^{T}	JQ693658	JQ646287	LR134185	LR134250	JQ671815	Poursafar *et al.* (2018), present study
A. indefessa	*Cheiranthus*	CBS 536.83^{T}	KC584234	KC584159	KC584458	KC584717	–	Woudenberg *et al.* (2013)
A. infectoria	*Infectoriae*	CBS 210.86^{T}	AF347034	AY278793	KC584404	KC584662	JQ671804	Woudenberg *et al.* (2013), Poursafar *et al.* (2018)
A. inflata	*Pseudoalternaria*	FMR 16477 ^{T}	LR133930	LR133938	–	–	LR133966	Present study
A. intercepta	*Infectoriae*	CBS 119406^{T}	JQ693656	JQ646297	LR134170	–	JQ671826	Poursafar *et al.* (2018), present study
A. ipomoeae	*Porri*	CBS 219.79^{T}	KJ718175	KJ718020	KJ718348	KJ718523	–	Woudenberg *et al.* (2014)
A. iridiaustralis	*Alternaria*	CBS 118486^{T}	KP124435	KP124284	KP124905	KP125214	–	Woudenberg *et al.* (2015)
A. japonica	*Japonicae*	CBS 118390	KC584201	KC584121	KC584405	KC584663	–	Woudenberg *et al.* (2013)
A. jacinthicola	*Alternaria*	CBS 133751^{T}	KP124438	KP124287	KP124908	KP125217	–	Woudenberg *et al.* (2015)
A. jesenskae	*Porri*	CBS 133855^{T}	KJ718177	KJ718022	KJ718350	KJ718525	–	Woudenberg *et al.* (2014)

(*continued on next page*)

Table 2. (Continued).

Species	Section	Isolates[1]	GenBank accession numbers[2]					References
			ITS	*gapdh*	*rpb2*	*tef1*	*ATPase*	
A. juxtiseptata	*Gypsophilae*	CBS 119673^{T}	KC584202	KC584122	KC584406	KC584664	–	Woudenberg *et al.* (2013)
A. kordkuyana	*Pseudoalternaria*	IRAN 16888F^{T}	MF033843	MF033826	–	–	MF033860	Poursafar *et al.* (2018)
		FMR 17061	LR133970	LR133998	–	–	LR134001	Present study
		FMR 17372	LR133995	LR133997	–	–	LR133999	Present study
A. kulundii	*Soda*	CBS 137525^{T}	KJ443262	KJ649618	KJ443176	KJ443219	–	Grum-Grzhimaylo *et al.* (2016)
A. lawrencei	*Infectoriae*	FMR 17004^{T}	LR133907	LR133908	LR133911	LR133912	LR133914	Present study
A. leptinellae	*Eureka*	CBS 477.90^{T}	KC584235	KC584160	KC584459	KC584718	–	Woudenberg *et al.* (2013)
A. leucanthemi	*Teretispora*	CBS 421.65^{T}	KC584240	KC584164	KC584472	KC584732	–	Woudenberg *et al.* (2013)
A. limaciformis	*Phragmosporae*	CBS 481.81^{T}	KC584203	KC584123	KC584407	KC584665	JQ671798	Woudenberg *et al.* (2013), Deng *et al.* (2018)
A. limicola	*Euphorbiicola*	CBS 483.90^{T}	KJ718178	JQ646329	KJ718351	KJ718526	–	Woudenberg *et al.* (2014)
A. linariae	*Porri*	CBS 105.41^{T}	KJ718180	KJ718024	KJ718353	KJ718528	–	Woudenberg *et al.* (2014)
A. longipes	*Alternaria*	CBS 540.94	AY278835	AY278811	KC584409	KC584667	–	Woudenberg *et al.* (2013)
A. lolii	*Embellisioides*	CBS 115266^{T}	JN383492	JN383473	KC584460	KC584719	–	Woudenberg *et al.* (2013)
A. macrospora	*Porri*	CBS 117228^{T}	KC584204	KC584124	KC584410	KC584668	–	Woudenberg *et al.* (2013)
A. malorum	*Chalastospora*	CBS 135.31	JQ693638	JQ646278	–	–	JQ671800	Poursafar *et al.* (2018)
		FMR 17369	LR134074	LR134077	–	–	LR134029	Present study
A. merytae	*Infectoriae*	CBS 119403^{T}	JQ693651	JQ646292	LR134119	LR134198	JQ671820	Poursafar *et al.* (2018), present study
A. metachromatica	*Infectoriae*	CBS 553.94^{T}	JQ693660	AY562404	JQ905189	FJ214931	JQ671809	Andersen *et al.* (2009), Poursafar *et al.* (2018), Geng *et al.* (unpubl. data)
A. mimicula	*Brassicicola*	CBS 118696^{T}	FJ266477	AY562415	KC584411	KC584669	–	Woudenberg *et al.* (2013)
A. molesta	*Phragmosporae*	CBS 548.81^{T}	KC584205	KC584125	KC584412	KC584670	–	Woudenberg *et al.* (2013)
A. montanica	*Porri*	CBS 121343^{T}	KJ718194	KJ718033	KJ718367	KJ718541	–	Woudenberg *et al.* (2014)
A. montsantina	*Infectoriae*	FMR 17060^{T}	LR133913	LR133915	LR133918	LR133919	LR133916	Present study
A. mouchaccae	*Phragmosporae*	CBS 119671^{T}	KC584206	AY562399	KC584413	KC584671	–	Woudenberg *et al.* (2013)
A. multiformis	*Ulocladioides*	CBS 102060^{T}	FJ266486	KC584174	KC584484	KC584744	–	Woudenberg *et al.* (2013)
A. multirostrata	*Porri*	CBS 712.68^{T}	KJ718195	JQ646362	KJ718368	EU130546	–	Woudenberg *et al.* (2014)
A. murispora	*Infectoriae*	MFLU 14-0758^{T}	NR_137964	–	–	–	–	Ariyawansa and Hyde (unpubl. data)
A. neoipomoeae	*Porri*	PPRI 11845^{T}	KJ718198	KJ718036	KJ718371	KJ718544	–	Woudenberg *et al.* (2014)
A. nepalensis	*Japonicae*	CBS 118700^{T}	KC584207	KC584126	KC584414	KC584672	–	Woudenberg *et al.* (2013)
A. nitrimali	*Porri*	CBS 109163^{T}	KJ718201	JQ646358	KJ718374	KJ718547	–	Woudenberg *et al.* (2014)
A. nobilis	*Gypsophilae*	CBS 116490	KC584208	KC584127	KC584415	KC584673	–	Woudenberg *et al.* (2013)

Table 2. (Continued).

Species	Section	Isolates[1]	GenBank accession numbers[2]					References
			ITS	*gapdh*	*rpb2*	*tef1*	*ATPase*	
A. novae-guineensis	*Porri*	CBS 116120^{T}	KJ718202	KJ718039	KJ718375	KJ718548	–	Woudenberg *et al.* (2014)
A. novae-zelandiae	*Infectoriae*	CBS 119405^{T}	JQ693655	JQ646296	LR134120	LR134197	JQ671825	Poursafar *et al.* (2018), present study
A. obclavata	*Chalastospora*	CBS 124120^{T}	KC584225	KC584149	KC584443	KC584701	LR134100	Woudenberg *et al.* (2013), present study
A. obovoidea	*Ulocladioides*	CBS 101229	FJ266487	FJ266498	KC584485	KC584745	–	Woudenberg *et al.* (2013)
A. obtecta	*Porri*	CBS 117367	KJ718204	KJ718041	KJ718377	KJ718550	–	Woudenberg *et al.* (2014)
A. oregonensis	*Infectoriae*	CBS 542.94^{T}	FJ266478	FJ266491	KC584416	KC584674	JQ671827	Woudenberg *et al.* (2013), Poursafar *et al.* (2018)
A. oudemansii	*Ulocladium*	CBS 114.07^{T}	FJ266488	KC584175	KC584486	KC584746	–	Woudenberg *et al.* (2013)
A. panax	*Panax*	CBS 482.81	KC584209	KC584128	KC584417	KC584675	–	Woudenberg *et al.* (2013)
A. papavericola	*Crivellia*	CBS 116606^{T}	FJ357310	FJ357298	KC584446	KC584705	–	Woudenberg *et al.* (2013)
A. paralinicola	*Porri*	CBS 116652^{T}	KJ718206	KJ718043	KJ718379	KJ718552	–	Woudenberg *et al.* (2014)
A. passiflorae	*Porri*	CBS 113.38	KJ718207	JQ646353	KJ718380	KJ718553	–	Woudenberg *et al.* (2014)
A. parvicaespitosa	*Pseudoalternaria*	LEP 014858^{T}	MF033859	MF033842	–	–	KJ908217	Poursafar *et al.* (2018)
A. penicillata	*Crivellia*	CBS 116608^{T}	FJ357311	FJ357299	KC584440	KC584698	–	Woudenberg *et al.* (2013)
A. perpunctulata	*Althernantherae*	CBS 115267^{T}	KC584210	KC584129	KC584418	KC584676	–	Woudenberg *et al.* (2013)
A. petroselini	*Radicina*	CBS 112.41^{T}	KC584211	KC584130	KC584419	KC584677	–	Woudenberg *et al.* (2013)
A. petuchovskii	*Soda*	CBS 137517^{T}	KJ443254	KJ649616	KJ443170	KJ443211	–	Grum-Grzhimaylo *et al.* (2016)
A. peucedani		CNU 111485^{T}	KF728231	KF889361	–	–	–	Deng *et al.* (2014)
A. photistica	*Panax*	CBS 212.86^{T}	KC584212	KC584131	KC584420	KC584678	JQ671807	Woudenberg *et al.* (2013), Deng *et al.* (2018)
A. phragmospora	*Phragmosporae*	CBS 274.70^{T}	JN383493	JN383474	KC584462	KC584721	–	Woudenberg *et al.* (2013)
A. pipionipisi	*Porri*	CBS 116115^{T}	KJ718214	KJ718049	KJ718387	KJ718560	–	Woudenberg *et al.* (2014)
A. planifunda	*Embellisioides*	CBS 537.83^{T}	FJ357315	FJ357303	KC584463	KC584722	–	Woudenberg *et al.* (2013)
A. poaceicola	*Infectoriae*	MFLUCC 13-0346^{T}	KY026587	–	KY460971	–	–	Thambugala *et al.* (2017)
A. pobletensis	*Chalastospora*	FMR 16448^{T}	LR133896	LR133897	–	–	LR133903	Present study
A. porri	*Porri*	CBS 116699^{T}	KJ718218	KJ718053	KJ718391	KJ718564	–	Woudenberg *et al.* (2014)
A. proteae	*Embellisioides*	CBS 475.90^{T}	AY278842	KC584161	KC584464	KC584723	–	Woudenberg *et al.* (2013)
A. protenta	*Porri*	CBS 116696	KJ718221	JQ646335	KJ718394	KJ718567	–	Woudenberg *et al.* (2014)
A. pseudorostrata	*Porri*	CBS 119411^{T}	JN383483	AY562406	KC584422	KC584680	–	Woudenberg *et al.* (2013)
A. pseudoventricosa	*Infectoriae*	FMR 16900^{T}	LR133928	LR133935	LR133934	LR133936	LR133937	Present study
A. radicina	*Radicina*	CBS 245.67^{T}	KC584213	KC584133	KC584423	KC584681	–	Woudenberg *et al.* (2013)
A. ranunculi	*Porri*	CBS 116330^{T}	KJ718225	KJ718058	KJ718398	KJ718571	–	Woudenberg *et al.* (2014)

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Table 2. (Continued).

Species	Section	Isolates[1]	GenBank accession numbers[2]					References
			ITS	*gapdh*	*rpb2*	*tef1*	*ATPase*	
A. ricini	*Porri*	CBS 215.31^{T}	KJ718226	KJ718059	KJ718399	KJ718572	–	Woudenberg *et al.* (2014)
A. rosae	*Pseudoalternaria*	CBS 121341^{T}	JQ646279	JQ646279	–	–	JQ671803	Poursafar *et al.* (2018)
		FMR 15720	LR134076	LR134070	–	–	LR134004	Present study
		FMR 17376	LR134071	LR13403	–	–	LR134003	Present study
		FMR 17377	LR134073	LR134072	–	–	LR134028	Present study
A. roseogrisea	*Infectoriae*	CBS 121921^{T}	LR134102	LR134103	LR134192	LR134260	LR134104	Present study
A. rostellata	*Porri*	CBS 117366^{T}	KJ718229	JQ646332	KJ718402	KJ718575	–	Woudenberg *et al.* (2014)
A. saponariae	*Gypsophilae*	CBS 116492	KC584215	KC584135	KC584425	KC584683	–	Woudenberg *et al.* (2013)
A. scirpicola	*Nimbya*	CBS 481.90	KC584237	KC584163	KC584469	KC584728	JQ671781	Woudenberg *et al.* (2013), Deng *et al.* (2018)
A. scirpinfestans	*Nimbya*	EGS 49-185^{T}	JN383499	JN383480	–	JQ672404	JQ671783	Lawrence *et al.* (2012), Lawrence *et al.* (unpubl. data)
A. scirpivora	*Nimbya*	EGS 50-021^{T}	JN383500	JN383481	–	JQ672405	JQ671782	Lawrence *et al.* (2012), Lawrence *et al.* (unpubl. data)
A. scorzonerae	*Porri*	CBS 103.46	KJ718190	JQ646363	KJ718363	KJ718537	–	Woudenberg *et al.* (2014)
A. selini	*Radicina*	CBS 109382^{T}	AF229455	AY278800	KC584426	KC584684	–	Woudenberg *et al.* (2013)
A. sennae	*Porri*	CBS 477.81^{T}	KJ718230	JQ646344	KJ718403	EU130543	–	Woudenberg *et al.* (2014)
A. septospora	*Pseudoulocladium*	CBS 109.38	FJ266489	FJ266500	KC584487	KC584747	–	Woudenberg *et al.* (2013)
A. septorioides	*Brassicicola*	CBS 106.41^{T}	KC584216	KC584136	KC584427	KC584685	–	Woudenberg *et al.* (2013)
A. sesami	*Porri*	CBS 115264	JF780939	KJ718061	KJ718405	KJ718577	–	Woudenberg *et al.* (2014)
A. shukurtuzii	*Soda*	CBS 137520^{T}	KJ443257	KJ649620	KJ443172	KJ443214	–	Grum-Grzhimaylo *et al.* (2016)
A. sidae	*Porri*	CBS 117730^{T}	KJ718232	KJ718062	KJ718406	KJ718578	–	Woudenberg *et al.* (2014)
A. simsimi	*Dianthicola*	CBS 115265^{T}	JF780937	KC584137	KC584428	KC584686	–	Woudenberg *et al.* (2013)
A. silybi	*Porri*	CBS 134092^{T}	KJ718233	KJ718063	KJ718407	KJ718579	–	Woudenberg *et al.* (2014)
A. slovaca	*Infectoriae*	CBS 567.66^{T}	KC584226	KC584150	KC584444	KC584702	LR134368	Woudenberg *et al.* (2013), present study
A. smyrnii	*Radicina*	CBS 109380	AF229456	KC584138	KC584429	KC584687	–	Woudenberg *et al.* (2013)
A. solani	*Porri*	CBS 106.21	KJ718236	KJ718066	KJ718410	KJ718582	–	Woudenberg *et al.* (2014)
A. solani-nigri	*Porri*	CBS 113403	KJ718243	KJ718071	KJ718418	KJ718589	–	Woudenberg *et al.* (2014)
A. soliaridae		CBS 118387^{T}	KC584218	KC584140	KC584431	KC584689	–	Woudenberg *et al.* (2013)
A. solidaccana	*Brassicicola*	CBS 118698^{T}	KC584219	KC584141	KC584432	KC584690	–	Woudenberg *et al.* (2013)
A. sonchi	*Sonchi*	CBS 119675	KC584220	KC584142	KC584433	KC584691	–	Woudenberg *et al.* (2013)
A. steviae	*Porri*	CBS 117362^{T}	KJ718252	KJ718079	KJ718427	KJ718598	–	Woudenberg *et al.* (2014)
A. subcucurbitae	*Ulocladioides*	CBS 121491^{T}	KC584249	EU855803	KC584489	KC584749	–	Woudenberg *et al.* (2013)
A. tagetica	*Porri*	CBS 479.81	KC584221	KC584143	KC584434	KC584692	–	Woudenberg *et al.* (2013)

Table 2. (Continued).

Species	**Section**	**Isolates**[1]	**GenBank accession numbers**[2]					**References**
			ITS	***gapdh***	***rpb2***	***tef1***	***ATPase***	
A. tellustris	*Embellisia*	CBS 538.83^{T}	FJ357316	AY562419	KC584465	KC584724	JQ671794	Woudenberg *et al.* (2013), Deng *et al.* (2018)
A. terricola	*Ulocladioides*	CBS 202.67^{T}	FJ266490	KC584177	KC584490	KC584750	–	Woudenberg *et al.* (2013)
A. tillandsiae	*Porri*	CBS 116116^{T}	KJ718260	KJ718087	KJ718435	KJ718606	–	Woudenberg *et al.* (2014)
A. thalictrigena		CBS 121712^{T}	EU040211	KC584144	KC584436	KC584694	–	Woudenberg *et al.* (2013)
A. thunbergiae	*Porri*	CBS 116331^{T}	KJ718257	KJ718084	KJ718432	KJ718603	–	Woudenberg *et al.* (2014)
A. tomato	*Alternaria*	CBS 103.30	KP124445	KP124294	KP124915	KP125224	–	Woudenberg *et al.* (2015)
A. triglochinicola	*Eureka*	CBS 119676^{T}	KC584222	KC584145	KC584437	KC584695	–	Woudenberg *et al.* (2013)
A. triticimaculans	*Infectoriae*	CBS 578.94^{T}	JQ693657	JQ646280	LR134183	–	JQ671806	Poursafar *et al.* (2018), present study
A. triticina	*Infectoriae*	CBS 763.84^{T}	AY278834	JQ646281	LR134186	FJ214942	JQ671808	Andersen *et al.* (2009), Poursafar *et al.* (2018), Present study
A. tropica	*Porri*	CBS 631.93^{T}	KJ718261	KJ718088	KJ718436	KJ718607	–	Woudenberg *et al.* (2014)
A. tumida	*Embellisioides*	CBS 539.83^{T}	FJ266481	FJ266493	KC584466	KC584725	–	Woudenberg *et al.* (2013)
A. quercicola	*Infectoriae*	CBS 141466^{T}	KX228295	KX228362	LR134188	LR134259	LR134115	Crous *et al.* (2013), present study
A. vaccariae	*Gypsophilae*	CBS 116533	KC584223	KC584146	KC584438	KC584696	–	Woudenberg *et al.* (2013)
A. vaccariicola	*Gypsophilae*	CBS 118714^{T}	KC584224	KC584147	KC584439	KC584697	–	Woudenberg *et al.* (2013)
A. venezuelensis	*Porri*	CBS 116121^{T}	KJ718263	KJ718090	KJ718438	KJ718609	–	Woudenberg *et al.* (2014)
A. ventricosa	*Infectoriae*	CBS 121546^{T}	JQ693649	JQ646290	LR134134	KY352501	JQ671818	Poursafar *et al.* (2018), Fotedar *et al.* (unpubl. data), present study
A. viburni	*Infectoriae*	CBS 119407^{T}	JQ693647	JQ646288	LR134166	LR134200	JQ671816	Poursafar *et al.* (2018), present study
A. zinniae	*Porri*	CBS 117223	KJ718270	KJ718096	KJ718445	KJ718616	–	Woudenberg *et al.* (2014)

[1] CBS: Culture collection of the Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CNU: Culture Collection Center of the Chungnam National University; DAOM: Canadian Collection of Fungal Cultures, Ottawa, Canada; EGS: Personal collection of Dr. E.G. Simmons; FMR: Facultat de Medicina, Universitat Rovira i Virgili, Reus, Spain; IRAN: Fungal Culture Collections of the Iranian Research Institute of Plant Protection; KUMCC, Culture collection of Kunming Institute of Botany, Kunming, China; LEP: Mycological Herbarium of All-Russian Institute of Plant Protection, Saint Petersburg, Russia; MFLU and MFLUCC: Herbarium and culture collection of Mae Fah Luang University, Chiang Rai, Thailand, respectively; PPRI: ARC-Plant Protection Research Institute, Roodeplaat, South Africa. ^{T} indicates ex-type strains.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *gapdh*: partial glyceraldehyde-3-phosphate dehydrogenase gene; *rpb2*: partial DNA-directed RNA polymerase II second largest subunit gene; *tef1*: partial translation elongation factor 1-alpha gene; *ATPase*: partial plasma membrane ATPase gene.

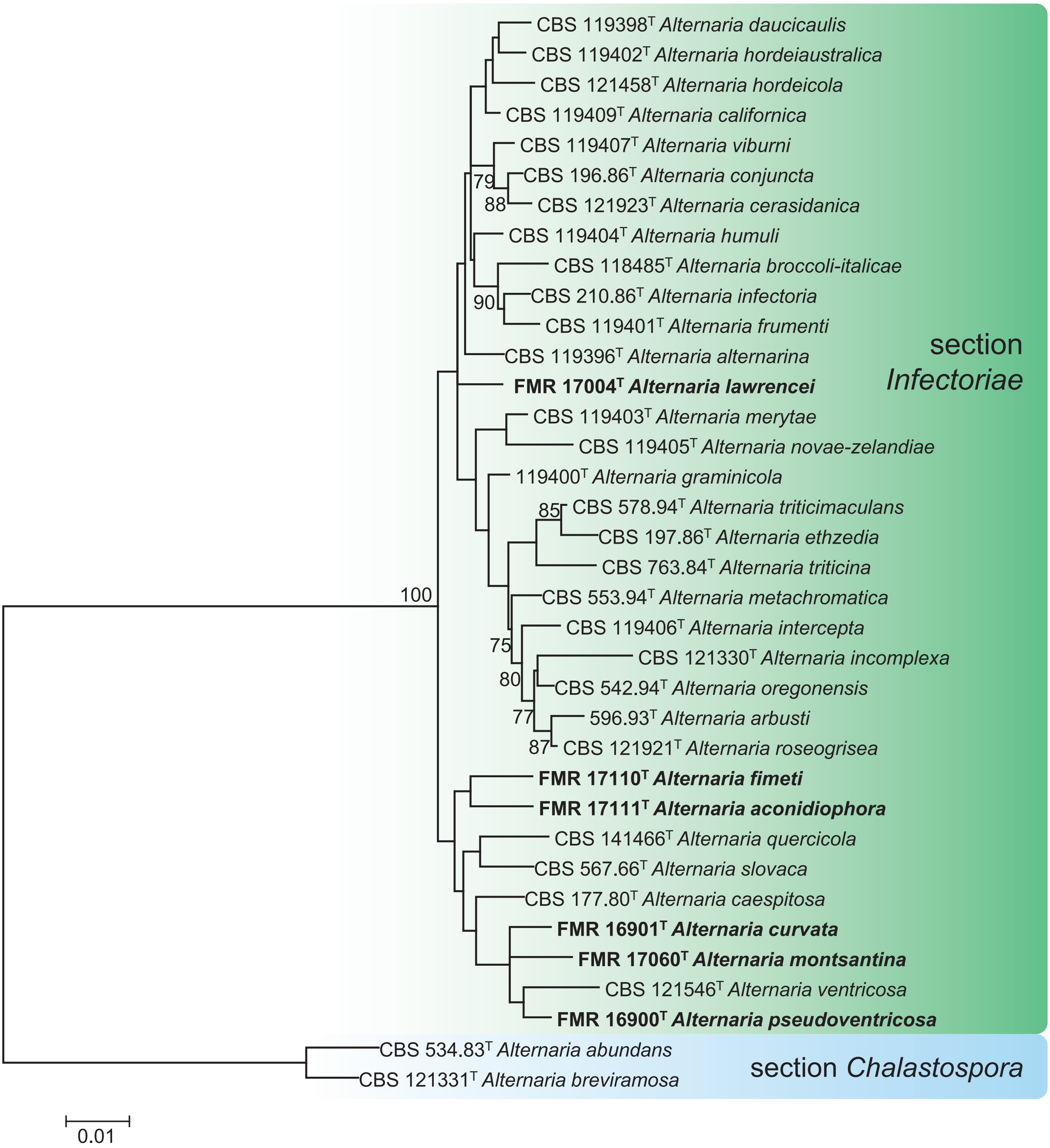

Fig. 5. Maximum Likelihood (ML) tree constructed with ITS (529 bp), *ATPase* (1180 bp), *gapdh* (489 bp), *rpb2* (573 bp) and *tef1* (239 bp) sequences of ex-type strains of the species in section *Infectoriae*. The phylogenetic tree was rooted to *Alternaria abundans* CBS 534.83 and *Alternaria breviramosa* CBS 121331 (section *Chalastospora*). Bootstrap support values above 70 % are shown at the nodes. GenBank accession numbers are indicated in Table 2. The novel species described in this study are indicated in **bold**. ^{T} indicates ex-type strain. TreeBASE: S23786.

seed-borne species may attack seedlings, resulting in damping-off, stem lesions or collar rot; sunken and dark lesions are present in roots, tubers, stems and fruits infections; some rots and decay are typical symptoms of post-harvest diseases (Laemmlen 2001, Thomma 2003, Lawrence *et al.* 2008). Phytotoxins are also produced during the invasion process as virulence factors which affect a wide spectrum of plant species. *Alternaria* toxins diffuse into host tissues resulting in a chlorotic or yellow halo around lesions, exacerbating the severity of the symptoms (Singh *et al.* 2015).

Notes: *Alternaria* is characterised mainly by its asexual morph with darkly pigmented multi-celled conidia, which are typically dictyosporous, some phragmosporous, and arranged single or in chains on the conidiophore. Some of these morphological features can also be observed in other closely related genera such as *Paradendryphiella* (Woudenberg *et al.* 2013) or *Stemphylium* (Woudenberg *et al.* 2017). However, *Paradendryphiella* mainly differs by its denticulate conidiogenous cells with prominent conidial scars aggregated at the apex of simple or branched conidiophores, and *Stemphylium* by showing

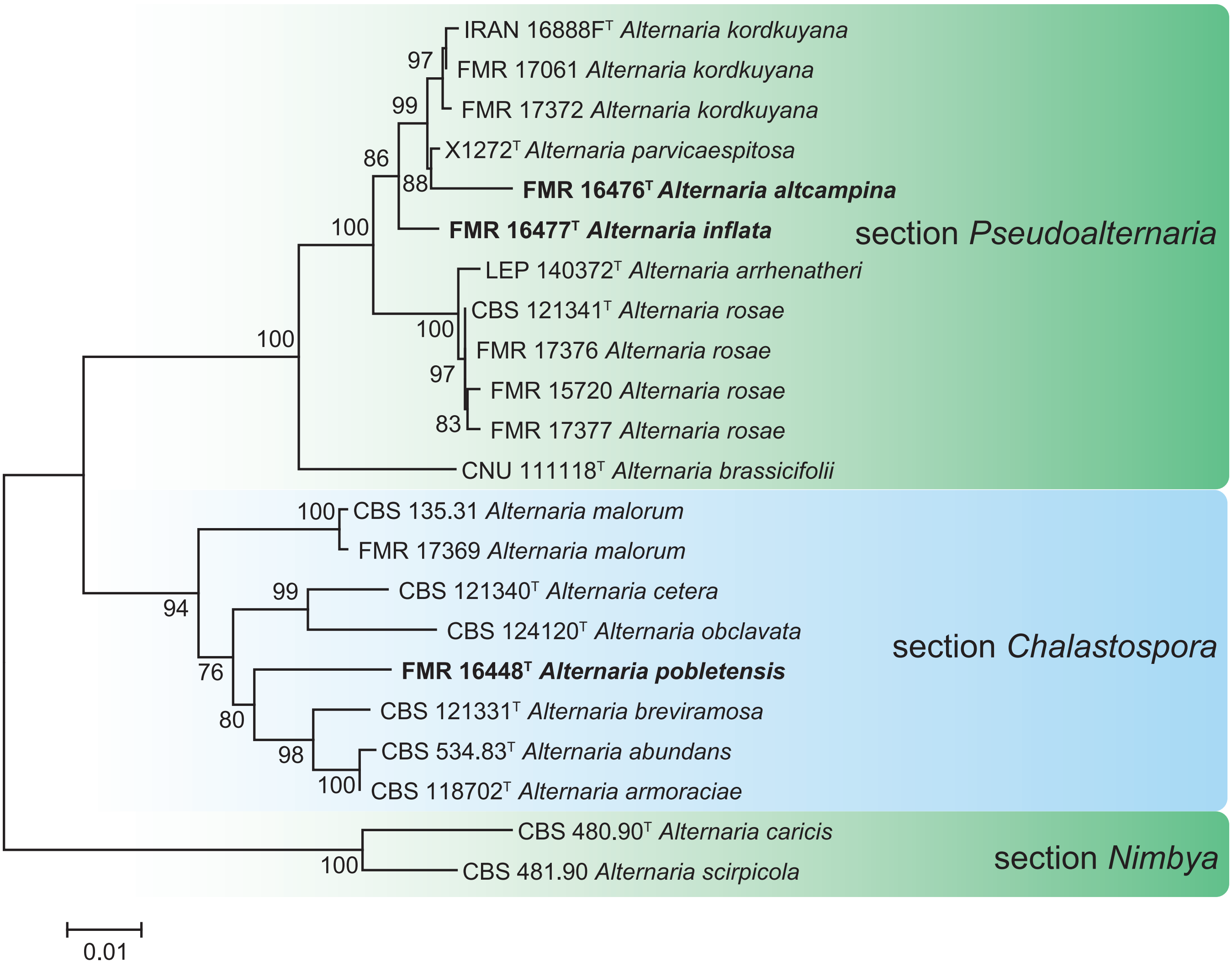

Fig. 6. Maximum Likelihood (ML) tree constructed with ITS (576 bp), *ATPase* (1198 bp) and *gapdh* (491 bp) sequences of ex-type strains of species in the sections *Pseudoalternaria* and *Chalastospora*. The phylogenetic tree was rooted to *Alternaria caricis* CBS 480.90 and *A. scirpicola* CBS 481.90 (section *Nimbya*). Bootstrap support values above 70 % are shown at the nodes. GenBank accession numbers are indicated in Table 2. The novel species described in this study are indicated in **bold**. ^{T} indicates ex-type strain. TreeBASE: S23787.

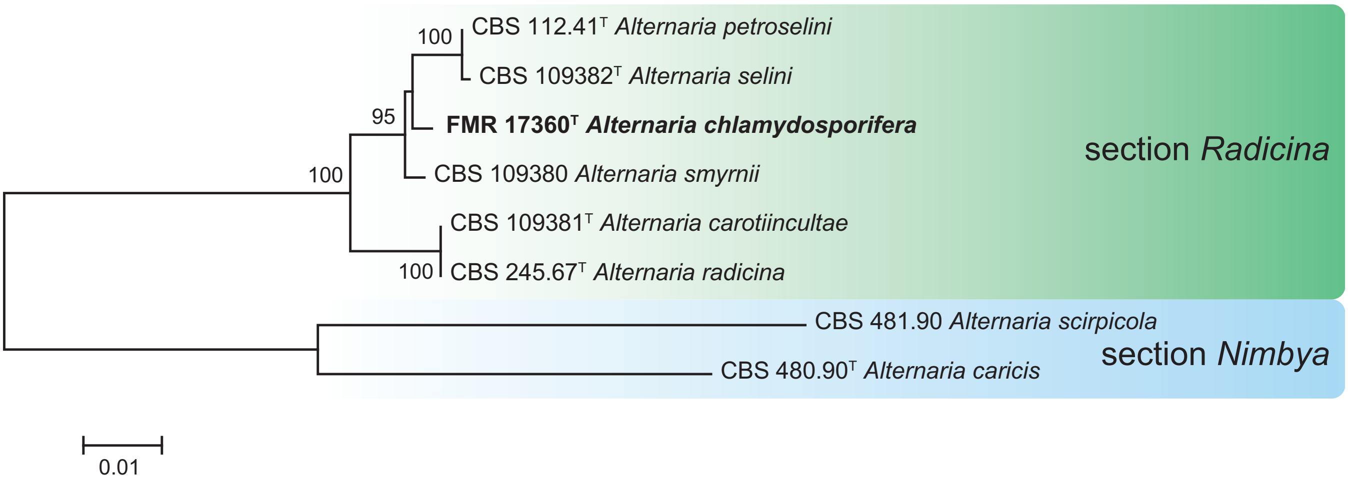

Fig. 7. Maximum Likelihood (ML) tree constructed with ITS (523 bp), *gapdh* (503 bp), *rpb2* (860 bp) and *tef1* (247 bp) sequences of ex-type strains of species in section *Radicina*. The phylogenetic tree was rooted to *Alternaria caricis* CBS 480.90 and *A. scirpicola* CBS 481.90 (section *Nimbya*). Bootstrap support values above 70 % are shown at the nodes. GenBank accession numbers are indicated in Table 2. The novel species described in this study are indicated in **bold**. ^{T} indicates ex-type strain. TreeBASE: S23788.

percurrent conidiophores with apically swollen conidiogenous cells.

Extensive morphological investigations of the genus *Alternaria* were carried out by Emory G. Simmons, which culminated with his monograph on *Alternaria* species identification (Simmons 2007). Based on the sporulation patterns and conidial morphology, he described several *Alternaria* species-groups which were typified by representative species (Simmons 1992). In recent years, based on molecular phylogenetic approaches using DNA sequence data, it has been shown that the main morphological groups identified by Simmons represent monophyletic species groups. Lawrence *et al.* (2013) provided the first strongly supported phylogenetic hypothesis among *Alternaria* lineages and elevated several of those monophyletic species groups to the taxonomic status of sections, each with a type species. Successive phylogenetic investigations added additional sections within the genus by synonymising genera such as *Allewia, Brachycladium, Chalastospora, Chmelia, Crivellia, Embellisia, Nimbya, Pseudoalternaria, Sinomyces, Teretispora, Ulocladium, Undiphilum* and *Ybotromyces* (Woudenberg *et al.* 2013, 2014, Lawrence *et al.* 2016). Therefore, the genus *Alternaria* currently comprises close to 280 species, most of them classified in 27 sections. Taxonomic traits and species composition of all *Alternaria* sections are summarised in Lawrence *et al.* (2016).

Considering, however, the overlap of morphological traits among *Alternaria* sections/species and that the culture conditions can greatly influence the morphology of these fungi, molecular identification is practically mandatory for the classification of *Alternaria* isolates. Although the ITS barcode is considered a good phylogenetic marker to define sections, it has limited discriminatory power to distinguish species, making multi-locus sequence analysis with several protein-coding loci essential for accurate species identification. While Woudenberg *et al.* (2013), in addition to the nrDNA regions, used the combination of *gapdh*, *rpb2* and *tef1* loci for redefining the genus, the combination of other phylogenetic markers has since been analysed to determine relationships and species delineation in studies on a particular section; *i.e.* ITS, *Alt a-1*, *endoPG, gapdh*, OPA10-2, *rpb*2 and *tef1* for section *Alternaria* (Woudenberg et al. 2015); ITS, *ATPase*, *tef1* and *gapdh* for sections *Infectoriae* and *Pseudoalternaria* (Andersen *et al.* 2009, Deng *et al.* 2018, Poursafar *et al.* 2018); ITS, *Alt a-1*, *gapdh*, *rpb2* and *tef1* for section *Porri* (Woudenberg *et al.* 2014); and ITS, *Alt a-1* and *gapdh* for section *Sonchi* (Lawrence *et al.* 2012, Deng *et al.* 2014). Nevertheless, according to Lawrence *et al.* (2013) the plasma membrane *ATPase*, *cmdA*, and *Alt a-1* loci are the most informative markers for *Alternaria* species delimitation. However, considering that the latter locus unreliably amplifies some species within sect. *Infectoriae*, they suggested that the most suitable genetic markers for molecular identification at the species level are *ATPase* and *cmdA* genes (Lawrence *et al.* 2013, 2016). Unfortunately, the latter marker has not been used for the phylogeny of any of the above-mentioned sections.

Alternaria is a very successful pathogenic genus that causes disease on a great number of economically important plants, causing large economic losses due to the number of plant species affected and worldwide distributions of several *Alternaria* species (Meena *et al.* 2017). They are commonly described causing stem canker, leaf blight or leaf spot on a large variety of crops, including cereals, ornamentals, oil crops, vegetables such as broccoli, cauliflower, carrot, onion and potato, and fruits like apple, citrus, pear and strawberry, among others. Species in section *Alternaria*, such as *A. alternata*, *A. arborescens* or *A. tenuissima*, as well as others from sections *Alternantherae*, *Brassiccicola*, *Crivellia*, *Gypsophilae*, *Nimbya*, *Radicina* or *Sonchi,* are frequently reported causing such diseases, but the largest group of phytopathogens in the genus is concentrated in section *Porri* (Lawrence *et al.* 2016, Meena *et al.* 2017). The most relevant plant pathogens in this latter section are *A. bataticola, A. porri, A. solani* and *A. tomatophila* (Woudenberg *et al.* 2014). *Alternaria* species also produce diverse phytotoxins, which affect their host plants at different stages of pathogenesis (Thomma 2003, Lawrence *et al.* 2008, Meena *et al.* 2017). Some of these phytotoxins have been evaluated by the European Food Safety Authority as potentially causing risks to human health (Meena *et al.* 2017).

In humans, *Alternaria* species are commonly associated with hypersensitivity pneumonitis, bronchial asthma, allergic sinusitis and rhinitis. To a lesser extent, they have been also described as causing paranasal sinusitis, ocular infections, onychomycosis, cutaneous and subcutaneous infections, granulomatous pulmonary disease, soft palate perforation and disseminated disease (Pastor & Guarro 2008, de Hoog *et al.* 2011).

In several surveys of microfungi from Spanish regions with different climates and biodiversity, samples of plant litter (leaves, bark and twigs) and dung of wild and farm herbivore animals (rabbits, rodents, goats, cattle and horses) were collected. From these samples, we found 16 interesting *Alternaria* isolates, belonging to sections *Infectoriae*, *Pseudoalternaria*, *Chalastospora* and *Radicina*. The multi-locus phylogenetic analysis based on five above-mentioned gene markers showed that 10 of them were undescribed species for the genus, and the others were identified as *A. kourtkuyana*, *A. rosae* and *A. malorum* (Figs 5–7). Most of these novel species have been isolated from herbivore dung, which appear to represent a reservoir of interesting *Alternaria* species which could represent potential plant pathogens.

References: Ellis 1976, Simmons 2007 (morphology); Laemmlen 2001, Thomma 2003, Lawrence *et al.* 2008, Meena *et al.* 2017 (plant infections); Pastor & Guarro 2008, de Hoog *et al.* 2011 (human infections); Woudenberg *et al.* 2013, 2014, 2015, Grum-Grzhimaylo *et al.* 2016, Lawrence *et al.* 2016, Poursafar *et al.* 2018 (morphology and phylogeny).

Alternaria aconidiophora Iturrieta-González, Dania García & Gené, ***sp. nov.*** MycoBank MB829626. Fig. 8.

Etymology: Name refers to the lack of conidiophores from vegetative hyphae.

Asexual morph on PCA: *Mycelium* superficial and immersed. *Hyphae* 1–4 µm wide, septate, branched, hyaline to greyish, smooth-walled. *Conidiophores* absent. *Conidiogenous loci* inconspicuous on vegetative hyphae, scarce. *Conidia* commonly solitary at centre of the colony, globose, ovoid, near ellipsoid or obclavate, 12–31 × 7–12 µm, with some darkened middle transverse septa, 1–5 transverse, 0–1(–2) longitudinal or oblique septa per transverse segment, brown, smooth-walled. *Secondary conidiophores* present, may be formed apically from the conidial body as a short extension often geniculate, with one or two, terminal or subterminal conidiogenous loci. *Sexual morph* not observed.

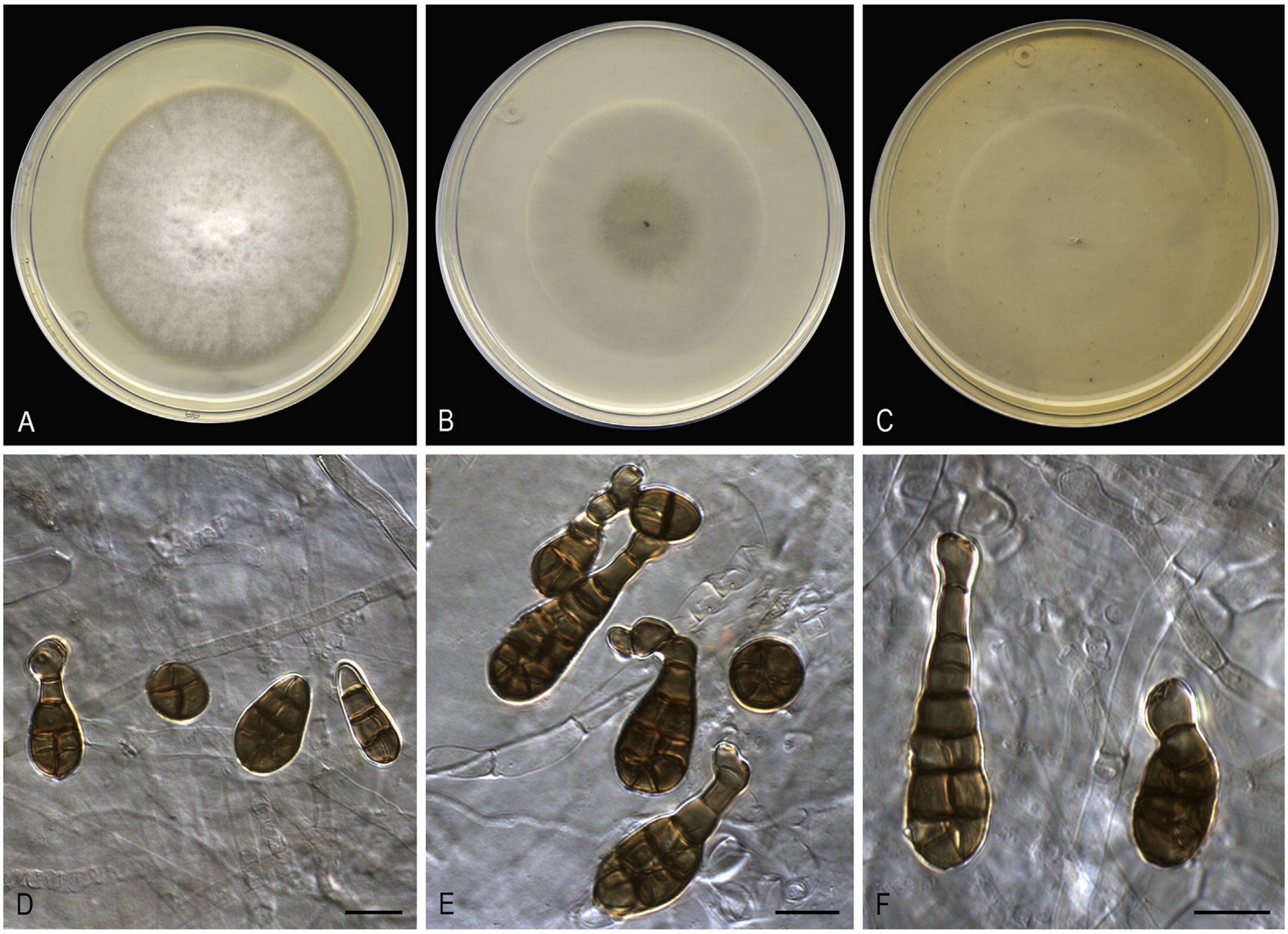

Fig. 8. *Alternaria aconidiophora* (ex-type FMR 17111). **A.** Colonies on PDA. **B.** Colonies on PCA. **C.** Colonies on OA. **D–F.** Conidia. Scale bars = 10 µm.

Culture characteristics: Colonies on PDA reaching 64 mm diam after 1 wk at 25 °C, flat, cottony at centre, slightly radially folded towards the periphery, aerial mycelium abundant, margins regular; surface white (1A1); reverse yellowish white (4A2). On PCA attaining 54 mm diam, flat, aerial mycelium scarce, margins regular; surface greyish green to greenish grey (1D3/1B1); reverse greenish grey (1C2/1B1). On OA reaching 61 mm diam, flat, aerial mycelium scarce, margins regular; surface and reverse colourless.

Cardinal temperature for growth: Optimum 25 °C, maximum 37 °C, minimum 5 °C.

Typus: **Spain**, Catalonia, Alta Ribagorça, Vall de Boí, isolated from forest leaf litter, Dec. 2017, J. Gené (**holotype** CBS H-23891, culture ex-type CBS 145419 = FMR 17111).

Notes: *Alternaria aconidiophora* together with *A. fimeti*, both species introduced here from herbivore dung, are placed in an unsupported clade in *Alternaria* section *Infectoriae* (Fig. 5). Morphologically, the latter differs from *A. aconidiophora* in having conspicuous sporulation with well-differentiated conidiophores and verrucose conidia up to 44 µm long. The conidia of *A. aconidiophora* are smooth-walled and 12–31 µm long.

Alternaria altcampina Iturrieta-González, Dania García & Gené, ***sp. nov.*** MycoBank MB829627. Fig. 9.

Etymology: Name refers to the region of Alt Camp (Catalonia), from where the fungus was collected.

Asexual morph on PCA: *Mycelium* superficial and immersed. *Hyphae* 2–4 µm wide, branched, pale yellowish brown to brown, septate, smooth-walled to verruculose. *Conidiophores* macronematous, arising laterally or terminally from aerial hyphae, erect to slightly flexuous, unbranched, occasionally branched, up to 10-septate, 12–88 × 3–4 µm, brown becoming pale towards apex, smooth-walled, with 1 terminal and up to 3 subterminal conidiogenous loci. *Conidia* in branched chains, occasionally solitary, ovoid, obclaviform, ellipsoidal or somewhat cylindrical, 9–43 × 6–8 µm, with darkened middle transverse septa, (1–)2–3(–6) transverse, 0–1 longitudinal or oblique septa in up to 4 of the transverse segments, usually inconspicuous, pale yellowish to yellowish brown, verrucose. *Secondary conidiophores* commonly formed apically as a beak from conidial body, or as a lateral conidiogenous loci from body cells bearing conidia in short chains. *Sexual morph* not observed.

Culture characteristics: Colonies on PDA reaching 73 mm diam after 1 wk at 25 °C, flat, densely floccose, aerial mycelium abundant, margins fimbriate; surface olive brown to blond (4D3/4C4), white at the periphery; reverse yellowish brown to orange-grey (5E4/5B2). On PCA attaining 66 mm diam, flat, granular, aerial mycelium scarce, margins regular; surface dark green (30F8); reverse dull green (30E4). On OA reaching 70 mm diam, flat, loosely floccose at centre, aerial mycelium scarce, margins regular; surface dark green (28F4); reverse dull green (29E3).

Cardinal temperature for growth: Optimum 25 °C, maximum 37 °C, minimum 5 °C.

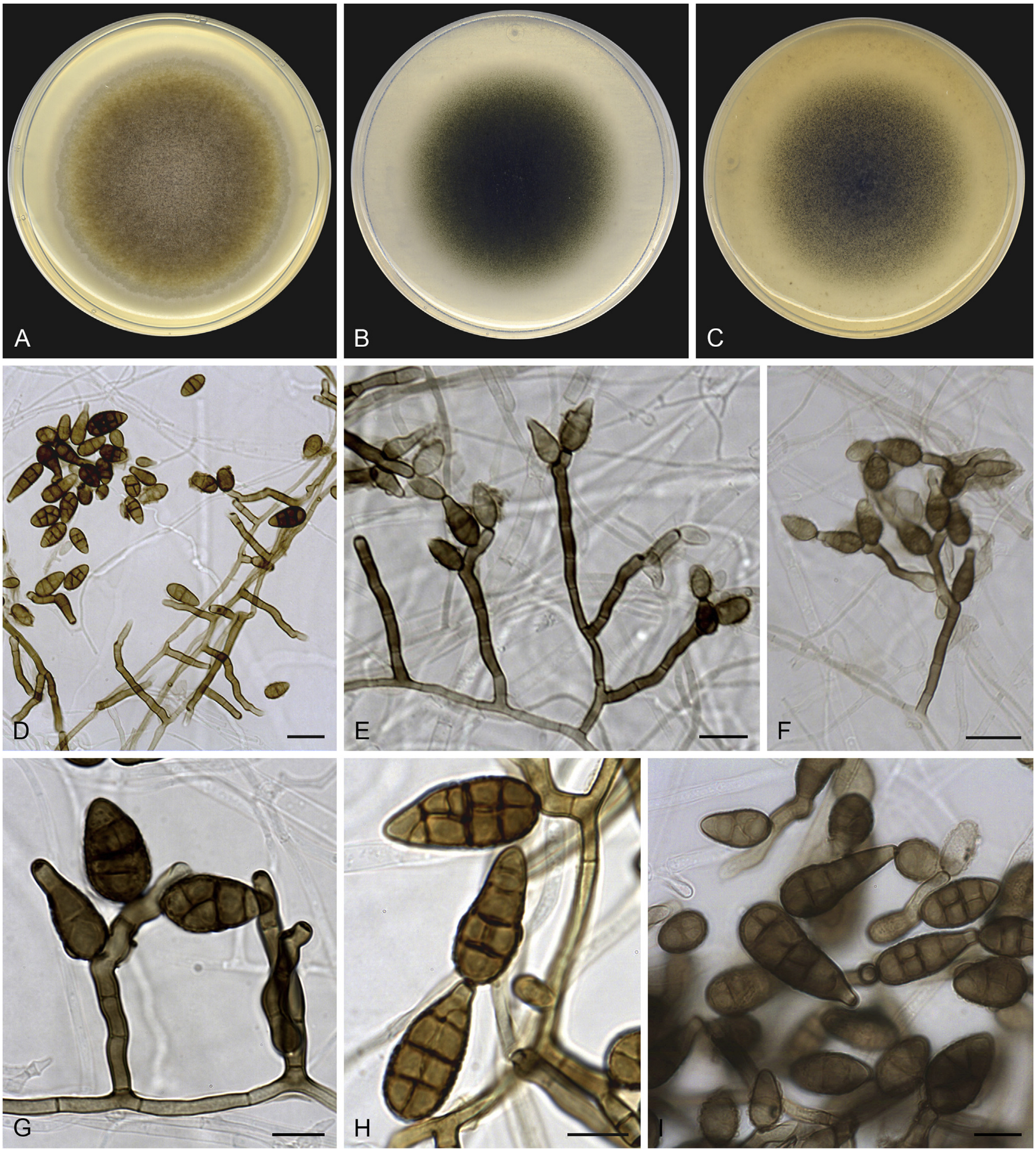

Fig. 9. *Alternaria altcampina* (ex-type FMR 16476). **A.** Colonies on PDA. **B.** Colonies on PCA. **C.** Colonies on OA. **D–I.** Conidiophores and conidia. Scale bars: D–E = 20 µm; F–I = 10 µm.

Typus: **Spain**, Catalonia, Alt Camp, isolated from goat dung, Mar. 2017, I. Iturrieta-González, M. Guevara-Suarez & J. Guarro (**holotype** CBS H-23892, culture ex-type CBS 145420 = FMR 16476).

Notes: Based on the phylogeny of ITS, *ATPase* and *gapdh*, *A. altcampina* is classified in *Alternaria* section *Pseudoalternaria* (Fig. 6). It is closely related to the recently described species *A. parvicaespitosa,* which was isolated from harvested blueberry fruit (California, USA), and *A. kordkuyana*, isolated from symptomatic wheat heads of *Triticum aestivum* (Kordkuy, Iran). *Alternaria parvicaespitosa* differs in having smaller conidia (10–25 × 7–12 µm) with smooth to slightly punctulate outer walls (Gannibal & Lawrence 2016), and *A. kordkuyana* by its larger conidia [30–50(–60) × 7–11 µm] and shorter conidiophores (10–40 × 3–4 µm) (Poursafar *et al.* 2018).

Alternaria chlamydosporifera Iturrieta-González, Dania García & Gené, ***sp. nov.*** MycoBank MB829628. Fig. 10.

Etymology: Name refers to the production of abundant chlamydospores in culture.

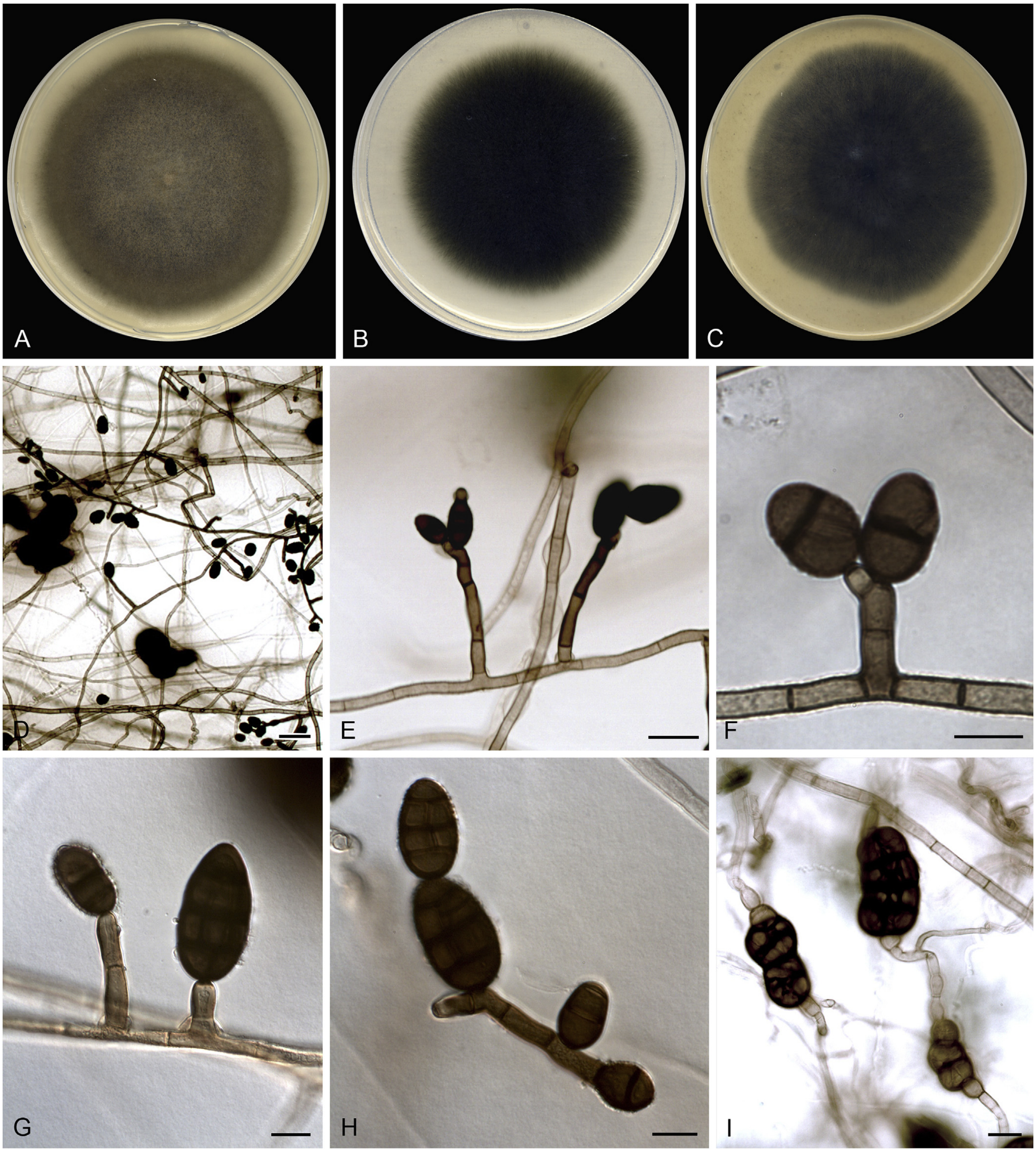

Fig. 10. *Alternaria chlamydosporifera* (ex-type FMR 17360). **A.** Colonies on PDA. **B.** Colonies on PCA. **C.** Colonies on OA. **D–H.** Conidiophores and conidia. **I.** Chlamydospores. Scale bars: D = 50 µm; E, I = 20 µm; F–H = 10 µm.

Asexual morph on PCA: *Mycelium* superficial and immersed. *Hyphae* 3–6 µm wide, septate, branched, pale brown to brown, smooth-walled. *Conidiophores* macronematous, arising directly from aerial hyphae, erect to slightly flexuous, occasionally geniculate at apex, 1–4-septate, unbranched or scarcely branched, 14–140 × 3–5 µm, dark brown, verruculose, with 1–2 conidiogenous loci. *Conidia* mostly solitary, occasionally in short chains with up to two conidia, ellipsoidal or ovoid, occasionally subglobose, 12–41 × 7–20 µm, with darkened middle transverse septa, 1–3(–4) transverse, and 0–1(–2) longitudinal septa per transverse segments, brown to dark brown, verruculose. *Secondary conidiophores* can be formed apically from conidial body as a beak, geniculate, with 1–3 terminal or lateral conidiogenous loci, bearing solitary or short chains of conidia. *Chlamydospores* abundant, immersed, intercalary, irregular shape, rarely broadly ellipsoidal or clavate, muriform, sometimes showing central constriction, 60–91 × 32–57 µm, dark brown to black. *Sexual morph* not observed.

Culture characteristics: Colonies on PDA reaching 82 mm diam after 1 wk at 25 °C, flat, densely floccose, aerial mycelium abundant, margins regular; surface greyish brown (5E3); reverse black to greyish brown (5E3). On PCA attaining 68 mm diam, flat, with granular appearance by the presence of abundant chlamydospores, aerial mycelium scarce, margins regular; surface dark green (29F5); reverse dark green (30F8). On OA reaching 71 mm diam, flat, loosely floccose at centre, slightly granular towards the periphery, aerial mycelium scarce, margins slightly lobate; surface dark green (29F4); reverse dark green (29F4).

Cardinal temperature for growth: Optimum 25 °C, maximum 37 °C, minimum 5 °C.

Typus: **Spain**, Huesca, Baells, isolated from rabbit dung, Apr. 2018, G. Sisó & D. García (**holotype** CBS H-23893, culture ex-type CBS 145421 = FMR 17360).

Notes: *Alternaria chlamydosporifera* belongs to *Alternaria* section *Radicina* (Fig. 7). It is included in a well-supported clade (95 % BS) with *A. petroselini, A. selini* and *A. smyrnii*, which are pathogens of *Apiaceae* (Lawrence *et al.* 2016). *Alternaria petroselini* and *A. selini* can be easily differentiated by the lack of chlamydospores in culture and their larger (50–66 µm in *A. petroselini vs.* 48–65 µm in *A. selini*) and usually ellipsoidal conidia (Simmons 1995). Although *A. smyrnii*, the closest relative to *A. chlamydosporifera*, has been described as producing sclerotial knots in culture that are able to form fertile conidiophores, its conidia are considerably longer (67–96 µm) (Simmons 1995) than those of *A. chlamydosporifera* (12–41 µm long). In addition, we have never observed conidiophores associated with the chlamydospores of the latter species.

Alternaria curvata Iturrieta-González, Dania García & Gené, ***sp. nov.*** MycoBank MB829628. Fig. 11.

Etymology: Name refers to the presence of curved conidia.

Asexual morph on PCA: *Mycelium* superficial and immersed. *Hyphae* 2–6 µm wide, septate, branched, hyaline to yellowish brown to brown, smooth-walled to verruculose. *Conidiophores* macronematous, arising laterally or terminally from aerial hyphae, erect to slightly flexuous, usually unbranched, up to 14-septate, 23–80 × 3–5 µm, brown to dark brown, smooth-walled, with a terminal or occasionally a sub-terminal conidiogenous loci. *Conidia* forming branched chains, with up to 5 conidia in unbranched part, ovoid or nearly ellipsoidal, often slightly curved, 13–47(–70) × 4–16 µm, with darkened middle transverse septa, (0–)1–5(–7) transverse, and 0–2(–3) longitudinal or oblique septa per transverse segment, brown to dark brown, verrucose to tuberculate. *Secondary conidiophores* can be formed apically or laterally from the conidial body as a short extension bearing conidia in short chains. *Sexual morph* not observed.

Culture characteristics: Colonies on PDA reaching 63 mm diam after 1 wk at 25 °C, flat, densely floccose, aerial mycelium abundant, margins regular; surface white to dull green (1A1/30D4); reverse dark green to olive yellow (30F8/2D6), white at the periphery. On PCA attaining 62 mm diam, flat, loosely floccose, aerial mycelium scarce, margins regular; surface olive (3F4); reverse dark green to grey (29F4/29B1). On OA reaching 61 mm diam, scarce aerial mycelium towards the periphery, margins regular; surface greyish green (30E5), with greyish mycelium tufts at centre; reverse dull green (29E4).

Cardinal temperature for growth: Optimum 25 °C, maximum 37 °C, minimum 5 °C.

Typus: **Spain**, Catalonia, Tarragona, Els Ports Natural Park, isolated from goat dung, Oct. 2017, G. Sisó & C. González-García (**holotype** CBS H-23894, culture ex-type CBS 145422 = FMR 16901).

Notes: *Alternaria curvata* was included in the section *Infectoriae*, forming an unsupported basal clade together with *A. montsantina* and *A. pseudoventricosa*, both introduced here, and *A. ventricosa* (Fig. 5). Morphologically, the former two species differ from *A. curvata* in lacking curved conidia. *Alternaria ventricosa* has asymmetrical conidia, due to the hyperplasia and hypertrophy of cells, especially on one side of the conidia (Roberts 2007). Other morphologically similar species are *A. fimeti* and *A. triticina*, which also have curved conidia. However, *A. triticina* is phylogenetically more distant and its conidia are strongly inequilateral and wider (up to 22 µm) (Simmons 2007) than those of *A. curvata* (4–16 µm wide). *Alternaria fimeti* can be differentiated from *A. curvata* by the production of longer conidiophores (22–182 µm in *A. fimeti vs.* 23–80 µm in *A. curvata*) and the absence or scarce development of secondary conidiophores.

Alternaria fimeti Iturrieta-González, Dania García & Gené, ***sp. nov.*** MycoBank MB829630. Fig. 12.

Etymology: Name refers to the substrate where the species was isolated, herbivore dung.

Asexual morph on PCA: *Mycelium* superficial and immersed. *Hyphae* 2–5 µm wide, septate, branched, hyaline to subhyaline to pale yellowish, verruculose. *Conidiophores* semi- to macronematous, arising laterally or terminally from aerial hyphae, erect to slightly flexuous, unbranched (can be slightly branched on OA), up to 9-septate, 22–182 × 1–5 µm, pale brown, smooth-walled, with 1 terminal conidiogenous locus. *Conidia* solitary or in short chains of up to six conidia, ovoid, obpyriform or obclavate, some slightly curved, 9–44 × 5–14(–23) µm, with darkened middle transverse septa, 0–5 transverse (up to 7 in OA), and 0–1(–2) longitudinal or oblique septa per segment, brown, verrucose. *Secondary conidiophores* only scarcely produced on OA as apical or lateral extension from conidial body, up to 25 µm long. *Sexual morph* not observed.

Culture characteristics: Colonies on PDA reaching 66 mm diam after 1 wk at 25 °C, flat, densely floccose, aerial mycelium abundant, margins fimbriate; surface yellowish grey to yellowish white (3C2/3A2); reverse yellowish brown to light yellow (5E8/4A5). On PCA attaining 65 mm diam, flat, slightly floccose at centre, aerial mycelium scarce, margins regular; surface olive-brown (4F5); reverse olive-brown (4F8/4E4). On OA reaching 64 mm diam, flat, slightly floccose, scarce aerial mycelium, margins regular; surface dull green (30E5) with grey floccose area; reverse dull green (30E4).

Cardinal temperature for growth: Optimum 25 °C, maximum 37 °C, minimum 5 °C.

Typus: **Spain**, Catalonia, Priorat, Montsant Natural Park, Arbolí, isolated from small rodent dung, Feb. 2018, I. Iturrieta-González, E. Carvalho & J. Gené (**holotype** CBS H-23895, culture ex-type CBS 145423 = FMR 17110).

Note: *Alternaria fimeti* is placed in a clade of section *Infectoriae* together with *A. aconidiophora* (see notes of this latter species).

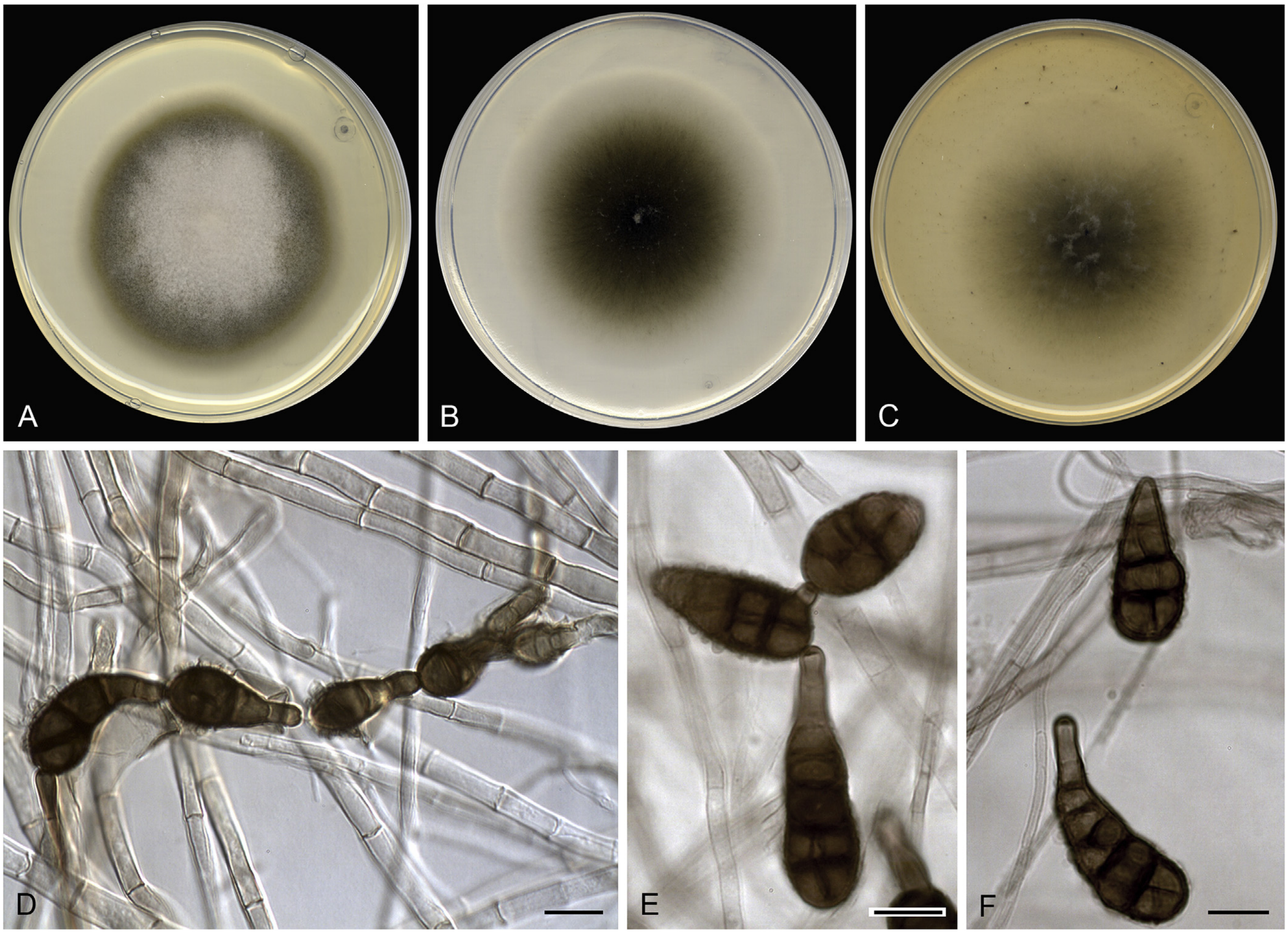

Fig. 11. *Alternaria curvata* (ex-type FMR 16901). **A.** Colonies on PDA. **B.** Colonies on PCA. **C.** Colonies on OA. **D–F.** Conidiophore and conidia. Scale bars = 10 µm.

Alternaria inflata Iturrieta-González, Dania García & Gené, ***sp. nov.*** MycoBank MB829631. Fig. 13.

Etymology: Name refers to the presence of swollen cells in the conidial body.

Asexual morph on PCA: *Mycelium* superficial and immersed. *Hyphae* of 1–3 µm wide, septate, branched, hyaline to pale brown, smooth-walled to verruculose. *Conidiophores* arising laterally or terminally from aerial hyphae, erect to slightly flexuous, semi- to macronematous, up to 10-septate, commonly unbranched, 9–73(–105) × 2–5 µm, pale brown to brown, smooth-walled, with one terminal conidiogenous loci or up to three subterminal conidiogenous loci. *Conidia* solitary or in short chains with up to four conidia, broadly ellipsoidal or ovoid, 13–41 × 5–14 µm, often with some swollen cells protruding the conidium outline, some with darkened middle transverse septa, (1–)2–3(–5) transverse septa, and 0–2 longitudinal or oblique septa per transverse segment, brown, verruculose. *Secondary conidiophores* scarcely produced, as an apical extension up to 15 µm long, bearing conidia in short chains. *Chlamydospores* present, consisting of intercalary, thick-walled, brown swollen cells, up to 8 × 6 µm, arranged in chains or in clusters. *Sexual morph* not observed.

Culture characteristics: Colonies on PDA reaching 62 mm diam after 1 wk at 25 °C, flat, aerial mycelium abundant, floccose, margins fimbriate; surface white (1A1); reverse greyish yellow to yellowish white (4C6/4A2). On PCA attaining 67 mm diam, flat, scarce aerial mycelium, margins regular; surface dull green to grey (30E4/30B1); reverse dark green to grey (30E4/30B1). On OA reaching 61 mm diam, flat, loosely floccose, margins regular; surface pale grey (1B1); reverse pale grey (1B1).

Cardinal temperature for growth: Optimum 25 °C, maximum 37 °C, minimum 5 °C.

Typus: **Spain**, Catalonia, Conca de Barberà, Poblet, isolated from rabbit dung, Mar. 2017, J. Guarro & I. Iturrieta-González (**holotype** CBS H-23896, culture ex-type CBS 145424 = FMR 16477).

Notes: Our phylogeny shows that *A. inflata* belongs to section *Pseudoalternaria* (Fig. 6). It clustered in a well-supported clade (86 % BS) with *A. altcampina*, *A. kordkuyana* and *A. parvicaespitosa,* but formed a single basal lineage representative of a distinct species. *Alternaria inflata* can be differentiated from all the species in the section by the production of chlamydospores and by the formation of broadly ellipsoidal conidia, usually with swollen cells protruding from the conidial body. In addition, *A. altcampina* also differs in the production of secondary conidiophores, *A. parvicaespitosa* in its shorter conidiophores (up to 70 µm) and conidia (10–25 µm) (Gannibal & Lawrence 2016), and *A. kordkuyana* in the production of longer conidial chains [up 5–8(–10) conidia] and conidia measuring 30–50(–60) × 7–11 µm with up to seven transverse septa (Poursafar *et al.* 2018).

Fig. 12. *Alternaria fimeti* (ex-type FMR 17110). **A.** Colonies on PDA. **B.** Colonies on PCA. **C.** Colonies on OA. **D–G.** Conidiophores and conidia. Scale bars: D = 20 µm; E–G = 10 µm.

With the additions of *A. altcampina* and *A. inflata* section *Pseudoalternaria* now comprises seven species. It is of note, however, that most of these taxa are only known from a single collection. In our survey of asexual fungi from herbivore dung, we identified several Spanish isolates belonging to other species in the section, namely *A. kordkuyana* and *A. rosae* (Fig. 6). Considering that most of the species in section *Pseudoalternaria* are mainly associated with herbaceous plants of the families *Brassicaceae, Ericaceae, Poacea* or *Rosaceae,* it is not surprising to find these fungi in faeces of herbivorous animals.

Alternaria lawrencei Iturrieta-González, Dania García & Gené, ***sp. nov.*** MycoBank MB829632. Fig. 14.

Etymology: Name in honour of Daniel P. Lawrence for his contribution to the taxonomy of the genus *Alternaria.*

Asexual morph on PCA: *Mycelium* superficial and immersed. *Hyphae* 1–3 µm wide, septate, branched, pale brown, smooth-walled. *Conidiophores* macronematous, solitary, arising directly from aerial hyphae, erect to slightly flexuous, occasionally geniculate at apex, usually unbranched, up to 10-septate, 9–125 × 3–4(–5) µm, brown, smooth-walled, with 1–2 lateral or terminal conidiogenous loci; *micronematous conidiophores* also present, reduced to intercalary conidiogenous cells with a single conidiogenous locus on hyphae. *Conidia* solitary or in short chains, up to six conidia in the unbranched part, ovoid, obpyriform or obclavate, 6–71 × 7–15 µm, with darkened middle transverse septa, (1–)2–7(–9) transverse, and 0–2(–3) longitudinal or oblique septa, pale brown to brown, verrucose to tuberculate. *Secondary conidiophores* commonly formed apically on conidia as a geniculate extension with several conidiogenous loci, or as lateral extensions from cells of conidial body, up to 35 µm long, producing conidia solitary or in short chains. *Sexual morph* not observed.

Culture characteristics: Colonies on PDA reaching 68 mm diam after 1 wk at 25 °C, low convex, cottony, aerial mycelium abundant, margins regular; surface white (1A1); reverse yellowish brown to greyish yellow (5E7/4B6). On PCA attaining 69 mm diam, low convex, slightly floccose, aerial mycelium relatively abundant at centre, margins regular; surface yellowish grey to olive (2D2/1E3); reverse dark green to olive (30F8/1E3). On OA reaching 63 mm diam, loosely floccose at centre, flat and scarce aerial mycelium towards the periphery, margins regular and diffuse; surface olive (2F4) to olive-grey (2B1); reverse olive to yellowish grey (2F8/2D2).

Cardinal temperature for growth: Optimum 25 °C, maximum 37 °C, minimum 5 °C.

Typus: **Spain**, Catalonia, Tarragona, Els Ports Natural Park, isolated from goat dung, Oct. 2017, G. Sisó & C. González-García (**holotype** CBS H-23897, culture ex-type CBS 145425 = FMR 17004).

Notes: Although *A. lawrencei* is clearly placed in section *Infectoriae*, the multi-locus analysis did not reveal any phylogenetic

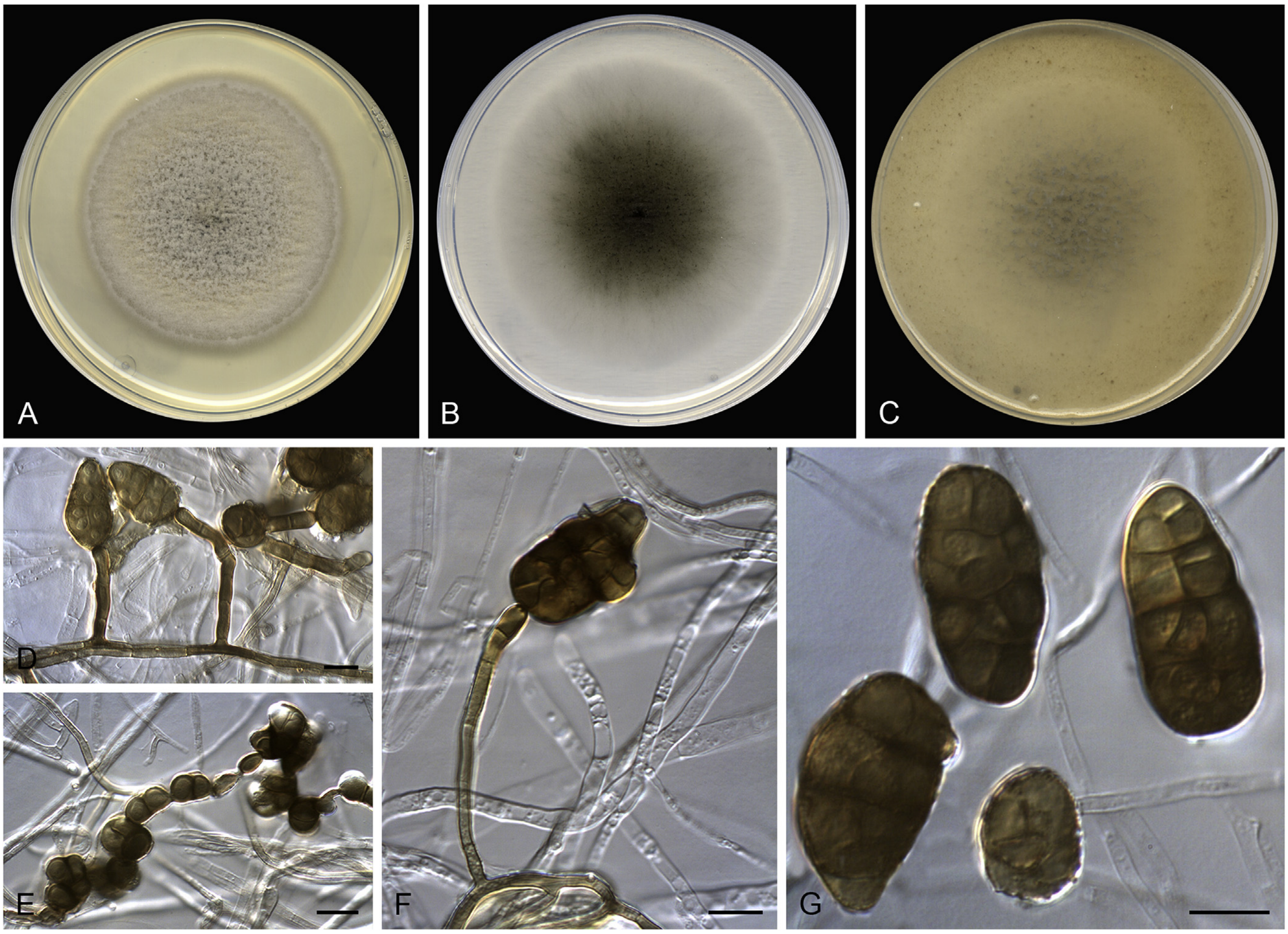

Fig. 13. *Alternaria inflata* (ex-type FMR 16477). **A.** Colonies on PDA. **B.** Colonies on PCA. **C.** Colonies on OA. **D, F–G.** Conidiophores and conidia. **E.** Chlamydospores. Scale bars = 10 µm.

relationship with any species included in the analysis (Fig. 4). It is of note, however, that eight species of the section (*i.e. A. cerasi, A. cesenica*, *A. dactylidicola*, *A. forlicesenensis*, *A. hampshirensis*, *A. litorea*, *A. murispora* and *A. poaceicola*) could not be included in our analysis due to their limited molecular data. Nevertheless, *A. cesenica*, *A. dactylidicola*, *A. forlicesenensis*, *A. hampshirensis*, *A. murispora* and *A. poaceicola* can be distinguished from *A. lawrencei* by the production of a sexual morph (Ariyawansa *et al.* 2015b, Liu *et al.* 2015, Thambugala *et al.* 2017, Wanasinghe *et al.* 2018), *A. cerasi* by its inequilateral conidia (Potebnia 1907, Simmons 2007), and *A. litorea* by the production of shorter primary conidiophores (40–50 µm long) and smooth-walled conidia that are 22–32 µm long (Simmons 2007).

Alternaria montsantina Iturrieta-González, Dania García & Gené, ***sp. nov.*** MycoBank MB829633. Fig. 15.

Etymology: Name refers to the place, Montsant Natural Park (Catalonia), where the fungus was collected.

Asexual morph on PCA: *Mycelium* superficial and immersed. *Hyphae* 1–7 µm wide, septate, branched, usually forming hyphal coils, subhyaline to pale brown, smooth-walled to verruculose. *Conidiophores* macronematous, arising laterally or terminally from aerial hyphae, erect to slightly flexuous, unbranched, up to 15-septate, 12–137 × 3–6 µm, often with geniculate apical portion containing intercalary and terminal conidiogenous loci, brown, smooth-walled to verruculose. *Conidia* solitary or in short chains with up to five conidia, subglobose, ovoid or obpyriform, 8–65 × 6–12 µm, with 1–3(–11) transverse septa, and 0–2 longitudinal or oblique septa, brown, verrucose to tuberculate. *Secondary conidiophores* commonly produced apically as a long, often geniculate extension, up to 105 µm long and 10-septate, bearing terminal conidial chains. *Sexual morph* not observed.

Culture characteristics: Colonies on PDA reaching 76 mm diam after 1 wk at 25 °C, flat, densely floccose, aerial mycelium abundant, margins regular; surface pastel grey to greyish yellow (1C1/2C4) and with a white edge; reverse blond to white (4C4/1A1). On PCA attaining 70 mm diam, flat, loosely floccose at centre, aerial mycelium moderate, margins regular; surface olive brown to white (4D4/1A1); reverse olive to white (3D4/1A1). On OA reaching 75 mm diam, flat, cottony, margins regular; surface yellowish grey to olive (3D2/2F4) and white edge; reverse olive to white (2F4/1A1).

Cardinal temperature for growth: Optimum 25 °C, maximum 37 °C, minimum 5 °C.

Typus: **Spain**, Catalonia, Priorat, Montsant Natural Park, Swamp of Siurana, isolated from an unidentified twig, Feb. 2018, I. Iturrieta-González, E. Carvalho & J. Gené (**holotype** CBS H-23898, culture ex-type CBS 145426 = FMR 17060).

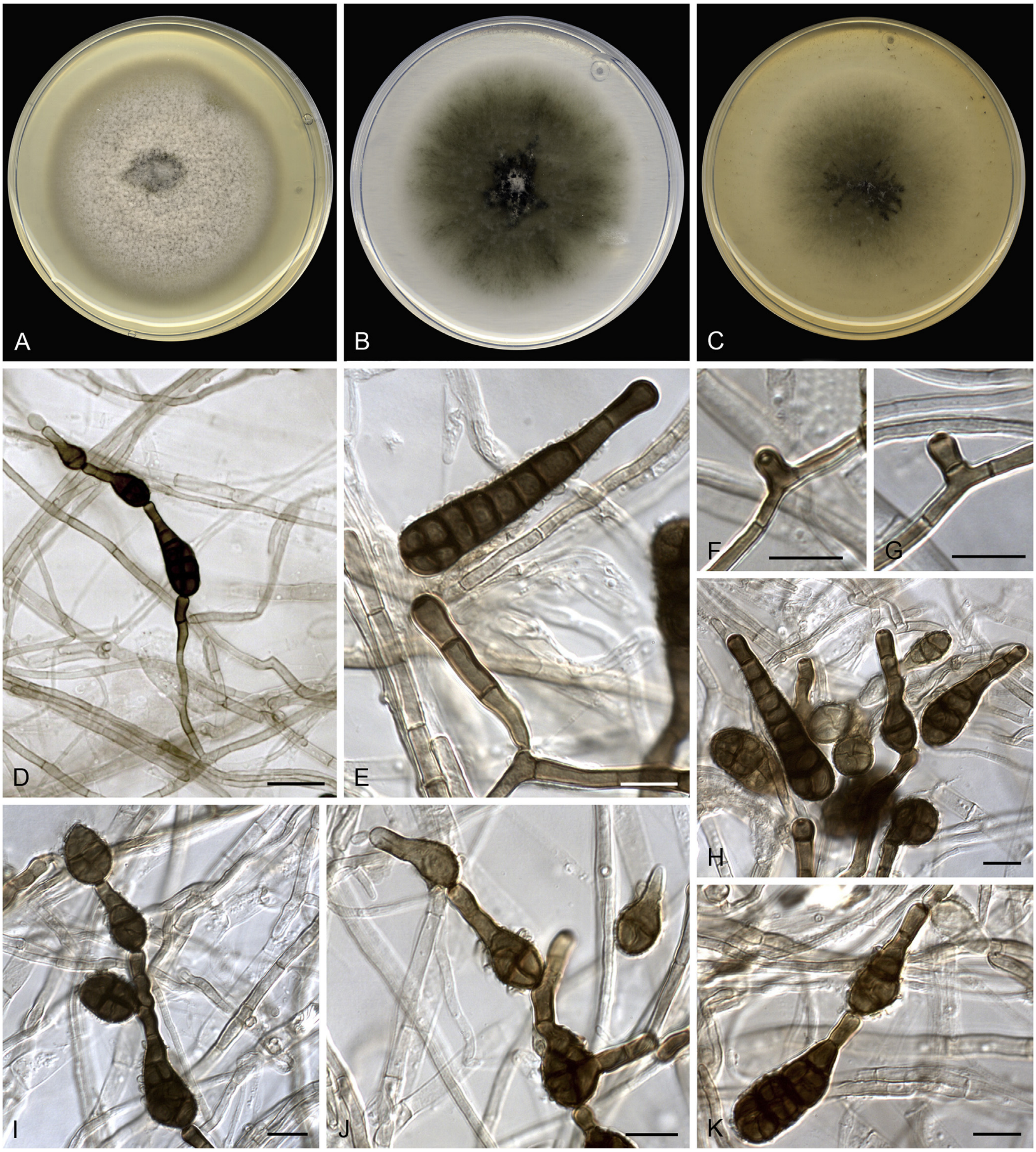

Fig. 14. *Alternaria lawrencei* (ex-type FMR 17004). **A.** Colonies on PDA. **B.** Colonies on PCA. **C.** Colonies on OA. **D–K.** Conidiophores and conidia. Scale bars: D = 20 μm; E–K = 10 μm.

Notes: *Alternaria montsantina* is placed in a weakly supported basal clade of the section *Infectoriae,* together with *A. curvata*, *A. pseudoventricosa* and *A. ventricosa* (Fig. 5). Morphologically, this new species can be distinguished from *A. curvata* and *A. ventricosa* by the absence of curved or inequilateral inflated conidia. *Alternaria montsantina* differs from *A. pseudoventricosa* in the production of longer (12–137 μm) and often geniculate primary and secondary conidiophores, bearing solitary conidia or arranged in short chains (up to five conidia). Conidiophores in *A. pseudoventricosa* are 30–44 μm long, and the conidial chains include up to 19 conidia.

Alternaria pobletensis Iturrieta-González, Dania García & Gené, ***sp. nov.*** MycoBank MB829634. Fig. 16.

Etymology: Name refers to the place, Poblet (Catalonia), from where the species was collected.

Asexual morph on PCA: *Mycelium* superficial and immersed. *Hyphae* 2–5 μm wide, branched, pale brown, septate, smooth-walled. *Conidiophores* semi- to macronematous, solitary, arising directly from aerial hyphae, erect to slightly flexuous, occasionally slightly geniculate at apex, unbranched or branched, up to 8-septate, 14–82 × 4–5(–6) μm, brown,

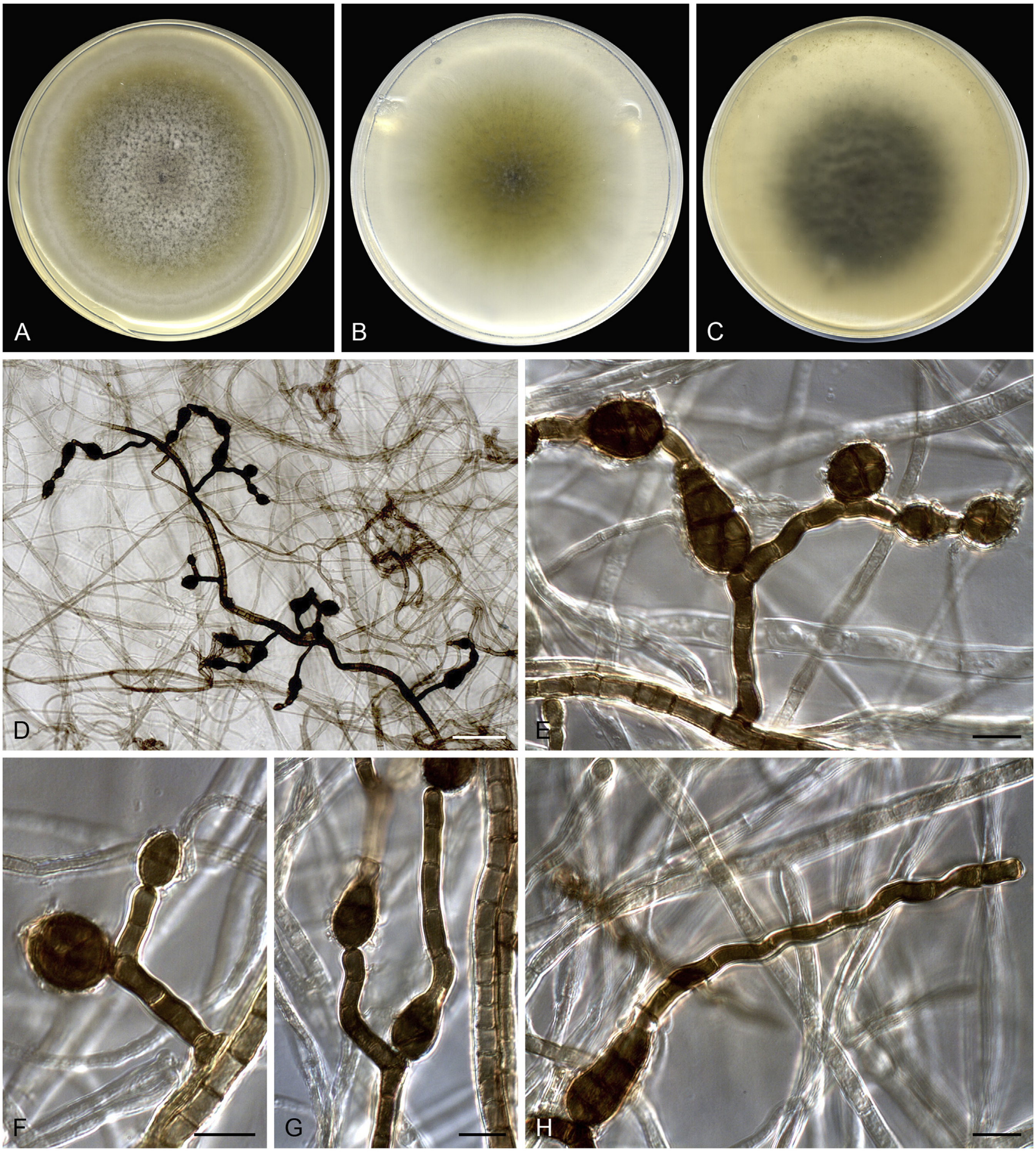

Fig. 15. *Alternaria montsantina* (ex-type FMR 17060). **A.** Colonies on PDA. **B.** Colonies on PCA. **C.** Colonies on OA. **D–H.** Conidiophores and conidia. Scale bars: D = 50 µm; E–H = 10 µm.

smooth-walled, with 1–2 lateral or terminal conidiogenous loci. *Conidia* commonly in short, scarcely branched chains, with up to seven conidia, obpyriform or obclavate, some ellipsoidal or subcylindrical, 8–50 × 5–20 µm, (1–)3–7(–9) transverse septa, often middle septa darker, and 0–1(–2) longitudinal or oblique septa per transverse segment, pale brown to brown, smooth-walled or verruculose. *Secondary conidiophores* commonly produced apically as a short beak up to 11 µm long, or laterally from cells of conidial body, bearing conidia in short chains. *Sexual morph* not observed.

Culture characteristics: Colonies on PDA reaching 46 mm diam after 1 wk at 25 °C, flat, floccose at the centre, velvety towards the periphery, aerial mycelium moderate, margins regular; surface olive (3F8), whitish at the periphery; reverse black to yellowish brown (5D5). On PCA attaining 58 mm diam, flat, velvety, margins regular; surface dark green to dull green (30F8/28D3); reverse dark green to dull green (30F8/28D3). On OA reaching 55 mm diam, flat, loosely floccose, margins regular; surface greyish green to dull green (29C3/29E4); reverse dark green to dull green (30F8/30E3).

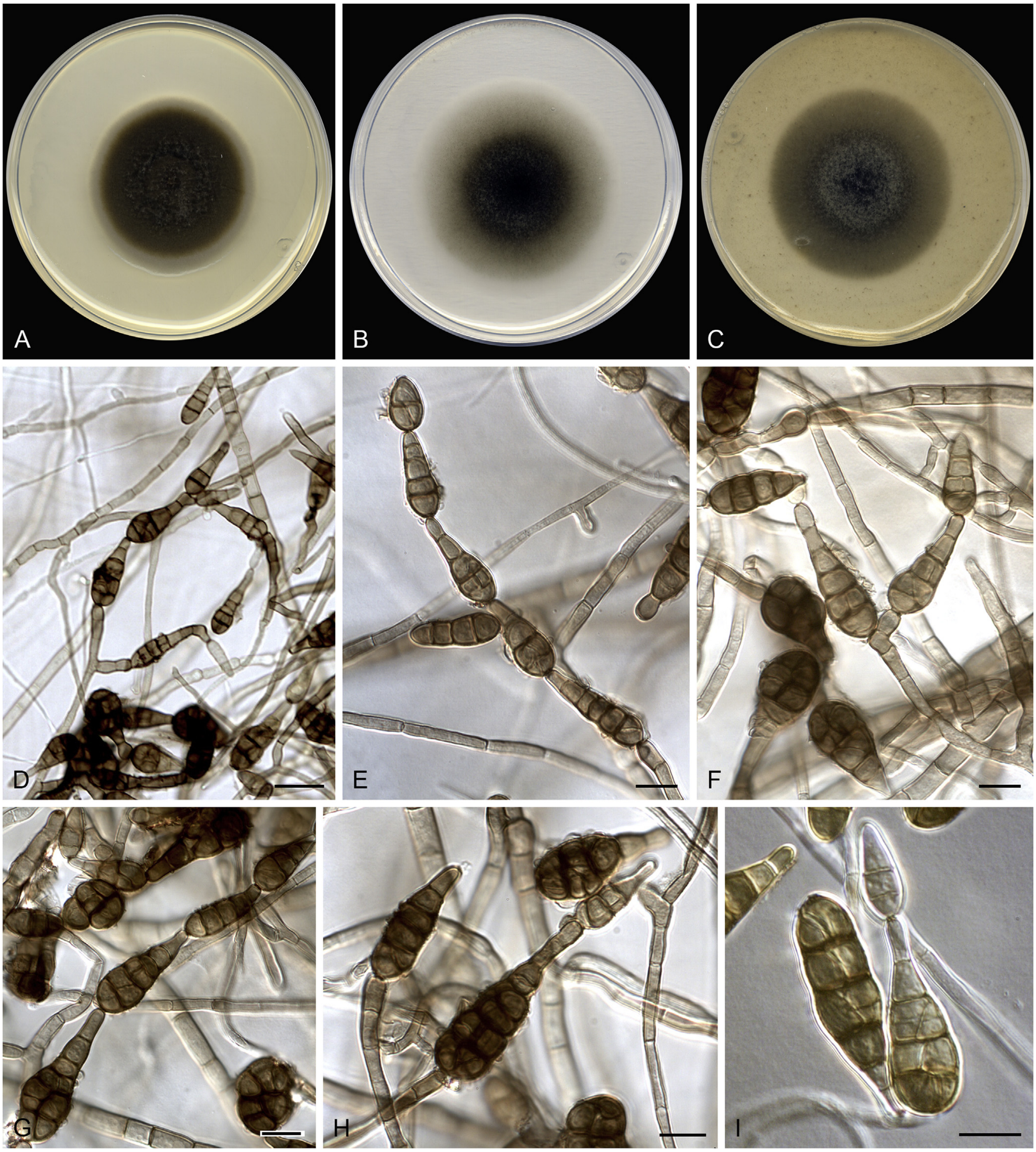

Fig. 16. *Alternaria pobletensis* (ex-type FMR 16448). **A.** Colonies on PDA. **B.** Colonies on PCA. **C.** Colonies on OA. **D–I.** Conidiophores and conidia. Scale bars: D = 20 µm; E–I = 10 µm.

Cardinal temperature for growth: Optimum 25 °C, maximum 35 °C, minimum 5 °C.

Typus: **Spain**, Catalonia, Conca de Barberà, Poblet, isolated from unidentified herbivore dung, Mar. 2017, J. Guarro & I. Iturrieta-González (**holotype** CBS H-23899, culture ex-type CBS 145427 = FMR 16448).

Notes: *Alternaria pobletensis* clustered in section *Chalastospora* in a single branch clearly separated from the other six species that currently comprise the section (Fig. 7). Other species of section *Chalastospora* rarely produce conidia with longitudinal septa (Woudenberg *et al.* 2013); however, the conidia in *A. pobletensis* usually have two or more longitudinal or oblique septa. Its closest relative is *A. breviramosa*. This was originally described as *Chalastospora ellipsoidea*, found on *Triticum* (*Poaceae*) in Australia (Crous *et al.* 2009a), but later its name was changed to avoid confusion with *Alternaria ellipsoidea*, an already described species from section *Gypsophilae* (Woudenberg *et al.* 2013). Section *Gypsophilae* contains all *Alternaria* species that occur on *Caryophyllaceae* (Lawrence *et al.* 2016). *Alternaria breviramosa* differs from *A. pobletensis* by having shorter conidiophores (up to 25 µm), often reduced to conidiogenous cells, and ellipsoidal, subcylindrical to fusoid conidia with only transverse septa (Crous *et al.* 2009a).

Alternaria pseudoventricosa Iturrieta-González, Dania García & Gené, ***sp. nov.*** MycoBank MB829635. Fig. 17.

Etymology: Name refers to the apparent phylogenetic relationship to *A. ventricosa.*

Asexual morph on PCA: *Mycelium* superficial and immersed. *Hyphae* 1–7 µm wide, septate, branched, hyaline to pale brown, smooth-walled. *Conidiophores* macronematous, arising laterally from aerial hyphae, erect to slightly flexuous, up to 4-septate, unbranched, 30–45 × 4–6 µm, brown, smooth-walled, with one terminal conidiogenous locus. *Conidia* commonly in unbranched chains, with up to 19 conidia, obpyriform or obclavate, 10–48(–66) × 5–14 µm, with darkened middle transverse septa, 1–7 transverse, 0–1 longitudinal or oblique septa, brown to dark brown, verrucose to tuberculate. *Secondary conidiophores* scarce, as a beak arising from the conidial body. *Sexual morph* not observed.

Culture characteristics: Colonies on PDA reaching 64 mm diam after 1 wk at 25 °C, flat, cottony at the centre, floccose towards the periphery, margins regular; surface white (1A1); reverse yellowish white (4A2). On PCA attaining 62 mm diam, flat towards the periphery, margins regular; surface dark green (29F4), with tuft of white aerial mycelium at centre; reverse dark green to grey (29F8/29B1). On OA reaching 67 mm diam, flat, loosely floccose, margins regular; surface dull green (29E4); reverse dull green (29E4).

Cardinal temperature for growth: Optimum 25 °C, maximum 37 °C, minimum 5 °C.

Typus: **Spain**, Catalonia, Tarragona, Els Ports Natural Park, isolated from horse dung, Oct. 2017, G. Sisó & C. González-García (**holotype** CBS H-23900, culture ex-type CBS 145428 = FMR 16900).

Notes: *Alternaria pseudoventricosa* and *A. ventricosa* clustered in an unsupported monophyletic basal clade in section *Infectoriae* (Fig. 5). They can be differentiated by their conidial morphology. Conidia in *A. ventricosa* are usually asymmetric, laterally swollen, and pale cinnamon brown (Roberts 2007). In contrast, those of *A. pseudoventricosa* are obpyriform or obclavate and brown to dark brown.

Authors: I. Iturrieta-González, D. García, M. Hernández-Restrepo & J. Gené

Brunneosphaerella Crous, Stud. Mycol. 64: 31. 2009. Fig. 18.

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

Type species: *Brunneosphaerella protearum* (Syd. & P. Syd.) Crous, basionym: *Leptosphaeria protearum* Syd. & P. Syd. Epitype and ex-epitype strain designated by Crous *et al.* (2011): CBS H-20335, CBS 130597 = CPC 16338.

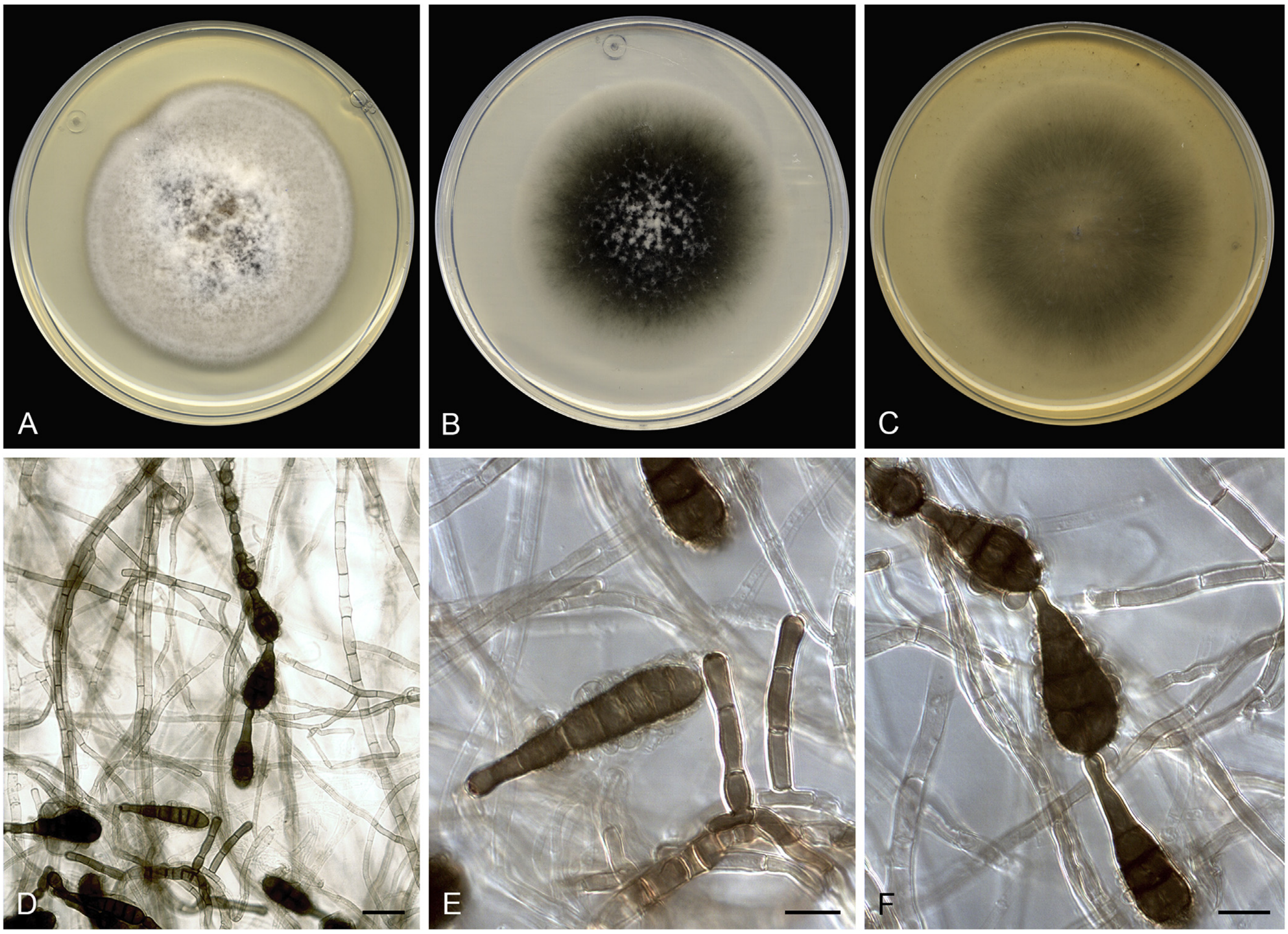

Fig. 17. *Alternaria pseudoventricosa* (ex-type FMR 16900). **A.** Colonies on PDA. **B.** Colonies on PCA. **C.** Colonies on OA. **D–F.** Conidiophores and conidia. Scale bars: D = 20 µm; E, F = 10 µm.

Fig. 18. *Brunneosphaerella* spp. **A–E.** Disease symptoms. **A, B.** *Brunneosphaerella protearum* (epitype CBS H-20335). **C.** *Brunneosphaerella nitidae* (holotype CBS H-20334). **D, E.** Ascomata visible on lesion surface. **D.** *Brunneosphaerella protearum* (CBS H-20335). **E.** *Brunneosphaerella nitidae* (holotype CBS H-20334). **F–H.** Vertical sections through ascomata showing wall structure. **F.** *Brunneosphaerella jonkershoekensis* (holotype PREM 59447). **G, H.** *Brunneosphaerella protearum* (CBS H-20335). **I–M.** Asci. **I.** *Brunneosphaerella jonkershoekensis* (holotype PREM 59447). **J, K.** *Brunneosphaerella nitidae* (holotype CBS H-20334). **L, M.** *Brunneosphaerella protearum* (CBS H-20335). **N–Q.** Ascospores. **N, O.** *Brunneosphaerella jonkershoekensis* (holotype PREM 59447). **P.** *Brunneosphaerella nitidae* (holotype CBS H-20334). **Q.** *Brunneosphaerella protearum* (CBS H-20335). **R, S.** Germinating ascospores. **R.** *Brunneosphaerella nitidae* (holotype CBS H-20334). **S.** *Brunneosphaerella protearum* (CBS H-20335). Scale bars: G = 75 μm; F, I = 50 μm; H, J–M, P–S = 10 μm; N, O = 5 μm. Pictures A, B, D, F–I, L–O, Q, S taken from Crous *et al.* (2009b); C, E, J, K, P, R from Crous *et al.* (2011).

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

Species	Isolates[1]	GenBank accession numbers[2]				References
		ITS	*chs*	*rpb2*	*tef1*	
Brunneosphaerella jonkershoekensis	CPC 13902^{ET}	JN712439	JN712609	MF951441	JN712571	Crous *et al.* (2011), Videira *et al.* (2017)
B. nitidae	CBS 130595^{T}	GU214625	JN712619	MF951442	JN712581	Crous *et al.* (2009b, 2011), Videira *et al.* (2017)
B. protearum	CBS 130597^{ET}	GU214626	JN712620	MF951443	JN712582	Crous *et al.* (2009b, 2011), Videira *et al.* (2017)
B. roupeliae	CBS 144602^{T}	MK539950	–	MK540080	–	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, respectively.

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

DNA barcodes (genus): LSU, ITS.

DNA barcodes (species): *chs*, *rpb2*, *tef1*. Table 3.

Ascomata amphigenous, immersed to semi-immersed, black, single, gregarious, substomatal, pyriform or globose with a papillate, periphysate ostiole; *ascomatal wall* consisting of three strata of slightly compressed *textura angularis*, an outer stratum of dark brown, thick-walled cells, becoming paler in the central stratum, and hyaline, thin-walled in the inner stratum. *Pseudoparaphyses* absent. *Asci* clavate to cylindro-clavate, often curved, tapering to a pedicel, narrowing slightly to a rounded apex with an indistinct ocular chamber, 8-spored, bitunicate with fissitunicate dehiscence. *Ascospores* biseriate, fusiform, broader at the apical end, initially hyaline and 1-septate, becoming yellow-brown and 3-septate at maturity, slightly constricted at median to supra-median septum (adapted from Crous *et al.* 2009b).

Culture characteristics: Colonies on OA spreading, flat, with sparse to moderate aerial mycelium, lobate and smooth, rarely feathery, margins. On OA surface pale luteous, smoke grey with submerged iron-grey margins, or olivaceous grey with iron-grey, pale olivaceous grey and smoke grey patches. On PDA surface olivaceous grey, sometimes with pale olivaceous grey to smoke grey patches, or smoke grey with iron-grey margins; reverse iron-grey. On MEA surface pale olivaceous grey, smoke grey, dirty white with patches of smoke grey, or smoke grey with dirty white and olivaceous grey patches and submerged iron-grey margins; reverse iron-grey or olivaceous grey.

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

Distribution: Africa, mainly reported from South Africa. Also reported from Pacific Islands (Hawaii) and Europe (Portugal and Spain).

Hosts: *Protea* spp. (*Proteaceae*).

Disease symptoms: Leaf spots and Brunneosphaerella leaf blight.

Notes: *Brunneosphaerella* was introduced by Crous *et al.* (2009b) to accommodate *Leptosphaeria protearum*, which is a major leaf spot and blight pathogen of *Protea* spp. causing severe losses in plantations of South African *Protea* spp. wherever they are cultivated. Morphologically, *Brunneosphaerella* is distinct from *Leptosphaeria* in that ascospores are always brown at maturity, and asexual morphs have brown, percurrently proliferating conidiogenous cells. A new species isolated from leaves of *Protea repens* in South Africa, *B. jonkershoekensis*, was included in the genus when it was introduced (Crous *et al.* 2009b). This species appears to be a serious pathogen of *Pr. repens* in the Western Cape Province of South Africa. Subsequently, Crous *et al.* (2011) described the third species known from the genus, *B. nitidae*. This was isolated from the same area as *B. jonkershoekensis*, but *B. nitidae* was isolated from leaves of *Pr. nitida*, causing leaf spots on this host. Thus, the genus comprises four species, all of which were isolated from species of *Protea* in South Africa. The ITS sequences of the four species are highly similar. However, these can be easily delimited based on the *chs*, *rpb2* and *tef1* sequences.

References: Crous *et al.* 2009b, 2011, Videira *et al.* 2017 (morphology and phylogeny).

Brunneosphaerella roupeliae Crous, ***sp. nov.*** MycoBank MB829609. Fig. 19.

Etymology: Name refers to *Protea roupeliae*, the host species from which it was collected.

Fig. 19. *Brunneosphaerella roupeliae* (ex-type CBS 144602). **A.** Close-up of leaf spot with ascomata. **B, C.** Asci with ascospores. **D.** Germinating ascospores. Scale bars = 10 μm.

Fig. 20. Disease symptoms of *Elsinoe* spp. **A.** *Elsinoe ampelina* on *Vitis vinifera*. **B.** *Elsinoe asclepiadea* on *Asclepias mellodora*. **C.** *Elsinoe bidentis* on *Bidens segetum*. **D.** *Elsinoe erythrinae* on *Erythrina* sp. **E.** *Elsinoe eucalypticola* on *Eucalyptus* sp. **F.** *Elsinoe fawcettii* on *Citrus* sp. **G.** *Elsinoe freyliniae* on *Freylinia lanceolata*. **H.** *Elsinoe perseae* on *Persea americana*. **I.** *Elsinoe othonnae* on *Othonna quinquedentata*. **J.** *Elsinoe poinsettiae* on *Euphorbia* sp. **K.** *Elsinoe punicae* on *Punica granatum*. **L.** *Elsinoe terminaliae* on *Terminalia catappa*. Pictures taken from Fan *et al*. (2017).

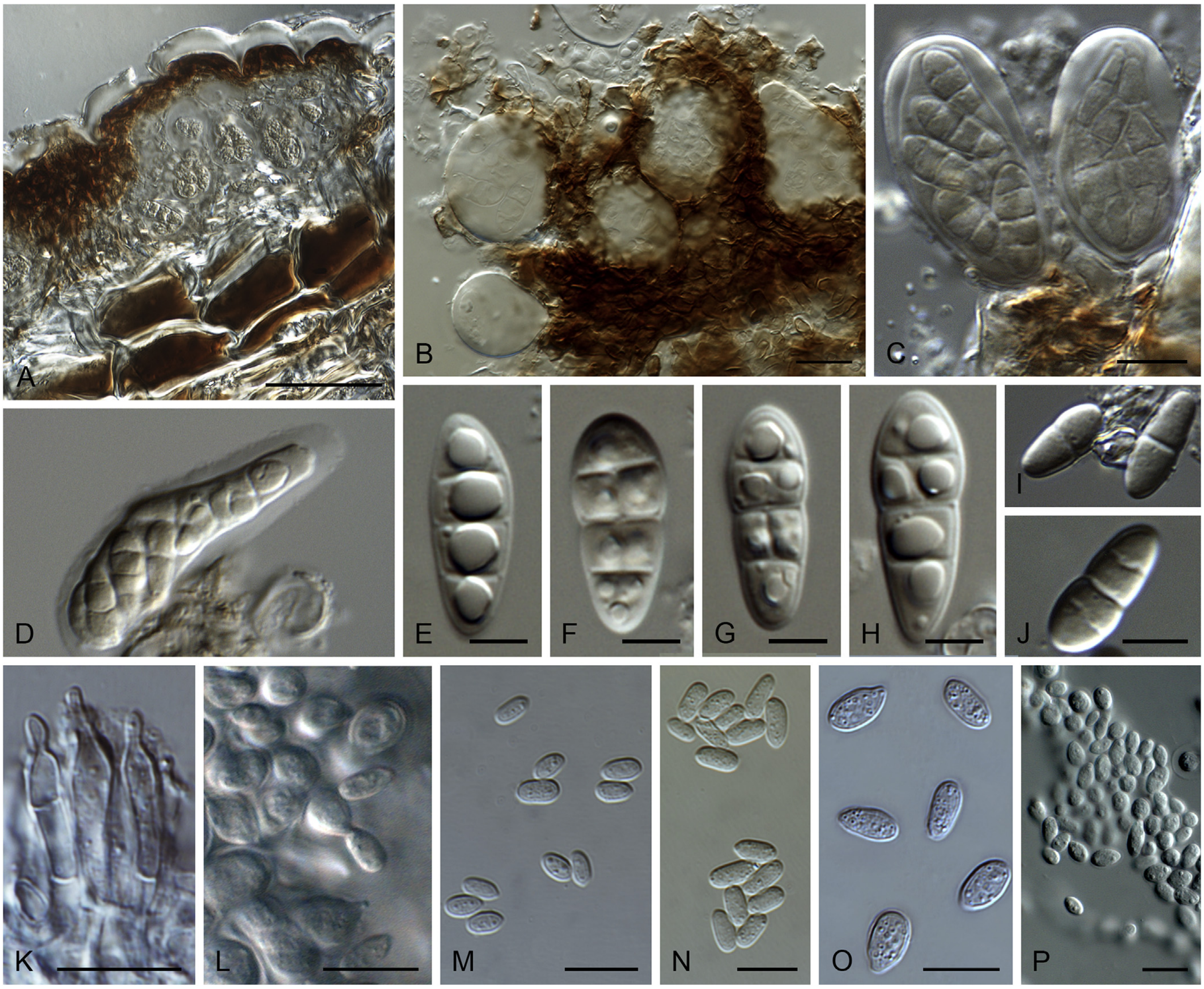

Fig. 21. *Elsinoe* spp. **A–J.** Sexual morph. **A.** Subcutilar ascoma of *Elsinoe fecunda*. **B–D.** Asci. **B.** *Elsinoe eucalypticola* (ex-type CBS 124765). **C, D.** *Elsinoe fecunda* (holotype, PREM 56503). **E–J.** Ascospores. **E–H.** *Elsinoe eucalypticola* (ex-type CBS 124765). **I, J.** *Elsinoe fecunda*. **K–P.** Asexual morph. **K, L.** Conidiophores. **K.** *Elsinoe asclepiadea* (ex-type CPC 18544). **L.** *Elsinoe othonnae* (ex-type CBS 139910). **M–P.** Conidia. **M.** *Elsinoe asclepiadea* (ex-type CPC 18544). **N.** *Elsinoe erythrinae* (ex-epitype CPC 18542). **O.** *Elsinoe tectificae* (ex-type CBS 124777). **P.** *Elsinoe othonnae* (ex-type CBS 139910). Scale bars: A = 100 µm; B–D, K–U = 10 µm; E–J = 5 µm; C applies to C and B; J applies I and J. Pictures taken from Fan *et al.* (2017).

Leaf spots amphigenous, sub-circular, 5–20 mm diam, medium brown, with raised, dark brown border. *Ascomata* pseudothecial, amphigenous, black, immersed to erumpent, globose, to 250 µm diam, with apical ostiole; *ascomatal wall* of 2–3 layers of brown cells of *textura angularis*. *Asci* aparaphysate, fasciculate, bitunicate, subsessile, ellipsoid-fusoid, straight to slightly curved, 8-spored, 65–110 × 11–15 µm. *Ascospores* bi- to triseriate, overlapping, guttulate, thick-walled, straight to slightly curved, obovoid with obtuse ends, widest in middle of apical cell, 3-septate, constricted at median septum, tapering towards both ends, but more prominently towards lower end, (19–)22–23(–25) × 5(–6) µm. *Ascospores* germinating from both ends, becoming brown and verruculose, constricted at primary septum, with germ tubes parallel to the long axis, ascospore becoming 7–9 µm diam.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium, and even, lobate margins, reaching 10 mm diam after 2 wk at 25 °C. On MEA surface pale olivaceous grey, reverse olivaceous grey; on PDA surface and reverse olivaceous grey, and on OA surface pale luteous.

Typus: **South Africa**, KwaZulu-Natal Province, Drakensberg, Monks Cowl, on leaves of *Protea roupeliae* (*Proteaceae*), 18 Jan. 2010, A. Wood, HPC 1522 (**holotype** CBS H-23847, culture ex-type CPC 32914 = CBS 144602).

Notes: *Brunneosphaerella roupeliae* was isolated from the same host genus in South Africa as the other three species of the genus, *Protea*. The ITS and LSU sequences located this species in the genus *Brunneosphaerella* since both sequences showed more than 99 % of nucleotide similarity with the ex-type strains of the other three species. The *rpb2* sequence showed a nucleotide similarity of 95.86 % with the ex-epitype strain of *B. protearum*, 95.45 % with the ex-epitype strain of *B. jonkershoekensis*, and 94.5 % with the ex-type strain of *B. nitidae*. The *tef1* sequence showed a nucleotide similarity of 95.66 % with the ex-epitype strain of *B. protearum* and the ex-type strain of *B. nitidae*, and

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

Species	Isolates[1]	GenBank accession numbers[2]				References
		ITS	LSU	*rpb2*	*tef1*	
Elsinoe abutilonis	CBS 510.50^{T}	KX887185	KX886949	KX887068	KX886831	Fan *et al.* (2017)
E. ampelina	CBS 208.25	KX887186	KX886950	KX887069	KX886832	Fan *et al.* (2017)
E. anacardii	CBS 470.62^{T}	KX887189	KX886953	KX887072	KX886835	Fan *et al.* (2017)
E. annonae	CBS 228.64	KX887190	KX886954	KX887073	KX886836	Fan *et al.* (2017)
E. arachidis	CBS 511.50^{T}	KX887191	KX886955	KX887074	KX886837	Fan *et al.* (2017)
E. arrudai	CBS 220.50^{T}	KX887194	KX886958	KX887077	KX886840	Fan *et al.* (2017)
E. asclepiadea	CBS 141937^{T}	KX887195	KX886959	KX887078	KX886841	Fan *et al.* (2017)
E. australis	CBS 314.32^{ET}	KX887198	KX886962	KX887081	KX886844	Fan *et al.* (2017)
E. banksiae	STE-U 2678^{T}	AF227197	–	–	–	Swart *et al.* (2001)
E. banksiicola	CBS 113734^{T}	KX887199	KX886963	KX887082	KX886845	Fan *et al.* (2017)
E. barleriicola	CBS 471.62^{T}	KX887200	KX886964	KX887083	KX886846	Fan *et al.* (2017)
E. bidentis	CBS 512.50^{T}	KX887201	KX886965	KX887084	KX886847	Fan *et al.* (2017)
E. brasiliensis	CPC 18528^{ET}	KX887204	–	KX887087	KX886850	Fan *et al.* (2017)
E. caleae	CBS 221.50^{T}	KX887205	KX886968	KX887088	KX886851	Fan *et al.* (2017)
E. centrolobii	CBS 222.50^{T}	KX887206	KX886969	KX887089	KX886852	Fan *et al.* (2017)
E. citricola	CPC 18535^{T}	KX887207	KX886970	KX887090	KX886853	Fan *et al.* (2017)
E. coryli	CBS 275.76^{T}	KX887209	KX886972	KX887092	KX886855	Fan *et al.* (2017)
E. diospyri	CBS 223.50^{T}	KX887210	KX886973	KX887093	KX886856	Fan *et al.* (2017)
E. eelemani	DAR 83016^{T}	KX372292	–	KX398204	KX398203	Crous *et al.* (2016a)
E. embeliae	CBS 472.62^{T}	KX887211	KX886974	–	KX886857	Fan *et al.* (2017)
E. erythrinae	CPC 18542^{ET}	KX887214	KX886977	KX887096	KX886860	Fan *et al.* (2017)
E. eucalypticola	CBS 124765^{T}	KX887215	KX886978	KX887097	KX886861	Fan *et al.* (2017)
E. eucalyptorum	CBS 120084^{T}	KX887216	KX886979	KX887098	KX886862	Fan *et al.* (2017)
E. euphorbiae	CBS 401.63^{T}	KX887217	KX886980	KX887099	KX886863	Fan *et al.* (2017)
E. fagarae	CBS 514.50^{T}	KX887218	KX886981	KX887100	KX886864	Fan *et al.* (2017)
E. fawcettii	CBS 139.25^{T}	KX887219	KX886982	KX887101	KX886865	Fan *et al.* (2017)
E. fici	CBS 515.50	KX887223	KX886986	KX887105	KX886869	Fan *et al.* (2017)
E. fici-caricae	CBS 473.62^{T}	KX887224	KX886987	KX887106	KX886870	Fan *et al.* (2017)
E. flacourtiae	CBS 474.62^{T}	KX887225	KX886988	KX887107	KX886871	Fan *et al.* (2017)
E. freyliniae	CBS 128204^{T}	KX887226	KX886989	KX887108	KX886872	Fan *et al.* (2017)
E. genipae	CBS 342.39^{T}	KX887227	KX886990	KX887109	KX886873	Fan *et al.* (2017)
E. genipae-americanae	CBS 516.50^{T}	KX887228	KX886991	KX887110	KX886874	Fan *et al.* (2017)
E. glycines	CBS 389.64^{ET}	KX887229	KX886992	KX887111	KX886875	Fan *et al.* (2017)
E. hederae	CBS 517.50^{T}	KX887231	KX886994	KX887113	KX886877	Fan *et al.* (2017)
E. ichnocarpi	CBS 475.62^{T}	KX887232	KX886995	KX887114	KX886878	Fan *et al.* (2017)
E. jasminae	CBS 224.50^{T}	KX887233	KX886996	KX887115	KX886879	Fan *et al.* (2017)
E. jasminicola	CBS 212.63^{T}	KX887234	KX886997	–	KX886880	Fan *et al.* (2017)
E. krugii	CPC 18531^{ET}	KX887235	KX886998	KX887116	KX886881	Fan *et al.* (2017)
E. lagoa-santensis	CBS 518.50^{T}	KX887239	KX887002	KX887120	KX886885	Fan *et al.* (2017)
E. ledi	CBS 167.33^{ET}	KX887240	KX887003	KX887121	KX886886	Fan *et al.* (2017)
E. lepagei	CBS 225.50^{T}	KX887241	KX887004	KX887122	–	Fan *et al.* (2017)
E. leucopogonis	CBS 144439^{T}	MH327822	MH327858	MH327885	MH327897	Crous *et al.* (2018)
E. leucospermi	CBS 111207^{T}	KX887242	KX887005	KX887123	KX886887	Fan *et al.* (2017)
E. lippiae	CBS 166.40^{T}	KX887248	KX887011	KX887129	KX886893	Fan *et al.* (2017)
E. mangiferae	CBS 226.50^{T}	KX887249	KX887012	KX887130	KX886894	Fan *et al.* (2017)
E. mattiroloanum	CBS 287.64	KX887250	KX887013	KX887131	KX886895	Fan *et al.* (2017)
E. menthae	CBS 322.37^{ET}	KX887253	KX887016	KX887134	KX886898	Fan *et al.* (2017)
E. mimosae	CPC 19478^{ET}	KX887255	KX887018	KX887136	KX886900	Fan *et al.* (2017)
E. oleae	CBS 227.59^{T}	KX887256	KX887019	KX887137	KX886901	Fan *et al.* (2017)

Table 4. (Continued).

Species	Isolates[1]	GenBank accession numbers[2]				References
		ITS	LSU	*rpb2*	*tef1*	
E. othonnae	CBS 139910^{T}	KR476726	–	MK540083	–	Crous *et al.* (2015c), present study
E. perseae	CBS 406.34^{T}	KX887258	KX887021	KX887139	KX886903	Fan *et al.* (2017)
E. phaseoli	CBS 165.31^{T}	KX887263	KX887026	KX887144	KX886908	Fan *et al.* (2017)
E. picconiae	CBS 145026^{T}	MK539951	MK540022	MK540081	MK540164	Present study
E. piri	CBS 163.29	KX887267	KX887030	KX887148	KX886912	Fan *et al.* (2017)
E. pitangae	CBS 227.50^{T}	KX887269	KX887032	KX887150	KX886914	Fan *et al.* (2017)
E. poinsettiae	CBS 109333	KX887270	KX887033	KX887151	KX886915	Fan *et al.* (2017)
E. pongamiae	CBS 402.63^{ET}	KX887272	KX887035	KX887153	KX886917	Fan *et al.* (2017)
E. populi	CBS 289.64	KX887273	KX887036	KX887154	KX886918	Fan *et al.* (2017)
E. preissianae	CBS 142129^{T}	KY173406	KY173498	–	–	Crous *et al.* (2016a)
E. proteae	STE-U 1349^{T}	AF097578	–	–	–	Swart *et al.* (2001)
E. protearum	CBS 113618^{T}	KX887275	KX887038	KX887156	KX886920	Fan *et al.* (2017)
E. punicae	CPC 19968	KX887276	KX887039	KX887157	KX886921	Fan *et al.* (2017)
E. quercus-ilicis	CBS 232.61^{T}	KX887277	KX887040	–	KX886922	Fan *et al.* (2017)
E. randii	CBS 170.38^{IsoT}	KX887278	KX887041	KX887158	KX886923	Fan *et al.* (2017)
E. rhois	CBS 519.50^{T}	KX887280	KX887043	KX887160	KX886925	Fan *et al.* (2017)
E. ricini	CBS 403.63	KX887281	KX887044	KX887161	KX886926	Fan *et al.* (2017)
E. rosarum	CBS 212.33^{ET}	KX887283	KX887046	KX887163	KX886928	Fan *et al.* (2017)
E. salicina	CPC 17824^{T}	KX887286	KX887049	KX887166	KX886931	Fan *et al.* (2017)
E. semecarpi	CBS 477.62^{T}	KX887287	KX887050	KX887167	KX886932	Fan *et al.* (2017)
E. sesseae	CPC 18549	KX887288	KX887051	KX887168	KX886933	Fan *et al.* (2017)
E. sicula	CBS 398.59^{T}	KX887289	KX887052	KX887169	KX886934	Fan *et al.* (2017)
E. solidaginis	CBS 191.37^{ET}	KX887290	KX887053	KX887170	KX886935	Fan *et al.* (2017)
E. tectificae	CBS 124777^{T}	KX887292	KX887055	KX887172	KX886937	Fan *et al.* (2017)
E. terminaliae	CBS 343.39^{ET}	KX887293	KX887056	KX887173	–	Fan *et al.* (2017)
E. theae	CBS 228.50^{T}	KX887295	KX887058	KX887175	KX886939	Fan *et al.* (2017)
E. tiliae	CBS 350.73	KX887296	KX887059	KX887176	KX886940	Fan *et al.* (2017)
E. veneta	CBS 164.29^{ET}	KX887297	KX887060	KX887177	KX886941	Fan *et al.* (2017)
E. verbenae	CPC 18561^{ET}	KX887298	KX887061	KX887178	KX886942	Fan *et al.* (2017)
E. veronicae	CBS 145362^{T}	MK539952	MK540023	MK540082	–	Present study
E. violae	CBS 336.35^{T}	KX887302	KX887065	KX887182	KX886946	Fan *et al.* (2017)
E. zizyphi	CBS 378.62^{T}	KX887303	KX887066	KX887183	KX886947	Fan *et al.* (2017)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CPC: Culture collection of Pedro Crous, housed at Westerdijk Fungal Biodiversity Institute; DAR: Plant Pathology Herbarium, New South Wales, Australia; STE-U: Department of Plant Pathology, Stellenbosch University, South Africa. $^{T,\ ET}$ and ^{IsoT} indicate ex-type, ex-epitype and ex-isotype strains, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; LSU: partial large subunit (28S) nrRNA gene; *rpb2*: partial DNA-directed RNA polymerase II second largest subunit gene; *tef1*: partial translation elongation factor 1-alpha gene.

94.44 % with the epitype strain of *B. jonkershoekensis*. *Brunneosphaerella roupeliae* produces the shortest ascospores of the genus [(19–)22–23(–25) µm in *B. roupeliae vs.* (25–)27–34(–37) µm in *B. jonkershoekensis vs.* (20–)24–28(–30) µm in *B. nitidae vs.* (20–)23–26(–30) µm in *B. protearum*].

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

Elsinoe Racib., Parasit. Alg. Pilze Java's (Jakarta) 1: 14. 1900. Figs 20, 21.

Synonyms: *Sphaceloma* de Bary, Ann. Oenol. 4: 165. 1874.
Manginia Viala & Pacottet, C. r. hebd. Séanc. Acad. Sci., Paris 139: 88. 1904.
Melanobasidium Maubl., Bull. Soc. mycol. Fr. 22: 69. 1906.
Plectodiscella Woron., Mykol. Zentbl. 4: 232. 1914.
Isotexis Syd., in Sydow & Petrak, Annls mycol. 29: 261. 1931.
Melanobasis Clem. & Shear, Gen. fung., Edn 2 (Minneapolis): 224. 1931.
Melanodochium Syd., Annls mycol. 36: 310. 1938.
Bitancourtia Thirum. & Jenkins, Mycologia 45: 781. 1953.
Kurosawaia Hara, List of Japanese Fungi, 4th Edn: 172. 1954.
Uleomycina Petr., Sydowia 8: 74. 1954.
Melanophora Arx, Verh. K. ned. Akad. Wet., tweede sect. 51: 43. 1957.

Classification: *Dothideomycetes*, *Dothideomycetidae*, *Myriangiales*, *Elsinoaceae*.

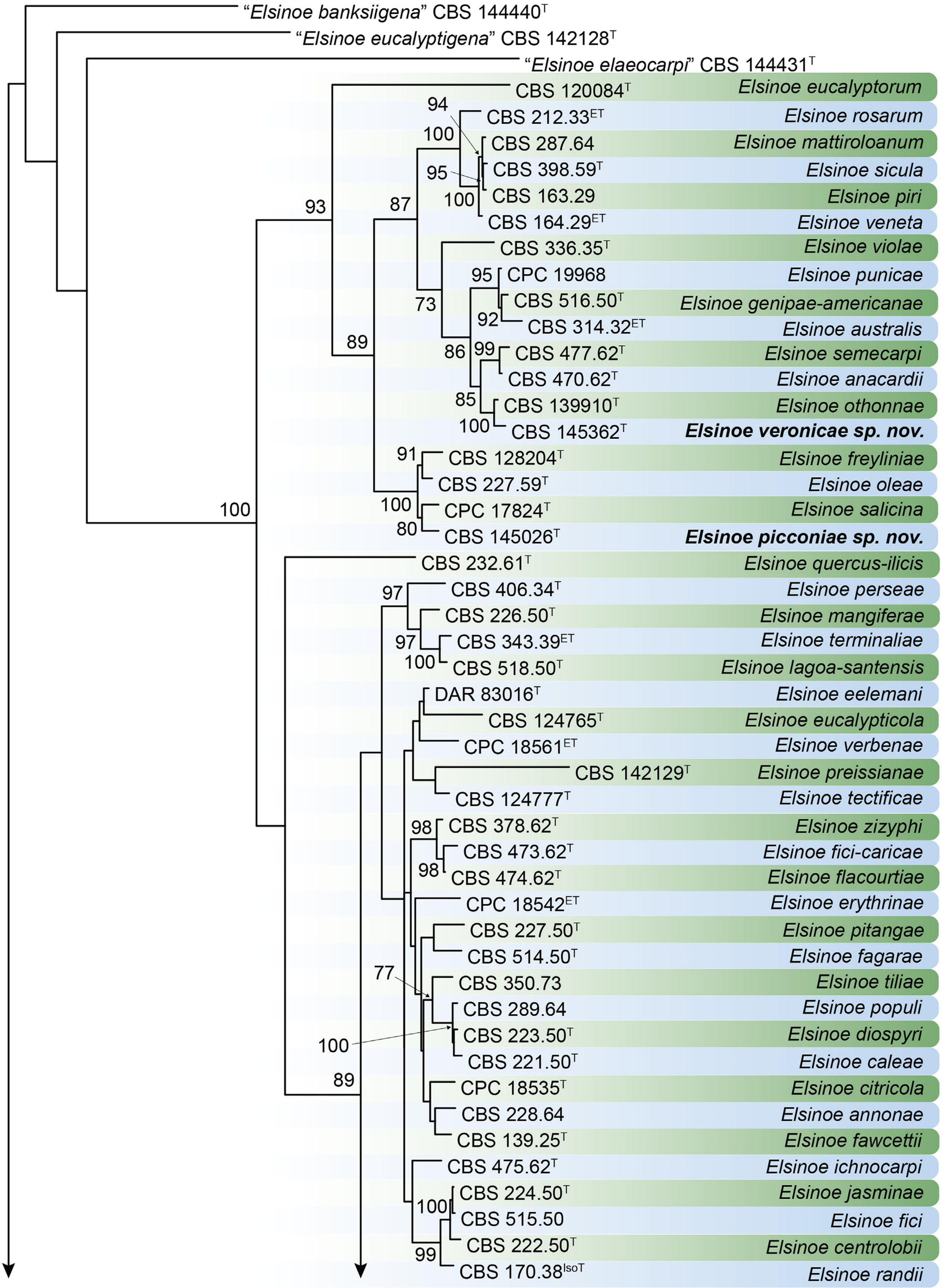

Fig. 22. RAxML phylogram obtained from the combined ITS (609 bp), LSU (741 bp), *rpb2* (747 bp) and *tef1* (422 bp) sequence alignment of all accepted species of *Elsinoe*. The tree was rooted to *Myriangium hispanicum* CBS 247.33. The novelties proposed in this study are indicated in **bold**. RAxML bootstrap support (BS) values above 70 % are shown at the nodes. GenBank accession numbers are listed in Table 4. $^{T,\ ET}$ and ^{IsoT} indicate ex-type, ex-epitype and ex-isotype strains, respectively. TreeBASE: S23834.

Type species: *Elsinoe canavaliae* Racib. Type or reference material not available.

DNA barcode (genus): LSU.

DNA barcodes (species): ITS, *rpb2*, *tef1*. Table 4. Fig. 22.

Ascostromata solitary, aggregated, or gregarious, wart-like, or as small distinctively coloured elevations, or pulvinate, immersed to semi-immersed, globose to subglobose, white, pale yellow or brown, soft, multi-loculate, locules scattered in upper part of ascostromata; *ascostromatal wall* composed of pseudoparenchymatous cells of *textura globulosa* to *textura angularis*; *locules* with few to numerous asci inside each locule, ostiolate; *ostiole* minute. *Periphyses* absent. *Asci* 8-spored, bitunicate, fissitunicate, saccate to globose, with a minute pedicel, and ocular chamber. *Ascospores* irregularly arranged, oblong or fusiform with slightly acutely rounded ends, with 2–3 transverse septa,

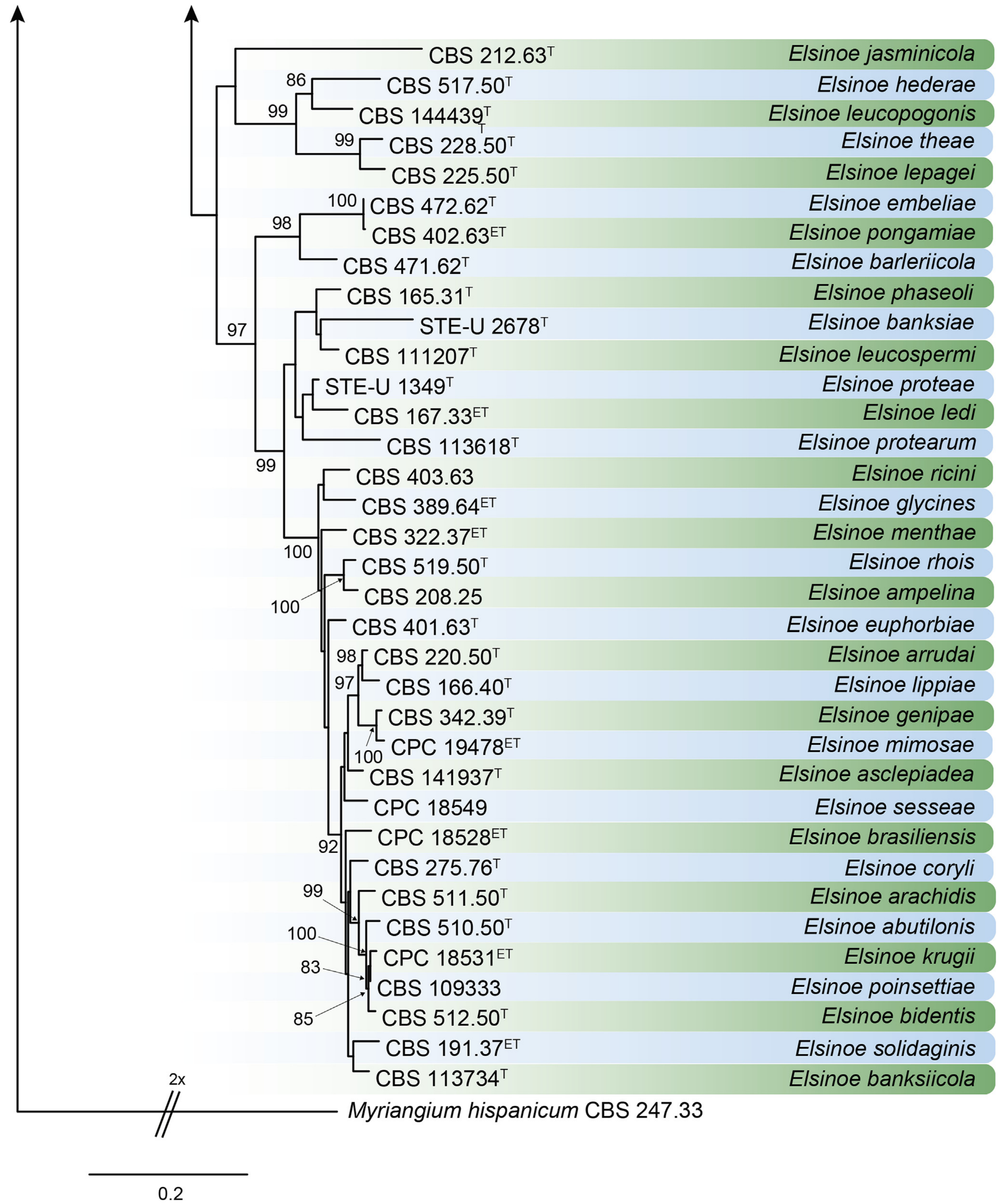

Fig. 22. (Continued).

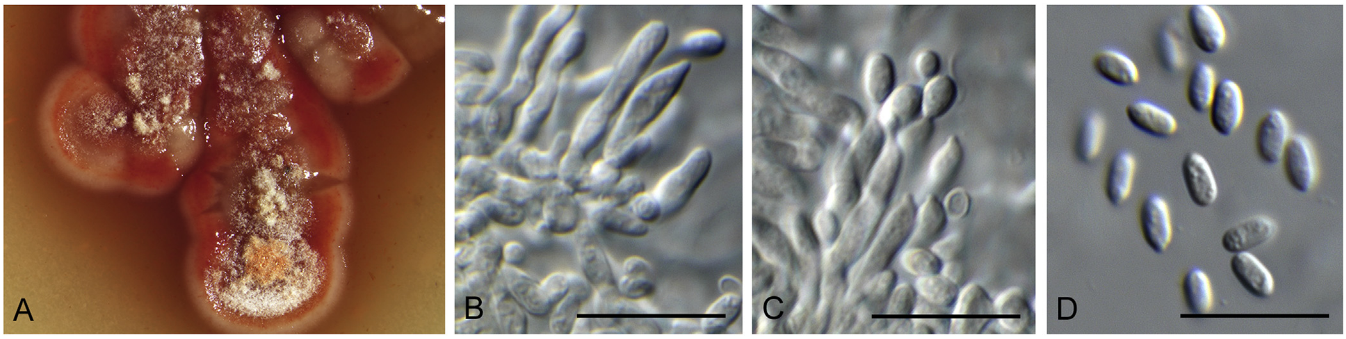

Fig. 23. *Elsinoe picconiae* (ex-type CBS 145026). **A.** Colony on OA. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars = 10 µm.

hyaline, smooth-walled, lacking a sheath. *Acervuli* or *sporodochia* subepidermal, pseudoparenchymatous. *Conidiophores* hyaline to pale brown, polyphialidic. *Conidiogenous cells* formed directly from the upper cells of the pseudoparenchyma, mono- to polyphialidic, integrated or discrete, determinate, hyaline to pale brown, without visible periclinal thickening. *Conidia* hyaline, smooth-walled, aseptate, ellipsoidal, guttulate (adapted from Fan *et al.* 2017).

Culture characteristics: Colonies on MEA, slow growing, raised, irregular, erumpent, folded or cerebriform, smooth and irregular margins, with sparse to moderate white to grey aerial mycelium. On MEA, surface white to pale luteous, cinnamon, sepia, apricot, saffron with or without purplish grey in centre, brown with apricot margins, rosy buff in centre with cinnamon margins, livid red, scarlet red with diffuse red pigment in agar, or iron-grey; reverse umber, ochreous, iron-grey, dark vinaceous, or centre scarlet and orange with cinnamon margins.

Optimal media and cultivation conditions: MEA, OA, PDA, SNA and WA at 22 °C under near-ultraviolet light (12 h light, 12 h dark).

Distribution: Worldwide.

Hosts: Wide range of hosts, including some economically important crops such as avocado, cassava, citrus, grapevines, ornamentals such as poinsettias, field crops and woody hosts.

Disease symptoms: Scab, leaf and fruit spot and anthracnose disease.

Notes: *Elsinoe* comprises plant pathogenic species that cause scab and spot anthracnose on a wide range of hosts, including some economically important crops and ornamentals. The disease symptoms that these species produce are easily recognisable, being known as "signature-bearing diseases", for the cork-like appearance of older infected tissues with scab-like appearance. Also, these can produce other disease symptoms often called anthracnose, as in the case of infected grapevines (Barrus & Horsfall 1928, Jenkins 1947, Farr *et al.* 1989, Pan 1994, Phillips 1994, Gottwald 1995). However, the use of this name is confusing since it is used much broader to include diseases caused by *Colletotrichum*. Although many species of *Elsinoe* causing scab disease have been described, only few of them cause important diseases (Holliday 1980), having the main impact on the appearance of the harvested product and its market acceptability rather than on crop productivity (Swart *et al.* 2001). Species of *Elsinoe* seem to be host-specific since 77 of the 81 species accepted in the present study occur on only one host species or genus.

Elsinoe and its asexual morph, *Sphaceloma,* were recently reviewed by Fan *et al.* (2017). In that study, 26 new combinations were proposed for the species originally placed in *Sphaceloma*. Moreover, eight new species were introduced and 13 epitypes were designated. Based on phylogenetic data, Fan *et al.* (2017) accepted 75 species in the genus. However, *E. banksiae*, which was described by Swart *et al.* (2001), and three species described by Crous *et al.* (2016a), *i.e. E. eelemani*, *E. eucalyptigena* and *E. preissianae*, were not included in that study. Our phylogenetic analysis corroborated the placement of these species in the main well-supported clade representing the genus *Elsinoe*, except for *E. eucalyptigena*, whose placement remains unknown and, therefore it is not considered an accepted species of *Elsinoe* in the present study. Moreover, another three new species have been subsequently described by Crous *et al.* (2018), *i.e. E. banksiigena*, *E. elaeocarpi* and *E. leucopogonis*. However, in our phylogenetic analysis, the two first species were not located in the *Elsinoe s. str.* clade, and are thus excluded from the genus at present. Therefore, hitherto a total of 79 species are accepted, plus the new species described in the

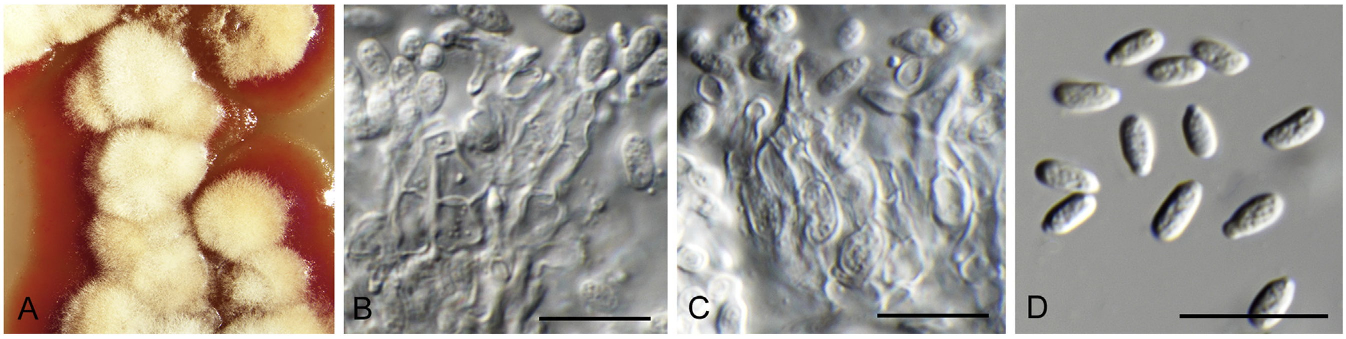

Fig. 24. *Elsinoe veronicae* (ex-type CBS 145362). **A.** Colony on OA. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars = 10 µm.

present study. Unfortunately, there are no cultures and molecular data of the type species of the genus, *E. canavaliae*, which needs to be epitypified in order to clarify its phylogenetic position.

References: Fan *et al.* 2017 (morphology and phylogeny).

Elsinoe picconiae Crous, ***sp. nov.*** MycoBank MB829611. Fig. 23.

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

Conidiomata sporodochial or acervular on leaves, medium brown, up to 250 μm diam; *conidiomatal wall* composed of *textura angularis*. *Conidiophores* subcylindrical to doliiform, hyaline to pale brown, smooth-walled, 0–1-septate, unbranched, 10–15 × 3–4 μm. *Conidiogenous cells* polyphialidic, hyaline, smooth-walled, subcylindrical to doliiform, 5–8 × 3–4 μm. *Conidia* hyaline, aseptate, ellipsoid, apex obtuse, base truncate, (4–)5–6(–7) × (2–)2.5 μm.

Culture characteristics: Colonies erumpent, spreading, with sparse aerial mycelium, folded surface, and smooth, lobate margins, reaching 7 mm diam after 2 wk at 25 °C. On MEA surface rust, reverse sienna; on PDA surface coral, reverse bay; on OA surface scarlet with diffuse scarlet pigment.

Typus: **Spain**, Tenerife, Los Silos, leaf of *Picconia excelsa* (*Oleaceae*), 12 Mar. 2017, A. van Iperen, HPC 2063 (**holotype** CBS H-23848, culture ex-type CBS 145026 = CPC 33648).

Notes: *Elsinoe picconiae* is related to *E. freyliniae*, *E. oleae* and *E. salicina*. However, *E. picconiae* can be easily distinguished by its narrower conidia [(2–)2.5 μm *vs.* (2.5–)3–4 μm in *E. freyliniae*, 3–6 μm in *E. oleae*, and (2.5–)3–4.5(–5) μm in *E. salicina*]. Moreover, *E. picconiae* is the first species of the genus isolated from *Picconia excelsa.*

Elsinoe veronicae Crous, Thangavel & Y. Marín, ***sp. nov.*** MycoBank MB829610. Fig. 24.

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

Conidiomata sporodochial, erumpent, 80–200 μm diam, based on a pale brown stroma, giving rise to densely aggregated conidiophores. *Conidiophores* hyaline to pale brown, smooth-walled, subcylindrical, 1–2-septate, 15–30 × 2.5–3.5 μm, unbranched or branched above. *Conidiogenous cells* integrated, subcylindrical, hyaline, smooth-walled, 7–10 × 2.5–3.5 μm, polyphialidic. *Conidia* solitary, aggregating in mucoid mass, aseptate, hyaline, smooth-walled, guttulate, ellipsoid, apex subobtuse, tapering at base to truncate hilum, (4–)5–5.5(–6.5) × 2.5(–3) μm.

Culture characteristics: Colonies erumpent, spreading, surface folded with moderate aerial mycelium, and even, lobate margins, reaching 25 mm diam after 2 wk. On MEA surface brick, reverse cinnamon; on PDA surface brick to scarlet, reverse brick in centre, scarlet in outer region; on OA surface scarlet with diffuse scarlet pigment.

Typus: **New Zealand**, Auckland, St. John, Morrin Road, on *Veronica* sp. (*Scrophulariaceae*), 2013, R. Thangavel (**holotype** CBS H-23865, culture ex-type CBS 145362 = CPC 34137 = T17_00408D).

Notes: *Elsinoe veronicae* is closely related to *E. othonnae*. Although the ITS sequences of both species showed more than 99 % nucleotide similarity, the *rpb2* sequences showed only 96.95 % similarity. Morphologically, these are also similar differing mainly in their conidial size [(4–)5–5.5(–6.5) × 2.5(–3) μm in *E. veronicae vs.* (5–)6–7 × (2.5–)3(–4) μm in *E. othonnae*]. Moreover, *E. veronicae* was found on *Veronica* (*Scrophulariaceae*) in New Zealand, while *E. othonnae* has only been reported on *Othonna* (*Asteraceae*) in South Africa (Crous *et al.* 2015c).

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

Exserohilum K.J. Leonard & Suggs, Mycologia 66: 290. 1974. Fig. 25.

Synonyms: *Setosphaeria* K.J. Leonard & Suggs, Mycologia 66: 294. 1974.

Luttrellia Khokhr. & Gornostaĭ (as '*Lutrellia*'; non *Luttrellia* Shearer), Vodorosli, Griby i Mkhi Dal'nego Vostoka [Algae, Fungi and Mosses of the Soviet Far-East] (Vladivostok): 80. 1978.

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

Type species: *Exserohilum turcicum* (Pass.) K.J. Leonard & Suggs, basionym: *Helminthosporium turcicum* Pass. Ex-epitype and ex-epitype strain designated by Hernández-Restrepo *et al.* (2018): CBS H-23323, CBS 690.71.

DNA barcodes (genus): LSU, ITS.

DNA barcodes (species): ITS, *gapdh*, *rpb2*. Table 5. Fig. 26.

Ascomata superficial, immersed or erumpent, globose to ellipsoid, unilocular, dark brown to black, with or without a neck, ostiolate, with simple rigid setae around the ostiolar apex and on the upper half of the ascoma where they are often mixed with hyaline, filiform, septate hyphae; *ascomatal wall* composed of pseudoparenchymatous cells, dark brown and thick-walled on the outside, but with more or less hyaline cells towards the inside, cells of *textura angularis*. *Pseudoparaphyses* filiform, hyaline, septate, branched, anastomosing. *Asci* arising from a basal cushion of thin-walled pseudoparenchymatous cells, bitunicate, 1–8-spored, cylindrical to cylindrical-clavate, short or moderately long-stalked, thick-walled, with an apical nasse and fissitunicate dehiscence. *Ascospores* fusoid, hyaline to pale brown, smooth-walled, 2–6 or rarely more transversely septate, constricted at the septa, surrounded by a hyaline mucilaginous sheath which often extends some distance beyond the ends of the spore. *Conidiophores* macronematous, mononematous, septate, cylindrical, olivaceous brown to brown, smooth-walled to verruculose, often geniculate above. *Conidiogenous cells* integrated, terminal and intercalary, sympodial, mono- or polytretic, cicatrised; *conidiogenous nodes* smooth to rough. *Conidia* fusiform, cylindrical or obclavate, straight to curved, multidistoseptate, with a protruding hilum (adapted from Hernández-Restrepo *et al.* 2018).

Culture characteristics: Colonies on PDA brown or grey olivaceous to olivaceous black, sometimes white, pale grey, hairy, cottony to powdery, margins fimbriate.

Optimal media and cultivation conditions: Sterilised *Zea mays* leaves placed on 1.5 % WA or PDA at 25 °C under near-ultraviolet light (12 h light, 12 h dark) to induce sporulation.

Distribution: Worldwide.

Fig. 25. *Exserohilum* spp. **A–E.** Sexual morph. **A.** Ascomata of *Exserohilum minor* (ex-isotype IMI 294530). **B, C.** Asci of *Exserohilum minor* (ex-isotype IMI 294530). **D, E.** Ascospores. **D.** *Exserohilum minor* (ex-isotype IMI 294530). **E.** *Exserohilum khartoumensis* (ex-isotype CBS 132708). **F–AA.** Asexual morph. **F–N.** Conidiophores and conidia. **F, L.** *Exserohilum oryzicola* (ex-isotype CBS 502.90). **G.** *Exserohilum turcicum* (ex-epitype CBS 690.71). **H, N.** *Exserohilum holmii* (ex-isotype CBS 413.65 and BRIP 12679).

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

Species	Isolates[1]	GenBank accession numbers[2]				References
		ITS	LSU	*gapdh*	*rpb2*	
Exserohilum corniculatum	BRIP 11426$^{\mathrm{T}}$	LT837453	LT883391	LT883533	LT852480	Hernández-Restrepo *et al.* (2018)
Ex. holmii	CBS 413.65$^{\mathrm{IsoT}}$	LT837459	LT715621	LT715890	LT852489	Hernández-Restrepo *et al.* (2018)
Ex. khartoumensis	IMI 249194$^{\mathrm{IsoT}}$	LT837461	LT715619	LT715888	LT852490	Hernández-Restrepo *et al.* (2018)
Ex. minor	BRIP 14616$^{\mathrm{T}}$	LT837470	LT883403	LT883545	LT852502	Hernández-Restrepo *et al.* (2018)
Ex. monoceras	BRIP 12271$^{\mathrm{A}}$	LT837475	LT883406	LT883548	LT852507	Hernández-Restrepo *et al.* (2018)
Ex. neoregeliae	CBS 132832$^{\mathrm{T}}$	LT837476	LT715617	LT715886	LT852508	Hernández-Restrepo *et al.* (2018)
Ex. oryzicola	CBS 502.90$^{\mathrm{IsoT}}$	HF934949	HF934886	LT715878	HF934851	Amaradasa *et al.* (2014), Hernández-Restrepo *et al.* (2018)
Ex. pedicellatum	CBS 322.64$^{\mathrm{ET}}$	KT265258	HF934889	LT715902	HF934854	Amaradasa *et al.* (2014), Chowdhary *et al.* (2015), Hernández-Restrepo *et al.* (2018)
Ex. protrudens	BRIP 14814$^{\mathrm{T}}$	LT631308	LT715611	LT715880	LT715741	Hernández-Restrepo *et al.* (2018)
Ex. rostratum	CBS 325.87	KT265237	LT715629	LT715898	LT852492	Chowdhary *et al.* (2015), Hernández-Restrepo *et al.* (2018)
Ex. turcicum	CBS 690.71$^{\mathrm{ET}}$	LT837487	LT883415	LT882581	–	Hernández-Restrepo *et al.* (2018)

[1] BRIP: Queensland Plant Pathology Herbarium, Brisbane, Australia; CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; IMI: International Mycological Institute, CABI-Bioscience, Egham, Bakeham Lane, UK. $^{\mathrm{T,\ ET,\ IsoT}}$ and $^{\mathrm{A}}$ indicate ex-type, ex-epitype, ex-isotype and authentic strains.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; LSU: partial large subunit (28S) nrRNA gene; *gapdh*: partial glyceraldehyde-3-phosphate dehydrogenase gene; *rpb2*: partial DNA-directed RNA polymerase II second largest subunit gene.

Host: Mainly pathogens of grasses, but some also on non-grass hosts. Other substrates where they can be found include river sediments, soil, grains, plant debris, and humans. *Exserohilum rostratum* has been reported as a human pathogen.

Disease symptoms: In plants: leaf blight, leaf spots, melting out, root rot, and foot rot, among others. In humans: skin infections, keratitis, non-invasive allergies, invasive sinusitis, and disseminated infections.

Notes: Exserohilum is differentiated from the closely related *Bipolaris*, *Curvularia* and *Pyrenophora* by producing conidia with a protruding hilum (Leonard & Suggs 1974). Recently the taxonomy and phylogeny of *Exserohilum* has been revisited by Hernández-Restrepo *et al.* (2018). Based on morphological and molecular data 11 phylogenetic species are accepted (Fig. 26, Table 5). Three species were excluded from the genus, namely *Ex. novae-zelandiae* relocated to *Sporidesmiella*, and *Ex. paspali* and *Ex. sorghicola* to *Curvularia*, while another 15 species were retained in *Exserohilum,* although some were doubtful. Species in *Exserohilum* are morphologically very variable and a molecular analysis is required for a correct species identification.

The type species of the genus, *Ex. turcicum* (= *Helminthosporium turcicum*), was described from Italy causing northern leaf blight of corn (Passerini 1876, Saccardo 1886). Other species attacking economically significant crops include *Ex. pedicellatum*, causing root rot on maize and brown lesions on wheat roots (Henry 1924, Sivanesan 1987), and *Ex. rostratum*, producing leaf spot on banana, maize and wheat, foot rot in wheat, damping off of sugarcane seedlings, blackening and seed germination failure in cereals (Drechsler 1923, Leonard 1976, Sivanesan 1987, Lin *et al.* 2011).

Previously, three different species, *Ex. longirostratum*, *Ex. macginnisii* and *Ex. rostratum,* were recognised as human pathogens (McGinnis *et al.* 1986, Padhye *et al.* 1986, de Hoog *et al.* 2000, da Cunha *et al.* 2012). However, a multi-locus phylogenetic analysis (Hernández-Restrepo *et al.* 2018) demonstrated that they are actually the same phylogenetic species. *Exserohilum rostratum* has been reported as an agent of phaeohyphomycosis and sometimes causing life-threatening infections in humans (McGinnis *et al.* 1986, Padhye *et al.* 1986, Aquino *et al.* 1995, Adler *et al.* 2006). This species was recently implicated in an outbreak of fungal meningitis associated with contaminated methylprednisolone in the USA (Kainer *et al.* 2012).

References: Drechsler 1923, 1934, Luttrell 1963, Leonard & Suggs 1974, Sivanesan 1987 (taxonomy, morphology and pathogenicity), Leonard 1976 (sexual/asexual connection), de Hoog *et al.* 2000, da Cunha *et al.* 2012 (human pathogens), Hernández-Restrepo *et al.* 2018 (morphology, phylogeny, review).

Author: M. Hernández-Restrepo

Neosetophoma Gruyter *et al.*, Mycologia 102: 1075. 2010. Fig. 27.

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

I. *Exserohilum pedicellatum* (CBS 375.76). **J, M.** *Exserohilum rostratum* (CBS 120380, CBS 196.29). **K.** *Exserohilum monoceras* (CBS 198.29). **O.** Detail of the conidial hilum of *Exserohilum oryzicola* (ex-isotype CBS 502.90). **P–AA.** Conidia. **P, Q, Z, AA.** *Exserohilum rostratum* (CBS 128054, CBS 120380, BRIP 11422). **R.** *Exserohilum holmii* (BRIP 12679). **S.** *Exserohilum pedicellatum* (BRIP 12040). **T, U.** *Exserohilum turcicum* (BPI 431157 holotype). **V.** *Exserohilum oryzicola* (BRIP 16229). **W.** *Exserohilum protrudens* (BRIP 14816). **X.** *Exserohilum corniculatum* (ex-type BRIP 11426). **Y.** *Exserohilum neoregelia* (CBS 132833). Scale bars A = 50 µm; others = 10 µm; C applies to B and C; E applies to D and E. Pictures taken from Hernández-Restrepo *et al.* (2018).

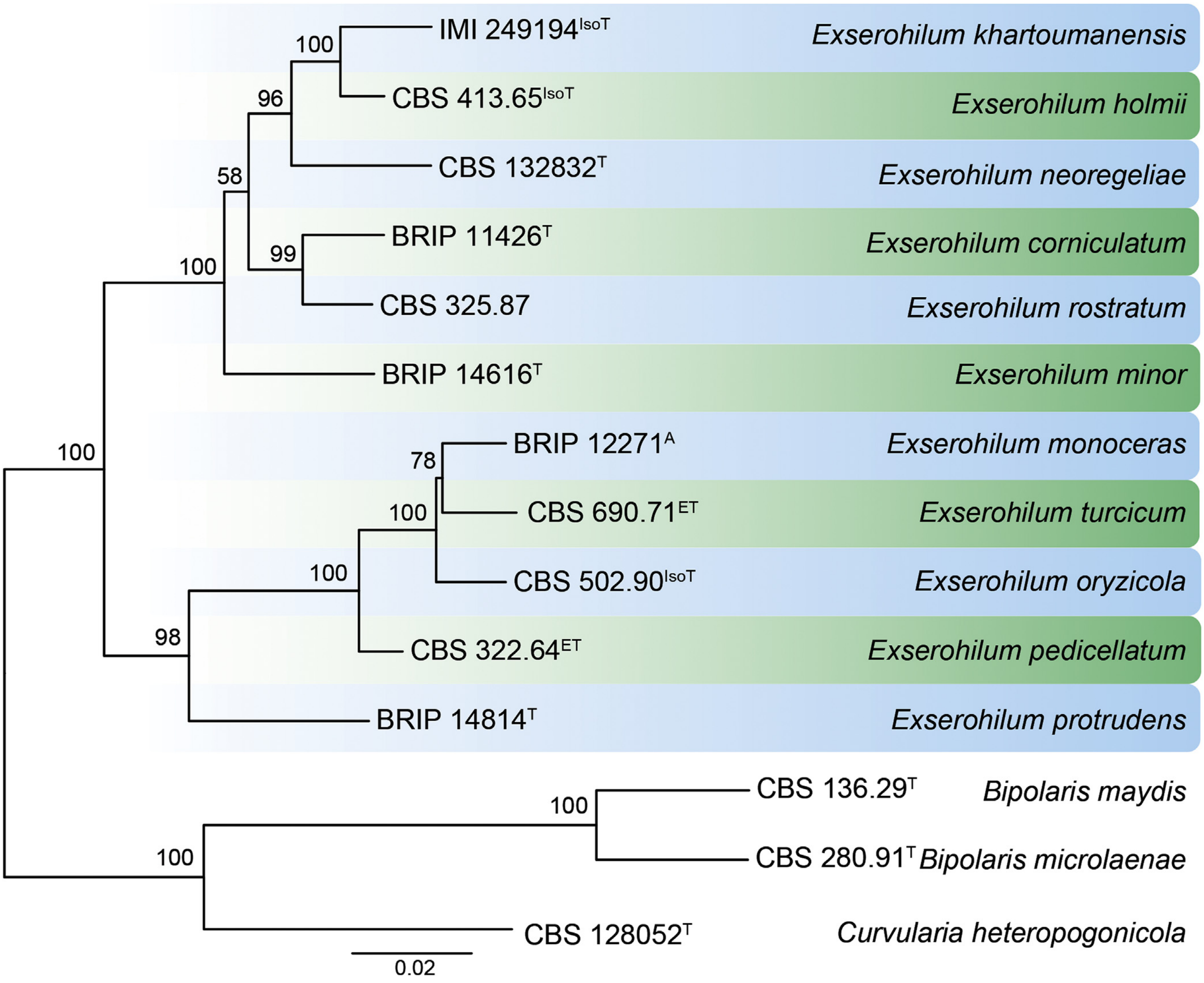

Fig. 26. RAxML phylogram obtained from the combined ITS (793 bp), *gapdh* (578 bp) and *rpb2* (860 bp) sequence alignment of all the accepted species of *Exserohilum*. The tree was rooted to *Curvularia* and *Bipolaris*. RAxML bootstrap support (BS) values above 70 % are shown in the nodes. GenBank accession numbers are indicated in Table 5. ^{T,} ^{ET,} ^{IsoT} and ^{A} indicate ex-type, ex-epitype, ex-isotype and authentic strains. TreeBASE: S23834.

Type species: *Neosetophoma samarorum* (Desm.) Gruyter *et al.*, basionym: *Phoma samarorum* Desm. Epitype and ex-epitype strain designated by Gruyter *et al.* (2010): CBS H-20319, CBS 138.96.

DNA barcode (genus): LSU. Fig. 28.

DNA barcodes (species): ITS, *rpb2*, *tef1*, *tub2*. Table 6. Fig. 29.

Ascomata ostiolate, globose to subglobose, solitary to gregarious, dark brown to black, immersed to slightly erumpent or superficial, smooth; *ascomatal wall* composed of 2–4 layers of brown to reddish-brown or dark brown to black cells of *textura*

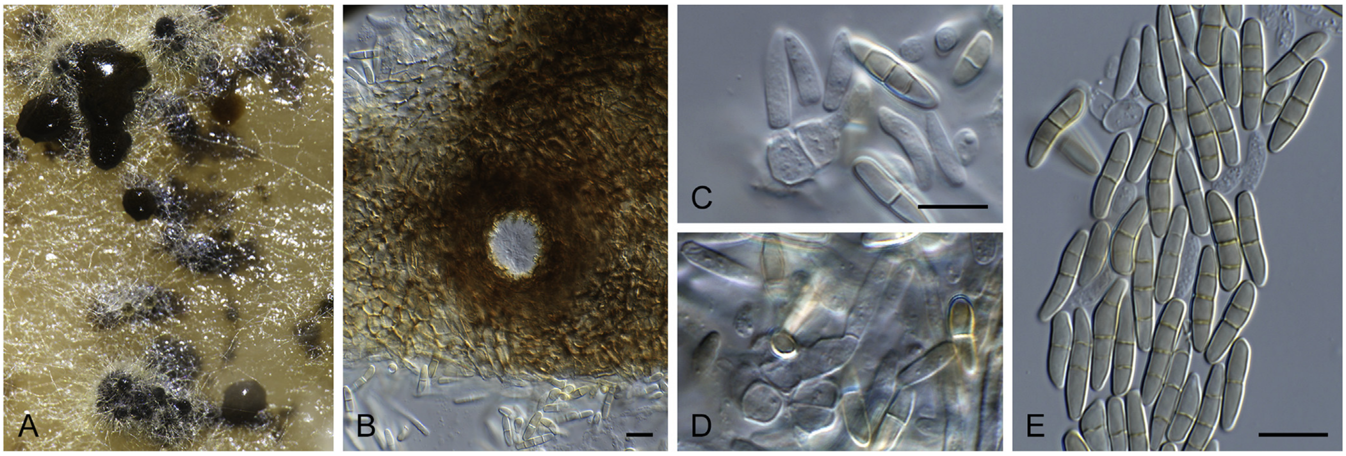

Fig. 27. *Neosetophoma lunariae* (ex-type CBS 141409). **A.** Conidiomata on OA. **B.** Conidiomata showing ostiolar region. **C, D.** Conidiogenous cells. **E.** Conidia. Scale bars = 10 µm; C applies to C and D. Pictures taken from Hernández-Restrepo *et al.* (2016a).

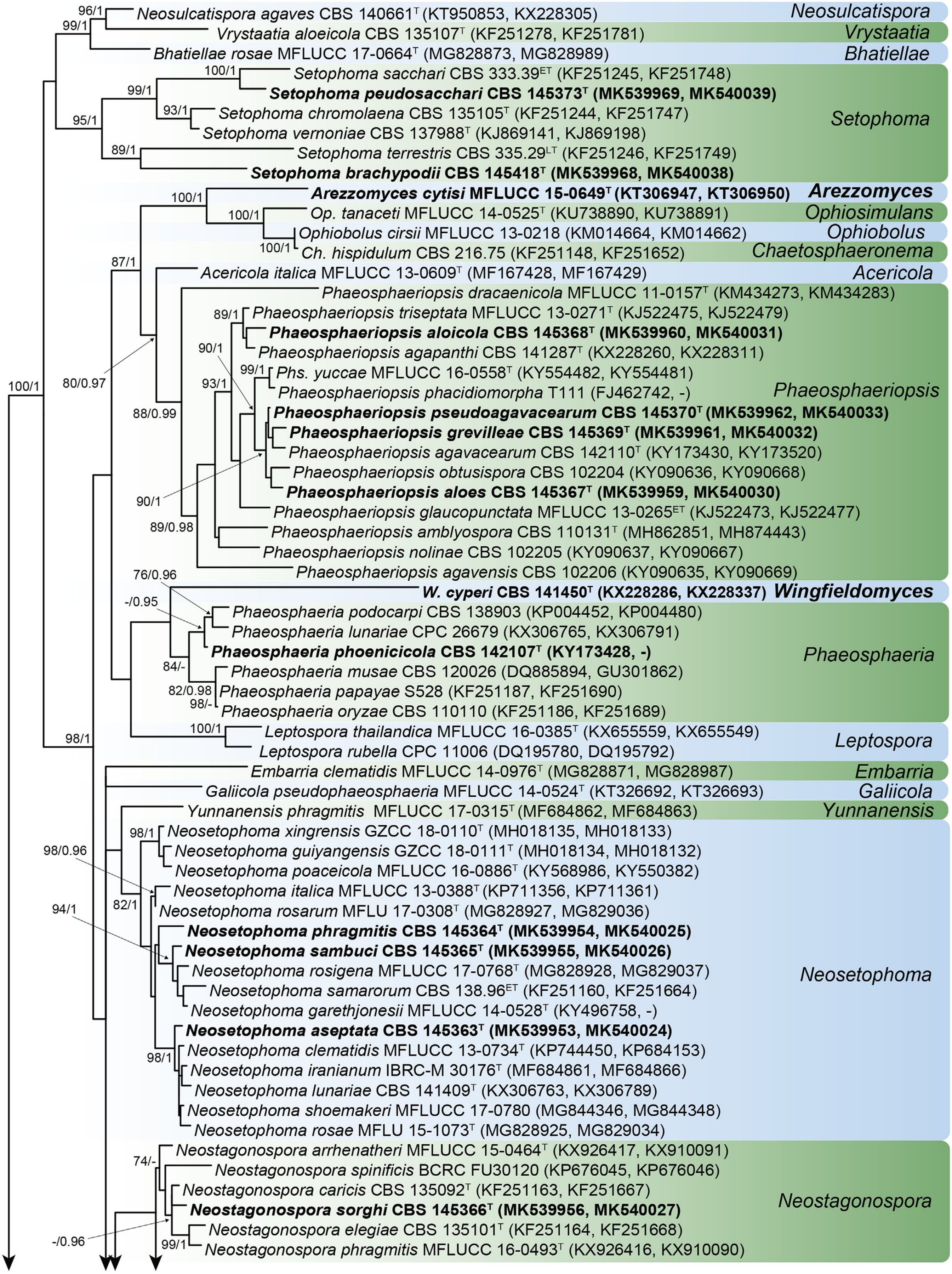

Fig. 28. RAxML phylogram obtained from the combined ITS (626 bp) and LSU (852 bp) sequence alignment of members of the family *Phaeosphaeriaceae*. The tree was rooted to *Coniothyrium glycines* CBS 124141 and *Coniothyrium sidae* CBS 135108. The novelties proposed in this study are indicated in **bold**. RAxML bootstrap support (BS) values above 70 %and Bayesian posterior probability scores above 0.95 are shown at the nodes. Numbers between parentheses correspond to GenBank accession numbers for ITS and LSU sequences, respectively. $^{T, ET, HT, IsoT, LT}$ and ^{NT} indicate ex-type, ex-epitype, holotype, ex-isotype, ex-lectotype and ex-neotype strains, respectively. TreeBASE: S23834.

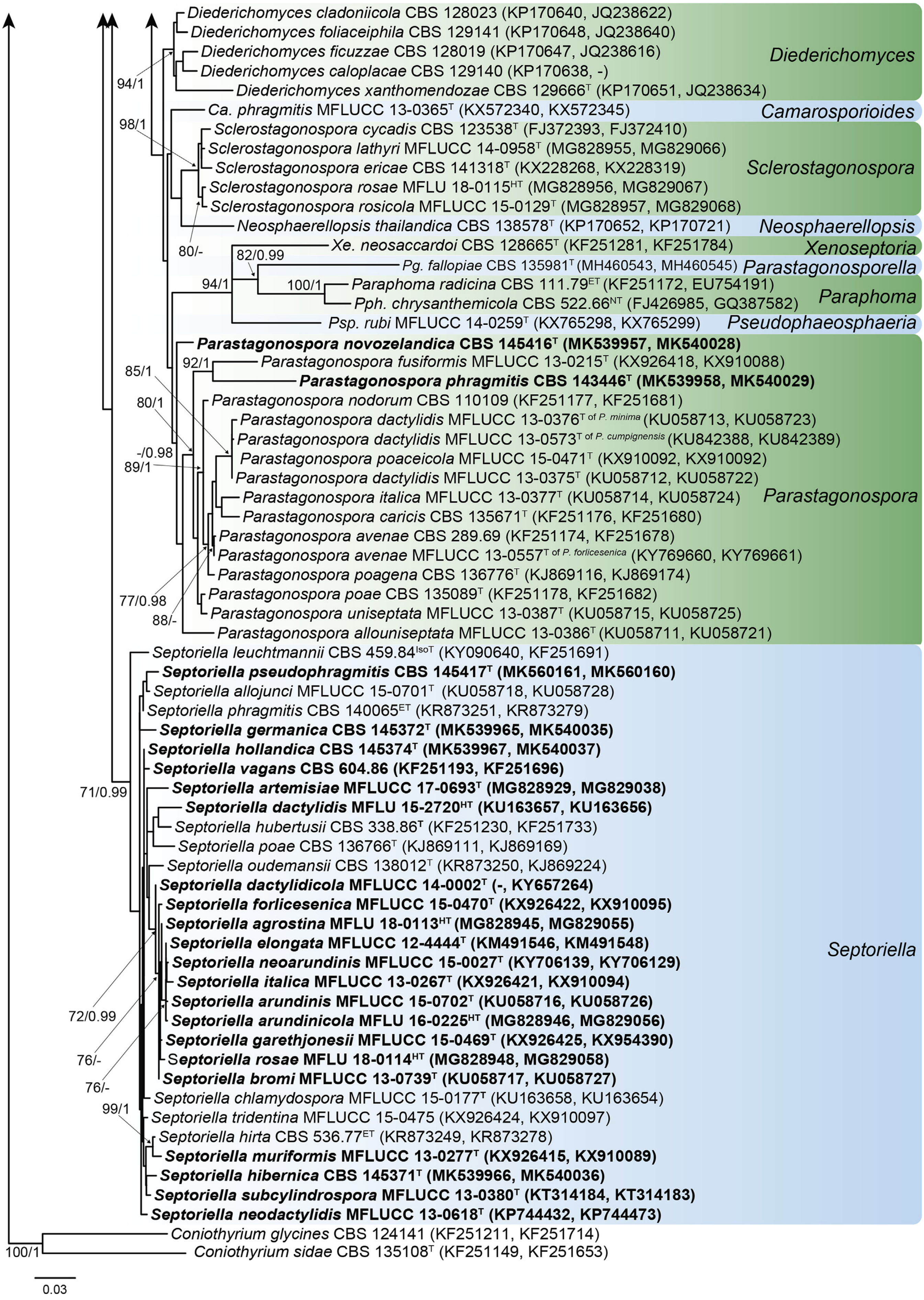

Fig. 28. (Continued).

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

Species	**Isolates**[1]	**GenBank accession numbers**[2]				**References**
		ITS	***rpb2***	***tef1***	***tub2***	
Neosetophoma aseptata	CBS 145363^{T}	MK539953	MK540084	–	–	Present study
Nph. clematidis	MFLUCC 13-0734^{T}	KP744450	–	–	–	Liu *et al.* (2015)
Nph. garethjonesii	MFLUCC 14-0528^{T}	KY496758	–	KY514402^{a}	–	Tibpromma *et al.* (2017)
Nph. guiyangensis	GZCC 18-0111^{T}	MH018134	–	–	–	Hyde *et al.* (2018)
Nph. iranianum	IBRC-M 30176^{T}	MF684861	–	–	–	Karunarathna *et al.* (2017)
Nph. italica	MFLUCC 13-0388^{T}	KP711356	–	–	–	Liu *et al.* (2015)
Nph. lunariae	CBS 141409^{T}	KX306763	–	–	–	Hernández-Restrepo *et al.* (2016a)
Nph. phragmitis	CBS 145364^{T}	MK539954	MK540085	MK540148^{b}	–	Present study
Nph. poaceicola	MFLUCC 16-0886^{T}	KY568986	–	–	–	Thambugala *et al.* (2017)
Nph. rosae	MFLUCC 15-1073^{T}	MG828925	–	MG829218^{a}	–	Wanasinghe *et al.* (2018)
Nph. rosarum	MFLUCC 17-0308^{T}	MG828927	–	–	–	Wanasinghe *et al.* (2018)
Nph. rosigena	MFLUCC 17-0768^{T}	MG828928	–	–	–	Wanasinghe *et al.* (2018)
Nph. samarorum	CBS 138.96^{ET}	KF251160	KF252168	KF253119^{b}	KF252655	Quaedvlieg *et al.* (2013)
Nph. sambuci	CBS 145365^{T}	MK539955	MK540086	MK540149^{b}	–	Present study
Nph. shoemakeri	MFLUCC 17-0780	MG844346	–	MG844352^{a}	–	Hyde *et al.* (2018)
Nph. xingrensis	GZCC 18-0110^{T}	MH018135	–	–	–	Hyde *et al.* (2018)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; GZCC: Guizhou Academy of Agricultural Sciences Culture Collection, Guiyang, China; IBRC: Herbarium of the Plant bank, Iranian Biological Resource Center, Karaj, Iran; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Ria, Thailand. ^{T} and ^{ET} indicate ex-type and ex-epitype strains, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *rpb2*: partial DNA-directed RNA polymerase II second largest subunit gene; *tef1*: partial translation elongation factor 1-alpha gene; *tub2*: partial β-tubulin gene. ^{a} and ^{b} in *tef1* column indicate the primers used for sequencing: ^{a}: EF1-983F / EF1-2218R; ^{b}: EF1-728F / EF-2.

angularis to *textura prismatica*. *Hamathecium* comprising numerous, septate, cellular or filamentous pseudoparaphyses, embedded in a hyaline gelatinous matrix. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical to clavate, short pedicellate, with a furcate pedicel, apically rounded, with a minute or indistinct ocular chamber. *Ascospores* overlapping, 1–3-seriate, hyaline or subhyaline when young, becoming pale yellow, pale brown or yellowish brown to brown at maturity, 1–5-septate, straight to slightly curved, fusoid or narrowly fusoid, with rounded or acute ends, constricted or not at the septum, enlarged at the second cell below apex, guttulate, smooth-walled, without any mucilaginous sheath and appendages. *Conidiomata* pycnidial, solitary to confluent, immersed or superficial, globose to subglobose or irregular, with mycelial outgrowths, or confluent, unilocular, occasionally multi-locular, with papillate ostioles, sometimes developing long necks, honey, olivaceous, olivaceous black, pale brown, brown, dark brown, or black, with up to 10 layers of pseudoparenchymatal cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* phialidic, extending percurrently at apex, hyaline, doliiform to ampulliform, determinate, hyaline, smooth-walled. *Conidia* hyaline, slightly yellowish or pale brown, 0–3(–4)-septate, ellipsoidal, cylindrical, subcylindrical, fusiform, or tear-drop shape, straight to curved, usually attenuate at one end, or apex and base obtuse, or sometimes with bluntly rounded to truncate base, continuous or constricted at the septa, smooth-walled, often guttulate (asexual morph description adapted from Gruyter *et al.* 2010).

Culture characteristics: Colonies flat, with a moderate amount of aerial mycelium. On PDA surface fluffy, circular or irregular, margins entire or filiform, white, pale grey, grey, greenish grey, or mouse grey; reverse yellowish, yellowish grey, greyish white, grey olivaceous, or dark brown. On MEA pale grey to almost white, buff, or brown to dark brown; reverse dark brown, or buff with patches of grey olivaceous.

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

Distribution: Asia, Europe and North America.

Hosts: Pathogens or saprophytes found on a wide range of host including *Cirsium arvense* (*Asteraceae*), *Clematis vitalba* (*Ranunculaceae*), *Iris germanica* (*Iridaceae*), *Lunaria annuna* (*Brassicaceae*), *Malva* sp. (*Malvaceae*), *Phlox paniculata* (*Polemoniaceae*), *Phragmites australis* (*Poaceae*), *Rosa canina* (*Rosaceae*), *Sambucus* spp., *Viburnum opulus* (*Caprifoliaceae*), and *Urtica dioica* (*Urticaceae*). Also isolated from soil.

Disease symptoms: Leaf spots.

Notes: *Neosetophoma* was introduced by de Gruyter *et al.* (2010) to accommodate *Phoma samarorum*, which is a pathogen causing leaf spots of grasses. Subsequently, 12 new species have been added to this genus, all of which appear to be saprobes, except for *Nph. iranianum*, which was isolated from soil (Karunarathna *et al.* 2017), and *Nph. lunariae*, which is endophytic (Hernández-Restrepo *et al.* 2016a).

This genus is characterised by globose to irregular conidiomata with papillate ostioles, and yellowish to brownish conidia usually attenuated at one end, less frequent with apex and base obtuse or with a bluntly rounded to truncate base. The sexual morph was observed for the first time by Tibpromma *et al.* (2017), when *Nph. garethjonesii* was introduced. Subsequently, four new species producing a sexual morph have been described, of which only one also produces the asexual morph, namely *Nph. shoemakeri* (Hyde *et al.* 2018).

References: de Gruyter *et al.* 2010, Quaedvlieg *et al.* 2013, Tibpromma *et al.* 2017, Hyde *et al.* 2018, Wanasinghe *et al.* 2018 (morphology and phylogeny).

Neosetophoma aseptata Crous, R.K. Schumach. & Y. Marín, ***sp. nov.*** MycoBank MB829639. Fig. 30.

Etymology: Name refers to its aseptate conidia, which have never been observed in the other species of the genus.

Conidiomata solitary, brown, erumpent, globose, 250–350 µm diam with 1–3 ostioles; *conidiomatal wall* of 3–4 layers of brown

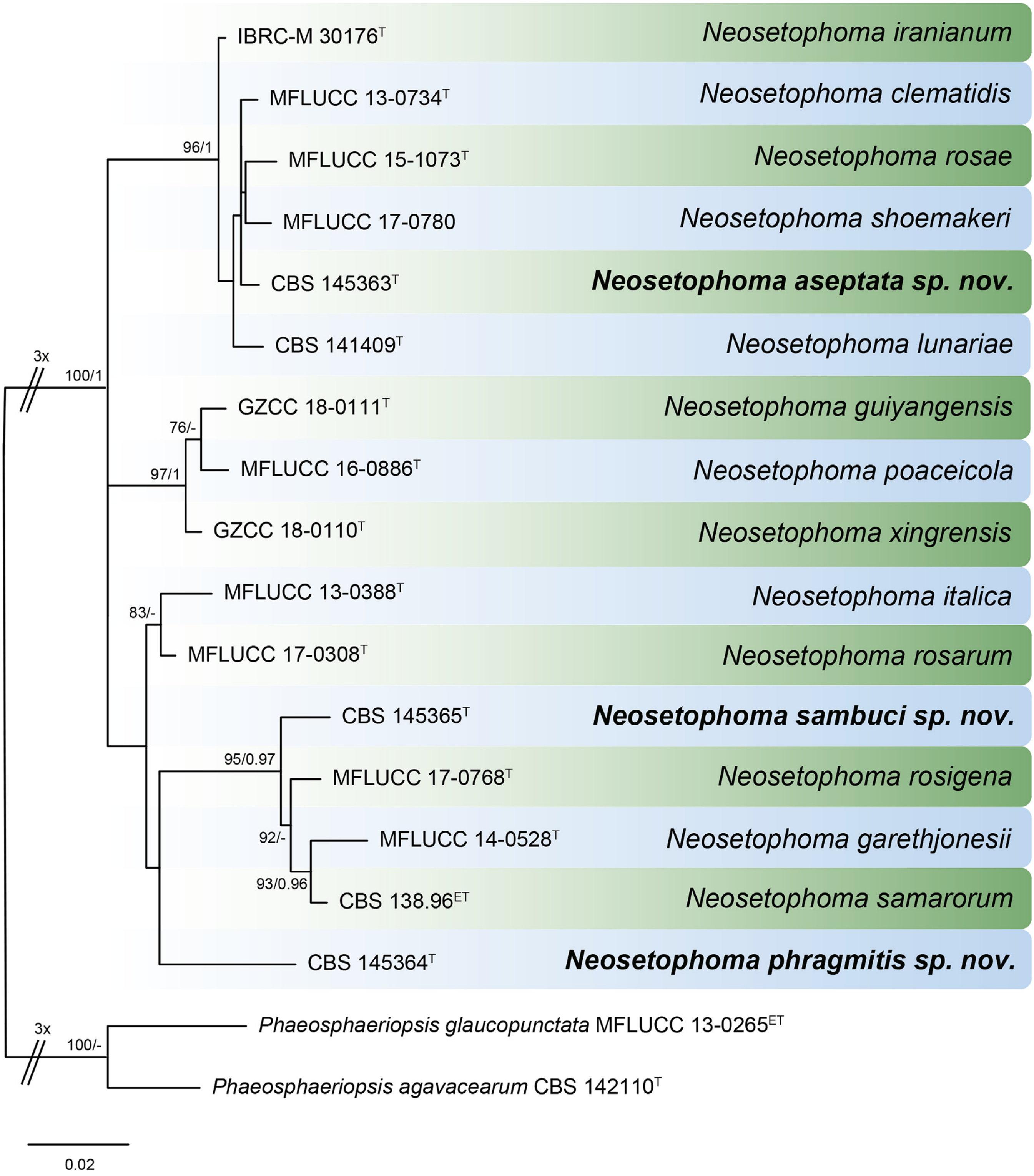

Fig. 29. RAxML phylogram obtained from the combined ITS (585 bp), LSU (848 bp) and *rpb2* (744 bp) sequence alignment of all accepted species of *Neosetophoma*. The tree was rooted to *Phaeosphaeriopsis glaucopunctata* MFLUCC 13-0265 and *Phaeosphaeriopsis agavacearum* CPC 29122. The novelties proposed 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 of LSU are listed in Fig. 28, and of the other loci in Tables 6 and 10. ^{T} and ^{ET} indicate ex-type and ex-epitype strains, respectively. TreeBASE: S23834.

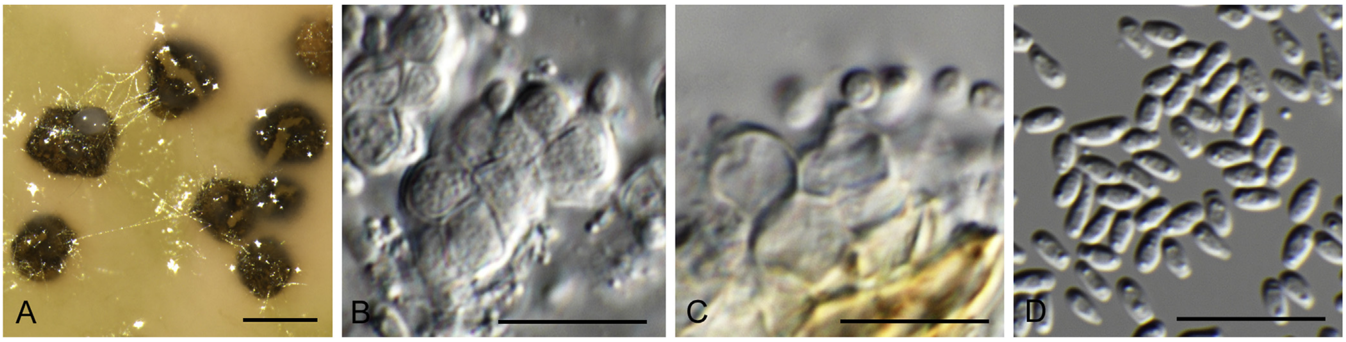

Fig. 30. *Neosetophoma aseptata* (ex-type CBS 145363). **A.** Conidiomata sporulating on OA. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars: A = 300 µm; others = 10 µm.

cells of *textura angularis. Conidiophores* reduced to conidiogenous cells lining inner cavity, hyaline, smooth-walled, subcylindrical to ellipsoid, phialidic with minute collarette, 4–8 × 4–5 µm. *Conidia* solitary, aseptate, hyaline, smooth-walled, subcylindrical to ellipsoid, apex obtuse, base truncate, (3.5–)4–5 × (1.5–)2 µm.

Culture characteristics: Colonies flat, spreading, surface folded, with moderate aerial mycelium and even, lobate margins, reaching 50 mm diam after 2 wk. On MEA surface pale olivaceous grey, reverse umber with diffuse umber pigment; on PDA surface olivaceous grey, reverse umber with diffuse umber pigment; on OA surface saffron with patches of grey olivaceous.

Typus: **Germany**, near Berlin, moist meadow, on *Viburnum opulus* (*Caprifoliaceae*), 7 Jun. 2017, R.K. Schumacher, HPC 2131, RKS 123 (**holotype** CBS H-23866, culture ex-type CBS 145363 = CPC 33919).

Notes: *Neosetophoma aseptata* was located in a large, well-supported clade (96 % BS / 1 PP) comprising *Nph. clematidis*, *Nph. iranianum*, *Nph. lunariae*, *Nph. rosae* and *Nph. shoemakeri*. *Neosetophoma aseptata* can be easily distinguished by its aseptate conidia, being 1-septate in *Nph. shoemakeri*, 1–3-septate in *Nph. iranianum* and *Nph. rosae*, 3-septate in *Nph. clematidis*, and (1–)3(–4)-septate in *Nph. lunariae.* Moreover, *Nph. aseptata* produces the smallest conidia in the complex [(3.5–)4–5 × (1.5–)2 µm in *Nph. aseptata vs.* 4–6 × 2–4 µm in *Nph. iranianum vs.* 7.5–10.5 × 2.5–3 µm in *Nph. shoemakeri vs.* 8–14 × 1.5–3 µm in *Nph. rosae vs.* 11–15 × 2–4 µm in *Nph. clematidis vs.* (10–)14–17(–22) × (2.5–)3 µm in *Nph. lunariae*]. *Neosetophoma clematidis* produces the largest conidiomata in this complex, being up to 475 µm diam (up to 300 µm in *Nph. aseptata* and *Nph. lunaria*, up to 180 µm in *Nph. shoemakeri*, up to 130 µm in *Nph. rosae*, up to 120 µm in *Nph. iranianum*).

Neosetophoma aseptata is the first species isolated from *Viburnum*. *Neosetophoma samarorum* and *Nph. sambuci* are reported in *Sambucus* spp., which is a member of the same family, *Caprifoliaceae.*

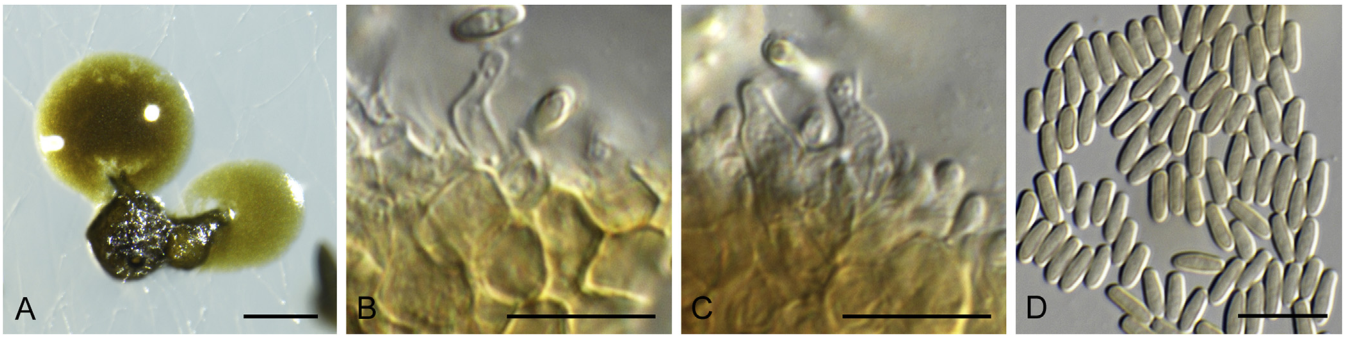

Fig. 31. *Neosetophoma phragmitis* (ex-type CBS 145364). **A.** Conidiomata sporulating on SNA. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars: A = 200 µm; others = 10 µm.

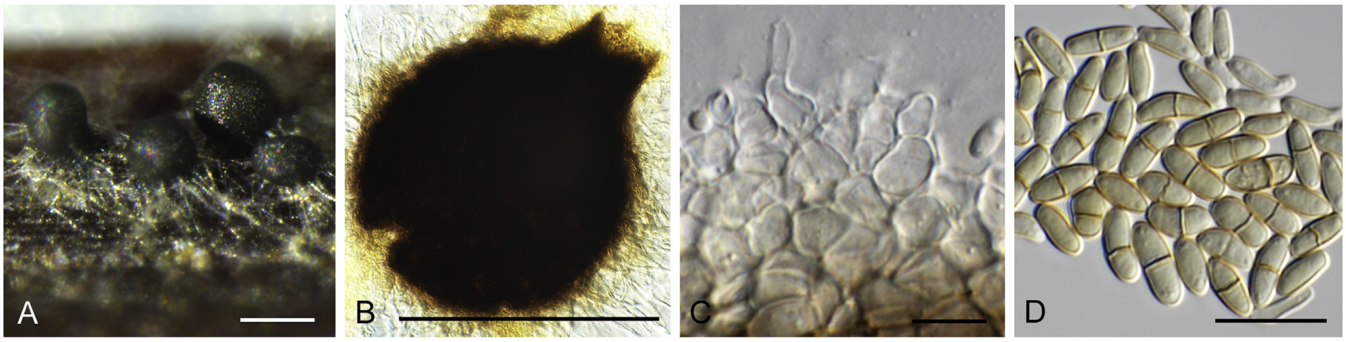

Fig. 32. *Neosetophoma sambuci* (ex-type CBS 145365). **A.** Conidiomata sporulating on PNA. **B.** Conidioma on SNA showing papillate neck. **C.** Conidiogenous cells. **D.** Conidia. Scale bars: A, B = 200 µm; others = 10 µm.

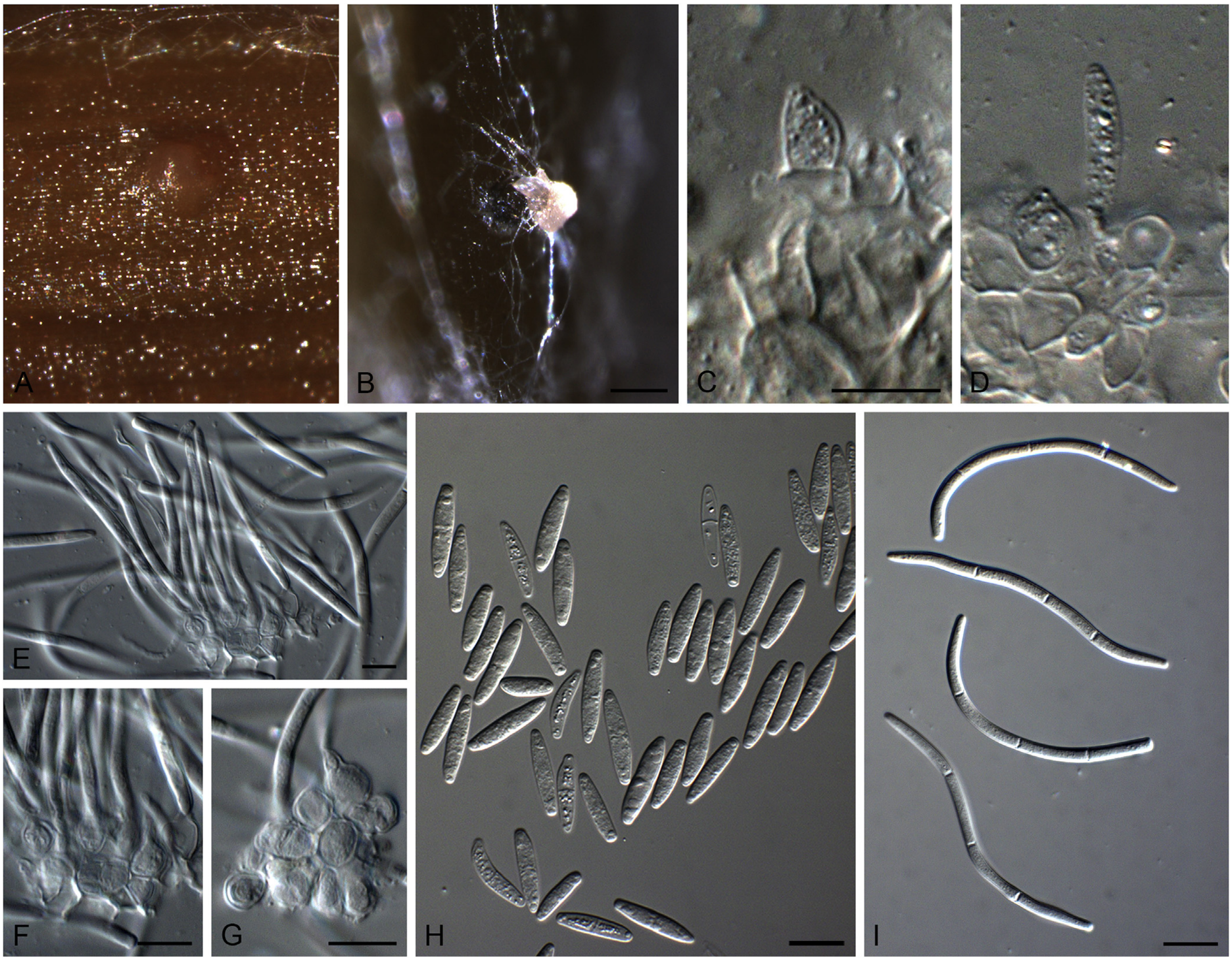

Fig. 33. *Neostagonospora* spp. **A, B.** Conidioma forming in culture. **A.** *Neostagonospora caricis* (ex-type CBS 135092). **B.** *Neostagonospora elegiae* (ex-type CBS 135101). **C–G.** Conidiogenous cells. **C, D.** *Neostagonospora caricis* (ex-type CBS 135092). **E–G.** *Neostagonospora elegiae* (ex-type CBS 135101). **H, I.** Conidia. **H.** *Neostagonospora caricis* (ex-type CBS 135092). **I.** *Neostagonospora elegiae* (ex-type CBS 135101). Scale bars: B = 150 µm; all others = 10 µm; C applies to C and D. Pictures taken from Quaedvlieg *et al.* (2013).

Neosetophoma phragmitis Crous, R.K. Schumach. & Y. Marín, ***sp. nov.*** MycoBank MB829640. Fig. 31.

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

Conidiomata solitary, pycnidial, brown, globose, 180–200 µm diam, neck papillate with central ostiole; *conidiomatal wall* of 3–4 layers of brown cells of *textura angularis. Conidiophores* reduced to conidiogenous cells lining inner cavity, hyaline, smooth-walled, ampulliform, 5–8 × 2.5–3 µm, proliferating percurrently at apex. *Conidia* solitary, pale brown, smooth-walled, aseptate, straight, apex obtuse, base truncate, (3–)4–5(–6) × 2 µm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and feathery margins, covering dish in 2 wk. On

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

Species	**Isolates**[1]	**GenBank accession numbers**[2]				**References**
		ITS	***rpb2***	***tef1***	***tub2***	
Neostagonospora arrhenatheri	MFLUCC 15-0464^{T}	KX926417	–	MG520901^{a}	–	Phookamsak *et al.* (2017), Thambugala *et al.* (2017)
Nst. caricis	CBS 135092^{T}	KF251163	KF252171	–	KF252658	Quaedvlieg *et al.* (2013)
Nst. elegiae	CBS 135101^{T}	KF251164	KF252172	KF253122^{b}	KF252659	Quaedvlieg *et al.* (2013)
Nst. phragmitis	MFLUCC 16-0493^{T}	KX926416	–	MG520902^{a}	–	Phookamsak *et al.* (2017), Thambugala *et al.* (2017)
Nst. sorghi	CBS 145366^{T}	MK539956	MK540087	MK540150^{b}	MK540168	Present study
Nst. spinificis	BCRC FU30120	KP676045	LC055104	–	–	Yang *et al.* (2016)

[1] BCRC: Bioresource Collection and Research Centre, Taiwan; CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Ria, Thailand. ^{T} indicates ex-type strains.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *rpb2*: partial DNA-directed RNA polymerase II second largest subunit gene; *tef1*: partial translation elongation factor 1-alpha gene; *tub2*: partial β-tubulin gene. ^{a} and ^{b} in *tef1* column indicate the primers used for sequencing: ^{a}: EF1-983F / EF1-2218R, ^{b}: EF1-728F / EF-2.

MEA surface and reverse ochreous; on PDA surface and reverse hazel; on OA surface hazel.

Typus: **Germany**, near Berlin, on leaf sheath of *Phragmites australis* (*Poaceae*), 16 Apr. 2016, R.K. Schumacher, HPC 1178 (**holotype** CBS H-23867, culture ex-type CBS 145364 = CPC 30680).

Notes: In the phylogenetic analysis based on ITS, LSU and *rpb2* sequences, *Nph. phragmitis* was located in an independent branch removed from the other species of the genus. This is the first species isolated from *Phragmitis australis* (*Poaceae*). *Neosetophoma poaceicola* is the only species that was reported before on a member of the *Poaceae*, being isolated from a grass host. However, both species are not related, and *Nph. phragmitis* only produces the asexual morph, while only the sexual morph was observed in *Nph. poaceicola*.

Neosetophoma sambuci Crous, R.K. Schumach. & Y. Marín, ***sp. nov.*** MycoBank MB829641. Fig. 32.

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

Conidiomata solitary, erumpent, brown, pycnidial, globose, 150–200 µm diam, with central ostiole; *conidiomatal wall* of 3–4 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth-walled, ampulliform, phialidic, 4–6 × 3–4 µm. *Conidia* solitary, pale brown, smooth-walled, guttulate, subcylindrical, apex obtuse, base truncate, aseptate, becoming 1-septate and swollen (ellipsoid) with age, (5–)7–8(–10) × (2–)2.5(–3) µm.

Culture characteristics: Colonies flat, spreading, covering dish in 2 wk, with sparse to moderate aerial mycelium. On MEA surface ochreous, reverse umber; on PDA surface and reverse olivaceous grey; on OA surface ochreous.

Typus: **Germany**, near Berlin, on twig of *Sambucus nigra* (*Caprifoliaceae*), 11 Mar. 2016, R.K. Schumacher, HPC 1072 (**holotype** CBS H-23868, culture ex-type CBS 145365 = CPC 30357).

Notes: In the phylogenetic analysis based on ITS, LSU and *rpb2* sequences, *Nph. sambuci* was located in a well-supported clade (97 % BS / 0.98 PP) together with *Nph. garethjonesii*, *Nph. samarorum* and *Nph. rosigena*. *Neosetophoma garethjonesii* can be easily distinguished from the other species by only producing a sexual morph. The other three species produce an asexual morph, and can be differentiated by the size of their conidia [4–16 × 1.5–3 µm in *Nph. samarorum vs.* (5–)7–8(–10) × (2–)2.5(–3) µm in *Nph. sambuci vs.* 4–6 × 1.5–2.5 µm in *Nph. rosigena*]. Moreover, conidia in *Nph. sambuci* are pale brown while in *Nph. samarorum* they are slightly yellowish and in *Nph. rosigena* they are olivaceous brown. *Neosetophoma sambuci* was isolated from twigs of *Sambucus nigra* (*Caprifoliaceae*). The only species previously reported on this host was *Nph. samarorum*.

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

Neostagonospora Quaedvl. *et al.*, Stud. Mycol. 75: 364. 2013. Fig. 33.

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

Type species: *Neostagonospora caricis* Quaedvlieg *et al.* Holotype and ex-type strain: CBS H-21306, CBS 135092.

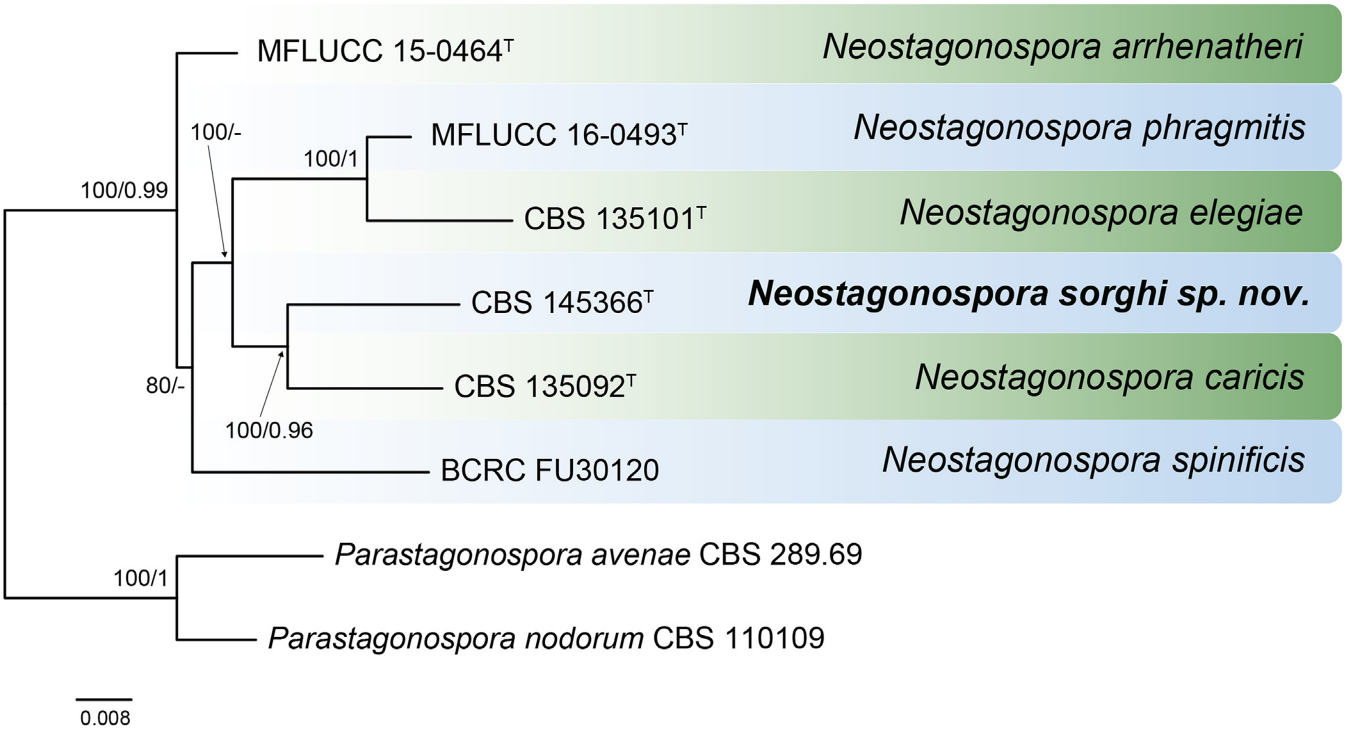

Fig. 34. RAxML phylogram obtained from the combined ITS (571 bp), LSU (847 bp), *rpb2* (337 bp) and *tub2* (304 bp) sequence alignment of all accepted species of *Neostagonospora*. The tree was rooted to *Parastagonospora avenae* CBS 289.69 and *Parastagonospora nodorum* CBS 110109. The novelty proposed 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 of LSU are listed in Fig. 28, and of the other loci in Tables 7 and 9. T indicates ex-type strains. TreeBASE: S23834.

DNA barcode (genus): LSU. Fig. 28.

DNA barcodes (species): ITS, *rpb2*, *tef1*, *tub2*. Table 7. Fig. 34.

Conidiomata immersed, pycnidial, globose, exuding a pale luteous to creamy conidial mass; *conidiomatal wall* composed of 2–3 layers of pale brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells*

Fig. 35. *Neostagonospora sorghi* (ex-type CBS 145366). **A.** Conidiomata sporulating on MEA. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars: A = 200 µm; others = 10 µm.

Fig. 36. *Nothophoma* spp. **A, B.** Disease symptoms. **A.** *Nothophoma quercina* (CGMCC 3.19246) on *Osmanthus fragrans*. **B.** *Nothophoma quercina* (LC12187) on *Jasminum mesnyi*. **C–I.** Asexual morph. **C, D.** Conidiomata of *Nothophoma anigozanthi* (ex-epitype CBS 381.91) sporulating on OA. **E–H.** Conidia. **E.** *Nothophoma infossa* (ex-neotype CBS 123395). **F.** *Nothophoma macrospora* (ex-type CBS 140674). **G.** *Nothophoma quercina* (CGMCC 3.19246). **H.** *Nothophoma variabilis* (ex-type CBS 142457). **I.** Conidiogenous cells of *Nothophoma macrospora* (ex-type CBS 140674). Scale bars: C = 200 µm; D = 20 µm; E–I = 10 µm. Pictures C, D taken from Chen *et al.* (2015); E from Aveskamp *et al.* (2009); F, I from Crous *et al.* (2016b); H from Valenzuela-Lopez *et al.* (2018).

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

Species	Isolates[1]	GenBank accession numbers[2]				References
		LSU	ITS	*rpb2*	*tub2*	
Nothophoma anigozanthi	CBS 381.91$^{\text{ET}}$	GU238039	GU237852	KT389655	GU237580	Aveskamp *et al.* (2010), Chen *et al.* (2015)
Not. arachidis-hypogaeae	CBS 125.93	GU238043	GU237771	KT389656	GU237583	Aveskamp *et al.* (2010), Chen *et al.* (2015)
Not. gossypiicola	CBS 377.67	GU238079	GU237845	KT389658	GU237611	Aveskamp *et al.* (2010), Chen *et al.* (2015)
Not. infossa	CBS 123395$^{\text{NT}}$	GU238089	FJ427025	KT389659	FJ427135	Aveskamp *et al.* (2009, 2010), Chen *et al.* (2015)
Not. macrospora	CBS 140674$^{\text{T}}$	LN880537	LN880536	LT593073	LN880539	Crous *et al.* (2016b)
Not. quercina	CBS 633.92	EU754127	GU237900	KT389657	GU237609	Aveskamp *et al.* (2010), Chen *et al.* (2015)
	CGMCC 3.19246	MK088581	MK088574	MK088588	MK088595	Present study
	LC12187	MK088582	MK088575	MK088589	MK088596	Present study
Not. raii	MCC 1082$^{\text{T}}$	–	MF664467	–	MF664468	Crous *et al.* (2017b)
Not. variabilis	CBS 142457$^{\text{T}}$	LN907428	LT592939	LT593078	LT593008	Valenzuela-Lopez *et al.* (2018)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CGMCC: Chinese General Microbiological Culture Collection Center, Beijing, China; LC: Dr Lei Cai's personal culture collection, housed at CAS, China; MCC: National Centre for Microbial Resources (formerly Microbial Culture Collection), Pune, India. $^{\text{T}}$, $^{\text{ET}}$ and $^{\text{NT}}$ indicate ex-type, ex-epitype and ex-neotype strains, respectively.

[2] LSU: partial large subunit (28S) nrRNA gene; ITS: internal transcribed spacers and intervening 5.8S nrDNA; *rpb2*: partial DNA-directed RNA polymerase II second largest subunit gene; *tub2*: partial β-tubulin gene.

phialidic, hyaline, smooth-walled, aggregated, lining the inner cavity, ampulliform to doliiform, tapering at apex with prominent periclinal thickening. *Conidia* hyaline, smooth-walled, granular, thin-walled, narrowly fusoid-ellipsoidal to subcylindrical, apex subobtusely rounded, base truncate, widest in middle, aseptate or transversely euseptate, becoming constricted with age (adapted from Quaedvlieg *et al.* 2013).

Culture characteristics: Colonies flat, spreading, erumpent, circular or undulate, smooth to velvety, even margins, with sparse to moderate aerial mycelium. On PDA, surface dirty white, greyish sepia to isabelline; reverse pale white to pale pink, pale pink with white edge, luteous or olivaceous grey to pale olivaceous grey.

Optimal media and cultivation conditions: PDA and sterilised *Carex* leaves or *Anthriscus* stem placed on 1.5 % water agar at 25 °C under continuous near-ultraviolet light to promote sporulation.

Distribution: Africa (South Africa), Asia (Russia and Taiwan), Australia and Europe (Italy and the Netherlands).

Hosts: *Arrhenatherum elatius*, *Phragmites australis*, *Sorghum halepense* and *Spinifex littoreus* (*Poaceae*), *Carex acutiformis* (*Cyperaceae*) and *Elegia cuspidata* (*Restionaceae*).

Disease symptoms: Leaf spots.

Notes: *Neostagonospora* was introduced by Quaedvlieg *et al.* (2013) to accommodate two taxa associated with leaf spots on *Carex acutiformis* (*Nst. caricis*) and *Elegia cuspidata* (*Nst. elegiae*). However, its pathogenicity remains unclear since Koch's postulates have not been completed. Subsequently, another foliicolous fungus was included in this genus, *Nst. spinificis* (Yang *et al.* 2016), associated with green tissues and leaf spots of *Spinifex littoreus*. The most recently introduced species are both saprobes on members of *Poaceae*: *Nst. arrhenatheri* and *Nst. phragmitis* (Thambugala *et al.* 2017). Further studies are needed to prove the pathogenicity of members included in this genus.

Neostagonospora is similar to *Stagonospora* since both produce pycnidial conidiomata with euseptate, hyaline, fusoid-ellipsoidal to subcylindrical conidia, but *Neostagonospora* is distinguished by having conidiogenous cells that are phialidic, with prominent periclinal thickening (Quaedvlieg *et al.* 2013).

In our phylogenetic analysis based on ITS and LSU sequences of members of the family *Phaeosphaeriaceae* (Fig. 28), *Nst. artemisiae*, which was the most recently described species (Wanasinghe *et al.* 2018), is not included in the clade that represents the genus *Neostagonospora*, being located in the *Septoriella* clade. Therefore, this species is excluded from *Neostagonospora* and transferred to *Septoriella* (see *Septoriella* below).

References: Quaedvlieg *et al.* 2013, Yang *et al.* 2016, Thambugala *et al.* 2017 (morphology and phylogeny).

Neostagonospora sorghi Crous & Y. Marín, ***sp. nov.*** MycoBank MB829612. Fig. 35.

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

Conidiomata solitary, erumpent, pycnidial, brown, globose, 180–200 μm diam, with central ostiole; *conidiomatal wall* of 2–3 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* hyaline to pale brown, smooth-walled, ampulliform, phialidic with visible periclinal thickening and collarette, 5–8 × 4–5 μm. *Conidia* solitary, aseptate, ellipsoid with obtuse ends, straight, guttulate, (4–)5–6 × (2–)2.5(–3) μm.

Culture characteristics: Colonies flat, spreading with moderate aerial mycelium and even, lobate margins, covering dish in 2 wk. On MEA surface hazel to isabelline, reverse isabelline; on PDA surface isabelline with scarlet outer margins, reverse brown vinaceous; on OA surface isabelline with patches of scarlet.

Typus: **Australia**, Western Australia, Denmark, Mount Lindesay Walk trail, on *Sorghum halepense* (*Poaceae*), 19 Sep. 2015, P.W. Crous, HPC 697A (**holotype** CBS H-23869, culture ex-type CBS 145366 = CPC 29239).

Notes: *Neostagonospora sorghi* is the first species of the genus reported from *Sorghum*, and occurring in Australia. It is closely

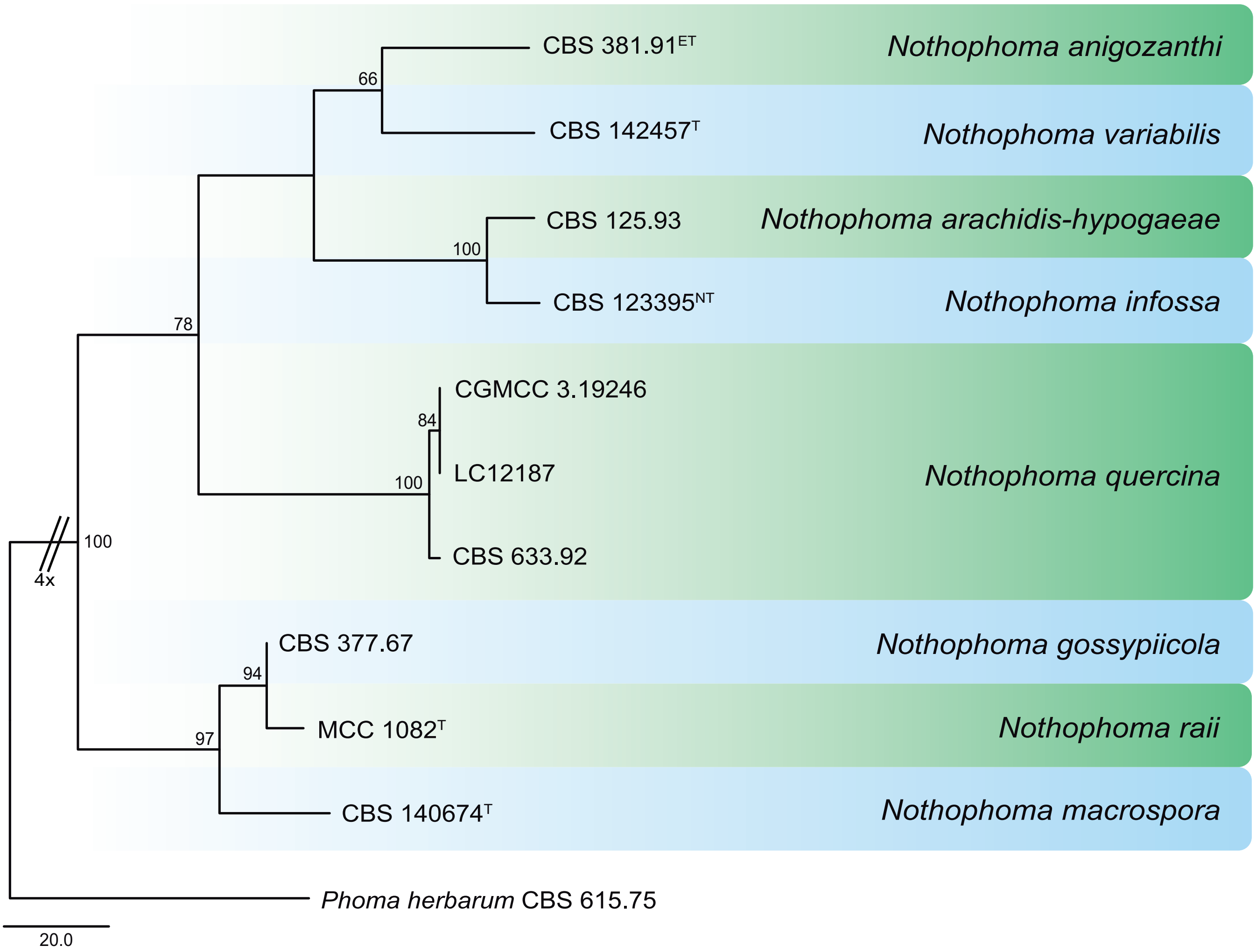

Fig. 37. Phylogenetic tree generated from a maximum parsimony analysis based on the combined LSU (868 bp), ITS (490 bp), *tub2* (336 bp) and *rpb2* (845 bp) sequences of all accepted species of *Nothophoma*. The tree was rooted to *Phoma herbarum* CBS 615.75. Values above the branches represent parsimony bootstrap support values (> 50 %). GenBank accession numbers are indicated in Table 8. $^{T,\ ET}$ and ^{NT} indicate ex-type, ex-epitype and ex-neotype strains, respectively. TreeBASE: S23494.

related to *Nst. caricis*, which is associated with leaf spots on *Carex acutiformis*. However, *Nst. sorghi* can be distinguished from this species and from other species of the genus by its aseptate conidia. Moreover, *Nst. sorghi* produces smaller conidia than *Nst. caricis* [(4–)5–6 × (2–)2.5(–3) µm in *Nst. sorghi vs.* (10–)13–16(–19) × (3–)3.5(–4) µm in *Nst. caricis*].

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

Nothophoma Q. Chen & L. Cai, Stud. Mycol. 82: 212. 2015. Fig. 36.

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

Type species: *Nothophoma infossa* (Ellis & Everh.) Q. Chen & L. Cai, basionym: *Phoma infossa* Ellis & Everh., J. Mycol. 4: 102. 1888. Neotype and ex-neotype strain designated by Aveskamp *et al.* (2009): CBS H-20145, CBS 123395.

DNA barcodes (genus): LSU, ITS.

DNA barcodes (species): *rpb2*, *tub2*. Table 8. Fig. 37.

Conidiomata pycnidial, globose to elongated, or irregular, superficial or immersed into the agar, solitary or confluent, ostiolate, sometimes with an elongated neck; *conidiomatal wall* pseudoparenchymatous, multi-layered, outer wall pigmented. *Conidiogenous cells* phialidic, hyaline, smooth-walled, ampulliform to doliiform, sometimes flask-shaped. *Conidia* hyaline but incidentally brown, smooth- and thin-walled, aseptate, ovoid or ellipsoidal, eguttulate or guttulate. *Chlamydospores* elongated barrel-shaped, olivaceous brown, in chains. *Sexual morph* unknown (adapted from Chen *et al.* 2015, Crous *et al.* 2017b).

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

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

Distribution: Worldwide.

Hosts: Wide host range, mainly occurring as pathogens, and also endophytes or saprobes, on *Amaryllidaceae*, *Anacardiaceae*, *Fabeceae*, *Fagaceae*, *Haemodoraceae*, *Malvaceae*, *Oleaceae*, *Rosaceae*, *Rhamnaceae* and *Rutaceae*. Also isolated from other substrates and environments, such as soil, fungi and human infections.

Disease symptoms: Leaf spots, stem cankers, brown spot of fruits, shoot canker.

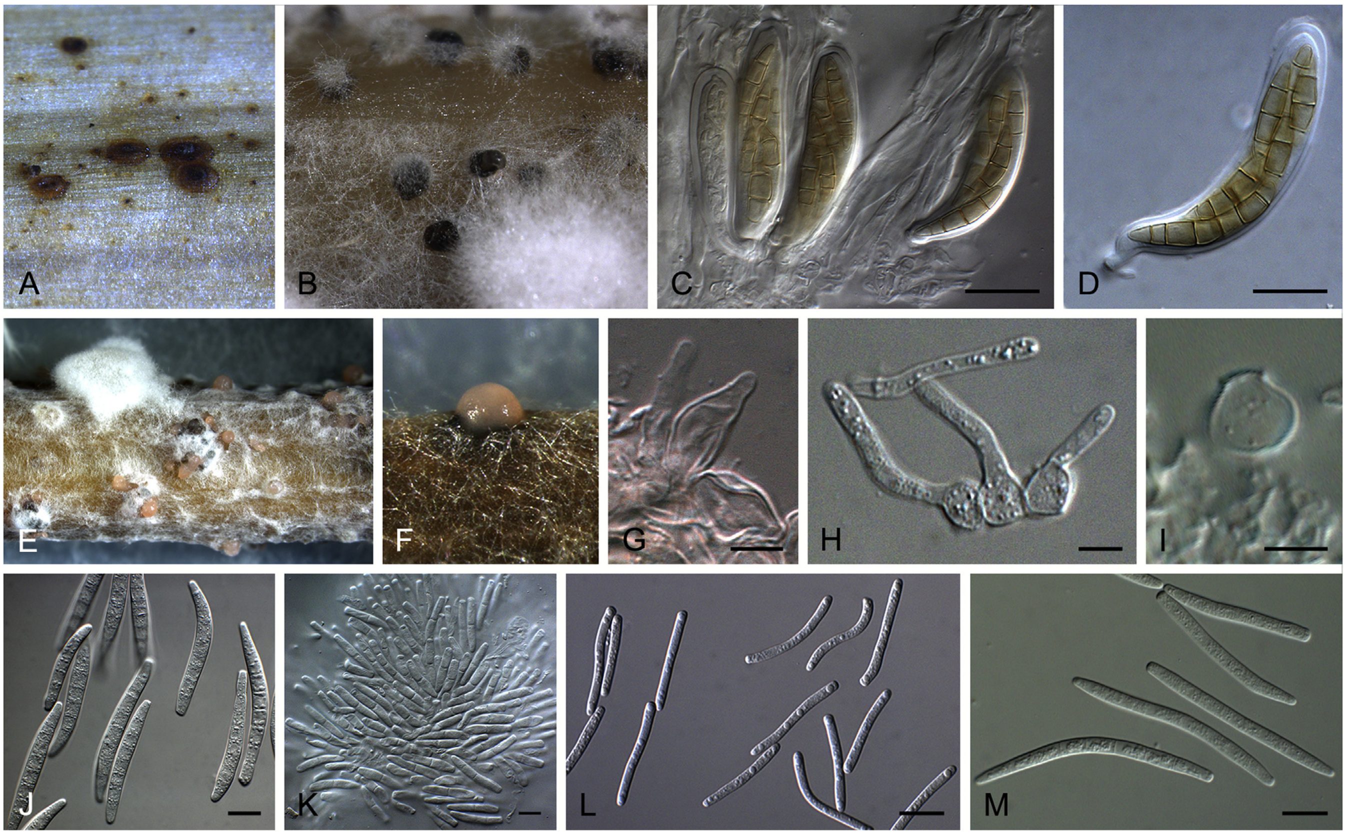

Fig. 38. *Parastagonospora* spp. **A–D.** Sexual morph of *Parastagonospora nodorum* (CBS H-13909). **A, B.** Ascomata. **C, D.** Asci and ascospores. **E–M.** Asexual morph. **E, F.** Conidiomata. **E.** *Parastagonospora poagena* (ex-type CBS 136776). **F.** *Parastagonospora poae* (CBS 135091). **G–I.** Conidiogenous cells. **G.** *Parastagonospora caricis* (ex-type CBS H-21304). **H.** *Parastagonospora poae* (CBS 135091). **I.** *Parastagonospora poagena* (ex-type CBS 136776). **J–M.** Conidia. **J.** *Parastagonospora caricis* (ex-type CBS H-21304). **K.** *Parastagonospora nodorum* (CBS H-13909). **L.** *Parastagonospora poae* (CBS 135091). **M.** *Parastagonospora poagena* (ex-type CBS 136776). Scale bars: C, D, J–M = 10 µm; G–I = 5 µm. Pictures A–D, F–H, J–L taken from Quaedvlieg *et al.* (2013); E, I, M from Crous *et al.* (2014b).

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

Species	**Isolates**[1]	**GenBank accession numbers**[2]				**References**
		ITS	***rpb2***	***tef1***	***tub2***	
Parastagonospora allouniseptata	MFLUCC 13-0386^{T}	KU058711	–	MG520914^{a}	–	Li *et al.* (2015), Phookamsak *et al.* (2017)
P. avenae	CBS 289.69	KF251174	KF252182	KF253132^{b}	KF252669	Quaedvlieg *et al.* (2013)
	MFLUCC 13-0557^{T} of *P. forlicesenica*	KY769660	–	–	–	Thambugala *et al.* (2017)
P. caricis	CBS 135671^{T}	KF251176	KF252184	KF253134^{b}	KF252671	Quaedvlieg *et al.* (2013)
P. dactylidis	MFLUCC 13-0375^{T}	KU058712	–	–	–	Li *et al.* (2015)
	MFLUCC 13-0376^{T} of *P. minima*	KU058713	–	MG520916^{a}	–	Li *et al.* (2015), Phookamsak *et al.* (2017)
	MFLUCC 13-0573^{T} of *P. cumpignensis*	KU842388	–	–	–	Li *et al.* (2016a)
P. fusiformis	MFLUCC 13-0215^{T}	KX926418	KX863711	–	–	Thambugala *et al.* (2017)
P. italica	MFLUCC 13-0377^{T}	KU058714	–	MG520915^{a}	–	Li *et al.* (2015), Phookamsak *et al.* (2017)
P. nodorum	CBS 110109	KF251177	KF252185	KF253135^{b}	KF252672	Quaedvlieg *et al.* (2013)
P. novozelandica	CBS 145416^{T}	MK539957	MK540088	MK540151	MK540169	Present study
P. phragmitis	CBS 143446^{T}	MK539958	MK540089	MK540152	–	Present study
P. poaceicola	MFLUCC 15-0471^{T}	KX926419	KX880499	–	–	Thambugala *et al.* (2017)
P. poae	CBS 135089^{T}	KF251178	KF252186	KF253136^{b}	KF252673	Quaedvlieg *et al.* (2013)
P. poagena	CBS 136776^{T}	KJ869116	–	–	–	Crous *et al.* (2014b)
P. uniseptata	MFLUCC 13-0387^{T}	KU058715	–	MG520917^{a}	–	Li *et al.* (2015), Phookamsak *et al.* (2017)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Ria, Thailand. ^{T} indicates ex-type strains.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *rpb2*: partial DNA-directed RNA polymerase II second largest subunit gene; *tef1*: partial translation elongation factor 1-alpha gene; *tub2*: partial β-tubulin gene. ^{a} and ^{b} in *tef1* column indicate the primers used in sequencing: ^{a}: EF1-983F / EF1-2218R, ^{b}: EF1-728F / EF-2.

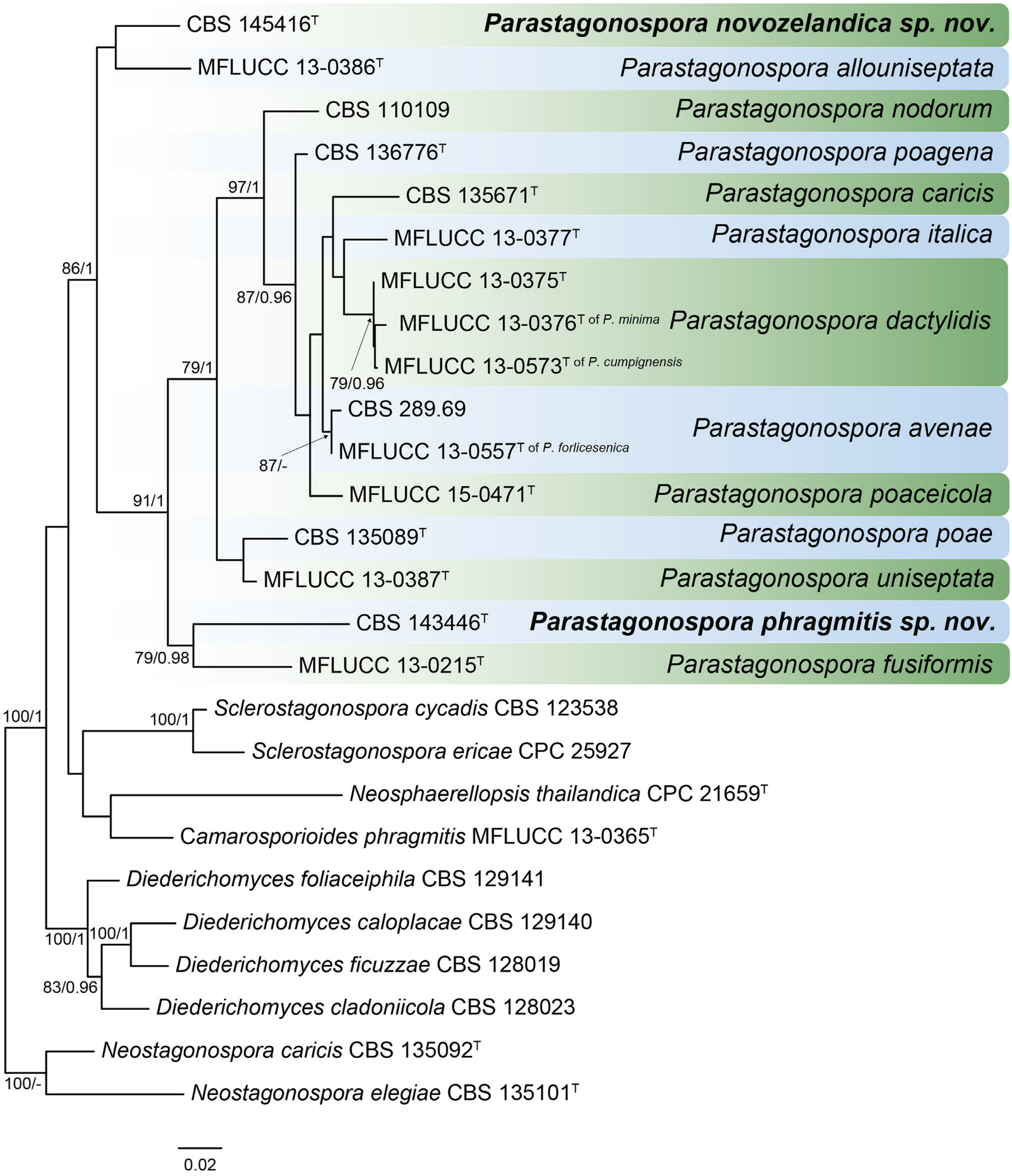

Fig. 39. RAxML phylogram obtained from the combined ITS (575 bp), LSU (848 bp), *rpb2* (337 bp) and *tef1* (866 bp) sequence alignment of all accepted species of *Parastagonospora*. The tree was rooted to *Neostagonospora carici* CBS 135092 and *Neostagonospora elegiae* CBS 135101. The novelties proposed 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 of LSU are listed in Fig. 28, and of the others loci are indicated in Tables 7 and 9. T indicates ex-type strains. TreeBASE: S23834.

Notes: *Nothophoma* was one of the genera established recently in order to delineate a more natural classification for the *Ascochyta-Didymella-Phoma* complex (Chen *et al.* 2015). Currently this genus comprises nine species, including five *Phoma* species previously classified in *Phoma*, and four species that were recently proposed (Crous *et al.* 2016b, 2017b, Valenzuela-Lopez *et al.* 2018). Within *Nothophoma* morphological differences between species are insignificant, and phylogenies based on multi-locus sequence data are primarily used to distinguish species.

Species in this genus are seed- and soil-borne endophytes or pathogens mainly causing leaf spots and stem canker of cultivated crops and plants, such as groundnut and cotton. Some species are mycophylic on other fungi or occur in soil, as well as

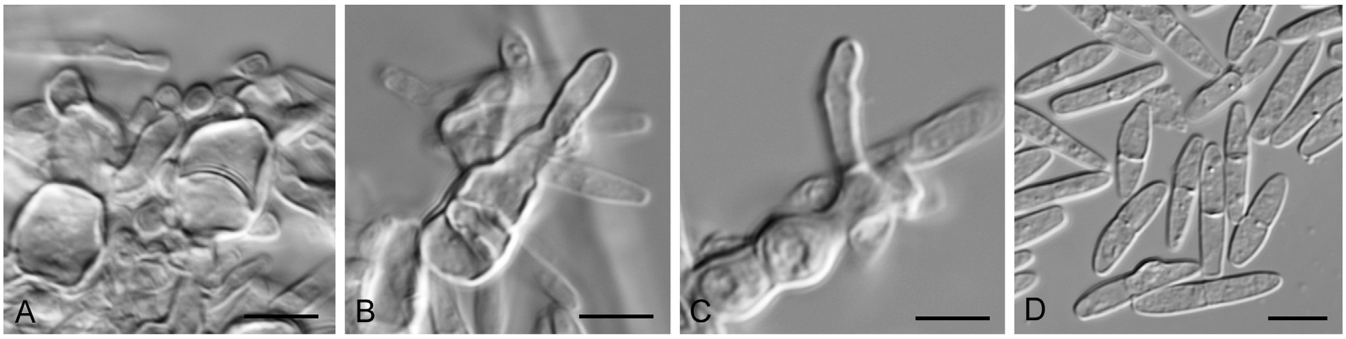

Fig. 40. *Parastagonospora novozelandica* (ex-type CPC 29613). **A–C.** Conidiogenous cells. **D.** Conidia. Scale bars = 10 µm.

in the respiratory secretion of a patient with pneumonia or in a human bronchial wash sample (Boerema *et al.* 2004, Aveskamp *et al.* 2009, 2010, Chen *et al.* 2015, Crous *et al.* 2016b, 2017b, Valenzuela-Lopez *et al.* 2018).

References: Boerema *et al.* 2004 (morphology and pathogenicity), Aveskamp *et al.* 2010, Chen *et al.* 2015, Crous *et al.* 2016b, 2017b, Valenzuela-Lopez *et al.* 2018 (morphology and phylogeny).

Authors: Q. Chen & L. Cai

Parastagonospora Quaedvl. *et al.*, Stud. Mycol. 75: 362. 2013. Fig. 38.

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

Type species: *Parastagonospora nodorum* (Berk.) Quaedvlieg *et al.*, basionym: *Depazea nodorum* Berk. Reference strain: CBS 110109.

DNA barcode (genus): LSU. Fig. 28.

DNA barcodes (species): ITS, *rpb2*, *tef1, tub2*. Table 9. Fig. 39.

Ascomata perithecial, immersed, globose, becoming depressed, dark brown to black, with central ostiole with upper region slightly papillate; *ascomatal wall* thin- or thick-walled, composed of 2–6 layers of brown cells of *textura angularis*. *Pseudoparaphyses* filiform, hyaline, septate. *Asci* bitunicate, clavate, cylindrical, narrowly fusoid or curved, shortly stipitate, thick-walled, 8-spored. *Ascospores* fusoid or ellipsoidal, hyaline or subhyaline to pale brown, smooth-walled, transversely 3-euseptate, cells above central septum often broader than the lower ones, with acute rounded ends, constricted or not at each septum, sometimes with distinct oil droplets in each cell. *Conidiomata* pycnidial, brown to black, erumpent or immersed to semi-immersed, subepidermal, globose to subglobose, ampulliform, or obpyriform, with central papillate ostiole, exuding creamy or pinkish conidial mass; *conidiomatal wall* composed of 2–4 layers of brown cells of *textura angularis,* or composed of 1–5 outer layers of dark brown cells and 1–3 inner layers of hyaline cells of *textura angularis,* or composed of an outer layer of brown to dark brown cells of *textura globosa* and an inner layer of pale brown to hyaline cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* phialidic, hyaline, smooth-walled, aggregated, lining the inner cavity, ampulliform to subcylindrical, broadly cylindrical or broadly conical, with percurrent proliferation near apex. *Conidia* hyaline or subhyaline, smooth-walled, thin- or thick-walled, cylindrical, subcylindrical or fusiform, granular to multi-guttulate, with obtuse or subobtuse apex and truncate base, rarely rounded at both ends, straight to gently curved, sigmoid, transversely 1–9-euseptate, sometimes constricted at the septa (adapted from Quaedvlieg *et al.* 2013).

Culture characteristics: Colonies flat, with aerial mycelium, white to pink, olivaceous, grey or vinaceous buff.

Optimal media and cultivation conditions: Sterilised *Carex* leaves placed on 1.5 % WA at 25 °C under continuous near-ultraviolet light to promote sporulation.

Distribution: Worldwide.

Hosts: Pathogens or saprophytes of grass (*Poaceae*). Species of *Parastagonospora* are directly or indirectly responsible for significant annual crop losses worldwide on wheat, barley and rye.

Disease symptoms: Leaf, glume and node spots.

Notes: *Parastagonospora* was recently introduced in order to accommodate a clade of several common and serious cereal

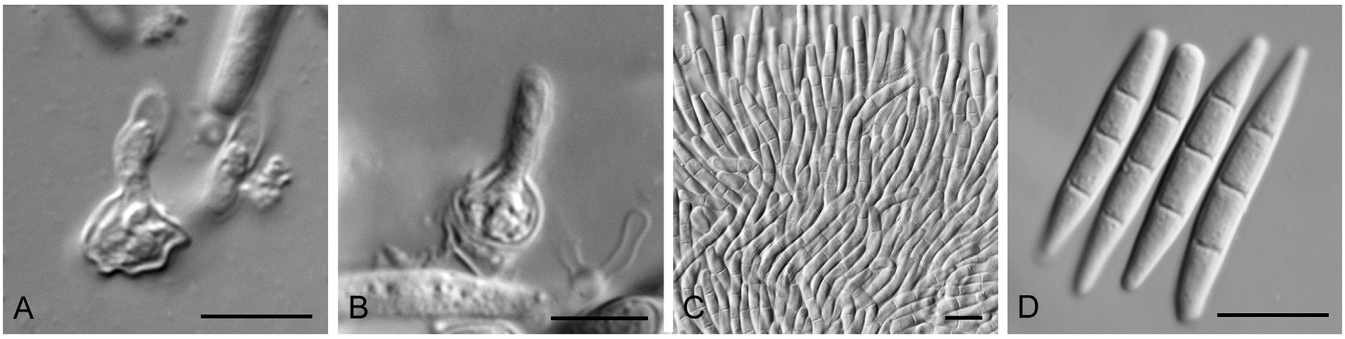

Fig. 41. *Parastagonospora phragmitis* (ex-type CPC 32075). **A, B.** Conidiogenous cells. **C, D.** Conidia. Scale bars = 10 µm.

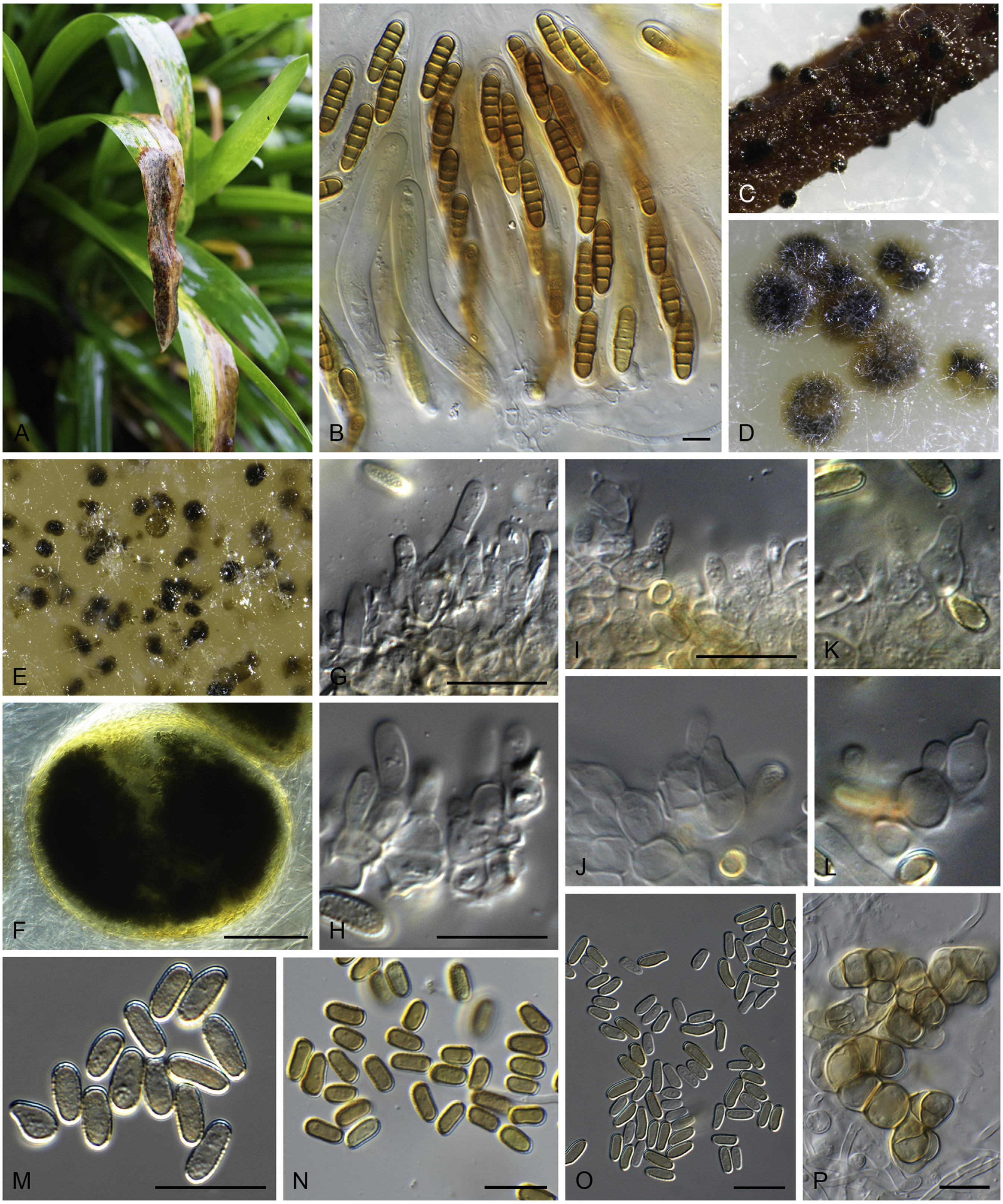

Fig. 42. *Phaeosphaeriopsis* spp. **A.** Symptomatic leaves of *Agapanthus precox* caused by *Phaeosphaeriopsis agapanthi*. **B.** Asci and ascospores of *Phaeosphaeriopsis agavacearum* (ex-type CBS 142110). **C–P.** Asexual morph. **C, D.** Conidiomata sporulating on PNA and OA, respectively, of *Phaeosphaeriopsis agapanthi* (ex-type CBS 141287). **E.** Conidiomata sporulating on OA of *Phaeosphaeriopsis agavacearum* (ex-type CBS 142110). **F.** Conidioma of *Phaeosphaeriopsis agavacearum* (ex-type CBS 142110). **G–L.** Conidiogenous cells giving rise to conidia. **G, H.** *Phaeosphaeriopsis agapanthi* (ex-type CBS 141287). **I–L.** *Phaeosphaeriopsis glaucopunctata* (CBS 653.86). **M–O**. Conidia. **M.** *Phaeosphaeriopsis agapanthi* (ex-type CBS 141287). **N.** *Phaeosphaeriopsis agavacearum* (ex-type CBS 142110). **O.** *Phaeosphaeriopsis glaucopunctata* (CBS 653.86). **P.** Chlamydospores of *Phaeosphaeriopsis agavacearum* (ex-type CBS 142110). Scale bars: F = 100 µm; others = 10 µm; I applies to I–L. Pictures A, C, D, G, H, M taken from Crous *et al.* (2016b); B, E, F, N, P from Crous *et al.* (2016a); I–L, O from Quaedvlieg *et al.* (2013).

pathogens that had been previously been placed in the genera *Septoria/Stagonospora* or *Leptosphaeria/Phaeosphaeria* (Quaedvlieg *et al.* 2013). This genus differs from *Stagonospora* mainly in the sexual morph, being phaeosphaeria-like in *Parastagonospora* and didymella-like in *Stagonospora*.

In the phylogenetic analysis based only on the ITS and LSU sequences of representative members of the family *Phaeosphaeriaceae* (Fig. 28), all the species of *Parastagonospora* were located in a well-supported clade (0.98 PP), except for *P. phoenicicola*. The ex-type strain of this latter species clustered in well-supported clade (84 % BS) representing the genus *Phaeosphaeria*. Therefore, a new combination is proposed for this taxon.

In our phylogenetic analysis (Fig. 39), *P. cumpignensis*, *P. dactylidis* and *P. minima* grouped in the same well-supported clade (79 % BS / 0.96 PP) without significant phylogenetic distance. The three species all have been isolated from Thailand on dead stems of *Dactylis* (Li *et al.* 2015, 2016a). Only ITS sequences are available for *P. cumpignensis* and *P. dactylidis*, and nucleotide similarity for this locus for all three species is 100 %. Therefore, these three species are reduced to synonymy. The same problem is found in *P. forlicesenica*, which is one of the most recently described species in the genus (Thambugala *et al.* 2017). Based on ITS, *P. forlicesenica* shares a nucleotide similarity of 99.8 % with *P. avenae*. Therefore, further studies should be done to confirm if *P. forlicesenica* represents a separate species or should be synonymised with *P. avenae*.

Species of *Parastagonospora* are pathogens or saprophytes of grasses, being directly or indirectly responsible for significant annual crop losses worldwide. *Parastagonospora avenae* causes minor leaf blotch of barley and rye, while it is considered an important pathogen of oats (Cunfer 2000). *Parastagonospora nodorum* is known primarily as a major necrotrophic pathogen of wheat that causes leaf and glume blotch, but also infects barley, on which it is considered as not economically important (Cunfer 2000, Oliver *et al.* 2012).

References: Cunfer 2000 (pathology and morphology), Oliver *et al.* 2012 (pathology, genomics and host resistence), Quaedvlieg *et al.* 2013, Li *et al.* 2015, Thambugala *et al.* 2017 (morphology and phylogeny).

Parastagonospora dactylidis W.J. Li *et al.*, Mycosphere 6: 691. 2015.

Synonyms: *Parastagonospora minima* W.J. Li, *et al.*, Mycosphere 6: 691. 2015.

Parastagonospora cumpignensis Tibpromma *et al.*, Fungal Diversity 78: 48. 2016.

Typus: **Italy**, Province of Arezzo, Passo della Consuma, on dead stem of *Dactylis* sp. (*Poaceae*), 19 Jun. 2012, Erio Camporesi (**holotype** MFLU 15-0693, culture ex-type MFLUCC 13-0375 = ICMP 20774 = KUMCC15-0131).

Additional materials: **Italy**, Province of Arezzo, Passo della Consuma, on dead stem of *Dactylis* sp. (*Poaceae*), 19 Jun. 2012, Erio Camporesi, MFLUCC 13-0376 = ICMP 20776 = KUMCC15-0132; *ibid*., Campigna, Santa Sofia, ForlìCesena Province, on dead stem of *Dactylis glomerata* (*Poaceae*), 23 Jun. 2012, Erio Camporesi, MFLUCC 13-0573.

Notes: In our phylogenetic analysis (Fig. 39), the ex-type strains of *P. cumpignensis* (MFLUCC 13- 0573), *P. dactylidis* (MFLUCC 13-0375) and *P. minima* (MFLUCC 13-0376) grouped in the same well-supported clade (79 % BS / 0.96 PP) without significant phylogenetic distance. The ITS sequences of the three species showed a nucleotide similarity of 100 %. Moreover, all of them were isolated from from Thailand on dead stems of *Dactylis* (Li *et al.* 2015, 2016a). Therefore, the three species are herewith reduced to synonymy.

Parastagonospora novozelandica Crous, Thangavel & Y. Marín, ***sp. nov.*** MycoBank MB829668. Fig. 40.

Etymology: Name refers to New Zealand, the country where this fungus was isolated.

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

Species	**Isolates**[1]	**GenBank accession numbers**[2]				**References**
		ITS	***rpb2***	***tef1***	***tub2***	
Phaeosphaeriopsis agapanthi	CBS 141287^{T}	KX228260	MK540094	MK540157^{a}	MK540173	Crous *et al.* (2016b), present study
Phs. agavacearum	CBS 142110^{T}	KY173430	KY173591	MK540158^{a}	KY173610	Crous *et al.* (2016a), present study
Phs. agavensis	CBS 102206	KY090635	KY090685	–	–	Ahmed *et al.* (2017)
Phs. aloes	CBS 145367^{T}	MK539959	MK540090	MK540153^{a}	–	Present study
Phs. aloicola	CBS 145368^{T}	MK539960	MK540091	MK540154^{a}	MK540170	Present study
Phs. amblyospora	CBS 110131^{T}	AY188993	–	–	–	Câmara *et al.* (2003)
Phs. dracaenicola	MFLUCC 11-0157^{T}	KM434273	KM434309	KM434301^{b}	–	Phookamsak *et al.* (2014b)
Phs. glaucopunctata	MFLUCC 13-0265^{ET}	KJ522473	–	MG520918^{b}	–	Thambugala *et al.* (2014), Phookamsak *et al.* (2017)
Phs. grevilleae	CBS 145369^{T}	MK539961	MK540092	MK540155^{a}	MK540171	Present study
Phs. nolinae	CBS 102205	KY090637	KY090686	–	–	Ahmed *et al.* (2017)
Phs. obtusispora	CBS 102204	KY090636	KY090687	–	–	Ahmed *et al.* (2017)
Phs. phacidiomorpha	T111	FJ462742	–	–	–	Zhang *et al.* (unpubl. data)
Phs. pseudoagavacearum	CBS 145370^{T}	MK539962	MK540093	MK540156^{a}	MK540172	Present study
Phs. triseptata	MFLUCC 13-0271^{T}	KJ522475	KJ522485	MG520919^{b}	–	Thambugala *et al.* (2014), Phookamsak *et al.* (2017)
Phs. yuccae	MFLUCC 16-0558^{T}	KY554482	–	MG520920^{b}	–	Phookamsak *et al.* (2017)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Ria, Thailand; T: isolate housed in China. ^{T} and ^{ET} indicate ex-type and ex-epitype strains.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *rpb2*: partial DNA-directed RNA polymerase II second largest subunit gene; *tef1*: partial translation elongation factor 1-alpha gene; *tub2*: partial β-tubulin gene. ^{a} and ^{b} in *tef1* column indicate the primers used in sequencing: ^{a}: EF1-728F / EF-2, ^{b}: EF1-983F / EF1-2218R.

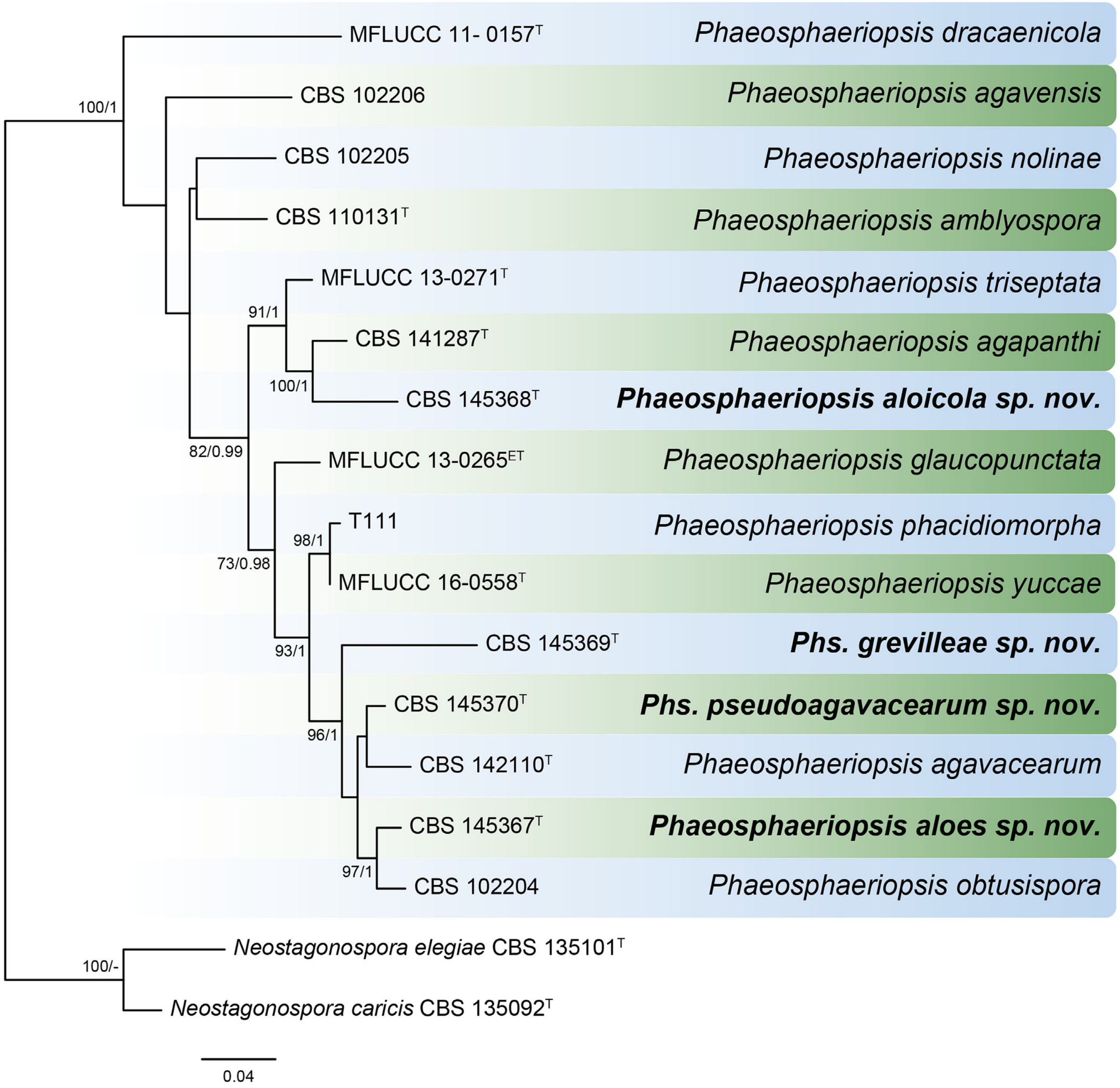

Fig. 43. RAxML phylogram obtained from the combined ITS (587 bp), LSU (849 bp), *rpb2* (838 bp), *tef1* (601 bp) and *tub2* (519 bp) sequence alignment of all accepted species of *Phaeosphaeriopsis*. The tree was rooted to *Neostagonospora caricis* CBS 135092 and *Neostagonospora elegiae* CBS 135101. 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 of LSU are listed in Fig. 28, and of the other loci in Tables 7 and 9. ^{T} and ^{ET} indicate ex-type and ex-epitype strains, respectively. TreeBASE: S23834.

Culture nearly sterile, with only a few conidiomata observed. *Conidiomata* solitary, pycnidial, dark brown, globose, 180–200 µm diam, with central ostiole; *conidiomatal wall* with 3–6 layers of pale brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* hyaline, smooth, ampulliform to subcylindrical, 6–8 × 2.5–5 µm, proliferating percurrently at apex. *Conidia* solitary, hyaline to pale olivaceous, smooth, guttulate, subcylindrical, straight, apex subobtuse, base truncate, 1-septate, (9–)11–13(–16) × (2–)2.5(–3) µm.

Culture characteristics: Colonies flat, spreading, reaching 60 mm diam after 2 wk, with moderate aerial mycelium, and even, smooth margins. On MEA surface greenish olivaceous to umber, reverse olivaceous to umber; on OA surface brown vinaceous.

Typus: **New Zealand**, Browns Bay, on unidentified grass (*Poaceae*), Nov. 2015, R. Thangavel (**holotype** CBS H-23903, culture ex-type T15–06960B = CPC 29613 = CBS 145416).

Notes: *Parastagonospora novozelandica* is related to *P. allouniseptata*. Both species produce 1-septate conidia, but these can be easily distinguished based on their conidial dimensions [(9–)11–13(–16) × (2–)2.5(–3) µm in *P. novozelandica vs.* 16–22 × 2.5–3.5 µm in *P. allouniseptata*].

Parastagonospora phragmitis Crous & Y. Marín, ***sp. nov.*** MycoBank MB829667. Fig. 41.

Etymology: Name reflects the genus *Phragmites* from which this fungus was isolated.

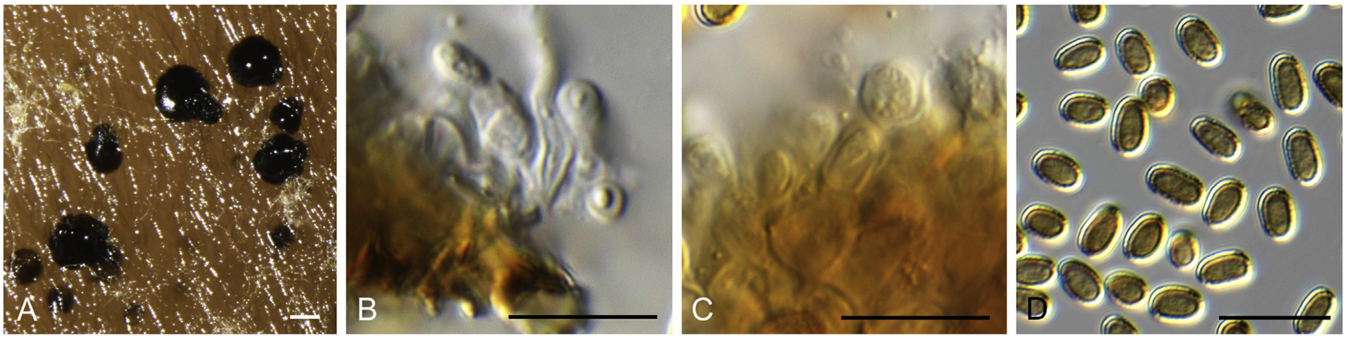

Fig. 44. *Phaeosphaeriopsis aloes* (ex-type CBS 145367). **A.** Conidiomata sporulating on MEA. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars: A = 180 µm; all others = 10 µm.

Conidiomata solitary, pycnidial, brown, globose, 250–300 µm diam, with central ostiole; *conidiomatal wall* with 3–6 layers of pale brown cells of *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* hyaline, smooth, ampulliform to doliiform, 7–10 × 8–9 µm, proliferating percurrently at apex. *Conidia* solitary, hyaline to pale olivaceous, smooth, guttulate, subcylindrical-fusoid, straight to slightly curved, with prominent taper in upper third to subobtuse apex, widest in middle to lower third, base truncate, 3-septate, (18–)23–25(–27) × (3–)4 µm.

Culture characteristics: Colonies flat, spreading, covering dish after 2 wk, with moderate aerial mycelium, and smooth, lobate margins. On MEA surface saffron, reverse sienna; on PDA surface saffron to sienna, reverse sienna; on OA surface pale luteous to saffron.

Typus: **Australia**, New South Wales, Sussex Inlet, on *Phragmites* sp. (*Poaceae*), 27 Nov. 2015, P.W. Crous, HPC 1785 (**holotype** CBS H-23902, culture ex-type CPC 32075 = CBS 143446).

Notes: *Parastagonospora phragmitis* is related to *P. fusiformis*. However, *P. phragmitis* produces an asexual morph, while in *P. fusiformis* only the sexual morph has been observed. Moreover, *P. phragmitis* is the first species of the genus reported on *Phragmites*.

Phaeosphaeria phoenicicola (Crous & Thangavel) Y. Marín & Crous, ***comb. nov.*** MycoBank MB829700.

Basionym: *Parastagonospora phoenicicola* Crous & Thangavel, Persoonia 37: 349. 2016.

Description and illustration: Crous *et al.* (2016a).

Typus: **New Zealand**, Auckland, Botany road, on leaves of *Phoenix canariensis* (*Arecaceae*), 2015, R. Thangavel (**holotype** CBS H-22892, culture ex-type CPC 28711 = CBS 142107).

Notes: In the phylogenetic analysis based on ITS and LSU sequences (Fig. 28), the ex-type strain of this species was located in the well-supported clade (84 % BS) representing the genus *Phaeosphaeria*. Morphologically, this species produces conidia more similar to *Phaeosphaeria* than to *Parastagonospora*, since these are subcylindrical, mostly straight, while in *Parastagonospora* the conidia tend to be sigmoid and longer than in *P. phoenicicola*. Based on morphology and molecular data, the new combination, *Phaeosphaeria phoenicicola,* is herewith proposed.

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

Phaeosphaeriopsis M.P.S. Câmara *et al.*, Mycol. Res. 107: 519. 2003. Fig. 42.

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

Type species: *Phaeosphaeriopsis glaucopunctata* (Grev.) M.P.S. Câmara *et al.*, basionym: *Cryptosphaeria glaucopunctata* Grev. [as *"glauco-punctata"*]. Epitype and ex-epitype strain designated

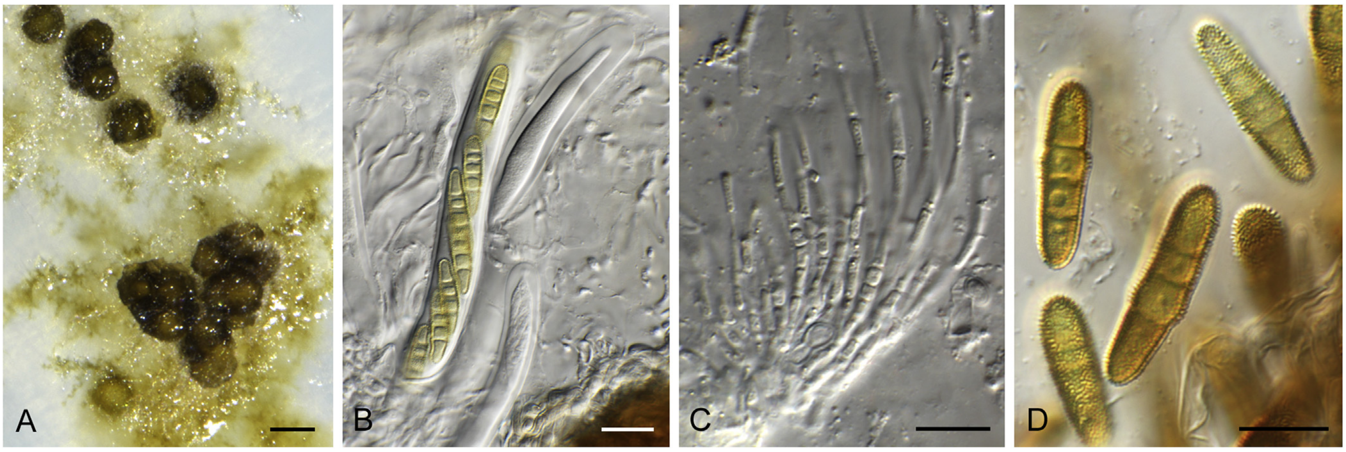

Fig. 45. *Phaeosphaeriopsis aloicola* (ex-type CBS 145368). **A.** Ascomata sporulating on SNA. **B.** Asci. **C.** Pseudoparaphyses. **D.** Ascospores. Scale bars: A = 200 µm; all others = 10 µm.

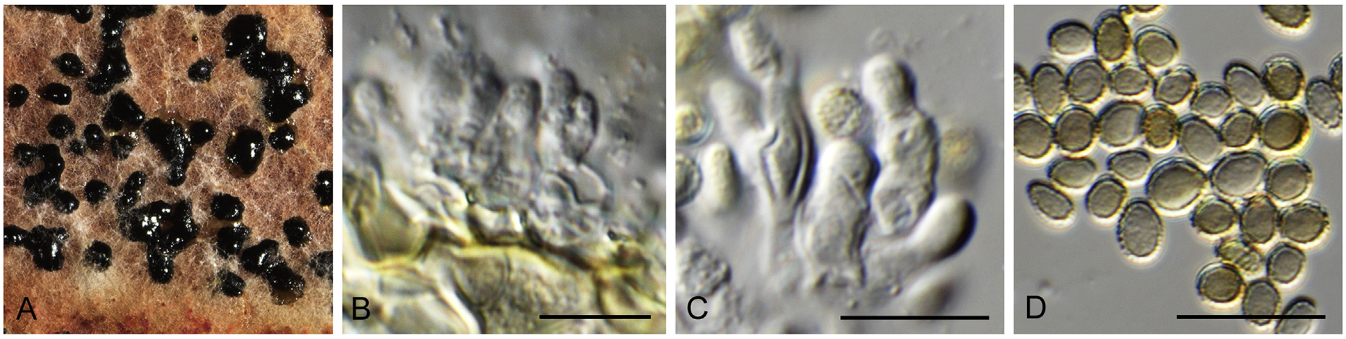

Fig. 46. *Phaeosphaeriopsis grevilleae* (ex-type CBS 145369). **A.** Conidiomata sporulating on PDA. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars = 10 µm.

by Thambugala *et al.* (2014): MFLU 14-0029, MFLUCC 13-0265 = ICMP 20199.

DNA barcode (genus): LSU. Fig. 28.

DNA barcodes (species): ITS, *rpb2*, *tef1, tub2*. Table 10. Fig. 43.

Ascomata solitary or aggregated, immersed, subepidermal to erumpent, pushing up flaps of the epidermis, globose to pyriform, often papillate, solitary or gregarious in a stroma of scleroplectenchyma or dark brown cells of *textura angularis*, often surrounded by septate, brown hyphae extending into the host tissues. *Asci* 8-spored, bitunicate, cylindrical to broadly fusoid, short stipitate, with visible apical chamber. *Ascospores* uni- to triseriate, cylindrical, broadly rounded at apex, tapering to narrowly rounded base, 4–5-septate, first septum submedian, often constricted, medium brown, echinulate, punctate or verrucose. *Asexual morph* coniothyrium-like or phaeostagonospora-like. *Conidiomata* pseudoparenchymatous, sometimes of scleroplectenchyma. *Conidiogenous cells* lining locule, ampulliform, hyaline, proliferating percurrently, resulting in inconspicuous annellations. *Conidia* cylindrical, with bluntly rounded ends, 0–3-septate, yellowish brown, punctate (Quaedvlieg *et al.* 2013).

Culture characteristics: Colonies flat or rarely slightly raised, spreading, feathery, velvety or floccose, with sparse to moderate aerial mycelium, circular or lobate, margins smooth or rarely slightly radiating. On PDA, surface white, dirty white, pinkish white, primrose, pale grey or pale luteous; reverse dirty white, light to dark grey, luteous or olivaceous buff. On MEA, surface dirty white, pale luteous, or white to cream at the margins, pale yellowish to yellowish brown in the middle and pale brown to brown or orange-brown at the centre, with small white to grey droplets; reverse luteous, umber with patches of dirty white, isabelline in the middle and cinnamon in outer region, or white to cream at the margins, brown to orange-brown in the middle and pale yellowish at the centre.

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

Distribution: Worldwide.

Hosts: Pathogens or saprophytes on *Agapanthus praecox* (*Alliaceae*), *Agave* spp. and *Yucca* spp. (*Agavaceae*), *Aloe* sp. (*Aloaceae*), *Dracaena lourieri*, *Dracaena* sp. and *Nolina erumpens* (*Dracaenaceae*), *Grevillea* sp. (*Proteaceae*), *Phormium* spp. (*Phormiaceae*) and *Ruscus* spp. (*Ruscaceae*).

Disease symptoms: Leaf spots and leaf blight.

Notes: The genus *Phaeosphaeriopsis* was introduced by Câmara *et al.* (2003) to accommodate some species of *Paraphaeosphaeria* that were not congeneric based on phylogenetic data. *Phaeosphaeriopsis* is characterised by having uni- or multi-loculate stromata and 4–5-septate ascospores, and coniothyrium-like and phaeostagonospora-like asexual morphs, while *Paraphaeosphaeria* produces 2-septate ascospores and has a microsphaeropsis-like asexual morph (Câmara *et al.* 2003, Quaedvlieg *et al.* 2013). *Phaeosphaeriopsis* is related to *Acericola*, which is a genus recently introduced to accommodate a saprobic fungus found on dead twigs of *Acer campestre* (Hyde *et al.* 2017). Unfortunately, it appears that the LSU sequence of *Acericola* is incorrect (Crous *et al.* 2019a).

In our phylogenetic analysis based on ITS and LSU sequences, 11 species are accepted in the genus *Phaeosphaeriopsis*, and four strains located in independent branches are introduced as new species.

Species included in *Phaeosphaeriopsis* are saprobes or presumed pathogens. The type species, *Phaeosphaeriopsis*

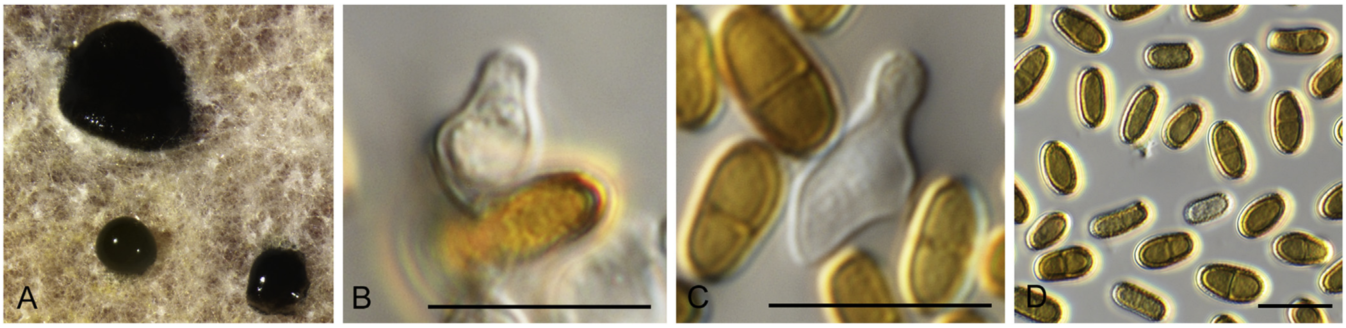

Fig. 47. *Phaeosphaeriopsis pseudoagavacearum* (ex-type CBS 145370). **A.** Conidiomata sporulating on MEA. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars = 10 µm.

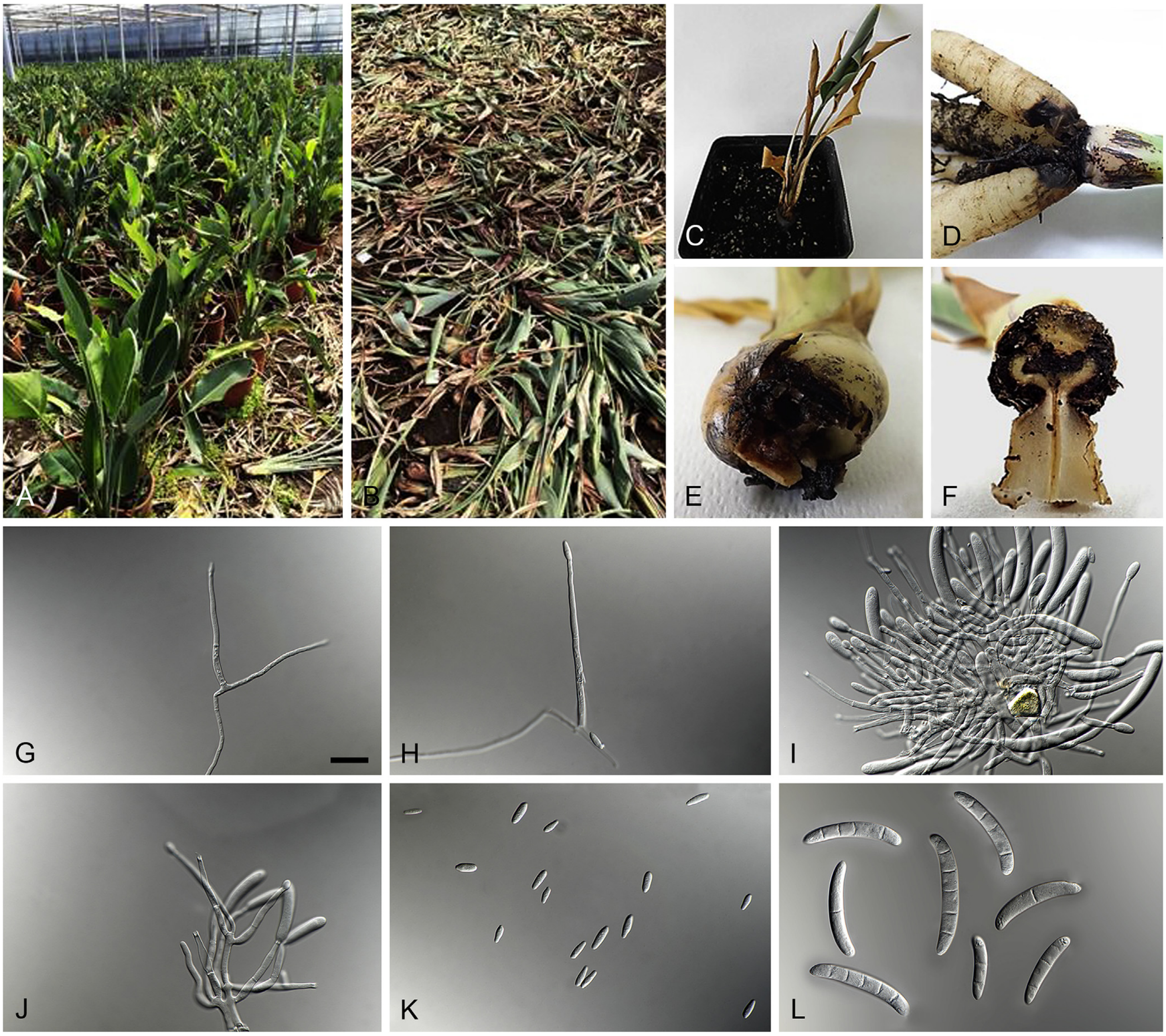

Fig. 48. *Pleiocarpon strelitziae* (ex-type CBS 142251). **A–F.** Disease symptoms. **A, B.** Wilting and dying *Strelitzia reginae* plants in the nursery. **C–F.** Basal rot and wilting of plant induced during the pathogenicity test. **G–L.** Asexual morph. **G, H.** Simple conidiophores. **I, J.** Sporodochia. **K.** Microconidia. **L.** Macroconidia. Scale bars: 10 µm; G applies to G–L. Pictures taken from Aiello *et al.* (2017).

glaucopunctata, is associated with leaf spot and necrosis of *Ruscus aculeatus* (Câmara *et al.* 2003, Golzar & Wang 2012). *Phaeosphaeriopsis agapanthi* and *Phs. dracaenicola* are also associated with necrotic leaf spots of *Agapanthus precox* and *Dracaena lourieri*, respectively (Phookamsak *et al.* 2014b, Crous *et al.* 2016b).

References: Câmara *et al.* 2003, Quaedvlieg *et al.* 2013, Thambugala *et al.* 2014 (morphology and phylogeny).

Phaeosphaeriopsis aloes Crous & Y. Marín, ***sp. nov.*** MycoBank MB829642. Fig. 44.

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

Conidiomata solitary, brown, pycnidial, globose, 150–180 µm diam, with central ostiole, 30–40 µm diam; *conidiomatal wall* of 3–4 layers of brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth-walled, ellipsoid, phialidic, 4–6 × 3–4 µm. *Conidia* solitary, aseptate, straight, verruculose, golden-brown, subcylindrical, apex obtuse, base bluntly rounded, (4–)5(–6) × 3(–3.5) µm.

Culture characteristics: Colonies flat, spreading, with sparse to moderate aerial mycelium, covering dish in 2 wk. On MEA surface honey, reverse cinnamon; on PDA surface and reverse sepia; on OA surface saffron.

Typus: **USA**, California, on leaves of *Aloe* sp. (*Aloaceae*), 6 Aug. 2016, P.W. Crous, HPC 1326 (**holotype** CBS H-23870, culture ex-type CBS 145367 = CPC 31480).

Notes: *Phaeosphaeriopsis aloes* is related to *Phs. obtusispora*. This latter species only produces the sexual morph, while only the asexual morph has been observed in our new species.

Phaesphaeriopsis aloes and *Phs. aloicola*, both described here, are the first species of the genus found on a member of the family *Aloaceae*, an *Aloe* sp. However, the two species are not related. *Phaeosphaeriopsis aloes* produces an asexual morph, while in *Phs. aloicola* only the sexual morph has been observed.

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

Species	Isolates[1]	GenBank accession numbers[2]					References
		ITS	*his3*	*rpb2*	*tef1*	*tub2*	
Pleiocarpon livistonae	CBS 145030^T	MK539963	MK540234	MK540095	MK540165	MK540179	Present study
Pl. strelitziae	CBS 142251^T	KY304644	KY304616	KY304697	KY304722	KY304750	Aiello *et al.* (2017)

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

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

Phaeosphaeriopsis aloicola Crous & Y. Marín, ***sp. nov.*** MycoBank MB829643. Fig. 45.

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

Ascomata solitary, aggregated, erumpent, brown, globose, 150–200 µm diam, with papillate neck and central ostiole, 40–50 µm diam; *ascomatal wall* of 4–6 layers of brown cells of *textura angularis. Pseudoparaphyses* hyaline, smooth-walled, hyphae-like, 2–3 µm diam, anastomosing, branched, intermingled among asci. *Asci* bitunicate, subcylindrical, apex obtuse with well-defined apical chamber, 2 µm diam, fasciculate, short stipitate, 70–100 × 10–12 µm. *Ascospores* bi- to triseriate, subcylindrical, straight to slightly curved, (2–)3-septate, at times slightly swollen in second cell from apex, medium brown, verruculose, ends obtuse, (19–)22–25(–26) × (4–)5(–6) µm.

Culture characteristics: Colonies flat, spreading, with sparse to moderate aerial mycelium and even, lobate margins, reaching 30 mm diam on PDA, covering dish on MEA and OA. On MEA surface buff, outer region sienna, reverse sienna; on PDA surface and reverse buff to sienna; on OA surface scarlet.

Typus: **USA**, California, on leaves of *Aloe* sp. (*Aloaceae*), 6 Aug. 2016, P.W. Crous, HPC 1306 (**holotype** CBS H-23871, culture ex-type CBS 145368 = CPC 31454).

Notes: *Phaeosphaeriopsis aloicola* is related to *Phs. agapanthi* and *Phs. triseptata*. Morphologically, *Phs. aloicola* is similar to *Phs. triseptata* since both produce verruculose, 3-septate ascospores. However, both species differ in the size of ascomata (up to 200 µm in *Phs. aloicola vs.* up to 110 µm in *Phs. triseptata*), asci (70–100 × 10–12 µm in *Phs. aloicola vs.* 56–70 × 7.5–9 µm in *Phs. triseptata*) and ascospores [(19–)22–25(–26) × (4–)5(–6) µm in *Phs. aloicola vs.* 14.5–18 × 3–4 µm in *Phs. triseptata*]. Moreover, *Phs. triseptata* also produces an asexual morph, which has not been observed in *Phs. aloicola*. *Phaeosphaeriopsis agapanthi* only produces an asexual morph. The three species were isolated from different hosts in different families. *Phaeosphaeriopsis agapanthi* was isolated from *Agapanthus precox* (*Amaryllidaceae*), *Phs. aloicola* from *Aloe* sp. (*Aloaceae*), and *Phs triseptata* from *Ruscus aculeatus* (*Asparagaceae*). Moreover, *Phs. aloicola* was found in the USA while the other species have been reported from Europe. *Phaeosphaeriopsis aloes* was also isolated from *Aloe* in California. For comparison see notes of *Phaeosphaeriopsis aloes*.

Phaeosphaeriopsis grevilleae Crous & Y. Marín, ***sp. nov.*** MycoBank MB829644. Fig. 46.

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

Conidiomata solitary, pycnidial, scattered, globose, 180–250 µm diam, with central ostiole, exuding black mucoid conidial mass; *conidiomatal wall* of 2–3 layers of brown cells of *textura angularis. Conidiophores* reduced to conidiogenous cells lining inner cavity, hyaline, smooth-walled, ampulliform, phialidic, 5–7 × 3–5 µm. *Conidia* solitary, aseptate, medium brown, verruculose, ellipsoid to ovoid, (4–)5(–6) × (3–)3.5(–4) µm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and feathery margins, reaching 35 mm diam on MEA, covering dish on PDA and OA. On MEA surface and reverse scarlet; on PDA surface ochreous, reverse sienna; on OA surface scarlet with patches of ochreous.

Typus: **Australia**, Queensland, leaves of *Grevillea* sp. (*Proteaceae*), 14 Jul. 2009, P.W. Crous, (**holotype** CBS H-23872, culture ex-type CBS 145369 = CPC 17003).

Notes: In the phylogenetic analysis based on ITS, LSU, *rpb2*, *tef1* and *tub2*, this species was located in an independent

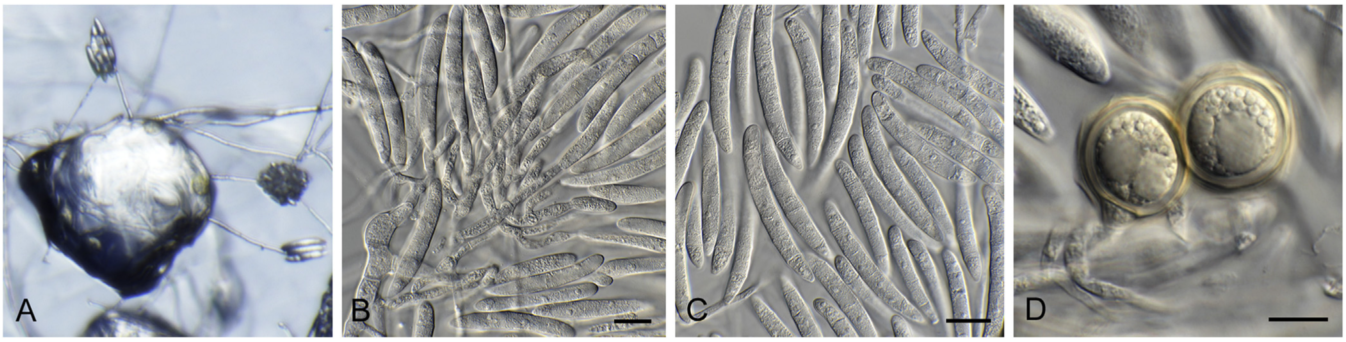

Fig. 49. *Pleiocarpon livistonae* (ex-type CBS 145030). **A.** Sporodochium on SNA. **B.** Conidiophores with conidiogenous cells. **C.** Conidia. **D.** Chlamydospores. Scale bars = 10 µm.

Fig. 50. *Pyrenophora* spp. **A–D.** Sexual morph. **A, B.** Sterile ascomata of *Pyrenophora campanulata* (CBS 127927). **C.** Protoascomata of *Pyrenophora erythrospila* on PDA (CBS 312.69). **D.** Protoascoma of *Pyrenophora erythrospila* (CBS 108941). **E–K.** Asexual morph. **E–H.** Conidiophores. **E.** *Pyrenophora fugax* (CBS 509.77). **F.** *Pyrenophora novozelandica* (CBS 127934). **G.** *Pyrenophora erythrospila* (CBS 312.69). **H.** *Pyrenophora fugax* (CBS 509.77). **I, J.** Conidia. **I.** *Pyrenophora erythrospila* (CBS 312.69). **J.** *Pyrenophora fugax* (CBS 509.77). **K.** Chlamydospores of *Pyrenophora tetrarrhenae* (CBS 127924). Scale bars: A = 50 µm; D = 20 µm; G–K = 10 µm.

branch. This is the first species reported on *Grevillea,* which is a member of the *Proteaceae*.

Phaeosphaeriopsis pseudoagavacearum Crous & Y. Marín, ***sp. nov.*** MycoBank MB829645. Fig. 47.

Etymology: Named after its similarity to *Phaeosphaeriopsis agavacearum*.

Conidiomata solitary, globose, brown, pycnidial, 200–250 µm diam, with central ostiole, 15–20 µm diam; *conidiomatal wall* of 2–3 layers of brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth-walled, ampulliform, phialidic, 5–7 × 3–4 µm. *Conidia* solitary, golden-brown, verruculose, thick-walled, straight to slightly curved, 1-septate, subcylindrical, apex obtuse, base bluntly rounded, (6–)8–9(–10) × 4(–4.5) µm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and even, smooth margins, covering dish in

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

Species	**Isolates**[1]	**GenBank accession numbers**[2]				**References**
		ITS	**LSU**	***gapdh***	***rpb2***	
Pyrenophora avenicola	CBS 307.84^{T}	MK539972	MK540042	MK540180	–	Present study
Py. biseptata	CBS 307.69	MK539973	MK540043	MK540181	–	Present study
	CBS 319.69	MK539974	MK540044	MK540182	MK540102	Present study
	CBS 108963	MK539975	JN712532	MK540183	–	Crous *et al.* (2011), present study
Py. bromi	CBS 311.68	MK539976	MH870851	MK540184	–	Vu *et al.* (2019), present study
	DAOMC 127414	JN943666	JN940074	AY004839	–	Zhang & Berbee (2001), Hambleton (unpubl. data)
Py. chaetomioides	CBS 279.31^{A}	MK539977	MK540045	MK540185	MK540103	Present study
	CBS 195.31	MK539978	MH866633	MK540186	MK540104	Vu *et al.* (2019), present study
	CBS 314.68	MK539979	MK540046	MK540187	MK540105	Present study
Py. cynosuri	CBS 127918^{T}	MK539980	MK540047	MK540188	MK540106	Present study
Py. dactylidis	DAOMC 92161	JN943667	JN940087	AY004812	–	Zhang & Berbee (2001), Hambleton (unpubl. data)
Py. dictyoides	DAOMC 63666	JN943653	JN940080	AY004836	–	Zhang & Berbee (2001), Hambleton (unpubl. data)
	CBS 258.80	MK539981	MK540048	MK540189	MK540107	Present study
	CBS 967.87	MK539982	MK540049	MK540190	MK540108	Present study
	CBS 127933	MH877971	MK540050	MK540191	MK540109	Vu *et al.* (2019), present study
Py. erythrospila	CBS 312.69	MK539983	MK540051	MK540192	–	Present study
	CBS 108941	MK539984	MK540052	MK540193	MK540110	Present study
Py. fugax	CBS 509.77	MK539985	MK540053	MK540194	MK540111	Present study
Py. grahamii	CBS 315.69	MK539986	MK540054	MK540195	–	Present study
	CBS 128043	MK539987	MH876230	MK540196	MK540112	Vu *et al.* (2019), present study
	CBS 128044	MK539988	MH876231	MK540197	MK540113	Vu *et al.* (2019), present study
Py. leucospermi	CBS 111083^{T}	JN712467	JN712533	MK540198	MK540114	Crous *et al.* (2011), present study
	CBS 111505	MK539989	JN712542	MK540199	MK540115	Crous *et al.* (2011), present study
	CBS 114493	MK539990	JN712545	MK540200	MK540116	Crous *et al.* (2011), present study
Py. lolii	CBS 240.48	MK539991	MK540055	MK540201	MK540117	Present study
	CBS 318.69	MK539992	MH871050	MK540202	MK540118	Vu *et al.* (2019), present study
	CBS 128046	MK539993	MH876233	MK540203	MK540119	Vu *et al.* (2019), present study
Py. nisikadoi	CBS 190.29^{ET}	KM257054	KM243296	KM257057	–	Manamgoda *et al.* (2014)
	CBS 119213	EU552124	MK540056	MK540204	MK540120	Marincowitz *et al.* (2008), present study
	CBS 127912	MH877963	MK540057	MK540205	MK540121	Vu *et al.* (2019), present study
Py. nobleae	CBS 259.80	MK539994	MK540058	MK540206	MK540122	Present study
	CBS 966.87	MK539995	MK540059	MK540207	MK540123	Present study
	CBS 127936	MK539996	MK540060	MK540208	MK540124	Present study
Py. novozelandica	CBS 127934^{T}	MK539997	MK540061	MK540209	MK540125	Present study
Py. phaeocomes	DAOMC 222769	JN943649	JN940093	–	DQ497614	Hambleton (unpubl. data), James *et al.* (unpubl. data)
Py. poae	CBS 319.68^{A}	MK539998	MK540062	MK540210	MK540126	Present study
	CBS 128045	MK539999	MH876232	MK540211	MK540127	Vu *et al.* (2019), present study
	DAOMC 145373	JN943650	JN940083	AY004832	JN993632	Zhang & Berbee (2001), Schoch *et al.* (2012), Hambleton (unpubl. data)
Py. pseudoerythrospila	CBS 127931^{T}	MK540000	MK540063	MK540212	–	Present study
Py. semeniperda	DAOMC 213153	JN943665	JN940088	AY004826	–	Zhang & Berbee (2001), Hambleton (unpubl. data)
	BRIP 10941	KJ415564	KJ415518	KJ415382	–	Tan *et al.* (2014)
	CBS 127927	MK540001	MK540064	MK540213	MK540128	Present study
Py. sieglingiae	CBS 127930	MK540002	MK540065	MK540214	MK540129	Present study
Py. teres	CBS 228.76$^{\mathrm{T\ of}\ \mathit{Py.\ teres}\ \mathrm{f.}\ \mathit{maculata}}$	MK540003	MK540066	MK540215	MK540130	Present study
	CBS 281.31$^{\mathrm{A\ of}\ \mathit{Py.\ japonica}}$	MK540004	MK540067	MK540216	MK540131	Present study

Table 12. (Continued).

Species	Isolates[1]	GenBank accession numbers[2]				References
		ITS	LSU	*gapdh*	*rpb2*	
	CBS 282.31	MK540005	MK540068	MK540217	MK540132	Present study
	CBS 314.69	MK540006	MK540069	MK540218	MK540133	Present study
	CBS 336.29	MK540007	MH877692	MK540219	MK540134	Vu *et al.* (2019), present study
	CBS 123929	MK540008	MK540070	MK540220	MK540135	Present study
	CBS 123932	MK540009	MK540071	MK540221	MK540136	Present study
Py. tetrarrhenae	DAOMC 171966	JN943663	JN940090	–	JN993620	Schoch *et al.* (2012), Hambleton (unpubl. data)
	CBS 127915	MK540010	MH877964	MK540222	MK540137	Vu *et al.* (2019), present study
	CBS 127924	MK540011	MH877965	MK540223	MK540138	Vu *et al.* (2019), present study
Py. trichostoma	CBS 328.53	MK540012	MK540072	MK540224	MK540139	Present study
	CBS 391.54	MK540013	MK540073	MK540225	–	Present study
	CBS 392.54	MK540014	MK540074	MK540226	MK540140	Present study
Py. triseptata	CBS 128047	MK540015	MH877983	MK540227	MK540141	Vu *et al.* (2019), present study
	CBS 128048	MK540016	MH876234	MK540228	MK540142	Vu *et al.* (2019), present study
Py. tritici-repentis	CBS 259.59$^{\text{SynT of } \textit{Py. tritici-vulgaris}}$	MK540017	MK540075	AM884276	MK540143	Lepoint *et al.* (2010), present study
	CBS 191.29	MK540018	MK540076	MK540229	MK540144	Present study
	CBS 127922	MK540019	MK540077	MK540230	MK540145	Present study
Py. variabilis	CBS 127920$^{\text{T}}$	MK540020	MK540078	MK540231	MK540146	Present study
Py. wirreganensis	CBS 109896	MK540021	MK540079	MK540232	MK540147	Present study

[1] BRIP: Queensland Plant Pathology Herbarium, Brisbane, Australia; CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands; DAOMC: Plant Research Institute, Department of Agriculture (Mycology), Ottawa, Canada. $^{\text{A, ET, SynT and T}}$ indicate authentic, ex-epitype, ex-syntype and ex-type strains, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; LSU: partial large subunit (28S) nrRNA gene; *gapdh*: partial glyceraldehyde-3-phosphate dehydrogenase gene; *rpb2*: partial DNA-directed RNA polymerase II second largest subunit gene.

2 wk. On MEA surface ochreous, reverse bay; on PDA surface sienna with bay outer region, reverse bay; on OA surface sienna with scarlet margins.

Typus: **France**, Domaine la Fraysse, Valgorge, on leaves of *Agave* sp. (*Asparagaceae*), 15 Jul. 2010, P.W. Crous (**holotype** CBS H-23873, culture ex-type CBS 145370 = CPC 18383).

Notes: *Phaeosphaeriopsis pseudoagavacearum* is closely related to *Phs. agavacearum*. Morphologically these species are also similar in producing verruculose, aseptate conidia. However, they differ in the size of their conidiomata (up to 180 μm diam in *Phs. agavacearum vs.* up to 250 μm diam in *Phs. pseudoagavacearum*) and conidia [(5–)6–7(–9) × 3(–4) μm in *Phs. agavacearum vs.* (6–)8–9(–10) × 4(–4.5) μm in *Phs. pseudoagavacearum*].

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Pleiocarpon L. Lombard & D. Aiello, IMA Fungus 8: 73. 2017. Fig. 48.

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

Type species: *Pleiocarpon strelitziae* L. Lombard & D. Aiello. Holotype and ex-type strain: CBS H-22967, CBS 142251.

DNA barcode (genus): LSU.

DNA barcodes (species): ITS, *his3*, *rpb2*, *tef1*, *tub2*. Table 11.

Conidiophores simple or aggregated, forming sporodochia; *simple conidiophores* arising laterally or terminally from aerial mycelium, solitary to loosely aggregated, unbranched or sparsely branched, septate, bearing up to two conidiogenous cells. *Conidiogenous cells* monophialidic, cylindrical, tapering slightly towards the apex. *Macroconidia* cylindrical to subcylindrical, hyaline, straight to curved, 1−6-septate, apex or apical cell typically slightly bent to one side and minutely beaked, base with sometimes visible, centrally located or laterally displaced hilum. *Microconidia* absent or abundant, aseptate, hyaline, ellipsoid to ovoid or subcylindrical, straight to slightly curved, with clearly laterally displaced hilum. *Chlamydospores* absent or solitary, globose, brown, thich-walled, guttulate. *Sexual morph* not observed (adapted from Aiello *et al.* 2017).

Culture characteristics: Colonies on PDA with sparse to moderate aerial mycelium, even, smooth, with lobate margins; surface and reverse umber or cinnamon to honey.

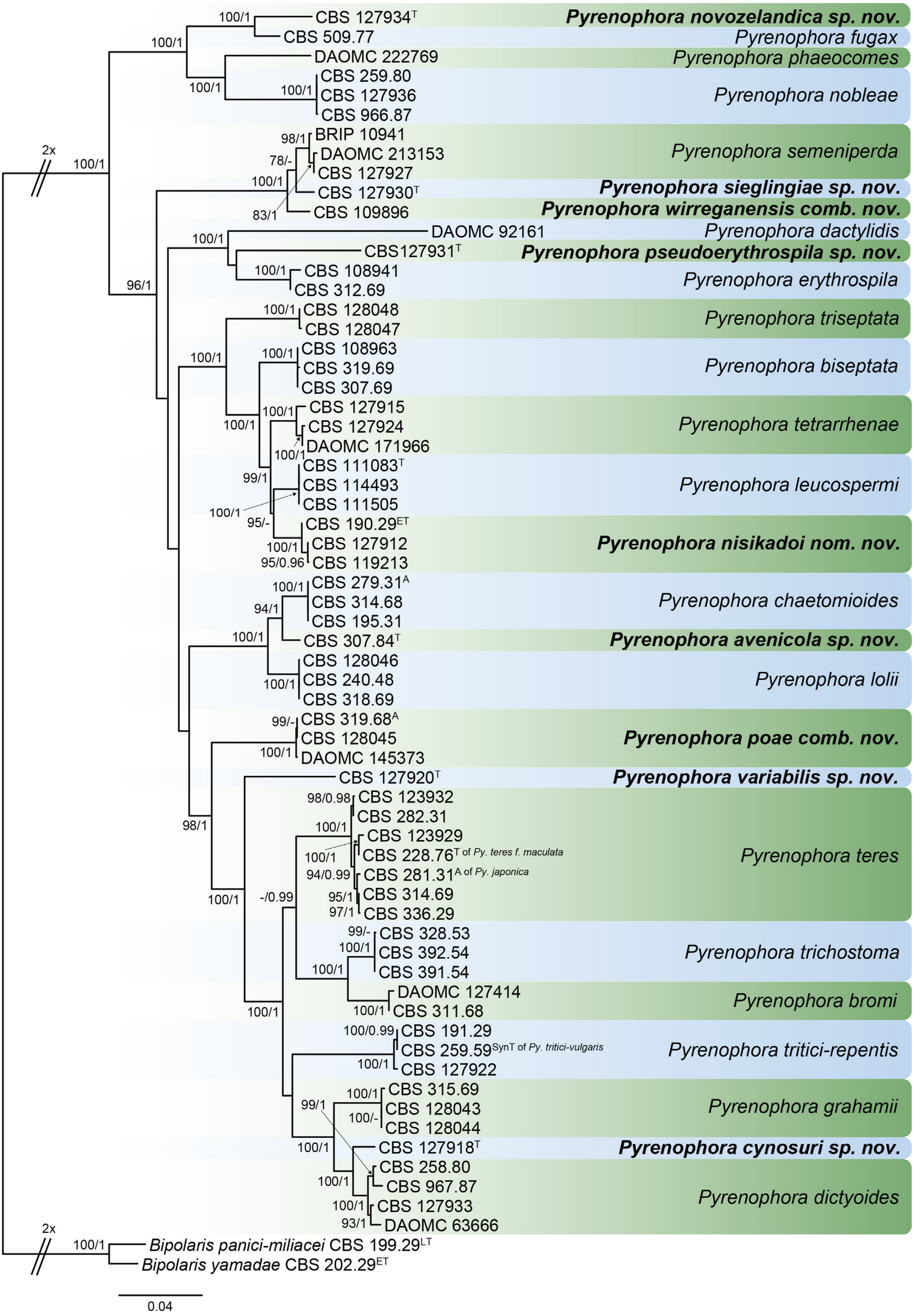
Optimal media and cultivation conditions: On PDA, MEA, OA or SNA with sterile filter paper and carnation leaf pieces at 25 °C.

Distribution: Italy and Sri Lanka.

Host: *Livistona rotundifolia* (*Arecaceae*) and *Strelitzia reginae* (*Strelitziaceae*).

Disease symptoms: Basal rot and wilt.

Notes: *Pleiocarpon* was recently introduced by Aiello *et al.* (2017) to accommodate a new species isolated from potted plants of *Strelitzia reginae* in an ornamental nursery located in eastern Sicily that had a new basal rot disease. This basal stem rot disease resulted in the detachment of the roots from the stem. Moreover, the diseased plants displayed symptoms of general wilting and rot of the internal foliage. Pathogenicity tests indicated


100/1
CBS 127934^{T}
Pyrenophora novozelandica sp. nov.
100/1
CBS 509.77
Pyrenophora fugax
DAOMC 222769
Pyrenophora phaeocomes
100/1
100/1
CBS 259.80
CBS 127936
CBS 966.87
Pyrenophora nobleae
2x
100/1
98/1
BRIP 10941
78/-
DAOMC 213153
CBS 127927
Pyrenophora semeniperda
100/1
CBS 127930^{T}
Pyrenophora sieglingiae sp. nov.
83/1
CBS 109896
Pyrenophora wirreganensis comb. nov.
100/1
DAOMC 92161
Pyrenophora dactylidis
CBS127931^{T}
Pyrenophora pseudoerythrospila sp. nov.
100/1
CBS 108941
96/1
CBS 312.69
Pyrenophora erythrospila
100/1
CBS 128048
CBS 128047
Pyrenophora triseptata
100/1
100/1
CBS 108963
CBS 319.69
CBS 307.69
Pyrenophora biseptata
100/1
CBS 127915
100/1
CBS 127924
DAOMC 171966
100/1
Pyrenophora tetrarrhenae
CBS 111083^{T}
99/1
CBS 114493
CBS 111505
100/1
Pyrenophora leucospermi
95/-
CBS 190.29^{ET}
100/1
CBS 127912
95/0.96
CBS 119213
Pyrenophora nisikadoi nom. nov.
100/1
CBS 279.31^{A}
94/1
CBS 314.68
CBS 195.31
Pyrenophora chaetomioides
100/1
CBS 307.84^{T}
Pyrenophora avenicola sp. nov.
CBS 128046
100/1
CBS 240.48
CBS 318.69
Pyrenophora lolii
99/-
CBS 319.68^{A}
CBS 128045
100/1
DAOMC 145373
Pyrenophora poae comb. nov.
CBS 127920^{T}
Pyrenophora variabilis sp. nov.
98/0.98
CBS 123932
98/1
CBS 282.31
100/1
CBS 123929
100/1
CBS 228.76^{T} of *Py. teres f. maculata*
94/0.99
CBS 281.31^{A} of *Py. japonica*
100/1
-/0.99
95/1
CBS 314.69
97/1
CBS 336.29
Pyrenophora teres
99/-
CBS 328.53
100/1
CBS 392.54
100/1
CBS 391.54
Pyrenophora trichostoma
DAOMC 127414
100/1
100/1
CBS 311.68
Pyrenophora bromi
100/0.99
CBS 191.29
CBS 259.59^{SynT} of *Py. tritici-vulgaris*
100/1
CBS 127922
Pyrenophora tritici-repentis
100/1
CBS 315.69
99/1
CBS 128043
100/-
CBS 128044
Pyrenophora grahamii
100/1
CBS 127918^{T}
Pyrenophora cynosuri sp. nov.
CBS 258.80
100/1
CBS 967.87
100/1
CBS 127933
93/1
DAOMC 63666
Pyrenophora dictyoides
2x
100/1
Bipolaris panici-miliacei CBS 199.29^{LT}
Bipolaris yamadae CBS 202.29^{ET}
0.04

that *Pl. strelitziae*, was highly aggressive, killing all inoculated test plants within 2 mo (Aiello *et al.* 2017).

The phylogenetic analysis based on ITS, LSU, *tef1* and *tub2* demonstrated that *Pleiocarpon* is closely related to the genus *Thelonectria*, with both genera being characterised by cylindrocarpon-like asexual morphs (Aiello *et al.* 2017). Recently, *Thelonectria* was segregated by introducing three new genera, *Cinnamomeonectria*, *Macronectria* and *Tumenectria* (Salgado-Salazar *et al.* 2016). These four related genera are mostly found on bark of exposed wood of dead, dying or diseased trees, and are rarely associated with small cankers and root rots (Chaverri *et al.* 2011, Salgado-Salazar *et al.* 2016). Moreover, *Pleiocarpon* can be distinguished from *Thelonectria* and these three new genera by the absence of a sexual morph.

Hitherto, *Pleiocarpon* was monospecific. Here we introduce a new species isolated from *Livistona rotundifolia* (*Arecaceae*) in Sri Lanka, causing root and corm rot.

References: Aiello *et al.* 2017 (morphology, pathogenicity and phylogeny).

Pleiocarpon livistonae Crous & Quaedvl., ***sp. nov.*** MycoBank MB829613. Fig. 49.

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

Conidiophores simple, solitary or aggregated, forming sporodochia, arising from superficial hyphae, branched, 2–4-septate, 50–120 × 6–8 µm. *Conidiogenous cells* monophialidic, cylindrical, tapering slightly towards apex, 10–30 × 4–5 µm, forming conidia in false chains that eventually aggregate in a mucoid mass. *Macroconidia* hyaline, smooth-walled, subcylindrical, 1–6-septate, curved, apex subobtuse, with base sometimes visible as lateral hilum; 1–3 septate conidia (21–)28–34(–45) × (5–)6 µm; 4–6-septate conidia (45–)55–65(–70) × (5–)6 µm. *Chlamydospores* solitary, globose, brown, thick-walled, guttulate, 15–20 µm diam.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margins, reaching 60 mm diam after 2 wk at 25 °C. On MEA surface ochreous, reverse umber; on PDA surface and reverse umber; on OA surface umber.

Typus: **Sri Lanka**, on *Livistona rotundifolia* (*Arecaceae*), W. Quaedvlieg, NAK Tuinbouw, INS-17-20656D (**holotype** CBS H-23849, culture ex-type CBS 145030 = CPC 34576).

Notes: *Pleiocarpon livistonae* is distinguished from *Pl. strelitziae* by the absence of microconidia, the production of chlamydospores, and the septation and size of its macroconidia (1–6-septate, up to 70 µm in *Pl. livistonae vs*. 1–5-septate, up to 50 µm in *Pl. strelitziae*). *Pleiocarpon livistonae* is phylogenetically close but clearly differentiated from *Pl. strelitziae* based on ITS, *his3*, *rpb2*, *tef1* and *tub2* sequence similarity (96 %, 85 %, 92 %, 94 %, and 91 %, respectively). Moreover, *Pl. livistonae* was isolated from *Livistona rotundifolia* (*Arecaceae*) in Sri Lanka, while *Pl. strelitziae* was found on *Strelitzia reginae* (*Strelitziaceae*) in Italy.

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

Pyrenophora Fr., Summa veg. Scand. 2: 397. 1849. Fig. 50.
Synonyms: *Polytrichia* Sacc., Syll. fung. (Abellini) 1: 451. 1882.
Pleospora subgen. Scleroplea Sacc., Syll. fung. (Abellini) 2: 277. 1883.
Neilreichina Kuntze, Revis. gen. pl. (Leipzig) 2: 862. 1891.
Scleroplea (Sacc.) Oudem., Verslag. Meded. K. Akad. Wetensch., Afd. Natuurk., ser. 3 9: 152. 1900.
Drechslera S. Ito, Proc. Imp. Acad. Japan 6: 355. 1930.
Marielliottia Shoemaker, Canad. J. Bot. 76: 1559. 1999.

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

Type species: *Pyrenophora phaeocomes* (Rebent.) Fr., basionym: *Sphaeria phaeocomes* Rebent. Neotype specimen designated by Shoemaker (1961): UPS 170980. Representative strain: DAOM 222769.

DNA barcodes (genus): LSU, ITS.

DNA barcodes (species): ITS, *gapdh, tef1.* Table 12. Fig. 51.

Ascomata perithecial, immersed, becoming erumpent to near superficial, solitary or scattered, globose to subglobose, broadly or narrowly conical, smooth-walled, with central ostiole; *necks* papillate, covered with brown to reddish brown setae, which are darkened at the base; *ascomatal wall* comprising 2–4 layers of brown, thick-walled cells of *textura angularis*. *Pseudoparaphyses* not observed. *Asci* 8-spored, bitunicate, fissitunicate, clavate to subcylindrical, with a short, broad pedicel, with a distinct ocular chamber surrounded by a large apical ring. *Ascospores* 2–3-seriate, muriform, constricted at the septum, smooth-walled, surrounded by a mucilaginous sheath. *Conidiophores* semi- to macronematous, mononematous, sometimes caespitose, straight or flexuous, often geniculate, usually unbranched, sometimes branched, pale brown to brown, rarely subhyaline to pale brown. *Conidiogenous cells* polytretic, integrated, terminal, frequently becoming intercalary, sympodial, cylindrical, smooth-walled, or less frequently verruculose, cicatrised. *Conidia* solitary, in certain species also sometimes catenate or forming secondary conidiophores which bear conidia, acropleurogenous, simple, straight or curved, cylindrical, ellipsoidal or obclavate, less frequently subglobose, obpyriform or fusiform, tapering towards apex, straw-coloured or pale to dark brown or olivaceous brown, sometimes the end cells are paler than the intermediate ones, smooth-walled or verruculose, pseudoseptate; *hila* protuberant or flat, darkened, thickened (adapted from Ellis 1971, Ariyawansa *et al.* 2014).

Culture characteristics: Colonies flat or umbonate, cottony, sometimes granular or powdery, with moderate to abundant aerial mycelium, sometimes with sparse aerial mycelium, margins fringed, sometimes arachnoid. On PDA smoke-grey to olivaceous or olivaceous grey, primrose to greyish yellow-green, greenish grey to olivaceous black, olivaceous black with patches white for the aerial mycelium, honey to isabelline, orange to umber, cinnamon with centre white due to the aerial mycelium, greyish sepia to fuscous black, or fuscous grey with margins buff;

Fig. 51. RAxML phylogram obtained from the combined ITS (788 bp), LSU (862 bp), *gapdh* (694 bp) and *tef1* (860 bp) sequences of all the accepted species of *Pyrenophora*. *Bipolaris panici-miliacei* CBS 199.29 and *Bipolaris yamadae* CBS 202.29 were used as outgroup. The novelties proposed in this study are indicated in **bold**. RAxML bootstrap support (BS) values above 70 % and Bayesian posterior probability scores $\geq$ 0.95 are shown in the nodes. GenBank accession numbers were indicated in Table 12 and Manamgoda *et al.* (2014). $^{\text{A, ET, LT, SynT and T}}$ indicate authentic, ex-epitype, ex-lectotype, ex-syntype and ex-type strains, respectively. TreeBASE: S23834.

Fig. 52. *Pyrenophora avenicola* (ex-type CBS 307.84). **A, B.** Conidiophores and conidia. **C–I.** Conidia. Scale bars: A, B = 10 µm; C–I = 5 µm; C applies to C–I.

reverse olivaceous, olivaceous black with or without margins, primrose or luteous, fuscous black with or without margins transparent or buff, honey to isabelline, sienna to umber with margins luteous, or cinnamon with centre brick to dark brick. On MEA white to pale greenish glaucous or buff, greyish sepia to pale mouse grey or mouse grey, smoke-grey to pale olivaceous grey, glaucous grey to greenish grey, pale vinaceous to vinaceous buff, purplish grey with margins vinaceous buff, luteous with margins white to pale smoke-grey, vinaceous buff to hazel with margins white and saffron, pale greenish grey to greenish grey, or fuscous black with margins luteous; reverse olivaceous black, smoke-grey to olivaceous grey with middle white due to the aerial mycelium, fuscous black with or without margins luteous or olivaceous or buff to cinnamon or honey to isabelline, chestnut with margins luteous to rust, blood colour with margins luteous or scarlet, chestnut with margins luteous, or orange to sienna. On OA smoke-grey, olivaceous, olivaceous black, hazel, buff, cinnamon, olivaceous grey with margins luteous, greyish sepia to fuscous black with margins brick, or orange to umber with margins transparent; reverse olivaceous to olivaceous black, smoke-grey to olivaceous grey, olivaceous black with margins transparent or luteous, leaden grey to leaden black, buff with centre fuscous black and margins olivaceous, isabelline with centre olivaceous, orange to umber or greyish sepia to fuscous black with margins transparent, olivaceous grey to olivaceous black with margins transparent, or fuscous black with margins brick, or transparent with centre brick to dark brick.

Optimal media and cultivation conditions: On PDA, PNA, OA and MEA to induce sporulation of the asexual morph, while for the sexual morph Sach's agar with sterilised rice or wheat straw at 25 °C is used.

Distribution: Worldwide, mainly in Australia, Europe, New Zealand and North America.

Hosts: Wide host range, occurring as pathogens, saprobes or endophytes. Mainly found in members of *Poaceae*, being pathogens of cereals and grasses, including barley, oats and wheat. The most common genera belonging to *Poaceae* which this genus is associated to are *Agropyron*, *Agrostis*, *Avena*, *Bromus*, *Dactylis*, *Festuca*, *Hordeum*, *Lolium*, *Poa* and *Triticum*, among others. *Pyrenophora* species are also reported from other genera outside this family, such as *Protea* and *Leucospermum* in the *Proteaceae*.

Fig. 53. *Pyrenophora cynosuri* (ex-type CBS 127918). **A–C.** Conidiophores and conidia. **D.** Conidium forming secondary conidium. **E–M.** Conidia. Scale bars: 10 µm; E applies to E–M.

Disease symptoms: Leaf spots, leaf blight, leaf blotch, net blotch, melting out, head rot, foot rot, seed-borne diseases, among others.

Notes: *Pyrenophora* is characterised by immersed to semi-immersed ascomata with necks covered with brown to reddish brown setae, lack of pseudoparaphyses, clavate to saccate asci, usually with a large apical ring, and muriform terete (cylindrical, frequently circular in section but narrowing to one end) ascospores (Ariyawansa *et al.* 2014). The asexual morph was known as *Drechslera* and it is characterised by brown, transversely septate conidia similar to those found in *Bipolaris* and *Curvularia*. In order to properly delineate these three genera, phylogenetic analyses using sequence data of different loci (*i.e.* LSU, SSU, ITS, *gapdh* and *rpb2*) were performed (Zhang & Berbee 2001, Ariyawansa *et al.* 2014, Manamgoda *et al.* 2014). The synonymy of *Drechslera* with *Pyrenophora* was recently discussed by Ariyawansa *et al.* (2014). However, there is still a large number of species which await treatment. Three new combinations are introduced here, *i.e. Py. nisikadoi*, *Py. poae* and *Py. wirreganensis*. The main problem encountered is the lack of type material of the already known species, and this resulted in few molecular studies being performed in the past.

Species delimitation in *Pyrenophora* based on morphology alone is complicated since many species have overlapping characters, similar to what is observed in *Bipolaris* and *Curvularia* (Marin-Felix *et al.* 2017). Therefore, molecular data (ITS, *gapdh* and *rpb2*) are essential for an accurate identification of species of *Pyrenophora.* In our phylogenetic analysis, 21 species are accepted and an additional six are newly described.

Pyrenophora includes saprobic and plant pathogenic species with a worldwide distribution, commonly associated with members of the family *Poaceae*. Some species are serious plant pathogens, *e.g.* *Py. teres*, which is a necrotrophic pathogen causing net blotch in barley (Crous *et al.* 1995, Louw *et al.* 1995, Campbell *et al.* 1999, 2002), and *Py. tritici-repentis*, which causes tan spot of wheat (Lamari & Bernier 1989, Balance *et al.* 1996, Abdullah *et al.* 2017) in all the major wheat growing areas of the world resulting in 3–50 % yield losses (Lamari & Bernier 1989).

References: Sivanesan 1987 (morphology and pathogenicity), Zhang & Berbee 2001, Ariyawansa *et al.* 2014 (morphology and phylogeny).

Pyrenophora avenicola Y. Marín & Crous, ***sp. nov.*** MycoBank MB829614. Fig. 52.

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

Hyphae hyaline, branched, septate, verrucose, 2–6(–7.5) µm. *Conidiophores* arising in groups, septate, straight or flexuous, sometimes geniculate at upper part, usually cells decrease in size towards apex, sometimes branched, cell walls thicker than those of vegetative hyphae, semi- to macronematous, subhyaline to pale brown, usually paler towards apex, not swollen at the base, up to 350 µm long, 4.5–7 µm wide. *Conidiogenous cells* verruculose, terminal or intercalary, proliferating sympodially, subhyaline to pale brown, subcylindrical to swollen, 14–33.5(–43.5) × 6.5–9.5 µm. *Conidia* verruculose, straight, middle cells enlarged, cylindrical to obclavate, tapering towards apex, pale brown to brown, end cells rarely slightly paler, 1–4(–5)-distoseptate, 21.5–71.5 × 9.5–15 µm, forming secondary conidiophores or conidia; *hila* protuberant, darkened, thickened, 3–4.5 µm. *Chlamydospores*, *microconidiation* and *sexual morph* not observed.

Culture characteristics: Colonies on MEA covering dish after 1 wk at 25 °C, with abundant aerial mycelium, umbonate; surface fuscous black, margins luteous; reverse smoke-grey to olivaceous grey, centre white due to the aerial mycelium. Colonies on PDA covering dish, with abundant aerial mycelium; surface smoke-grey to olivaceous grey; reverse fuscous black to black, margins transparent. Colonies on OA covering all dish, with moderate to abundant aerial mycelium; surface smoke-grey to olivaceous grey; reverse olivaceous grey to olivaceous black, margins transparent.

Typus: **Sweden**, Uppsala, on seed of *Avena* sp. (*Poaceae*), unknown date, C. Svensson (**holotype** CBS H-23840, culture ex-type CBS 307.84).

Notes: *Pyrenophora avenicola* is closely related to *Py. chaetomioides*. Moreover, both species have been found on the same host, *Avena*. However, *Py. avenicola* can be easily distinguished by its shorter conidiophores (up to 350 µm in *Py. avenicola vs.* 1 mm in *Py. chaetomioides*) and smaller conidia (21.5–71.5 × 9.5–15 µm in *Py. avenicola vs.* 25–140 × 12–22 µm in *Py. chaetomioides*) with less septa [1–4(–5) in *Py. avenicola vs.* 2–9 in *Py. chaetomioides*]. The sexual morph has only been observed in *Py. chaetomioides*.

Pyrenophora cynosuri Y. Marín & Crous, ***sp. nov.*** MycoBank MB829615. Fig. 53.

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

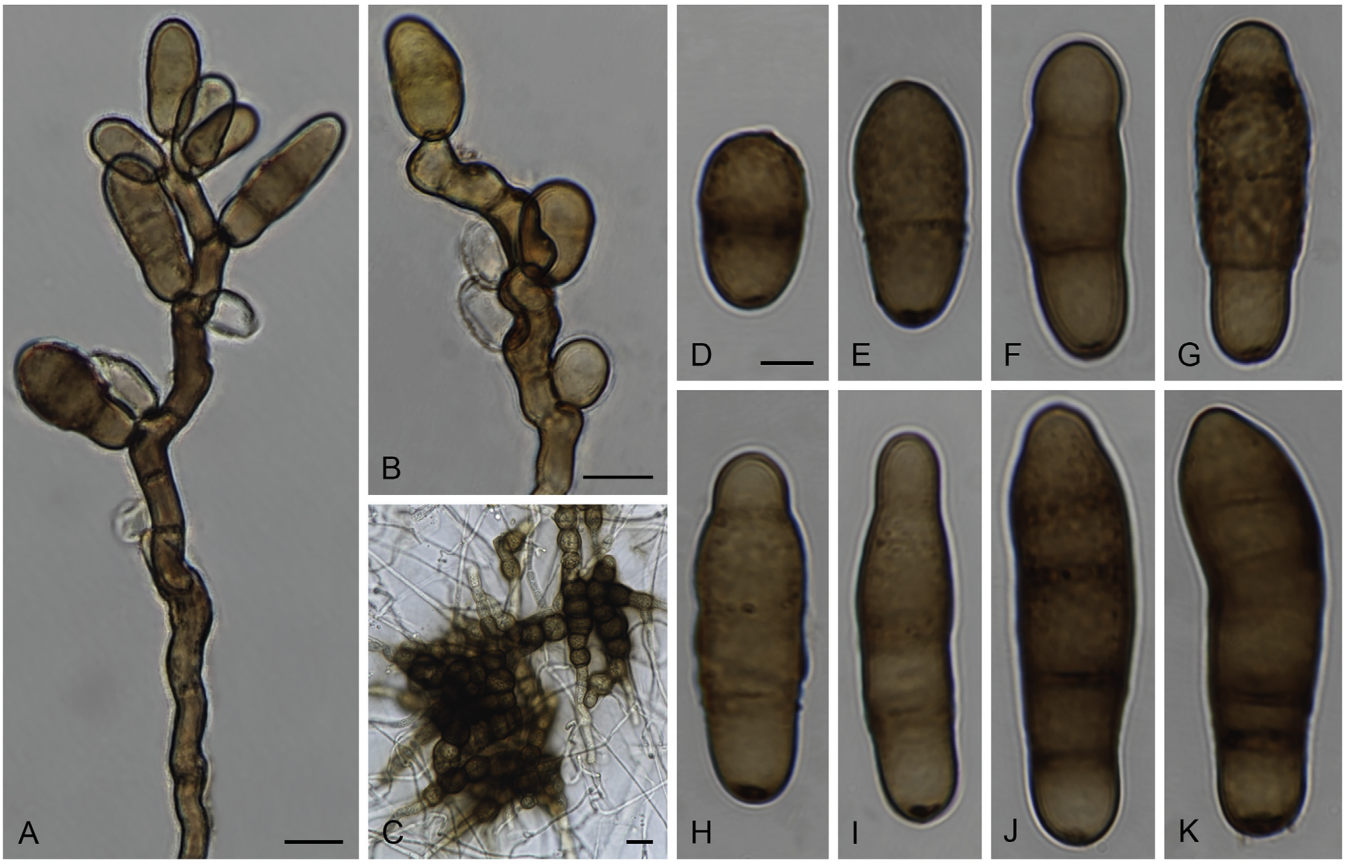


Fig. 54. *Pyrenophora nisikadoi* (CBS 119213). **A, B.** Conidiophores and conidia. **C.** Chlamydospores. **D–K.** Conidia. Scale bars: A, B = 10 µm; C = 20 µm; D = 5 µm; D applies to D–K.

Hyphae hyaline to pale brown, branched, septate, smooth-walled or verrucose, 1.5–5 µm. *Conidiophores* arising in groups, septate, straight or flexuous, usually geniculate in upper part, size of cells rarely decrease towards apex, rarely branched, cell walls thicker than those of vegetative hyphae, macronematous, rarely micronematous, pale brown to brown, slightly paler towards apex, not swollen at the base, (70–) 95–700 × 4.5–8 µm. *Conidiogenous cells* smooth-walled to slightly verruculose, terminal or intercalary, proliferating sympodially, pale brown to brown, subcylindrical to swollen, 10–30(–37) × 5.5–10 µm. *Conidia* verruculose, mostly curved, middle cells sometimes enlarged, cylindrical to obclavate, tapering towards apex, subhyaline to pale brown, end cells rarely paler, 2–5-distoseptate, (25–) 28–80(–83) × 9–16.5 µm, forming secondary conidiophores or conidia; *hila* protuberant, darkened, thickened, (3–) 3.5–6 µm. *Chlamydospores*, *microconidiation* and *sexual morph* not observed.

Culture characteristics: Colonies on MEA reaching 55–60 mm diam after 1 wk at 25 °C, with moderate aerial mycelium, flat to umbonate, margins arachnoid; surface greyish sepia to mouse grey; reverse blood colour, margins luteous. Colonies on PDA reaching 60–65 mm diam, with sparse aerial mycelium, flat, margins arachnoid; surface greyish sepia to fuscous black; reverse fuscous black. Colonies on OA covering dish, with moderate aerial mycelium; surface greyish sepia to fuscous black, margins brick; reverse fuscous black, margins brick.

Typus: **New Zealand**, on seeds of *Cynosurus cristatus* (*Poaceae*), 1975, E.H.C. McKenzie (**holotype** CBS H-23841, culture ex-type CBS 127918 = BRIP 12355 a = NZ 14880).

Notes: *Pyrenophora cynosuri* was isolated from seeds of *Cynosurus cristatum*, a member of the *Poaceae*, which includes host genera commonly infected by species of *Pyrenophora*. However, *Cynosurus* represents a new host genus for *Pyrenophora*.

Pyrenophora cynosuri is closely related and morphologically similar to *Py. dictyoides*. However, both species differ in the size of their conidiophore length (up to 700 µm in *Py. cynosuri vs.* up to 250 µm in *Py. dictyoides*) and conidial length (up to 83 µm in *Py. cynosuri vs.* up to 250 µm in *Py. dictyoides*), as well as conidial septation (up to 5 in *Py. cynosuri vs.* up to 15 in *Py. dictyoides*).

Fig. 55. *Pyrenophora novozelandica* (ex-type CBS 127934). **A–D.** Conidiophores and conidia. **E–M.** Conidia. Scale bars: A–D = 10 µm; E = 5 µm; E applies to E–M.

Pyrenophora dictyoides A.R. Paul & Parbery, Trans. Brit. Mycol. Soc. 51: 708. 1968.
Synonyms: *Helminthosporium dictyoides* Drechsler, J. Agric. Res. 24: 679. 1923.
Helminthosporium dictyoides var. dictyoides Drechsler, J. Agric. Res. 24: 679. 1923.
Helminthosporium dictyoides f. dictyoides Drechsler, J. Agric. Res. 24: 679. 1923.
Drechslera dictyoides (Drechsler) Shoemaker, Canad. J. Bot. 37: 881. 1959.
Helminthosporium dictyoides f. perenne Braverman & J.H. Graham, Phytopathology 50: 695. 1960.
Drechslera andersenii Scharif, Studies on Graminicolous Species of *Helminthosporium* (Tehran): 29. 1963. (nom. inval., Art. 36.1).
Drechslera andersenii A. Lam, Trans. Brit. Mycol. Soc. 85: 601. 1986.

Notes: Isolates belonging to *Py. dictyoides* (CBS 127933 and DAOM 63666) and *Drechslera andersenii* (CBS 258.80 and CBS 967.87) clustered together in a well-supported clade (100 % BS / 1 PP). Moreover, the morphology of the asexual morph is similar in both species, differing only in the production of conidia with much less tapered apices in *D. andersenii* (Sivanesan 1987). Therefore, we reduce these species to synonymy.

Pyrenophora nisikadoi Y. Marín & Crous, ***nom. nov.*** MycoBank MB829616. Fig. 54.
Replaced synonym: Helminthosporium brizae Y. Nisik., Ber. Ohara Inst. Landw. Biol.: 121, 133. 1928, non *Pyrenophora brizae* C. Massal. ex Sacc. 1911.
Additional synonyms: *Bipolaris brizae* (Y. Nisik.) Shoemaker, Canad. J. Bot. 37: 882. 1959.
Drechslera brizae (Y. Nisik.) Subram. & B.L. Jain, Curr. Sci. 35: 354. 1966.

Etymology: Named after the Japanese plant pathologist and mycologist, Y. Nisikado, who first described and named this fungus.

Hyphae hyaline to pale brown, branched, septate, verrucose, 2–5.5 µm. *Conidiophores* arising in groups, septate, mostly flexuous, rarely straight, geniculate at upper part, sometimes size of cells decrease towards apex, frequently branched, cell walls thicker than those of vegetative hyphae, macronematous, pale brown to brown, sometimes paler towards apex, rarely swollen at the base, 50–330 × 3.5–6.5(–8.5) µm. *Conidiogenous cells* smooth-walled to verruculose, terminal or intercalary, proliferating sympodially, pale brown to brown, subcylindrical to swollen, 7.5–20.5(–25) × 5–7.5 µm. *Conidia* verruculose, straight or curved, middle cells enlarged, cylindrical to obclavate, tapering towards apex, pale brown to brown, basal cell sometimes paler, less frequently apical cell also paler, (1–)2–4(–5)-distoseptate, (15–)17.5–42.5 × 8.5–12 µm, not forming secondary conidiophores or conidia; *hila* flat, darkened, thickened, 2–4 µm. *Chlamydospores* immersed in all media tested (MEA, OA and PDA), brown to dark brown, lineally or irregularly disposed, verrucose, globose to subglobose, up to 30 µm. *Microconidiation* and *sexual morph* not observed.

Culture characteristics: Colonies on MEA reaching 80–90 mm diam after 1 wk at 25 °C, with abundant aerial mycelium, cottony, lobate; surface pale greenish grey to greenish grey; reverse olivaceous black. Colonies on PDA covering dish, with moderate aerial mycelium, cottony, powdery at margins, flat; surface greenish grey to olivaceous black; reverse olivaceous black. Colonies on OA covering the dish, with sparse aerial mycelium, powdery to granular, flat; surface grey olivaceous to olivaceous black; reverse leaden grey to leaden black.

Typus: **Japan**, from *Briza minor* (*Poaceae*), Y. Nisikado [**epitype** designated by Manamgoda *et al.* (2014) CBS H-7218, culture ex-epitype CBS 190.29 = MUCL 9613].

Additional materials examined: **South Africa**, Western Cape Province, J.S. Marais Nature Reserve, from *Protea burchellii* senescent flowerheads (*Proteaceae*), 6 Jun. 2000, S. Lee, CBS 119213. **New Zealand**, Auckland, Waitakere Ranges, from *Briza minor* (*Poaceae*), 1 Nov. 1975, E.H.C. McKenzie, CBS 127912 = ICMP 6183.

Notes: This species was originally described in *Helminthosporium* as *Hel. brizae* (Nisikado 1928), then transferred to *Bipolaris* (Shoemaker 1959), and finally placed in *Drechslera* (Subramanian & Jain 1966). Type material was not available, thus Manamgoda *et al.* (2014) designated CBS 190.29 as ex-epitype since this strain was isolated by the original author from the same host and location. In our phylogenetic analysis based on ITS, *gapdh* and *rpb2*, CBS 190.29 together with other two strains were located in a well-supported clade (100 % BS / 1 PP) within the main clade representing the genus *Pyrenophora*. Therefore, we propose to transfer this species to *Pyrenophora*,

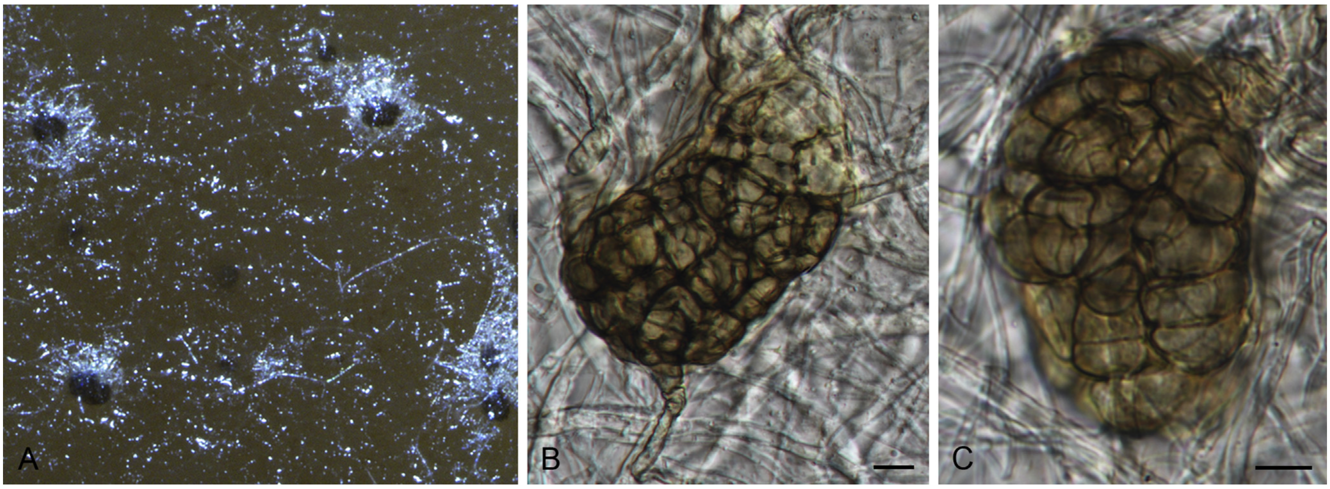


Fig. 56. *Pyrenophora pseudoerythrospila* (ex-type CBS 127931). **A.** Protoascomata on OA. **B, C.** Protoascomata. Scale bars = 10 µm.

Fig. 57. *Pyrenophora sieglingiae* (ex-type CBS 127930). **A–C.** Sterile ascomata. **D.** Neck of ascoma. **E, F.** Conidiophores and conidia. **G–O.** Conidia. Scale bars: C = 100 µm; D–F = 20 µm; G = 10 µm; G applies to G–O.

changing the epithet to *Py. nisikadoi* since *Py. brizae* already exists.

Isolate CBS 119213 sporulated, enabling us to conduct a morphological comparison and provide a modern description of this species in PDA. Moreover, *Py. nisikadoi* was formerly only recorded from *Briza minor*, a member of the *Poaceae*, while it is here also recorded from *Protea birchellii*, which belongs to the *Proteaceae*.

Pyrenophora novozelandica Y. Marín & Crous, ***sp. nov.*** MycoBank MB829620. Fig. 55.

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

Hyphae hyaline to pale brown, branched, septate, verrucose, 1–6(–8.5) µm. *Conidiophores* arising in groups, septate, straight or flexuous, sometimes geniculate at upper part, size of cells not decreasing towards apex, rarely branched, cell walls thicker than those of vegetative hyphae, macronematous, pale brown to brown, paler towards apex, not swollen at the base, 35–700 × 4.5–7.5 µm. *Conidiogenous cells* smooth-walled, terminal or intercalary, proliferating sympodially, brown, terminal conidiogenous cells hyaline, cylindrical to subcylindrical, 11–22 × 5–8.5 µm. *Conidia* smooth-walled, straight, rarely slightly curved, sometimes middle cells slightly enlarged, cylindrical to obclavate, tapering towards apex, pale brown to brown, sometimes basal cell slightly paler, (2–)3–5(–6)-distoseptate, 20.5–58 × 9.5–14 µm, not forming secondary conidiophores or conidia; *hila* usually inconspicuous, flat, slightly darkened, slightly thickened, 2–4 µm. *Chlamydospores*, *microconidiation* and *sexual morph* not observed.

Culture characteristics: Colonies on MEA reaching 27–30 mm diam after 1 wk at 25 °C, with sparse aerial mycelium, raised, margins fringed; surface grey olivaceous;

reverse dark mouse grey, margins buff. Colonies on PDA reaching 38–40 mm diam, with sparse aerial mycelium, flat, margins fringed; surface smoke grey to olivaceous grey; reverse olivaceous black. Colonies on OA reaching 37–40 mm diam, with moderate aerial mycelium, flat, margins fringed; surface grey olivaceous; reverse olivaceous black.

Typus: **New Zealand**, Wanganui, Palmerston North, Seed Testing Station, on seed of *Triticum* sp. (*Poaceae*), 5 Oct. 1976,

Fig. 58. *Pyenophora variabilis* (ex-type CBS 127920). **A–C.** Conidiophores and conidia. **D–N.** Conidia. Scale bars = 10 µm; C applies to A–C; N applies to D–N.

G.F. Laundon (**holotype** CBS H-23843, culture ex-type CBS 127934 = LEV 11079b = PDD 50697).

Notes: *Pyrenophora novozelandica* is similar and closely related to *Py. fugax*. However, both species can be easily distinguished based on the size of their conidiophores (up to 250 µm in *Py. fugax vs.* up to 700 µm in *Py. novozelandica*) and conidia (50–170 × 14–24 µm in *Py. fugax vs.* 20.5–58 × 9.5–14 µm in *Py. novozelandica*), as well as conidial septation [4–8(–10) in *Py. fugax vs.* (2–)3–5(–6) in *Py. novozelandica*]. *Pyrenophora novozelandica* is known to occur on *Triticum* in New Zealand, which is a common host of species belonging to *Pyrenophora*, including *Py. fugax*.

Pyrenophora poae (Baudyš) Y. Marín & Crous, ***comb. nov.*** MycoBank MB829617.
Basionym: *Helminthosporium poae* Baudyš, Lotos 63: 104. 1916.
Synonyms: *Helminthosporium vagans* Drechsler, J. Agric. Res., Washington 24: 688. 1923.
Drechslera vagans (Drechsler) Shoemaker, Canad. J. Bot. 37: 881. 1959.
Drechslera poae (Baudyš) Shoemaker, Canad. J. Bot. 40: 827. 1962.

Description and illustration: Sivanesan (1987).

Materials examined: **Canada**, Saskatchewan, Saskatoon, from *Poa pratensis* (*Poaceae*), Oct. 1973, J.D. Smith, DAOMC 145373. **Germany**, Husum, from *P. pratensis*, Aug. 1966, U.G. Schlösser, CBS 319.68. **USA**, Maryland, Beltsville, from *P. pratensis*, Apr. 1979, A. Hagan, CBS 128045 = BRIP 12969a.

Notes: *Pyrenophora poae* was introduced as *Helminthosporium poae* by Baudys (1916), then transferred to *Drechslera* (Shoemaker 1959). The original description was based on a specimen isolated from *Poa trivialis* in the Czech Republic. Type material is not available, but CBS 319.68 is considered here as an authentic strain since was isolated from the same host genus and continent. Unfortunately, it did not sporulate and thus we chose to not designate it as epitype. All the strains identified as *D. poae* were located in the main clade belonging to *Pyrenophora*, and a new combination is proposed here.

Pyrenophora pseudoerythrospila Y. Marín & Crous, ***sp. nov.*** MycoBank MB829675. Fig. 56.

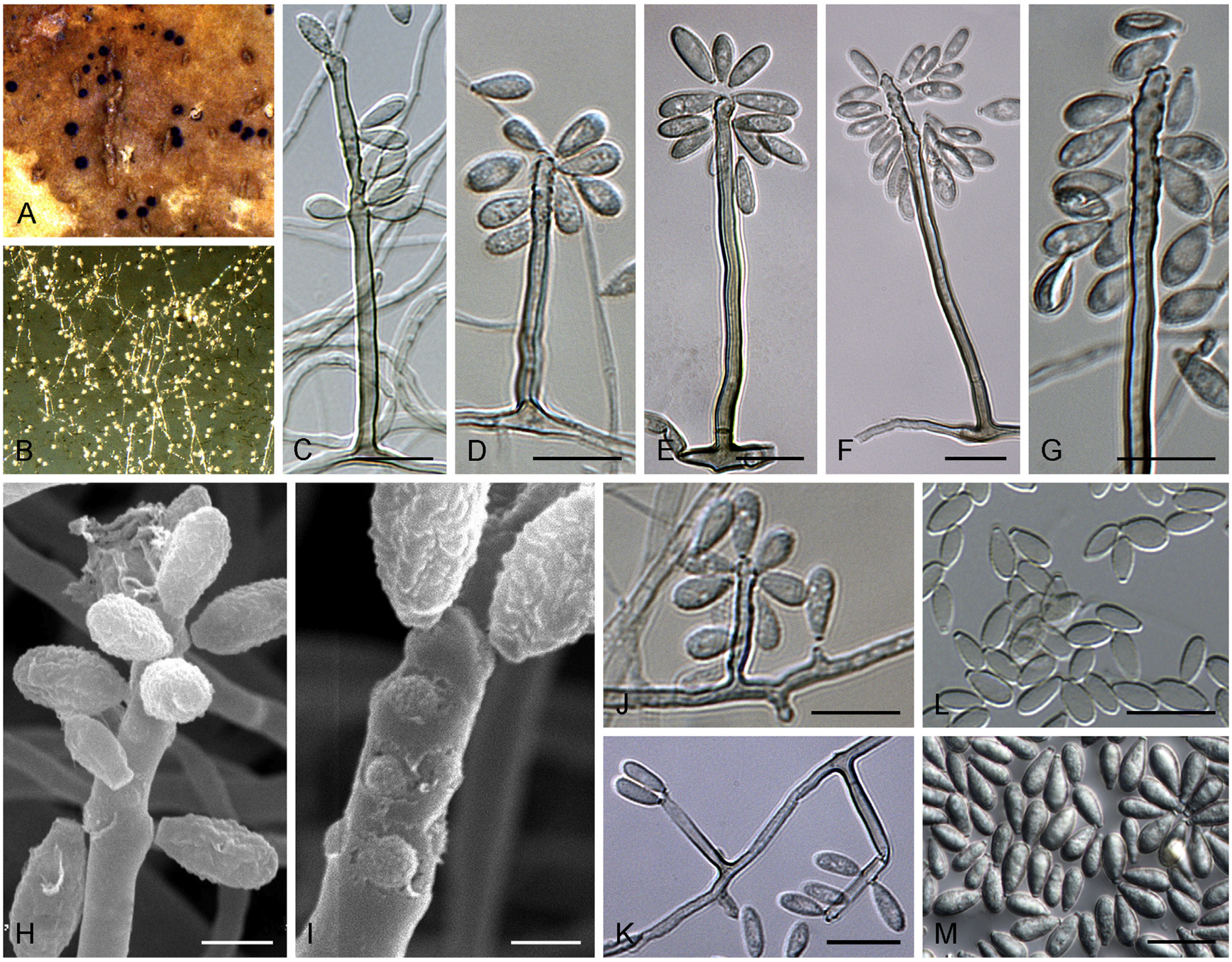


Fig. 59. *Ramichloridium* spp. **A.** *Ramichloridium luteum* on apple. **B.** Sporulating colonies of *Ramichloridium luteum* (ex-type CBS 132088) on PDA. **C–G.** Macronematous conidiophores with sympodially proliferating conidiogenous cells, which give rise to a conidium-bearing rachis with crowded and prominent scars. **C.** *Ramichloridium apiculatum* (ex-type CBS 156.59). **D.** *Ramichloridium cucurbitae* (ex-type CBS 132087). **E, F.** *Ramichloridium luteum* (ex-type CBS 132088). **G.** *Ramichloridium punctatum* (ex-type CBS 132090). **H, I.** Scanning electron micrographs of *Ramichloridium luteum* (ex-type CBS 132088) showing sympodial proliferation with scars on conidiogenous cells. **J, K.** Conidiophores reduced to conidiogenous cells. **J.** *Ramichloridium cucurbitae* (ex-type CBS 132087). **K.** *Ramichloridium luteum* (ex-type CBS 132088). **L, M.** Conidia. **L.** *Ramichloridium apiculatum* (ex-type CBS 156.59). **M.** *Ramichloridium punctatum* (ex-type CBS 132090). Scale bars: H = 2 µm; I = 1 µm; all others = 10 µm. Pictures C, L taken from Li *et al.* (2012); all others from Arzanlou *et al.* (2007).

Etymology: Named after its close phylogenetic relation to *Py. erythrospila*.

Only forming protoascomata in OA. *Protoascomata* composed of pale brown to brown cells of up to 100 µm diam, of *textura angularis* to *textura globulosa*. *Pyrenophora pseudoerythrospila* differs from its closest phylogenetic neighbour, *Py. erythrospila* by unique fixed alleles in three loci based on alignments of the separate loci deposited in TreeBASE (S23834): LSU positions 70 (G), 395 (C), 396 (T), 397 (T), 500 (G), 536 (C), 537 (T); ITS positions 141 (A), 146 (A), 147 (T), 148 (A), 149 (G), 152 (G), 153 (A), 154 (G), 155 (T), 164 (T), 168 (T), 169 (G), 173 (G), 174 (C), 176 (A), 178 (T), 179 (G), 184 (T), 187 (T), 189 (T), 197 (C), 198 (C), 199 (C), 205 (C), 206 (T), 208 (C), 223 (T), 224 (T), 225 (T), 226 (T), 234 (A), 252 (T), 264 (T), 268 (C), 279 (G), 288 (C), 289 (A), 293 (A), 302−304 (indels), 327 (T), 330−332 and 341 (indels),511 (T), 536−540 (indels), 558 (C), 591 (A), 594 (G), 601 (T), 621 (A), 630 (C), 641 (G), 643 (A), 644 (G), 645 and 646 (indels), 659 (T), 660 (G), 664 (T), 666 (A), 667 (T); *gapdh* positions 30 (C), 49 (A), 54 and 55 (indels), 59 (G), 60 (A), 69 (C), 71 (C), 74 (A), 85 (T), 87 (A), 177 (G), 178 (G), 179 (C), 180 (C), 182 (C), 187 (G), 189 (C), 190 (T), 191 (A), 192 (T), 193 (C), 194 (A), 195 (G), 196 (A), 197 (C), 201 (G), 203 (A), 204 (G), 205 (A), 256 (G), 319 (G), 373 (T), 406 (C), 487 (T), 493 (T), 496 (T), 523 (G), 526 (C), 532 (C), 538 (A).

Culture characteristics: Colonies on MEA reaching 55−60 mm diam after 1 wk at 25 °C, with sparse aerial mycelium, flat, margins fringed; surface pale vinaceous to vinaceous buff; reverse orange to sienna, margins transparent. Colonies on PDA reaching 56−59 mm diam, with sparse aerial mycelium, flat, margins fringed; surface cinnamon, white mycelium in the centre; reverse cinnamon, centre brick to dark brick. Colonies on OA reaching 50−55 mm diam, without aerial mycelium, flat; surface cinnamon; reverse transparent, centre brick to dark brick.

Typus: **Germany**, West Germany, on *Lolium* sp. (*Poaceae*), 9 Sep. 1968, U.G. Schlosser (**holotype** CBS H-23844, culture ex-type CBS 127931 = DAOMC 126772).

Notes: The ex-type strain of *Pyrenophora pseudoerythrospila* did not sporulate on any of the media tested, producing only few protoascomata in OA. However, these remained sterile after several months of incubation. *Pyrenophora pseudoerythrospila* is closely related to *Py. erythrospila*, which produces both sexual and asexual morphs. The protoascomata were also reported in *Py. erythrospila*, but these finally developed mature ascospores after 25 wk. *Pyrenophora erythrospila* is commonly found on *Agrostis* spp. in Australia and North America, but has also been reported on *Lolium* in Germany (Farr & Rossman 2019), having the same host and distribution as *Py. pseudoerythrospila*.

Pyrenophora sieglingiae Y. Marín & Crous, ***sp. nov.*** MycoBank MB829618. Fig. 57.

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

Hyphae hyaline to pale brown, branched, septate, verrucose, (1−)1.5–5.5 µm. *Sterile ascomata* solitary or arising in groups, brown to dark brown or black, sometimes apical part of neck yellowish brown, composed of cells of *textura intricata*, up to 1200 µm long, up to 300 µm wide, conidiophores arising from the body and neck; inside consisting of angular to globose, hyaline cells. *Conidiophores* arising in groups, septate, straight or flexuous, rarely geniculate in the upper part, cell size rarely decreases towards the apex, unbranched, cell walls thicker than those of vegetative hyphae, macronematous, brown, mostly paler towards apex, not swollen at the base, 100−700 × (5−)7−9(−11) µm. *Conidiogenous cells* verruculose, terminal or intercalary, proliferating sympodially, pale brown to brown, subcylindrical to slightly swollen, (12−)15−33.5(−36.5) × 9−12(−13.5) µm. *Conidia* verruculose, straight or curved, sometimes with middle cells enlarged, cylindrical to obclavate, tapering towards apex, pale brown to brown, end cells usually paler, 4−8-distoseptate, 56−108(−120) × 15−23(−25.5) µm, forming secondary conidiophores or conidia; *hila* not protuberant or flat, darkened, thickened, (4−)4.5−6.5(−7) µm. *Chlamydospores*, *microconidiation* and *sexual morph* not observed.

Culture characteristics: Colonies on MEA reaching 26−29 diam after 1 wk at 25 °C, with abundant aerial mycelium, raised, slightly lobate; surface white to buff; reverse fuscous black. Colonies on PDA reaching 27−30 diam, with abundant aerial mycelium, lobate; surface olivaceous black with patches of white due to aerial mycelium; reverse olivaceous black, margins luteous. Colonies on OA reaching 54−57 diam, with moderate to abundant aerial mycelium, flat; surface smoke-grey to olivaceous grey; reverse smoke-grey to olivaceous grey.

Typus: **New Zealand**, Auckland, Waikumete, from leaf of *Sieglingia decumbens* (*Poaceae*), E.H.C. McKenzie (**holotype** CBS H-23842, culture ex-type CBS 127930 = ICMP 6170 = PDDCC 6170).

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

Species	Isolates[1]	GenBank accession numbers[2]				References
		ITS	LSU	*rpb2*	*tef1*	
Ramichloridium apiculatum	CBS 156.59^{T}	EU041791	EU041848	MF951416	–	Arzanlou *et al.* (2007), Videira *et al.* (2017)
R. cucurbitae	CBS 132087^{T}	JQ622087	JQ622095	–	JQ622112	Li *et al.* (2012)
R. luteum	CBS 132088^{T}	EU329730	JQ622099	MF951417	JQ622116	Li *et al.* (2012), Videira *et al.* (2017)
R. malus	LQ73^{T}	EF627452	–	–	–	Zhang *et al.* (2007)
R. punctatum	CBS 132090^{T}	JQ622086	JQ622094	–	JQ622111	Li *et al.* (2012)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; LQ: collection not specified in the work in which it was introduced. ^{T} indicates ex-type strains.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; LSU: partial large subunit (28S)nrDNA; *rpb2*: partial DNA-directed RNA polymerase II second largest subunit gene; *tef1*: partial elongation factor 1-alpha gene.

Notes: *Pyrenophora sieglingiae* is closely related to *Py. semeniperda* and *Py. wirreganensis*. Morphologically, these species are similar, producing sterile ascomata with long necks. However, they can be distinguished by the size of their conidiophores (up to 700 µm in *Py. sieglingiae vs.* up to 180 µm in *Py. semeniperda vs.* up to 1 000 µm in *Py. wirreganensis*) and conidia [56–108(–120) × 15–23(–25.5) µm in *Py. sieglingiae vs.* 70–160 × 13–17 µm in *Py. semeniperda vs.* (30–)40–80(–100) × (10–)12–19(–22) µm in *Py. wirreganensis*). Moreover, *Py. semeniperda* produces conidia with more septa (up to 12 in *Py. semeniperda vs.* up to 8 in *Py. sieglingiae vs.* up to 9 in *Py. wirreganensis*), and it is the only one that produces a sexual morph. *Pyrenophora sieglingiae* has been isolated from *Sieglingia* from New Zealand while *Py. wirreganensis* occurs on *Hordeum* in Australia. *Pyrenophora semeniperda* has been isolated from both hosts in both locations, apart from other hosts that are widely distributed, *i.e.* *Agropyron*, *Avena*, *Bromus*, *Cortaderia*, *Ehrhartia*, *Pennisetum* and *Triticum*.

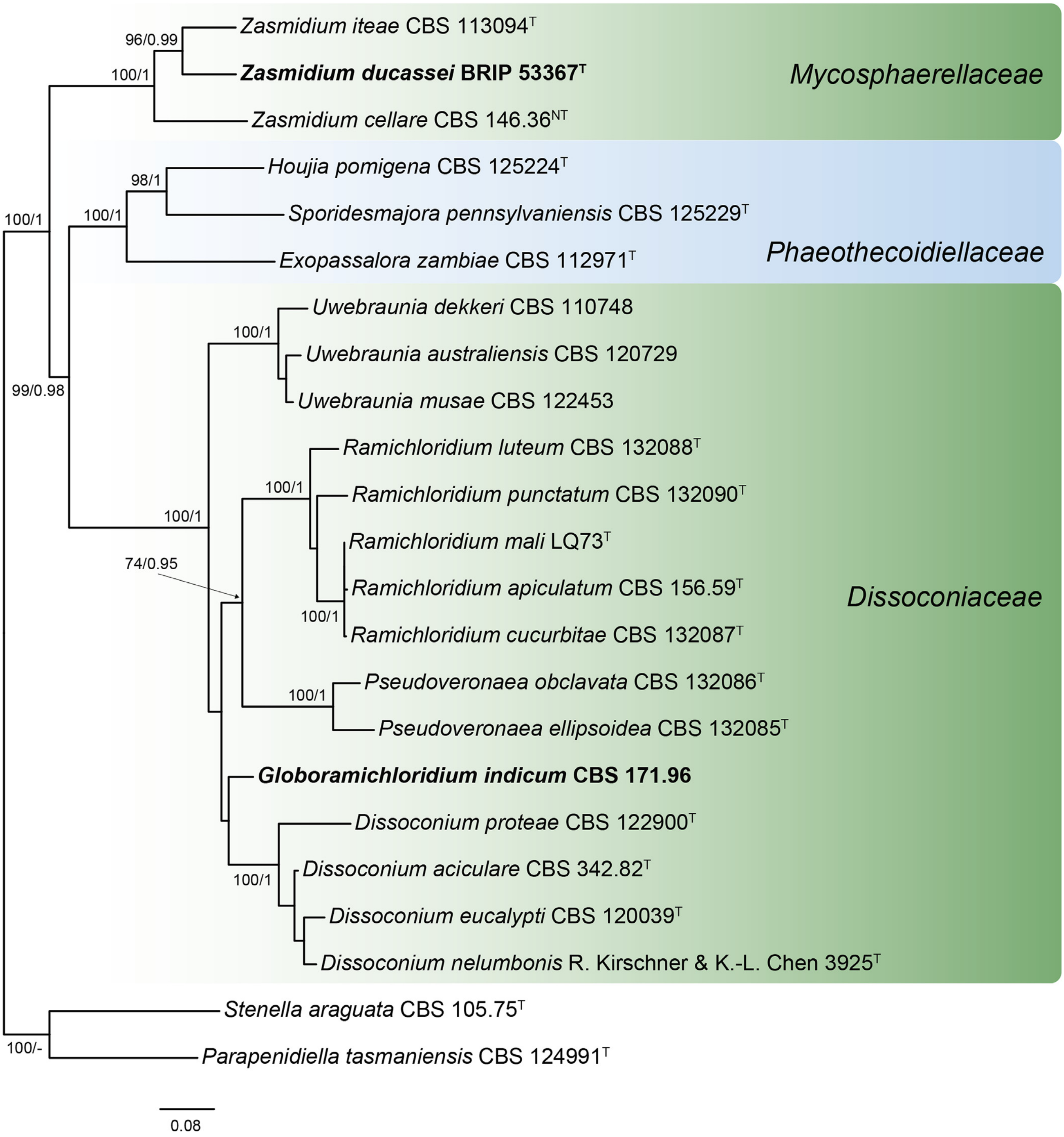


Fig. 60. RAxML phylogram obtained from the combined ITS (594 bp), LSU (761 bp), *rpb2* (819 bp) and *tef1* (470 bp) sequence alignment of all accepted species of *Ramichloridium* and related taxa. The tree was rooted to *Parapenidiella tasmaniensis* CBS 124991 and *Stenella araguata* CBS 105.75. The 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 listed in Table 13, Li *et al.* (2012), Videira *et al.* (2017) and Chen & Kirschner (2018). ^{T} and ^{NT} indicate ex-type and ex-neotype strains, respectively. TreeBASE: S23834.

Pyrenophora teres Drechsler, J. Agric. Res., Washington 24: 656. 1923.

Synonyms: *Helminthosporium secalis* Fée, Mém. Soc. Mus. Hist. Nat. Strassbourg 3: 36. 1843.

Alternaria secalis (Fée) Sacc. & Traverso, Syll. fung. (Abellini) 20: 1184. 1911.

Helminthosporium gramineum Rabenh., Klotzschii Herb. Viv. Mycol., Edn Nov, Ser. Sec., Cent. 4: no. 332. 1857.

Brachysporium gracile var. gramineum (Rabenh. ex Schltdl.) Sacc., Syll. fung. (Abellini) 4: 430. 1886.

Drechslera graminea (Rabenh. ex Schltdl.) S. Ito, Proc. Imper. Acad. Tokyo 6: 355. 1930.

Drechslera teres subsp. *graminea* (Rabenh. ex Schltdl.) Simay, Barley Newsletter 36: 174. 1992.

Helminthosporium teres Sacc., Syll. fung. (Abellini) 4: 412. 1886.

Drechslera teres (Sacc.) Shoemaker, Can. J. Bot. 37: 881. 1959.

Drechslera teres f. teres (Sacc.) Shoemaker, Canad. J. Bot. 37: 881. 1959.

Drechslera teres subsp. teres (Sacc.) Shoemaker, Canad. J. Bot. 37: 881. 1959.

Helminthosporium hordei Eidam, Der Landw. (Schles. Landw. Ztg), Breslau 27: 509. 1891.

Helminthosporium tuberosum G.F. Atk., Bulletin of Cornell University 3: 47. 1897.

Drechslera tuberosa (G.F. Atk.) Shoemaker, Canad. J. Bot. 37: 881. 1959.

Helminthosporium fragosoi Bubák, Hedwigia 57: 13. 1915.

Pyrenophora teres f. teres Drechsler, J. Agric. Res., Washington 24: 656. 1923.

Pyrenophora teres subsp. teres Drechsler, J. Agric. Res., Washington 24: 656. 1923.

Helminthosporium japonicum S. Ito & Kurib., Proc. Imper. Acad. Tokyo 6: 353. 1930.

Pyrenophora japonica S. Ito & Kurib., Proc. Imper. Acad. Tokyo 6: 353. 1930.

Drechslera japonica (S. Ito & Kurib.) Shoemaker, Canad. J. Bot. 37: 881. 1959.

Pyrenophora graminea S. Ito & Kurib., Proc. Imp. Acad. Japan 6: 353. 1930.

Pyrenophora teres subsp. *graminea* (S. Ito & Kurib.) Simay, Barley Newsletter 36: 174. 1992.

Pyrenophora secalis M.D. Whitehead & J. Dicks., Mycologia 44: 752. 1952.

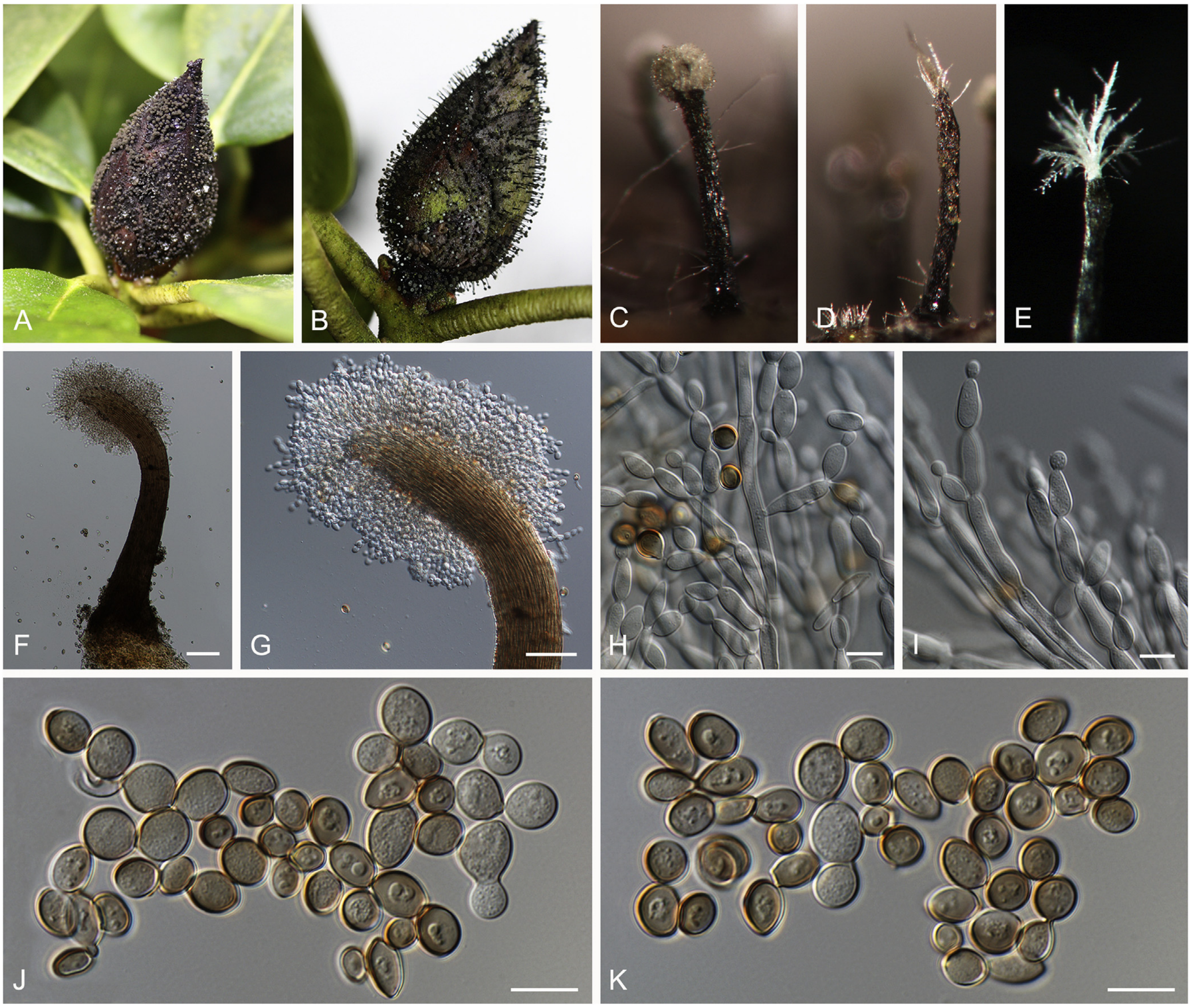


Fig. 61. *Seifertia azalae*. **A, B.** Disease symptoms caused on *Rhododendron*. **C–G.** Synnemata. **H, I.** Conidiogenous cells and conidia. **J, K.** Conidia. Scale bars: F = 100 µm; G = 50 µm; H–K = 10 µm.

Drechslera teres f. maculata Smed.-Pet., Arb. Tiflis Bot. Gard.: 139. 1971.
Pyrenophora teres f. maculata Smed.-Pet., The Royal Veterinary and Agricultural University Yearbook: 139. 1971.

Description and illustrations: Sivanesan (1987).

Materials examined: **Denmark**, from *Hordeum vulgare* (*Poaceae*), unknown date, V. Smedegaard-Petersen (**ex-type** culture of *Py. teres f. maculata* CBS 228.76). **Japan**, from *H. vulgare* (*Poaceae*), unknown date, S. Ito, CBS 281.31; unkown substrate and date, S. Ito, CBS 282.31; from *H. vulgare* (*Poaceae*), unknown date, Y. Nisikado, CBS 336.29 = MUCL 9687. **Germany**, Niedersachsen, Rotenburg, from *H. vulgare* (*Poaceae*), Jul. 1968, U.G. Schlösser, CBS 314.69. **Hungary**, Eszteragpuszta, from *Hordeum vulgare* leaf (*Poaceae*), unknown date, col. M. Csosz, dep. J. Bakonyi, CBS 123929; Taplanszentkereszt, from *Hordeum vulgare* leaf (*Poaceae*), unknown date, col. A. Tomcsanyi, dep. J. Bakonyi, CBS 123932.

Notes: In our phylogenetic analysis, isolates identified as *Py. teres* and *Py. graminea* were located in the same well-supported clade (100 % BS / 1 PP), suggesting that these represent the same species. In fact, *Py. graminea* has been recently considered as a subspecies of *Py. teres* (Simay 1992) since its morphology is similar and both species share the same host, *Hordeum*. Therefore, we propose the synonymy of both species under the name of *Py. teres*, which is well established and the most commonly used name for this taxon. Moreover, an authentic strain of *Py. japonica* was also located in this clade, supporting the synonymy of *Py. japonica* with *Py. teres* proposed by Crous *et al.* (1995), which was based on their morphological, molecular and pathological similarity.

Pyrenophora teres produces net blotch on barley worldwide, causing cell death and feeding off the nutrients released (Sivanesan 1987, Louw *et al.* 1995, Campbell *et al.* 1999, Ellwood *et al.* 2012). Two different forms of *Py. teres* were recognised depending on the disease symptoms produced, *i.e. Py. teres f. teres* producing the net form of net blotch, characterised by elongated lesions where necrosis develops along leaf veins with occasional transverse striations, while *Py. teres f. maculata* produces the spot form of net blotch, typified by more ovoid lesions, often surrounded by a chlorotic zone (Campbell *et al.* 1999, Ellwood *et al.* 2012). However, both forms are considered the same species, *Py. teres*. This disease becomes systemic in plants infected from seed (Sivanesan 1987).

Pyrenophora variabilis Hern.-Restr. & Y. Marín, ***sp. nov.*** MycoBank MB829619. Fig. 58.

Etymology: Name refers to the highly variable conidial morphology.

Hyphae hyaline to brown, branched, septate, smooth-walled to verrucose, 2.5–7 µm. *Conidiophores* arising in groups, septate, straight or flexuous, sometimes geniculate in upper part, simple, cell walls thicker than those of vegetative hyphae, semi- to macronematous, brown, not swollen at the base, up to 321 µm long, 5–10 µm wide. *Conidiogenous cells* smooth-walled, terminal or intercalary, proliferating sympodially, brown, subcylindrical, 18–27 × 8–10 µm. *Conidia* smooth-walled, straight to curved, cylindrical, subcylindrical, obclavate, obpyriform to subglobose, pale brown to brown, 1–3-distoseptate, 20–75 × 13–19.5 µm; *hila* flat, darkened, thickened, 4–7 µm. *Chlamydospores* and *sexual morph* not observed.

Typus: **Canada**, British Columbia, Agassiz Research Station, from leaves of *Poa trivialis* (*Poaceae*), Jul. 1972, J.D. Smith (**holotype** CBS H-23843, culture ex-type CBS 127920 = DAOMC 139513).

Notes: *Pyrenophora variabilis* was located on an independent branch far removed from the other species in the genus. It can be easily distinguished from all the species of the genus by its highly variable conidial morphology in size and shape, from cylindrical, subcylindrical or obclavate to subglobose or obpyriform. It was isolated from *Poa trivialis* (*Poaceae*) leaves in Canada, a common host of *Pyrenophora* spp.

Pyrenophora wirreganensis (Wallwork *et al.*) Y. Marín & Crous, ***comb. nov.*** MycoBank MB829621.
Basionym: *Drechslera wirreganensis* Wallwork *et al.*, Mycol. Res. 96. 888. 1992.

Description and illustration: Wallwork *et al.* (1992).

Material examined: **Australia**, South Australia, from *Hordeum* sp. (*Poaceae*), unknown date, J. Bakonyi, CBS 109896.

Notes: *Pyrenophora wirreganensis* was introduced as *Drechslera wirreganensis* by Wallwork *et al.* (1992) to accommodate a specimen isolated from *Hordeum* in Australia. In the phylogenetic analysis, the strain CBS 109896 identified as *Py. wirreganensis* and isolated from the same host and location than the ex-type strain (IMI 348323), was located in an independent branch within the main clade representing the genus *Pyrenophora*. Therefore, this species is here transferred to the latter genus. For comparison with close species see notes of *Py. sieglingiae*.

Authors: Y. Marin-Felix, M. Hernández-Restrepo, P.W. Crous

Ramichloridium Stahel ex de Hoog, Stud. Mycol. 15: 59. 1977. Fig. 59.

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

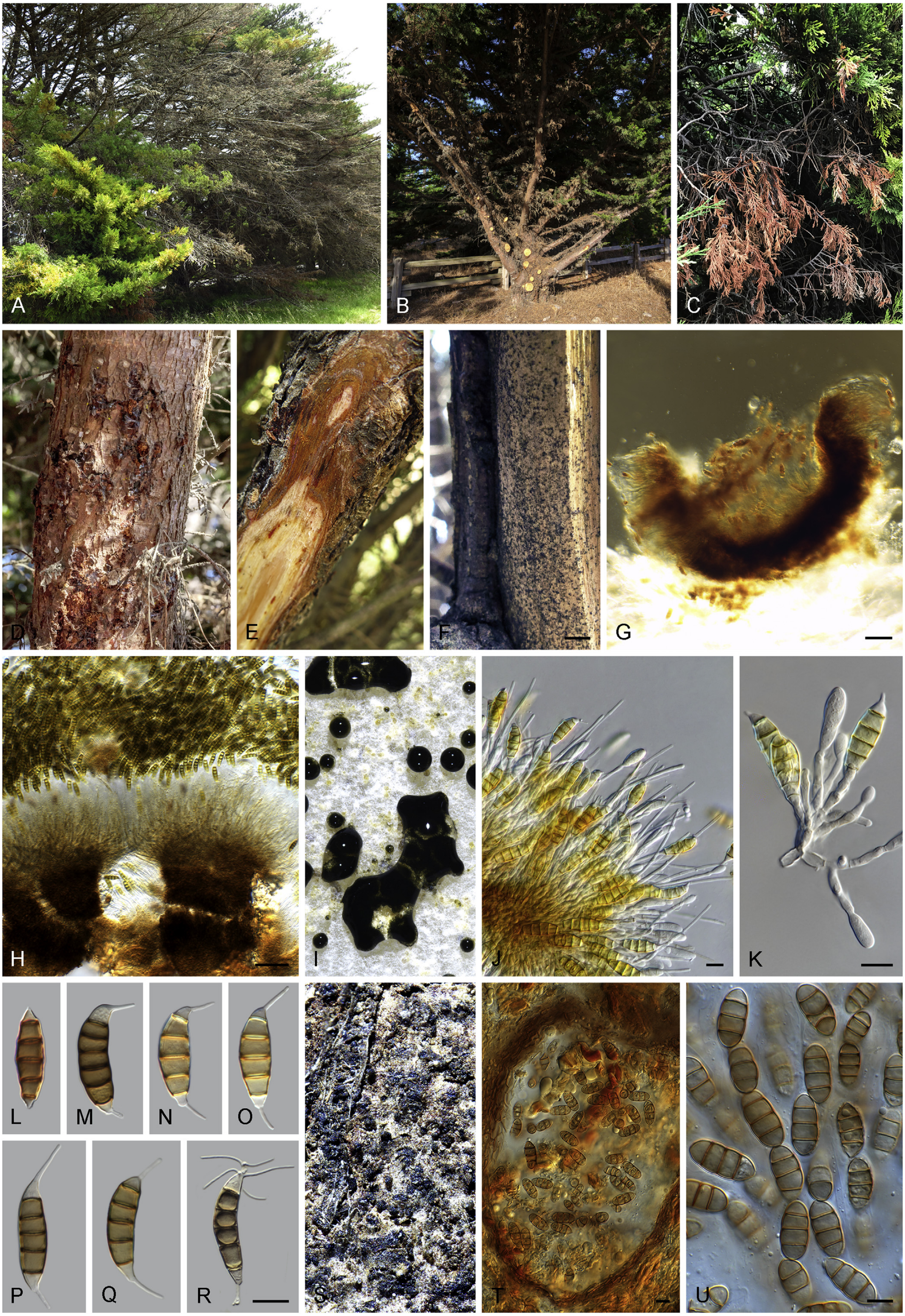
Type species: *Ramichloridium apiculatum* (J.H. Mill. *et al.*) de Hoog, basionym: *Chloridium apiculatum* J.H. Mill. *et al.* Ex-type strain: CBS 156.59 = ATCC 13211 = IMI 100716 = JCM 6972 = MUCL 15753 = MUCL 7991 = QM 7716.

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

Species	Isolates[1]	GenBank accession numbers[2]			References
		LSU	ITS	*tef1*	
Seifertia azaleae	DAOM 239136	EU030276	–	–	Seifert *et al.* (2007)
	CPC 35017	MK540034	MK539964	MK540166	Present study
Sei. shangrilaensis	MFLUCC 16-0238^T	KU954100	–	KU954101	Li *et al.* (2016b)

[1] CPC: Culture collection of Pedro Crous, housed at Westerdijk Fungal Biodiversity Institute; DAOM: Plant Research Institute, Department of Agriculture (Mycology), Ottawa, Canada; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Ria, Thailand. ^{T} indicates ex-type strains.

[2] LSU: partial large subunit (28S) nrRNA gene; ITS: internal transcribed spacers and intervening 5.8S nrDNA; *tef1*: partial translation elongation factor 1-alpha gene.


A
B
C
D
E
F
G
H
I
J
K
L
M
N
O
P
Q
R
S
T
U

DNA barcode (genus): LSU.

DNA barcodes (species): ITS, *rpb2*, *tef1*. Table 13. Fig. 60.

Mycelium consisting of hyaline, subhyaline, pale brown, or brown, smooth-walled, septate, branched, submerged and aerial hyphae. *Conidiophores* straight to gently curved, subcylindrical, unbranched, smooth- and thick-walled, brown to dark brown, 0–3-septate, or sometimes reduced to intercalary conidiogenous cells. *Conidiogenous cells* integrated, terminal, pale to medium brown, or golden-brown, apical part subhyaline to pale brown, subcylindrical, rarely somewhat clavate, sometimes with irregular, nodulose swellings along the length of the conidiogenous cells, tapering towards apex, with sympodial proliferation, forming a rachis with slightly thickened and darkened, circular, somewhat protruding scars. *Conidia* solitary, aseptate, pale brown, smooth-walled to finely verrucose, clavate or oblong to ellipsoid, or obovate to obconical, apex obtuse or subobtuse, base truncate, with a conspicuous, slightly darkened and thickened, not refractive hilum.

Culture characteristics: Colonies after 1 mo at 25 °C in the dark flat, spreading, with sparse to moderate aerial mycelium, margins smooth and even, or lobate and feathery. On SNA grey olivaceous, pale mouse grey, or smoke-grey. On PDA olivaceous grey or smoke-grey; reverse olivaceous grey or iron-grey. On OA olivaceous grey or iron-grey; reverse iron-grey, with pale luteous pigment diffusing into agar. On MEA olivaceous green; reverse olivaceous black, often with a diffusing citron-yellow pigment.

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

Distribution: Africa, America and Asia.

Hosts: *Aloe* sp. (*Aloaceae*), *Cucumis sativus*, *Cucurbita maxima* (*Cucurbitaceae*), *Malus domestica*, *Malus pumila* and *Pyrus pyrifolia* (*Rosaceae*). Also isolated from soil.

Disease symptoms: Sooty blotch and flyspeck diseases.

Notes: *Ramichloridium* was initially introduced by Stahel (1937), designating *R. musae* as type species. However, the name was invalid due to the lack of Latin description or diagnosis. Subsequently, de Hoog (1977) validated this genus to include species with erect, dark conidiophores and predominantly aseptate conidia, designating as new type species *R. apiculatum*. In that study, 13 species were recognised in *Ramichloridium*, and subsequently more species were included. However, several molecular studies demonstrated that some of them belonged to different genera, *i.e. Myrmecridium*, *Pachyramichloridium*, *Pleurothecium*, *Radulidium*, *Rhinocladiella* and *Zasmidium*, and were subsequently transferred (Arzanlou *et al.* 2007, Cheewangkoon *et al.* 2009, Videira *et al.* 2017). Some species still need to be molecularly studied to confirm their phylogenetic position. In the present study, only five species have been demonstrated to belong to *Ramichloridium*, which is characterised by aseptate, pale brown, smooth-walled to finely verrucose, clavate or oblong to ellipsoid, or obovate to obconical conidia. Based on molecular data, *R. indicum* is proposed here as a new genus, *Globoramichloridium indicum*, and *R. ducassei* as a new combination in *Zasmidium* (see *Zasmidium* below). Moreover, *R. apiculatum*, *R. cucurbitae* and *R. mali* were located in a well-supported clade (100 % BS / 1 PP) without phylogenetic distance. Unfortunately, the only loci available and common in the three species are the ITS and LSU. Therefore, other loci should be sequenced to verify their status as separate species.

Species of *Ramichloridium* cause sooty blotch and flyspeck disease (SBFS) on members of the family *Rosaceae*, which produces blemishes on the epicuticular wax layer and is regarded as an economically serious disease (Wang *et al.* 2014). *Ramichloridium cucurbitae* and *R. punctatum* have been found as SBFS pathogens only in the USA (Li *et al.* 2012), while *R. apiculatum*, *R. luteum* and *R. mali* have been reported as causal agents of SBFS in China (Zhang *et al.* 2007, Li *et al.* 2012, Wang *et al.* 2014).

References: Arzanlou *et al.* 2007, Li *et al.* 2012 (morphology and phylogeny).

Globoramichloridium Y. Marín & Crous, ***gen. nov.*** MycoBank MB829622.

Etymology: Name reflects the characteristic globose conidia produced by this genus.

Illustration: Arzanlou *et al.* (2007).

Mycelium consisting of submerged and aerial hyphae; *submerged hyphae* smooth- and thin-walled, hyaline, with thin septa; *aerial hyphae* coarsely verrucose, olivaceous green, rather thick-walled, with thin septa. *Conidiophores* arising vertically from creeping hyphae at right angles, straight, unbranched, thick-walled, smooth-walled, dark brown, with up to 10 thin septa, often with inflated basal cells. *Conidiogenous cells* terminally integrated, smooth-walled, dark brown, sympodially proliferating, rachis straight or flexuose, geniculate or nodose, subhyaline; *scars* thickened and darkened, clustered at nodes. *Microcyclic conidiation* observed in culture. *Conidia* solitary, (0–)1-septate, not constricted at the septum, subhyaline to pale brown, smooth-walled or coarsely verrucose, rather thin-walled, broadly ellipsoidal to globose, with truncate base; *hila* conspicuous, slightly darkened, not thickened.

Culture characteristics: Colonies on MEA reaching 35 mm diam after 2 wks at 24 °C. Colonies velvety, rather compact, slightly elevated, with entire, smooth, whitish margins, dark olivaceous green in the central part.

Type species: *Globoramichloridium indicum* (Subram.) Y. Marín & Crous. Holotype: IMI 114625. Representative strain: CBS 171.96.

Fig. 62. *Seiridium* spp. **A–F.** Disease symptoms on *Cupressaceae* hosts. **A–C.** Flagging of branches. **D.** Trunk canker with gummosis. **E.** Branch canker. **F.** Conidiomata. **G–I.** *Seiridium pezizoides* (CBS 145115). **G, H.** Acervuli on *Cupressaceae* sp. **I.** Conidial masses on artificial media. **J, K.** Conidiophores and conidiogenous cells. **J.** *Seiridium neocupressi* (CBS 142625). **K.** *Seiridium eucalypti* (CBS 343.97). **L–R.** Conidia. **L.** *Seiridium cardinale* (CBS 909.85). **M.** *Seiridium spyridicola* (CBS 142628). **N.** *Seiridium unicorne* (CBS 538.82). **O.** *Seiridium neocupressi* (CBS 142625). **P.** *Seiridium eucalypti* (CBS 343.97). **Q.** *Seiridium kartense* (CBS 142629). **R.** *Seiridium pezizoides* (CBS 145115). **S–U.** *Seiridium cupressi* (IMI 40096). **S, T.** Ascomata. **U.** Ascospores. Scale bars: F = 2 mm; G, H = 50 μm; J–U = 10 μm. Pictures J–U taken from Bonthond *et al.* (2018).

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

Species	Isolates.[1]	GenBank accession numbers[2]				References
		ITS	*rpb2*	*tef1*	*tub2*	
Seiridium camelliae	MFLUCC 12-0647^{T}	JQ683725	–	JQ683741	JQ683709	Maharachchikumbura *et al.* (2015)
S. cancrinum	CBS 226.55^{T}	LT853089	LT853137	LT853186	LT853236	Bonthond *et al.* (2018)
S. cardinale	CBS 909.85^{R}	LT853064	LT853113	LT853161	LT853211	Bonthond *et al.* (2018)
S. ceratosporum	PHSI2001Pathcw07	AY687314	–	–	DQ534043	Liu *et al.* (2007)
S. cupressi	CBS 224.55^{ET}	LT853083	LT853131	LT853180	LT853230	Bonthond *et al.* (2018)
S. eucalypti	CBS 343.97^{ET}	LT853099	LT853146	LT853196	LT853246	Bonthond *et al.* (2018)
S. kartense	CBS 142629^{T}	LT853100	LT853147	LT853197	LT853247	Bonthond *et al.* (2018)
S. kenyanum	CBS 228.55^{T}	LT853098	LT853145	LT853195	LT853245	Bonthond *et al.* (2018)
S. marginatum	CBS 140403^{GT}	KT949914	LT853149	LT853199	LT853249	Jaklitsch *et al.* (2016), Bonthond *et al.* (2018)
S. neocupressi	CBS 142625^{T}	LT853079	LT853127	LT853176	LT853226	Bonthond *et al.* (2018)
S. papillatum	CBS 340.97^{T}	LT853102	LT853150	LT853200	LT853250	Bonthond *et al.* (2018)
S. persooniae	CBS 143445^{T}	MG386033	–	–	MG386163	Crous *et al.* (2017b)
S. pezizoides	CBS 145115	MK079342	MK058475	MK058480	MK058485	Present study
S. phylicae	CBS 133587^{T}	LT853091	LT853139	LT853188	LT853238	Bonthond *et al.* (2018)
S. podocarpi	CBS 137995^{T}	LT853101	LT853148	LT853198	LT853248	Bonthond *et al.* (2018)
S. pseudocardinale	MFLUCC 13-0525^{T}	KU848210	–	–	–	Wijayawardene *et al.* (2016)
	CBS 145114	MK079341	MK058479	MK058484	MK058489	Present study
S. rosarum	MFLUCC 17-0654^{T}	MG828961	–	–	–	Wanasinghe *et al.* (2018)
S. spyridicola	CBS 142628^{T}	LT853095	LT853142	LT853192	LT853242	Bonthond *et al.* (2018)
S. unicorne	CBS 143871^{ET}	MK079339	MK058477	MK058482	MK058487	Present study
	CBS 143872	MK079338	MK058476	MK058481	MK058486	Present study
	CBS 143873	MK079340	MK058478	MK058483	MK058488	Present study
	CBS 538.82^{R}	LT853088	LT853136	LT853185	LT853235	Bonthond *et al.* (2018)
S. venetum	MFLU 15-0369^{R}	KT438836	–	–	KT438837	Maharachchikumbura *et al.* (2015)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; MFLU and MFLUCC: Herbarium and culture collection of Mae Fah Luang University, Chiang Rai, Thailand, respectively; PHSI: from Liu *et al.* (2007). $^{T, ET, GT}$ and ^{R} indicate type or ex-type, ex-epitype, ex-generic type and reference strains, respectively.

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

Notes: This genus is introduced to accommodate *R. indicum*, which differs from *Ramichloridium* spp. by its broadly ellipsoidal to globose, mostly 1-septate, smooth-walled or coarsely verrucose conidia, being clavate or oblong to ellipsoid, or obovate to obconical, aseptate, smooth-walled to finely verrucose in *Ramichloridium*. This genus is related to *Dissoconium*, but the latter can be easily distinguished by its percurrent and sympodial proliferation, and the ellipsoid to obclavate, smooth-walled conidia.

Globoramichloridium indicum (Subram.) Y. Marín & Crous, ***comb. nov.*** MycoBank MB829623.
Basionym: *Chloridium indicum* Subram., Proc. Indian Acad. Sci., Sect. B 42: 286. 1955.
Synonyms: *Veronaea verrucosa* Geeson, Trans. Brit. Mycol. Soc. 64: 349. 1975.
Veronaea indica (Subram.) M.B. Ellis, in Ellis, More Dematiaceous Hyphomycetes: 209. 1976.
Ramichloridium indicum (Subram.) de Hoog, Stud. Mycol. 15: 70. 1977.

Description and illustration: Arzanlou *et al.* (2007).

Material examined: Unknown collection details, Feb. 1996, L. Marvanová, CBS 171.96.

Notes: The strain examined and included in the phylogenetic analysis, CBS 171.96, was not derived from type material. However, the morphology of this strain fits perfectly with the morphology of the holotype IMI 114625 (de Hoog 1977). Therefore, CBS 171.96 is considered here as a representative strain, and we propose the new genus and combination based on the phylogenetic data derived from this isolate, as well as on the morphological differences observed.

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Seifertia Partr. & Morgan-Jones, Mycotaxon 83: 348. 2002. Fig. 61.

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

Type species: *Seifertia azaleae* (Peck) Partr. & Morgan-Jones, basionym: *Periconia azaleae* Peck. Representative strain: DAOM 239136.

DNA barcode (genus): LSU.

DNA barcodes (species): LSU, *tef1*. Table 14.

Mycelium superficial or immersed, composed of branched, septate, smooth- and thin-walled, pale white to white or brown

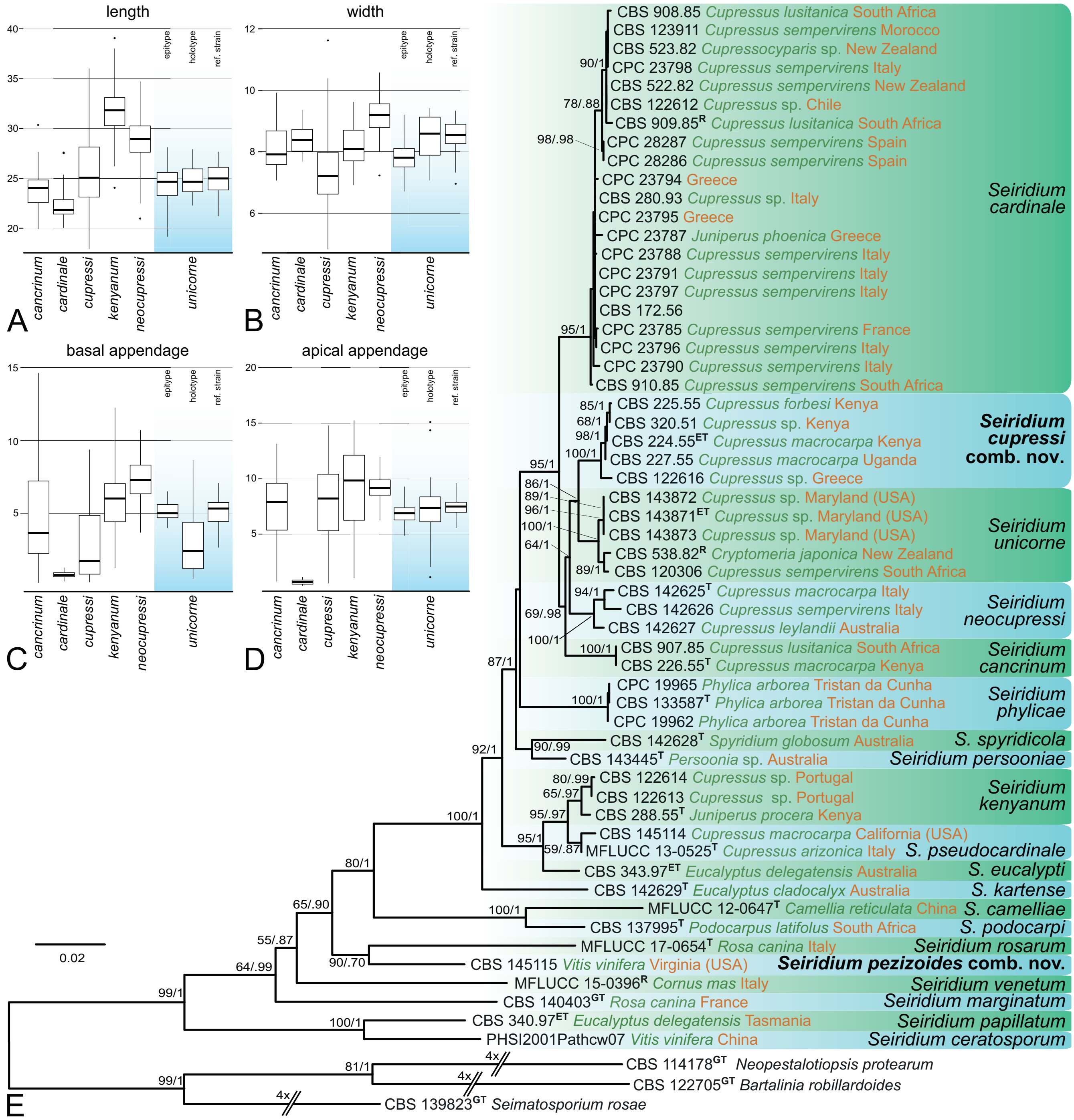

Fig. 63. **A–D.** Boxplots of conidial measurement data in µm from *S. unicorne* and other *Cupressaceae* pathogens. The boxes show the lower and upper quantiles and whiskers extend to 1.5x the interquartile range. Except for the new epitype all measurements are adapted from Bonthond *et al.* (2018). The ex-epitype strain (CBS 143871), holotype (IMI 5816) and reference strain (CBS 538.82) of *S. unicorne* are highlighted in blue. **E.** The best Maximum Likelihood (ML) tree based on four loci (ITS: 616 bp, *rpb2*: 802 bp, *tef1*: 633 bp, *tub2*: 809 bp). Nodes are labelled with ML bootstrap values (BS > 49 %)/Bayesian posterior probabilities (PP > 0.49) using the same model selection, settings and software as in Bonthond *et al.* (2018). Strains are displayed by number, host and country of collection. GenBank accession numbers are listed in Bonthond *et al.* (2018) and in Table 15. $^{T, ET, GT}$ and ^{R} indicate ex-type, ex-epitype, ex-generic type and reference strains, respectively. TreeBASE: S23390.

hyphae. *Synnemata* erect, simple, unbranched or very rarely branched, greenish when young, becoming dark brown to black at maturity, capitate at the apex. *Conidiophores* macronematous, synnematous, straight or slightly flexuous, unbranched or branched toward the upper region, cylindrical, septate, smooth- and thin-walled, hyaline to pale brown or olivaceous brown to brown. *Conidiogenous cells* mono- or polyblastic, integrated, terminal, determinate, cylindrical to subclavate or doliiform, smooth-walled. *Conidia* acropleurogenous, holoblastic, in simple or branched acropetal chains, dry, sometimes aggregated into slimy masses at the apex of the synnema, aseptate or very rarely 1-septate, smooth- and thin-walled, oblong, ellipsoidal, subglobose or fusiform, hyaline to subhyaline, pale brown or olivaceous (adapted from Partridge & Morgan-Jones 2002).

Culture characteristics: Colonies effuse, powdery or cottony to fairy fluffy, grey to dark brown.

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

Distribution: North America, Europe and Asia.

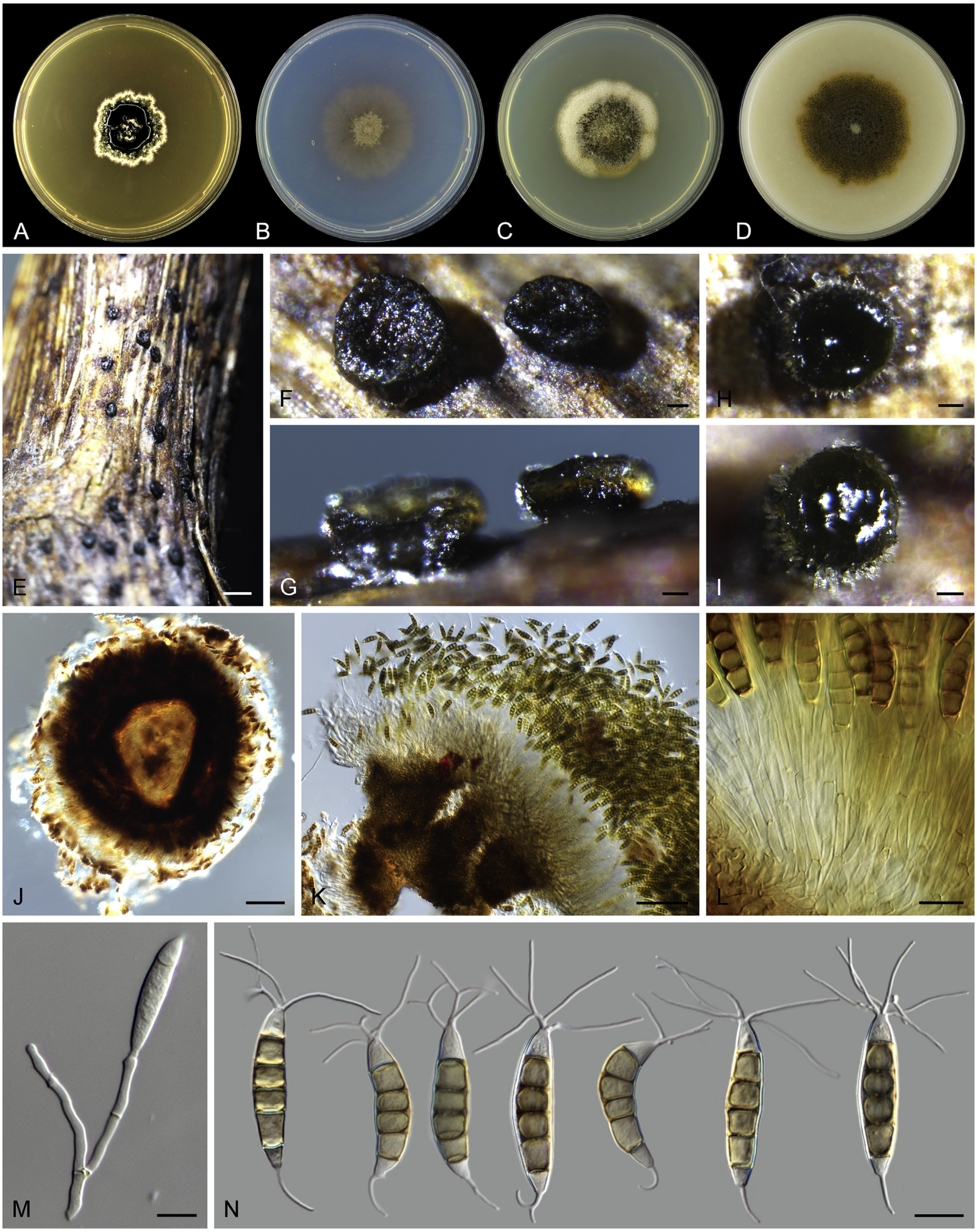

Fig. 64. *Seiridium pezizoides* (CBS 145115). **A–D.** Colony morphology in 90-mm-diam Petri dishes after 10 d at 22 °C on MEA, SNA, PDA and CMA, respectively. **E–K.** Conidiomata on *Vitis vinifera*. **L, M.** Conidiophores. **N.** Conidia. Scale bars: E = 1 mm; F–K = 100 µm; L–N = 10 µm.

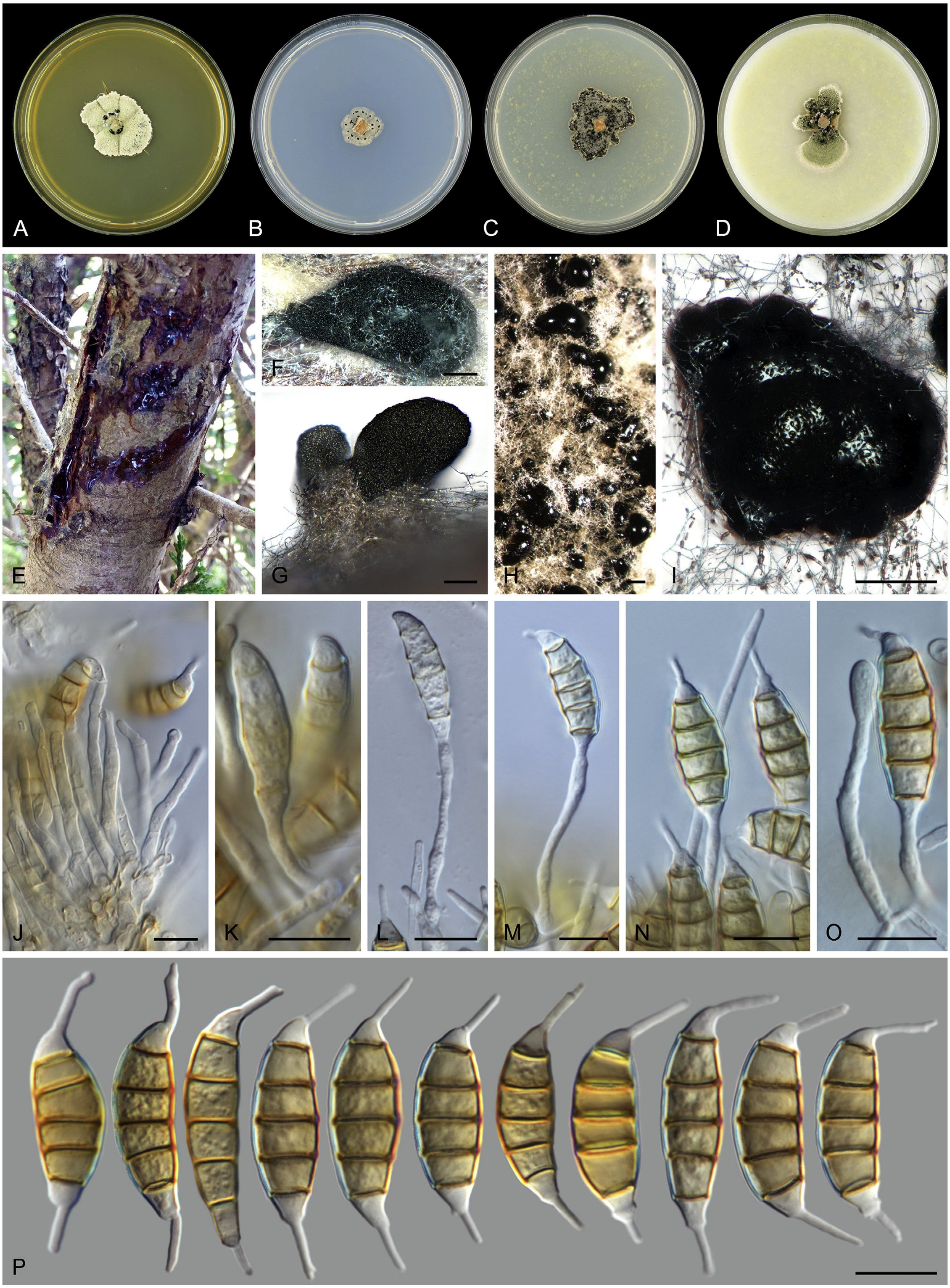

Fig. 65. *Seiridium unicorne* (ex-epitype CBS 143871). **A–D.** Colony morphology in 90-mm-diam Petri dishes after 10 d at 22 °C on MEA, SNA, PDA and CMA, respectively. **E.** Symptoms on naturally infected host. **F, G.** Conidiomata on artificially infected *Cupressaceae* sp. **H.** Sporulation on PDA. **I.** Conidioma on SNA partially immersed in agar. **J–O.** Conidiophores and conidia. **P.** Conidia. Scale bars: F–H = 100 µm; I–P = 10 µm.

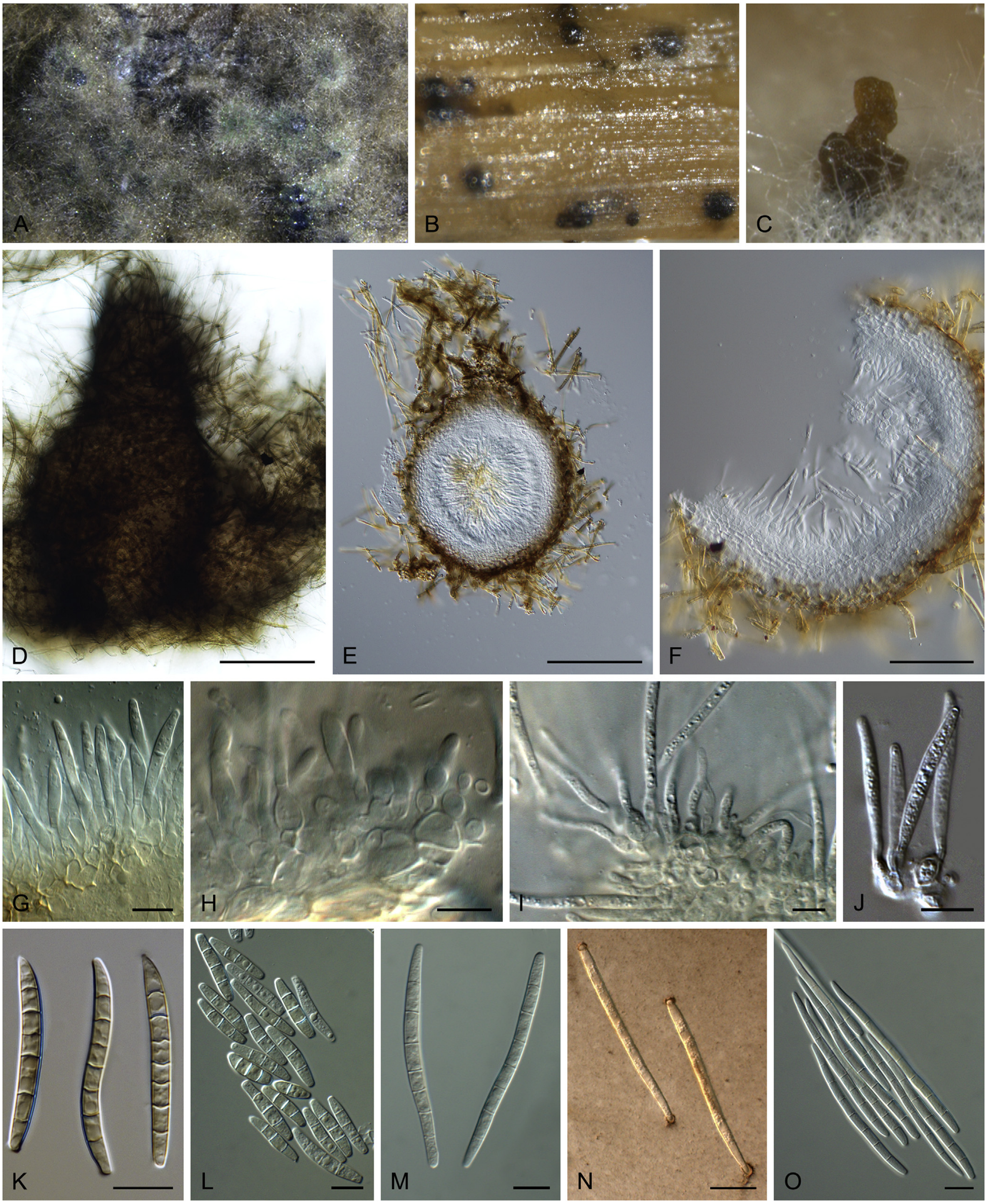

Fig. 66. *Septoriella* spp. **A.** Conidiomata on OA of *Septoriella hirta* (ex-neotype CBS 536.77). **B.** Conidiomata *in vivo* of *Septoriella phragmitis* (ex-epitype CBS 140065). **C.** Conidial cirrhus of *Septoriella phragmitis* (ex-epitype CBS 140065). **D.** Conidioma of *Septoriella hirta* (ex-neotype CBS 536.77). **E, F.** Section through conidiomata of *Septoriella hirta* (ex-neotype CBS 536.77). **G–I.** Conidiogenous cells. **G.** *Septoriella oudemansii* (ex-type CBS 138012). **H, I.** *Septoriella phragmitis* (ex-epitype CBS 140065). **J.** Developing conidia of *Septoriella hirta* (ex-neotype CBS 536.77). **K–O.** Conidia. **K.** *Septoriella hirta* (ex-neotype CBS 536.77). **L.** *Septoriella oudemansii* (ex-type CBS 138012). **M.** *Septoriella poae* (ex-type CBS 136766). **N, O.** *Septoriella phragmitis* (ex-epitype CBS 140065). Scale bars: D, E = 100 µm; F = 50 µm; all others = 10 µm. Pictures A–F, H–K, N, O taken from Crous *et al.* (2015a,b,c); G, L from Crous *et al.* (2014b).

Hosts: Species of *Rhododendron*.

Disease symptoms: Bud and twig blight; Rhododendron bud blight disease.

Notes: *Seifertia* was introduced by Partridge & Morgan-Jones (2002) to accommodate *Pycnostysanus azaleae* based on morphological differences. *Seifertia azaleae* is morphologically similar to *Sorocybe resinae*. However, Partridge & Morgan-Jones (2002) decided to erect the new genus *Seifertia* since *Sei. azaleae* produces much narrower conidia and has minute denticles on the conidiogenous cells. *Seifertia* is characterised by erect, simple, and dark synnemata, macronematous conidiophores, holoblastic, integrated, terminal and determinate conidiogenous cells, and unicellular or very rarely 1-septate, pale brown or olivaceous conidia. This cosmopolitan genus occurs on azaleas and rhododendrons causing a disease known as Rhododendron bud blight disease, in which the flower buds die, and twig blight occurs. Infected buds are easily recognisable by the blackening of the bud and the development of numerous synnemata which appear as tiny black spines over the entire surface (Partridge & Morgan-Jones 2002, Glawe & Hummel 2006).

This genus, which is relatively poorly studied, was recently placed in *Melanommataceae* by Li *et al.* (2016b), when they introduced the second species belonging to *Seifertia*, *Sei. shangrilaensis*. However, the relation of *Seifertia* with *Mycopappus* and its synasexual morph *Xenostigmina*, which are foliar pathogens belonging to *Melanommataceae*, was demonstrated previously by Crous *et al.* (2009a).

References: Partridge & Morgan-Jones 2002 (morphology), Glawe & Hummel 2006 (pathogenicity), Seifert *et al.* 2007, Li *et al.* 2016b (morphology and phylogeny).

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

Species	Isolates[1]	GenBank accession numbers[2]				References
		ITS	*rpb2*	*tef1*	*tub2*	
Septoriella agrostina	MFLU 18-0113^{HT}	MG828945	–	MG829227[a]	–	Wanasinghe *et al.* (2018)
Sep. allojunci	MFLUCC 15-0701^{T}	KU058718	–	MG520935[a]	–	Li *et al.* (2015), Phookamsak *et al.* (2017)
Sep. artemisiae	MFLUCC 17-0693^{T}	MG828929	–	–	–	Wanasinghe *et al.* (2018)
Sep. arundinicola	MFLU 16-0225^{HT}	MG828946	MG829261	MG829228[a]	–	Wanasinghe *et al.* (2018)
Sep. arundinis	MFLUCC 15-0702^{T}	KU058716	–	MG520921[a]	–	Li *et al.* (2015), Phookamsak *et al.* (2017)
Sep. bromi	MFLUCC 13-0739^{T}	KU058717	–	–	–	Li *et al.* (2015)
Sep. chlamydospora	MFLUCC 15-0177^{T}	KU163658	–	–	–	Hyde *et al.* (2018)
Sep. dactylidicola[3]	MFLUCC 14-0002^{T}	–	–	–	–	–
Sep. dactylidis	MFLU 15-2720^{HT}	KU163657	–	–	–	Jayasiri *et al.* (2015)
Sep. elongata	MFLUCC 12-4444^{T}	KM491546	–	–	–	Li *et al.* (2015)
Sep. forlicesenica	MFLUCC 15-0470^{T}	KX926422	KY131966	MG520922[a]	–	Phookamsak *et al.* (2017), Thambugala *et al.* (2017)
Sep. garethjonesii	MFLUCC 15-0469^{T}	KX926425	KX898363	MG520923[a]	–	Phookamsak *et al.* (2017), Thambugala *et al.* (2017)
Sep. germanica	CBS 145372^{T}	MK539965	MK540096	MK540159[b]	MK540174	Present study
Sep. hibernica	CBS 145371^{T}	MK539966	MK540097	–	–	Present study
Sep. hirta	CBS 536.77^{ET}	KR873249	KR873324	–	–	Crous *et al.* (2015a)
Sep. hollandica	CBS 145374^{T}	MK539967	MK540098	MK540160[b]	MK540175	Present study
Sep. hubertusii	CBS 338.86^{T}	KF251230	KF252235	–	KF252717	Quaedvlieg *et al.* (2013)
Sep. italica	MFLUCC 13-0267^{T}	KX926421	KX891169	MG520924[a]	–	Phookamsak *et al.* (2017), Thambugala *et al.* (2017)
Sep. leuchtmannii	CBS 459.84^{IsoT}	KF251188	KF252195	KF253144[b]	KF252682	Quaedvlieg *et al.* (2013)
Sep. muriformis	MFLUCC 13-0277^{T}	KX926415	KX863710	–	–	Thambugala *et al.* (2017)
Sep. neoarundinis	MFLUCC 15-0027^{T}	KY706139	–	MG520936[a]	–	Phookamsak *et al.* (2017), Thambugala *et al.* (2017)
Sep. neodactylidis	MFLUCC 13-0618^{T}	KP744432	–	–	–	Liu *et al.* (2015)
Sep. oudemansii	CBS 138012^{T}	KR873250	–	–	–	Crous *et al.* (2015a)
Sep. phragmitis	CBS 140065^{ET}	KR873251	–	–	–	Crous *et al.* (2015a)
Sep. poae	CBS 136766^{T}	KJ869111	KJ869233	–	–	Crous *et al.* (2014b)
Sep. pseudophragmitis	CBS 145417^{T}	MK560161	MK559450	MK559452[b]	MK559451	Present study
Sep. rosae	MFLU 18-0114^{HT}	MG828948	–	MG829230[a]	–	Wanasinghe *et al.* (2018)
Sep. subcylindrospora	MFLUCC 13-0380^{T}	KT314184	–	–	–	Ariyawansa *et al.* (2015a)
Sep. tridentina	MFLUCC 15-0475^{T}	KX926424	KX891171	–	–	Thambugala *et al.* (2017)
Sep. vagans	CBS 604.86	KF251193	KF252200	KF253149[b]	KF252687	Quaedvlieg *et al.* (2013)

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; MFLU and MFLUCC: Herbarium and culture collection of Mae Fah Luang University, Chiang Rai, Thailand, respectively. ^{T}, ^{ET}, ^{HT} and ^{IsoT} indicate ex-type, ex-epitype, holotype and ex-isotype strains, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *rpb2*: partial DNA-directed RNA polymerase II second largest subunit gene; *tef1*: partial translation elongation factor 1-alpha gene; *tub2*: partial β-tubulin gene. [a] and [b] in *tef1* column indicate the primers used in sequencing: a: EF1-983F, EF1-2218R, b: EF1-728F, EF-2.

[3] Only LSU and SSU sequences available: KY657264 and KY657265, respectively (Thambugala *et al.* 2017).

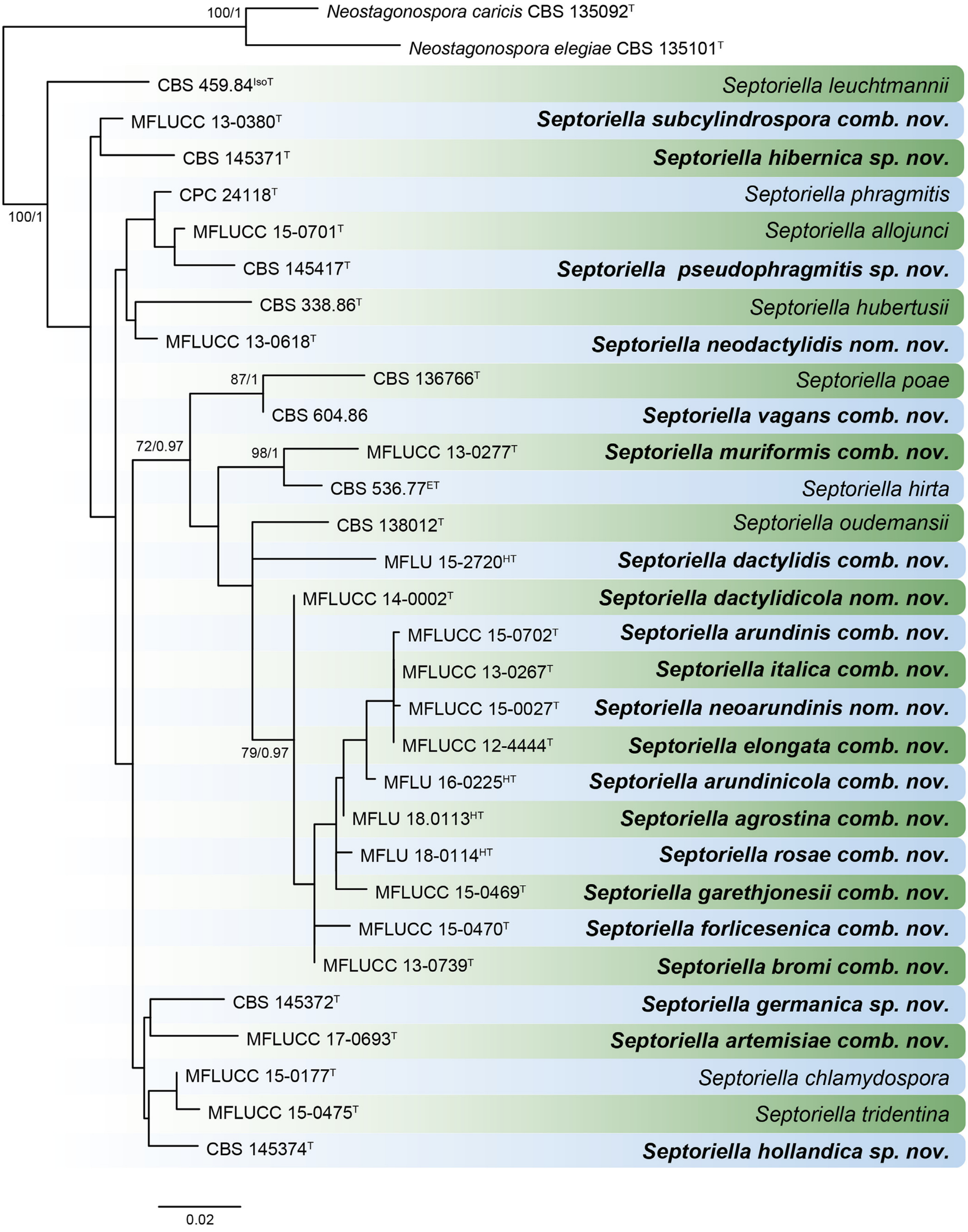

Fig. 67. RAxML phylogram obtained from the combined ITS (580 bp), LSU (849 bp) and *rpb2* (1083 bp) sequence alignment of all accepted species of *Septoriella*. The tree was rooted to *Neostagonospora caricis* CBS 135092 and *Neostagonospora elegiae* CBS 135101. The novelties proposed in this study are 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 of LSU are listed in Fig. 28, and of the other loci in Tables 7 and 16. T, ET, HT and IsoT indicate ex-type, ex-epitype, holotype and ex-isotype strains, respectively. TreeBASE: S23834.

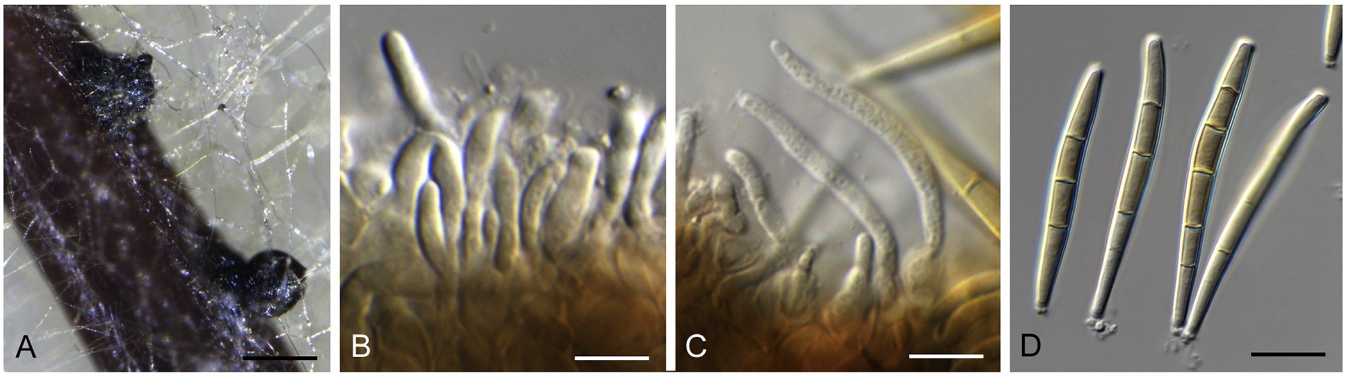

Fig. 68. *Septoriella germanica* (ex-type CBS 145372). **A.** Conidiomata sporulating on PNA. **B, C.** Conidiogenous cells. **D.** Conidia with mucoid caps. Scale bars: A = 200 µm; all others = 10 µm.

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Seiridium Nees, Das System der Pilze und Schwämme: 22. 1817. Fig. 62.
Synonym: *Pestalotia* De Not., Mém. Reale Accad. Sci. Torino 3: 80. 1841.
Additional synonyms in Bonthond *et al.* (2018).

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

Type species: *Seiridium marginatum* Nees, Syst. Pilze (Würzburg): 23. 1817. Neotype designated by Shoemaker *et al.* (1966): K 200376. Epitype and ex-epitype culture designated by Jaklitsch *et al.* (2016): WU 33575, CBS 140403.

DNA barcode (genus): ITS.

DNA barcodes (species): ITS, *rpb2*, *tef1*, *tub2*. Table 15. Fig. 63.

Ascomata perithecial, immersed to semi-erumpent, depressed, globose to pyriform, scattered or confluent, with central ostiole; *necks* slightly papillate, black, periphysate; *ascomatal wall* dark brown, pseudoparenchymatous. *Paraphyses* hyaline, smooth-walled, filiform. *Asci* cylindrical, 8-spored, unitunicate, thin-walled, stipitate, with an apical amyloid ring. *Ascospores* cylindrical-oblong, euseptate, septa often thicker than the wall, yellow- to dark brown, guttulate. *Conidiomata* acervuloid to pycnidioid, semi-immersed to erumpent, uni- to plurilocular, brown or black, glabrous, dehiscing by irregular splits in the upper wall. *Conidiophores* lining the cavity of the conidioma, septate and sparsely branched at the base, or reduced to conidiogenous cells, hyaline, smooth-walled. *Conidiogenous cells* discrete, integrated, ampulliform to lageniform or sub-cylindrical, hyaline, smooth-walled, proliferating percurrently at the apex. *Conidia* fusiform, euseptate (septal pores present or not), end cells hyaline, median cells dark brown to brown, wall thick, smooth or with striations, constricted at septa or not; *apical cell* with single or multiple, unbranched or branched appendages; *basal cell* with or without a centric, unbranched or sometimes branched appendage (adapted from Bonthond *et al.* 2018).

Culture characteristics: Colonies on PDA circular to irregular, reaching 12–68 mm diam after 14 d at 22 °C, mostly flat, in some cultures elevated at margins, often white coloured or with other colours, sporulation rare, with pycnidioid conidiomata. On SNA circular to irregular to rhizoid, reaching 20–54 mm diam after 14 d at 22 °C, mostly flat, white coloured, with moderate to abundant aerial mycelium, sporulation for some species within and others after 2 wk, sporodochia often compact and scattered.

Optimal media and cultivation conditions: Colonies grow well on CMA, MEA, PDA and SNA at 22 °C. Most species sporulate on SNA and some species on CMA, MEA or PDA as well.

Distribution: Worldwide.

Hosts: A diversity of gymnosperms and angiosperms. The genus is most well-known from members of *Cupressaceae*.

Disease symptoms: Cankers on stems and twigs.

Notes: *Pestalotia* was introduced in 1841 and is similar to *Seiridium* (1817), one of the older names in the *Sporocadaceae*.

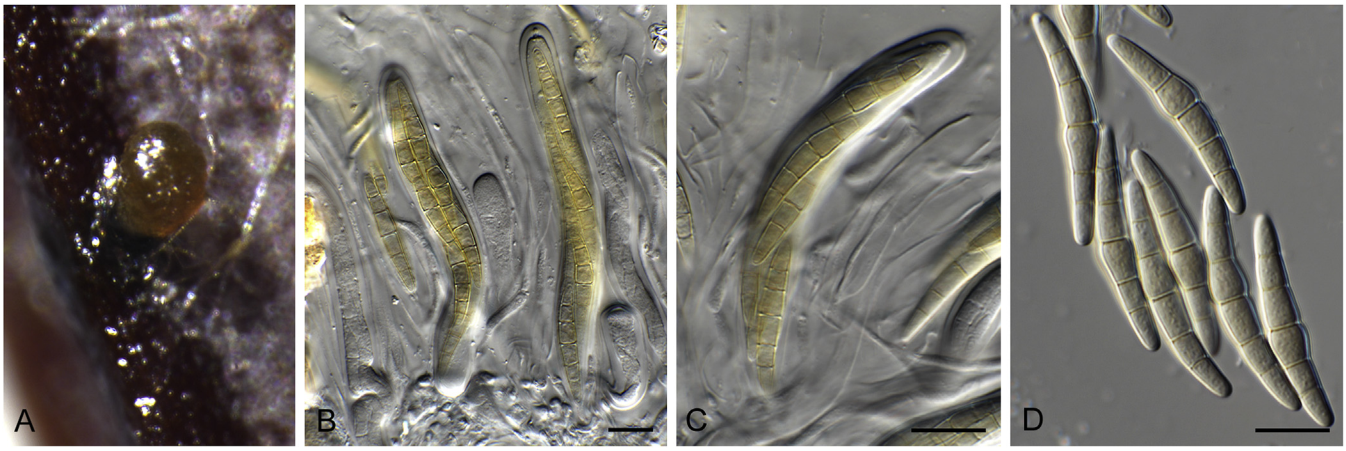


Fig. 69. *Septoriella hollandica* (ex-type CBS 145374). **A.** Ascomata sporulating on PNA. **B, C.** Asci. **D.** Ascospores. Scale bars = 10 µm.

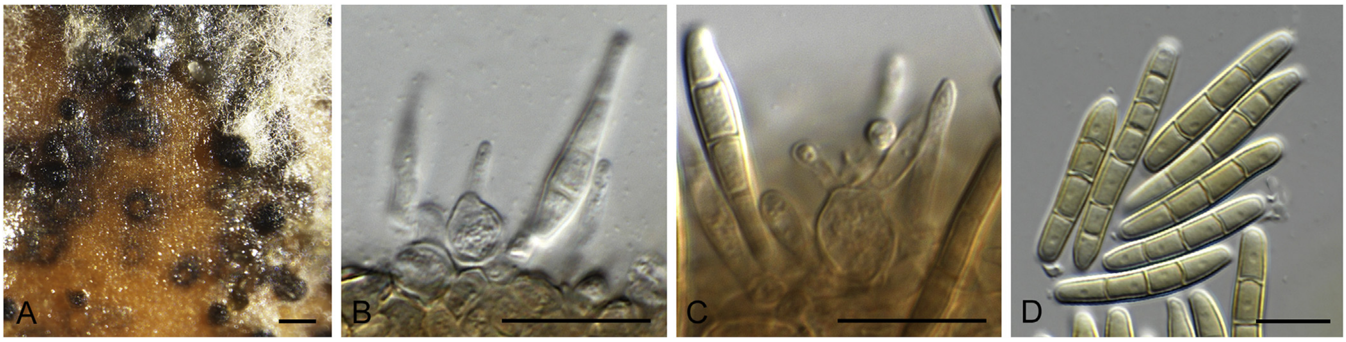


Fig. 70. *Septoriella pseudophragmitis* (ex-type CPC 24166). **A.** Conidiomata sporulating on MEA. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars: A = 250 µm; all others = 10 µm.

The genus has been subjected to many rearrangements (reviewed in Sutton 1969) which eventually resulted in the genus accommodating only the type species, *Pe. pezizoides*. One of the important characters used to separate *Pestalotia* from the related genera *Pestalotiopsis* and *Truncatella* was the production of 5-septate (or 6-celled) conidia. However, this morphology is typical for *Seiridium* as well, and for this reason it was speculated that *Pestalotia* and *Seiridium* could be congeneric (Maharachchikumbura *et al.* 2014). A fresh collection of *Pe. pezizoides* from *Vitis vinifera* collected in the USA was recently obtained (Table 1), which matches in all respects with the type of *Pe. pezizoides*. DNA sequence data generated here confirm that *Pe. pezizoides* clusters within *Seiridium* (Fig. 63). Therefore, *Pestalotia* is reduced to synonymy with *Seiridium.* For *Seiridium*, the here synonymised *Pestalotia* and related genera, not only the number but also the type of conidial septation has been a commonly reported descriptor. Different authors have interpreted the appearance of the cell walls as either distoseptate (*e.g.* Nag Raj 1993) or euseptate (*e.g.* Sutton 1980). Although when examined by light microscopy, conidia can appear as

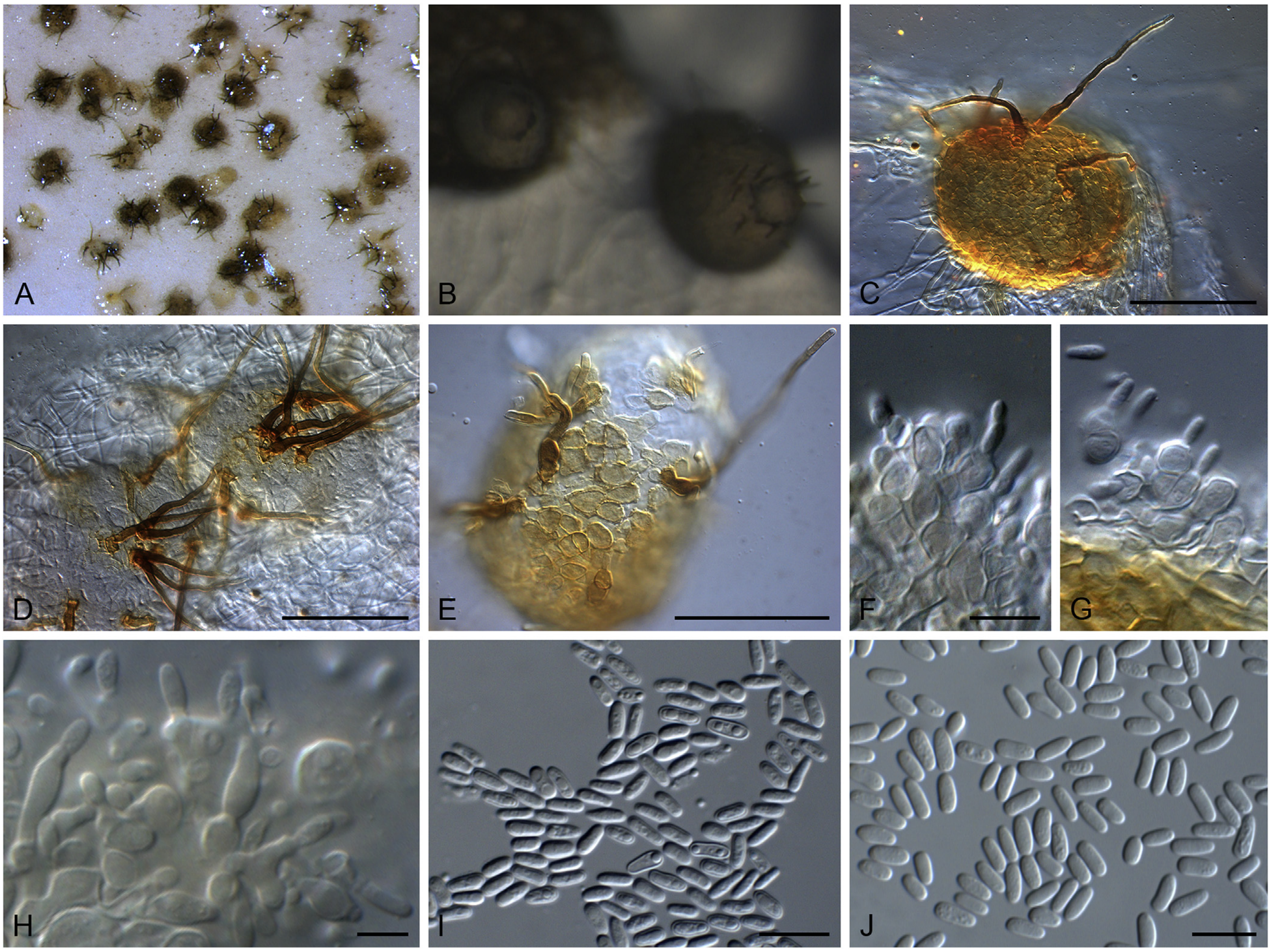


Fig. 71. *Setophoma* spp. **A, B.** Conidioma forming in culture. **A.** *Setophoma chromolaenae* (ex-type CBS 135105). **B.** *Setophoma vernoniae* (ex-type CBS 137988). **C–E.** Conidiomata with setae of *Setophoma chromolaenae* (ex-type CBS 135105). **F–H.** Conidiogenous cells. **F, G.** *Setophoma chromolaenae* (ex-type CBS 135105). **H.** *Setophoma vernoniae* (ex-type CBS 137988). **I, J.** Conidia. **I.** *Setophoma chromolaenae* (ex-type CBS 135105). **J.** *Setophoma vernoniae* (ex-type CBS 137988). Scale bars: C–E = 20 µm; all others = 10 µm; F applies to F and G.

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

Species	Isolates[1]	GenBank accession numbers[2]				References
		ITS	*rpb2*	*tef1*	*tub2*	
Setophoma brachypodii	CBS 145418^{T}	MK539968	MK540099	MK540161	–	Present study
Set. chromolaenae	CBS 135105^{T}	KF251244	KF252249	KF253195	KF252728	Quaedvlieg *et al.* (2013)
Set. pseudosacchari	CBS 145373^{T}	MK539969	MK540100	–	MK540176	Present study
Set. sacchari	CBS 333.39^{ET}	KF251245	KF252250	–	–	Quaedvlieg *et al.* (2013)
Set. terrestris	CBS 335.29^{LT}	KF251246	KF252251	KF253196	KF252729	Quaedvlieg *et al.* (2013)
Set. vernoniae	CBS 137988^{T}	KJ869141	–	MK540162	MK540177	Crous *et al.* (2014b), present study

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

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

distoseptate, electron microscopic studies on *S. cupressi* (Roberts & Swart 1980) and *S. pezizoides* (Griffiths & Swart 1974) have shown that the conidial cell walls are differentiated into multiple zones but arise from a single layered cell wall and are thus euseptate. Since the sexual morph is known for only a few species, the taxonomy in *Seiridium* has been based mainly on asexual morphology. However, the generic type (*S. marginatum*) is one of the exceptions where both morphs have been characterised. This species was re-described and epitypified by Jaklitsch *et al.* (2016), who also provided detailed illustrations of sexual and asexual morphology.

References: Nag Raj 1993 (morphology), Danti & Della Rocca 2017 (pathogenicity), Bonthond *et al.* 2018 (morphology and phylogeny),

Seiridium cupressi (Nattrass *et al.*) Bonthond, Sand.-Den. & Crous, ***comb. nov.*** MycoBank MB830554.
Basionym: *Rhynchosphaeria cupressi* Nattrass *et al.*, Trans. Brit. Mycol. Soc. 46: 103. 1963.
Synonyms: *Cryptostictis cupressi* Guba, Monograph of *Monochaetia* and *Pestalotia*: 47. 1961. *Nom. inval.* Art. 40.3 (Shenzhen).
Lepteutypa cupressi (Nattrass *et al.*) H.J. Swart, Trans. Brit. Mycol. Soc. 61: 79. 1973.
Seiridium cupressi (Guba) Boesew, Trans. Brit. Mycol. Soc. 80: 545. 1983. *Nom. inval.* Art. 40.3 (Shenzhen).

Description: Sexual morph Nattrass *et al.* (1963). Asexual morph Bonthond *et al.* (2018).

Known distribution: Africa (Kenya, Uganda) and Europe (Greece).

Typus: **Africa**, Kenya, on *Cupressus macrocarpa*, July 1954, R.M. Nattrass (**holotype** of *Rhynchosphaeria cupressi* IMI 56917); from cankers in branches of *Cupressus macrocarpa*, 1949, D.R. Jones [**epitype** of *Rhynchosphaeria cupressi* designated here IMI 52254, MBT386544 (dried culture), culture ex-epitype CBS 224.55].

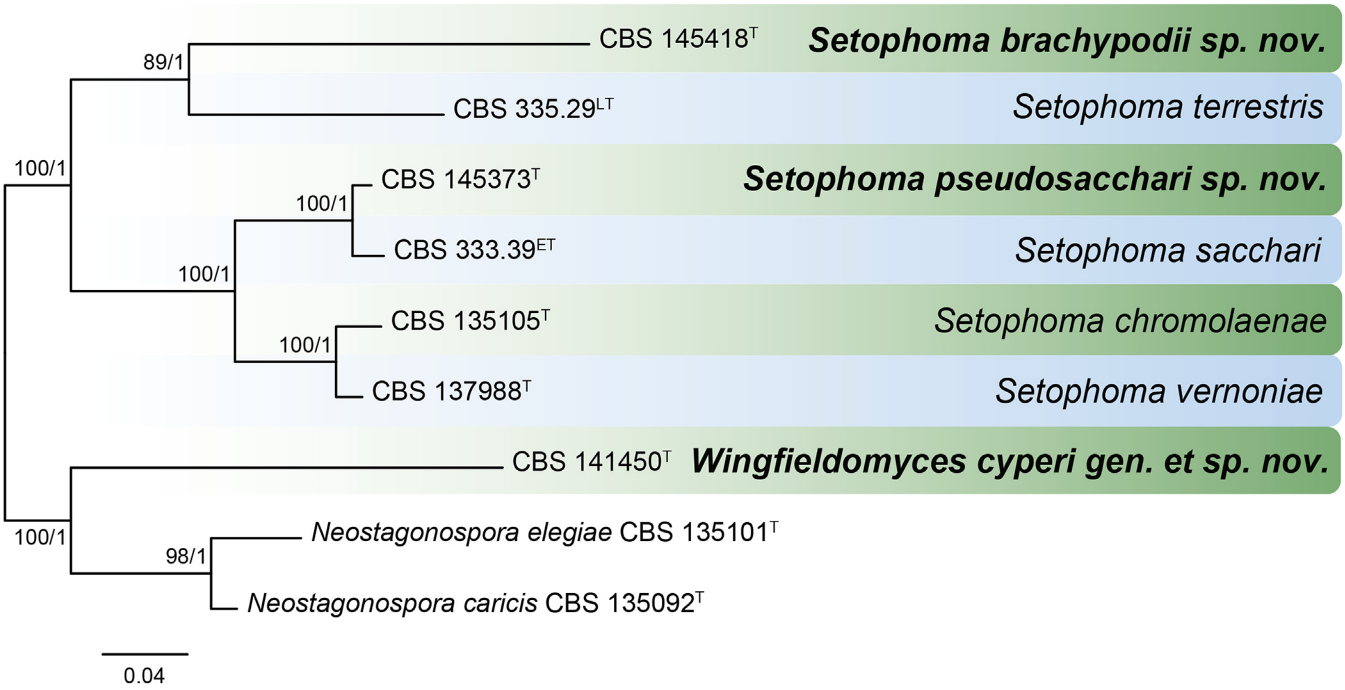


Fig. 72. RAxML phylogram obtained from the combined ITS (589 bp), LSU (835 bp), *tef1* (788 bp) and *tub2* (532 bp) sequence alignment of all accepted species of *Setophoma*. The tree was rooted to *Neostagonospora caricis* CBS 135092 and *Neostagonospora elegiae* CBS 135101. The novelties proposed in 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 of LSU are listed in Fig. 28, and of the other loci in Tables 7, 17 and 18. $^{T, ET}$ and ^{LT} indicate ex-type strains, ex-epitype and ex-lectotype, respectively. TreeBASE: S23834.

Fig. 73. *Setophoma pseudosacchari* (ex-type CBS 145373). **A.** Ascomata sporulating on OA. **B.** Asci with ascospores. **C.** Conidia. Scale bars: A = 300 μm; all others = 10 μm.

Additional materials examined: **Europe**, Greece, from *Cupressus* sp., A. Graniti, CBS 122616 = CMW 1646. **Africa**, Kenya, non-pathogenic isolate from *Cupressus* sp., collection data unknown, CBS 320.51; on *Cupressus macrocarpa*, July 1948, R.M. Nattrass, IMI 37158; on *Cupressus macrocarpa*, Dec. 1949, R.M. Nattrass, IMI 40096; from cankers in branches of *Cupressus forbesii*, 1949, D.R. Jones, IMI 52255 (dried culture); CBS 225.55.

Notes: This species has been a source of confusion since its introduction (Guba 1961). Bonthond *et al.* (2018) showed that Guba's diagnosis included three different species (*S. cancrinum*, *S. cupressi* and *S. kenyanum*) and selected an epi- and lectotype for *Cryptosticis cupressi*. The latter name, however, was invalidly published (article 40.1). Nattrass *et al.* (1963) re-examined the material from Guba (1961) and synonymised *C. cupressi* with *Monochaetia unicornis*. Despite noting small morphological differences between the asexual stage of *R. cupressi* and the type of *M. unicornis* (*i.e.* smaller and slender conidia), they were not able to confirm the exogenous origin of the basal appendage, which was the main argument for Guba (1961) to place the species in *Cryptostictis* instead of *Monochaetia*. In the same study, Nattrass *et al.* (1963) described the sexual morph of *M. unicornis* as *Rhynchosphaeria cupressi* based on three specimens: IMI 37158, IMI 40096 and the holotype IMI 56917. Bonthond *et al.* (2018) examined each of these specimens but incorrectly cited the holotype as IMI 37158. While only the sexual morph was found in these materials, the original description from Nattrass *et al.* (1963) includes drawings, photographs and measurements of the conidia. These measurements (22–32 × 6–9.5 μm) fall perfectly within the range documented for the lineage currently assigned to *S. cupressi* (Guba) Boesew. (18–36 × 5–11.5 μm) (Bonthond *et al.* 2018). Consequently, being the oldest valid name for this lineage and in accordance with the rule of priority *Ry. cupressi* is recombined in *Seiridium,* as *S. cupressi* (Nattrass *et al.*) Bonthond, Sand.-Den. & Crous, and an epitype is designated (IMI 52254). The similar species *S. cancrinum* and *S. unicorne* show smaller conidia (20–30.5 μm and 19–28 μm, respectively), whereas conidia of *S. kenyanum* are considerably larger (24–39 μm).

Seiridium pezizoides (De Not.) Crous, ***comb. nov.*** MycoBank MB828021. Fig. 64.
Basionym: *Pestalotia pezizoides* De Not., Mém. Reale Accad. Sci. Torino 2, 3: 80. 1839.

Caulicolous. Isolated from branches of *Vitis vinifera*. On the host (described in more detail by Nag Raj 1993): *Conidiomata* irregularly scattered over the surface, gregarious to confluent, discoid to cupulate and occasionally globose, erumpent from tissue, acervular to sporodochial, occasionally with aerial mycelium, black to brown, (300–)350–500(–650) μm. On SNA: *Conidiophores* tightly aggregated in the conidioma, cylindrical, irregularly branched, hyaline or pale brown at the base, smooth- and thin-walled. *Conidiogenous cells* discrete, hyaline, cylindrical, smooth- and thin-walled. *Conidia* lunate to falcate, often curved, 5-septate, not striate, bearing a basal and two or more apical appendages, euseptate with pores sometimes visible, (24–)28–33.5(–38.5) × (6–)7–8(–9) μm, mean ± SD = 30.7 ± 2.8 × 7.5 ± 0.4 μm; *basal cell* obconic with truncate base, hyaline, smooth-walled, bearing marginal frills, 4–7 μm; *four median cells* pale brown, smooth-walled, cylindrical to doliiform; *second cell* from base 3.5–8 μm; *third cell* 3.5–7 μm; *fourth cell* 3.5–6.5 μm; *fifth cell* 3.5–7.5 μm; *apical cell* conical, hyaline, smooth-walled, 4.5–8.5 μm long; *apical appendages* single or multiple, centric, branched or unbranched, 8.5–27 μm; *basal appendage* single, cylindrical, centric, occasionally branched, 5.5–14 μm.

Culture characteristics: Colonies on PDA circular, reaching 34–37 mm diam after 10 d at 22 °C, flat, olivaceous to luteous in the centre, white to brown at the margins, with abundant aerial mycelium at the margins, not sporulating within 10 d. On CMA circular, reaching 39–41 mm diam after 10 d at 22 °C, flat at centre and margins, dark brown to black, without aerial mycelium, not sporulating within 10 d. On MEA circular to slightly irregular, reaching 25–27 mm diam after 10 d at 22 °C, flat, olivaceous to pale green, with a white outer ring, with moderate aerial mycelium, massive spore production in the centre. On SNA circular, reaching 31–33 mm diam after 10 d at 22 °C,

Table 18. DNA barcodes of the accepted *Wingfieldomyces* sp.

Species	Isolates[1]	GenBank accession numbers[2]				References
		ITS	*rpb2*	*tef1*	*tub2*	
Wingfieldomyces cyperi	CBS 141450^T	KX228286	MK540101	MK540163	MK540178	Crous *et al.* (2016b), present study

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

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

raised in the centre, flat at the margins, with moderate aerial mycelium, no sporulation within 10 d.

Distribution: Europe (France, Italy), USA.

Typus: **Italy**, near Mailand, twig of *Vitis vinifera* (*Vitaceae*), *leg*. Oct. 1838, De Notaris, **holotype**, RO.

Additional material examined: **USA**, Virginia, Charlottesville, from a complex hybrid of *Vitis æstivalis* × *Vitis cinerea* × *Vitis vinifera*, 2018, L. Morton, CBS 145115 = CPC 35011.

Notes: After several rearrangements and the introduction of the genera *Pestalotiopsis* and *Truncatella* (see Sutton 1969 and references therein), the generic type *Pe. pezizoides* was the only remaining species in *Pestalotia*. A specimen of *Pe. pezizoides* (IMI 83642, from branches of *Vitis vinifera*, Italy, non-type) was examined and redescribed by Sutton (1980). A more detailed description was provided by Nag Raj (1993), based on several materials, including this specimen. The present study is the first to provide DNA sequence data on this species. We sequenced four loci (ITS, *rpb2, tef1* and *tub2*) and included *Pe. pezizoides* in an updated phylogeny of *Seiridium* (Fig. 63) which supports the conclusion that *Pestalotia* and *Seiridium* are congeneric. Consequently, the species is transferred to *Seiridium* as *S. pezizoides*. The *S. pezizoides* strain (CBS 145115 = CPC 35011) that was included in this analysis conforms morphologically with the description and was isolated from the same host, *Vitis*. However, since the specimen was collected in Virginia (USA) and the holotype is from Italy, it is not suitable for epitypification. The phylogeny generated here suggests that *S. pezizoides* is most closely related to *S. rosarum* (*Rosa canina*, Italy).

Seiridium unicorne (Cooke & Ellis) B. Sutton, Mycol. Pap. 138: 74. 1975. Fig. 65.
Basionym: *Pestalotia unicornis* Cooke & Ellis, Grevillea 7: 6. 1878, as "*Pestalozzia*".
Synonym: *Monochaetia unicornis* (Cooke & Ellis) Sacc. & D. Sacc., Syll. Fung. 18: 485. 1906.

Caulicolous. Most commonly isolated from cankers on branches of species from *Cupressaceae*. *Conidiomata* on PDA numerous, sporodochial, globose or clavate, mostly solitary, erumpent from agar, partially immersed in mycelium, producing

Fig. 74. *Wingfieldomyces cyperi* (ex-type CBS 141450). **A.** Symptomatic leaf of *Cyperus sphaerocephala*. **B–D.** Asci. **E.** Pseudoparaphyses. **F–I.** Ascospores. Scale bars: 10 µm; F applies to F–I. Pictures B, C, E–I taken from Crous *et al.* (2016b).

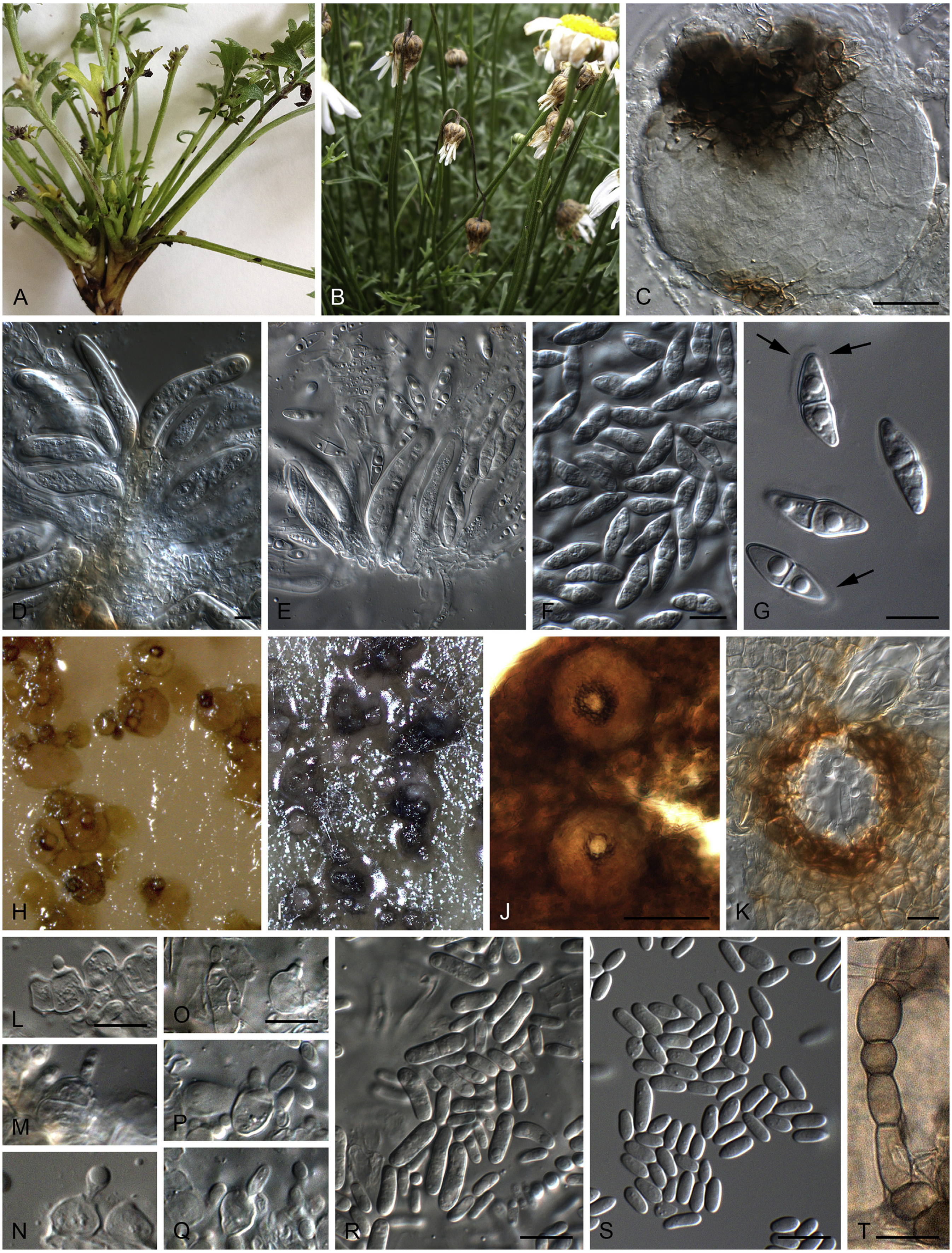


Fig. 75. *Stagonosporopsis* spp. **A, B.** Disease symptoms of *Stagonosporopsis tanaceti* (ex-type CBS 131484). **A.** Leaf necrosis. **B.** Drooping flower heads. **C–G.** Sexual morph of *Stagonosporopsis inoxydabilis* (ex-type CBS 425.90). **C.** Close-up of ascoma with darkened ostiolar area. **D, E.** Stipitate, bitunicate asci. **F, G.** Ascospores (arrows denote sheath). **H–T.** Asexual morph. **H, I.** Colony sporulating on OA. **H.** *Stagonosporopsis chrysanthemi* (CBS 500.63). **I.** *Stagonosporopsis tanaceti* (ex-type CBS 131484). **J.** Close-up of pycnidial conidiomata of *Stagonosporopsis tanaceti* (ex-type CBS 131484). **K.** Close-up of darkened ostiolar area of *Stagonosporopsis chrysanthemi* (CBS 500.63). **L–Q.** Conidiogenous cells. **L–N.** *Stagonosporopsis chrysanthemi* (CBS 500.63). **O–Q.** *Stagonosporopsis tanaceti* (ex-type CBS 131484). **R, S.** Conidia. **R.** *Stagonosporopsis chrysanthemi* (CBS 500.63). **S.** *Stagonosporopsis tanaceti* (ex-type CBS 131484). **T.** Chain of chlamydospores of *Stagonosporopsis tanaceti* (ex-type CBS 131484). Scale bars: C = 35 μm; J = 150 μm; all others = 10 μm; D applies to D and E; L applies to L–N; O applies to O–Q. Pictures taken from Vaghefi *et al.* (2012).

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

Species	**Strain**[1]	**GenBank accession numbers**[2]					**References**
		ITS	**LSU**	***act***	***rpb2***	***tub2***	
Stagonosporopsis actaeae	CBS 106.96^{T}	GU237734	GU238166	JN251974	KT389672	GU237671	Aveskamp *et al.* (2010), de Gruyter *et al.* (2012), Chen *et al.* (2015)
Sta. ailanthicola	MFLUCC 16-1439^{T}	KY100872	KY100874	–	KY100876	KY100878	Tibpromma *et al.* (2017)
Sta. ajacis	CBS 177.93^{NT}	GU237791	GU238168	JN251962	KT389673	GU237673	Aveskamp *et al.* (2010), de Gruyter *et al.* (2012), Chen *et al.* (2015)
Sta. andigena	CBS 101.80	GU237714	GU238169	JN251958	–	GU237674	Aveskamp *et al.* (2010), de Gruyter *et al.* (2012)
Sta. artemisiicola	CBS 102636	GU237728	GU238171	JN251971	KT389674	GU237676	Aveskamp *et al.* (2010), de Gruyter *et al.* (2012), Chen *et al.* (2015)
Sta. astragali	CBS 178.25	GU237792	GU238172	JN251963	–	GU237677	Aveskamp *et al.* (2010), de Gruyter *et al.* (2012)
Sta. bomiensis	CGMCC 3.18366^{T}	KY742123	KY742277	–	KY742189	KY742365	Chen *et al.* (2017)
Sta. centaureae	MFLUCC 16-0787^{T}	KX611240	KX611238	–	–	–	Hyde *et al.* (2016)
Sta. citrulli	ATCC TSD-2^{T}	KJ855546	–	–	–	KJ855602	Stewart *et al.* (2015)
Sta. caricae	CBS 248.90	GU237807	GU238175	JN251969	–	GU237680	Aveskamp *et al.* (2010), de Gruyter *et al.* (2012)
	DAR 28714	MK253236	MK253237	MK255065	MK255066	MK255067	Present study
Sta. chrysanthemi	ATCC 10748^{ET}	JQ897484	JQ897460	JQ897508	–	JQ897504	Vaghefi *et al.* (2012)
Sta. crystalliniformis	CBS 713.85^{T}	GU237903	GU238178	JN251960	KT389675	GU237683	Aveskamp *et al.* (2010), de Gruyter *et al.* (2012), Chen *et al.* (2015)
Sta. cucurbitacearum	CBS 133.96	GU237780	GU238181	JN251968	KT389676	GU237686	Aveskamp *et al.* (2010), de Gruyter *et al.* (2012), Chen *et al.* (2015)
Sta. dennisii	CBS 631.68^{ET}	GU237899	GU238182	Q-bank[3]	KT389677	GU237687	Aveskamp *et al.* (2010), Chen *et al.* (2015)
Sta. dorenboschii	CBS 426.90^{T}	GU237862	GU238185	JN251980	KT389678	GU237690	Aveskamp *et al.* (2010), de Gruyter *et al.* (2012), Chen *et al.* (2015)
Sta. helianthi	CBS 200.87^{T}	KT389545	KT389761	–	KT389683	KT389848	Chen *et al.* (2015)
Sta. heliopsidis	CBS 109182	GU237747	GU238186	JN251980	KT389679	GU237691	Aveskamp *et al.* (2010), de Gruyter *et al.* (2012), Chen *et al.* (2015)
Sta. hortensis	CBS 572.85	GU237730	GU238198	JN251966	KT389680	GU237703	Aveskamp *et al.* (2010), de Gruyter *et al.* (2012), Chen *et al.* (2015)
Sta. inoxydabilis	CBS 425.90^{T}	GU237861	GU238188	JN251972	KT389682	GU237693	Aveskamp *et al.* (2010), de Gruyter *et al.* (2012), Chen *et al.* (2015)
Sta. loticola	CBS 562.81^{IsoT}	GU237890	GU238192	JN251978	KT389684	GU237697	Aveskamp *et al.* (2010), de Gruyter *et al.* (2012), Chen *et al.* (2015)
Sta. lupini	CBS 101494^{T}	GU237724	GU238194	JN251967	KT389685	GU237699	Aveskamp *et al.* (2010), de Gruyter *et al.* (2012), Chen *et al.* (2015)
Sta. oculo-hominis	CBS 634.92^{T}	GU237901	GU238196	JN251976	KT389686	GU237701	Aveskamp *et al.* (2010), de Gruyter *et al.* (2012), Chen *et al.* (2015)
Sta. papillata	CGMCC 3.18367^{T}	KY742125	KY742279	–	KY742191	KY742367	Chen *et al.* (2017)
Sta. rudbeckiae	CBS 109180	GU237745	GU238197	Q-bank[3]	–	GU237702	Aveskamp *et al.* (2010)
Sta. tanaceti	CBS 131484^{T}	JQ897481	JQ897461	JQ897512	–	JQ897496	Vaghefi *et al.* (2012)
Sta. trachelii	CBS 379.91	GU237850	GU238173	JN251977	KT389687	GU237678	Aveskamp *et al.* (2010), de Gruyter *et al.* (2012), Chen *et al.* (2015)
Sta. valerianellae	CBS 329.67^{IsoT}	GU237832	GU238201	JN251965	–	GU237706	Aveskamp *et al.* (2010), de Gruyter *et al.* (2012)

[1] ATCC: American Type Culture Collection, Virginia, USA; CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CGMCC: Chinese General Microbiological Culture Collection Center, Beijing, China; DAR: New South Wales Plant Pathology Herbarium, NSW, Australia; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Rai, Thailand. $^{T,\ ET,\ IsoT}$ and ^{NT} indicate ex-type, ex-epitype, ex-isotype and ex-neotype strains, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; LSU: partial large subunit (28S) nrRNA gene; *act*: partial actin gene; *rpb2*: partial DNA-directed RNA polymerase II second largest subunit; *tub2*: partial β-tubulin gene.

[3] Q-bank: Sequences retrieved from Q-bank Fungi database (http://www.q-bank.eu/fungi/).

large black spore masses; on SNA, sporodochial, mostly aggregated, erumpent from agar, producing large black spore masses. On SNA: *Conidiophores* septate, cylindrical, irregularly branched, hyaline or brown, thin-walled, 22–68 µm long, ex-epitype: 22–50 µm long. *Conidiogenous cells* discrete, hyaline, cylindrical, smooth- and thin-walled, 3.5–29.5 × 1.5–3.5 µm, ex-epitype: 16.2–28.9 × 1.7–3.5 µm, proliferating percurrently, with visible collarettes and minute periclinal thickenings. *Conidia* lunate to falcate, curved, 5-septate, rarely 4- or 6-septate, not striate, bearing two appendages, euseptate with no visible pores, (19–)22.5–26.5(–28) × (6.5–)7.5–8.5(–9.5) µm, mean ± SD = 24.5 ± 1.8 × 7.9 ± 0.5 µm, ex-epitype: (19–)22.5–26.5(–28) × (6.5–)7.5–8.5(–9) µm, mean ± SD = 24.4 ± 1.9 × 7.8 ± 0.4 µm; *basal cell* obconic with a truncate base, hyaline, walls smooth, bearing minute marginal frills, 2.5–9.5 µm, ex-epitype: 2.5–6 µm (n = 119); *four median cells* colour varying from pale to dark brown, smooth-walled, cylindrical to doliiform; *second cell* from base 3.5–6 µm (n = 152); *third cell* 3–5.5 µm; *fourth cell* 3–5.5 µm; *fifth cell* 3–5.5 µm, ex-epitype: *second cell* from base 3.5–6 µm; *third cell* 3–5.5 µm; *fourth cell* 3–5 µm; *fifth cell* 3–5.5 µm; *apical cell* conical, hyaline, smooth-walled, 2–5.5 µm long, ex-epitype: 2–5.5 µm long; *apical appendage* single, mostly centric, 5–10 µm, ex-epitype: 5–9.5 µm; *basal appendage* single, cylindrical, mostly excentric, 2.7–7.1 µm, ex-epitype: 4–6.5 µm (adapted from Bonthond *et al.* 2018).

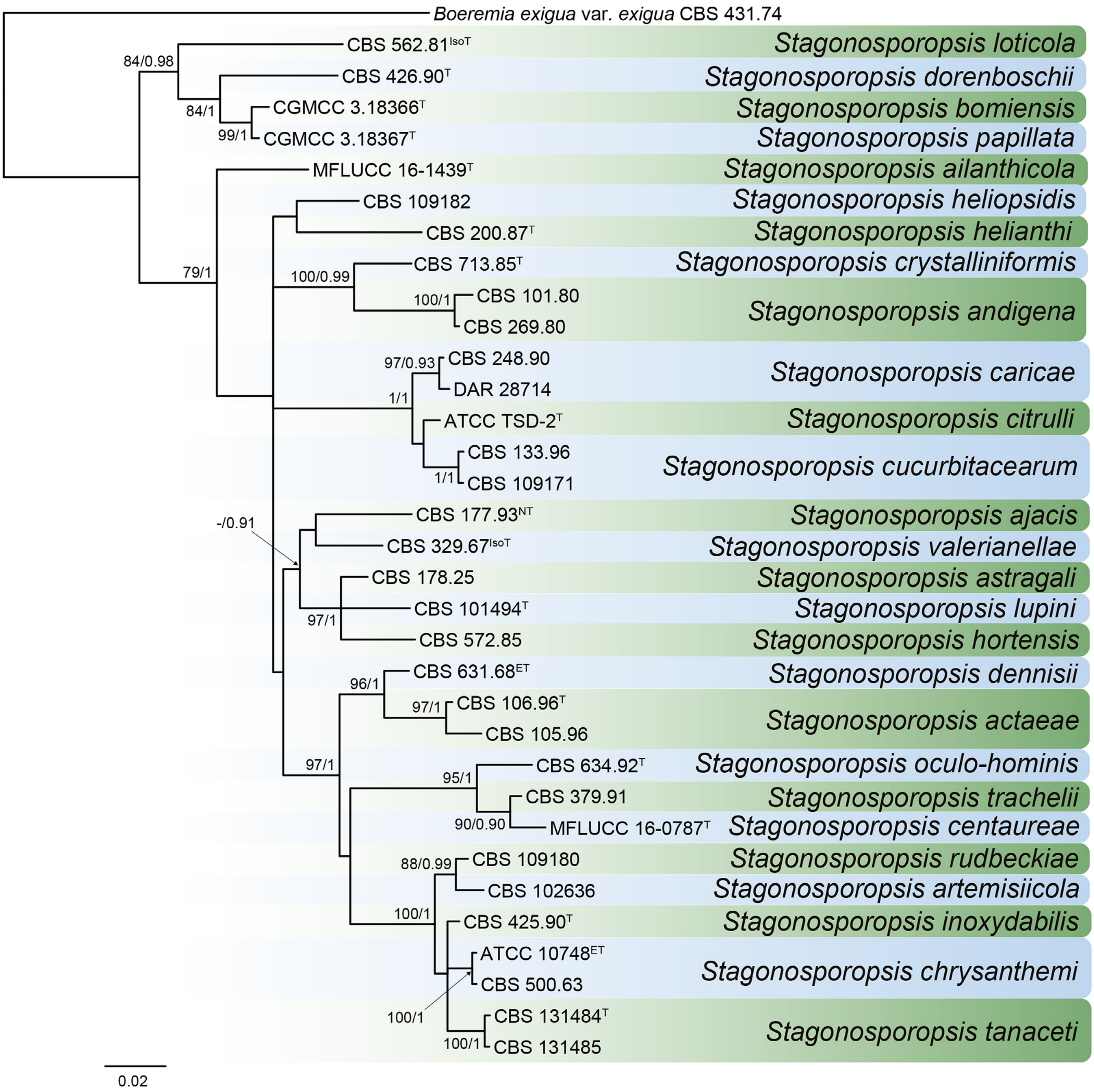


Fig. 76. The majority rule consensus phylogram of *Stagonosporopsis* spp. inferred from the concatenated LSU (876 bp), ITS (459 bp), *tub2* (299 bp) and *rpb2* (596 bp) sequence alignment using Bayesian Inference. The tree is rooted to *Boeremia exigua* var. *exigua* CBS 431.74. Bootstrap support values > 75 % and PP values > 0.90 are shown above or below the branches. $^{T, ET, IsoT}$ and ^{NT} indicate ex-type, ex-epitype, ex-isotype and ex-neotype strains, respectively. Genbank accession numbers are indicated in Table 19, Aveskamp *et al.* (2010) and Vaghefi *et al.* (2012). TreeBASE: S23800.

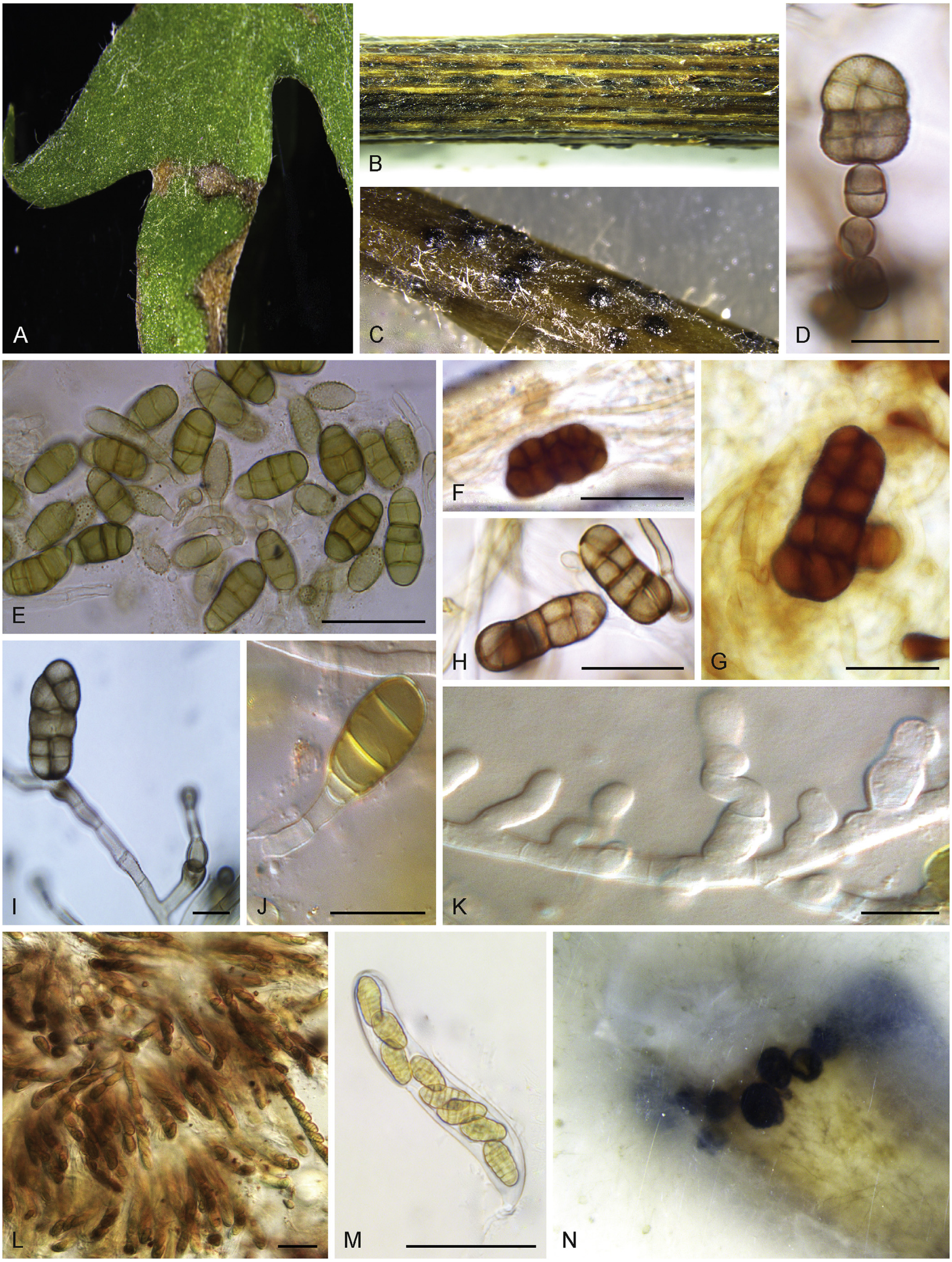


Fig. 77. *Stemphylium* spp. **A.** Disease symptoms caused by *Stemphylium vesicarium* (BRIP 65181) on pyrethrum leaves. **B, C.** Pseudothecial ascomata of *Stemphylium vesicarium* (BRIP 65181) on pyrethrum flower stems *in vivo* and *in vitro* respectively. **D–H.** Conidia of *Stemphylium* spp. **D, H.** *Stemphylium vesicarium* (BRIP 65181). **E.** *Stemphylium truncatulae* (holotype BRIP 14850). **F, G.** *Stemphylium waikerieanum* (ex-type VPRI 21969). **I–K.** Conidiophores of *Stemphylium* spp. **I.** 1-branched conidiophore of *Stemphylium vesicarium* (BRIP 65181). **J.** Simple conidiophore of *Stemphylium truncatuale* (holotype BRIP 14850). **K.** Branched and immature conidiophores of *Stemphylium waikerieanum* (ex-type VPRI 21969). **L–N.** Sexual morphs. **L, M.** Asci and ascospores of *Stemphylium vesicarium* isolated from the dead flower stems of pyrethrum. **N.** Immature pseudothecial ascomata of *Stemphylium truncatulae* on SNA after 1 wk. Scale bars: D–K = 20 µm; L, M = 100 µm. Pictures A–D, H, I, M taken from Moslemi *et al.* (2017).

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

Species	**Isolates**[1]	**GenBank accession numbers**[2]			**References**
		ITS	***gapdh***	***cmdA***	
Stemphylium amaranthi	CBS 124746^{T}	KU850505	KU850652	KU850793	Woudenberg *et al.* (2017)
Ste. armeriae	CBS 338.73	KU850511	KU850658	KU850799	Woudenberg *et al.* (2017)
Ste. astragali	CBS 116583^{ET}	KU850512	KU850659	KU850800	Woudenberg *et al.* (2017)
Ste. beticola	CBS 141024^{T}	KU850520	KU850667	KU850808	Woudenberg *et al.* (2017)
	VPRI 42502	MK336834	MK336880	MK336857	Present study
Ste. botryosum	CBS 714.68^{T}	KC584238	AF443881	KU850826	Woudenberg *et al.* (2017)
Ste. callistephi	CBS 527.50^{T}	KU850539	KU850686	KU850828	Woudenberg *et al.* (2017)
Ste. canadense	CBS 116602^{T}	KU850641	KU850782	KU850932	Woudenberg *et al.* (2017)
Ste. chrysanthemicola	CBS 117255^{T}	KU850640	KU850781	KU850931	Woudenberg *et al.* (2017)
	VPRI 10316	MK336835	MK336881	MK336858	Present study
Ste. drummondii	CBS 346.83^{T}	GQ395365	KU850687	KU850829	Woudenberg *et al.* (2017)
Ste. eturmiunum	CBS 109845^{T}	KU850541	KU850689	KU850831	Woudenberg *et al.* (2017)
	BRIP 27557	MK336820	MK336866	MK336843	Present study
	BRIP 27560	MK336821	MK336867	MK336844	Present study
	BRIP 55702	MK336826	MK336872	MK336849	Present study
	BRIP 60383	MK336827	MK336873	MK336850	Present study
	BRIP 62759	MK336830	MK336876	MK336853	Present study
	BRIP 63689	MK336831	MK336877	MK336854	Present study
Ste. gracilariae	CBS 482.90^{T}	KU850549	AF443883	KU850839	Woudenberg *et al.* (2017)
Ste. halophilum	CBS 337.73^{T}	KU850553	KU850700	KU850843	Woudenberg *et al.* (2017)
Ste. ixeridis	CBS 124748^{T}	KU850590	KU850737	KU850881	Woudenberg *et al.* (2017)
Ste. lancipes	CBS 133314^{ET}	KU850596	KU850742	KU850887	Woudenberg *et al.* (2017)
Ste. loti	CBS 407.54^{T}	KU850597	KU850743	KU850888	Woudenberg *et al.* (2017)
Ste. lucomagnoense	CBS 116601^{T}	KU850629	KU850770	KU850920	Woudenberg *et al.* (2017)
Ste. lycii	CBS 125241^{T}	KU850602	KU850748	KU850893	Woudenberg *et al.* (2017)
Ste. lycopersici	CBS 122639^{NT}	KU850611	KU850756	KU850902	Woudenberg *et al.* (2017)
	BRIP 13821	MK336813	MK336859	MK336836	Present study
	BRIP 13902	MK336814	MK336860	MK336837	Present study
	BRIP 15113	MK336817	MK336863	MK336840	Present study
	BRIP 62317	MK336828	MK336874	MK336851	Present study
Ste. majusculum	CBS 717.68^{T}	KU850618	AF443891	KU850909	Woudenberg *et al.* (2017)
Ste. novae-zelandiae	CBS 138295^{T}	KU850631	KU850772	KU850922	Woudenberg *et al.* (2017)
Ste. paludiscirpi	CBS 109842^{T}	KU850620	KU850762	KU850911	Woudenberg *et al.* (2017)
Ste. rombundicum	BRIP 27486^{HT}	MK336819	MK336865	MK336842	Present study
Ste. sarciniforme	CBS 110049	KU850591	KU850738	KU850882	Woudenberg *et al.* (2017)
Ste. simmonsii	CBS 133518^{T}	KU850637	KU850778	KU850928	Woudenberg *et al.* (2017)
Ste. solani	CBS 116586^{ET}	KU850627	KU850768	KU850918	Woudenberg *et al.* (2017)
Ste. symphyti	CBS 115268^{T}	KU850643	KU850784	KU850934	Woudenberg *et al.* (2017)
Ste. trifolii	CBS 116580^{T}	KU850647	KU850788	KU850938	Woudenberg *et al.* (2017)
Ste. triglochinicola	CBS 718.68^{T}	KU850648	KU850789	KU850939	Woudenberg *et al.* (2017)
Ste. truncatulae	BRIP 14850^{HT}	MK336815	MK336861	MK336838	Present study
Ste. vesicarium	CBS 715.68	KU850565	KU850712	KU850855	Woudenberg *et al.* (2017)
	BRIP 5891	MK336829	MK336875	MK336852	Present study
	BRIP 14857	MK336816	MK336862	MK336839	Present study
	BRIP 26714	MK336818	MK336864	MK336841	Present study
	BRIP 40125	MK336822	MK336868	MK336845	Present study
	BRIP 40155	MK336823	MK336869	MK336846	Present study
	BRIP 52457	MK336824	MK336870	MK336847	Present study
	BRIP 53984	MK336825	MK336871	MK336848	Present study
	VPRI 31963	MK336833	MK336879	MK336856	Present study
Ste. waikerieanum	VPRI 21969^{HT}	MK336832	MK336878	MK336855	Present study

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

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; *gapdh*: partial glyceraldehyde-3-phosphate dehydrogenase gene; *cmdA*: partial calmodulin gene.

Culture characteristics: Colonies on PDA irregular, reaching 65–68 mm diam after 14 d at 22 °C, slightly umbonate, colour citrine, olivaceous buff to olivaceous, with compact aerial mycelium on the surface, abundant sporulation surrounding centre and at the margins of the colony. On CMA circular or irregular, reaching 58–59 mm diam after 14 d at 22 °C, flat at the centre and margins, citrine to olivaceous coloured, with moderate aerial mycelium on the surface, sporulating abundantly. On MEA irregular, reaching 35–40 mm diam after 14 d at 22 °C, flat to crateriform, slightly sunk into the agar, buff to olivaceous coloured at the centre becoming white at the margins, with dense mycelium on the surface, sporulating near the centre. On SNA circular to slightly irregular, reaching 20–21 mm diam after 14 d at 22 °C, umbonate, with moderate aerial mycelium, sporulation abundant between centre and margins.

Distribution: New Zealand, South Africa and USA.

Typus: **USA,** Maryland, Pocomoke City, 38.072952N, 75.555852W, from branch canker of *Cupressus* sp., 2017, S.A. Krueger-Hadfield (**epitype** of *Pestalotia unicornis* designated here CBS H-23739, MBT383596, cultures ex-epitype CBS 143871 = CPC 34650, CBS 143872 = CPC 34649, CBS 143873 = CPC 34651); New Jersey, from *Chamaecyparis thyoides*, 1878, J.B. Ellis (**holotype** of *Pestalotia unicornis* IMI 5816).

Additional materials examined: **New Zealand**, from *Cryptomeria japonica*, 1981, H.J. Boesewinkel (CBS H-23151 reference specimen, culture CBS 538.82 = CPC 23783 = NBRC 32684). **South Africa**, from *Cupressus sempervirens*, 1999, I. Barnes (culture CBS 120306 = CMW 5596).

Notes: *Seiridium unicorne* (basionym: *Pestalotia unicornis*) is the earliest described cypress pathogen (Cooke & Ellis 1878) of

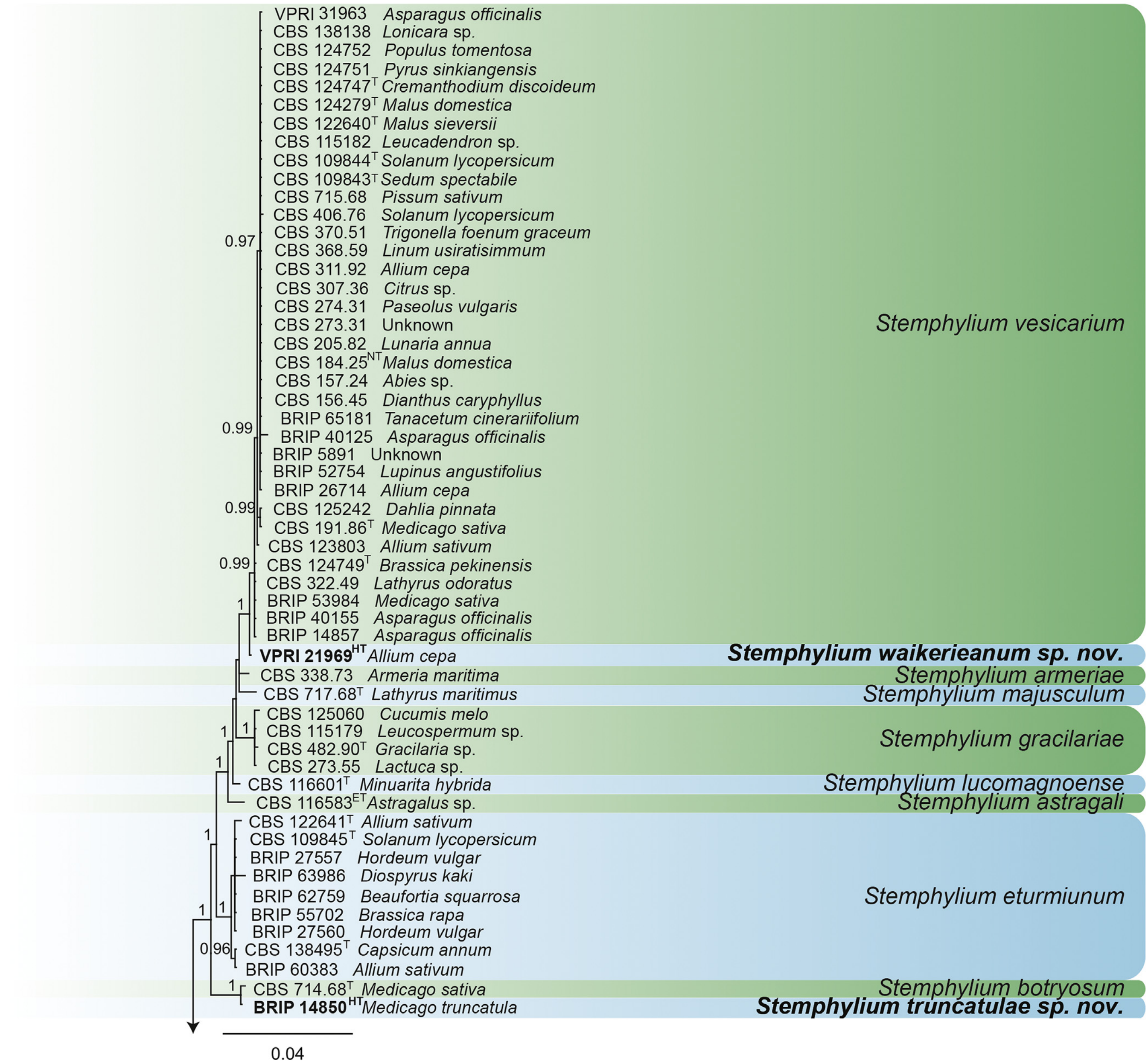


Fig. 78. Bayesian phylogenetic tree inferred from ITS (565 bp), *gapdh* (613 bp) and *cmdA* (863) using partitioned analysis with N92+G+I substituition model for ITS and *gapdh* and GTR+G+I for *cmdA*. Highest log likelihood -34098.05. The analysis involved 122 nucleotide sequences including 98 sequences obtained from GenBank and 24 sequences obtained in the present study. Scale bar indicates expected changes per site. The tree was rooted to *Alternaria alternata* (GV14 634a1). The novel species described in this study are shown in **bold**. Bayesian posterior probability scores above 0.95 are shown at the nodes. GenBank accession numbers are indicated in Table 20. $^{T, ET, HT}$ and ^{NT} indicate ex-type, ex-epitype, ex-holotype and ex-neotype strains, respectively. TreeBASE:S23794.

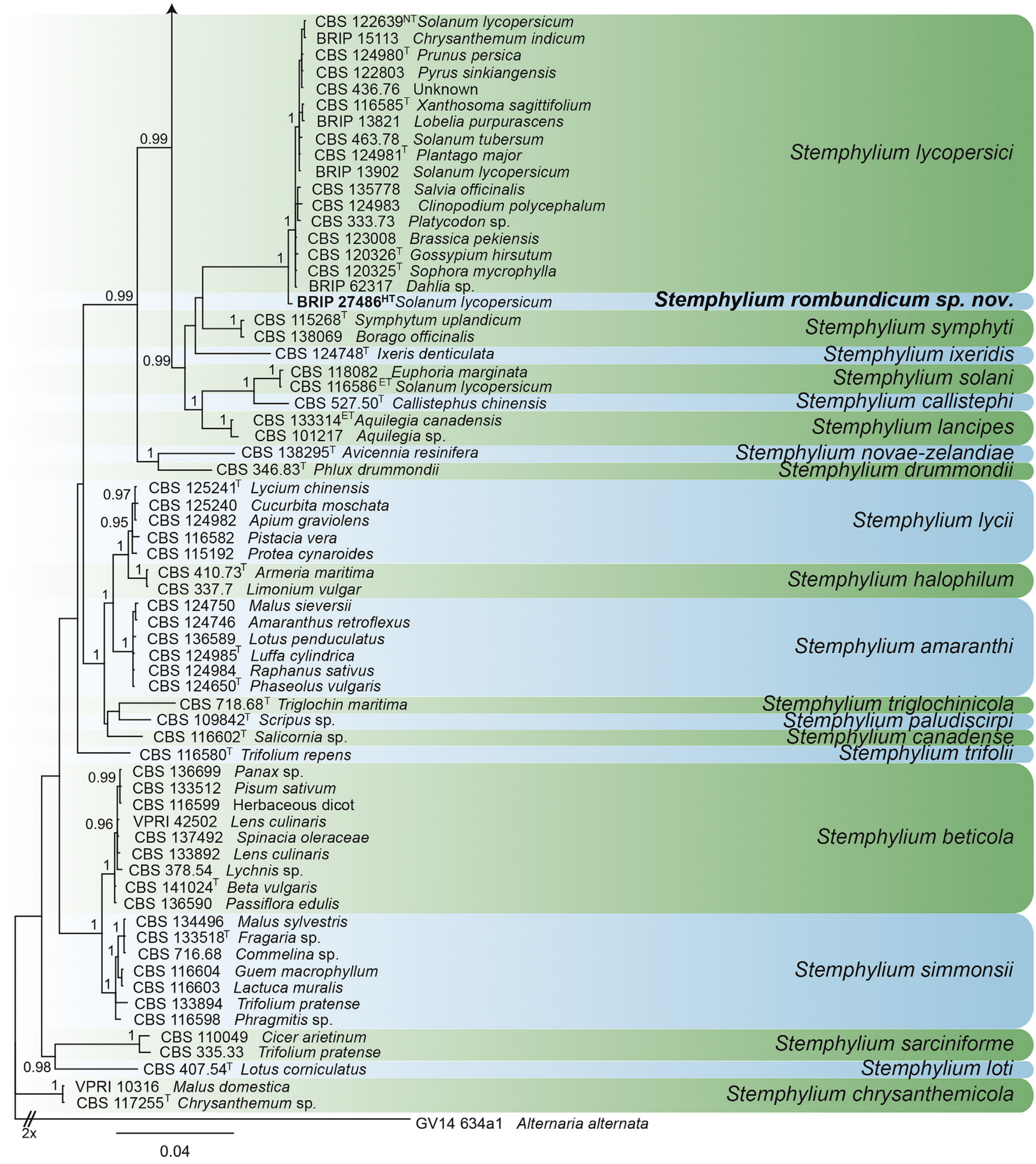


Fig. 78. (Continued).

Seiridium and was isolated from "cedar wood" collected in New Jersey (USA). The host was later identified by W.W. Wagener as *Chamaecyparis thyoides,* as indicated on the holotype label (see Bonthond *et al.* 2018). The genus *Seiridium* accommodates multiple species infecting *Cupressaceae* and *S. unicorne* has traditionally been regarded as a mild pathogen but capable of infecting a broad range of hosts, including plant species beyond the *Cupressaceae* (Guba 1961). The holotype (IMI 5816) was obtained and examined during a preceding study (Bonthond *et al.* 2018) and found to be limited to two microscope slides. Therefore, the selection of an epitype for *S. unicorne* is important to consolidate a stable taxonomic concept for this taxon. Given the occurrence of related species which are pathogenic on the same hosts (*i.e. S. cancrinum, S. cardinale, S. cupressi* and *S. neocupressi*) the availability of ex-epitype DNA sequence data provides a valuable reference for the identification of future collections. The specimen we introduce here as epitype (CBS H-23739) was collected from necrotic lesions of a *Cupressus* sp. in Maryland, USA and matches morphologically in all respects with the holotype (IMI 5816) and the reference strain (CBS 538.82) of *S. unicorne*. Furthermore, in the four-locus phylogeny (Fig. 63E) the ex-epitype strain clusters under a fully supported node in the

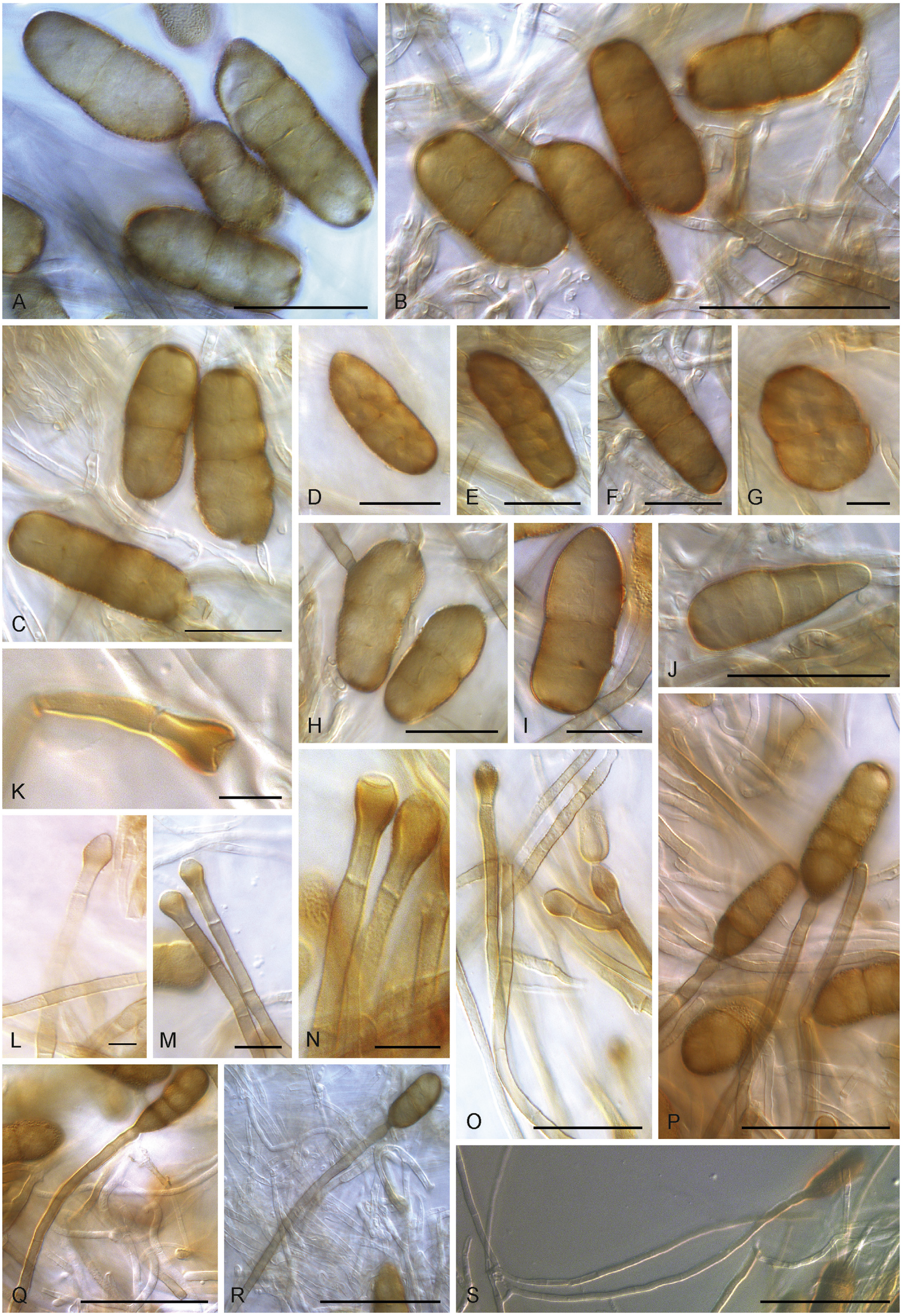


Fig. 79. *Stemphylium rombundicum* (ex-type BRIP 27486). **A–J.** Conidia. **K–S.** Verrucose conidiogenous cells and straight and simple conidiophores with conidia attached. Scale bars: A–N, P = 20 µm; others 100 µm.

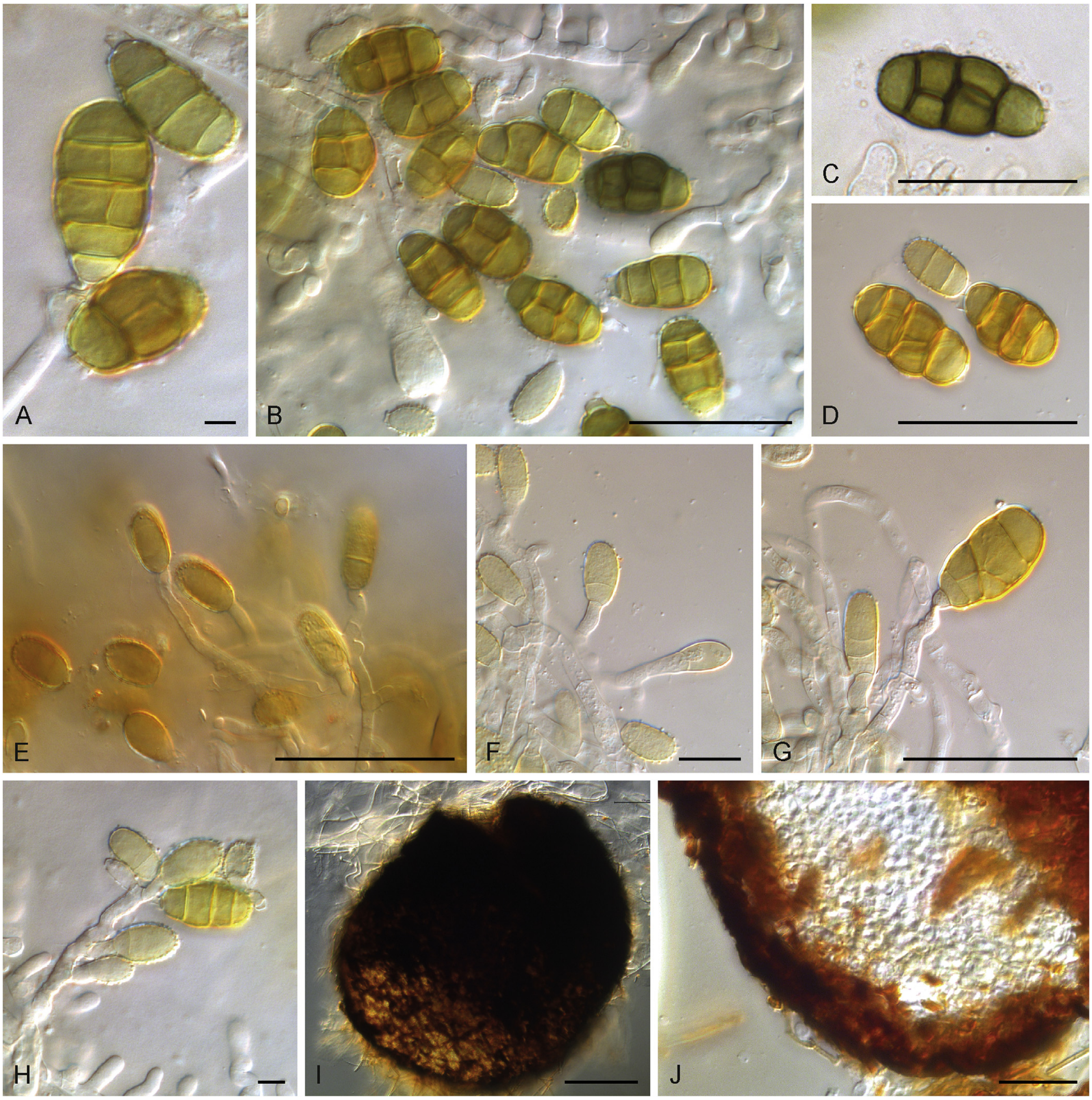


Fig. 80. *Stemphylium truncatulae* (ex-type BRIP 14850). **A–H.** Asexual morph. **A–D.** Conidia on SNA. **E–H.** Straight and simple or multibranched conidiophores and conidiogenous cells. **I–J.** Sexual morph. **I.** Immature pseudothecium. **J.** Ascomatal wall. Scale bars: I = 100 µm; others 20 µm.

clade that was assigned to *S. unicorne* based on morphology (Bonthond *et al.* 2018). Conidial measurements strongly overlap between the selected epitype, holotype and reference strain (Fig. 63A–D), although the median width of the epitype being slightly narrower in comparison to the holotype and reference strain. Measurements of basal and apical appendages and distributions of those measurements are highly similar between epitype and reference strain. For both appendages, the variation in measurements is higher for the holotype compared to the reference strain and the epitype, which, however, likely results from the age and condition of the material as we observed that conidial appendages from the holotype were often damaged.

Authors: G. Bonthond, M. Sandoval-Denis, S.A. Krueger-Hadfield, L. Morton, C. Ambers & P.W. Crous

Septoriella Oudem., Ned. kruidk. Archf, ser. 2, 5: 504. 1889. Fig. 66.

Synonyms: *Allophaeosphaeria* Ariyaw. *et al.*, Fungal Diversity 72: 137. 2015.
Poaceicola W.J. Li *et al.*, Mycosphere 6: 696. 2015.
Vagicola Chethana & K.D. Hyde, Fungal Diversity 75: 113. 2015.

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

Type species: *Septoriella phragmitis* Oudem. Epitype and ex-epitype strain designated by Crous *et al.* (2015a): CBS H-22281, CBS 140065.

DNA barcode (genus): LSU. Fig. 28.

DNA barcodes (species): ITS, *rpb2*, *tef1, tub2*. Table 16. Fig. 67.

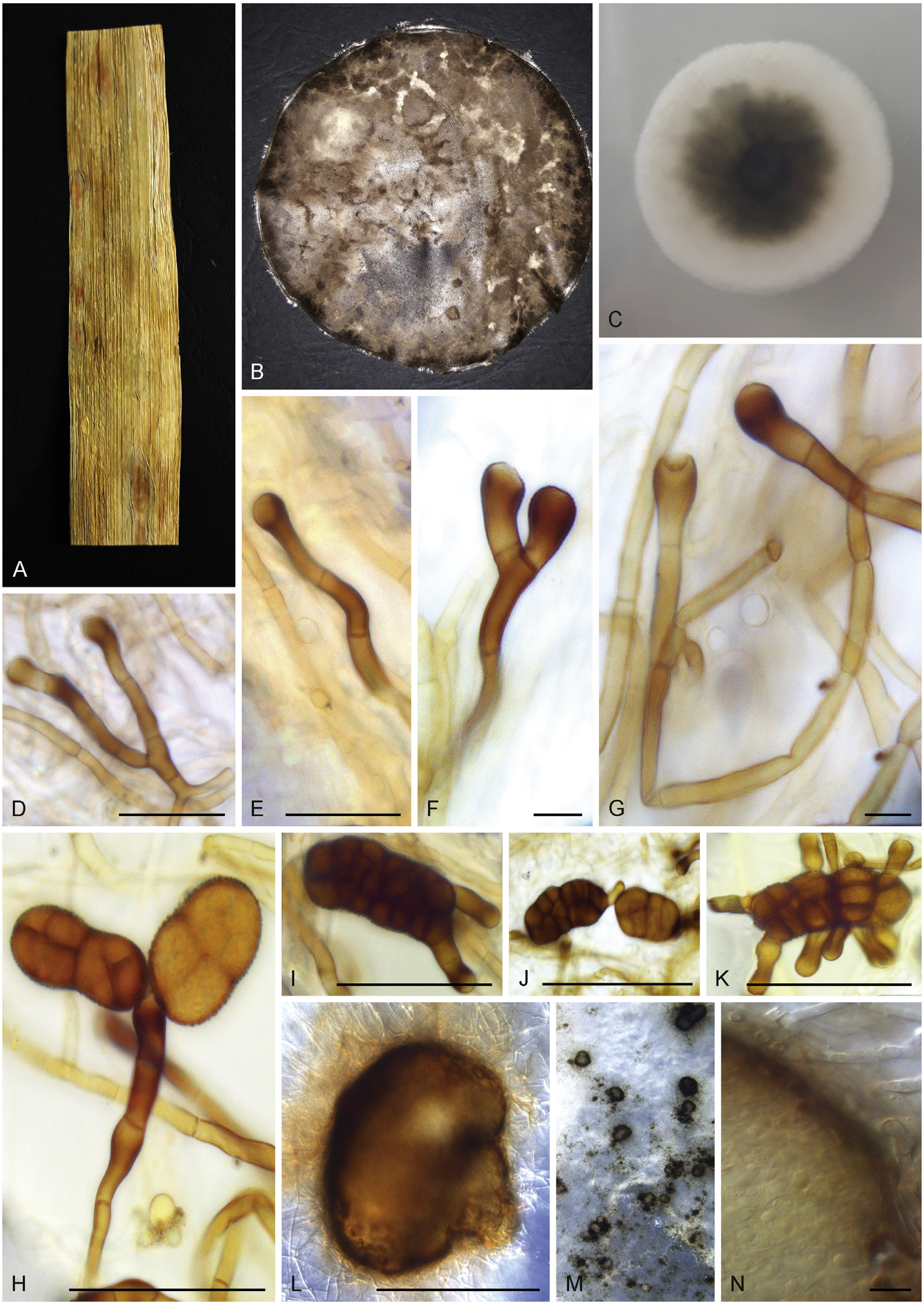


Fig. 81. *Stemphylium waikerieanum* (ex-type VPRI 21969). **A.** Dried leaf of *Allium cepa* showing leaf lesions caused by the pathogen. **B.** Dried type culture. **C.** Revived colony after 1 wk on PDA. **D–K.** Asexual morph. **D–H.** Simple or 1-branched conidiophores on PDA and SNA. **I–K.** Phaeodictyospores. **L–N.** Sexual morph. **L, M.** Immature ascomata on SNA after 1 wk. **N.** Ascomatal wall. Scale bars: N = 100 µm; others 20 µm.

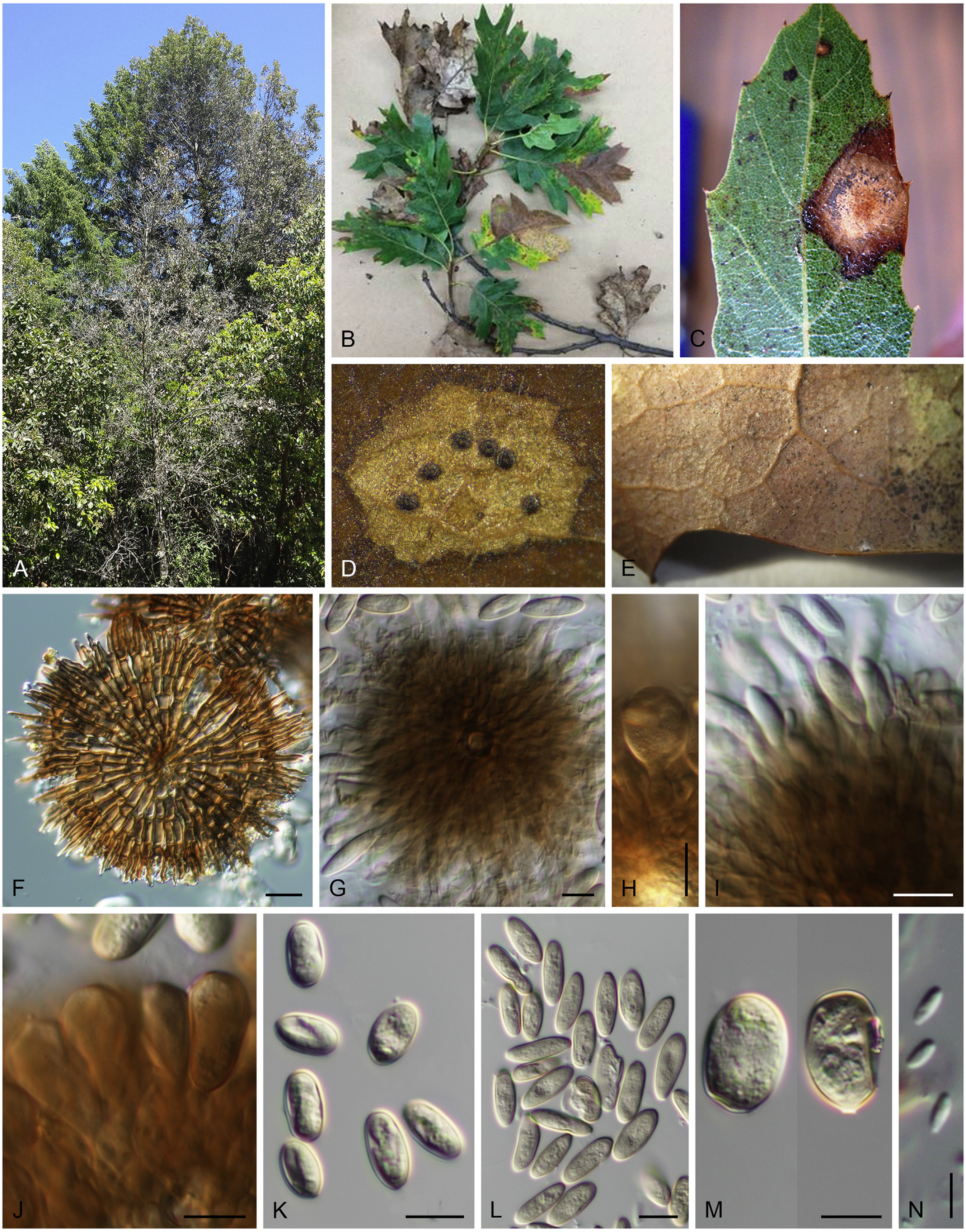


Fig. 82. *Tubakia* spp. **A–E.** Disease symptoms. **A.** *Tubakia californica* on Tanoak tree (*Notholithocarpus densiflorus*). **B.** *Tubakia californica* on California black oak (*Quercus kelloggii*). **C.** *Tubakia sierrafriensis* (holotype CFNL 2944) on *Quercus eduardi*. **D.** *Tubakia japonica* (epitype NBRC H-11611) on *Castanea crenata*. **E.** *Tubakia melnikiana* (holotype HAL 3179 F) causing necrotic leaf lesion. **F–N.** Asexual morph. **F.** Scutellum of *Tubakia paradryinoides* (holotype TFM:FPH 3923). **G.** Central columella of *Tubakia oblongispora* (holotype NBRC H-11881). **H–J.** Conidiophores. **H.** *Tubakia japonica* (epitype NBRC H-11611). **I.** *Tubakia oblongispora* (holotype NBRC H-11881). **J.** *Tubakia paradryinoides* (holotype TFM:FPH 3923). **K–M.** Conidia. **K.** *Tubakia dryinoides* (holotype NBRC H-11618). **L.** *Tubakia oblongispora* (holotype NBRC H-11881). **M.** *Tubakia paradryinoides* (holotype TFM:FPH 3923). **N.** Microconidia of *Tubakia dryinoides* (holotype NBRC H-11618). Scale bars: 10 µm. Pictures taken from Braun *et al.* (2018).

Ascomata ostiolate, solitary to gregarious, immersed to semi-immersed or superficial, broadly ellipsoidal to globose, subglobose, or obpyriform, brown to dark brown or black, smooth-walled, coriaceous, uni- to biloculate; *necks* central, flush to papillate, brown to dark brown or black, with or without periphyses, rarely comprising short, hyaline setae; *ascomatal wall* thin-walled, outer layers composed of brown to dark brown or blackish cells of *textura angularis*, inner layers composed of brown cells of *textura prismatica*, or of hyaline or brown cells of *textura angularis*, rarely composed of hyaline gelatinous cells. *Hamathecium* composed of numerous, 1–3 μm wide, filiform to broadly cylindrical, septate, cellular pseudoparaphyses, or lacking pseudoparaphyses. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical, broadly cylindrical, cylindrical-fusiform, cylindrical-clavate, clavate, or broadly clavate, pedicellate, apically rounded with an ocular chamber. *Ascospores* overlapping, 1–3-seriate, hyaline to yellowish brown or pale brown, brown, golden brown, or reddish brown, narrowly or broadly fusiform or oblong to narrowly oblong, straight or slightly curved, smooth-walled or echinulate, multi-septate, with transverse septa, with or without longitudinal septa, sometimes with enlarged medium cells, constricted or not at septa, conical or obtuse, rounded ends, with or without sheath. *Conidiomata* pycnidial, solitary or aggregated, immersed to semi-immersed, globose to subglobose, unilocular, pale brown to brown or dark brown, with central, papillate, circular ostiole; *conidiomatal wall* of brown cells of *textura angularis*, rarely of *textura oblita*, inner layers becoming hyaline. *Conidiophores* lining the inner cavity, reduced to conidiogenous cells, invested in mucus. *Conidiogenous cells* ampulliform to lageniform, hyaline, smooth-walled, proliferating via inconspicuous percurrent proliferations near apex. *Conidia* cylindrical to subcylindrical, fusiform, or subfusiform, apex obtuse to subobtuse, base truncate, straight or curved, euseptate, pale brown to brown, thin-walled, smooth-walled or minutely verruculose, bearing mucoid appendages at both ends (type H sensu Nag Raj 1993) (description of asexual morph adapted from Crous *et al.* 2015a).

Culture characteristics: Colonies with moderate to abundant aerial mycelium, variable in colour, circulate or lobate. On PDA surface white to iron-grey or grey olivaceous, greyish white, pale olivaceous grey, or dull green margins, mouse grey in the middle and pale mouse grey at the center; reverse grey, olivaceous grey, dull green, buff to dark brown, olivaceous to pale brown or black, brown or olivaceous brown to black. On MEA surface white, dirty white, or white to pale yellow or iron-grey; reverse yellow, umber, buff, or dark grey to black.

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

Distribution: Mostly Europe, but also reported in Asia and North America.

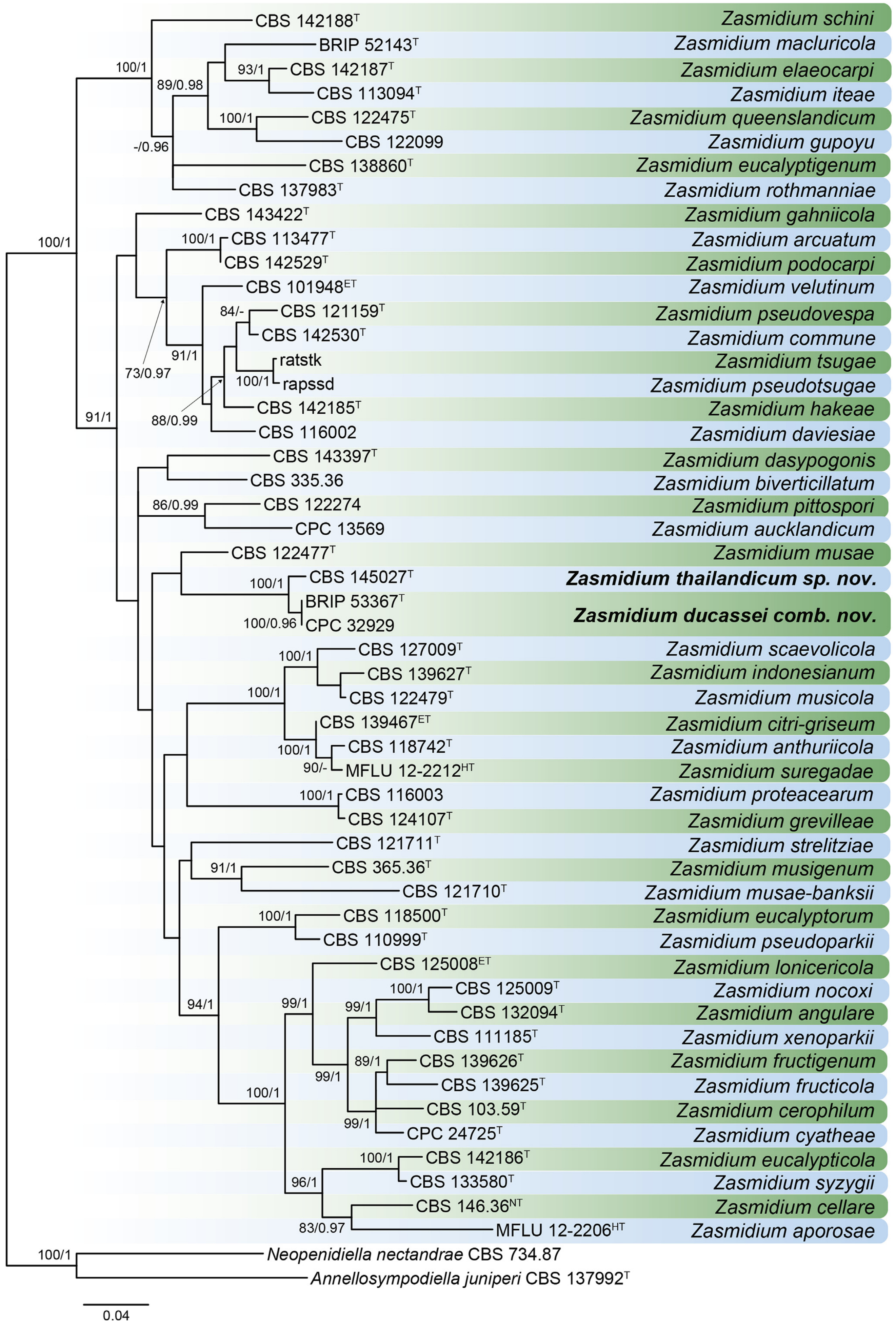
Hosts: Mostly saprophytes of grasses (*Poaceae*), including *Arundo* spp., *Agrostis stolonifera*, *Bromus sterilis*, *Calamagrostis* spp., *Dactylis glomerata*, *Elymus glaucus*, *E. repens*, *Poa* sp., *Phragmites* spp. and *Setaria verticillata*. Also found on *Rosa canina* (*Rosaceae*) and *Juncus* sp. (*Juncaceae*), and others hosts not molecularly corroborated. *Septoriella hirta* is considered and important secondary pathogen of grasses, including *Agropyron* spp., *Bromus* spp., *Dactylis glomerata*, *Festuca* spp., *Poa* spp., *Stipa* spp., and *Triticum* spp., among others.

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

Species	**Isolates**[1]	**GenBank accession number**[2]				**References**
		ITS	***rpb2***	***tef1***	***tub2***	
Tubakia americana	CBS 129014	MG591873	MG976449	MG592058	MG592152	Braun *et al.* (2018)
T. braunii	CBS 115011^{T}	MG591912	MG976488	MG592101	MG592193	Braun *et al.* (2018)
T. californica	CBS 143670^{T}	MG591835	MG976451	MG592023	MG592117	Braun *et al.* (2018)
T. dryina	CBS 112097^{ET}	MG591851	MG976455	MG592039	MG592133	Braun *et al.* (2018)
T. dryinoides	NBRC 9267^{T}	MG591878	MG976461	MG592063	MG592157	Braun *et al.* (2018)
T. hallii	CBS 129013^{T}	MG591880	MG976462	MG592065	MG592159	Braun *et al.* (2018)
T. iowensis	CBS 129012^{T}	MG591879	–	MG592064	MG592158	Braun *et al.* (2018)
T. japonica	NBRC 9268^{ET}	MG591886	MG976465	MG592071	MG592165	Braun *et al.* (2018)
T. liquidambaris	CBS 139744	MG605068	–	MG603578	–	Harrington & McNew (2018)
T. macnabbii	CBS 137349^{T}	MG605069	–	MG603579	–	Harrington & McNew (2018)
T. melnikiana	CPC 32255^{T}	MG591893	MG976472	MG592080	MG592174	Braun *et al.* (2018)
T. oblongispora	NBRC 9885^{T}	MG591897	MG976474	MG592084	MG592178	Braun *et al.* (2018)
T. paradryinoides	NBRC 9884^{T}	MG591898	MG976475	MG592085	MG592179	Braun *et al.* (2018)
T. seoraksanensis	CBS 127492^{IsoT}	MG591908	MG976485	MG592096	MG592188	Braun *et al.* (2018)
T. sierrafriensis	CPC 33020^{T}	MG591910	MG976486	MG592099	MG592191	Braun *et al.* (2018)
T. suttoniana	CBS 639.93^{IsoT}	MG591921	MG976493	MG592110	MG592202	Braun *et al.* (2018)
T. tiffanyae	CBS 137345^{T}	MG605081	–	–	–	Harrington & McNew (2018)

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

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


CBS 142188^{T} Zasmidium schini
BRIP 52143^{T} Zasmidium macluricola
CBS 142187^{T} Zasmidium elaeocarpi
CBS 113094^{T} Zasmidium iteae
CBS 122475^{T} Zasmidium queenslandicum
CBS 122099 Zasmidium gupoyu
CBS 138860^{T} Zasmidium eucalyptigenum
CBS 137983^{T} Zasmidium rothmanniae
CBS 143422^{T} Zasmidium gahniicola
CBS 113477^{T} Zasmidium arcuatum
CBS 142529^{T} Zasmidium podocarpi
CBS 101948^{ET} Zasmidium velutinum
CBS 121159^{T} Zasmidium pseudovespa
CBS 142530^{T} Zasmidium commune
ratstk Zasmidium tsugae
rapssd Zasmidium pseudotsugae
CBS 142185^{T} Zasmidium hakeae
CBS 116002 Zasmidium daviesiae
CBS 143397^{T} Zasmidium dasypogonis
CBS 335.36 Zasmidium biverticillatum
CBS 122274 Zasmidium pittospori
CPC 13569 Zasmidium aucklandicum
CBS 122477^{T} Zasmidium musae
CBS 145027^{T} Zasmidium thailandicum sp. nov.
BRIP 53367^{T}
CPC 32929 Zasmidium ducassei comb. nov.
CBS 127009^{T} Zasmidium scaevolicola
CBS 139627^{T} Zasmidium indonesianum
CBS 122479^{T} Zasmidium musicola
CBS 139467^{ET} Zasmidium citri-griseum
CBS 118742^{T} Zasmidium anthuriicola
MFLU 12-2212^{HT} Zasmidium suregadae
CBS 116003 Zasmidium proteacearum
CBS 124107^{T} Zasmidium grevilleae
CBS 121711^{T} Zasmidium strelitziae
CBS 365.36^{T} Zasmidium musigenum
CBS 121710^{T} Zasmidium musae-banksii
CBS 118500^{T} Zasmidium eucalyptorum
CBS 110999^{T} Zasmidium pseudoparkii
CBS 125008^{ET} Zasmidium lonicericola
CBS 125009^{T} Zasmidium nocoxi
CBS 132094^{T} Zasmidium angulare
CBS 111185^{T} Zasmidium xenoparkii
CBS 139626^{T} Zasmidium fructigenum
CBS 139625^{T} Zasmidium fructicola
CBS 103.59^{T} Zasmidium cerophilum
CPC 24725^{T} Zasmidium cyatheae
CBS 142186^{T} Zasmidium eucalypticola
CBS 133580^{T} Zasmidium syzygii
CBS 146.36^{NT} Zasmidium cellare
MFLU 12-2206^{HT} Zasmidium aporosae
Neopenidiella nectandrae CBS 734.87
Annellosympodiella juniperi CBS 137992^{T}
100/1
89/0.98
93/1
100/1
-/0.96
100/1
100/1
73/0.97
91/1
84/-
100/1
88/0.99
91/1
86/0.99
100/1
100/0.96
100/1
100/1
100/1
90/-
100/1
91/1
100/1
94/1
99/1
100/1
99/1
99/1
89/1
99/1
100/1
96/1
83/0.97
100/1
0.04

Disease symptoms: Secondary foot rot and rot of mature straw. Discoloured culms and predisposition of the plant to premature collapse.

Notes: *Septoriella* was considered an asexual genus characterised by pycnidial, unilocular conidiomata, and cylindrical to fusoid, euseptate conidia bearing mucoid appendages at both ends (Crous *et al.* 2015a). However, in our phylogenetic studies based on ITS and LSU, and on the combined dataset, the ex-type strains of the sexual genera *Allophaeosphaeria*, *Poaceicola* and *Vagicola* were located in the clade representing the genus *Septoriella*. Therefore, these genera are synonymised with *Septoriella* in the present study.

Allosphaeosphaeria was recently introduced by Liu *et al.* (2015) to incorporate two new saprophytic species found on *Dactylis glomerata* from Italy, *i.e. Al. dactylidis* and *Al. muriformia*, the latter designated as type species. These species only produce the sexual morph characterised by ascospores with transverse and longitudinal septa, and a gelatinous sheath. Subsequently, three other new species were introduced in the genus, *i.e. Al. clematidis*, *Al. cytisi* and *Al. subcylindrospora*. *Allosphaeosphaeria clematidis* and *Al. cytisi* only produce the sexual morph, while *Al. subcylindrospora* only produces an asexual morph. The morphology of this asexual morph fits perfectly in the description of *Septoriella*, corroborating the synonymy proposed in the present study based on the phylogenetic data. *Allosphaeosphaeria clematidis* was recently excluded from the genus and transferred to the new genus *Embarria* (Wanasinghe *et al.* 2018). Moreover, in our phylogenetic studies, *Al. cytisi* formed an independent lineage in *Phaeosphaeriaceae* far from the clade representing *Septoriella*. Therefore, a new genus is proposed to accommodate this species.

The genus *Poaceicola* was introduced by Li *et al.* (2015) to accommodate *Phaeosphaeria elongata* and two new species, *i.e. Po. arundinis* and *Po. bromi*. The two latter species are characterised by the production of an asexual morph similar to *Septoriella*. *Poaceicola elongata* produces a sexual morph characterised by ascospores with transverse septa. The presence of only transverse septa could be a morphologic difference from *Allophaeosphaeria*. However, seven more new species have been included in the genus, including one species presenting ascospores with transverse and longitudinal septa, *Po. arundinis*, demonstrating that the longitudinal septation of the ascospores is not phylogenetically informative in these genera.

Vagicola was recently introduced by Ariyawansa *et al.* (2015a), in the same year as the other two genera. Ariyawansa *et al.* (2015a) raised the subgenus *Vagicola* (Shoemaker & Babcock 1989) to generic rank to accommodate *Phaeosphaeria vagans*, a species characterised by a sexual morph similar to the species of *Poaceicola,* having ascospores with transverse septa only. Subsequently, Jayasiri *et al.* (2015) introduced two new species: *V. chlamydospora*, which presents both morphs, and *V. dactylidis*, which produces only the sexual morph. The sexual morph of *V. chlamydospora* is similar to the two former species of the genus, while *V. dactylidis* produces ascospores with transverse and longitudinal septa as seen in species of *Allophaeosphaeria*, indicating again that the longitudinal septation of ascospores is not phylogenetically informative. *Vagicola chlamydospora* was recently transferred to *Septoriella* based on phylogenetic data (Jayasiri *et al.* 2015). Surprisingly, the asexual morph reported in that species does not fit with the morphology of *Septoriella*, since it produces micro- to macronematous conidiophores and chlamydospore-like conidia. Recently, Thambugala *et al.* (2017) introduced the last species of the genus, *V. arundinis*, which produces both morphs and is characterised by ascospores with transverse septa and an asexual morph similar to *Septoriella*, which demonstrates the link of *Vagicola* with *Septoriella*. This last species was invalid because two holotypes were designated. Therefore, this taxon is validated in the present study.

Moreover, in our phylogenetic analyses, the ex-type strain of the most recently described species of *Neostagonospora* was located in the clade representing *Septoriella*. This species is characterised by the production of conidia that are subcylindrical or fusiform, euseptate, with a subobtuse apex and truncate base. However, the presence of mucoid appendages at both ends, as the other species of *Septoriella*, has not been reported. *Septoriella artemisiae* is saprobic or weakly necrotrophic on dead and dying stems of *Artemisia austriaca*.

Most of the species now included in *Septoriella* are saprophytes, except for *Sep. hirta*, which is an important secondary pathogen of grasses (Sprague 1950). This species is often found in association with other fungi such as *Gaeumannomyces graminis* (Johnston *et al.* 2014) and *Oculimacula yallundae* causing foot rot of wheat (Crous *et al.* 2003, 2015a). Other disease symptoms observed in plants affected by *Sep. hirta* are discoloured culms and predisposition to premature collapse, especially in rainy and windy seasons, since this species produces a weakness in the culms of plants with ripe grains. The result of all these symptoms resulted in the increasing of the cost of harvesting and decreasing of the grain quality (Sprague 1950).

References: Sprague 1950 (pathogenicity), Crous *et al.* 2014b, Ariyawansa *et al.* 2015a, Li *et al.* 2015, Liu *et al.* 2015, Thambugala *et al.* 2017 (morphology and phylogeny).

Septoriella agrostina (Mapook *et al.*) Y. Marín & Crous, ***comb. nov.*** MycoBank MB829676.
Basionym: *Poaceicola agrostina* Mapook *et al.*, Fungal Diversity 89: 132. 2018.

Description and illustration: Wanasinghe *et al.* (2018).

Septoriella artemisiae (Wanas. *et al.*) Y. Marín & Crous, ***comb. nov.*** MycoBank MB829677.
Basionym: *Neostagonospora artemisiae* Wanas. *et al*, Fungal Diversity 89: 130. 2018.

Description and illustration: Wanasinghe *et al.* (2018).

Septoriella arundinicola (Wanas. *et al.*) Y. Marín & Crous, ***comb. nov.*** MycoBank MB829678.

Fig. 83. RAxML phylogram obtained from the combined ITS (534 bp), LSU (741 bp) and *rpb2* (739 bp) sequence alignment of all accepted species of *Zasmidium*. The tree was rooted to *Anellosympodiella juniperi* CBS 137992 and *Neopenidiella nectandrae* CBS 734.78. 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 listed in Table 22 and Videiraet al. (2017). $^{T, ET, HT}$ and ^{NT} indicate ex-type, ex-epitype, holotype and ex-neootype strains, respectively. TreeBASE: S23834.

Table 22. DNA barcodes of accepted *Zasmidium* spp.

Species	**Isolates**[1]	**GenBank accession numbers**[2]						**References**
		ITS	**LSU**	***rpb2***	***act***	***tef1***	***tub2***	
Zasmidium angulare	CBS 132094^{T}	JQ622088	JQ622096	MF951690	–	JQ622113	–	Li *et al.* (2012), Videira *et al.* (2017)
Z. anthuriicola	CBS 118742^{T}	FJ839626	FJ839662	MF951691	–	KF253229	KF252763	Crous *et al.* (2009a), Quaedvlieg *et al.* (2013), Videira *et al.* (2017)
Z. aporosae	MFLU 12-2206^{HT}	KC677912	–	–	–	–	–	Phengsintham *et al.* (2013)
Z. arcuatum	CBS 113477^{T}	EU041779	EU041836	MF951692	–	–	–	Arzanlou *et al.* (2007), Videira *et al.* (2017)
Z. aucklandicum	CPC 13569	MF951409	MF951280	MF951733	–	–	–	Videira *et al.* (2017)
Z. biverticillatum	CBS 335.36	EU041796	EU041853	–	–	–	–	Arzanlou *et al.* (2007)
Z. cellare	CBS 146.36^{NT}	EU041821	EU041878	MF951693	–	–	–	Arzanlou *et al.* (2007), Videira *et al.* (2017)
Z. cerophillum	CBS 103.59^{T}	EU041798	GU214485	MF951694	–	–	–	Arzanlou *et al.* (2007), Crous *et al.* (2009b), Videira *et al.* (2017)
Z. citri-griseum	CBS 139467^{ET}	KF901796	KF902155	KF902518	–	KF903385	KF903079	Quaedvlieg *et al.* (2014)
Z. commune	CBS 142530^{T}	KY979765	KY979820	–	KY979860	–	–	Crous *et al.* (2017a)
Z. cyatheae	CPC 24725^{T}	KT037530	KT037571	–	KT037629	KT037490	–	Guatimosim *et al.* (2016)
Z. dasypogonis	CBS 143397^{T}	MG386048	MG386101	–	–	–	–	Crous *et al.* (2017b)
Z. daviesiae	CBS 116002	FJ839633	FJ839669	MF951698	KF903477	KF903373	KF903069	Crous *et al.* (2009a), Quaedvlieg *et al.* (2014), Videira *et al.* (2017)
Z. ducassei	BRIP 53367^{T}	HQ149687	–	–	–	–	–	Shivas *et al.* (2011)
	CPC 32929	MK539971	MK540041	–	MK540233	MK540167	-	Present study
Z. elaeocarpi	CBS 142187^{T}	MF951398	MF951263	MF951699	–	–	–	Videira *et al.* (2017)
Z. eucalypticola	CBS 142186^{T}	MF951400	MF951265	MF951701	–	–	–	Videira *et al.* (2017)
Z. eucalyptigenum	CBS 138860^{T}	KP004458	KP004486	–	KT037630	–	–	Crous *et al.* (2014c), Guatimosim *et al.* (2016)
Z. eucalyptorum	CBS 118500^{T}	KF901652	MF951266	MF951702	KF903495	KF903101	–	Quaedvlieg *et al.* (2014), Videira *et al.* (2017)
Z. fructicola	CBS 139625^{T}	KP896052	KP895922	MF951703	KP896003	KP896099	–	Huang *et al.* (2015), Videira *et al.* (2017)
Z. fructigenum	CBS 139626^{T}	KP896056	KP895926	MF951704	KP896007	KP896103	KP896149	Huang *et al.* (2015), Videira *et al.* (2017)
Z. gahniicola	CBS 143422^{T}	MG386050	MG386103	–	–	–	–	Crous *et al.* (2017b)
Z. grevilleae	CBS 124107^{T}	FJ839634	FJ839670	MF951705	–	–	–	Crous *et al.* (2009a), Videira *et al.* (2017)
Z. gupoyu	CBS 122099	MF951401	MF951267	MF951706	–	–	–	Videira *et al.* (2017)
Z. hakeae	CBS 142185^{T}	MF951402	MF951268	MF951707	–	–	–	Videira *et al.* (2017)
Z. indonesianum	CBS 139627^{T}	KF901739	KF902086	MF951710	–	KF903377	–	Quaedvlieg *et al.* (2014), Videira *et al.* (2017)
Z. iteae	CBS 113094^{T}	MF951405	MF951271	MF951711	–	–	–	Videira *et al.* (2017)
Z. lonicericola	CBS 125008^{ET}	KF251283	KF251787	MF951712	–	KF253231	KF252765	Quaedvlieg *et al.* (2013), Videira *et al.* (2017)
Z. macluricola	BRIP 52143^{T}	GU108499	–	–	–	–	–	Shivas *et al.* (2009)
Z. musae	CBS 122477^{T}	EU514291	–	–	EU514346	–	–	Arzanlou *et al.* (2008)
Z. musae-banksii	CBS 121710^{T}	EU041795	EU041852	MF951716	–	–	–	Arzanlou *et al.* (2007), Videira *et al.* (2017)
Z. musicola	CBS 122479^{T}	EU514294	MF951275	MF951717	–	–	–	Arzanlou *et al.* (2008), Videira *et al.* (2017)
Z. musigenum	CBS 365.36^{T}	EU041801	EU041858	–	–	–	–	Arzanlou *et al.* (2007)
Z. nocoxi	CBS 125009^{T}	KF251284	KF251788	MF951719	–	KF253232	KF252766	Quaedvlieg *et al.* (2013), Videira *et al.* (2017)
Z. pitospori	CBS 122274	MF951406	MF951276	MF951720	–	–	–	Videira *et al.* (2017)
Z. podocarpi	CBS 142529^{T}	KY979766	KY979821	–	KY979861	–	KY979930	Crous *et al.* (2017a)
Z. proteacearum	CBS 116003	FJ839635	FJ839671	MF951721	KF903478	–	KF903070	Crous *et al.* (2009a), Quaedvlieg *et al.* (2014), Videira *et al.* (2017)
Z. pseudoparkii	CBS 110999^{T}	DQ303023	JF700965	MF951723	KF903419	KF903273	KF902977	Crous *et al.* (2006), Quaedvlieg *et al.* (2011, 2013), Videira *et al.* (2017)
Z. pseudotsugae	rapssd	EF114687	EF114704	–	–	–	–	Winton *et al.* (2007)
Z. pseudovespa	CBS 121159^{T}	MF951407	KF901836	MF951724			KF902812	Quaedvlieg *et al.* (2013, 2014), Videira *et al.* (2017)
Z. queenslandicum	CBS 122475^{T}	EU514295	MF951277	MF951725	–	–	–	Arzanlou *et al.* (2008), Videira *et al.* (2017)
Z. rothmanniae	CBS 137983^{T}	KJ869135	MH878613	–	–	–	–	Crous *et al.* (2014c), Vu *et al.* (2019)
Z. scaevolicola	CBS 127009^{T}	KF251285	KF251789	MF951726	–	KF253233	KF252767	Quaedvlieg *et al.* (2013), Videira *et al.* (2017)
Z. schini	CBS 142188^{T}	MF951408	MF951278	MF951727	–	–	–	Videira *et al.* (2017)

Table 22. (Continued).

Species	**Isolates**[1]	**GenBank accession numbers**[2]						**References**
		ITS	**LSU**	***rpb2***	***act***	***tef1***	***tub2***	
Z. strelitziae	CBS 121711^{T}	EU041803	EU041860	MF951729	–	–	–	Arzanlou *et al.* (2007), Videira *et al.* (2017)
Z. suregadae	MFLU 12-2212^{HT}	KC677914	KC677939	–	–	–	–	Phengsintham *et al.* (2013)
Z. syzygii	CBS 133580^{T}	KC005777	KC005798	MF951730	–	–	–	Crous *et al.* (2012), Videira *et al.* (2017)
Z. thailandicum	CBS 145027^{T}	MK539970	MK540040	–	–	–	–	Present study
Z. tsugae	ratstk	EF114688	EF114705	–	–	–	–	Winton *et al.* (2007)
Z. velutinum	CBS 101948^{ET}	EU041781	EU041838	MF951731	–	–	–	Arzanlou *et al.* (2007), Videira *et al.* (2017)
Z. xenoparkii	CBS 111185^{T}	DQ303028	JF700966	MF951732	KF903438	KF903274	KF902978	Crous *et al.* (2006), Quaedvlieg *et al.* (2011, 2014), Videira *et al.* (2017)

[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; MFLU: Mae Fah Luang University herbarium, Chiang Rai, Thailand; rapssd and ratstk were not specified in the original publications. $^{T,\ ET,\ HT}$ and ^{NT} indicate ex-type, ex-epitype, holotype and ex-neotype strains, respectively.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; LSU: partial large subunit (28S) nrRNA gene; *rpb2*: partial DNA-directed RNA polymerase II second largest subunit gene; *act*: partial actin gene; *tef1*: partial translation elongation factor 1-alpha gene; *tub2*: partial β-tubulin gene.

Basionym: *Poaceicola arundinicola* Wanas. *et al.*, Fungal Diversity 89: 135. 2018.

Description and illustration: Wanasinghe *et al.* (2018).

Septoriella arundinis (W.J. Li *et al.*) Y. Marín & Crous, ***comb. nov.*** MycoBank MB829679.
Basionym: *Poaceicola arundinis* W.J. Li *et al.*, Mycosphere 6: 698. 2015.

Description: Li *et al.* (2015).

Septoriella bromi (Wijayaw. *et al.*) Y. Marín & Crous, ***comb. nov.*** MycoBank MB829680.
Basionym: *Poaceicola bromi* Wijayaw. *et al.*, Mycosphere 6: 698. 2015.

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

Septoriella dactylidicola Y. Marín & Crous, ***nom. nov.*** MycoBank MB829681.
Replaced synonym: *Poaceicola dactylidis* Tibpromma *et al.*, Mycosphere 8: 755. 2017, non *Septoriella dactylidis* (Wanas. *et al.*) Y. Marín & Crous. 2019.

Description and illustration: Thambugala *et al.* (2017).

Septoriella dactylidis (Wanas. *et al.*) Y. Marín & Crous, ***comb. nov.*** MycoBank MB829682.
Basionym: *Vagicola dactylidis* Wanas. *et al.*, Phytotaxa 6: 725. 2015.

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

Septoriella elongata (Wehm.) Y. Marín & Crous, ***comb. nov.*** MycoBank MB829683.
Basionym: *Leptosphaeria elongata* Wehm., Mycologia 44: 633. 1952.
Synonym: *Poaceicola elongata* (Wehm.) W.J. Li *et al.*, Mycosphere 6: 701. 2015.

Description and illustration: Wehmeyer (1952).

Septoriella forlicesenica (Thambug. *et al.*) Y. Marín & Crous, ***comb. nov.*** MycoBank MB829684.
Basionym: *Poaceicola forlicesenica* Thambug *et al.*, Mycosphere 8: 756. 2017.

Description and illustration: Thambugala *et al.* (2017).

Septoriella garethjonesii (Thambug. *et al.*) Y. Marín & Crous, ***comb. nov.*** MycoBank MB829685.
Basionym: *Poaceicola garethjonesii* Thambug *et al.*, Mycosphere 8: 756. 2017.

Description and illustration: Thambugala *et al.* (2017).

Septoriella germanica Crous, R.K. Schumach. & Y. Marín, ***sp. nov.*** MycoBank MB829701. Fig. 68.

Etymology: Name refers to Germany, from where this fungus was isolated.

Conidiomata solitary, pycnidial, erumpent, globose, brown, 180–220 μm diam, *in vivo* gregarious, caespitose or in rows, but also pseudostromatic, up to 300 μm diam, with central ostiole, 30–40 μm diam; *conidiomatal wall* of 3–4 layers of brown cells of *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth-walled, globose to ampulliform, phialidic, 4–6 × 4–5 μm. *Conidia* solitary, scolecosporous, fusoid to subcylindrical, apex subobtuse, base truncate, straight to sligthly curved, 3–6-septate, golden-brown, smooth-walled, granular with mucoid caps at each end, (35–)37–42(–46) × 3(–3.5) μm, *in vivo* 29–46 × 3–4.5 μm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium, covering dish in 2 wk. On MEA, PDA and OA surface olivaceous grey, reverse iron-grey.

Typus: **Germany**, near Berlin, on dead culm of *Phragmites australis* (*Poaceae*), 16 Apr. 2016, R.K. Schumacher, HPC 1168 (**holotype** CBS H-23875, culture ex-type CBS 145372 = CPC 30511).

Notes: *Septoriella germanica* is related to *Sep. artemisiae.* However, both species differ in the size of the conidia [15–25 × 2–2.5 μm in *Sep. artemisiae vs.* (35–)37–42(–46) × 3(–3.5) μm in *Sep. germanica*], as well as in the conidial septation (2–4 in *Sep. artemisiae vs.* 3–6 μm in *Sep. germanica*). *Septoriella germanica* was isolated from *Phragmites australis* (*Poaceae*), while *Sep. artemisiae* was found on *Artemisia austriaca* (*Asteraceae*).

Septoriella hibernica Crous, Quaedvl. & Y. Marín, ***sp. nov.*** MycoBank MB829703.

Etymology: Name refers to Ireland, where this fungus was collected.

Culture sterile. *Septoriella hibernica* differs from its closest phylogenetic neighbour, *Septoriella subcylindrispora* by unique fixed alleles in the ITS locus based on the alignment deposited in TreeBASE (S23834): positions 5 (T), 33 (T), 34 (A), 46 (T), 61 (A), 89 (T), 477 (A), 479 (T), 480 (A), 512 (T), 528 (G), 534 (G).

Culture characteristics: Colonies erumpent, spreading, covering dish in 2 wk, with fluffy aerial mycelium and even margins. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus: **Ireland**, on unidentified grass species (*Poaceae*), Mar. 2014, W. Quaedvlieg (**holotype** CBS H-23874, culture ex-type CBS 145371 = CPC 24290).

Notes: *Septoriella hibernica* remained sterile on all media tested. It is related to *Sep. subcylindrispora*, but the ITS sequences of both species showed only 97.75 % of nucleotide similarity (Identities = 522/538, 3 gaps).

Septoriella hollandica Crous, Quaedvl. & Y. Marín, ***sp. nov.*** MycoBank MB829702. Fig. 69.

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

Ascomata solitary, erumpent, globose, brown, 150–180 µm diam with central ostiole; *conidiomatal wall* of 3–4 layers of brown cells of *textura angularis. Pseudoparaphyses* hyphae-like, hyaline, smooth-walled, branched, septate, 1.5–2 µm diam. *Asci* subcylindrical, flexuous, bitunicate, with well-defined apical chamber, 1–1.5 µm diam, fasciculate, short stipitate, 70–90 × 8–10 µm. *Ascospores* bi- to triseriate, fusoid-ellipsoid, 5-septate, constricted at median septum, medium brown, smooth-walled, guttulate, widest above median septum, (27–)28–30(–32) × (4–)4.5(–5) µm.

Culture characteristics: Colonies flat, spreading, covering dish in 2 wk with moderate aerial mycelium. On MEA surface vinaceous buff, reverse sienna; on PDA surface isabelline, reverse hazel; on OA surface saffron.

Typus: **The Netherlands**, Oosterbeek, on leaves of *Phragmites australis* (*Poaceae*), 24 Jan. 2014, W. Quaedvlieg (**holotype** CBS H-23877, culture ex-type CBS 145374 = CPC 24109).

Notes: *Septoriella hollandica* is related to *Sep. chlamydospora* and *Sep. tridentina*. *Septoriella hollandica*, as well as *Sep. chlamydospora* and *Sep. tridentina*, produce sexual morphs in culture. *Septoriella hollandica* can be easily distinguished from *Sep. chlamydospora* by its 5-septate ascospores, being 9-septate in *Sep. chlamydospora*. *Septoriella tridentina* is the only species of this complex that produces ascospores surrounded by a mucilaginous sheath. The asexual morph was reported only for *Sep. chlamydospora*. However, as it was mentioned above, the asexual morph described in *Sep. chlamydospora* (Jayasiri *et al.* 2015) corresponds to chains of chlamydospores instead of scolecosporous conidia typical of *Septoriella*. *Septoriella hollandica* was isolated from *Phragmites australis*, while the other two species were found on *Dactylidis* spp.

Septoriella italica (Thambug. *et al.*) Y. Marín & Crous, ***comb. nov.*** MycoBank MB829704.

Basionym: *Poaceicola italica* Thambug. *et al.*, Mycosphere 8: 759. 2017.

Description: Thambugala *et al.* (2017).

Septoriella muriformis (Ariyaw. *et al.*) Y. Marín & Crous, ***comb. nov.*** MycoBank MB829705.
Basionym: *Allophaeosphaeria muriformis* Ariyaw. *et al.*, Fungal Diversity 72: 137.

Descriptions and illustrations: Liu *et al.* (2015), Thambugala *et al.* (2017).

Septoriella neoarundinis Y. Marín & Crous, ***nom. nov.*** MycoBank MB829706.
Replaced synonym: ***Vagicola arundinis*** Phukhams., Camporesi & K.D. Hyde, ***sp. nov.*** MycoBank MB831056, non *Septoriella arundinis* (W.J. Li *et al.*) Y. Marín & Crous. 2019.
Synonym: *Vagicola arundinis* Phukhams. *et al.* Mycosphere 8: 763. 2017. (nom. inval., Art. 40).

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

Description and illustration: Thambugala *et al.* (2017).

Typus: **Italy**, Province of Marsignano, Predappio, on a dead stem of *Arundo plinii* (*Poaceae*), 10 Nov. 2014, E. Camporesi IT 2223A (**holotype** MFLU 17-0016, ex-type living culture MFLUCC 15-0027).

Notes: This species was initially introduced by Thambugala *et al.* (2017) as *Vagicola arundinis*. However, it was invalid since two different holotype numbers were cited. Therefore, this species is validated here and a new name in *Septoriella* is proposed, using a new epithet since *Sep. arundinis* is occupied.

Septoriella neodactylidis Y. Marín & Crous, ***nom. nov.*** MycoBank MB829707.
Replaced synonym: *Allophaeosphaeria dactylidis* Wanas. *et al.*, Fungal Diversity 72: 137. 2015, non *Septoriella dactylidis* (Wanas. *et al.*) Y. Marín & Crous. 2019.

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

Septoriella pseudophragmitis Crous, Quaedvl. & Y. Marín, ***sp. nov.*** MycoBank MB829708. Fig. 70.

Etymology: Name refers to its morphological similarity with *Sep. phragmitis*, which occurs on the same host.

Conidiomata solitary, pycnidial, erumpent, globose, brown-black, 200–250 µm diam with central ostiole; *conidiomatal wall* of 6–8 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth-walled, globose to ampulliform, phialidic, 4–10 × 4 µm. *Conidia* solitary, subcylindrical, golden-brown, guttulate, smooth-walled, apex obtuse, base truncate, 3(–6)-septate, with mucoid caps at each end, (20–)24–28(–32) × (3–)3.5(–4) µm.

Culture characteristics: Colonies erumpent, spreading, covering dish after 2 wk at 25 °C, with moderate aerial mycelium and feathery margins. On MEA surface olivaceous grey, reverse iron-grey.

Typus: **The Netherlands**, on leaves of *Phragmites* sp. (*Poaceae*), 5 Mar. 2014, W. Quaedvlieg (**holotype** CBS-H 23904, culture ex-type CBS 145417 = CPC 24166).

Notes: *Septoriella pseudophragmitis* is similar to *Sep. phragmitis*, which is reported from the same host, *Phragmites* (*Poaceae*).

These species differ in the size of their conidiomata (up to 250 µm diam in *Sep. pseudophragmitis vs.* 350 µm diam in *Sep. phragmitis*) and conidia [(20–)24–28(–32) × (3–)3.5(–4) µm in *Sep. pseudophragmitis vs.* (29–)32–40(–46) × 3(–3.5) µm diam in *Sep. phragmitis*], as well as in the conidial septation, being mostly 3-septate in *Sep. pseudophragmitis* and 5-septate in *Sep. phramitis*. Based on our phylogenetic analysis, *Septoriella pseudophragmitis* is related to *Sep. allojunci*. However, *Sep. allojunci* produces smaller conidiomata (up to 150 µm) and larger conidia (48–70 × 3–6.6 µm). Moreover, *Sep. allojunci* was isolated from *Juncus* (*Juncaceae*).

Septoriella rosae (Mapook *et al.*) Y. Marín & Crous, ***comb. nov.*** MycoBank MB829713.
Basionym: *Poaceicola rosae* Mapook *et al.*, Fungal Diversity 89: 136. 2018.

Description and illustration: Wanasinghe *et al.* (2018).

Septoriella subcylindrospora (W.J. Li *et al.*) Y. Marín & Crous, ***comb. nov.*** MycoBank MB829709.
Basionym: *Allophaeosphaeria subcylindrospora* W.J. Li *et al.*, Fungal Diversity 75: 100. 2015.

Description and illustration: Ariyawansa *et al.* (2015a).

Septoriella vagans (Niessl) Y. Marín & Crous, ***comb. nov.*** MycoBank MB829710.
Basionym: *Pleospora vagans* Niessl, Verh. nat. Ver. Brünn 14: 174. 1876.
Synonym: *Vagicola vagans* (Niessl) O.E. Erikss. *et al.*, Fungal Diversity 75: 115. 2015.

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

Arezzomyces Y. Marín & Crous, ***gen. nov.*** MycoBank MB829711.

Etymology: Name reflects the Italian province Arezzo where it was collected.

Ascomata solitary, scattered, immersed to erumpent, obpyriform, dark brown to black, coriaceous, with ostiole filled with hyaline cells, appearing as a white ring around ostiole; *necks* papillate, black, smooth; *ascomatal wall* comprising 6–8 layers, outer layer heavily pigmented, comprising blackish to dark brown, thick-walled cells of *textura angularis*, inner layer composed of brown, thin-walled cells of *textura angularis*. *Hamathecium* comprising numerous, filamentous, branched, septate pseudoparaphyses. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical, pedicel furcate, rounded and thick-walled at the apex, with an ocular chamber. *Ascospores* mostly uniseriate, initially hyaline, becoming yellowish brown at maturity, ellipsoidal, muriform, with 6–8 transverse septa, 3–7 vertical septa, strongly constricted at the central septa, weakly constricted at the other septa, with conical and narrowly rounded ends, lacking a mucilaginous sheath. *Asexual morph* not observed.

Culture characteristics: Colonies spreading, surface erumpent, with moderate aerial mycelium, and feathery margins. On MEA, PDA and OA surface dirty white; reverse dirty white to luteous.

Type species: *Arezzomyces cytisi* (Wanas. *et al.*) Y. Marín & Crous. Holotype and ex-type cultures: MFLU 15-1502, MFLUCC 15-0649.

Notes: *Arezzomyces* is introduced to accommodate *Allophaeosphaeria cytisi* since, based on phylogenetic data, it is located in an independent lineage distant to the clade representing the genus *Septoriella*. Moreover, based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Ophiosimulans tanaceti* [GenBank KU738890; Identities = 534/586 (91 %), 11 gaps (1 %)], *Ophiobolus cirsii* [GenBank KM014664; Identities = 514/566 (91 %), 22 gaps (1 %)], and *Chaetosphaeronema hispidulum* [GenBank KX096655; Identities 535/588 (91 %), 22 gaps (3 %)]. *Arezzomyces cytisi* is a saprobe found on dead herbaceous branches of *Cytisus*.

Arezzomyces cytisi (Wanas. *et al.*) Y. Marín & Crous, ***comb. nov.*** MycoBank MB829712.
Basionym: *Allophaeosphaeria cytisi* Wanas. *et al.,* Fungal Diversity 75: 97. 2015.

Description and illustration: Ariyawansa *et al.* (2015a).

Typus: **Italy**, Arezzo Province, Casuccia di Micheli in Quota, dead and hanging branches of *Cytisus* sp. (*Fabaceae*), 20 Jun. 2012, E. Camporesi (**holotype** MFLU 15-1502, culture ex-type MFLUCC 15-0649).

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Setophoma Gruyter *et al.*, Mycologia 10: 1077. 2010. Fig. 71.

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

Type species: *Setophoma terrestris* (H.N. Hansen) Gruyter *et al.*, basionym: *Phoma terrestris* H.N. Hansen. Lectotype and ex-lectotype strain designated by de Gruyter *et al.* (2010): CBS H-20311, CBS 335.29.

DNA barcode (genus): LSU. Fig. 28.

DNA barcodes (species): ITS, *rpb2*, *tef1, tub2*. Table 17. Fig. 72.

Ascomata scattered, gregarious, immersed, visible as raised, minute black dots on host surface, uniloculate, globose to subglobose, glabrous, brown to dark brown, ostiole central, with minute papilla; *ascomatal wall* thin, of equal thickness, composed of pseudoparenchymatous cells, arranged in flattened *textura angularis* to *textura prismatica*. *Hamathecium* composed of numerous, filiform, broad cellular pseudoparaphyses, with distinct septa, anastomosing at apex. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short pedicellate, apically rounded, with well-developed narrowly ocular chamber. *Ascospores* overlapping, 2-seriate, phragmosporous, cylindrical to cylindrical-clavate, hyaline, 3-septate, usually enlarged at the second cell from apex, smooth-walled with large guttules. *Conidiomata* pycnidial, solitary to confluent, superficial or submerged in agar, globose to subglobose, setose, with papillate necks, honey to olivaceous or olivaceous black, with 2–7(–11) layers of pseudoparenchymatal cells. *Conidiogenous cells* hyaline, monophialidic. *Conidia* aseptate, ellipsoidal to subcylindrical or subfusoid, guttulate (adapted from Quaedvlieg *et al.* 2013, Phookamsak *et al.* 2014a).

Culture characteristics: Colonies spreading with sparse to moderate aerial mycelium, smooth or folded surface, even or lobate margins. On PDA surface iron-grey or grey olivaceous with outer region iron-grey; reverse olivaceous grey or iron-grey. On MEA surface olivaceous grey or umber with patches of apricot and dirty white; reverse ochreous or cinnamon with patches of olivaceous grey. On OA surface isabelline or iron-grey surrounded by orange to apricot diffuse pigment layer in agar.

Optimal media and cultivation conditions: OA and SNA at 25 °C under continuous near-ultraviolet light to promote sporulation. Sterile bamboo pieces on WA to induce sporulation of the sexual morph.

Distribution: Worldwide.

Hosts: Mainly on members of *Poaceae*, but also of *Amaryllidaceae* and *Asteraceae*, among others.

Disease symptoms: Leaf spots and necrosis, leaf dieback, and pink root.

Notes: *Setophoma* was introduced by de Gruyter *et al.* (2010) to accommodate two species previously placed in *Pyrenochaeta*, *i.e*. *Pyr. sacchari* and *Pyr. terrestris*. *Setophoma* is characterised by pycnidial conidiomata covered by setae, phialidic conidiogenous cells, and hyaline, ellipsoidal to subcylindrical, aseptate, guttulate conidia (de Gruyter *et al.* 2010, Quaedvlieg *et al.* 2013). When *Setophoma* was introduced, the sexual morph had not been observed. Subsequently, Phookamsak *et al.* (2014a) reported the sexual morph of this genus. It was found causing leaf spots of sugarcane (*Saccharum officinarum*), and based on the phylogenetic data it was shown to be the sexual morph of *Set. sacchari*. This sexual morph is similar to *Phaeosphaeria* species, producing ascospores with three septa with the second cell from the apex being swollen; these cells differ in colour (hyaline in *Setophoma vs.* yellowish to brown in *Phaeosphaeria*).

Setophoma encompasses pathogenic or saprobic species associated with monocotyledonous plants (de Gruyter *et al.* 2010). The type species, *Set. terrestris*, causes pink root on *Allium* spp., and also on *Zea mays* and *Oryza sativa*, but it is asymptomatic on other hosts (Farr & Rossman 2019). *Setophoma vernoniae* produces leaf spots on *Vernonia polyanthes* (Crous *et al.* 2014b), while *Set. sacchari* is considered a weak pathogen of members of the *Poaceae* that is only noticeable when conditions are favourable for disease spread, and causes leaf spots and necrosis and leaf dieback (Farr & Rossman 2019).

In our phylogenetic analysis based on ITS and LSU (Fig. 28), the clade representing the genus *Setophoma* is well-supported (95 % BS / 1 PP). However, the most recently described species, *Set. cyperi*, is not located in that clade, representing a new genus in the family *Phaeosphaeriaceae*.

At the proof stage of this paper, a new publication appeared on *Setophoma* (Liu *et al.* 2019), which contains four new species.

References: de Gruyter *et al.* 2010, Quaedvlieg *et al.* 2013, Phookamsak *et al.* 2014a (morphology and phylogeny).

Setophoma brachypodii Crous, R.K. Schumach. & Y. Marín, ***sp. nov.*** MycoBank MB829669.

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

Culture sterile. *Setophoma brachypodii* differs from its closest phylogenetic neighbour, *Setophoma terrestris* by unique fixed alleles in two loci based on alignments of the separate loci deposited in TreeBASE (S23834): LSU positions 42 (G), 67 (C), 75 (C), 77 (T), 79 (G), 81 (C), 82 (A), 89 (C), 133 (C), 144 (G), 145 (C), 146 (C), 147 (T), 150 (G), 302 (C), 348 (T), 380 (C), 392 (A), 437 (T), 445 (T), 446 (C), 473 (A), 477 (G), 601 (G), 636 (T), 637 (T), 638 (A); ITS positions 32 (C), 34 and 35 (indels), 36 (T), 37 (T), 38 (T), 42 (G), 43 (T), 44 (A), 54 (C), 56 (G), 57 (T), 58 (T), 59 (C), 60 (G), 61 (C), 62 (T), 63 (G), 64 (T), 66 (G), 67 (T), 72 (T), 77 (G), 78 (T), 80 (T), 99 (T), 100 (G), 101 (A), 103 (C), 114 (C), 117 (G), 118 (T), 119 (A), 121 (C), 122 (T), 124 (C), 130 (A) 138 (C), 140 (A), 143 (T), 146 (A), 148 (C), 172 (A), 176 (T), 178 (A), 180 (T), 182 (A), 186 (indel), 354 (T), 379 (T), 381 (indel), 388 (T), 389 (G), 390 (G), 391 (T), 392 (C), 393 (C), 394 (T), 395 (C), 396 (T), 399 (G), 400 (A), 401 (C), 402 (C), 409 (A), 418 (A), 419 (T), 433 (G), 434 (T), 435 (A), 441 (G), 444 (T), 467 (A), 470 (indel), 473 (T), 475 (C), 477 (A), 478 (C), 479 (T), 482 (A), 485 (C), 486 (C), 490 (A), 495–498 (indels), 499 (C), 500 (C), 502 (T), 504 (A), 506 (T), 507 (A), 511 (C).

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and even, lobate margins, reaching 60 mm diam after 2 wk. On MEA, PDA and OA, surface and reverse olivaceous grey.

Typus: **Belgium**, Dinant, 173 m a.s.l., on border of calcareous meadow, on a dead and attached leaf of *Brachypodium sylvaticum* (*Poaceae*), 2 Nov. 2016, L. Bailly & R.K. Schumacher, HPC 1503, RKS 1 (**holotype** CBS H-23905, culture ex-type CBS 145418 = CPC 32492).

Notes: *Setophoma brachypodii* remained sterile on all media tested, and the original specimen was depleted, hence we could not describe it based on morphology. This is the first species of *Setophoma* reported on *Brachypodium*.

Setophoma pseudosacchari Crous & Y. Marín, ***sp. nov.*** MycoBank MB829670. Fig. 73.

Etymology: Named after its closely phylogenetic relation to *Setophoma sacchari*.

Ascomata developing on OA, solitary, erumpent, brown, 200–300 µm diam, globose, with large central ostiole, 30–40 µm diam; *ascomatal wall* of 3–4 layers of brown cells of *textura angularis*, ascomata setose; *setae* brown, flexuous, thick-walled, septate, base verruculose, with slight taper to obtuse apex, up to 150 µm long. *Pseudoparaphyses* hyphae-like, anastomosing, branched, septate, hyaline, occurring intermingled among asci. *Asci* bitunicate, ellipsoid to subcylindrical, hyaline, curved to straight, fasciculate, apex obtuse, with well-defined ocular chamber, 2 µm diam, stipitate, 70–100 × 10–13 µm. *Ascospores* bi- to triseriate, fusoid-ellipsoid with subobtuse ends, straight, 3-septate, widest in second cell from apex, prominently guttulate, hyaline, smooth-walled, (22–)25–30 × (5.5–)6 µm. *Conidiomata* developing on SNA, solitary to aggregated, erumpent, brown, globose, 200–300 µm diam, with 1–2 ostioles, lacking setae; *conidiomatal wall* of 2–3 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining inner cavity, dissolving at maturity, hyaline, smooth-walled, globose to ampulliform, phialidic, 4–6 × 5–6 µm. *Conidia* solitary, aseptate, straight to slightly curved, subcylindrical to fusoid-ellipsoid, apex obtuse, base truncate, hyaline, smooth-walled, guttulate, (8–)11–12(–14) × (3–)4 µm.

Culture characteristics: Colonies erumpent, spreading, surface folded, with moderate aerial mycelium and even, lobate margins, reaching 55 mm diam. On MEA surface peach, outer region scarlet, reverse sienna; on PDA surface umber, outer region saffron, reverse sienna with patches of saffron; on OA surface sienna with patches of saffron.

Typus: **France**, La Réunion Island, leaf spots on *Saccharum officinarum* (*Poaceae*), May 2015, P.W. Crous, HPC 296 (**holotype** CBS H-23876, CBS 145373 = CPC 26421).

Notes: This species is closely related to *Nph. sacchari*, which is a species also isolated from sugarcane. However, the ITS sequences of the type material of both species showed only a 97.68 % of nucleotide similarity. Unfortunately, *tef1* and *tub2* sequences of *Nph. sacchari* are not available in order to compare both species. These species produce both the sexual and asexual morphs, with morphological differences most obvious in the sexual morph. *Neosetophoma pseudosacchari* can be easily distinguished by its larger ascomata (up to 300 µm diam in *Nph. pseudosacchari vs.* up to 180 µm diam in *Nph. sacchari*), asci [70–100 × 10–13 µm in *Nph. pseudosacchari vs.* 60–75(–85) × 12–15(–17) µm in *Nph. sacchari*] and ascospores [(22–)25–30 × (5.5–)6 µm in *Nph. pseudosacchari vs.* 20–23(–25) × 5–6 µm in *Nph. sacchari*].

Wingfieldomyces Y. Marín & Crous, ***gen. nov.*** MycoBank MB829671. Table 18. Fig. 74.

Etymology: Named in honour of its collector, Prof. dr M.J. Wingfield, who contributed greatly to the elucidation of African fungal biodiversity.

Ascomata immersed on host, erumpent in culture, black, globose, with central ostiole; *ascomatal wall* of 3–4 layers of dark brown cells of *textura angularis*. *Pseudoparaphyses* intermingled among asci, hyaline, septate, branched prominently, constricted at septa. *Asci* bitunicate with apical chamber, subcylindrical, hyaline, smooth, fasciculate, stipitate, 8-spored. *Ascospores* tri- to multiseriate, fusoid with subobtusely rounded ends, finely verruculose, red-brown, guttulate, 2-septate, slightly constricted at septa, with central cell somewhat swollen.

Culture characteristics: Colonies spreading, erumpent surface, with moderate aerial mycelium, margins feathery. On MEA, PDA and OA surface dirty white; reverse dirty white to luteous.

Type species: *Wingfieldomyces cyperi* (Crous & M.J. Wingf.) Y. Marín & Crous. Holotype and ex-type cultures: CBS H-22622, CBS 141450 = CPC 25702.

Notes: *Wingfieldomyces* is introduced to accommodate *Set. cyperi* since, based on phylogenetic data, it is located in an independent lineage distant to the clade representing the genus *Setophoma*. Moreover, based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *Pringsheimia euphorbiae* [GenBank NR_145344; Identities = 456/500 (91 %), 8 gaps (1 %)] and *Phaeosphaeria caricis* [GenBank KY090633; Identities 439/485 (91 %), 12 gaps (2 %)]. It only produces a sexual morph in culture, characterised by tri- to multiseriate, 2-septate, red-brown ascospores, while *Setophoma* produces both morphs and 2-seriate, 3-septate, hyaline ascospores with the second cell from the apex becoming swollen. *Wingfieldomyces* is associated with leaf scorch symptoms on *Cyperus*.

Wingfieldomyces cyperi (Crous & M.J. Wingf.) Y. Marín & Crous, ***comb. nov.*** MycoBank MB829672. Fig. 74.
Basionym: *Setophoma cyperi* Crous & M.J. Wingf., Persoonia 36: 385. 2016.

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

Typus: **South Africa**, Eastern Cape Province, Haga Haga, on leaves of *Cyperus sphaerocephala* (*Cyperaceae*), Dec. 2014, M.J. Wingfield (**holotype** CBS H-22622, culture ex-type CPC 25702 = CBS 141450).

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Stagonosporopsis Died., Ann. Mycol. 10: 142. 1912. Emend. Aveskamp *et al.*, Stud. Mycol. 65: 44. 2010. Fig. 75.

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

Type species: *Stagonosporopsis boltshauseri* (Sacc.) Died., designated as lectotype by Clements & Shear (1931), basionym: Ascochyta *boltshauseri* Sacc. = *Stagonosporopsis hortensis* (Sacc. & Malbr.) Petr., basionym: *Hendersonia hortensis* Sacc. & Malbr. Representative strain of *Sta. hortensis*: CBS 572.85 = PD 79/269.

DNA barcode (genus): LSU.

DNA barcodes (species): ITS*, rpb2, tub2*. Table 19. Fig. 76.

Ascomata pseudothecial, globose to subglobose, sometimes with a somewhat conical neck. *Asci* cylindrical or subclavate, 8-spored, biseriate. *Ascospores* ellipsoid, fusoid or obovoid, uniseptate, guttulate, sometimes with a gelatinous sheath. *Conidiomata* pycnidial, globose to subglobose, glabrous or with hyphal outgrowths, superficial on agar surface or immersed, solitary or confluent, ostiolate or poroid, occasionally papillate; *conidiomatal wall* pseudoparenchymatous, 2–6 layered, with an outer wall composed of 1–3 layers of brown to olivaceous cells. *Conidiogenous cells* phialidic, hyaline, simple, smooth-walled, ampulliform or doliiform. *Conidia* often dimorphic: mainly aseptate, hyaline, ellipsoid to subglobose, thin-walled, smooth-walled, eguttulate or with several polar or scattered guttules; second type of *conidia* larger in size, can be produced both *in vivo* and *in vitro* in the same pycnidia as the other type of conidia, 0–3-septate.

Culture characteristics: Colonies on OA regular to somewhat irregular, colourless, buff, luteous to ochraceous or amber, or olivaceous grey to greenish grey, with scarce or abundant floccose white to pale salmon, or olivaceous grey aerial mycelium.

Optimal media and cultivation conditions: On OA at 20–24 °C under near-ultraviolet light (13 h light, 11 h dark) to induce sporulation of the asexual morph, while MEA stimulates pigmentation and crystal formation. Changes in colour of the fungal cultures upon a sudden increase of pH (NaOH spot test), which may be used for taxonomic characterisation, are best observed on OA.

Distribution: Worldwide.

Hosts: Associated with at least 30 plant genera in *Asteraceae*, *Brassicaceae*, *Campanulaceae*, *Caricaceae*, *Cucurbitaceae*, *Fabaceae*, *Lamiaceae*, *Ranunculaceae*, *Solanaceae* and *Valerianaceae* as saprobes or pathogens. *Stagonosporopsis oculohominis* is the only species that is not associated with a plant host and was isolated from human corneal ulcer in the USA.

Disease symptoms: Plant stunting, seedling damping-off, leaf spots and dieback, crown rot, stem canker, flower blight, and fruit rot.

Notes: Many species of *Stagonosporopsis* are phytopathogens, causing devastating diseases on plants from various families.

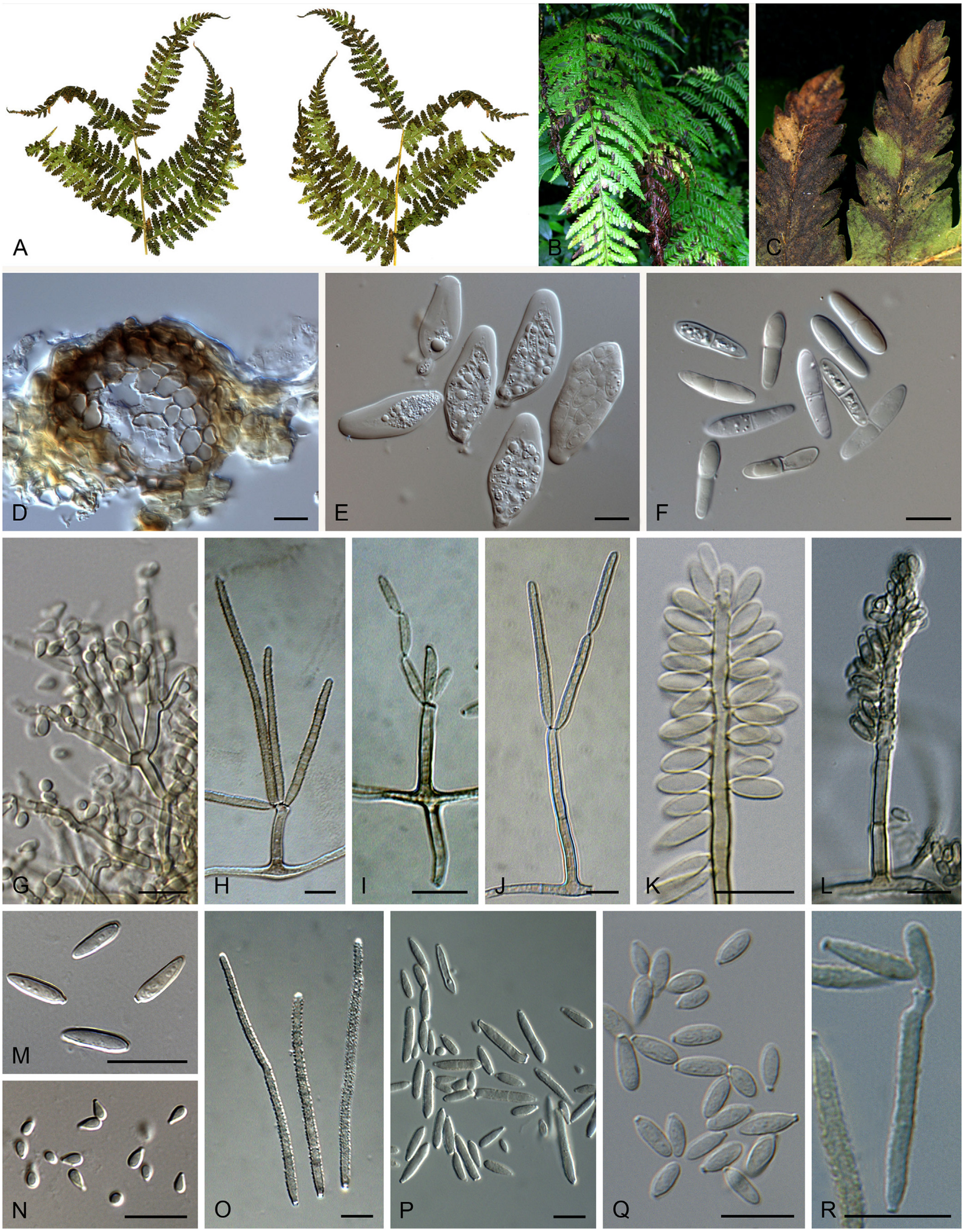

Fig. 84. *Zasmidium* spp. **A–C**. Disease symptoms caused by *Zasmidium cyatheae* (ex-type CPC 24725). **A**, **B**. Frond spots on *Cyathea delgadii*. **C**. Erumpent subcuticular ascomata, fruiting epiphyllous. **D–F**. Sexual morph of *Zasmidium cyatheae* (ex-type CPC 24725). **D**. Ascoma. **E**. Asci. **F**. Ascospores. **G–R**. Asexual morph. **G–L**. Conidiophores. **G**. *Zasmidium biverticillatum* (CBS 335.36). **H**. *Zasmidium citri-griseum* (ex-epitype CBS 139467). **I**. *Zasmidium fructigenum* (ex-type CBS 139626). **J**. *Zasmidium indonesianum* (ex-type CBS 139627). **K**. *Zasmidium musigenum* (ex-type CBS 365.36). **L**. *Zasmidium strelitziae* (ex-type CBS 121711). **M–Q**. Conidiophores. **M**. *Zasmidium biverticillatum* (CBS 335.36). **N**. *Zasmidium biverticillatum* (CBS 335.36). **O**. *Zasmidium citri-griseum* (ex-epitype CBS 139467). **P**. *Zasmidium fructicola* (ex-type CBS 139625). **Q**. *Zasmidium musigenum* (ex-type CBS 365.36). **R**. Primary and secondary conidia of *Zasmidium cellare* (ex-neotype CBS 146.36). Scale bars: 10 μm. Pictures A–F taken from Guatimosim et al. (2016); G, K–N, Q, R from Arzanlou et al. (2007); H–J, O, P from Huang et al. (2015).

Some species have a worldwide distribution, *e.g.*, *Sta. cucurbitacearum* on *Cucurbitaceae*, and *Sta. hortensis* on *Fabaceae*, while others represent important quarantine plant pathogens limited to certain geographical areas. For example, *Sta. andigena* and *Sta. chrysanthemi* are classified as A1 and A2 quarantine pathogens, respectively, by the European and Mediterranean Plant Protection Organisation (EPPO; 2016). *Stagonosporopsis tanaceti* is a destructive pathogen of pyrethrum (*Tanacetum cinerariifolium*) in Australia but has not been reported elsewhere in the world (Vaghefi *et al.* 2012). Some *Stagonosporopsis* species have been isolated from plants but their pathogenicity has not been established. For example, *Sta. dennisii* has been reported from dead stems of *Solidago* spp. but no data are available on its pathogenicity (Boerema *et al.* 2004).

Species identification based on only morphology is unreliable. *Stagonosporopsis* was originally separated from *Ascochyta* based on occasional formation of multi-septate (stagonospora-like) conidia (Diedicke 1912). However, later phylogenetic studies revealed that some *Stagonosporopsis* spp. lack the stagonospora-like spores or any features except for globose pycnidial conidiomata, and aseptate, hyaline conidia (Aveskamp *et al.* 2010). Thus, multi-locus sequence typing is essential for identification of *Stagonosporopsis* species. The emended description of the genus *Stagonosporopsis* by Aveskamp *et al.* (2010) states that the sexual morph of *Stagonosporopsis*, if present, occurs only *in vivo.* However, some strains of *Sta. chrysanthemi*, *Sta. caricae* and *Sta. inoxydabilis* have been shown to produce pseudothecial ascomata intermingled with pycnidial conidiomata on agar media (Boerema *et al.* 2004, Vaghefi *et al.* 2012).

Currently, more than 40 species are linked to the genus *Stagonosporopsis.* However, only 27 species are recognised based on molecular data (Table 19). Previous phylogenetic studies have used one locus (*act* in De Gruyter *et al.* 2012), three loci (LSU, ITS and *tub2* in Aveskamp *et al.* 2010), four loci (LSU, ITS, *tub2* and *act* in Hyde *et al.* 2014; LSU, ITS, *tub2* and *rpb2* in Chen *et al.* 2015; ITS, *tub2*, *chs* and *cal* in Stewart *et al.* 2015) and five loci (LSU, ITS, *tub2*, *act* and *tef1* in Vaghefi *et al.* 2012) for phylogenetic species recognition in *Stagonosporopsis*. However, in most cases, ITS and *tub2* sequences are sufficient for achieving resolution to species level. While ITS sequences alone may be used to distinguish *Stagonosporopsis* as a monophyletic clade within *Didymellaceae*, *tub2* fails to distinguish *Stagonosporopsis* and, thus, needs to be always combined with ITS (Chen *et al.* 2015). A phylogeny produced by *rpb2* alone is highly similar to the combined four-locus phylogeny based on LSU, ITS, *tub2* and *rpb2*. However, amplification of *rpb2* has not been successful for many *Stagonosporopsis* spp. (Chen *et al.* 2015). Likewise, while partial *cal* sequences provide high resolution for *Stagonosporopsis* species delineation, it has not been successfully amplified in some strains (Aveskamp *et al.* 2010, Vaghefi *et al.* 2012). Thus, the use of ITS and *tub2* is recommended as they will provide sufficient resolution for almost all *Stagonosporopsis* species, are easier to amplify, and are available for the majority of *Stagonosporopsis* spp. described to date (Table 19). The only two species that cannot be separated based on the LSU-ITS-*tub2* phylogeny are *S. bomiensis* and *S. papillata*, for which sequencing of *rpb2* was necessary (Chen *et al.* 2017).

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

Stagonosporopsis chrysanthemi (F. Stevens) Crous *et al.*, Australas. Pl. Pathol. 41: 681. 2012.
Basionym: *Ascochyta chrysanthemi* F. Stevens, Bot. Gaz. 44: 246. 1907.
Synonyms: *Mycosphaerella ligulicola*, K.F. Baker *et al.*, Phytopathology 39: 799. 1949.
Didymella ligulicola (K.F. Baker *et al.*) Arx, Beitr. Kryptfl. Schweiz 11: 364. 1962.
Didymella ligulicola var. ligulicola (K.F. Baker *et al.*) Arx, Stud. Mycol. 32: 199. 1990.
Phoma ligulicola var. ligulicola Boerema, Stud. Mycol. 32: 9. 1990.
Stagonosporopsis ligulicola var. ligulicola (K.F. Baker *et al.*) Aveskamp *et al.*, Stud. Mycol. 65: 46. 2010.

Typus: **USA**, North Carolina, West Raleigh, on *Chrysanthemum indicum*, Dec. 1906, F.L. Stevens (Bartholomew, Fungi Columbiani no. 2502, Field Museum of Natural History, C0004169F; designated here as **lectotype**, MBT385563); on *Chrysanthemum morifolium*, 1949, L.H. Davis [**epitype** of *Ascochyta chrysanthemi* designated here ATCC 10748, MBT385567 (preserved in a metabolically inactive state)].

Notes: Stevens (1907) described *Ascochyta chrysanthemi* on *Chrysanthemum indicum* from North Carolina; however, he did not refer to a holotype specimen in the original description. A specimen at Field Museum of Natural History (C0004169F) is chosen as lectotype, among numerous other duplicates deposited at BPI, CUP, NYBG, MSC, and various other herbaria that include collections distributed as E. Bartholomew, Fungi Columbiani 2502. Since no living cultures derived from these specimens are available, we designate ATCC 10748, isolated from *Chrysanthemum morifolium* from North Carolina, as ex-epitype culture of *Ascochyta chrysanthemi* here.

Authors: N. Vaghefi, Y. Marin-Felix, P.W. Crous & P.W.J. Taylor

Stemphylium Wallr., Flora Cryptogamica Germaniae 2: 300. 1833. Fig. 77.
Synonyms: *Scutisporium* Preuss, Linnaea 24: 112. 1821.
Epochniella Sacc., Michelia 2: 127. 1880.
Soreymatosporium Sousa da Câmara, Proposta *Stemphylium*: 18. 1930.
Thyrodochium Werderm., *Annls mycol.* 22: 188. 1942.

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

Type species: *Stemphylium botryosum* Wallr. = *Pleospora tarda* E.G. Simmons. Holotype of *Ste. botryosum*: "Ad sparagam" in herb. Wallroth, STR. Ex-type strain of *Ple. tarda*: CBS 714.68.

DNA barcode (genus): ITS.

DNA barcodes (species): *cmdA*, *gapdh.* Table 20. Fig. 78.

Ascomata pseudothecial, globose or ovoid, membranous, dark brown to black, sometimes with a slender neck. *Asci* oblong to clavate, with distinct outer and inner walls. *Ascospores* elongate to oval, with 7 horizontal and 3–5 longitudinal septa, yellowish to brown, muriform on maturity. *Conidiophores* dark due to percurrent proliferation forming *phaeodictyospores*, mostly solitary, straight or flexuous, short or long, branched or unbranched, aseptate or septate. *Conidiophores* proliferate further after a conidium is produced, producing new cells and new conidia. *Conidiogenous cells* swollen at apex, single or in group. *Conidia* olive, dark or pale brown, verrucose, oblong or muriform, with 3 or more constricted transverse and 1–2 longitudinal or oblique septa.

Culture characteristics: *Stemphylium* colonies grow rapidly on a variety of media. On most media, the colonies are velvety to cottony in texture with a pale or dark olivaceous grey, brown or brownish black colour and black pigmentation on the colony reverse. Conidial density is low in cultures produced under laboratory conditions even when the isolate is grown under alternate cycle of 12 h light and 12 h darkness on PDA. Aerial mycelia flat/effuse, woolly or compact. Margins smooth and sharp or crenate and lobate.

Optimal media and cultivation conditions: SNA for pigmentation and morphological identification, PCA for morphological identification and alternatively PDA for pigmentation and morphological identification. Incubation for 1–2 wk at moderate temperatures from 23–27 °C (depending on the species) under cool white florescent light with an 8-hr or 12-hr photoperiod.

Distribution: Worldwide.

Hosts: Many *Stemphylium* species are saprophytes and grow on plant debris and cellulose material. However, plant pathogenic species, such as *Ste. beticola*, *Ste. botryosum*, *Ste. loti*, *Ste. solani* and *Ste. vesicarium*, can cause devastating damage and significant loss of agriculturally important crops annually. *Stemphylium* spp. are pathogenic to a wide range of hosts, such as tomato, garlic, asparagus, alfalfa, lupin, lentil and cotton. The ability of pathogens to infect a wide range of crops reflects its adaptability to wide range of climatic conditions and provides better survival chances.

Disease symptoms: Leaf spot, defoliation, curling and bending of the leaf margins and stems. Lesion size differs in various hosts and can grow to encompass the entire leaf and reduce photosynthesis.

Notes: Simmons (1967) established criteria for morphological identification of various *Stemphylium* spp. and introduced *Pleospora herbarum* as the sexual morph of *Ste. botryosum*. However, Simmons (1985) subsequently reclassified *Stemphylium*/*Pleospora* holomorphs and reported *P. tarda* as the sexual morph of *Ste. botryosum* and *P. herbarum* the sexual morph of *Ste. herbarum* (Moslemi *et al.* 2017). The asexual morph *Stemphylium* has been well studied, though the sexual morph *Pleospora* is poorly defined. The number of *Pleospora* spp. identified may be as many as 1000 and they are reported to be polyphyletic. *Stemphylium* is morphologically similar to the closely related genus *Alternaria*. However, unlike *Alternaria* in which its conidia remain attached and form a chain, *Stemphylium* conidia are always solitary, arising from a conidiogenous cell with a swollen apex (Inderbitzin *et al.* 2009). Morphological features such as spore shape and size, conidiophores, ascospores and the size and time of pseudothecial maturation are important characteristics in species identification. Other features such as variation in conidial wall ornamentation and septum development are not considered as important parameters in *Stemphylium* identification (Câmara *et al.* 2002).

For phylogenetic analyses of *Stemphylium* species, *cmdA* and *gapdh* were identified as the most informative genes, and *rpb2* and *actA* as the least informative (Woudenberg *et al.* 2017). Among ITS, *cmdA* and *gapdh*, *cmdA* provides the highest resolution; however, more significant support is obtained when all three loci are combined.

Environmental factors such as temperature and moisture are key in *Stemphylium* disease development. Plant debris and seeds are primary sources of inoculum of *Stemphylium* in most host plant species. When environmental conditions are favourable, the pathogen can cause significant loss to various agricultural crops such as lupin and cotton (Boshuizen *et al.* 2004).

References: Simmons (1967), Ellis (1971), Bayaa & Erskine (1998), Câmara *et al.* (2002) (morphology); Bashi & Rotem (1975), Mwakutuya (2006) (culture characteristics); Boshuizen *et al.* (2004) (biology and life cycle); Wang *et al.* (2010) (host range); Woudenberg *et al.* (2017), Crous *et al.* (2019b) (optimal media and growing conditions).

Stemphylium rombundicum Moslemi, Y.P. Tan & P.W.J. Taylor, ***sp. nov.*** MycoBank MB829291. Fig. 79.

Etymology: Named after the famous beverage, Bundaberg Rum (Bundy Rum), produced in Bundaberg, Queensland, Australia, where the fungus was first isolated.

Conidiophores long, solitary, straight, septate, verrucose, light or dark brown, (62–)111–258(–307) µm, bearing one thickened, darkened, percurrent rejuvenation site. *Conidiogenous cells* swollen at apex, darkened, (5–)6–9(–10) µm wide. *Conidia* solitary, conidium body light brown to golden, turning into dark brown around longitudinal and transverse septa, verrucose, oblong or cylindrical, occasionally ovoid with curved apex, (27.5–)35–55.5(–61) × (10–)12.5–24(–26.5) µm, with 3–4 transverse septa, 1–2(–3) longitudinal or oblique septa per transverse sector. *Sexual morph* not observed.

Culture characteristics: Colonies on SNA after 1 wk reaching 35 mm diam, effuse, hairy or velvety, white, colourless, mycelia mostly immersed in the agar. On PDA reaching 35 mm diam, fast growing, with compact, entire, aerial mycelium, fine, woolly on the surface; reverse dark orange to dark brown in the centre with central pale brown rings growing towards the sides; thick yellow margins, and grey zones can also be seen.

Typus: **Australia**, Queensland, Bundaberg (Burnett Heads), from fruit lesions of *Solanum lycopersicum* (*Solanaceae*), 9 Aug. 2000, J. Maltby (**holotype** BRIP 27486, culture ex-type BRIP 27486).

Notes: Colonies of *Ste. lycopersici* produce a yellow dark red pigmentation diffusing out in PDA and other media (Yamamoto 1960). As *Ste. rombundicum* is closely related to species in the *Ste. lycopersici* complex, similar physiological characters can be observed on PDA. Colonies only sporulated at 23 °C under 12 h photoperiod on PDA. Against *Ste. lycopersici* in which the conidia are mostly ovoid with a pointed apex, *Ste. rombondicum* mostly contains cylindrical or oblong conidia. It is difficult to observe the longitudinal septa in conidia of *Ste. rombundicum*. Conidiophores are significantly long compared to the type *Ste. lycopersici* in which the conidiophores length do not exceed 140 µm. Conidia of *Ste. lycopersici* are significantly longer (50–74 µm × 16–23 µm) than those of *Ste. rombundicum*.

Stemphylium truncatulae Moslemi, Y.P. Tan & P.W.J. Taylor, ***sp. nov.*** MycoBank MB829282. Fig. 80.

Etymology: Named after the host species, *Medicago truncatula*, from which it was first collected.

Immature ascomata observed on SNA and PDA embedded in the agar. *Ascomata* pseudothecial, dark brown to black, globose or flask shaped, solitary or aggregated in groups of 3–5, (83.5–)185.5–186(–304) × (351–)453–483(–603) µm, with outgrowing dark mycelia; *ascomatal wall* 27–32 µm thick. *Conidiophores* solitary, straight to flexuous, mostly branched, septate or occasionally aseptate, smooth-walled, light brown, mostly 7–11 µm length, some 17–39 µm in length, bearing 2–6 thickened, pale, percurrent rejuvenation sites. *Conidiogenous cells* slender or slightly swollen at apex, pale, (5.5–)6.5–7(–9.5) µm. *Conidia* solitary, conidium body pale brown to golden or olivaceous brown, mostly smooth-walled, sometimes minutely verrucose, usually ovoid, occasionally with pointed apex, (8–)9.5–18(–21) × (14–)15.5–29.5(–32) µm, with 2–4 transverse septa, one longitudinal or oblique septa per transverse sector.

Culture characteristics: Colonies on SNA reaching 21–25 mm diam after 1 wk, with white and fluffy aerial mycelia in the centre; reverse colourless with pale olivaceous grey centre. Colonies on PDA reaching 25 mm diam after 1 wk, with white fluffy mycelia in the centre; reverse dark green to grey with thin white margins.

Typus: **Australia**, Victoria, from seeds of *Medicago truncatula* (*Fabaceae*), 10 Sep. 1982, M. Mebalds (**holotype** BRIP 14850, culture ex-type BRIP 14850).

Notes: Differs from the type species *Ste. botryosum* described by Simmons (1969) by producing significantly smaller conidia. According to Simmons (1969), conidia of *Ste. botryosum* are 24–26 µm wide and 33–35 µm long. Additionally, colonies of *Ste. botryosum* grow rapidly to 48 mm diam after 6 d of incubation at 25 °C (Hosen *et al.* 2013), while *Ste. truncatulae* is slow growing. The morphological identifications along with sequence analyses support *Ste. truncatulae* as a unique taxon closely related to the type species *Ste. botryosum* (CBS 714.68).

Stemphylium waikerieanum Moslemi, Jacq. Edwards & P.W.J Taylor, ***sp. nov.*** MycoBank MB829283. Fig. 81.

Etymology: Named after the location, Waikerie in South Australia, from where it was collected.

Immature ascomata observed on SNA after 2 wk embedded in the agar. *Ascomata* pseudothecial, dark brown to black, mostly flask-shaped or occasionally globose, solitary or aggregated in groups of 4–6, (267.5–)292–349.5(–374) × (191.5–)235.5–337(–381) µm, with outgrowing mycelia; *ascomatal wall* thin, 10–15 µm thick. *Conidiophores* solitary, straight, simple or occasionally 1-branched, septate, smooth-walled, pale brown, (29–)42–85(–98) µm long, cylindrical, enlarging apically to the site of conidium production. *Conidiogenous cells* swollen at apex, darkened, (6–)6.5–7(–7.5) µm wide. *Conidia* solitary, dark reddish brown, verrucose, ovoid, oblong or cylindrical, (18–)25–49(–52) × (10.5–)14–26(–30) µm, with 2–5 transverse septa, 1–2(–3) longitudinal or oblique septa per transverse sector, constricted at multiple darkened transverse septa.

Culture characteristics: Colonies on SNA reaching 28 mm diam after 1 wk with flat, entire and fluffy aerial mycelia in the centre, sub-hyaline. On PDA reaching 20 mm diam after 1 wk, compact, entire, aerial mycelium white, woolly, with rings of light olivaceous grey in the centre and dark olivaceous grey to black on the reverse side, margins regular, thick and white.

Typus: **Australia,** South Australia, Waikerie, from leaf spots on *Allium sativum* (*Alliaceae*), 14 Nov. 1997, H. Suheri (**holotype** VPRI 21969, culture ex-type VPRI 21969).

Notes: *Stemphylium waikerieanum* is morphologically similar to species in the *Ste. vesicarium* species complex. However, the conidium length in *Ste. vesicarium* complex does not exceed 45 µm (Simmons 1969), whereas conidia of *Ste. waikerieanum* were observed up to 49 µm long. The multigene phylogenetic analysis of ITS, *gapdh* and *cmdA* also support (PP value =1) this species as a novel taxon.

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Tubakia B. Sutton, Trans. Brit. Mycol. Soc. 60: 164. 1973. Fig. 82.
Synonyms: *Actinopelte* Sacc., Annls mycol. 11: 315. 1913.

Classification: *Dothideomycetes*, *Diaporthomycetidae*, *Diaporthales*, *Tubakiaceae*.

Type species: *Tubakia japonica* (Sacc.) B. Sutton, basionym: *Actinopelte japonica* Sacc. Epitype and ex-epitype strains designated by Braun *et al.* (2018): NBRC H-11611, NBRC 9268 = MUCC2296 = ATCC 22472.

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

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

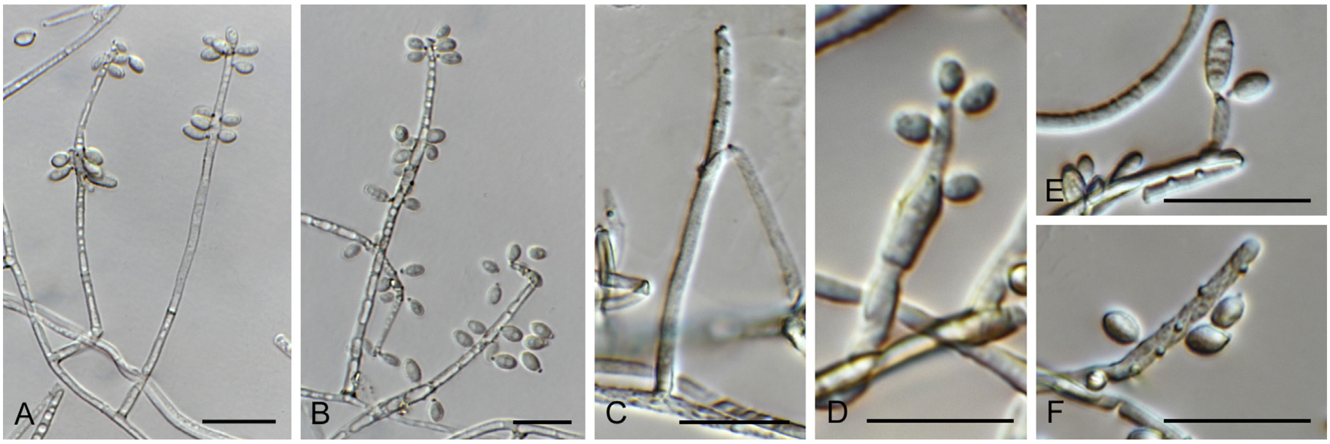

Fig. 85. *Zasmidium thailandicum* (ex-type CBS 145027). **A–C.** Conidiophores sporulating on SNA. **D–F.** Conidiogenous cells with apical rachis giving rise to conidia. Scale bars = 10 µm.

Ascomata perithecial, pigmented, dark, on fallen overwintered leaves, rostrate, beak short, usually lateral-eccentric, slightly protuberant, with periphysate ostiolate; *ascomatal wall* variable in thickness, paler than stromatic layers, polyascal. *Paraphyses* lacking. *Asci* unitunicate, 8-spored, oblong-ellipsoid, stalk short to oblong, ascal apex with two refractive conoid structures, asci deliquescing at maturity. *Ascospores* more or less uniseriate, becoming irregularly biseriate, one-celled, hyaline, ellipsoid to fusiform, often inequilateral or slightly curved, wall finely ornamented, content granular-guttulate. *Conidiomata* pycnothyrial, usually circular or subcircular when viewed from above, superficial, easily removable, scutellate, fixed to the leaf by a central columella; *scutellum* composed of loose to dense hyphal strands, mostly branched, thick-walled, pigmented, margin compact or outer portions of the radiating hyphal strands looser to free, tips rounded, truncate or pointed, margin usually not recurved. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* phialidic, usually subcylindrical-conical, lageniform, hyaline to pale brown, arising from small, colourless fertile cells around the upper part of the central pycnothyrial columella, percurrently proliferating, sometimes forming indistinct periclinal thickenings or annellations (collarettes). *Conidia* formed singly, globose to broad ellipsoid-obovoid, sometimes subcylindrical or somewhat irregular, wall thin to somewhat thickened, smooth to faintly rough, hyaline to pigmented, apex rounded, base rounded to attenuated, sometimes with distinct frill or peg-like basal hilum (adapted from Braun *et al.* 2018).

Culture characteristics: Colonies on MEA flat, with dense or fluffy, sparse to moderate aerial mycelium, margins regular or scalloped; surface ivory white, dingy white to pale yellow, straw, cream to light grey, smoke grey, white with center green olive and brown hyphal stripes, creamy white with or without concentric rings of olivaceous mycelium, or white to grey with wet conidial masses olive green to black; reverse pale grey, greyish white with olivaceous margins, smoke grey with olivaceous grey margins, golden yellow to slightly darker, yellowish grey with concentric rings, yellow with dark grey concentric rings, straw with dark brown concentric rings, or middle dark grey and yellow to medium brown towards the rim.

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

Distribution: North America, Asia, Australia and Europe.

Hosts: *Castanea* spp., *Chrysolepis chrysophylla*, *Lithocarpus densiflorus* and *Quercus* spp (*Fagaceae*), *Liquidambar styraciflua* (*Hamamelidaceae*), *Lindera glauca* (*Lauraceae*), and *Pinus tabuliformis* (*Pinaceae*). Reported from other hosts not verified such as *Acer* spp. (*Aceraceae*), *Carya* spp. (*Juglandaceae*) and *Fraxinus* spp. (*Oleaceae*).

Disease symptoms: Leaf spots, necrosis and death. *Tubakia iowensis* also causes petiole necrosis and death of whole leaves on bur oak (bur oak blight).

Notes: *Tubakia* was recently revised by Braun *et al.* (2018), resulting in the introduction of five new genera to accommodate species previously placed in *Tubakia*, *i.e. Apiognomonioides*, *Involutiscutellula*, *Oblongisporothyrium*, *Paratubakia* and *Saprothyrium*. All these genera together with *Racheliella* and *Sphaerosporithyrium*, both genera also described during the revision of the genus *Tubakia*, were accommodated in the new family *Tubakiaceae* (Braun *et al.* 2018). Presently, 16 species are accepted in the genus based on molecular data (ITS, *tef1* and *tub2* sequences). These species may form different types of asexual morphs, being the punctiform conidiomata (pycnothyria) composed of convex scutella with radiating threads of cells fixed to the substratum by a central columella the most common and characteristic structure formed. Other asexual morphs include sporodochial conidiomata and crustose or pustulate pycnidioid conidiomata. The conidia are globose to broad ellipsoid-obovoid, sometimes subcylindrical or somewhat irregular, aseptate, hyaline, subhyaline to pigmented. *Tubakia suttoniana* is the only species that produces sexual morph characterised by ostiolate ascomata, unitunicate asci with two refractive conoid structures in the ascal apex, and one-celled, hyaline ascospores.

Species of *Tubakia* are endophytes and/or pathogens in leaves and twigs of many tree species, causing distinct leaf lesions in different hosts including oak (*Quercus* spp.), chestnut (*Castanea* spp.) and other hardwood species. Moreover, *T. iowensis* is also capable of causing petiole necrosis and death of whole leaves on bur oak (*Q. macrocarpa*), sometimes killing nearly every leaf on a susceptible tree. This disease is known as bur oak blight and is most common in Iowa and Minnesota, but it has been noted in western and southern Wisconsin, northern Illinois, northeast Kansas, eastern Nebraska, and eastern South Dakota, with isolated groups of affected trees in counties of Illinois and Missouri that border Iowa (Harrington & McNew 2016).

References: Harrington *et al.* 2012 (morphology and pathogenicity), Harrington & McNew 2016 (pathogenicity, bur oak blight), Harrington & McNew 2018 (morphology and phylogeny), Braun *et al.* 2018 (morphology, pathogenicity and phylogeny).

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Zasmidium Fr., Summa veg. Scand., Sectio Post. (Stockholm): 407. 1849. Fig. 83.

Synonyms: *Periconiella* Sacc., Atti Ist. Veneto Sci. Lett. Arti 3: 727. 1885.

Biharia Thirum. & Mishra, Sydowia 7: 79. 1953.

Stenellopsis B. Huguenin, Bull. Trimestriel Soc. Mycol. France 81: 695. 1966.

Verrucispora D.E. Shaw & Alcorn, Proc. Linn. Soc. New South Wales 92: 171. 1967. (nom. illegit., Art. 53.1).

Verrucisporota D.E. Shaw & Alcorn, Austral. Syst. Bot. 6: 273. 1993.

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

Type species: *Zasmidium cellare* (Pers.) Fr., basionym: *Racodium cellare* Pers. Neotype designated by Videira *et al.* (2017): CBS 146.36 (duplicate cultures ATCC 36951 = IFO 4862 = IMI 044943 = LCP 52.402 = LSHB BB274 = MUCL 10089).

DNA barcode (genus): LSU.

DNA barcodes (species): ITS, *rpb2*, *act*, *tef1*, *tub2*. Table 22. Fig. 84.

Ascomata pseudothecial, amphigenous or epiphyllous, dark brown or black, globose, single to aggregated; *necks* rarely perceptible, usually a paler coloured circular area, composed of convergent yellow hyphae; *ascomatal wall* composed of 2–3 layers of cells of *textura angularis*. *Asci* bitunicate, fasciculate, subsessile, obpyriform, obovoid to ellipsoidal, obclavate to fusoid-ellipsoidal, saccate or clavate to cylindrical, aparaphysate, 8-spored. *Ascospores* 2–3-seriate to multiseriate, hyaline, smooth-walled, guttulate, without sheath, fusoid to ellipsoidal with obtuse ends, straight to slightly curved, uniseptate, constricted or not at the septum, widest in the middle of apical cell. In plant pathogenic species, *mycelium* mostly immersed as well as superficial, rarely only immersed; *hyphae* branched, septate, hyaline or almost so to pigmented, pale olivaceous to brown, wall thin to somewhat thickened, immersed hyphae smooth-walled or almost so to faintly rough, external hyphae distinctly verruculose to verrucose (in culture immersed hyphae usually smooth-walled or almost so, aerial hyphae verruculose). *Stromata* lacking to well-developed, pigmented. *Conidiophores* solitary, arising from superficial hyphae, lateral, occasionally terminal, *in vivo* (in plant pathogenic taxa) sometimes also fasciculate, arising from internal hyphae or stromata, semimacronematous to macronematous, in culture occasionally micronematous, cylindrical, filiform, subuliform, straight to strongly geniculate-sinuous, mostly unbranched, aseptate, *i.e.* reduced to conidiogenous cells, to pluriseptate, subhyaline to pigmented, pale olivaceous to medium dark brown, wall thin to somewhat thickened, smooth to verruculose. *Conidiogenous cells* integrated, terminal, occasionally intercalary, rarely pleurogenous, or conidiophores reduced to conidiogenous cells, mostly polyblastic, sympodial, with conspicuous, somewhat thickened and darkened-refractive, planate loci. *Conidia* solitary or catenate, in simple or branched acropetal chains, shape and size variable, ranging from amero- to scolecosporous, aseptate to transversely pluri-euseptate, subhyaline to pigmented, pale olivaceous to brown, wall thin to somewhat thickened, smooth or almost so to usually distinctly verruculose (in plant pathogenic species without superficial mycelium always verruculose); *hila* somewhat thickened and darkened-refractive, planate, conidial secession schizolytic (asexual morph description adapted from Braun *et al.* 2013).

Culture characteristics: Colonies slow growing, with sparse to moderate aerial mycelium, rarely with aerial mycelium absent, sometimes with mucoid exudate, margins smooth and regular, lobate or feathery. On MEA olivaceous, olivaceous green with margins whitish, brown olivaceous, olivaceous grey, iron mouse grey, grey, cream, yellowish brown, vinaceous buff to olivaceous buff, dark brown, or dark brown with margins grey; reverse pale or dark grey olivaceous, olivaceous black, mouse grey, iron-grey, greenish black, pale orange, isabelline, buff, dark brown, or brown vinaceous. On PDA pale white with margins pale olivaceous grey, pale mouse grey, olivaceous grey, iron-grey, iron-grey with patches orange, or brown olivaceous; reverse olivaceous grey, iron-grey, iron-grey with patches orange, or isabelline. On OA mouse grey, olivaceous grey, smoke grey with margins olivaceous grey, iron-grey, or iron-grey with broad margins of orange; reverse olivaceous, olivaceous grey, dark mouse grey, or iron-grey.

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

Distribution: Worldwide.

Hosts: Wide range of hosts belonging to 25 different families, including *Alocasia odora* and *Anthurium* sp. (*Araceae*), *Aporosa villosa* (*Euphorbiaceae*), *Brabejum stellatifolium*, *Grevillea* spp. and *Hakea undulata* (*Proteaceae*), *Citrus* spp. (*Rutaceae*), *Cyathea delgadii* (*Cyatheaceae*), *Dasypogon* sp. (*Dasypogonaceae*), *Daviesia latifolia* (*Fabaceae*), *Elaeocarpus kirtonii* (*Elaeocarpaceae*), *Eucalyptus* spp. (*Myrtaceae*), *Gahnia sieberiana* (*Cyperaceae*), *Geniostoma rupestre* (*Loganiaceae*), *Itea parvifolia* (*Escalloniaceae*), *Lonicera japonica* (*Caprifoliaceae*), *Maclura cochinchinensis* (*Moraceae*), *Malus* spp. (*Rosaceae*), *Pittosporum tenuifolium* (*Pittosporaceae*), *Podocarpus* sp. (*Podocarpaceae*), *Pseudotsuga menziesii* and *Tsuga heterophylla* (*Pinaceae*), *Restio subverticillatus* (*Restionaceae*), *Rothmannia engleriana* (*Rubiaceae*), *Sasa* sp. (*Poaceae*), *Scaevola taccada* (*Goodeniaceae*), *Schinus terebinthifolius* (*Anacardiaceae*), *Strelitzia* sp. (*Strelitziaceae*), and *Syzygium cordatum* (*Myrtaceae*).

Disease symptoms: Causing various lesions, ranging from yellowish discolorations to distinct leaf spots. Also associated with sooty blotch and flyspeck diseases. Also isolated from wall in wine cellar.

Notes: The genus *Zasmidium* is morphologically similar to *Stenella*, producing thickened and darkened conidiogenous loci and hila (Braun *et al.* 2013). However, these genera differ in the conidial hila and scars, being flat in *Stenella* and planate and somewhat thickened, darkened in *Zasmidium*. Moreover, *Stenella* belongs to *Teratosphaeriaceae* while *Zasmidium* is located within *Mycosphaerellaceae* (Arzanlou *et al.* 2007, Quaedvlieg *et al.* 2013, Videira *et al.* 2017).

A recent phylogenetic analysis based on LSU, ITS and *rpb2* showed that species belonging to other genera, *i.e. Mycosphaerella*, *Parastenella*, *Periconiella*, *Ramichloridium*, *Rasutoria*, *Stenella* and *Verrucisporota*, were located in the monophyletic clade representing the genus *Zasmidium* (Videira *et al.* 2017). Therefore, 12 new combinations were introduced, and the genera *Periconiella* and *Verrucisporota* reduced to synonymy with *Zasmidium*. Based on our phylogenetic analysis, 48 species are accepted in the genus together with one new species described here, and a new combination based on *Ramichloridium ducassei*.

The type species of the genus, *Z. cellare*, has been isolated from wine cellars in Europe and America, while the other species of the genus are associated to plants as saprobic or mostly biotrophic, usually foliicolous, symptomless or causing various lesions, ranging from yellowish discolorations to distinct leaf spots. *Zasmidium* spp. are pathogens of a wide range of hosts such as *Z. biverticillatum* and *Z. musigenum*, which cause tropical speckle disease on members of *Musaceae* (Stahel 1937, Jones 2000), and *Z. fructicola* and *Z. fructigenum*, both pathogens of *Citrus* causing a disease known as citrus greasy spot (Huang *et al.* 2015).

References: Arzanlou *et al.* 2007, Videira *et al.* 2017 (morphology and phylogeny), Braun *et al.* 2013 (morphology).

Zasmidium ducassei (R.G. Shivas *et al.*) Y. Marín & Crous, ***comb. nov.*** MycoBank MB829646.
Basionym: *Ramichloridium ducassei* R.G. Shivas *et al.*, Australas. Pl. Path. 40: 63. 2010.

Description and illustration: Shivas *et al.* (2011).

Typus: **Australia**, Queensland, Daintree, on leaves of *Musa acuminata* × *balbisiana* (*Musaceae*), 14 Apr. 2010, M. Berridge & K.R.E. Grice (**holotype** BRIP 53367, culture ex-type BRIP 53367).

Additional material examined: **Malaysia**, on leaves of *Musa* sp., 2016, P.W. Crous, CPC 32929.

Notes: This species was initially introduced as *R. ducassei* to accommodate some isolates associated with a severe leaf speckle disease of Ducasse banana (*Musa acuminata* × *babisiana* cv. Pisang awak) in northern Queensland (Shivas *et al.* 2011). The authors noticed that this species was similar to *Zasmidium* in having pigmented conidiophores with integrated conidiogenous cells that sympodially proliferate near the apex, with slightly thickened and refractive scars and aseptate, subhyaline conidia also with slightly thickened and refractive hila. However, it was classified in *Ramichloridium* in preference to *Zasmidium* because, at the time, *Zasmidium* was a paraphyletic genus in the *Mycosphaerellaceae*. In our phylogenetic analysis based on the combined dataset, the ex-type strain of this species was located in the well-supported clade (100 % BS / 1 PP) representing *Zasmidium*, and therefore a new combination *Z. ducassei* is proposed. Moreover, additional isolates belonging to this species were obtained from the same host genus, but from different locale, Malaysia.

Zasmidium thailandicum Crous, ***sp. nov.*** MycoBank MB829647. Fig. 85.

Etymology: Named reflects the country from where it was collected, Thailand.

On SNA. *Conidiophores* solitary, arising from superficial hyphae, subcylindrical, pale brown, 1–3-septate, unbranched or branched below, 20–100 × (1.5–)2 µm. *Conidiogenous cells* subhyaline, smooth-walled, subcylindrical, apical and intercalary, apical part with well-defined rachis bearing minute (0.5 µm diam) slightly darkened scars, 10–30 × 1.5–2 µm. *Ramoconidia* fusoid to obclavate, hyaline, smooth-walled, aseptate, guttulate, 8–12(–17) × 2.5–3 µm. *Conidia* solitary, hyaline, smooth-walled, guttulate, aseptate, ellipsoid, apex obtuse, base protruding, truncate, 0.5–1 µm diam, (3–)4–4.5(–5) × (2–)2.5 µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margins, reaching 20 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface pale mouse grey, reverse mouse grey.

Typus: **Thailand**, Rachaburi province, Bangkok, on leaves of *Musa* sp. (*Musaceae*), 2010, P.W. Crous, HPC 2158 (**holotype** CBS H-23850, culture ex-type CBS 145027 = CPC 33960).

Notes: Zasmidium thailandicum is closely related to *Z. ducassei*. Moreover, both species have been reported from the same host genus, *Musa*, causing leaf spots on banana leaves. However, these species can be easily distinguished by the length of their conidia [5–10 µm in *Z. ducassei vs.* (3–)4–4.5(–5) µm in *Z. thailandicum*].

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