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New and Interesting Fungi. 2

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Abstract: One order, seven families, 28 new genera, 72 new species, 13 new combinations, four epitypes, and 21 interesting new host and / or geographical records are introduced in this study. *Pseudorobillardaceae* is introduced for *Pseudorobillarda* (based on *P. phragmitis*). New genera include: *Jeremyomyces* (based on *J. labinae*) on twigs of *Salix alba* (Germany); *Neodothidotthia* (based on *N. negundinicola*) on *Acer negundo* (Ukraine); *Neomedicopsis* (based on *N. prunicola*) on fallen twigs of *Prunus padus* (Ukraine); *Neophaeoappendicospora* (based on *N. leucaenae*) on *Leucaena leucocephala* (France) (incl. *Phaeoappendicosporaceae*); *Paradevriesia* (incl. *Paradevriesiaceae*) (based on *P. americana*) from air (USA); *Phaeoseptoriella* (based on *P. zeae*) on leaves of *Zea mays* (South Africa); *Piniphoma* (based on *P. wesendahlina*) on wood debris of *Pinus sylvestris* (Germany); *Pseudoconiothyrium* (based on *P. broussonetiae*) on branch of *Broussonetia papyrifera* (Italy); *Sodiomyces* (based on *S. alkalinus*) from soil (Mongolia), and *Turquoiseomyces* (incl. *Turquoiseomycetales* and *Turquoiseomycetaceae*) (based on *T. eucalypti*) on leaves of *Eucalyptus leptophylla* (Australia); *Typhicola* (based on *T. typharum*) on leaves of *Typha* sp. (Germany); *Xenodevriesia* (incl. *Xenodevriesiaceae*) (based on *X. strelitziicola*) on leaves of *Strelitzia* sp. (South Africa). New species include: *Bacillicladium clematidis* on branch of *Clematis vitalbae* (Austria); *Cercospora gomphrenigena* on leaves of *Gomphrena globosa* (South Africa); *Cyphellophora clematidis* on *Clematis vitalba* (Austria); *Exophiala abietophila* on bark of *Abies alba* (Norway); *Exophiala lignicola* on fallen decorticated trunk of *Quercus* sp. (Ukraine); *Fuscostagonospora banksiae* on *Banksia* sp. (Australia); *Gaeumannomycella caricicola* on dead leaf of *Carex remota* (Germany); *Hansfordia pruni* on *Prunus persica* twig (Italy) (incl. *Hansfordiaceae*); *Microdochium rhopalostylidis* on *Rhopalostylis sapida* (New Zealand); *Neocordana malayensis* on leaves of *Musa* sp. (Malaysia); *Neocucurbitaria prunicola* on fallen twigs of *Prunus padus* (Ukraine); *Neocucurbitaria salicis-albae* on *Salix alba* twig (Ukraine); *Neohelicomyces deschampsiae* on culm base of dead leaf sheath of *Deschampsia cespitosa* (Germany); *Pararoussoella juglandicola* on twig of *Juglans regia* (Germany); *Pezicula eucalyptigena* on leaves of *Eucalyptus* sp. (South Africa); *Phlogicylindrium dunnii* on leaves of *Eucalyptus dunnii* (Australia); *Phyllosticta hagahagaensis* on leaf litter of *Carissa bispinosa* (South Africa); *Phyllosticta austroafricana* on leaf spots of unidentified deciduous tree host (South Africa); *Pseudosigmoidea alnicola* on *Alnus glutinosa* leaf litter (Germany); *Pseudoteratosphaeria africana* on leaf spot on unidentified host (Angola); *Porodiplodia vitis* on canes of *Vitis vinifera* (USA); *Sodiomyces alkalinus* from soil (Mongolia), *Sodiomyces magadiensis* and *Sodiomyces tronii* from soil (Kenya), *Sympodiella quercina* on fallen leaf of *Quercus robur* (Germany) and *Zasmidium hakeicola* on leaves of *Hakea corymbosa* (Australia). Epitypes are designated for: *Cryptostictis falcata* on leaves of *E. alligatrix* (Australia), *Hendersonia phormii* on leaves of *Phormium tenax* (New Zealand), *Sympodiella acicola* on needles of *Pinus sylvestris* (Netherlands), and *Sphaeria scirpicola* var. *typharum* on leaf of *Typha* sp. (Germany). Several taxa originally described from rocks are validated in this study. New taxa include: *Extremaceae fam. nov.*, and new genera, *Arthrocatena, Catenulomyces, Constantinomyces, Extremus, Hyphoconis, Incertomyces, Lapidomyces, Lithophila,*

Monticola, Meristemomyces, Oleoguttula, Perusta, Petrophila, Ramimonilia, Saxophila and *Vermiconidia.* New species include: *Arthrocatena tenebrosa*, *Catenulomyces convolutus*, *Constantinomyces virgultus*, C. *macerans*, *C. minimus, C. nebulosus, C. virgultus, Exophiala bonariae, Extremus adstrictus, E. antarcticus, Hyphoconis sterilis, Incertomyces perditus, Knufia karalitana, K. marmoricola*, *K. mediterranea, Lapidomyces hispanicus, Lithophila guttulata, Monticola elongata, Meristemomyces frigidus*, *M. arctostaphyli, Neodevriesia bulbillosa, N. modesta, N. sardiniae, N. simplex, Oleoguttula mirabilis, Paradevriesia compacta, Perusta inaequalis*, *Petrophila incerta, Rachicladosporium alpinum, R. inconspicuum*, *R. mcmurdoi, R. monterosanum, R. paucitum, Ramimonilia apicalis, Saxophila tyrrhenica, Vermiconidia antarctica, V. calcicola, V. foris,* and *V. flagrans.*

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INTRODUCTION

This paper represents the second contribution to the New and Interesting Fungi (NIF) series, aimed at expanding the body of knowledge of fungal biodiversity and fungal conservation. The series focuses on new records, new sexual-asexual connections, consolidation of sexual and asexual genera following the abandonment of dual nomenclature for fungi (Hawksworth *et al.* 2011, Wingfield *et al*. 2012), and the description of fungal taxa, or notes relating to interesting observations (Crous *et al.* 2018c). The series represents a regular feature of the journal Fungal Systematics and Evolution (www.FUSE-journal.org). It is hoped that it will provide an attractive resource for mycologists to publish single new species or to highlight the relevance of important fungi. Mycologists and other researchers wishing to contribute to future issues of NIF are encouraged to contact the Editor-in-Chief (p.crous@westerdijkinstitute.nl).

MATERIALS AND METHODS

Isolates

Samples were placed in damp chambers and incubated at room temperature for 1–3 d. Single conidial colonies were grown from sporulating conidiomata in Petri dishes containing 2 % malt extract agar (MEA) as described by Crous *et al.* (1991). Leaf and stem tissues bearing ascomata were soaked in water for approximately 2 h, after which they were attached to the undersides of the lids of Petri dishes containing MEA. After ascospores had been ejected onto the MEA surface, germination patterns were determined after 24 h, and single ascospore or conidial cultures were established following the method described by (Crous 1998). Colonies were sub-cultured on 2 % potato-dextrose agar (PDA), oatmeal agar (OA), MEA (Crous *et al*. 2009c), autoclaved pine needles on 2 % tap water agar (PNA) (Smith *et al.* 1996), or autoclaved banana leaves (BLA), and incubated at 25 °C under continuous near-ultraviolet light to promote sporulation. Reference strains and specimens of the studied fungi are maintained in the CBS culture collection (CBS) of the Westerdijk Fungal Biodiversity Institute (WI), Utrecht, the Netherlands.

DNA extraction, amplification (PCR) and phylogeny

Fungal mycelium (Table 1) was scraped from the agar surface of cultures with a sterile scalpel and the genomic DNA was isolated using the Wizard® Genomic DNA Purification Kit (Promega Corporation, WI, USA) following the manufacturers' protocols. Nine loci were amplified following previously published protocols. First, the 28S nrRNA gene (LSU) and internal transcribed spacer regions with intervening 5.8S nrRNA gene (ITS) of the nrDNA operon were sequenced for all the isolates included in this study (for amplification conditions, see Fan *et al*. 2018). Other loci were sequenced for various species or genera using primers and conditions specific for those groups of fungi (Table 1). Amplification of the partial DNA-directed RNA polymerase II second largest subunit gene (*rpb2*), the partial translation elongation factor 1-alpha gene (*tef1*) and the partial beta-tubulin gene (*tub2*) followed Braun *et al.* (2018), while the amplification of the partial actin gene (*act*), the partial calmodulin gene (*cmdA*), the partial glyceraldehyde-3-phosphate dehydrogenase gene (gapdh) and the partial histone H3 gene (*his3*) followed Videira *et al*. (2016). The resulting fragments were sequenced in both directions using the respective PCR primers and the BigDye Terminator Cycle Sequencing Kit v. 3.1 (Applied Biosystems Life Technologies, Carlsbad, CA, USA); DNA sequencing amplicons were purified through Sephadex G-50 Superfine columns (Sigma-Aldrich, St. Louis, MO) in MultiScreen HV plates (Millipore, Billerica, MA). Purified sequence reactions were analysed on an Applied Biosystems 3730xl DNA Analyzer (Life Technologies, Carlsbad, CA, USA). The DNA sequences were analysed and consensus sequences were computed using SeqMan Pro v. 13 (DNASTAR, Madison, WI, USA).

The sequences for each gene region were subjected to megablast searches (Zhang *et al*. 2000) to identify closely related sequences in the NCBI's GenBank nucleotide database. The results are provided as part of the species notes or as selected phylogenetic trees. Phylogenetic trees were generated using Bayesian analyses performed with MrBayes v. 3.2.6 (Ronquist *et al*. 2012) for the overview trees and Maximum Parsimony analyses performed with PAUP v. 4.0b10 (Swofford 2003) as explained in Braun *et al*. (2018) for the genus and species trees. All resulting trees were printed with Geneious v. 11.0.3 (http://www.geneious.com, Kearse *et al.* 2012) and the layout of the trees was done in Adobe Illustrator v. CC 2017. Statistical measures calculated included tree length (TL), consistency index (CI), retention index (RI) and rescaled consistency index (RC).

Morphology

Slide preparations were mounted in lactic acid, Shear's mounting fluid or water, from colonies sporulating on MEA, PDA, PNA, BLA or OA. Sections through conidiomata were made by hand. Observations were made with a Nikon SMZ25 dissection-microscope, and with a Zeiss Axio Imager 2 light microscope using differential interference contrast (DIC) illumination and images recorded on a Nikon DS-Ri2 camera with associated software. Colony characters and pigment production were noted after 2–4 wk of growth on MEA, PDA and OA (Crous *et al*. 2009c)

Table 1. Collection details and GenBank accession numbers of isolates considered in this study.

Species	Locality	Substrate	Culture accession number(s)[1]	GenBank accession number[2]		
				ITS, LSU, *act*	*cmdA*, *gapdh*, *his3*	*rpb2*, *tef1*, *tub2*
Allelochaeta falcata	Australia	*Eucalyptus alligatrix*	CPC 13578 = CBS 131117, ex-epitype	JN871204.1, JN871213.1, –	–, –, –	–, –, –
Amycosphaerella africana	New Zealand	*Metrosideros excelsa*	CPC 32782 = CBS 144635 = T16_03926C	MK442569.1, MK442511.1, –	–, –, –	–, MK442688.1, MK442725.1
Bacillicladium clematidis, sp. nov.	Austria	*Clematis vitalba*	CPC 33882 = CBS 145035, ex-type	MK442570.1, MK442512.1, –	–, –, –	–, –, MK442726.1
Beltrania rhombica	Chile	*Eucalyptus urophylla*	CPC 31775 = CBS 144521	MK442571.1, MK442513.1, –	–, –, –	–, –, –
Brevistachys lateralis	Thailand	*Musa* sp.	CPC 33958 = CBS 145062	MK442572.1, MK442514.1, –	MK442649.1, –, –	MK442661.1, MK442689.1, MK442727.1
Cercospora gomphrenigena, sp. nov.	South Africa	*Gomphrena globosa*	CPC 32470 = CBS 144613, ex-type	MK442573.1, MK442515.1, –	MK442650.1, –, MK442658.1	–, MK442690.1, MK442728.1
Cladoriella xanthorrhoeae	Australia	*Xanthorrhoea* sp.	CPC 32609 = CBS 144523	MK442574.1, MK442516.1, –	–, –, –	–, –, –
Creosphaeria sassafras	Spain	*Laurus nobilis*	CPC 33410 = CBS 144984	MK442575.1, MK442517.1, –	–, –, –	–, –, –
Cylindrocladiella peruviana	South Africa	*Pelargonium* sp.	CPC 33527 = CBS 145053 = SPXX	MK442576.1, MK442518.1, –	–, –, MK442659.1	MK442662.1, MK442691.1, MK442729.1
Cyphellophora clematidis, sp. nov.	Austria	*Clematis vitalba*	CPC 33880 = CBS 144983, ex-type	MK442577.1, MK442519.1, –	–, –, –	–, –, MK442730.1
Diaporthe anacardii	South Africa	Unidentified leaf litter	CPC 33074 = CBS 144610	MK442578.1, MK442520.1, –	MK442651.1, –, –	–, MK442692.1, –
Diaporthe eres	Netherlands	*Lactuca sativa*	CPC 34055 = CBS 145040	MK442579.1, MK442521.1, MK442634.1	MK442652.1, –, –	MK442663.1, MK442693.1, MK442731.1
Dichotomophthora basellae	Thailand	Unidentified host plant	CPC 33044 = CBS 145050	MK442580.1, MK442522.1, –	–, –, –	MK442664.1, –, –
Exophiala abietophila, sp. nov.	Norway	*Abies alba*	CPC 34580 = CBS 145038, ex-type	MK442581.1, MK442523.1, –	–, –, –	–, –, –
Exophiala lignicola, sp. nov.	Ukraine	*cf. Quercus* sp.	CPC 32464 = CBS 144622, ex-type	MK442582.1, MK442524.1, –	MK442653.1, –, –	–, MK442694.1, –
Fuscostagonospora banksiae, sp. nov.	Australia	*Banksia* sp.	CPC 31724 = CBS 144621, ex-type	MK442583.1, MK442525.1, –	–, –, –	–, –, –
Gaeumannomycella caricicola, sp. nov.	Germany	*Carex remota*	CPC 33925 = CBS 145041, ex-type	MK442584.1, MK442526.1, –	–, –, MK442660.1	–, –, MK442732.1
Hansfordia pruni, sp. nov.	Italy	*Prunus persica*	CBS 194.56 = IMI 146912, ex-type	MK442585.1, MH869122.1, KU760903.1	–, –, –	KU684307.1, –, –
Hansfordia pulvinata	Italy	*Cercospora unamunoi* on *Capsicum annuum*	CBS 134.62 = IMI 146913	MK442586.1, MH869699.1, –	–, –, –	–, –, –
	Australia	*Macrozamia miquelii*	CPC 32119 = CBS 144422	MK442587.1, MK442527.1, –	–, –, –	–, –, –
Hypsotheca maxima, comb. nov.	Brazil	*Niphidium crassifolium*	CPC 24674 = COAD 1983, ex-epitype	KX891229.1, KX891228.1, –	–, –, –	–, –, –
Hypsotheca nigra, comb. nov.	Spain	Epiphytic lichens growing on bark of holm oak	MA 18191	–, KP144011.1, –	–, –, –	–, –, –
Hypsotheca pleomorpha, comb. nov.	Australia	*Eucalyptus piperita*	CPC 32144 = CBS 144636	MK442588.1, MK442528.1, –	–, –, –	–, –, –
Jeremyomyces labinae, gen. et sp. nov.	Germany	*Salix alba*	CPC 33154 = CBS 144617, ex-type	MK442589.1, MK442529.1, –	MK442654.1, –, –	MK442665.1, MK442695.1, MK442733.1
Macgarvieomyces luzulae	Ukraine	*Luzula sylvatica*	CPC 34292 = CBS 145042	MK442591.1, MK442531.1, MK442635.1	–, –, –	–, –, –
Microdochium rhopalostylidis, sp. nov.	New Zealand	*Rhopalostylis sapida*	CPC 34449 = CBS 145125, ex-type	MK442592.1, MK442532.1, MK442636.1	MK442655.1, –, –	MK442667.1, –, MK442735.1

Table 1. (Continued).

Species	Locality	Substrate	Culture accession number(s)[1]	GenBank accession number[2]		
				ITS, LSU, *act*	*cmdA*, *gapdh*, *his3*	*rpb2*, *tef1*, *tub2*
Neocordana malayensis, sp. nov.	Malaysia	*Musa* sp.	CPC 32837 = CBS 144604, ex-type	MK442593.1, MK442533.1, MK442637.1	–, –, –	–, –, MK442736.1
Neocucurbitaria prunicola, sp. nov.	Ukraine	*Prunus padus*	CPC 33709 = CBS 145033, ex-type	MK442594.1, MK442534.1, –	–, –, –	MK442668.1, –, MK442737.1
Neocucurbitaria salicis-albae, sp. nov.	Germany	*Salix alba*	CPC 33162 = CBS 144611, ex-type	MK442595.1, MK442535.1, –	–, –, –	MK442669.1, –, MK442738.1
Neodevriesia metrosideri	New Zealand	*Metrosideros excelsa*	CPC 32786 = CBS 144638	MK442596.1, MK442536.1, MK442638.1	–, –, –	–, –, MK442739.1
Neodothidotthia negundinicola, gen. et sp. nov.	Ukraine	*Acer negundo*	CPC 34071 = CBS 145039, ex-type	MK442597.1, MK442537.1, –	–, –, –	–, MK442697.1, –
Neodothidotthia negundinis, comb. nov.	USA	*Fendlera rupicola*	CPC 12928 = CBS 119686	MK442598.1, EU673272.1, –	–, –, –	–, –, –
	USA	*Euonymus alatus*	CPC 12930 = CBS 119688	MK442599.1, EU673274.1, –	–, –, –	–, –, –
	USA	*Acer negundo*	CPC 12932 = CBS 119690	MK442600.1, EU673275.1, –	–, –, –	–, –, –
	USA	*Acer negundo*	CPC 12933 = CBS 119691	MK442601.1, EU673276.1, –	–, –, –	–, –, –
Neohelicomyces deschampsiae, sp. nov.	Germany	*Deschampsia cespitosa*	CPC 33686 = CBS 145029, ex-type	MK442602.1, MK442538.1, –	–, –, –	–, –, –
Neomedicopsis prunicola, gen. et sp. nov.	Ukraine	*Prunus padus*	CPC 33711 = CBS 145031, ex-type	MK442603.1, MK442539.1, –	–, –, –	MK442670.1, –, –
Neophaeoappendicospora leucaenae, gen. et sp. nov.	La Réunion	*Leucaena leucocephala*	CPC 27240, ex-type	MK442604.1, MK442540.1, –	–, –, –	–, –, –
Ochroconis musae	Thailand	*Persea americana*	CPC 33947 = CBS 145061	MK442605.1, MK442541.1, MK442639.1	–, –, –	–, MK442698.1, –
Paradevriesia americana, gen. et comb. nov.	USA	Air	CBS 117726 = CPC 5121 = ATCC 96545, ex-type	MH863026.1, EU040227.1, –	–, –, –	–, –, –
Paradevriesia compacta, sp. nov.	Mallorca	Rock	CBS 118294 = TRN 111 = dH 14587, ex-type	GU323967.1, GU323967.1, –	–, –, –	KF310095.1, –, KF546761.1
Paradevriesia pseudoamericana, comb. nov.	Germany	*Malus domestica*	CPC 16174 = CBS 126270, ex-type	GU570527.1, GU570544.1, –	–, –, –	–, HM177416.1, –
Pararamichloridium livistonae	Australia	*Livistona australis*	CPC 32152 = CBS 144522, ex-type	MK442606.1, MK442542.1, –	–, –, –	–, –, –
Pararoussoella juglandicola, sp. nov.	Germany	*Juglans regia*	CPC 33400 = CBS 145037, ex-type	MK442607.1, MK442543.1, –	–, –, –	MK442671.1, MK442699.1, –
Pararoussoella mukdahanensis, comb. nov.	Thailand	Bamboo, dead culms	MFLUCC 11-0201, ex-type	KU940129.1, KU863118.1, –	–, –, –	–, –, –
Petriella sordida	Ukraine	*Luzula* sp.	CPC 32460 = CBS 144612	MK442608.1, MK442544.1, –	MK442656.1, –, –	–, MK442700.1, MK442740.1
	Ukraine	*Luzula* sp.	CPC 32461 = CBS 145121	MK442609.1, MK442545.1, –	–, –, –	MK442672.1, MK442701.1, –
Pezicula eucalyptigena, sp. nov.	South Africa	*Eucalyptus* sp.	CPC 32129 = CBS 144637, ex-type	MK442610.1, MK442546.1, –	–, –, –	MK442673.1, –, –
Phaeoseptoriella zeae, gen. et sp. nov.	South Africa	*Zea mays*	CPC 33064 = CBS 144614, ex-type	MK442611.1, MK442547.1, –	–, –, –	MK442674.1, MK442702.1, MK442741.1
Phlogicylindrium dunnii, sp. nov.	Australia	*Eucalyptus dunnii*	CPC 31818 = CBS 144620, ex-type	MK442612.1, MK442548.1, –	–, –, –	MK442675.1, MK442703.1, –

Table 1. (Continued).

Species	Locality	Substrate	Culture accession number(s)[1]	GenBank accession number[2]		
				ITS, LSU, *act*	*cmdA*, *gapdh*, *his3*	*rpb2*, *tef1*, *tub2*
Phyllosticta austroafricana, sp. nov.	South Africa	Leaf spots of unidentified deciduous tree host	CPC 31920 = CBS 144593, ex-type	MK442613.1, MK442549.1, MK442640.1	–, –, –	–, MK442704.1, –
Phyllosticta hagahagaensis, sp. nov.	South Africa	*Carissa bispinosa*	CPC 32799 = CBS 144592, ex-type	MK442614.1, MK442550.1, MK442641.1	–, MK442657.1, –	–, MK442705.1, –
Piniphoma wesendahlina, gen. et sp. nov.	Germany	*Pinus sylvestris*	CPC 33693 = CBS 145032, ex-type	MK442615.1, MK442551.1, –	–, –, –	MK442676.1, MK442706.1, MK442742.1
Porodiplodia vitis, sp. nov.	USA	*Vitis vinifera*	CPC 31642 = CBS 144634, ex-type	MK442616.1, MK442552.1, –	–, –, –	–, MK442707.1, –
Pseudoanungitea variabilis	Spain	Leaf litter	CBS 132716 = FMR 11934, ex-type	KY853424.1, KY853484.1, –	–, –, –	MK442678.1, MK442710.1, –
Pseudocercospora hakeae	Australia	*Hakea* sp.	CPC 32100 = CBS 144520	MK442617.1, MK442553.1, MK442642.1	–, –, –	MK442677.1, MK442708.1, MK442743.1
Pseudoconiothyrium broussonetiae, gen. et sp. nov.	Italy	*Broussonetia papyrifera*	CPC 33570 = CBS 145036, ex-type	MK442618.1, MK442554.1, –	–, –, –	–, MK442709.1, –
Pseudophaeophleospora phormii, comb. nov.	New Zealand	*Phormium tenax*	CPC 32742 = CBS 144606 = T16_03297D, ex-epitype	MK442619.1, MK442555.1, MK442643.1	–, –, –	–, MK442711.1, –
Pseudosigmoidea alnicola, sp. nov.	Germany	*Alnus glutinosa*	CPC 33776 = CBS 145034, ex-type	MK442620.1, MK442556.1, –	–, –, –	–, –, –
Pseudoteratosphaeria africana, sp. nov.	Angola	Leaf spot on unidentified host	CPC 33072 = CBS 144597	MK442621.1, MK442557.1, MK442644.1	–, –, –	–, MK442712.1, MK442744.1
	Angola	Leaf spot on unidentified host	CPC 33144 = CBS 144595, ex-type	MK442622.1, MK442558.1, MK442645.1	–, –, –	–, MK442713.1, MK442745.1
	Angola	Leaf spot on unidentified host	CPC 33145 = CBS 144596	MK442623.1, MK442559.1, MK442646.1	–, –, –	–, MK442714.1, MK442746.1
Selenodriella fertilis	Australia	*Eucalyptus* sp.	CPC 32663 = CBS 144589	MK442624.1, MK442560.1, –	–, –, –	–, –, –
Septonema crispulum	Italy	*Pinus pinea*	CBS 735.96, ex-isotype	MH862607.1, MH874232.1, –	–, –, –	MK442679.1, –, –
Stagonospora pseudoperfecta	Germany	*Typha* sp.	CPC 33138 = CBS 144607	MK442625.1, MK442561.1, –	–, –, –	–, MK442715.1, MK442747.1
Sympodiella acicola	Netherlands	*Pinus sylvestris*	CBS 425.76	KY853467.1, KY853529.1, –	–, –, –	MK442680.1, MK442716.1, –
	Netherlands	*Pinus sylvestris*	CBS 487.82, ex-epitype	KY853468.1, KY853530.1, –	–, –, –	MK442681.1, MK442717.1, –
Sympodiella alternata, comb. nov.	Japan	*Pinus densifolia*	IFO 8933 = CBS 326.69, ex-type	MK442626.1, MH871053.1, –	–, –, –	MK442682.1, MK442718.1, –
	–	–	HKUCC 10828 = NN43193	–, DQ408574.1, –	–, –, –	DQ435078.1, –, –
Sympodiella goidanichii, comb. nov.	Italy	*Fagus sylvatica*	CBS 136.58, ex-type	MH857722.1, MH869262.1, –	–, –, –	–, MK442719.1, –
Sympodiella quercina, sp. nov.	UK	*Betula* sp.	CBS 987.70	MH860019.1, MH871803.1, –	–, –, –	MK442683.1, MK442720.1, –
	Germany	*Quercus robur*	CPC 33903 = CBS 145028, ex-type	MK442627.1, MK442562.1, –	–, –, –	MK442684.1, MK442721.1, –

Table 1. (Continued).

Species	Locality	Substrate	Culture accession number(s)[1]	GenBank accession number[2]		
				ITS, LSU, *act*	*cmdA*, *gapdh*, *his3*	*rpb2*, *tef1*, *tub2*
Sympoventuria regnans	Australia	*Eucalyptus pauciflora*	CPC 31820 = CBS 144605	MK442628.1, MK442563.1, –	–, –, –	–, MK442722.1, MK442748.1
Tubakia suttoniana	New Zealand	*Quercus* sp.	CPC 32745 = CBS 144591 = T16_01981A	MK442629.1, MK442564.1, –	–, –, –	MK442685.1, MK442723.1, MK442749.1
Turquoiseomyces eucalypti, gen. et sp. nov.	Australia	*Eucalyptus leptophylla*	CPC 34399 = CBS 145126, ex-type	MK442630.1, MK442565.1, –	–, –, –	MK442686.1, –, MK442750.1
Typhicola typharum, gen. et comb. nov.	Germany	*Typha* sp.	CPC 33271 = CBS 145043, ex-neotype	MK442590.1, MK442530.1, –	–, –, –	MK442666.1, MK442696.1, MK442734.1
Wojnowiciella dactylidis	New Zealand	*Dypsis* sp. (*Arecaceae*)	CPC 32741 = CBS 145077 = T16_03296B	MK442631.1, MK442566.1, –	–, –, –	–, MK442724.1, MK442751.1
Xenodevriesia strelitziicola, gen. et comb. nov.	South Africa	*Strelitzia* sp.	CBS 122480 = X1045, ex-type	GU214635.1, GU214417.1, –	–, –, –	–, –, –
Zasmidium hakeicola, sp. nov.	Australia	*Hakea corymbosa*	CPC 32703 = CBS 144590, ex-type	MK442632.1, MK442567.1, MK442647.1	–, –, –	MK442687.1, –, MK442752.1
Zygosporium pseudogibbum	Australia	*Macrozamia miquelii*	CPC 32120 = CBS 144442	MK442633.1, MK442568.1, MK442648.1	–, –, –	–, –, MK442753.1

[1] ATCC: American Type Culture Collection, Virginia, USA; CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands; CPC: Culture collection of Pedro Crous, housed at CBS; dH: Culture collection of Sybren de Hoog, housed at CBS; IFO: Institute for Fermentation, Osaka, Yodogawa-ku, Osaka, Japan (collection transferred to NBRC); IMI: International Mycological Institute, CABI-Bioscience, Egham, Bakeham Lane, United Kingdom; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Rai, Thailand.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; LSU: large subunit (28S) of the nrRNA gene operon; *act*: partial actin gene; *cmdA*: partial calmodulin gene; *gapdh*: partial glyceraldehyde-3-phosphate dehydrogenase gene; *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 beta-tubulin gene.

incubated at 25 °C. Colony colours (surface and reverse) were scored using the colour charts of Rayner (1970). Sequences derived in this study were deposited in GenBank (Table 1), the alignment in TreeBASE (www.treebase.org; study number S23853), and taxonomic novelties in MycoBank (www.MycoBank.org; Crous *et al*. 2004).

RESULTS

Phylogeny

Dothideomycetes LSU phylogeny (Fig. 1): The alignment contained 254 isolates and *Helotium subcorticale* (CBS 248.62, GenBank MH869740.1) was used as outgroup. The final alignment contained a total of 809 characters used for the phylogenetic analyses, including alignment gaps. The alignment contained a total of 392 unique site patterns. Based on the results of MrModelTest, dirichlet base frequencies and the GTR+I+G model was used for the Bayesian analysis. The Bayesian analyses generated 133 802 trees from which 100 352 were sampled after 25 % of the trees were discarded as burn-in. The posterior probability values (PP) higher than 0.84 are plotted on the tree (Fig. 1).

Eurotiomycetes LSU phylogeny (Fig. 2): The alignment contained 71 isolates and *Saccharata proteae* (CBS 119218, GenBank EU552145.1) was used as outgroup. The final alignment contained a total of 772 characters used for the phylogenetic analyses, including alignment gaps. The alignment contained a total of 265 unique site patterns. Based on the results of MrModelTest, dirichlet base frequencies and the GTR+I+G model was used for the Bayesian analysis. The Bayesian analyses generated 30 502 trees from which 22 878 were sampled after 25 % of the trees were discarded as burn-in. The posterior probability values (PP) higher than 0.84 are plotted on the tree (Fig. 2).

Lecanoromycetes and *Leotiomycetes* LSU phylogeny (Fig. 3): The alignment contained 42 isolates and *Saccharata proteae* (CBS 119218, GenBank EU552145.1) was used as outgroup. The final alignment contained a total of 838 characters used for the phylogenetic analyses, including alignment gaps. The alignment contained a total of 222 unique site patterns. Based on the results of MrModelTest, dirichlet base frequencies and the GTR+I+G model was used for the Bayesian analysis. The Bayesian analyses generated 9 102 trees from which 6 828 were sampled after 25 % of the trees were discarded as burn-in. The posterior probability values (PP) higher than 0.84 are plotted on the tree (Fig. 3).

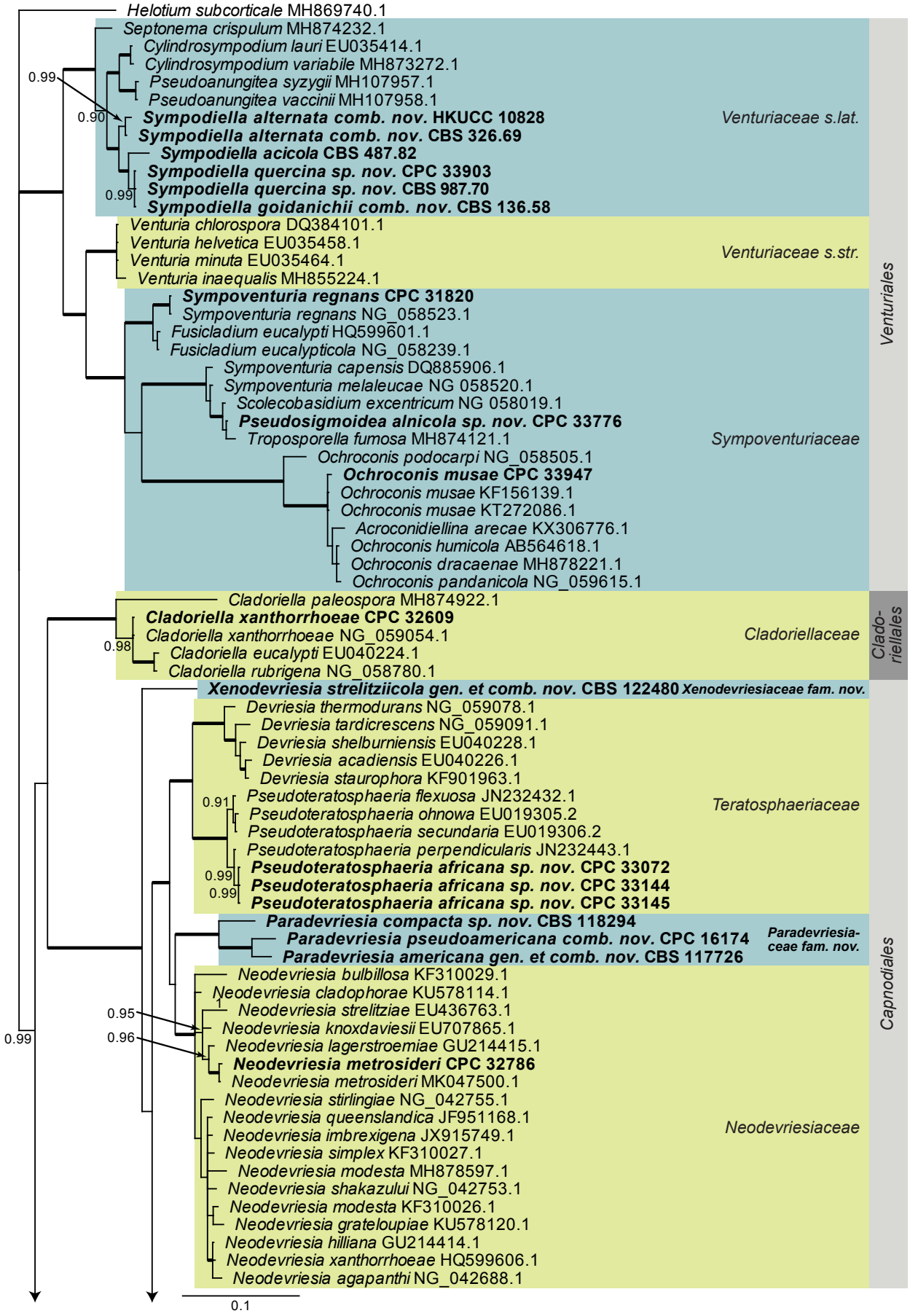

Fig. 1. Consensus phylogram (50 % majority rule) obtained from a Bayesian analysis of the *Dothideomycetes* alignment. Bayesian posterior probabilities (PP) >0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or culture accession numbers are indicated behind the species names. The tree was rooted to *Helotium subcorticale* (GenBank MH869740.1) and the novelties treated in the Taxonomy section are indicated in bold face.

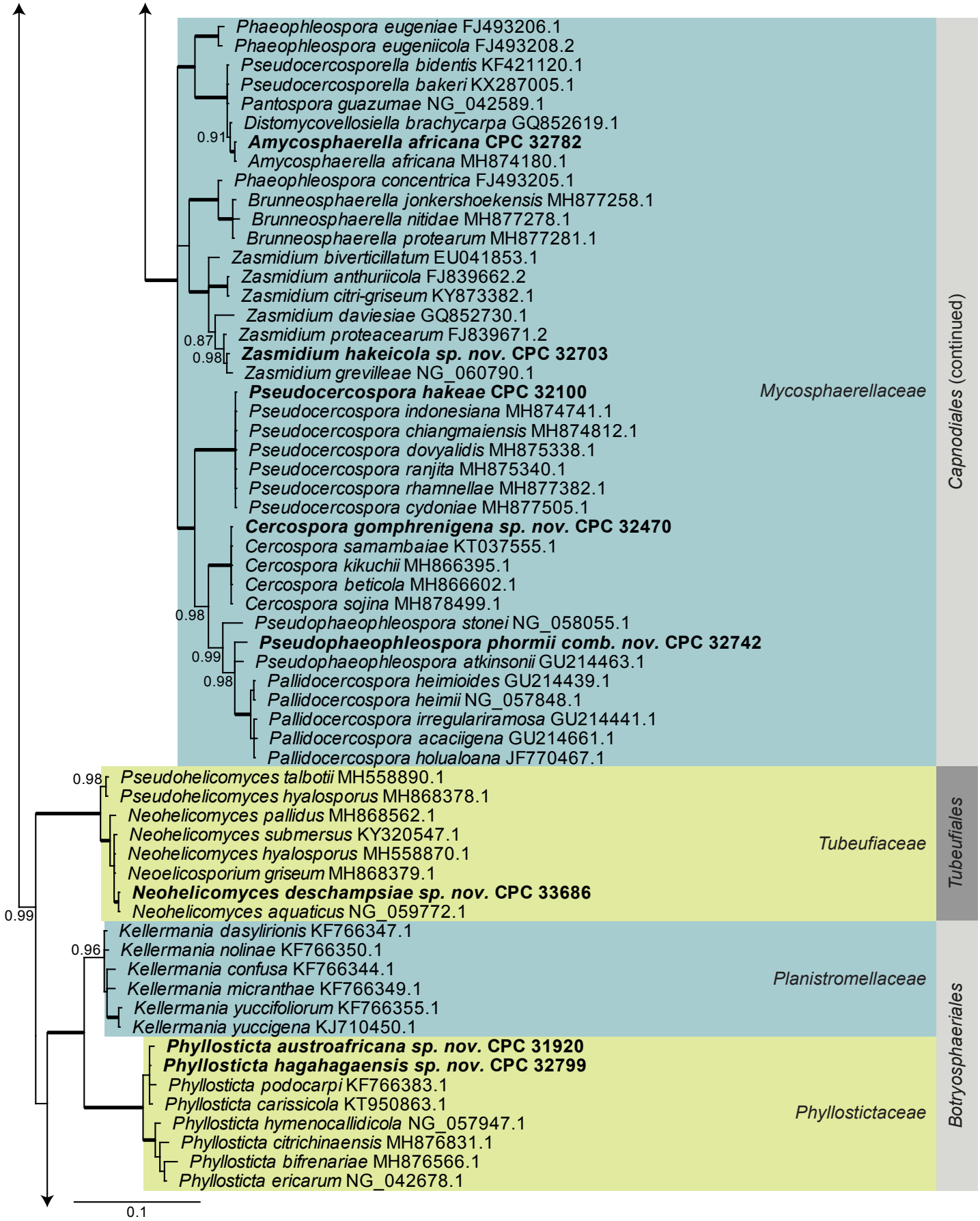

Fig. 1. (Continued).

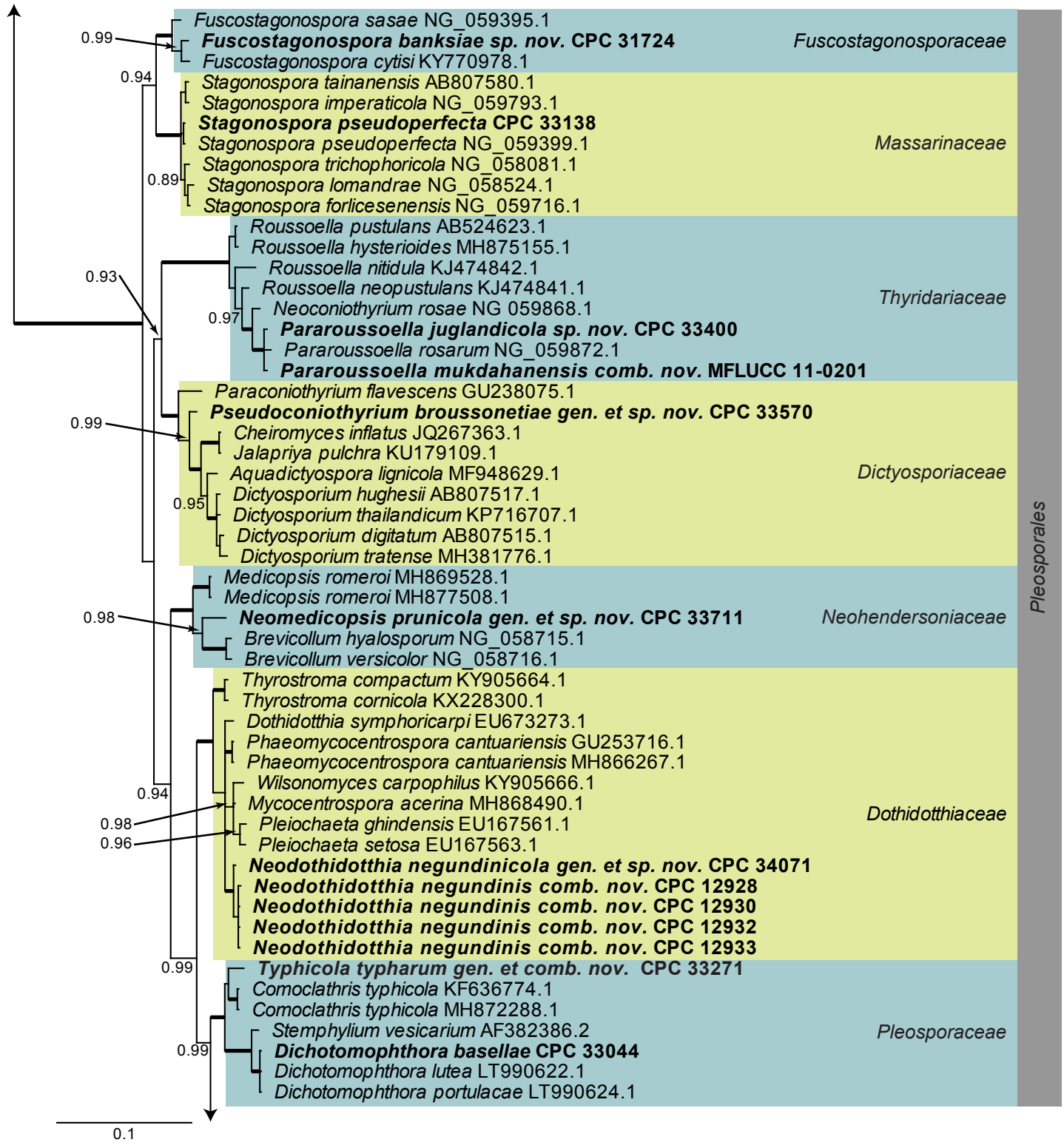

Fig. 1. (Continued).

Sordariomycetes LSU phylogeny (Fig. 4): The alignment contained 174 isolates and *Saccharata proteae* (CBS 119218, GenBank EU552145.1) was used as outgroup. The final alignment contained a total of 778 characters used for the phylogenetic analyses, including alignment gaps. The alignment contained a total of 334 unique site patterns. Based on the results of MrModelTest, dirichlet base frequencies and the GTR+I+G model was used for the Bayesian analysis. The Bayesian analyses generated 161 202 trees from which 120 902 were sampled after 25 % of the trees were discarded as burn-in. The posterior probability values (PP) higher than 0.84 are plotted on the tree (Fig. 4).

Species phylogenies: Specific phylogenetic analyses were run for selected species and the resulting phylogenies are discussed in the species notes where applicable. Statistics associated with those phylogenies are provided in the figure legends.

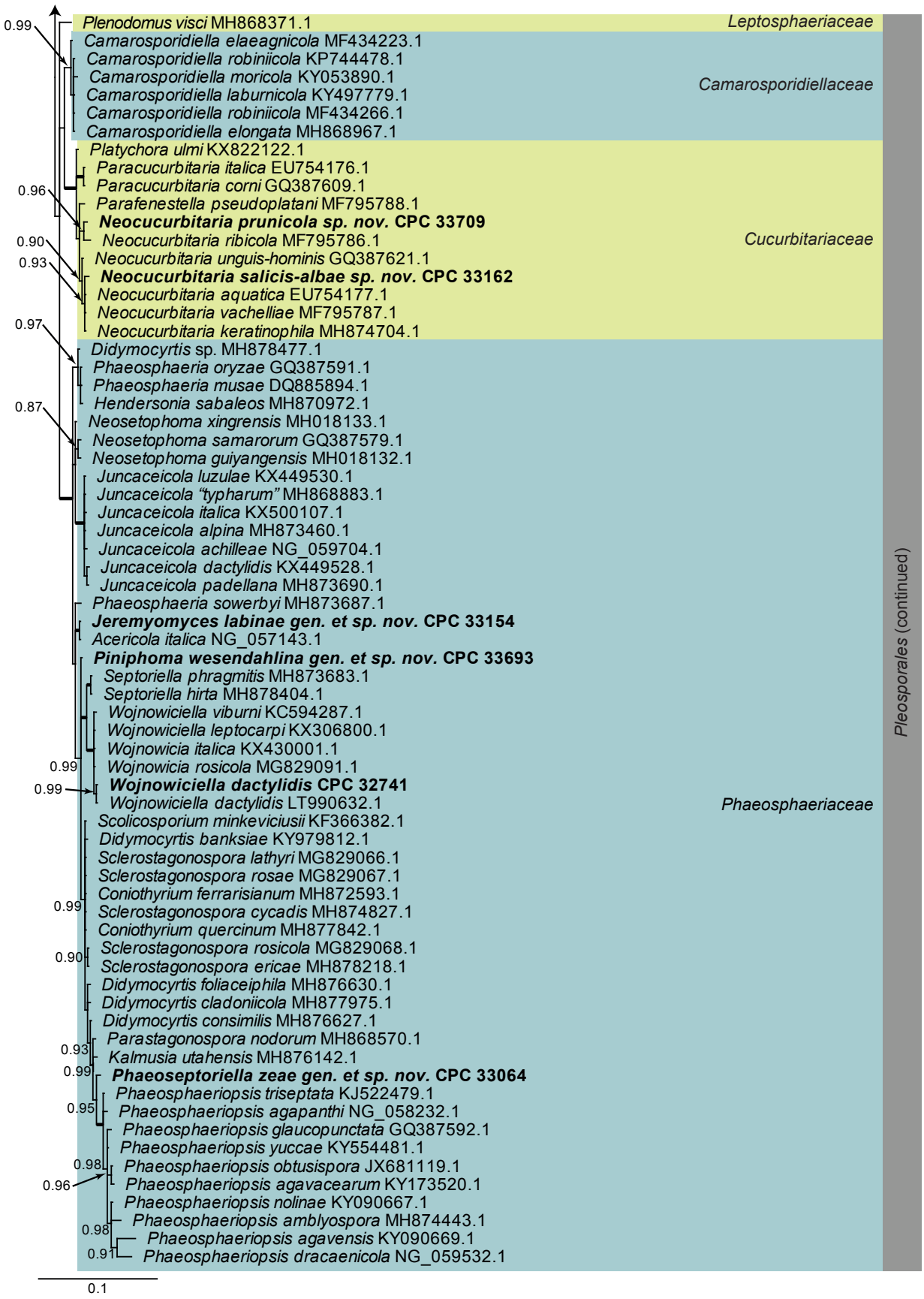

Fig. 1. (Continued).

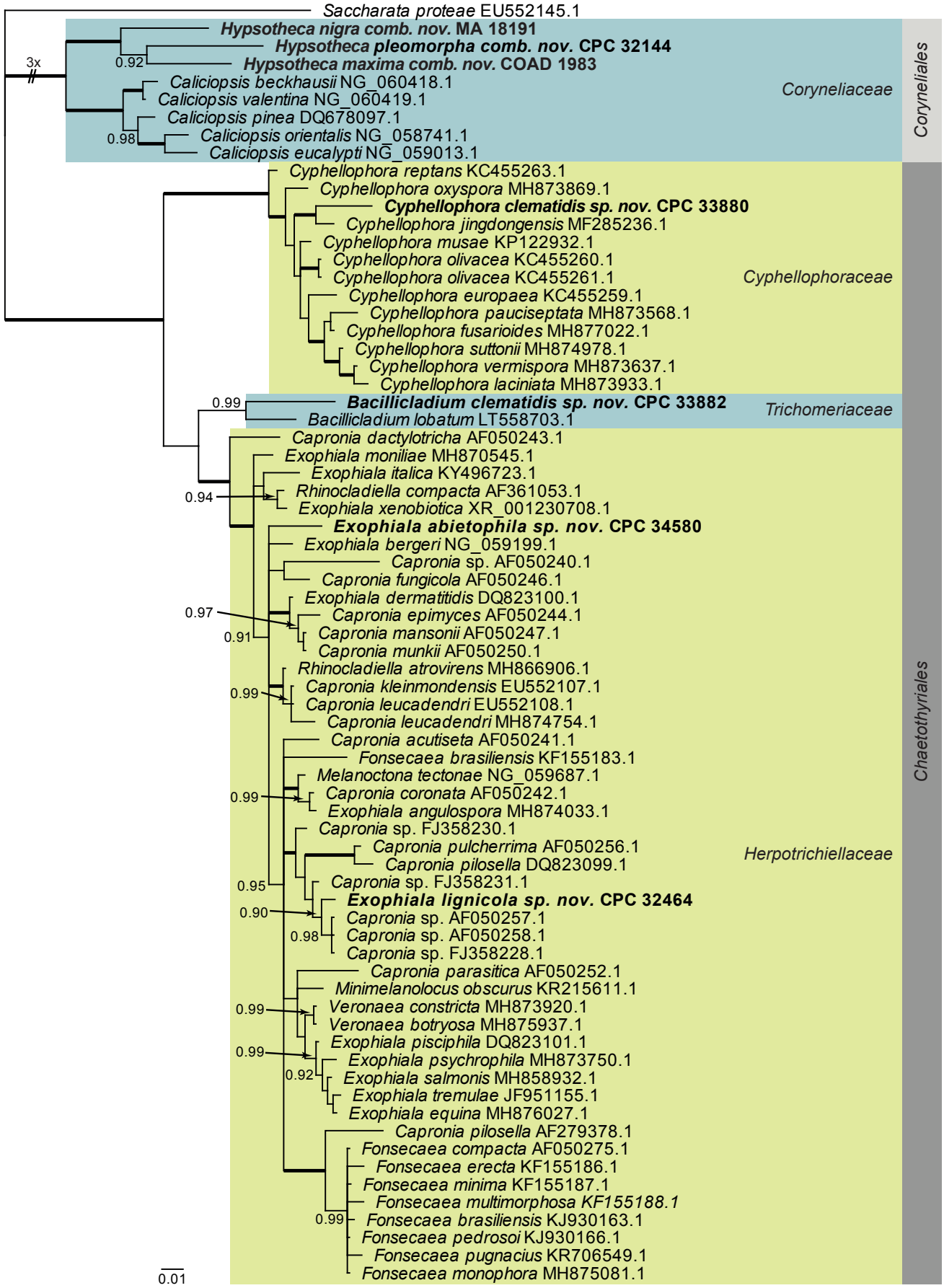

Fig. 2. Consensus phylogram (50 % majority rule) obtained from a Bayesian analysis of the *Eurotiomycetes* alignment. Bayesian posterior probabilities (PP) >0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or culture accession numbers are indicated behind the species names. The tree was rooted to *Saccharata proteae* (GenBank EU552145.1) and the novelties treated in the Taxonomy section are indicated in bold face.

Fig. 3. Consensus phylogram (50 % majority rule) obtained from a Bayesian analysis of the *Lecanoromycetes* and *Leotiomycetes* alignment. Bayesian posterior probabilities (PP) >0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families, orders and classes are indicated with coloured blocks to the right of the tree. GenBank accession and/or culture accession numbers are indicated behind the species names. The tree was rooted to *Saccharata proteae* (GenBank EU552145.1) and the novelties treated in the Taxonomy section are indicated in bold face.

Taxonomy

Amycosphaerella africana (Crous & M.J. Wingf.) Quaedvl. & Crous, *Persoonia* **33**: 23. 2014. Fig. 5.
Basionym: *Mycosphaerella africana* Crous & M.J. Wingf., *Mycologia* **88**: 450. 1996.

In vitro. Ascomata pseudothecial, erumpent to superficial on agar, black, globose, 70–90 µm diam; apical ostiole; wall of 2–4 layers of medium brown *textura angularis*. *Asci* aparaphysate, fasciculate, bitunicate, narrowly ellipsoid to subcylindrical, straight to incurved, 8-spored, 28–37 × 6–7 µm. *Ascospores* multiseriate, overlapping, hyaline, guttulate, thin-walled, straight to slightly curved, fusoid-ellipsoid with obtuse ends, widest in middle of the apical cell, medianly 1-septate, not to slightly constricted at septum, tapering toward both ends, 10–12 × (2–)2.5 µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium, and smooth, lobate margins, covering dish in 2 wk. On MEA surface pale olivaceous grey to olivaceous grey, reverse iron-grey; on PDA surface olivaceous grey with patches of pale olivaceous grey, reverse iron-grey; on OA surface olivaceous grey with patches of dirty white.

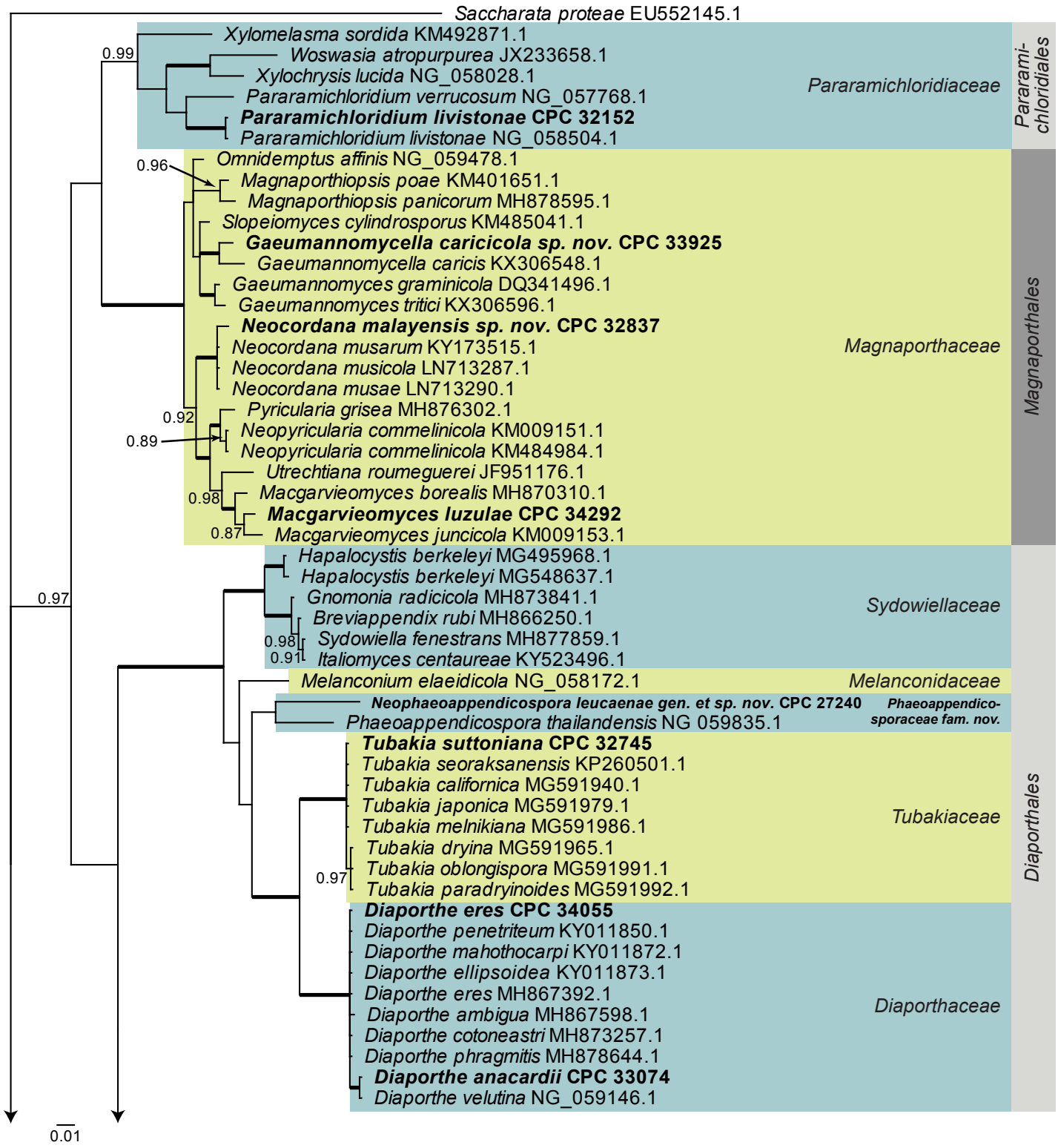

Fig. 4. Consensus phylogram (50 % majority rule) obtained from a Bayesian analysis of the *Sordariomycetes* alignment. Bayesian posterior probabilities (PP) >0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or culture accession numbers are indicated behind the species names. The tree was rooted to *Saccharata proteae* (GenBank EU552145.1) and the novelties treated in the Taxonomy section are indicated in bold face.

Material examined: **New Zealand**, Auckland, Bucklands Beach, 22 Wells Road, on leaves of *Metrosideros excelsa* (*Myrtaceae*), 2015, *R. Thangavel*, T16_03926C = CBS H-23809, culture CBS 144635 = CPC 32782.

Notes: *Amycosphaerella africana*, which is the oldest name for this taxon, is known from Australia (*Buckinghamia* sp., *Eucalyptus grandis, E. globulus*), Colombia (*E. grandis*), New Zealand (*Dracaena draco*), Portugal (*E. globulus*), South Africa (*E. cladocalyx*, *E. deanei*, *E. grandis*, *E. radiata*, *E. smithii, E. viminalis*), and Zambia (*E. globulus*) (Videira *et al*. 2017).

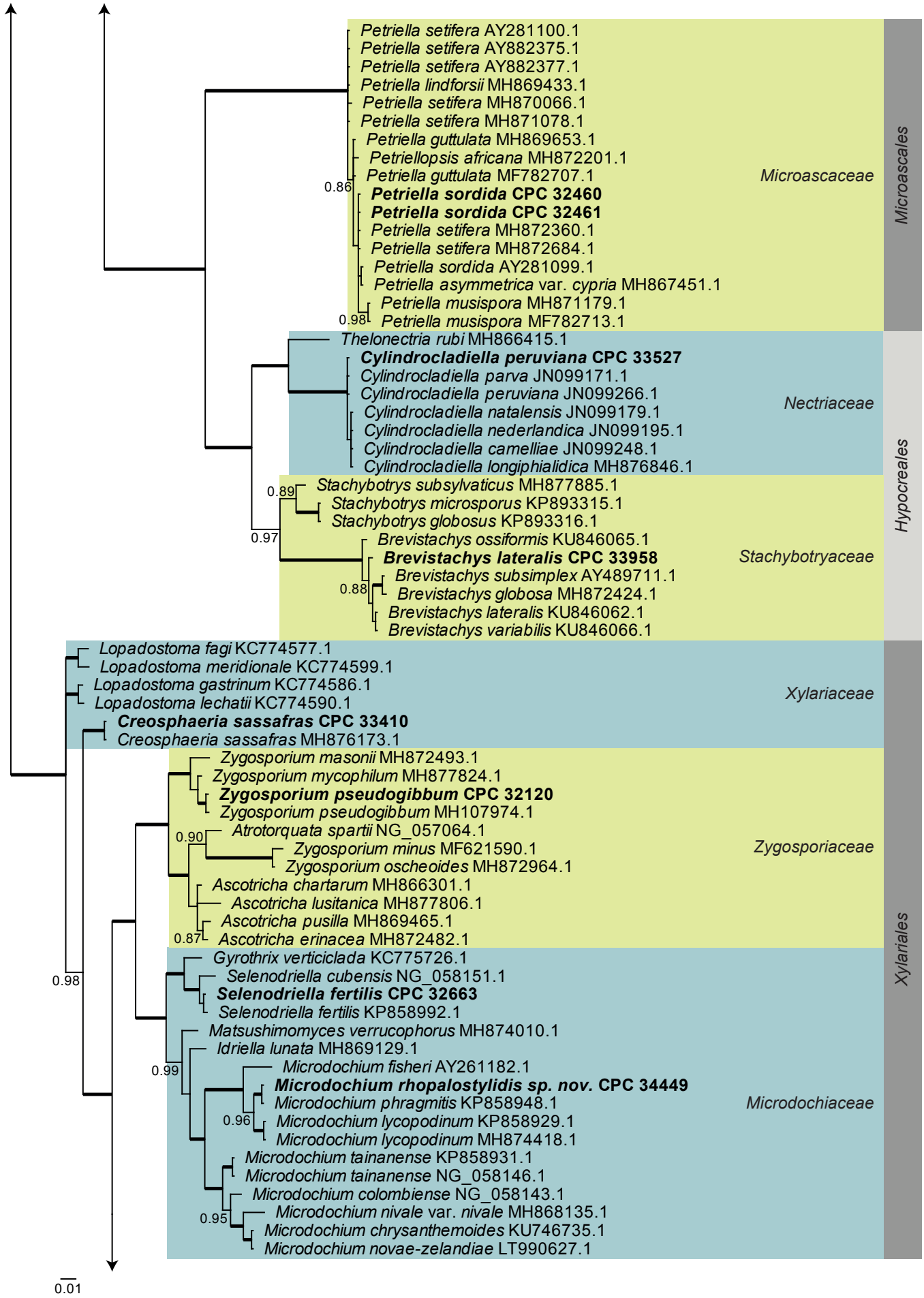

Fig. 4. (Continued).

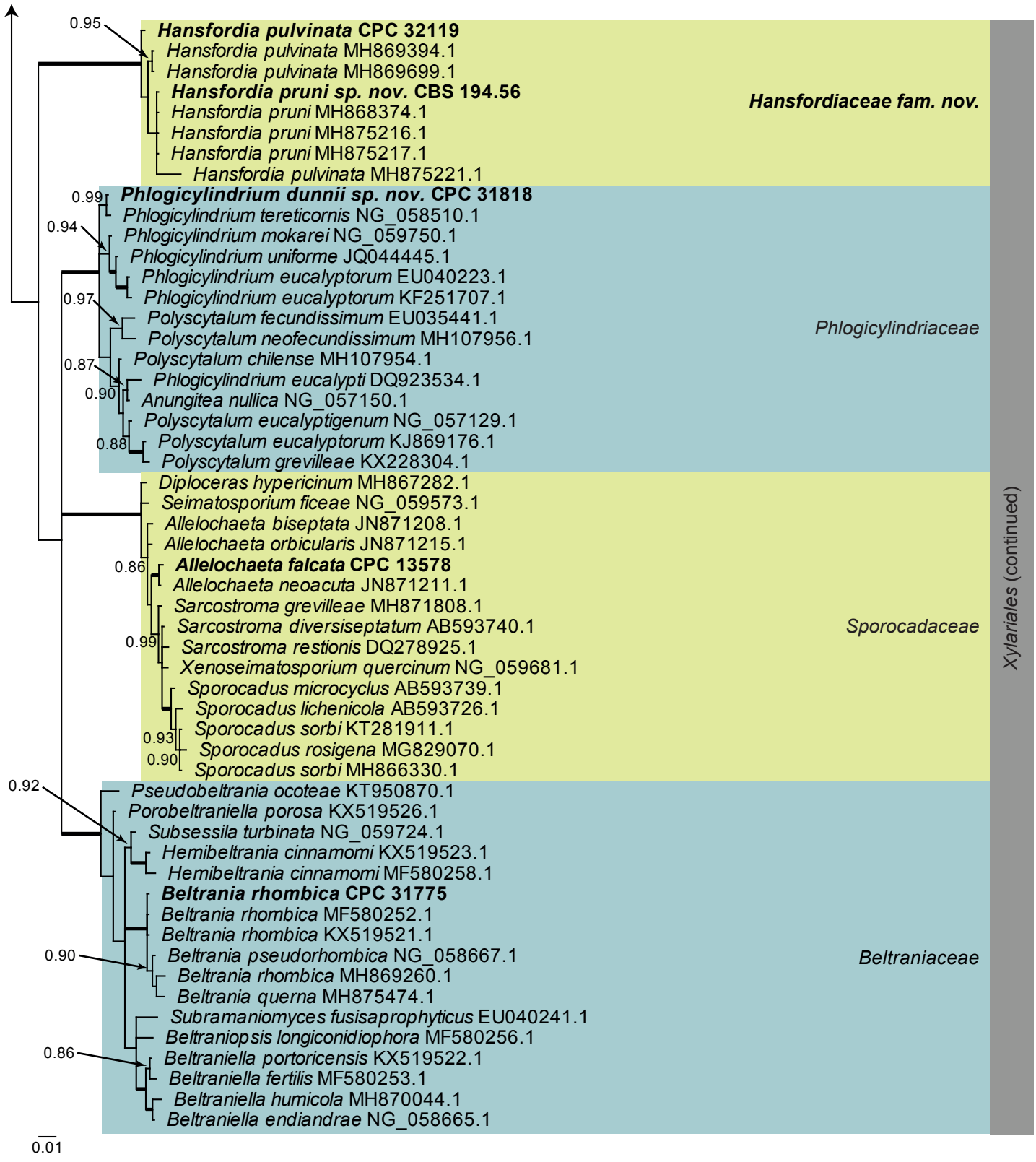

Fig. 4. (Continued).

Based on a megablast search of NCBI's GenBank nucleotide database, the **ITS** sequence was identical to *Mycosphaerella buckinghamiae* (GenBank EU707856.2; Identities = 523/523 (100 %)), *Amycosphaerella africana* (as *Mycosphaerella africana*, GenBank AY626981.1; Identities = 523/523 (100 %)), and related to *Pantospora guazumae* (GenBank NR_119971.1; Identities = 521/523 (99 %), no gaps). Closest hits using the **LSU** sequence are *Amycosphaerella africana* (GenBank MH874180.1; Identities = 785/785 (100 %)), *Mycosphaerella buckinghamiae* (GenBank EU707856.2; Identities = 785/785 (100 %)), and *Distomycovellosiella brachycarpa* (as *Passalora brachycarpa*, GenBank GU214664.1; Identities = 782/785 (99 %), 2 gaps (0 %)). The ***tef1*** sequence was identical to numerous sequences of *Amycosphaerella africana* (e.g. as *Mycosphaerella ellipsoidea*, GenBank JX901653.1; Identities = 394/394 (100 %)). Closest hits using the ***tub2***

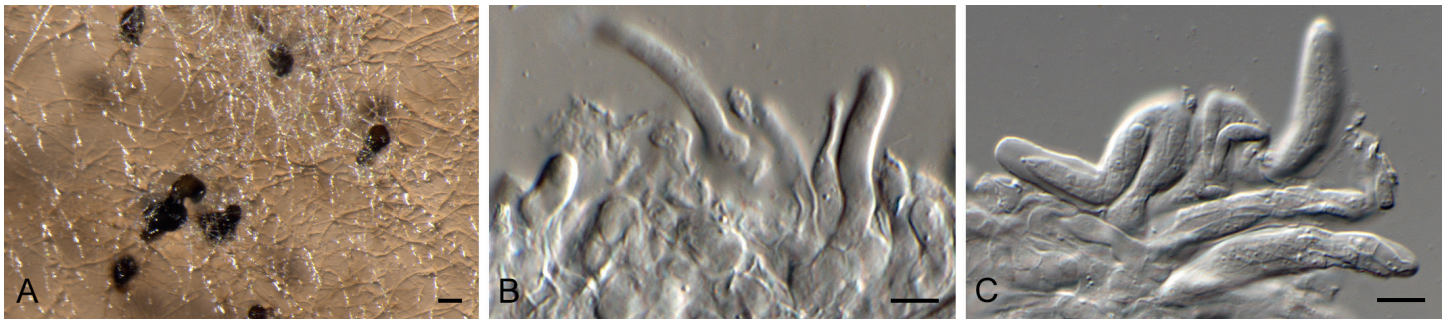

Fig. 5. *Amycosphaerella africana* (CPC 32782). **A.** Ascomata forming on SNA. **B, C.** Asci and ascospores. Scale bars: A = 90 µm, B, C = 10 µm.

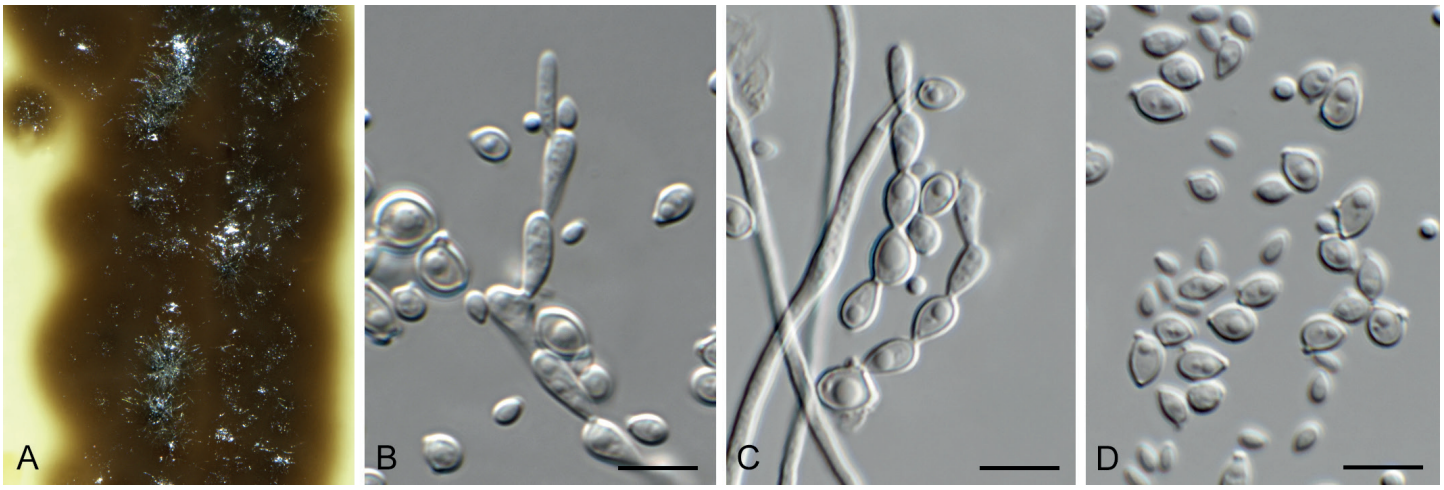

Fig. 6. *Bacillicladium clematidis* (CPC 33882). **A.** Colony on OA. **B, C.** Conidiogenous cells giving rise to conidia. **D.** Budding conidia. Scale bars = 10 µm.

sequence had highest similarity to *Amycosphaerella africana* (GenBank LC121222.1; Identities = 571/572 (99 %), no gaps), *Pseudocercospora fijiensis* (GenBank XM_007921924.1; Identities = 566/616 (92 %), no gaps), and *Zymoseptoria tritici* (GenBank XM_003856727.1; Identities = 552/616 (90 %), no gaps).

Bacillicladium clematidis Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB829299. Fig. 6.

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

Mycelium consisting of pale brown, smooth, branched, 1.5–2 µm diam hyphae that become swollen and constricted at septa in the conidiogenous region, where individual cells become more ellipsoid and clavate to globose, up to 5 µm diam. *Conidiophores* reduced to conidiogenous cells on hyphae, pale brown, smooth, phialidic, 0.5–1 × 1 µm, with inconspicuous collarette, not flared. *Conidia* solitary, ellipsoid, pale brown, smooth, guttulate, aseptate, apex obtuse, basal locus truncate, 0.5 µm diam; older conidia undergoing microcyclic conidiation, (3–)4–4.5(–5) × (1.5–)2.5–3(–5) µm.

Culture characteristics: Colonies flat, spreading, lacking aerial mycelium and even, lobate margin, reaching 6 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse umber.

Typus: **Austria**, Gaaden, branch of *Clematis vitalbae* (*Ranunculaceae*), 21 Apr. 2017, *M. Mann & R.K. Schumacher*, HPC 2101, RKS 102 (**holotype** CBS H-23828, culture ex-type CPC 33882 = CBS 145035).

Notes: *Bacillicladium clematidis* is phylogenetically allied to the genus *Bacillicladium*, based on *B. lobatum. Bacillicladium lobatum*, which grows on bare granite walls, has three different growth habits *in vitro*, dependent on cultivation medium, temperature and colony age. But morphologically, *B. clematidis* provides an appropriate fit for the genus, sharing the black yeast-like growth in culture (Réblová *et al.* 2016).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Camptophora hylomeconis* (GenBank NR_132881.1; Identities = 352/402 (88 %), 20 gaps (5 %)), *Aphanophora eugeniae* (GenBank NR_132829.1; Identities = 394/466 (85 %), 24 gaps (5 %)), and *Ceramothyrium thailandicum* (GenBank NR_137768.1; Identities = 346/415 (83 %), 36 gaps (8 %)). Closest hits using the **LSU** sequence are *Bacillicladium lobatum* (GenBank LT558703.1; Identities = 822/863 (95 %), 2 gaps (0 %)), *Veronaea botryosa* (GenBank MH875937.1; Identities = 818/869 (94 %), 5 gaps (0 %)), and *Veronaea constricta* (GenBank MH873920.1; Identities = 811/862 (94 %), 5 gaps (0 %)). No significant hits were obtained when the ***tub2*** sequence was used in blastn and megablast searches.

Beltrania rhombica Penz., *Michelia* **2**(8): 474. 1882. Fig. 7.

Setae rarely observed, erect, dark brown, thick-walled, 7–10-septate, straight to flexuous, tapering to an acute apex, 200–300 × 4–5 µm, with lobed basal cell, 6–8 µm diam.

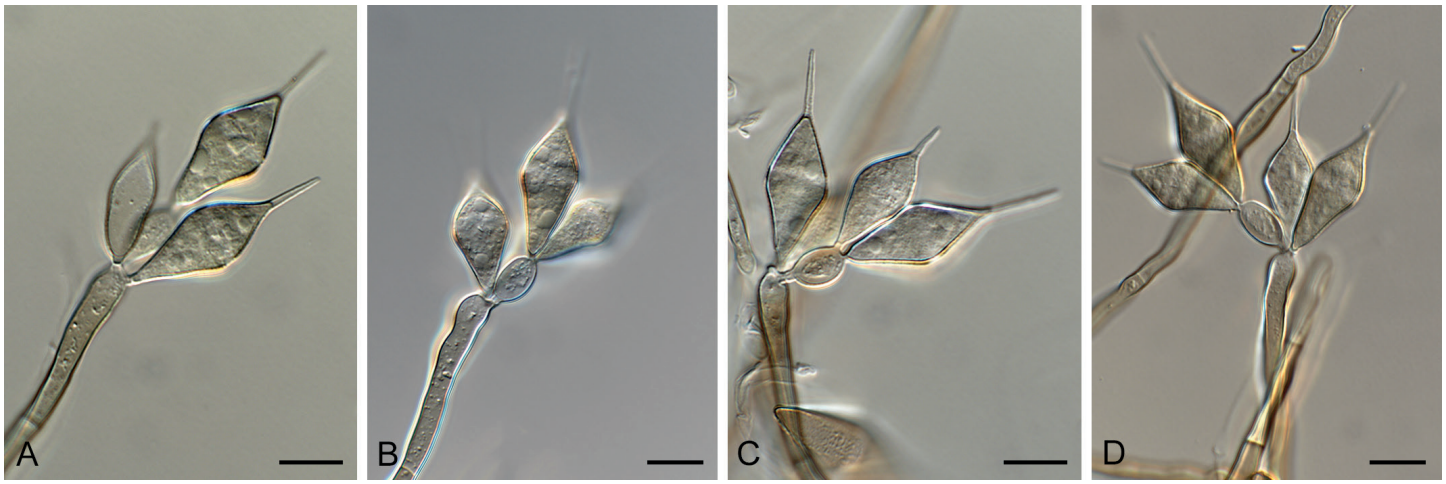

Fig. 7. *Beltrania rhombica* (CPC 31775). **A–D.** Conidiophores, separating cells and conidia. Scale bars = 10 µm.

Conidiophores erect, unbranched, medium brown, smooth, multi-septate, 50–300 × 4–7 µm. *Conidiogenous cells* terminal, pale brown, smooth, 15–30 × 4–6 µm, polyblastic with several flat-tipped denticles, 1.5–2 µm. *Separating cells* pale brown, finely roughened, 7–13 × 5–7 µm, with several apical, flat-tipped denticles, 1–2 µm diam. *Conidia* solitary, biconic, pale brown, aseptate, with a distinct median transverse band of paler pigment, (22–)24–27(–29) × (9–)10–11 µm; apical appendage (10–)12–14(–15) × 1 µm, tapering to an acutely rounded tip.

Culture characteristics: Colonies spreading, with moderate aerial mycelium, covering dish after 2 wk at 25 °C. On MEA surface dark brick, reverse fawn; on PDA surface and reverse umber; on OA surface umber.

Material examined: **Chile**, Llanos, on leaves of *Eucalyptus urophylla* (*Myrtaceae*), Jul. 2010, *M.J. Wingfield*, HPC 1412, CBS H-23264, culture CPC 31775 = CBS 144521.

Notes: *Beltrania pseudorhombica* was described from needles of *Pinus tabulaeformis* collected in Beijing, China (Crous *et al*. 2014), and distinguished from *B. rhombica*, which has longer setae (can be up to 330 µm long, and wider conidia 15–30 × 7–14 µm; Ellis 1971). There is no ex-type strain for *B. rhombica*, and it needs to be recollected on *Citrus limon* in Italy to clarify its taxonomy.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Beltrania rhombica* (GenBank MH857718.1; Identities = 574/577 (99 %), no gaps), *Beltrania pseudorhombica* (GenBank NR_148074.1; Identities = 574/577 (99 %), no gaps), and *Beltrania querna* (GenBank MH856775.1; Identities = 530/538 (99 %), no gaps). Closest hits using the **LSU** sequence are *Beltrania rhombica* (GenBank MF580252.1; Identities = 823/823 (100 %), no gaps), *Beltrania pseudorhombica* (GenBank NG_058667.1; Identities = 810/812 (99 %), no gaps), and *Beltrania querna* (GenBank MH875474.1; Identities = 859/866 (99 %), 2 gaps (0 %)).

Brevistachys lateralis L. Lombard & Crous, *Persoonia* **36**: 183. 2016. Fig. 8.

Mycelium consisting of hyaline, branched, septate, smooth, 2.5–3 µm diam hyphae (hyphae thick-walled and brown in conidiogenous region). *Conidiophores* erect, simple, single, rarely in groups, mostly unbranched, straight to slightly flexuous, 2–3-septate, thick-walled on PDA, thin-walled on OA, olivaceous brown, verruculose, 80–100 × 2.5–3.5 µm, with bulbous apex, 6–7 µm diam, bearing a whorl of 10–12 conidiogenous cells. *Conidiogenous cells* terminal, elongate, doliiform to subcylindrical, pale brown, smooth, 9–12 × 4–4.5 µm, with conspicuous collarettes. *Conidia* aggregating in slimy mass with brown exudate on PDA, but in long unbranched dry chains on OA (without exudate), dimorphic, conidia globose, becoming dark brown and verruculose, (4–)5(–6) µm diam, or ellipsoid, pale brown, verruculose, 9–10 ×4–5 µm.

Culture characteristics: Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface olivaceous grey, reverse umber in middle, sienna in outer region; on PDA surface ochreous with diffuse saffron pigment, reverse vinaceous; on OA surface saffron.

Material examined: **Thailand**, Rachaburi Province, Bangkok, on leaves of *Musa* sp. (*Musaceae*), 2008, *P.W. Crous*, HPC 2156, CBS H-23831, culture CPC 33958 = CBS 145062.

Notes: *Brevistachys lateralis* was described from leaves of *Musa* sp. collected in Queensland, Australia (Lombard *et al*. 2016). This is the first record of the fungus from Thailand where it also occurs on *Musa* leaves.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Brevistachys variabilis* (GenBank NR_153620.1; Identities = 531/542 (98 %), 6 gaps (1 %)), *Brevistachys globosa* (GenBank NR_145070.1; Identities = 555/569 (98 %), 4 gaps (0 %)), and *Brevistachys subsimplex* (as *Stachybotrys subsimplex*, GenBank AF205439.1; Identities = 558/573 (97 %), 2 gaps (0 %)). Closest hits using the **LSU** sequence are *Brevistachys lateralis* (GenBank KU846062.1; Identities = 823/825 (99 %), 1 gap (0 %)), *Brevistachys variabilis* (GenBank KU846066.1; Identities = 822/825 (99 %), 1 gap (0 %)), and *Brevistachys subsimplex* (as *Stachybotrys subsimplex*, GenBank AY489711.1; Identities = 829/833 (99 %), no gaps). Closest hits using the ***cmdA*** sequence had highest similarity to *Brevistachys lateralis* (GenBank KU846027.1; Identities = 360/360 (100 %), no gaps), *Brevistachys variabilis* (GenBank KU846030.1; Identities = 360/360 (100 %), no

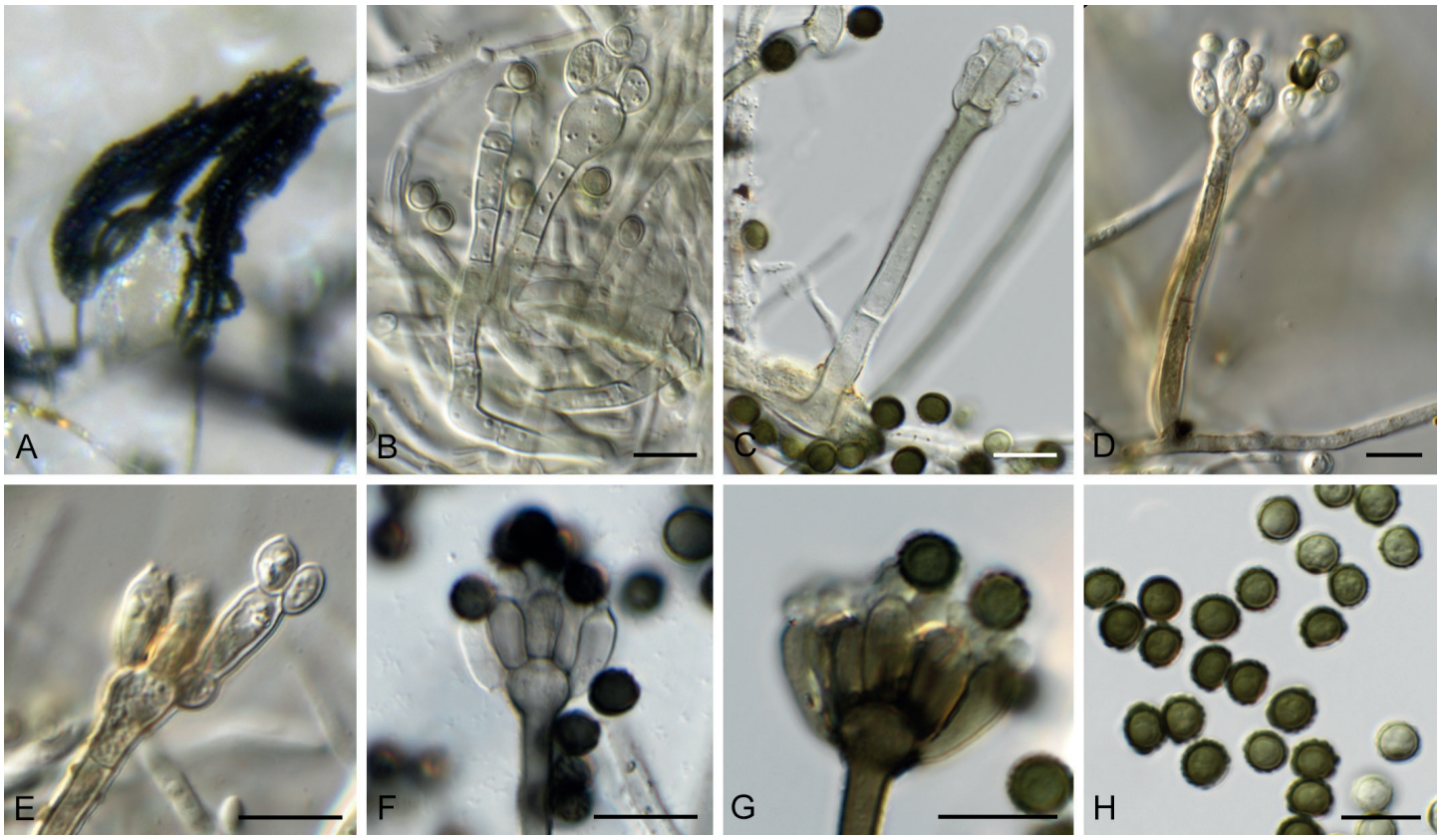

Fig. 8. *Brevistachys lateralis* (CPC 33958). **A–G.** Conidiophores with phialides, forming chains of conidia. **H.** Conidia. Scale bars = 10 µm.

gaps), *Brevistachys globosa* (GenBank KU846023.1; Identities = 315/326 (97 %), 1 gap (0 %)) and *Brevistachys ossiformis* (GenBank KU846028.1; Identities = 307/326 (94 %), 1 gap (0 %)), and distant hits with *Stachybotrys chlorohalonata* (GenBank AY180255.1; Identities = 125/133 (94 %), no gaps), *Stachybotrys chartarum* (GenBank KM231452.1; Identities = 124/133 (93 %), no gaps), and *Xenoacremonium recifei* (GenBank KM231420.1; Identities = 122/131 (93 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Brevistachys lateralis* (GenBank KU846074.1; Identities = 760/760 (100 %), no gaps), *Brevistachys subsimplex* (as *Stachybotrys subsimplex*, GenBank EF692519.1; Identities = 762/785 (97 %), no gaps), and *Brevistachys ossiformis* (GenBank KU846075.1; Identities = 738/760 (97 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Brevistachys lateralis* (GenBank KU846090.1; Identities = 439/442 (99 %), no gaps), *Brevistachys globosa* (GenBank KU846085.1; Identities = 423/442 (96 %), 4 gaps (0 %)), and *Brevistachys ossiformis* (GenBank KU846091.1; Identities = 412/443 (93 %), 10 gaps (2 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Brevistachys lateralis* (GenBank KU846106.1; Identities = 361/361 (100 %), no gaps), *Brevistachys variabilis* (GenBank KU846110.1; Identities = 359/361 (99 %), no gaps), and *Brevistachys globosa* (GenBank KU846101.1; Identities = 351/362 (97 %), 1 gap (0 %)).

Cercospora gomphrenigena Crous, ***sp. nov.*** MycoBank MB829300. Fig. 9.

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

Leaf spots circular, 1–4 mm diam, medium brown, with broad purple-red border. *Fascicles* only developing in moist chambers. *Conidiophores* solitary, arising from weakly developed stroma of a few brown globoid cells, subcylindrical, medium brown, smooth, flexuous, multiseptate, up to 800 µm tall, 3–6 µm diam. *Conidiogenous cells* subcylindrical, brown, smooth, terminal and intercalary, 30–160 × 4–5 µm; scars thickened, darkened and refractive, 3–4 µm diam. *Conidia* solitary, acicular, hyaline, smooth, flexuous, multiseptate, apex subobtuse, base truncate, 150–300 × 4–5 µm; hila thickened, darkened and refractive, 3–4 µm diam.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and even, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface smoke grey, reverse scarlet with diffuse scarlet pigment; on PDA surface smoke grey, reverse olivaceous grey; on OA surface olivaceous grey with patches of dirty white, with diffuse scarlet pigment.

Typus: **South Africa**, Gauteng Province, Gauteng, on leaves of *Gomphrena globosa* (*Amaranthaceae*), 2010, *P.W. Crous*, HPC 1516 (**holotype** CBS H-23803, culture ex-type CPC 32470 = CBS 144613).

Notes: A DNA phylogeny for most common species of *Cercospora* known from culture was presented by Groenewald *et al*. (2013), with secondary barcode genes treated by Bakhshi *et al.* (2018). *Cercospora gomphrenigena* was collected from leaves of *Gomphrena globosa* in South Africa in an attempt to resolve the identity of *Cercospora pretoriensis* that occurs on this host (conidia narrowly cylindrical to subacicular, 15–90 × 2–4.5 µm; Braun *et al.* 2015), from which *C. gomphrenigena* is morphologically distinct, having much longer and wider conidia. It is morphologically closer to C. *gomphrenae* [conidiophores in

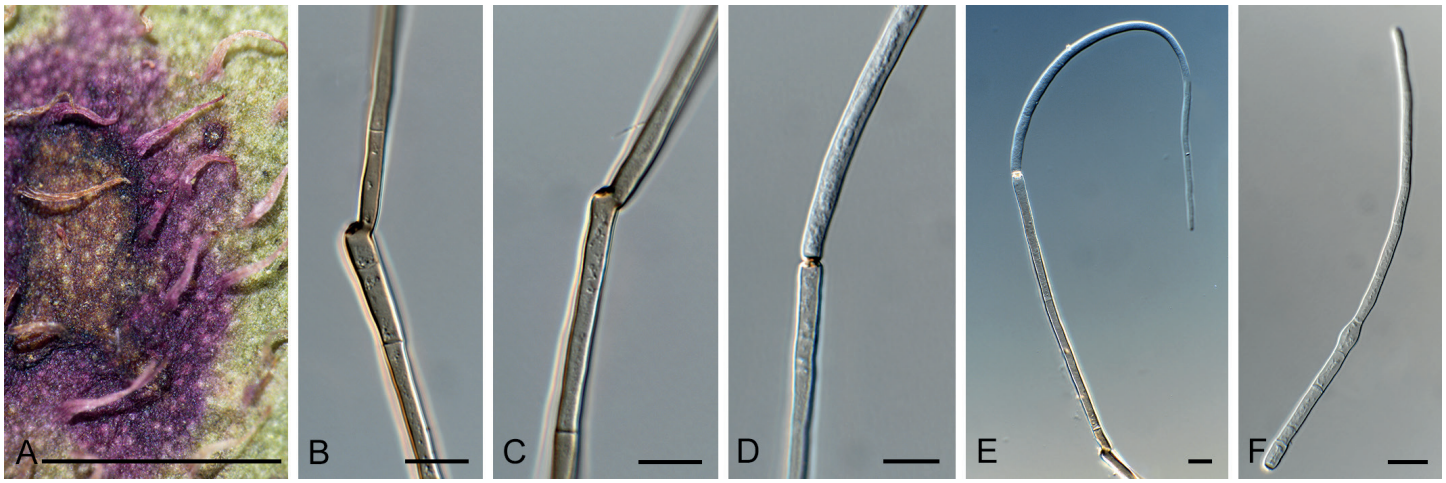

Fig. 9. *Cercospora gomphrenigena* (CPC 32470). **A.** Leaf spot. **B–E.** Conidiophores with conidial loci. **F.** Conidium. Scale bars: A = 4 mm, B–F = 10 µm.

small, divergent fascicles, 30–300 × 3–7 µm, conidiogenous cells 10–30 µm long, conidia 30–300(–450) × 2–5 µm, 3–20-septate; Braun *et al.* 2015], but is distinct in having longer conidiophores and conidiogenous cells, wider scars, and wider conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the **ITS** sequence was identical to *Cercospora dichondrae* (GenBank MK039698.1; Identities = 525/525 (100 %)), *Cercospora beticola* (GenBank MH424448.1; Identities = 525/525 (100 %)), and *Cercospora malayensis* (GenBank MH129519.1; Identities = 525/525 (100 %)). The **LSU** sequence is identical to those of numerous *Cercospora* species, e.g. *Cercospora sesami* (GenBank MK029365.1; Identities = 783/783 (100 %)). Closest hits using the ***cmdA*** sequence had highest similarity to *Cercospora samambaiae* (GenBank KT037463.1; Identities = 448/448 (100 %)), *Cercospora* sp. G NV-2018 (GenBank MF681410.1; Identities = 443/444 (99 %), no gaps), and *Cercospora cyperina* (GenBank KT193729.1; Identities = 444/448 (99 %), no gaps). Closest hits using the ***his3*** sequence had highest similarity to *Cercospora* sp. 3 LO-2017 (GenBank KX522813.1; Identities = 375/375 (100 %)), *Cercospora kikuchii* (GenBank KP825147.1; Identities = 375/375 (100 %)), and *Cercospora* cf. *physalidis* (GenBank JX142654.1; Identities = 380/381 (99 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Cercospora* sp. 3 LO-2017 (GenBank KX522847.1; Identities = 280/280 (100 %)), *Cercospora* cf. *alchemillicola* (GenBank KR733109.1; Identities = 279/279 (100 %)), and *Cercospora samambaiae* (GenBank KT037468.1; Identities = 487/488 (99 %), no gaps). Closest hits using the ***tub2*** sequence had highest similarity to *Cercospora kikuchii* (GenBank AB240222.1; Identities = 581/581 (100 %)), *Cercospora beticola* (GenBank XM_023592737.1; Identities = 754/784 (96 %), no gaps), and *Cercospora* sp. Q (GenBank JX142482.1; Identities = 1016/1054 (96 %), 4 gaps (0 %)).

Cladoriella xanthorrhoeae Crous, *Persoonia* **39**: 417. 2017. Fig. 10.

Mycelium consisting of pale brown, smooth, septate, branched, 2.5–3 µm diam hyphae. *Conidiophores* solitary, erect, flexuous, medium brown, smooth, subcylindrical, unbranched, 1–4-septate, 20–40 × 2.5–3 µm; at times conidiophores can be reduced to conidiogenous cells arising from hyphae, 5–8 × 2.5–3 µm. *Conidiogenous cells* terminal, integrated, medium brown, smooth to finely roughened, subcylindrical, with 1–2 flat-tipped loci, 2–2.5 µm diam, darkened, somewhat thickened, 7–12 × 3.5–4 µm. *Ramoconidia* medium brown, finely verruculose, 1(–2)-septate, subcylindrical to somewhat fusoid-ellipsoid, 12–19 × 3.5–4 µm; loci thickened, darkened, 1.5–2 µm diam. *Conidia* in short (2–6), branched chains, medium brown, verruculose, fusoid-ellipsoid, 1-septate; hila truncate, thickened, darkened, 1.5–2 µm diam, (9–)12–15(–17) × (3.5–)4 µm; hila thickened, somewhat darkened, 1.5–2 µm diam.

Culture characteristics: Colonies erumpent, spreading, with sparse aerial mycelium and feathery margin, reaching 7 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface iron-grey; diffuse red pigment visible in agar on PDA and OA.

Material examined: **Australia**, New South Wales, Nullica State Forest, on leaves of *Xanthorrhoea* sp. (*Asphodelaceae*), Nov. 2016, *P.W. Crous*, HPC 1830, CBS H-23804, culture CPC 32609 = CBS 144523.

Notes: *Cladoriella xanthorrhoeae* was recently described on *Xanthorrhoea* sp. from Australia (Crous *et al*. 2017), and CPC 32609 represents the second collection of this fungus from the type locality, where it appears to be well established on Xanthorrhoea.

Based on a megablast search of NCBI's GenBank nucleotide database, the **ITS** sequence was identical to *Cladoriella xanthorrhoeae* (GenBank NR_156392.1; Identities = 602/602 (100 %)); and related to *Cladoriella rubrigena* (GenBank NR_156219.1; Identities = 498/552 (90 %), 15 gaps (2 %)) and *Cladoriella eucalypti* (GenBank EU040224.1; Identities = 589/641 (92 %), 15 gaps (2 %)). Closest hits using the **LSU** sequence are *Cladoriella rubrigena* (GenBank NG_058780.1; Identities = 867/881 (98 %), 2 gaps (0 %)), *Cladoriella eucalypti* (GenBank EU040224.1; Identities = 861/876 (98 %), 2 gaps (0 %)), and *Cladoriella paleospora* (GenBank MH874922.1; Identities = 823/880 (94 %), 3 gaps (0 %)).

Creosphaeria sassafras (Schwein.) Y.M. Ju *et al.*, *Mycotaxon* **47**: 223. 1993. Fig. 11.
Basionym: *Sphaeria sassafras* Schwein., *Schr. naturf. Ges. Leipzig* **1**: 36 (10 of repr.). 1822.

In vitro: Mycelium consisting of hyaline to brown, smooth to warty, 1.5–3 µm diam hyphae. *Conidiophores* reduced to

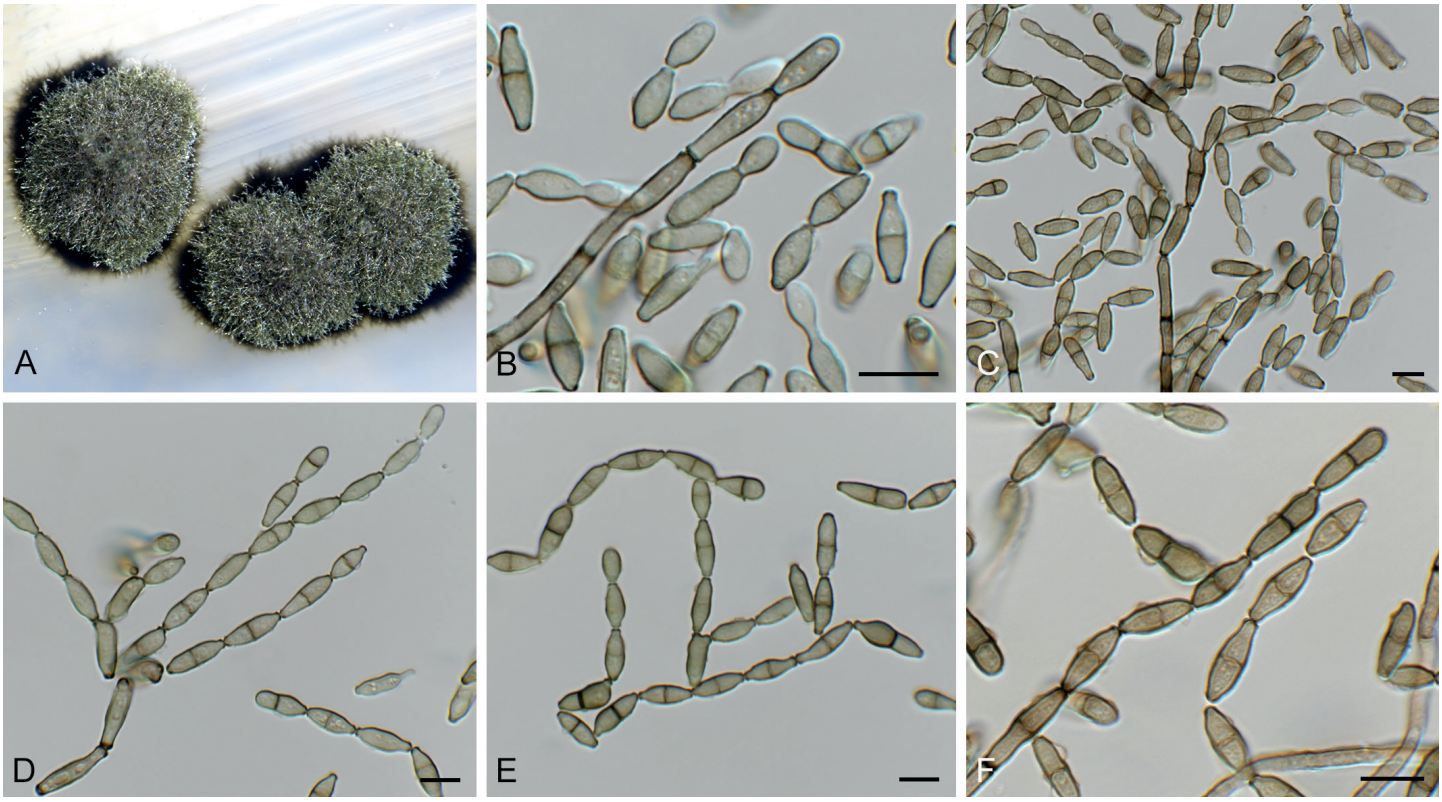

Fig. 10. *Cladoriella xanthorrhoeae* (CPC 32609). **A.** Colonies on SNA. **B–F.** Conidiophores giving rise to branched conidial chains. Scale bars = 10 µm.

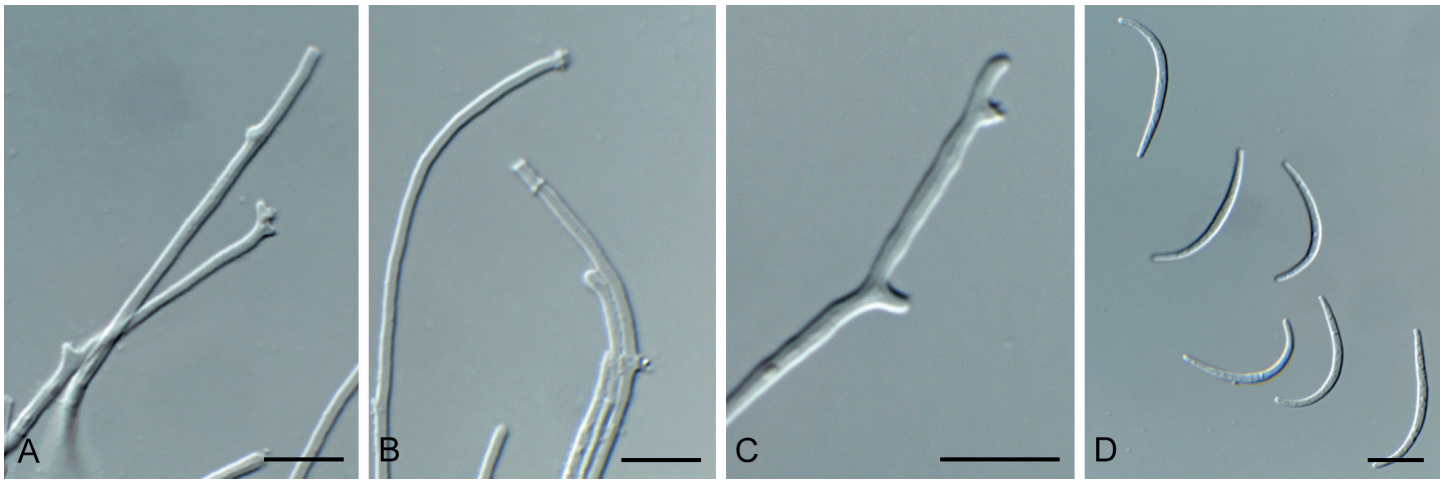

Fig. 11. *Creosphaeria sassafras* (CPC 33410). **A–C.** Conidiophores with conidial loci. **D.** Conidia. Scale bars = 10 µm.

conidiogenous cells occurring on narrower hyphae (1.5–2 µm diam), solitary, erect, pale brown to hyaline, smooth, nodes 1–3 × 1–1.5 µm. *Conidia* hyaline, smooth, aseptate, curved, spindle-shaped, apex subobtuse, base truncate, 20–30 × 2 µm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA surface hazel, reverse sepia in inner region, orange in outer zone; on PDA surface hazel, reverse brown vinaceous; on OA surface hazel.

Material examined: **Spain**, Barcelona, dead branch of *Laurus nobilis* (*Lauraceae*), Mar. 2017, *M. Vera Intrago & R.K. Schumacher*, HPC 2043, RKS 90, culture CPC 33410 = CBS 144984.

Notes: Bills & Peláez (1996) reported conidia of the asexual morph to be 16–22 × 1.2–1.8 µm. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had the greatest similarity to several sequences of *Creosphaeria sassafras* (e.g. GenBank HQ660446.1; Identities = 515/516 (99 %), no gaps). Closest hits using the **LSU** sequence are *Creosphaeria sassafras* (GenBank MH876173.1; Identities = 854/854 (100 %), no gaps), *Lopadostoma lechatii* (GenBank KC774590.1; Identities = 833/854 (98 %), no gaps), and *Lopadostoma meridionale* (GenBank KC774599.1; Identities = 833/855 (97 %), 3 gaps (0 %)).

Cylindrocladiella peruviana (Bat. *et al.*) Boesew., *Canad. J. Bot.* **60**: 2289. 1982. Fig. 12.
Basionym: *Cylindrocladium peruvianum* Bat. *et al.*, *Atas Inst. Micol. Univ. Recife* **2**: 386. 1965.

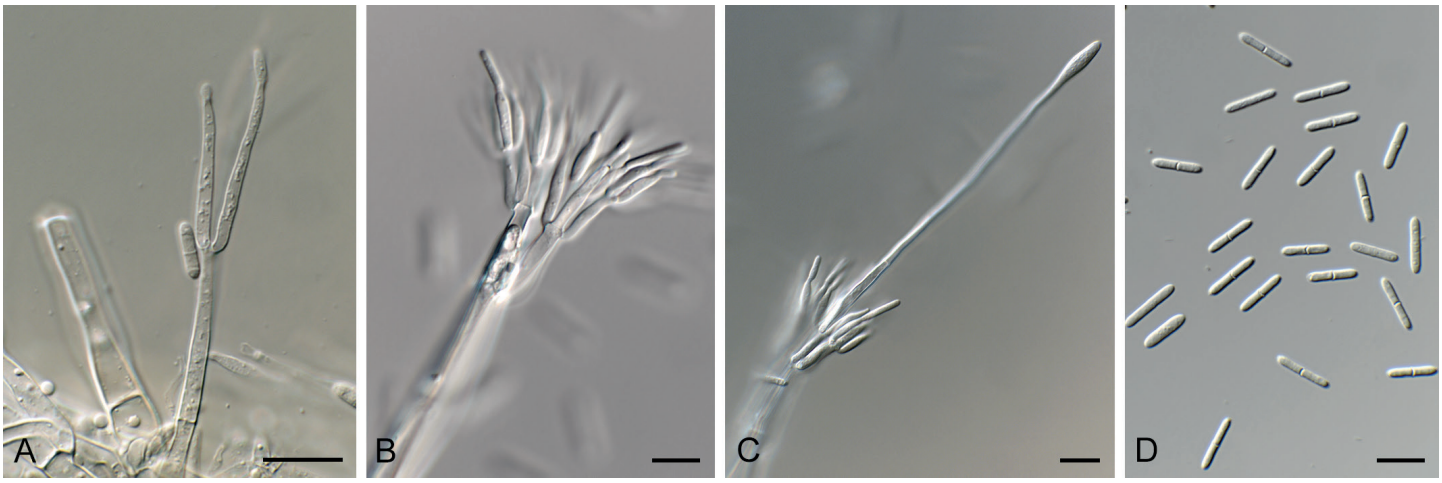

Fig. 12. *Cylindrocladiella peruviana* (CPC 33527). **A.** Subverticillate conidiophore. **B, C.** Penicillate conidiophores. **D.** Conidia. Scale bars = 10 µm.

Conidiophores dimorphic, penicillate and subverticillate, mononematous and hyaline, comprising a stipe, a penicillate arrangement of fertile branches, a stipe extension and a terminal vesicle; *stipe extension* aseptate, straight, 50–70 × 2–3 µm, thick-walled with one basal septum, terminating in thin-walled, ellipsoid to lanceolate vesicles, 3–4 µm wide. *Penicillate conidiogenous apparatus* with primary branches 0–1-septate, 15–25 × 3–4 µm, secondary branches aseptate, 8–15 × 2.5–3 µm, each terminal branch producing 2–4 phialides; *phialides* cylindrical, doliiform to reniform to cymbiform, hyaline, aseptate, 9–12 × 2.5–3 µm, apex with minute periclinal thickening and collarette. *Subverticillate conidiophores* comprising of a septate stipe and rarely primary branches terminating in 2–4 phialides; *phialides* cymbiform to cylindrical, hyaline, aseptate, 20–30 × 2–2.5 µm, apex with minute periclinal thickening and collarette. *Conidia* cylindrical, rounded at both ends, straight, (0–)1-septate, (9–)10–12(–13) × 2(–2.5) µm, held in asymmetrical clusters by colourless slime. *Sexual morph* unknown.

Culture characteristics: Colonies flat, spreading, with fluffy, moderate aerial mycelium, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface sienna with patches of ochreous, reverse umber to sienna.

Material examined: **South Africa**, Western Cape Province, Stellenbosch, *Pelargonium* sp. (*Geraniaceae*), 1 Feb. 2010, *P.W. Crous*, CBS H-23821, culture CPC 33527 = CBS 145053.

Notes: *Cylindrocladiella peruviana* is known to occur in South Africa (van Coller *et al.* 2005), and has been confirmed from hosts such as *Acacia mearnsii, Eucalyptus* spp., and *Vitis vinifera*, but this is the first record from *Pelargonium*.

Based on a megablast search of NCBI's GenBank nucleotide database, the **ITS** sequence was identical to *Cylindrocladiella peruviana* (GenBank KU896173.1; Identities = 550/550), *Cylindrocladiella parvispora* (GenBank MH017028.1; Identities = 546/546), and *Cylindrocladiella malesiana* (GenBank MH017019.1; Identities = 546/546). Closest hits using the **LSU** sequence are *Cylindrocladiella peruviana* (GenBank JN099266.1; Identities = 841/841 (100 %), no gaps), *Cylindrocladiella longiphialidica* (GenBank MH876846.1; Identities = 840/841 (99 %), no gaps), and *Cylindrocladiella camelliae* (GenBank JN099248.1; Identities = 840/841 (99 %), no gaps). Closest hits using the ***his3*** sequence had highest similarity to *Cylindrocladiella peruviana* (GenBank MH017011.1; Identities = 480/480 (100 %), no gaps), *Cylindrocladiella microcylindrica* (as *Nectricladiella camelliae*, GenBank AY793523.1; Identities = 442/457 (97 %), 5 gaps (1 %)), and *Cylindrocladiella solicola* (GenBank MH017002.1; Identities = 469/485 (97 %), 5 gaps (1 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Cylindrocladiella camelliae* (GenBank KM232304.1; Identities = 819/837 (98 %), no gaps), *Cylindrocladiella lageniformis* (GenBank KM232303.1; Identities = 648/722 (90 %), no gaps), and *Calonectria brevistipitata* (GenBank KY653367.1; Identities = 744/861 (86 %), 2 gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Cylindrocladiella peruviana* (GenBank JN099007.1; Identities = 482/483 (99 %), 1 gap (0 %)), *Cylindrocladiella obpyriformis* (GenBank MH016985.1; Identities = 475/489 (97 %), 7 gaps (1 %)), and *Cylindrocladiella arbusta* (GenBank MH016978.1; Identities = 475/489 (97 %), 7 gaps (1 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Cylindrocladiella peruviana* (GenBank JN098801.1; Identities = 618/618 (100 %), no gaps), *Cylindrocladiella terrestris* (GenBank MF444930.1; Identities = 482/493 (98 %), no gaps), and *Cylindrocladiella camelliae* (GenBank JN098749.1; Identities = 604/618 (98 %), no gaps).

Cyphellophora clematidis Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB829301. Fig. 13.

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

Mycelium consisting of pale brown, smooth, septate, branched, (1.5–)2–3 µm diam hyphae. *Conidiomata* sporodochial, round, erumpent, olivaceous, 30–120 µm diam, consisting of a basal stroma of globose to ellipsoid, olivaceous, smooth-walled cells, 2–4 µm diam, giving rise to aggregated conidiogenous cells. *Conidiogenous cells* ellipsoid to ampulliform, olivaceous brown, smooth, 4–6(–10) × 2.5–4 µm, phialidic with darker brown, flared collarette, 1.5–2 µm diam. *Conidia* aseptate, aggregated in mucoid mass, olivaceous, smooth, guttulate, ellipsoid, apex obtuse, tapering toward a truncate base, 0.5 µm diam, (3–)4–5(–6.5) × (1.5–)2(–2.5) µm.

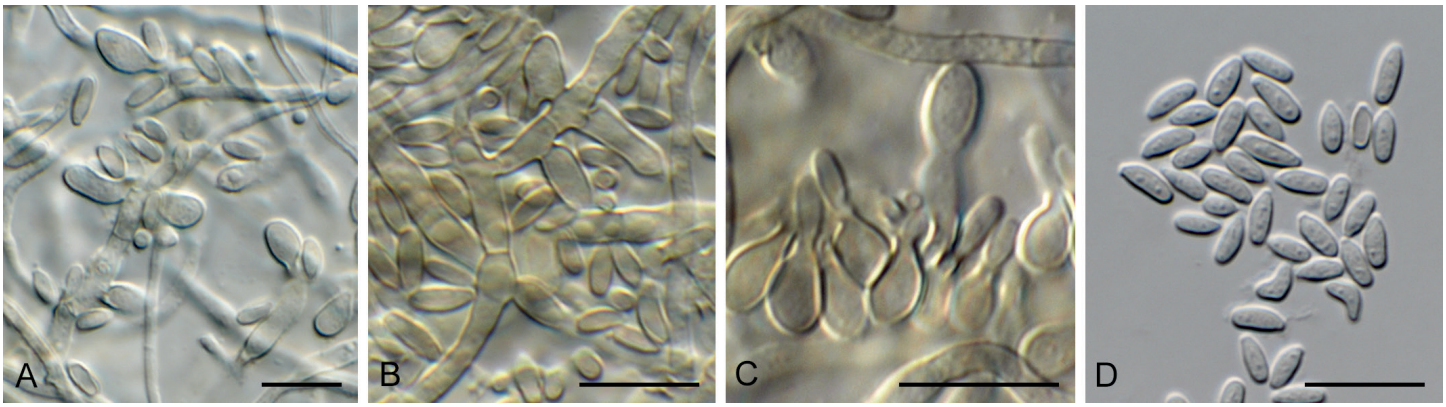

Fig. 13. *Cyphellophora clematidis* (CPC 33880). **A–C.** Hyphae with clusters of conidiogenous cells. **D.** Conidia. Scale bars = 10 µm.

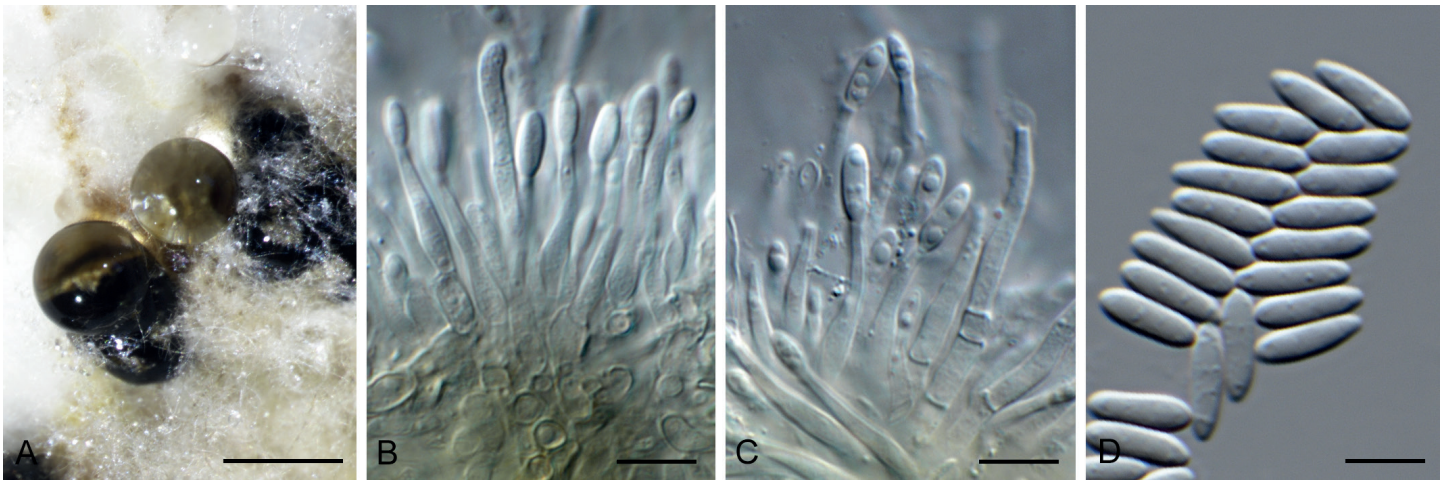

Fig. 14. *Diaporthe anacardii* (CPC 33074). **A.** Conidiomata on PDA. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars: A = 250 µm, B–D = 10 µm.

Culture characteristics: Colonies flat, spreading with sparse to moderate aerial mycelium, and smooth, lobate margin, reaching 40 mm diam after 2 wk at 25 ºC. On MEA surface umber, reverse chestnut; on PDA surface hazel, reverse iron-grey; on OA surface olivaceous grey.

Typus: **Austria**, lower Austria, Gaaden, on *Clematis vitalba* (*Ranunculaceae*), 21 Apr. 2017, *M. Mann & R.K. Schumacher*, HPC 2101 = RKS 102 (**holotype** CBS H-23827, culture ex-type CPC 33880 = CBS 144983).

Notes: Although *Cyphellophora clematidis* was isolated from *Clematis vitalba*, *Cyphellophora* also contains species that are associated with human and animal skin and nails (Gao *et al.* 2015). *Cyphellophora clematidis* is phylogenetically distinct from other species presently known based on their DNA sequences, and is introduced here as new, being morphologically distinct in that it has predominantly aseptate conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Anthopsis deltoidea* (GenBank NR_153555.1; Identities = 492/557 (88 %), 40 gaps (7 %)), *Cyphellophora pluriseptata* (GenBank MH063042.1; Identities = 481/562 (86 %), 24 gaps (4 %)), and *Cyphellophora eucalypti* (GenBank GQ303274.1; Identities = 530/633 (84 %), 48 gaps (7 %)). Closest hits using the **LSU** sequence are *Cyphellophora fusarioides* (GenBank MH877022.1; Identities = 836/861 (97 %), 4 gaps (0 %)), *Cyphellophora musae* (GenBank KP122932.1; Identities = 835/861 (97 %), 3 gaps (0 %)), and *Cyphellophora suttonii* (GenBank MH874978.1; Identities = 834/861 (97 %), 4 gaps (0 %)). No significant hits were obtained when the ***tub2*** sequence was used in blastn and megablast searches.

Diaporthe anacardii (Early & Punith.) R.R. Gomes *et al.*, *Persoonia* **31**: 15. 2013. Fig. 14.
Basionym: *Phomopsis anacardii* Early & Punith., *Trans. Brit. Mycol. Soc.* **59**: 345. 1972.

Conidiomata black, globose, erumpent, 250–350 µm diam, exuding a creamy conidial mass. *Conidiophores* hyaline, smooth, branched, 2–3-septate, subcylindrical, 25–50 × 2.5–3.5 µm. *Conidiogenous cells* subcylindrical, smooth, terminal, intercalary, 15–35 × 2–2.5 µm, apex 1.5 µm diam, mostly without collarette. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, fusoid-ellipsoid, straight, apex subobtuse, base truncate, 1 µm diam, (7–)8–10(–11) × (2.5–)3 µm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface buff with patches of pale olivaceous grey, reverse cinnamon.

Material examined: **South Africa**, Western Cape Province, Stellenbosch, on unidentified leaf litter, 2010, *P.W. Crous*, HPC 1692, culture CPC 33074 = CBS 144610.

Notes: This collection is closely related to *Diaporthe anacardii* (from *Anacardi occidentalis* in Kenya, and also recorded from Nigeria, Guinea and Cuba; Gomes *et al.* 2013), and *Diaporthe velutina* (from leaves of *Neolitsea* sp., *Callerya cinerea* and *Camellia sinensis* collected in China; Gao *et al*. 2017). Based on the *cmdA* and *tef1* sequence data, this isolate is identified as *Diaporthe anacardii*, which represents the first record from South Africa.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Diaporthe velutina* (GenBank NR_152470.1; Identities = 561/563 (99 %), 2 gaps (0 %)), *Diaporthe foeniculina* (GenBank KP050598.1; Identities = 534/538 (99 %), 2 gaps (0 %)), and *Diaporthe inconspicua* (GenBank KC343125.1; Identities = 556/561 (99 %), no gaps). Closest hits using the **LSU** sequence are *Diaporthe velutina* (GenBank NG_059146.1; Identities = 788/788 (100 %)), *Diaporthe phragmitis* (GenBank MH878644.1; Identities = 785/788 (99 %), no gaps), and *Diaporthe cotoneastri* (GenBank MH873257.1; Identities = 785/788 (99 %), no gaps). Closest hits using the ***cmdA*** sequence had highest similarity to *Diaporthe anacardii* (GenBank KC343266.1; Identities = 681/682 (99 %), no gaps), *Diaporthe portugallica* (as *Diaporthe* sp. VG-2018, GenBank MH063893.1; Identities = 469/486 (97 %), no gaps), and *Diaporthe velutina* (GenBank KX999286.1; Identities = 444/461 (96 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Diaporthe anacardii* (GenBank KC343750.1; Identities = 335/341 (98 %), 2 gaps (0 %)), *Diaporthe portugallica* (as *Diaporthe* sp. VG-2018, GenBank MH063911.1; Identities = 324/339 (96 %), no gaps), and *Diaporthe velutina* (GenBank KX999178.1; Identities = 324/339 (96 %), 2 gaps (0 %)).

Diaporthe eres Nitschke, *Pyrenomyc. Germ.* **2**: 245. 1870. Fig. 15.

Conidiomata pycnidial, globose, erumpent, brown, up to 400 µm diam; creamy conidial droplets exude from ostiole; walls of 3–6 layers of brown *textura angularis. Conidiophores* lining the inner cavity, hyaline, smooth, 1–3-septate, branched, densely aggregated, subcylindrical, straight to sinuous, 15–35 × 3–4 µm. *Conidiogenous cells* 6–20 × 2–2.5 µm, phialidic, subcylindrical, terminal and intercalary, with slight apical taper towards apex, 0.5 µm diam with visible periclinal thickening; collarette inconspicuous. *Conidia* aseptate, hyaline, smooth, fusoid, tapering towards both ends, straight, apex subobtuse, base truncate, (7–)8–9(–10) × (2–)2.5(–3) µm.

Culture characteristics: Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface isabelline with patches of sepia and honey, reverse brown vinaceous with patches of hazel and ochreous.

Material examined: **Netherlands**, on *Lactuca sativa* (*Asteraceae*), Jun. 2017, *W. Quaedvlieg*, NAK Tuinbouw INS-17-08263A, culture CPC 34055 = CBS 145040.

Notes: *Diaporthe* includes important plant pathogens, saprobes, and endophytes on a wide range of plant hosts (Guarnaccia & Crous 2017). *Diaporthe eres*, the type species of *Diaporthe*, was circumscribed by Udayanga *et al*. (2014). The present collection from *Lactuca sativa* in the Netherlands fits within the broad concept of *D. eres*.

Based on a megablast search of NCBI's GenBank nucleotide database, the **ITS** sequence was identical to *Diaporthe eres* (GenBank MG281122.1; Identities = 576/576 (100 %)) and *Diaporthe cotoneastri* (GenBank KC145903.1; Identities = 576/576 (100 %)). Closest hits using the **LSU** sequence are *Diaporthe eres* (GenBank MH867392.1; Identities = 893/893 (100 %), no gaps), *Diaporthe cotoneastri* (GenBank MH873257.1; Identities = 891/891 (100 %), no gaps), and *Diaporthe ambigua* (GenBank MH867598.1; Identities = 892/893 (99 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Diaporthe eres* (GenBank KJ420750.1; Identities = 234/234 (100 %)), *Diaporthe cotoneastri* (GenBank KC843231.1; Identities = 273/275 (99 %), no gaps), and *Phomopsis fukushii* (GenBank JN230379.1; Identities = 265/268 (99 %), no gaps). Closest hits using the ***cmdA*** sequence had highest similarity to *Diaporthe* cf. *nobilis* (GenBank KC343391.1; Identities = 409/409 (100 %), no gaps), *Diaporthe eres* (GenBank KC343331.1; Identities = 409/409 (100 %), no gaps), and *Diaporthe cotoneastri* (GenBank KC763137.1; Identities = 403/409 (99 %), 4 gaps (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Diaporthe ampelina* (as *Phomopsis viticola*, GenBank HQ446836.1; Identities = 632/683 (93 %), no gaps), *Diaporthe limonicola* (GenBank MH797629.1; Identities = 622/683 (91 %), no gaps), and *Diaporthe foeniculina* (GenBank MG922553.1; Identities = 619/680 (91 %), no gaps). Closest hits using the ***tef1***

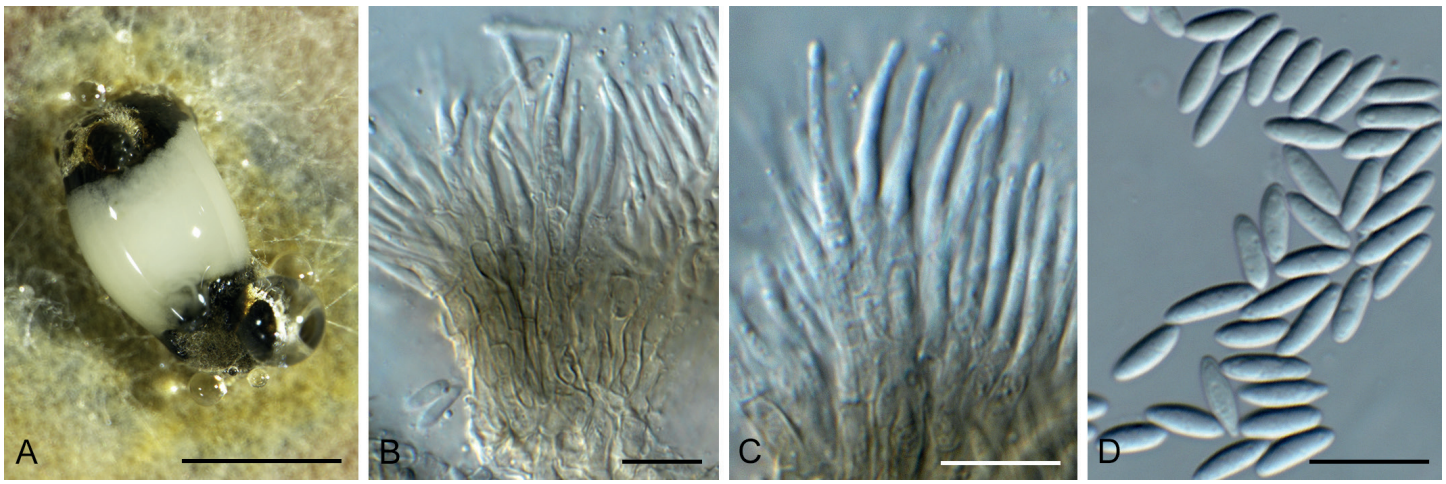

Fig. 15. *Diaporthe eres* (CPC 34055). **A.** Conidioma on OA. **B, C.** Conidiophores with conidiogenous cells. **D.** Conidia. Scale bars: A = 400 µm, B–D = 10 µm.

sequence had highest similarity to *Diaporthe eres* (GenBank MG281568.1; Identities = 610/610 (100 %), no gaps), *Diaporthe* cf. *nobilis* (GenBank KC343875.1; Identities = 346/347 (99 %), no gaps), and *Diaporthe phaseolorum* (GenBank HQ445915.1; Identities = 355/359 (99 %), no gaps). Closest hits using the ***tub2*** sequence had highest similarity to *Diaporthe hungariae* (GenBank MG281303.1; Identities = 317/317 (100 %), no gaps), *Diaporthe rosicola* (GenBank MG843877.1; Identities = 311/313 (99 %), no gaps), and *Diaporthe betulae* (GenBank KT733021.1; Identities = 429/439 (98 %), no gaps).

Dichotomophthora basellae Hern.-Restr. *et al.*, *Stud. Mycol.* **92**: 69. 2018. Fig. 16.

Hyphae hyaline to brown, septate, smooth to verruculose, 6–8 µm wide. *Conidiophores* macronematous, unbranched or irregularly branched, lobed at the apex, forming a stipe and head; *stipe* pale brown, smooth, 500–2000 × 9–17 µm; head 30–60 µm diam, pale brown. *Conidiogenous cells* polytretic, integrated and terminal, lobed, cicatrized, individual lobes 15–25 × 9–20 µm. *Conidia* (50–)80–95(–105) × (9–)12–14(–15), solitary, dry, subcylindrical, rounded at the ends, pale yellow-brown, 3–5-distoseptate, at times forking at apex, giving rise to bifurcate appearance, two apical branches 0–2-septate, 7–30 µm long. *Microconidia* obovoid to ellipsoid, 0–2-distoseptate, 10–30 × 10–11 µm. *Sclerotia* and s*exual morph* unknown.

Culture characteristics: Colonies spreading, with sparse to moderate aerial mycelium and smooth, even margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface and reverse umber, with diffuse apricot pigment; on PDA surface and reverse orange, with patches of umber, and orange pigment; on OA surface orange, with patches of umber, apricot to orange pigment.

Material examined: **Thailand**, Chiang Mai Province, Chiang Mai, on unidentified host plant, 2008, *R. Cheewangkoon*, CBS H-23813, culture CPC 33044 = CBS 145050.

Notes: The genus *Dichotomophthora* was recently revised by Marin-Felix *et al.* (2019), who accepted four species associated with leaf spots on various host plants. D*ichotomophthora basellae* was described as having conidia that are 32–86 × 10–18 µm, ellipsoid to cylindrical rounded at ends, and 2–5-distoseptate. The present isolate is morphologically atypical, as its conidia are frequently forking at the apex. Phylogenetically however, it is identical to *D. basellae*, and was collected at the same locality.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Dichotomophthora basellae* (GenBank NR_158422.1; Identities = 595/595 (100 %), no gaps) and *Dichotomophthora lutea* (GenBank NR_158420.1; Identities = 590/596 (99 %), 1 gap (0 %)). Closest hits using the **LSU** sequence of CPC 33044 are *Dichotomophthora portulacae* (GenBank LT990624.1; Identities = 833/833 (100 %), no gaps), *Dichotomophthora lutea* (GenBank LT990622.1; Identities = 810/810 (100 %), no gaps), *Curvularia papendorfii* (GenBank MH875471.1; Identities = 855/855 (100 %), no gaps), *Bipolaris cactivora* (GenBank LT715590.1; Identities = 855/855 (100 %), no gaps), and *Drechslera helianthi* (GenBank MH876194.1; Identities = 854/855 (99 %), no gaps). There are no LSU sequences of *Dichotomophthora basellae* available on GenBank. Closest hits using the ***rpb2*** sequence had highest similarity to *Dichotomophthora basellae* (GenBank LT990640.1; Identities = 860/860 (100 %), no gaps), *Dichotomophthora lutea* (GenBank LT990636.1; Identities = 906/911 (99 %), no gaps), and *Bipolaris cactivora* (GenBank LT715726.1; Identities = 718/739 (97 %), no gaps).

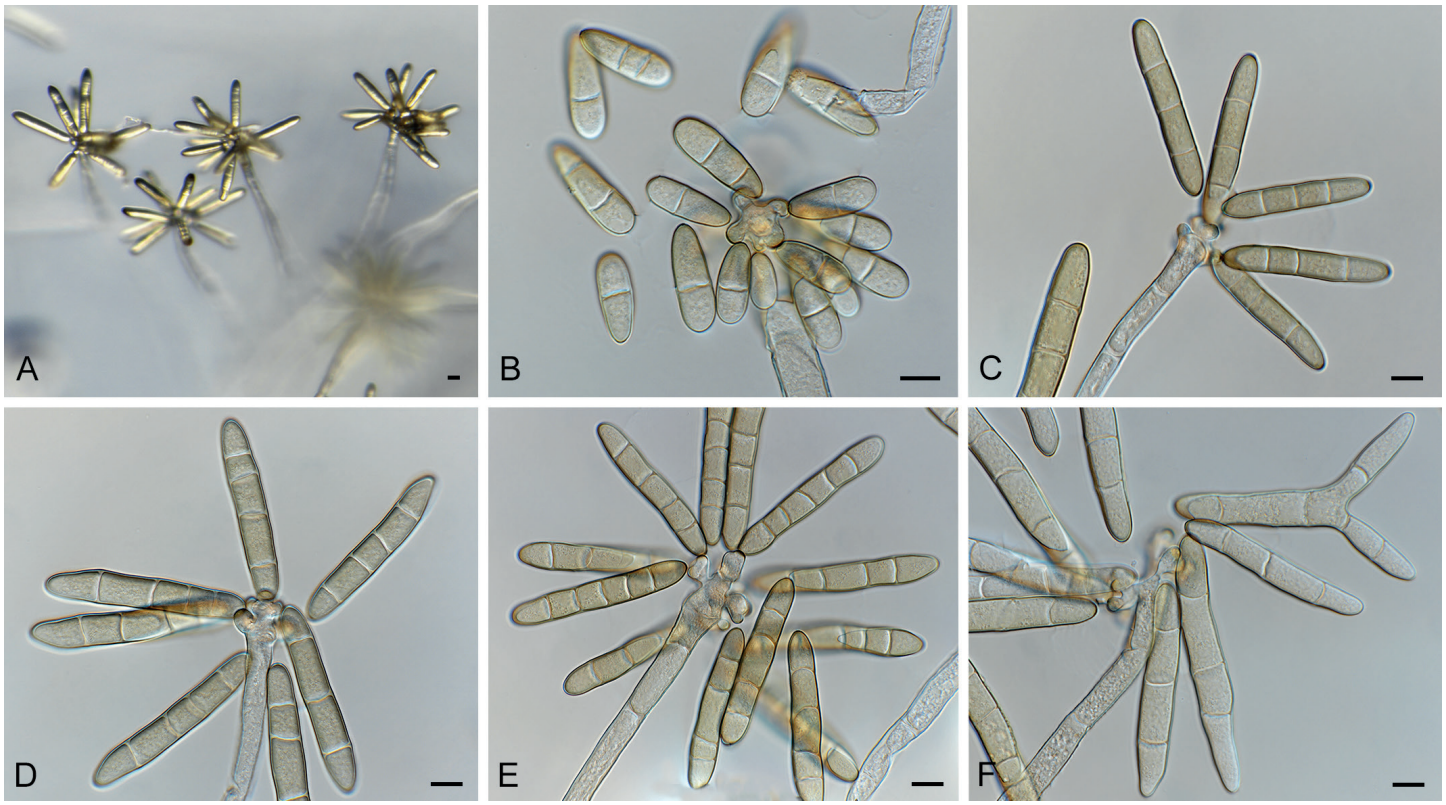

Fig. 16. *Dichotomophthora basellae* **(**CPC 33044). **A.** Conidiophores on SNA. **B.** Microconidia. **C–F.** Macroconidia. Scale bars = 10 µm.

Exophiala abietophila Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB829302. Fig. 17.

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

Mycelium consisting of smooth, septate, brown, branched, 2–3 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells or with a supporting cell. *Conidiogenous cells* pale brown, smooth, reduced to conidiogenous loci, 0.5 µm diam, or ampulliform to doliiform, 4–6 × 2.5–3 µm. *Conidia* aseptate, (2.5–)3(–3.5) × 1.5–2 µm, ellipsoid, hyaline, smooth-walled, guttulate, apex obtuse, tapering to a truncate base, 0.5 µm diam.

Culture characteristics: Colonies flat, spreading, with folded surface, sparse aerial mycelium and smooth, lobate margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse umber.

Typus: **Norway**, Oppland, Vestre Sildre, on bark of *Abies alba* (*Pinaceae*), 29 Jul. 2017, *F. Sanchez et al.,* HPC 2230 (**holotype** CBS H-23836, culture ex-type CPC 34580 = CBS 145038).

Notes: *Exophiala* includes several species of dematiaceous hyphomycetes that are clinically relevant (de Hoog 1977). Species of *Exophiala* are however commonly isolated from plant litter and soil. Phylogenetically *E. abietophila* is distinct from all species presently known from their DNA sequence data.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Exophiala moniliae* (GenBank HE605213.1; Identities = 567/643 (88 %), 34 gaps (5 %)), *Exophiala bergeri* (GenBank MH857080.1; Identities = 484/544 (89 %), 25 gaps (4 %)), and *Atrokylindriopsis setulosa* (GenBank KP337330.1; Identities = 516/576 (90 %), 19 gaps (3 %)). Closest hits using the **LSU** sequence are *Exophiala dermatitidis* (GenBank DQ823100.1; Identities = 1112/1194 (93 %), 24 gaps (2 %)), *Exophiala bergeri* (GenBank NG_059199.1; Identities = 1099/1184 (93 %), 27 gaps (2 %)), and *Capronia pilosella* (GenBank DQ823099.1; Identities = 1106/1199 (92 %), 27 gaps (2 %)).

Exophiala lignicola Crous & Akulov, ***sp. nov.*** MycoBank MB829303. Fig. 18.

Etymology: Name refers to rotten wood from which it was isolated.

Mycelium consisting of smooth, pale brown, septate, branched, 2–3 µm diam hyphae. *Conidiophores* penicillate with conidia in apical slimy mass, or reduced to solitary conidiogenous cells

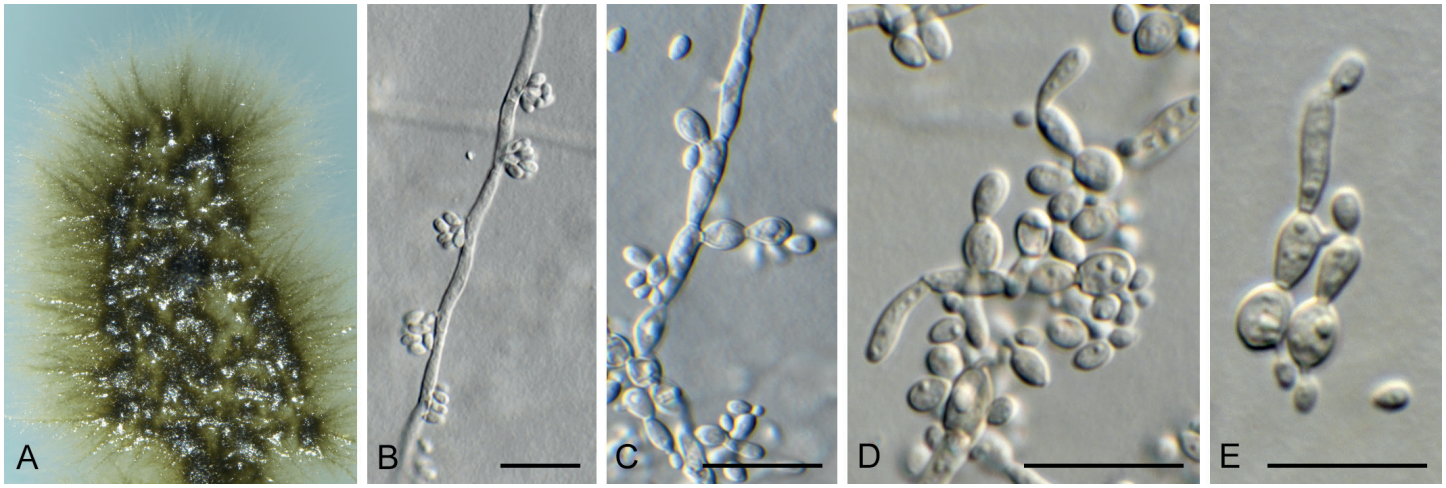

Fig. 17. *Exophiala abietophila* (CPC 34580). **A.** Colony on SNA. **B, C.** Conidiogenous loci on hyphae. **D, E.** Budding conidia. Scale bars = 10 µm.

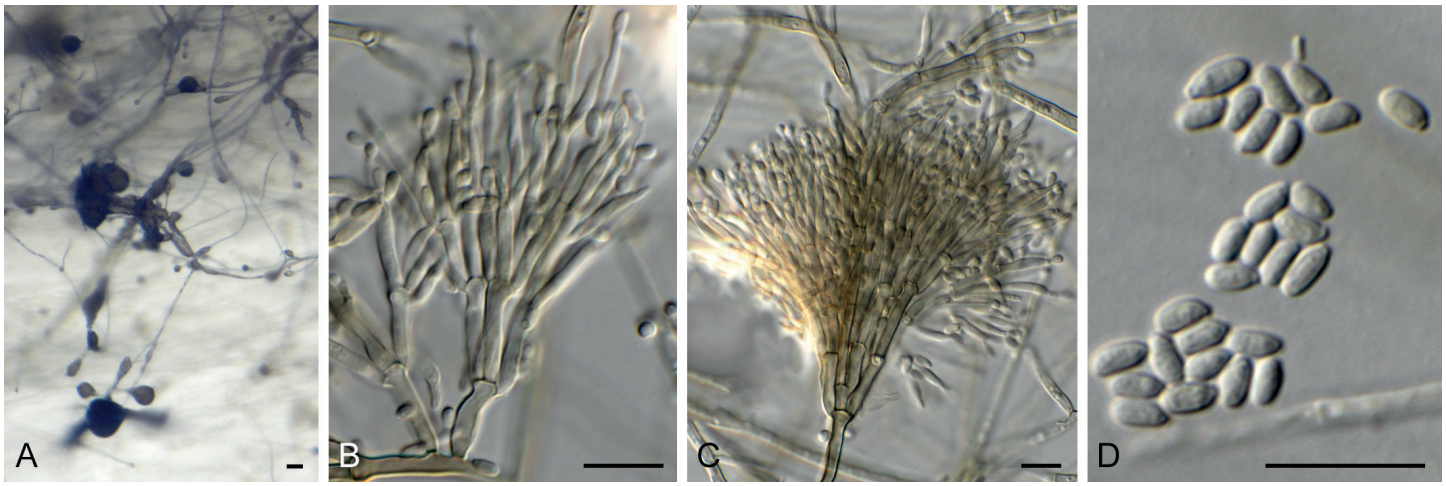

Fig. 18. *Exophiala lignicola* (CPC 32464). **A.** Conidiophores on SNA. **B, C.** Penicillate conidiophores. **D.** Conidia. Scale bars: A = 20 µm, B–D = 10 µm.

or loci on hyphae; conidiophores erect, arising from superficial hyphae, pale to medium brown, smooth, subcylindrical, flexuous, branched or not, stipe 10–20 × 2–3 µm, with apical and lateral penicillate conidiophores; primary branches aseptate, medium brown, smooth, 5–15 × 2–2.5 µm; secondary and tertiary branches subcylindrical, medium brown, smooth, aseptate, 8–12 × 1.5–2 µm, giving rise to 1–4 phialides, pale brown, smooth, subcylindrical to fusoid-ellipsoid, with prominent taper at apex to form a narrow cylindrical channel with percurrent proliferations, (1–)8–16 × (1.5–)2 µm. *Conidia* solitary, aseptate, pale brown, smooth, fusoid-ellipsoid, apex obtuse, base truncate, slightly reflective, (3.5–)4(–5.5) × 2(–3) µm.

Culture characteristics: Colonies erumpent, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 12 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus: **Ukraine**, Kharkiv, Forest park, on fallen decorticated trunk of cf. *Quercus* sp. (*Fagaceae*) in a native oak-maple-ash forest, 28 Oct. 2016, *A. Akulov*, CWU (MYC) AS 6112 = HPC 1509 (**holotype** CBS H-23802, culture ex-type CPC 32464 = CBS 144622).

Notes: *Exophiala* (*Herpotrichiellaceae*) is commonly isolated from decaying wood, soil, and plant litter. This genus of dematiaceous hyphomycetes, commonly referred to as black yeasts, is morphologically variable, with conidiophores ranging from well-defined penicillate structures as in *E. lignicola*, or solitary loci on hyphae. The genus presently contains approximately 60 epithets, several of which have Capronia sexual morphs (Untereiner 1997). Numerous species of *Exophiala* / *Capronia* are known as host-specific fungicolous or lichenicolous fungi (Halici *et al*., 2010; Friebes, 2012). Phylogenetically, *E. lignicola* is distinct from those species known from their DNA sequences, and based on its unique conidiophores, it is treated as a unique taxon.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Rhinocladiella coryli* (GenBank NR_155727.1; Identities = 542/612 (89 %), 18 gaps (2 %)), *Exophiala eucalypticola* (GenBank NR_158438.1; Identities = 518/589 (88 %), 21 gaps (3 %)), and *Rhinocladiella aquaspersa* (GenBank MH374866.1; Identities = 539/619 (87 %), 32 gaps (5 %)). Closest hits using the **LSU** sequence are *Exophiala angulospora* (GenBank MH874033.1; Identities = 875/885 (99 %), no gaps), *Capronia coronata* (GenBank AF050242.1; Identities = 875/885 (99 %), no gaps), and *Fonsecaea pedrosoi* (GenBank AF050276.1; Identities = 872/887 (98 %), 2 gaps (0 %)). No significant hits were obtained when the ***cmdA*** sequence was used in blastn and megablast searches. Closest hits using the ***tef1*** sequence had highest similarity to *Exophiala dermatitidis* (GenBank DQ840566.1; Identities = 186/192 (97 %), no gaps), *Capronia munkii* (GenBank EF413607.1; Identities = 184/193 (95 %), no gaps), and *Capronia coronata* (GenBank XM_007726769.1; Identities = 187/198 (94 %), 2 gaps (1 %)).

Fuscostagonospora banksiae Crous & Carnegie, ***sp. nov.*** MycoBank MB829304. Fig. 19.

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

Conidiomata solitary, pycnidial, globose, brown, 180–200 µm diam, exuding a milky white conidial mass. *Conidiophores* lining the inner cavity, reduced to conidiogenous cells or with a supporting cell, branched at base or not, 5–12 × 3–4 µm. *Conidiogenous cells* ampulliform to doliiform, hyaline, smooth, 5–7 × 3–4 µm; proliferating indistinctly percurrently at apex. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, ellipsoid, apex obtuse, base bluntly rounded, (3–)4(–5) × (2–)2.5(–3) µm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and lobed, feathery margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface ochreous to dirty white with chestnut sectors, reverse ochreous with chestnut; on PDA surface umber with sections of dirty white and scarlet, reverse chestnut with sectors of scarlet and umber; on OA surface umber to pale luteous.

Typus: **Australia**, New South Wales, Riamukka State Forest, 31.376993S 151.693569E, on *Banksia* sp. (*Proteaceae*), 2015, *A.J. Carnegie,* HPC 1445 (**holotype** CBS H-23796, culture ex-type CPC 31724 = CBS 144621).

Notes: *Fuscostagonospora* was introduced for a sexual species occurring on bamboo (Tanaka *et al*. 2015). The present collection represents an asexual morph, and is thus difficult to compare with the known sexual species in the genus, but it is placed in *Fuscostagonospora* based on its phylogeny.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Periconia pseudobyssoides* (GenBank KY364628.1; Identities = 426/464 (92 %), 10 gaps (2 %)), *Periconia byssoides* (GenBank KY364620.1; Identities = 426/464 (92 %), 10 gaps (2 %)), and *Fuscostagonospora sasae* (GenBank NR_153964.1; Identities = 425/468 (91 %), 16 gaps (3 %)). Closest hits using the **LSU** sequence are *Fuscostagonospora cytisi* (GenBank KY770978.1; Identities = 839/846 (99 %), no gaps), *Fuscostagonospora sasae* (GenBank AB807548.1; Identities = 838/850 (99 %), no gaps), and *Corynespora olivacea* (GenBank JQ044448.1; Identities = 858/879 (98 %), 5 gaps (0 %)).

Gaeumannomycella caricicola Hern.-Restr., Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB829305. Fig. 20.

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

In vivo. *Ascomata* perithecial, immersed or semi-immersed on the substrate, globose, subglobose to elliptical, pale brown, 275–390 × 135–235 µm, with a lateral, central cylindrical neck, 108–167 × 57–97 µm; *ascomatal wall textura intrincata* to *epidermoidea*. *Paraphyses* sparse, basally moniliform, upwards filiform, unbranched, multi-celled, hyaline, thin-walled and smooth, evanescent. *Asci* numerous, unitunicate, cylindrical to elongated clavate, stalked, 8-spored, 73–210 × 9–18 µm. *Ascospores* cylindrical, to slightly curved at one or both ends, widest in the middle, tapering to the base, ends rounded, multi-guttulate, 0–3-septate, septa often indistinct, hyaline, 32–45 × 3–3.5 µm. *Hyphopodia* brown, lobed (few hyphopodia were observed close to the perithecial neck).

Culture characteristics: Colonies flat, spreading, with folded surface, sparse to moderate aerial mycelium and smooth,

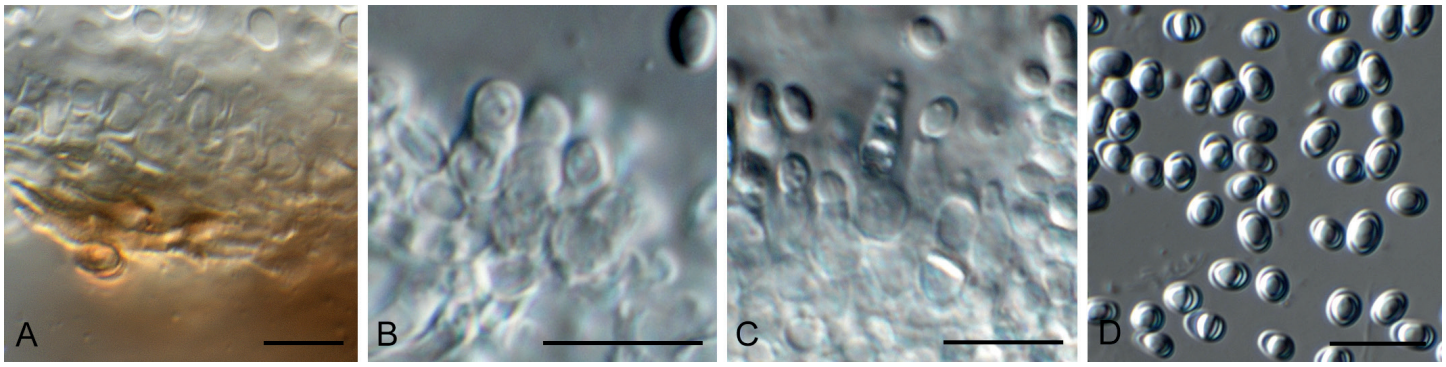

Fig. 19. *Fuscostagonospora banksiae* (CPC 31724). **A.** Conidiomatal wall giving rise to conidiogenous cells. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars = 10 µm.

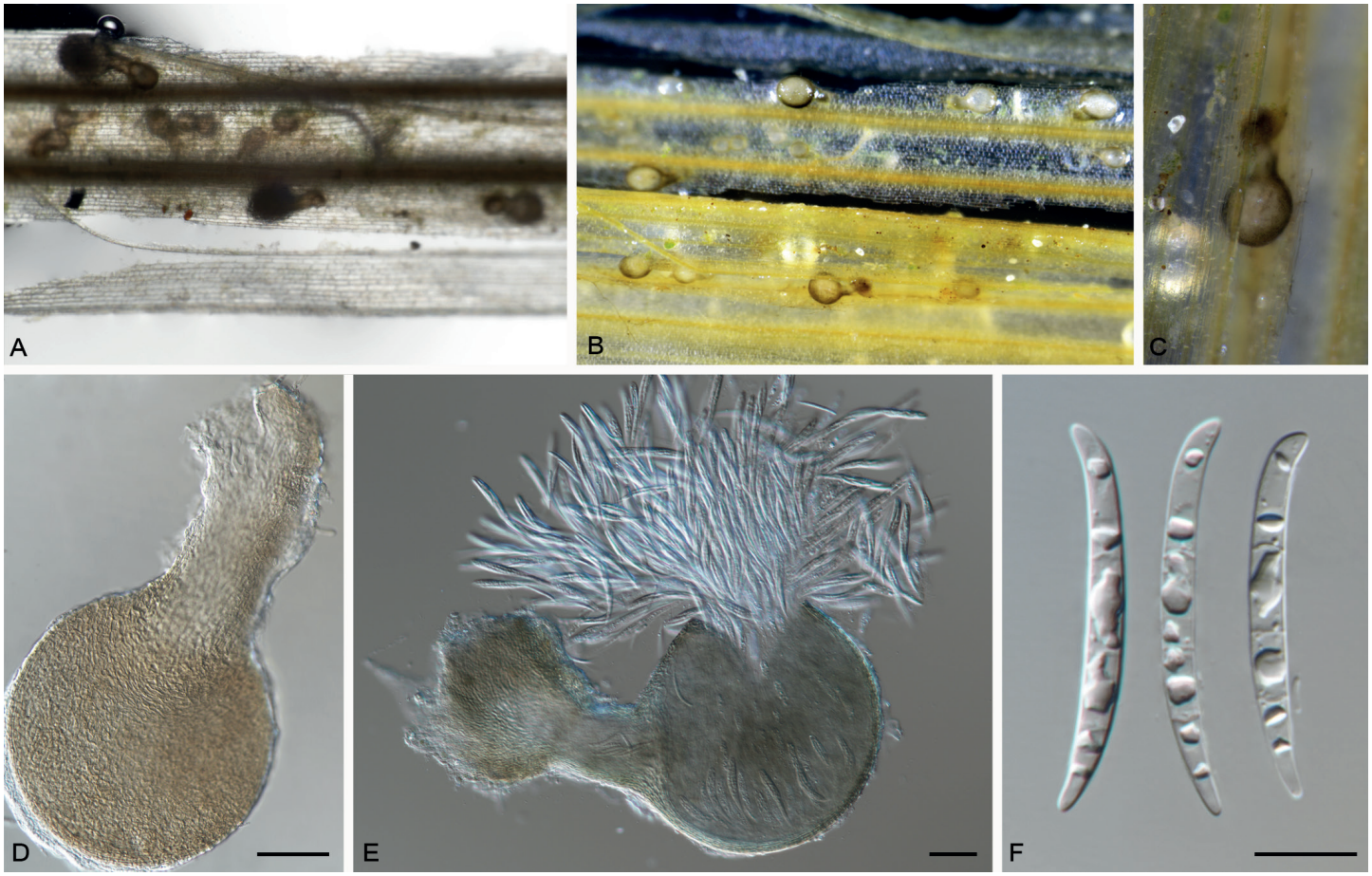

Fig. 20. *Gaeumannomycella caricicola* **(**CPC 33925). **A–C.** Perithecial ascomata embedded on the substrate (grass leaves). **D.** Perithecia. **E.** Perithecia with asci. **F.** Ascospores. Scale bars. A–E = 50 µm, F = 10 µm.

lobate margin, covering dish after 2 wk at 25 °C. On MEA surface pale olivaceous, reverse luteous; on PDA surface and reverse olivaceous grey; on OA surface olivaceous grey.

Typus: **Germany**, near Berlin, on dead leaf of *Carex remota* (*Cyperaceae*), 2 Jun. 2017, *R.K. Schumacher*, HPC 2136 = RKS 122 (**holotype** CBS H-23793, culture ex-type CPC 33925 = CBS 145041).

Notes: *Gaeumannomycella* was introduced by Hernández-Restrepo *et al.* (2016) for a genus of fungi morphologically similar to *Gaeumannomyces*, and associated with a disease on *Cyperaceae. Gaeumannomycella caricicola* is phylogenetically distinct from *Gaeumannomycella caricis*, the only other species presently known in the genus. Of interest is the fact that both species occur on *Carex*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Slopeiomyces cylindrosporus* (as *Gaeumannomyces cylindrosporus*, GenBank JF508361.1; Identities = 506/519 (97 %), 3 gaps (0 %)), *Gaeumannomycella caricis* (GenBank KX306478.1; Identities = 523/553 (95 %), 10 gaps (1 %)), and *Nakataea oryzae* (GenBank FJ746639.1; Identities = 511/550 (93 %), 9 gaps (1 %)). Closest hits using the **LSU** sequence are *Slopeiomyces cylindrosporus* (GenBank KM009159.1; Identities = 835/848 (98 %), no gaps), *Omnidemptus affinis* (GenBank NG_059478.1; Identities = 832/848 (98 %), no gaps), and *Gaeumannomyces graminicola* (GenBank DQ341496.1; Identities = 832/848 (98

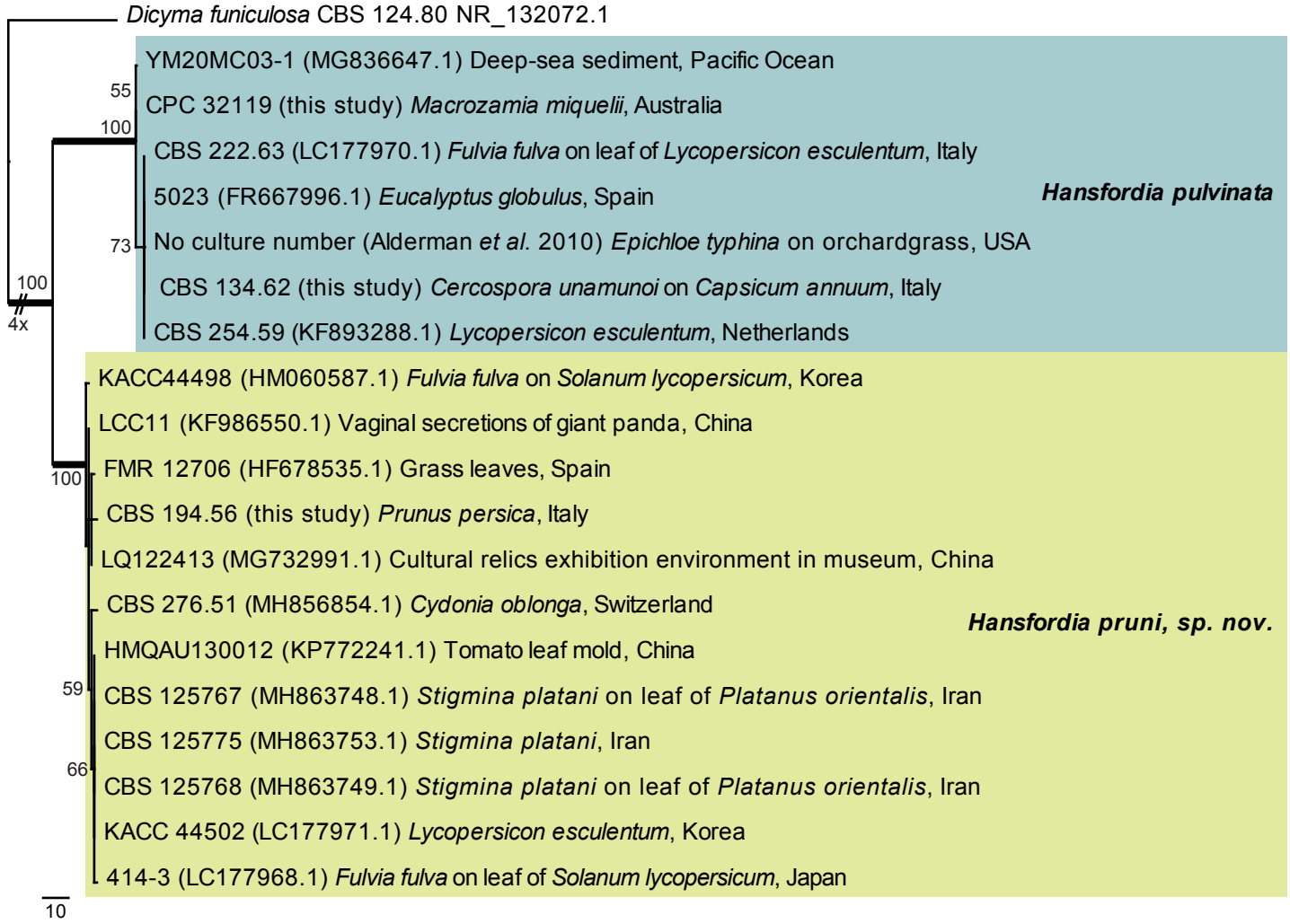

Fig. 21. The first of five equally most parsimonious trees obtained from a phylogenetic analysis of the *Hansfordia* ITS alignment (20 strains including the outgroup; 477 characters analysed: 337 constant, 93 variable and parsimony-uninformative and 47 parsimony-informative). The tree was rooted to *Dicyma funiculosa* (GenBank NR_132072.1) and the scale bar indicates the number of changes. Bootstrap support values higher than 49 % are shown at the nodes and the species clades are highlighted with coloured boxes. Species names are indicated to the right of the tree. Strain numbers, followed by the sources between round brackets, substrate/source and country of origin are indicated for each sequence. Branches present in the strict consensus tree are thickened. The length of the most basal branch was shortened to facilitate layout. Tree statistics: TL = 159, CI = 0.975, RI = 0.986, RC = 0.961.

%), no gaps). Distant hits using the ***his3*** sequence had highest similarity to *Colletotrichum arxii* (GenBank KF687846.1; Identities = 173/183 (95 %), no gaps), *Verticillium albo-atrum* (GenBank DQ266200.1; Identities = 173/184 (94 %), no gaps), and *Colletotrichum vietnamense* (GenBank KF687854.1; Identities = 172/183 (94 %), no gaps). Distant hits using the ***tub2*** sequence had highest similarity to *Gibellina cerealis* (GenBank KT377187.1; Identities = 334/409 (82 %), 28 gaps (6 %)), *Slopeiomyces cylindrosporus* (*Gaeumannomyces cylindrosporus* as, GenBank AY435448.1; Identities = 333/425 (78 %), 32 gaps (7 %)), and *Magnaporthiopsis maydis* (as *Cephalosporium maydis*, GenBank AY435435.1; Identities = 265/351 (75 %), 27 gaps (7 %)).

Hansfordiaceae Crous, ***fam. nov.*** MycoBank MB829455.

Mycelium superficial to immersed. *Conidiophores* solitary, erect, straight to flexuous, branched, medium brown, smooth, arising from superficial mycelium, at times setiform, multi-septate with lateral branches, each giving rise to several smaller, pale brown branches that form *conidiogenous cells*, subhyaline, subcylindrical or clavate; subdenticulate apical loci with rhexolytic conidiogenesis. *Conidia* aseptate, solitary, dry, globose to ellipsoid to fusoid, hyaline to pale brown, smooth or finely roughened, with minute basal frill derived from the apex of the separating cell.

Type genus: *Hansfordia* S. Hughes.

Type species: *H. ovalispora* S. Hughes.

Hansfordia pruni Crous, ***sp. nov.*** MycoBank MB829306. Figs 21, 22.

Etymology: Name refers to the genus *Prunus* from which it was isolated.

Conidiophores solitary, erect, straight to flexuous, branched, medium brown, smooth, arising from superficial mycelium, 100–1000 × 2.5–3 µm, multi-septate with lateral branches in upper half, each giving rise to several smaller, pale brown branches that form 1–2 *conidiogenous cells*, subhyaline, subcylindrical with

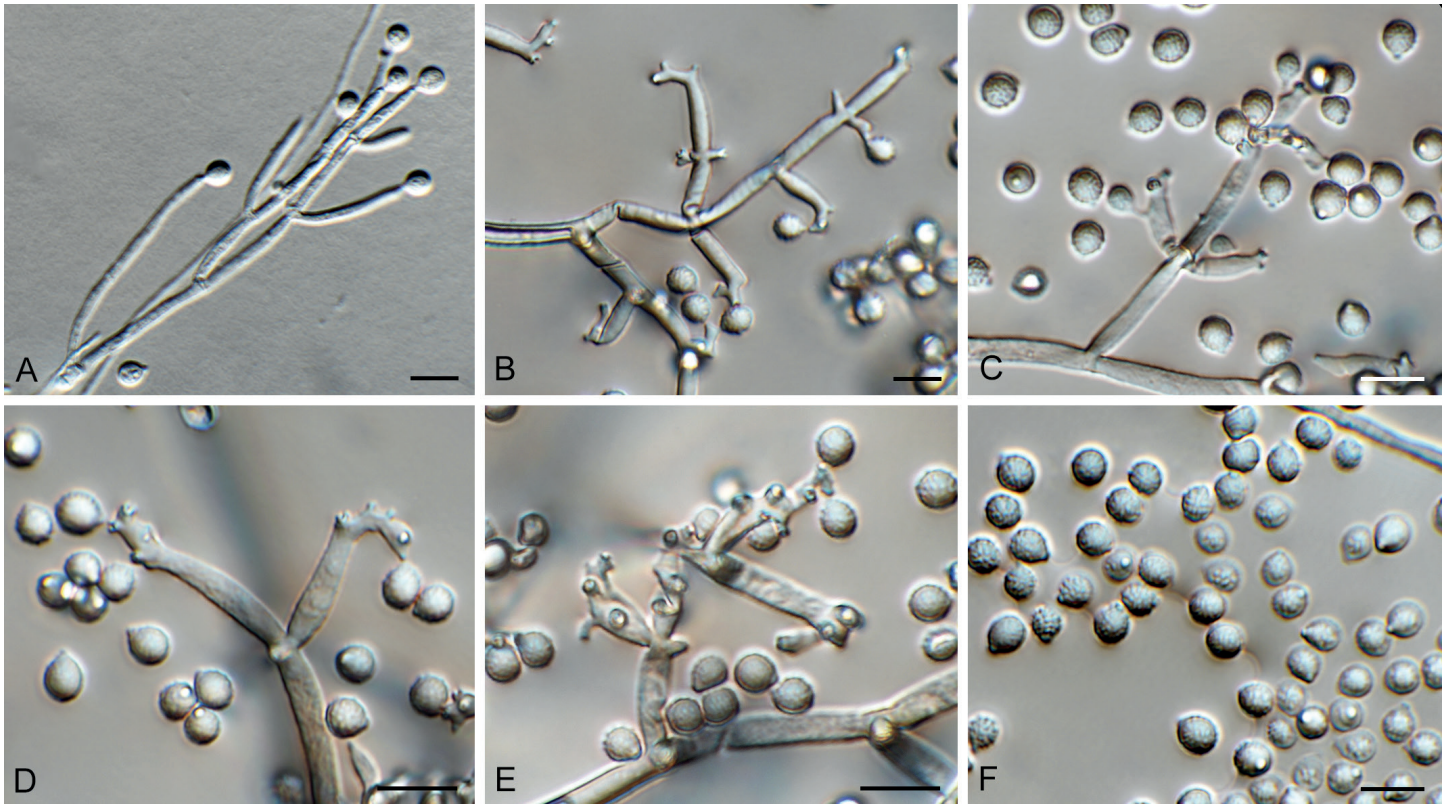

Fig. 22. *Hansfordia pruni* (CBS 194.56). **A–E.** Conidiophores with conidiogenous cells. **F.** Conidia. Scale bars = 10 µm.

apical taper, 5–20 × 2.5–3 µm, with 2–6 subdenticulate apical loci with rhexolytic conidiogenesis. *Conidia* aseptate, solitary, dry, globose to subglobose, subhyaline, finely roughened, (4–)5(–6) × 4 µm diam, with minute basal frill derived from the apex of the separating cell.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and feathery, lobate margins, reaching 35 mm diam after 2 wk. On MEA fawn, reverse cinnamon; on PDA isabelline, reverse brown vinaceous; on OA vinaceous buff.

Typus: **Italy**, on twig of *Prunus persica* (*Rosaceae*), deposited in 1956, *M. Ribaldi* (**holotype** CBS H-23837, culture ex-type IMI 146912 = CBS 194.56).

Notes: *Hansfordia pulvinata* has many proposed synonyms (Deighton 1972), which based on morphology, appear similar to the type. However, *H. pruni* differs in that it has longer conidiophores, more aggregated sub-denticulate loci on its conidiogenous cells, and smaller conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the **ITS** sequence was identical to *Hansfordia pulvinata* (GenBank KU683763.1; Identities = 1040/1040 (100 %)); other closest hits included *Entosordaria quercina* (GenBank MF488994.1; Identities = 842/915 (92 %), 20 gaps (2 %)), and *Entosordaria perfidiosa* (GenBank MF488993.1; Identities = 840/914 (92 %), 18 gaps (1 %)).

Hansfordia pulvinata (Berk. & M.A. Curtis) S. Hughes, *Canad. J. Bot.* **36**: 771. 1958. Fig. 21, 23.
Basionym: *Polyactis pulvinata* Berk. & M.A. Curtis, *Grevillea* **3**(27): 110. 1875.

Conidiophores solitary, erect, flexuous, branched, medium brown, smooth, arising from superficial mycelium, 200–600 × 3–4 µm, multi-septate with lateral branches in upper half, each giving rise to several smaller, pale brown branches that form 1–2 *conidiogenous cells*, subhyaline, subcylindrical with apical taper, 10–17 × 3–3.5 µm, with 1–2 subdenticulate apical loci with rhexolytic conidiogenesis. *Conidia* solitary, dry, globose, subhyaline, finely roughened, (5–)6(–7) µm diam, with minute basal frill derived from apex of the separating cell.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and feathery, lobate margin, reaching 25 mm diam after 2 wk at 25 °C. On MEA surface olivaceous grey in centre, smoke grey in outer region, luteous in reverse; on PDA surface olivaceous grey in centre, smoke grey in outer region, reverse olivaceous grey in centre, luteous in outer region; on OA surface pale olivaceous grey, outer region pale luteous.

Material examined: **Australia**, New South Wales, Australian Botanical Garden Mount Annan, on leaves of *Macrozamia miquelii* (*Zamiaceae*), 25 Nov. 2016, *P.W. Crous*, HPC 1734, CBS H-23581, culture CPC 32119 = CBS 144422.

Notes: *Hansfordia pulvinata* (a mycoparasite on other fungi, including *Fulvia fulva* on tomatoes; Peresse & le Picard 1980) was originally described from branches of *Alnus* sp. collected in North America. It needs to be recollected in the USA to fix the application of the name. Morphologically however, the culture considered in this study applies best to the current concept for this taxon (Ellis 1971, 1976, Deighton 1972). *Hansfordia pulvinata* has been suggested as possible biological control agent for plant pathogenic fungi (Mitchell & Taber 1986, Alderman *et al.* 2010).

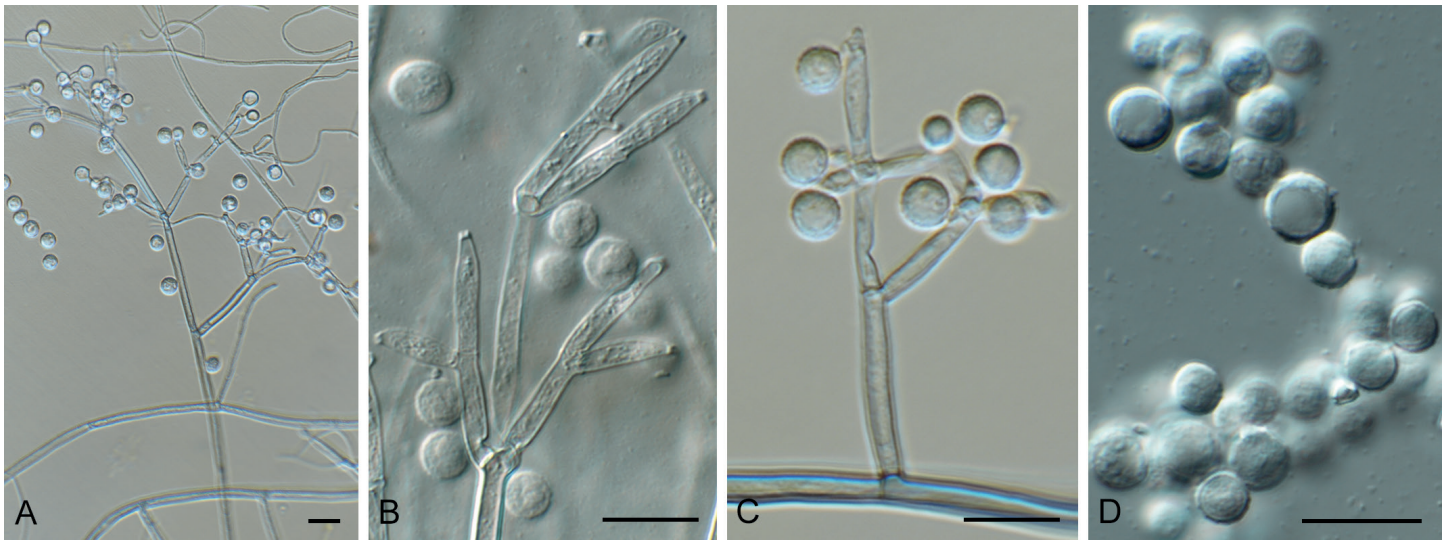

Fig. 23. *Hansfordia pulvinata* (CPC 32119). **A.** Conidiophore. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars = 10 µm.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Hansfordia pulvinata* (GenBank LC177970.1; Identities = 468/471 (99 %), no gaps), *Hansfordia pulvinata* (GenBank MH863749.1; Identities = 510/546 (93 %), 11 gaps (2 %)), *Gyrothrix verticiclada* (GenBank KC775750.1; Identities = 407/463 (88 %), 17 gaps (3 %)), *Selenodriella fertilis* (GenBank KP859055.1; Identities = 473/544 (87 %), 24 gaps (4 %)), and *Daldinia bambusicola* (GenBank KY610385.1; Identities = 474/553 (86 %), 22 gaps (3 %)). Closest hits using the **LSU** sequence are *Gyrothrix circinata* (GenBank KJ476964.1; Identities = 793/830 (96 %), 5 gaps (0 %)), *Circinotrichum maculiforme* (GenBank KR611896.1; Identities = 805/844 (95 %), 5 gaps (0 %)), and *Oxydothis garethjonesii* (GenBank KY206762.1; Identities = 799/842 (95 %), 2 gaps (0 %)).

Hypsotheca Ellis & Everh., *J. Mycol.* **1**: 128. 1885.
Synonyms: *Capnodiella* (Sacc.) Sacc. & D. Sacc., *Syll. fung.* (Abellini) **17**: 621. 1905. [based on *Capnodium maximum*]
Sorica Giesenh., *Ber. dt. bot. Ges.* **22**: 195. 1904. [based on *Sorica dusenii*]

Ascomata separate or loosely grouped, not arising from a visible stroma, dark brown to black, ventricose, straight or curved, elongate with a submedian to suprabasal swollen ascigerous locule. Ascomatal wall of *textura porrecta* to *textura intricata. Asci* 8-spored, elongating at maturity and extending up the ascoma neck to the apex before deliquescing to release ascospores at or below the ostiole; discharged ascospores accumulating in a dry reddish brown mass at the ostiole. *Ascospores* golden brown, thick-walled, smooth, depressed globose to subellipsoid. Pycnidial and hyphomycetous morphs produced. *Pycnidial conidiomata* solitary, dark brown to black, globose or depressed globose, or short stipitate, with a prominent papillate ostiole, wall of *textura angulata* to *textura intricata. Conidiophores* hyaline, arising from the inner cells of the pycnidial wall, simple ampulliform or elongate, septate. *Conidiogenous cells* phialidic with an inconspicuous collarette. *Conidia* hyaline, asymmetrical, oblong to allantoid or fusoid, aseptate, smooth. *Hyphomycetous morph* with mucoid heads of conidia scattered on short lateral phialodes, phaeoacremonium-like, sub-hyaline to pale brown, smooth or rough. *Conidiogenous cells* lageniform, the collarettes usually inconspicuous or flared (phialophora-like). *Conidia* aseptate, ellipsoid-ovoid, smooth.

Type species: *Hypsotheca subcorticalis* [*Basionym*: *Sphaeronaema subcorticale,* perithecia occurring inside the bark of *Quercus*, New Jersey, USA, type at K].

Hypsotheca nigra (Schrad. ex DC.) Crous, ***comb. nov.*** MycoBank MB829445.
Basionym: *Stilbum nigrum* Schrad. ex DC., *Flore française* **2**: 593. 1805.
Synonyms: *Lagenula nigra* (Schrad. ex DC.) G. Arnaud, *Annls Épiphyt.* **16**: 267. 1930.
Caliciopsis nigra (Schrad. ex DC) Fitzp., *Mycologia* **34**: 501. 1942.

Hypsotheca maxima (Berk. & M.A. Curtis) Crous, ***comb. nov.*** MycoBank MB829446.
Basionym: *Capnodium maximum* Berk. & M.A. Curtis, *J. Linn. Soc., Bot.* **10**: 391. 1868 (1869).
Polychaeton maximum (Berk. & M.A. Curtis) Kuntze, *Revis. gen. pl.* (Leipzig) **1**: 13. 1891.
Sorica maxima (Berk. & M.A. Curtis) Giesenh., *Ber. dt. bot. Ges.* **22**: 358. 1904.
Capnodiella maxima (Berk. & M.A. Curtis) Sacc. & D. Sacc., *Syll. fung.* (Abellini) **17**: 621. 1905.
Caliciopsis maxima (Berk. & M.A. Curtis) Höhn., *Sitzungsber. Akad. Wiss. Wien, Math.-Naturwiss. Kl.*, Abt. 1, **128**: 84. 1919.

Typus: **Cuba**, on fronds of *Niphidium* sp. (*Polypodiaceae*) (originally identified as *Polypodium* sp.), 1941, *Wright* (**holotype** CUP-029913). **Brazil**, Rio de Janeiro, Nova Friburgo, on fronds of *Niphidium crassifolium* (*Polypodiaceae*), 5 Nov. 2011, *R.W. Barreto* (**epitype** VIC 42568, culture ex-epitype COAD 1983 = CPC 24674).

Material examined: **Brazil**, Rio de Janeiro, Nova Friburgo, on fronds of *Microgramma squamulosa* (*Polypodiaceae*), 10 Oct. 2013, *R.W. Barreto*, VIC 42602.

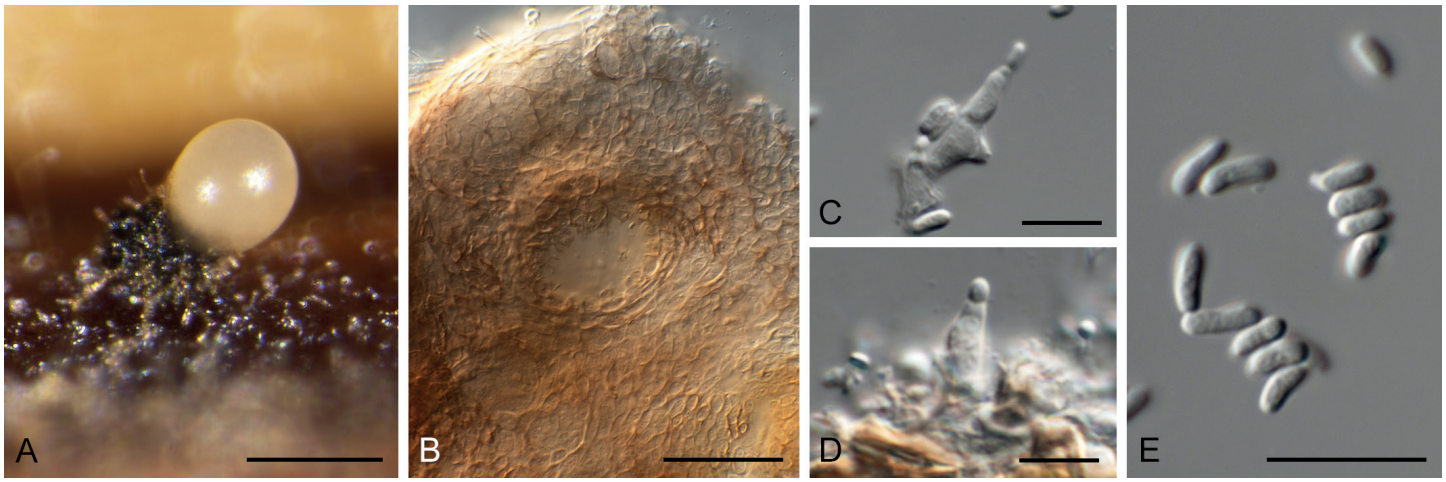

Fig. 24. *Hypsotheca pleomorpha* **(**CPC 32144). **A.** Conidioma forming on PDA. **B.** Conidioma with ostiole. **C, D.** Conidiogenous cells. **E.** Conidia. Scale bars: A = 200 µm, B = 50 µm, C–E = 10 µm.

Hypsotheca pleomorpha (Patricia McGee & I. Pascoe) Crous, ***comb. nov.*** MycoBank MB829312. Fig. 24.
Basionym: *Caliciopsis pleomorpha* Patricia McGee & I. Pascoe, *Fungal Syst. Evol.* **2**: 50. 2018.

Conidiomata pycnidial, globose, ostiolate, brown, 50–200 µm diam, separate (on PNA), or aggregated in a brown stroma (on PDA, MEA). *Conidiophores* arising from inner layer, hyaline, smooth, subcylindrical, branched, 1–4-septate, 5–20 × 3–4 µm. *Conidiogenous cells* subcylindrical to doliiform, hyaline, smooth, terminal and intercalary, phialidic with prominent periclinal thickening, 3–6 × 2–4 µm. *Conidia* solitary, aseptate, hyaline, smooth, granular, fusoid-ellipsoid, mostly somewhat curved, apex obtuse, tapered towards base, truncate, 0.5 µm diam, (3–) 4–5(–6) × 1.5(–2) µm.

Culture characteristics: Colonies spreading, surface folded, with sparse to moderate aerial mycelium and smooth, lobate margins, reaching 50 mm diam after 2 wk. On MEA, PDA and OA surface and reverse chestnut.

Material examined: **Australia**, New South Wales, on leaves of *Eucalyptus piperita* (*Myrtaceae*), 2014, *P.W. Crous*, HPC 1762, culture CBS 144636 = CPC 32144.

Notes: The genus *Caliciopsis* (based on *C. pinea*) represents two phylogenetically distinct, well-supported clades, one of which is ascribed here to the former generic synonym, *Hypsotheca*, which appears to be the oldest name available for this clade. *Hypsotheca* (based on *Hypsotheca subcorticalis*; globose ascospores) was formerly distinguished from *Caliciopsis* (*Caliciopsis pinea*; ellipsoid ascospores) based on ascospore shape, although Fitzpatrick (1942) did not consider this character to be significant at generic level. Morphologically there are few differences between these genera, except that species of *Hypsotheca* known from culture also form a phaeoacremonium-like synasexual morph in culture, which has not yet been observed for species of *Caliciopsis s.str*. *Hypsotheca pleomorpha* was recently described as the causal agent of a canker disease of *Eucalyptus* spp. in Australia (Pascoe *et al*. 2018), and is reported here from leaves of *Eucalyptus piperita*, although its possible role as foliar pathogen remains unknown.

Based on a megablast search of NCBI's GenBank nucleotide database, the **ITS** sequence was identical to *Caliciopsis pleomorpha* (GenBank MG641785.1; Identities = 523/523 (100 %)), and related to *Corynelia uberata* (GenBank KU204606.1; Identities = 511/526 (97 %), 5 gaps (0 %)) and *Caliciopsis maxima* (GenBank KX891229.1; Identities = 467/533 (88 %), 20 gaps (3 %)). Closest hits using the **LSU** sequence are *Caliciopsis nigra* (GenBank KP144011.1; Identities = 769/826 (93 %), 9 gaps (1 %)), *Caliciopsis pinea* (GenBank DQ678097.1; Identities = 781/843 (93 %), 8 gaps (0 %)), and *Caliciopsis beckhausii* (GenBank NG_060418.1; Identities = 789/855 (92 %), 5 gaps (0 %)).

Jeremyomyces Crous & R.K. Schumach., ***gen. nov.*** MycoBank MB829307.

Etymology: Name refers to Jeremy, a young man who due to social circumstances has to live in a children's home in Germany. Despite these difficult circumstances, he has proven to be an attentive observer with a special interest in fungi.

Ascomata pseudothecial, intracorticolous, singly, gregarious, unilocular, sphaerical, black; ostiole indistinct. *Peridium* few-layered, consisting of a *textura angularis* with thick-walled, smooth, and eguttulate cells, inner layers hyaline, outer layers red brown. *Paraphysoids* numerous, distinctly longer than the asci, basally moniliform, upwards tapered and filiform, end cells gnarled, multi-celled, hyaline, thin-walled, smooth, eguttulate, branched, with anastomoses. *Asci* 8-spored, clavate, apically rounded with an ocular chamber, pedicel short and furcate, thick-walled, bitunicate, fissitunicate, apical chamber well-defined, clavate to subcylindrical, spores oblique biseriate overlapped. *Ascospores* hyaline, smooth, guttulate, 1-septate (3-septate with age), fusoid, widest above septum, prominently constricted with well-defined mucoid sheath; basal cell somewhat longer and apical cell. *Conidiomata* developing in culture, pycnidial, brown, globose with central ostiole. *Conidiophores* reduced to conidiogenous cells, lining the inner cavity, ampulliform to doliiform, hyaline, smooth, phialidic. *Conidia* solitary, aseptate, hyaline, smooth, subcylindrical with obtuse ends.

Type species: *Jeremyomyces labinae* Crous & R.K. Schumach.

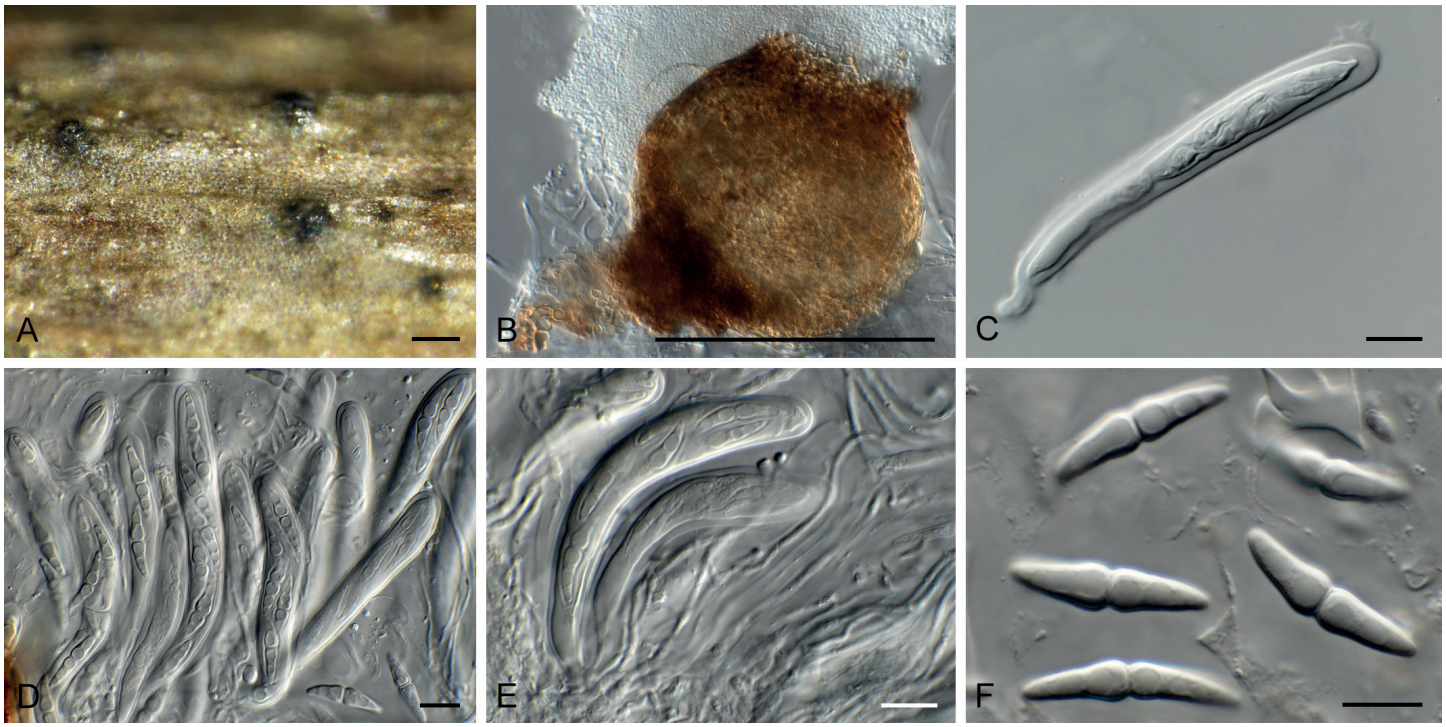

Fig. 25. *Jeremyomyces labinae* (CPC 33154). **A.** Ascomata on host tissue. **B.** Conidioma in culture. **C–E.** Asci. **F.** Ascospores with sheath. Scale bars: A, B = 200 µm, C–F = 10 µm.

Jeremyomyces labinae Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB829309. Fig. 25.

Etymology: Name refers to Mrs. Elena Labina, a Russian colleague who has dedicated much of her personal time to collaborating with the authorities of this species in fungal research.

Ascomata pseudothecial, intracorticolous, singly, gregarious, unilocular, sphaerical, black, soft, +/-thin, ostiole indistinct, basally with a few short and red brown hyphae, up to 200 µm diam. *Peridium* few-layered, consisting of a *textura angularis* with thick-walled, smooth, and eguttulate cells, inner layers hyaline, outer layers red brown. *Paraphysoids* numerous, distinctly longer than the asci, basally moniliform, upwards tapered and filiform, end cells gnarled, multi-celled, 2–3 µm diam, hyaline, thin-walled, smooth, eguttulate, branched, with anastomoses. *Asci* 8-spored, clavate, apically rounded with an ocular chamber, pedicel short and furcate, thick-walled, bitunicate, fissitunicate, 75–115 × 10–13 µm, apical chamber well-defined, 2 µm diam, clavate to subcylindrical, spores oblique biseriate overlapped. *Ascospores* hyaline, smooth, guttulate (at least 2 guttules per cell), 1-septate (3-septate with age), fusoid, widest above septum, prominently constricted with well-defined mucoid sheath, 5 µm diam; basal cell somewhat longer and apical cell, (19–)22–24(–26) × (4–)5(–6) µm. In culture: *Conidiomata* developing in culture, pycnidial, brown, globose with central ostiole, 150–180 µm diam. *Conidiophores* reduced to conidiogenous cells, lining the inner cavity, ampulliform to doliiform, hyaline, smooth, phialidic, 3–4 × 3–5 µm. *Conidia* solitary, aseptate, hyaline, smooth, subcylindrical with obtuse ends, (3–)4–5 × 2 µm.

Culture characteristics: Colonies spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface pale olivaceous grey, reverse olivaceous grey; on PDA surface olivaceous grey in centre, scarlet in outer region, reverse scarlet with diffuse scarlet pigment; on OA surface olivaceous grey with patches of scarlet and diffuse scarlet pigment.

Typus: **Germany**, near Berlin, on twig of *Salix alba* (*Salicaceae*), 21 Jan. 2017, *R.K. Schumacher*, HPC 1956 (**holotype** CBS H-23817, culture ex-type CPC 33154 = CBS 144617).

Notes: Morphologically *Jeremyomyces* is similar to *Angustimassarina* (Thambugala *et al*. 2015), except that it has a coelomycetous asexual morph. Strangely, the LSU sequence clusters with the type sequence of *Acericola italica,* a fungus that is morphologically quite distinct, having brown, three-septate ascospores. This suggests that the GenBank sequence of *Acericola* is incorrect. Based on this sequence however, this fungus was placed in a new genus, *Acericola*, rather than *Setomelanomma*, which is probably where it belongs.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Acericola italica* (GenBank NR_156344.1; Identities = 523/534 (98 %), 3 gaps (0 %)), *Xenophoma puncteliae* (as *Phoma* sp. JDL-2012a, GenBank JQ238617.1; Identities = 553/578 (96 %), 9 gaps (1 %)), and *Phaeosphaeria caricis* (GenBank KY090633.1; Identities = 536/583 (92 %), 13 gaps (2 %)). Closest hits using the **LSU** sequence are *Acericola italica* (GenBank MF167429.1; Identities = 883/883 (100 %), no gaps), *Phaeosphaeria sowerbyi* (GenBank MH873687.1; Identities = 891/896 (99 %), no gaps), and *Phaeosphaeria herpotrichoides* (GenBank MH873664.1; Identities = 891/896 (99 %), no gaps). No significant hits were obtained when the ***cmdA*** sequence was used in blastn and megablast searches. Distant hits using the ***rpb2*** sequence had highest similarity to *Phaeosphaeriopsis triseptata* (GenBank KJ522486.1; Identities = 877/1003 (87 %), 2 gaps (0 %)), *Hawksworthiana alliariae* (as *Dematiopleospora*

alliariae, GenBank KX507261.1; Identities = 846/1008 (84 %), 1 gap (0 %)), and *Dematiopleospora salsolae* (GenBank MG829254.1; Identities = 830/1005 (83 %), 2 gaps (0 %)). Distant hits using the ***tef1*** sequence had highest similarity to *Didymocyrtis cladoniicola* (as *Diederichomyces cladoniicola*, GenBank KP170668.1; Identities = 435/521 (83 %), 16 gaps (3 %)), *Phaeosphaeria ammophilae* (GenBank MF795877.1; Identities = 411/495 (83 %), 30 gaps (6 %)), and *Chaetosphaeronema hispidulum* (GenBank KF253108.1; Identities = 394/472 (83 %), 23 gaps (4 %)). Distant hits using the ***tub2*** sequence had highest similarity to *Xenophoma puncteliae* (GenBank KP170711.1; Identities = 249/278 (90 %), 1 gap (0 %)), *Didymocyrtis banksiae* (GenBank KY979923.1; Identities = 245/279 (88 %), 9 gaps (3 %)), and *Phoma haematocycla* (GenBank KT309405.1; Identities = 239/272 (88 %), 3 gaps (1 %)).

Macgarvieomyces luzulae (Ondřej) Y. Marín *et al*., Stud. Mycol. 92: 84. 2018 (2019). Fig. 26.
Basionym: *Pyricularia luzulae* Ondřej, Ceská Mykol. 42: 81. 1988.

Conidiophores solitary, erect, straight to flexuous, subcylindrical, unbranched, thick-walled, brown, smooth-walled, 1–3-septate, arising from hyphae looking lacking a swollen base, 60–120 × 5–6 µm. *Conidiogenous cells* integrated, terminal, pale brown, smooth-walled, subcylindrical with apical taper towards a rachis of sympodially arranged denticles, 1–2 × 1–1.5 µm. *Conidia* solitary, pale brown, finely roughened, guttulate, fusoid, apex appendiculate, base tapering to protruding hilum, 1–1.5 µm diam, somewhat darkened, (21–)22–23(–25) × (5.5–)6–7(–8) µm with a single supramedian transverse septum; when sporulating on PNA, germinating conidia form appressoria that are brown, irregularly lobed, 5–10 µm diam, with a hyaline central infection pore, 1 µm diam.

Culture characteristics: Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA surface and reverse saffron; on PDA and OA surface and reverse pale luteous.

Material examined: **Ukraine**, Rakhiv district, Transcarpathian region, Sidlovyana stow, Petros mountains, on *Luzula sylvatica* (*Juncaceae*), 9 Aug. 2017, *A. Akulov*, CWU (MYC) AS 6437 = HPC 2197, CBS H-23833, culture CPC 34292 = CBS 145042.

Notes: *Macgarvieomyces* was introduced by Klaubauf *et al*. (2014) for a genus of fungi resembling *Pyricularia* in general morphology, but which was distinct from the latter genus in having fusoid, 1-septate conidia, and occurring on *Juncaceae*. *Macgarvieomyces luzulae* was recently treated by Marin-Felix *et al.* (2019), and this is the second collection from *Luzula sylvatica*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Macgarvieomyces luzulae* (GenBank MG934442.1; Identities = 548/548 (100 %)), *Macgarvieomyces borealis* (GenBank NR_145384.1; Identities = 485/517 (94 %), 10 gaps (1 %)), and *Macgarvieomyces juncicola* (GenBank KM009165.1; Identities = 462/494 (94 %), 11 gaps (2 %)). Closest hits using the **LSU** sequence are *Macgarvieomyces juncicola* (GenBank KM009153.1; Identities = 854/864 (99 %), 1 gap (0 %)), *Macgarvieomyces borealis* (GenBank NG_058088.1; Identities = 853/863 (99 %), no gaps), and *Deightoniella roumeguerei* (as *Utrechtiana cibiessia*, GenBank JF951176.1; Identities = 877/895 (98 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Macgarvieomyces luzulae* (GenBank MG934464.1; Identities = 348/350 (99 %), no gaps), *Macgarvieomyces borealis* (GenBank KM485170.1; Identities = 221/251 (88 %), 9 gaps (3 %)), and *Macgarvieomyces juncicola* (GenBank KM485171.1; Identities = 252/318 (79 %), 29 gaps (9 %)).

Microdochium rhopalostylidis Crous & Thangavel, ***sp. nov.*** MycoBank MB829310. Fig. 27.

Etymology: Name refers to the genus *Rhopalostylis* from which it was isolated.

Mycelium immersed and superficial, consisting of hyaline, smooth, branched, septate, 2–3 µm diam hyphae. *Sporodochia* slimy, hyaline, becoming pale brown with age. *Conidiophores* tightly aggregated, irregularly branched, hyaline, smooth, 0–4-septate, 5–25 × 2.5–3.5 µm. *Conidiogenous cells* smooth, hyaline, ampulliform, terminal and lateral with sympodial proliferation and inconspicuous flat-tipped loci, 4–10 × 3–3.5 µm. *Conidia* solitary, aggregating in mucoid packets, hyaline, smooth-walled, guttulate, fusoid, curved, apex subobtuse, base truncate, 1–3-septate, (13–)16–20(–23) × (2.5–)3(–4) µm.

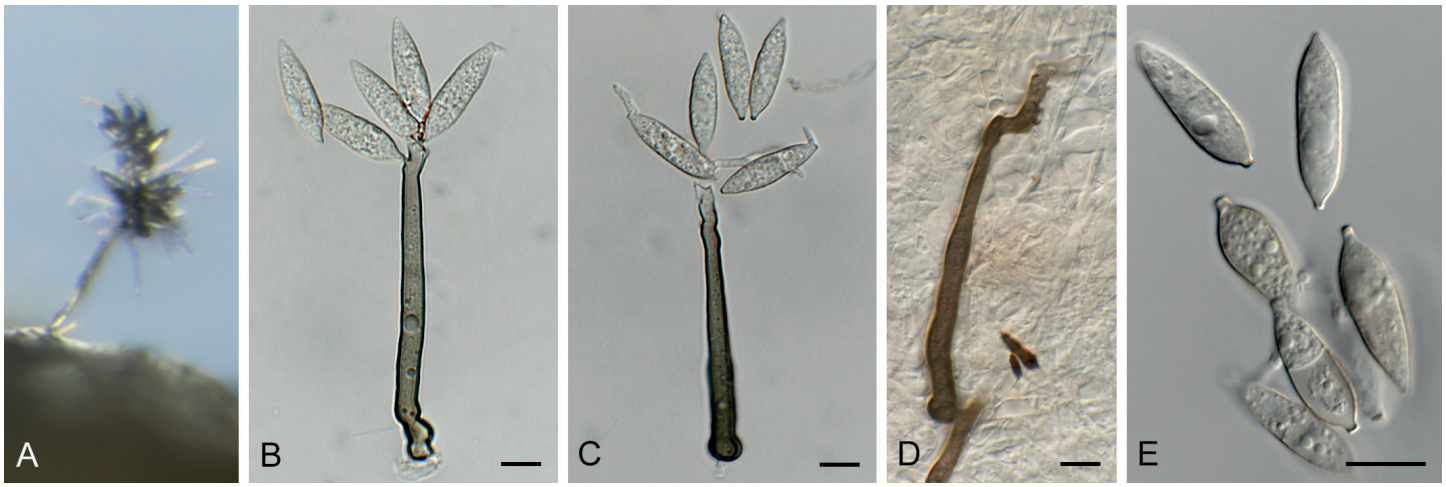

Fig. 26. *Macgarvieomyces luzulae* **(**CPC 34292). **A.** Conidiophore on PNA. **B–D.** Conidiophores. **E.** conidia. Scale bars = 10 µm.

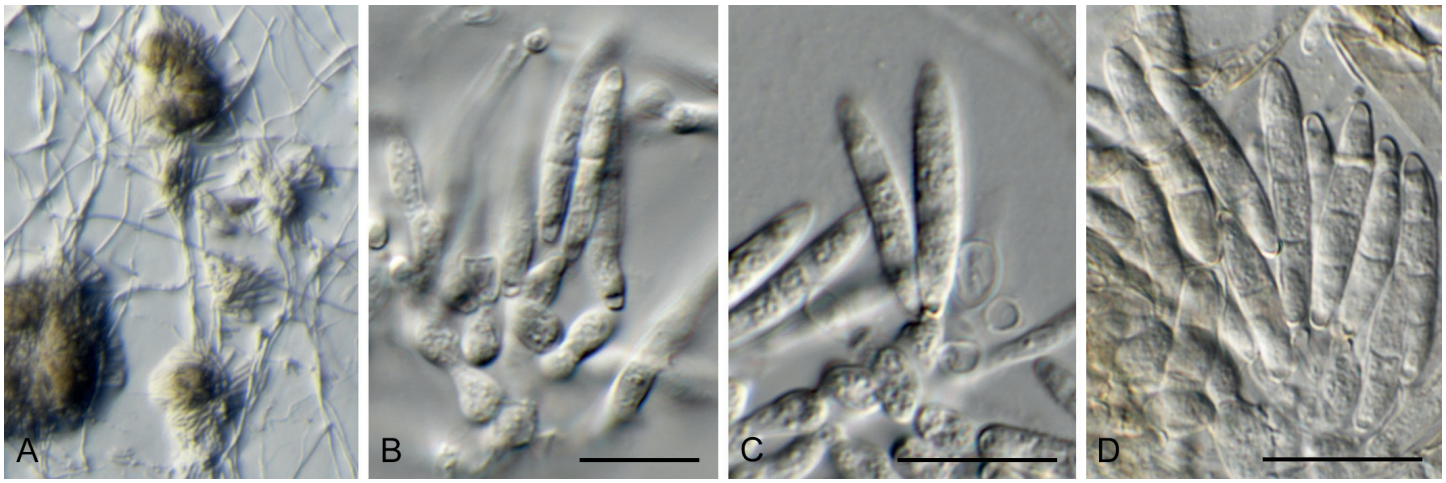

Fig. 27. *Microdochium rhopalostylidis* (CPC 34449). **A.** Sporodochia on SNA. **B–D.** Conidiogenous cells giving rise to conidia. Scale bars = 10 µm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA and PDA surface saffron to luteous, reverse sienna; on OA surface umber to saffron.

Typus: **New Zealand**, Auckland, Auckland Botanical Garden, on leaves of *Rhopalostylis sapida* (*Arecaceae*), 2017, *R. Thangavel*, T17_03052B (**holotype** CBS H-23835, culture ex-type CPC 34449 = CBS 145125).

Note: *Microdochium* and allied genera were revised by Hernández-Restrepo *et al*. (2016). Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pseudofusarium fusarioideum* (GenBank MH860033.1; Identities = 537/551 (97 %), 7 gaps (1 %)), *Microdochium phragmitis* (GenBank NR_132916.1; Identities = 529/544 (97 %), 7 gaps (1 %)), and *Microdochium lycopodinum* (GenBank KP859005.1; Identities = 529/544 (97 %), 8 gaps (1 %)). Closest hits using the **LSU** sequence are *Microdochium phragmitis* (GenBank KP858948.1; Identities = 893/893 (100 %), no gaps), *Microdochium lycopodinum* (GenBank KP858929.1; Identities = 847/855 (99 %), no gaps), and *Microdochium fisheri* (GenBank KP858951.1; Identities = 825/844 (98 %), 2 gaps (0 %)). Distant hits using the ***actA*** sequence had highest similarity to *Penicillifer pulcher* (GenBank KM231107.1; Identities = 406/420 (97 %), no gaps), *Penicillifer bipapillatus* (GenBank KM231105.1; Identities = 404/420 (96 %), no gaps), and *Gliocephalotrichum longibrachium* (GenBank KM231117.1; Identities = 403/419 (96 %), no gaps). Only very distant hits were obtained using the ***cmdA*** sequence, for example with *Penicillium johnkrugii* (GenBank JN686399.1; Identities = 135/142 (95 %), no gaps), *Penicillium exsudans* (GenBank KX885052.1; Identities = 133/139 (96 %), no gaps), and *Penicillium austrosinicum* (GenBank KX885051.; Identities = 133/139 (96 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Microdochium phragmitis* (GenBank KP859122.1; Identities = 798/849 (94 %), no gaps), *Microdochium lycopodinum* (GenBank KP859102.1; Identities = 789/837 (94 %), no gaps), and *Microdochium fisheri* (GenBank KP859124.1; Identities = 750/841 (89 %), 2 gaps (0 %)). The best hit using the ***tub2*** sequence had highest similarity to *Microdochium musae* (GenBank MH108044.1; Identities = 115/135 (85 %), 5 gaps (3 %)).

Neocordana malayensis Crous, ***sp. nov.*** MycoBank MB829313. Fig. 28.

Etymology: Name refers to Malaysia where it was isolated.

Mycelium consisting of pale brown, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* subcylindrical, flexuous, erect, medium brown, smooth, multiseptate, 200–500 × 7–9 µm. *Conidiogenous cells* polyblastic, terminal and intercalary, 10–40 × 6–8 µm, denticulate; denticles up to 1 µm long, 0.5–1 µm wide. *Conidia* oblong to obovoid, (12–)14–18(–20) × (8–)10 µm, 1-septate, thick-walled, brown with truncate hilum, 1 µm diam.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and feathery margin, reaching 65 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white with patches of pale olivaceous grey or pale luteous.

Typus: **Malaysia**, on leaves of *Musa* sp. (*Musaceae*), Feb. 2010, *P.W. Crous*, HPC 1595 (**holotype** CBS H-23812, culture ex-type CPC 32837 = CBS 144604).

Notes: *Neocordana* was introduced by Hernández-Restrepo *et al.* (2015) to accommodate several species of hyphomycetes causing a foliar disease on *Canna* and *Musa*. The morphological characteristics of *N. malayensis* overlap with those of *N. musae* and *N. musicola* in conidial dimensions, but are distinct from them in having very long, flexuous conidiophores. Phylogenetically, it also clusters apart from *N. musae* and *N. musicola.*

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neocordana musigena* (GenBank KY979749.1; Identities = 553/575 (96 %), 15 gaps (2 %)), *Neocordana musarum* (GenBank KY173425.1; Identities = 553/575 (96 %), 15 gaps (2 %)), and *Neocordana musae* (GenBank LN713276.1; Identities = 553/575 (96 %), 15 gaps (2 %)). Closest hits using the **LSU** sequence are *Neocordana musicola* (GenBank LN713287.1; Identities = 843/847 (99 %), no gaps), *Neocordana musarum* (GenBank KY173515.1; Identities = 820/824 (99 %), no gaps), and *Neocordana musae* (GenBank LN713290.1; Identities = 873/878 (99 %), 1 gap (0 %)). Closest hits using the ***actA*** sequence had highest similarity to *Neocordana musigena* (GenBank

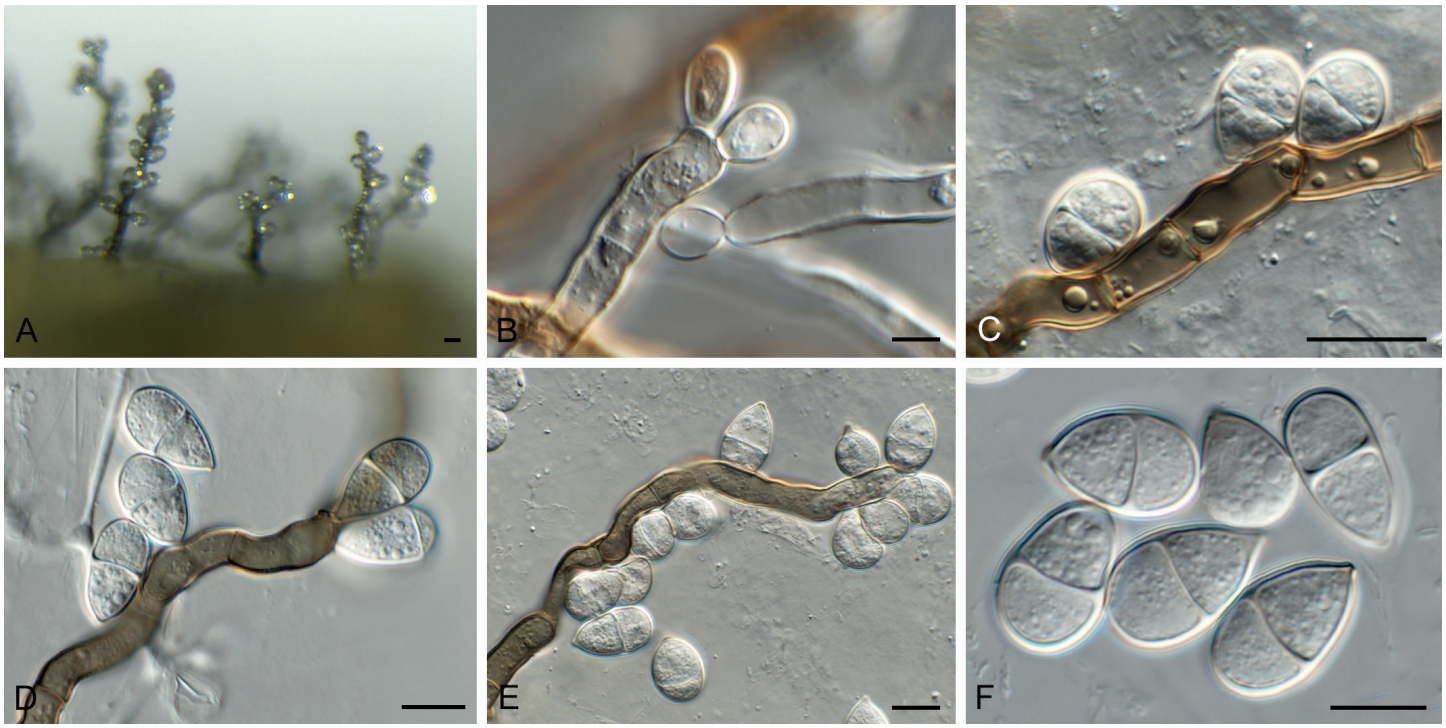

Fig. 28. *Neocordana malayensis* (CPC 32837). **A.** Conidiophores on PNA. **B–E.** Conidiophores with conidiogenous loci. **F.** Conidia. Scale bars = 10 µm.

KY979854.1; Identities = 746/746 (100 %), no gaps), *Neocordana musarum* (GenBank KY173568.1; Identities = 357/358(99%), no gaps), and *Gaeumannomyces tritici* (GenBank XM_009225830.1; Identities = 386/414 (93 %), no gaps). Closest hits using the ***tub2*** sequence had highest similarity to *Neocordana musigena* (GenBank KY979915.1; Identities = 553/559 (99 %), 1 gap (0 %)), *Hypoxylon calileguense* (GenBank KU604578.1; Identities = 714/797 (90 %), 1 gap (0 %)), and *Chaetomium globosum* (GenBank XM_001226965.1; Identities = 654/735 (89 %), 2 gaps (0 %)).

Neocucurbitaria prunicola Crous & Akulov, ***sp. nov.*** MycoBank MB829314. Fig. 29.

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

Conidiomata pycnidial, solitary to aggregated, globose, medium brown, 100–200 µm diam, with central ostiole, 20–40 µm diam, surrounded with erect, unbranched, brown, smooth, 1–2-septate, thick-walled setae, 20–40(–70) × 3–4 µm, with obtuse ends; conidiomatal wall of 3–4 layers of flattened, brown *textura angularis. Conidiophores* lining the inner cavity, hyaline, smooth, subcylindrical, branched, 1–3-septate, 10–20 × 2–3 µm. *Conidiogenous cells* hyaline, smooth, subcylindrical to doliiform, phialidic, terminal and intercalary, 3–10 × 2–3 µm. *Conidia* hyaline, smooth, aseptate, guttulate, subcylindrical with obtuse ends, (2–)3–3.5(–4) × 1.5(–2) µm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse grey olivaceous.

Typus: **Ukraine**, Ternopil region, Dniester Canyon N.P., forest, fallen twigs of *Prunus padus* (= *Padus avium*) (*Rosaceae*), 6 Oct. 2016, *A. Akulov*, CWU AS 6209 = HPC 2045 (**holotype** CBS H-23824, culture ex-type CPC 33709 = CBS 145033).

Notes: *Neocucurbitaria* was treated by Jaklitsch *et al.* (2018), and shown to have phoma-like asexual morphs. *Neocucurbitaria prunicola* is phylogenetically distinct from other species presently known in the genus.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neocucurbitaria rhamni* (GenBank MF795778.1; Identities = 446/483 (92 %), 5 gaps (1 %)), *Neocucurbitaria rhamnioides* (GenBank MF795784.1; Identities = 447/486 (92 %), 7 gaps (1 %)), and *Astragalicola vasilyevae* (GenBank NR_157504.1; Identities = 453/494 (92 %), 13 gaps (2 %)). Closest hits using the **LSU** sequence are *Neocucurbitaria unguis-hominis* (GenBank GQ387621.1; Identities = 850/854 (99 %), no gaps), *Neocucurbitaria keratinophila* (GenBank MH874704.1; Identities = 849/854 (99 %), no gaps), and *Neocucurbitaria quercina* (GenBank GQ387620.1; Identities = 849/854 (99 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Neocucurbitaria unguis-hominis* (as *Pyrenochaeta unguis-hominis*, GenBank LT717682.1; Identities = 760/866 (88 %), 2 gaps (0 %)), *Cucurbitaria berberidis* (GenBank LT854936.1; Identities = 768/876 (88 %), 7 gaps (0 %)), and *Neocucurbitaria cava* (as *Pyrenochaeta cava*, GenBank LT717681.1; Identities = 744/856 (87 %), 2 gaps (0 %)). Distant hits using the ***tub2*** sequence had highest similarity to *Neocucurbitaria juglandicola* (GenBank MF795901.1; Identities = 452/495 (91 %), 2 gaps (0 %)), *Neocucurbitaria populi* (GenBank MF795902.1; Identities = 451/495 (91 %), 2 gaps (0 %)), *Neocucurbitaria rhamnioides* (GenBank MF795908.1; Identities = 448/493 (91 %), 7 gaps (1 %)), *Leptosphaeria biglobosa* (as *Leptosphaeria maculans*, GenBank FO906902.1; Identities = 887/999 (89 %), 11 gaps (1 %)), *Leptosphaeria biglobosa* (GenBank FO905876.1; Identities = 877/987 (89 %), 10 gaps (1 %)), and *Helminthosporium solani* (GenBank AF461130.1; Identities = 702/803 (87 %), 10 gaps (1 %)).

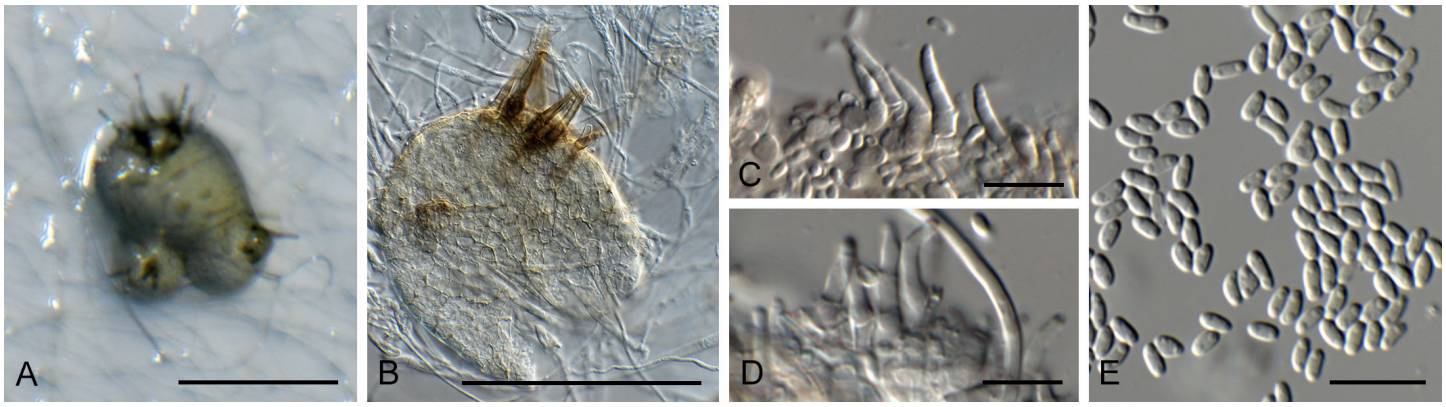

Fig. 29. *Neocucurbitaria prunicola* (CPC 33709). **A, B.** Conidiomata on SNA. **C, D.** Conidiogenous cells. **E.** Conidia. Scale bars: A, B = 200 µm, C–E = 10 µm.

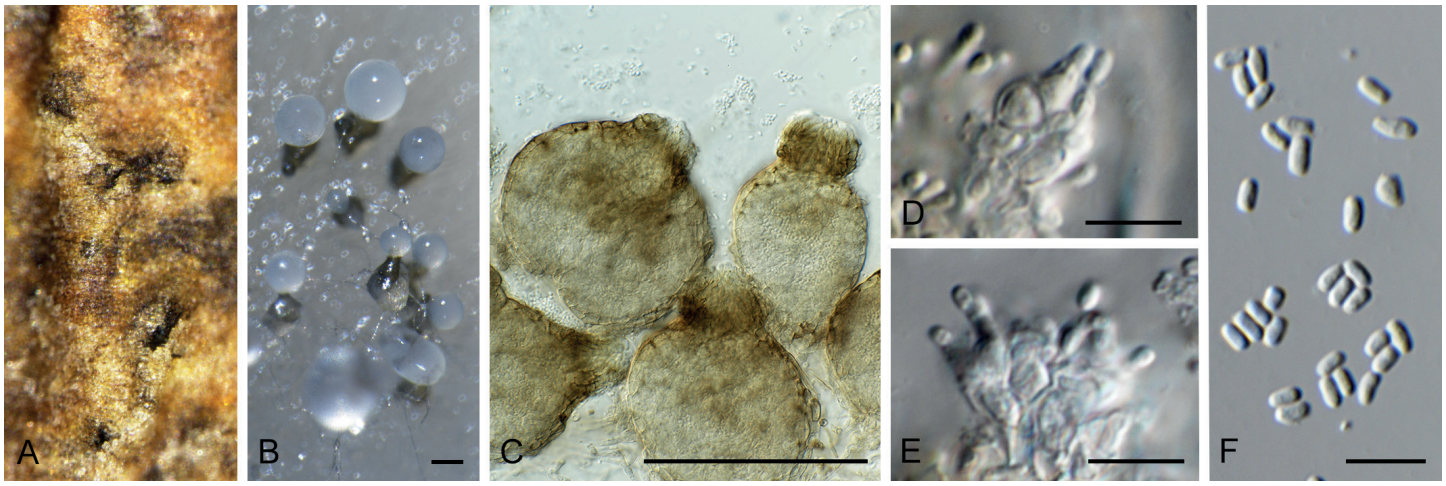

Fig. 30. *Neocucurbitaria salicis-albae* (CPC 33162). **A.** Immersed conidiomata on host tissue. **B, C.** Conidiomata in culture. **D, E.** Conidiogenous cells. **F.** Conidia. Scale bars: B, C = 120 µm, C–F = 10 µm.

Neocucurbitaria salicis-albae Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB829315. Fig. 30.

Etymology: Name refers to *Salix alba* from which it was isolated.

Conidiomata pycnidial, solitary or aggregated, brown, globose, 70–120 µm diam, with prominent papillate darker brown central ostiole 1(–3), 20–30 µm diam; wall of 3–6 layers of pale brown *textura angularis*. *Conidiophores* lining the inner cavity, hyaline, smooth, reduced to conidiogenous cells, ampulliform, phialidic, 5–7 × 2.5–4 µm. *Conidia* solitary, aseptate, hyaline, smooth, prominently guttulate, thin-walled, subcylindrical to fusoid-ellipsoid, (2.5–)3–3.5(–4) × 2 µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 17–30 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus: **Germany**, near Berlin, on *Salix alba* twig, 21 Jan. 2017, *R.K. Schumacher*, HPC 1963 (**holotype** CBS H-23818, culture ex-type CPC 33162 = CBS 144611).

Notes: *Pyrenochaeta* (= *Cucurbitaria*) was resurrected as discrete genus by De Gruyter *et al.* (2010). *Neocucurbitaria* was established by Wanasinghe *et al.* (2017) for a sister genus with pyrenochaeta-like asexual morphs, and cucurbitaria-like sexual morphs. *Neocucurbitaria* and several pyrenochaeta-like genera and their respective families were clarified further by Valenzuela-Lopez *et al.* (2018). *Neocucurbitaria salicis-albae* is a new species from *Salix*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neocucurbitaria quercina* (as *Pyrenochaeta quercina*, GenBank LT623220.1; Identities = 519/533 (97 %), no gaps), *Neocucurbitaria acanthocladae* (GenBank MF795766.1; Identities = 515/535 (96 %), 2 gaps (0 %)), and *Neocucurbitaria unguis-hominis* (as *Pyrenochaeta unguis-hominis*, GenBank KP794081.1; Identities = 472/490 (96 %), 7 gaps (1 %)). The ITS sequence is identical to "*Cucurbitariaceae* sp. MUT 4403" (GenBank KC339238.1; Identities = 491/491 (100 %)), isolated from *Posidonia oceanica* in the Punta Manara-Riva Trigoso Bay, Italy. Closest hits using the **LSU** sequence are *Neocucurbitaria keratinophila* (GenBank MH874704.1; Identities = 859/861 (99 %), no gaps)), *Neocucurbitaria quercina* (GenBank GQ387620.1; Identities = 859/861 (99 %), no gaps), and *Neocucurbitaria aquatica* (GenBank EU754177.1; Identities = 859/861 (99 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Neocucurbitaria quercina* (as *Pyrenochaeta quercina*, GenBank LT623277.1; Identities = 919/956 (96 %), no gaps), *Neocucurbitaria unguis-hominis* (as *Pyrenochaeta unguis-hominis*, GenBank LT623279.1; Identities = 872/952 (92 %), no gaps), and *Neocucurbitaria aetnensis* (GenBank MF795811.1; Identities = 832/900 (92 %), no gaps). Closest hits using the

tub2 sequence had highest similarity to *Neocucurbitaria acanthocladae* (GenBank MF795894.1; Identities = 440/457 (96 %), 1 gap (0 %)), *Neocucurbitaria cinereae* (GenBank MF795899.1; Identities = 438/457 (96 %), 1 gap (0 %)), *Neocucurbitaria ribicola* (GenBank MF795912.1; Identities = 432/457 (95 %), 2 gaps (0 %)), *Leptosphaeria biglobosa* (GenBank FO905876.1; Identities = 932/1036 (90 %), 6 gaps (0 %)), *Westerdykella cylindrica* (GenBank JX235707.1; Identities = 689/777 (89 %), 10 gaps (1 %)), and *Helminthosporium solani* (GenBank AF461130.1; Identities = 745/861 (87 %), 12 gaps (1 %)).

Neodevriesia metrosideri Crous, *Persoonia* **41**: 303. 2018. Fig. 31.

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

Mycelium consisting of branched, septate, brown, smooth, 3(–5) µm diam hyphae. *Conidiophores* erect, solitary, arising directly from superficial hyphae, subcylindrical, straight to somewhat curved, smooth, brown, 0–2-septate, 10–30 × 2–3 µm. *Conidiogenous cells* terminal, integrated, subcylindrical, brown, smooth, 5–10 × 2–3 µm; hila truncate, 2–3 µm diam, not darkened nor thickened. *Conidia* occurring in branched chains (–15), medium brown, smooth, subcylindrical to fusoid-ellipsoid, 0–1(–2)-septate, (10–)13–15(–20) × 2–3(–4) µm; hila unthickened, not darkened, 1.5–2 µm diam.

Culture characteristics: Colonies erumpent, with moderate aerial mycelium, and smooth, lobate margins, reaching 20 mm diam after 2 wk. On MEA, PDA and OA surface and reverse iron-grey.

Material examined: **New Zealand**, Auckland, Bucklands Beach, 22 Wells Road, on leaves of *Metrosideros excelsa* (*Myrtaceae*), 2015, *R. Thangavel*, T16_03926G, CBS H-23810, culture CBS 144638 = CPC 32786.

Notes: *Neodevriesia metrosideri* was recently described from *Metrosideros* sp. on the Great Barrier Island in New Zealand (Crous *et al*. 2018b), and this is the second collection of this taxon from this country.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neodevriesia lagerstroemiae* (GenBank GU214634.1; Identities = 518/533 (97 %), 4 gaps (0 %)), *Neodevriesia fraserae* (as *Devriesia fraseriae*, GenBank NR_144961.1; Identities = 508/535 (95 %), 9 gaps (1 %)), and *Devriesia sardiniae* (GenBank KP791766.1; Identities = 504/531 (95 %), 4 gaps (0 %)). Closest hits using the **LSU** sequence are *Neodevriesia lagerstroemiae* (GenBank KF902149.1; Identities = 732/741 (99 %), no gaps), *Neodevriesia knoxdaviesii* (as *Teratosphaeria knoxdaviesii*, GenBank EU707865.1; Identities = 801/814 (98 %), 2 gaps (0 %)), and *Neodevriesia cladophorae* (as *Devriesia* sp. MW-2016a, GenBank KU578114.1; Identities = 798/813 (98 %), no gaps). No ***actA*** sequences of *Neodevriesia* or *Devriesia* are currently available for comparison on GenBank. No significant hits were obtained when the ***tub2*** sequence was used in blastn and megablast searches.

Neodothidotthia Crous, ***gen. nov.*** MycoBank MB829317.

Etymology: Name reflects its morphological similarity to the genus *Dothidotthia*.

Sporodochia dark brown, punctiform. *Stromata* immersed to superficial, brown. *Conidiophores* brown, finely roughened, subcylindrical, septate. *Conidiogenous cells* brown, subcylindrical, finely roughened, proliferating percurrently at apex. *Conidia* fusoid to ellipsoid, medium brown, transversely septate, apex obtuse, base truncate.

Type species: *Neodothidotthia negundinicola* Crous & Akulov.

Neodothidotthia negundinicola Crous & Akulov, ***sp. nov.*** MycoBank MB829318. Fig. 32.

Etymology: Name refers to *Acer negundo* from which it was isolated.

Sporodochia dark brown, punctiform, 100–300 µm diam. *Stromata* immersed to superficial, brown, 80–150 µm diam. *Conidiophores* brown, finely roughened, subcylindrical, 4–6-septate, 60–150 × 7–12 µm. *Conidiogenous cells* brown, subcylindrical, finely roughened, 8–15 × 5–7 µm, proliferating

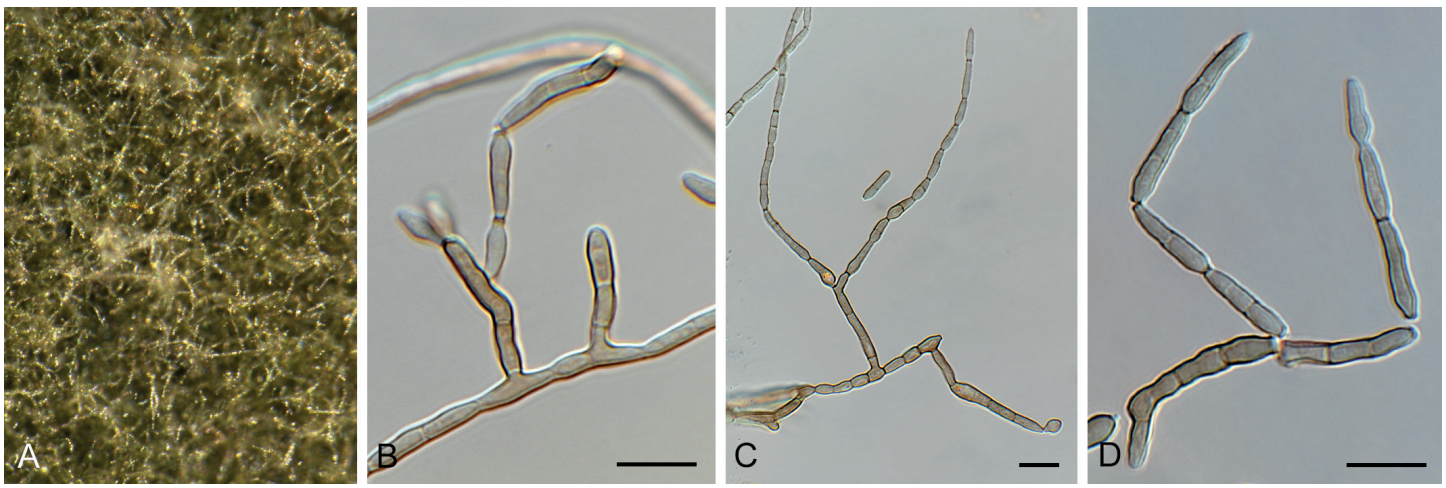

Fig. 31. *Neodevriesia metrosideri* (CPC 32786). **A.** Colony on PDA. **B–D.** Conidiophores giving rise to branched conidial chains. Scale bars = 10 µm.

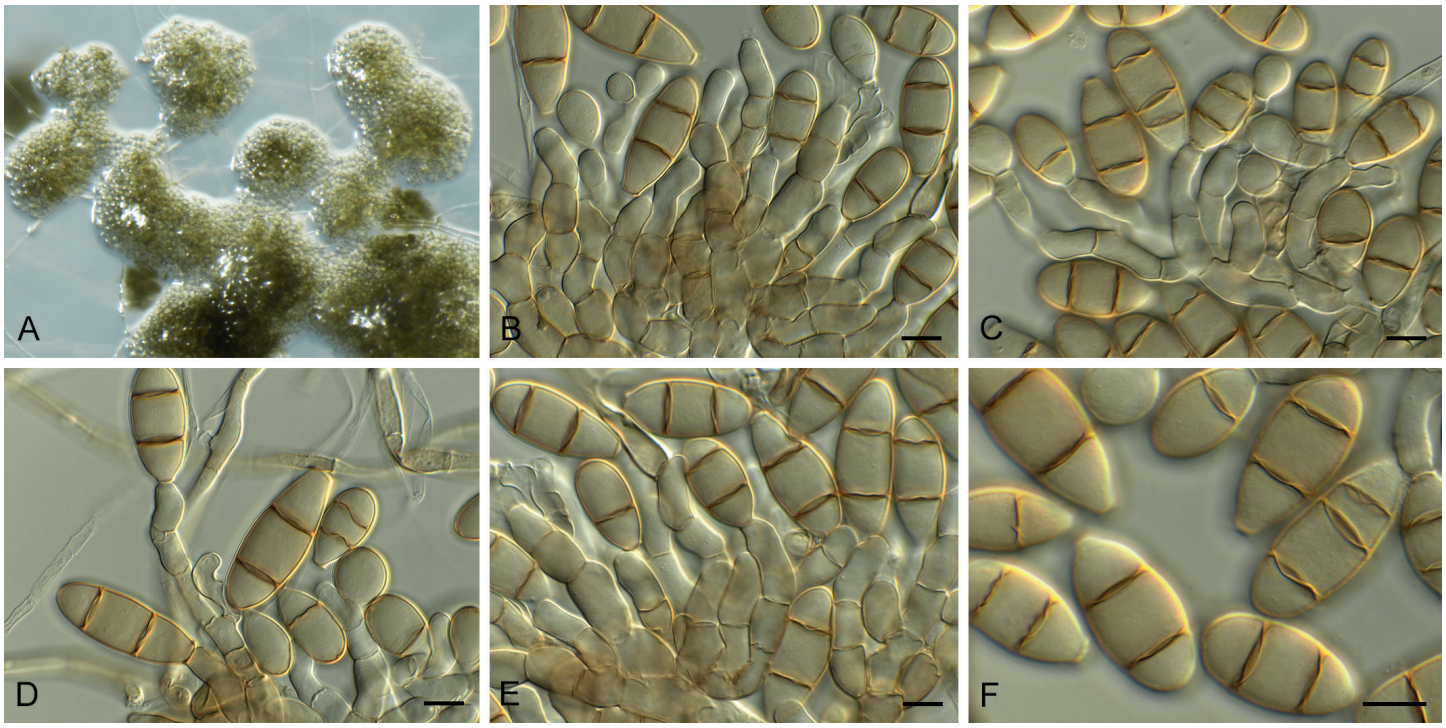

Fig. 32. *Neodothidotthia negundinicola* (CPC 34071). **A.** Sporodochia on SNA. **B–E.** Conidiogenous cells giving rise to conidia. **F.** Conidia. Scale bars = 10 µm.

percurrently at apex. *Conidia* fusoid to ellipsoid, medium brown, transversely (1–)2-septate, apex obtuse, base truncate, 4–5 µm diam, (25–)30–35(–37) × (12–)13–15(–16) µm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth to feathery, lobate margin, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus: **Ukraine**, Kharkiv region, Zolochiv district, on the dead branches of *Acer negundo* (*Sapindaceae*) still attached to the tree, 28 May 2017, *A. Akulov & R.K. Schumacher*, CWU AS 6293 = HPC 2127 = RKS 116 (**holotype** CBS H-23832, culture ex-type CPC 34071 = CBS 145039).

Neodothidotthia negundinis (Berk. & M.A. Curtis) Crous, ***comb. nov.*** MycoBank MB829319.
Basionym: Coryneum negundinis Berk. & M.A. Curtis, *Grevillea* **2**(22): 153. 1874.
Synonym: *Thyrostroma negundinis* (Berk. & M.A. Curtis) A.W. Ramaley, *Mycotaxon* **94**: 131. 2006 (2005).

Illustration: See Phillips *et al.* (2008).

Material examined: **USA**, Colorado, Durango, 7 Animas Place, dead twigs of *Euonymus alatus*, 29 Jun. 2004, *A.W. Ramaley 0411*, BPI 871820, culture CPC 12930 = CBS 119688; Colorado, Durango, between Animas Place and Animas River, dead twigs of *Acer negundo*, 8 Jul. 2004, *A.W. Ramaley 0414*, BPI 871819, asexual morph culture CPC 12933 = CBS 119691, sexual morph CPC 12932 = CBS 119690; Colorado, La Plata Co, *ca.* 1.75 mile up Carbon Junction Trail, dead twigs of *Fendlera rupicola*, 11 May 2004, *A.W. Ramaley 0403*, BPI 871821, culture CPC 12928 = CBS 119686.

Notes: *Thyrostroma negundinis* (as *Stigmina negundinis*, on twigs of *Acer negundo*, North America) has conidia that are ellipsoid, 2-septate, 25–38 × 12–18 µm, base 4–5 µm diam (Ellis 1971), thus closely fitting with the present collection, although they are phylogenetically distinct. Ramaley (2005) found conidia on the type specimen of *Amphisphaeria aspera* to be much smaller, namely (10–)12–15 × 6–7 µm, suggesting that the latter collection represents a different species in this complex.

Ramaley (2005) and Phillips *et al.* (2008) showed that *Dothidotthia* (based on *D. symphoricarpi* from the USA; CBS 119687) has a *Thyrostroma* (based on *T. compactum*, reference strain CBS 335.37) asexual morph, which they ascribed to *Thyrostroma negundinis*. The link between the two genera has however, not been confirmed in culture. It has thus been proposed to continue using both names until this question has been resolved (Wijayawardene *et al.* 2014, Rossman *et al.* 2015). As we show here, *Thyrostroma* is closely allied, but not congeneric with *Dothidotthia*, thus both generic names should be retained. Furthermore, the European collection of "*Thyrostroma negundinis*" is allied to *D. symphoricarpi*, but is phylogenetically distinct, and therefore described here as a new genus, *Neodothidotthia*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Thyrostroma cornicola* (GenBank NR_154514.1; Identities = 517/540 (96 %), 6 gaps (1 %)), *Thyrostroma compactum* (GenBank MH859911.1; Identities = 516/540 (96 %), 6 gaps (1 %)), and *Phaeomycocentrospora cantuariensis* (GenBank MH866055.1; Identities = 515/539 (96 %), 6 gaps (1 %)). Closest hits using the **LSU** sequence are *Phaeomycocentrospora cantuariensis* (GenBank GU253716.1; Identities = 866/877 (99 %), 2 gaps (0 %)), *Pleiochaeta setosa* (GenBank EU167563.1; Identities = 847/859 (99 %), 3 gaps (0 %)), and *Pleiochaeta ghindensis* (GenBank EU167561.1; Identities = 845/858 (98 %), 2 gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Phaeomycocentrospora cantuariensis* (GenBank GU384382.1; Identities = 265/308 (86 %), 9 gaps (2 %)), *Thyrostroma cornicola*

(GenBank KX228372.1; Identities = 312/372 (84 %), 12 gaps (3 %)), and *Pyrenophora biseptata* (as *Drechslera biseptata*, GenBank JN712588.1; Identities = 321/402 (80 %), 30 gaps (7 %)).

Neohelicomyces deschampsiae Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB829320. Fig. 33.

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

Conidiophores erect, flexuous, mostly unbranched, subcylindrical with slight apical taper, 10–15-septate, 150–220 × 3–4 µm, brown, smooth-walled, tapering toward subobtuse apex. *Conidiogenous cells* intercalary, consisting of short, lateral, cylindrical pegs, pale brown, monoblastic, rarely polyblastic, 2–5 × 1.5–2.5 µm. *Conidia* solitary, coiled 2–3 times, multiseptate, coils 19–22 µm diam, cells 2–2.5 µm diam.

Culture characteristics: Colonies erumpent, spreading, with folded surface and feathery lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA surface umber, reverse sienna; on PDA surface umber, reverse ochreous; on OA surface umber.

Typus: **Germany**, near Berlin, culm base of dead leaf sheath of *Deschampsia cespitosa* (*Poaceae*), 3 May 2017, *R.K. Schumacher*, HPC 2109 = RKS 101 (**holotype** CBS H-23590, culture ex-type CPC 33686 = CBS 145029).

Notes: *Neohelicomyces* differs from *Tubeufia* and allied genera, especially from *Helicomyces*, in having elongate, erect, conspicuous conidiophores, and differs from *Helicosporium* based on conidial morphology (Tsui *et al*. 2006). Based on the species known from their DNA, *N. deschampsiae* appears to represent a new species, being phylogenetically distinct from *T. helicomyces* and *T. paludosa*, which have also been reported from this host (Ellis & Ellis 1997).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Tubeufia helicomyces* (GenBank MH857031.1; Identities = 556/591 (94 %), 18 gaps (3 %)), *Helicosporium lumbricoides* (GenBank MH856861.1; Identities = 554/590 (94 %), 16 gaps (2 %)), *Helicosporium pallidum* (GenBank AY916462.1; Identities = 550/586 (94 %), 16 gaps (2 %)), and *Neohelicomyces aquaticus* (as *Tubeufiaceae* sp. ZL-2017b, GenBank KY320528.1; Identities = 422/452 (93 %), 20 gaps (4 %)). Closest hits using the **LSU** sequence are *Neohelicomyces aquaticus* (as *Tubeufiaceae* sp. ZL-2017b, GenBank KY320545.1; Identities = 849/849 (100 %), no gaps), *Neohelicomyces hyalosporus* (as *Neohelicomyces* sp. YZL-2018a, GenBank MH558870.1; Identities = 841/843 (99 %), no gaps), *Neohelicomyces submersus* (as *Tubeufiaceae* sp. ZL-2017c, GenBank KY320547.1; Identities = 827/830 (99 %), no gaps), and *Tubeufia helicomyces* (GenBank MH868562.1; Identities = 854/860 (99 %), no gaps).

Neomedicopsis Crous & Akulov, ***gen. nov.*** MycoBank MB829321.

Etymology: Name refers to the genus *Medicopsis*, which is phylogenetically allied to it.

Conidiomata pycnidial, globose, erumpent with central ostiole; wall of 6–12 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells, hyaline, smooth, ampulliform with long cylindrical neck, proliferating percurrently. *Conidia* solitary, globose to subglobose, initially pale brown, becoming dark brown, thick-walled, guttulate, granular, apex obtuse, base truncate.

Type species: *Neomedicopsis prunicola* Crous & Akulov.

Neomedicopsis prunicola Crous & Akulov, ***sp. nov.*** MycoBank MB829322. Fig. 34.

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

Conidiomata pycnidial, globose, 200–300 µm diam, erumpent with central ostiole; wall of 6–12 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells, hyaline, smooth, ampulliform with long cylindrical neck, 10–30 × 3–6 µm, proliferating percurrently. *Conidia* solitary, globose to subglobose, initially pale brown, becoming dark brown, thick-walled, guttulate, granular, apex obtuse, base truncate, 3–4 µm diam, (12–)17–20(–22) × (12–)14–16(–17) µm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 25 mm

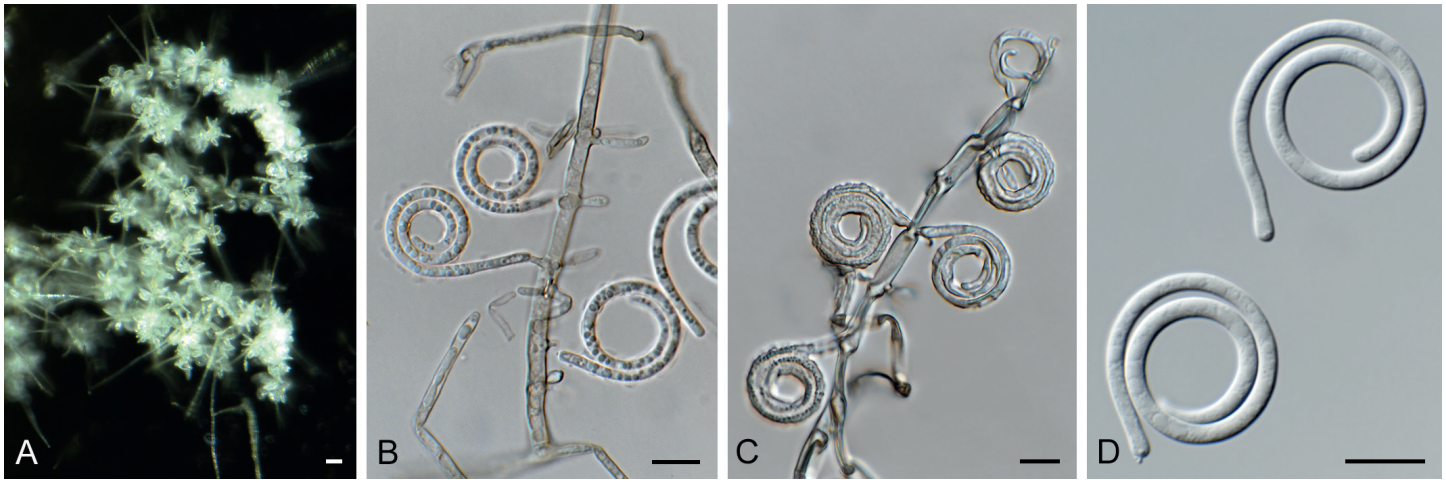

Fig. 33. *Neohelicomyces deschampsiae* (CPC 33686). **A.** Conidiophores on SNA. **B, C.** Conidiophores giving rise to conidia. **D.** Conidia. Scale bars: A = 20 µm, B–D = 10 µm.

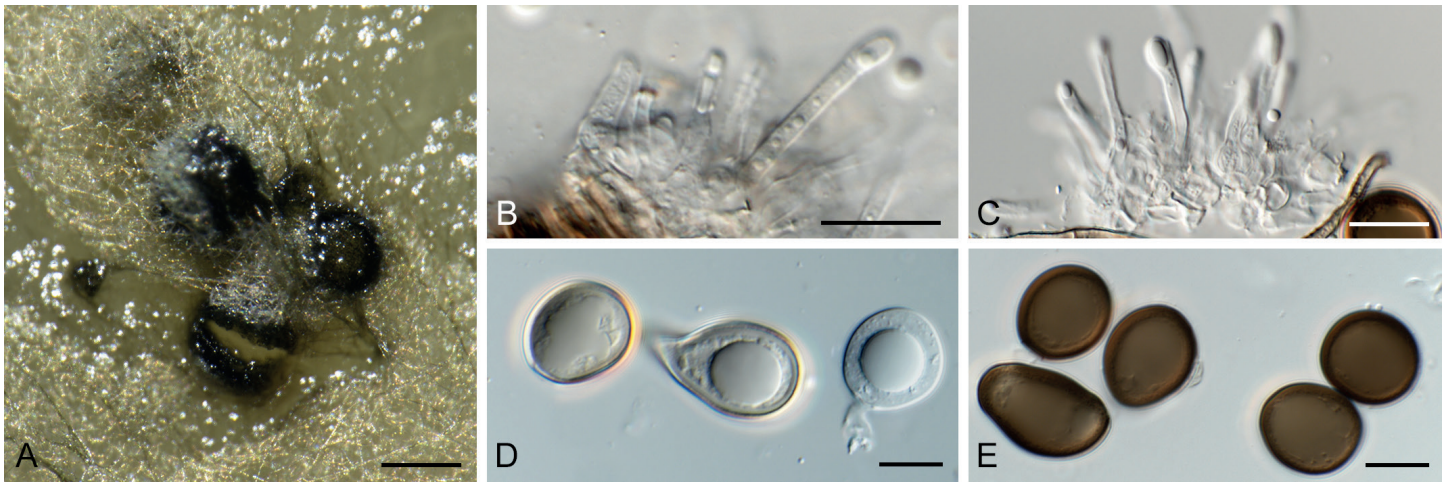

Fig. 34. *Neomedicopsis prunicola* (CPC 33711). **A.** Conidiomata on OA. **B, C.** Conidiogenous cells. **D, E.** Conidia. Scale bars: A = 300 µm, B–E = 10 µm.

diam after 2 wk at 25 °C. On MEA surface pale olivaceous grey, reverse olivaceous grey; on PDA surface and reverse olivaceous grey; on OA surface olivaceous grey.

Typus: **Ukraine**, Ternopil region, Dniester Canyon N.P., forest, fallen twigs of *Prunus padus* (= *Padus avium*) (*Rosaceae*), 6 Oct. 2016, *A. Akulov*, HPC 2045 = CWU AS 6209 (**holotype** CBS H-23825, culture ex-type CPC 33711 = CBS 145031).

Notes: de Gruyter *et al*. (2013) introduced the genus *Medicopsis* to accommodate *P. romeroi*, a pathogen associated with mycetoma in humans (Ahmed *et al.* 2014). *Medicopsis* is phoma-like in morphology, and *Neomedicopsis* is distinct in having globose, dark brown, thick-walled conidia that arise from long cylindrical conidiogenous cells that proliferate percurrently. *Neomedicopsis* is somewhat reminiscent of *Lasmeniella*, except that it lacks multilocular conidiomata.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Medicopsis romeroi* (GenBank JX088727.1; Identities = 506/557 (91 %), 13 gaps (2 %)), *Pleomassaria acericola* (GenBank MH863515.1; Identities = 490/555 (88 %), 22 gaps (3 %)), and *Neohendersonia kickxii* (GenBank KX820257.1; Identities = 483/555 (87 %), 21 gaps (3 %)). Closest hits using the **LSU** sequence are *Medicopsis romeroi* (GenBank MH869528.1; Identities = 837/861 (97 %), 1 gap (0 %)), *Lentithecium aquaticum* (GenBank MH874800.1; Identities = 837/867 (97 %), 12 gaps (1 %)), and *Murilentithecium clematidis* (GenBank KM408758.1; Identities = 834/864 (97 %), 7 gaps (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Medicopsis romeroi* (GenBank LT797035.1; Identities = 584/706 (83 %), 4 gaps (0 %)), *Crassiparies quadrisporus* (GenBank LC271252.1; Identities = 578/718 (81 %), 4 gaps (0 %)), and *Farasanispora avicenniae* (GenBank MG973031.1; Identities = 576/726 (79 %), 12 gaps (1 %)).

Phaeoappendicosporaceae Crous & M.J. Wingf., ***fam. nov.*** MycoBank MB829458.

Pseudostroma immersed, becoming erumpent; ectostroma pale brown to grey, containing periphyses; ostioles cylindrical. *Perithecia* globose to lenticular, dark brown, wall of *textura angularis. Paraphyses* hyaline, septate, unbranched, hypha-like. *Asci* ellipsoid to fusoid, 8-spored, without a refractive canal at apex. *Ascospores* ellipsoid-fusoid, brown, 1-euseptate, with gelatinous appendage at each truncate end. *Conidiomata* pycnidial, multilocular, forming a long neck. *Paraphyses* hyaline, cylindrical, septate, unbranched, hypha-like. *Conidiophores* subcylindrical, hyaline to pale brown, septate, unbranched. *Conidiogenous cells* cylindrical, hyaline to pale brown, proliferating percurrently at apex. *Conidia* ellipsoid to oblong, straight to slightly curved, thick-walled, transversely euseptate with oblique septa.

Type genus: *Phaeoappendicospora* Senan., Q.R. Li & K.D. Hyde

Neophaeoappendicospora Crous & M.J. Wingf., ***gen. nov.*** MycoBank MB829323.

Etymology: Name reflects its morphological similarity to *Phaeoappendicospora.*

Pseudostroma immersed, becoming erumpent, causing fissures; ectostroma pale brown to grey, containing tightly packed periphyses; ostioles cylindrical, inconspicuous with brown walls, not projecting; entostroma confined to a network of pale brown hyphae, enclosing a circular group of tightly packed perithecial ascomata with convergent ostioles. *Perithecia* globose to lenticular, dark brown, wall of *textura angularis. Paraphyses* intermingled among asci, hyaline, septate, unbranched, constricted at septa, hypha-like. *Asci* ellipsoid to fusoid, with 8 biseriate ascospores, without a refractive canal at apex (Melzer's reagent). *Ascospores* ellipsoid-fusoid, brown, 1-euseptate, thick-walled, with gelatinous appendage at each truncate end, smooth, becoming verruculose with age, granular to guttulate, with truncate apices and central apiculus. *Conidiomata* immersed in bark, pycnidial, multilocular, forming a long neck. *Paraphyses* hyaline, cylindrical, septate, unbranched, hypha-like. *Conidiophores* subcylindrical, hyaline to pale brown, septate, unbranched. *Conidiogenous cells* cylindrical, hyaline to pale brown, proliferating percurrently with numerous percurrent proliferations at apex. *Conidia* ellipsoid to oblong, straight to slightly curved, thick-walled, guttulate, transversely euseptate with oblique septa.

Type species: *Neophaeoappendicospora leucaenae* Crous & M.J. Wingf.

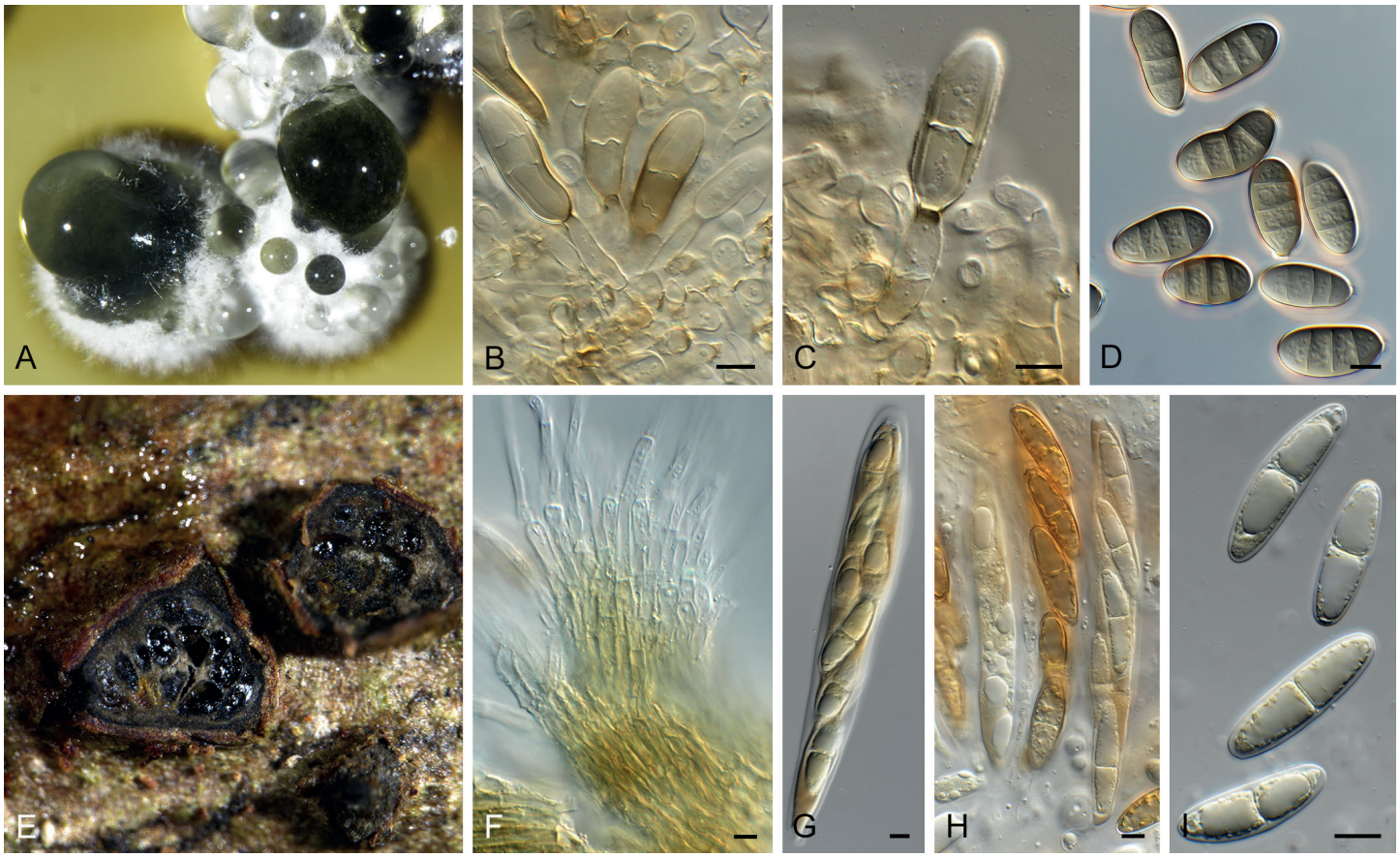

Fig. 35. *Neophaeoappendicospora leucaenae* (CPC 27240). **A.** Conidiomata on MEA. **B, C.** Conidiogenous cells giving rise to conidia. **D.** Conidia. **E.** Ascomata on host tissue. **F.** Pseudoparaphyses. **G, H.** Asci. **I.** Ascospores. Scale bars = 10 µm.

Neophaeoappendicospora leucaenae Crous & M.J. Wingf., ***sp. nov.*** MycoBank MB829324. Fig. 35.

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

Pseudostroma immersed in bark, up to 2 mm diam, becoming erumpent, causing fissures; ectostroma pale brown to grey, containing tightly packed periphyses; ostioles cylindrical, inconspicuous with brown walls, not projecting; entostroma confined to a network of pale brown hyphae, enclosing a circular group of up to 12 tightly packed perithecial ascomata with convergent ostioles. *Perithecia* globose to lenticular, dark brown, wall of *textura angularis. Paraphyses* intermingled among asci, hyaline, septate, unbranched, constricted at septa, hypha-like, 5–6 µm diam. *Asci* ellipsoid to fusoid, with 8 biseriate ascospores, without a refractive canal at apex (Melzer's reagent), 130–180 × 17–25 µm. *Ascospores* ellipsoid-fusoid, brown, 1-euseptate, thick-walled, with gelatinous appendage at each truncate end, smooth, becoming verruculose with age, granular to guttulate, (34–)36–42(–47) × (9–)10(–11) µm; at times slightly swollen at septum (wall appearing thickened), and truncate apices with central apiculus. *Conidiomata* immersed in bark, pycnidial, up to 800 µm diam, multilocular, forming a long neck on host, up to 1 mm tall. *Paraphyses* hyaline, cylindrical, septate, unbranched, hypha-like, 3–4 µm diam. *Conidiophores* subcylindrical, hyaline to pale brown, 0–2-septate, unbranched, 15–50 × 4–6 µm. *Conidiogenous cells* cylindrical, hyaline to pale brown, proliferating percurrently with numerous percurrent proliferations at apex, 15–30 × 4–6 µm. *Conidia* ellipsoid to oblong, straight to slightly curved, thick-walled, guttulate, 3-transversely euseptate with 1–3 oblique septa, apex obtuse, base truncate, 3–4 µm diam, (24–)26–29(–34) × (11–)12(–13) µm.

Culture characteristics: Colonies erumpent, with sparse aerial mycelium, slow-growing, with lobate margins. On MEA surface umber with patches of dirty white, reverse chestnut. On PDA surface umber, reverse umber with patches of diffuse sienna pigment. On OA surface isabelline.

Typus: **France**, La Réunion, stems of *Leucaena leucocephala* (*Fabaceae*), 13 Mar. 2014, *M.J. Wingfield*, HPC 309 (**holotype** CBS H-23794, culture ex-type CPC 27240).

Notes: *Neophaeoappendicospora* is morphologically similar to *Phaeoappendicospora*, which was established as monotypic genus by Senanayake *et al*. (2017) for a fungus occurring on dead twigs of *Quercus* in Thailand. *Neophaeoappendicospora leucaenae* is distinct from *P. thailandensis* (ascospores 26–34.5 × 11–13 µm) by its larger ascospores, and the fact that *Neophaeoappendicospora* readily forms an asexual morph in culture, which is absent in *Phaeoappendicospora*. *Phaeoappendicospora* and *Neophaeoappendicospora* represent genera in a new family, introduced here as *Phaeoappendicosporaceae.*

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Diaporthe australafricana* (GenBank KR534731.1; Identities = 395/458 (86 %), 22 gaps (4 %)), *Diaporthe phaseolorum* (GenBank LC171670.1; Identities = 505/615 (82 %), 55 gaps (8 %)), and *Diaporthe helianthi* (GenBank MF033502.1;

Identities = 505/615 (82 %), 55 gaps (8 %)). Closest hits using the **LSU** sequence are *Pachytrype rimosa* (GenBank FJ532381.1; Identities = 806/851 (95 %), 8 gaps (0 %)), *Hapalocystis berkeleyi* (GenBank MG548637.1; Identities = 797/844 (94 %), 6 gaps (0 %)), and *Melanconium elaeidicola* (GenBank NG_058172.1; Identities = 803/851 (94 %), 5 gaps (0 %)).

Ochroconis musae (G.Y. Sun & Lu Hao) Samerp. & de Hoog, *Mycol. Progr.* **14** (no. 6): 8. 2015. Fig. 36.
Basionym: *Scolecobasidium musae* G.Y. Sun & Lu Hao, *Mycol. Progr.* **12**: 492. 2012 (2013).
Synonym: *Ochroconis mirabilis* Samerp. & de Hoog, *Fungal Divers*. **65**: 110. 2013 (2014).

Mycelium consisting of pale brown, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* erect to flexuous, arising from vegetative hyphae, subcylindrical, 1–3-septate, 7–40 × 2.5–3 µm, branched or not, brown, smooth-walled, proliferating sympodially with several denticles that are 1–2 × 1 µm; conidiogenous cells 7–12 × 1.5–3 µm. *Conidia* subcylindrical, (8–)11–13(–16) × (2.5–)3(–4) µm, smooth-walled, pale brown, 1(–3)-septate, becoming verruculose and constricted at septa with age, apex obtuse, tapering to truncate hilum, 1 µm diam.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 25 mm diam after 2 wk at 25 °C. On MEA surface umber with diffuse sienna pigment, reverse chestnut; on PDA surface and reverse umber; on OA surface umber.

Material examined: **Thailand**, Chiang Mai, on leaf trichomes of *Persea americana* (*Lauraceae*), 2008, *P.W. Crous*, CBS H-23830, culture CPC 33947 = CBS 145061.

Notes: *Ochroconis* has pigmented conidiophores, and sympodial conidiogenesis with denticles that give rise to septate, pigmented, verruculose conidia (Giraldo *et al*. 2014, Crous *et al*. 2017). The present collection is closely related to *O. musae* (Samerpitak *et al*. 2015).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Ochroconis musae* (GenBank KT272078.1; Identities = 581/588 (99 %), no gaps), *Acroconidiellina arecae* (GenBank KX306747.1; Identities = 663/672 (99 %), 2 gaps (0 %)), and *Ochroconis musae* (as *Ochroconis mirabilis*, GenBank KF156028.1; Identities = 580/589 (98 %), 1 gap (0 %)). Closest hits using the **LSU** sequence are *Ochroconis musae* (as *Ochroconis mirabilis*, GenBank KF156139.1; Identities = 791/793 (99 %), no gaps), *Ochroconis musae* (GenBank KT272086.1; Identities = 815/818 (99 %), 2 gaps (0 %)), and *Ochroconis dracaenae* (GenBank MH878221.1; Identities = 808/813 (99 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Ochroconis mirabilis* (GenBank HQ916972.1; Identities = 263/264 (99 %), no gaps), *Ochroconis constricta* (GenBank KF155942.1; Identities = 263/264 (99 %), no gaps), and *Ochroconis musae* (as *Ochroconis mirabilis*, GenBank KT272055.1; Identities = 263/264 (99 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Ochroconis humicola* (GenBank AB564640.1; Identities = 430/433 (99 %), no gaps), *Ochroconis dracaenae* (GenBank KX228377.1; Identities = 492/510 (96 %), 1 gap (0 %)), and *Ochroconis musae* (GenBank KF156002.1; Identities = 367/370 (99 %), no gaps).

Paradevriesiaceae Crous, ***fam. nov.*** MycoBank MB829459.

Paradevriesia Crous, ***gen. nov.*** MycoBank MB829325.

Etymology: Name reflects the fact that it is phylogenetically allied to *Devriesia s.str*.

Mycelium consisting of branched, septate, hyphae, irregular in width, smooth to verruculose, at times forming hyphal strands and hyphal coils; hyphae frequently forming dark brown, thick-walled, intercalary, muriformly septate chlamydospores in culture. *Conidiophores* macro- and micronematous subcylindrical, medium brown, straight to irregularly curved, septate, or reduced to conidiogenous cells. *Conidiogenous cells* terminal or lateral on hyphae, medium brown, smooth, guttulate, subcylindrical, mono- to polyblastic; scars somewhat darkened and thickened, but not refractive. *Conidia* medium brown, guttulate, smooth, in mostly unbranched chains, subcylindrical to narrowly ellipsoidal, septate; hila darkened, somewhat thickened, not refractive.

Type species: *Paradevriesia americana* (Arzanlou & Crous) Crous.

Paradevriesia americana (Crous & Dugan) Crous, ***comb. nov.*** MycoBank MB829326.
Basionym: *Devriesia americana* Crous & Dugan, *Stud. Mycol.* **58**: 42. 2007.

Fig. 36. *Ochroconis musae* (CPC 33947). **A–D.** Conidiophores giving rise to conidia. Scale bars = 10 µm.

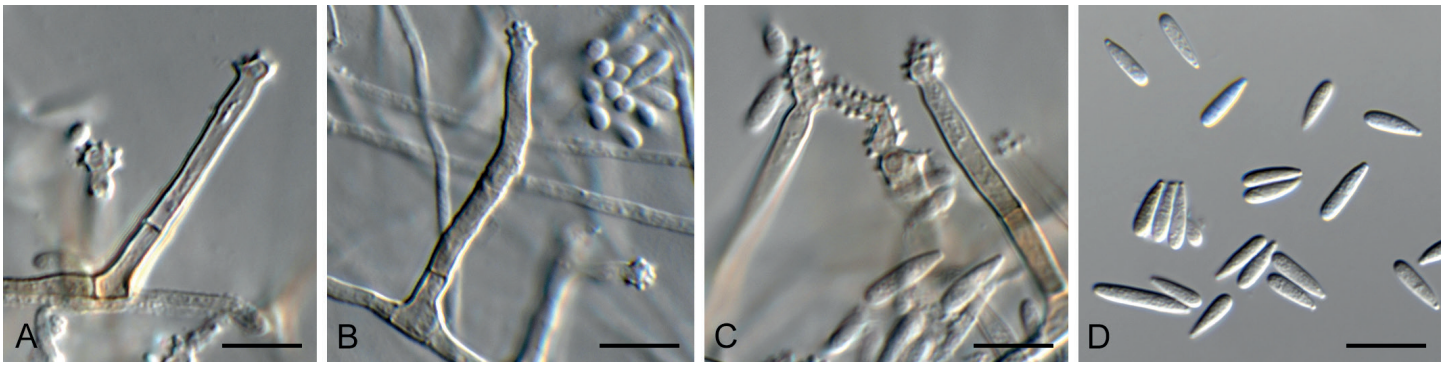

Fig. 37. *Pararamichloridium livistonae* (CPC 32152). **A–C.** Conidiophores. **D.** Conidia. Scale bars = 10 µm.

Paradevriesia pseudoamericana (J. Frank *et al.*) Crous, ***comb. nov.*** MycoBank MB829328.
Basionym: *Devriesia pseudoamericana* J. Frank *et al.*, *Persoonia* **24**: 97. 2010.

Notes: Although morphologically similar, members of *Paradevriesia* have a different ecology to members of *Devriesia s. str*. (Seifert *et al.* 2004), which usually occur in soil, and are thermotolerant. Species of *Paradevriesia* are presently known from plant and rock surfaces, and do not grow at high temperatures. Phylogenetically, *Paradevriesia* also represents a distinct family in *Capnodiales*.

Pararamichloridium livistonae Crous, *Persoonia* **39**: 357. 2017. Fig. 37.

Mycelium consisting of hyaline, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* solitary, cylindrical, erect, straight to flexuous, arising from superficial hyphae, pale brown, smooth, 2–6-septate, 25–65 × 2.5–3 µm. *Conidiogenous cells* terminal, integrated, cylindrical, pale brown, smooth, 14–20 × 2.5–3 µm, with terminal rachis of aggregated, short denticles, 1 × 1 µm, flat-tipped, not darkened nor thickened. *Conidia* aseptate, solitary, hyaline, smooth-walled, fusoid-ellipsoid to clavate, apex obtuse, tapering from middle to truncate hilum, 0.5 µm diam, slightly reflective, 7–8 × 2–2.5 µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA surface and reverse sienna with diffuse sienna pigment; on PDA surface pale luteous, reverse sienna with diffuse sienna pigment; on OA surface pale luteous.

Material examined: **Australia**, New South Wales, Murramarang National Park, on leaves of *Livistona australis* (*Arecaceae*), Nov. 2016, *P.W. Crous*, CBS H-23800, culture CPC 32152 = CBS 144522.

Notes: *Pararamichloridium livistonae* was described from leaves of *Livistona australis* collected in Australia (Crous *et al.* 2017), and isolate CPC 32152 represents the second collection of this fungus from the type locality.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pararamichloridium livistonae* (GenBank NR_156652.1; Identities = 616/617 (99 %), no gaps), *Pararamichloridium verrucosum* (GenBank NR_156653.1; Identities = 380/447 (85 %), 22 gaps (4 %)), and *Paramicrothyrium chinense* (GenBank KM246198.1; Identities = 507/632 (80 %), 63 gaps (9 %)). Closest hits using the **LSU** sequence are *Pararamichloridium livistonae* (GenBank NG_058504.1; Identities = 834/835(99%), 1 gap (0 %)), *Pararamichloridium verrucosum* (GenBank MH873621.1; Identities = 844/877 (96 %), 2 gaps (0 %)), and *Magnaporthiopsis poae* (GenBank KM401651.1; Identities = 824/870 (95 %), 3 gaps (0 %)).

Pararoussoella juglandicola Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB829329. Fig. 38.

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

Conidiomata erumpent, globose, brown, pycnidial, 150–300 µm diam with central ostiole, exuding a black conidial mass. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, ampulliform to doliiform, phialidic with periclinal thickening at apex, 5–7 × 4–5 µm. *Conidia* aseptate,

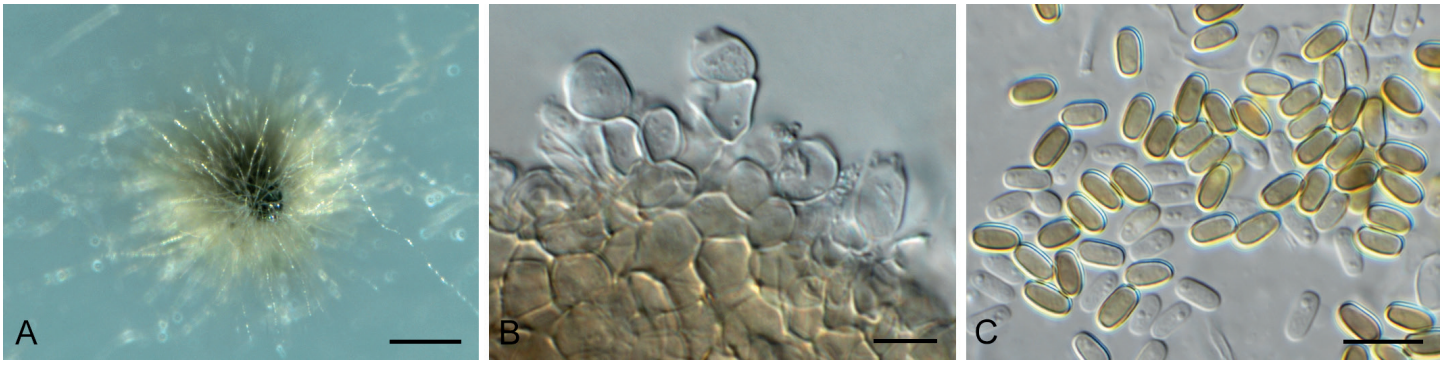

Fig. 38. *Pararoussoella juglandicola* (CPC 33400). **A.** Conidioma on SNA. **B.** Conidiogenous cells. **C.** Conidia. Scale bars: A = 300 µm, B, C = 10 µm.

solitary, subcylindrical, guttulate, apex bluntly rounded, base truncate, hyaline becoming brown, smooth, (5–)6(–7) × (2.5–)3 µm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and feathery, lobate margin, reaching 60 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus: **Germany**, near Berlin, on twig of *Juglans regia* (*Juglandaceae*), 21 Jan. 2017, *R.K. Schumacher*, HPC 1953 = RKS 12 (**holotype** CBS H-23820, culture ex-type CPC 33400 = CBS 145037).

Pararoussoella mukdahanensis (Phook. *et al.*) Crous, ***comb. nov.*** MycoBank MB829330.
Basionym: *Roussoella mukdahanensis* Phook. *et al.*, *Fungal Diversity* **82**: 32. 2016 (2017).

Notes: Species of *Thyridariaceae* are commonly isolated from various plant substrates. The family was recently treated by Wanasinghe *et al*. (2018), in which the genus *Pararoussoella* was established based on its distinct phylogenetic relationship to *Roussoella*. *Pararoussoella juglandicola* represents a new member of the genus, which is phylogenetically distinct from other species, including *Roussoella mukdahanensis*, for which a new combination is required.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Roussoella mukdahanensis* (GenBank NR_155722.1; Identities = 488/497 (98 %), 1 gap (0 %)), *Pararoussoella rosarum* (GenBank NR_157529.1; Identities = 492/505 (97 %), 4 gaps (0 %)), and *Aaosphaeria arxii* (GenBank MH872962.1; Identities = 541/587 (92 %), 7 gaps (1 %)). Closest hits using the **LSU** sequence are *Roussoella neopustulans* (GenBank KJ474841.1; Identities = 824/837 (98 %), no gaps), *Arthopyrenia salicis* (GenBank KP671722.1; Identities = 852/866 (98 %), no gaps), and *Roussoella pustulans* (GenBank AB524623.1; Identities = 820/834 (98 %), no gaps). Distant hits using the ***rpb2*** sequence had highest similarity to *Roussoella percutanea* (GenBank KF366453.1; Identities = 575/710 (81 %), 10 gaps (1 %)), *Parathyridaria percutanea* (GenBank LT797063.1; Identities = 730/905 (81 %), 6 gaps (0 %)) and *Flammeascoma lignicola* (GenBank KT324586.1; Identities = 696/898 (78 %), 8 gaps (0 %)). Very distant hits using the ***tef1*** sequence had highest similarity to *Roussoella scabrispora* (GenBank KX650537.1; Identities = 130/140 (93 %), no gaps), *Thyrostroma franseriae* (GenBank KY905680.1; Identities = 203/235 (86 %), 3 gaps (1 %)), *Stachybotrys limonispora* (GenBank KU847058.1; Identities = 131/136 (96 %), no gaps), and *Trichoderma applanatum* (GenBank KJ634759.1; Identities = 141/150 (94 %), 3 gaps (2 %)).

Petriella sordida (Zukal) G.L. Barron & J.C. Gilman, *Canad. J. Bot.* **39**: 839. 1961. Fig. 39.
Basionym: *Microascus sordidus* Zukal, *Ber. dt. bot. Ges.* **8**: 297. 1890.

Conidiophores synnematal, erect, flexuous, olivaceous brown, smooth, arising from a reduced basal stroma, consisting of numerous (30–100) individual conidiophores, septate (septa 10–30 µm apart), 250–350 µm long, stipe (7–)15–30(–90) µm diam, with flaring conidiogenous head, containing an olivaceous brown, mucoid conidial mass. *Conidiogenous cells* subcylindrical, olivaceous, smooth, 10–25 × 2–2.5 µm, proliferating inconspicuously percurrently at apex. *Conidia* solitary, aseptate, guttulate, smooth, subcylindrical, apex obtuse, slightly constricted in middle, base truncate, 2 µm diam, slightly darkened, (7–)9–10(–12) × (3–)3.5(–4) µm.

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

Material examined: **Ukraine**, Rakhiv district, Transcarpathian region, on leaves of *Luzula* sp. (*Juncaceae*), Nov. 2016, *A. Akulov*, HPC 1497, CBS H-23801, culture CBS 144612 = CPC 32460).

Notes: Species of *Petriella* are commonly isolated from soil and dung (Lackner & de Hoog 2011), and thus it is assumed that the isolate in the present study was probably an opportunist on leaves of *Luzula* sp. *Petriella sordida* was described to have synnemata with conidia being (5–)6.5–11.5(–14) × 2.5–5.5 µm (Corlett & MacLatchy 1987).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 32460

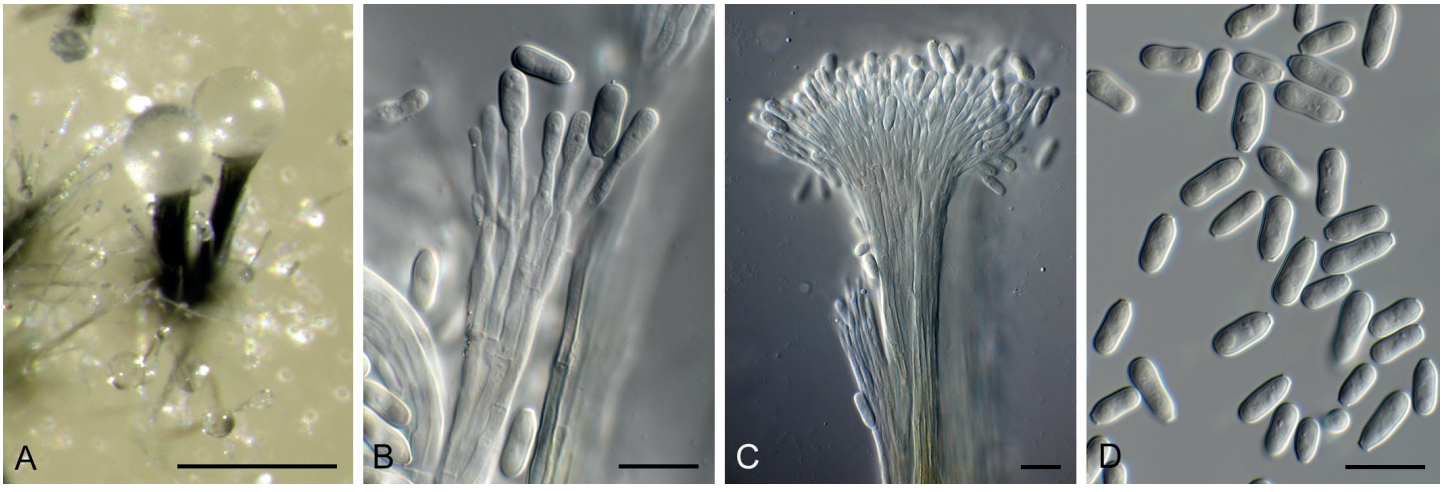

Fig. 39. *Petriella sordida* (CPC 32460). **A.** Synnemata on OA. **B, C.** Conidiophores with conidiogenous cells. **D.** Conidia. Scale bars = 10 µm.

had highest similarity to *Petriella sordida* (GenBank MH863637.1; Identities = 564/565 (99 %), no gaps), *Melanospora asymmetrica* (GenBank KY628677.1; Identities = 554/556 (99 %), no gaps), and *Petriella guttulata* (GenBank MF782707.1; Identities = 558/565 (99 %), 1 gap (0 %)). The ITS sequence was identical to that of "*Petriella* sp. Vega423" (GenBank EU002908.1, 565/565) isolated as root endophyte of *Coffea arabica* in Colombia. The ITS sequences of CPC 32460 and 32461 are identical. Closest hits using the **LSU** sequence of CPC 32460 are *Petriella setifera* (GenBank MH872684.1; Identities = 794/794 (100 %)), *Petriella sordida* (GenBank MH875102.1; Identities = 793/794 (99 %), no gaps), and *Petriella asymmetrica* var. *cypria* (GenBank MH867451.1; Identities = 793/794 (99 %), no gaps). The LSU sequences of CPC 32460 and 32461 are identical. The ***cmdA*** sequence of CPC 32460 was identical to that of *Petriella sordida* (strain UTHSC 03-394, GenBank AM409103.1; Identities = 449/449 (100 %)). Closest hits using the ***rpb2*** sequence of CPC 32461 had highest similarity to *Petriella setifera* (GenBank DQ368640.1; Identities = 701/702 (99 %), no gaps), *Scedosporium boydii* (GenBank KP981186.1; Identities = 510/600 (85 %), no gaps), and *Pseudallescheria fusoidea* (GenBank KP981195.1; Identities = 509/600 (85 %), no gaps). No ***tef1*** sequences of *Petriella* which cover the same region amplified here are available for comparison in GenBank; distant hits include *Scedosporium aurantiacum* (GenBank KJ784086.1; Identities = 278/334 (83 %), 8 gaps (2 %)), *Scopulariopsis brevicaulis* (GenBank KP009002.1; Identities = 148/159 (93 %), no gaps), and *Thyronectria rhodochlora* (GenBank KM225694.1; Identities = 144/154 (94 %), no gaps). The *tef1* sequences of CPC 32460 and 32461 are identical. The ***tub2*** sequence of CPC 32460 was identical to both *Petriella setifera* (GenBank EU977491.1; Identities = 488/488 (100 %)) and *Petriella sordida* (GenBank AM409104.1; Identities = 399/399 (100 %)).

Pezicula eucalyptigena Crous, ***sp. nov.*** MycoBank MB829331. Fig. 40.

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

In vitro. *Conidiomata* sporodochial, forming superficially on agar, scattered, dark brown, 100–250 µm diam, exuding a creamy conidial mass. *Macroconidiophores* hyaline, smooth, subcylindrical, branched, 1–4-septate, 40–90 × 3–4 µm. *Macroconidiogenous cells* integrated, terminal and intercalary, subcylindrical, hyaline, smooth, phialidic with indistinct percurrent proliferations, 10–25 × × 3.5–4 µm. *Macroconidia* aseptate, hyaline, smooth, guttulate, ellipsoid-clavate, straight to slightly curved, with prominently protruding truncate hilum, 2 µm diam, (23–)24–27(–30) × (6–)7(–8) µm. *Microconidiophores* hyaline, smooth, subcylindrical, branched, 6–12-septate, 60–130 × 2.5–3.5 µm. *Microconidiogenous cells* integrated, terminal and intercalary, subcylindrical, hyaline, smooth, phialidic, 10–20 × 2.5–3 µm. *Microconidia* hyaline, smooth, aseptate, subcylindrical, apex obtuse, base truncate, straight to irregularly curved, (7–)10–12(–15) × 2(–2.5) µm.

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

Typus: **South Africa**, Western Cape Province, Malmesbury, on leaves of *Eucalyptus* sp. (*Myrtaceae*), 2006, *P.W. Crous* (**holotype** CBS H-23799, culture ex-type CBS 144637 = CPC 32129).

Notes: The *Pezicula* generic complex was recently revised by Chen *et al*. (2016). Species from this complex known to occur on *Eucalyptus* include *Parafabraea caliginosa*, *Parafabraea eucalypti*, and *Pezicula californiae* (from *Eucalyptus* leaves in California, USA). *Pezicula eucalyptigena* is phylogenetically closely related to *P. californiae* (conidia 12.5–27.5 × 4.2–5.8 µm), but morphologically distinct in that it has larger conidia (Cheewangkoon *et al*. 2010, Chen *et al.* 2016).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pezicula cinnamomea* (GenBank KR859109.1; Identities = 498/524 (95 %), 5 gaps (0 %)), *Pezicula sporulosa* (GenBank JN693514.1; Identities = 495/519 (95%), 4 gaps (0 %)), and *Pezicula californiae* (GenBank JX144747.1; Identities = 495/519 (95 %), 4 gaps (0 %)). Closest hits using the **LSU** sequence are *Pezicula brunnea* (GenBank KR858894.1; Identities = 842/848 (99 %), no gaps), *Pezicula ericae* (GenBank MH874637.1; Identities = 876/883 (99 %), no gaps), and *Pezicula melanigena* (GenBank KR859003.1; Identities = 838/845 (99 %), no gaps. Closest hits using the ***rpb2*** sequence had highest similarity to *Pezicula eucrita*

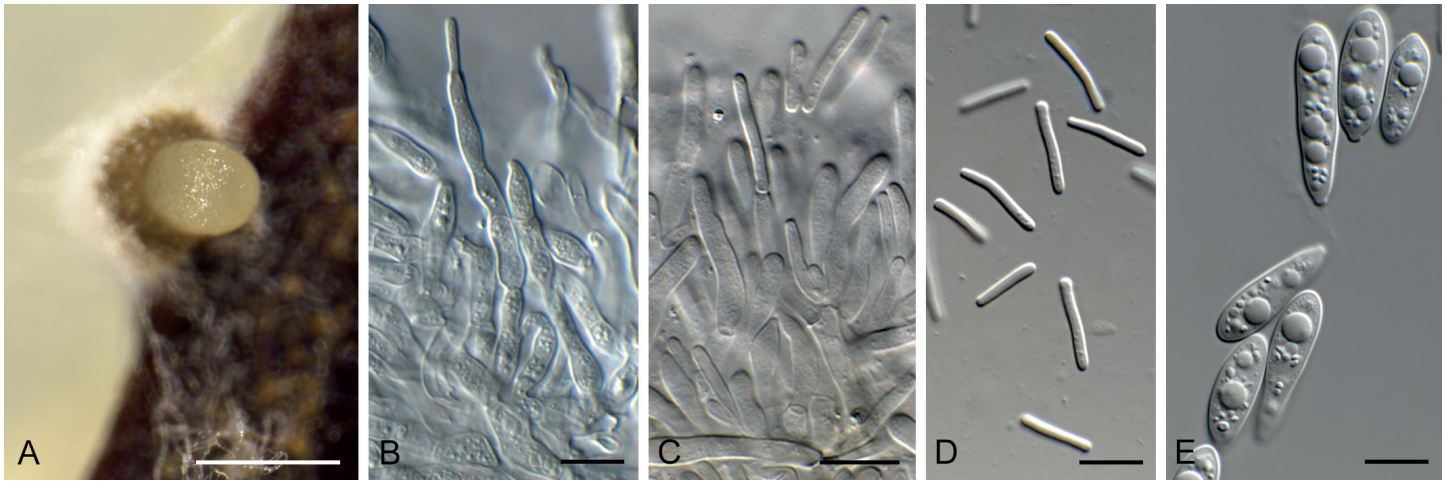

Fig. 40. *Pezicula eucalyptigena* (CPC 32129). **A.** Conidioma on PNA. **B, C.** Conidiogenous cells. **D.** Microconidia. **E.** Macroconidia. Scale bars: A = 250 µm, B–E = 10 µm.

(GenBank KF376205.1; Identities = 866/915 (95 %), no gaps), *Pezicula neoheterochroma* (GenBank KR859338.1; Identities = 850/899 (95 %), no gaps), and *Pezicula* aff. *cinnamomea* (GenBank KF376209.1; Identities = 864/915 (94 %), no gaps).

Phaeoseptoriella Crous, ***gen. nov.*** MycoBank MB829332.

Etymology: Name refers to its morphological similarity to small species of *Phaeoseptoria*.

Associated with leaf spots. *Conidiomata* solitary, globose, brown with central ostiole. *Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* ampulliform to doliiform, pale brown, smooth, proliferating percurrently at apex. *Conidia* solitary, pale brown, finely roughened, straight to slightly curved, fusoid-ellipsoid, septate, apex subobtuse, base truncate.

Type species: *Phaeoseptoriella zeae* Crous.

Phaeoseptoriella zeae Crous, ***sp. nov.*** MycoBank MB829333. Fig. 41.

Etymology: Name refers to the host *Zea mays* from which it was isolated.

Associated with small, subcircular, pale brown, amphigenous leaf spots, 2–6 mm diam. *Conidiomata* solitary, globose, 200–250 µm diam, brown with central ostiole. *Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* ampulliform to doliiform, pale brown, smooth, proliferating percurrently at apex, 4–6 × 4–6 µm. *Conidia* solitary, pale brown, finely roughened, straight to slightly curved, fusoid-ellipsoid, apex subobtuse, base truncate, 1.5–2 µm diam, (1–)3-septate, (14–)17–20(–23) × (3–)4 µm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA surface dirty white, reverse cinnamon; on PDA surface dirty white, reverse rosy buff; on OA surface rosy vinaceous.

Typus: **South Africa**, Gauteng Province, Gauteng, on leaves of *Zea mays* (*Poaceae*), 12 Apr. 2010, *T.A. Coutinho*, HPC 2038 (**holotype** CBS H-23814, culture ex-type CPC 33064 = CBS 144614).

Notes: Phaeosphaeria leaf spot (PLS) has previously been attributed to *Phaeosphaeria maydis* (described from leaves of *Zea mays* in Sao Paulo, Brazil), which has been linked to various asexual morphs including a *Phyllosticta* sp. (= *Guignardia* sexual morph), and *Phoma maydis*. Amaral *et al*. (2005) reported a phoma-like asexual morph associated with PLS as similar in culture to colonies of *Phaeosphaeria maydis*, and postulated that several fungal species were involved in causing PLS. However, in a recent study, Gonçalves *et al.* (2013) showed that a bacterium, *Pantoea ananatis*, was the primary disease-causing agent, and that the fungi isolated from these lesions, were secondary colonist of the diseased tissue, stating also that the disease symptoms shown by Amaral *et al*. (2005) were atypical for PLS. In South Africa, prominent tan-coloured subcircular leaf spots were found on *Z. mays* to be associated with a new genus, described here as *Phaeoseptoriella zeae.* Further studies are now required to determine the relative importance of this fungus, and confirm its role as maize pathogen.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Parastagonospora avenae* (as *Phaeosphaeria avenaria*, GenBank FJ605258.1; Identities = 526/546 (96 %), 6 gaps (1 %)), *Camarosporioides phragmitis* (GenBank NR_153925.1; Identities = 425/474 (90 %), 15 gaps (3 %)), and *Coniothyrium ferrarisianum* (GenBank MH860854.1; Identities = 424/474 (89 %), 15 gaps (3 %)). Closest hits using the **LSU** sequence are *Didymocyrtis consimilis* (GenBank MH876627.1; Identities = 878/882 (99 %), no gaps), *Parastagonospora nodorum* (GenBank MH868570.1; Identities = 878/882 (99 %), no gaps), and *Kalmusia utahensis* (GenBank MH876142.1; Identities = 877/882 (99 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Didymocyrtis banksiae* (GenBank KY979850.1; Identities = 759/902 (84 %), 2 gaps (0 %)), *Parastagonospora nodorum* (as *Phaeosphaeria nodorum*, GenBank DQ499803.1; Identities = 757/903 (84 %), 2 gaps (0 %)), and *Parastagonospora avenaria* f. sp. *tritici* (as *Phaeosphaeria avenaria* f. sp. *triticae*, GenBank DQ499799.1; Identities = 757/905 (84 %), 6 gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Sclerostagonospora ericae* (GenBank KX228375.1; Identities = 417/515 (81 %), 28 gaps (5 %)), *Didymocyrtis cladoniicola* (as

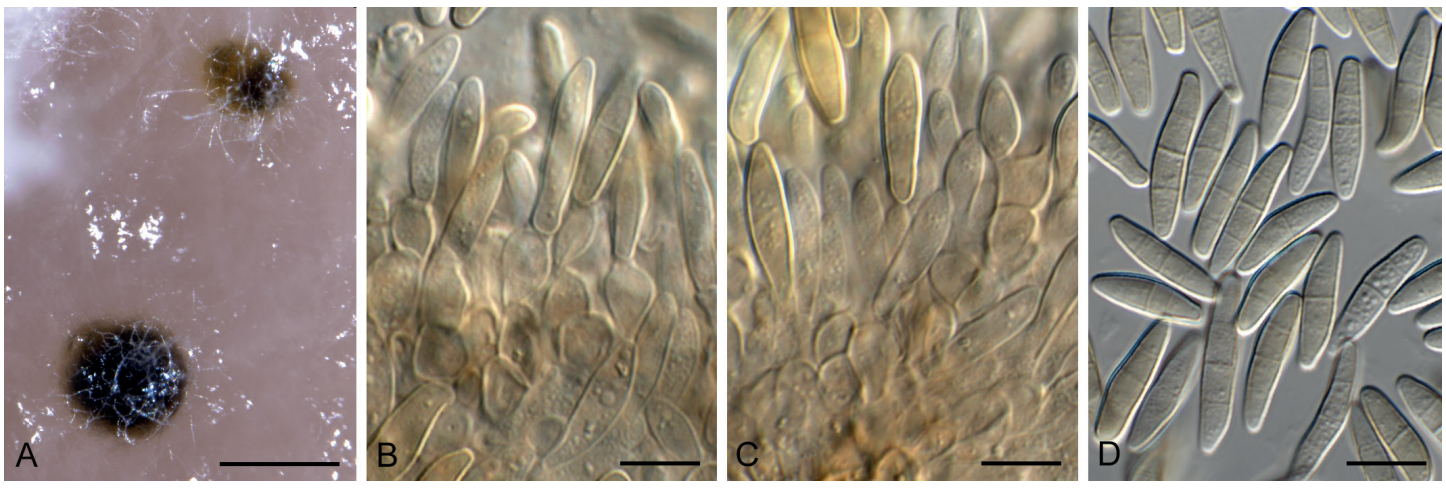

Fig. 41. *Phaeoseptoriella zeae* (CPC 33064). **A.** Conidiomata on OA. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars: A = 250 µm, B–D = 10 µm.

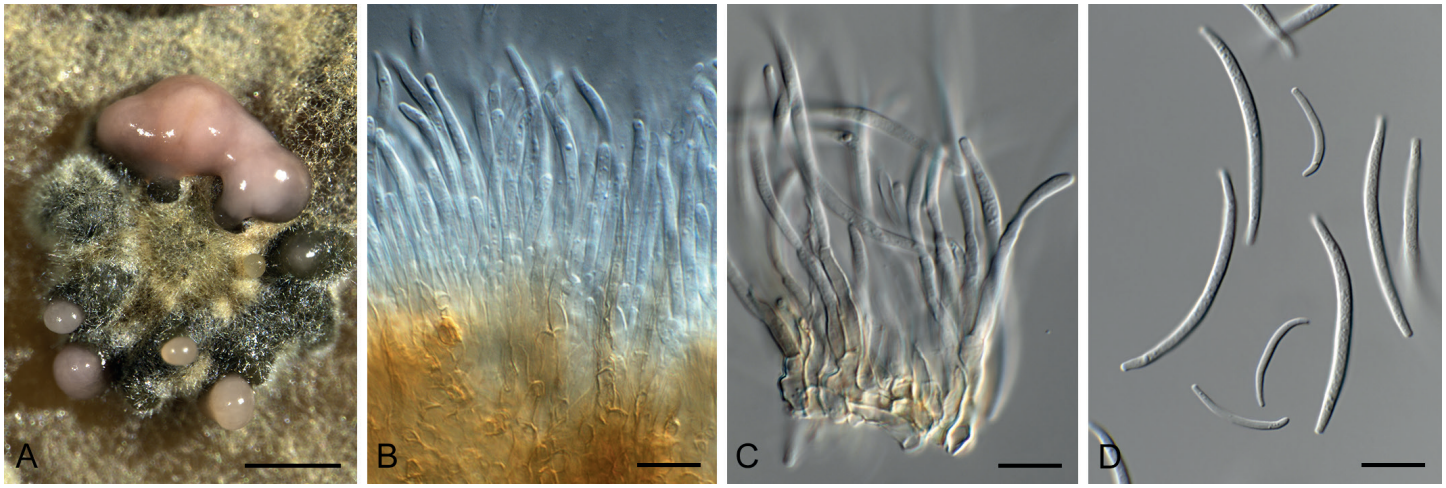

Fig. 42. *Phlogicylindrium dunnii* (CPC 31818). **A.** Eustromatic conidioma on PDA. **B, C.** Conidiophores. **D.** Micro- and macroconidia. Scale bars: A = 200 µm, B–D = 10 µm.

Diederichomyces cladoniicola, GenBank KP170668.1; Identities = 409/516 (79 %), 10 gaps (1 %)), and *Septoria oudemansii* (GenBank KF253436.1; Identities = 333/409 (81 %), 8 gaps (1 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Sclerostagonospora ericae* (GenBank KX228383.1; Identities = 263/287 (92 %), 4 gaps (1 %)), *Diederichomyces ficuzzae* (GenBank KP170697.1; Identities = 262/290 (90 %), 6 gaps (2 %)), and *Didymocyrtis foliaceiphila* (as *Diederichomyces foliaceiphila*, GenBank KP170698.1; Identities = 260/288 (90 %), 3 gaps (1 %)).

Phlogicylindrium dunnii Crous, ***sp. nov.*** MycoBank MB829334. Fig. 42.

Etymology: Name refers to *Eucalyptus dunnii* from which it was isolated.

Conidiomata eustromatic, multilocular, locules 100–200 µm diam, occurring solitary on leaves, but in clusters on agar, exuding a slimy pink conidial mass. *Conidiophores* arising from a brown stroma of 3–6 layers of *textura angularis*, subcylindrical, branched, 1–3-septate, brown, smooth, 30–70 × 3–4 µm. *Conidiogenous cells* pale brown, smooth, subcylindrical, 15–30 × 2.5–3 µm, proliferating sympodially and percurrently near apex. *Macroconidia* hyaline, smooth, narrowly fusoid to widest in the middle with slight taper towards ends, subcylindrical, 1-septate, apex subobtuse, base truncate, curved, (32–)35–42(–47) × (2–)2.5(–3) µm. *Microconidia* hyaline, smooth, aseptate, cylindrical, curved, apex obtuse, base truncate, 15–18 × 1.5 µm, forming in same conidioma as macroconidia.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and folded surface and smooth, lobate margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA surface ochreous, reverse umber; on PDA surface ochreous, reverse salmon to ochreous; on OA surface smoke grey.

Typus: **Australia**, New South Wales, Tooloom State Forest, on leaves of *Eucalyptus dunnii* (*Myrtaceae*), 20 Jan. 2016, *A.J. Carnegie*, HPC 1447 (**holotype** CBS H-23264, culture ex-type CPC 31818 = CBS 144620).

Notes: *Phlogicylindrium* was established by Summerell *et al.* (2006) to accommodate a genus with erect, flame-like conidiomatal tufts to sporodochial conidiomata, and cylindrical, hyaline conidia forming on brown, percurrently proliferating conidiogenous cells. *Phlogicylindrium dunnii* is rather atypical in the fact that it has eustromatic, multilocular conidiomata, that with age appear sporodochial as they age.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phlogicylindrium tereticornis* (GenBank NR_156660.1; Identities = 550/566 (97 %), 3 gaps (0 %)), *Phlogicylindrium eucalyptorum* (GenBank EU040223.1; Identities = 411/432 (95 %), 3 gaps (0 %)), and *Phlogicylindrium mokarei* (GenBank KY173431.1; Identities = 409/432 (95 %), 3 gaps (0 %)). Closest hits using the **LSU** sequence are *Phlogicylindrium tereticornis* (GenBank NG_058510.1; Identities = 788/789 (99 %), no gaps), *Phlogicylindrium mokarei* (GenBank NG_059750.1; Identities = 782/789 (99 %), no gaps), and *Phlogicylindrium uniforme* (GenBank JQ044445.1; Identities = 780/789 (99 %), no gaps). The best hit using the ***rpb2*** sequence was with *Phlogicylindrium tereticornis* (GenBank MG386142.1; Identities = 861/871 (99 %), no gaps). The best hit using the ***tef1*** sequence was with *Phlogicylindrium tereticornis* (GenBank MG386151.1; Identities = 396/402 (99 %), no gaps).

Phyllosticta austroafricana Crous, ***sp. nov.*** MycoBank MB829336. Fig. 43.

Etymology: Name refers to the continent Africa where it was collected.

Associated with leaf spots on leaf litter of unidentified deciduous tree host. *Conidiomata* pycnidial, solitary, black, erumpent, globose, exuding hyaline conidial masses; pycnidia up to 200 µm diam; wall of several layers of brown *textura angularis*. *Ostiole* central, up to 20 µm diam. *Conidiophores* subcylindrical, with 1–2 supporting cells, at times branched at base, 20–30 × 3–5 µm. *Conidiogenous cells* terminal, subcylindrical, hyaline, smooth, coated in a mucoid layer, 10–15 × 3–4 µm, proliferating several times percurrently near apex. *Conidia* (11–)14–17(–23) × (6–)8–10(–11) µm, solitary, hyaline, aseptate, thin- and smooth-walled, coarsely guttulate, ellipsoid to obovoid, tapering towards a truncate base, 2–3 µm diam, enclosed in a mucoid sheath, 2–3 µm thick, and bearing a hyaline apical mucoid appendage, (5–)7–8(–10) × 1.5(–2) µm, tapering towards an acutely rounded tip.

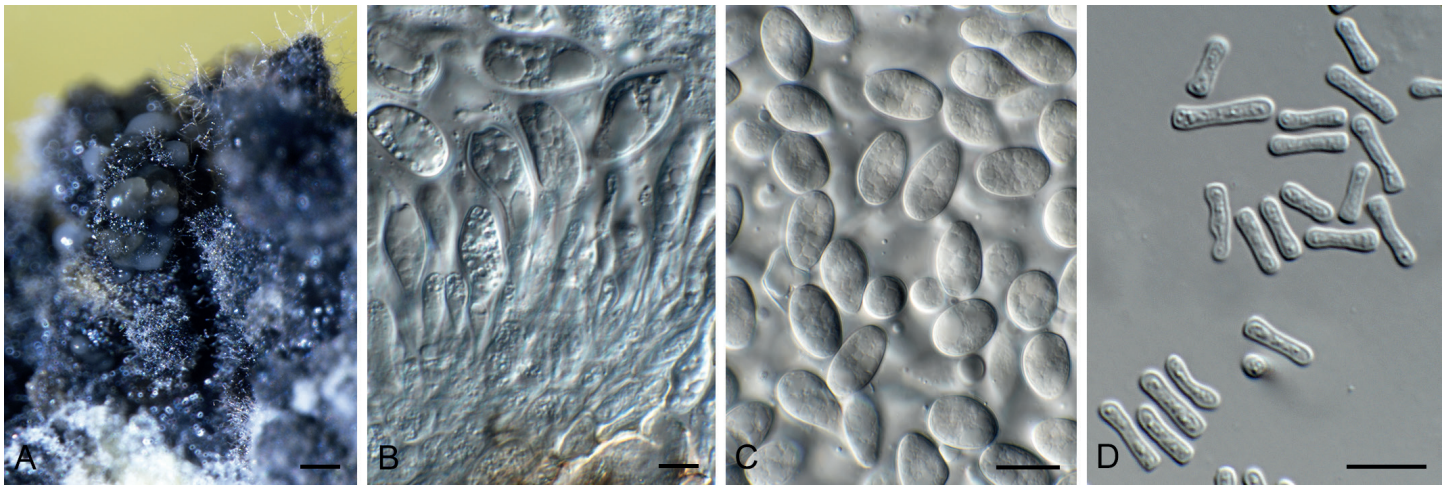

Fig. 43. *Phyllosticta austroafricana* (CPC 31920). **A.** Conidiomata on MEA. **B.** Conidiogenous cells. **C.** Conidia. **D.** Spermatia. Scale bars: A = 200 µm, B–D = 10 µm.

Spermatia bacilliform, hyaline, smooth, guttulate, 6–8 × 2–3 µm.

Culture characteristics: Colonies erumpent, spreading, with sparse aerial mycelium and uneven surface and lobed margin, reaching 5 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface iron-grey, and reverse iron-grey, with diffuse yellow pigment on OA.

Typus: **South Africa**, Western Cape Province, on leaf spots of unidentified deciduous tree host, 2010, *P.W. Crous* (**holotype** CBS H-23797, culture ex-type CPC 31920 = CBS 144593).

Notes: *Phyllosticta* includes several important plant pathogens causing leaf and fruit spot diseases. Important species are *P. ampelicida* causing black rot disease on grapevines (Zhou *et al*. 2015), species in the *P. musarum* species complex causing banana freckle disease (Wong *et al.* 2012), and *P. citricarpa* causing citrus black spot (Guarnaccia *et al*. 2017). *Phyllosticta austroafricana* is a phylogenetically distinct species, associated with leaf spots on an unidentified tree host.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phyllosticta pseudotsugae* (GenBank KF154277.1; Identities = 539/573 (94 %), 5 gaps (0 %)), *Phyllosticta carissicola* (GenBank NR_147363.1; Identities = 574/613 (94 %), 4 gaps (0 %)), and *Phyllosticta podocarpi* (GenBank KF154276.1; Identities = 535/572 (94 %), 3 gaps (0 %)). Closest hits using the **LSU** sequence are *Phyllosticta carissicola* (GenBank KT950863.1; Identities = 848/851 (99 %), no gaps), *Phyllosticta podocarpi* (GenBank KF766383.1; Identities = 835/840 (99 %), no gaps), and *Phyllosticta hymenocallidicola* (GenBank NG_057947.1; Identities = 869/882 (99 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Phyllosticta acaciigena* (GenBank KY173570.1; Identities = 517/562 (92 %), 5 gaps (0 %)), *Exserohilum khartoumense* (as *Setosphaeria khartoumensis*, GenBank LT837600.1; Identities = 474/526 (90 %), 11 gaps (2 %)), *Exserohilum rostratum* (as *Setosphaeria rostrata*, GenBank LT837683.1; Identities = 473/526 (90 %), 11 gaps (2 %)), and *Exserohilum prolatum* (GenBank LT837660.1; Identities = 473/526 (90 %), 11 gaps (2 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Phyllosticta ericarum* (GenBank KR025452.1; Identities = 303/331 (92 %), 5 gaps (1 %)), *Phyllosticta carissicola* (GenBank KT950879.1; Identities = 367/403 (91 %), 19 gaps (4 %)), and *Phyllosticta catimbauensis* (GenBank MF466155.1; Identities = 299/331 (90 %), 4 gaps (1 %)).

Phyllosticta hagahagaensis Crous & M.J. Wingf., ***sp. nov.*** MycoBank MB829335. Fig. 44.

Etymology: Name reflects Haga Haga in the Eastern Cape Province of South Africa where it was collected.

Conidiomata pycnidial, solitary, black, erumpent, globose, exuding hyaline conidial masses; pycnidia 250–350 µm diam; wall of several layers of brown *textura angularis*. *Ostiole* central, up to 20 µm diam. *Conidiophores* subcylindrical, unbranched or branched below, 0–2-septate, 15–30 × 4–5 µm. *Conidiogenous cells* terminal and intercalary, subcylindrical, hyaline, smooth, coated in a mucoid layer, 7–16 × 3.5–4 µm, proliferating several times percurrently near apex. *Conidia* (11–)13–14(–15) × (7–)8(–9) µm, solitary, hyaline, aseptate, thin- and smooth-walled, guttulate, granular, ellipsoid to obovoid, tapering towards a truncate base, 3–3.5 µm diam, enclosed in a mucoid sheath, 2.5–5 µm thick, and bearing a hyaline apical mucoid appendage, 5–15 × 1.5–2 µm, tapering towards an acutely rounded tip.

Culture characteristics: Colonies erumpent, spreading, with sparse to moderate aerial mycelium and uneven surface and margin, reaching 18 mm diam after 2 wk at 25 °C. On MEA surface smoke grey to grey olivaceous, reverse olivaceous grey; on PDA surface and reverse olivaceous grey; on OA surface olivaceous grey to grey olivaceous.

Typus: **South Africa**, Eastern Cape Province, Haga Haga, on leaf litter of *Carissa bispinosa* (*Apocynaceae*), 23 Dec. 2010, *M.J. Wingfield*, HPC 1545 (**holotype** CBS H-23811, culture ex-type CPC 32799 = CBS 144592).

Notes: *Phyllosticta carissicola* [conidia (11–)12–14(–15) × (9–)10(–11) µm, sheath 2–3 µm thick apical mucoid appendage, (10–)12–17(–25) × 1.5(–2) µm] was described from leaves of *Carissa macrocarpa* (CPC 25665) in South Africa by Crous *et al.* (2015). *Phyllosticta hagahagaensis* differs morphologically from *P. carissicola* in having wider conidia, a wider mucoid sheath, and shorter appendages.

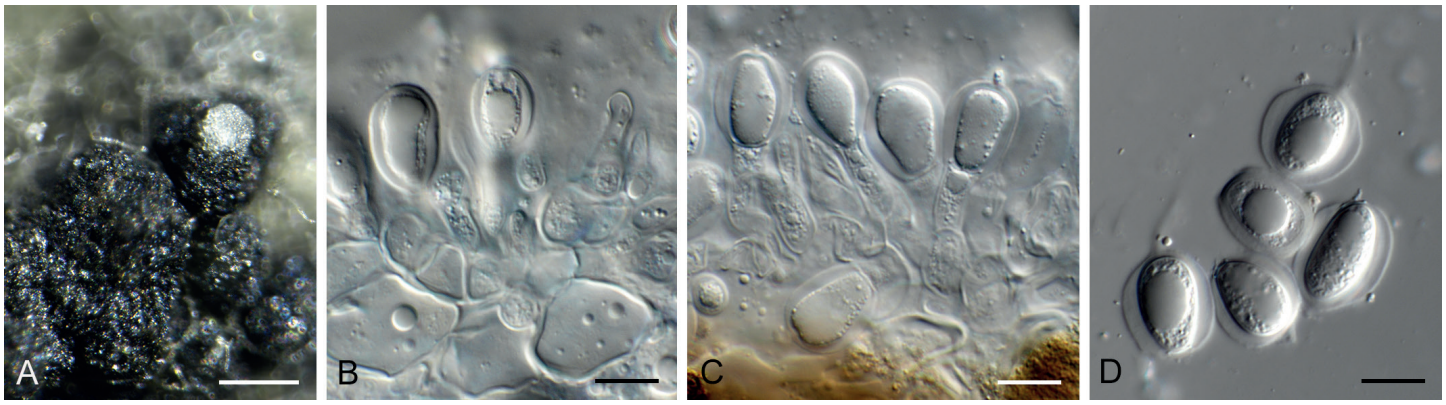

Fig. 44. *Phyllosticta hagahagaensis* (CPC 32799). **A.** Conidioma on OA. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars: A = 300 µm, B–D = 10 µm.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phyllosticta podocarpi* (GenBank KF766217.1; Identities = 591/603 (98 %), 1 gap (0 %)), *Phyllosticta pseudotsugae* (GenBank KF154277.1; Identities = 559/572 (98 %), 1 gap (0 %)), and *Phyllosticta owaniana* (GenBank JF261462.1; Identities = 569/588 (97 %), no gaps). Closest hits using the **LSU** sequence are *Phyllosticta carissicola* (GenBank KT950863.1; Identities = 855/856 (99 %), no gaps), *Phyllosticta podocarpi* (GenBank KF766383.1; Identities = 837/840 (99 %), no gaps), and *Phyllosticta hymenocallidicola* (GenBank NG_057947.1; Identities = 876/887 (99 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Phyllosticta acaciigena* (GenBank KY173570.1; Identities = 521/560 (93 %), 1 gap (0 %)), *Phyllosticta carissicola* (GenBank KT950872.1; Identities = 233/243 (96 %), no gaps), *Cladosporium velox* (GenBank KT600654.1; Identities = 459/510 (90 %), 3 gaps (0 %)), and *Alternaria frumenti* (GenBank JQ671649.1; Identities = 467/523 (89 %), 9 gaps (1 %)). Closest hits using the ***gapdh*** sequence had highest similarity to *Phyllosticta owaniana* (GenBank JF343766.1; Identities = 299/300 (99 %), no gaps), *Phyllosticta podocarpi* (GenBank KF289168.1; Identities = 298/300 (99 %), no gaps), and *Phyllosticta carissicola* (GenBank KT950876.1; Identities = 501/510 (98 %), 1 gap (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Phyllosticta carissicola* (GenBank KT950879.1; Identities = 379/389 (97 %), 2 gaps (0 %)), *Phyllosticta hakeicola* (GenBank MH108025.1; Identities = 328/353 (93 %), 10 gaps (2 %)), and *Phyllosticta yuccae* (GenBank JX227948.1; Identities = 355/398 (89 %), 14 gaps (3 %)).

Piniphoma Crous & R.K. Schumach., ***gen. nov.*** MycoBank MB829337.

Etymology: Name combined the name of the host genus *Pinus*, and the fungal genus *Phoma*.

Conidiomata solitary, pycnidial, globose with central ostiole, pale brown, exuding a creamy conidial mass. *Conidiophores* reduced to conidiogenous cells lining inner cavity, ampulliform, hyaline, smooth, phialidic. *Conidia* solitary, aseptate, smooth, hyaline, straight, guttulate, subcylindrical with obtuse ends.

Type species: *Piniphoma wesendahlina* Crous & R.K. Schumach.

Piniphoma wesendahlina Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB829338. Fig. 45.

Etymology: Name reflects to the city of Berlin where it was collected.

Conidiomata solitary, pycnidial, 80–120 µm diam, globose with central ostiole, pale brown, only observed on PNA, exuding a creamy conidial mass. *Conidiophores* reduced to conidiogenous cells lining inner cavity, ampulliform, hyaline, smooth, phialidic, 4–5 × 3–4 µm. *Conidia* solitary, aseptate, smooth, hyaline, straight, guttulate, subcylindrical with obtuse ends, (3–)4(–5) × 2 µm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 45 mm

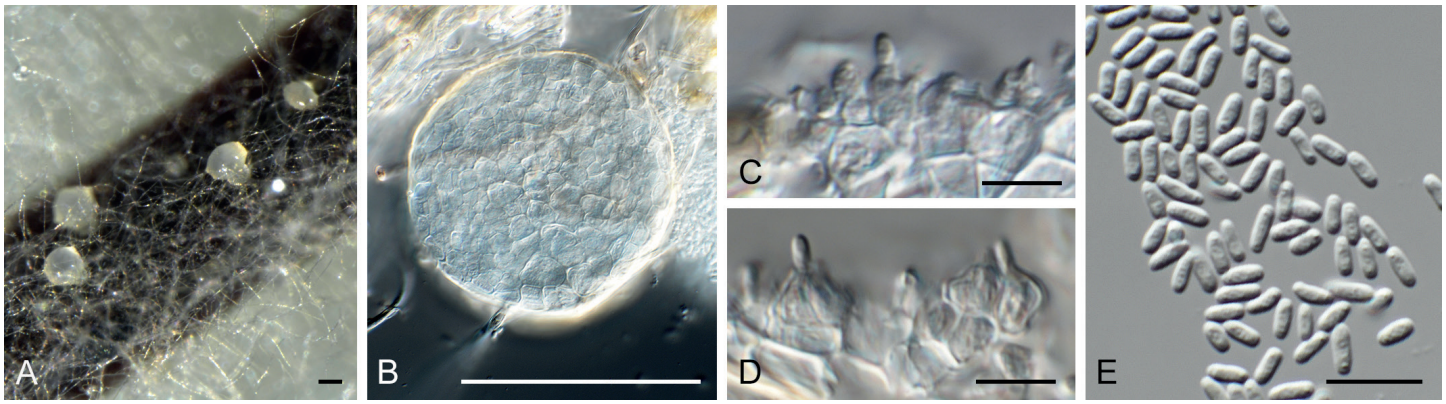

Fig. 45. *Piniphoma wesendahlina* (CPC 33693). **A.** Conidiomata on PNA. **B.** Conidioma. **C, D.** Conidiogenous cells. **E.** Conidia. Scale bars: A, B = 100 µm, C–E = 10 µm.

diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus: **Germany**, Berlin, wood debris of *Pinus sylvestris* (*Pinaceae*), 1 May 2017, *H. Schreiber & R.K. Schumacher*, HPC 2114 = RKS 106 (**holotype** CBS H-23823, culture ex-type CPC 33693 = CBS 145032).

Notes: *Piniphoma wesendahlina* is a phoma-like genus occurring on *Pinus sylvestris* wood debris collected in Berlin, Germany. Phylogenetically, it appears distinct from other phoma-like genera presently known (Chen *et al.* 2015, Valenzuela-Lopez *et al.* 2018), and is thus introduced as new.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Setophoma vernoniae* (GenBank KJ869141.1; Identities = 445/486 (92 %), 8 gaps (1 %)) and *Shiraia bambusicola* (GenBank MF062656.1; Identities = 451/491 (92 %), 11 gaps (2 %)). It was identical to several unidentified sequences, e.g. GenBank GU566235.1 from the rhizosphere of *Phalaris arundinacea* in Czech Republic, GenBank FN394707.1 from a fungal endophyte of *Holcus lanatus* in Spain and GenBank MH063650.1 from surface-sterilised, asymptomatic roots of *Arrhenatherum elatius* in France. Closest hits using the **LSU** sequence are *Coniothyrium quercinum* (GenBank MH877842.1; Identities = 858/860 (99 %), no gaps), *Sclerostagonospora cycadis* (GenBank MH874827.1; Identities = 858/860 (99 %), no gaps), and *Coniothyrium ferrarisianum* (GenBank MH872593.1; Identities = 858/860 (99 %), no gaps). Distant hits using the ***rpb2*** sequence had highest similarity to *Exserohilum fusiforme* (GenBank LT852483.1; Identities = 732/899 (81 %), 22 gaps (2 %)), *Exserohilum oryzicola* (GenBank LT715748.1; Identities = 717/883 (81 %), 19 gaps (2 %)), and *Bipolaris maydis* (GenBank XM_014222497.1; Identities = 740/918 (81 %), 17 gaps (1 %)). Very distant hits using the ***tef1*** sequence had highest similarity to *Dendryphion penicillatum* (GenBank AY375376.1; Identities = 207/234 (88 %), 4 gaps (1 %)), *Libertasomyces quercus* (GenBank KY929197.1; Identities = 208/235 (89 %), 8 gaps (3 %)), and *Alternaria alternariae* (as *Ulocladium alternariae*, GenBank AY375370.1; Identities = 207/234 (88 %), 6 gaps (2 %)). Distant hits using the ***tub2*** sequence had highest similarity to *Sclerostagonospora ericae* (GenBank KX228383.1; Identities = 467/551 (85 %), 26 gaps (4 %)), *Parastagonospora avenae* f. sp. *avenae* (as *Phaeosphaeria avenaria* f. sp. *avenaria*, GenBank AY870404.1; Identities = 468/557 (84 %), 31 gaps (5 %)), and *Seltsamia ulmi* (GenBank MF795918.1; Identities = 409/487 (84 %), 17 gaps (3 %)).

Pseudocercospora hakeae (U. Braun & Crous) U. Braun & Crous, *Stud. Mycol.* **75**: 88. 2012 (2013). Fig. 46.
Basionym: *Cercostigmina protearum* var. *hakeae* U. Braun & Crous, *Sydowia* **46**: 206. 1994.

Leaf spots amphigenous, elongated, confined by leaf veins, 2–3 mm diam, medium brown with raised, dark brown border. *Caespituli* olivaceous brown, amphigenous, developing on a well-defined brown stroma up to 250 µm diam. *Conidiophores* densely aggregated, subcylindrical, branched or not, geniculous-sinuous, 3–7-septate, medium brown, thick-walled, finely verruculose, 30–70 × 6–8 µm. *Conidiogenous cells* subcylindrical, medium brown, finely verruculose, thick-walled, terminal and intercalary, proliferating percurrently and or sympodially, 12–20 × 5–7 µm; loci truncate, unthickened, not darkened, 2–3 µm diam. *Conidia* solitary, subcylindrical, medium brown, finely verruculose, apex obtuse, base truncate, 2(–2.5) µm diam, straight to geniculous-sinuous, (1–)3–6(–7)-septate, (15–)30–50(–65) × 4(–5) µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 7 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, and reverse iron-grey.

Material examined: **Australia**, New South Wales, Fitzroy Falls, Morton National Park, on leaves of *Hakea* sp. (*Proteaceae*), 26 Nov. 2016, *P.W. Crous*, HPC 1756 = CBS H-23798, culture CPC 32100 = CBS 144520).

Notes: *Pseudocercospora hakeae* (as *Cercostigmina protearum* var. *hakeae*) was described from leaves on *Hakea saligna* collected in the Limpopo Province of South Africa (Crous & Braun 1994). The culture linked to this species (CBS 112226), was, however, collected on *Grevillea* sp. in Australia (Crous *et al.* 2013). The present collection provided the first culture from a *Hakea* sp., also collected in Australia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pseudocercospora fuligena* (GenBank GU214675.1; Identities = 533/535 (99 %), 1 gap (0 %)), *Pseudocercospora*

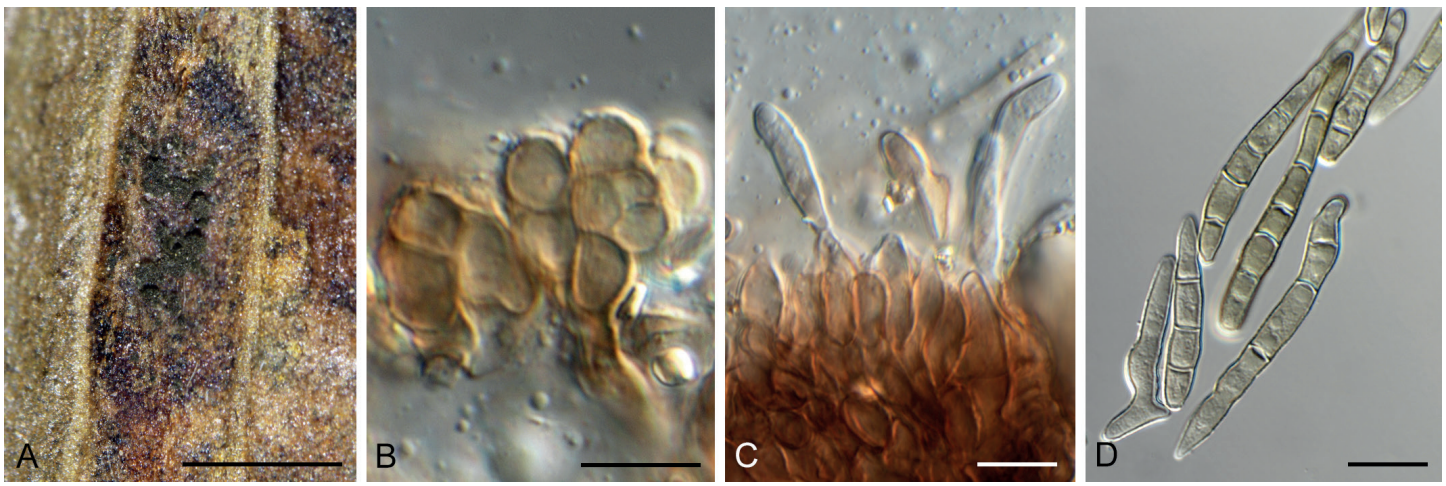

Fig. 46. *Pseudocercospora hakeae* (CPC 32100). **A.** Leaf spot. **B.** Stroma. **C.** Conidiogenous cells. **D.** Conidia. Scale bars = 10 µm.

chengtuensis (GenBank GU214672.1; Identities = 533/535 (99 %), 1 gap (0 %)), and *Pseudocercospora atromarginalis* (GenBank GU214671.1; Identities = 533/535 (99 %), 1 gap (0 %)). Closest hits using the **LSU** sequence are *Pseudocercospora cydoniae* (GenBank MH877505.1; Identities = 852/852 (100 %), no gaps), *Pseudocercospora rhamnellae* (GenBank MH877382.1; Identities = 852/852 (100 %), no gaps), and *Pseudocercospora ranjita* (GenBank MH875340.1; Identities = 852/852 (100 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Pseudocercospora hakeae* (GenBank JQ325017.1; Identities = 587/588 (99 %), no gaps), *Pseudocercospora cruenta* (GenBank JQ325012.1; Identities = 574/590 (97 %), 2 gaps (0 %)), and *Pseudocercospora neriicola* (GenBank KJ869231.1; Identities = 573/589 (97 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Pseudocercospora prunicola* (GenBank MF951621.1; Identities = 851/893 (95 %), no gaps), *Pseudocercospora nymphaeacea* (GenBank LC199939.1; Identities = 813/860 (95 %), no gaps), and *Pseudocercospora flavomarginata* (GenBank MF951619.1; Identities = 841/893 (94 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Pseudocercospora hakeae* (GenBank GU384495.1; Identities = 314/315 (99 %), no gaps), *Pseudocercospora basiramifera* (GenBank DQ211677.2; Identities = 458/510 (90 %), 9 gaps (1 %)), and *Pseudocercospora pallida* (GenBank GU384469.1; Identities = 280/315 (89 %), 3 gaps (0 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Pseudocercospora atromarginalis* (GenBank KM452894.1; Identities = 226/235 (96 %), no gaps), *Pseudocercospora pyracanthigena* (GenBank JX902271.1; Identities = 225/235 (96 %), no gaps), and *Pseudocercospora tereticornis* (GenBank JX902280.1; Identities = 224/235 (95 %), no gaps).

Pseudoconiothyrium Crous & R.K. Schumach., ***gen. nov.*** MycoBank MB829339.

Etymology: Name refers to its morphological similarity to the genus *Coniothyrium*, from which it is phylogenetically distinct.

Conidiomata eustromatica, pycnidial, aggregated, globose with central opening; wall of 6–10 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining inner cavity, hyaline, smooth, doliiform to ampulliform, phialidic with periclinal thickening, and at times with percurrent proliferation. *Conidia* solitary, aseptate, subcylindrical to ellipsoid to subglobose, apex obtuse, base truncate to bluntly rounded, medium brown, verruculose.

Type species: *Pseudoconiothyrium broussonetiae* Crous & R.K. Schumach.

Pseudoconiothyrium broussonetiae Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB829340. Fig. 47.

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

Conidiomata eustromatica, pycnidial, aggregated, 250–400 µm diam, globose with central opening; wall of 6–10 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining inner cavity, hyaline, smooth, doliiform to ampulliform, phialidic with periclinal thickening, and at times with percurrent proliferation, 5–10 × 4–6 µm. *Conidia* solitary, aseptate, subcylindrical to ellipsoid to subglobose, apex obtuse, base truncate to bluntly rounded, medium brown, verruculose, (5–)6–7(–8) × (4.5–)5(–6) µm.

Culture characteristics: Colonies spreading, with folded surface, moderate aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface dirty white to ochreous, reverse ochreous; on PDA surface pale luteous to ochreous, reverse ochreous; on OA surface ochreous with diffuse ochreous pigment.

Typus: **Italy**, Firenze, Plaza della indipendenza, branch of *Broussonetia papyrifera* (*Moraceae*), 16 Feb. 2017, *G. Bonari & R.K. Schumacher*, HPC 2009 = RKS 68 (**holotype** CBS H-23822, culture ex-type CPC 33570 = CBS 145036).

Notes: *Pseudoconiothyrium* is allied to *Paraconiothyrium* in the phylogenetic tree, but it is phylogenetically distinct from the latter genus. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pseudocoleophoma typhicola* (GenBank NR_154350.1; Identities = 508/563 (90 %), 13 gaps (2 %)), *Coniothyrium crepinianum* (GenBank MH860873.1; Identities = 507/574 (88 %), 25 gaps (4 %)), and *Pseudocoleophoma polygonicola* (GenBank NR_154274.1; Identities = 429/470 (91 %), 11 gaps (2 %)). Closest hits using the **LSU** sequence are *Aquadictyospora lignicola* (as *Pleosporales* sp. ZLL-2017a, GenBank MF948629.1; Identities = 774/789 (98 %), 1 gap (0 %)), *Dictyosporium tratense* (as *Dictyocheirospora* sp. YJ-2018b, GenBank MH381776.1; Identities = 814/831 (98 %), 4 gaps (0 %)), and *Cheiromyces inflatus* (GenBank JQ267363.1; Identities = 802/819 (98 %), 1 gap (0 %)). Very distant hits

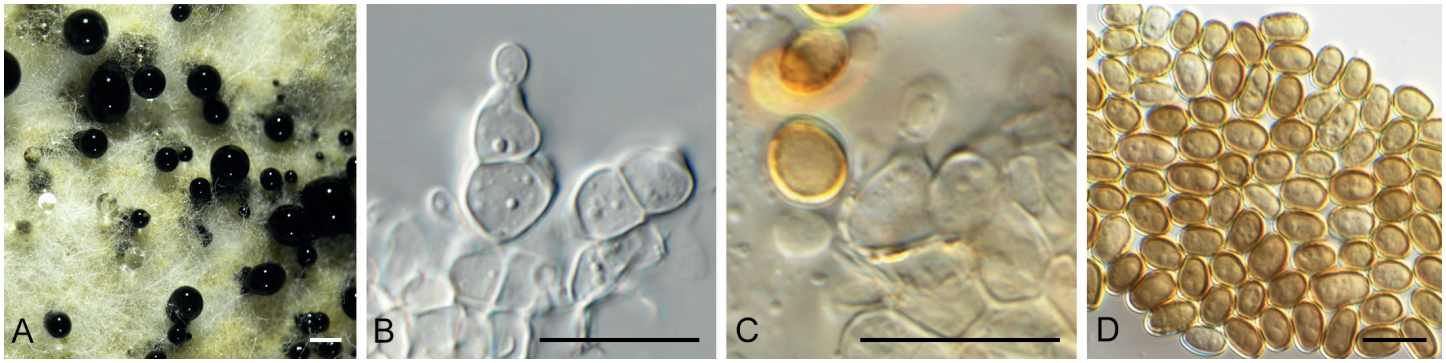

Fig. 47. *Pseudoconiothyrium broussonetiae* (CPC 33570). **A.** Conidiomata on PDA. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars: A = 300 µm, B–D = 10 µm.

using the ***tef1*** sequence had highest similarity to *Xenophoma puncteliae* (GenBank KP170686.1; Identities = 265/321 (83 %), 18 gaps (5 %)) and *Pseudochaetosphaeronema ginkgonis* (as *Pseudochaetosphaeronema* sp. XYD-2016a, GenBank KU365984.1; Identities = 278/345 (81 %), 18 gaps (5 %)).

Pseudophaeophleospora phormii (Naito) Crous, ***comb. nov.*** MycoBank MB829341. Fig. 48.
Basionym: *Hendersonia phormii* Naito, *Science Rep. Kagoshima Univ.* **1**: 77. 1952.
Synonyms: *Kirramyces phormii* (Naito) M.E. Palm, *Mycol. Res.* **100**: 374. 1996.
Phaeophleospora phormii (Naito) Crous *et al.*, *S. Afr. J. Bot.* **63**: 115. 1997.

Leaf spots brown, elliptical to elongate, surrounded by a dark red-purple border. *Conidiomata* pycnidial, immersed, solitary, globose to subglobose, up to 200 µm diam; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* cylindrical to lageniform, medium brown, finely roughened, 10–15 × 4–5 µm, proliferating percurrently near apex. *Conidia* solitary, medium brown, verruculose, aggregating in mucoid mass, cylindrical, apex obtuse, base truncate, 2–3 µm diam, with marginal frill, 3(–6)-septate, (30–)38–55(–60) × (3–)3.5(–4) µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium, folded surface and smooth, lobate margin, reaching 7 mm diam after 2 wk at 25 °C. On MEA surface grey olivaceous, reverse olivaceous grey; on PDA surface dirty white, reverse olivaceous grey; on OA surface dirty white with diffuse red pigment.

Typus: **New Zealand**, Levin, Earl St, on *Phormium tenax*, 12 Dec. 1971, *G. Laudon*, PDD 39822 (**neotype** designated by Palm 1996); Auckland, Grey Lynn Park, on *Phormium tenax* (*Asphodelaceae*), 5 Oct. 2016, *R. Thangavel* T16_03297D (**epitype designated here** CBS H-23264, MBT385290, culture ex-epitype CPC 32742 = CBS 144606).

Notes: *Pseudophaeophleospora* was established by Videira *et al.* (2017) to accommodate a phaeophleospora-like genus occurring on *Eucalyptus*. The two genera are morphologically similar, and best distinguished based on their DNA sequences.

The present collection closely matches the morphology of the neotype of *Hendersonia phormii*, described by Palm (1996). Unfortunately, the culture used in the latter paper is no longer viable, and could thus not be deposited. The culture from the present collection is thus herewith designated as epitype, to fix the phylogenetic application of the name.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pseudophaeophleospora atkinsonii* (as *Phaeophleospora atkinsonii*, GenBank GU214643.1; Identities = 480/505 (95 %), no gaps), *Pallidocercospora acaciigena* (GenBank MH862893.1; Identities = 478/520 (92 %), 5 gaps (0 %)), and *Pallidocercospora heimii* (as *Mycosphaerella heimii*, GenBank GQ852745.1; Identities = 479/521 (92 %), 7 gaps (1 %)). Closest hits using the **LSU** sequence are *Pseudophaeophleospora atkinsonii* (as *Phaeophleospora atkinsonii*, GenBank GU214463.1; Identities = 839/849 (99 %), no gaps), *Pallidocercospora irregulariramosa* (GenBank GU214441.1; Identities = 878/892 (98 %), 1 gap (0 %)), and *Pallidocercospora holualoana* (as *Mycosphaerella holualoana*, GenBank JF770467.1; Identities = 877/892 (98 %), 1 gap (0 %)). No ***actA*** sequences of *Pseudophaeophleospora* are available for comparison on GenBank; distant hits include *Pseudocercospora udagawana* (GenBank GU320527.1; Identities = 544/604 (90 %), 12 gaps (1 %)), *Parapallidocercospora thailandica* (as *Pallidocercospora thailandica*, GenBank EU514333.1; Identities = 496/535 (93 %), 7 gaps (1 %)), and *Pallidocercospora heimii* (GenBank KF903399.1; Identities = 487/525 (93 %), 6 gaps (1 %)). No ***tef1*** sequences of *Pseudophaeophleospora* are available for comparison on GenBank; distant hits include *Pallidocercospora crystallina* (GenBank MF135483.1; Identities = 376/463 (81 %), 27 gaps (5 %)), *Parapallidocercospora thailandica* (as *Mycosphaerella thailandica*, GenBank AY840477.2; Identities = 329/399 (82 %), 24 gaps (6 %)), and *Neoceratosperma cyatheae* (GenBank KT037504.1; Identities = 184/196 (94 %), no gaps).

Pseudorobillardaceae Crous, ***fam. nov.*** MycoBank MB829342.

Etymology: Name refers to the genus *Pseudorobillarda*.

Conidiomata immersed, globose, unilocular, with central ostiole; wall of 3–6 layers of thin-walled, flattened *textura angularis*; conidiomata giving rise to both micro- and macroconidia. *Macroconidiophores* lining the inner cavity, reduced to conidiogenous cells, hyaline, smooth, doliiform, phialidic with periclinal thickening and flared collarette, or proliferating percurrently when older. *Paraphyses* numerous, hyphae-like, intermingled among conidiophores, aseptate, flexuous.

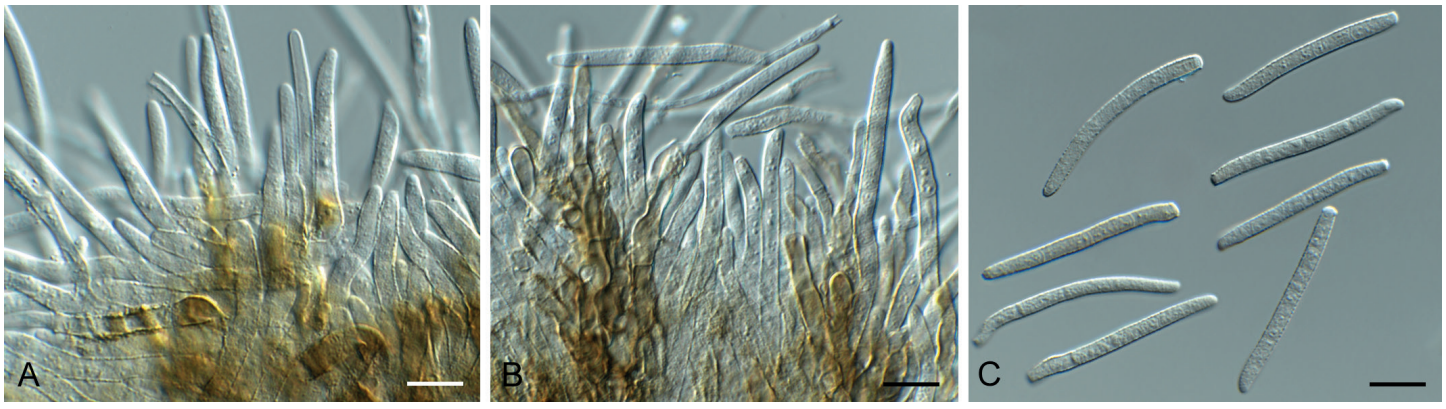

Fig. 48. *Pseudophaeophleospora phormii* (CPC 32742). **A, B.** Conidiogenous cells. **C.** Conidia. Scale bars = 10 µm.

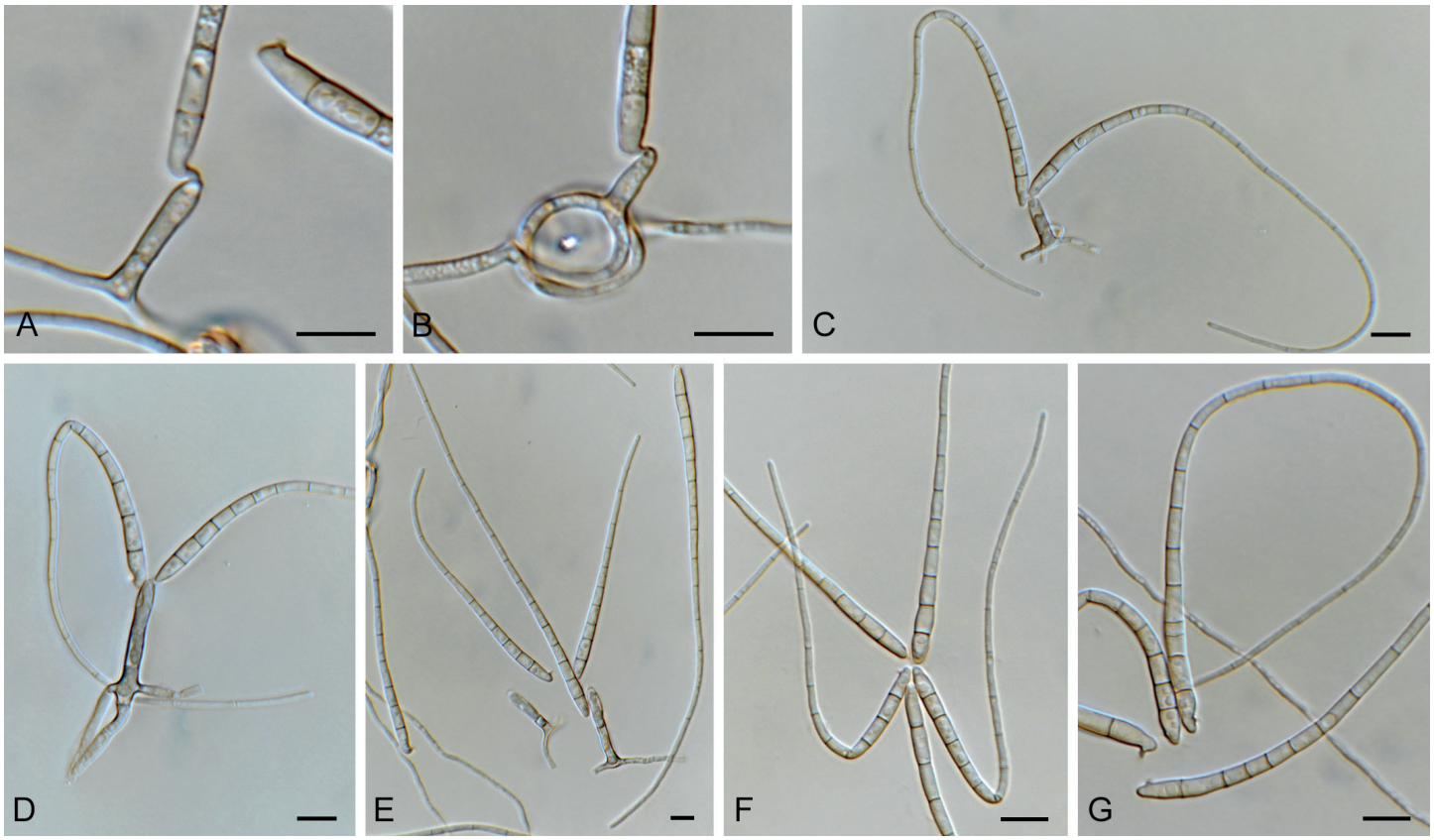

Fig. 49. *Pseudosigmoidea alnicola* (CPC 33776). **A–E.** Conidiogenous cells giving rise to conidia. **F, G.** Conidia. Scale bars = 10 µm.

Macroconidia solitary, septate, guttulate, hyaline, smooth, apex subobtuse, tapering to a truncate base; apical appendages arising from splitting of the conidial sheath, hair-like, flexuous, unbranched, fragile, flexuous, unbranched, mostly absent. *Microconidiogenous cells* hyaline, smooth, subcylindrical to ampulliform, proliferating percurrently. *Microconidia* solitary, aseptate, hyaline, smooth, guttulate, subcylindrical, apex obtuse, base truncate; apical appendages hair-like, flexuous, unbranched, fragile, flexuous, unbranched.

Type genus: *Pseudorobillarda* M. Morelet (1968)

Type species: *Pseudorobillarda phragmitis* (Cunnell) M. Morelet.

Notes: *Pseudorobillarda bolusanthi* was recently introduced by Crous *et al*. (2018b), and placed in the *Pseudorobillardaceae* (*Dothideomycetes*). The family, however, was unpublished, and is therefore formally introduced here.

Pseudosigmoidea alnicola Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB829346. Fig. 49.

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

Mycelium consisting of pale brown, smooth, 1.5–2 µm diam hyphae, frequently forming hyphal coils, giving rise to solitary, erect conidiophores, subcylindrical, unbranched, pale brown, smooth, 0–1-septate, 10–20 × 2.5–3 µm. *Conidiogenous cells* integrated, terminal, pale brown, smooth, subcylindrical, 5–15 × 1.5–3 µm; apex with one to several denticles-like loci, 0.5–1 × 1 µm. *Conidia* obclavate, flexuous, multi-septate, pale brown, smooth-walled, guttulate, apex subobtuse, base obconically truncate, widest at first basal septum, base bluntly rounded, attached to conidiogenous cell via excentric locus which leaves a cylindrical separating cell on the side of the conidium, 1–2 × 1–1.5 µm, 80–250 × 3–4 µm, apical region of conidium 1.5–2 µm diam.

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

Typus: **Germany**, near Berlin, alder wood, leaf litter of *Alnus glutinosa* (*Betulaceae*), 3 May 2017, *R.K. Schumacher*, HPC 2100 (**holotype** CBS H-23826, culture ex-type CPC 33776 = CBS 145034).

Notes: *Pseudosigmoidea* (based on *P. cranei*), has rhexolytic conidiogenesis with a separating cell, and long, flexuous, subcylindrical to obclavate, septate, hyaline to pale brown, smooth conidia (Ando & Nakamura 2000). Although the genus is listed as *Ascomycota* "*incertae sedis*", this study shows that it resides in the *Sympoventuriaceae* (*Venturiales, Dothidiomycetes*). *Pseudosigmoidea* is known from two species, *P. cranei* (conidia 26–116.5 × 1.5–2.5 µm, 3–8-septate) and *P. ibarakiensis* (conidia 68–133 × 4–8 µm, up to 6-septate; Diene *et al.* 2013), both of which can easily be distinguished from *P. alnicola* based on their conidial morphology.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Troposporella fumosa* (GenBank DQ351724.1; Identities = 564/585 (96 %), 1 gap (0 %)), *Helicoma monilipes*

(GenBank DQ351723.1; Identities = 556/587 (95 %), 4 gaps (0 %)), and *Pseudosigmoidea ibarakiensis* (GenBank LC146758.1; Identities = 546/577 (95 %), 10 gaps (1 %)). Closest hits using the **LSU** sequence are *Scolecobasidium excentricum* (GenBank MH874174.1; Identities = 854/856 (99 %), no gaps), *Troposporella fumosa* (GenBank MH874121.1; Identities = 850/856 (99 %), no gaps), and *Sympoventuria melaleucae* (GenBank NG_058520.1; Identities = 840/849 (99 %), no gaps).

Pseudoteratosphaeria africana Crous, ***sp. nov.*** MycoBank MB829347. Fig. 50.

Etymology: Name refers to the continent of Africa where it was collected.

Leaf spots amphigenous, circular, 2–5 mm diam, medium brown, with thin, raised dark brown border. *Ascomata* pseudothecial, predominantly hypophyllous, black, immersed to erumpent, globose, 70–100 µm diam, with apical ostiole; wall of 2–3 layers of brown *textura angularis. Asci* aparaphysate, fasciculate, bitunicate, subsessile, obovoid, straight to slightly curved, 8-spored, 30–35 × 8–11 µm. *Ascospores* bi- to triseriate, overlapping, hyaline, guttulate, thin-walled, straight to slightly curved, obovoid with obtuse ends, widest in middle of apical cell, medianly 1-septate, constricted at septum, tapering towards both ends, but more prominently towards lower end, (11–)12–13(–14) × (2.5–)3–3.5(–4) µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium, folded surface, and smooth, lobate margin, reaching 20–30 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus: **Angola**, Longa River, leaf spot on unidentified host, 6 Nov. 2010, *J. Roux*, HPC 1697 (**holotype** CBS H-23816, culture ex-type CPC 33144 = CBS 144595).

Additional materials examined: **Angola**, Longa River, leaf spot on unidentified host, 6 Nov. 2010, *J. Roux*, cultures CPC 33145 = CBS 144596, CPC 33072 = CBS 144597.

Notes: *Pseudoteratosphaeria* was introduced by Quaedvlieg *et al*. (2014) to accommodate a genus morphologically similar to *Teratosphaeria*, which lacked any known asexual morphs, and occurred primarily on *Myrtaceae*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 33072 had highest similarity to *Pseudoteratosphaeria perpendicularis* (GenBank NR_155617.1; Identities = 485/496 (98 %), 1 gap (0 %)), *Pseudoteratosphaeria stramenticola* (as *Mycosphaerella stramenticola*, GenBank DQ632669.1; Identities = 488/500 (98 %), 2 gaps (0 %)), and *Pseudoteratosphaeria gamsii* (as *Teratosphaeria gamsii*, GenBank DQ302959.1; Identities = 481/497 (97 %), 2 gaps (0 %)). The ITS sequences of CPC 33072, 33144 and 33145 are identical. Closest hits using the **LSU** sequence are *Pseudoteratosphaeria perpendicularis* (as *Teratosphaeria perpendicularis*, GenBank JN232443.1; Identities = 859/861 (99 %), no gaps), *Pseudoteratosphaeria ohnowa* (GenBank EU019305.2; Identities = 866/873 (99 %), no gaps), and *Pseudoteratosphaeria flexuosa* (as *Teratosphaeria flexuosa*, GenBank JN232432.1; Identities = 877/885 (99 %), no gaps). The LSU sequences of CPC 33072, 33144 and 33145 are identical. Closest hits using the ***actA*** sequence had highest similarity to *Pseudoteratosphaeria stramenticola* (GenBank KF903530.1; Identities = 515/541 (95 %), 2 gaps (0 %)), *Pseudoteratosphaeria perpendicularis* (GenBank KF903491.1; Identities = 513/540 (95 %), no gaps), and *Pseudoteratosphaeria gamsii* (GenBank KF903494.1; Identities = 510/540 (94 %), no gaps). The *actA* sequences of CPC 33072, 33144 and 33145 are identical. Closest hits using the ***tef1*** sequence had highest similarity to *Pseudoteratosphaeria perpendicularis* (GenBank KF903232.1; Identities = 320/347 (92 %), 5 gaps (1 %)), *Pseudoteratosphaeria stramenticola* (GenBank KF903237.1; Identities = 319/354 (90 %), 16 gaps (4 %)), and *Pseudoteratosphaeria gamsii* (GenBank KF903229.1; Identities = 311/352 (88 %), 13 gaps (3 %)). The *tef1* sequences of CPC 33072, 33144 and 33145 are identical. Closest hits using the ***tub2*** sequence had highest similarity to *Pseudoteratosphaeria ohnowa* (as *Teratosphaeria ohnowa*, GenBank KF442464.1; Identities = 304/338 (90 %), 6 gaps (1 %)), *Pseudoteratosphaeria gamsii* (GenBank KF902933.1; Identities = 221/246 (90 %), 3 gaps (1 %)), and *Pseudoteratosphaeria perpendicularis* (GenBank KF902936.1; Identities = 218/247 (88 %), 5 gaps (2 %)). The *tub2* sequences of CPC 33072 and 33145 are identical; the sequence of CPC 33144 differs at one nucleotide from the others.

Porodiplodia vitis Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB829349. Fig. 51.

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

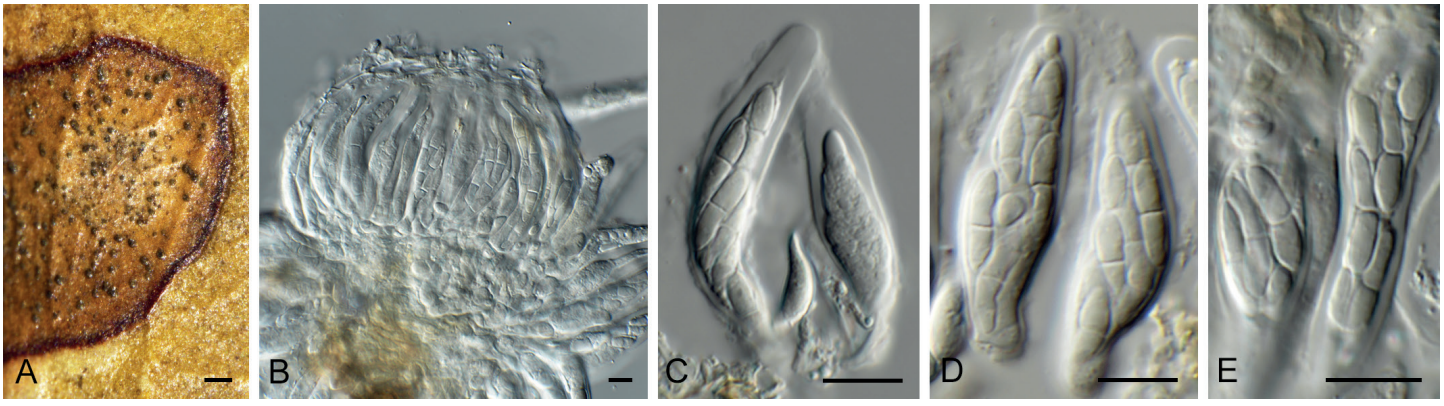

Fig. 50. *Pseudoteratosphaeria africana* (CPC 33144). **A.** Leaf spot. **B–E.** Asci and ascospores. Scale bars: A = 5 mm, B–E = 10 µm.

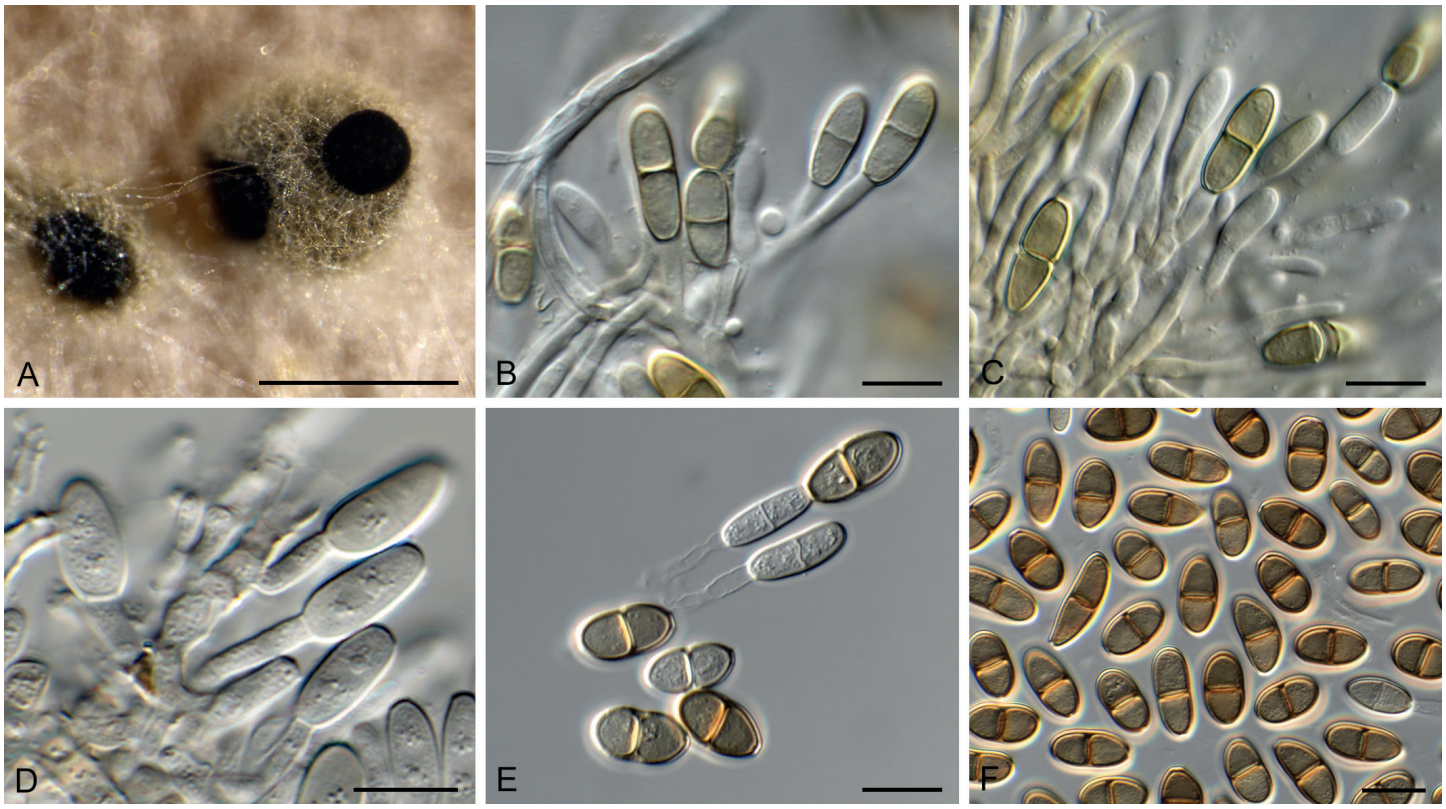

Fig. 51. *Porodiplodia vitis* (CPC 31642). **A.** Conidiomata on OA. **B–E.** Conidiogenous cells giving rise to conidia. **F.** Conidia. Scale bars: A = 300 µm, B–F = 10 µm.

Conidiomata eustromatic, uni- to multilocular, brown, globose, 150–300 µm, aggregated on agar, ostiolate. *Conidiophores* lining inner cavity, subcylindrical, hyaline, smooth, branched, 1–3-septate, 15–20 × 2.5–4 µm, proliferating percurrently near apex. *Paraphyses* intermingled among conidiophores, hyaline, smooth, septate, subcylindrical with obtuse ends, 25–30 × 3–4 µm. *Conidia* in short chains (–3), fusoid-ellipsoid to subcylindrical, medium brown, finely verruculose, guttulate, thick-walled, 1-septate, apex obtuse (at times with central pore), base truncate with central pore, 2 µm diam, (13–)14–16(–19) × (5–)6(–8) µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface cinnamon to buff, reverse sienna; on PDA surface saffron, reverse cinnamon; on OA surface cinnamon, with diffuse cinnamon pigment.

Typus: **USA**, New York, Bronx, Van Cortlandt Park, on canes of *Vitis vinifera* (*Vitaceae*), 2016, *E. Crenson & R.K. Schumacher*, HPC 1372 (**holotype** CBS H-23795, culture ex-type CBS 144634 = CPC 31642).

Notes: *Porodiplodia* was recently established for a genus occurring on leaves of *Livistona australis* in Australia, characterised by having eustromatic conidiomata, and conidia occurring in short chains, with a pore at each end of its conidia (Crous *et al.* 2018c). *Porodiplodia vitis* differs from *P. livistonae* (conidia (14–)15–17(–20) × 5(–6) µm) in having shorter, wider conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Porodiplodia livistonae* (GenBank MH327809.1; Identities = 533/536 (99 %), no gaps), *Chalara clidemiae* (GenBank NR_145313.1; Identities = 528/547 (97 %), 1 gap (0 %)), and *Mollisia caespiticia* (GenBank KY965813.1; Identities = 506/542 (93 %), 2 gaps (0 %)). Closest hits using the **LSU** sequence are *Porodiplodia livistonae* (GenBank MH327845.1; Identities = 859/859 (100 %), no gaps), *Chalara clidemiae* (GenBank MH878219.1; Identities = 765/772 (99 %), no gaps), and *Chaetochalara africana* (as *Chalara africana*, GenBank FJ176249.1; Identities = 834/849 (98 %), 2 gaps (0 %)). No ***tef1*** sequences of *Porodiplodia* are available on GenBank for comparison; distant hits using the *tef1* sequence had highest similarity to *Davidhawksworthia ilicicola* (GenBank KU728592.1; Identities = 205/233 (88 %), 7 gaps (3 %)), *Hymenoscyphus menthae* (GenBank KM114512.1; Identities = 203/231 (88 %), 6 gaps (2 %)), and *Fusarium napiforme* (GenBank KM099398.1; Identities = 201/231 (87 %), 4 gaps (1 %)).

Selenodriella fertilis (Piroz. & Hodges) R.F. Castañeda & W.B. Kendr., *Univ. Waterloo Biol. Ser.* **33**: 34. 1990. Fig. 52.
Basionym: *Circinotrichum fertile* Piroz. & Hodges, *Canad. J. Bot.* **51**: 160. 1973.

Conidiophores dimorphic. *Microconidiophores* reduced to conidiogenous cells or with a supporting cell, arising directly from mycelium, hyaline, smooth, subcylindrical, tapering toward denticulate apex, 7–12 × 2.5–3.5 µm. *Macroconidiophores* erect, arising from superficial hyphae, flexuous, branched or not, base with T-cell or rhizoids, subcylindrical, 60–140 × 4–5 µm, 4–10-septate, lateral branches 0–3-septate, 15–60 × 2.5–3 µm. *Conidiogenous cells* pale brown, smooth, subcylindrical to elongated fusoid-ellipsoid, terminal and intercalary, with apical rachis of denticulate loci; denticles 1–2 × 1–1.5 µm, scars somewhat darkened, not thickened nor refractive, 20–30 × 2.5–

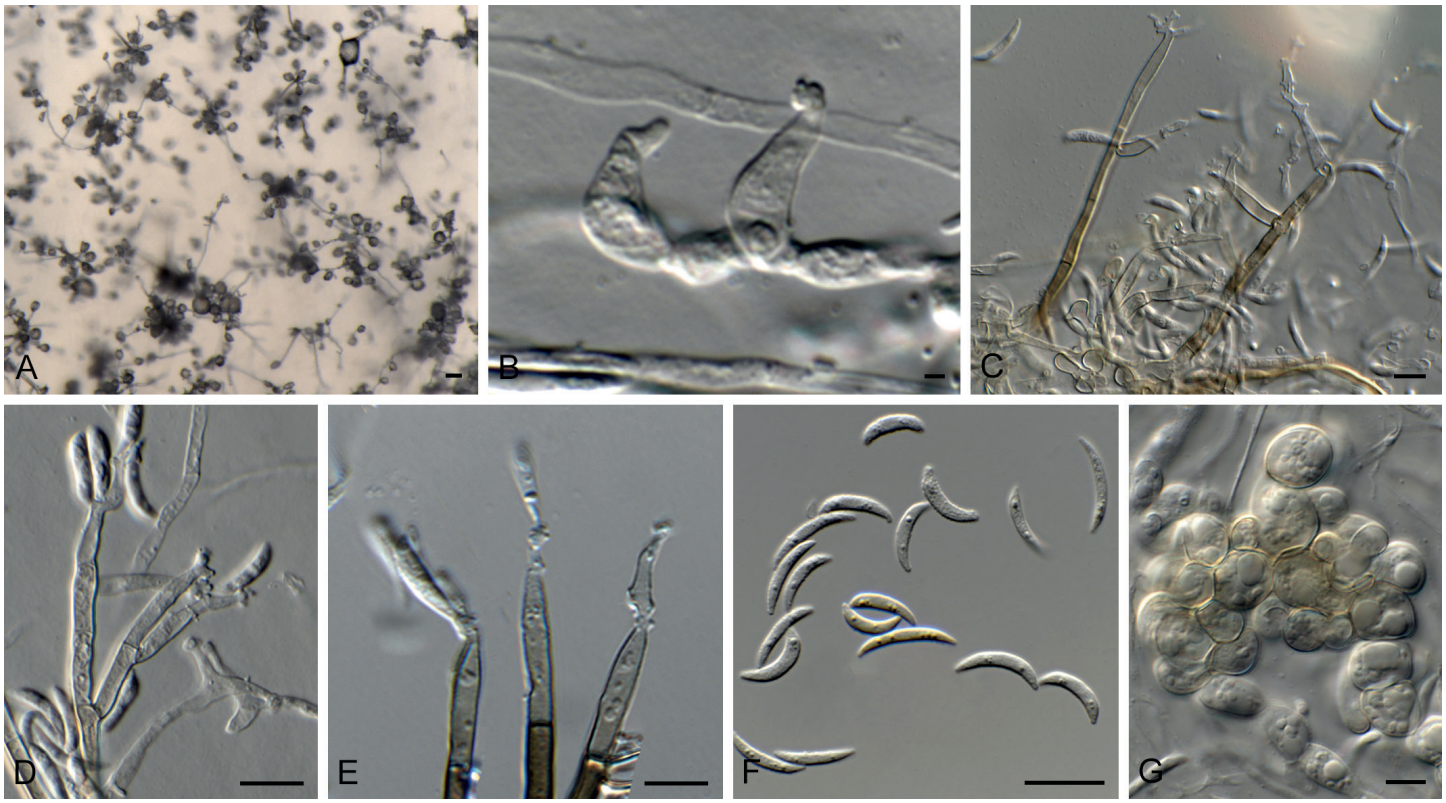

Fig. 52. *Selenodriella fertilis* (CPC 32663). **A.** Colony on SNA. **B.** Conidiogenous cells. **C–E.** Conidiophores. **F.** Conidia. **G.** Chlamydospores. Scale bars: A = 100 µm, B–G = 10 µm.

3 µm. *Conidia* aggregating in mucoid masses, aseptate, fusoid-ellipsoid, prominently curved, apex subobtuse, base truncate, 1 µm diam, not thickened nor darkened, (9–)12–14(–15) × 2(–3) µm. *Chlamydospores* in chains, globose, thin-walled, hyaline, becoming pale brown and forming microsclerotia, 7–12 µm diam.

Culture characteristics: Colonies flat, spreading, with sparse aerial mycelium, folded surface and smooth, even margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface and reverse isabelline to buff; on PDA surface and reverse olivaceous grey; on OA surface olivaceous grey.

Material examined: **Australia**, Victoria, Nowa Nowa, on leaf litter of *Eucalyptus* sp. (*Myrtaceae*), 30 Nov. 2016, *P.W. Crous*, HPC 1876, culture CPC 32663 = CBS 144589.

Notes: For notes on *Selenodriella*, see Hernández-Restrepo *et al*. (2016), who confirmed the occurrence of *Selenodriella fertilis* in Australia on *Hakea baxteri*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Selenodriella fertilis* (GenBank MH861691.1; Identities = 525/526 (99 %), no gaps), *Gyrothrix circinata* (GenBank KJ476968.1; Identities = 477/483 (99 %), 5 gaps (1 %)), and *Selenodriella cubensis* (GenBank NR_154414.1; Identities = 515/522 (99 %), 1 gap (0 %)). Closest hits using the **LSU** sequence are *Selenodriella fertilis* (GenBank KP858992.1; Identities = 849/851 (99 %), 1 gap (0 %)), *Selenodriella cubensis* (GenBank NG_058151.1; Identities = 844/852 (99 %), 1 gap (0 %)), and *Gyrothrix verticiclada* (GenBank KC775726.1; Identities = 800/821 (97 %), 6 gaps (0 %)).

Stagonospora pseudoperfecta Kaz. Tanaka & K. Hiray., *Stud. Mycol.* **82**: 106. 2015. Fig. 53.

Conidiomata globose, brown, 250–300 µm diam (with papillate neck on host tissue); wall of 2–3 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, ampulliform to subcylindrical, 5–10 × 3–5 µm; proliferating percurrently. *Conidia* solitary, hyaline, smooth, fusoid-ellipsoid, guttulate, 3-septate, apex obtuse, tapering from basal septum to truncate hilum, 2 um diam, (13–)20–22(–250 × (4–)5(–6) µm.

Culture characteristics: Colonies erumpent, spreading, with abundant, fluffy aerial mycelium covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface smoke grey, and reverse olivaceous grey.

Material examined: **Germany**, near Berlin, on *Typha* sp. (*Typhaceae*), 1 Apr. 2017, *R.K. Schumacher*, RKS 85 = HPC 2026, culture CPC 33138 = CBS 144607.

Notes: *Stagonospora pseudoperfecta* was described from dead leaves of *Typha latifolia* collected in Japan (Tanaka *et al.* 2015), and this is the first record of the fungus from Europe.

Based on a megablast search of NCBI's GenBank nucleotide database, the **ITS** sequence was identical to *Stagonospora pseudoperfecta* (GenBank NR_155768.1; Identities = 497/497 (100 %)); and related to *Stagonospora trichophoricola* (GenBank KY750315.1; Identities = 533/538 (99 %), 1 gap (0 %)) and *Stagonospora bicolor* (as *Saccharicola bicolor*, GenBank KT367526.1; Identities = 530/535 (99 %), 1 gap (0 %)). Closest hits using the **LSU** sequence are *Stagonospora pseudoperfecta* (GenBank NG_059399.1; Identities = 797/797 (100 %)),

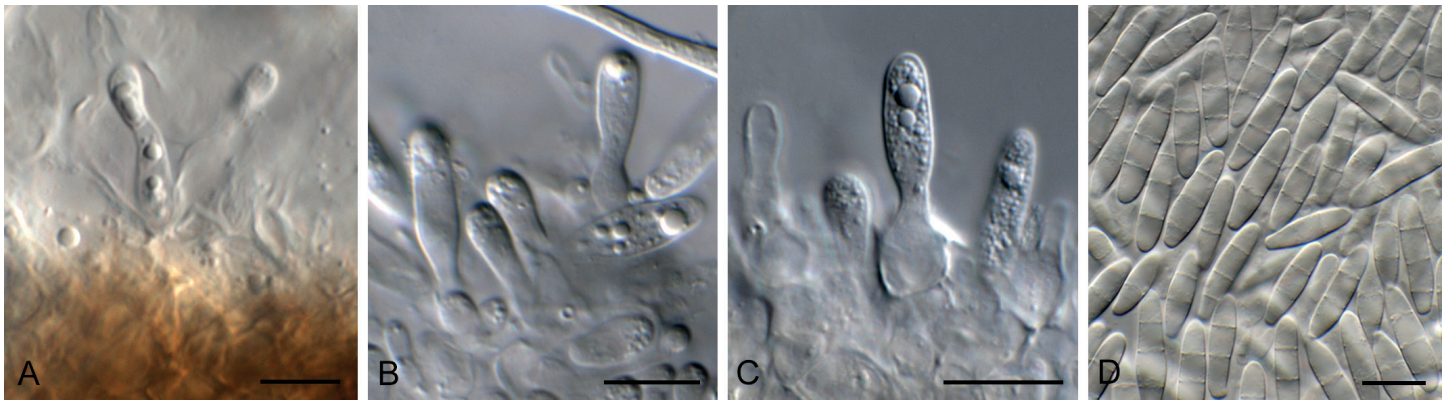

Fig. 53. *Stagonospora pseudoperfecta* (CPC 33138). **A–C.** Conidiogenous cells. **D.** Conidia. Scale bars = 10 µm.

Stagonospora forlicesenensis (GenBank NG_059716.1; Identities = 794/797 (99 %), no gaps), and *Stagonospora imperaticola* (GenBank NG_059793.1; Identities = 793/797 (99 %), no gaps). No ***tef1*** sequences of *Stagonospora pseudoperfecta* are available for comparison on GenBank; distant hits include *Helminthosporium oligosporum* (GenBank KY984449.1; Identities = 304/364 (84 %), 19 gaps (5 %)), *Helminthosporium tiliae* (GenBank KY984456.1; Identities = 304/364 (84 %), 19 gaps (5 %)), and *Corynespora leucadendri* (GenBank KF253110.1; Identities = 313/381 (82 %), 22 gaps (5 %)). No ***tub2*** sequences of *Stagonospora pseudoperfecta* are available for comparison on GenBank; distant hits include *Stagonospora victoriana* (GenBank MG386166.1; Identities = 331/389 (85 %), 13 gaps (3 %)), *Stagonospora chrysopyla* (GenBank KM033943.1; Identities = 322/387 (83 %), 14 gaps (3 %)), and *Stagonospora* cf. *paludosa* (GenBank KF252737.1; Identities = 245/296 (83 %), 11 gaps (3 %)).

Sympodiella W.B. Kendr., *Trans. Br. Mycol. Soc*. **41**: 519. 1958. ***emend***. Hern.-Restr. & Crous

Mycelium consisting of pale to medium brown, smooth, septate, branched hyphae. *Sympodiella* morph. *Conidiophores* solitary, erect, medium brown, smooth, subcylindrical, straight to flexuous, unbranched, septate, sometimes proliferating percurrently (in culture). *Conidiogenous cells* terminal, subcylindrical, medium brown, polyblastic, sympodial. *Conidia* aseptate or septate, sometimes constricted at the septa, subcylindrical to acicular, apex obtuse, base truncate, smooth, hyaline to subhyaline. Repetophragma-like *Synasexual morph*. *Conidiophores* solitary, erect, medium brown, smooth, subcylindrical, straight to geniculous-sinuous, unbranched, septate, proliferating percurrently. *Conidiogenous cells* terminal, subcylindrical, straight or flexuous, medium brown, mono- or polyblastic, sometimes sympodial (mainly in culture). *Conidia* solitary, septate, subcylindrical, straight, apex obtuse, sometimes with a dark cap, base truncate, with or without a minute marginal frill, smooth, pale- to medium brown, guttulate; hilum unthickened, not darkened.

Type species: *Sympodiella acicola* W.B. Kendr.

Notes: We emend *Sympodiella* to include species with a repetophragma-like synasexual morph. A new species is introduced as *S. quercina* and additionally two new combinations are proposed and discussed below.

Sympodiella acicola W.B. Kendr., *Trans. Br. Mycol. Soc*. **41**: 519. 1958. Figs 54–56.

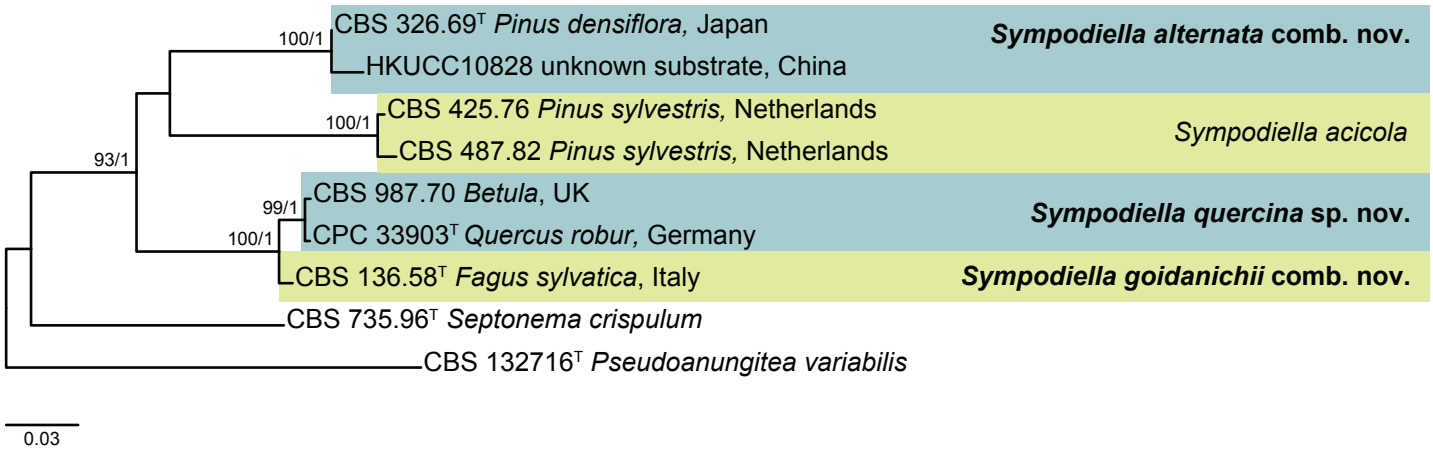

Fig. 54. RAxML phylogenetic tree obtained from a phylogenetic analysis of the *Sympodiella* ITS, LSU, *rpb2* and *tef1* alignment (9 strains including outgroup; 4014 characters analysed: 699 from ITS, 886 from LSU, 921 from *rpb2*, and 1508 from *tef1*). The tree was rooted to *Pseudoanungitea variabilis* CBS 132716 and *Septonema crispulum* CBS 735.96 and the scale bar indicates the number of changes. Bootstrap support values higher than 70 % and Bayesian posterior probabilities higher than 0.95 are shown at the nodes and the species clades are highlighted with coloured boxes. Species names are indicated to the right of the tree. Strain numbers are followed by the substrate/source and country of origin are indicated for each strain.

Fig. 55. *Sympodiella acicola* (CBS H-1620 - *Pinus* needles). **A–L.** *Sympodiella* asexual morph. **A–G**. Conidiophores, conidiogenous cells and conidia. **H–L**. Conidia. **M–V.** Repetophragma-like synasexual morph. **M–S.** Conidiophores and conidia. **T–V.** Conidia. Scale bars = 10 µm.

Fig. 56. *Sympodiella acicola* (CBS 487.82 on OA). **A–E, G, H.** Conidiophores, conidiogenous cells and conidia (arrows showing percurrent proliferations). **F, I–K.** Conidia. Scale bars: A, B = 20 µm, C–K = 10 µm.

Typus: **UK**, Cheshire, on *Pinus sylvestris* (*Pinaceae*), 1956, *W.B. Kendrick*, **holotype** IMI 69967. **Netherlands**, Baarn, De Vuursche, on *Pinus sylvestris,* 12 Apr. 1982, *G.S. de Hoog* (**epitype** designated here CBS H-1620 MBT385535, ex-epitype culture CBS 487.82).

Synasexual morph repetophragma-like. *Conidiophores* brown, smooth, proliferating percurrently, up to 25 µm long, 2–3.5 µm wide at the base. *Conidiogenous cells* terminal, brown. *Conidia* 3–4(–7)-septate, subcylindrical, straight, apex obtuse, base truncate, with a minute marginal frill, smooth, pale- to medium brown, 13–35 × 3–4 µm.

Notes: Conidia in *S. acicola* have been considered arranged in unbranched chains (Kendrick 1958, Seifert *et al.* 2011). During an examination of the specimen CBS H-1620, some of these conidia resemble phragmoconidia constricted at the septa similar to those described in *Wiesneriomyces*, since they often remain connected together after they separate from the conidiogenous cells. In culture however (CBS 487.82), they are readily deciduous. Furthermore, in a specimen of *Sympodiella acicola* (CBS H-1620) the conidiophores were mixed with a repetophragma-like conidiophores described here as the synasexual morph of *Sympodiella acicola*. Interestingly, in culture (CBS 487.82) we observed some conidiophores with percurrent proliferations and the 1-septate conidia were more abundant than in natural substrate. This species has been reported mainly from *Pinus* spp. (Kendrick 1958, Ellis 1976).

Sympodiella alternata (Tubaki & Saito) Crous & Hern.-Restr., ***comb. nov.*** MycoBank MB829352. Fig. 57.
Basionym: *Endophragmia alternata* Tubaki & Saito, *Trans. Brit. Mycol. Soc.* **52**: 477. 1969.

Typus: **Japan**, Sendai, on fallen needles of *Pinus densifolia* (*Pinaceae*), 1966, *T. Saitô* (**holotype** IFO H-11600, ex-type culture IFO 8933 = CBS 326.69).

Note: *Sympodiella alternata* is only known by the repetophragma-like synasexual morph from Asia (Tubaki & Saitô 1969). During this study we examined the ex-type culture of *Sympodiella alternata* (CBS 326.69). Conidia were similar to those described in the protologue with a dark cap in the apex of the conidia, but they were slightly smaller with less septa (30–36 × 5–6 µm, 5–8-septate vs. (37–)40–46(–70) × 5–6(–7) µm, (7–)8-septate; Tubaki & Saitô 1969). The conidiophores proliferate percurrently and sometimes geniculate conidiophores were observed. This species is known from *Pinus densifolia* from Japan (Tubaki & Saitô 1969) and from an unknown substrate from China (Shenoy *et al.* 2006).

Sympodiella goidanichii (Rambelli) Crous & Hern.-Restr., ***comb. nov.*** MycoBank MB829353.
Basionym: *Ceratosporella goidanichii* Rambelli, *R.C. Secc. Accad. Sci. Ist. Bologna*, sér. 6, **5**: 3. 1958.
Synonyms: *Sporidesmium goidanichii* (Rambelli) S. Hughes, *N.Z. J. Bot*. **17**: 162. 1979.

Fig. 57. *Sympodiella alternata* (CBS 326.69 on OA). **A–C.** Conidiophores with percurrent proliferations. **D, E.** Conidiophores with sympodial proliferations. F. Conidiophore with lateral conidia. **G–I.** Conidiophores giving rise to conidia. **J–P.** Conidia. Scale bars = 10 µm.

Repetophragma goidanichii (Rambelli) W.P. Wu, *Fungal Diversity Res. Ser.* **15**: 80. 2005.

Typus: **Italy**, on cupule of *Fagus sylvatica* (*Fagaceae*), collection date unknown, *A. Rambelli*, ex-type culture CBS 136.58.

Note: *Sympodiella goidanichii* was described from *Fagus sylvatica* in Italy as *Ceratosporella goidanichii* (Rambelli 1958). Hughes (1979) considered *Ceratosporella goidanichii* and *Endophragmia alternata* as conspecific species and include them in *Sporidesmium* due to the successive proliferation of the conidiophores. During his studies the type strain of *Ceratosporella goidanichhii* failed to produce conidia and the observations were based on the sporulating culture of *Endophragmia alternata* and the descriptions given by Rambelli (1958) and Ellis (1976). Later this species was transferred to *Repetophragma*, because of the percurrent proliferations of the conidiophores and the presence of euseptate conidia (Wu & Zhuang 2005). In our study the ex-type strain of *Ceratosporella goidanichii* (CBS 136.58) remains sterile and the new combination in *Sympodiella* is mainly based on the phylogenetic analysis.

Sympodiella quercina Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB829351. Figs 58–60.

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

Mycelium consisting of pale to medium brown, smooth, septate, branched, 2.5–3 µm diam hyphae. Sympodiella-like morph. *Conidiophores* solitary, erect, medium brown, smooth, subcylindrical, straight to flexuous, unbranched, septate, 48.5–68 × 3–5 µm. *Conidiogenous cells* terminal, subcylindrical, medium brown, polyblastic, sympodial, 15–20 × 3–3.5 µm. *Conidia* septate, subcylindrical to acicular, tapering, apex obtuse, base truncate, smooth, hyaline, 30–74 × 2–3.5 µm, apex 1.5–2.5 µm wide. Repetophragma-like synasexual morph. *Conidiophores* solitary, erect, medium brown, smooth, subcylindrical, straight to geniculous-sinuous, unbranched, 2–6-septate, 25–90 × 5–6 µm. *Conidiogenous cells* terminal, subcylindrical, medium brown, 6–17 × 5–6 µm, proliferating percurrently. *Conidia* solitary, subcylindrical, apex obtuse, base truncate, medium brown (end cells frequently subhyaline), smooth, guttulate, straight, (4–)6-septate, (40–)47–55(–65) × (5–)6–6.5(–7) um; hilum unthickened, not darkened, 5–6.5 µm diam, with minute marginal frill.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 12 mm diam after 2 wk at 25 °C. On MEA surface umber, reverse chestnut; on PDA surface umber, reverse iron-grey; on OA surface umber.

Typus: **Germany**, near Berlin, in *Pinus sylvestris* forest, on fallen leaf of *Quercus robur* (*Fagaceae*), 19 Aprs. 2017, *H. Schreiber & R.K. Schumacher*, HPC 2106 = RKS 94 (**holotype** CBS H-23829, culture ex-type CPC 33903 = CBS 145028).

Additional material examined: **UK**, Lancashire, on leaf litter of *Betula* sp., 17 Jan. 1968, deposited by *J.C. Frankland*, CBS 987.70.

Notes: In natural substrate this species has repetophragma-like conidiophores up to 210 µm long with percurrent proliferations and conidia measuring 32–44 × 5–7 µm, with or without a dark cap in the apex of the conidia. Next to repetophragma-like conidiophores, *Sympodiella* conidiophores were also found, and since the close phylogenetic relationship with *Sympodiella acicola* we also described the synasexual morph. In this species the *Sympodiella* type of conidiophores produce fragile hyaline phragmoconidia similar to those observed in *Cylindrosympodium* (Kendrick & Castañeda 1990) and some species of *Subulispora* (Sutton 1973, Kirk 1985). Additionally, the superficial network of darkly pigmented hyphae described in *S. acicola* (Kendrick 1985) was also observed in *S. quercina*.

An additional strain (CBS 987.70) previously identified as *Repetophragma goidanichii* was phylogenetically related with *S. quercina*. However, the conidial sizes observed in this culture are below the range observed in CPC 33903, and also have more septa (35–50 × 4–7 µm, 6–7(–9)-septate), the dark apical cap was only evident in some of the younger conidia, and conidiophores were not well-developed. The synasexual morph was not observed in any of the cultures of *S. quercina*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Sporidesmium goidanichii* (GenBank MH860019.1; Identities = 486/489 (99 %), 2 gaps (0 %)), *Septonema crispulum* (GenBank MH862607.1; Identities = 402/445 (90 %), 8 gaps (1 %)), and *Sympodiella acicola* (GenBank KY853468.1; Identities = 432/488 (89 %), 18 gaps (3 %)). Closest hits using the **LSU** sequence are *Repetophragma goidanichii* (GenBank DQ408574.1; Identities = 836/848 (99 %), 1 gap (0 %)), *Sympodiella acicola* (GenBank KY853530.1; Identities = 844/858 (98 %), no gaps), and *Cylindrosympodium lauri* (GenBank EU035414.1; Identities = 836/859 (97 %), 2 gaps (0 %)).

Sympoventuria regnans Crous, *Persoonia* **39**: 425. 2017. Fig. 61.

Mycelium consisting of medium brown, smooth, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells, or a supporting cell. *Conidiogenous cells* arising directly from hyphae, subcylindrical, medium brown, smooth, 7–18 × 3(–4) µm, with 1(–3) terminal, flat-tipped loci, 1(–1.5) µm diam, thickened and darkened. *Conidia* pale brown, guttulate, smooth-walled, 0(–1)-septate, fusoid-ellipsoid, occurring in chiefly unbranched acropetal chains of up to 10, (10–)13–16(–18) × (2–)3 µm; loci thickened and somewhat darkened, 1(–1.5) µm diam.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA surface isabelline, reverse umber; on PDA surface umber, reverse dark brick; on OA surface umber.

Material examined: **Australia**, New South Wales, 31.366346S 151.580038E, Ngulin Nature Reserve, Hell Hole Forest Rd, on leaves of *Eucalyptus pauciflora* (*Myrtaceae*), 13 Jul. 2016, *A.J. Carnegie*, HPC 1454, culture CPC 31820 = CBS 144605.

Notes: *Sympoventuria* was introduced for a genus of ascomycetes with sympodiella-like asexual morphs occurring on *Eucalyptus* leaf litter in South Africa (Crous *et al*. 2007). *Sympoventuria regnans* is described from leaves of *E. regnans* collected in La Trobe State Forest, Victoria, Australia (Crous *et al.* 2017), and has a similar morphology to the present collection.

Fig. 58. *Sympodiella quercina* (HPC 2106 - *Quercus* leaf). **A–G.** Repetophragma-like synasexual morph. **A–C, E, F.** Conidiophores and conidia. **D.** Network of brown hyphae on the substrate. **G.** Conidia. **H.** Repetophragma-like and *Sympodiella* conidiophores and conidia. **I–M**. *Sympodiella* asexual morph. **I–L.** Conidiophores and conidia. **M.** Conidia. Scale bars D, E, H, I = 20 µm, others = 10 µm.

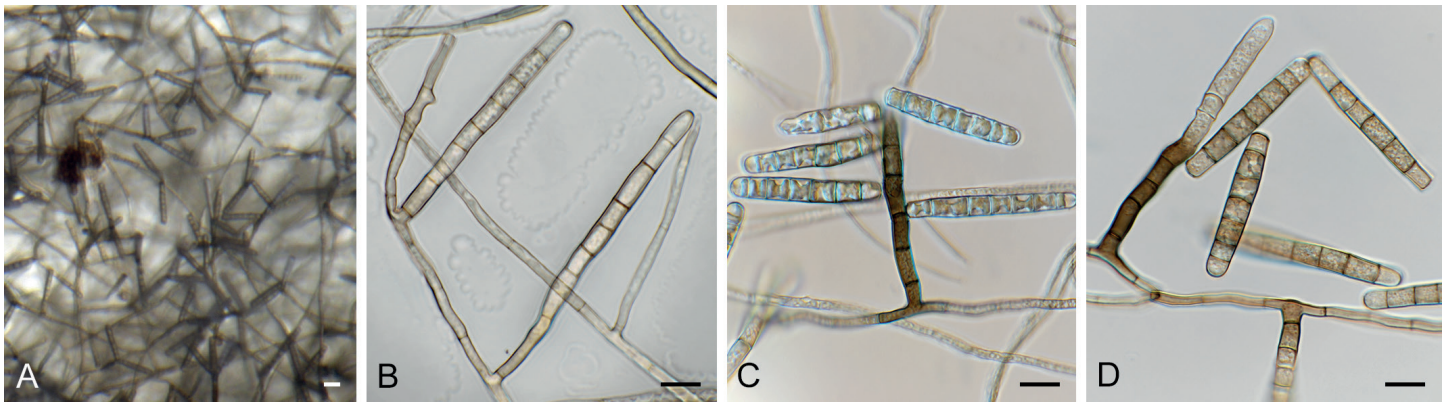

Fig. 59. *Sympodiella quercina* (CPC 33903). **A.** Colony on SNA. **B–D.** Conidiophores giving rise to conidia. Scale bars: A = 20 μm, B–D = 10 μm.

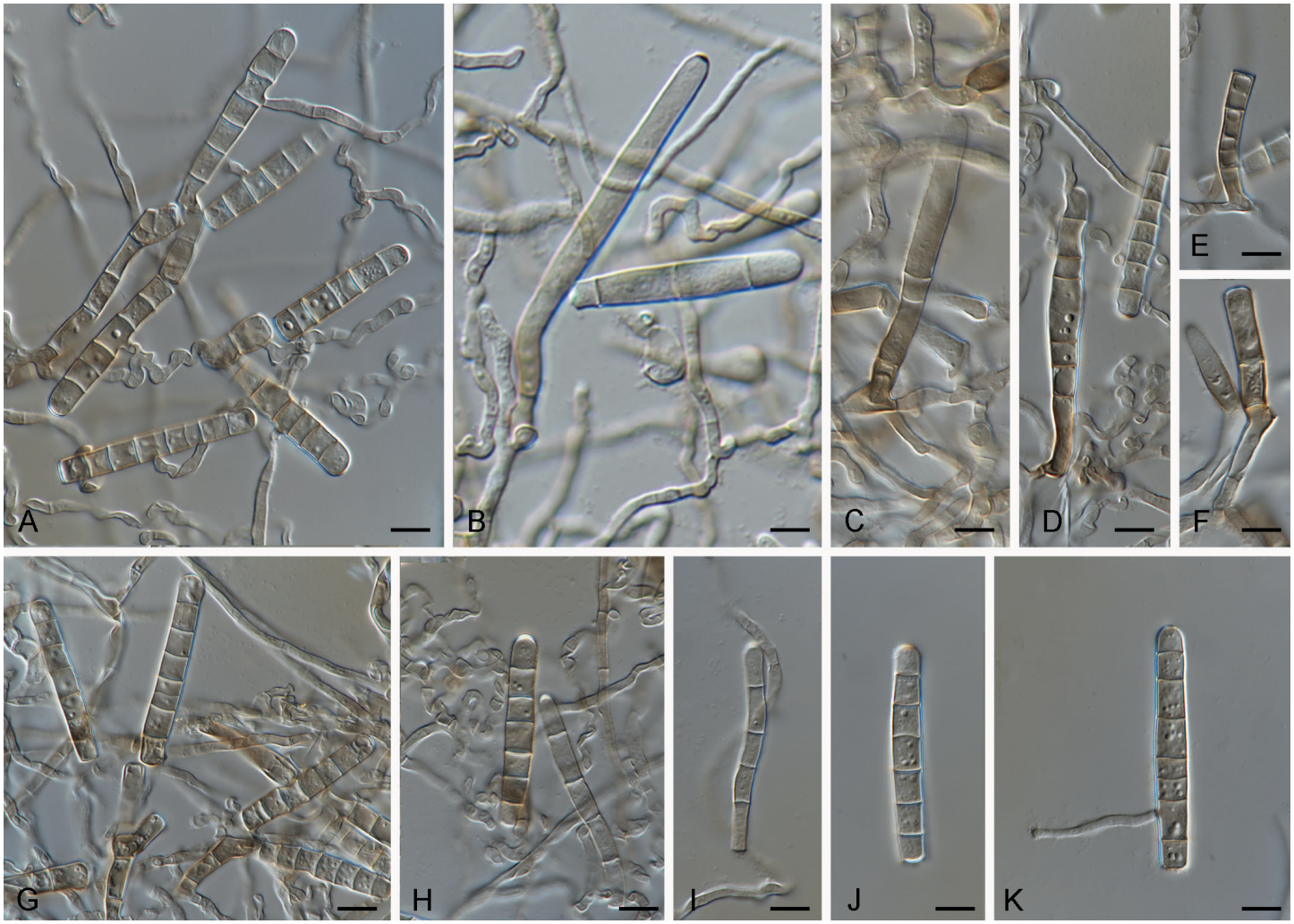

Fig. 60. *Sympodiella quercina* (CBS 987.70 on SNA). **A–D.** Conidiophores giving rise to conidia. **E, F.** Conidiogenous cells. **G–K.** Conidia. Scale bars = 10 μm.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Sympoventuria regnans* (GenBank MG386066.1; Identities = 568/569 (99 %), no gaps), *Fusicladium eucalypti* (GenBank HQ599600.1; Identities = 548/573 (96 %), 5 gaps (0 %)), and *Fusicladium eucalypticola* (GenBank NR_145402.1; Identities = 516/538 (96 %), 4 gaps (0 %)). Closest hits using the **LSU** sequence are *Sympoventuria regnans* (GenBank NG_058523.1; Identities = 852/852 (100 %), no gaps), *Fusicladium eucalypticola* (GenBank KX228329.1; Identities = 861/872 (99 %), 1 gap (0 %)), and *Fusicladium eucalypti* (GenBank HQ599601.1; Identities = 863/877 (98 %), 3 gaps (0 %)). No ***tef1*** sequences of *Sympoventuria* are available for comparison on GenBank; distant hits include *Pallidocercospora crystallina* (GenBank MF135483.1; Identities = 189/201 (94 %), 3 gaps (1 %)), *Parapallidocercospora thailandica* (as *Mycosphaerella thailandica*, GenBank AY840477.2; Identities = 176/184 (96 %), no gaps), and *Phyllosticta ericarum* (GenBank KR025451.1; Identities = 179/189 (95 %), no gaps). Distant hits using the ***tub2*** sequence had highest similarity to *Sympoventuria regnans* (GenBank MG386169.1; Identities = 328/373 (88 %), 9 gaps (2 %)), *Didymocyrtis brachylaenae*

Fig. 61. *Sympoventuria regnans* (CPC 31820). **A–C.** Conidiophores. **D.** Conidia. Scale bars = 10 µm.

(GenBank MH327896.1; Identities = 837/946 (88 %), 12 gaps (1 %)), and *Phoma nigrificans* (GenBank AY749030.1; Identities = 836/945 (88 %), 11 gaps (1 %)).

Tubakia suttoniana U. Braun & Crous, *Fungal Syst. Evol.* **1**: 90. 2018. Fig. 62.

On SNA: *Pycnothyria* not developing. Central columella developing with aggregated brown, smooth conidiophores. *Conidiophores* tapering toward apex, branched or not, 0–2-septate, 10–30 × 2.5–3 µm. *Conidiogenous cells* medium brown, smooth, subcylindrical with apical taper, phialidic, at times with percurrent proliferations, 10–15 × 2.5–3 µm. *Conidia* aseptate, solitary, pale brown, smooth, granular, guttulate, ellipsoid, with minute truncate hilum, 1–2 µm diam, (11–)13–14(–15) × 7(–8) µm.

Culture characteristics: Colonies erumpent, spreading in concentric circles, with moderate to profuse aerial mycelium, covering the dish after 2 wk at 25 °C. On MEA surface zones of pale olivaceous grey to olivaceous grey, reverse olivaceous grey; on PDA surface zones of olivaceous grey to smoke grey, reverse olivaceous grey; on OA surface olivaceous grey.

Material examined: **New Zealand**, Auckland, Takanini, Marango PK way, on leaves of *Quercus* sp. (*Fagaceae*), 16 May 2016, *R. Thangavel*, CBS H-23808, culture CPC 32745 = T16_01981A = CBS 144591.

Notes: *Tubakia suttoniana* is known from branch and stem cankers on *Quercus cerris* in New Zealand (CBS 229.77; Braun *et al*. 2018), and CPC 32745 represents an additional record from that country.

Based on a megablast search of NCBI's GenBank nucleotide database, the **ITS** sequence was identical to *Tubakia suttoniana* (GenBank MG591919.1; Identities = 605/605 (100 %)); other closest hits included *Tubakia californica* (GenBank MG591847.1; Identities = 602/603 (99 %), 1 gap (0 %)), and *Tubakia melnikiana* (GenBank MG591893.1; Identities = 600/601 (99 %), 1 gap (0 %)). Closest hits using the **LSU** sequence are *Tubakia japonica* (GenBank MG591979.1; Identities = 882/882 (100 %), no gaps), *Tubakia seoraksanensis* (GenBank KP260501.1; Identities = 845/845 (100 %), no gaps), and *Tubakia californica* (GenBank MG591940.1; Identities = 844/844 (100 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Tubakia suttoniana* (GenBank MG976493.1; Identities = 940/941 (99 %), no gaps), *Tubakia californica* (GenBank MG976452.1; Identities = 933/934 (99 %), no gaps), and *Tubakia japonica* (GenBank MG976469.1; Identities = 991/993 (99 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Tubakia suttoniana* (GenBank MG592108.1; Identities = 467/467 (100 %), no gaps), *Tubakia* sp. 1 (GenBank MG592101.1; Identities = 550/562 (98 %), no gaps), and *Tubakia japonica* (GenBank MG592075.1; Identities = 550/562 (98 %), no gaps). Closest hits using the ***tub2*** sequence had highest similarity to *Tubakia suttoniana* (GenBank MG592201.1; Identities = 505/507 (99 %), 1 gap (0 %)), *Tubakia seoraksanensis* (GenBank MG592190.1; Identities = 487/492 (99 %), 1 gap (0 %)), and

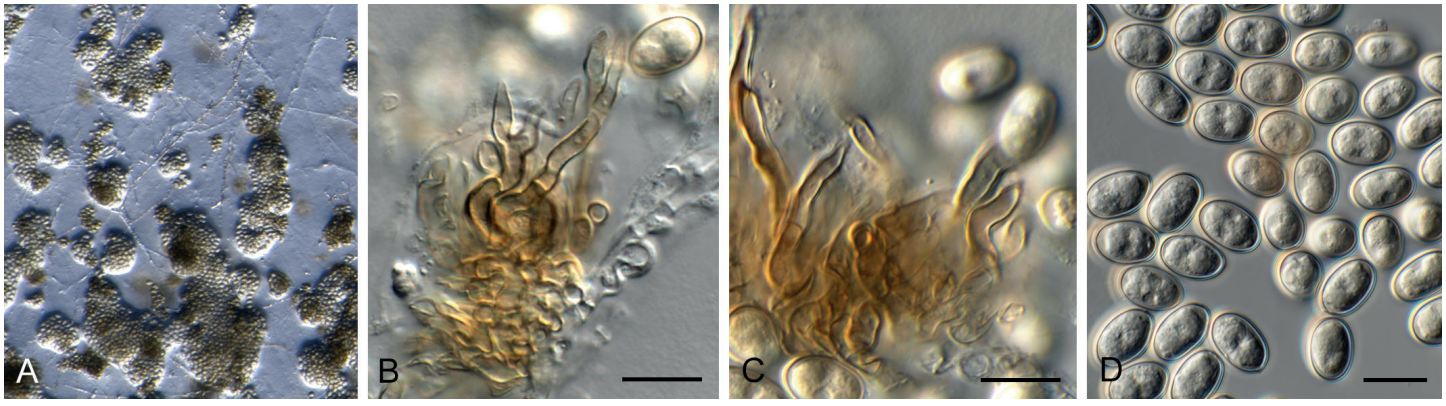

Fig. 62. *Tubakia suttoniana* (CPC 32745). **A.** Conidiomatal initials developing on SNA. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars = 10 µm.

Tubakia japonica (GenBank MG592165.1; Identities = 508/515 (99 %), 1 gap (0 %)).

Turquoiseomycetales Crous, ***ord. nov.*** MycoBank MB829363.

Turquoiseomycetaceae Crous, ***fam. nov.*** MycoBank MB829461.

Turquoiseomyces Crous, ***gen. nov.*** MycoBank MB829363.

Etymology: Name refers to the characteristic green-blue discolouration of the host tissue surrounding conidiomata.

Conidiomata solitary to aggregated, dark brown, globose, pycnidial, opening by irregular rupture; wall of 6–8 layers of brown *textura intricata. Conidiophores* lining the inner cavity, extensively branched, septate, tightly aggregated, pale green-brown, finely roughened, subcylindrical. *Conidiogenous cells* ampulliform to subcylindrical, pale green-brown, finely roughened, terminal and intercalary, proliferating percurrently. *Conidia* solitary, subcylindrical, guttulate, smooth-walled, medianly 1-septate, apex swollen with mucoid cap, base somewhat tapered, truncate, reflective.

Type species: *Turquoiseomyces eucalypti* Crous.

Turquoiseomyces eucalypti Crous, ***sp. nov.*** MycoBank MB829364. Fig. 63.

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

Conidiomata solitary to aggregated, dark brown, globose, pycnidial, opening by irregular rupture, 250–350 µm diam; wall of 6–8 layers of brown *textura intricata. Conidiophores* lining the inner cavity, extensively branched, septate, tightly aggregated, 10–25 × 3–4 µm, pale green-brown, finely roughened, subcylindrical. *Conidiogenous cells* ampulliform to subcylindrical, pale green-brown, finely roughened, terminal and intercalary, 5–10 × 3–4 µm, proliferating percurrently. *Conidia* solitary, subcylindrical, guttulate, smooth-walled, medianly 1-septate, apex swollen with mucoid cap, base somewhat tapered, truncate, reflective, 1.5–2 µm diam, straight to flexuous, (50–) 55–60(–80) × 3(–4) µm.

Culture characteristics: Colonies erumpent, spreading, surface folded, with sparse aerial mycelium and smooth, lobate margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA surface greenish grey, reverse smoke grey; on PDA surface olivaceous grey, reverse smoke grey; on OA surface iron-grey in centre, buff in outer region.

Typus: **Australia** New South Wales, Cobb Highway, on leaves of *Eucalyptus leptophylla* (*Myrtaceae*), Aug. 2017, *B.A. Summerell*, HPC 2220 (**holotype** CBS H-23834, culture ex-type CPC 34399 = CBS 145126).

Notes: This very obvious fungus was first seen on leaves where conidia were surrounded by tissue with a green-blue discolouration, which was different from the normal foliicolous coelomycetes on *Eucalyptus* that generally have structures with shades of brown to black. In culture, it again produced greenish grey colonies on MEA. The present collection is not known from DNA data available in GenBank, and is also distinct morphologically, representing a distinct family and order in *Lecanoromycetes*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Lecanora subcarnea* (GenBank AY541267.1; Identities = 313/374 (84 %), 25 gaps (6 %)), *Pseudogymnoascus pannorum* var. *pannorum* (GenBank MH866140.1; Identities = 313/374 (84 %), 27 gaps (7 %)), and *Ciliciopodium hyalinum* (GenBank KM231857.1; Identities = 313/374 (84 %), 27 gaps (7 %)). Closest hits using the **LSU** sequence are *Umbilicaria torrefacta* (GenBank JQ740001.1; Identities = 818/886 (92 %), 5 gaps (0 %)), *Umbilicaria muehlenbergii* (GenBank JQ739997.1; Identities = 814/886 (92 %), 4 gaps (0 %)), and *Acarospora anomala* (GenBank LN810758.1; Identities = 813/885 (92 %), 3 gaps (0 %)). No significant hits were obtained when the ***tub2*** sequence was used in blastn and megablast searches.

Typhicola Crous, ***gen. nov.*** MycoBank MB829599.

Etymology: Name refers to the genus *Typha* on which it was collected.

Ascomata gregarious along leaf veins, immersed, globose with central ostiole, somewhat papillate to erumpent, black,

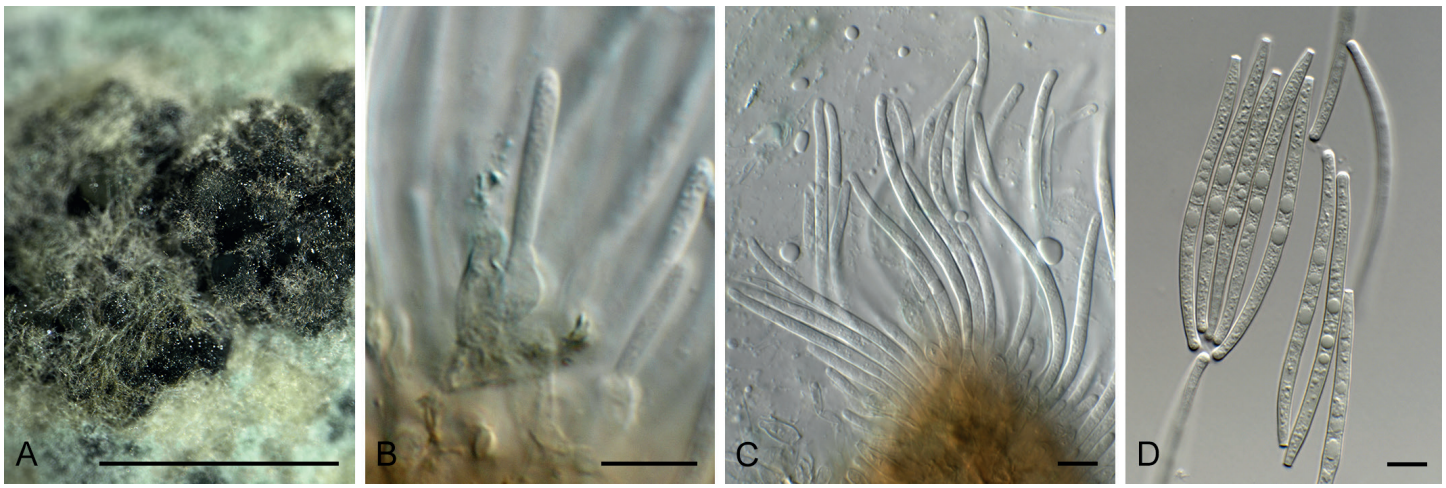

Fig. 63. *Turquoiseomyces eucalypti* (CPC 34399). **A.** Conidiomata in culture on OA (note colour). **B, C.** Conidiogenous cells giving rise to conidia. **D.** Conidia. Scale bars: A = 300 µm, B–D = 10 µm.

soft. *Pseudoparaphyses* numerous, hyaline, smooth, branched with anastomoses, hyphae-like. *Asci* 8-spored, bitunicate, fissitunicate, subcylindrical, with well-developed ocular chamber, thick-walled, short papillate. *Ascospores* ellipsoid, septate, straight to slightly curved, end cells conically rounded, brown, thick-walled, prominently constricted at thick septa, with mucilaginous sheath.

Type species: *Typhicola typharum* (Desm.) Crous.

Typhicola typharum (Desm.) Crous, ***comb. nov.*** MycoBank MB829600. Fig. 64.
Basionym: *Sphaeria scirpicola* var. *typharum* Desm., *Pl. cryptog. Fr,* ed. 2, nr. 1428. 1848.
Synonym: *Juncaceicola typharum* (Desm.) Tennakoon *et al.*, *Cryptog. Mycol.* **37**: 151. 2016.

Ascomata on dead leaves, gregarious along leaf veins, immersed, globose with central ostiole, somewhat papillate to erumpent, black, soft, 100–150 µm diam. *Pseudoparaphyses* numerous, hyaline, smooth, branched with anastomoses, hyphae-like, 2–3 µm diam. *Asci* 8-spored, bitunicate, fissitunicate, subcylindrical, with well-developed ocular chamber, 2 µm diam, thick-walled, short papillate, 80–100 × 20–25 µm. *Ascospores* ellipsoid, 3-septate, with central pore in septum, widest in second cell from apex, straight to slightly curved, end cells conically rounded, golden brown, thick-walled (< 0.5 µm), prominently constricted at thick septa, exospore warty, endospore smooth, finely guttulate, with mucilaginous sheath (up to 3 µm diam), covering entire ascospore (when mounted in water), (23–)27–29(–31) × (8–)9–10(–11) µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and feathery, lobate margin, reaching 45 mm diam after 2 wk at 25 °C. On MEA and PDA surface and reverse olivaceous grey; on OA surface iron-grey.

Typus: **France**, on leaves of *Typha* sp. (*Typhaceae*), *Desm.*, exsiccata "Plantes Cryptogames de France, ed. 2: no. 1428 (1848)" (**lectotype** designated here in PC, MBT385534). **Germany**, near Berlin, leaf of *Typha* sp. (*Typhaceae*), 1 Apr. 2017, *R.K. Schumacher*, HPC 2025 = RKS 84 (**epitype** designated here CBS H-23819, MBT385272, culture ex-epitype CPC 33271 = CBS 145043).

Notes: This fungus occurs commonly in Europe, sporulates well in culture, but produced only the sexual morph in the present study. Tennakoon *et al*. (2016) introduced the genus *Juncaceicola* and the combination *J. typharum*, but could not locate any type material of *Sphaeria scirpicola* var. *typharum*, and based their new combination on CBS 296.54 (on *Nardus stricta*, Switzerland), which probably represents an undescribed species of *Juncaceicola.* Although phylogenetically distinct, there is morphologically little to choose between *Typhicola* and *Juncaceicola*, and the two genera are best distinguished based on DNA data.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Juncaceicola typharum* (as *Leptosphaeria typharum*, GenBank AF439465.1; Identities = 507/518 (98 %), 1 gap (0 %)), *Pleospora typhicola* (GenBank KF636768.1; Identities = 453/486 (93 %), 12 gaps (2 %)), and *Neocamarosporium goegapense* (GenBank KJ869163.1; Identities = 519/587 (88 %), 26 gaps (4 %)). Closest hits using the **LSU** sequence are *Pleospora typhicola* (GenBank KF636774.1; Identities = 848/862 (98 %), 2 gaps (0 %)), *Camarosporidiella robiniicola* (GenBank MF434266.1; Identities = 832/849 (98 %), no gaps), *Camarosporium laburnicola* (GenBank KY497779.1; Identities = 845/863 (98 %), 1 gap

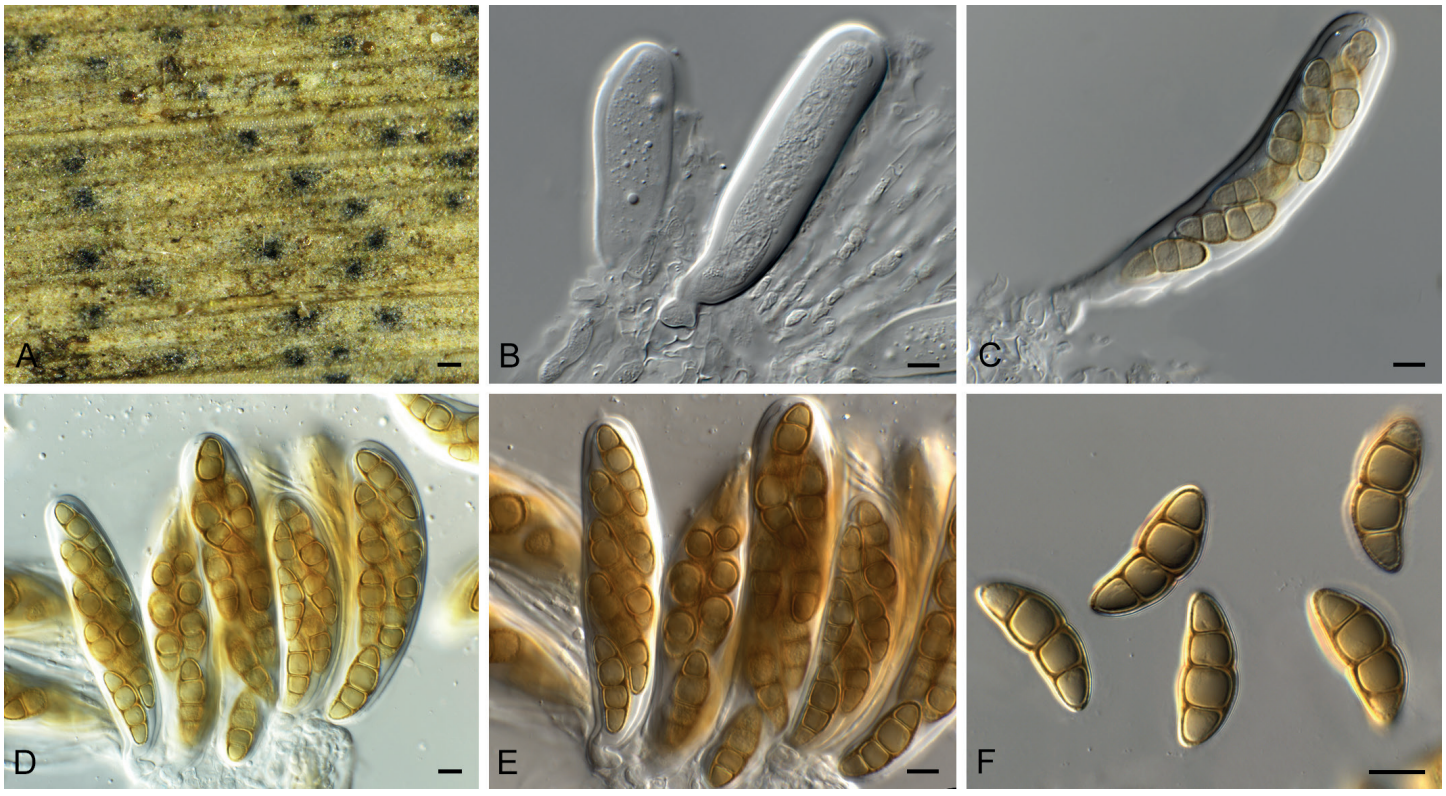

Fig. 64. *Typhicola typharum* (CPC 33271). **A.** Ascomata on host tissue. **B–E.** Asci. **F.** Ascospores. Scale bars: A = 150 µm, B–F = 10 µm.

(0 %)), and *Juncaceicola typharum* (GenBank MH868883.1; Identities = 834/863 (97 %), 3 gaps (0 %)). Distant hits using the ***rpb2*** sequence had highest similarity to *Pleospora incompta* (GenBank KC584504.1; Identities = 740/867 (85 %), 4 gaps (0 %)), *Comoclathris compressa* (GenBank KC584498.1; Identities = 736/867 (85 %), 4 gaps (0 %)), and *Pleospora typhicola* (GenBank KC584505.1; Identities = 733/865 (85 %), no gaps). Distant hits using the ***tef1*** sequence had highest similarity to *Juncaceicola typharum* (as *Phaeosphaeria typharum*, GenBank KF253148.1; Identities = 123/131 (94 %), no gaps), *Dendryphion penicillatum* (GenBank AY375371.1; Identities = 261/281 (93 %), 6 gaps (2 %)), *Alternaria ventricosa* (GenBank KY352501.1; Identities = 272/301 (90 %), 5 gaps (1 %)), and *Lasiodiplodia iranensis* (GenBank KU997110.1; Identities = 266/295 (90 %), 4 gaps (1 %)). Distant hits using the ***tub2*** sequence had highest similarity to *Alternaria solani* (GenBank CP022033.1; Identities = 916/981 (93 %), 9 gaps (0 %)), *Alternaria alternata* (GenBank KJ396337.1; Identities = 905/977 (93 %), 7 gaps (0 %)), and *Alternaria cucumerina* (GenBank HQ413318.1; Identities = 903/977 (92 %), 7 gaps (0 %)).

Wojnowiciella dactylidis (Wijayaw. *et al.*) Hern.-Restr. & Crous, *Sydowia* **68**: 221. 2016. Fig. 65.
Basionym: *Wojnowicia dactylidis* Wijayaw. *et al*., *Fungal Diversity* **72**: 144. 2015.

Conidiomata erumpent, pycnidial, solitary, globose, papillate, 200–300 µm diam, with 1–2 ostioles; wall of 3–6 layers of brown *textura angularis. Microconidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, doliiform to ampulliform, 4–5 × 3–4 µm, phialidic, with periclinal thickening. *Microconidia* solitary, hyaline, smooth, guttulate, aseptate, subcylindrical, apex obtuse, base truncate, (3–)4(–5) × 2 µm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface isabelline, reverse isabelline to hazel, with zones of cinnamon.

Material examined: **New Zealand**, Auckland, Grey Lynn, Grey Lynn park, on *Dypsis* sp. (*Arecaceae*), 5 Oct. 2016, *R. Thangavel*, CBS H-23807, culture T16_03296B = CPC 32741 = CBS 145077.

Notes: *Wojnowiciella dactylidis* was described from *Dactylis glomerata* collected in Italy, and this is the first record from New Zealand. Unfortunately, only the microconidial morph was observed in culture.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Wojnowiciella dactylidis* (GenBank LT990660.1; Identities = 572/572 (100 %), no gaps), *Wojnowiciella cissampeli* (GenBank NR_155972.1; Identities = 568/579 (98 %), 6 gaps (1 %)), and *Wojnowicia rosicola* (GenBank MG828979.1; Identities = 554/568 (98 %), 8 gaps (1 %)). Closest hits using the **LSU** sequence are *Wojnowicia rosicola* (GenBank MG829091.1; Identities = 846/847 (99 %), no gaps), *Wojnowicia italica* (GenBank KX430001.1; Identities = 846/847 (99 %), no gaps), and *Wojnowiciella dactylidis* (GenBank LT990632.1; Identities = 844/845 (99 %), 1 gap (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Wojnowicia italica* (GenBank KX430003.1; Identities = 438/440 (99 %), no gaps), *Wojnowiciella dactylidis* (GenBank LT990613.1; Identities = 423/425 (99 %), no gaps), and *Wojnowiciella cissampeli* (GenBank LT990616.1; Identities = 463/469 (99 %), no gaps). No ***tub2*** sequences of *Wojnowiciella* or *Wojnowicia* are available for comparison on GenBank; distant hits using the *tub2* sequence had highest similarity to *Fenestella fenestrata* (GenBank MF795893.1; Identities = 247/280 (88 %), 7 gaps (2 %)), *Didymocyrtis banksiae* (GenBank KY979923.1; Identities = 251/284 (88 %), 18 gaps (6 %)), and *Didymocyrtis foliaceiphila* (as *Diederichomyces foliaceiphila*, GenBank KP170700.1; Identities = 246/280 (88 %), 8 gaps (2 %)).

Xenodevriesiaceae Crous, ***fam. nov.*** MycoBank MB829462.

Xenodevriesia Crous, ***gen. nov.*** MycoBank MB829365.

Etymology: Name reflects the fact that this is similar to, but distinct from the genus *Devriesia*.

Mycelium consisting of medium brown, smooth, septate, branched hyphae. *Conidiophores* dimorphic. *Microconidiophores* reduced to conidiogenous cells on hyphae, erect, cylindrical, medium brown, smooth with truncate ends, proliferating sympodially. *Macroconidiophores* erect, cylindrical, straight to geniculate-sinuous, medium brown, smooth, unbranched or branched above, septate. *Conidiogenous cells* terminal or lateral on branched conidiophores, medium brown, smooth, cylindrical, proliferating sympodially; loci truncate, inconspicuous, somewhat darkened, not refractive. *Conidia* medium brown, smooth, guttulate, subcylindrical to narrowly obclavate, apex obtuse to truncate, base truncate, occurring in branched chains, septate; hila inconspicuous to somewhat darkened and thickened, not refractive.

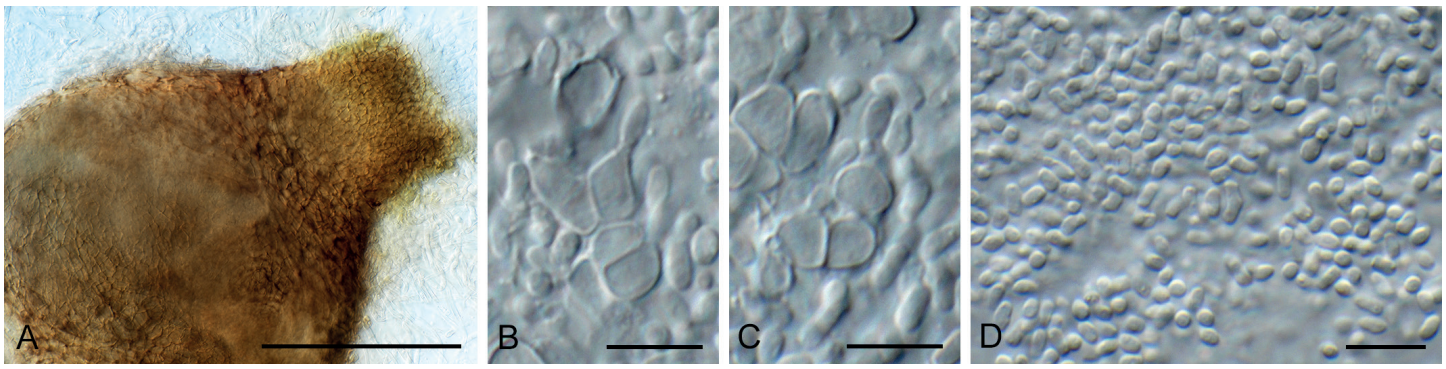

Fig. 65. *Wojnowiciella dactylidis* (CPC 32741). **A.** Conidioma on SNA. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars: A = 150 µm, B–D = 10 µm.

Type species: *Xenodevriesia strelitziicola* (Arzanlou & Crous) Crous.

Xenodevriesia strelitziicola (Arzanlou & Crous) Crous, ***comb. nov.*** MycoBank MB829366.
Basionym: *Devriesia strelitziicola* Arzanlou & Crous, *Stud. Mycol.* **64**: 38. 2009.

Notes: *Devriesia strelitziicola* was introduced by Crous *et al.* (2009b) for a fungus that was devriesia-like and pseudocercospora-like in morphology, but which proved to be phylogenetically distinct from both genera. It is morphologically distinct from *Devriesia* in that it does not produce chlamydospores, and from *Peudocercospora* in that the conidial hila are somewhat darkened and thickened. Phylogenetically, it is also clearly distinct, and represents a new family in *Capnodiales*.

Zasmidium hakeicola Crous, ***sp. nov.*** MycoBank MB829367. Fig. 66.

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

Mycelium consisting of smooth, pale brown, septate, branched, 2–2.5 µm diam hyphae. *Conidiophores* solitary, erect, geniculous-flexuous, branched or not, subcylindrical, medium brown, finely verruculose, thick-walled, guttulate, multiseptate, 100–200 × 3–5 µm, arising from superficial hyphae or as a few cells of a weakly developed stroma. *Conidiogenous cells* terminal, at times intercalary, subcylindrical, medium brown, finely verruculose, proliferating sympodially, 25–50 × 5–7 µm; loci prominently thickened and darkened, refractive, 2.5–3 µm diam. *Conidia* solitary, obclavate, apex obtuse, base obconically truncate, verruculose, medium brown, straight, (40–)47–55(–65) × 8(–9) µm; hilum thickened, darkened and refractive, 3–4 µm diam; conidia at times bifurcate, 3(–5)-septate.

Culture characteristics: Colonies erumpent, spreading, with sparse to moderate aerial mycelium and feathery margin, reaching 4 mm diam after 2 wk at 25 °C. On MEA and PDA surface pale olivaceous grey to olivaceous grey, reverse olivaceous grey; on OA surface pale olivaceous grey to olivaceous grey.

Typus: **Australia**, New South Wales, Australian Botanical Garden Mount Annan, on leaves of *Hakea corymbosa* (*Proteaceae*), 25 Nov. 2016, *P.W. Crous*, HPC 1722 (**holotype** CBS H-23806, culture ex-type CPC 32703 = CBS 144590).

Notes: A morphologically similar species, *Zasmidium grevilleae* (conidia 3–7(–12)-septate, (30–)50–65(–80) × (5–)6–7 µm), was described from leaves of *Grevillea decurrens* collected in Australia (Crous *et al*. 2009a, Videira *et al.* 2017). The present

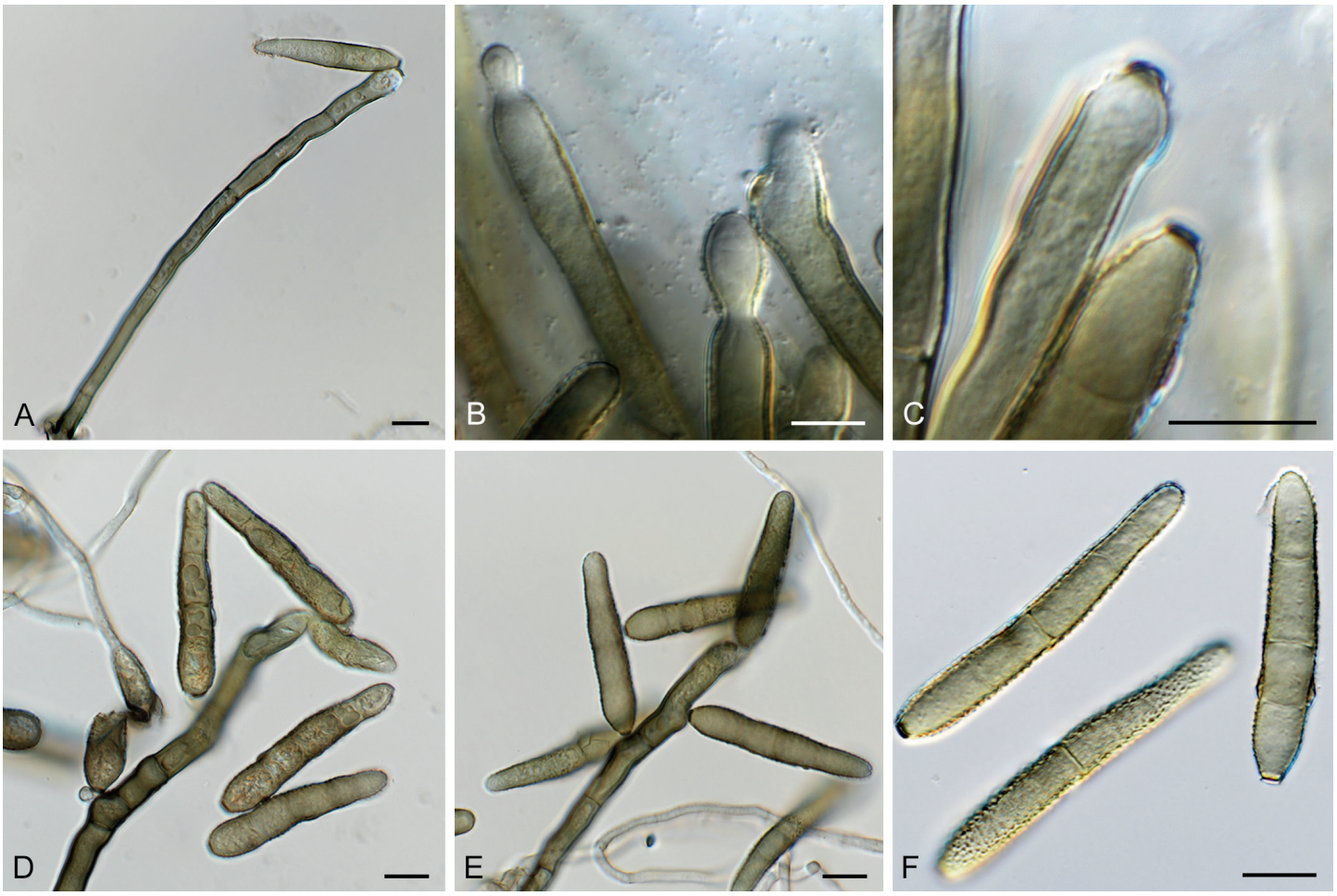

Fig. 66. *Zasmidium hakeicola* (CPC 32703). **A.** Conidiophore giving rise to conidium. **B–E.** Conidiogenous cells and conidial loci. **F.** Conidia. Scale bars = 10 µm.

collection from *Hakea* differs from that species in having shorter, wider conidia, with fewer septa.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Zasmidium grevilleae* (GenBank NR_156522.1; Identities = 533/538 (99 %), 1 gap (0 %)), *Zasmidium proteacearum* (as *Verrucisporota proteacearum*, GenBank FJ839635.1; Identities = 513/539 (95 %), 23 gaps (4 %)), and *Zasmidium velutinum* (as *Periconiella velutina*, GenBank EU041781.1; Identities = 492/545 (90 %), 16 gaps (2 %)). Closest hits using the **LSU** sequence are *Zasmidium proteacearum* (as *Verrucisporota proteacearum*, GenBank FJ839671.2; Identities = 858/860 (99 %), no gaps), *Zasmidium grevilleae* (GenBank MH874876.1; Identities = 857/860 (99%), no gaps), and *Zasmidium biverticillatum* (as *Ramichloridium biverticillatum*, GenBank EU041853.1; Identities = 834/846 (99 %), 2 gaps (0 %)). Closest hits using the ***actA*** sequence had highest similarity to *Zasmidium proteacearum* (as *Verrucisporota proteacearum*, GenBank KF903478.1; Identities = 433/439 (99 %), 1 gap (0 %)), *Zasmidium citri-griseum* (GenBank KF903676.1; Identities = 392/430 (91 %), 2 gaps (0 %)), and *Parapallidocercospora thailandica* (as *Mycosphaerella thailandica*, GenBank EU514333.1; Identities = 373/410 (91 %), 6 gaps (1 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Zasmidium proteacearum* (GenBank MF951721.1; Identities = 677/683 (99 %), no gaps), *Zasmidium grevilleae* (GenBank MF951705.1; Identities = 662/668 (99 %), no gaps), and *Zasmidium musicola* (GenBank MF951717.1; Identities = 663/761 (87 %), no gaps). Closest hits using the ***tub2*** sequence had highest similarity to *Zasmidium commune* (GenBank KY979928.1; Identities = 721/787 (92 %), no gaps), *Pseudocercospora fijiensis* (GenBank XM_007921924.1; Identities = 702/789 (89 %), no gaps), and *Ramularia collo-cygni* (GenBank JN003648.1; Identities = 701/789 (89 %), no gaps).

Zygosporium pseudogibbum Crous, *Fungal Syst. Evol.* **1**: 213. 2018. Fig. 67.

Conidiophores solitary, erect, consisting of 1–2 pale brown basal cells forming a stipe, 8–20 × 3–4 µm, giving rise to a curved, dark brown terminal vesicle, 12–15 × 5–7 µm. *Conidiogenous cells* arranged in a whorl of 3–4 on a terminal vesicle, hyaline, smooth, reniform, 5–6 × 3.5–4 µm. *Vesicle* with single apical cell, 4–6 × 3–4 µm, pale brown, cylindrical, with obtuse apex and prominent collarette. *Conidia* solitary, globose, verruculose, faintly olivaceous, (5–)5.5(–6) µm diam.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium, folded surface and even, smooth margin, reaching 25 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white, reverse pale luteous.

Material examined: **Australia**, New South Wales, Australian Botanical Garden Mount Annan, on leaves of *Macrozamia miquelii* (*Zamiaceae*), 25 Nov. 2016, *P.W. Crous*, HPC 1734, CBS H-23580, culture CPC 32120 = CBS 144442.

Notes: *Zygosporium pseudogibbum* (on *Eucalyptus* leaves from Malaysia; Crous *et al*. 2018c) is closely related to *Z. gibbum*, a European taxon (reference isolate, FMR 13130 = CBS 137306; leaf litter Canary Islands; Hernández-Restrepo *et al.* 2017). Morphologically these taxa are very similar and they are thus best distinguished based on their DNA sequences.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Zygosporium mycophilum* (GenBank MH856563.1; Identities = 562/565 (99 %), 2 gaps (0 %)), *Zygosporium pseudogibbum* (GenBank NR_159072.1; Identities = 551/554 (99 %), 2 gaps (0 %)), and *Zygosporium masonii* (GenBank MH860771.1; Identities = 527/567 (93 %), 16 gaps (2 %)).

Closest hits using the **LSU** sequence are *Zygosporium pseudogibbum* (GenBank MH107974.1; Identities = 839/840 (99 %), no gaps), *Atrotorquata spartii* (GenBank KP325443.1; Identities = 845/872 (97 %), 2 gaps (0 %)), and *Lopadostoma fagi* (GenBank KC774577.1; Identities = 829/874 (95 %), 4 gaps (0 %)). The ***actA*** sequence had highest similarity to *Zygosporium pseudogibbum* (GenBank MH107989.1; Identities = 526/540 (97 %), no gaps); other distant hits include *Nalanthamala psidii* (GenBank KM231245.1; Identities = 346/369 (94 %), no gaps), *Dactylonectria alcacerensis* (GenBank KM231158.1; Identities = 346/369 (94 %), no gaps), and *Dactylonectria novozelandica* (GenBank KM231157.1; Identities = 346/369 (94 %), no gaps). The ***tub2*** sequence had highest similarity to *Zygosporium pseudogibbum* (GenBank MH108055.1; Identities = 461/475 (97 %), 1 gap (0 %)); other distant hits include *Hypoxylon crocopeplum* (GenBank AY951711.1; Identities = 739/798 (93 %), no gaps), *Hypoxylon calileguense* (GenBank KU604579.1; Identities = 739/799 (92 %), no gaps), and *Dicyma funiculosa* (GenBank KU684134.1; Identities = 830/937 (89 %), 11 gaps (1 %)).

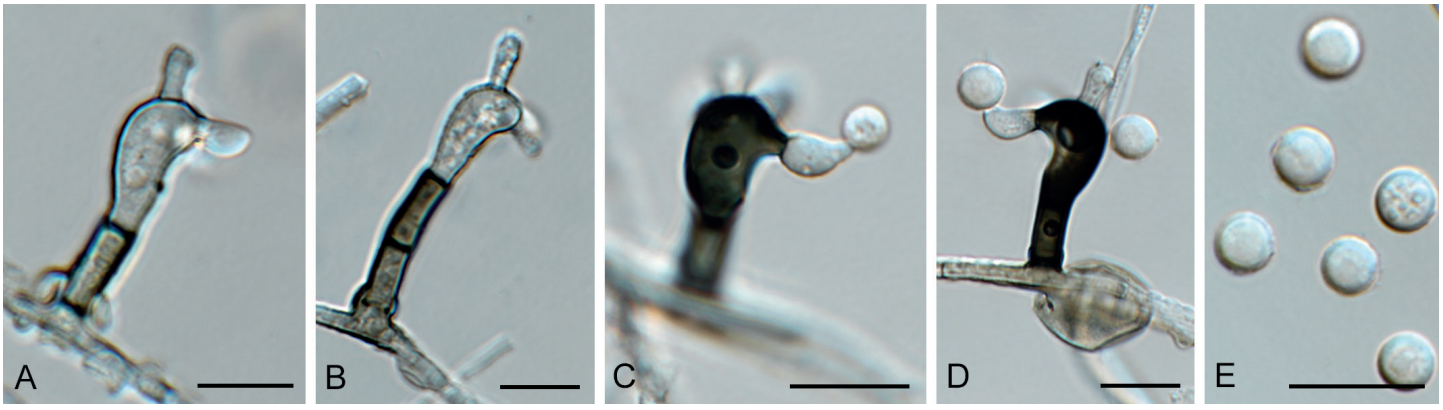

Fig. 67. *Zygosporium pseudogibbum* (CPC 32120). **A–D.** Conidiophores giving rise to conidia. **E.** Conidia. Scale bars = 10 µm.

Addendum: validation of names and typifications

During the course of this study we encountered several names that were invalid based on the International Code of nomenclature for algae, fungi, and plants (see MycoBank and Index Fungorum) due to a variety of reasons. As this has led to problems with new combinations or genera and families subsequently based on these names also being rendered invalid, and thus we decided to validate these names below.

Allelochaeta falcata (B. Sutton) Crous, *Fungal Syst. Evol.* **2**: 288. 2018.
Basionym: *Cryptostictis falcata* B. Sutton, *Mycol. Pap*. **88**: 25. 1963.

Morphological descriptions and illustrations: See Barber *et al*. (2011), Crous *et al.* (2018a).

Typus. **Australia**, Victoria, on *Eucalyptus* sp., 1963, *collector unknown* (**holotype** Herb IMI 59166); New South Wales, Central Tablelands, *ca*. 200 metres WSW of 'Coomber' homestead, on Coomber property, *ca*. 8 km SW of Rylstone, S32°50'04" E149°56'13", alt. 600 ± 10 m, 17 Aug. 2006, *R. Johnstone* & *A.E. Orme*, 734259, on *Eucalyptus alligatrix* (**epitype** designated here CBS H-20744, MBT385261, cultures ex-epitype CPC 13578 = CBS 131117).

Notes: *Allelochaeta* was treated by Crous *et al.* (2018a). Unfortunately, the holotype specimen was incorrectly cited and thus the epitype is consequently invalid. This is corrected here.

Arthrocatena Egidi & Selbmann, ***gen. nov.*** MycoBank MB829384.
Synonym: *Arthrocatena* Egidi & Selbmann, *Fungal Diversity* **65**: 159. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after dark, arthric conidia in chains.

Description and illustration: Egidi *et al*. (2014).

Type species: *Arthrocatena tenebrosa* Egidi & Selbmann.

Arthrocatena tenebrosa Egidi & Selbmann, ***sp. nov.*** MycoBank MB829385.
Synonym: *Arthrocatena tenebrio* Egidi & Selbmann, *Fungal Diversity* **65**: 159. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after dark, arthric conidia in chains.

Description and illustration: Egidi *et al*. (2014).

Typus: **Italy**, Monte Rosa, Punta Indren, from rock (**holotype** CBS 136100, culture and specimen preserved as metabolically inactive).

Catenulomyces Egidi & de Hoog, ***gen. nov.*** MycoBank MB829386.
Synonym: *Catenulomyces* Egidi & de Hoog, *Fungal Diversity* **65**: 154. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after its conidial chains.

Description and illustration: Egidi *et al*. (2014).

Type species: *Catenulomyces convolutus* Egidi & de Hoog.

Catenulomyces convolutus Egidi & de Hoog, ***sp. nov.*** MycoBank MB829387.
Synonym: Catenulomyces *convolutus* Egidi & de Hoog, *Fungal Diversity* **65**: 154. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the conidial chains and curly shape of conidia.

Description and illustration: Egidi *et al.* (2014).

Typus: **Spain,** La Cabrera, from rock (**holotype** CBS 118609, culture and specimen preserved as metabolically inactive).

Constantinomyces Egidi & Onofri, ***gen. nov.*** MycoBank MB829388.
Synonym: *Constantinomyces* Egidi & Onofri, *Fungal Diversity* **65**: 155. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Genus named after Constantino Ruibal who was one of the first to uncover the stunning diversity of rock-inhabiting fungi.

Description and illustration: Egidi *et al*. (2014).

Type species: *Constantinomyces virgultus* Egidi & Onofri.

Constantinomyces macerans de Hoog & Onofri, ***sp. nov.*** MycoBank MB829389.
Synonym: *Constantinomyces macerans* de Hoog & Onofri, *Fungal Diversity* **65**: 157. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the mere thin hyphal morphology of the fungus.

Description and illustration: Egidi *et al*. (2014).

Typus: **Spain**, Patones, from rock (**holotype** CBS 119304, culture and specimen preserved as metabolically inactive).

Constantinomyces minimus de Hoog & Isola, ***sp. nov.*** MycoBank MB829390.
Synonym: *Constantinomyces minimus* de Hoog & Isola, *Fungal Diversity* **65**: 157. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named refers to the scant appearance of the fungus.

Description and illustration: Egidi *et al*. (2014).

Typus: **Spain**, La Cabrera, from rock (**holotype** CBS 118766, culture and specimen preserved as metabolically inactive).

Constantinomyces nebulosus Isola & Zucconi, ***sp. nov.*** MycoBank MB829391.
Synonym: *Constantinomyces nebulosus* Isola & Zucconi, *Fungal Diversity* **65**: 157. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: The species name refers to the dark and poorly shaped morphology of the fungus.

Description and illustration: Egidi *et al*. (2014).

Typus: **Spain**, Atazar, from rock (**holotype** CBS 117941, culture and specimen preserved as metabolically inactive).

Constantinomyces virgultus Egidi & Onofri, ***sp. nov.*** MycoBank MB829392.
Synonym: *Constantinomyces* virgultus Egidi & Onofri, *Fungal Diversity* **65**: 155. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: The species' microscopic morphology is shrub-like.

Description and illustration: Egidi *et al*. (2014).

Typus: **Spain**, Mallorca, from rock (**holotype** CBS 117930, culture and specimen preserved as metabolically inactive).

Exophiala bonariae Isola & Zucconi, ***sp. nov.*** MycoBank MB829393.
Synonym: *Exophiala bonariae* Isola & Zucconi, *Fungal Diversity* **76**: 85. 2015 (2016). *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the cemetery of Bonaria, where the type strain was isolated.

Description and illustration: Isola *et al*. (2016).

Typus: **Italy**, Cagliari, (Zelina Ferri funerary monument) in the cemetery of Bonaria, isolated from marble (**holotype** CBS 139957, culture and specimen preserved as metabolically inactive).

Extremaceae Quaedvl. & Crous, ***fam. nov.*** MycoBank MB829394.
Synonym: *Extremaceae* Quaedvl. & Crous, *Persoonia* **33**: 21. 2014. *Nom. inval*. Art. 32.1(c), see Art. 10.6 (Shenzen).

Etymology: Named after the genus *Extremus*.

Description and illustration: Quaedvlieg *et al.* (2014).

Type genus: *Extremus* Quaedvl. & Crous.

Extremus Quaedvl. & Crous, ***gen. nov.*** MycoBank MB829395.
Synonym: *Extremus* Quaedvl. & Crous, *Persoonia* **33**: 21. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after its ecologically extreme, rock-inhabiting habitat.

Description and illustration: Quaedvlieg *et al.* (2014).

Type species: *Extremus adstrictus* Quaedvl. & Crous.

Extremus adstrictus Quaedvl. & Crous, ***sp. nov.*** MycoBank MB829396.
Synonyms: *Devriesia adstricta* Egidi & Onofri, *Fungal Diversity* **65**: 150. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).
Extremus adstrictus (Egidi & Onofri) Quaedvl. & Crous, *Persoonia* **33**: 22. 2014. *Nom. inval.*, Art. 40.7 (Shenzhen).

Etymology: Named after conidial chains where conidia are densely packed at septa.

Description and illustration: Egidi *et al*. (2014).

Typus: **Spain**, Mallorca, from rock (**holotype** CBS 118292, culture and specimen preserved as metabolically inactive).

Extremus antarcticus Quaedvl. & Crous, ***sp. nov.*** MycoBank MB829397.
Synonyms: *Devriesia antarctica* Selbmann & de Hoog, *Fungal Diversity* **65**: 150. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).
Extremus antarcticus (Selbmann & de Hoog) Quaedvl. & Crous, *Persoonia* **33**: 22. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the geographical origin of the strain.

Description and illustration: Egidi *et al*. (2014).

Typus: **Antarctica**, Linnaeus Terrace, from rock (**holotype** CBS 136103, culture and specimen preserved as metabolically inactive).

Hyphoconis Egidi & Quaedvl., ***gen. nov.*** MycoBank MB829398.
Synonym: *Hyphoconis* Egidi & Quaedvl., *Fungal Diversity* **65**: 153. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after absence of sporulation.

Description and illustration: Egidi *et al.* (2014).

Type species: *Hyphoconis sterilis* Egidi & Quaedvl.

Hyphoconis sterilis Egidi & Quaedvl., ***sp. nov.*** MycoBank MB829399.
Synonym: *Hyphoconis sterilis* Egidi & Quaedvl., *Fungal Diversity* **65**: 153. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after poor sporulation by hyphal fragments.

Description and illustration: Egidi *et al*. (2014).

Typus: **Spain**, Atazar, from rock (**holotype** CBS 118321, culture and specimen preserved as metabolically inactive).

Incertomyces Egidi & Zucconi, ***gen. nov.*** MycoBank MB829400.
Synonym: *Incertomyces* Egidi & Zucconi, *Fungal Diversity* **65**: 157. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the poor morphological features of the species.

Description and illustration: Egidi *et al.* (2014).

Type species: *Incertomyces perditus* Egidi & Zucconi.

Incertomyces perditus Egidi & Zucconi, ***sp. nov.*** MycoBank MB829401.
Synonym: *Incertomyces perditus* Egidi & Zucconi, *Fungal Diversity* **65**: 157. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the poor morphological features of the species.

Description and illustration: Egidi *et al*. (2014).

Typus: **Italy**, Monte Rosa, from rock (**holotype** CBS 136105, culture and specimen preserved as metabolically inactive).

Knufia karalitana Isola & Onofri, ***sp. nov.*** MycoBank MB829402.
Synonym: *Knufia karalitana* Isola & Onofri, *Fungal Diversity* **76**: 88. 2015 (2016). *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the ancient name of Cagliari (Karalis), the city where the strain was isolated.

Description and illustration: Isola *et al*. (2016).

Typus: **Italy**, Cagliari, isolated from marble lion in front of the Cathedral of Santa Maria (**holotype** CBS 139720, culture and specimen preserved as metabolically inactive).

Knufia marmoricola Onofri & Zucconi, ***sp. nov.*** MycoBank MB829403.
Synonym: *Knufia marmoricola* Onofri & Zucconi, *Fungal Diversity* **76**: 88. 2015 (2016). *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the substratum, from which the type strain was isolated.

Description and illustration: Isola *et al*. (2016).

Typus: **Italy**, isolated from travertine of St Peter colonnade (Vatican City State) (**holotype** CBS 139726, culture and specimen preserved as metabolically inactive).

Knufia mediterranea Selbmann & Zucconi, ***sp. nov.*** MycoBank MB829404.
Synonym: *Knufia mediterranea* Selbmann & Zucconi, *Fungal Diversity* **76**: 88. 2015 (2016). *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the Mediterranean basin, the site from which the strain was isolated.

Description and illustration: Isola *et al*. (2016).

Typus: **Italy**, Cagliari, isolated from Francesca Warzee funerary marble monument, cemetery of Bonaria (**holotype** CBS 139721, culture and specimen preserved as metabolically inactive).

Lapidomyces de Hoog & Stielow, ***gen. nov.*** MycoBank MB829405.
Synonym: *Lapidomyces* de Hoog & Stielow, *Fungal Diversity* **65**: 159. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Rock-inhabiting fungus.

Description and illustration: Egidi *et al*. (2014).

Type species: *Lapidomyces hispanicus* de Hoog & Stielow.

Lapidomyces hispanicus de Hoog & Stielow, ***sp. nov.*** MycoBank MB829406.
Synonym: *Lapidomyces hispanicus* de Hoog & Stielow, *Fungal Diversity* **65**: 159. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Rock-inhabiting fungus from Spain.

Description and illustration: Egidi *et al*. (2014).

Typus: **Spain**, Puebla la Sierra, from rock (**holotype** CBS 118355, culture and specimen preserved as metabolically inactive).

Lithophila Selbmann & Isola, ***gen. nov.*** MycoBank MB829407.
Synonym: *Lithophila* Selbmann & Isola, *Fungal Diversity* **76**: 88. 2015 (2016). *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after its guttulate cells.

Description and illustration: Isola *et al*. (2016).

Type species: *Lithophila guttulata* Selbmann & Isola.

Lithophila guttulata Selbmann & Isola, ***sp. nov.*** MycoBank MB829408.
Synonym: *Lithophila guttulata* Selbmann & Isola, *Fungal Diversity* **76**: 90. 2015 (2016). *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after its guttulate cells.

Description and illustration: Isola *et al*. (2016).

Typus: **Italy**, Vatican City State, isolated from marble stone (cat. 37106) exposed in the Vatican Museums – Cortile della Pigna (**holotype** CBS 139723, culture and specimen preserved as metabolically inactive).

Monticola Selbmann & Egidi, ***gen. nov.*** MycoBank MB829409.
Synonym: *Monticola* Selbmann & Egidi, *Fungal Diversity* **65**: 155. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Inhabitant of the mountain.

Description and illustration: Egidi *et al*. (2014).

Type species: *Monticola elongata* Selbmann & Egidi.

Monticola elongata Selbmann & Egidi, ***sp. nov.*** MycoBank MB829410.
Synonym: *Monticola elongata* Selbmann & Egidi, *Fungal Diversity* **65**: 155. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Inhabitant of the mountain with elongate conidium-like structures.

Description and illustration: Egidi *et al*. (2014).

Typus: **Italy**, Monte Rosa, Stolenberg, from rock (**holotype** CBS 136206, culture and specimen preserved as metabolically inactive).

Meristemomyces Isola & Onofri, ***gen. nov.*** MycoBank MB829411.
Synonym: *Meristemomyces* Isola & Onofri, *Fungal Diversity* **65**: 158. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the typical meristematic growth of the fungus.

Description and illustration: Egidi *et al*. (2014).

Type species: *Meristemomyces frigidus* Isola & Onofri.

Meristemomyces arctostaphyli Crous & M.J. Wingf., ***sp. nov.*** MycoBank MB829412.
Synonym: *Meristemomyces arctostaphylos* Crous & M.J. Wingf., *Persoonia* 36: 347. 2016. *Nom. inval*. Art 35.1 (Shenzen).

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

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

Typus: **USA**, Utah, near Long Valley, on leaves of *Arctostaphylos patula* (*Ericaceae*), Oct. 2014, *M.J. Wingfield* (**holotype** CBS H-22600, culture ex-type CPC 25574 = CBS 141290).

Meristemomyces frigidus Isola & Onofri, ***sp. nov.*** MycoBank MB829413.
Synonym: *Meristemomyces frigidus* Isola & Onofri, *Fungal Diversity* **65**: 159. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the typical meristematic growth and the cold environment from which the strain was isolated.

Description and illustration: Egidi *et al*. (2014).

Typus: **Himalaya**, Aconcagua, from rock (**holotype** CBS 136109, culture and specimen preserved as metabolically inactive).

Neodevriesia bulbillosa Egidi & Zucconi, ***sp. nov.*** MycoBank MB829414.
Synonyms: *Devriesia bulbillosa* Egidi & Zucconi, *Fungal Diversity* **65**: 148. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).
Neodevriesia bulbillosa (Egidi & Zucconi) Crous, *Sydowia* **67**: 108. 2015. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after large, ellipsoidal multicellular structures present in culture.

Description and illustration: Egidi *et al*. (2014).

Typus: **Spain**, Mallorca, Cala Sant Vicenç (**holotype** CBS 118285, culture and specimen preserved as metabolically inactive).

Neodevriesia modesta Isola & Zucconi, ***sp. nov.*** MycoBank MB829415.
Synonyms: *Devriesia modesta* Isola & Zucconi, *Fungal Diversity* **65**: 148. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).
Neodevriesia modesta (Isola & Zucconi) Crous, *Sydowia* 67: 108. 2015. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after its scarce exhibition of *Neodevriesia* morphology.

Description and illustration: Egidi *et al*. (2014).

Typus: **Italy**, Viterbo, Vallerano, Grotta del Salvatore (**holotype** CBS 137182, culture and specimen preserved as metabolically inactive).

Neodevriesia sardiniae Isola & de Hoog, ***sp. nov.*** MycoBank MB829416.
Synonyms: *Devriesia sardiniae* Isola & de Hoog, *Fungal Diversity* **76**: 85. 2015 (2016). *Nom. inval*., Art. 40.7 (Shenzhen).
Neodevriesia sardiniae (Isola & de Hoog) M.M. Wang & L. Cai, *Mycologia* **109**: 972. 2017. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after Sardinia, the island where the strain was isolated.

Description and illustration: Isola *et al*. (2016).

Typus: **Italy**, Cagliari, (Frau-Carta funerary monument) in the cemetery of Bonaria, isolated from a marble cross (**holotype** CBS 139724, culture and specimen preserved as metabolically inactive).

Neodevriesia simplex Selbmann & Zucconi, ***sp. nov.*** MycoBank MB829417.
Synonyms: *Devriesia simplex* Selbmann & Zucconi, *Fungal Diversity* **65**: 148. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).
Neodevriesia simplex (Selbmann & Zucconi) Crous, *Sydowia* **67**: 107. 2015. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after simple unbranched chains of aseptate conidia.

Description and illustration: Egidi *et al*. (2014).

Typus: **Italy**, Viterbo, Vallerano, Grotta del Salvatore, from rock (**holotype** CBS 13718, culture and specimen preserved as metabolically inactive).

Oleoguttula Selbmann & de Hoog, ***gen. nov.*** MycoBank MB829418.
Synonym: *Oleoguttula* Selbmann & de Hoog, *Fungal Diversity* **65**: 152. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after black conidia looking like oil droplets; it is one of the very few sporulating rock-inhabiting fungi.

Description and illustration: Egidi *et al*. (2014).

Type species: *Oleoguttula mirabilis* Selbmann & de Hoog.

Oleoguttula mirabilis Selbmann & de Hoog, ***sp. nov.*** MycoBank MB829419.
Synonym: *Oleoguttula mirabilis* Selbmann & de Hoog, *Fungal Diversity* **65**: 152. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after black conidia looking like oil droplets; as one of the very few sporulating rock-inhabiting fungi, the morphology is impressive.

Description and illustration: Egidi *et al*. (2014).

Typus: **Antarctica**, Lachman Crags, from rock (**holotype** CBS 136102, culture and specimen preserved as metabolically inactive).

Paradevriesia compacta Crous, ***sp. nov.*** MycoBank MB829327.
Synonym: *Devriesia compacta* de Hoog & Quaedvl., *Fungal Diversity* **65**: 148. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after densely packed, barrel-shaped conidia.

Description and illustration: Egidi *et al*. (2014).

Typus: **Spain**, Mallorca, Manut II, from rock (**holotype** CBS 118294, culture and specimen preserved as metabolically inactive).

Perusta Egidi & Stielow, ***gen. nov.*** MycoBank MB829420.
Synonym: *Perusta* Egidi & Stielow, *Fungal Diversity* **65**: 155. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the not uniformly burnt-like colour of the colony.

Description and illustration: Egidi *et al*. (2014).

Type species: *Perusta inaequalis* Egidi & Stielow.

Perusta inaequalis Egidi & Stielow, ***sp. nov.*** MycoBank MB829421.
Synonym: *Perusta inaequalis* Egidi & Stielow, *Fungal Diversity* **65**: 155. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the unilaterally inflating conidium-like cells.

Description and illustration: Egidi *et al*. (2014).

Typus: **Spain**, Atazar, from rock (**holotype** CBS 118271, culture and specimen preserved as metabolically inactive).

Petrophila de Hoog & Quaedvl., ***gen. nov.*** MycoBank MB829422.
Synonym: *Petrophila* de Hoog & Quaedvl., *Fungal Diversity* **65**: 152. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the rock substrate it was isolated from.

Description and illustration: Egidi *et al.* (2014).

Type species: *Petrophila incerta* de Hoog & Quaedvl.

Petrophila incerta de Hoog & Quaedvl., ***sp. nov.*** MycoBank MB829423.
Synonym: *Petrophila incerta* de Hoog & Quaedvl., *Fungal Diversity* **65**: 152. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the rock substrate it was isolated from.

Description and illustration: Egidi *et al*. (2014).

Typus: **Spain**, Mallorca, from rock (**holotype** CBS 118608, culture and specimen preserved as metabolically inactive).

Rachicladosporium alpinum Egidi & Zucconi, ***sp. nov.*** MycoBank MB829424.
Synonym: *Rachicladosporium alpinum* Egidi & Zucconi, *Fungal Diversity* **65**: 159. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the mountain chain from which the rock was collected.

Description and illustration: Egidi *et al*. (2014).

Typus: **Italy**, Siusi Alps, from rock (**holotype** CBS 136040, culture and specimen preserved as metabolically inactive).

Rachicladosporium inconspicuum de Hoog & Stielow, ***sp. nov.*** MycoBank MB829425.
Synonym: *Rachicladosporium inconspicuum* de Hoog & Stielow, *Fungal Diversity* **65**: 162. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Name reflects the scarce morphological differentiation observed in the colony.

Description and illustration: Egidi *et al*. (2014).

Typus: **Italy**, Monte Rosa, from rock (**holotype** CBS 136043, culture and specimen preserved as metabolically inactive).

Rachicladosporium mcmurdoi Selbmann & Onofri, ***sp. nov.*** MycoBank MB829426.
Synonym: *Rachicladosporium mcmurdoi* Selbmann & Onofri, *Fungal Diversity* **65**: 159. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the valley from which the rock was collected.

Description and illustration: Egidi *et al*. (2014).

Typus: **Antarctica**, Southern Victoria Land, McMurdo Dry Valleys, Battleship Promontory, from rock (**holotype** CBS 119432, culture and specimen preserved as metabolically inactive).

Rachicladosporium monterosanum Isola & Zucconi, ***sp. nov.*** MycoBank MB829427.
Synonym: *Rachicladosporium monterosium* Isola & Zucconi, *Fungal Diversity* **65**: 161. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the mountain Monte Rosa from which the rock was collected.

Description and illustration: Egidi *et al*. (2014).

Typus: **Italy**, Stolemberg, Monte Rosa, from rock (**holotype** CBS 137178, culture and specimen preserved as metabolically inactive).

Rachicladosporium paucitum Isola & Egidi, ***sp. nov.*** MycoBank MB829428.
Synonym: *Rachicladosporium paucitum* Isola & Egidi, *Fungal Diversity* **65**: 162. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after poor sporulation by hyphal fragments.

Description and illustration: Egidi *et al*. (2014).

Typus: **Italy**, Monte Rosa, from rock (**holotype** CBS 136041, culture and specimen preserved as metabolically inactive).

Ramimonilia Stielow & Quaedvl., ***gen. nov.*** MycoBank MB829429.
Synonym: *Ramimonilia* Stielow & Quaedvl., *Fungal Diversity* **65**: 155. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Name reflects the typically chained disposition of hyphae.

Description and illustration: Egidi *et al*. (2014).

Type species: *Ramimonilia apicalis* Stielow & Quaedvl.

Ramimonilia apicalis Stielow & Quaedvl., ***sp. nov.*** MycoBank MB829430.
Synonym: *Ramimonilia apicalis* Stielow & Quaedvl., *Fungal Diversity* **65**: 155. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Name reflects the typical branched hyphae with apical germination.

Description and illustration: Egidi *et al*. (2014).

Typus: **Spain**, Patones, from rock (**holotype** CBS 118327, culture and specimen preserved as metabolically inactive).

Saxophila Selbmann & de Hoog, ***gen. nov.*** MycoBank MB829431.
Synonym: *Saxophila* Selbmann & de Hoog, *Fungal Diversity* **76**: 90. 2015 (2016). *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the rock substrate where it was isolated.

Description and illustration: Isola *et al*. (2016).

Type species: *Saxophila tyrrhenica* Selbmann & de Hoog.

Saxophila tyrrhenica Selbmann & de Hoog, ***sp. nov.*** MycoBank MB829432.
Synonym: *Saxophila tyrrhenica* Selbmann & de Hoog, *Fungal Diversity* **76**: 90. 2015 (2016). *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the Tyrrhenian basin, the site from which the strain was isolated.

Description and illustration: Isola *et al*. (2016).

Typus: **Italy**, Cagliari, isolated from little marble angels of an anonymous funerary monument in the cemetery of Bonaria (**holotype** CBS 139725, culture and specimen preserved as metabolically inactive).

Sodiomyces A.A. Grum-Grzhim, Debets & Bilanenko, ***gen. nov.*** MycoBank MB829354.
Synonym: *Sodiomyces* Grum-Grzhim., Debets & Bilanenko, *Persoonia* **31**: 154. 2013. *Nom. inval*., Art. 40.1 (Shenzen).

Etymology: From the English soda and Latin *mycetes*, referring to the ability of filamentous fungus grow at high ambient pH and salts.

Description and illustration: Giraldo & Crous (2019).

Types species: *Sodiomyces alkalinus* Grum-Grzhim., Debets & Bilanenko.

Sodiomyces alkalinus Grum-Grzhim., Debets & Bilanenko, ***sp. nov.*** MycoBank MB829355.

Etymology: From the Latin, alcalinus = alkaline.

Description and illustrations: Bilanenko *et al.* (2005) and Grum-Grzhimaylo *et al*. (2013).

Typus: **Mongolia**, Choibalsan area, the soda soil (pH 10.7) on the edge of Shar-Burdiyn lake, 1999, *D. Sorokin* (**holotype** CBS 110278, culture and specimen preserved as metabolically inactive), culture ex-type CBS 110278 = F11 = VKM F-3762.

Sodiomyces alcalophilus (G. Okada) Giraldo López & Crous, ***comb. nov.*** MycoBank MB829356.
Basionym: *Acremonium alcalophilum* G. Okada, *Trans. Mycol. Soc. Japan* **34**: 173. 1993.

Description and illustrations: Okada *et al.* (1993).

Typus: **Japan**, Kanagawa Pref., Tsukui-gun, near Tsukui Lake, from sludge of pig faeces compost, 9 Dec. 1984, *A. Yoneda* (**holotype** TNS-F-176428, isotype CBS H-5163, ex-isotype culture CBS 114.92 = JCM 7366).

Sodiomyces magadiensis S.A. Bondarenko, Grum-Grzhim., Debets & Bilanenko, ***sp. nov.*** MycoBank MB829359.
Synonym: *Sodiomyces magadii* S.A. Bondarenko, *et al.*, *Fungal Diversity* **76**: 52. 2015 (2016). *Nom. inval*., Art. 35.1 (Shenzhen).

Etymology: Name refers to the Magadi Lake in Kenya (Africa), where the fungus was isolated.

Description and illustrations: Grum-Grzhimaylo *et al.* (2016).

Typus: **Kenya**, soda soil (pH 11) at the edge of Magadi Lake, Jan. 2013, S. Bondarenko (**holotype** CBS H-21958, culture ex-type MAG2 = CBS 137619 = VKM F-4583).

Sodiomyces tronii S.A. Bondarenko, Grum-Grzhim., Debets & Bilanenko, ***sp. nov.*** MycoBank MB829361.
Synonym: *Sodiomyces tronii* S.A. Bondarenko, *et al.*, *Fungal Diversity* **76**: 52. 2015 (2016). *Nom. inval*., Art. 35.1 (Shenzhen)

Etymology: Name refers to the 'trona' salt (carbonate mineral), which is abundant in Magadi Lake in Kenya (Africa), where the fungus was isolated.

Description and illustrations: Grum-Grzhimaylo *et al.* (2016).

Typus: **Kenya**, soda soil (pH 11) at the edge of Magadi Lake, Jan. 2013, *S. Bondarenko* (**holotype** CBS H-21957, culture ex-type MAG1 = CBS 137618 = VKM F-4582).

Notes: Although *Sodiomyces alkalinus* was redescribed in Giraldo & Crous (2019), all species in the genus are invalid. This is due to the fact that the generic name *Sodiomyces* was invalid because it lacked a valid type species. The genus and all species are thus validated here.

Vermiconidia Egidi & Onofri, ***gen. nov.*** MycoBank MB829433.
Synonym: *Vermiconia* Egidi & Onofri, *Fungal Diversity* **65**: 150. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Morphology of conidial chains reminiscent of worms.

Description and illustration: Egidi *et al.* (2014).

Type species: *Vermiconidia foris* Egidi & Onofri.

Vermiconidia antarctica Egidi & Selbmann, ***sp. nov.*** MycoBank MB829434.
Synonym: *Vermiconia antarctica* Egidi & Selbmann, *Fungal Diversity* **65**: 152. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the cold continent the strain was isolated from.

Description and illustration: Egidi *et al.* (2014).

Typus: **Antarctica**, McMurdo Dry Valleys, Battleship Promontory, from rock (**holotype** CBS 136107, culture and specimen preserved as metabolically inactive).

Vermiconidia calcicola de Hoog & Onofri, ***sp. nov.*** MycoBank MB829435.
Synonym: *Vermiconia calcicola* de Hoog & Onofri, *Fungal Diversity* **76**: 90. 2015 (2016). *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the substrate where the ex-type strain was isolated.

Description and illustration: Isola *et al*. (2016).

Typus: **Italy**, Cagliari, isolated from Giuseppina Ara funerary marble monument in the cemetery of Bonaria (**holotype** CBS 140080, culture and specimen preserved as metabolically inactive).

Vermiconidia foris Egidi & Onofri, ***sp. nov.*** MycoBank MB829436.
Synonym: *Vermiconia foris* Egidi & Onofri, *Fungal Diversity* **65**: 150. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Morphology of propagating cultures reminiscent of extraterrestrial worms.

Description and illustration: Egidi *et al*. (2014).

Typus: **Italy**, Monte Rosa, from rock (**holotype** CBS 136106, culture and specimen preserved as metabolically inactive).

Vermiconidia flagrans Selbmann & Isola, ***sp. nov.*** MycoBank MB829437.
Synonym: *Vermiconia flagrans* Selbmann & Isola, *Fungal Diversity* **65**: 152. 2014. *Nom. inval*., Art. 40.7 (Shenzhen).

Etymology: Named after the survival of high summer temperatures prevailing in its natural habitat.

Description and illustration: Egidi *et al.* (2014).

Typus: **Spain**, Mallorca, from rock (**holotype** CBS 118296, culture and specimen preserved as metabolically inactive).

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