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## New and Interesting Fungi. 5

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**Abstract:** Nine new genera, 17 new species, nine new combinations, seven epitypes, three lectotypes, one neotype, and 14 interesting new host and / or geographical records are introduced in this study. New genera: *Neobarrmaelia* (based on *Neobarrmaelia hyphaenes*), *Neobryochiton* (based on *Neobryochiton narthecii*), *Neocamarographium* (based on *Neocamarographium carpini*), *Nothocladosporium* (based on *Nothocladosporium syzygii*), *Nothopseudocercospora* (based on *Nothopseudocercospora dictamni*), *Paracamarographium* (based on *Paracamarographium koreanum*), *Pseudohormonema* (based on *Pseudohormonema sordidus*), *Quasiphoma* (based on *Quasiphoma hyphaenes*), *Rapidomyces* (based on *Rapidomyces narthecii*). New species: *Ascocorticium sorbicola* (on leaves of *Sorbus aucuparia*, Belgium), *Dactylaria retrophylli* (on leaves of *Retrophyllum rospigliosii*, Colombia), *Dactylellina miltoniae* (on twigs of *Miltonia clowesii*, Colombia), *Exophiala eucalyptigena* (on dead leaves of *Eucalyptus viminalis* subsp. *viminalis* supporting *Idolothrips spectrum*, Australia), *Idriellomyces syzygii* (on leaves of *Syzygium chordatum*, South Africa), *Microcera lichenicola* (on *Parmelia sulcata*, Netherlands), *Neobarrmaelia hyphaenes* (on leaves of *Hyphaene* sp., South Africa), *Neobryochiton narthecii* (on dead leaves of *Narthecium ossifragum*, Netherlands), *Niesslia pseudoexilis* (on dead leaf of *Quercus petraea*, Serbia), *Nothocladosporium syzygii* (on leaves of *Syzygium chordatum*, South Africa), *Nothotrimmatostroma corymbiae* (on leaves of *Corymbia henryi*, South Africa), *Phaeosphaeria hyphaenes* (on leaves of *Hyphaene* sp., South Africa), *Pseudohormonema sordidus* (on a from human pacemaker, USA), *Quasiphoma hyphaenes* (on leaves of *Hyphaene* sp., South Africa), *Rapidomyces narthecii* (on dead leaves of *Narthecium ossifragum*, Netherlands), *Reticulascus parahennebertii* (on dead culm of *Juncus inflexus*, Netherlands), *Scytalidium philadelphianum* (from compressed air in a factory, USA). New combinations: *Neobarrmaelia serenoae*, *Nothopseudocercospora dictamni*, *Dothiora viticola*, *Floricola sulcata*, *Neocamarographium carpini*, *Paracamarographium koreanum*, *Rhexocercosporidium bellocense*, *Russula lilacina*. Epitypes: *Elsinoe corni* (on leaves of *Cornus florida*, USA), *Leptopeltis litigiosa* (on dead leaf fronds of *Pteridium aquilinum*, Netherlands), *Nothopseudocercospora dictamni* (on living leaves of *Dictamnus albus*, Russia), *Ramularia arvensis* (on leaves of *Potentilla reptans*, Netherlands), *Rhexocercosporidium bellocense* (on leaves of *Verbascum* sp., Germany), *Rhopoglyphus filicinus* (on dead leaf fronds of *Pteridium aquilinum*, Netherlands), *Septoria robiniae* (on leaves of *Robinia pseudoacacia*, Belgium). Lectotypes: *Leptopeltis litigiosa* (on *Pteridium aquilinum*, France), *Rhopoglyphus filicinus* (on dead leaf fronds of *Pteridium aquilinum*, Netherlands), *Septoria robiniae* (on leaves of *Robinia pseudoacacia*, Belgium). Neotype: *Camarographium stephensii* (on dead leaf fronds of *Pteridium aquilinum*, Netherlands).

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## INTRODUCTION

The present study represents the fifth instalment of the New and Interesting Fungi (NIF) series that is published annually in the journal *Fungal Systematics and Evolution*. Papers report new knowledge on fungal biodiversity, list new host or geographical records, and new sexual-asexual connections. This study also includes validations and descriptions of new fungal taxa and lists interesting observations relating to fungal biology. Mycologists and other researchers wishing to contribute to future issues of NIF are encouraged to contact the Editor-in-Chief (p.crous@wi.knaw.nl).

## MATERIALS AND METHODS

### Isolates

Twig, culm and leaf samples (see Table 1) were treated as previously detailed (Crous *et al.* 2019b). Single conidial colonies were established on Petri dishes containing 2 % malt extract agar (MEA) as described by Crous *et al.* (1991), and single ascospore 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.* 2019b), or autoclaved pine needles on 2 % tap water agar (PNA) (Smith *et al.* 1996), 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 culture collection and fungarium (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 surface of agar 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. All 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. Amplification of the partial DNA-directed RNA polymerase II second largest subunit gene (*rpb2*), the partial translation elongation factor 1-alpha gene (*tef1*, first part) and the partial beta-tubulin gene (*tub2*) followed Braun *et al.* (2018), while amplification of the partial actin gene (*actA*), 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). Amplification of the partial DNA-directed RNA polymerase II largest subunit gene (*rpb1*) followed Klaubauf *et al.* (2014), and the partial translation elongation factor

1-alpha gene (*tef1*, second part) followed Réblová *et al.* (2020). 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 Geneious Prime v. 2022.0.2 (<http://www.geneious.com>, Kearse *et al.* 2012).

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. Maximum-likelihood phylogenetic trees were constructed generated using IQ-TREE v. 2.1.3 (Nguyen *et al.* 2015, Minh *et al.* 2020) and branch support values were calculated with 5 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) and optimal model-finding using the TESTNEW option using ModelFinder (Kalyaanamoorthy *et al.* 2017) as implemented in IQ-TREE. The only exception was the *Leotiomyces* LSU alignment which was analysed with MrBayes v. 3.2.7a (Ronquist *et al.* 2012) as explained in Braun *et al.* (2018) due to issues with longer branches in the IQ-TREE analysis. All resulting trees were printed with Geneious Prime v. 2022.0.2 and the layout of the trees was done in Adobe Illustrator 2022 v. 26.3.1.

### Morphology

Slide preparations were mounted in lactic acid, Shear's mounting fluid or water, from colonies sporulating on MEA, PDA, PNA or OA. 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. Cryo Scanning Electron Microscopy methods followed Bensch *et al.* (2018). Colony characters and pigment production were noted after 2–4 wk of growth on MEA, PDA and OA (Crous *et al.* 2019b) 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 alignments in figshare.com (doi: 10.6084/m9.figshare.20024564), and taxonomic novelties in MycoBank ([www.MycoBank.org](http://www.MycoBank.org); Crous *et al.* 2004).

## RESULTS

### Phylogeny

Statistics associated with the phylogenetic analyses presented in this study are provided in supplementary Table S1.

**Table 1.** Collection details and GenBank accession numbers of isolates treated in this study, and associated ex-type strains where available. Species for which additional sequences were generated during the course of this study are also listed here. Novel GenBank accession numbers are indicated in bold font.

Species	Culture or voucher accession number(s) <sup>1</sup>	Locality	Substrate	Collector(s)	GenBank accession number <sup>2</sup>			
					ITS	LSU	<i>rpb2</i>	<i>tub2</i>
<i>Annellophorella ellisii</i>	CBS 738.70 = IMI 140024, ex-type	France	Wood scrap on forest soil	–	MH871721.1	–	–	–
<i>Ascochyta nigriptycnidia</i>	CBS 116.96 = CCMF 243 = PD 95/7930, ex-type	Czech Republic	<i>Vicia cracca</i> , leaf spot	M. Ondrej	NG_070603.1	MT018253.1	GU237637.1	–
<i>Ascocorticium sorbicola</i> , gen. et sp. nov.	CPC 39716 = CBS 148249	Russia	<i>Vicia tenuifolia</i>	T.S. Bulgakov	<b>ON811483.1</b>	<b>ON811542.1</b>	<b>ON803534.1</b>	<i>tef1</i> (first part): <b>ON803560.1</b> <i>tef1</i> (second part): <b>ON803584.1</b>
<i>Camarographium stephensii</i>	CPC 40075 = CBS 148303, ex-type	Belgium	<i>Sorbus aucuparia</i> , leaves	B. Declercq	<b>ON811506.1</b>	<b>ON811565.1</b>	<b>ON803545.1</b>	<i>tef1</i> (first part): <b>ON803561.1</b>
<i>Cercosporidium chaetomium</i>	CPC 41598 = CBS 149168, ex-neotype	Netherlands	<i>Pteridium aquilinum</i> , dead leaf fronds	P.W. Crous	<b>ON811484.1</b>	<b>ON811543.1</b>	<b>ON803587.1</b>	<i>tef1</i> (first part): <b>ON803561.1</b>
	CPC 41923	Netherlands	<i>Pteridium aquilinum</i> , stem	P.W. Crous	<b>ON811485.1</b>	<b>ON811544.1</b>	<b>ON803588.1</b>	<i>tef1</i> (first part): <b>ON803562.1</b>
	CPC 18624 = CBS 142177, ex-epitype	Canada	<i>Euphorbia</i> sp.	P.W. Crous & K. Seifert	NR_156367.1	NG_069527.1	MF951474.1	–
	CPC 39688 = CBS 148457	Russia	<i>Polygonum aviculare</i>	T.S. Bulgakov	<b>ON811486.1</b>	<b>ON811545.1</b>	<b>ON803535.1</b>	–
<i>Coniella eucaalyptorum</i>	CPC 3904 = CBS 112640 = DFR 100185, ex-type	Australia	<i>Eucalyptus grandis</i> x <i>tereticornis</i>	P.Q. Thu & R.J. Gibbs	AY339338.1	AY339290.1	KX833452.1	<i>tef1</i> (first part): KX833637.1
<i>Curvularia eragrostidicola</i>	CPC 39780 = CBS 149182	South Africa	<i>Eucalyptus benthamii</i> , leaves	J. Roux	<b>ON811487.1</b>	<b>ON811546.1</b>	<b>ON803589.1</b>	<i>tef1</i> (first part): <b>ON803563.1</b>
	BRIP 12538, ex-type	Australia	<i>Eragrostis pilosa</i> , inflorescence	J.L. Alcorn	NR_158446.1	–	–	<i>gapdh</i> : MH433643.1, <i>tef1</i> (first part): MH433661.1
	CPC 39009 = CBS 147069	Namibia	Dung of <i>Pracavia</i> sp.	P.W. Crous	<b>ON811488.1</b>	<b>ON811547.1</b>	<b>ON803536.1</b>	<i>tef1</i> (second part): <b>ON803581.1</b>
<i>Dactylaria retrophylli</i> , sp. nov.	CPC 39510 = CBS 148271, ex-type	Colombia	<i>Retrophyllum rospigliosii</i>	M.J. Wingfield	<b>ON811489.1</b>	<b>ON811548.1</b>	–	–
<i>Dactylellina miltoniae</i> , sp. nov.	CPC 39508 = CBS 148270, ex-type	Colombia	<i>Miltonia clowesii</i> , twigs	M.J. Wingfield	<b>ON811490.1</b>	<b>ON811549.1</b>	<b>ON803537.1</b>	<i>tef1</i> (second part): <b>ON803582.1</b>
<i>Dothiora viticola</i> , comb. nov.	CBS 140676 = FMR 13040 = L9D-17, ex-type	Spain: Canary Islands	<i>Vitis vinifera</i> cv. Malvasia, fruit (grapes)	F. Laich	NR_137620.1	MH878164.1	–	–
<i>Elsinoe corni</i>	CPC 41728 = CBS 148184, ex-epitype	USA: North Carolina	<i>Cornus florida</i>	A. Loyd	<b>ON811491.1</b>	<b>ON811550.1</b>	<b>ON803538.1</b>	–
<i>Elsinoe parthenocissi</i>	CPC 38770 = T19_06384B = CBS 146969	New Zealand	<i>Parthenocissus quinquefolia</i>	C. Inglis	<b>ON811492.1</b>	<b>ON811551.1</b>	<b>ON803539.1</b>	–

Table 1. (Continued).

Species	Culture or voucher accession number(s) <sup>1</sup>	Locality	Substrate	Collector(s)	ITS	LSU	GenBank accession number <sup>2</sup>			Other loci
							<i>rpb2</i>	<i>tub2</i>		
<i>Exophiala eucalyptigena</i> , sp. nov.	CPC 41024 = CBS 148273, ex-type	Australia	Dead leaves of <i>Eucalyptus viminalis</i> subsp. <i>viminalis</i> supporting <i>Idolothrips spectrum</i> population	A. Wells & L.A. Mound	ON811493.1	ON811552.1	–	ON803590.1	<i>tef1</i> (first part): ON803564.1	
<i>Floricola juncicola</i>	CPC 38197 = CBS 146811, ex-type	France	<i>Juncus</i> sp., dead culm	A. Gardiennet	NR_173010.1	NG_076710.1	MW890063.1	–	<i>tef1</i> (first / second part): MW890092.1 / MW890108.1	
	CPC 41356 = CBS 148318	Netherlands	<i>Juncus effusus</i> , dead culm	E.R. Osieck	ON811494.1	ON811553.1	ON803540.1	–	<i>tef1</i> (first part): ON803565.1	
	CPC 41357 = CBS 148287	Netherlands	<i>Juncus effusus</i> , dead culm	E.R. Osieck	ON811495.1	ON811554.1	ON803541.1	–	<i>tef1</i> (first part): ON803566.1	
<i>Floricola sulcata</i> , comb. nov.	CBS 118224 = CMW 18063, ex-type	South Africa	<i>Ischyrolepis subverticillata</i> , dead culm	S. Marinowitz	JX517284.1	JX517293.1	–	–	–	
	CPC 41345 = CBS 148286	Netherlands	<i>Juncus effusus</i> , dead culm	E.R. Osieck	ON811496.1	ON811555.1	ON803542.1	–	<i>tef1</i> (first part): ON803567.1	
<i>Idriellomyces syzygii</i> , sp. nov.	CPC 40065 = CBS 148252, ex-type	South Africa	<i>Syzygium cordatum</i> , leaves	M.J. Wingfield	ON811497.1	ON811556.1	–	–	–	
<i>Leptopeltis litigiosa</i>	CPC 41927 = CBS 149171, ex-epitype	Netherlands	<i>Pteridium aquilinum</i> , dead leaf fronds	P.W. Crous	ON811498.1	ON811557.1	–	–	–	
<i>Macgarvieomyces juncicola</i>	CPC 40815 = CBS 148264	Netherlands	<i>Juncus effusus</i> , dead culm	E.R. Osieck	ON811499.1	ON811558.1	–	–	<i>actA</i> : ON803512.1, <i>cmdA</i> : ON803526.1, <i>rpb1</i> : ON803532.1	
<i>Magnibotryascoma mali</i>	CPC 38756 = T19_05741A = CBS 147001	New Zealand	<i>Metrosideros</i> sp.	L. Rabbidge	ON811500.1	ON811559.1	–	–	<i>tef1</i> (first part): ON803568.1	
	CPC 38757 = T19_05741B = CBS 146778	New Zealand	<i>Metrosideros</i> sp.	L. Rabbidge	ON811501.1	ON811560.1	–	–	<i>tef1</i> (first / second part): ON803569.1 / ON803583.1	
<i>Microcera lichenicola</i> , sp. nov.	MFLUCC 17-0933, ex-type	China	<i>Malus halliana</i> , decaying twigs	C. Phukhamsakda	NR_156346.1	NG_059830.1	MF173437.1	–	SSU: NG_063644.1, <i>tef1</i> (second part): MF173435.1	
	CPC 41114 = CBS 149169, ex-type	Netherlands	<i>Parmelia sulcata</i>	J. Boers	ON811502.1	ON811561.1	–	ON803591.1	–	
<i>Microcera</i> sp.	CPC 41230 = CBS 148313	Netherlands	<i>Physcia tenella</i>	J. Boers	ON811503.1	ON811562.1	ON803543.1	ON803592.1	<i>rpb1</i> : ON803533.1, <i>tef1</i> (first part): ON803570.1	
<i>Mycodiella eucalypti</i>	CPC 29458 = CBS 142098, ex-type	Australia	<i>Eucalyptus diversicolor</i> , leaves	P.W. Crous	NR_155408.1	NG_059747.1	KY173586.1	–	<i>actA</i> : KY173565.1	



Table 1. (Continued).

Species	Culture or voucher accession number(s) <sup>1</sup>	Locality	Substrate	Collector(s)	GenBank accession number <sup>2</sup>				Other loci
					ITS	LSU	rpb2	tub2	
<i>Syzygium cordatum</i> , leaf litter	CPC 38962 = CBS 146986	South Africa		P.W. Crous	ON811505.1	ON811564.1	ON803544.1	ON803593.1	cmdA: ON803527.1
<i>Neobarrmaelia hyphaenes</i> , <i>gen. et sp. nov.</i>	CPC 40101 = CBS 148304, ex-type	South Africa	<i>Hyphaene crenata</i> , leaves	M.J. Wingfield & J. Roux	ON811507.1	ON811566.1	ON803546.1	ON803594.1	–
<i>Neobarrmaelia serenoae</i> , <i>comb. nov.</i>	CPC 37572 = CBS 146017, ex-type	USA	<i>Serenoa repens</i> , leaf	M.J. Wingfield	MT223781.1	MT223876.1	–	MT223730.1	<i>tef1</i> (first part): MT223709.1
<i>Neobryochiton narthecii</i> , <i>gen. et sp. nov.</i>	CPC 41972 = CBS 149172, ex-type	Netherlands	<i>Narthecium ossifragum</i> , dead leaves	J. Boers	ON811508.1	ON811567.1	ON803547.1	–	–
<i>Neocamarographium carpini</i> , <i>gen. et comb. nov.</i>	CPC 18919, 18918 = CBS 128781, ex-isotype	Russia	<i>Carpinus betulus</i> , thin, dried twigs	V. Mel'nik	NR_156250.1	NG_058837.1	–	–	–
<i>Neocamarographium carpini</i> , <i>gen. et comb. nov.</i>	CPC 25067	Germany	<i>Carpinus betulus</i> , attached twig	R.K. Schumacher	ON811509.1	–	–	–	–
<i>Neofusicoccum mediterraneum</i>	CMW 26679 = CBS 125263	South Africa	<i>Terminalia sericea</i>	D. Begoude & J. Roux	MH863478.1	MH874970.1	KX464045.1	KX465052.1	<i>tef1</i> (first part): GQ471780.1
<i>Niesslia neoexosporioides</i>	CPC 13137 = CBS 121718, ex-type	Greece	<i>Eucalyptus</i> sp. branches and leaves	P.W. Crous, M.J. Wingfield & A.J.L. Phillips	EU040221.1	EU040221.1	KY855815.1	–	<i>actA</i> : KY855639.1, <i>gapdh</i> : KY855694.1
<i>Niesslia pseudoexilis</i> , <i>sp. nov.</i>	CPC 38177 = CBS 146810, ex-type	Germany	<i>Carex paniculata</i> , dead leaves	R.K. Schumacher	NR_173014.1	NG_076714.1	–	MW890137.1	<i>actA</i> : MW890027.1, <i>tef1</i> (first part): MW890097.1
<i>Nothocladosporium syzygii</i> , <i>gen. et sp. nov.</i>	CPC 41317 = CBS 148284	Netherlands	<i>Phragmites australis</i> , dead culms	E. R. Osieck	ON811510.1	ON811568.1	–	ON803595.1	<i>actA</i> : ON803513.1, <i>tef1</i> (first part): ON803571.1
<i>Nothopseudocercospora dictamni</i> , <i>gen. et comb. nov.</i>	CPC 40376 = CBS 148333, ex-type	Serbia	<i>Quercus petraea</i> , dead leaf	D. Savić	ON811511.1	ON811569.1	ON803548.1	ON803596.1	<i>actA</i> : ON803514.1
<i>Nothocladosporium syzygii</i> , <i>gen. et sp. nov.</i>	CPC 40091 = CBS 148289, ex-type	South Africa	<i>Syzygium cordatum</i> , leaves	M.J. Wingfield	ON811512.1	ON811570.1	–	ON803597.1	<i>actA</i> : ON803515.1, <i>tef1</i> (first part): ON803572.1
<i>Nothopseudocercospora dictamni</i> , <i>gen. et comb. nov.</i>	CPC 39776 = CBS 148299, ex-epitype	Russia	<i>Dictamnus albus</i>	T.S. Bulgakov	ON811513.1	ON811571.1	ON803549.1	–	<i>actA</i> : ON803516.1, <i>cmdA</i> : ON803528.1, <i>tef1</i> (first part): ON803573.1
<i>Nothotrimmatostroma corymbiae</i> , <i>sp. nov.</i>	CPC 40077 = CBS 148336	South Africa	<i>Corymbia henryi</i>	M.J. Wingfield	ON811514.1	ON811572.1	–	–	–
<i>Paracamarographium koreanum</i> , <i>gen. et comb. nov.</i>	CPC 40085 = CBS 148335 CPC 40087 = CBS 148334, ex-type	South Africa	<i>Corymbia henryi</i> <i>Corymbia henryi</i>	M.J. Wingfield M.J. Wingfield & J. Roux	ON811515.1 ON811516.1	ON811573.1 ON811574.1	– –	– –	– –
<i>Paracamarographium koreanum</i> , <i>gen. et comb. nov.</i>	CBS 117159, ex-type	Korea	<i>Cornus kousa</i> , dead twigs	V. Mel'nik	JQ044432.1	JQ044451.1	–	–	–

Table 1. (Continued).

Species	Culture or voucher accession number(s) <sup>1</sup>	Locality	Substrate	Collector(s)	ITS	LSU	GenBank accession number <sup>2</sup>		
							<i>rpb2</i>	<i>tub2</i>	Other loci
<i>Paraphoma salicis</i>	CPC 38651 = CBS 146797 = CWU AS 7121, ex-type	Ukraine	<i>Salix cf. alba</i> , leaves	A. Akulov	NR_173017.1	MW883829.1	MW890069.1	MW890140.1	<i>actA</i> : MW890028.1
<i>Periconia pseudobyssooides</i>	CPC 39991 = CBS 148454	Netherlands	<i>Salix</i> sp.	A.L. van Iperen	<b>ON811517.1</b>	<b>ON811575.1</b>	<b>ON803550.1</b>	<b>ON803598.1</b>	–
	BILAS 50334 = S1-11P, ex-type	Lithuania	<i>Heraclium sosnowskyi</i> , dead stalks	S. Markovskaja	KC954161.1	–	–	–	–
	CPC 38820 = CBS 147067	South Africa	<i>Euphorbia ingens</i> , leaf litter	P.W. Crous	<b>ON811518.1</b>	<b>ON811576.1</b>	–	–	<i>tef1</i> (first / second part): <b>ON803574.1</b> / <b>ON803585.1</b> SSU: <b>ON787969.1</b>
<i>Phaeoisaria clematidis</i>	CPC 39680	Netherlands	<i>Sambucus nigra</i> , stems	P.W. Crous	<b>ON811519.1</b>	<b>ON811577.1</b>	<b>ON803551.1</b>	–	–
<i>Phaeophleospora hymenocallidicola</i>	CPC 39937 = CBS 149173	Netherlands	<i>Sambucus nigra</i> , stems	A.L. van Iperen	<b>ON811520.1</b>	<b>ON811578.1</b>	<b>ON803552.1</b>	–	–
	CPC 25014 = CBS 139912, ex-type	Thailand	Leaves of epiphyte	P.W. Crous	NR_137994.1	NG_070062.1	–	–	–
	CPC 40026 = CBS 148250	USA: Puerto Rico	<i>Mangifera indica</i> var. <i>palmeri</i> , leaf necrosis	–	<b>ON811521.1</b>	<b>ON811579.1</b>	–	–	–
<i>Phaeosphaeria hyphaenes</i> , sp. nov.	CPC 40027 = CBS 149175	USA: Puerto Rico	Necrosis on fruit peduncle of <i>Mangifera indica</i>	–	<b>ON811522.1</b>	–	–	–	–
	CPC 40354 = CBS 148254, ex-type	South Africa	<i>Hyphaene crenata</i> , leaves	M.J. Wingfield & J. Roux	<b>ON811523.1</b>	<b>ON811580.1</b>	<b>ON803553.1</b>	<b>ON803599.1</b>	<i>tef1</i> (first part): <b>ON803575.1</b>
	CPC 29372 = T15_05353B = CBS 142134, ex-type	New Zealand	<i>Phoenix canariensis</i>	R. Thangaval	NR_155690.1	NG_067319.1	–	KY173611.1	–
<i>Pseudohormonema sordidus</i> , gen. et sp. nov.	CPC 38747 = CBS 147066	New Zealand	<i>Libertia ixioides</i>	C. Inglis	<b>ON811524.1</b>	<b>ON811581.1</b>	–	<b>ON803600.1</b>	<i>actA</i> : <b>ON803517.1</b>
	CBS 130468 = UTHSC 07-2004, ex-type	USA	Human pacemaker	D. Sutton	<b>ON811525.1</b>	<b>ON811582.1</b>	–	<b>ON803601.1</b>	<i>actA</i> : <b>ON803518.1</b>
	CBS 140365	Saudi Arabia	Polluted soil	S. de Hoog & T.A. Mousa	<b>ON811526.1</b>	<b>ON811583.1</b>	–	<b>ON803602.1</b>	–
<i>Pseudoplagiostoma eucalypti</i>	CBS 140366	Saudi Arabia	Polluted soil	S. de Hoog & T.A. Mousa	<b>ON811527.1</b>	–	–	<b>ON803603.1</b>	–
	CPC 13341 = CBS 124807, ex-type	Venezuela	<i>Eucalyptus urophylla</i> , living leaves	M.J. Wingfield	GU973512.1	GU973606.1	–	GU973575.1	<i>tef1</i> (first part): GU973542.1
	CPC 39762 = CBS 149183	South Africa	<i>Eucalyptus benthamii</i> , leaves	J. Roux	<b>ON811528.1</b>	<b>ON811584.1</b>	–	<b>ON803604.1</b>	<i>tef1</i> (first part): <b>ON803576.1</b>
<i>Pseudosolaoacrosporiella cryptomeriae</i>	CPC 39587 = CBS 148441, ex-type	Netherlands	<i>Cryptomeria japonica</i> , leaves	P.W. Crous	NR_175206.1	<b>ON811585.1</b>	–	–	<i>tef1</i> (first part): OK651183.1

Table 1. (Continued).

Species	Culture or voucher accession number(s) <sup>1</sup>	Locality	Substrate	Collector(s)	GenBank accession number <sup>2</sup>				
					ITS	LSU	<i>rpb2</i>	<i>tub2</i>	Other loci
<i>Pseudosydowia phantasmae</i> , <i>comb. nov.</i>	CPC 38883 = CBS 146830, ex-type	Namibia	<i>Moringa ovalifolia</i> , leaves	P.W. Crous	NR_171999.1	NG_074499.1	–	–	–
	CPC 38950 = CBS 146982	Namibia	<i>Moringa ovalifolia</i> , flower	P.W. Crous	<b>ON811504.1</b>	<b>ON811563.1</b>	–	–	–
<i>Quasiphoma hyphaenes</i> , <i>gen. et sp. nov.</i>	CPC 40045 = CBS 148253, ex-type	South Africa	<i>Hyphaene crenata</i> , leaves	M.J. Wingfield & J. Roux	<b>ON811529.1</b>	<b>ON811586.1</b>	<b>ON803554.1</b>	<b>ON803605.1</b>	<i>actA</i> : <b>ON803519.1</b>
<i>Racheliella wingfieldiana</i>	CPC 13806 = CBS 143669, ex-type	South Africa	<i>Syzygium guineense</i>	M.J. Wingfield	MG591911.1	MG976487.1	MG592192.1		<i>tef1</i> (first part): MG592100.1
	CPC 40039 = CBS 148251	South Africa	<i>Syzygium</i> sp.	M.J. Wingfield	<b>ON811530.1</b>	<b>ON811587.1</b>	–	<b>ON803606.1</b>	<i>tef1</i> (first part): <b>ON803577.1</b>
<i>Ramularia arvensis</i>	CPC 39985 = CBS 148455, ex-epitype	Netherlands	<i>Potentilla reptans</i>	A.L. van Iperen	<b>ON811531.1</b>	<b>ON811588.1</b>	–	–	<i>actA</i> : <b>ON803520.1</b> , <i>gapdh</i> : <b>ON803530.1</b> , <i>his3</i> : <b>ON803531.1</b> , <i>tef1</i> (first part): <b>ON803578.1</b>
<i>Rapidomyces narthecii</i> , <i>gen. et sp. nov.</i>	CPC 41974 = CBS 149174, ex-type	Netherlands	<i>Narthecium ossifragum</i> , dead leaves	J. Boers	<b>ON811532.1</b>	<b>ON811589.1</b>	<b>ON803555.1</b>	–	–
<i>Reticulascus parahennebertii</i> , <i>sp. nov.</i>	CPC 41226 = CBS 148282, ex-type	Netherlands	<i>Juncus inflexus</i> , dead culm	E.R. Osieck	<b>ON811533.1</b>	<b>ON811590.1</b>	–	–	<i>tef1</i> (second part): <b>ON803586.1</b>
<i>Rhexocercosporidium bellocense</i> , <i>comb. nov.</i>	CPC 39764 = CBS 148297, ex-epitype	Germany	<i>Verbascum cf. densiflorum</i>	J. Kruse	<b>ON811535.1</b>	<b>ON811592.1</b>	<b>ON803557.1</b>	–	–
<i>Rhexocercosporidium</i> aff. <i>bellocense</i>	CPC 39690 = CBS 148246	Russia	<i>Verbascum</i> sp.	T.S. Bulgakov	<b>ON811534.1</b>	<b>ON811591.1</b>	<b>ON803556.1</b>	<b>ON803607.1</b>	–
<i>Rhopoglyphus filicinus</i>	CBS 384.59 = ETH 2752	India	<i>Pteridium aquilinum</i>	E. Müller	MH857898.1	<b>ON811593.1</b>	–	–	–
	CPC 41596, ex-epitype	Netherlands	<i>Pteridium aquilinum</i> , dead leaf fronds	P.W. Crous	<b>ON811536.1</b>	<b>ON811594.1</b>	<b>ON803558.1</b>	–	<i>actA</i> : <b>ON803521.1</b>
	CPC 41925	Netherlands	<i>Pteridium aquilinum</i> , stem	P.W. Crous	<b>ON811537.1</b>	<b>ON811595.1</b>	–	–	<i>actA</i> : <b>ON803522.1</b>
<i>Scytalidium philadelphianum</i> , <i>sp. nov.</i>	CPC 40793 = CBS 148262, ex-type	USA: Pennsylvania	Compressed air in a factory	Ž. Jurjević	<b>ON811538.1</b>	–	–	–	–
<i>Septoria chelidonii</i>	CPC 12337 = CBS 132027	South Korea	<i>Chelidonium majus</i>	H.D. Shin	GU269860.1	GU253870.1	KF252374.1	KF252845.1	<i>actA</i> : KF253676.1, <i>cmdA</i> : KF254025.1, <i>tef1</i> (first part): KF253319.1
	CPC 39746 = CBS 148456	Russia	<i>Chelidonium majus</i>	T.S. Bulgakov	<b>ON811539.1</b>	<b>ON811596.1</b>	–	–	<i>actA</i> : <b>ON803523.1</b> , <i>tef1</i> (first part): <b>ON803579.1</b>
<i>Septoria robiniae</i>	CPC 39783 = CBS 148300, ex-epitype	Belgium	<i>Robinia pseudoacacia</i>	C. van Steenwinkel	<b>ON811540.1</b>	<b>ON811597.1</b>	–	–	<i>actA</i> : <b>ON803524.1</b> , <i>tef1</i> (first part): <b>ON803580.1</b>

Table 1. (Continued).

Species	Culture or voucher accession number(s) <sup>1</sup>	Locality	Substrate	Collector(s)	GenBank accession number <sup>2</sup>				
					ITS	LSU	<i>rpb2</i>	<i>tub2</i>	Other loci
<i>Teratosphaeria alcornii</i>	CPC 13384 = CBS 121100, Australia ex-epitype CPC 39789 = CBS 149184	South Africa	<i>Corymbia variegata</i> , leaves <i>Corymbia citriodora</i> , leaves	G. Price J. Roux	EF394866.1 ON811541.1	KF901882.1 ON811598.1	KF902407.1 ON803559.1	KF902982.1 ON803608.1	<i>actA</i> : KF903646.1, <i>cmdA</i> : KF902698.1 <i>actA</i> : ON803525.1, <i>cmdA</i> : ON803529.1

<sup>1</sup> BILAS: Herbarium of Institute of Botany, Nature Research Centre, Vilnius, Lithuania; BRIP: Plant Pathology Herbarium, Department of Primary Industries, Queensland, Australia; CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands; CMW: Culture Collection of the Forestry and Agricultural Biotechnology Institute (FABI) of the University of Pretoria, Pretoria, South Africa; CPC: Culture collection of Pedro Crous, housed at CBS; ETH: Swiss Federal Institute of Technology Culture Collection, Zurich, Switzerland; FMR: Facultat de Medicina, Universitat Rovira i Virgili, Reus, Spain; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Rai, Thailand; MUCI: Université Catholique de Louvain, Louvain-la-Neuve, Belgium; UTHSC: Fungus Testing Laboratory at the University of Texas Health Science Center, San Antonio, TX, USA.

<sup>2</sup> 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; *rpb1*: partial DNA-directed RNA polymerase II largest subunit gene; *rpb2*: partial DNA-directed RNA polymerase II second largest subunit gene; SSU: small subunit (18S) of the nrRNA gene operon; *tef1*: partial translation elongation factor 1- $\alpha$  gene; *tub2*: partial beta-tubulin gene.

Overview phylogenies: Phylogenies based on LSU sequence alignments per class are provided for the species treated here and are discussed in the species notes where applicable. Some classes were split into order-specific trees to facilitate layout or improve the alignment. Overview phylogenies are provided for *Dothideomycetes* (diverse orders; Fig. 1, two parts), *Dothideomycetes* (*Pleosporales*; Fig. 2), *Eurotiomycetes* (*Chaetothyriales*; Fig. 3), *Leotiomycetes* (diverse orders; Fig. 4), *Orbiliomycetes* (*Orbiliales*; Fig. 5), *Sordariomycetes* (diverse orders; Fig. 6), *Sordariomycetes* (*Hypocreales* and *Glomerales*; Fig. 7), and *Sordariomycetes* (*Xylariales*; Fig. 8). The major differences between the IQ-TREE and MrBayes analyses of the *Leotiomycetes* LSU alignment pertained to the placement of, for example, *Ascocorticiaceae* (basal to *Pseudeurotiaceae* in the Bayesian analysis but terminal inside this family in the IQ-TREE analysis). Also, the positions of *Chaetomellaceae* and *Phacidiales* were not consistent between the two analyses, as is evident from the basal polytomies involving those lineages in Fig. 4.

Species phylogenies: Specific phylogenetic analyses were run for selected species and the resulting phylogenies are discussed in the species notes where applicable.

The optimal identity thresholds to discriminate filamentous fungal species followed Vu *et al.* (2019), with secondary DNA barcodes generated where necessary (Stielow *et al.* 2015).

## Taxonomy

***Ascochyta nigripyncnidia*** (Boerema *et al.*) Qian Chen & L. Cai, *Stud. Mycol.* **82**: 187. 2015. Fig. 9.

*Basionym*: *Phoma nigripyncnidia* Boerema *et al.*, *Persoonia* **16**: 356. 1997.

*Synonyms*: *Ascochyta nigripyncnidiicola* Ondřej, *Biológia*, Bratislava **23**: 816. 1968.

*Stagonosporopsis nigripyncnidiicola* (Ondřej) Boerema *et al.*, *Persoonia* **16**: 356. 1997.

*Taxonomic lineage*: *Dothideomycetes*, *Pleosporales*, *Didymellaceae*.

On PNA. *Conidiomata* pycnidial, solitary to aggregated, globose to subglobose, glabrous, black, 150–300  $\mu$ m diam with prominent papillate neck giving rise to central ostiole; wall of 3–6 layers of brown *textura angularis*. *Conidiogenous cells* phialidic, hyaline, smooth-walled, ampulliform with prominent neck (2–4  $\mu$ m long), 7–10  $\times$  7–9  $\mu$ m. *Conidia* cylindrical, hyaline, smooth- and thin-walled, aseptate, biguttulate, ends obtuse, (7–)8(–9)  $\times$  2(–2.5)  $\mu$ m.

*Culture characteristics*: Colonies flat, spreading, with moderate to abundant aerial mycelium and smooth, lobate margin, covering dish after 1 wk at 25 °C. On MEA, PDA and OA surface and reverse iron grey.

*Material examined*: **Russia**, Rostov region, Krasnosulinsky district, state natural wildlife area “Gornensky”, edge of ravine forest, on *Vicia tenuifolia* (*Fabaceae*), 27 Jun. 2020, T.S. Bulgakov, HPC 3374 = PC 073 = CBS H-24794 = LE F-332412, culture CPC 39716 = CBS 148249.

*Notes*: *Ascochyta nigripyncnidia* (conidia 5.5–9  $\times$  1.5–2  $\mu$ m) was described from *Vicia cracca* in the Czech Republic (ex-type CBS 116.96) (Boerema *et al.* 1997, Chen *et al.* 2015), and is a good match for the present collection from Russia (*Didymellaceae*, *Pleosporales*; Fig. 2).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Ascochyta nigripyncnidia* [strain CBS 116.96, GenBank NR\_135978.1; Identities = 485/486 (99 %), no gaps], *Dothiorella gregaria* [strain TS08-158-2, GenBank AB470899.1; Identities =

515/522 (99 %), one gap (0 %)], *Phomatodes nebulosa* [strain 21, GenBank MW580418.1; Identities = 514/521 (99 %), no gaps], and *Ascochyta rabiei* [voucher BAR-5, GenBank MK074843.1; Identities = 513/521 (98 %), no gaps]. Closest hits using the LSU sequence are *Ascochyta nigripyncnidia* [strain CBS 116.96, GenBank



**Fig. 1.** Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis of the *Dothideomycetes* (diverse orders) LSU nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast bootstrap replicates are shown at the nodes. Culture collection numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Diaporthe perijuncta* (voucher BPI 748437; GenBank NG\_059064.1) and the species treated here are highlighted with coloured blocks and bold face. Accession numbers of sequence from material with a type status are also shown in bold face. Families and orders are indicated with coloured blocks to the right of the tree.



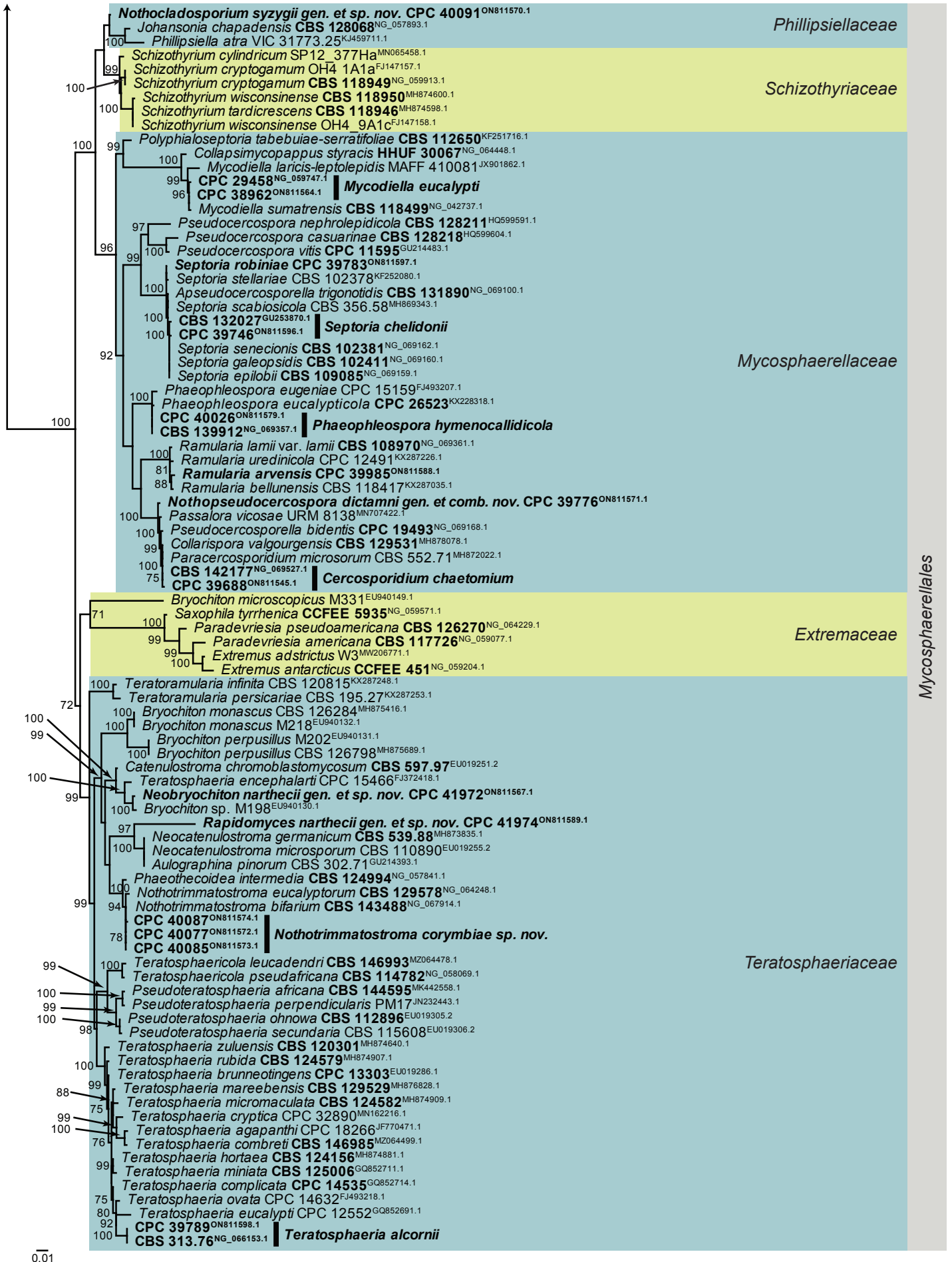
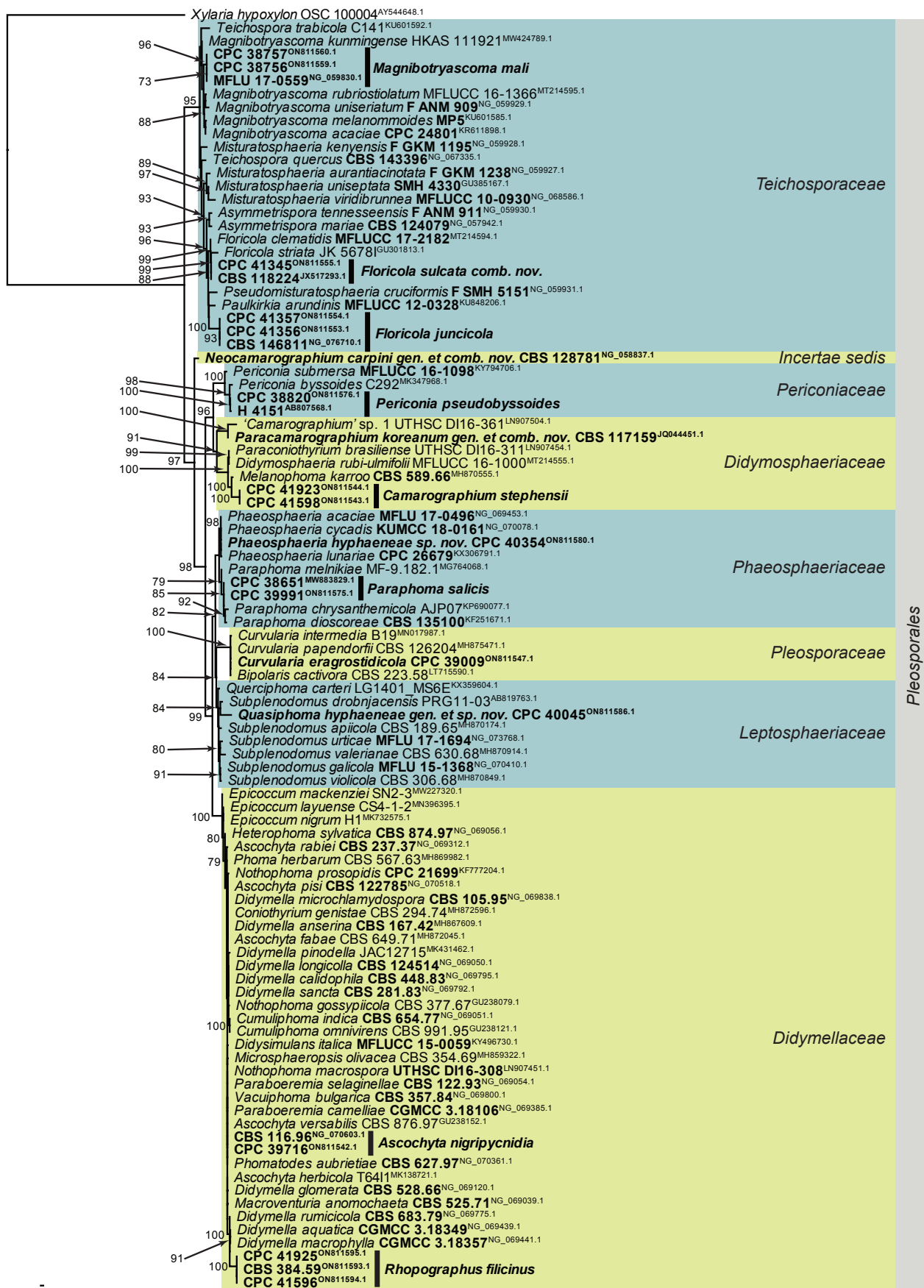
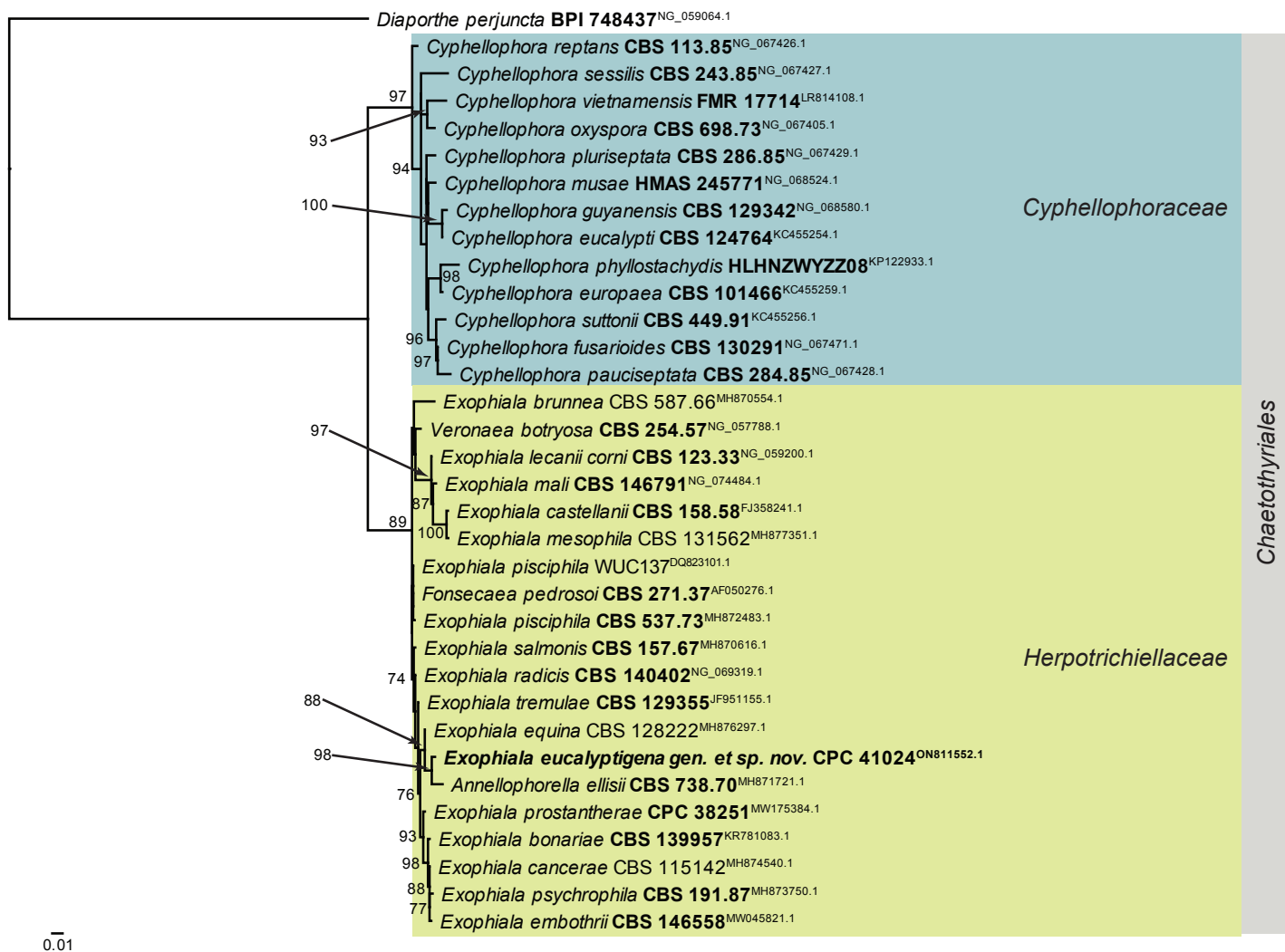


Fig. 1. (Continued).



**Fig. 2.** Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis of the *Dothideomycetes* (*Pleosporales*) LSU nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast bootstrap replicates are shown at the nodes. Culture collection numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Xylaria hypoxylon* (voucher OSC 100004; GenBank AY544648.1) and the species treated here are highlighted with coloured blocks and bold face. Accession numbers of sequence from material with a type status are also shown in bold face. Families and orders are indicated with coloured blocks to the right of the tree.



**Fig. 3.** Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis of the *Eurotiomycetes* LSU nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast bootstrap replicates are shown at the nodes. Culture collection numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Diaporthe perijuncta* (voucher BPI 748437; GenBank NG\_059064.1) and the species treated here is highlighted with bold face. Accession numbers of sequence from material with a type status are also shown in bold face. Families and orders are indicated with coloured blocks to the right of the tree.

NG\_070603.1; Identities = 818/818 (100%), no gaps], *Vacuiphoma bulgarica* [strain CBS 357.84, GenBank NG\_069800.1; Identities = 818/818 (100%), no gaps], *Paraboeremia camelliae* [strain CGMCC 3.18106, GenBank NG\_069385.1; Identities = 818/818 (100%), no gaps], and *Paraboeremia litseae* [strain CGMCC 3.18109, GenBank NG\_069384.1; Identities = 818/818 (100%), no gaps]. Closest hits using the *rpb2* sequence had highest similarity to *Ascochyta nigripyncnidia* [strain CBS 116.96, GenBank MT018253.1; Identities = 592/596 (99%), no gaps], *Ascochyta koolunga* [strain BRIP 70265, GenBank MN604922.1; Identities = 736/794 (93%), no gaps], and *Ascochyta lentis* [as *Didymella lentis*; strain ATCC 96419, GenBank EU874862.1; Identities = 777/839 (93%), no gaps]. No significant hits were obtained when the *tef1* (first part) sequence was used in blastn and megablast searches.

**Authors:** P.W. Crous & J.Z. Groenewald

***Ascocorticium sorbicola*** Crous & Declercq, *sp. nov.* MycoBank MB 844288. Fig. 10.

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

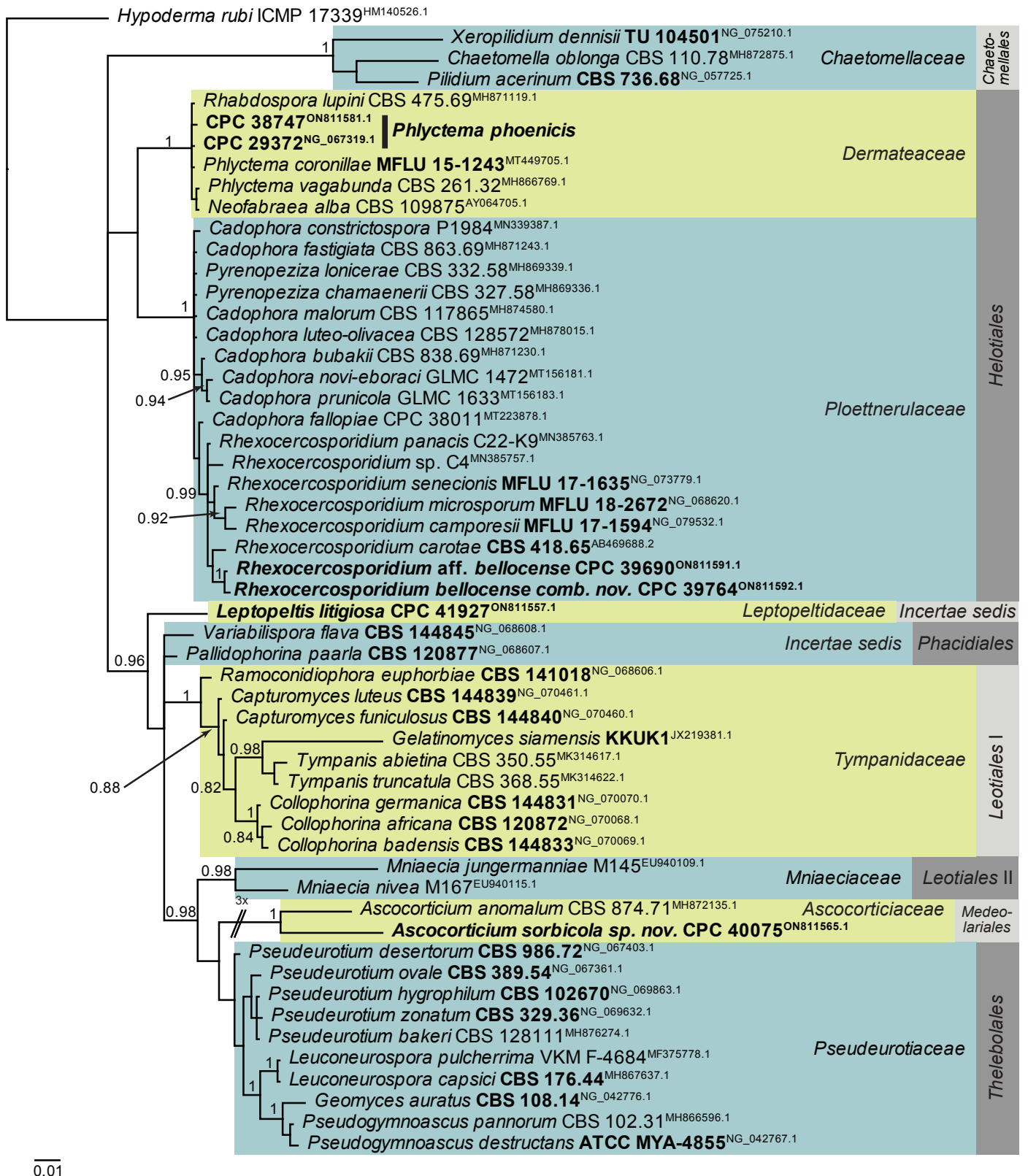
*Mycelium* consisting of hyaline, smooth-walled, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells arising directly from hyphae, hyaline, smooth- and thin-walled, subulate, straight to flexuous, proliferating sympodially, forming a rachis in upper part, 20–42 × 2–3 µm, with multiple subdenticulate loci, slightly thickened and refractive, not darkened. *Conidia* solitary, hyaline, aseptate, smooth- and thin-walled, guttulate, subglobose, (3–) 3.5(–4) × 2.5(–3) µm; hilum slightly thickened, not darkened, 0.5 µm diam.

**Culture characteristics:** Colonies erumpent, spreading, surface folded, with sparse aerial mycelium and feathery, lobate margin, reaching 4 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white, reverse buff.

**Typus:** Belgium, Genk, Bokrijk, Het Wik, on leaves of *Sorbus aucuparia* (*Rosaceae*), 17 Sep. 2020, B. Declercq, HPC 3511 (**holotype** CBS H-24842, culture ex-type CPC 40075 = CBS 148303).

**Notes:** *Ascocorticium anomalum* is the type of *Ascocorticium*, an ascomycete species which forms white corticioid patches

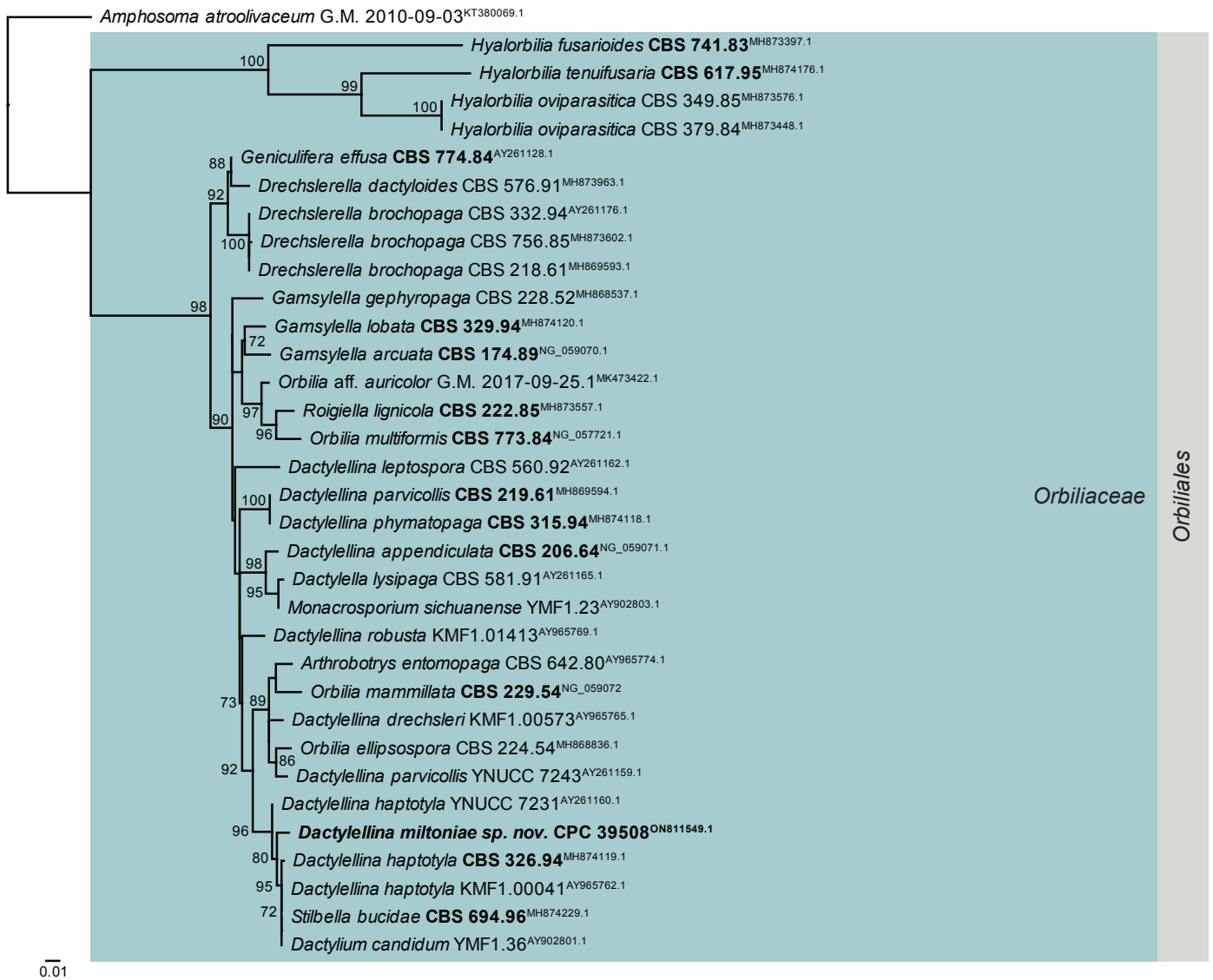




**Fig. 4.** Consensus phylogram (50 % majority rule) obtained from the Bayesian analysis of the *Leotiomyces* LSU nucleotide alignment. Bayesian Posterior Probability values (> 0.79) are shown at the nodes. Culture collection numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Hypoderma rubi* (culture ICMP 17339; GenBank HM140526.1) and the species treated here are highlighted with bold face. Accession numbers of sequence from material with a type status are also shown in bold face. Families and orders are indicated with coloured blocks to the right of the tree.

on wood or bark of gymnosperms and angiosperms, having acrodontium-like asexual morphs. *Ascocorticium sorbicola* is related to *A. anomalum* (conidia broadly ellipsoid, 3.5–5 × 3–3.5 µm), but has slightly smaller, subglobose conidia (Jülich & de

Vries 1982). Phylogenetically (Fig. 4), the two species appear to not be congeneric, but as only a single isolate is available, we choose to describe it in *Ascocorticium* pending further collections.



**Fig. 5.** Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh *et al.* 2020) of the *Orbiliomycetes* LSU nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast bootstrap replicates are shown at the nodes. Culture collection numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Amphosoma atroolivaceum* (voucher G.M. 2010-09-03; GenBank KT380069.1) and the species treated here is highlighted with bold face. Accession numbers of sequence from material with a type status are also shown in bold face. Families and orders are indicated with coloured blocks to the right of the tree.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest (distant) hits using the ITS sequence had highest similarity to *Neohelicosporium krabiense* [voucher HKAS 100725, GenBank NR\_160380.1; Identities = 214/236 (91 %), two gaps (0 %)], *Mikhtomia multicolor* [strain SKA19, GenBank KJ021238.1; Identities = 219/242 (90 %), six gaps (2 %)], and *Ascocorticium anomalum* [strain CBS 874.71, GenBank MH860391.1; Identities = 277/311 (89 %), 12 gaps (3 %)]. Closest hits using the LSU sequence are *Ascocorticium anomalum* [strain CBS 874.71, GenBank MH872135.1; Identities = 757/806 (94 %), six gaps (0 %)], *Sarcoleotia globosa* [strain MBH52476, GenBank AY789428.1; Identities = 759/819 (93 %), six gaps (0 %)], and *Glutinoglossum americanum* [voucher ILLS 64444, GenBank KP690098.1; Identities = 762/823 (93 %), 10 gaps (1 %)]. No significant hits were obtained when the *rpb2* and *tef1* (second part) sequences were used in blastn and megablast searches.

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*Camarographium stephensii* (Berk. & Broome) Bubák, *Ber. dt. bot. Ges.* **34**: 306. 1916. Fig. 11.

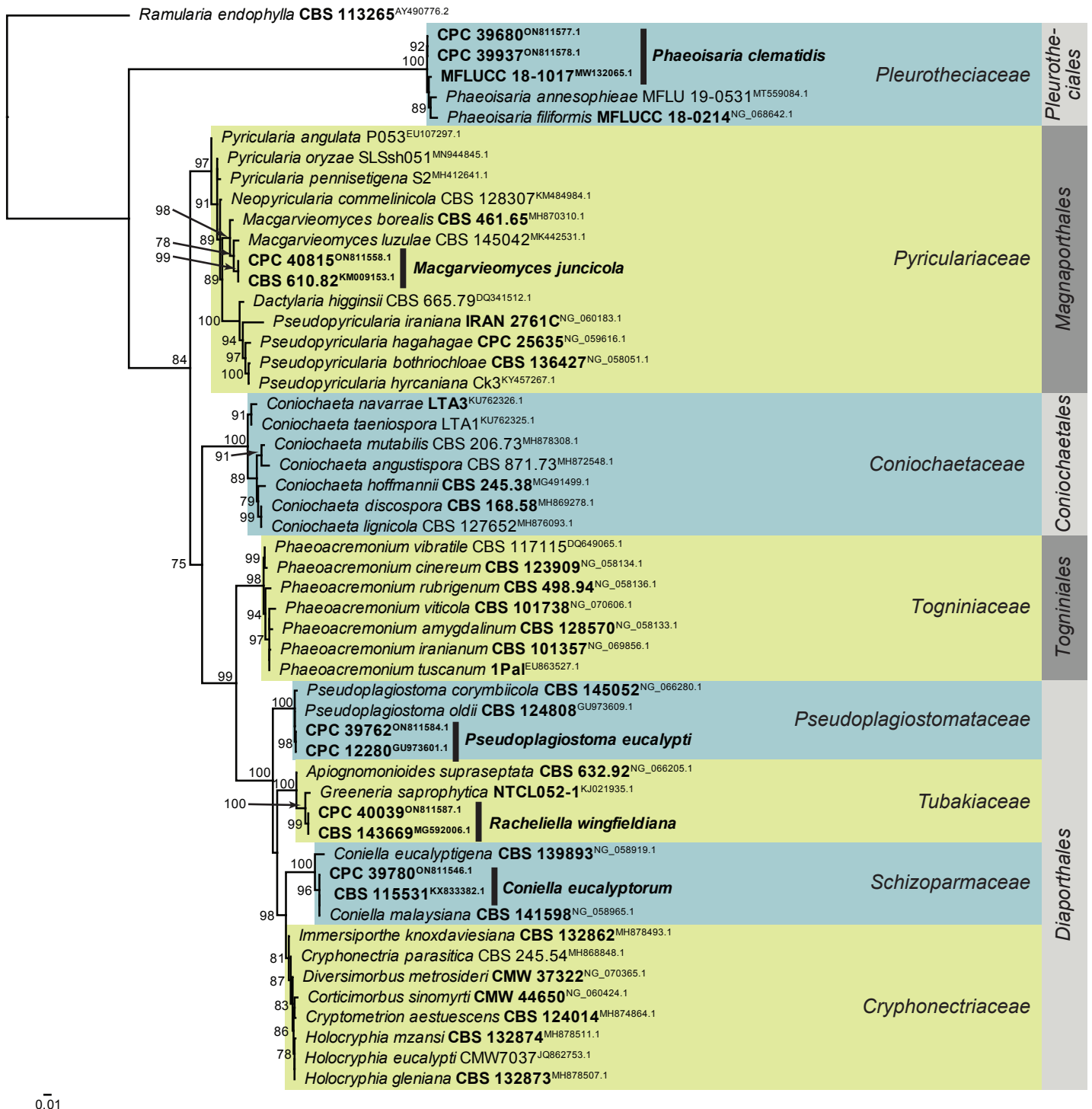
*Basionym*: *Hendersonia stephensii* Berk. & Broome, *Ann. Mag. Nat. Hist., Ser. 2* **7**: 95. 1851.

*Synonym*: *Camarosporium stephensii* (Berk. & Broome) Sacc., *Syll. Fung.* (Abellini) **3**: 469. 1884.

*Taxonomic lineage*: *Dothideomycetes*, *Pleosporales*, *Didymosphaeriaceae*.

*Conidiomata* solitary or aggregated in linear eustromata, separate, globose, papillate, thick-walled, wall of hyaline to pale brown, thin-walled *textura angularis*; stromata linear, eye-shaped, immersed, subepidermal opening by irregular rupture through which ostioles appear, with thick-walled *textura angularis*, connecting pycnidia; elsewhere of hyaline, irregular pseudoparenchyma. *Conidiophores* reduced to conidiogenous cells, solitary, phialidic, enteroblastic, rarely



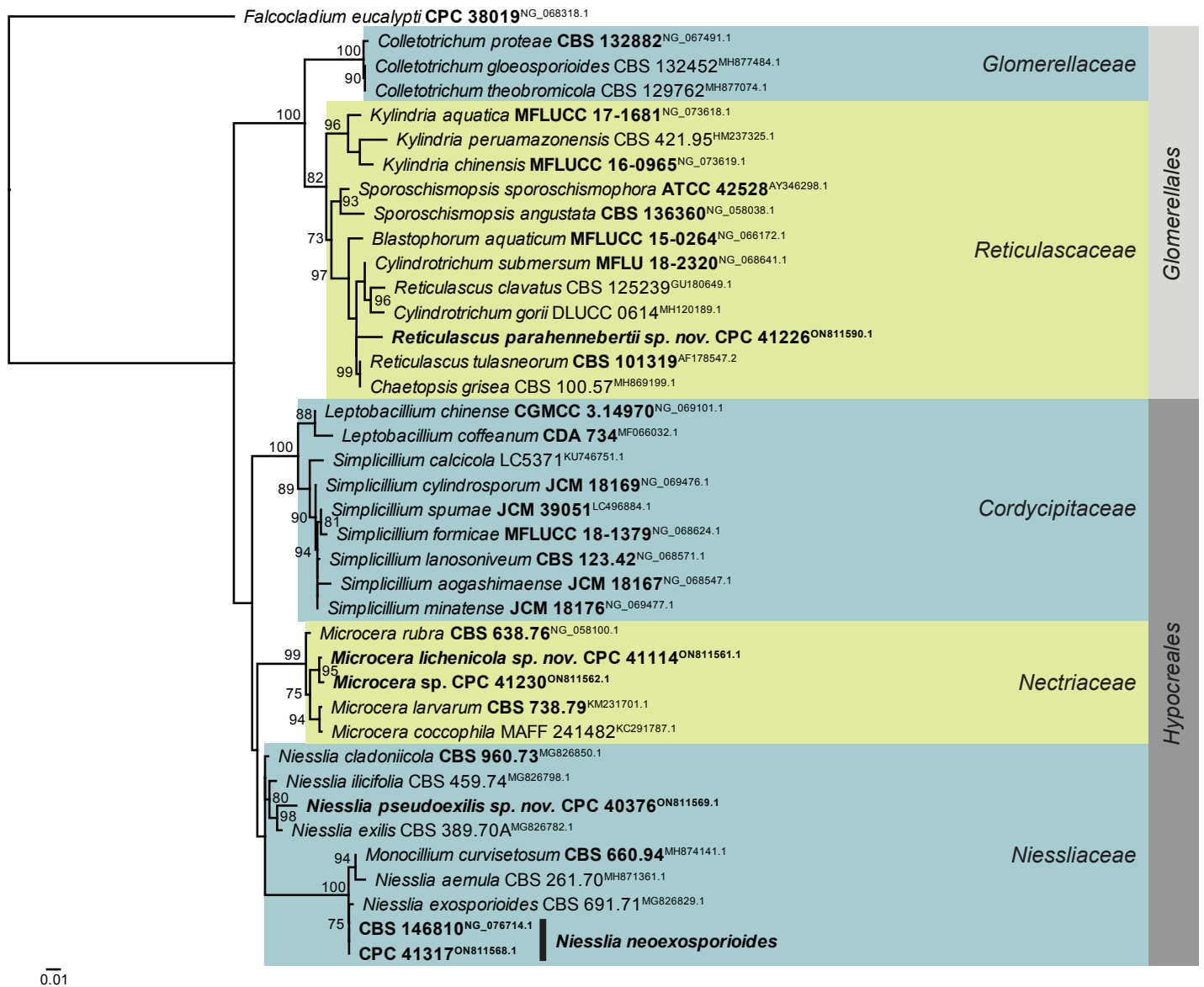


**Fig. 6.** Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis of the *Sordariomycetes* (diverse orders) LSU nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast bootstrap replicates are shown at the nodes. Culture collection numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Ramularia endophylla* (culture CBS 113265; GenBank AY490776.2) and the species treated here are highlighted with coloured blocks and bold face. Accession numbers of sequence from material with a type status are also shown in bold face. Families and orders are indicated with coloured blocks to the right of the tree.

percurrent, ampulliform to doliiform, hyaline, smooth, channel wide, collarette minute to prominent, lining the inner cavity of pycnidium, 7–10 × 4–8 µm. *Conidia* solitary, hyaline, becoming pale brown to brown, smooth to finely roughened, ellipsoid to irregularly so, or globose to obpyriform, apex obtuse, base flattened, 5 µm diam, distoseptate, thick-walled, with 3(–5) thick, transverse septa, and many thinner, longitudinal or oblique septa, (36–)45–50(–52) × (23–)25–28(–31) µm.

*Typus:* **Netherlands**, Utrecht Province, Bilthoven, on dead leaf fronds of *Pteridium aquilinum* (*Hypolepidaceae*), Jun. 2021, P.W. Crous, HPC 3632 (**neotype** designated here CBS H-24988, MBT 10007396, culture ex-neotype CPC 41598, CPC 41599 = CBS 149168).

*Additional material examined:* **Netherlands**, Utrecht Province, Lage Vuursche, on stem of *Pteridium aquilinum*, 13 Jun. 2021, P.W. Crous, HPC 3645, cultures CPC 41923, CPC 41924.

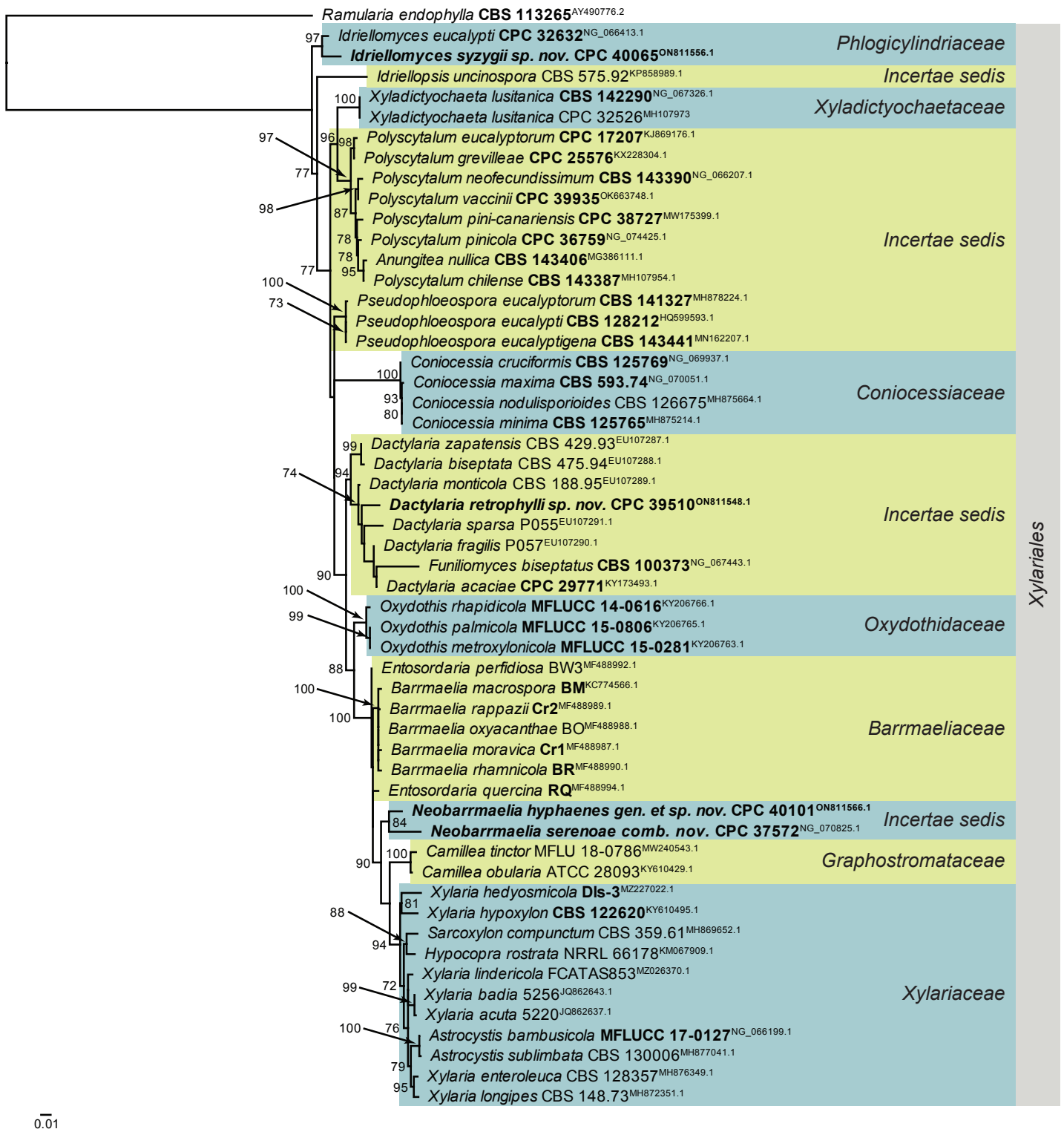


**Fig. 7.** Consensus phylogram (50% majority rule) obtained from the maximum likelihood analysis of the *Sordariomycetes* (*Glomerales* and *Hypocreales*) LSU nucleotide alignment. Bootstrap support values (> 69% are shown; only values > 94% are significant) from 5 000 ultrafast bootstrap replicates are shown at the nodes. Culture collection numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Falcocladium eucalypti* (culture CPC 38019; GenBank NG\_068318.1) and the species treated here are highlighted with coloured blocks and bold face. Accession numbers of sequence from material with a type status are also shown in bold face. Families and orders are indicated with coloured blocks to the right of the tree.

**Notes:** The genus *Camarographium* (*Didymosphaeriaceae*, *Pleosporales*), was introduced by Bubák (1916) with *C. stephensii* as type species. Because type material has presumably been lost, a neotype is designated here. Given the phylogenetic placement (Fig. 2) of *C. stephensii*, other species of *Camarographium* that are known from DNA sequence data need to be accommodated elsewhere (see below).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 41598 had highest similarity to *Didymosphaeria rubi-ulmifolii* [strain 8910, GenBank MK646046.1; Identities = 422/443 (95%), no gaps], *Paraconiothyrium brasiliense* [strain A1202B, GenBank MT230470.1; Identities = 422/443 (95%), no gaps], and *Albifimbria verrucaria* [as *Myrothecium verrucaria*; strain F0705, GenBank AB693919.1; Identities = 421/443 (95%), no gaps]. The ITS sequences of CPC 41598 and 41923 are identical. Closest hits using the **LSU** sequence

of CPC 41923 are *Melanophoma karroo* [strain CBS 589.66, GenBank MH870555.1; Identities = 790/805 (98%), two gaps (0%)], *Paraconiothyrium brasiliense* [strain UTHSC DI16-311, GenBank LN907454.1; Identities = 783/802 (98%), one gap (0%)], and *Didymosphaeria rubi-ulmifolii* [strain MFLUCC 16-1000, GenBank MT214555.1; Identities = 785/805 (98%), two gaps (0%)]. The LSU sequences of CPC 41598 and 41923 are identical. Closest hits using the **tef1** (first part) sequence of CPC 41923 had distant similarity to *Paraconiothyrium hakeae* [strain CBS 142521, GenBank KY979892.1; Identities = 363/442 (82%), 25 gaps (5%)], *Paraphaeosphaeria xanthorrhoeae* [strain CBS 142164, GenBank KY979888.1; Identities = 255/299 (85%), five gaps (1%)], and *Paraphaeosphaeria parmeliae* [strain CBS 131728, GenBank KP170679.1; Identities = 281/336 (84%), 20 gaps (5%)]. The **tef1** sequences of CPC 41598 and 41923 are identical. Closest hits using the **tub2** sequence of CPC 41923 had distant similarity to *Paraconiothyrium hakeae* [strain CBS



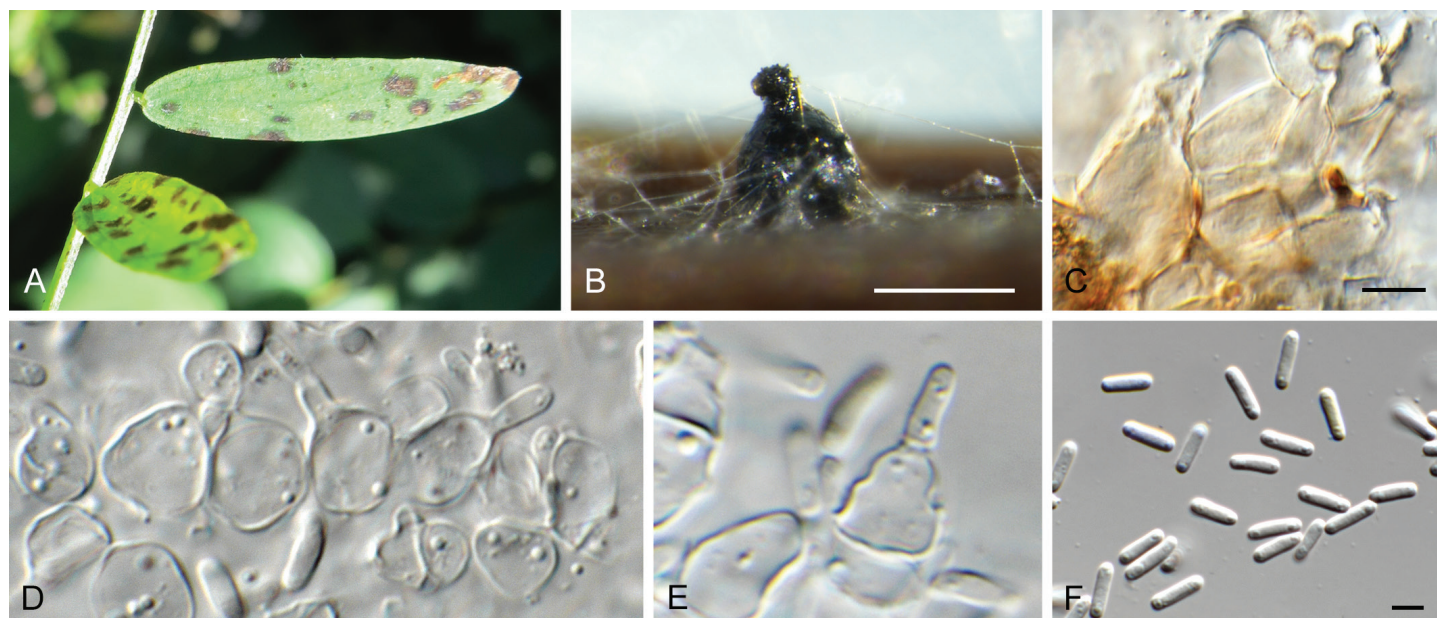
**Fig. 8.** Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis of the *Sordariomycetes* (*Xylariales*) LSU nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast bootstrap replicates are shown at the nodes. Culture collection numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Ramularia endophylla* (culture CBS 113265; GenBank AY490776.2) and the species treated here are highlighted with coloured blocks and bold face. Accession numbers of sequence from material with a type status are also shown in bold face. Families and orders are indicated with coloured blocks to the right of the tree.

142521, GenBank KY979920.1; Identities = 458/535 (86 %), 14 gaps (2 %)], *Paraconiothyrium variabile* [strain CBS 504.84, GenBank JX496434.1; Identities = 389/455 (85 %), 14 gaps (3 %)], and *Paraphaeosphaeria xanthorrhoeae* [strain CBS 142164, GenBank KY979909.1; Identities = 441/538 (82 %), 17

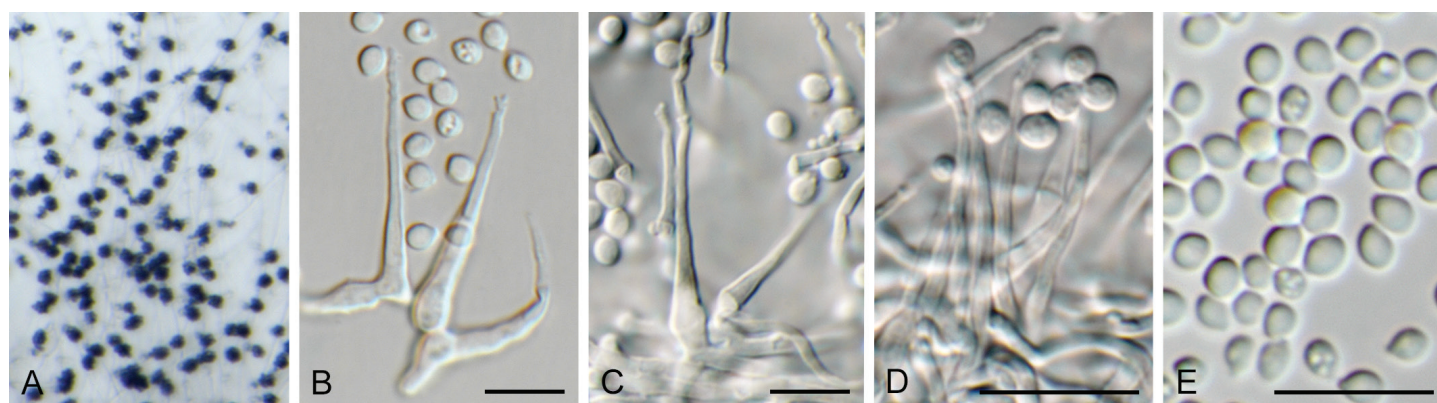
gaps (3 %)]. The *tub2* sequences of CPC 41598 and 41923 are identical.

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**Fig. 9.** *Ascochyta nigripyncnidia* (CPC 39716). **A.** Leaf spot symptoms on *Vicia tenuifolia*. **B.** Conidioma on PNA. **C–E.** Conidiogenous cells. **F.** Conidia. Scale bars: B = 300  $\mu\text{m}$ , all others = 10  $\mu\text{m}$ .



**Fig. 10.** *Ascocorticium sorbicola* (CPC 40075). **A.** Conidiophores on SNA. **B–D.** Conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars = 10  $\mu\text{m}$ .

***Cercosporidium chaetomium*** (Cooke) Deighton, Mycol. Pap. 112: 27. 1967. Fig. 12.

**Basionym:** *Cladosporium chaetomium* Cooke, Grevillea 17(no. 83): 66. 1889.

**Taxonomic lineage:** *Dothideomycetes*, *Mycosphaerellales*, *Mycosphaerellaceae*.

**Leaf spots** amphigenous, round, 2–3 mm diam, fair grey with red-purple margin. **Conidiophores** fasciculate, amphigenous, brown with minute brown stroma, subcylindrical, verruculose, 0–2-septate, unbranched, 10–25  $\times$  4–6  $\mu\text{m}$ . **Conidiogenous cells** terminal, integrated, brown, verruculose, subcylindrical, 10–15  $\times$  3–4  $\mu\text{m}$ ; scars terminal, round, thickened, darkened, 1.5–2  $\mu\text{m}$  diam. **Conidia** solitary, straight to slightly curved, obclavate, apex subobtuse, base obconically tapered to truncate hilum, pale brown, finely roughened, guttulate, (0–)3(–6)-septate, (20–)35–50(–60)  $\times$  (3–)3.5(–4)  $\mu\text{m}$ ; hila thickened, darkened, refractive, 2  $\mu\text{m}$  diam. Conidia much longer in culture (–200  $\mu\text{m}$ ), and at times undergoing microcyclic conidiation.

**Culture characteristics:** Colonies erumpent, surface folded, with sparse aerial mycelium and feathery, lobate margin, reaching 7

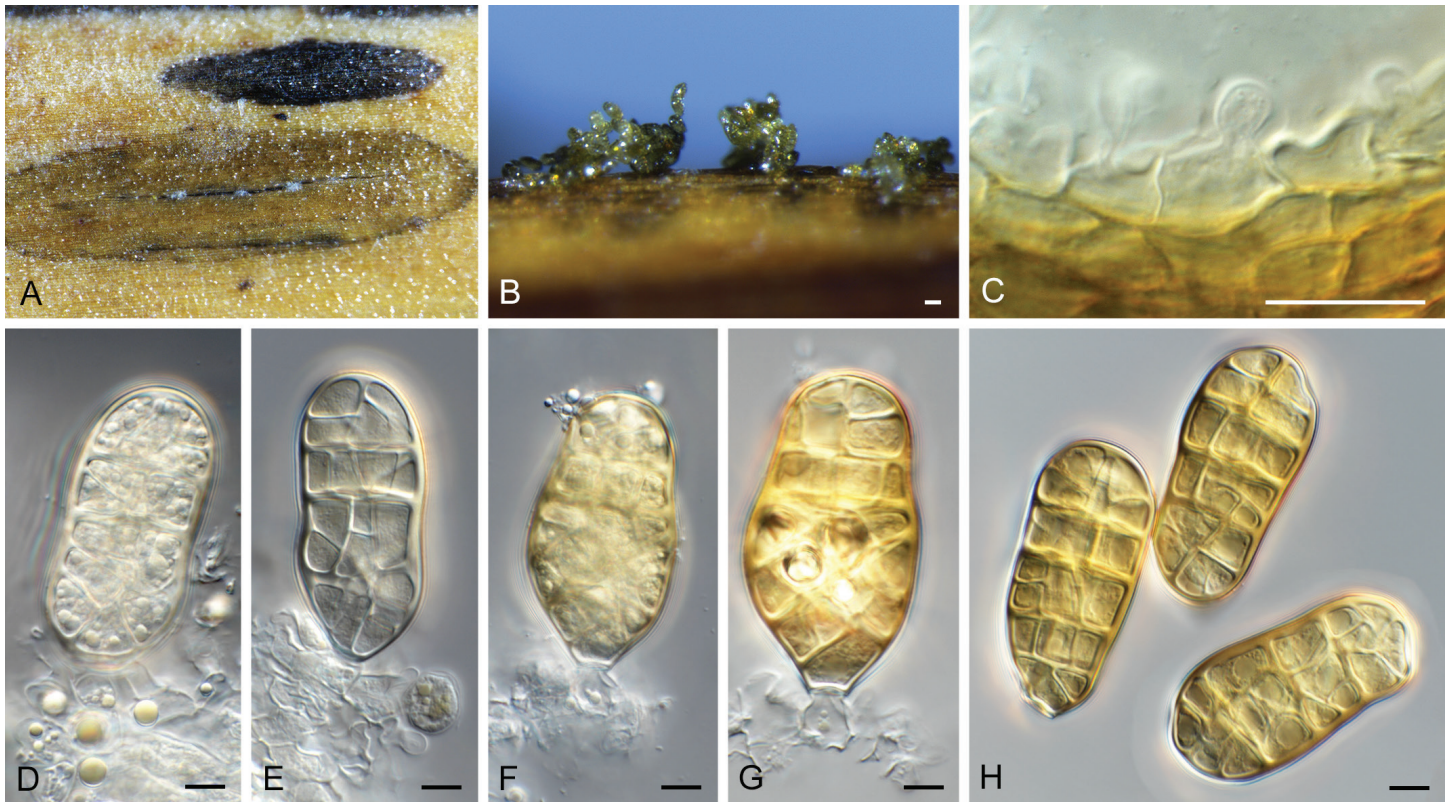
mm diam after 7 d at 25  $^{\circ}\text{C}$ . On MEA surface smoke grey, reverse olivaceous grey with diffuse red pigment; on PDA surface and reverse olivaceous grey; on OA surface smoke grey.

**Material examined:** **Russia**, Rostov region, Krasnosulinsky district, state natural wildlife area “Gornensky”, roadside, on *Polygonum aviculare* (*Polygonaceae*), 13 Jun. 2020, T.S. Bulgakov, HPC 3312 = PC 054 = CBS H-24899 = LE F-332404, culture CPC 39688 = CBS 148457.

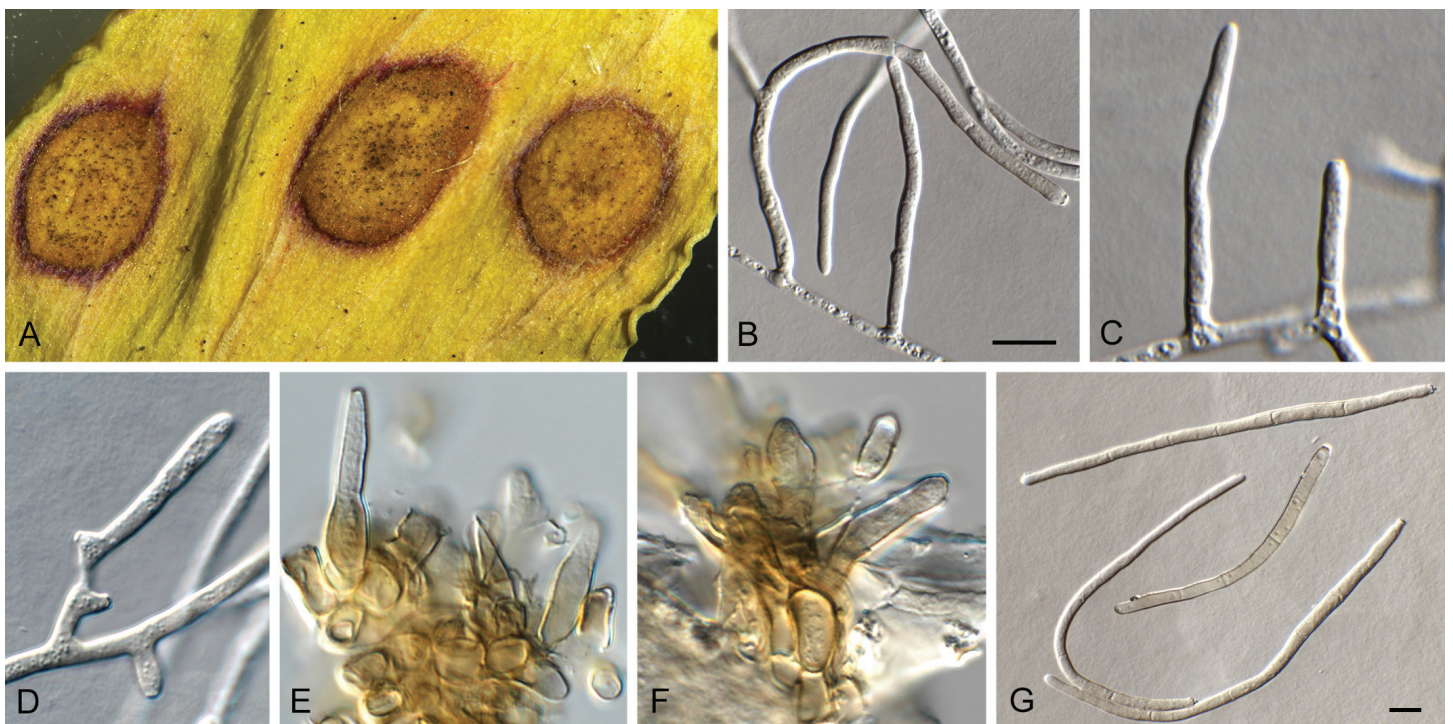
**Notes:** *Cercosporidium chaetomium* is the type species of the genus *Cercosporidium*, which was resurrected as distinct from *Passalora* by Videira et al. (2017). *Cercosporidium* is a common foliar pathogen, reported here from leaf spots on *Polygonum aviculare* in Russia. The genus belongs to *Mycosphaerellaceae* (*Mycosphaerellales*; Fig. 1 part 2) and the species is sister to *Cercosporidium californicum* and *Cercosporidium miurae* (Fig. 13).

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cercosporidium chaetomium* [strain CBS 142177, GenBank NR\_156367.1; Identities = 470/474 (99 %), one gap (0 %)], *Cercosporidium californicum* [strain CPC 18389, GenBank NR\_156239.1; Identities = 500/506 (99 %), one gap (0 %)], *Claroehilum henningsii* [strain IR-9, GenBank LC565143.1;





**Fig. 11.** *Camarographium stephensii* (CPC 41599). **A.** Immersed conidiomata. **B.** Conidial cirrus. **C.** Conidiogenous cells. **D–G.** Conidiogenous cells giving rise to conidia. **H.** Conidia. Scale bars: B = 30  $\mu\text{m}$ , all others = 10  $\mu\text{m}$ .

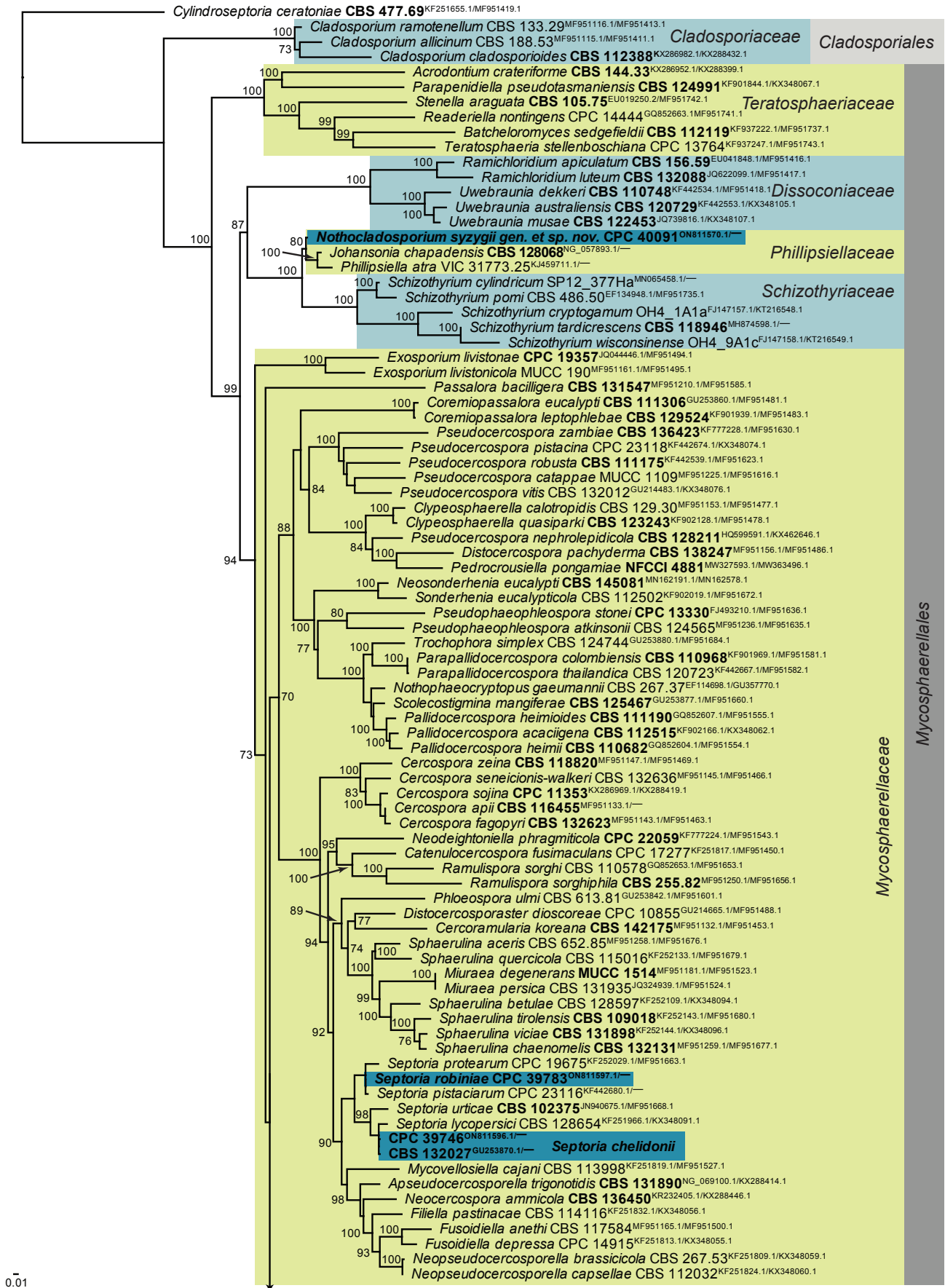


**Fig. 12.** *Cercosporidium chaetomium* (CPC 39688). **A.** Leaf spots on *Polygonum aviculare*. **B–D.** Conidiophores and conidiogenous cells in culture. **E, F.** Conidiophores *in vivo*. **G.** Conidia. Scale bars = 10  $\mu\text{m}$ .

Identities = 499/505 (99 %), no gaps], and *Passalora dissiliens* [as *Phaeoramularia dissiliens*; strain CBS 219.77, GenBank AF222835.1; Identities = 483/489 (99 %), no gaps]. Closest hits using the **LSU** sequence are *Collarispora valgourgensis* [strain CBS 129531, GenBank MH878078.1; Identities = 688/689 (99 %), no gaps], *Paracercosporidium microsorum* [as *Mycosphaerella*

*microsora*; strain CBS 552.71, GenBank MH872022.1; Identities = 688/689 (99 %), no gaps], and *Cercosporidium chaetomium* [strain CBS 142177, GenBank NG\_069527.1; Identities = 686/687 (99 %), no gaps]. Closest hits using the **rpb2** sequence had highest similarity to *Cercosporidium chaetomium* [strain CBS 142177, GenBank MF951474.1; Identities = 718/718 (100 %),





**Fig. 13.** Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Mycosphaerellales* and *Cladosporiales* concatenated (LSU, *rpb2*) nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast bootstrap replicates are shown at the nodes. Culture collection numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Cylindroseptoria ceratoniae* (culture CBS 477.69; GenBank KF251655.1 and MF951419.1, respectively) and the species treated here are highlighted with coloured blocks and bold face. Accession numbers of sequence from material with a type status are also shown in bold face. Families and orders are indicated with coloured blocks to the right of the tree.

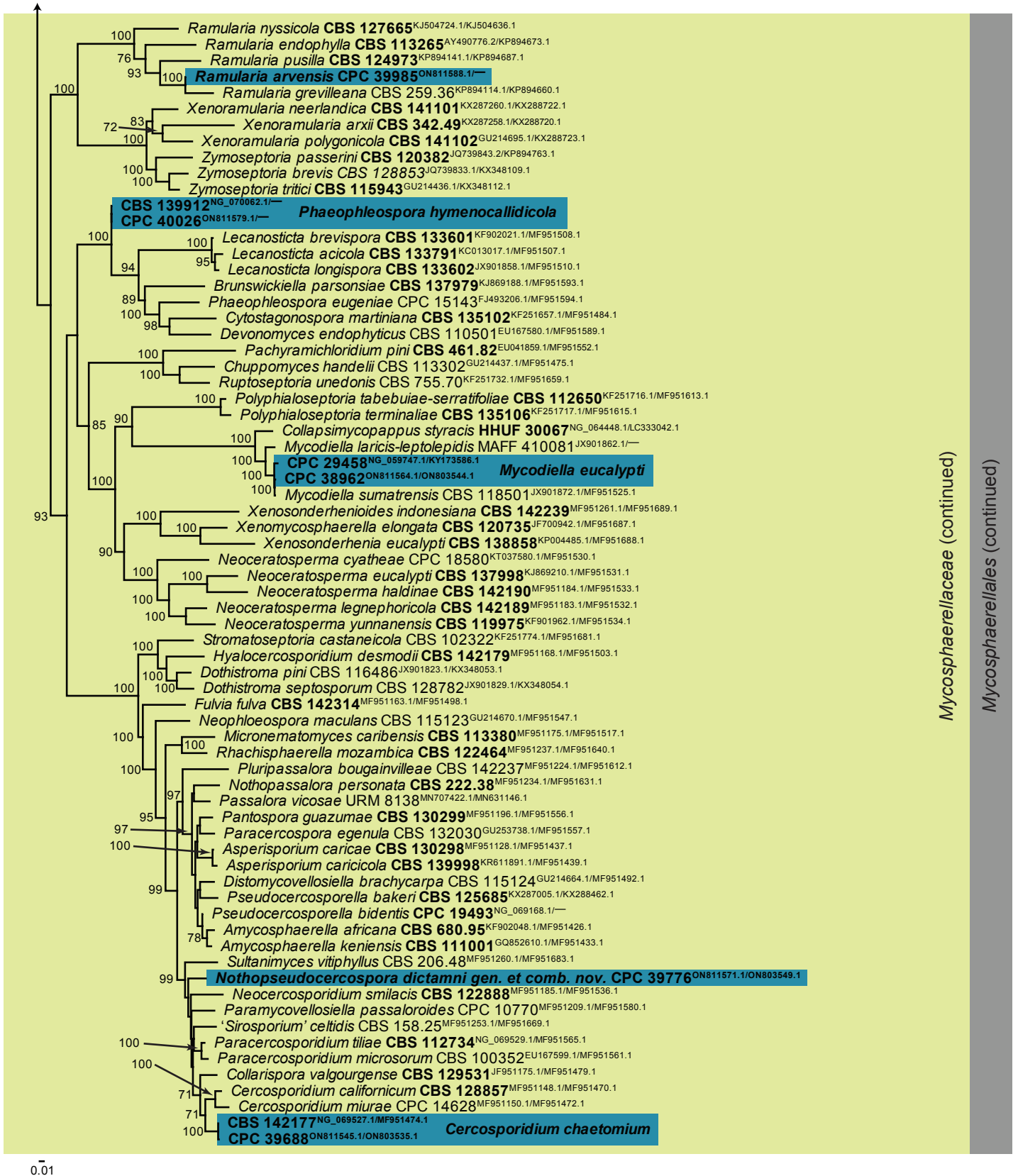


Fig. 13. (Continued).

no gaps], *Cercosporidium californicum* [strain CPC 18389, GenBank MF951471.1; Identities = 667/718 (93 %), no gaps], and *Collarispora valgourgensis* [strain CBS 125311, GenBank MF951480.1; Identities = 575/624 (92 %), no gaps].

*Coniella eucalyptorum* (Crous & M.J. Wingf.) L.V. Alvarez & Crous, *Stud. Mycol.* **85**: 15. 2016. Fig. 14.  
*Basionym*: *Pilidiella eucalyptorum* Crous & M.J. Wingf., *Mycol. Res.* **108**: 296. 2004.

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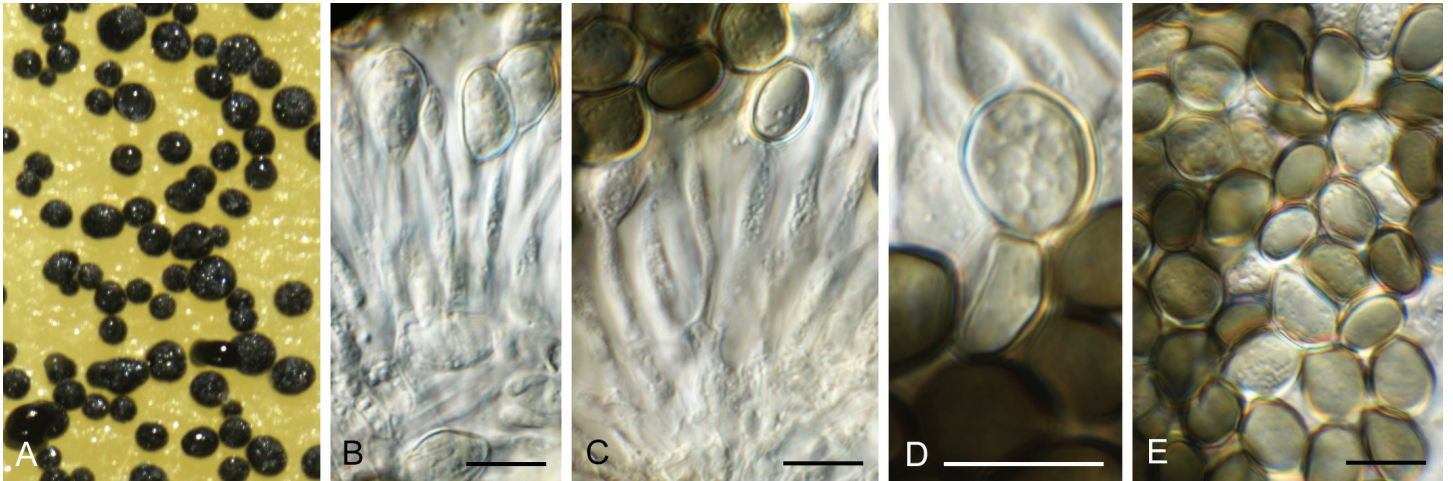


Fig. 14. *Coniella eucalyptorum* (CPC 39780). A. Conidiomata on OA. B–D. Conidiogenous cells giving rise to conidia. E. Conidia. Scale bars = 10  $\mu$ m.

**Taxonomic lineage:** Sordariomycetes, Diaporthales, Schizoparmaceae.

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

**Material examined:** South Africa, KwaZulu-Natal Province, Kwambonambi, on leaves of *Eucalyptus benthamii* (Myrtaceae), 8 Jun. 2020, J. Roux, HPC 3442, culture CPC 39780 = CBS 149182.

**Notes:** The genus *Coniella* includes saprobes, endophytes and plant pathogens (Alvarez et al. 2016). Of these, *Coniella eucalyptorum* is regarded as one of the more important foliar pathogens of *Eucalyptus*, and has been shown to cause significant defoliation on certain *Eucalyptus* species (Crous et al. 2019c). This is the first record of *C. eucalyptorum* occurring in South Africa. The species belongs to Schizoparmaceae (Diaporthales; Fig. 6).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Coniella eucalyptorum* [strain CBS 112733, GenBank KX833548.1; Identities = 590/590 (100 %), no gaps], *Coniella malaysiana* [strain CBS 141598, GenBank NR\_154820.1; Identities = 549/553 (99 %), no gaps], and *Coniella eucalyptigena* [strain CBS 139893, GenBank NR\_137983.1; Identities = 558/574 (97 %), two gaps (0 %)]. Closest hits using the LSU sequence are *Coniella eucalyptorum* [strain CBS 115531, GenBank KX833382.1; Identities = 815/815 (100 %), no gaps], *Coniella malaysiana* [strain CBS 141598, GenBank NG\_058965.1; Identities = 785/785 (100 %), no gaps], and *Coniella eucalyptigena* [strain CBS 139893, GenBank NG\_058919.1; Identities = 799/811 (99 %), no gaps]. Closest hits using the *tef1* (first part) sequence had highest similarity to *Coniella eucalyptorum* [strain CBS 114841, GenBank KX833646.1; Identities = 495/495 (100 %), no gaps], *Coniella malaysiana* [strain CBS 141598, GenBank KX833688.1; Identities = 408/465 (88 %), 14 gaps (3 %)], and *Coniella granati* [strain CBS 252.38, GenBank KX833681.1; Identities = 259/304 (85 %), 17 gaps (5 %)]. No significant hits were obtained when the *tub2* sequence was used in blastn and megablast searches.

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***Curvularia eragrostidicola*** Y.P. Tan & R.G. Shivas, *MycoKeys* 35: 14. 2018. Fig. 15.

**Taxonomic lineage:** Dothideomycetes, Pleosporales, Pleosporaceae.

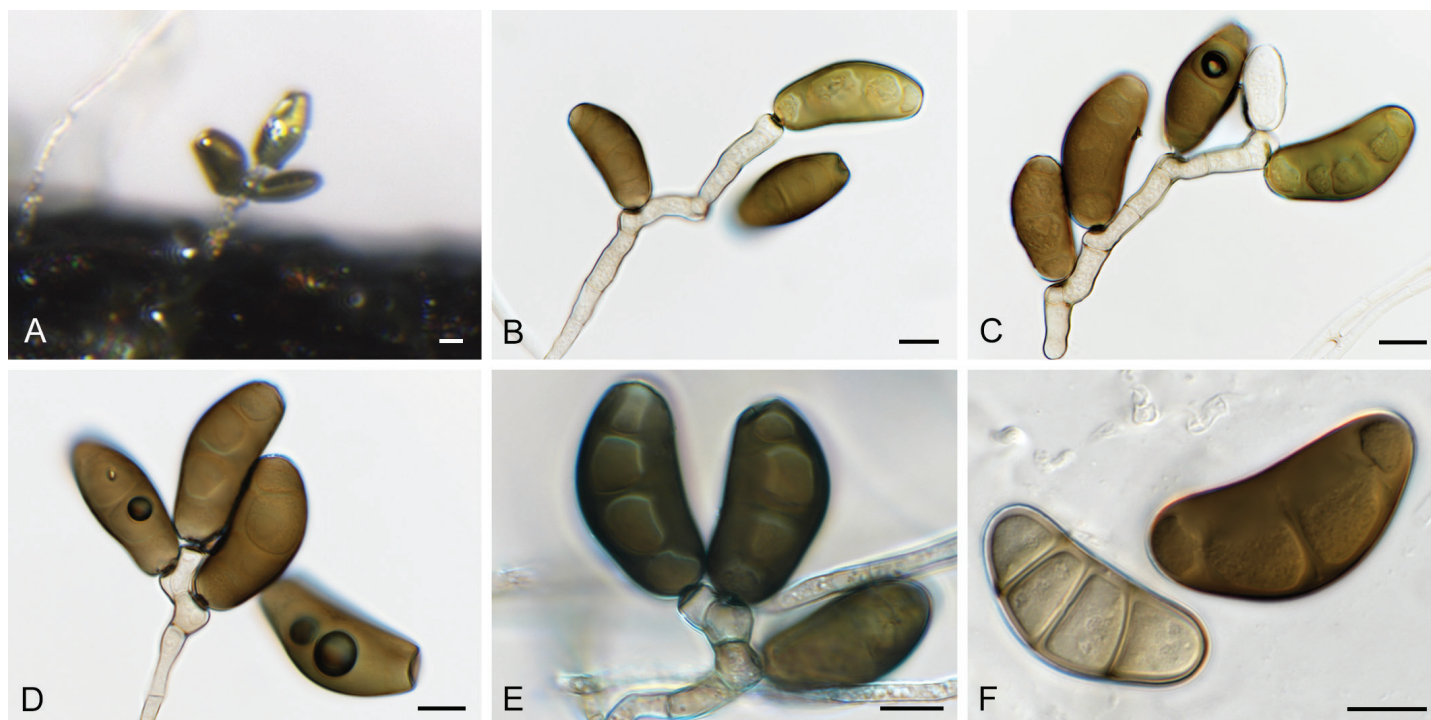
**Mycelium** consisting of pale brown, smooth, branched, septate, 3–4  $\mu$ m diam hyphae. **Conidiophores** solitary, erect, flexuous, subcylindrical, branched or not, pale brown to brown, smooth, geniculous-sinuuous, 3–12-septate, 25–130  $\times$  5–6  $\mu$ m. **Conidiogenous cells** integrated, terminal and intercalary, polytretic, sympodial, pale to medium brown, 7–15  $\times$  5–6  $\mu$ m; scars darkened, thickened, 3–4  $\mu$ m diam. **Conidia** ellipsoid-fusoid, widest in middle, tapering to obtuse ends, 3(–4)-distoseptate, septa not darkened, nor constricted, uniformly medium brown throughout, smooth-walled, swollen in second cell from apex, curved, hila thickened and darkened, 2–3  $\mu$ m diam, (33–)36–38(–40)  $\times$  (15–)16–17(–18)  $\mu$ m.

**Culture characteristics:** Colonies erumpent, spreading, with moderate to abundant aerial mycelium and smooth, even margin, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, reverse iron-grey.

**Material examined:** Namibia, Gobabeb Desert Namib Research Institute, Mirabib, on the dung of *Procapra* sp. (Procapridae), 19 Nov. 2019, P.W. Crous, HPC 3110 = CBS H-24532, culture CPC 39009 = CBS 147069.

**Notes:** *Curvularia eragrostidicola* was described from inflorescences of *Eragrostis pilosa* collected in Australia (conidia (25–)26–30(–34)  $\times$  (9–)13–15(–19)  $\mu$ m, 3-distoseptate; Tan et al. 2018), and this is the first record from Namibia. The species belongs to Pleosporaceae (Pleosporales; Fig. 2).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Curvularia eragrosticola* [strain BRIP 12538, GenBank NR\_158446.1; Identities = 557/561 (99 %), three gaps (0 %)], *Curvularia papendorffii* [strain ACSIKS\_2102013, GenBank MN547549.1; Identities = 467/474 (99 %), one gap (0 %)], and *Curvularia affinis* [strain 14, GenBank FJ467358.1; Identities = 528/542 (97 %), six gaps (1 %)]. Closest hits using the LSU sequence are *Curvularia papendorffii* [strain CBS 126204,



**Fig. 15.** *Curvularia eragrosticola* (CPC 39009). **A.** Conidiophores on PNA. **B–E.** Conidiophores and conidiogenous cells giving rise to conidia. **F.** Conidia. Scale bars = 10 µm.

GenBank MH875471.1; Identities = 864/864 (100 %), no gaps], *Bipolaris cactivora* [strain CBS 223.58, GenBank LT715590.1; Identities = 864/864 (100 %), no gaps], and *Curvularia intermedia* [strain B19, GenBank MN017987.1; Identities = 863/864 (99 %), no gaps]. Closest hits using the *rpb2* sequence had highest similarity to *Curvularia moringae* [strain CPC 38873, GenBank MW173117.1; Identities = 852/900 (95 %), no gaps], *Curvularia spicifera* [strain C-6, GenBank KU133372.1; Identities = 760/812 (94 %), no gaps], and *Curvularia crassiseptum* [strain CBS 503.90, GenBank LT852473.1; Identities = 812/868 (94 %), no gaps]. Closest hits using the *tef1* (second part) sequence had highest similarity to *Curvularia eragrosticola* [strain BRIP12538, GenBank MH433661.1; Identities = 860/869 (99 %), no gaps], *Curvularia papendorffii* [strain CBS 308.67, GenBank KM196594.1; Identities = 879/898 (98 %), one gap (0 %)], and *Curvularia micropus* [as *Bipolaris micropus*; strain UTHSC 07-1352, GenBank HE792957.1; Identities = 874/894 (98 %), one gap (0 %)].

**Authors:** P.W. Crous, J.Z. Groenewald, N. Yilmaz & M.J. Wingfield

***Dactylaria retrophylli*** Crous, *sp. nov.* MycoBank MB 844283. Fig. 16.

**Taxonomic lineage:** Sordariomycetes, Xylariales, *incertae sedis*.

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

**Mycelium** consisting of hyaline, septate, smooth-walled, branched, 1.5–2.5 µm diam hyphae. **Conidiophores** reduced to conidiogenous cells or with supporting cell, solitary, erect, geniculous-sinuuous, subcylindrical, 6–20 × 2.5–3.5 µm; hyaline, smooth-walled, apex denticulate, 1–2 × 1 µm; not thickened nor darkened. **Conidia** solitary, dry, hyaline, smooth-walled,

guttulate, medianly 1-septate, straight to narrowly fusoid, widest in middle, tapering towards both truncate ends, (26–)30–33(–37) × (1.5–)2 µm.

**Culture characteristics:** Colonies flat, spreading, surface folded, with sparse aerial mycelium and smooth, even margin, reaching 30 mm diam after 7 d at 25 °C. On MEA surface salmon, reverse ochreous; on PDA and OA surface and reverse pale luteous.

**Typus:** **Colombia**, Finca El Cedral, on leaves of *Retrophyllum rospigliosii* (*Podocarpaceae*), Feb. 2020, M.J. Wingfield, HPC 3260 (**holotype** CBS H-24817, culture ex-type CPC 39510 = CBS 148271).

**Notes:** *Dactylaria* (De Hoog 1985) is heterogeneous (Crous *et al.* 2016, 2017, 2018a), and the phylogenetic position of its type species, *D. purpurella*, remains unresolved. The present collection is tentatively named in *Dactylaria*, where it is phylogenetically distinct from other dactylaria-like taxa (Fig. 8). Morphologically, it is most similar to *D. monticola* in having medianly 1-septate, straight to narrowly fusoid conidia (30–37 × 1–1.5 µm) (Goh & Hyde 1997). Phylogenetically, it is related to *D. monticola* (CBS 188.95) in *Xylariales*, but distinct (Fig. 8).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Fusidium griseum* [strain ICMP 15049, GenBank EF029217.1; Identities = 505/559 (90 %), 22 gaps (3 %)], *Dactylaria acaciae* [strain CPC 29771, GenBank KY173400.1; Identities = 507/563 (90 %), 18 gaps (3 %)], and *Fusidium griseum* [strain Trtsf08, GenBank GU479905.1; Identities = 504/563 (90 %), 21 gaps (3 %)]. Closest hits using the **LSU** sequence are *Dactylaria monticola* [strain P060, GenBank EU107289.1; Identities = 814/831 (98 %), three gaps (0 %)], *Dactylaria zapatensis* [strain P056, GenBank EU107287.1; Identities = 812/830 (98 %), six gaps (0 %)], and *Dactylaria bisepitata* [strain P062, GenBank EU107288.1; Identities = 810/828 (98 %), six gaps



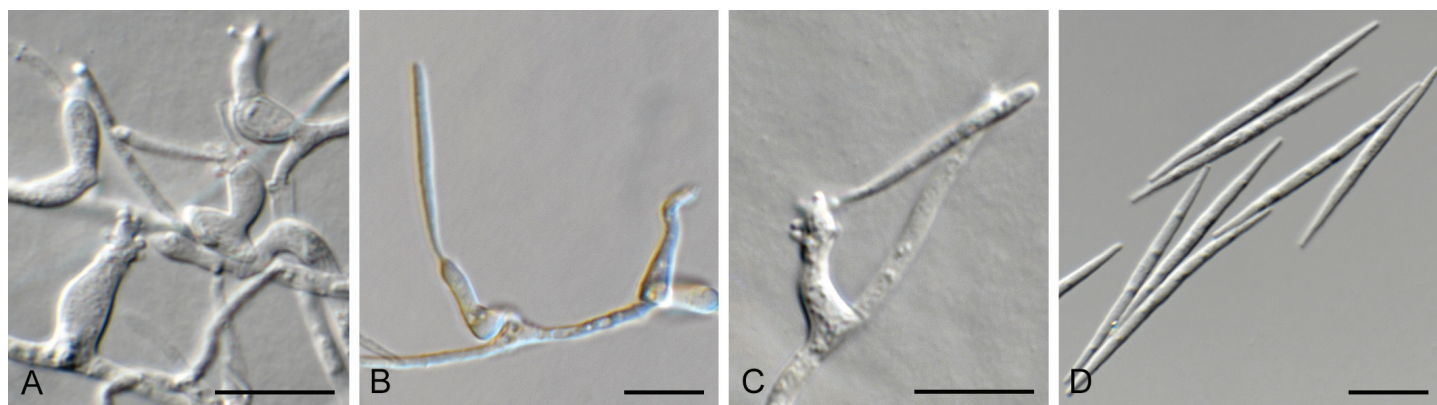


Fig. 16. *Dactylaria retrophylli* (CPC 39510). A–C. Conidiogenous cells giving rise to conidia. D. Conidia. Scale bars = 10  $\mu$ m.

(0 %)]. No *Fusidium* LSU sequences were available on GenBank for comparison.

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*Dactylellina miltoniae* Crous, *sp. nov.* MycoBank MB 844280. Fig. 17.

*Taxonomic lineage:* Orbiliomycetes, Orbiliales, Orbiliaceae.

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

*Mycelium* consisting of hyaline, septate, branched, 2–3  $\mu$ m diam hyphae. *Conidiophores* erect, flexuous, subcylindrical, hyaline, smooth, septate, unbranched, 100–150  $\times$  2–2.5  $\mu$ m. *Conidiogenous cells* terminal, integrated, blastic, at times subdentate, giving rise to clusters of conidia. *Conidia* hyaline, smooth, guttulate, (2–)3–4-septate, ellipsoid to spindle-shaped or obconical, (23–)34–40(–47)  $\times$  (5–)8–10(–11)  $\mu$ m. *Adhesive knobs* solitary, globose, hyaline, smooth, (4–)6–6.5  $\mu$ m. *Constricting rings*, *chlamydospores* or *sexual morph* not observed.

*Culture characteristics:* Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, lobate margin, reaching 55 mm diam after 7 d at 25  $^{\circ}$ C. On MEA surface saffron, reverse ochreous; on PDA surface and reverse peach; on OA surface peach.

*Typus:* Colombia, Restrepo, on twigs of *Miltonia clowesii* (Orchidaceae), Feb. 2020, M.J. Wingfield, HPC 3270 (**holotype** CBS H-24816, culture ex-type CPC 39508 = CBS 148270).

*Notes:* *Dactylellina miltoniae* was isolated from twigs of *Miltonia clowesii*, and is characterised by small adhesive knobs, and 2–4-septate conidia on flexuous conidiophores. It is morphologically similar to *D. haptotyla* (distinct in that it has small adhesive knobs), and *D. yuannanensis* (distinct in that it lacks con-constricting rings). Phylogenetically, it clusters close to Clade C of the *D. haptotyla* s.l. complex, as defined by Baral et al. (2020) in Orbiliaceae (Orbiliales; Fig. 5). It is closely allied to *Dactylella lysipaga* and *Dactylium candidum* (Fig. 18).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Dactylium candidum* [strain 1.00579, GenBank MH179721.1; Identities = 537/545 (99 %), no gaps], *Dactylella lysipaga* [strain BCRC 34374, GenBank FJ380944.1; Identities = 540/549 (98 %), one gap (0 %)], and *Dactylellina haptotyla* [as *Monacrosporium haptotylum*; strain XJ03-96-1, GenBank DQ999827.1; Identities = 497/519 (96 %), nine gaps (1 %)]. Closest hits using the LSU sequence are *Stilbella bucidiae* [strain CBS 694.96, GenBank MH874229.1; Identities = 730/737 (99 %), no gaps], *Dactylellina haptotyla* [as *Monacrosporium sclerohyphum*; strain KMF1.00041, GenBank AY965762.1; Identities = 730/737 (99 %), no gaps], and *Dactylium candidum* [strain YMF1.36, GenBank AY902801.1; Identities = 730/737 (99 %), no gaps]. Closest hits using the *rpb2* sequence had highest similarity to *Dactylellina haptotyla* [strain XJ03-96-1, GenBank DQ999804.1; Identities = 741/779 (95 %), one

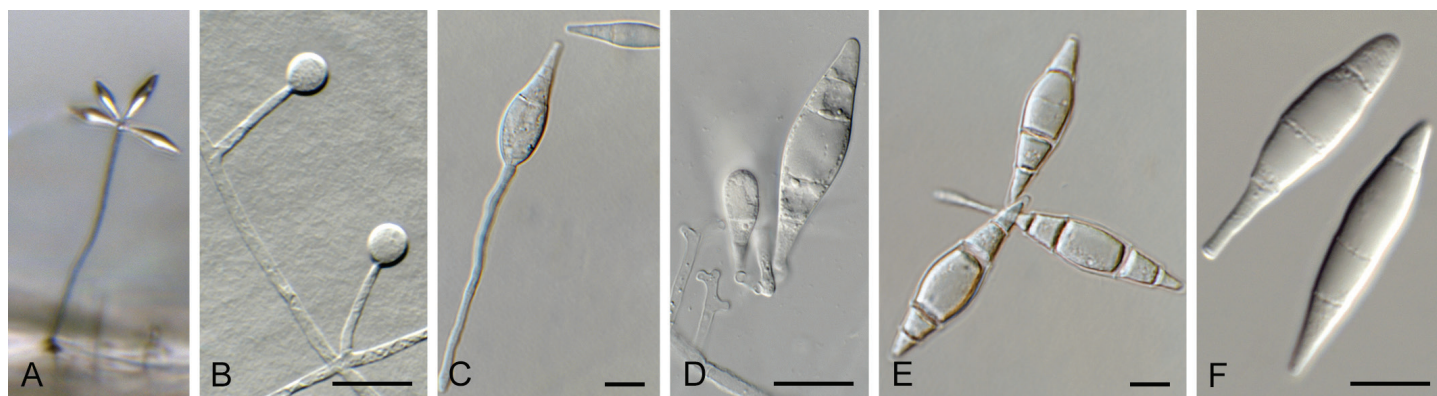
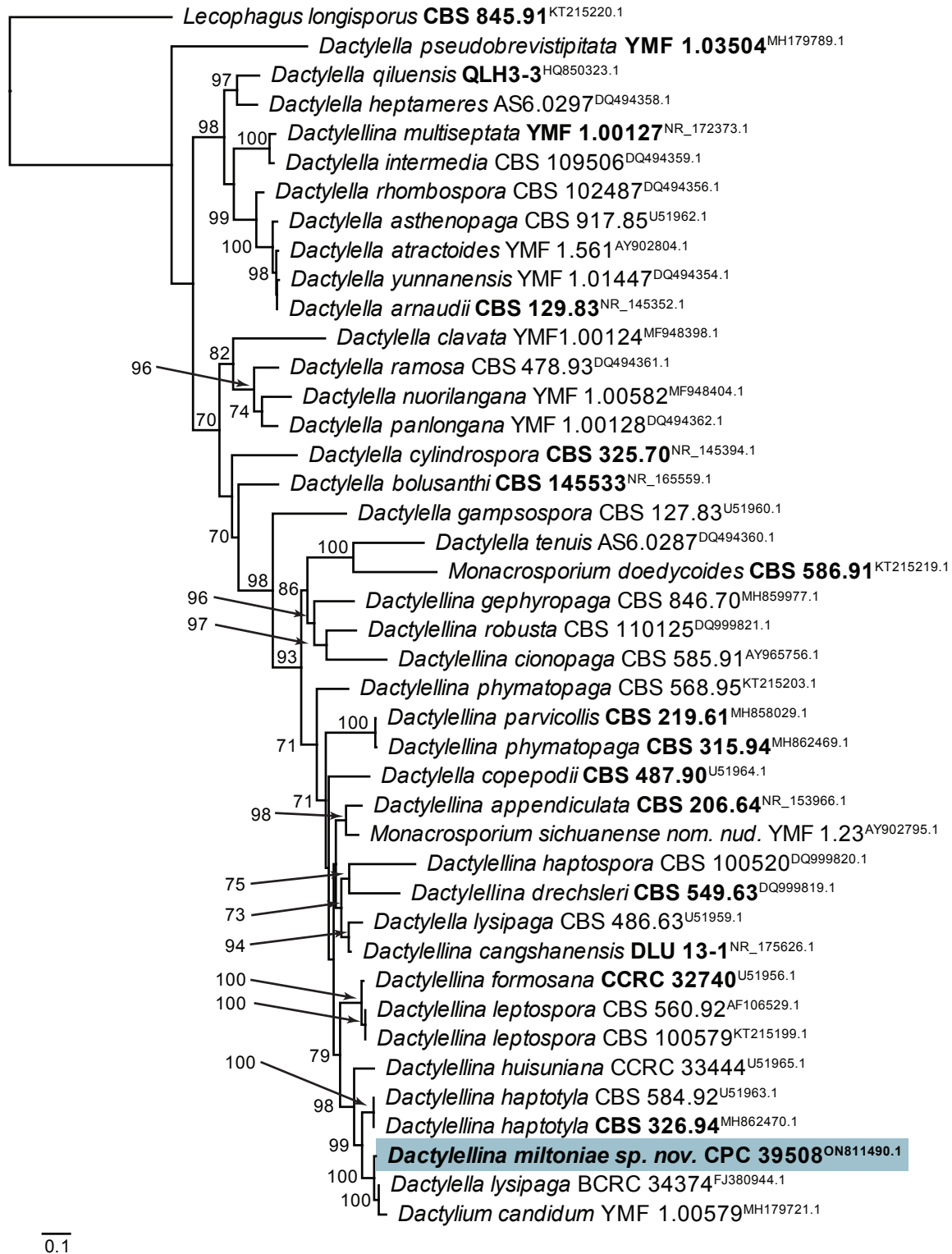


Fig. 17. *Dactylellina miltoniae* (CPC 39508). A. Conidiophore giving rise to conidia. B. Adhesive knobs. C. Conidiogenous cell with attached conidium. D–F. Conidia. Scale bars = 10  $\mu$ m.





**Fig. 18.** Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh *et al.* 2020) of the *Dactylella/Dactylellina* ITS nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast bootstrap replicates are shown at the nodes. Culture collection numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Lecophagus longisporus* (culture CBS 845.91; GenBank KT215220.1) and the species treated here is highlighted with bold face. Accession numbers of sequence from material with a type status are also shown in bold face.

gap (0 %)], *Dactylellina haptotyla* [as *Monacrosporium haptotylum*; strain SQ95-2, GenBank AY773441.1; Identities = 695/737 (94 %), one gap (0 %)], and *Dactylellina appendiculata* [strain CBS 206.64, GenBank DQ358229.1; Identities = 653/761 (86 %), one gap (0 %)]. Closest hits using the *tef1* (second part) sequence had highest similarity to *Dactylella lysipaga* [GenBank AY695066.1; Identities =

652/713 (91 %), no gaps], *Orbilina ellipsospora* [as *Monacrosporium ellipsosporum*; GenBank AY695064.1; Identities = 645/713 (90 %), no gaps], and *Dactylellina drechsleri* [as *Monacrosporium drechsleri*; GenBank AY695062.1; Identities = 645/713 (90 %), no gaps].

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***Dothiora viticola*** (Laich & Stchigel) Crous, *comb. nov.* MycoBank MB 844304.

*Basionym:* *Hormonema viticola* Laich & Stchigel, *Persoonia* **34**: 229. 2015.

*Taxonomic lineage:* *Dothideomycetes*, *Dothideales*, *Dothideaceae*.

*Description and illustration:* See Crous *et al.* (2015).

*Typus:* **Spain**, Canary Islands, Lanzarote, La Geria, 28.9764; -13.6917, from fruit (grapes) of *Vitis vinifera* cv. Malvasia, Aug. 2009, coll. F. Laich, isol. S.S. González-González & F. Laich (**holotype** CBS H-22115, cultures ex-type CBS 140676 = FMR 13040 = L9D-17).

*Notes:* The *Dothideales* was treated by Hongsanan *et al.* (2020b), and four families recognised, namely *Dothideaceae*, *Neocelosporiaceae*, *Sacotheciaceae* and *Zalariaceae* (also see Fig. 1 part 1). However, many of the genera in these families remain poorly understood due to the lack of DNA data related to their respective type species.

*Dothiora viticola* appears similar to other species of *Dothideaceae* in that cultures produce endoconidia. *Dothiora viticola* appears to have a wider host range and distribution than originally assumed, also occurring in grassland rhizospheres (Spain), orchids (Chile), as an endophyte of *Dactylis glomerata*, and associated with beetle galleries on walnut (*Juglans regia*) twigs in the USA. Also see the phylogenetic trees in Crous *et al.* (2015) for the placement of this species.

*Authors:* P.W. Crous & J.Z. Groenewald

***Elsinoe corni*** Jenkins & Bitanc., *J. Wash. Acad. Sci.* **38**: 362. 1948. Fig. 19.

*Taxonomic lineage:* *Dothideomycetes*, *Myriangiales*, *Elsinoaceae*.

*Description and illustration:* Jenkins & Bitancourt (1948).

*Typus:* **USA**, North Carolina, Highlands, MACON Co., on *Cornus florida* (*Cornaceae*), 5 Sep. 1947, J.A. Stevenson (**holotype** BPI 679270); North Carolina, Charlotte, 35.078519, -81.001553, on leaves of *Cornus florida*, 17 Apr. 2021, A. Loyd (**epitype** designated here, CBS H-24990, MBT 10007399, culture ex-epitype CPC 41728 = CBS 148184).

*Notes:* *Elsinoe* causes scab (or anthracnose) disease on numerous plant hosts (Fan *et al.* 2017). *Elsinoe corni* is the causal agent of spot anthracnose of flowering dogwood (*Cornus florida*) in the USA, causing small, circular spots on bracts, petioles, peduncles, stems and leaves. The pathogen was originally described by Jenkins & Bitancourt (1948) from *Cornus florida* collected in North Carolina. The present collection provides good material to serve as epitype to resolve the phylogeny of the species (Fig. 1 part 1).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Elsinoe fawcettii* [strain CBS 139.25, GenBank MH854816.1; Identities = 570/594 (96 %), six gaps (1 %)], *Elsinoe australis* [voucher 1629, GenBank MG956760.1; Identities = 570/594 (96 %), six gaps (1 %)], and *Elsinoe diospyri* [strain CBS 223.50, GenBank MH856596.1; Identities = 537/558 (96 %), six gaps (1 %)]. Closest hits using the **LSU** sequence are *Elsinoe populi*

[strain CBS 289.64, GenBank KX887036.1; Identities = 734/736 (99 %), no gaps], *Elsinoe diospyri* [strain CBS 223.50, GenBank KX886973.1; Identities = 733/736 (99 %), no gaps], and *Elsinoe tiliae* [strain CBS 350.73, GenBank KX887059.1; Identities = 732/736 (99 %), no gaps]. Closest hits using the **rpb2** sequence had highest similarity to *Elsinoe populi* [strain CBS 289.64, GenBank KX887154.1; Identities = 700/744 (94 %), no gaps], *Elsinoe diospyri* [strain CBS 223.50, GenBank KX887093.1; Identities = 699/744 (94 %), no gaps], and *Elsinoe caleae* [strain CBS 221.50, GenBank KX887088.1; Identities = 699/744 (94 %), no gaps].

*Authors:* P.W. Crous, J.Z. Groenewald & A. Loyd

***Elsinoe parthenocissi*** Jenkins & Bitanc., *Phytopathology* **32**: 424. 1942. Fig. 20.

*Taxonomic lineage:* *Dothideomycetes*, *Myriangiales*, *Elsinoaceae*.

*Conidiomata* sporodochial, erumpent, hyaline to pale brown, 200–300 µm diam. *Conidiophores* subcylindrical, hyaline to pale brown, smooth, 0–1-septate, at times reduced to conidiogenous cells. *Conidiogenous cells* integrated, terminal, subcylindrical to doliiform, hyaline, smooth, with age somewhat pigmented, mono- to polyphialidic, 9–17 × 4–5 µm. *Conidia* hyaline, granular, aseptate, ellipsoid, apex obtuse, tapering towards base with truncate hilum, (6–)7–8(–9) × (3–)4(–4.5) µm.

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

*Material examined:* **New Zealand**, Auckland, Devan Port, on *Parthenocissus quinquefolia* (*Vitaceae*), 2019, C. Inglis, CBS H-24481, culture CPC 38770 = T19\_06384B = CBS 146969.

*Notes:* *Elsinoe parthenocissi* (Fig. 1 part 1) was described from symptomatic leaves, stems and petioles of *Parthenocissus quinquefolia* collected in New Hampshire, USA (BPI 680610 type) (Jenkins & Bitancourt 1942). *Elsinoe parthenocissi* is the only species known from *Parthenocissus*, and has previously been reported from New Zealand by Dingley (1965). Only the asexual morph was collected in the present study, so the species identification remains unconfirmed, as it could also be an undescribed species of *Elsinoe* occurring on this host in New Zealand.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Elsinoe diospyri* [strain CBS 223.50, GenBank NR\_148135.1; Identities = 519/528 (98 %), four gaps (0 %)], *Elsinoe caleae* [strain CBS 221.50, GenBank NR\_148131.1; Identities = 518/527 (98 %), three gaps (0 %)], and *Elsinoe tiliae* [strain CBS 350.73, GenBank KX887296.1; Identities = 515/526 (98 %), four gaps (0 %)]. Closest hits using the **LSU** sequence are *Elsinoe tiliae* [strain CBS 350.73, GenBank KX887059.1; Identities = 732/736 (99 %), no gaps], *Elsinoe populi* [strain CBS 289.64, GenBank KX887036.1; Identities = 732/736 (99 %), no gaps], and *Elsinoe perseae* [strain CBS 288.64, GenBank KX887020.1; Identities = 731/736 (99 %), no gaps]. Closest hits using the **rpb2** sequence had highest similarity to *Elsinoe populi* [strain CBS 289.64, GenBank KX887154.1; Identities = 689/744 (93 %), no



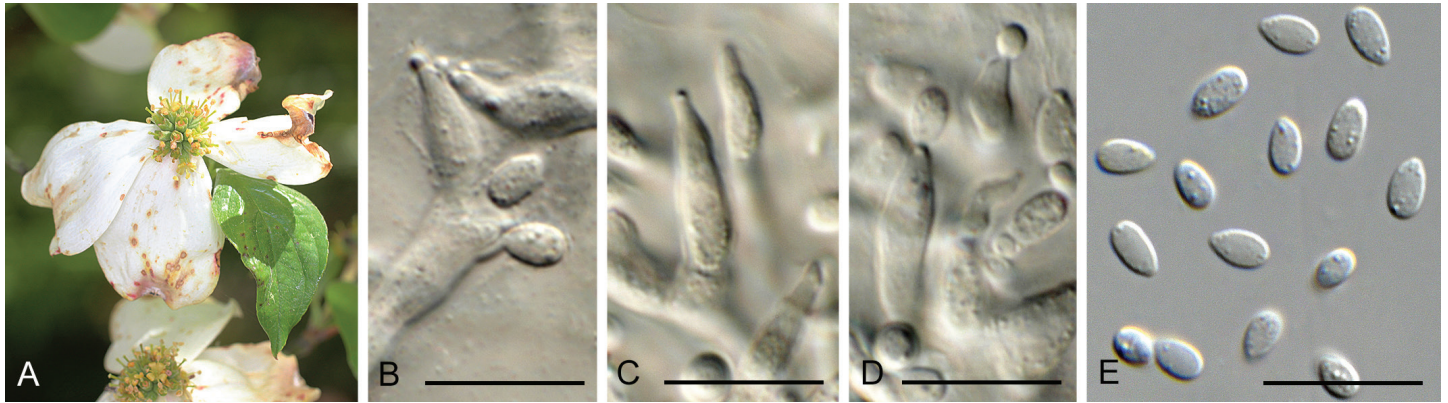


Fig. 19. *Elsinoe corni* (CBS 41728). A. Disease spots on *Cornus florida*. B–D. Conidiogenous cells giving rise to conidia. E. Conidia. Scale bars = 10  $\mu$ m.

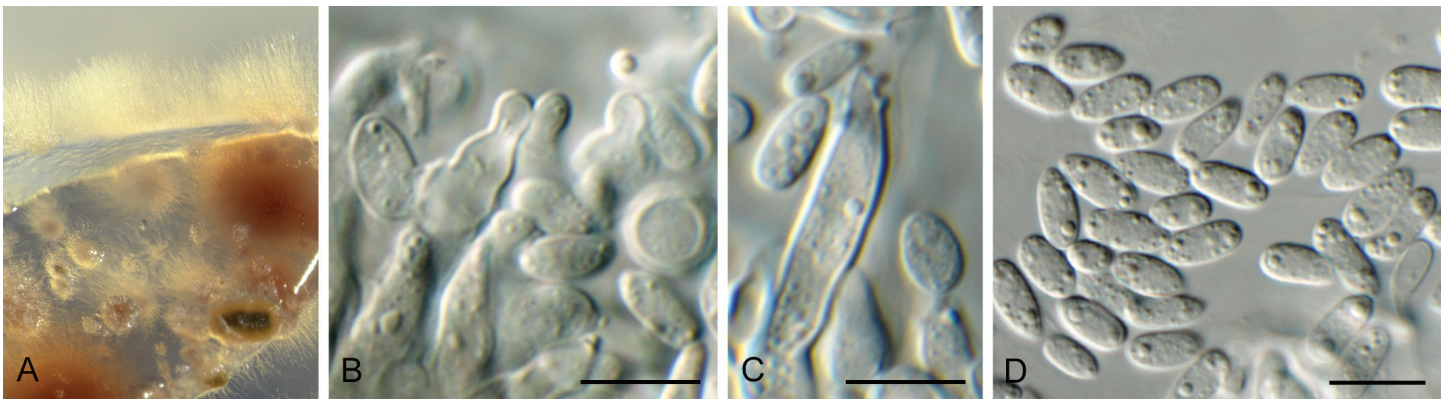


Fig. 20. *Elsinoe parthenocissi* (CPC 38770). A. Sporodochia on SNA. B, C. Conidiogenous cells giving rise to conidia. D. Conidia. Scale bars = 10  $\mu$ m.

gaps], *Elsinoe diospyri* [strain CBS 223.50, GenBank KX887093.1; Identities = 688/744 (92 %), no gaps], and *Elsinoe caleae* [strain CBS 221.50, GenBank KX887088.1; Identities = 688/744 (92 %), no gaps].

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***Exophiala eucalyptigena*** Crous, *sp. nov.* MycoBank MB 844281. Fig. 21.

**Taxonomic lineage:** Eurotiomycetes, Chaetothyriales, Herpotrichiellaceae.

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

**Mycelium** consisting of pale brown, smooth-walled, guttulate, septate, branched, 1.5–3  $\mu$ m diam hyphae. Hyphal cells becoming constricted at septa, and more ellipsoid closer to conidiogenous region. **Conidiogenous cells** solitary or in clusters, ampulliform with elongated neck, with numerous percurrent proliferations, pale to medium brown, smooth, base subglobose, 3–4  $\times$  4–5  $\mu$ m; neck cylindrical, 2–4  $\times$  1.5–2  $\mu$ m; rarely reduced to cylindrical, erect conidiogenous loci, direct on hyphae. **Conidia** solitary, aseptate, ellipsoid, smooth-walled, pale brown, guttulate, apex obtuse, tapering to narrowly truncate hilum, 0.5  $\mu$ m diam, (3–)3.5–4(–5)  $\times$  2(–2.5)  $\mu$ m.

**Culture characteristics:** Colonies flat, spreading, surface folded, with sparse aerial mycelium and smooth, lobate margin,

reaching 5 mm diam after 2 wk at 25  $^{\circ}$ C. On MEA, PDA and OA surface olivaceous grey, reverse iron-grey.

**Typus:** Australia, Australian Capital Territory, on dead leaves of *Eucalyptus viminalis* subsp. *viminalis* (Myrtaceae) supporting *Idolothrips spectrum* population, 17 Jan. 2015, A. Wells & L.A. Mound (**holotype** CBS H-24819, culture ex-type CPC 41024 = CBS 148273).

**Notes:** *Exophiala eucalyptigena* clusters among species of *Exophiala* s. str. (Crous et al. 2020a; Figs 3, 22). It is morphologically distinct from other species of *Exophiala* in that the conidiogenous cells are frequently arranged in clusters, and have elongated, cylindrical necks.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Exophiala pisciphila* [strain CBS 100.68, GenBank MH859072.1; Identities = 571/624 (92 %), 16 gaps (2 %)], *Veronea botryosa* [strain MFLUCC 11-0072, GenBank MG922570.1; Identities = 571/624 (92 %), 18 gaps (2 %)], and *Exophiala tremulae* [strain CBS 129355, GenBank NR\_159874.1; Identities = 570/624 (91 %), 16 gaps (2 %)]. Closest hits using the **LSU** sequence are *Exophiala equina* [strain CBS 128222, GenBank MH876297.1; Identities = 807/813 (99 %), no gaps], *Annellophorella ellisii* [strain CBS 738.70, GenBank MH871721.1; Identities = 805/813 (99 %), no gaps], and *Helicoarctatus thailandicus* [strain MFLUCC 18-0332, GenBank MK559870.1; Identities = 804/813 (99 %), no gaps]. Closest hits using the **tef1** (first part) sequence had highest similarity to *Exophiala salmonis* [strain AFTOL-ID 671, GenBank EF413612.1; Identities = 258/288 (90 %), six gaps (2 %)], *Exophiala pisciphila* [strain AFTOL-ID 669,

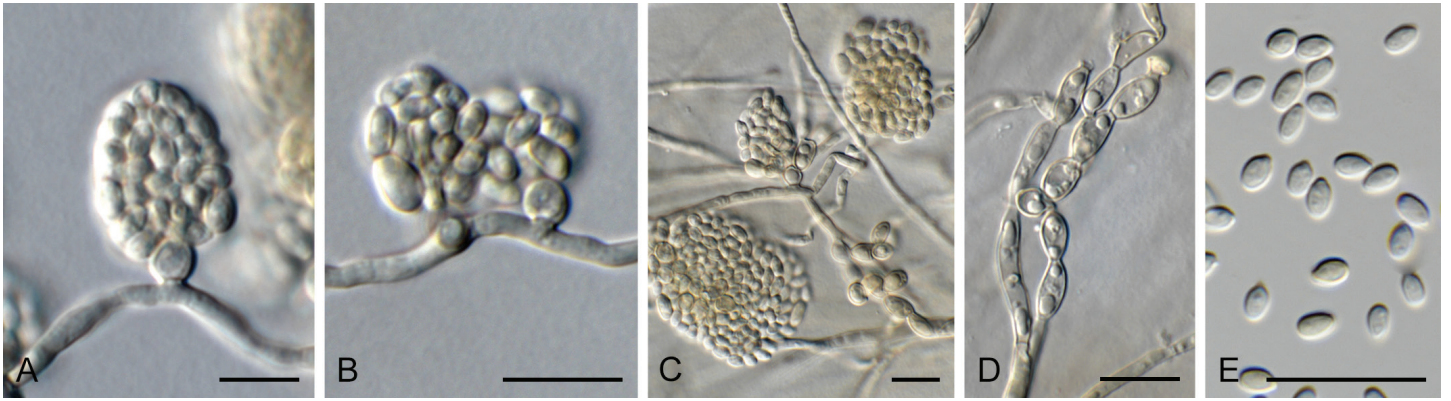


Fig. 21. *Exophiala eucalyptigena* (CPC 41024). A–D. Conidiogenous cells giving rise to conidia. E. Conidia. Scale bars = 10  $\mu$ m.

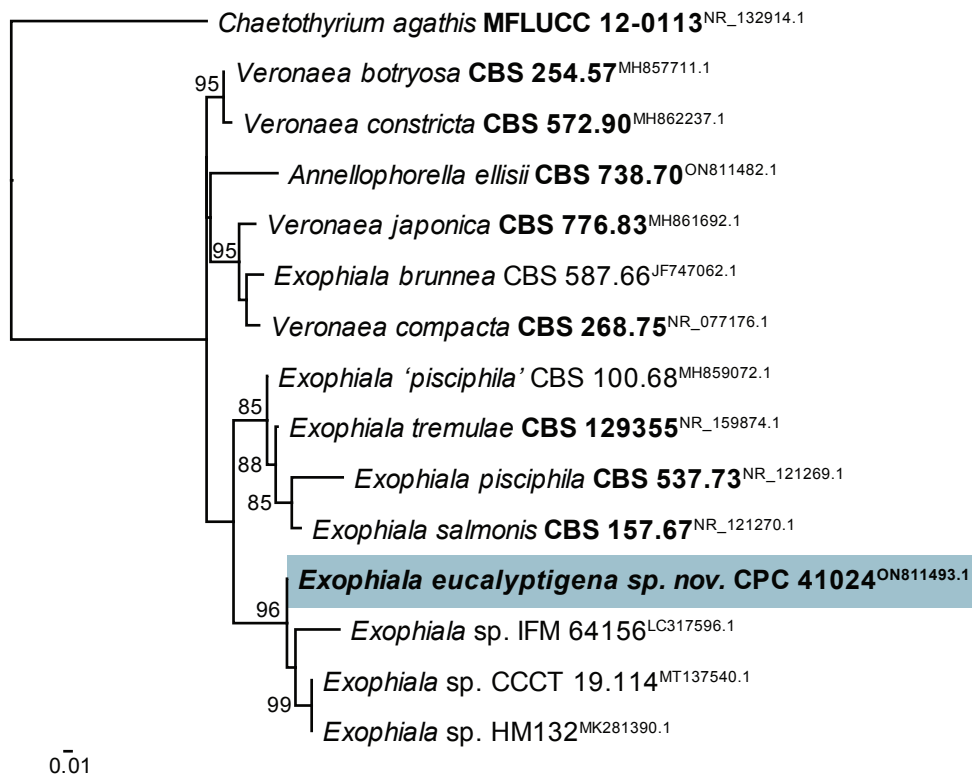


Fig. 22. Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Exophiala* ITS nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast bootstrap replicates are shown at the nodes. Culture collection numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Chaetothyrium agathis* (culture MFLUCC 12-0113; GenBank NR\_132914.1) and the species treated here is highlighted with bold face. Accession numbers of sequence from material with a type status are also shown in bold face.

GenBank DQ840567.1; Identities = 268/320 (84 %), 16 gaps (5 %)], and *Exophiala abietophila* [voucher HGUP-R300, GenBank MK887139.1; Identities = 239/283 (84 %), 11 gaps (3 %)]. Closest hits using the *tub2* sequence had highest similarity to *Veronaea botryosa* [strain 608911, GenBank MN477320.1; Identities = 326/414 (79 %), 16 gaps (3 %)], *Exophiala salmonis* [strain CBS 120274, GenBank KF928562.1; Identities = 304/387 (79 %), 18 gaps (4 %)], and *Exophiala oligosperma* [strain CBS 124085, GenBank KF928552.1; Identities = 287/364 (79 %), 15 gaps (4 %)].

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*Floricola juncicola* Crous & R.K. Schumach., *Fungal Syst. Evol.* **7**: 289. 2021. Fig. 23.

*Taxonomic lineage*: Dothideomycetes, Pleosporales, Teichosporaceae.

*Description and illustration*: Crous et al. (2021b).

*Material examined*: Netherlands, Gelderland, Hoge Veluwe, Deelense Wasch, 52°05'37"N, 5°51'17"E, on dead culm of *Juncus effusus* (*Juncaceae*), 1 Mar. 2021, E.R. Osieck, HPC 3609 = WI-29/#4220, cultures CPC 41356 = CBS 148318, CPC 41357 = CBS 148287.





**Fig. 23.** *Floricola juncicola* (CPC 41357). **A–C.** Conidiogenous cells giving rise to conidia. **D, E.** Conidia. Scale bars = 10 µm.

**Notes:** *Floricola juncicola* was described from dead culms of *Juncus* collected in France (Crous *et al.* 2021b), and found here to also be common on *Juncus* spp. in the Netherlands. The species belongs to *Teichosporaceae* (*Pleosporales*; Figs 2, 24).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 41356 had highest similarity to *Floricola juncicola* [strain CBS 146811, GenBank NR\_173010.1; Identities = 433/434 (99 %), no gaps], *Teichospora viticola* [strain MFLUCC 15-0039, GenBank NR\_154624.1; Identities = 367/385 (95 %), two gaps (0 %)], and *Teichospora kingiae* [strain CPC 29104, GenBank NR\_154656.1; Identities = 362/386 (94 %), six gaps (1 %)]. The ITS sequences of CPC 41356 and 41357 are identical (434/434 bp). Closest hits using the **LSU** sequence of CPC 41356 are *Floricola juncicola* [strain CBS 146811, GenBank NG\_076710.1; Identities = 831/832 (99 %), one gap (0 %)], *Paulkirkia arundinis* [strain MFLUCC 12-0328, GenBank KU848206.1; Identities = 810/829 (98 %), two gaps (0 %)], and *Floricola clematidis* [strain MFLUCC 17-2182, GenBank MT214594.1; Identities = 809/829 (98 %), two gaps (0 %)]. The LSU sequences of CPC 41356 and 41357 are identical (814/814 bp). Closest hits using the **rpb2** sequence of CPC 41356 had highest similarity to *Floricola juncicola* [strain CPC 38197, GenBank MW890063.1; Identities = 645/647 (99 %), no gaps], *Teichospora mariae* [strain C136, GenBank KU601595.1; Identities = 742/858 (86 %), two gaps (0 %)], and *Teichospora striata* [strain JK 5678I, GenBank GU371758.1; Identities = 712/878 (81 %), seven gaps (0 %)]. The **rpb2** sequences of CPC 41356 and 41357 are almost identical (842/845 bp, no gaps). Closest hits using the **tef1** (first part) sequence of CPC 41356 had highest similarity to *Floricola juncicola* [strain CPC 38197, GenBank MW890092.1; Identities = 502/503 (99 %), no gaps], *Astragalicola amorpha* [strain C227a, GenBank MF795842.1; Identities = 257/320 (80 %), 30 gaps (9 %)], and *Setophoma longinqua* [strain LC6593, GenBank MK525069.1; Identities = 253/319 (79 %), 22 gaps (6 %)]. The **tef1** sequences of CPC 41356 and 41357 differ with a single nucleotide (502/503 bp, no gaps).

**Authors:** P.W. Crous, J.Z. Groenewald & E.R. Osieck

***Floricola sulcata*** (Marinc. *et al.*) Crous & Osieck, **comb. nov.** MycoBank MB 844284. Fig. 25.

**Basionym:** *Sclerostagonospora sulcata* Marinc. *et al.*, *Sydowia* **69**: 252. 2017.

**Taxonomic lineage:** *Dothideomycetes*, *Pleosporales*, *Teichosporaceae*.

**Conidiomata** pycnidial, solitary, globose, dark brown with central ostiole, 150–250 µm diam; wall of 3–6 layers of brown *textura angularis*. **Conidiophores** subcylindrical, hyaline, smooth-walled, 0–1-septate, branched at base or not, 7–20 × 3–5 µm. **Conidiogenous cells** integrated, terminal, subcylindrical, hyaline, smooth-walled, 7–15 × 2.5–4 µm, proliferating percurrently at apex. **Conidia** solitary, subcylindrical, apex obtuse, at times slightly clavate, tapering to truncate hilum, 2–3 µm diam, with marginal frill, golden brown, roughened with striations along its entire length, (1–)3-septate, (11–)13–14(–15) × 4(–6) µm.

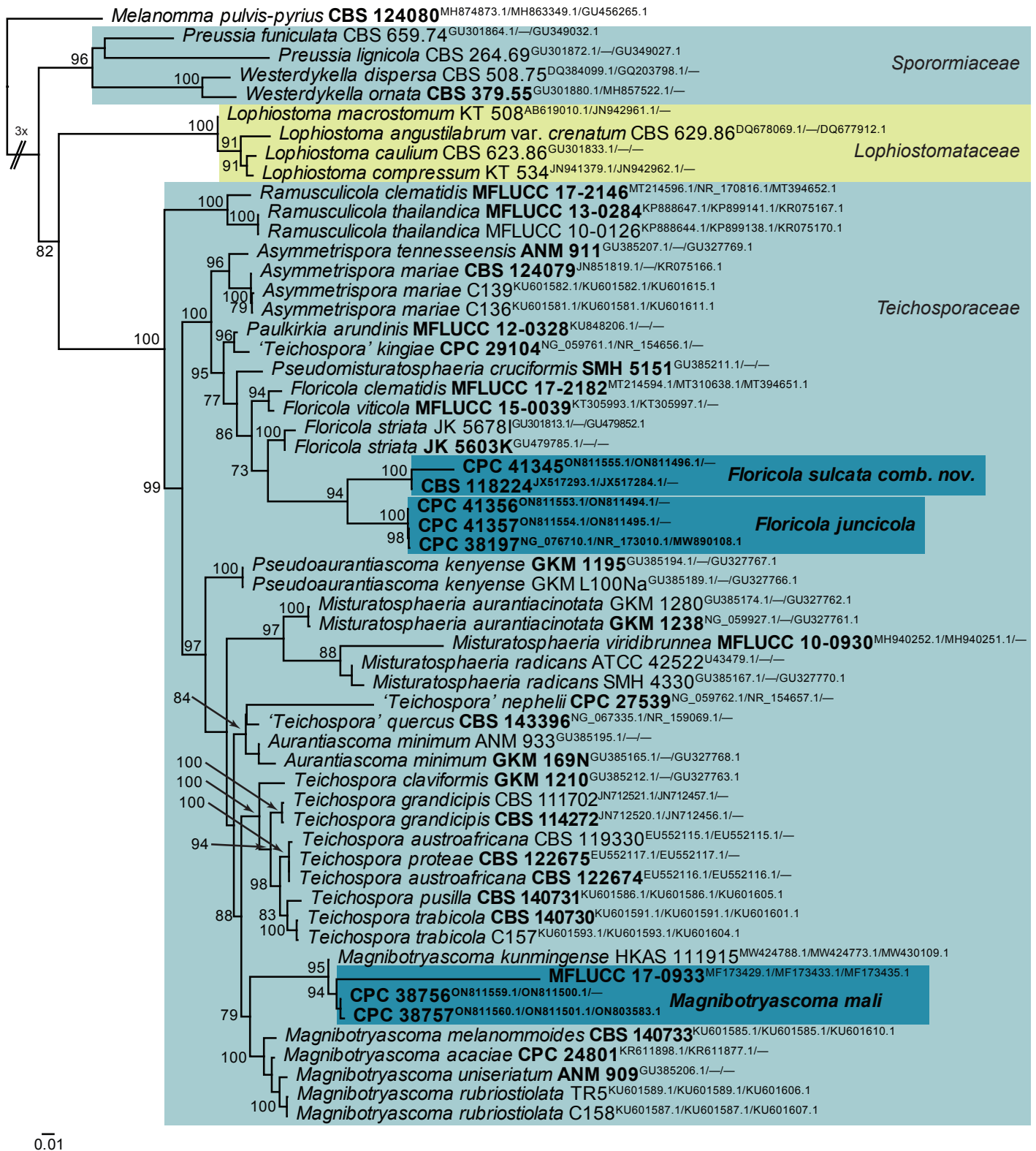
**Culture characteristics:** Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface olivaceous grey, reverse smoke grey; on PDA surface olivaceous grey, reverse iron grey with diffuse red pigment; on OA surface olivaceous grey.

**Material examined:** **Netherlands**, Overijssel Province, Engbertsdijkvenen, near Kloosterhaar, 52°28'57"N, 6°40'02"E, 17 m a.s.l., on dead culm of *Juncus effusus* (*Juncaceae*), 9 Mar. 2021, E.R. Osieck, HPC 3611 = WI-30/#4226 = CBS H-24832, culture CPC 41345 = CBS 148286.

**Notes:** *Sclerostagonospora sulcata* was described from culm litter of *Restio subverticellatus* collected in South Africa (Krisai-Greilhuber *et al.* 2017), with conidia being brown, striate, 3-septate, (13–)14–15(–17) × (4–)5–6(–7) µm. This taxon appears to be better accommodated in the genus *Floricola* (Phukhamsakda *et al.* 2020, Crous *et al.* 2021b; *Teichosporaceae*, *Pleosporales*, Figs 2, 24). This is the fourth species of the genus collected from monocotyledons (and the third from *Juncus*). The other two *Floricola* species were described from *Clematis vitalba* and *Vitis vinifera*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Sclerostagonospora sulcata* [as *Sclerostagonospora* sp.; ex-type strain CBS 118224, GenBank JX517284.1; Identities = 487/488 (99 %), no gaps], *Teichospora viticola* [strain MFLUCC 15-0039, GenBank NR\_154624.1; Identities = 395/411 (96 %), two gaps (0 %)], and "*Floricola*" *clematidis* [as *Teichospora* sp.

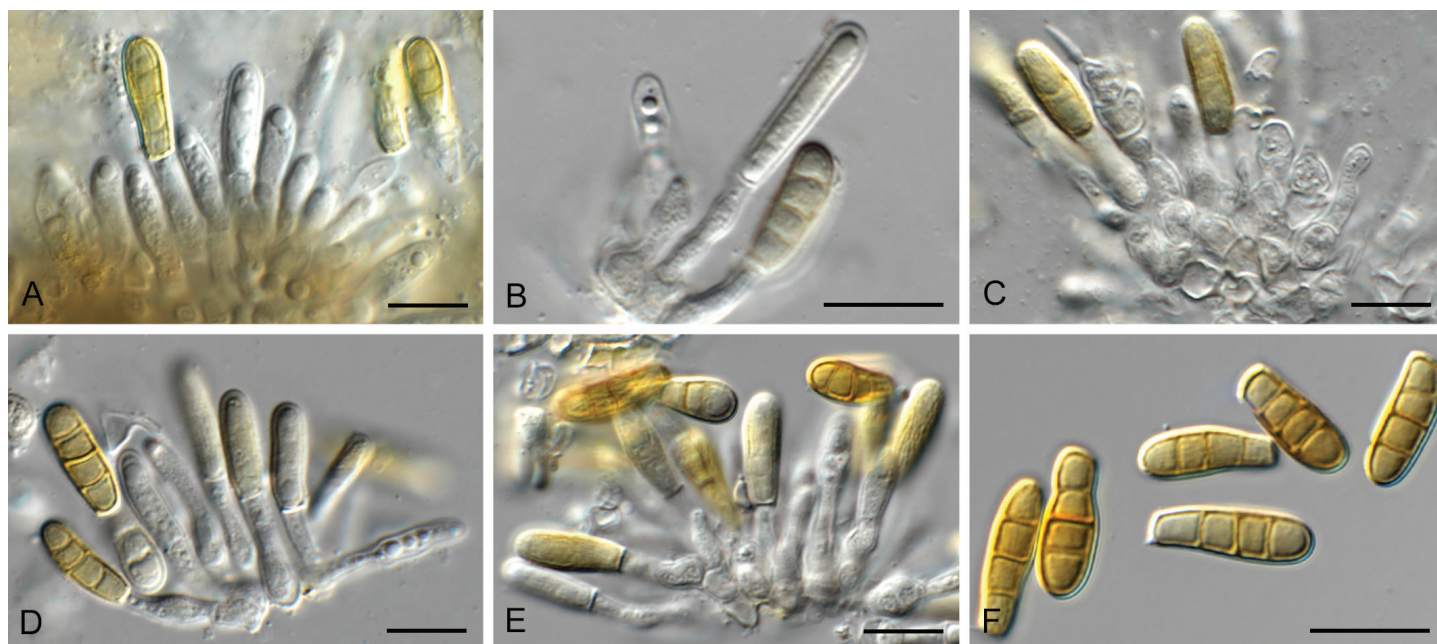




**Fig. 24.** Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Teichosporaceae* concatenated (LSU, ITS, *tef1*) nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast bootstrap replicates are shown at the nodes. Culture collection numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Melanomma pulvis-pyrius* (culture CBS 124080; GenBank MH874873.1, MH863349.1, GU456265.1, respectively) and the species treated here are highlighted with coloured blocks and bold face. Accession numbers of sequence from material with a type status are also shown in bold face. Families are indicated with coloured blocks to the right of the tree.

CP-2020b; strain MFLUCC 17-2182, GenBank MT310638.1; Identities = 394/411 (96 %), two gaps (0 %). Closest hits using the **LSU** sequence are *Sclerostagonospora sulcata* [ex-type strain CBS 118224, GenBank JX517293.1; Identities = 815/815

(100 %), no gaps], "*Floricola*" *clematidis* [strain MFLUCC 17-2182, GenBank MT214594.1; Identities = 814/815 (99 %), no gaps], and *Paulkirkia arundinis* [strain MFLUCC 12-0328, GenBank KU848206.1; Identities = 806/815 (99 %), no gaps].



**Fig. 25.** *Floricola sulcata* (CPC 41345). **A–E.** Conidiogenous cells giving rise to conidia. **F.** Conidia. Scale bars = 10 µm.

Closest hits using the *rpb2* sequence had highest similarity to “*Floricola*” *juncicola* [strain CPC 38197, GenBank MW890063.1; Identities = 583/648 (90 %), two gaps (0 %)], *Teichospora striata* [strain JK 56781, GenBank GU371758.1; Identities = 713/848 (84 %), two gaps (0 %)], and *Teichospora quercus* [strain CBS 143396, GenBank MH108010.1; Identities = 660/837 (79 %), 22 gaps (2 %)]. Closest hits using the *tef1* (first part) sequence had highest similarity to “*Floricola*” *juncicola* [strain CPC 38197, GenBank MW890092.1; Identities = 348/392 (89 %), 24 gaps (6 %)], *Teichospora trabicola* [strain C141, GenBank KU601603.1; Identities = 297/362 (82 %), 17 gaps (4 %)], and *Teichospora melanommoides* [strain MP5, GenBank KU601610.1; Identities = 289/352 (82 %), 14 gaps (3 %)].

**Authors:** P.W. Crous, J.Z. Groenewald & E.R. Osieck

***Idriellomyces syzygii*** Crous, *sp. nov.* MycoBank MB 844285. Fig. 26.

**Taxonomic lineage:** Sordariomycetes, Xylariales, Phlogicylindriaceae.

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

**Mycelium** consisting of hyaline, smooth-walled, septate, branched, 1.5–2 µm diam hyphae, forming hyphal coils. **Conidiophores** reduced to conidiogenous cells, arising directly from superficial mycelium, straight to geniculous-sinuous, hyaline, smooth- and thin-walled, 3–20 × 2–3 µm; apical part forming a rachis with truncate, denticulate loci, 0.5–1 × 0.5 µm, not thickened nor darkened. **Conidia** solitary, hyaline, smooth-walled, aseptate, falcate, apex subobtuse, base truncate, 0.5 µm diam, curved more prominently on dorsiventral side than inner plane, guttulate, (7–)8–10(–11) × (1.5–)2 µm.

**Culture characteristics:** Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA surface and reverse buff; on PDA and OA surface and reverse dirty white.

**Typus:** South Africa, KwaZulu-Natal Province, near Mozambique border, on leaves of *Syzygium cordatum* (Myrtaceae), 19 Oct. 2017,



**Fig. 26.** *Idriellomyces syzygii* (CPC 40065). **A–D.** Conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars = 10 µm.



M.J. Wingfield, HPC 3503 (holotype CBS H-24797, culture ex-type CPC 40065 = CBS 148252).

Notes: *Idriellomyces* is based on *I. eucalypti*, known from *Eucalyptus obliqua* leaves collected in Australia (Crous et al. 2018c). *Idriellomyces syzygii* also occurs on *Myrtaceae*, namely *Syzygium cordatum* leaves collected in South Africa, where it was mycophylic on a *Meliola* species. *Idriellomyces syzygii* differs from *I. eucalypti* in that the scars on the conidiogenous cells are more pronounced, denticulate, the conidiophores are hyaline, and it has larger conidia than those of *I. eucalypti*, (5–)6.5–7(–8) × 1.5(–2) µm (Crous et al. 2018c). Based on the phylogenetic trees generated here, the species is best accommodated in *Idriellomyces* (*Phlogicylindriaceae*, *Xylariales*; Figs 8, 27).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Idriellopsis uncinospora* [strain CBS 575.92, GenBank KP859052.1; Identities = 370/414 (89 %), 14 gaps (3 %)], *Idriellomyces eucalypti* [strain CPC 32632, GenBank NR\_160356.1; Identities = 462/534 (87 %), 30 gaps (5 %)], and *Cylindrium elongatum* [strain CBS 115974, GenBank KM231853.1; Identities = 463/545 (85 %), 31 gaps (5 %)]. Closest hits using the LSU sequence are *Idriellomyces eucalypti* [strain CPC 32632, GenBank NG\_066413.1; Identities = 786/804 (98 %), two gaps (0 %)], *Castanediella cagnizarii* [strain CBS 101043, GenBank KP858988.1; Identities = 770/804 (96 %), two gaps (0 %)], and *Castanediella tereticornis* [strain CBS 145068, GenBank NG\_068600.1; Identities = 769/804 (96 %), no gaps].

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*Leptopeltis litigiosa* (Desm.) L. Holm & K. Holm, *Bot. Notiser* **130**: 221. 1977. Fig. 28.

Basionym: *Leptostroma litigiosum* Desm., *Annls Sci. Nat., Bot.*, sér. 2 **19**: 338. 1843.

Synonyms: *Dothithyrella litigiosa* (Desm.) Höhn., *Annls mycol.* **16**: 171. 1918.

*Leptostroma litigiosum* Desm., *Annls Sci. Nat., Bot.*, sér. 2 **19**: 338. 1843.

*Leptostroma litigiosum* var. *exasperatum* Berk., in Hooker, *Bot. Antarct. Voy. Erebus Terror 1839-1843*, II, Fl. Nov-Zeal.: 193. 1855.

*Microthyrium litigiosum* (Desm.) Sacc., *Michelia* **1**: 496. 1879.

*Leptothyrium litigiosum* (Desm.) Sacc., *Michelia* **2**: 113. 1880.

*Pycnothyrium litigiosum* (Desm.) Died., *Annls mycol.* **11**: 175. 1913. (asexual morph)

Taxonomic lineage: *Leotiomyces*, *incertae sedis*, *Leptopeltidaceae*.

*Thyrothecia* subcuticular, brown, round, 100–250 µm diam, becoming confluent and forming larger crusts, opening by irregular rupture; surface of radiating rows of brown *textura angularis*; margin even, undulate. *Paraphyses* intermingled among asci, hyaline, smooth, septate, 2–2.5 µm diam, disintegrating at maturity. *Asci* hyaline, smooth, subcylindrical, apex subobtusate, somewhat tapered, slightly curved, 30–50 × 8–10 µm, base truncate to bluntly rounded, unitunicate, apex slightly thickened, at times straining slightly in Melzer's (unclear reaction). *Ascospores* tri to multiseriate, hyaline, smooth, guttulate, fusoid-ellipsoid, slightly curved, ends subobtusate, granular, (0–)1–3-septate, (10–)12–15(–20) × (3–)3.5–4 µm. *Pycnothyria* intermingled among thyrothecia, round, brown, 150–250 µm diam, with central ostiole. *Conidiophores* reduced to conidiogenous cells lining basal cavity, ampulliform,

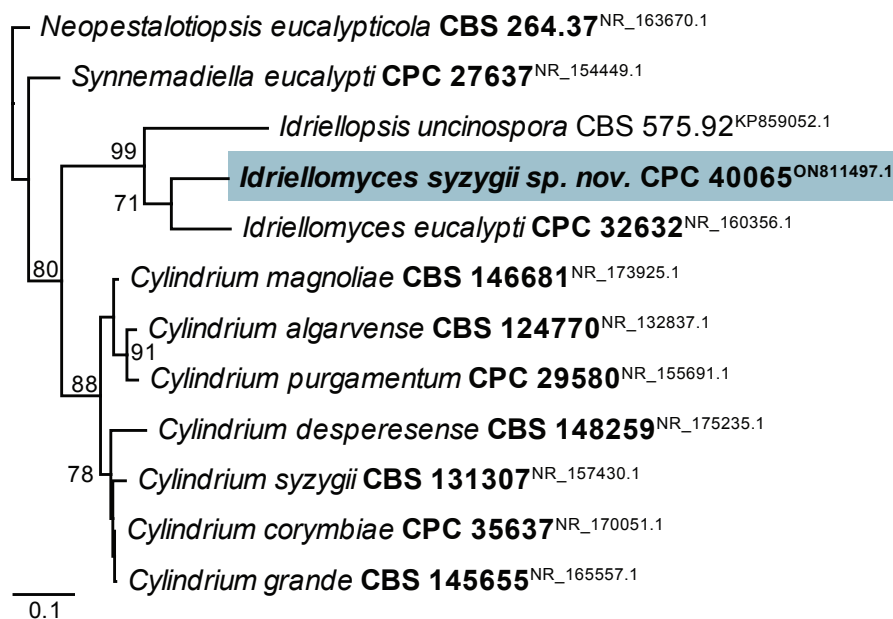
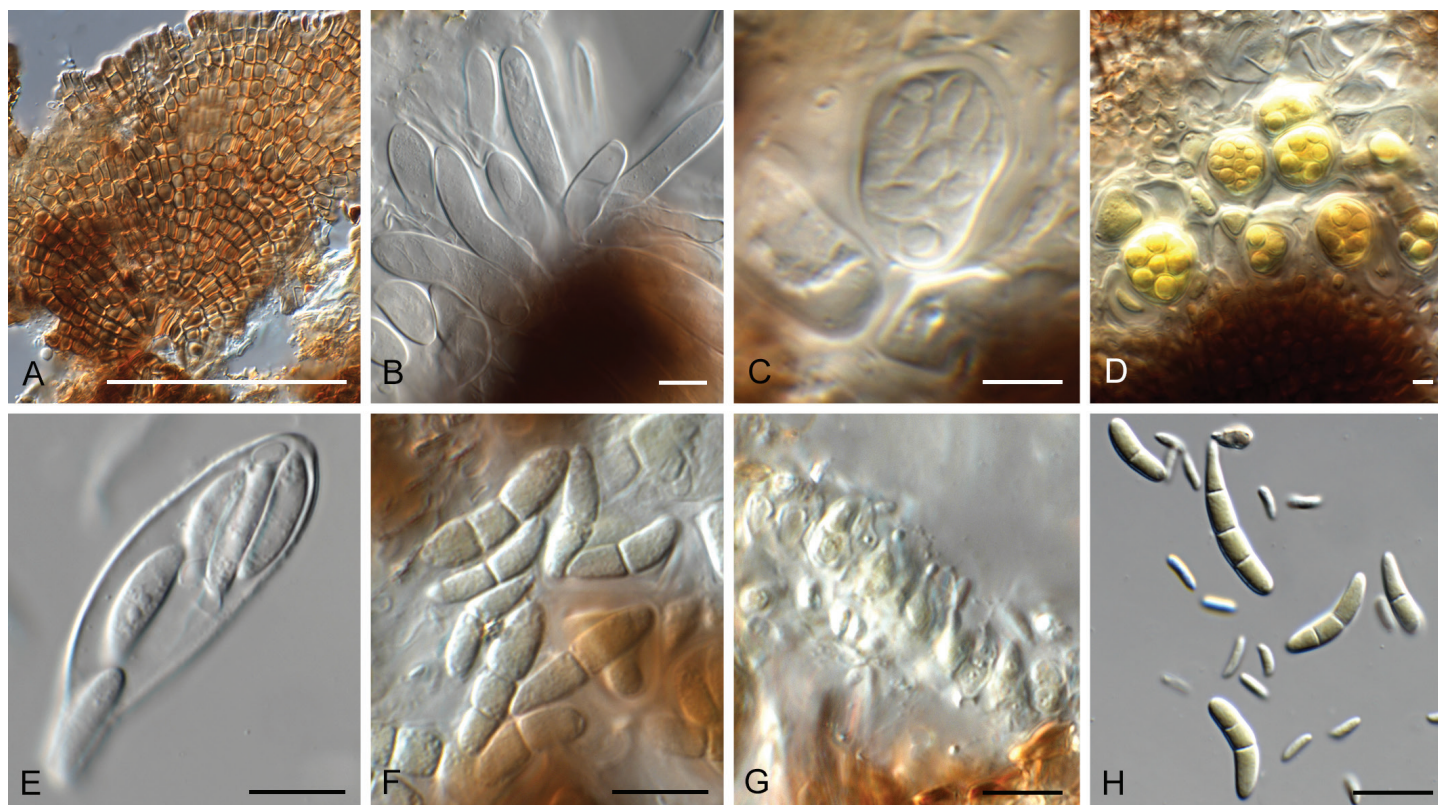


Fig. 27. Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Cylindrium* ITS nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast bootstrap replicates are shown at the nodes. Culture collection numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Neopestalotiopsis eucalypticola* (culture CBS 264.37; GenBank NR\_163670.1) and the species treated here is highlighted with bold face. Accession numbers of sequence from material with a type status are also shown in bold face.



**Fig. 28.** *Leptopeltis litigiosa* (CPC 41928). **A.** Superficial wall of thyrothecium. **B–E.** Asci. **F.** Ascospores. **G.** Conidiogenous cells. **H.** Ascospores and conidia. Scale bars: A = 125  $\mu$ m, all others = 10  $\mu$ m.

hyaline, smooth, 3–5  $\times$  3–4  $\mu$ m. *Conidia* solitary, hyaline, smooth, subcylindrical, apex obtuse, base tapering to truncate hilum, straight to curved, aseptate, granular, 4–7  $\times$  1.5–2  $\mu$ m. Ascospores in thyrothecia give rise to conidia via budding.

**Typus:** France, J.B.H.B. Desmazières, on *Pteridium aquilinum* (*Hypolepidaceae*), Moug. & Nestl., Stirpes Crypt. 673 (UPS), designated as **lectotype** here, MBT 10007403. **Netherlands**, Utrecht Province, Bilthoven, on dead leaf fronds of *Pteridium aquilinum*, Jun. 2021, P.W. Crous, HPC 3645 (**epitype** designated here CBS H-24991, MBT 10007404, culture ex-epitype CPC 41927, 41928 = CBS 149171).

**Notes:** The genus *Leptopeltis* was introduced based on *L. filicina* (*Leptopeltidaceae*), which we regard as a distinct genus, *sensu* Hongsanan *et al.* (2020a), and reject the suggested synonymy with *Fouragea filicina* (based on *Opegrapha filicina* 1845), as the basionym of *L. filicina* is older (1834). However, as molecular data for the type species *L. filicina* is lacking, its phylogeny remains unresolved. For the present, we have assigned this taxon to *Leptopeltidaceae* with no clear ordinal affinity in *Leotiomycetes* (Fig. 4)

*Leptopeltis litigiosa* is common on dead leaf fronds of *Pteridium aquilinum*, and often occurs intermixed with *L. pteridis* (= *L. aquilina*), which has larger, elongated black ascomata with a non-radiate shield, and slightly smaller ascospores, 12–15  $\times$  3–4  $\mu$ m (Holm & Holm 1977). Holm & Holm (1977) regarded asci to be unitunicate, while Eriksson (1981) stated that they were bitunicate. Although difficult to determine, in the present study asci appeared more unitunicate than bitunicate. Furthermore, based on single ascospore cultures, the asexual morph of *L. litigiosa* could be resolved as coelomycetous.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pragmopora cf. pini* [voucher G.M. 2019-05-19.1, GenBank MN547972.1; Identities = 473/525 (90 %), nine gaps (1 %)], *Claussenomyces* sp. keyed as *caeruleomarginatus* [voucher G.M. 2019-06-13.3, GenBank MN238834.1; Identities = 466/515 (90 %), 10 gaps (1 %)], and *Pragmopora cf. bacillifera* [voucher G.M. 2019-04-30.1, GenBank MK900749.1; Identities = 462/515 (90 %), nine gaps (1 %)]. Closest hits using the **LSU** sequence are *Pallidophorina paarla* [strain CBS 120877, GenBank NG\_068607.1; Identities = 688/708 (97 %), two gaps (0 %)], *Ramoconidiophora euphorbiae* [strain CBS 141018, GenBank NG\_068606.1; Identities = 684/708 (97 %), two gaps (0 %)], and *Capturomyces luteus* [strain GLMC 1842, GenBank MK314603.1; Identities = 683/708 (96 %), two gaps (0%)].

**Authors:** P.W. Crous, J.Z. Groenewald, M. Starink-Willemsse & A.L. van Iperen

**Macgarvieomyces juncicola** (MacGarvie) Klaubauf *et al.*, *Stud. Mycol.* **79**: 107. 2014. Fig. 29.

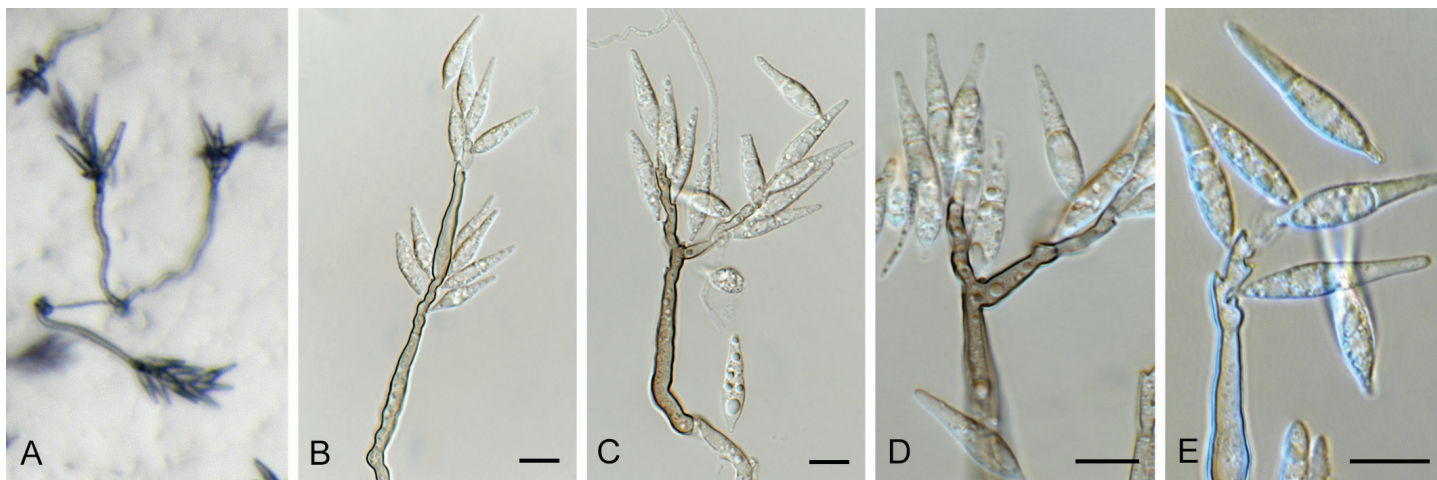
**Basionym:** *Pyricularia juncicola* MacGarvie, *Scientific Proc. R. Dublin Soc.*, Ser. B **2**(no. 16): 155. 1968.

**Taxonomic lineage:** Sordariomycetes, Magnaporthales, Pyriculariaceae.

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

**Material examined:** **Netherlands**, Utrecht Province, Nieuw Wulven, near Houten, 52°02'45"N, 5°10'34"E, 1.5 m a.s.l., on dead culm of





**Fig. 29.** *Macgarvieomyces juncicola* (CPC 40815). **A.** Conidiophores on SNA. **B–E.** Conidiophores and conidiogenous cells giving rise to conidia. Scale bars = 10  $\mu$ m.

*Juncus effusus* (Juncaceae), 8 Jan. 2021, E.R. Osieck, HPC 3564 = WI-10/#4195, culture CPC 40815 = CBS 148264.

**Notes:** *Macgarvieomyces juncicola* is known from culms of *Juncus effusus* in Ireland and the Netherlands (Klaubauf *et al.* 2014), and the present isolate represents a new collection for the species (Fig. 6).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Macgarvieomyces juncicola* [strain CBS 610.82, GenBank KM484855.1; Identities = 461/461 (100 %), no gaps], *Dactylaria junci* [strain P17, GenBank AY265321.1; Identities = 498/508 (98 %), no gaps], and *Macgarvieomyces luzulae* [strain CBS 145042, GenBank MK442591.1; Identities = 495/532 (93 %), 16 gaps (3 %)]. Closest hits using the **LSU** sequence are *Macgarvieomyces juncicola* [strain CBS 610.82, GenBank KM009153.1; Identities = 815/815 (100 %), no gaps], *Macgarvieomyces luzulae* [strain CBS 145042, GenBank MK442531.1; Identities = 805/815 (99 %), one gap (0 %)], and *Macgarvieomyces borealis* [strain CBS 461.65, GenBank MH870310.1; Identities = 803/815 (99 %), one gap (0 %)]. Closest hits using the **actA** sequence had highest similarity to *Macgarvieomyces juncicola* [strain CBS 610.82, GenBank KM485171.1; Identities = 317/317 (100 %), no gaps], *Macgarvieomyces luzulae* [strain CBS 145042, GenBank MK442635.1; Identities = 634/724 (88 %), 31 gaps (4 %)], and *Pseudopyricularia bothriochloae* [strain CBS 136427, GenBank KY905700.1; Identities = 598/713 (84 %), 45 gaps (6 %)]. Closest hits using the **cmdA** sequence had highest similarity to *Macgarvieomyces juncicola* [strain CBS 610.82, GenBank KM485240.1; Identities = 477/477 (100 %), no gaps], and *Macgarvieomyces luzulae* [strain CPC 31555, GenBank MG934520.1; Identities = 384/461 (83 %), 19 gaps (4 %)]. Closest hits using the **rpb1** sequence had highest similarity to *Macgarvieomyces juncicola* [strain CBS 610.82, GenBank KM485071.1; Identities = 749/749 (100 %), no gaps], *Macgarvieomyces luzulae* [strain CPC 31571, GenBank MG934471.1; Identities = 555/605 (92 %), no gaps], and *Pyricularia borealis* [strain CBS 461.65, GenBank KM009186.1; Identities = 652/716 (91 %), no gaps].

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***Magnibotryascoma mali*** Phukhams. *et al.*, *Fungal Diversity* **87**: 105. 2017. Fig. 30.

**Taxonomic lineage:** Dothideomycetes, Pleosporales, Teichosporaceae.

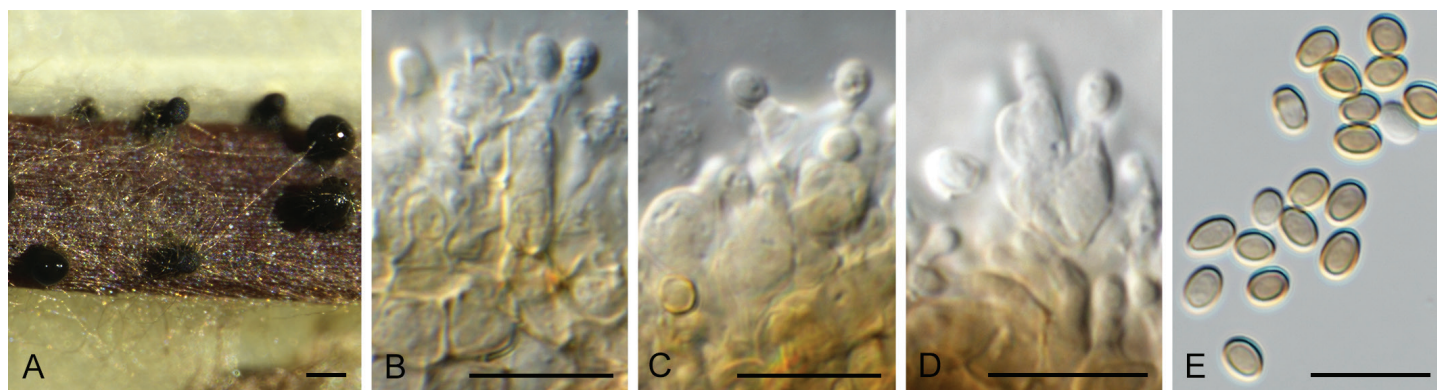
**Conidiomata** solitary, erumpent, globose, brown, 150–200  $\mu$ m diam, with central ostiole; wall of 6–8 layers of brown *textura angularis*. **Conidiophores** lining the inner cavity, reduced to conidiogenous cells or with a basal supporting cell, branched or not. **Conidiogenous cells** hyaline, smooth, phialidic with prominent periclinal thickening, ampulliform to subcylindrical, 5–10  $\times$  3–5  $\mu$ m. **Conidia** solitary, aseptate, thick-walled, guttulate, initially hyaline, smooth, becoming golden brown, ellipsoid to subovoid, 3–4  $\times$  2.5–3  $\mu$ m.

**Culture characteristics:** Colonies flat, spreading, with moderate aerial mycelium and lobate, smooth margin, reaching 50 mm diam after 2 wk at 25  $^{\circ}$ C. On MEA surface and reverse isabelline; on PDA surface isabelline, reverse brown vinaceous; on OA surface isabelline.

**Material examined:** **New Zealand**, Tuaranga port, on *Metrosideros* sp. (Myrtaceae), 22 Aug. 2019, L. Rabbidge, CBS H-24440, culture CPC 38757 = T19\_05741B = CBS 146778; Tauranga port, on *Metrosideros* sp., 2019, L. Rabbidge, CBS H-24506, culture CPC 38756 = T19\_05741A = CBS 147001.

**Notes:** *Magnibotryascoma mali* was recently described on *Malus halliana* collected in China (conidia 3–5  $\times$  2.3–3.8  $\mu$ m, oval to broadly obovoid, hyaline when young, become reddish brown at maturity, aseptate, smooth-walled; Hyde *et al.* 2017). The New Zealand collection is phylogenetically similar and has overlapping conidial dimensions. Based on the blast results and the phylogenetic trees (Figs 2, 24), our cultures can best be accommodated in this species. The long branch for the ex-type culture of this species (Fig. 24) is most likely due to an issue with the ex-type ITS sequence. Based on blast searches using the ex-type sequence, the best hit is with *Pseudochaetosphaeronema kunmingense* (Pleosporales), which contradicts the placement of this strain based on the other loci.

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



**Fig. 30.** *Magnibotryascoma mali* (CPC 38756). **A.** Conidiomata on PNA. **B–D.** Conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars: A = 200  $\mu\text{m}$ , all others = 10  $\mu\text{m}$ .

of CPC 38757 had highest similarity to *Magnibotryascoma* sp. DNW-2020a [strain HKAS 111915, GenBank MW424773.1; Identities = 547/549 (99 %), one gap (0 %)], *Teichospora rubriostiolata* [strain CBS 140734, GenBank NR\_154634.1; Identities = 552/605 (91 %), 20 gaps (3 %)], and *Teichospora melanommoides* [strain CBS 140733, GenBank NR\_154632.1; Identities = 554/607 (91 %), 25 gaps (4 %)]. The ITS sequences of CPC 38756 and 38757 are identical (591/591 bp). Closest hits using the **LSU** sequence of CPC 38757 are *Magnibotryascoma mali* [voucher MFLU 17-0559, GenBank NG\_059830.1; Identities = 817/817 (100 %), no gaps], *Magnibotryascoma* sp. DNW-2020a [strain HKAS 111921, GenBank MW424789.1; Identities = 857/865 (99 %), no gaps], and *Teichospora acaciae* [strain CBS 140000, GenBank MH878675.1; Identities = 772/780 (99 %), two gaps (0 %)]. The LSU sequences of CPC 38756 and 38757 are identical (850/850 bp). Closest hits using the **tef1** (first part) sequence of CPC 38757 had highest similarity to *Teichospora rubriostiolata* [strain C158x, GenBank KU601608.1; Identities = 405/462 (88 %), eight gaps (1 %)], *Teichospora melanommoides* [strain MP5, GenBank KU601610.1; Identities = 405/463 (87 %), 13 gaps (2 %)], and *Teichospora pusilla* [strain C140, GenBank KU601605.1; Identities = 403/467 (86 %), 17 gaps (3 %)]. The **tef1** sequences of CPC 38756 and 38757 are identical (492/492 bp). Closest hits using the **tef1** (second part) sequence of CPC 38757 had highest similarity to *Magnibotryascoma mali* [strain MFLUCC 17-0933, GenBank MF173435.1; Identities = 899/907 (99 %), no gaps], *Ramusculicola thailandica* [strain MFLUCC 13-0284, GenBank KR075167.1; Identities = 785/849 (92 %), no

gaps], and *Rhytidhysteron rufulum* [voucher MFLU 18-2190, GenBank MK360087.1; Identities = 791/857 (92 %), no gaps].

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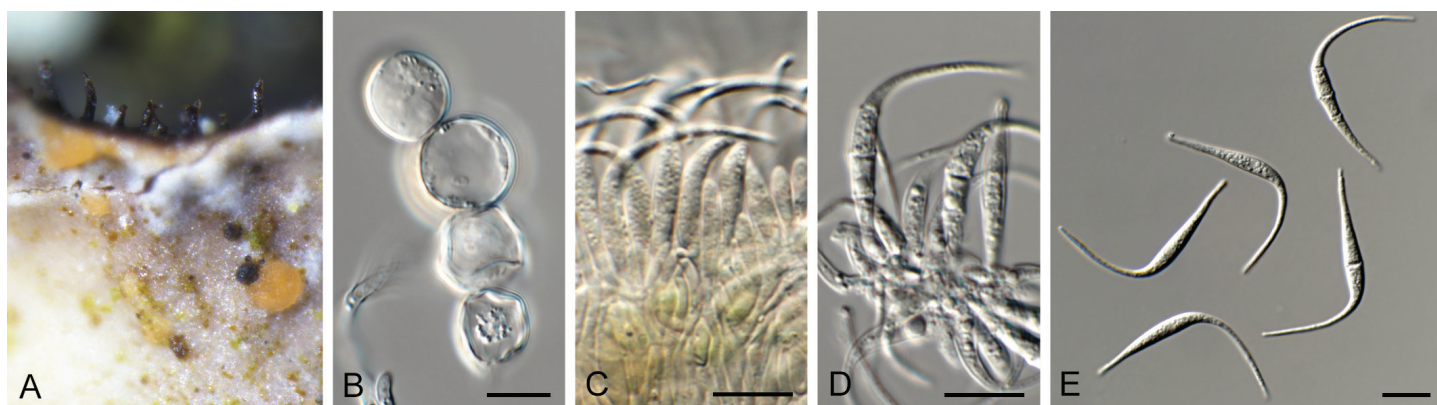
***Microcera lichenicola*** Crous & Boers, *sp. nov.* MycoBank MB 844286. Fig. 31.

**Taxonomic lineage:** Sordariomycetes, Hypocreales, Nectriaceae.

**Etymology:** Name refers to the lichen hosts from which it was isolated.

Associated with discoloured thalli of *Parmelia sulcata*. **Mycelium** consisting of hyaline, smooth-walled, branched, septate, 2–3  $\mu\text{m}$  diam hyphae. **Conidiomata** sporodochial, orange on host, consisting of tightly aggregated conidiophores that are reduced to conidiogenous cells or with a short stipe, giving rise to 1–4 conidiogenous cells. **Conidiogenous cells** subulate, tapering towards apex, flexuous, monopialidic with periclinal thickening and minute non-flared collarete, 10–20  $\times$  2–3  $\mu\text{m}$ . **Conidia** hyaline, smooth-walled, guttulate, (0–)3-septate, distinctly curved and twisted, apex attenuated, subobtuse, dorsiventrally curved, basal cell attenuated to subobtuse, non-foot-shaped to slightly notched basal cell, (35–)40–45(–55)  $\times$  3(–3.5)  $\mu\text{m}$ .

**Culture characteristics:** Colonies flat, spreading, surface folded, with sparse aerial mycelium and smooth, lobate margin, reaching 22 mm diam after 14 d at 25  $^{\circ}\text{C}$ . On MEA surface orange, reverse



**Fig. 31.** *Microcera lichenicola* (CPC 41114). **A.** Discoloured thalli of *Parmelia sulcata* with orange sporodochia. **B.** Chlamydospores. **C, D.** Conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars = 10  $\mu\text{m}$ .



orange with patches of ochreous; on PDA and OA surface and reverse orange. Cultures sterile, forming chains of hyaline, subglobose to globose chlamydospores, 6–15 µm diam.

*Typus*: **Netherlands**, Friesland Province, Ameland, Ballum, on *Parmelia sulcata* (*Parmeliaceae*), 21 Feb. 2021, J. Boers, HPC 3594 (**holotype** CBS H-24992, culture ex-type CPC 41114 = CBS 149169).

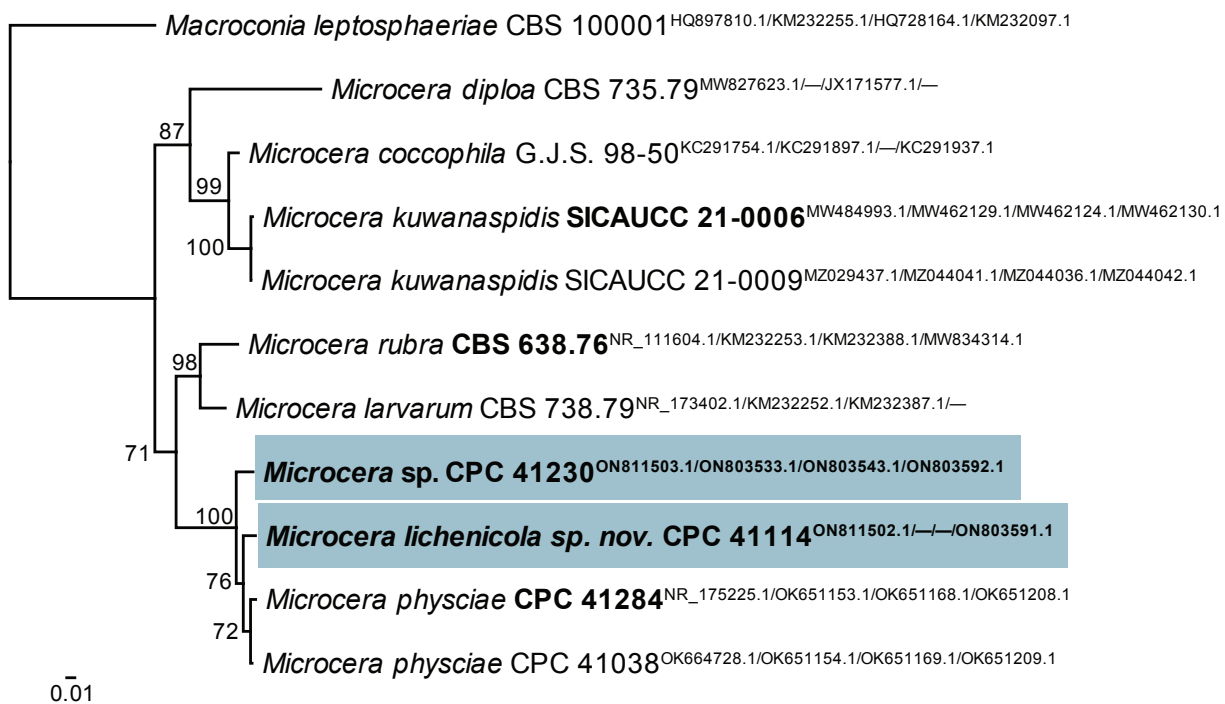
*Material examined of Microcera sp.*: **Netherlands**, Friesland Province, Ameland, Ballum, on *Physcia tenella* (*Physciaceae*), 21 Feb. 2021, J. Boers, HPC 3596, culture CPC 41230 = CBS 148313; North Holland Province, Ameland, Ballum, on *Parmelia sulcata* (*Parmeliaceae*), 21 Feb. 2021, J. Boers, HPC 3594, culture CPC 41115 = CBS 149170.

*Notes*: Although species of *Microcera* are usually pathogens of scale insects (Gräfenhan *et al.* 2011, Crous *et al.* 2021c), this is the second species described from a lichen thallus. *Microcera lichenicola* is phylogenetically (Figs 7, 32) and morphologically similar to *M. physciae* (on *Physcia tenella*), but distinct in that the latter has shorter conidia, (20–)24–26(–33) × 3(–3.5) µm (Crous *et al.* 2021d). Although the ITS and LSU sequences of CPC 41114 and 41230 are highly similar, their *tub2* sequences are only 96 % similar. Unfortunately we were unable to generate a complete dataset for both strains and therefore prefer not to apply the name *Microcera lichenicola* to CPC 41230 pending the collection of more strains from this host (family).

The ITS sequence of CPC 41114 differs with a single nucleotide from the ex-type sequence of *Microcera physciae* [strain CBS 148283, GenBank NR\_175225.1; Identities = 496/497 (99 %); based on a megablast search of NCBI's GenBank nucleotide

database, the closest hits using the ITS sequence of CPC 41114 had highest similarity to "*Fusarium sp.*" [strain F-267,620, GenBank EU860076.1; Identities = 544/545 (99 %), one gap (0 %)], *Microcera larvarum* [strain ICMP 5444, GenBank MT107902.1; Identities = 534/546 (98 %), three gaps (0 %)], and *Cosmospora aurantiicola* [strain F-251,305, GenBank EU860061.1; Identities = 533/545 (98 %), three gaps (0 %)]. The LSU sequence of CPC 41114 differs with a single nucleotide from the ex-type sequence of *Microcera physciae* [strain CBS 148283, GenBank OK663766.1; Identities = 813/814 (99 %); closest hits using the LSU sequence of CPC 41114 are *Microcera rubra* [strain CBS 638.76, GenBank NG\_058100.1; Identities = 806/816 (99 %), no gaps], *Microcera larvarum* [strain CBS 738.79, GenBank KM231701.1; Identities = 806/816 (99 %), no gaps], and *Microcera coccophila* [strain MAFF 241482, GenBank KC291787.1; Identities = 781/793 (98 %), no gaps]. The *tub2* sequence of CPC 41114 is 97 % similar to the ex-type sequence of *Microcera physciae* strain CBS 148283, GenBank OK651208.1; Identities = 510/526 (97 %), two gaps (0 %)]; closest hits using the *tub2* sequence of CPC 41114 had highest similarity to "*Fusarium sp.*" [strain F-267,620, GenBank EU860029.1; Identities = 527/542 (97 %), one gap (0 %)], *Microcera larvarum* [as *Fusarium larvarum* var. *larvarum*; strain F-266,784, GenBank EU860024.1; Identities = 470/542 (86 %), eight gaps (1 %)], and *Microcera coccophila* [strain MAFF 241482, GenBank KC291936.1; Identities = 449/515 (87 %), eight gaps (1 %)].

The ITS sequences of CPC 41230 and 41114 differ at two nucleotide positions (543/545 bp identical) while the LSU sequences of CPC 41230 and 41114 differ at three nucleotide positions (798/801 bp identical). The *rpb1* sequence of CPC



**Fig. 32.** Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh *et al.* 2020) of the *Microcera* concatenated (ITS, *rpb1*, *rpb2*, *tub2*) nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast bootstrap replicates are shown at the nodes. Culture collection numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Macroconia leptosphaeriae* (culture CBS 100001; GenBank HQ897810.1, KM232255.1, HQ728164.1, KM232097.1, respectively) and the species treated here is highlighted with bold face. Accession numbers of sequence from material with a type status are also shown in bold face.



41230 is 96 % similar to the ex-type sequence of *Microcera physciae* [strain CBS 148283, GenBank OK651153.1; Identities = 710/738 (96 %), no gaps]; closest hits using the **rpb1** sequence of CPC 41230 had highest similarity to *Microcera coccophila* [strain MAFF 241482, GenBank KC291895.1; Identities = 631/688 (92 %), no gaps], *Microcera larvarum* [strain A.R. 4580, GenBank KC291894.1; Identities = 627/688 (91 %), no gaps], and *Microcera rubra* [strain CBS 638.76, GenBank KM232253.1; Identities = 654/724(90 %), no gaps]. The **rpb2** sequence of CPC 41230 is 96 % similar to the ex-type sequence of *Microcera physciae* [strain CBS 148283, GenBank OK651168.1; Identities = 845/883 (96 %), one gap (0 %)]; closest hits using the **rpb2** sequence of CPC 41230 had highest similarity to *Microcera* sp. [strain NRRL 26790, GenBank JX171636.1; Identities = 832/863 (96 %), no gaps], *Microcera larvarum* [strain NRRL 20473, GenBank JX171587.1; Identities = 775/861 (90 %), no gaps], and *Microcera rubra* [strain CBS 638.76, GenBank KM232388.1; Identities = 773/859 (90 %), no gaps]. The **tef1 (first part)** sequence of CPC 41230 is 94 % similar to the ex-type sequence of *Microcera physciae* [strain CBS 148283, GenBank OK651190.1; Identities = 434/464 (94 %), four gaps (0 %)]; closest hits using the **tef1 (first part)** sequence of CPC 41230 had highest similarity to "*Fusarium* sp." [strain NRRL 20473, GenBank JF740695.1; Identities = 379/465 (82 %), 19 gaps (3 %)], *Microcera larvarum* [strain CBS 738.79, GenBank KM231957.1; Identities = 334/412 (81 %), 19 gaps (4 %)], and *Microcera coccophila* [strain ZJUP0179, GenBank MN614420.1; Identities = 221/255 (87 %), two gaps (0 %)]. The **tub2** sequences of CPC 41230 and 41114 are 96 % similar (505/525 bp, including three gaps).

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***Mycodiella eucalypti*** Crous, *Persoonia* **37**: 337. 2016. Fig. 33.

**Taxonomic lineage:** *Dothideomycetes*, *Mycosphaerellales*, *Mycosphaerellaceae*.

**Leaf spots** amphigenous, irregular, brown with raised red-brown border, 2–5 mm diam. **Ascomata** amphigenous, erumpent, globose, brown, 100–130 µm diam, with central periphysate ostiole, 10–15 µm diam; wall of 3–4 layers of brown *textura angularis*. **Asci** fasciculate, 8-spored, bitunicate, obovoid, curved to straight, with apical ocular chamber, 35–45 × 13–16 µm. **Ascospores** multiseriate, hyaline, smooth, guttulate, medianly 1-septate, thin-walled, not constricted at septum, subcylindrical to narrowly obovoid, widest in upper part of apical cell, (15–) 17–18(–20) × (3–)3.5–4 µm; ascospores germinating from both ends, with germ tubes parallel to the long axis, flexuous, becoming constricted at septum, 6–7 µm diam, remaining hyaline.

**Culture characteristics:** Colonies erumpent, spreading, with moderate aerial mycelium and lobate, even margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, reverse iron-grey.

**Material examined:** **South Africa**, Northern Province, Nelspruit, Buffelskloof Nature Reserve, on leaf litter of *Syzygium cordatum* (*Myrtaceae*), Nov. 2018, P.W. Crous, HPC 3148 = CBS H-24498, culture CPC 38962 = CBS 146986.

**Notes:** *Mycodiella eucalypti* (on *Eucalyptus diversicolor*, Australia, ascospores (11–)12–13(–15) × (2.5–)3(–3.5) µm; Crous *et al.* 2016) was originally described as having smaller ascospores than the present collection. However, the two collections are phylogenetically closely related (Figs 1 part 2, 13), suggesting that the South African collection is best treated as *M. eucalypti* until more strains of the species become available for comparison.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Mycodiella eucalypti* [strain CPC 29458, GenBank NR\_155408.1; Identities = 526/536 (98 %), gap (0 %)], *Mycodiella sumatrensis* [strain CBS 118499, GenBank NR\_111803.1; Identities = 455/468 (97 %), two gaps (0 %)], and *Mycosphaerella polygoni-cuspidati* [strain IMI 401968, GenBank LC146384.1; Identities = 494/512 (96 %), two gaps (0 %)]. Closest hits using the **LSU** sequence are *Mycodiella sumatrensis* [strain CBS 118499, GenBank NG\_042737.1; Identities = 712/714 (99 %), one gap (0 %)], *Mycodiella eucalypti* [strain CPC 29458, GenBank NG\_059747.1; Identities = 964/971 (99 %), no gaps], and *Mycosphaerella laricis-leptolepidis* [strain MAFF 410081, GenBank JX901862.1; Identities = 705/713 (99 %), no gaps]. Closest hits using the **actA** sequence had highest similarity to *Mycodiella eucalypti* [strain CPC 29525, GenBank KY173566.1; Identities = 491/497 (99 %), no gaps], *Mycodiella sumatrensis* [strain CBS 118499, GenBank KF903498.1; Identities = 514/522 (98 %), no gaps], and *Mycosphaerella laricis-leptolepidis* [strain MAFF 410234, GenBank JX902112.1; Identities = 509/541 (94 %), three gaps (0 %)]. Closest hits using the **cmdA** sequence had highest similarity to *Mycodiella sumatrensis* [strain CBS 118502, GenBank KF902552.1; Identities = 352/365 (96 %), no gaps], *Mycosphaerella laricis-leptolepidis* [strain MAFF 410081, GenBank JX901548.1; Identities = 255/263 (97 %), one gap (0 %)], and *Zasmidium corymbiae* [strain CBS 145049, GenBank MK047526.1; Identities = 281/306 (92 %), no gaps]. Closest hits using the **rpb2** sequence had highest similarity to *Mycodiella sumatrensis* [strain CBS 118501, GenBank MF951525.1; Identities = 770/771 (99 %), no gaps], *Mycodiella eucalypti* [strain CPC 29458, GenBank KY173586.1; Identities = 746/753 (99 %), no gaps], and *Collapsimycopappus styracis* [strain YS 4, GenBank LC333044.1; Identities = 703/767 (92 %), no gaps]. Closest hits using the **tub2** sequence had highest similarity to *Mycodiella sumatrensis* [strain CBS 118499, GenBank KF902814.1; Identities = 318/323 (98 %), no gaps], *Toxicocladosporium rubrigenum* [strain CBS 124158, GenBank KY706607.1; Identities = 326/395 (83 %), 21 gaps (5 %)], and *Pseudocercospora nelumbicola* [strain RK4111, GenBank LC200982.1; Identities = 321/390 (82 %), 32 gaps (8 %)].

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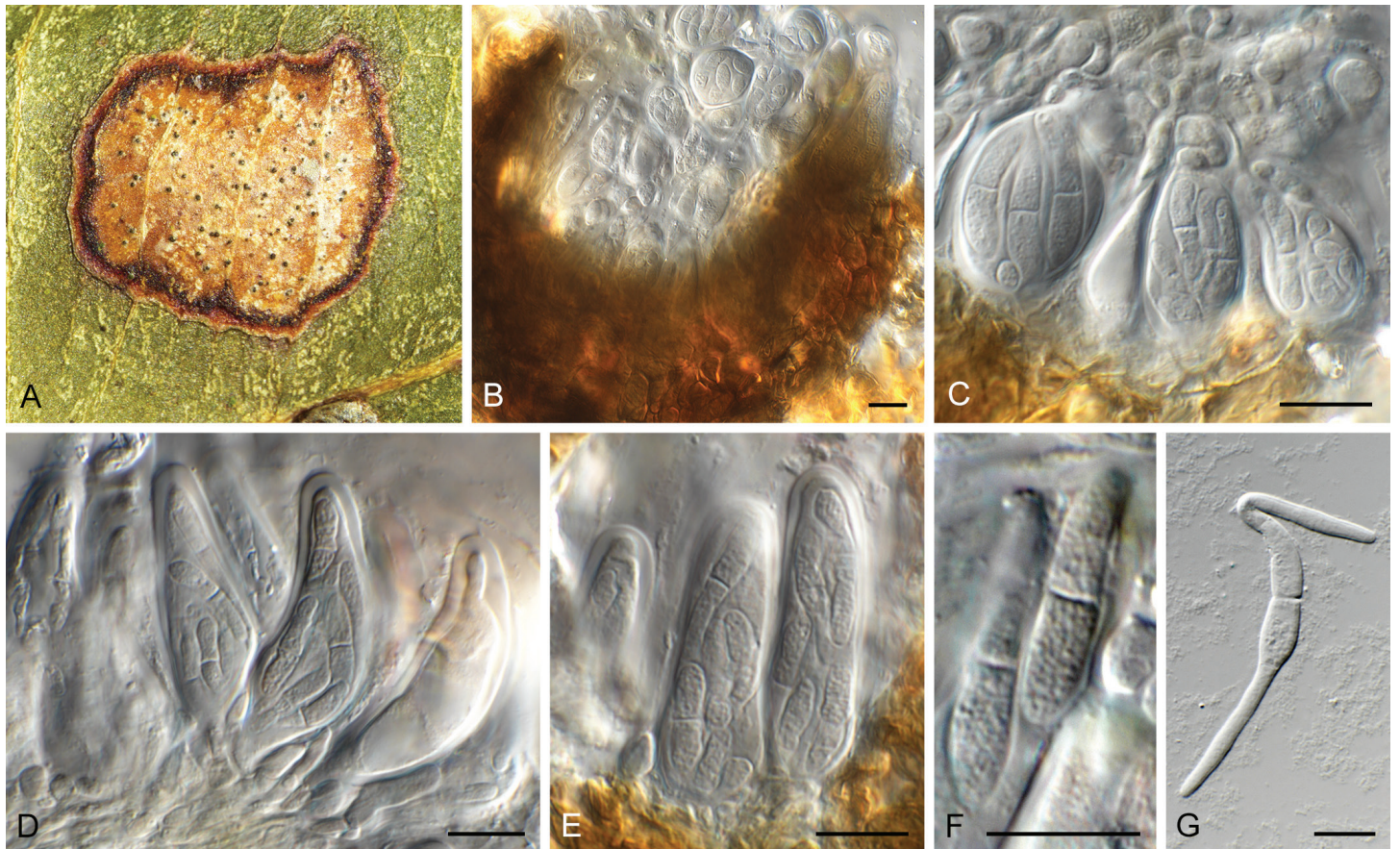
***Neobarrmaelia*** Crous, *gen. nov.* MycoBank MB 844289.

**Taxonomic lineage:** *Sordariomycetes*, *Xylariales*, *incertae sedis*.

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

**Mycelium** consisting of hyaline, smooth-walled, branched, septate hyphae. **Conidiophores** erect, brown, smooth-walled, subcylindrical, unbranched, straight to slightly flexuous, 0–2-septate. **Conidiogenous cells** integrated, terminal, brown, smooth-walled, subcylindrical, forming a rachis of denticles, truncate, not thickened nor darkened. **Conidia** in dry rosettes,





**Fig. 33.** *Mycodiella eucalypti* (CPC 38962). **A.** Leaf spot with ascomata. **B.** Broken ascoma with asci. **C–E.** Asci. **F.** Ascospores. **G.** Germinating ascospore. Scale bars = 10 µm.

guttulate, hyaline, smooth-walled, subcylindrical, falcate, apical part strongly hooked, aseptate, tapering to subobtuse apex and truncate hilum.

*Type species:* *Neobarrmaelia hyphaenes* Crous

***Neobarrmaelia hyphaenes*** Crous, *sp. nov.* MycoBank MB 844290. Fig. 34.

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

*Mycelium* consisting of hyaline, smooth-walled, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* erect, brown, smooth-walled, subcylindrical, unbranched, straight to slightly flexuous, 0–2-septate, 25–50 × 3–3.5 µm. *Conidiogenous cells* integrated, terminal, brown, smooth-walled, subcylindrical, 20–35 × 3–3.5 µm, forming a rachis of denticles, 0.5–1 × 0.5 µm, truncate, not thickened nor darkened. *Conidia* in dry rosettes, guttulate, hyaline, smooth-walled, subcylindrical, falcate, apical part strongly hooked, aseptate, tapering to subobtuse apex and truncate hilum, 0.5 µm diam, (15–)17–18(–20) × 1.5–2 µm.

*Culture characteristics:* Colonies erumpent, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse umber with diffuse umber pigment; on PDA surface and reverse dirty white with patches of umber; on OA surface dirty white with patches of isabelline.

*Typus:* **South Africa**, KwaZulu-Natal Province, Manguzi, on leaves of *Hyphaene* sp. (*Areaceae*), 19 Oct. 2017, M.J. Wingfield & J. Roux, HPC 3501 (**holotype** CBS H-24843 culture ex-type CPC 40101 = CBS 148304).

*Notes:* *Neobarrmaelia* is a typical xylariaceous asexual morph, resembling the genus *Barrmaelia*, which is based on *B. rhamnicola* (Voglmayr *et al.* 2018, Crous *et al.* 2020b). Phylogenetically, it groups in a separate clade with *B. serenoae*, for which the genus *Neobarrmaelia* is introduced (Fig. 8). Morphologically the two species differ in their conidial dimensions, with those of *N. serenoae* [(20–)25–30 × 1.5 µm] being longer than conidia of *N. hyphaenes* [(15–)17–18(–20) × 1.5–2 µm].

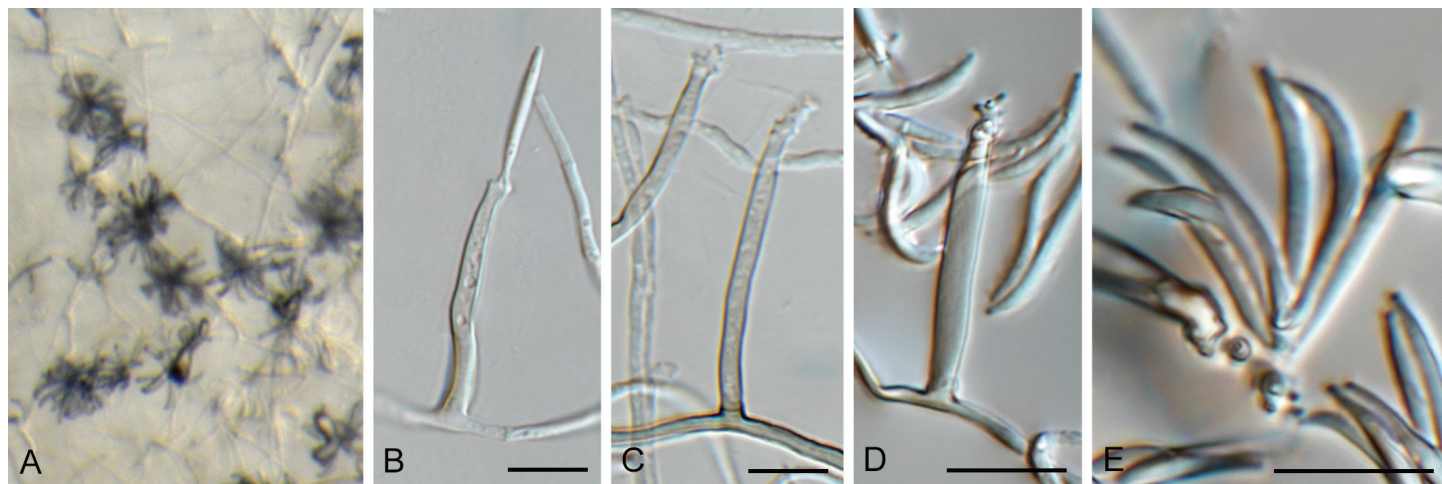
***Neobarrmaelia serenoae*** (Crous) Crous, **comb. nov.** MycoBank MB 844291.

*Basionym:* *Barrmaelia serenoae* Crous, *Fungal Syst. Evol.* **6**: 179. 2020.

*Material examined:* **USA**, Florida, Gainesville, on leaf of *Serenoa repens* (*Areaceae*), 24 Feb. 2019, M.J. Wingfield, HPC 2792 (**holotype** CBS H-24201, culture ex-type CPC 37572 = CBS 146017).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Barrmaelia macrospora* [strain CBS 142768, GenBank NR\_167684.1; Identities = 536/618 (87 %), 18 gaps (2 %)], *Barrmaelia moravica* [strain CBS 142769, GenBank NR\_153495.1; Identities = 536/618 (87 %), 20 gaps (3 %)], and *Entosordaria quercina* [strain CBS 142774, GenBank NR\_153499.1; Identities = 534/619 (86 %), 24 gaps (3 %)].





**Fig. 34.** *Neobarrmaelia hyphaenes* (CPC 40101). **A.** Conidiophores on SNA. **B–D.** Conidiophores and conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars = 10  $\mu$ m.

Closest hits using the **LSU** sequence are *Sarcoxydon compunctum* [strain CBS 359.61, GenBank MH869652.1; Identities = 801/821 (98 %), four gaps (0 %)], *Xylaria badia* [strain 5256, GenBank JQ862643.1; Identities = 798/819 (97 %), no gaps], and *Xylaria acuta* [strain 5220, GenBank JQ862637.1; Identities = 798/819 (97 %), no gaps]; LSU sequences of *Barrmaelia* match around 97 %. No significant hits were obtained when the *rpb2* and *tub2* sequences were used in blastn and megablast searches.

**Authors:** P.W. Crous, J.Z. Groenewald, J. Roux & M.J. Wingfield

***Neobryochiton*** Crous & Boers, **gen. nov.** MycoBank MB 844292.

**Taxonomic lineage:** *Dothideomycetes*, *Mycosphaerellales*, *Teratosphaeriaceae*.

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

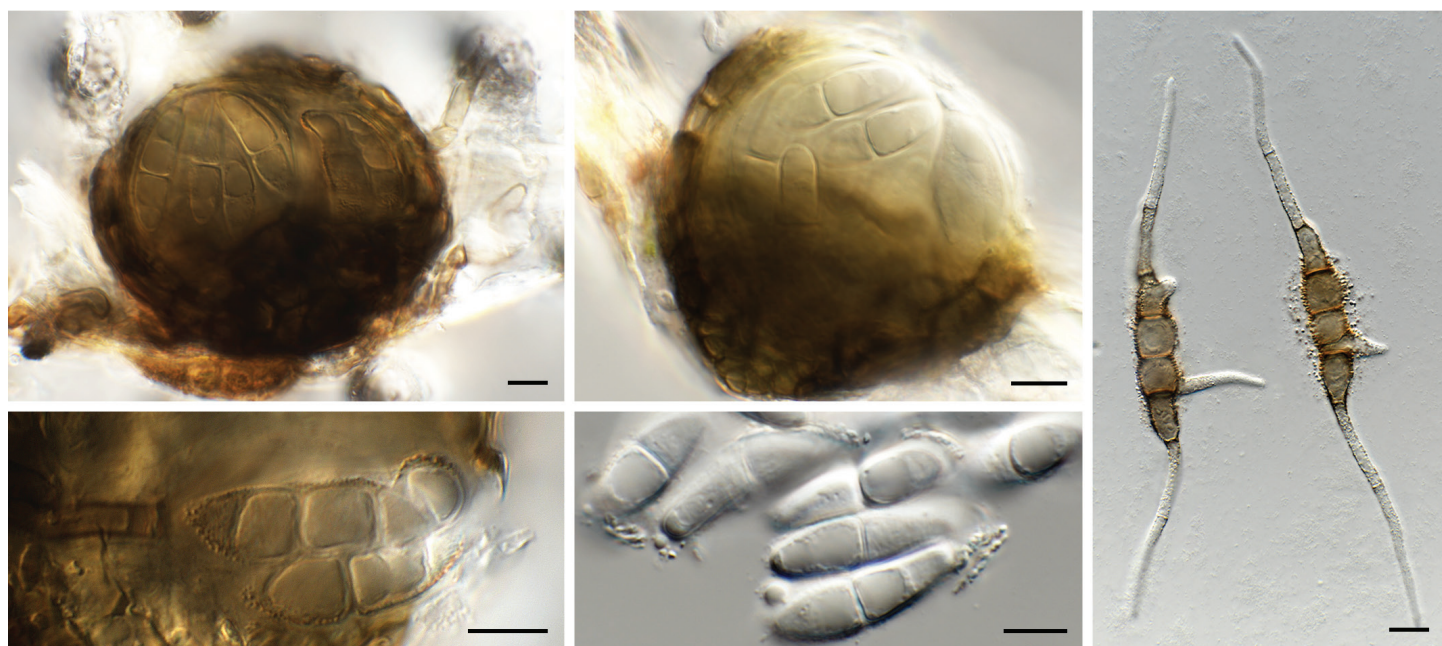
*Ascomata* pseudothecial, solitary, superficial, globose with central ostiole, brown; wall of 2–3 layers of brown *textura angularis*. *Asci* 8-spored, bitunicate with ocular chamber, ellipsoid. *Ascospores* multiseriate, hyaline, smooth-walled, guttulate, medianly 1-septate, constricted at septum, fusoid-ellipsoid, widest above septum, becoming 3-septate, brown and verruculose with age, surrounded by mucoid sheath.

**Type species:** *Neobryochiton narthecii* Crous & Boers

***Neobryochiton narthecii*** Crous & Boers, **sp. nov.** MycoBank MB 844293. Fig. 35.

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

*Ascomata* pseudothecial, solitary, superficial, globose with central ostiole, brown, 40–70  $\mu$ m diam; wall of 2–3 layers of brown *textura angularis*. *Asci* 8-spored, bitunicate with ocular



**Fig. 35.** *Neobryochiton narthecii* (CPC 41972). **A, B.** Superficial ascomata. **C, D.** Ascospores. **E.** Germinating ascospores. Scale bars = 10  $\mu$ m.



chamber, ellipsoid, 25–40 × 20–30 µm. *Ascospores* multiseriate, hyaline, smooth-walled, guttulate (with two large guttules per cell when mounted in water), medianly 1-septate, constricted at septum, fusoid-ellipsoid, widest above septum, becoming 3-septate, brown and verruculose with age, surrounded by mucoid sheath, (22–)25–28(–30) × (7–)8–9 µm. Germinating ascospores with polar germ tubes, germinating parallel to long axis of the spore, later developing secondary lateral germ tubes from middle of ascospore body; ascospores 9–11 µm diam, verruculose, with prominent mucoid sheath.

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

**Typus:** **Netherlands**, Drenthe Province, Dwingelderveld National Park, 52.829188, 6.432495, on dead leaves of *Narthecium ossifragum* (*Nartheciaceae*), 4 Jul. 2021, J. Boers, HPC 3653 (**holotype** CBS H-24993, cultures ex-type CPC 41972, 41973 = CBS 149172).

**Notes:** Döbbele (1978) introduced the genus *Bryochiton* (based on *B. monascus*; ascomata up to 40 µm diam, with brown, 3-septate, ellipsoid ascospores, 9–12.5 × 3.5–4.5 µm, asci 15–20 × 10–15 µm). *Bryochiton* presently accommodates five bryosymbiotic species (Döbbele 2007) with much smaller ascospores, which also differ from *N. narthecii* in general morphology.

*Neobryochiton narthecii* is closely related to “*Teratosphaeria* encephalarti” (Crous *et al.* 2008), and several isolates identified as “*Bryochiton* sp.”, in a study that revealed *Bryochiton* to be paraphyletic (Wäli *et al.* 2014). *Neobryochiton* is morphologically distinct from *T. encephalarti* and *Teratosphaeria* in general by having 3-septate ascospores as observed in *Bryochiton* s.str., from which it is phylogenetically distinct (Figs 1 part 2, 36). *Neobryochiton narthecii* is easily overlooked as it inhabits decaying leaves of *N. ossifragum* in peat bogs, intermixed with many other fungi. It can be found by carefully searching for the minute ascomata on leaves from the previous growing season which are lying on top of the *Sphagnum* layer.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to “*Bryochiton*” sp. [strain BRD3-083K, GenBank MT133280.1; Identities = 469/480 (98 %), two gaps (0 %)], “*Bryochiton*” sp. PW-2014 [strain M237, GenBank KM186837.1; Identities = 458/480 (95 %), four gaps (0 %)], and *Teratosphaeria encephalarti* [strain CPC 15465, GenBank FJ372400.1; Identities = 442/484 (91 %), 13 gaps (2 %)]. Closest hits using the **LSU** sequence are *Bryochiton* sp. [strain M198, GenBank EU940130.1; Identities = 793/796 (99 %), no gaps], *Teratosphaeria encephalarti* [strain CPC 15466, GenBank FJ372418.1; Identities = 786/796 (99 %), no gaps], and *Catenulostroma chromoblastomycosum* [strain CBS 597.97, GenBank EU019251.2; Identities = 784/796 (98 %), no gaps]. Closest hits using the **rpb2** sequence had distant similarity to *Constantinomyces oldenburgensis* [strain T2.4, GenBank LT976528.1; Identities = 626/799 (78 %), 12 gaps (1 %)], *Aulographina pinorum* [strain CBS 174.90, GenBank GU371737.1; Identities = 625/817 (76 %), 18 gaps (2 %)], and *Teratosphaeria nubilosa* [strain CBS 116005, GenBank KT216527.1; Identities = 629/837 (75 %), 24 gaps (2 %)].

**Authors:** P.W. Crous, J.Z. Groenewald & J. Boers

***Neocamarographium*** Crous, **gen. nov.** MycoBank MB 844294.

**Taxonomic lineage:** Dothideomycetes, Pleosporales, incertae sedis.

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

*Conidiomata* pycnidial, numerous, separate, dispersed, single, subepidermal, unilocular, completely immersed in the bark of the host, globose, rarely slightly depressed, with central, ostiolum. *Conidiomatal* wall up to 100 µm thick, composed at the outer layers of thick-walled, dark brown *textura angularis*, and at the inner layers of thin-walled, subhyaline *textura angularis*. *Paraphyses* intermingled among conidiogenous cells in some conidiomata, hyaline, smooth, subcylindrical with obtuse ends, septate, extending above the conidiogenous cells. *Conidiogenous cells* hyaline, discrete, holoblastic, annellidic, broadly ampulliform or doliiform. *Conidia* initially subhyaline, but later becoming yellowish brown in pycnidia, extruding in a slimy mass; young, subhyaline conidia have 3–5 transversal distosepta, whereas in mature conidia the compartments between the septa develop bodies (possible endoconidia) that are ellipsoid to subglobose, thick-walled, verruculose, at times guttulate, and get released in clusters of four, in sacks that appear to be the remnants of the conidial compartments. Outer conidial wall smooth, subhyaline, 1 µm thick; conidia oblong-ellipsoidal or slightly clavate, sometimes with light constriction in median point, with scar at the base.

**Type species:** *Neocamarographium carpini* (Melnik *et al.*) Crous

***Neocamarographium carpini*** (Melnik *et al.*) Crous, **comb. nov.** MycoBank MB 844295.

**Basionym:** *Camarographium carpini* Melnik *et al.*, *Persoonia* **27**: 149. 2011.

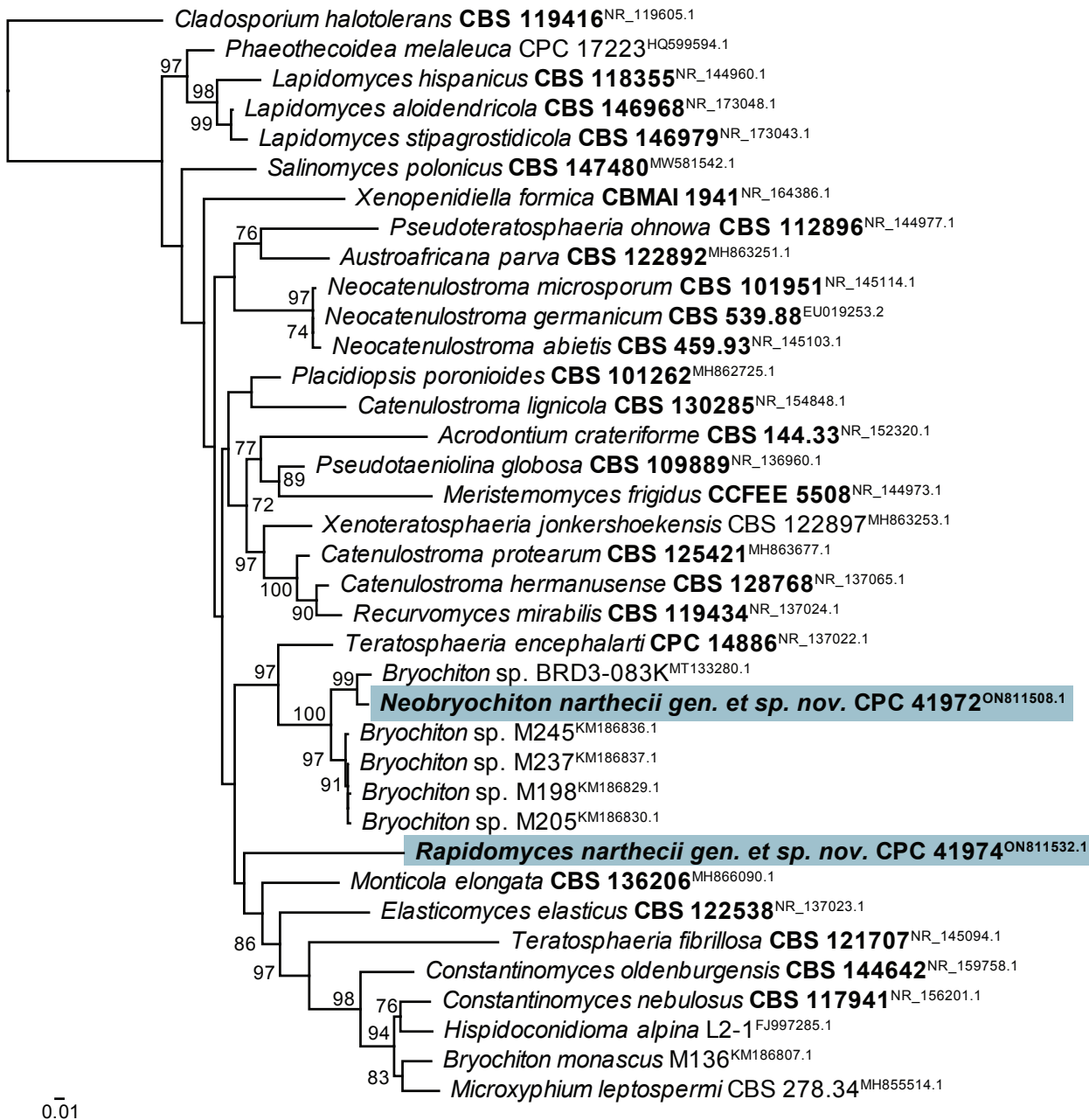
**Description and illustration:** Mel’nik *et al.* (2011).

**Typus:** **Russia**, St. Petersburg, Botanical Garden of the Komarov Botanical Institute, on thin, dried twigs of *Carpinus betulus* (*Betulaceae*), 27 Sept. 2010, V. Mel’nik (**holotype** LE 226162; **paratypes** LE 261808, LE 261817; **isotypes** HAL 2424 F, CBS H-20506), cultures ex-isotype CPC 18919, 18918 = CBS 128781.

**Material examined:** **Germany**, hornbeam wood (Carpinion), alt. 44 m a.s.l., sandy soil, acid fresh, mesotroph, on attached, corticated, initial, 1.5–4 mm diam twigs of *Carpinus betulus* (*Betulaceae*), 19 Jul. 2014, R.K. Schumacher, RKS 367, culture CPC 25067.

**Notes:** *Neocamarographium* is distinct from *Camarographium* in lacking an eustroma, but with well-defined unilocular conidiomata, and macroconidia that appear to develop internal structures that are possible endoconidia (Melnik *et al.* 2011). Phylogenetically, it also forms a distinct lineage (Fig. 2).

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Camarographium carpini* [strain CBS 128781, GenBank NR\_156250.1; Identities = 514/515 (99 %), no gaps], *Pleospora iqbalii* [strain CBS 362.69, GenBank MH859323.1; Identities = 700/808 (87 %), 55 gaps (6 %)], and *Melanomma populicola* [culture CPC 27203, GenBank MT223817.1; Identities = 685/828 (83 %), 40 gaps (4 %)].



**Fig. 36.** Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh *et al.* 2020) of the *Teratosphaeriaceae* ITS nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast bootstrap replicates are shown at the nodes. Culture collection numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Cladosporium halotolerans* (culture CBS 119416; GenBank NR\_119605.1) and the species treated here are highlighted with coloured blocks and bold face. Accession numbers of sequence from material with a type status are also shown in bold face.

*Authors:* P.W. Crous, R.K. Schumacher, J.Z. Groenewald, M. Starink-Willemse & A.L. van Iperen

*Neofusicoccum mediterraneum* Crous *et al.*, *Fungal Planet*, no. 19: [2]. 2007. Fig. 37.

*Taxonomic lineage:* Dothideomycetes, Botryosphaeriales, Botryosphaeriaceae.

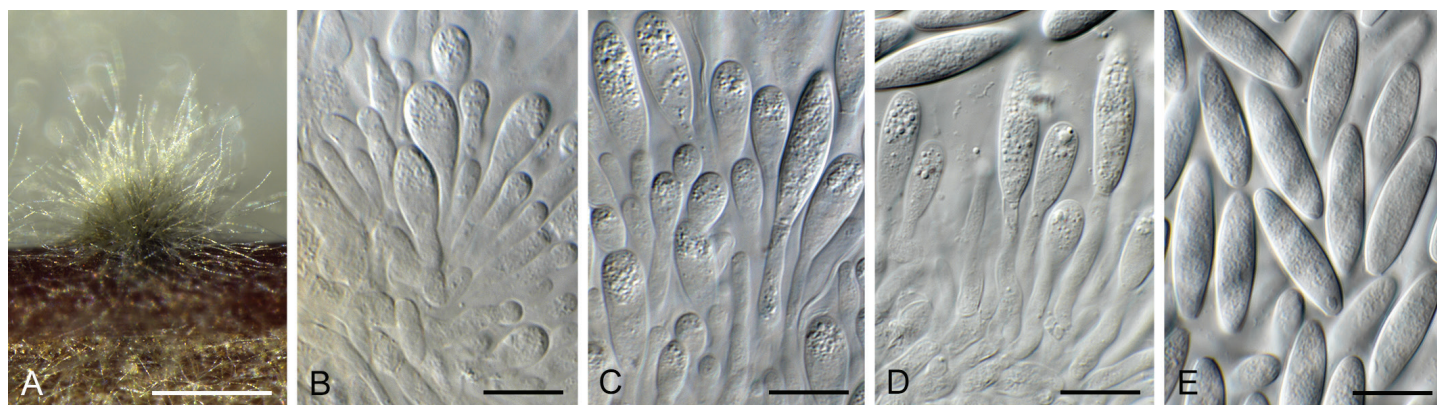
On PNA: *Conidiomata* stromatic, pycnidial, immersed, becoming somewhat erumpent, covered with hyphae on PNA, solitary, globose, 200–300 µm diam; wall of 6–8 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells or

with a supporting cell at base, hyaline, smooth, subcylindrical, proliferating percurrently at apex, 10–30 × 3–4 µm. *Conidia* hyaline, smooth, granular, straight, fusoid-ellipsoid, apex subobtuse, base truncate, aseptate, (23–)24–26(–27) × (6–)6.5–7 µm. *Dichomera* asexual morph not observed.

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

*Description and illustration:* Crous *et al.* (2007b).





**Fig. 37.** *Neofusicoccum mediterraneum* (CBS 125263). **A.** Conidioma on PNA. **B–D.** Conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars: A = 300  $\mu$ m, all others = 10  $\mu$ m.

**Material examined:** South Africa, Gauteng Province, Leeuwfontein Reserve, on *Terminalia sericea* (Combretaceae), 2010, D. Begoude & J. Roux (CBS H-24558, culture CMW 26679 = CBS 125263).

**Notes:** Although the name “*Neofusicoccum terminaliae*” has been used in literature (e.g. Zhang et al. 2021), it is an unpublished taxon from an earlier study on *Botryosphaeriaceae* occurring on *Terminalia* in Cameroon, South Africa and Madagascar (Begoude et al. 2010). Morphologically, “*N. terminaliae*” closely resembles *N. mediterraneum* (Fig. 37; Crous et al. 2007b) but genetically the introduction of a new taxon for the material from *Terminalia* is not warranted (Fig. 1 part 1; blast results below) and is herewith assigned to *N. mediterraneum*. *Neofusicoccum mediterraneum* was described from branches and leaves of *Eucalyptus* in Greece and rotting drupes of *Olea europaea* in Italy (Crous et al. 2007b).

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neofusicoccum mediterraneum* [strain ALG77, GenBank KJ657706.1; Identities = 563/565 (99 %), no gaps], *Neofusicoccum vitifusiforme* [strain CMW 875, GenBank HM176534.1; Identities = 559/565 (99 %), one gap (0 %)], and *Neofusicoccum corticosae* [now a synonym of *Neofusicoccum vitifusiforme*; strain CBS 120081, GenBank MN161920.1; Identities = 555/561 (99 %), one gap (0 %)]. Closest hits using the **LSU** sequence are *Neofusicoccum mediterraneum* [strain CBS 121718, GenBank NG\_069899.1; Identities = 908/908 (100 %), no gaps], *Neofusicoccum ningerense* [strain CSF6030, GenBank MT029168.1; Identities = 894/896 (99 %), one gap (0 %)], and *Neofusicoccum magniconidium* [strain CSF5876, GenBank MT029166.1; Identities = 894/896 (99 %), one gap (0 %)]. Closest hits using the **rpb2** sequence had highest similarity to *Neofusicoccum mediterraneum* [strain CBS 121718, GenBank KX464024.1; Identities = 592/594 (99 %), no gaps], *Botryosphaeria dothidea* [strain B71, GenBank AY217047.1; Identities = 592/594 (99 %), no gaps], and *Neofusicoccum ursorum* [strain CBS 122811, GenBank KX464047.1; Identities = 589/594 (99 %), no gaps]. Closest hits using the **tef1** sequence had highest similarity to *Neofusicoccum* sp. [strain BJFU B6209, GenBank MH459051.1; Identities = 263/265 (99 %), no gaps], *Neofusicoccum ursorum* [strain CBS 122812, GenBank KX464760.1; Identities = 262/264 (99 %), no gaps], and *Neofusicoccum mediterraneum* [strain MAN21312, GenBank KU997247.1; Identities = 272/275 (99 %), no gaps]. Closest hits using the **tub2** sequence had highest similarity to *Neofusicoccum mediterraneum* [strain ColPat-454,

GenBank MN839590.1; Identities = 434/434 (100 %), no gaps], *Neofusicoccum pistaciarium* [now a synonym of *Neofusicoccum mediterraneum*; strain CBS 113083, GenBank KX464998.1; Identities = 433/434 (99 %), no gaps], and *Neofusicoccum ursorum* [strain CBS 122811, GenBank KX465056.1; Identities = 432/434 (99 %), no gaps].

**Authors:** P.W. Crous, J.Z. Groenewald, J. Roux & D. Begoude

**Niesslia neoexosporioides** Crous & R.K. Schumach., *Fungal Syst. Evol.* **7**: 302. 2021. Fig. 38.

**Taxonomic lineage:** Sordariomycetes, Hypocreales, Niessliaceae.

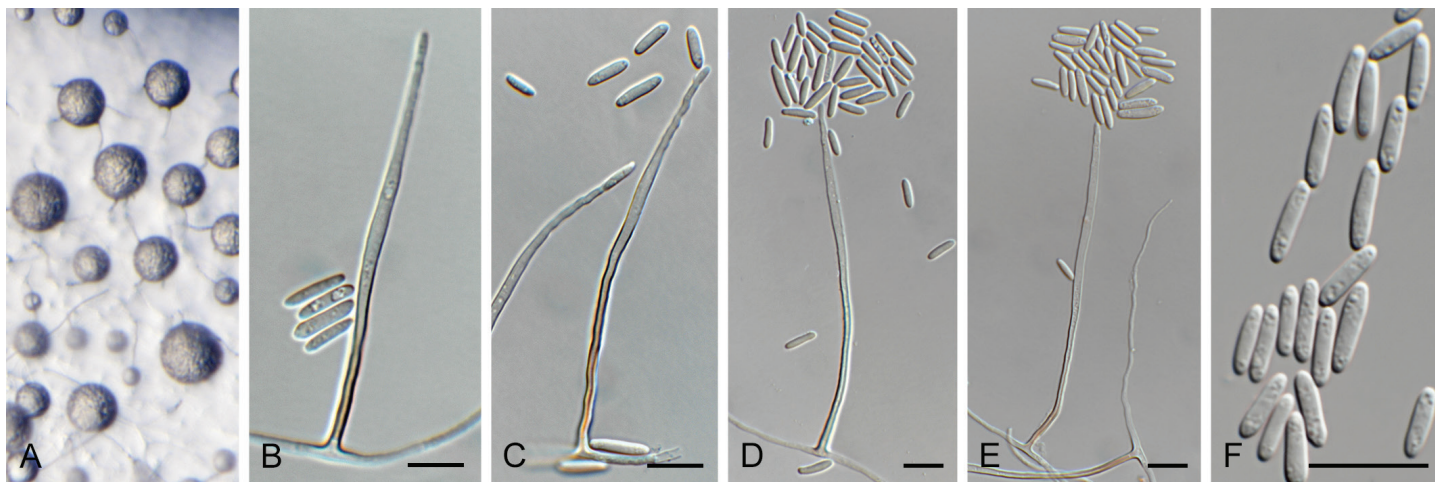
**Description and illustration:** Crous et al. (2021e).

**Material examined:** Netherlands, Utrecht Province, Nieuw Wulven, near Houten, 52°03’03’’N, 05°09’46’’E, 1.5 m a.s.l., on dead culms of *Phragmites australis* (Poaceae), 25 Feb. 2021, E.R. Osieck, HPC 3613 = WI-32/#4221, culture CPC 41317 = CBS 148284.

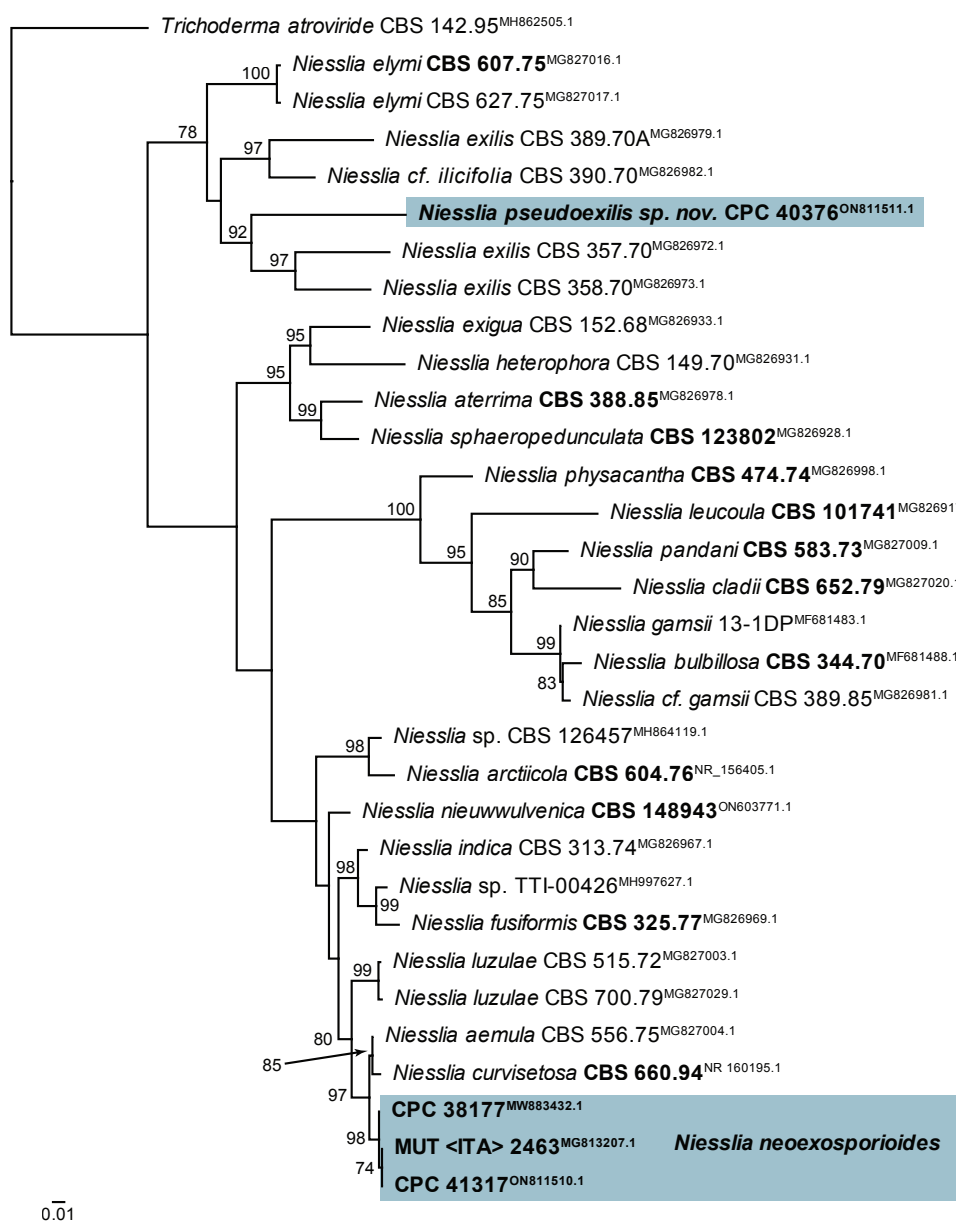
**Notes:** *Niesslia neoexosporioides* was described from dead leaves of *Carex paniculata* collected in Germany (Crous et al. 2021e), and the present collection of the asexual morph on dead culms of *Phragmites australis* from the Netherlands represents a new host record for the species with which it also clusters in the phylogenetic trees (Figs 7, 39).

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Niesslia neoexosporioides* [strain CBS 146810, GenBank NR\_173014.1; Identities = 366/366 (100 %), no gaps], *Niesslia aemula* [strain CBS 556.75, GenBank MG827004.1; Identities = 362/367 (99 %), one gap (0 %)], and *Monocillium curvisetosum* [strain CBS 660.94, GenBank NR\_160195.1; Identities = 360/365 (99 %), one gap (0 %)]. Closest hits using the **LSU** sequence are *Niesslia neoexosporioides* [strain CBS 146810, GenBank NG\_076714.1; Identities = 799/799 (100 %), no gaps], *Niesslia exosporioides* [strain CBS 691.71, GenBank MG826829.1; Identities = 797/799 (99 %), no gaps], and *Monocillium curvisetosum* [strain CBS 660.94, GenBank MH874141.1; Identities = 795/799 (99 %), no gaps]. The best hit using the **actA** sequence had highest similarity to *Niesslia neoexosporioides* [strain CPC 38177, GenBank MW890027.1; Identities = 669/676 (99 %), four gaps (0 %)]; all other hits were too distant. The best hit using the **tef1** (first part) sequence





**Fig. 38.** *Niesslia neoexosporioides* (CPC 41317). **A.** Conidiophores on SNA. **B.** Stipe with vesicle. **C–E.** Conidiophores with conidia. **F.** Conidia. Scale bars = 10 µm.



**Fig. 39.** Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh *et al.* 2020) of the *Niesslia* ITS nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast bootstrap replicates are shown at the nodes. Culture collection numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Trichoderma atroviride* (culture CBS 142.95; GenBank MH862505.1) and the species treated here are highlighted with coloured blocks and bold face. Accession numbers of sequence from material with a type status are also shown in bold face.

had highest similarity to *Niesslia neoexosporioides* [strain CPC 38177, GenBank MW890097.1; Identities = 475/494 (96 %)]; all other hits were too distant. The best hit using the **tub2** sequence had highest similarity to *Niesslia neoexosporioides* [strain CPC 38177, GenBank MW890137.1; Identities = 642/660 (97 %), seven gaps (1 %)]; all other hits were too distant.

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***Niesslia pseudoexilis*** Crous & R.K. Schumach., *sp. nov.* MycoBank MB 844297. Fig. 40.

*Taxonomic lineage:* Sordariomycetes, Hypocreales, Niessliaceae.

*Etymology:* Name refers to the fact that it is closely related to *Niesslia exilis*.

In OA (sterile on SNA). *Mycelium* consisting of hyaline, smooth-walled, branched, septate, 1.5–2 µm diam hyphae, forming hyphal coils, and aggregating into hyphal strands that give rise to conidiophores. *Conidiophores* reduced to conidiogenous cells, hyaline, smooth- and thick-walled, flexuous, 15–30 × 1.5–2 µm, monophialidic, apex 1 µm diam with minute flared collarette that gives rise to a mucoid conidial mass. *Conidia* solitary, aseptate, hyaline, smooth-walled, guttulate, subcylindrical, apex obtuse, tapering to a truncate hilum, 0.5 µm diam, (3.5–)4–5(–6) × 1.5(–2) µm.

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

*Typus:* Serbia, Fruška Gora, 45.144876, 19.776186, on dead fallen leaf of *Quercus petraea* (Fagaceae), 6 Nov. 2020, D. Savić HPC 3543, RKS 1155 (**holotype** CBS H-24866, culture ex-type CPC 40376 = CBS 148333).

*Notes:* *Niesslia pseudoexilis* is phylogenetically closely related to *N. exilis* (conidia 0–1-septate, rarely multi-septate, 5–11 × 1.2–2 µm; Gams *et al.* 2019) based on the LSU and ITS phylogenies (Figs 7, 39), but has smaller conidia. Although a sexual morph was present on the type specimen, the material proved inadequate to facilitate a morphological description.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Niesslia exilis* [strain CBS 389.70B, GenBank MG826980.1; Identities = 477/533 (89 %), 13 gaps (2 %)], *Myrtacremonium eucalypti* [strain CBS 142161, GenBank NR\_154212.1; Identities = 470/529 (89 %), 26 gaps (4 %)], and *Thyronectria rhodochlora* [strain NP8, GenBank KM225682.1; Identities = 476/538 (88 %), 19 gaps (3 %)]. Closest hits using the **LSU** sequence are *Niesslia exilis* [strain CBS 389.70B, GenBank MG826782.1; Identities = 788/799 (99 %), one gap (0 %)], *Niesslia cladoniicola* [strain CBS 960.73, GenBank MG826850.1; Identities = 785/799 (98 %), one gap (0 %)], and *Niesslia ilicifolia* [strain CBS 459.74, GenBank MG826798.1; Identities = 784/799 (98 %), one gap (0 %)]. Closest hits using the **actA** sequence had highest similarity to *Nectria dacryocarpa* [strain CBS 113532, GenBank KM231257.1; Identities = 585/658 (89 %), 27 gaps (4 %)], *Dactylonectria alcacerensis* [strain CBS 129087, GenBank KM231158.1; Identities = 557/645 (86 %), 32 gaps (4 %)], and *Dactylonectria novozelandica* [strain CBS 113552, GenBank KM231157.1; Identities = 557/645 (86 %), 32 gaps (4 %)]. Closest hits using the **rpb2** sequence had highest similarity to *Purpureocillium lilacinum* [strain BUP614, GenBank MH879624.1; Identities = 691/833 (83 %), six gaps (0 %)], *Isaria takamizusanensis* [strain NHJ 3497, GenBank EU369074.1; Identities = 675/817 (83 %), six gaps (0 %)], and *Tolypocladium paradoxum* [strain NBRC 106958, GenBank AB968561.1; Identities = 691/840 (82 %), two gaps (0 %)]. No significant hits were obtained when the **tub2** sequence was used in blastn and megablast searches.

Authors: P.W. Crous, J.Z. Groenewald & R.K. Schumacher

***Nothocladosporium*** Crous, *gen. nov.* MycoBank MB 844298.

*Taxonomic lineage:* Dothideomycetes, *Mycosphaerellales*, *Phillipsiellaceae*.

*Etymology:* Name refers to its morphological similarity to *Cladosporium*.

*Mycelium* consisting of hyaline, smooth-walled, branched, septate hyphae. *Conidiophores* macronematous, solitary, erect, subcylindrical, straight, unbranched, base bulbous,

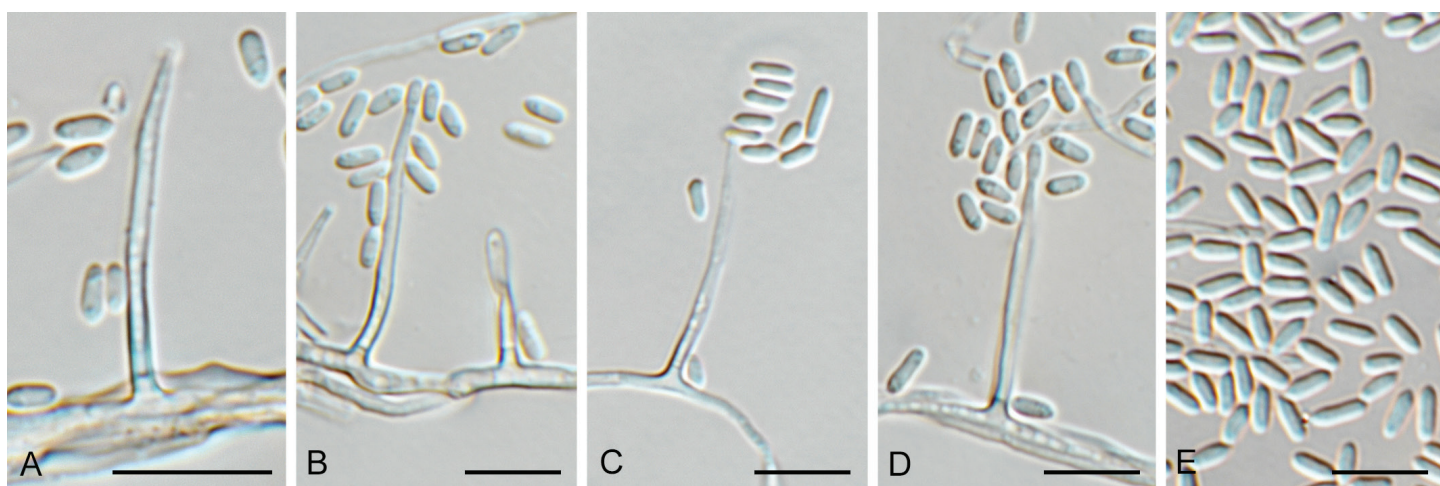


Fig. 40. *Niesslia pseudoexilis* (CPC 40376). A–D. Conidiogenous cells giving rise to conidia. E. Conidia. Scale bars = 10 µm.



lacking rhizoids; stipe dark brown, smooth- and thick-walled, multiseptate, bearing an apical penicillate arrangement of branches that give rise to dry, branched conidial chains. *Penicillate apparatus* of primary and secondary branches, giving rise to conidiogenous cells; primary branches brown, aseptate, subcylindrical; secondary branches brown, aseptate, subcylindrical. *Conidiogenous cells* pale brown, smooth-walled, subcylindrical to clavate; polyblastic, with loci darkened and thickened, not refractive. *Conidia* occurring in branched chains, aseptate, pale brown, smooth-walled, guttulate; ramoconidia subcylindrical to narrowly fusoid-ellipsoid; conidia fusoid-ellipsoid, hila thickened, darkened, not refractive.

*Type species: Nothocladosporium syzygii* Crous

***Nothocladosporium syzygii*** Crous, *sp. nov.* MycoBank MB 844299. Fig. 41.

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

*Mycelium* consisting of hyaline, smooth-walled, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* macronematous, solitary, erect, subcylindrical, straight, unbranched, base bulbous (10–12 µm diam), lacking rhizoids; stipe dark brown, smooth- and thick-walled, multiseptate, bearing an apical penicillate arrangement of branches that give rise to dry, branched conidial chains. *Penicillate apparatus* of primary and secondary branches, giving rise to 1–4 conidiogenous cells; primary branches brown, aseptate, subcylindrical, 15–20 × 5–6 µm; secondary branches brown, aseptate, subcylindrical, 8–12 × 4–5 µm. *Conidiogenous cells* pale brown, smooth-walled, subcylindrical to clavate, 10–16 × 3.5–6 µm; polyblastic, with loci darkened and thickened, not refractive, 2 µm diam. *Conidia* occurring in branched chains, aseptate, pale brown, smooth-walled, guttulate; ramoconidia subcylindrical to narrowly fusoid-ellipsoid, 10–13 × 4–5 µm; conidia fusoid-ellipsoid, (8–)9–10(–11) × (3–)3.5(–4) µm; hila thickened, darkened, not refractive, 1–1.5 µm diam.

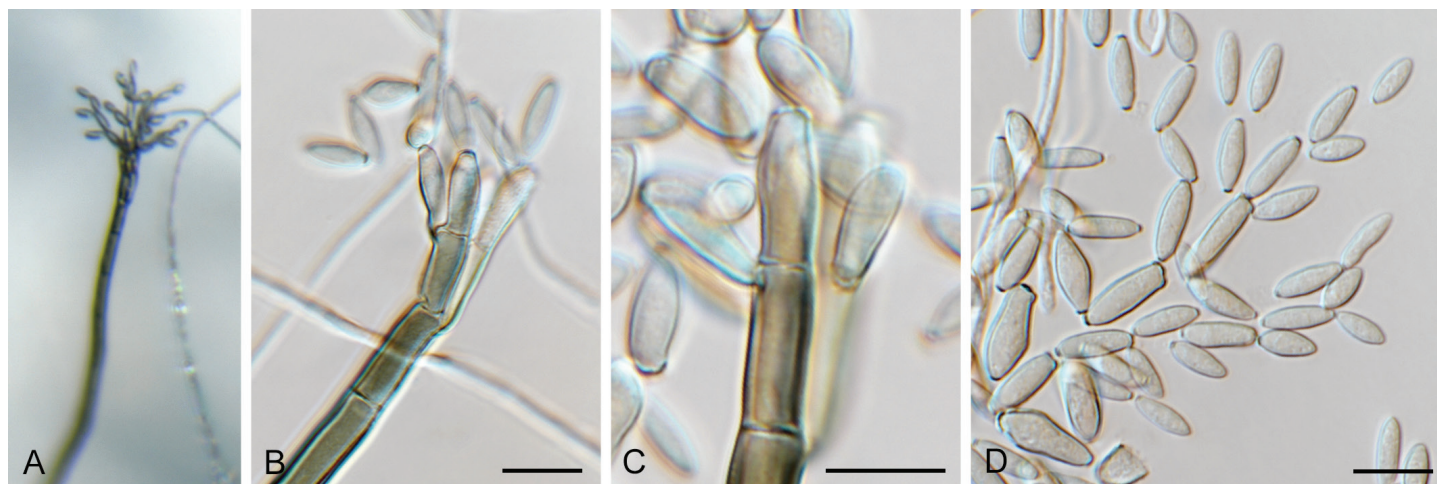
*Culture characteristics:* Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA surface pale luteous

with patches of ochreous, reverse umber; on PDA surface and reverse pale luteous; on OA surface pale luteous.

*Typus: South Africa*, near Mozambique, on leaves of *Syzygium cordatum* (Myrtaceae), 19 Oct. 2017, M.J. Wingfield, HPC 3503 (**holotype** CBS H-24835, culture ex-type CPC 40091 = CBS 148289).

*Notes:* *Penidiella* (Teratosphaeriaceae, Mycosphaerellales), accommodates hyphomycetes with brown, macronematous conidiophores with a conidiogenous apparatus composed of several branches, giving rise to ramoconidia and conidia with hila that are unthickened or almost so, barely to somewhat darkened-refractive (Crous *et al.* 2007a). *Cladosporium s.str.* (Cladosporiaceae, Cladosporiales) is distinguished by having conidia with typical coronate conidiogenous loci and conidial hila, *i.e.*, with a convex central dome surrounded by a raised periclinal rim (Bensch *et al.* 2012). In *Nothocladosporium* the conidiophores appear cladosporium-like, but the conidiogenous loci and conidial hila resemble those of *Penidiella*. Phylogenetically, however, it clusters apart, being more closely related to ascomycetes such as *Johansonia* and *Schizothyrium* (Crous *et al.* 2010), and therefore a new genus is introduced here to accommodate it (Figs 1 part 2, 13 part 1).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Johansonia chapadensis* [strain CBS 128068, GenBank HQ423449.1; Identities = 386/452 (85 %), 31 gaps (6 %)], *Schizothyrium pomi* [strain SP12\_375Aa, GenBank MN065457.1; Identities = 451/517 (87 %), 18 gaps (3 %)], *Zygophiala trispora* [strain HMAS 244987, GenBank NR\_159004.1; Identities = 451/516 (87 %), 21 gaps (4 %)], and *Zygophiala trispora* [as *Zygophiala* sp. GS-2014b; strain HL-HKBJ-23D, GenBank KF646711.1; Identities = 451/516 (87 %), 21 gaps (4 %)]. Closest hits using the **LSU** sequence are *Johansonia chapadensis* [strain CBS 128068, GenBank NG\_057893.1; Identities = 785/798 (98 %), no gaps], *Schizothyrium pomi* [strain SP12\_375Aa, GenBank MN065457.1; Identities = 784/799 (98 %), one gap (0 %)], and *Schizothyrium cylindricum* [strain SP12\_377Ha, GenBank MN065458.1; Identities = 783/799 (98 %), one gap (0 %)]. Closest hits using the **actA** sequence had highest similarity to *Pseudocercospora myopori* [strain CBS 114644, GenBank JX143245.2; Identities = 367/399 (92 %),



**Fig. 41.** *Nothocladosporium syzygii* (CPC 40091). **A.** Conidiophore on SNA. **B, C.** Conidiophore branches and conidiogenous cells. **D.** Conidia in chains. Scale bars = 10 µm.



no gaps], *Pseudocercospora neriicola* [strain CBS 138010, GenBank KJ869231.1; Identities = 367/399 (92 %), no gaps], and *Pseudocercospora paraguayensis* [strain CBS 111317, GenBank JQ325021.1; Identities = 367/399 (92 %), no gaps]. Closest hits using the *tef1* (first part) sequence had highest similarity to *Neotrimmatostroma paraexcentricum* [strain CPC 25594, GenBank KX228378.1; Identities = 345/422 (82 %), 27 gaps (6 %)], *Neotrimmatostroma dalrympleanae* [strain CBS 144609, GenBank MN162339.1; Identities = 327/397 (82 %), 22 gaps (5 %)], and *Phaeothecoidea intermedia* [strain CBS 124994, GenBank KF903171.1; Identities = 302/372 (81 %), 21 gaps (5 %)]. No significant hits were obtained when the *tub2* sequence was used in blastn and megablast searches.

Authors: P.W. Crous, J.Z. Groenewald & M.J. Wingfield

**Nothopseudocercospora** Crous & U. Braun, *gen. nov.* MycoBank MB 844415.

*Taxonomic lineage:* Dothideomycetes, Mycosphaerellales, Mycosphaerellaceae.

*Etymology:* Resembling the genus *Pseudocercospora*.

*Phytopathogenic.* Leaf spots amphigenous, angular to irregular, pale brown with dark brown border. *Conidiomata* with well-developed stroma, erumpent, brown, consisting of pale brown pseudoparenchymatal cells. *Conidiophores* subcylindrical, pale brown, smooth-walled, unbranched, septate. *Conidiogenous cells* terminal, integrated, subcylindrical, pale brown, smooth-walled, holoblastic, at times sympodial, or with minute percurrent proliferation. *Conidia* solitary, subcylindrical, straight to gently curved, apices subobtuse, base truncate, not thickened nor darkened, pale olivaceous, guttulate, septate, with flared basal marginal frill.

*Type species:* *Nothopseudocercospora dictamni* (Fuckel) Crous & U. Braun

***Nothopseudocercospora dictamni*** (Fuckel) Crous & U. Braun, *comb. nov.* MycoBank MB 844279. Fig. 42.

*Basionym:* *Septoria dictamni* Fuckel, *Enumeratio Fungorum Nassoviae*: 330. 1860 (*Jahrb. Vereins Naturk. Herzogth. Nassau*: 15. 1860).

*Synonyms:* *Cercospora dictamni* (Fuckel) Vassiljevsky, in Vassiljevsky & Karakulin, *Parazitnye nesovershennye griby*, 2, *Melankonialnye*: 574, Leningrad 1950.

*Cercostigmia dictamni* (Fuckel) U. Braun, *Cryptogam. Bot.* 4: 108. 1993.

*Pseudocercospora dictamni* (Fuckel) U. Braun & Crous, *Mycol. Prog.* 1: 22. 2002.

*Leaf spots* amphigenous, angular to irregular, 5–12 mm diam, pale brown with dark brown border. *Conidiomata* mainly epiphyllous, stroma well-developed, erumpent, brown, consisting of pale brown pseudoparenchymatal cells, up to 120 × 70 µm. *Conidiophores* subcylindrical, pale brown, smooth-walled, unbranched, 1–2-septate, 20–40 × 4–6 µm. *Conidiogenous cells* terminal, integrated, subcylindrical, pale brown, smooth-walled, holoblastic, at times sympodial, or with minute percurrent proliferation, 15–25 × 4–6 µm. *Conidia* solitary, subcylindrical, straight to gently curved, apices

subobtuse, base truncate, not thickened nor darkened, pale olivaceous, guttulate, (1–)3–4(–7)-septate, (50–)55–85(–120) × (3.5–)4(–5) µm, with flared basal marginal frill.

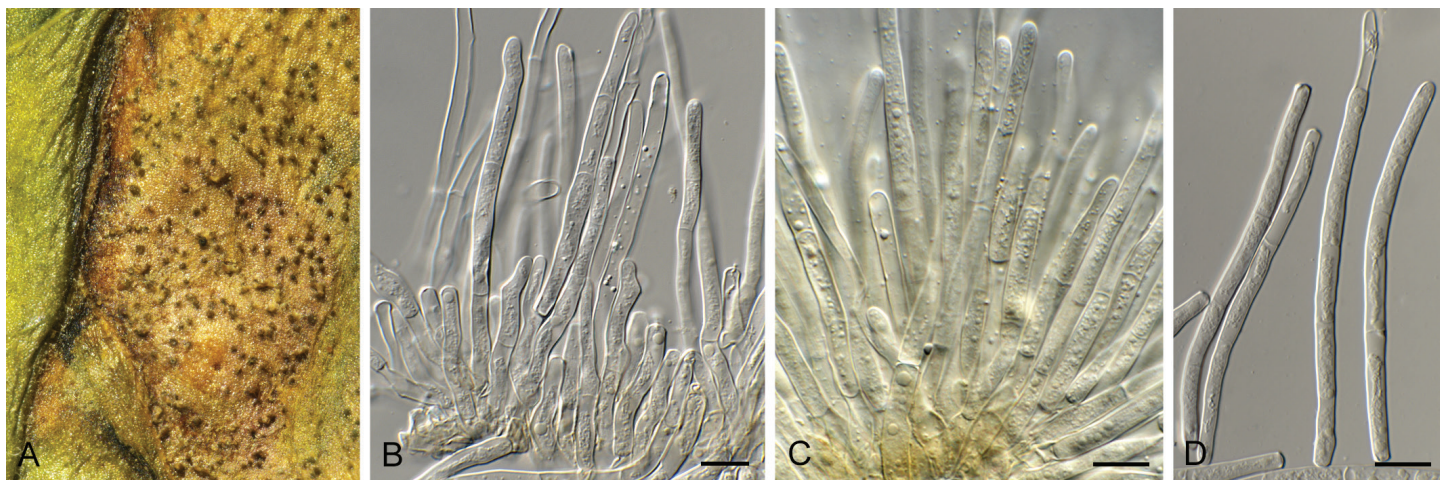
*Culture characteristics:* Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 20 mm diam after 7 d at 25 °C. On MEA surface pale white, reverse red; on PDA surface pale white with patches of olivaceous, reverse red with diffuse red pigment; on OA surface pale white with diffuse red pigment.

*Material examined:* **Germany**, on *Dictamnus albus* (*Rutaceae*), Fungi Rhen. 519 **lectotype** (HAL), designated in Braun, *Crypt. Bot* 3: 243. 1993. **Russia**, Rostov region, Krasnosulinsky district, state natural wildlife area “Gornensky”, stony steppe on a slope of a gully, on living leaves of *Dictamnus albus*, 27 Jun. 2020, T.S. Bulgakov, HPC 3399 = PC 062 (**epitype** designated here MBT 10007397, CBS H-24838, **isoepitype** LE F-332410, culture ex-epitype CPC 39776 = CBS 148299).

*Notes:* *Nothopseudocercospora dictamni* was originally described as a foliar pathogen of *Dictamnus albus* collected in Germany. The present collection matches the morphology of the lectotype (Braun 1993, Braun & Hill 2002), except for having slightly wider conidiophores, and is thus an appropriate candidate for epitypification. Although it fits the genus *Pseudocercospora* based on gross morphology, it also resembles *Collarispora*, which is characterised by subcylindrical conidia that are initially hyaline but later become pale brown, with a basal marginal frill. *Nothopseudocercospora* is closer related to *Sultanimyces* (conidiogenous cells polyblastic; conidiogenous loci conspicuous and slightly protruding; conidia pale to moderate olivaceous, ellipsoid, fusoid, subcylindrical or obclavate, smooth to verruculose, usually septate, median septum usually thicker, sometimes slightly constricted at median septum, with conspicuous and slightly protruding hila) and *Neocercosporidium* (conidiogenous cells integrated, terminal, proliferating sympodially, occasionally percurrently, conidiogenous loci minute but slightly thickened, darkened and refractive, front view resembling minute circles; conidia subhyaline to pale olivaceous or brownish, smooth, thin-walled, multi-septate, obclavate-cylindrical; hila slightly thickened, darkened and refractive) (Videira *et al.* 2017), but does not fit in either, and is thus introduced here as a new genus (Figs 1 part 2, 13 part 2).

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Amycosphaerella africana* [strain CBS 144635, GenBank MK442569.1; Identities = 495/509 (97 %), no gaps], *Claroihilumhenningsii* [strain IR-9, GenBank LC565143.1; Identities = 494/509 (97 %), no gaps], and *Cercosporidium californicum* [strain CBS 128857, GenBank MH865121.1; Identities = 494/510 (97 %), one gap (0 %)]. Closest hits using the **LSU** sequence are *Passalora vicosa* [strain URM 8138, GenBank MN707422.1; Identities = 805/808 (99 %), no gaps], *Pseudocercospora bidensis* [strain CPC 19493, GenBank NG\_069168.1; Identities = 804/808 (99 %), no gaps], and *Collarispora valgourgensis* [strain CBS 129531, GenBank MH878078.1; Identities = 804/808 (99 %), no gaps]. Closest hits using the **actA** sequence had highest similarity to *Amycosphaerella africana* [as *Mycosphaerella ellipsoidea*; strain CBS 110843, GenBank JX902106.1; Identities = 489/527 (93 %), six gaps (1 %)], *Rhachisphaerella mozambica* [as *Mycosphaerella mozambica*; strain CBS 121391, GenBank





**Fig. 42.** *Nothopseudocercospora dictamni* (CPC 39776). **A.** Leaf spot with conidiophores fascicles. **B, C.** Conidiogenous cells giving rise to conidia. **D.** Conidia. Scale bars = 10  $\mu$ m.

EU514319.1; Identities = 483/522 (93 %), five gaps (0 %), and *Pantospora guazumae* [strain CIRAD-AUS 130, GenBank MW070787.1; Identities = 528/571 (92 %), five gaps (0 %)]. Closest hits using the *cmdA* sequence had highest similarity to *Nothopassalora personata* [strain IRAN 3479C, GenBank MN422408.1; Identities = 396/433 (91 %), five gaps (1 %)], *Dothistroma pini* [strain CBS 121011, GenBank KF253965.1; Identities = 369/406 (91 %), nine gaps (2 %)], and *Dothistroma septosporum* [strain CBS 383.74, GenBank KF253966.1; Identities = 380/435 (87 %), 12 gaps (2 %)]. Closest hits using the *rpb2* sequence had highest similarity to *Cercosporidium californicum* [strain CPC 18390, GenBank MF951471.1; Identities = 793/857 (93 %), no gaps], *Paracercosporidium tiliae* [strain CBS 112734, GenBank MF951565.1; Identities = 793/863 (92 %), no gaps], and *Collarispora valgourgensis* [strain CBS 125311, GenBank MF951480.1; Identities = 611/665 (92 %), no gaps]. Closest hits using the *tef1* (first part) sequence had

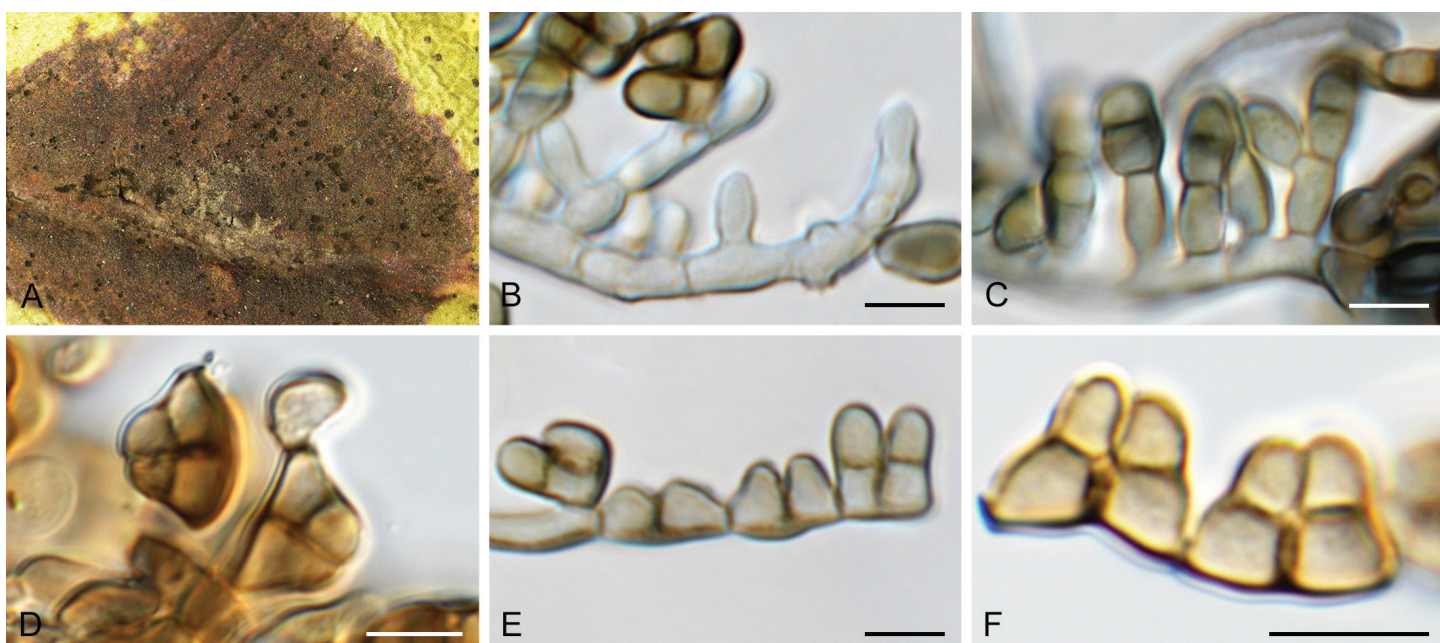
highest similarity to *Paracercospora egenula* [strain CBS 485.81, GenBank GU384415.2; Identities = 289/340 (85 %), 22 gaps (6 %)], *Amycosphaerella africana* [strain CBS 144635, GenBank MK442688.1; Identities = 297/357 (83 %), 39 gaps (10 %)], and *Ragnhildiana diffusa* [strain IL-GG-1, GenBank MG836579.1; Identities = 290/349 (83 %), 29 gaps (8 %)].

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

***Nothotrimmatostroma corymbiae*** Crous, *sp. nov.* MycoBank MB 844300. Fig. 43.

*Taxonomic lineage:* Dothideomycetes, Mycosphaerellales, Teratosphaeriaceae.

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



**Fig. 43.** *Nothotrimmatostroma corymbiae* (CPC 40087). **A.** Leaf spot. **B–E.** Conidiogenous cells giving rise to chains of conidia. **F.** Conidia. Scale bars = 10  $\mu$ m.

*Leaf spots* corky, dark brown, irregular to subcircular, 5–12 mm diam, not extending through leaf lamina, margin irregular. *Sporodochia* dark brown, in concentric clusters, 150–200 µm diam. *Conidiophores* micronematous, branched, septate, medium brown, smooth-walled, densely aggregated, up to 60 µm tall, 2–3 µm wide. *Conidiogenous cells* holothallic, integrated, terminal and lateral, doliform to subcylindrical, pale brown, smooth-walled, 5–10 × 2.5–3.5 µm. *Conidia* in branched chains, smooth-walled, medium brown, 4-celled, upper two primary cells 6–8 × 6–8 µm, with truncate ends where attached, 2–3 µm diam, separated from each other by a broad brown area, each primary cell giving rise to a smaller basal cell, globose, thin-walled, pale brown, 6–7 × 2.5–4 µm.

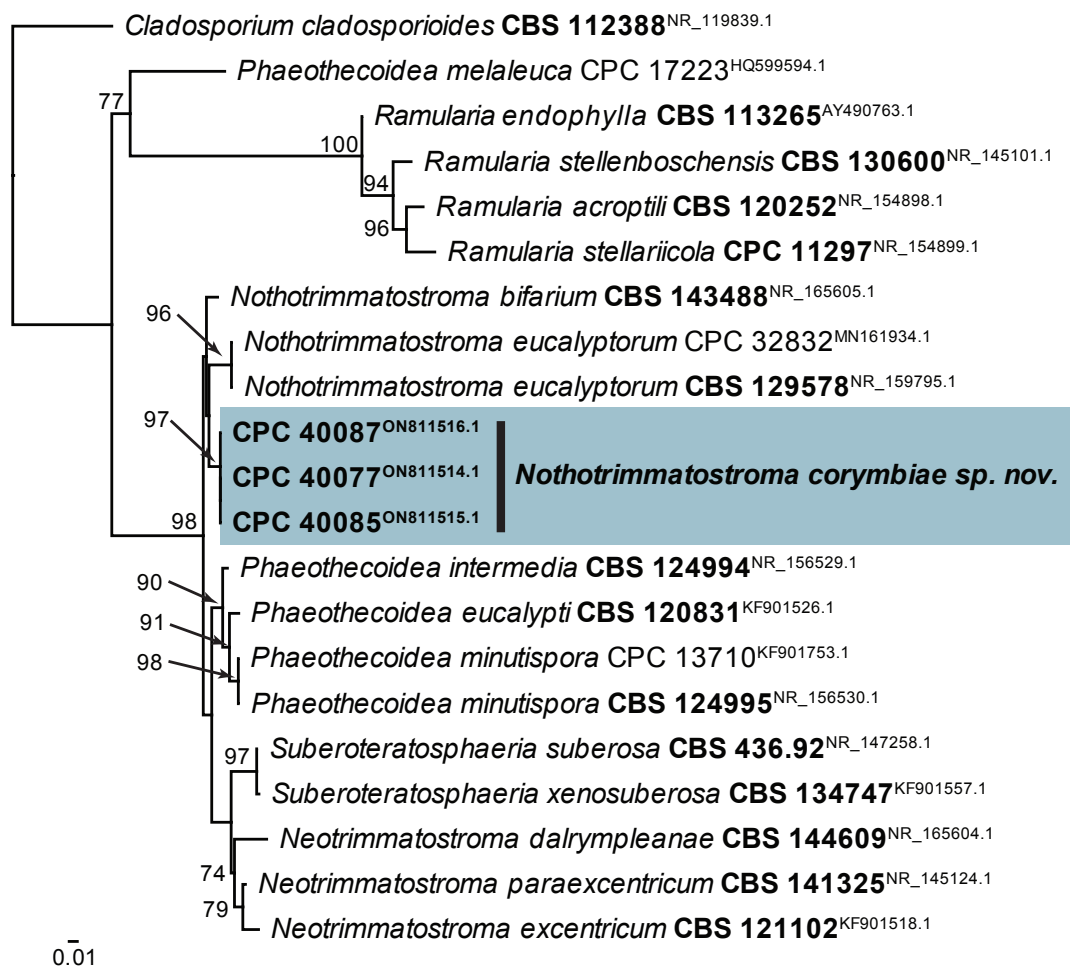
**Culture characteristics:** Colonies erumpent, spreading, with sparse to moderate aerial mycelium and smooth, lobate margin, reaching 6 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

**Typus:** **South Africa**, KwaZulu-Natal Province, Manguzi, on leaves of *Corymbia henryi* (*Myrtaceae*), 19 Oct. 2015, M.J. Wingfield & J. Roux, HPC 3504 (**holotype** CBS H-24867, culture ex-type CPC 40087 = CBS 148334).

**Additional materials examined:** **South Africa**, near Mozambique, on *C. henryi*, 19 Oct. 2015, M.J. Wingfield, HPC 3502, culture CPC 40085 = CBS 148335; near Mozambique, on *C. henryi*, 19 Oct. 2015, M.J. Wingfield, HPC 3496, culture CPC 40077 = CBS 148336.

**Notes:** *Nothotrimmatostroma* spp. are generally regarded as foliar pathogens of minor importance of *Eucalyptus* spp. *Nothotrimmatostroma corymbiae* is closely related to *N. bifarium* (conidia 12–24 × 6–14 µm, 6–10-celled when mature; Crous *et al.* 2019c) based on the LSU alignment (Fig. 1, part 2), and is the first species of the genus reported from South Africa. Based on the ITS alignment (Fig. 44), the closest phylogenetic neighbour is *Nothotrimmatostroma eucalyptorum*, although the connecting node is not supported.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence of CPC 40087 had highest similarity to *Nothotrimmatostroma bifarium* [strain CBS 143488, GenBank NR\_165605.1; Identities = 496/507 (98 %), no gaps], *Nothotrimmatostroma eucalyptorum* [strain CBS 129578, GenBank NR\_159795.1; Identities = 497/512 (97 %), one gap (0 %)], and *Phaeothecoidea intermedia* [strain CBS 124994, GenBank MH863442.1; Identities = 495/511 (97 %), no gaps]. The ITS sequence of CPC 40087 is identical to those of CPC 40077 and 40085 (506/506 and 501/501



**Fig. 44.** Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh *et al.* 2020) of the *Nothotrimmatostroma* ITS nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast bootstrap replicates are shown at the nodes. Culture collection numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Cladosporium cladosporioides* (culture CBS 112388; GenBank NR\_119839.1) and the species treated here is highlighted with bold face. Accession numbers of sequence from material with a type status are also shown in bold face.



nucleotides, respectively). Closest hits using the LSU sequence of CPC 40087 are *Nothotrimmatostroma bifarium* [strain CBS 143488, GenBank NG\_067914.1; Identities = 813/814 (99 %), no gaps], *Nothotrimmatostroma eucalyptorum* [strain CBS 129578, GenBank NG\_064248.1; Identities = 816/818 (99 %), no gaps], and *Phaeothecoidea intermedia* [strain CBS 124994, GenBank NG\_057841.1; Identities = 866/871 (99 %), no gaps]. The LSU sequences of CPC 40077, 40085 and 40087 are identical.

Authors: P.W. Crous, J.Z. Groenewald, J. Roux & M.J. Wingfield

***Paracamarographium*** Crous, *gen. nov.* MycoBank MB 844301.

*Taxonomic lineage:* Dothideomycetes, Pleosporales, Didymosphaeriaceae.

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

*Conidiomata* pycnidial, subperidermal, separate, single or in small clusters but without connecting stroma, completely immersed in the bark of the host, globose or slightly depressed, with a central, ostiolum; *conidiomatal wall* composed of a thick outer layer of *textura angularis* with dark brown cells, and a thick inner layer of *textura angularis-globulosa* of yellowish to hyaline, thinwalled cells, giving rise to conidiogenous cells all over the inner wall surface. *Macroconidiogenous cells* hyaline, discrete, holoblastic, annellidic, broadly ampulliform to doliiform. *Macroconidia* initially hyaline, elongated ellipsoidal to cylindrical, broadly rounded at the apex, rounded and with a scar at the base, 1-celled and thin-walled and containing numerous small oil-droplets when seceded, conidia attaining an up to 1  $\mu\text{m}$  thickened outer wall, and becoming medianly 1-euseptate, then transversely 3-septate, and finally multi-celled because of the formation of numerous distosepta oriented in all directions; each cell filled with 1 or more relatively large oil-droplets, outer conidium wall slowly becoming pale olivaceous brown. *Microconidiogenous cells* mostly arising from the upper part of the conidiomatal wall, hyaline, discrete, holoblastic, non-proliferating, ampulliform to doliiform. *Microconidia* hyaline, subglobose to ellipsoidal, rounded at the apex, broadly truncate at the base.

*Type species:* *Paracamarographium koreanum* (Verkley *et al.*) Crous

***Paracamarographium koreanum*** (Verkley *et al.*) Crous, *comb. nov.* MycoBank MB 844302.

*Basionym:* *Camarographium koreanum* Verkley *et al.*, *Sydowia* **57**: 260. 2005.

*Description and illustration:* Verkley *et al.* (2005).

*Typus:* Korea, Seoul, Hongneung Arboretum, Korea Forest Research Institute, on dead twigs of *Cornus kousa* (*Cornaceae*), *V. Mel'nik* s. n., 10 Sep. 2004 (**holotype** LE 226162; **isotypes** L, CBS H-14254; living ex-type cultures CBS 117158, 117159).

*Notes:* *Paracamarographium* is distinct from *Neocamarographium* and *Camarographium* by having microconidia, and forming separate, single or aggregated pycnidial conidiomata without connecting stroma as observed in

*Camarographium*. Initial analyses (data not shown) of the ITS sequence of *Paracamarographium koreanum* (GenBank JQ044432.1) indicated a distant relation to isolates identified as *Hendersonia pinicola* (conidia brown, fusoid-ellipsoid to clavate, 3-septate, from living needles of *Pinus murrayana*, USA; Wehmeyer 1946). The latter isolates appear to be incorrectly identified, and therefore no new combination is proposed for *H. pinicola*. *Paracamarographium* is related to species in *Didymosphaeriaceae* (*Pleosporales*; Fig. 2).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence of CBS 117159 (GenBank JQ044432.1) had distant similarity to *Corynespora smithii* [strain L133, GenBank KY984299.1; Identities = 882/1108 (80 %), 80 gaps (7 %)], *Bambusicola thailandica* [strain MFLUCC 11-0147, GenBank KU940119.1; Identities = 669/805 (83 %), 41 gaps (5 %)], and *Bambusicola subthailandica* [voucher SICAU 16-0005, GenBank MK253474.1; Identities = 739/909 (81 %), 49 gaps (5 %)]. Closest hits using the LSU sequence of CBS 117159 (JQ044451.1) are *Pseudochaetosphaeronema ginkgonis* [strain SYP-F-7195, GenBank KU365985.1; Identities = 912/931 (98 %), 10 gaps (1 %)], *Massaria platani* [strain AFTOL-ID 1574 = CBS 221.37, GenBank DQ678065.1; Identities = 897/917 (98 %), four gaps (0 %)], and *Macrodiplodiopsis desmazieri* [strain L138, GenBank KR873274.1; Identities = 872/893 (98 %), four gaps (0 %)].

Authors: P.W. Crous, J.Z. Groenewald, M. Starink-Willemsse & A.L. van Iperen

***Paraphoma salicis*** Crous & Akulov, *Fungal Syst. Evol.* **7**: 312. 2021. Fig. 45.

*Taxonomic lineage:* Dothideomycetes, Pleosporales, Phaeosphaeriaceae.

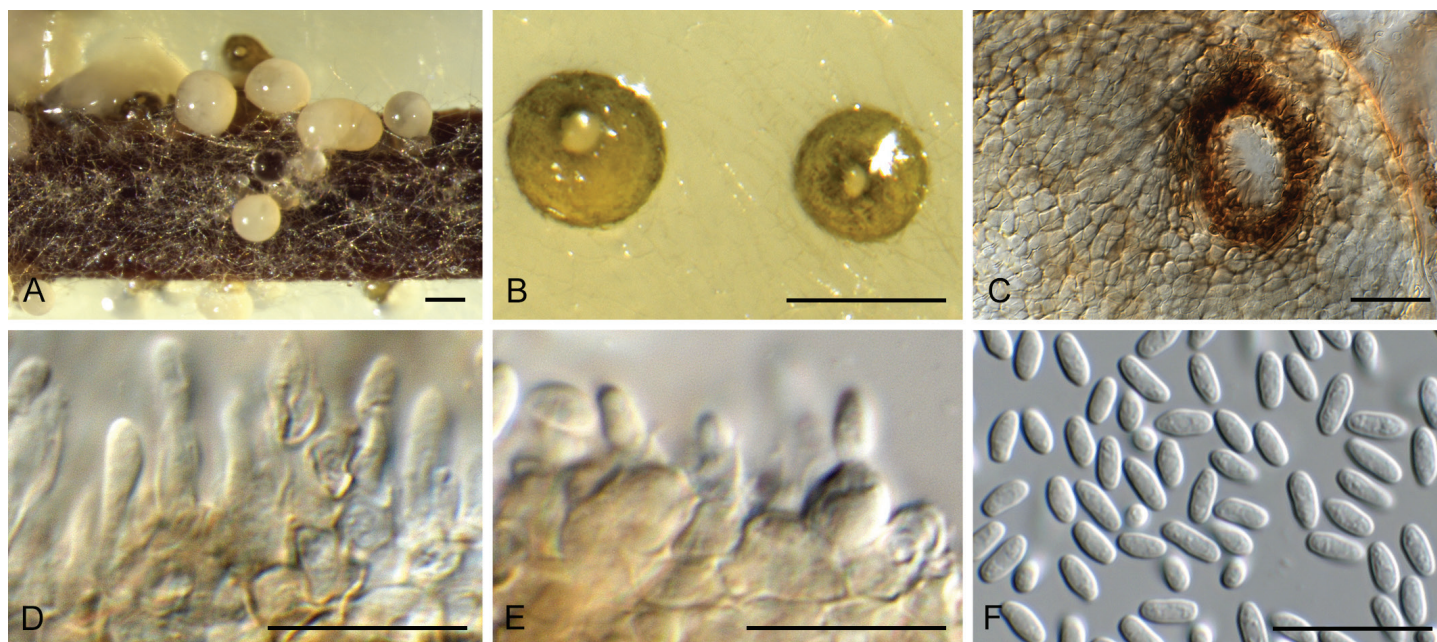
*Conidiomata* solitary, erumpent, globose, brown, 150–250  $\mu\text{m}$  diam, with central, dark brown ostiole, 30–40  $\mu\text{m}$  diam. *Conidiophores* reduced to *conidiogenous cells* lining inner cavity, hyaline, smooth, ampulliform, 4–7  $\times$  4–5  $\mu\text{m}$ , proliferating percurrently at apex. *Conidia* aseptate, solitary, hyaline, smooth, finely guttulate, straight, apex obtuse, base bluntly rounded to truncate, (5–)5.5–6(–7)  $\times$  2(–2.5)  $\mu\text{m}$ .

*Culture characteristics:* Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 7 d at 25 °C. On MEA surface ochreous, reverse isabelline; on PDA surface and reverse isabelline; on OA surface isabelline.

*Material examined:* Netherlands, Gelderland Province, Beuningen, river Waal, on *Salix* sp. (*Salicaceae*), 17 Oct. 2020, A.L. van Iperen, HPC 3485 = CBS H-24896, culture CPC 39991 = CBS 148454.

*Notes:* *Paraphoma salicis* [conidia (4–)5(–6)  $\times$  (2–)2.5(–3)  $\mu\text{m}$ ] was described on leaves of *Salix cf. alba* collected from Ukraine (Crous *et al.* 2021b), and is newly recorded here on a *Salix* sp. from the Netherlands (Fig. 2).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Paraphoma salicis* [strain CBS 146797, GenBank NR\_173017.1; Identities = 572/573 (99 %), no gaps], *Paraphoma radicina* [strain LYZ1871187, GenBank MH429796.1; Identities =



**Fig. 45.** *Paraphoma salicis* (CPC 39991). **A.** Conidiomata on PNA. **B.** Conidiomata on SNA. **C.** Ostiole. **D, E.** Conidiogenous cells giving rise to conidia. **F.** Conidia. Scale bars: A, B = 250  $\mu$ m, C = 40  $\mu$ m, all others = 10  $\mu$ m.

440/483 (91%), 10 gaps (2%)], and *Paraphoma chrysanthemicola* [strain MX, GenBank MK426809.1; Identities = 494/550 (90%), 20 gaps (3%)]. Closest hits using the **LSU** sequence are *Paraphoma chrysanthemicola* [strain AJP07, GenBank KP690077.1; Identities = 839/842 (99%), no gaps], *Paraphoma dioscoreae* [strain CBS 135100, GenBank KF251671.1; Identities = 827/830 (99%), no gaps], and *Paraphoma melnikiae* [voucher MF-9.182.1, GenBank MG764068.1; Identities = 838/842 (99%), no gaps]. Closest hits using the **rpb2** sequence had highest similarity to *Paraphoma salicis* [strain CPC 38651, GenBank MW890069.1; Identities = 876/876 (100%), no gaps], *Paraphoma melnikiae* [voucher MF-9.95, GenBank MG779462.1; Identities = 668/735 (91%), no gaps], and *Paraphoma fimeti* [strain UTHSC DI16-296, GenBank LT797032.1; Identities = 762/877 (87%), four gaps (0%)]. Closest hits using the **tub2** sequence had highest similarity to *Paraphoma salicis* [strain CPC 38651, GenBank MW890140.1; Identities = 440/443 (99%), no gaps], *Paraphoma chrysanthemicola* [strain CBS 172.70, GenBank KF252660.1; Identities = 217/230 (94%), two gaps (0%)], and *Paraphoma melnikiae* [voucher MF-9.240, GenBank MG779453.1; Identities = 398/428 (93%), two gaps (0%)].

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***Periconia pseudobyssoides*** S. Markovskaja & A. Kačergius, *Mycol. Prog.* **13**: 293. 2014. Fig. 46.

**Taxonomic lineage:** Dothideomycetes, Pleosporales, Periconiaceae.

**Mycelium** consisting of brown, smooth, branched, septate, 3–5  $\mu$ m diam hyphae. **Conidiophores** 450–650  $\times$  17–27  $\mu$ m, solitary, or in aggregated clusters on host tissue, brown, arising from a brown stroma, with base slightly swollen, 30–50  $\mu$ m diam, with rhizoids; stalk cylindrical, straight, flexuous, thick-walled, smooth, but verruculose in upper cell, 3–4-septate, with large guttules. Primary branches doliiform, brown, verruculose,

aseptate, 8–12  $\times$  7–9  $\mu$ m. **Conidiogenous cells** terminal and intercalary, or directly on conidiophore, 10–12  $\times$  9–11  $\mu$ m, tretic. **Conidia** aseptate, spherical, brown, with delicate spines, in short chains, (11–)13–16(–18)  $\mu$ m diam.

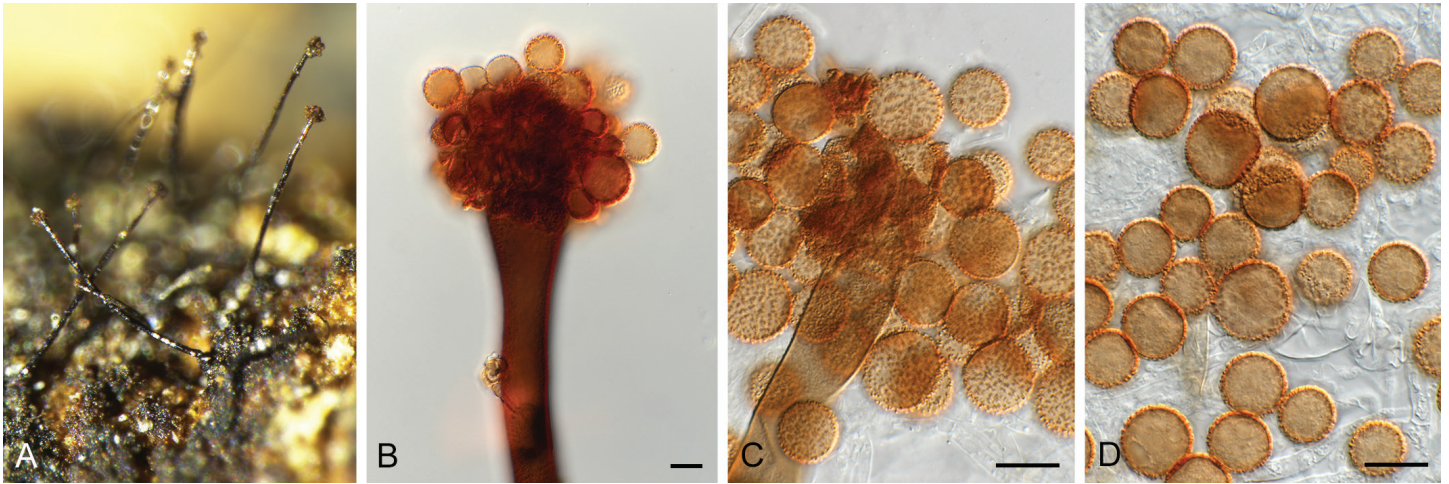
**Culture characteristics:** Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, even margin, covering dish after 2 wk at 25  $^{\circ}$ C. On MEA, PDA and OA surface umber with patches of dirty white, reverse umber with patches of chestnut.

**Material examined:** **South Africa**, Northern Province, Nelspruit, Lowveld Botanical Garden, on leaf litter of *Euphorbia ingens* (Euphorbiaceae), Nov. 2018, P.W. Crous, HPC 3140 = CBS H-24530, culture CPC 38820 = CBS 147067.

**Notes:** Phylogenetically (Fig. 2) and morphologically, the present collection is close to *P. pseudobyssoides* (conidiophores 300–600  $\mu$ m long, conidiogenous cells 10–12  $\times$  6–7.5  $\mu$ m, conidia (12–) 15–17(–20)  $\mu$ m; Markovskaja & Kačergius 2014).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Periconia byssoides* [strain 7GJ-1, GenBank KR708986.1; Identities = 524/526 (99%), two gaps (0%)], *Periconia pseudobyssoides* [strain DUCC 0850, GenBank MG333491.1; Identities = 495/498 (99%), no gaps], and *Acremoniella rugulosa* [strain CBS 110.35, GenBank MH855598.1; Identities = 501/506 (99%), one gap (0%)]. Closest hits using the **LSU** sequence are *Periconia pseudobyssoides* [strain H 4151, GenBank AB807568.1; Identities = 879/880 (99%), no gaps], *Periconia byssoides* [strain C292, GenBank MK347968.1; Identities = 884/889 (99%), no gaps], and *Periconia submersa* [strain MFLUCC 16-1098, GenBank KY794706.1; Identities = 825/836 (99%), no gaps]. No significant hits were obtained when the **tef1** (first part) sequence was used in blastn and megablast searches. Closest hits using the **tef1** (second part) sequence had highest similarity to *Periconia byssoides* [strain MFLUCC 17-2292, GenBank MK360069.1; Identities = 366/370 (99%), no gaps], *Periconia*





**Fig. 46.** *Periconia pseudobyssoidea* (CPC 38820). **A.** Conidiophores. **B.** Conidiophore and conidiogenous cells giving rise to conidia. **C.** Conidiogenous cells and conidia. **E.** Conidia. Scale bars = 10  $\mu$ m.

*pseudobyssoidea* [strain EF61a, GenBank AB808544.1; Identities = 430/436 (99 %), no gaps], and *Periconia homothallica* [strain EF58a, GenBank AB808541.1; Identities = 415/436 (95 %), no gaps].

**Authors:** P.W. Crous, J.Z. Groenewald & M.J. Wingfield

***Phaeoisaria clematidis*** (Fuckel) S. Hughes, *Canad. J. Bot.* **36**: 794. 1958. Fig. 47.

**Basionym:** *Stysanus clematidis* Fuckel, *Jb. nassau. Ver. Naturk.* **23–24**: 365. 1870. (1869–1870).

**Taxonomic lineage:** *Sordariomycetes*, *Pleurotheciales*, *Pleurotheciaceae*.

**Synnemata** erect, cylindrical to slightly clavate, up to 2 mm long, 20–40  $\mu$ m diam at base, composed of dark brown stipe of parallel, smooth-walled, septate, branched, 2–3  $\mu$ m diam hyphae, giving rise to terminal and lateral conidiogenous cells in the upper region of conidiophore. **Conidiogenous cells** pale brown, smooth, subhyaline towards apex, cylindrical to clavate, 5–15  $\times$  2–2.5  $\mu$ m; apical rosette of denticles cylindrical, 1–2  $\times$  1  $\mu$ m, not thickened nor darkened. **Conidia** aseptate, smooth- and thin-walled, hyaline to subhyaline, subcylindrical or obovoid,

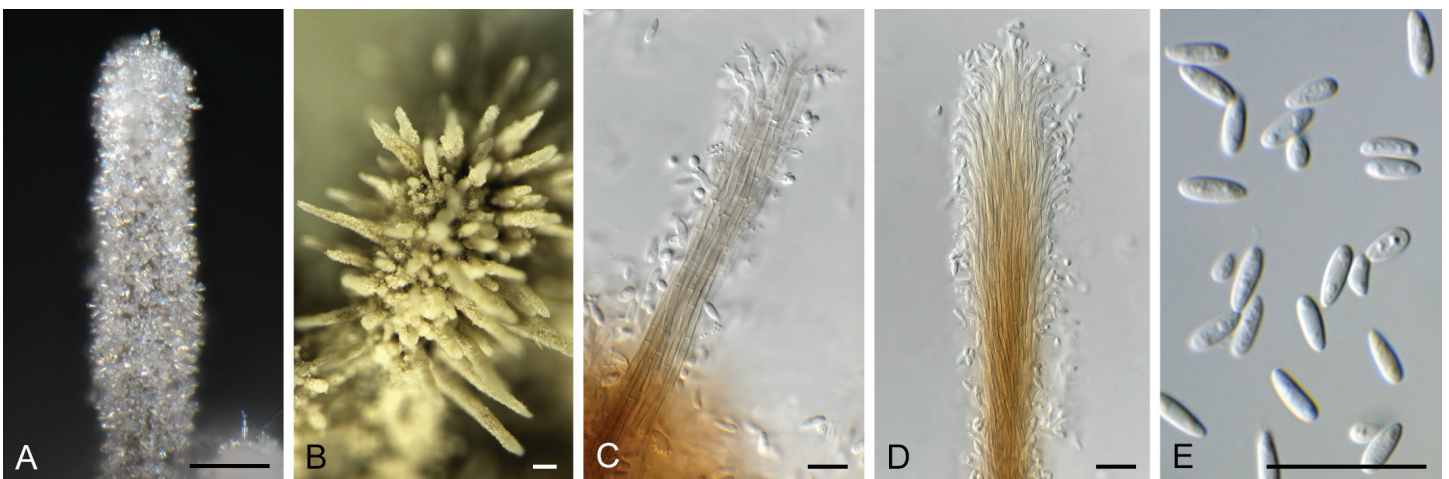
straight, (5–)6–7  $\times$  2(–2.5)  $\mu$ m. **Chlamydospores** produced in agar, thick- and smooth-walled, aseptate, ovoid to subglobose, 10–15  $\times$  8–10  $\mu$ m.

**Culture characteristics:** Colonies flat, spreading, with sparse aerial mycelium, surface folded, margin smooth, lobate, reaching up to 8 mm diam after 7 d. On MEA and PDA surface and reverse isabelline; on OA surface honey.

**Materials examined:** **Netherlands**, Utrecht Province, De Bilt, Beukenburglaan, on stems of *Sambucus nigra* (*Adoxaceae*), 23 Jul. 2020, P.W. Crous, culture CPC 39680; Zeeland Province, Oranjezon, on stems of *Sambucus nigra*, 17 Sep. 2020, A.L. van Iperen, HPC 3508, CBS H-24994, culture CPC 39937 = CBS 149173.

**Notes:** The genus *Phaeoisaria* is easily recognised by its erect synnemata, denticulate conidiogenous cells, and aseptate conidia. *Phaeoisaria clematidis*, the type species of the genus (*Pleurotheciaceae*, *Pleurotheciales*; Fig. 6), appears to be common on dead stems of *Sambucus nigra* in the Netherlands.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 39680 had highest similarity to *Phaeoisaria clematidis* [strain GZCC19-0541, GenBank MW133889.1; Identities = 525/530 (99 %), two



**Fig. 47.** *Phaeoisaria clematidis* (CPC 39680). **A, B.** Synnemata. **C, D.** Synnemata with conidiogenous cells. **E.** Conidia. Scale bars: A–D = 40  $\mu$ m, E = 10  $\mu$ m.



gaps (0 %)], *Hoehneliella perplexa* [strain NN057688, GenBank OL627919.1; Identities = 483/489 (99 %), three gaps (0 %)], and *Phaeoisaria annesophieae* [voucher MFLU 19-0531, GenBank MT559109.1; Identities = 518/549 (94 %), nine gaps (1 %)]. The ITS sequences of CPC 39680 and 39937 are identical (560/560 bp). Closest hits using the **LSU** sequence of CPC 39680 are *Phaeoisaria clematidis* [strain MFLUCC 18-1017, GenBank MW132065.1; Identities = 795/799 (99 %), no gaps], *Phaeoisaria annesophieae* [voucher MFLU 19-0531, GenBank MT559084.1; Identities = 813/822 (99 %), no gaps], and *Phaeoisaria filiformis* [strain MFLUCC 18-0214, GenBank NG\_068642.1; Identities = 774/784 (99 %), no gaps]. The LSU sequences of CPC 39680 and 39937 are identical (808/808 bp). Closest hits using the **rpb2** sequence of CPC 39680 had highest similarity to *Phaeoisaria clematidis* [strain MFLUCC 17-1341, GenBank MF401400.1; Identities = 485/497 (98 %), no gaps], *Phaeoisaria aquatica* [strain MFLUCC 16-1298, GenBank MF401406.1; Identities = 620/678 (91 %), no gaps], and *Phaeoisaria microspora* [strain M0104, GenBank MF167352.1; Identities = 668/757 (88 %), seven gaps (0 %)]. The **rpb2** sequences of CPC 39680 and 39937 differ at two nucleotides (849/851 bp identical). Closest hits using the **SSU** sequence of CPC 39680 are *Phaeoisaria clematidis* [strain MFLUCC 17-1968, GenBank MG837027.1; Identities = 991/991 (100 %), no gaps], *Phaeoisaria fasciculata* [strain DAOM 230055, GenBank KT278694.1; Identities = 925/928 (99 %), no gaps], and *Phaeoisaria guttulata* [voucher MFLU 18-0139, GenBank MG837026.1; Identities = 987/991 (99 %), no gaps].

**Authors:** P.W. Crous, J.Z. Groenewald, M. Starink-Willemse & A.L. van Iperen

***Phaeophleospora hymenocallidicola*** Crous, *Persoonia* **34**: 211. 2015. Fig. 48.

**Taxonomic lineage:** *Dothideomycetes*, *Mycosphaerellales*, *Mycosphaerellaceae*.

**Material examined:** **USA**, Puerto Rico, Agricultural experiment station, Juana Diaz, leaf necrosis on *Mangifera indica* var. Palmer (*Anacardiaceae*), Jun. 2020, A.M. Quimbita, CBS H-24795, culture CPC 40026 = CBS 148250; Puerto Rico, Commercial farm, Santa Isabel, necrosis on fruit peduncle of *M. indica*, Jun. 2020, A.M. Quimbita, culture CPC 40027 = CBS 149175.

**Notes:** *Phaeophleospora hymenocallidicola* (*Mycosphaerellaceae*, *Mycosphaerellales*; Fig. 1 part 2) was originally described as a foliar pathogen of a fern collected in Thailand (Crous et al. 2015), and is linked here to a foliar and fruit peduncle disease of mango in Puerto Rico.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phaeophleospora hymenocallidicola* [strain CBS 139912, GenBank NR\_137994.1; Identities = 571/571 (100 %), no gaps], *Phaeophleospora eucalypticola* [strain CBS 141294, GenBank NR\_145123.1; Identities = 570/572 (99 %), no gaps], and *Phaeophleospora pteridivora* [strain COAD 1182, GenBank NR\_155664.1; Identities = 450/481 (94 %), 12 gaps (2 %)]. The ITS sequences of CPC 40026 and 40027 are identical (573/573 bp). Closest hits using the **LSU** sequence of CPC 40026 are *Phaeophleospora eucalypticola* [strain CBS 141294, GenBank NG\_069357.1; Identities = 813/813 (100 %), no gaps], *Phaeophleospora hymenocallidicola* [strain CBS 139912, GenBank KR476772.1; Identities = 805/805 (100 %), no gaps], and *Phaeophleospora eugeniae* [strain CPC 15159, GenBank FJ493207.1; Identities = 810/813 (99 %), no gaps].

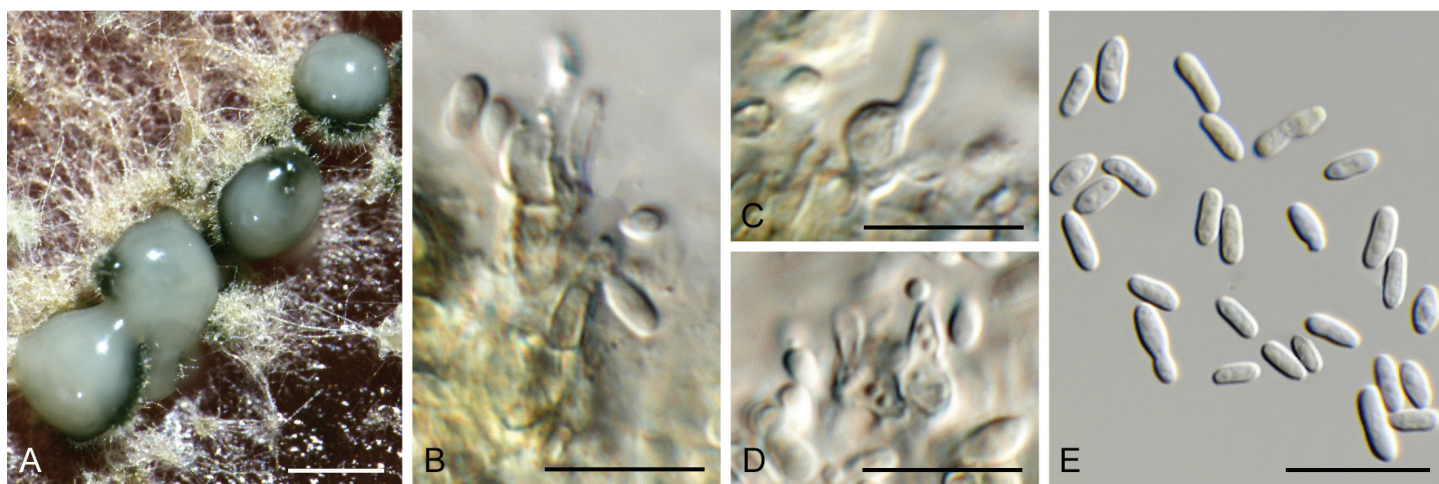
**Authors:** P.W. Crous, J.Z. Groenewald, A.M. Quimbita & L.I. Rivera-Vargas

***Phaeosphaeria hyphaenes*** Crous, *sp. nov.* MycoBank MB 844305. Fig. 49.

**Taxonomic lineage:** *Dothideomycetes*, *Pleosporales*, *Phaeosphaeriaceae*.

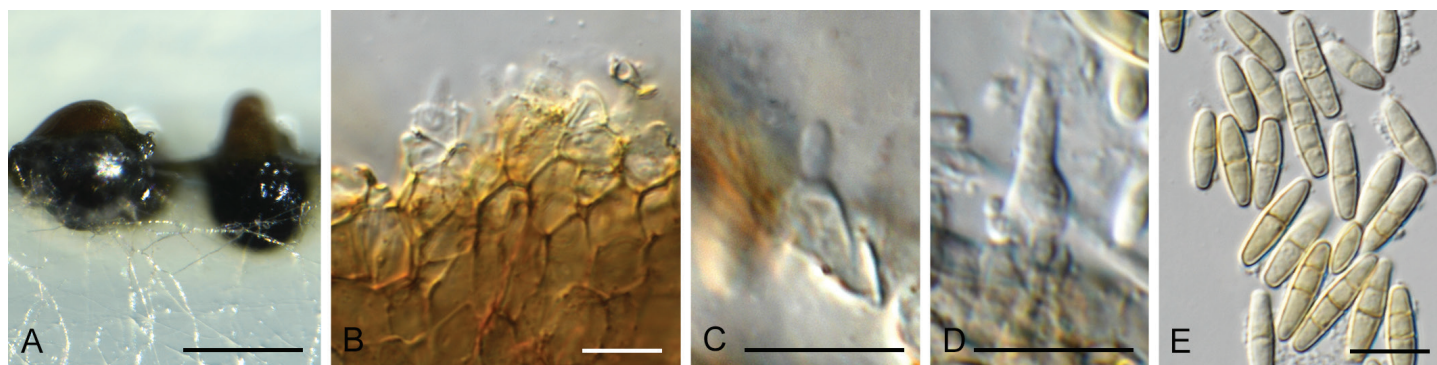
**Etymology:** Name refers to the host genus *Hyphaene* from which it was isolated.

**Conidiomata** pycnidial, solitary, immersed to erumpent, globose, brown with central ostiole, 150–300 µm diam; wall of 3–5 layers of brown *textura angularis*. **Conidiophores** reduced to conidiogenous cells lining the inner cavity. **Conidiogenous cells** subhyaline, smooth, ampulliform to doliiform, 4–5 × 3–5 µm; proliferating inconspicuously percurrently at apex. **Conidia** solitary, pale brown, smooth-walled, guttulate, subcylindrical, straight, apex obtuse, base truncate with flat scar, 0.5 µm diam, 1–3-septate, (7–)9–12(–13) × (2.5–)3 µm.



**Fig. 48.** *Phaeophleospora hymenocallidicola* (CPC 40026). **A.** Conidiomata on MEA. **B–D.** Conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars: A = 300 µm, all others = 10 µm.





**Fig. 49.** *Phaeosphaeria hyphaenes* (CPC 40354). **A.** Conidiomata on SNA. **B–D.** Conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars: A = 300  $\mu$ m, all others = 10  $\mu$ m.

**Culture characteristics:** Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 45 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

**Typus:** **South Africa**, KwaZulu-Natal Province, Manguzi, on leaves of *Hyphaene* sp. (*Arecaceae*), 19 Oct. 2017, M.J. Wingfield & J. Roux, HPC 3501 (**holotype** CBS H-24800, culture ex-type CPC 40354 = CBS 148254).

**Notes:** *Phaeosphaeria* was treated by Marin-Felix *et al.* (2019). *Phaeosphaeria hyphaenes* is closely related (Figs 2, 50) to *P. phoenicicola* (on *Phoenix canariensis*, New Zealand, conidia (8–)12–14(–16)  $\times$  (2–)2.5(–3)  $\mu$ m; Crous *et al.* 2016, Marin-Felix *et al.* 2019), but is distinct in that it has shorter conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phaeosphaeria* sp. 1 NV-2015 [strain UTHSC DI16-336, GenBank LT796889.1; Identities = 507/511 (99 %), no gaps], *Phaeosphaeria phoenicicola* [strain CPC 28711, GenBank NR\_156608.1; Identities = 502/512 (98 %), one gap (0 %)], and *Hendersonia culmiseda* [strain CBS 100.72, GenBank MH860403.1; Identities = 500/512 (98 %), one gap (0 %)]. Closest hits using the **LSU** sequence are *Phaeosphaeria cycadis* [strain KUMCC 18-0161, GenBank NG\_070078.1; Identities = 808/808 (100 %), no gaps], *Phaeosphaeria acaciae* [voucher MFLU 17-0496, GenBank NG\_069453.1; Identities = 808/808 (100 %), no gaps], and *Phaeosphaeria lunariae* [strain CPC 26679, GenBank KX306791.1; Identities = 808/808 (100 %), no gaps]. Closest hits using the **rpb2** sequence had highest similarity to *Phaeosphaeria* sp. 1 NV-2015 [strain UTHSC DI16-325, GenBank LT797042.1; Identities = 808/837 (97 %), no gaps], *Phaeosphaeria caricissectae* [strain CPC 38771, GenBank MZ078195.1; Identities = 763/837 (91 %), no gaps], and *Phaeosphaeria oryzae* [strain MFLUCC 11-0170, GenBank KM434306.1; Identities = 568/624 (91 %), no gaps]. No significant hits were obtained when the **tef1** first part) sequence was used in blastn and megablast searches. Closest hits using the **tub2** sequence had highest similarity to *Phaeosphaeria oryzae* [strain CBS 110110, GenBank KF252680.1; Identities = 220/234 (94 %), no gaps], *Phaeosphaeria* sp. 1 NV-2015 [strain UTHSC DI16-325, GenBank LT796962.1; Identities = 322/343 (94 %), four gaps (1 %)], and *Phaeosphaeria podocarpi* [strain CBS 138903, GenBank KP004508.1; Identities = 408/457 (89 %), 12 gaps (2 %)].

**Authors:** P.W. Crous, J.Z. Groenewald, J. Roux & M.J. Wingfield

***Phlyctema phoenicis*** Crous & Thangavel, *Persoonia* **37**: 349. 2016. Fig. 51.

**Taxonomic lineage:** Leotiomycetes, Helotiales, Dermateaceae.

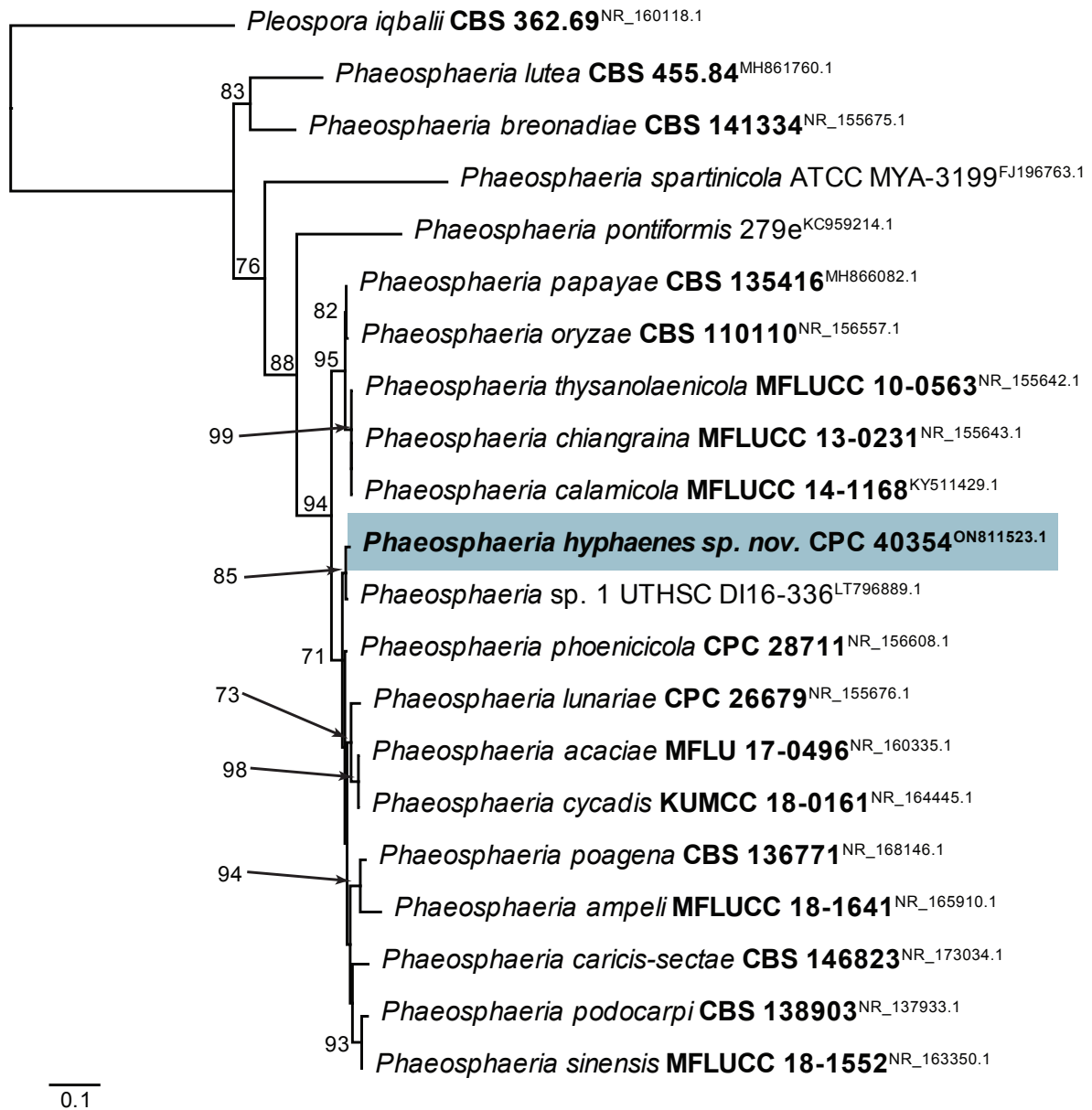
**Conidiomata** eustromatica, erumpent, acervuloid, separate, yellowish brown, pulvinate, round, unilocular, 200–300  $\mu$ m diam; wall of brown *textura angularis*. **Conidiophores** hyaline, smooth, 1–6-septate, irregularly branched, cylindrical, filiform, 18–40  $\times$  3–4  $\mu$ m. **Conidiogenous cells** subcylindrical, hyaline, smooth, phialidic, terminal and intercalary, with minute collarette and periclinal thickening, 6–17  $\times$  2.5–3  $\mu$ m. **Conidia** hyaline, smooth, aseptate, fusoid, curved, ends subobtusate, guttulate, (20–)25–30(–43)  $\times$  (2–)2.5  $\mu$ m.

**Culture characteristics:** Colonies flat, spreading, with moderate aerial mycelium and lobate, even margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white to buff, reverse sienna. 38747

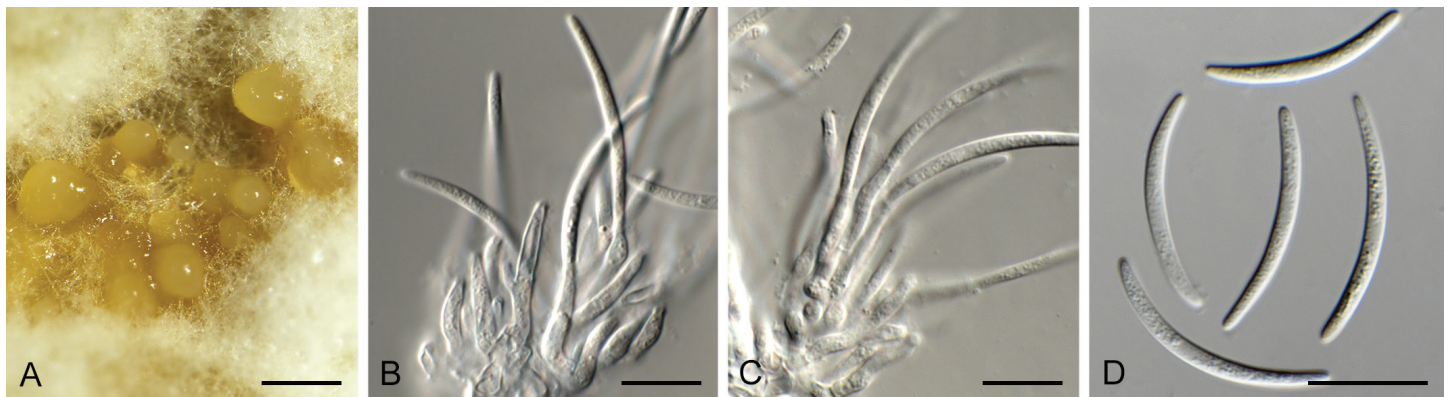
**Material examined:** **New Zealand**, Tauranga port, on *Libertia ixioides* (*Iridaceae*), 2019, C. Inglis, CBS H-24529, culture CPC 38747 = CBS 147066.

**Notes:** *Phlyctema phoenicis* was described from New Zealand, where it occurs on *Phoenix canariensis*, having conidia that are (17–)24–26(–27)  $\times$  2(–2.5)  $\mu$ m (Crous *et al.* 2016). Although the conidia of the holotype are smaller than those of the present collection on *Libertia ixioides*, the two collections are phylogenetically closely related (Fig 4).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Golovinomyces cynoglossi* [strain 5\_50, GenBank KY660948.1; Identities = 545/547 (99 %), no gaps], *Rhabdospora lupini* [strain CBS 475.69, GenBank MH859359.1; Identities = 544/546 (99 %), no gaps], and *Phlyctema phoenicis* [strain CPC 29372, GenBank NR\_155690.1; Identities = 540/542 (99 %), no gaps]. Closest hits using the **LSU** sequence are *Phlyctema coronillae* [voucher MFLU 15-1243, GenBank MT449705.1; Identities = 857/858 (99 %), no gaps], *Pseudofabraea citricarpa* [strain WZ-12-C-Co, GenBank MK968360.1; Identities = 848/849 (99 %), no gaps], and *Phlyctema vagabunda* [strain CBS 261.32, GenBank MH866769.1; Identities = 876/878 (99 %), no gaps]. Distant hits obtained using the **actA** sequence had highest



**Fig. 50.** Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 of the *Phaeosphaeria* ITS nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast bootstrap replicates are shown at the nodes. Culture collection numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Pleospora iqbalii* (culture CBS 362.69; GenBank NR\_160118.1) and the species treated here is highlighted with bold face. Accession numbers of sequence from material with a type status are also shown in bold face.



**Fig. 51.** *Phlyctema phoenicis* (CPC 38747). **A.** Conidiomata on OA. **B, C.** Conidiogenous cells giving rise to conidia. **D.** Conidia. Scale bars: A = 300  $\mu$ m, all others = 10  $\mu$ m.



similarity to *Coleophoma eucalyptigena* [strain CBS 146018, GenBank MT223749.1; Identities = 474/529 (90 %), 13 gaps (2 %)], *Satchmopsis brasiliensis* [strain CPC 24855, GenBank MT432192.1; Identities = 389/420 (93 %), no gaps], and *Satchmopsis pini* [strain CBS 146687, GenBank MT375096.1; Identities = 398/435 (91 %), one gap (0 %)]. Closest hits using the **tub2** sequence had highest similarity to *Phlyctema phoenicis* [strain CPC 29372, GenBank KY173611.1; Identities = 428/434 (99 %), no gaps], *Neofabraea eucalyptorum* [strain CBS 146634, GenBank MT375121.1; Identities = 374/454 (82 %), 14 gaps (3 %)], and *Coleophoma xanthosiae* [strain CPC 29214, GenBank KY173598.1; Identities = 234/269 (87 %), three gaps (1 %)].

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***Pseudohormonema*** Crous, *gen. nov.* MycoBank MB 844306.

*Taxonomic lineage:* Dothideomycetes, Dothideales, incertae sedis.

*Etymology:* Resembling the genus *Hormonema*.

*Mycelium* consisting of golden brown, finely verruculose, thick-walled, mucoid, guttulate hyphae. *Conidiophores* reduced to conidiogenous loci on hyphae, intercalary, phialidic, with truncate locus, giving rise to solitary conidia that aggregate in mucoid mass. *Conidia* initially hyaline, smooth, aseptate, guttulate to granular, ellipsoid, with age becoming medianly septate, each cell dividing further, golden brown, finely verruculose, then elongating to form chains of such chlamydospore-like structures.

*Type species:* *Pseudohormonema sordidus* Crous

***Pseudohormonema sordidus*** Crous, *sp. nov.* MycoBank MB 844307. Fig. 52.

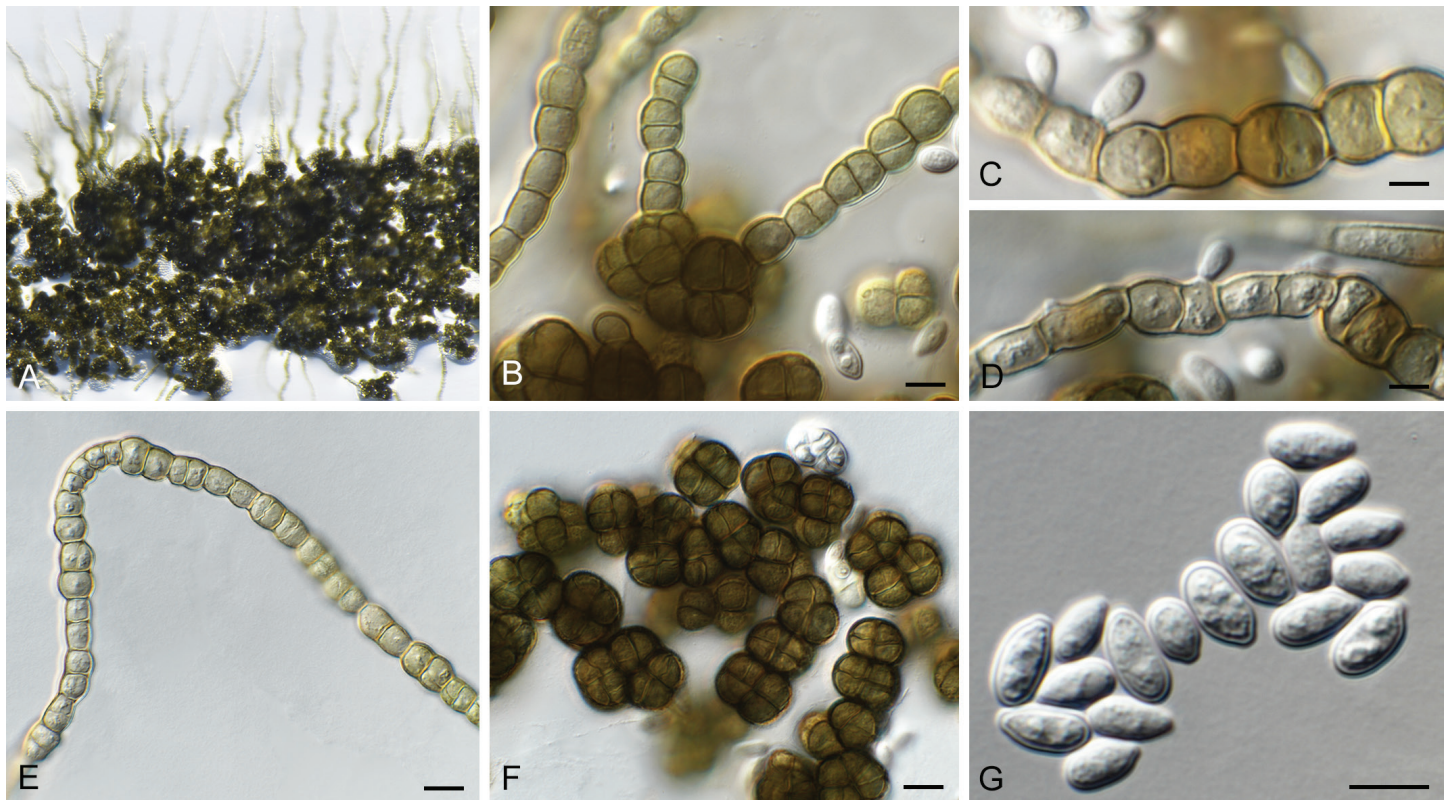
*Etymology:* *Sordida* (L.) dirty, impure, referring to its ecology.

*Mycelium* consisting of golden brown, finely verruculose, thick-walled, mucoid, guttulate, 5–7  $\mu\text{m}$  diam hyphae. *Conidiophores* reduced to conidiogenous loci on hyphae, intercalary, phialidic, with truncate locus, 2  $\mu\text{m}$  diam, giving rise to solitary conidia that aggregate in mucoid mass. *Conidia* initially hyaline, smooth, aseptate, guttulate to granular, ellipsoid, (6–)7–8(–10)  $\times$  (3.5–)4(–4.5)  $\mu\text{m}$ , apex obtuse, tapering in lower third to truncate hilum, 1–1.5  $\mu\text{m}$  diam, with age becoming medianly septate, each cell dividing, conidium becoming 4–8-celled, golden brown, finely verruculose, then elongating to form chains of such microsclerotium-like structures, each 1–4 or more-septate, eventually giving rise to hyphae with intercalary conidiogenous cells that again form aseptate, hyaline conidia.

*Culture characteristics:* Colonies erumpent, spreading, slimy, smooth, even to lobate margins, aerial mycelium absent, reaching 5 mm diam after 7 d at 25 °C in the dark. On MEA, PDA and OA surface and reverse fuscous black.

*Typus:* **USA**, from human pacemaker, date unknown, *D. Sutton* (**holotype** CBS-H 25001, culture ex-type CBS 130468 = UTHSC 07-2004).

*Additional materials examined:* **Saudi Arabia**, from polluted soil, Aug. 2014, coll. *S. de Hoog & T.A. Moussa*, isol. *M. Machado*, cultures CBS 140365, CBS 140366.



**Fig. 52.** *Pseudohormonema sordidus* (CBS 130468). **A.** Colony on SNA. **B–D.** Brown hyphae giving rise to hyaline, aseptate conidia. **E.** Hypha. **F.** Conidia becoming septate, brown, thick-walled, and anastomosing to form chains. **G.** Hyaline, aseptate conidia. Scale bars = 10  $\mu\text{m}$ .

*Notes:* *Pseudohormonema* represents a hormonema-like genus in *Dothideales* (see discussion under *Dothiora* above; Fig. 1 part 1), described as an opportunistic human pathogen, and from polluted soils. Although morphologically similar to *Hormonema*, it is different in that conidia become multiseptate, golden brown, finely verruculose, forming chains of microsclerotium-like structures in culture. Although the two strains from Saudi Arabia differ from the ex-type based on *tub2* (see below), we for now refrain from introducing an additional species for those strains pending the collection of more isolates to determine the genetic diversity of the present species.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CBS 130468 had highest similarity to *Sarcinomyces crustaceus* [strain UAMH 4286, GenBank NR\_121503.1; Identities = 535/615 (87 %), 27 gaps (4 %)], *Zalaria alba* [strain DAOM C250847, GenBank NR\_153465.1; Identities = 531/613 (87 %), 22 gaps (3 %)], and *Zalaria obscura* [strain DAOM C250849, GenBank NR\_153466.1; Identities = 529/611 (87 %), 22 gaps (3 %)]. The ITS sequence of CBS 130468 differs with one and two nucleotides respectively from CBS 140365 and 140366 (599/600 and 600/602 bp identical). Closest hits using the **LSU** sequence of CBS 130468 are *Neodothiora populina* [strain CPC 39399, GenBank MW175405.1; Identities = 549/570 (96 %), four gaps (0 %)], *Neocylindroseptoria pistaciae* [strain CBS 471.69, GenBank NG\_057996.1; Identities = 549/572 (96 %), two gaps (0 %)], and *Kabatina mahoniae* [strain CBS 264.92, GenBank MH874022.1; Identities = 549/572 (96 %), four gaps (0 %)]. The LSU sequences of CBS 130468 and 140365 are identical (570/570 bp). No significant hits were obtained when the **actA** and **tub2** sequences of CBS 130468 were used in a blast search. The *tub2* sequence of CBS 130468 is 93 % similar to those of CBS 140365 and 140366 (496/532 bp and 494/529 bp, both including one gap)

*Authors:* P.W. Crous & J.Z. Groenewald

***Pseudoplagiostoma eucalypti*** Cheew. *et al.*, *Fungal Diversity* **44**: 98. 2010. Fig. 53.

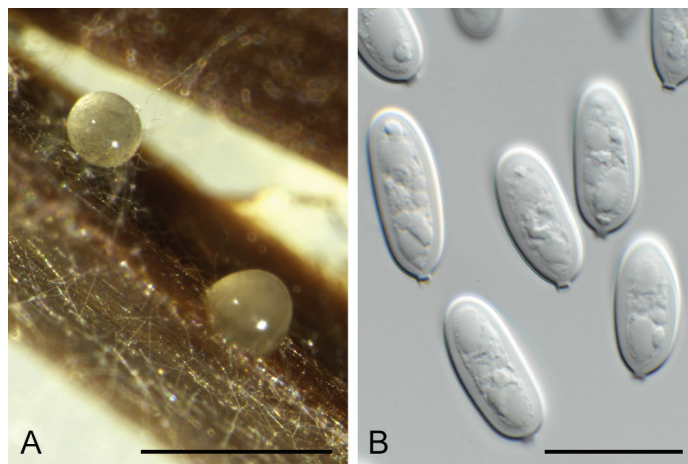
*Taxonomic lineage:* Sordariomycetes, Diaporthales, Pseudoplagiostomataceae.

*Description and illustration:* Cheewangkoon *et al.* (2010).

*Material examined:* **South Africa**, KwaZulu-Natal Province, Kwambonambi, on leaves of *Eucalyptus benthamii* (Myrtaceae), 8 Jun. 2020, J. Roux, HPC 3444, culture CPC 39762 = CBS 149183.

*Notes:* Species of *Pseudoplagiostoma* (*Pseudoplagiostomataceae*, *Diaporthales*; Fig. 6) are common foliar pathogens of *Eucalyptus* (Cheewangkoon *et al.* 2010, Crous *et al.* 2019c). This is the first record of a *Pseudoplagiostoma* species occurring on *Eucalyptus* in South Africa.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pseudoplagiostoma eucalypti* [strain LTL560, GenBank MF663591.1; Identities = 603/603 (100 %), no gaps], *Pseudoplagiostoma oldii* [strain CBS 124808, GenBank GU973534.1; Identities = 565/568 (99 %), two gaps (0 %)], and *Pseudoplagiostoma corymbiicola* [strain CBS 145052, GenBank NR\_161119.1; Identities = 597/604 (99 %), two gaps (0 %)].



**Fig. 53.** *Pseudoplagiostoma eucalypti* (CPC 39762). **A.** Conidiomata on PNA. **B.** Conidia. Scale bars: A = 300  $\mu$ m, B = 10  $\mu$ m.

Closest hits using the **LSU** sequence are *Pseudoplagiostoma eucalypti* [strain CPC 12280, GenBank GU973601.1; Identities = 734/734 (100 %), no gaps], *Pseudoplagiostoma oldii* [strain CBS 124808, GenBank GU973609.1; Identities = 733/734 (99 %), no gaps], and *Pseudoplagiostoma corymbiicola* [strain CBS 145052, GenBank NG\_066280.1; Identities = 813/816 (99 %), no gaps]. Closest hits using the **tef1** (first part) sequence had highest similarity to *Pseudoplagiostoma eucalypti* [strain CPC 14161, GenBank GU973540.1; Identities = 321/325 (99 %), one gap (0 %)], *Pseudoplagiostoma oldii* [strain CBS 124808, GenBank GU973564.1; Identities = 319/325 (98 %), no gaps], and *Pseudoplagiostoma corymbiicola* [strain CBS 145052, GenBank MK047558.1; Identities = 485/523 (93 %), five gaps (0 %)]. Closest hits using the **tub2** sequence had highest similarity to *Pseudoplagiostoma eucalypti* [strain PE1, GenBank KT831772.1; Identities = 731/731 (100 %), no gaps], *Pseudoplagiostoma oldii* [as *Diaporthales* sp. CR-2010a; strain CBS 124808, GenBank GU993862.1; Identities = 718/736 (98 %), one gap (0 %)], and *Pseudoplagiostoma variabile* [as *Diaporthales* sp. CR-2010b; strain CBS 113067, GenBank GU993863.1; Identities = 709/736 (96 %), one gap (0 %)].

*Authors:* P.W. Crous, J.Z. Groenewald & J. Roux

***Pseudosoloacrosporiella cryptomeriae*** Crous, *Persoonia* **47**: 195. 2021. Fig. 54.

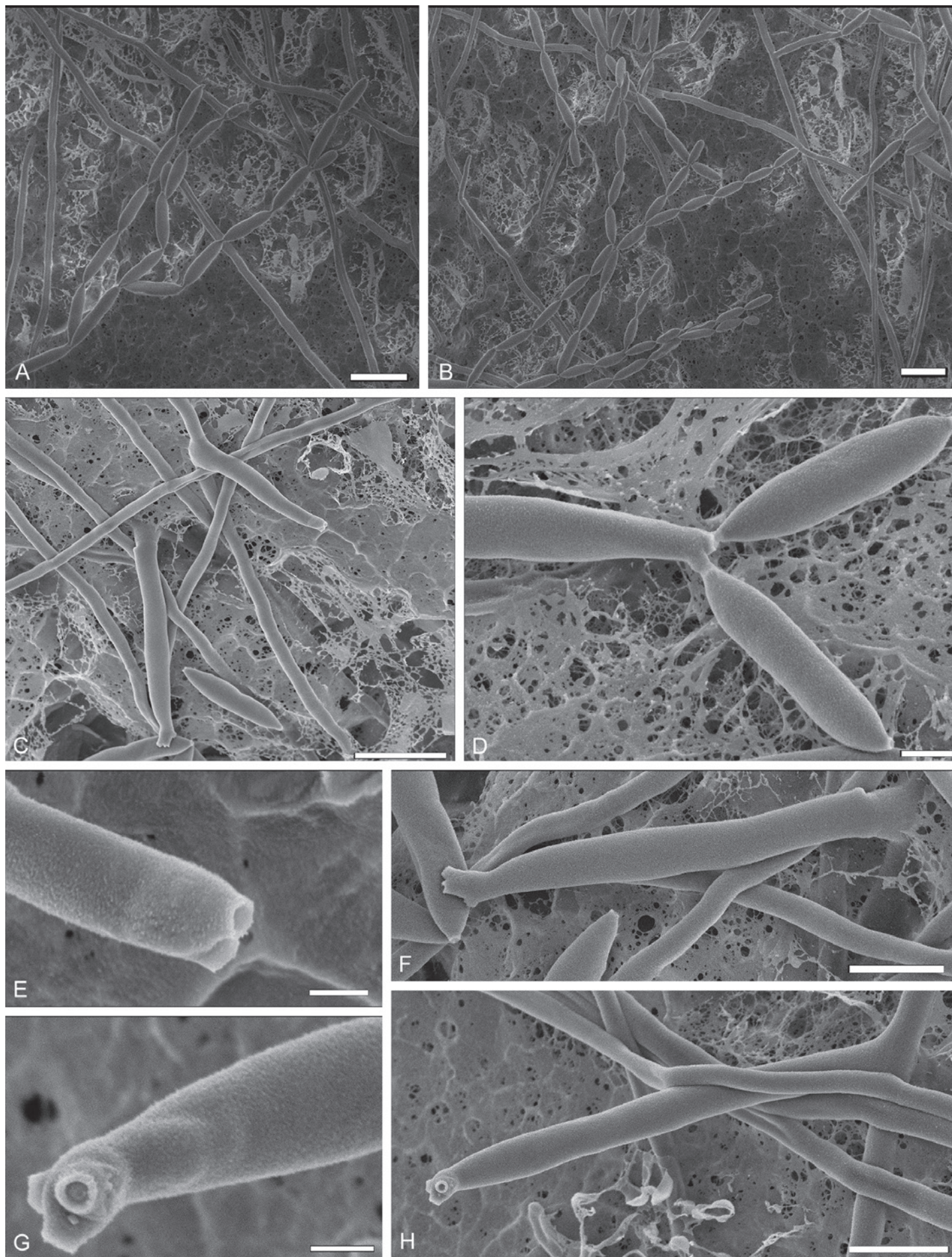
*Taxonomic lineage:* Dothideomycetes, Microthyriales, Microthyriaceae.

*Description and illustration:* Crous *et al.* (2021).

*Material examined:* **Netherlands**, Gelderland Province, Wageningen, Belmonte Botanical Garden, on leaves of *Cryptomeria japonica* (Cupressaceae), 28 July 2020, P.W. Crous, HPC 3301 (**holotype** CBS H-24883, culture ex-type CPC 39587 = CBS 148441).

*Notes:* *Pseudoacrosporiella* (*Microthyriaceae*, *Microthyriales*; Fig. 1 part 1) was recently introduced as a new genus of hyphomycetes resembling *Soloacrosporiella*, but being distinct in that it lacks setae, and its conidia do not have thickened and darkened hila, but rather have a characteristic marginal frill resulting from rhexolytic conidiogenesis (Crous *et al.* 2021d). The





**Fig. 54.** *Pseudosoloacrosporiella cryptomeriae* (CPC 39587). **A, B.** Scanning Electron Micrographs showing conidial chains. **C–H.** Conidiophores and conidiogenous cells showing rhexolytic conidiogenesis. Scale bars: A–C = 10  $\mu\text{m}$ , F, H = 5  $\mu\text{m}$ , D = 2  $\mu\text{m}$ , E, G = 1  $\mu\text{m}$ .



scanning electron micrographs clearly show this characteristic feature (Fig. 54).

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***Pseudosydowia*** Thambug. & K.D. Hyde, *Fungal Diversity* **68**: 140. 2014.

New synonym: *Moringomyces* Crous, *Persoonia* **45**: 323. 2020.

*Taxonomic lineage*: Dothideomycetes, Dothideales, Saccotheciaceae.

***Pseudosydowia phantasmae*** (Crous) Crous, *comb. nov.* MycoBank MB 845100. Fig. 55.

*Basionym*: *Moringomyces phantasmae* Crous, *Persoonia* **45**: 323. 2020.

*Conidiomata* immersed on seed pods, pycnidial to acervular, 180–200 µm diam. In culture forming acervular conidiomata, arising from a brown stroma consisting of brown, smooth to verruculose, thin-walled cells, 5–8 µm diam. *Conidiophores* reduced to conidiogenous cells, ampulliform to doliiform, hyaline, smooth, mono- to polyphialidic, 7–10 × 10–14 µm. *Conidia* aggregating in mucoid mass, hyaline, smooth, 0(–1)-septate, ellipsoid to ovoid, frequently curved, becoming brown with age, apex subobtuse, base truncate, (9–)12–14(–15) 4–5 µm.

*Material examined*: **Namibia**, Namib Research Institute, on flower of *Moringa ovalifolia* (*Moringaceae*), 19 Nov. 2019, P.W. Crous, HPC 3130 = CBS H-24494, culture CPC 38950 = CBS 146982.

*Culture characteristics*: Colonies erumpent, spreading, surface folded, with sparse aerial mycelium and smooth, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse iron-grey.

*Notes*: *Moringomyces phantasmae* was recently described from *Moringa ovalifolia* in Namibia (Crous *et al.* 2020a), for which this isolate represents the second collection (Fig. 1 part 1). In previous analyses (Crous *et al.* 2020a, 2021a), *Moringomyces phantasmae* clustered distinct from *Pseudosydowia*. However, by including an additional isolate in the present analysis,

*Moringomyces* is placed within *Pseudosydowia* (type species: *P. eucalypti*), albeit on a long branch with no support. *Pseudosydowia* is morphologically highly variable (Crous *et al.* 2019c), but includes the variation we see in *Moringomyces*, and hence the latter is reduced to synonymy.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Moringomyces phantasmae* [strain CBS 146830, GenBank NR\_171999.1; Identities = 603/604 (99 %), no gaps], *Pseudosydowia eucalypti* [strain CBS 131832, GenBank MH865934.1; Identities = 485/529 (92 %), 15 gaps (2 %)], and *Cryptocline arctostaphyli* [strain 19GCAS004, GenBank MW077685.1; Identities = 553/609 (91 %), 22 gaps (3 %)]. Closest hits using the **LSU** sequence are *Moringomyces phantasmae* [strain CPC 38883, GenBank MW175404.1; Identities = 834/834 (100 %), no gaps], *Pseudosydowia eucalypti* [strain CPC 14028, GenBank GQ303327.2; Identities = 837/855 (98 %), three gaps (0 %)], and *Pseudosydowia eucalyptorum* [strain CBS 145546, GenBank NG\_067893.1; Identities = 830/848 (98 %), three gaps (0 %)].

Authors: P.W. Crous, J.Z. Groenewald, N. Yilmaz & M.J. Wingfield

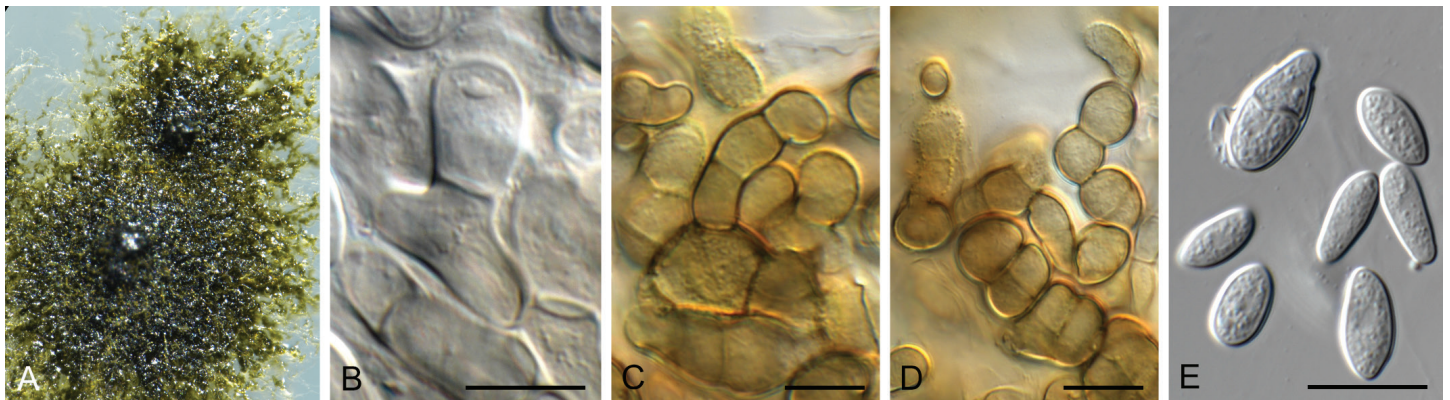
***Quasiphoma*** Crous, *gen. nov.* MycoBank MB 844308.

*Taxonomic lineage*: Dothideomycetes, Pleosporales, Leptosphaeriaceae.

*Etymology*: Name refers to the fact that it is phoma-like in morphology, but different, being allied to other phoma-like genera.

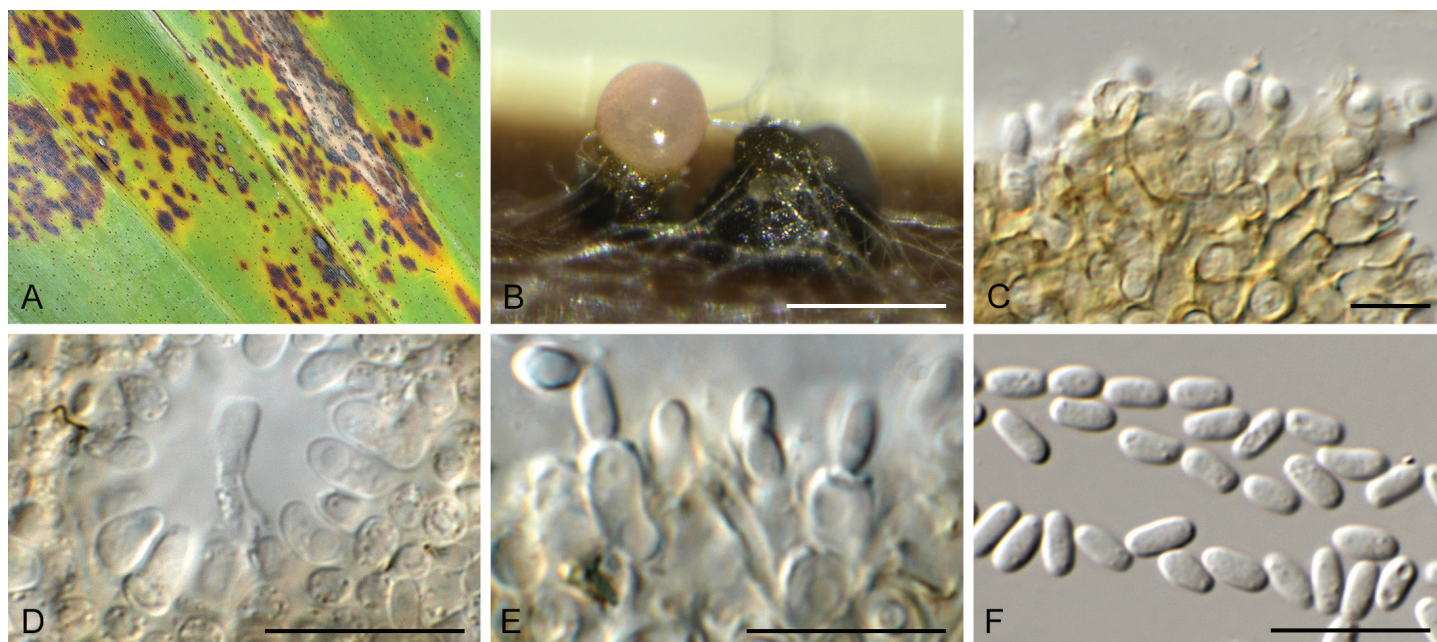
*Conidiomata* pycnidial, solitary, brown, globose, with central ostiole; wall of 3–6 layers of medium brown *textura angularis*; conidiomata exuding a creamy to pinkish conidial mass. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline smooth, ampulliform to doliiform, phialidic. *Conidia* solitary, or in short, false, disarticulating chains, hyaline, smooth- and thin-walled, guttulate, ellipsoid, with obtuse ends, aseptate.

*Type species*: *Quasiphoma hyphaenes* Crous



**Fig. 55.** *Pseudosydowia phantasmae* (CPC 38950). **A.** Colony on SNA. **B–D.** Swollen hyphae that develop conidiogenous loci giving rise to conidia. **E.** Conidia. Scale bars = 10 µm.





**Fig. 56.** *Quasiphoma hyphaenes* (CPC 40045). **A.** Leaf spots on *Hyphaene crenata*. **B.** Conidiomata on PNA. **C, E.** Conidiogenous cells giving rise to conidia. **D.** Ostiole viewed from above. **F.** Conidia. Scale bars: B = 250  $\mu$ m, all others = 10  $\mu$ m.

***Quasiphoma hyphaenes*** Crous, *sp. nov.* MycoBank MB 844309. Fig. 56.

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

**Conidiomata** pycnidial, solitary, brown, globose, 200–250  $\mu$ m diam, with central ostiole; wall of 3–6 layers of medium brown *textura angularis*; conidiomata exuding a creamy to pinkish conidial mass. **Conidiophores** reduced to conidiogenous cells lining the inner cavity, hyaline smooth, ampulliform to doliiform, phialidic, 5–7  $\times$  3–3.5  $\mu$ m. **Conidia** solitary, or in short, false, disarticulating chains, hyaline, smooth- and thin-walled, guttulate, ellipsoid, with obtuse ends, aseptate, (4–)5(–6)  $\times$  2(–2.5)  $\mu$ m.

**Culture characteristics:** Colonies erumpent, spreading, with abundant aerial mycelium and smooth, lobate margin, covering dish within 2 wk at 25  $^{\circ}$ C. On MEA, PDA and OA surface and reverse olivaceous grey.

**Typus:** **South Africa**, KwaZulu-Natal Province, Manguzi, on leaves of *Hyphaene* sp. (*Arecaceae*), 19 Oct. 2017, M.J. Wingfield & J. Roux, HPC 3501 (**holotype** CBS H-24798, culture ex-type CPC 40045 = CBS 148253).

**Notes:** Based on preliminary analyses (data not shown) of ITS, LSU, *rpb2* and *tub2*, *Quasiphoma hyphaenes* clustered between a reference strain of *Coniothyrium telephii* (characterised by setose pycnidia), and *Querciphoma minuta* (conidiomata are eustromatic, uni- to multi-locular, and conidia become brown and verruculose with age; Crous & Groenewald 2017). *Quasiphoma hyphaenes* is a nondescript phoma-like taxon, except that at times conidia appear to remain attached in short chains, which is unusual. It is associated with *Querciphoma* and *Subplenodomus* in the LSU phylogeny (Fig. 2).

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

similarity to *Phoma schachtii* [strain CBS 502.84, GenBank MH861770.1; Identities = 430/469 (92 %), 11 gaps (2 %)], *Longiseptatispora curvata* [strain CPC 36457, GenBank NR\_169725.1; Identities = 427/467 (91 %), nine gaps (1 %)], and *Coniothyrium wernsdorffiae* [strain CBS 150.34, GenBank MH855474.1; Identities = 428/469 (91 %), 12 gaps (2 %)]. Closest hits using the **LSU** sequence are *Subplenodomus drobnjacensis* [strain PRG11-03, GenBank AB819763.1; Identities = 795/814 (98 %), no gaps], *Alternariaster helianthi* [strain CBS 119672, GenBank KC584368.1; Identities = 795/815 (98 %), four gaps (0 %)], and *Querciphoma minuta* [as *Coniothyrium carteri*; strain LG1401\_MS6E, GenBank KX359604.1; Identities = 794/814 (98 %), no gaps]. Closest hits using the **rpb2** sequence had highest similarity to *Coniothyrium telephii* [strain CBS 188.71, GenBank KT389593.1; Identities = 512/598 (86 %), no gaps], *Exserohilum minor* [as *Setosphaeria minor*; strain BRIP 14615, GenBank LT852501.1; Identities = 662/812 (82 %), two gaps (0 %)], and *Exserohilum rostratum* [as *Setosphaeria rostrata*; strain BRIP 13592, GenBank LT882528.1; Identities = 661/813 (81 %), four gaps (0 %)]. No significant hits were obtained when the **actA** and **tub2** sequences were used in blastn and megablast searches.

**Authors:** P.W. Crous, J.Z. Groenewald, J. Roux & M.J. Wingfield

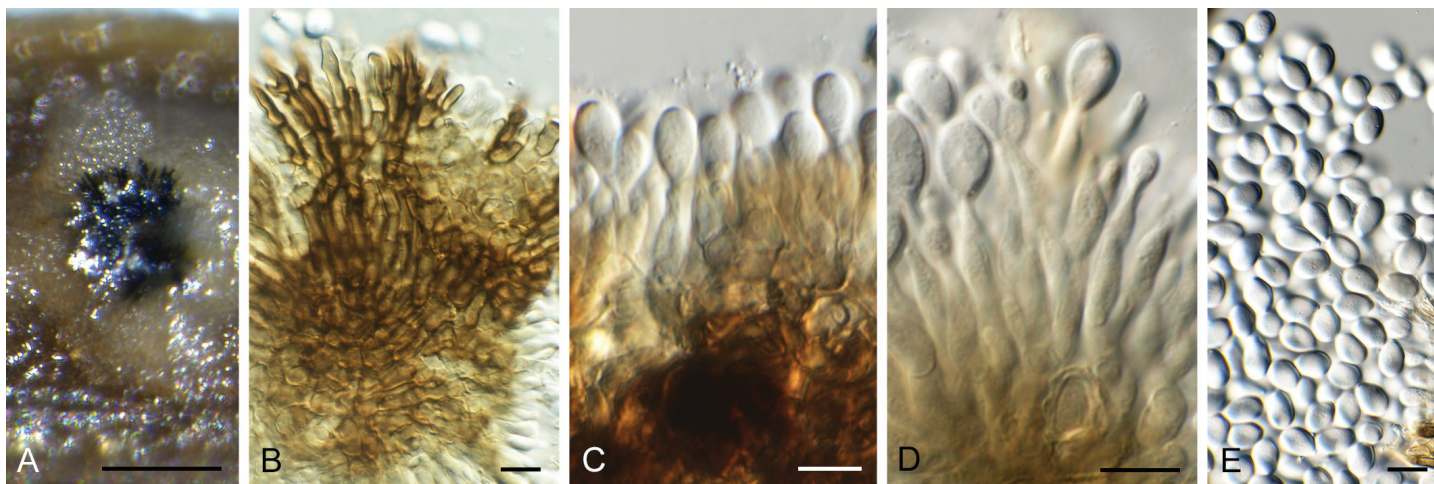
***Racheliella wingfieldiana*** Crous & U. Braun, *Fungal Syst. Evol.* 1: 71. 2018. Fig. 57.

**Taxonomic lineage:** Sordariomycetes, Diaporthales, Tubakiaceae.

**Description and illustration:** Crous *et al.* (2018b).

**Material examined:** **South Africa**, near Mozambique, on *Syzygium* sp. (*Myrtaceae*), 19 Oct. 2015, M.J. Wingfield, HPC 3498 = CBS H-24796, culture CPC 40039 = CBS 148251.





**Fig. 57.** *Racheliella wingfieldiana* (CPC 40039). **A.** Pycnothyrium on PNA. **B.** Radiating wall of pycnothyrium. **C, D.** Conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars = 10 µm.

**Notes:** *Racheliella wingfieldiana* (*Tubakiaceae*, *Diaporthales*; Fig. 6) was described from leaves of *Syzygium guineense* in the Eastern Cape Province of South Africa (Crous *et al.* 2018b). The present collection appears to represent a closely related cryptic lineage, but more isolates are required to determine the genetic variation within *R. wingfieldiana*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Racheliella wingfieldiana* [strain CBS 143669, GenBank MG591911.1; Identities = 575/583 (99 %), two gaps (0 %)], *Paratubakia subglobosa* [strain ATCC 22474, GenBank NR\_161043.1; Identities = 375/420 (89 %), 17 gaps (4 %)], and *Oblongisporothyrium castanopsisidis* [strain CBS 124732, GenBank MG591849.1; Identities = 373/419 (89 %), 16 gaps (3 %)]. Closest hits using the **LSU** sequence are *Racheliella wingfieldiana* [strain CBS 143669, GenBank MG592006.1; Identities = 805/805 (100 %), no gaps], *Greeneria saprophytica* [strain NTCL052-1, GenBank KJ021935.1; Identities = 810/815 (99 %), no gaps], and *Apiognomonioides suprasedata* [strain CBS 632.92, GenBank NG\_066205.1; Identities = 808/815 (99 %), no gaps]. The best hit using the **tef1** (first part) sequence had highest similarity to *Racheliella wingfieldiana* [strain CBS 143669, GenBank MG592100.1; Identities = 579/588 (98 %), three gaps (0 %)]; no other significant hits were obtained. The best hit using the **tub2** sequence had highest similarity to *Racheliella wingfieldiana* [strain CBS 143669, GenBank MG592192.1; Identities = 418/432 (97 %), one gap (0 %)]; no other significant hits were obtained.

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***Ramularia arvensis*** Sacc., *Michelia* 2(no. 8): 548. 1882. Fig. 58.

**Taxonomic lineage:** *Dothideomycetes*, *Mycosphaerellales*, *Mycosphaerellaceae*.

**Leaf spots** amphigenous, circular, brown to dark brown, 2–4 mm diam. **Conidiophores** fasciculate, amphigenous. On SNA. **Mycelium** consisting of hyaline, smooth, branched, septate, 2.5–3.5 µm diam hyphae. **Conidiophores** reduced to conidiogenous cells on hyphae, solitary, erect, subcylindrical, 5–25 × 3–4 µm; loci terminal, thickened, darkened, refractive, 1–1.5 µm diam. **Ramoconidia** subcylindrical, hyaline, smooth-walled, 1–3-septate, 20–55 × 3.5–4.5 µm; conidia in branched chains,

subcylindrical, hyaline, smooth-walled, (0–)1-septate, (10–)15–20(–30) × 3(–4) µm; hila thickened, darkened, refractive, 1 µm diam.

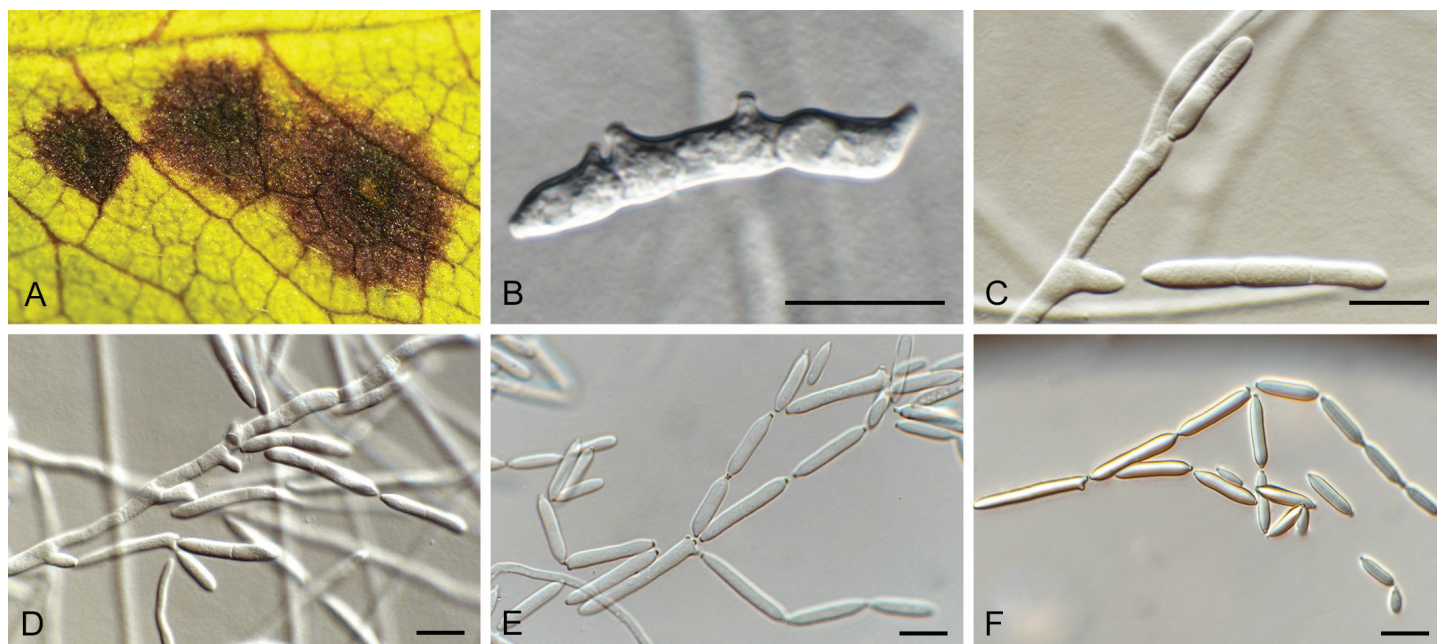
**Culture characteristics:** Colonies erumpent, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 10 mm diam after 7 d at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

**Typus:** **Italy**, Selva, Treviso, on *Potentilla reptans* (*Rosaceae*) (**holotype**, herb. Saccardo PAD). **Netherlands**, Gelderland Province, Beuningen, river Waal, on leaves of *Potentilla reptans*, 17 Oct. 2020, A.L. van Iperen, HPC 3475 (**epitype** designated here CBS H-24897, MBT 10007416, culture ex-epitype CPC 39985 = CBS 148455).

**Notes:** The present collection was initially thought to be *R. grevilleana*, which has a broad host range and distribution. The latter species was treated in detail by Braun (1998) who also listed several synonyms described from Europe on *Potentilla* (e.g. *R. anserina*, *R. arvensis* and *R. punctiformis*). Phylogenetically (Figs 1 part 2, 13 part 2) and morphologically however, our collection is distinct from *R. grevilleana* (on *Fragaria* spp.), having branched conidial chains, ramoconidia, and smaller subcylindrical terminal conidia. The oldest name which can be applied to this specimen is *Ramularia arvensis*, described from Italy on *Potentilla reptans*. One yet older name exists (*Ramularia martianoffiana*), described from Asia, Siberia on another Asian *Potentilla* species, but the type has not been preserved, and its morphology cannot be confirmed.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Ramularia collo-cygni* [strain CBS 101180, GenBank NR\_154944.1; Identities = 516/522 (99 %), three gaps (0 %)], *Ramularia glennii* [strain SFI-D21, GenBank MT535837.1; Identities = 517/524 (99 %), three gaps (0 %)], and *Ramularia eucalypti* [strain SFI-D21, GenBank MT535837.1; Identities = 517/524 (99 %), three gaps (0 %)]. Closest hits using the **LSU** sequence are *Ramularia uredinicola* [strain CPC 12491, GenBank KX287226.1; Identities = 809/812 (99 %), no gaps], *Ramularia bellunensis* [strain CBS 118417, GenBank KX287035.1; Identities = 824/828 (99 %), one gap (0 %)], and *Ramularia lamii* var. *lamii* [strain CBS 108970, GenBank NG\_069361.1; Identities = 817/822 (99 %), one gap (0 %)].





**Fig. 58.** *Ramularia arvensis* (CPC 39985). **A.** Leaf spots. **B.** Ramoconidium. **C, D.** Conidiophores giving rise to conidia. **E, F.** Catenulate conidia. Scale bars = 10  $\mu$ m.

Closest hits using the *actA* sequence had highest similarity to *Ramularia grevilleana* [strain CBS 719.84, GenBank KP894331.1; Identities = 587/617 (95 %), 10 gaps (1 %)], *Ramularia eucalypti* [strain CPC 13044, GenBank KJ504458.1; Identities = 560/610 (92 %), 20 gaps (3 %)], and *Ramularia glennii* [strain CBS 129441, GenBank KJ504433.1; Identities = 557/609 (91 %), 19 gaps (3 %)]. Closest hits using the *gapdh* sequence had highest similarity to *Ramularia grevilleana* [strain CBS 259.36, GenBank KP894549.1; Identities = 505/524 (96 %), no gaps], *Ramularia pratensis* var. *pratensis* [strain CPC 19448, GenBank KX288330.1; Identities = 423/464 (91 %), six gaps (1 %)], and *Ramularia hydrangeae-macrophyllae* [strain CPC 25903, GenBank KX288295.1; Identities = 421/463 (91 %), seven gaps (1 %)]. Closest hits using the *his3* sequence had highest similarity to *Ramularia grevilleana* [strain CBS 259.36, GenBank KP894771.1; Identities = 339/356 (95 %), eight gaps (2 %)], *Ramularia vallisumbrosae* [strain CBS 271.38, GenBank KX288988.1; Identities = 332/357 (93 %), four gaps (1 %)], and *Ramularia pratensis* [strain CBS 136.23, GenBank KJ504633.1; Identities = 328/356 (92 %), 14 gaps (3 %)]. Closest hits using the *tef1* (first part) sequence had highest similarity to *Ramularia grevilleana* [strain CBS 114732, GenBank KP894438.1; Identities = 304/320 (95 %), no gaps], *Ramularia rumicicola* [strain CPC 11294, GenBank KX288063.1; Identities = 172/186 (92 %), four gaps (2 %)], and *Ramularia haroldporterii* [strain CPC 16296, GenBank KJ504681.1; Identities = 150/153 (98 %), no gaps].

**Authors:** P.W. Crous, J.Z. Groenewald, U. Braun, M. Starink-Willemse & A.L. van Iperen

**Rapidomyces** Crous & Boers, *gen. nov.* MycoBank MB 844310.

**Taxonomic lineage:** Dothideomycetes, Mycosphaerellales, Teratosphaeriaceae.

**Etymology:** Rapid-, relating to the rate of ascomatal development in damp chambers.

*Ascomata* substomatal, immersed to superficial, solitary, brown, linked by brown hyphal network, globose to subglobose, with central ostiole; wall of 2–3 layers of brown *textura angularis*. *Asci* 8-spored, broadly ellipsoid to subglobose, bitunicate. *Ascospores* multiseriate, hyaline, smooth-walled, guttulate, fusoid-ellipsoid, medianly 1-septate, constricted at septum. *Ascospores* becoming brown and verruculose upon discharge, with prominent mucoid sheath.

**Type species:** *Rapidomyces narthecii* Crous & Boers

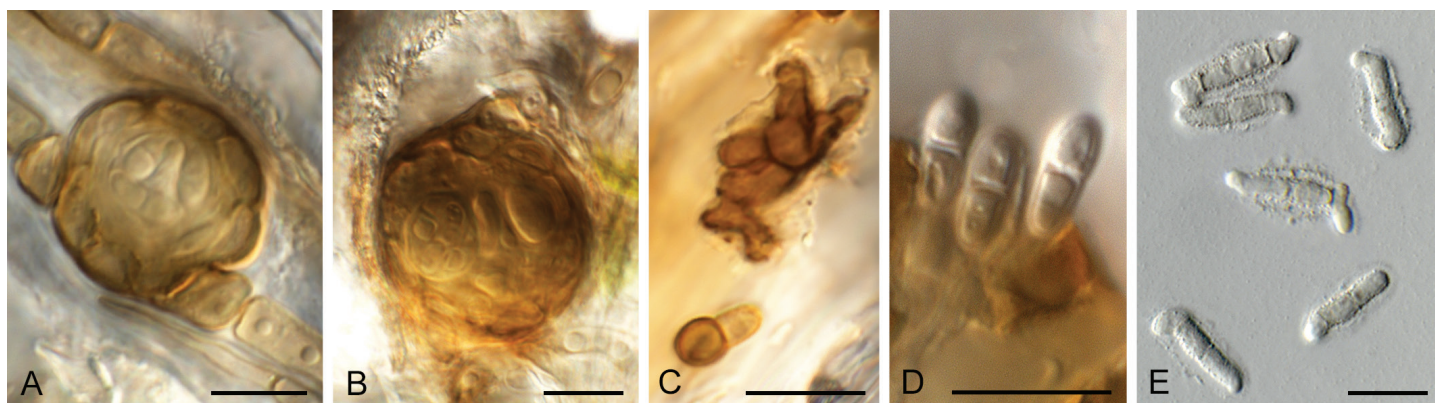
***Rapidomyces narthecii*** Crous & Boers, *sp. nov.* MycoBank MB 844311. Fig. 59.

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

*Ascomata* substomatal, immersed to superficial, solitary, brown, linked by brown hyphal network, 5–6  $\mu$ m diam, globose to subglobose, 15–40  $\mu$ m diam, with central ostiole; wall of 2–3 layers of brown *textura angularis* (developing in damp chambers from superficial hyphae on host tissue within 3–5 d of incubation). *Asci* 8-spored, broadly ellipsoid to subglobose, bitunicate, 10–20  $\times$  8–12  $\mu$ m. *Ascospores* multiseriate, hyaline, smooth-walled, guttulate, fusoid-ellipsoid, medianly 1-septate, constricted at septum, widest just above septum, 8–9  $\times$  3–3.5  $\mu$ m. *Ascospores* becoming brown and verruculose upon discharge, with prominent mucoid sheath; ascospores 4  $\mu$ m diam, germinating from polar ends, with germ tubes at various angles to the long axis of the spore.

**Culture characteristics:** Colonies spreading, with moderate aerial mycelium and even, lobate margins, reaching 15 mm diam after 2 wk. On MEA, PDA and OA surface and reverse olivaceous grey.

**Typus:** Netherlands, Drenthe Province, Dwingelderveld National Park, 52.829188, 6.432495, on dead leaves of *Narthecium ossifragum*



**Fig. 59.** *Rapidomyces narthecii* (CPC 41974). **A. B.** Superficial ascomata. **C.** Superficial ascospores on host tissue. **D.** Ascospores. **E.** Germinating ascospores. Scale bars = 10 µm.

(*Nartheciaceae*), 4 Jul. 2021, J. Boers, HPC 2353 (**holotype** CBS H-24997, cultures ex-type CPC 41974, 41975 = CBS 149174).

**Notes:** *Rapidomyces* represents a new, phylogenetically distinct sexual genus in Teratosphaeriaceae (Figs 1 part 2, 36). It is related to several extremophilic genera, namely *Lapidomyces* (rock inhabiting hyphomycetous fungus; Crous et al. 2019a), *Xenopenidiella formica* (ant inhabiting hyphomycetous fungus; Duarte et al. 2017), *Acrodontium crateriforme* (hyphomycete occurring on various substrates; Videira et al. 2016), *Pseudotaeniolina* (rock inhabiting hyphomycete; De Leo et al. 2003), and *Neocatenulostroma* (saprobic and plant pathogenic; Crous et al. 2007a). Morphologically, it lacks an asexual morph, and resembles other sexual genera in *Teratosphaeriaceae*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pseudotaeniolina globosa* [strain CBS 109889, GenBank MH862844.1; Identities = 382/420 (91 %), four gaps (0 %)], *Teratosphaeria jonkershoekensis* [strain CBS 122897, GenBank EU707864.1; Identities = 378/415 (91 %), seven gaps (1 %)], and *Neocatenulostroma microsporium* [strain HFJN1, GenBank MH349092.1; Identities = 374/413 (91 %), four gaps (0 %)]. Closest hits using the **LSU** sequence are *Neocatenulostroma germanicum* [strain CBS 539.88, GenBank MH873835.1; Identities = 797/835 (95 %), 10 gaps (1 %)], *Aulographina pinorum* [strain CBS 302.71, GenBank GU214393.1; Identities = 797/835 (95 %), 10 gaps (1 %)], and *Neocatenulostroma microsporium* [strain CBS 110890, GenBank EU019255.2; Identities = 797/835 (95 %), 10 gaps (1 %)]. Closest hits using the **rpb2** sequence had distant similarity to *Teratosphaeria fibrillosa* [strain CPC 13960, GenBank LT799765.1; Identities = 558/711 (78 %), 24 gaps (3 %)], *Ramularia chamaedrys* [strain CBS 116577, GenBank KX288512.1; Identities = 360/456 (79 %), four gaps (0 %)], and *Collarispora valgourgensis* [strain CBS 129531, GenBank MF951479.1; Identities = 359/460 (78 %), seven gaps (1 %)].

**Authors:** P.W. Crous, J.Z. Groenewald & J. Boers

***Reticulascus parahennebertii*** Crous & Osieck, *sp. nov.* MycoBank MB 844312. Fig. 60.

**Taxonomic lineage:** Sordariomycetes, Glomerellales, Reticulascaceae.

**Etymology:** Refers to its morphological similarity to *Reticulascus hennebertii*.

*Mycelium* consisting of hyaline, smooth-walled, branched, septate, 2.5–3 µm diam hyphae, frequently forming hyphal coils. *Conidiophores* solitary or in clusters, subcylindrical, unbranched, medium brown, thick-walled, straight to flexuous, base bulbous, 6–8 µm diam, 3–4-septate, intermingled among sterile setae, similar in morphology but with obtuse apical cells, 50–100 × 4–5 µm. *Conidiogenous cells* terminal, intercalary, subcylindrical, pale brown, smooth, with apical monophialides, 35–45 µm long, with flared collarettes, 3–4 µm diam. *Conidia* solitary, aggregating in mucoid mass, subcylindrical, hyaline, smooth, guttulate, apex obtuse, tapering to truncate hilum, 1.5–2 µm diam, 3-septate, (12–)13–14(–15) × (3.5–)4 µm.

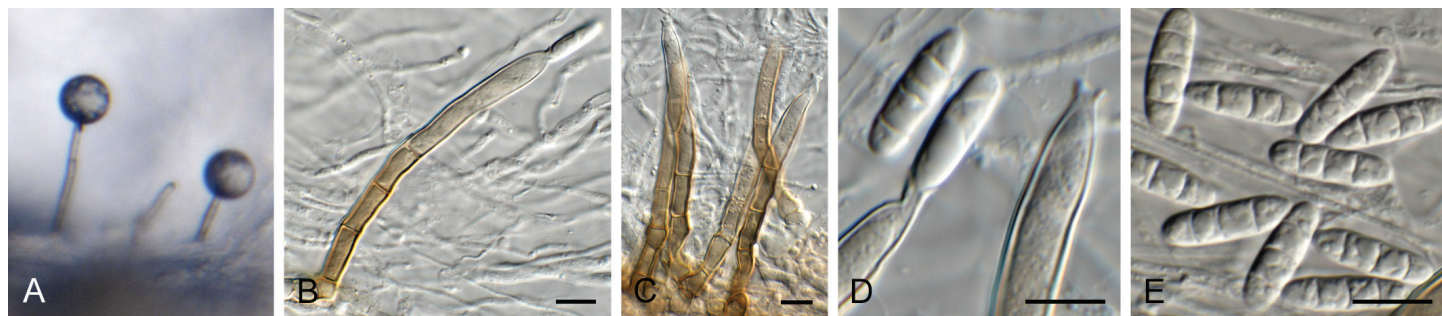
**Culture characteristics:** Colonies flat, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 25 mm diam after 2 wk at 25 °C. On MEA surface and reverse smoke grey; on PDA surface pale smoke grey, reverse pale smoke grey with dirty white margin; on OA surface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

**Material examined:** **Netherlands**, Utrecht Province, Nieuw Wulven, near Houten, 52°02'44"N, 5°09'40"E, 1.5 m a.s.l., on dead culm of *Juncus inflexus* (*Juncaceae*), 4 Feb. 2021, E.R. Osieck, HPC 3590 = WI-21/#4205 (**holotype** CBS H-24828, culture ex-type CPC 41226 = CBS 148282).

**Notes:** Réblová et al. (2011) reduced *Cylindrotrichum hennebertii* (CBS 570.76) to synonymy under *Reticulascus tulasneorum* (asexual morph *C. oligospermum*) (ex-type strain CBS 101319). *Cylindrotrichum hennebertii* was described as having conidia that are variable in size, 0–3-septate, 7–13 × 2–3 µm, and lacking sterile setae *in vivo* (Gams & Holubová-Jechová 1976). *Reticulascus parahennebertii* is distinct in having slightly wider conidia and sterile setae, which also resolves it as a distinct species of *Reticulascus* (Fig. 7).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to "*Cylindrotrichum* sp." [strain 1552, GenBank AM262411.1; Identities = 451/452 (99 %), no gaps], *Blastophorum aquaticum* [strain MFLUCC 15-0264, GenBank NR\_153629.1; Identities = 487/548 (89 %), 14 gaps (2 %)], and *Cylindrotrichum submersum* [voucher MFLU 18-2320, GenBank





**Fig. 60.** *Reticulascus parahennebertii* (CPC 41226). **A.** Conidiophores on SNA. **B–D.** Conidiophores and conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars = 10  $\mu$ m.

NR\_168818.1; Identities = 481/541 (89%), 10 gaps (1%)). Closest hits using the **LSU** sequence are *Reticulascus tulasneorum* [strain CBS 101319, GenBank AF178547.2; Identities = 790/805 (98%), two gaps (0%)], *Cylindrotrichum submersum* [voucher MFLU 18-2320, GenBank NG\_068641.1; Identities = 758/776 (98%), two gaps (0%)], and *Chaetopsis grisea* [strain CBS 100.57, GenBank MH869199.1; Identities = 790/810 (98%), seven gaps (0%)]. Closest hits using the **tef1** (second part) sequence had highest similarity to *Leptosillia pistaciae* [strain ISPaVe 1958, GenBank MK523320.1; Identities = 801/888 (90%), two gaps (0%)], *Cylindrotrichum submersum* [voucher MFLU 18-2320, GenBank MN200280.1; Identities = 741/823 (90%), two gaps (0%)], and *Leptosillia macrospora* [strain CRM2, GenBank MK523314.1; Identities = 794/888 (89%), two gaps (0%)].

**Authors:** P.W. Crous, J.Z. Groenewald & E.R. Osieck

***Rhexocercosporidium bellocense*** (C. Massal. & Sacc.) Crous, J. Kruse & U. Braun, **comb. nov.** MycoBank MB 844313. Fig. 61. **Basionym:** *Septocylindrium bellocense* C. Massal. & Sacc., *Annls mycol.* **6:** 558. 1908.

**Synonym:** *Thedongia bellocensis* (C. Massal. & Sacc.) U. Braun, *Nova Hedwigia* **54**(3–4): 471. 1992.

**Taxonomic lineage:** Leotiomyces, Helotiales, Ploettnerulaceae.

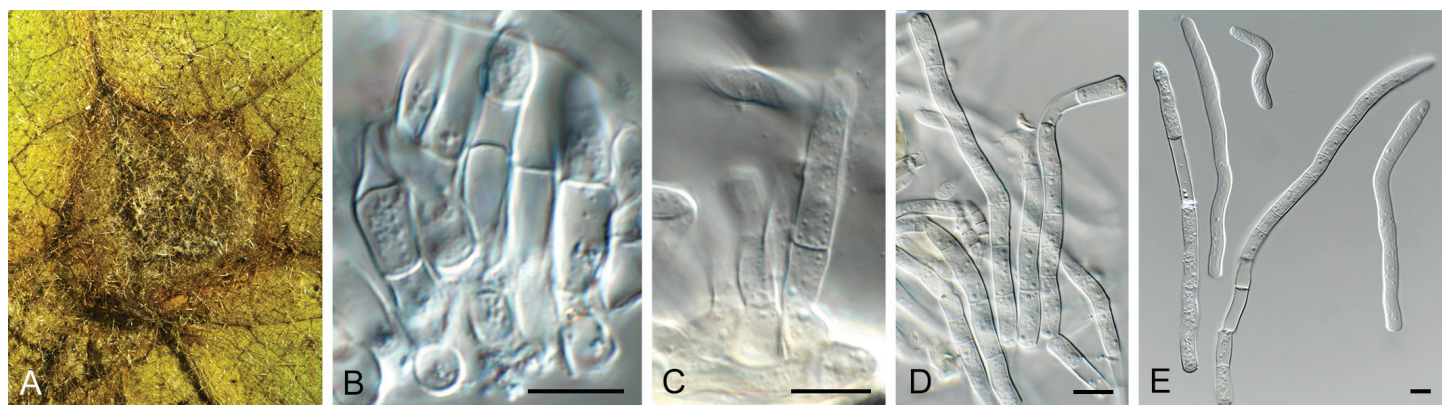
**Leaf spots** variable, subcircular, amphigenous, pale to medium brown, 2–10 mm diam, margin dark brown, diffuse. **Conidiomata** fasciculate, predominantly epiphyllous, whitish on leaf surface. **Conidiophores** arising from poorly developed

brownish stroma, in dense fascicles, 20–60  $\times$  3–6  $\mu$ m, straight to geniculate-sinuous, subcylindrical, 1–2-septate, subhyaline. **Conidiogenous cells** terminal, integrated, holothallic, rarely sympodial, scars unthickened, 7–20  $\times$  3–4  $\mu$ m; conidiogenous cells difficult to discern from conidia. **Conidia** in disarticulating chains, cylindrical, apex obtuse, base truncate, (20–)50–100(–160)  $\times$  3.5–6  $\mu$ m, hyaline, smooth, 3–6(–10)-septate; hila not thickened nor darkened.

**Culture characteristics:** Cultures sterile. Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 20 mm diam after 7 d at 25  $^{\circ}$ C. On MEA surface and reverse olivaceous grey; on PDA surface olivaceous grey, reverse iron grey; on OA surface iron grey.

**Typus:** **Italy**, Verona, M. Bellocca, on *Verbascum nigrum* (*Scrophulariaceae*), 1908, *Massalongo* (**holotype** VER). **Germany**, Rhineland-Palatinate, Bad Kreuznach, 49 $^{\circ}$ 48'13"N, 7 $^{\circ}$ 44'8"E, on leaves of *Verbascum cf. densiflorum*, 14 Jun. 2020, J. Kruse, HPC 3451 (**epitype** designated here, CBS H-24836, MBT 10007419; isoeotype POLL 9787; culture ex-epitype CPC 39764 = CBS 148297).

**Notes:** *Septocylindrium bellocense* was described from leaves of *Verbascum nigrum* collected in Italy, for which the present collection from Germany is an appropriate specimen to serve for epitypification. Braun (1995) noted conidia to be catenate, (20–)30–130(–200)  $\times$  3–7  $\mu$ m, 3–20-septate, sometimes even more, and occurring on different *Verbascum* spp. in Europe. Because *S. bellocense* has hyaline conidia occurring in chains, Braun (1992) placed it in *Thedongia*. However, it is not congeneric with the



**Fig. 61.** *Rhexocercosporidium bellocense* (CPC 39764). **A.** Leaf spot on *Verbascum cf. densiflorum*. **B–D.** Conidiophores and conidiogenous cells giving rise to conidia. **E.** Conidia in disarticulating chains. Scale bars = 10  $\mu$ m.



type of *Theclonia* (*T. ligustrina*; *Leotiomyces*), but clusters with *Rhexocerosporidium carotae*, the type of *Rhexocerosporidium* (Fig. 4). The latter genus was introduced to accommodate *Arothecium carotae*, a pathogen of carrots, characterised by hyaline to subhyaline, solitary conidia. As shown here, however, species of *Rhexocerosporidium* can also have conidia arranged in chains.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Rhexocerosporidium carotae* [strain Rc1-18Dc, GenBank MN594496.1; Identities = 467/486 (96 %), no gaps], *Phialophora cinerescens* [strain CBS 280.35, GenBank MH855676.1; Identities = 475/497 (96 %), no gaps], and *Polyscytalum pustulans* [strain PP3, GenBank EU196535.1; Identities = 474/498 (95 %), no gaps]. Closest hits using the **LSU** sequence are *Rhexocerosporidium panacis* [strain C22-K9, GenBank MN385763.1; Identities = 758/764 (99 %), no gaps], *Cadophora constrictospora* [strain P2414, GenBank MN339394.1; Identities = 757/764 (99 %), no gaps], and *Cadophora luteo-olivacea* [strain P2092, GenBank MN339390.1; Identities = 757/764 (99 %), no gaps]. Closest hits using the **rpb2** sequence had highest similarity to *Cadophora cf. interclivum* [strain P6081, GenBank MN367269.1; Identities = 531/583 (91%), no gaps], *Rhexocerosporidium panacis* [strain C22-K9, GenBank MN787159.1; Identities = 770/852 (90 %), no gaps], and *Rhexocerosporidium carotae* [strain C22-K8, GenBank MN787158.1; Identities = 770/852 (90 %), no gaps].

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

***Rhexocerosporidium* aff. *bellocense*.** Fig. 62.

**Taxonomic lineage:** *Leotiomyces*, *Helotiales*, *Ploettnerulaceae*.

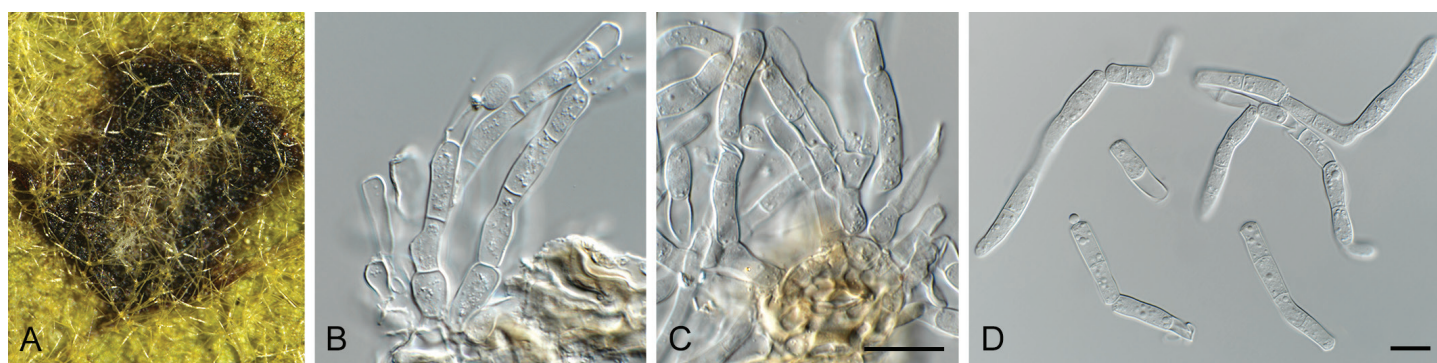
**Leaf spots** amphigenous, subcircular, 2–5 mm diam, dark purple, with indistinct border. **Conidiomata** fasciculate, amphigenous, predominantly whitish on leaf surface. **Conidiophores** arising from stomata that are erumpent, pale brown, up to 60 µm diam; conidiophores subcylindrical, straight to geniculate-sinuous, 1–4-septate, hyaline, 12–50 × 6–7 µm. **Conidiogenous cells** terminal, integrated, with flat, unthickened scars, 12–25 × 5–6 µm. **Conidia** solitary in disarticulating chains, cylindrical, straight to curved, apex obtuse, base truncate, (20–)70–100(–160) × 5(–6) µm, hyaline, smooth, 1–11-septate; hilum unthickened, nor darkened.

**Culture characteristics:** Cultures sterile. Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 17 mm diam after 7 d at 25 °C. On MEA, PDA and OA surface dirty white and reverse olivaceous grey.

**Material examined:** **Russia**, Rostov region, Krasnosulinsky district, state natural wildlife area "Gornensky", disturbed steppe near road, on leaves of *Verbascum* sp. (*Scrophulariaceae*), 13 Jun. 2020, *T.S. Bulgakov*, HPC 3414 = PC 032 = CBS H-24791 = LE F-332411, culture CPC 39690 = CBS 148246.

**Notes:** The Russian collection of *Rhexocerosporidium* aff. *bellocense* is morphologically similar to *R. bellocense*, but differs in having somewhat wider conidiophores, and shorter and wider conidia compared to the description of *R. bellocense* in Braun (1995), which was based on measurements of a number of collections on *Verbascum* spp. in Europe [conidiophores 20–60 × 3–6 µm, conidia (20–)30–130(–200) × 3–7 µm, 3–20-septate]. The Russian collection might well fall into the variability of *R. bellocense*, above all, since the two species are genetically highly similar (based on a comparison with CPC 39764; ITS: 831/844 bp, LSU: 762/764 bp, *rpb2*: 873/874 bp, respectively similar; Fig. 4), but cryptic speciation can also not be excluded with certainty. However, a final conclusion is not yet possible, based on a single specimen and culture.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Rhexocerosporidium carotae* [strain Rc2-18Dc, GenBank MN594497.1; Identities = 546/574 (95 %), two gaps (0 %)], *Phialophora cinerescens* [strain CBS 280.35, GenBank MH855676.1; Identities = 557/586 (95 %), two gaps (0 %)], and *Cadophora luteo-olivacea* [strain STAF242, GenBank KU214556.1; Identities = 554/584 (95 %), one gap (0 %)]. Closest hits using the **LSU** sequence are *Rhexocerosporidium panacis* [strain C22-K9, GenBank MN385763.1; Identities = 814/818 (99 %), no gaps], *Cadophora luteo-olivacea* [strain CBS 128572, GenBank MH878015.1; Identities = 813/818 (99 %), no gaps], and *Cadophora malorum* [strain CBS 117865, GenBank MH874580.1; Identities = 813/818 (99 %), no gaps]. Closest hits using the **rpb2** sequence had highest similarity to *Cadophora cf. interclivum* [strain P6081, GenBank MN367269.1; Identities = 531/583 (91 %), no gaps], *Cadophora cf. meredithiae* [strain P1313, GenBank MN367229.1; Identities = 552/612 (90 %), no gaps], and *Rhexocerosporidium panacis* [strain C22-K9, GenBank MN787159.1; Identities = 772/856 (90 %), no gaps]. Closest hits



**Fig. 62.** *Rhexocerosporidium* aff. *bellocensis* (CPC 39690). **A.** Leaf spot on *Verbascum* sp. **B, C.** Conidiophores and conidiogenous cells giving rise to conidia. **D.** Conidia in disarticulating chains. Scale bars = 10 µm.



using the *tub2* sequence had highest similarity to *Pyrenopeziza brassicae* [strain PbFr002, GenBank KC342227.1; Identities = 432/505 (86 %), 14 gaps (2 %)], *Cadophora meredithiae* [strain BAG2, GenBank MF677914.1; Identities = 421/493 (85 %), 18 gaps (3 %)], and *Rhexocercosporidium panacis* [strain RP17, GenBank MT822282.1; Identities = 383/450 (85 %), seven gaps (1 %)].

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

***Rhopoglyphus filicinus*** (Fr.) Nitschke ex Fuckel, *Jb. nassau. Ver. Naturk.* **23–24**: 219. 1870 (1869–1870). Fig. 63.

*Basionym*: *Sphaeria filicina* Fr., *Syst. Mycol.* (Lundae) **2**: 427. 1823 [replaced synonym *Sphaeria pteridis* Sowerby, *Col. Fig. Engl. Fung. Mushr.* (London) **3**(no. 27): tab. 394, fig. 10. 1803, designated as **lectotype** here, MBT 10007421].

*Taxonomic lineage*: Dothideomycetes, Pleosporales, Didymellaceae.

*Stromata* linear, subepidermal, black, glossy, 0.5–3 mm diam wide, 1 mm to several cm long, becoming confluent, forming conspicuous crusts on dead petioles. *Ascomata* immersed in linear rows in stroma, opening via linear split with periphyses at apex, globose, 120–220 µm diam, wall of 8–15 layers of medium brown *textura angularis* to *textura globulosa*. *Pseudoparaphyses* intermingled among asci, hyaline, branched, septate, anastomosing, 2–3 µm diam, constricted at septa, hyphae-like. *Asci* bitunicate, 8-spored straight to slightly curved, subcylindrical to narrowly cymbiform, apex obtuse, apical chamber 1.5–2 µm diam, pedicellate, 70–95 × 15–18 µm. *Ascospores* tri- to multiseriate, golden brown, smooth, granular, fusoid-ellipsoid with obtuse ends, straight to slightly curved, initially 3-septate, constricted at medium septum, swollen in cell

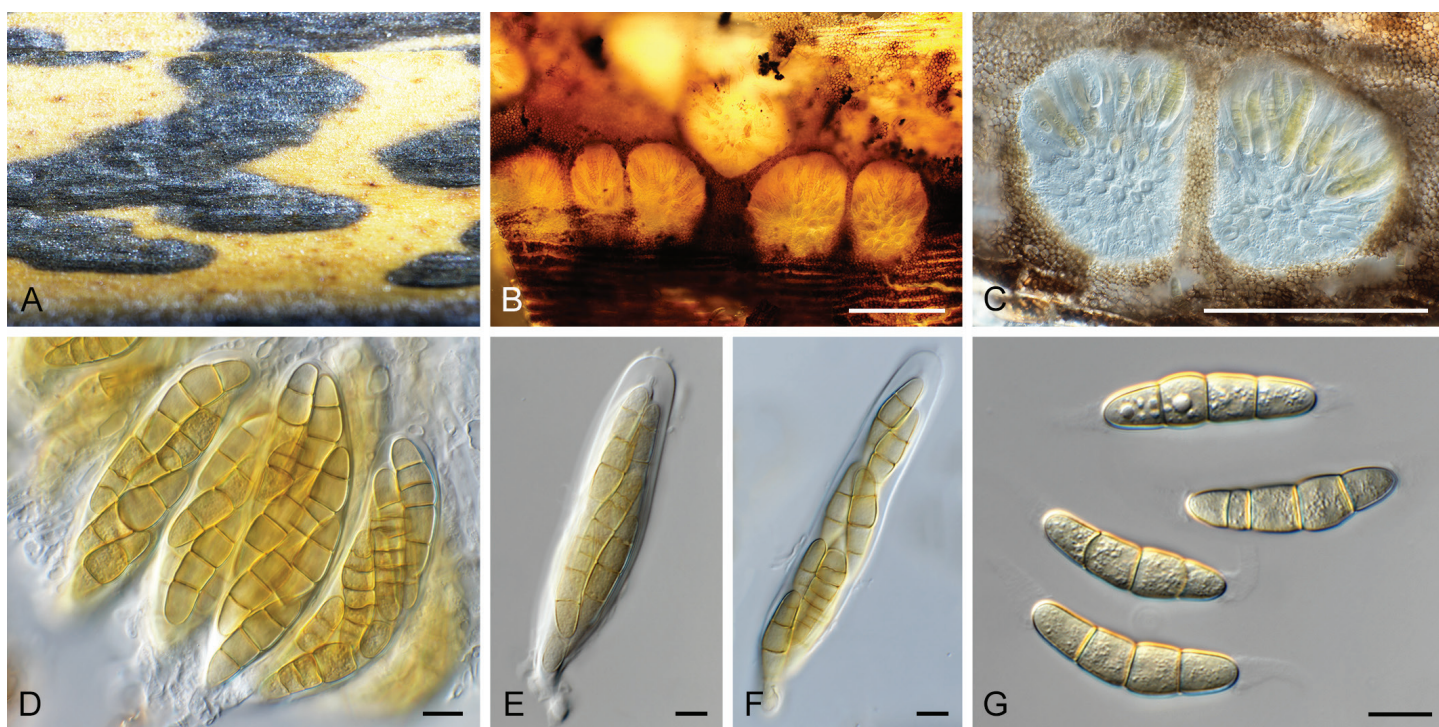
above medium septum, 3(–7)-septate, septa darker brown, with mucoid appendages at both ends, up to 15 µm long, (26–)28–33(–36) × (6–)7–8(–9) µm.

*Typus*: Netherlands, Utrecht Province, Bilthoven, on dead leaf fronds of *Pteridium aquilinum* (*Hypolepidaceae*), Jun. 2021, P.W. Crous, HPC 3632 (**epitype** designated here CBS H-24998, MBT 10007422, culture ex-epitype CPC 41596, 41597 = CBS 149224).

*Additional material examined*: Netherlands, Utrecht Province, Lage Vuursche, on stem of *Pteridium aquilinum*, 13 Jun. 2021, P.W. Crous, HPC 3645, cultures CPC 41925, 41926.

*Notes*: *Rhopoglyphus filicinus* is the type species of the genus *Rhopoglyphus*, which has to date had an unresolved higher phylogeny, being a member of *Dothideomycetes* (*Didymellaceae*, *Pleosporales*; Fig. 2). *Rhopoglyphus filicinus* causes black, raised mosaic lesions on stems of *Pteridium aquilinum*, and is common in the Netherlands, and probably also elsewhere in Europe.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 41596 had highest similarity to *Rhopoglyphus filicinus* [strain CBS 384.59, GenBank MH857898.1; Identities = 514/514 (100 %), no gaps], *Phoma herbarum* [strain CBS 368.61, GenBank MH858087.1; Identities = 483/518 (93 %), eight gaps (1 %)], and *Ascochyta orobi* [strain CBS 105.30, GenBank MH855088.1; Identities = 483/518 (93 %), eight gaps (1 %)]. The ITS sequences of CPC 41596 and 41925 are identical. Closest hits using the **LSU** sequence of CPC 41596 are *Didymella rumicicola* [strain CBS 683.79, GenBank NG\_069775.1; Identities = 794/805 (99 %), no gaps], *Didymella macrophylla* [strain CGMCC 3.18357, GenBank NG\_069441.1; Identities = 793/805 (99 %), no gaps], and *Didymella aquatica* [strain CGMCC 3.18349, GenBank NG\_069439.1; Identities = 793/805 (99 %), no gaps]. The LSU sequences of CPC 41596 and



**Fig. 63.** *Rhopoglyphus filicinus* (CPC 41597). **A.** Erumpent stroma with ascomata. **B, C.** Section through stroma, showing ascomatal cavities. **D–F.** Asci. **G.** Ascospores. Scale bars: B, C = 200 µm, all others = 10 µm.

41925 are identical to each other and also to the LSU sequence of CBS 384.59 generated in this study. Closest hits using the *actA* sequence of CPC 41596 had distant similarity to species in *Didymellaceae*, e.g. *Boeremia exigua* var. *pseudolilacis* [strain CPC 25089, GenBank KT193804.1; Identities = 552/630 (88 %), 16 gaps (2 %)], *Ascochyta rabiei* [as *Didymella rabiei*; strain AR628, GenBank KM244530.1; Identities = 551/629 (88 %), 16 gaps (2 %)], and *Calophoma sandffordenica* [strain CBS 145571, GenBank MK876453.1; Identities = 553/630 (88 %), 16 gaps (2 %)]. The *actA* sequences of CPC 41596 and 41925 are identical. No significant hits were obtained when the *rpb2* sequence of CPC 41596 was used in blastn and megablast searches.

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***Russula lilacina*** (A.H. Sm.) Trappe & T.F. Elliott, *comb. nov.* MycoBank MB 821382.

**Basionym:** *Macowanites lilacinus* A.H. Sm., *Mycologia* **55**: 426. 1963.

**Taxonomic lineage:** Agaricomycetes, Agaricales, Russulaceae.

**Description and illustration:** Smith (1963).

**Notes:** In light of efforts to resolve the nomenclatural issues surrounding sequestrate generic names in the *Russulaceae*, Elliott & Trappe (2018a, b) combined all members of *Bucholtzia*, *Cystangium*, *Elasmomyces*, *Gymnomyces*, *Macowanites*, and *Martellia* with the traditionally agaricoid genus *Russula*. However, *Macowanites lilacinus* was overlooked. We here combine the last remaining member of the genus *Macowanites* with *Russula* and name it: *Russula lilacina* (A.H. Smith) Trappe & T.F. Elliott. To see the justification for this combination, please review Elliott & Trappe (2018a).

**Authors:** T.F. Elliott & J.M. Trappe

***Scytalidium philadelphianum*** Crous & Jurjević, *sp. nov.* MycoBank MB 844315. Fig. 64.

**Taxonomic lineage:** Leotiomyces, Helotiales, Helotiaceae.

**Etymology:** Name refers to the location where it was isolated, Philadelphia, Pennsylvania.

*Mycelium* consisting of hyaline, smooth-walled, branched, septate, 2–2.5 µm diam hyphae. *Conidiophores* erect, solitary, subcylindrical, straight to flexuous, unbranched, 1–2-septate, 10–30 × 2.5–4 µm. *Conidiogenous cells* integrated, terminal, subcylindrical, hyaline, smooth, 10–15 × 3–4 µm, holoblastic, proliferating sympodially at apex, which is slightly swollen; scars inconspicuous, truncate, 2–3 µm diam. *Conidia* occurring in long disarticulating conidial chains, hyaline, smooth-walled, guttulate, subcylindrical, not constricted at septa, segments 3–6 × (2–)2.5–3 µm. *Chlamydozoospores* dark brown, globose to ellipsoid, 0–1-septate, 4–6 µm diam, thick-walled, smooth to roughened, intercalary to terminal, in terminal, frequently adjacent to erect conidiophores.

**Culture characteristics:** Colonies flat, spreading, with abundant aerial mycelium, covering dish after 7 d at 25 °C. On MEA, CYA (Czapek yeast agar), PDA and OA surface and reverse iron grey. On CYA covering dish after 7 d at 37 °C.

**Typus:** USA, Pennsylvania, Philadelphia, from compressed air in a factory, Oct. 2020, Ž. Jurjević 5560 (**holotype** CBS H-24808, culture ex-type CPC 40793 = CBS 148262).

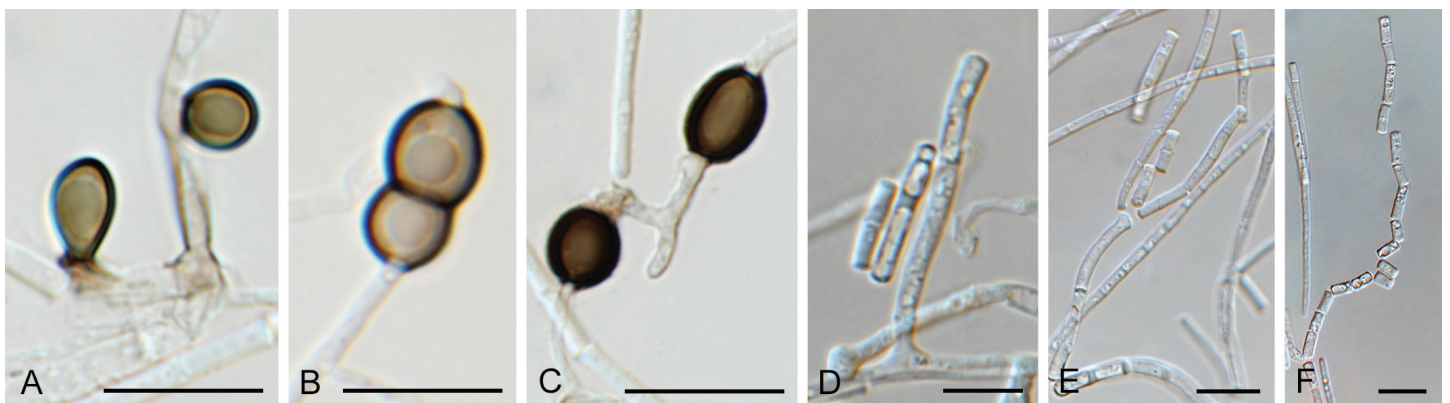
**Notes:** *Scytalidium philadelphianum* is congeneric to *S. lignicola*, but clusters distinct from the ex-type isolate CBS 233.57 = UAMH 1502 (Fig. 65). Morphologically it is similar, but distinct in that it has wider conidia and 0–1-septate, narrower chlamydozoospores (arthroconidia 5–8 × 2 µm, chlamydozoospores up to 7 µm wide; Pesante 1957).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Scytalidium lignicola* [strain UAMH 1502, GenBank NR\_121314.1; Identities = 548/581 (94 %), 16 gaps (2 %)], *Scytalidium cuboideum* [as *Arthrographis cuboidea*; GenBank AY557369.1; Identities = 483/544 (89 %), 25 gaps (4 %)], and *Trichoderma afroharzianum* [voucher research collection Farrer lab 122, GenBank MN644645.1; Identities = 526/596 (88 %), 39 gaps (6 %)].

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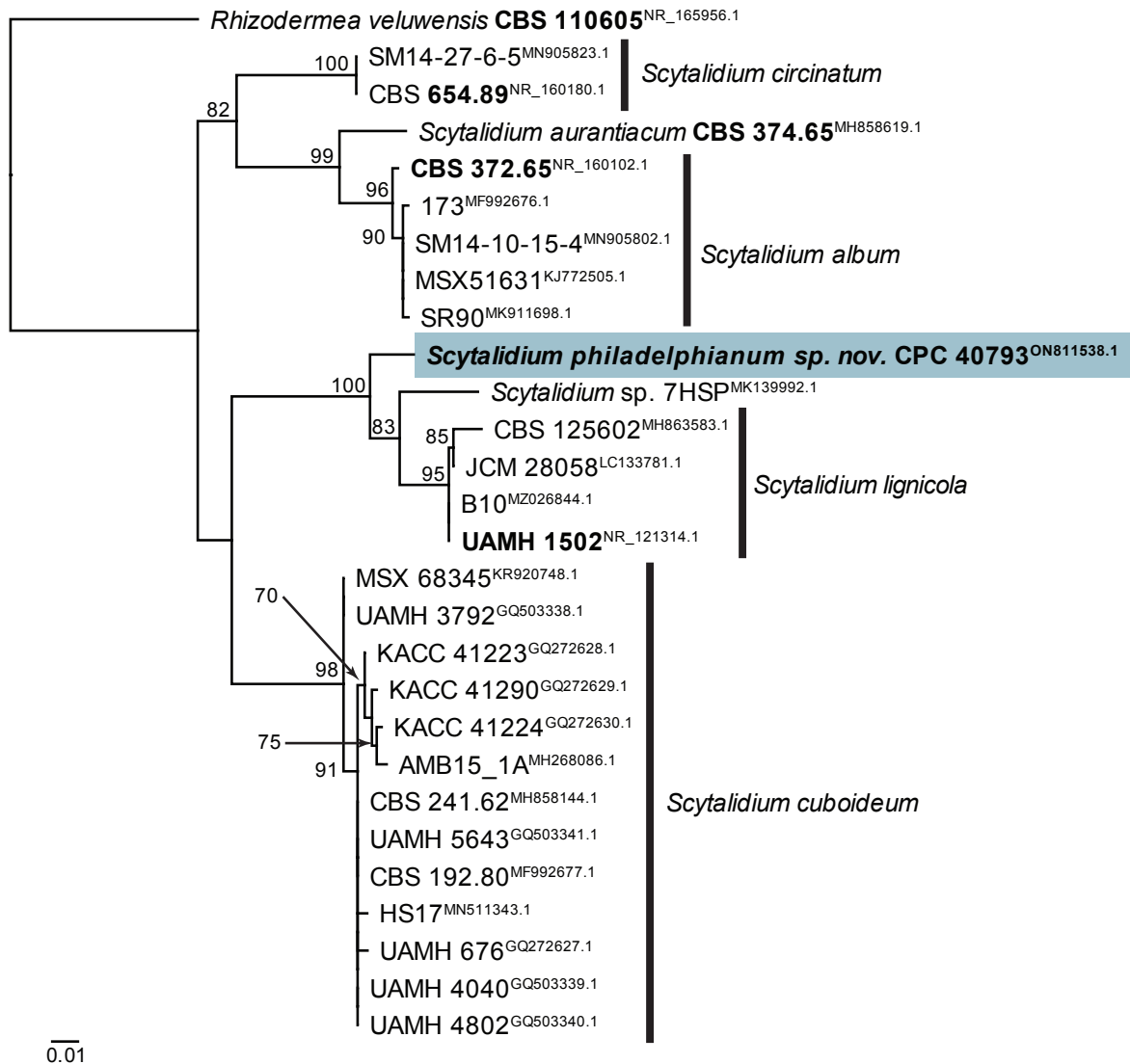
***Septoria chelidonii*** (Lib.) Desm., *Annls Sci. Nat., Bot., sér. 2* **17**: 110. 1842. Fig. 66.

**Basionym:** *Ascochyta chelidonii* Lib., *Pl. crypt. Arduenna, fasc. (Liège)* **3**(nos 201–300): no. 204. 1834.



**Fig. 64.** *Scytalidium philadelphianum* (CPC 40793). **A–C.** Chlamydozoospores. **D–F.** Conidial chains. Scale bars = 10 µm.





**Fig. 65.** Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh *et al.* 2020) of the *Scytalidium* ITS nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast bootstrap replicates are shown at the nodes. Culture collection numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Rhizodermea veluwensis* (culture CBS 110605; GenBank NR\_165956.1) and the species treated here is highlighted with bold face. Accession numbers of sequence from material with a type status are also shown in bold face.

*Synonym:* *Spilosphaeria chelidonii* (Lib.) Rabenh., *Klotzschii* Herb. *Viv. Mycol., Edn Nov, Ser. Sec., Cent.* 6: no. 552. 1857.

*Taxonomic lineage:* Dothideomycetes, Mycosphaerellales, Mycosphaerellaceae.

*Leaf spots* amphigenous, angular, elongated, 2–4 mm diam, medium brown with raised, dark brown border. *Conidiomata* pycnidial, brown, erumpent, 200–250 µm diam, opening by central ostiole; wall of 2–3 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells or with a supporting cell, branched or not, 7–15 × 3–4 µm, hyaline, smooth. *Conidiogenous cells* terminal or lateral, ampulliform, hyaline, smooth, proliferating percurrently near apex, 7–10 × 3–4 µm. *Conidia* solitary, hyaline, smooth, guttulate, subcylindrical, straight to slightly curved, apex subobtuse, base truncate, (1–)3-septate, (21–)26–29(–35) × 2(–2.5) µm.

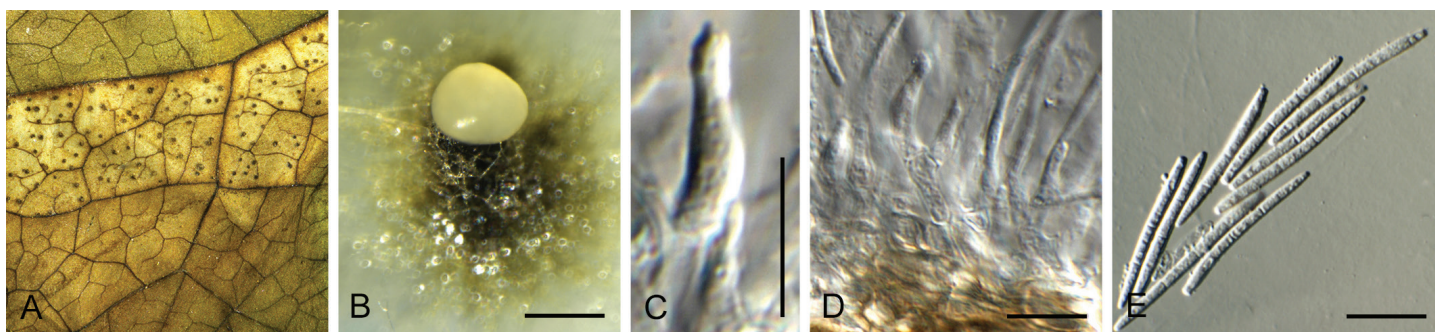
*Culture characteristics:* Colonies flat, spreading, with moderate aerial mycelium and feathery, lobate margin, reaching 15 mm

diam after 7 d at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

*Material examined:* **Russia**, Rostov region, Krasnosulinsky district, state natural wildlife area “Gornensky”, roadside of artificial forest road, on *Chelidonium majus* (*Papaveraceae*), 10 Jul. 2020, T.S. Bulgakov, HPC 3326 = CBS H-24898 = PC-010 = LE F-332406, culture CPC 39746 = CBS 148456.

*Notes:* *Septoria chelidonii* (*Mycosphaerellaceae*, *Mycosphaerellales*; Figs 1 part 2, 13 part 1) is a well-known pathogen of *Chelidonium* spp. (Verkley *et al.* 2013), and has previously been reported from Russia (Mel’nik *et al.* 2008).

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Septoria chelidonii* [strain CBS 132027, GenBank GU269860.1; Identities = 493/493 (100 %), no gaps], *Septoria cerastii* [strain CBS 128626, GenBank MH865054.1; Identities = 506/510 (99 %), no gaps], *Septoria sigesbeckiae* [strain CBS 128661, GenBank MH865108.1; Identities = 529/534 (99 %),



**Fig. 66.** *Septoria chelidonii* (CPC 39746). **A.** Leaf spot with conidiomata. **B.** Conidioma on OA. **C, D.** Conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars: B = 250 µm, all others = 10 µm.

no gaps], and *Septoria perillae* [strain CBS 128655, GenBank MH865103.1; Identities = 529/534 (99 %), no gaps]. Closest hits using the **LSU** sequence are *Septoria senecionis* [strain CBS 102381, GenBank NG\_069162.1; Identities = 802/803 (99 %), no gaps], *Septoria galeopsidis* [strain CBS 102411, GenBank NG\_069160.1; Identities = 802/803 (99 %), no gaps], and *Septoria epilobii* [strain CBS 109085, GenBank NG\_069159.1; Identities = 802/803 (99 %), no gaps]. Closest hits using the **actA** sequence had highest similarity to *Septoria chelidonii* [strain CBS 128607, GenBank KF253676.1; Identities = 214/214 (100 %), no gaps], *Septoria gaurina* [strain QD-3, GenBank MW187076.1; Identities = 558/566 (99 %), no gaps], *Septoria cerastii* [strain CBS 132028, GenBank JQ325030.1; Identities = 546/556 (98 %), four gaps (0 %)], and *Septoria melissae* [voucher KACC47728, GenBank MH359403.1; Identities = 573/586 (98 %), one gap (0 %)]. Closest hits using the **tef1** (first part) sequence had highest similarity to *Septoria chelidonii* [strain CBS 128607, GenBank KF253319.1; Identities = 330/331 (99 %), no gaps], *Septoria gaurina* [strain QD-3, GenBank MW187078.1; Identities = 326/333 (98 %), two gaps (0 %)], and *Septoria agrimoniicola* [strain CBS 128585, GenBank KF253283.1; Identities = 325/333 (98 %), two gaps (0 %)].

**Authors:** P.W. Crous & J.Z. Groenewald

***Septoria robiniae*** (Lib.) Desm., *Anns Sci. Nat., Bot.*, sér. 3 **11**: 349. 1849. Fig. 67.

**Basionym.** *Ascochyta robiniae* Lib., *Pl. crypt. Arduenna*, fasc. (Liège) 4(nos 301–400): no. 357. 1837.

**Synonyms.** *Phloeospora robiniae* (Lib.) Höhn., *Anns mycol.* **3**: 333. 1905.

*Cylindrosporium robiniae* (Lib.) Died., *Krypt.-Fl. Brandenburg* (Leipzig) **9**: 846. 1915.

**Taxonomic lineage:** *Dothideomycetes*, *Mycosphaerellales*, *Mycosphaerellaceae*.

**Leaf spots** amphigenous, medium brown, with diffuse chlorotic borders, 5–10 mm diam. **Conidiomata** amphigenous, acervular, 50–120 µm diam, immersed in epidermis, giving rise to a pale creamy conidial cirrhous; wall of 3–4 layers of pale brown *textura angularis*. **Conidiophores** reduced to conidiogenous cells, hyaline to pale brown, smooth-walled, ampulliform to subcylindrical, 6–12 × 5–7 µm, proliferating inconspicuously percurrently at apex. **Conidia** solitary, hyaline, smooth-walled, granular to guttulate, straight to curved, subcylindrical to acicular, apex subobtuse, base truncate to long obconically truncate, hilum with minute marginal frill, 1–2(–3)-septate, *in vivo* (36–)45–55(–

66) × (3–)4(–4.5) µm, *in vitro* 65–90 × 3(–3.5) µm. The isotype (BR-MYCO 147039-84) had *leaf spots* that were amphigenous, subcircular to irregular, medium brown with diffuse margins, 4–8 mm diam. **Conidiomata** were similar to that of the epitype. **Conidiogenous cells** 7–10 × 3.5–5 µm, and **conidia** subcylindrical to acicular, 1–2(–3)-septate, (28–)38–55(–60) × (3–)3.5–4 µm.

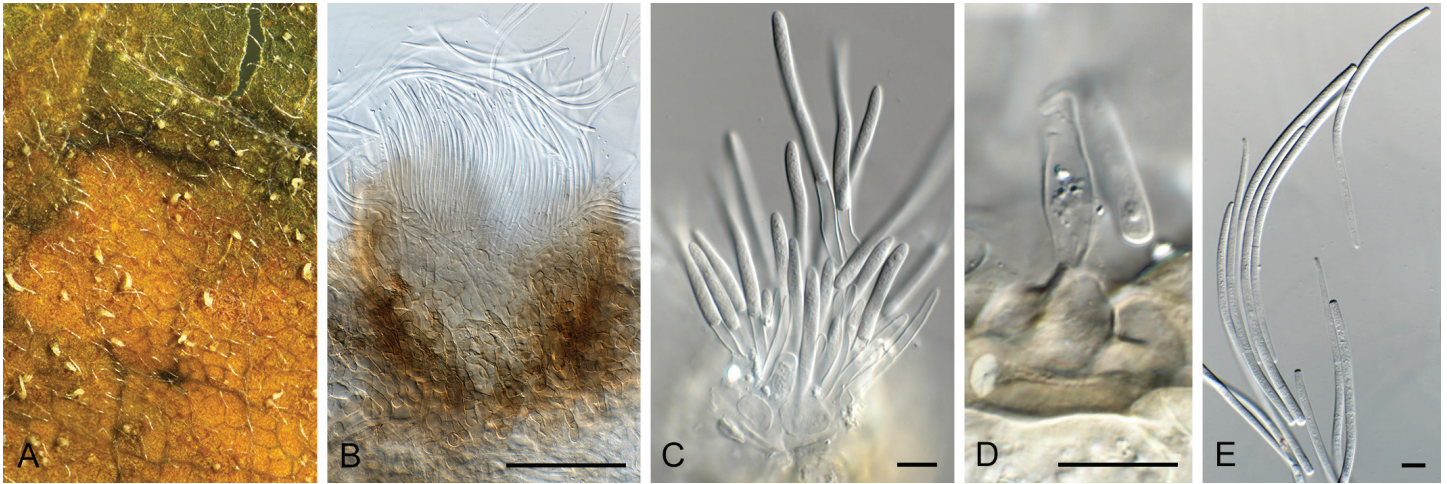
**Culture characteristics:** Colonies erumpent, with sparse aerial mycelium and feathery, lobate margin, reaching 5 mm diam after 7 d at 25 °C. On MEA surface and reverse umber; on PDA surface and reverse olivaceous grey; on OA surface olivaceous grey.

**Typus:** **Belgium**, on leaves of *Robinia pseudoacacia* (*Fabaceae*), exsiccata M.A. Libert – Pl. Crypt. Arduenna fasc. (Liège) 4: 357 (1837), designated here as **lectotype**, BR-MYCO 147039-84, MBT 10007424; Limburg, Heusden-Zolder, on leaves of *R. pseudoacacia*, 22 Jul. 2020, C. Van Steenwinkel, HPC 3454 (**epitype** designated here CBS H-24839, MBT 10007425; culture ex-epitype CPC 39783 = CBS 148300).

**Notes:** *Septoria robiniae* (as *Phloeospora robiniae*) is an important foliar pathogen of *Robinia pseudoacacia* in Europe, causing leaf necrosis and deformation from early spring onwards (Kehr & Butin 1996). Because this pathogen produces prominent acervuli with erect, creamy conidial cirrhi, it has for long been assumed to be a member of *Phloeospora*. However, Verkley *et al.* (2013) demonstrated that species of *Septoria* could have conidiomatal pycnidia and/or acervuli, thus this feature alone is insufficient to separate members of this complex. The present collection closely matches the morphology of the holotype, and thus it is a good choice for typification to fix the genetic application of the name (*Mycosphaerellaceae*, *Mycosphaerellales*; Figs 1 part 2, 13 part 1).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Septoria apocyni* [strain LB-02, GenBank KR611856.1; Identities = 503/505 (99 %), no gaps], *Septoria pistaciarum* [strain SE, GenBank MZ268218.1; Identities = 513/516 (99 %), no gaps], and *Septoria posoniensis* [strain CBS 128645, GenBank MH865067.1; Identities = 512/516 (99 %), one gap (0 %)]. Closest hits using the **LSU** sequence are *Apeudocercospora trigonotidis* [strain CBS 131890, GenBank NG\_069100.1; Identities = 788/789 (99 %), no gaps], *Septoria scabiosicola* [strain CBS 356.58, GenBank MH869343.1; Identities = 788/789 (99 %), no gaps], and *Septoria stellariae* [strain CBS 102378, GenBank KF252080.1; Identities = 788/789 (99 %), no gaps]. Closest hits using the **actA** sequence had highest similarity to *Septoria protearum* [strain T19\_05709B, GenBank MW890033.1; Identities = 536/580 (92 %), 11 gaps





**Fig. 67.** *Septoria robiniae* (CPC 39783). **A.** Leaf spot with conidiomata. **B.** Conidioma with exuding conidial mass. **C, D.** Conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars: B = 60 µm, all others = 10 µm.

(1 %), *Septoria citri* [strain CBS 315.37, GenBank JX902161.1; Identities = 498/541 (92 %), 11 gaps (2 %)], and *Septoria carvi* [strain KML1860, GenBank KX822110.1; Identities = 485/527 (92 %), four gaps (0 %)]. Closest hits using the *tef1* (first part) sequence had highest similarity to *Septoria rumicum* [strain CBS 503.76, GenBank KF253478.1; Identities = 368/418 (88 %), 18 gaps (4 %)], *Septoria pistaciarum* [strain CPC 23116, GenBank KF442635.1; Identities = 433/514 (84 %), 24 gaps (4 %)], and *Septoria hippocastani* [strain CBS 411.61, GenBank KF253383.1; Identities = 363/417 (87 %), nine gaps (2 %)].

**Authors:** P.W. Crous, J.Z. Groenewald & C. Van Steenwinkel

***Teratosphaeria alcornii*** Crous, *Persoonia* **23**: 114. 2009. Fig. 68. **Basionym:** *Stigmia eucalypti* Alcorn, *Trans. Br. mycol. Soc.* **60**: 151. 1973.

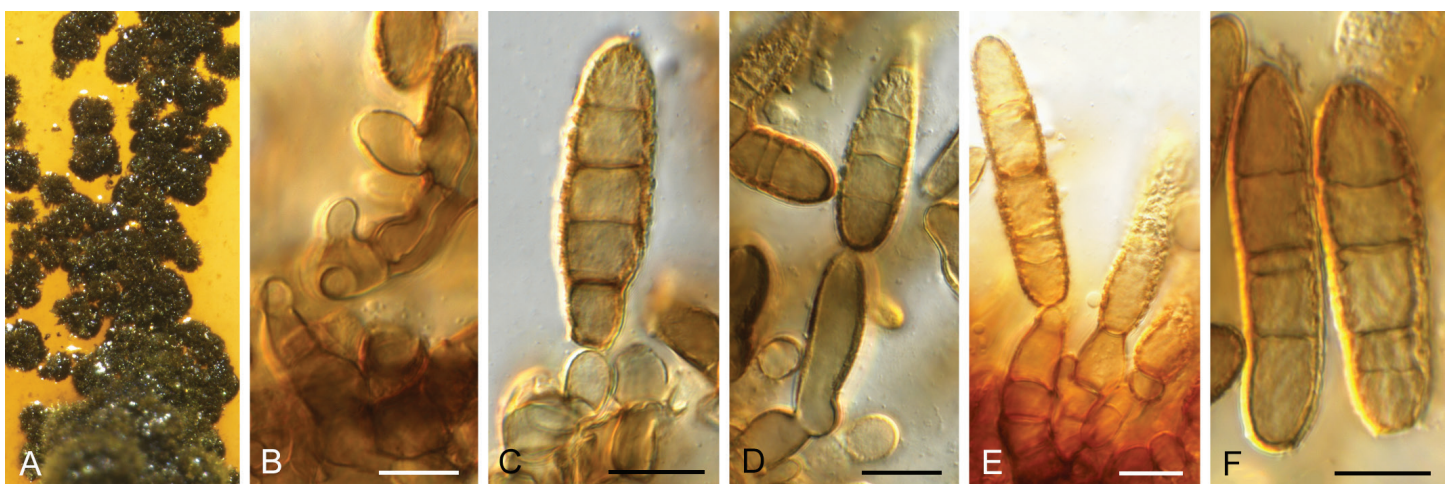
**Taxonomic lineage:** *Dothideomycetes*, *Mycosphaerellales*, *Teratosphaeriaceae*.

**Descriptions and illustrations:** Crous *et al.* (2009, 2019).

**Material examined:** **South Africa**, KwaZulu-Natal Province, Kwambonambi, on leaves of *Corymbia citriodora* (*Myrtaceae*), 9 Jun. 2020, J. Roux, HPC 3448, culture CPC 39789 = CBS 149184.

**Notes:** *Teratosphaeria alcornii* (*Teratosphaeriaceae*, *Mycosphaerellales*; Fig. 1 part 2) is generally considered to be a minor pathogen on commercially propagated eucalypt hosts, although it can cause serious leaf spots on some species in Australia (Crous *et al.* 2009, 2019). This is the first record of *T. alcornii* occurring in South Africa.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Teratosphaeria alcornii* [strain CPC 13384, GenBank EF394866.1; Identities = 477/478 (99 %), no gaps], *Teratosphaeria pseudocryptica* [strain CPC 29430, GenBank MN162082.1; Identities = 477/508 (94 %), 11 gaps (2 %)], and *Teratosphaeria rubida* [strain CBS 124579, GenBank MH863388.1; Identities = 476/507 (94 %), 11 gaps (2 %)]. Closest hits using the **LSU** sequence are *Teratosphaeria alcornii* [strain CBS 313.76, GenBank NG\_066153.1; Identities = 803/803 (100 %), no gaps], *Teratosphaeria complicata* [strain CPC 14535, GenBank GQ852714.1; Identities = 793/801 (99 %), one gap (0 %)], and *Teratosphaeria ovata* [strain CPC 14632, GenBank FJ493218.1; Identities = 793/801 (99 %), one gap (0 %)]. Closest hits using the **actA** sequence had highest similarity to *Teratosphaeria alcornii* [strain CBS 121100, GenBank KF903646.1; Identities = 530/533 (99 %), no gaps], *Teratosphaeria corymbicola* [strain CBS 146047, GenBank MN556788.1; Identities = 517/578 (89 %), 15 gaps (2 %)], and *Teratosphaeria dunnii* [strain CBS



**Fig. 68.** *Teratosphaeria alcornii* (CPC 39789). **A.** Colonies on MEA. **B–E.** Conidiogenous cells giving rise to conidia. **F.** Conidia. Scale bars = 10 µm.

145548, GenBank MK876463.1; Identities = 513/852 (88 %), 15 gaps (2 %)]. Closest hits using the *cmdA* sequence had highest similarity to *Teratosphaeria alcornii* [strain CBS 121100, GenBank KF902698.1; Identities=384/388 (99 %), no gaps], *Teratosphaeria angophorae* [strain CBS 120493, GenBank KF902699.1; Identities = 346/388 (89 %), one gap (0 %)], and *Teratosphaeria fimbriata* [strain CBS 120736, GenBank KF902720.1; Identities = 344/388 (89 %), one gap (0 %)]. Closest hits using the *rpb2* sequence had highest similarity to *Teratosphaeria fimbriata* [strain CPC 13324, GenBank LT799766.1; Identities = 612/671 (91 %), no gaps], *Teratosphaeria cryptica* [strain CBS 111663, GenBank KX348101.1; Identities = 728/845 (86 %), no gaps], and *Teratosphaeria corymbicola* [strain CBS 146047, GenBank MN556802.1; Identities = 727/845 (86 %), no gaps]. Closest hits using the *tub2* sequence had highest similarity to *Teratosphaeria alcornii* [strain CBS 121100, GenBank KF902982.1; Identities = 246/251 (98 %), no gaps], *Teratosphaeria molleriana* [strain CBS 111164, GenBank KF252755.1; Identities = 239/278 (86 %), 15 gaps (5 %)], and *Teratosphaeria consideniana* [strain CBS 120087, GenBank FJ952510.1; Identities = 285/333 (86 %), 13 gaps (3 %)].

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**Supplementary Material:** <http://fuse-journal.org/>

**Table S1.** Statistics for the different phylogenetic analyses performed in this study.



**Table S1**

**Table S1.** Statistics for the different phylogenetic analyses performed in this study.

Analysis <sup>1</sup>	Number of strains (including outgroup)	Total number of characters (including gaps)	IQ-TREE analysis				Bayesian analysis			
			Distinct patterns	Parsimony-informative sites	Singleton sites	Constant sites	Best-fit model <sup>2</sup>	Unique site patterns	Trees sampled	Substitution model <sup>3</sup>
Fig. 1. <i>Dothideomycetes</i> (other orders) - LSU	161	872	478	317	64	491	TN+R4	n/a	n/a	n/a
Fig. 2. <i>Dothideomycetes</i> ( <i>Pleosporales</i> ) - LSU	97	880	267	151	90	639	TIM3e+I+G4	n/a	n/a	n/a
Fig. 3. <i>Eurotiomycetes</i> - LSU	34	958	208	95	129	734	TNe+R3	n/a	n/a	n/a
Fig. 4. <i>Leotiomycetes</i> - LSU	54	831	254	150	72	609	TN+R4	254	125 252 of 167 002	GTR + I + gamma with dirichlet state frequency distribution
Fig. 5. <i>Orbiliomycetes</i> - LSU	34	819	197	151	46	622	TIMe+I+G4	n/a	n/a	n/a
Fig. 6. <i>Sordariomycetes</i> (other orders) - LSU	53	899	320	242	63	594	TIMe+R3	n/a	n/a	n/a
Fig. 7. <i>Sordariomycetes</i> ( <i>Hypocreales</i> & <i>Glomerales</i> ) LSU	39	862	228	142	80	640	TIM3e+R2	n/a	n/a	n/a
Fig. 8. <i>Sordariomycetes</i> ( <i>Xylariales</i> ) - LSU	54	855	218	134	89	632	TIM3e+R3	n/a	n/a	n/a
Fig. 13. <i>Mycosphaerellales</i> & <i>Cladosporiales</i> - LSU/ <i>rpb2</i>	155	1 461	778	631	81	748	GTR+R4 for both loci	n/a	n/a	n/a
Fig. 18. <i>Dactylella/Dactylellina</i> - ITS	42	684	451	275	123	286	TIM2e+I+G4	n/a	n/a	n/a
Fig. 22. <i>Exophiala</i> - ITS	15	629	185	93	70	466	TIM2e+G4	n/a	n/a	n/a
Fig. 24. <i>Teichosporaceae</i> - LSU/ITS/ <i>tef1</i>	57	2 970	1 066	692	226	2 052	TNe+G4 (ITS), TN+R4 and TIM3e+I+G4 (LSU)	n/a	n/a	n/a
Fig. 27. <i>Idriellomyces</i> - ITS	12	579	200	114	56	409	TIM2e+G4	n/a	n/a	n/a
Fig. 32. <i>Microcera</i> - ITS/ <i>rpb1/rpb2/tub2</i>	11	2 812	605	402	351	2 059	TNe+G4 for all loci	n/a	n/a	n/a
Fig. 36. <i>Teratosphaeriaceae</i> - ITS	37	575	293	158	71	345	TIM2e+I+G4	n/a	n/a	n/a
Fig. 39. <i>Niesslia</i> - ITS	32	701	378	202	83	416	TIM2+R4	n/a	n/a	n/a
Fig. 44. <i>Nothotrimmatostroma</i> - ITS	21	565	180	116	50	399	TNe+G4	n/a	n/a	n/a
Fig. 50. <i>Phaeosphaeria</i> - ITS	21	609	279	114	126	369	TIM2+R4	n/a	n/a	n/a
Fig. 65. <i>Scytalidium</i> - ITS	28	630	203	105	50	475	TNe+G4	n/a	n/a	n/a

<sup>1</sup> ITS: internal transcribed spacers and intervening 5.8S nrDNA; LSU: large subunit (28S) of the nrRNA gene operon; *rpb1*: partial DNA-directed RNA polymerase II largest subunit 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.

<sup>2</sup> The best-fit model(s) identified for the alignment in IQ-TREE using the TESTNEW option.

<sup>3</sup> The best-fit model identified according to the Akaike Information Criterion as implemented in MrModeltest.