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New and Interesting Fungi. 6

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Abstract: Three new genera, six new species, three combinations, six epitypes, and 25 interesting new host and / or geographical records are introduced in this study. New genera: *Neoleptodontidium* (based on *Neoleptodontidium aquaticum*), and *Nothoramularia* (based on *Nothoramularia ragnhildianicola*). New species: *Acremonium aquaticum* (from cooling pad water, USA), *Cladophialophora laricicola* (on dead wood of *Larix* sp., Netherlands), *Cyphellophora neerlandica* (on lichen on brick wall, Netherlands), *Geonectria muralis* (on moss growing on a wall, Netherlands), *Harposporium illinoisense* (from rockwool, USA), and *Neoleptodontidium aquaticum* (from hydroponic water, USA). New combinations: *Cyphellophora deltoidea* (based on *Anthopsis deltoidea*), *Neoleptodontidium aciculare* (based on *Leptodontidium aciculare*), and *Nothoramularia ragnhildianicola* (based on *Ramularia ragnhildianicola*). Epitypes: *Cephalophora tropica* (from water, USA), *Miricatena prunicola* (on leaves of *Prunus serotina*, Netherlands), *Nothoramularia ragnhildianicola* (on *Ragnhildiana ferruginea*, parasitic on *Artemisia vulgaris*, Germany), *Phyllosticta multicorniculata* (on needles of *Abietis balsamea*, Canada), *Thyronectria caraganae* (on twigs of *Caragana arborescens*, Ukraine), and *Trichosphaeria pilosa* (on decayed *Salix* branch, Netherlands). Furthermore, the higher order phylogeny of three genera regarded as *incertae sedis* is resolved, namely *Cephalophora* (*Ascodesmidaceae*, *Pezizales*), *Miricatena* (*Helotiales*, *Leotiomycetes*), and *Trichosphaeria* (*Trichosphaeriaceae*, *Trichosphaeriales*), with *Trichosphaeriaceae* being an older name for *Plectosphaerellaceae*.

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INTRODUCTION

Although the *Fungi* are highly diverse and estimated to represent between 2.2 and 3.8 million species, only around 150 000 species have been described to date. *Fungi* are essential for ecosystem processes, and are of economic importance as plant, human or animal pathogens, or as agents for industrial or pharmaceutical

industries (Lücking *et al.* 2021). In spite of their importance, only 2 000–2 500 species of fungi are described annually, illustrating a great challenge to understand and preserve this important biodiversity resource. Resolving this problem relies on increased efforts to collect, preserve and describe novel species (Cheek *et al.* 2020). In order to facilitate the description of novel species, the New and Interesting Fungi (NIF) series is published annually

in the journal *Fungal Systematics and Evolution*. Papers include the description of new species, report new host or geographical records, and new sexual-asexual connections. These and the present study also include validations (typifications) of fungal taxa and list interesting observations relating to fungi and their biology.

MATERIALS AND METHODS

Isolates

Samples (see Table 1) were treated as previously detailed (Crous *et al.* 2019c). 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.* 2019c), 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. The first part of the 28S nrRNA gene (LSU) and complete 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 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 first part of the 18S nrRNA gene (SSU) was amplified as described by Hernández-Restrepo *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 (ML) phylogenetic trees were constructed generated using IQ-TREE v. 2.1.3 (Nguyen *et al.* 2015) and branch support values were calculated with 1 000 non-parametric bootstrap replicates and optimal model-finding using the TESTNEW option using ModelFinder (Kalyaanamoorthy *et al.* 2017) as implemented in IQ-TREE. Bayesian analyses were performed with MrBayes v. 3.2.7a (Ronquist *et al.* 2012) as explained in Braun *et al.* (2018), while RAxML v. 8.0.0.0 (Stamatakis 2014) was used with default parameters to provide additional ML support values for selected trees, while parsimony analyses using PAUP* v. 4.0a build 168 (Swofford *et al.*) were performed as explained in Videira *et al.* (2016). All resulting trees were printed with Geneious Prime v. 2022.0.2 and the layout of the trees was done using Adobe Illustrator 2022 v. 26.3.1. Sequences derived in this study were submitted to GenBank (Table 1) and the alignments and phylogenetic trees in figshare.com (doi: 10.6084/m9.figshare.23447330). The optimal identity thresholds to discriminate filamentous fungal species followed Vu *et al.* (2019).

Morphology

Slide preparations were mounted in lactic acid, Shear's mounting fluid, Melzer's solution, 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. Colony characters and pigment production were noted after 2–4 wk of growth on MEA, PDA and OA (Crous *et al.* 2019c) incubated at 25 °C. Colony colours (surface and reverse) were scored using the colour charts of Rayner (1970). Taxonomic novelties were submitted to MycoBank (www.MycoBank.org; Crous *et al.* 2004).

RESULTS

Phylogeny

Phylogenetic trees were generated for the taxonomic novelties, or to better clarify the position of a taxon in a broader context where needed. These trees are discussed in the species notes and the statistics associated with the phylogenetic analyses presented in this study are provided in supplementary Table S1.

Taxonomy

Acremonium aquaticum Crous & Jurjević, *sp. nov.* MycoBank MB 848820. Fig. 1.

Etymology: Name refers to the fact that it was isolated from water.

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells, solitary, erect, subcylindrical with apical taper, hyaline, smooth, phialidic, 20–30 × 1.5–2 µm. *Conidia* in long, unbranched

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) ¹	Locality and Substrate	Collector(s) and collection date	GenBank accession number ²				
				ITS	LSU	rpb2	tub2	Other loci
<i>Acremonium aquaticum</i> , <i>sp. nov.</i>	CBS 149454 = CPC 42867, ex-type	USA: Cooling pad water from greenhouse	Z. Jurjević, 4 Oct. 2021	QQ990087	QQ990041	QQ989208	QQ989251	<i>actA</i> : QQ989189 , <i>tef1</i> (second part): QQ989237
<i>Acrostalagmus luteoalbus</i>	CBS 149685 = CPC 43187	South Africa: <i>Portulacaria afra</i> , leaf	P.W. Crous, 27 Feb. 2022	QQ990088	QQ990042	QQ989209	–	<i>tef1</i> (second part): QQ989238
<i>Appendopyricularia juncicola</i>	CBS 149232 = CPC 41278, ex-type	Netherlands: <i>Juncus effusus</i> , dead culms	E.R. Osieck, 25 Feb. 2021	NR_182605	NG_149075	–	ON605635	<i>actA</i> : ON605619, <i>tef1</i> (first part): ON605627
	CBS 149686 = CPC 44053	Netherlands: <i>Carex elongata</i> , culms	E.R. Osieck, 20 Mar. 2022	QQ990091	QQ990045	–	–	<i>tef1</i> (first part): QQ989225
	CPC 44055	Netherlands: <i>Carex elongata</i> , culms	E.R. Osieck, 20 Mar. 2022	QQ990092	QQ990046	–	QQ989254	<i>tef1</i> (first part): QQ989226
	CPC 44106	Netherlands: <i>Juncus effusus</i> , culms	E.R. Osieck, 28 Apr. 2022	QQ990093	QQ990047	–	QQ989255	<i>tef1</i> (first part): QQ989227
	CPC 44107	Netherlands: <i>Juncus effusus</i> , culms	E.R. Osieck, 28 Apr. 2022	QQ990094	QQ990048	–	QQ989256	–
<i>Biscogniauxia anceps</i>	CPC 42686	Netherlands: <i>Juncus effusus</i> , culms	E.R. Osieck, 9 Dec. 2021	QQ990095	QQ990049	–	QQ989257	<i>tef1</i> (first part): QQ989228
	CBS 149687 = CPC 43197	Spain: <i>Eucalyptus</i> sp., bark	M.A. Delgado, 25 Mar. 2022	QQ990096	–	–	–	–
<i>Cephalophora tropica</i>	CBS 149457 = CPC 42877, ex-epitype	USA: Pan water of crocodile farm	Z. Jurjević, 24 Nov. 2021	QQ990097	QQ990050	QQ989210	–	<i>rpb1</i> : QQ989203 , SSU: QQ990136 , <i>tef1</i> (second part): QQ989239
<i>Ceratocystis ficicola</i>	CBS 149669 = CPC 44213	Italy (Sicily): Trunk necrosis in <i>Ficus carica</i>	G. Polizzi, 2022	QQ990098	QQ990051	QQ989211	QQ989258	<i>tef1</i> (second part): QQ989240
	CBS 149670 = CPC 44214	Italy (Sicily): Trunk necrosis in <i>Ficus carica</i>	G. Polizzi, 2022	QQ990099	–	–	–	–
<i>Chloridium caudigerum</i>	MAFF 625119, ex-type	Japan: <i>Ficus carica</i> , twigs	Y. Kajitani, Nov. 1990	NR_119410	–	–	–	–
	CBS 149688 = CPC 42899	Netherlands: <i>Ulmus</i> sp., branch	E.R. Osieck, 19 Feb. 2022	QQ990100	QQ990052	–	QQ989259	<i>tef1</i> (second part): QQ989241
<i>Chloridium gamsii</i>	CBS 667.75, ex-type	Belgium: Decaying wood	W. Gams, Sep. 1975	OP455415	OP455522	–	OP465095	<i>tef1</i> (second part): OP464990
	CBS 149043 = CPC 41933	Netherlands: <i>Cladonia portentosa</i>	J. Boers, 7 Jun. 2021	QQ990101	QQ990053	–	–	<i>tef1</i> (second part): QQ989242
<i>Cladophialophora larricola</i> , <i>sp. nov.</i>	CBS 148944 = CPC 41384, ex-type	Netherlands: <i>Larix</i> sp., dead wood	J. Boers, 16 Mar. 2021	QQ990102	QQ990054	–	QQ989260	<i>tef1</i> (first part): QQ989229
<i>Cylindromonium eugenicola</i>	CBS 146075 = CPC 37170, ex-type	South Africa: <i>Eugenia capensis</i> , leaf litter	M.J. Wingfield, 2010	NR_166338	NG_068337	–	–	–
	CBS 149689 = CPC 43326	Spain (Gran Canaria): <i>Eucalyptus</i> sp., dead twig	A.L. van Iperen, 1 Apr. 2022	QQ990103	QQ990055	–	–	–
<i>Cyphellophora deltoidea</i> , <i>comb. nov.</i>	CBS 263.77 = CMT 1111.74, ex-type	Italy: Soil	Unknown	NR_153555	NG_057113	–	–	–
<i>Cyphellophora neerlandica</i> , <i>sp. nov.</i>	CBS 149512 = CPC 42634, ex-type	Netherlands: Lichen on brick wall	J. Boers, 12 Nov. 2021	QQ990089	QQ990043	–	QQ989252	–

Table 1. (Continued).

Species	Culture or voucher accession number(s) ¹	Locality and Substrate	Collector(s) and collection date	GenBank accession number ²				
				ITS	LSU	rpb2	tub2	Other loci
<i>Didymella brevipilosa</i>	CPC 42641 CBS 148654 = FMR 17415, ex-type CBS 149049 = CPC 41600	Netherlands: Lichen on brick wall Spain: Plant debris submerged in freshwater Canada: <i>Abies balsamea</i> , buds	J. Boers, 12 Nov. 2021 V. Magaña-Dueñas, May. 2018 D. Malloch, 4 May 2021	OO990090 OU612373 OO990104	OO990044 OU612372 OO990056	– OU612359 OO989212	OO989253 OU612358 OO989261	– – <i>actA</i> : OO989190
<i>Drepanopeziza populi-albae</i>	CBS 149510 = CPC 42336	Russia: <i>Populus alba</i>	T.S. Bulgakov, 26 Jun. 2021	OO990105	OO990057	–	–	–
<i>Endoconidioma populi</i>	CBS 149070 = CPC 41602	Canada: <i>Abies balsamea</i> , buds	D. Malloch, 4 May 2021	OO990106	OO990058	–	–	–
<i>Fusariella atrovirens</i>	UAMH 10297, ex-type CBS 149690 = CPC 43304	USA: <i>Populus tremuloides</i> , twig Namibia: Lichenicolous on unknown lichen growing on rock	A. Tsuneda, 7 Aug. 2001 P.W. Crous, 4 Apr. 2022	NR_121303	NG_059198	–	–	–
<i>Fusariella hughesii</i>	CBS 149074 = CPC 41594	Ukraine: <i>Adonis vernalis</i> , overwintered stems	A. Akulov, 11 Apr. 2021	OO990107	OO990059	OO989213	–	<i>tef1</i> (second part): OO989243
<i>Geonectria muralis</i> , sp. nov.	CBS 149515 = CPC 42404, ex-type CPC 42405	Netherlands: Moss growing on the bottom part of wall Netherlands: Moss growing on the bottom part of wall	J. Boers, 7 Sep. 2021 J. Boers, 7 Sep. 2021	OO990108 OO990109	OO990060 OO990061	–	–	–
<i>Harposporium illinoisensis</i> , sp. nov.	CPC 42406 CBS 149456 = CPC 42872, ex-type	Netherlands: Moss growing on the bottom part of wall USA: Rockwool	J. Boers, 7 Sep. 2021 Z. Jurjević, Oct. 2021	OO990110 OO990111	OO990062	–	–	–
<i>Hysterobrevium rosae</i>	CBS 149699 = CPC 42948 MFLUCC 14-0551, ex-type	Netherlands: Bamboo stick Italy: <i>Rosa canina</i> , dead aerial branch	E.R. Osieck, 11 Feb. 2022 E. Camporesi, 15 Jun. 2014	OO990112 OO990113	OO990063 OO990064	OO989214 OO989215	OO989262	<i>actA</i> : OO989191, <i>tef1</i> (second part): OO989244 <i>tef1</i> (second part): OO989245
<i>Microcera physciae</i>	CBS 148283 = CPC 41284, ex-type CBS 149570 = CPC 42638	Netherlands: <i>Physcia tenella</i> Spain: <i>Phragmites australis</i>	J. Boers, 10 Mar. 2021 M. Delgado, 8 Oct. 2021	NR_175225 OO990114	NG_081335 OO990065	OK651168 OO989216	OK651208 OO989263	<i>tef1</i> (second part): MH535879 <i>rpb1</i> : OK651153, <i>tef1</i> (first part): OK651190 <i>rpb1</i> : OO989204, <i>tef1</i> (first part): OO989230
<i>Miricatena prunicola</i>	CBS 149448 = CPC 42627, ex-epitype CBS 149455 = CPC 42868, ex-type CPC 42875	Netherlands: <i>Prunus serotina</i> , leaves USA: Hydroponic water in greenhouse USA: Greenhouse peat	E. Slootweg, 7 Nov. 2021 Z. Jurjević, 4 Oct. 2021 Z. Jurjević, 4 Oct. 2021	OO990115 OO990116 OO990117	OO990066 OO990067 OO990068	–	–	<i>tef1</i> (first part): OO989231
<i>Neoleptodontidium aquaticum</i> , gen. et sp. nov.	CBS 123.86, ex-type	India: Rotten wood	V. Rao, Jan. 1984	MH861931	–	–	–	–
<i>Neoleptodontidium aciculare</i> , comb. nov.								
<i>Nothoramularia raghnildiana</i> , gen. et comb. nov.	CBS 149075 = CPC 42463	Germany: On <i>Raghnildiana ferruginea</i> , parasitic on <i>Artemisia vulgaris</i>	J. Kruse, 7 Sep. 2021	OO990119	OO990070	–	–	–

Table 1. (Continued).

Species	Culture or voucher accession number(s) ¹	Locality and Substrate	Collector(s) and collection date	GenBank accession number ²					
				ITS	LSU	rpb2	tub2	Other loci	
<i>Ophiognomonia setacea</i>	CBS 149076 = CPC 42462, ex-epitype	Germany: On <i>Raghnildiana ferruginea</i> , parasitic on <i>Artemisia vulgaris</i>	J. Kruse, 7 Sep. 2021						
	CBS 859.79, ex-epitype	Switzerland: <i>Quercus</i> sp.	M. Monod, 8 May 1979	OO990118	OO990069	-	-	-	<i>tef1</i> (second part): JQ414154
	CBS 149691 = CPC 43206	Spain: <i>Quercus robur</i> , leaves	J. Castillo, 21 Jan. 2022	AY818958	AY818962	-	-	-	<i>tef1</i> (second part): OO989232 , <i>tef1</i> (second part): OO989246
<i>Paradissoconium narthecii</i>	CBS 148449 = CPC 41970, ex-type	Netherlands: <i>Narthecium ossifragum</i> , dead leaves	J. Boers, 4 Jul. 2021	OO990120	OO990071	-	-	-	<i>actA</i> : OK651125, <i>rpb1</i> : OK651151
	CBS 149692 = CPC 42494	Netherlands: <i>Narthecium ossifragum</i> , dead leaves	J. Boers, 26 Sep. 2021	NR_175214	NG_081323	-	-	-	<i>actA</i> : OO989192 , <i>rpb1</i> : OO989205
<i>Paraeotypella citricola</i>	CBS 149693 = CPC 43208	Spain: Bark of unknown tree	26 Jan. 2022, J. Castillo	OO990121	OO990072	-	-	-	
<i>Phomatospora endopteris</i>	CBS 149073 = CPC 41832	Netherlands: <i>Pteridium aquilinum</i> , stems	P.W. Crous, 24 May 2021	OO990122	OO990073	OO989217	OO989264	-	
	CBS 149077 = CPC 41921, ex-epitype	Canada: <i>Abies balsamea</i> , buds	D. Malloch, 4 May 2021	OO990123	OO990074	OO989218	-	SSU: OO990137	
<i>Phyllosticta multicorniculata</i>	CBS 149078 = CPC 41919	Canada: <i>Abies balsamea</i> , buds	D. Malloch, 4 May 2021	OO990124	OO990075	-	-	-	<i>actA</i> : OO989193 , <i>gapdh</i> : OO989198 , <i>tef1</i> (first part): OO989233
	CBS 149694 = CPC 44105	UK: <i>Allium schoenoprasum</i>	P.W. Crous, May 2022	OO990125	OO990076	-	-	-	<i>actA</i> : OO989194 , <i>gapdh</i> : OO989199 , <i>tef1</i> (first part): OO989234
<i>Pleurotheciella aquatica</i>	MFLUCC 17-0464, ex-type	China: Saprolic on decaying wood submerged in Jinsha River	H.Y. Su, Apr. 2015	OO990126	OO990077	OO989219	-	-	
	CBS 145564 = CPC 35443, ex-type	Italy: <i>Pistacia lentiscus</i> , leaves	P.W. Crous, 13 Apr. 2018	NR_160591	NG_066193	MF401405	-	SSU: MF399220	<i>actA</i> : MK876462, <i>gapdh</i> : MK876473
<i>Ramularia pistaciae</i>	CBS 149696 = CPC 44067	UK: <i>Arbutus unedo</i> , leaf spot	P.W. Crous & S. Denman, 14 May 2022	OO990127	OO990078	OO989220	-	-	<i>actA</i> : OO989195 , <i>gapdh</i> : OO989200 , <i>his3</i> : OO989201 , <i>tef1</i> (first part): OO989235
<i>Ruptoseptoria unedonis</i>	CBS 149697 = CPC 44069	UK: <i>Arbutus unedo</i> , leaf spot	P.W. Crous & S. Denman, 14 May 2022	OO990128	OO990079	OO989221	-	-	
<i>Schizothecium conicum</i>	CBS 149695 = CPC 44110	Netherlands: <i>Juncus effusus</i> , stems	E.R. Osieck, 28 Apr. 2022	OO990129	OO990080	-	-	-	
	CBS 148302 = CPC 40067, ex-type	Netherlands: <i>Pinus sylvestris</i>	A.L. van Iperen, 1 Nov. 2020	OK664747	NG_081347	OK651177	-	-	
<i>Sporidesmiella pini</i>	CBS 149045 = CPC 41495	Netherlands: <i>Juncus effusus</i> , dead culms	E.R. Osieck, 9 Mar. 2021	OO990131	OO990082	-	-	-	
<i>Thyronectria caraganae</i>	CPC 41494	Netherlands: <i>Juncus effusus</i> , dead culms	E.R. Osieck, 9 Mar. 2021	OO990130	OO990081	OO989222	-	-	<i>tef1</i> (second part): OO989247
	CBS 148949 = CPC 41504, ex-epitype	Ukraine: <i>Caragana arborescens</i> , twigs	A. Akulov, 11 Apr. 2021	OO990132	OO990083	-	OO989265	-	<i>actA</i> : OO989196 , <i>rpb1</i> : OO989206
	CBS 149509 = CPC 42342	Ukraine: <i>Caragana arborescens</i> , dead branch	A. Akulov, 1 Aug. 2021	OO990133	OO990084	OO989223	OO989266	-	<i>rpb1</i> : OO989207 , <i>tef1</i> (second part): OO989248

Table 1. (Continued).

Species	Culture or voucher accession number(s) ¹	Locality and Substrate	Collector(s) and collection date	ITS	LSU	rpb2	tub2	Other loci	GenBank accession number ²
<i>Trichosphaeria pilosa</i>	TCA1, ex-type	Ukraine: <i>Caragana arborescens</i> , dead branch	L.V. Smyk, 6 May 1990	NR_155911	KX514385	-	KX514399	actA: KX514382, rpb1: KX514390, tef1 (second part): KX514396	
	CBS 149698 = CPC 42927, ex-epitype	Netherlands: <i>Salix</i> sp., decayed branch	E.R. Osieck, 28 Jan. 2022					actA: OQ989197, his3: OQ989202, tef1 (first part): OQ989236, tef1 (second part): OQ989249	
<i>Zaanenomyces versatilis</i>	CBS 148312 = CPC 41224, ex-type	Netherlands: <i>Juncus inflexus</i> , dead culms	E.R. Osieck, 4 Feb. 2021	OQ990134 NR_175227	OQ990085 NG_081336	OQ989224	OQ989267		
	CBS 149453 = CPC 42831	Netherlands: <i>Juncus effusus</i> , dead stems	E.R. Osieck, 9 Mar. 2021	OQ990135	OQ990086	-	-	tef1 (second part): OQ989250	

¹ C.P.K.: Collection maintained at the University of Technology Vienna, Austria; CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands; CPC: Culture collection of Pedro Crous, housed at CBS; FMR: Facultat de Medicina, Universitat Rovira i Virgili, Reus, Spain; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Rai, Thailand; UAMH: University of Alberta Microfungus Collection and Herbarium, Edmonton, Alberta, Canada.

² ITS: internal transcribed spacers and intervening 5.8S nrDNA; LSU: large subunit (28S) of the nrRNA gene operon; act: partial actin 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.

chains, aseptate, smooth, fusoid-ellipsoid, initially hyaline, but becoming olivaceous with age, (4–)5–6 × (2–)2.5 μm; forming olivaceous mucoid droplets with age.

Culture characteristics: Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, lobate margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse dirty white, but sectoring with age to form olivaceous zones, most prominent on MEA.

Typus: USA, North Carolina, Durham, cooling pad water, greenhouse, Oct. 2021, Z. Jurjević 5662 (**holotype** CBS H-25167, culture ex-type CPC 42867 = CBS 149454).

Notes: *Acremonium* and allied genera were recently revised by Hou et al. (2023). *Acremonium aquaticum* is phylogenetically (92 % bootstrap support; Fig. 2) closely related to *A. charticola* (conidia in mucoid heads, 3.2–4.5 × 1.4–2.0 μm; Gams 1971) but is morphologically distinct in having larger conidia that are formed in chains.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Acremonium* sp. from indoor plaster in Russia (strain tk2, GenBank LT549084.1; Identities = 537/537 (100 %), no gaps), *Acremonium charticola* (strain CBS 881.73, GenBank AJ621774.1; Identities = 472/506 (93 %), 11 gaps (2 %)), and *Acremonium alternatum* (strain NIOSN M-120, GenBank MG589592.1; Identities = 412/446 (92 %), six gaps (1 %)). It is also identical to isolates from a pine tree in South Korea (GenBank MK848676.1), a tempera painting on canvas in Slovenia (GenBank MZ687371.1), soil collected in a 40-yr-old *Pinus merkusii* forest in Viet Nam (GenBank MW504687.1), from *Ageratina adenophora* in China (GenBank MK304178.1), and marine sediment in China (GenBank KX098125.1). Closest hits using the LSU sequence were *Acremonium charticola* (strain CBS 881.73, GenBank MH872552.1; Identities = 817/823 (99 %), two gaps (0 %)), *Acremonium sordidulum* (strain SP17, GenBank MZ269296.1; Identities = 814/822 (99 %), one gap (0 %)), and *Acremonium alternatum* (strain MUT<ITA> 6246, GenBank MN947574.1; Identities = 792/800 (99 %), one gap (0 %)). Closest hits using the actA sequence had highest similarity to *Tilachlidium brachiatum* (strain CBS 505.67, GenBank KM231249.1; Identities = 543/637 (85 %), 20 gaps (3 %)), *Acremonium chrysogenum* (no strain number specified, GenBank AF056976.1; Identities = 558/658 (85 %), 35 gaps (5 %)), and *Acremonium* sp. from *Leymus chinensis* in China (strain 324, GenBank JN836732.1; Identities = 587/633 (93 %), 15 gaps (2 %)). Closest hits using the rpb2 (first part) sequence had highest similarity to *Acremonium alternatum* (strain AFTOL-ID 1396, GenBank FJ238366.1; Identities = 573/676 (85 %), 11 gaps (1 %)), and *Caespitomonium euphorbiae* (culture CPC 39083, GenBank OK651157.1; Identities = 627/866 (72 %), 42 gaps (4 %)). Closest hits using the tef1 (second part) sequence had highest similarity to *Acremonium charticola* (strain 06700, GenBank KT878367.1; Identities = 722/753 (96 %), no gaps), *Amphichorda guana* (strain LC5819, GenBank KX855212.1; Identities = 696/748 (93 %), no gaps), and *Acremonium sclerotigenum* (strain 06239, GenBank KT878358.1; Identities = 712/769 (93 %), five gaps (0 %)). No significant hits were obtained using the tub2 sequence.

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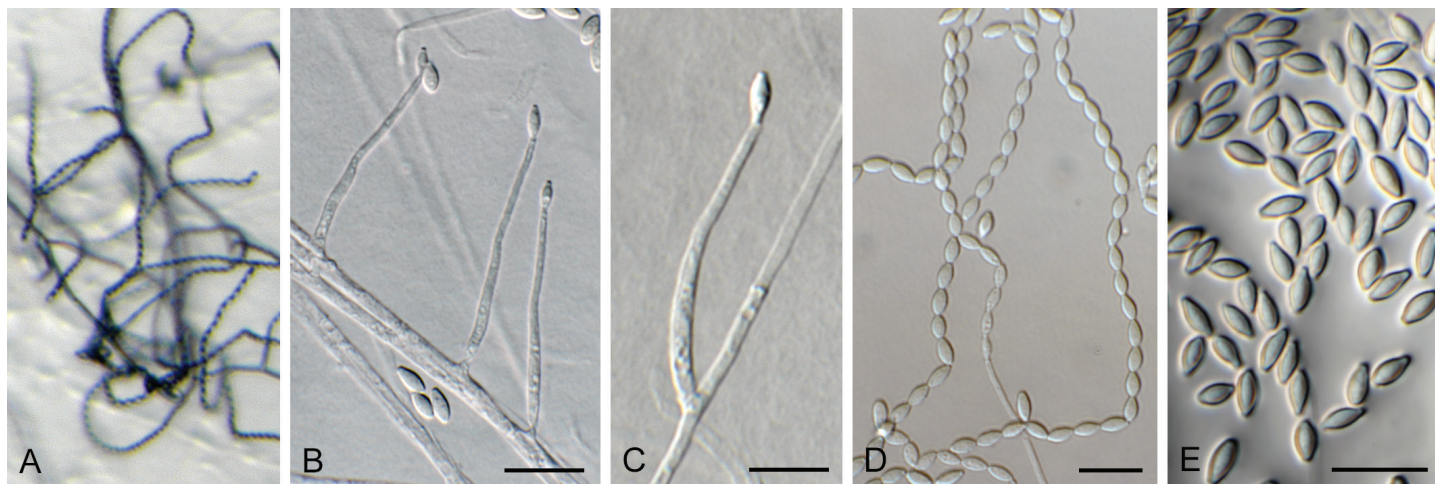


Fig. 1. *Acremonium aquaticum* (CPC 42867). **A.** Colony on SNA. **B–D.** Conidiogenous cells giving rise to chains of conidia. **E.** Conidia. Scale bars = 10 μ m.

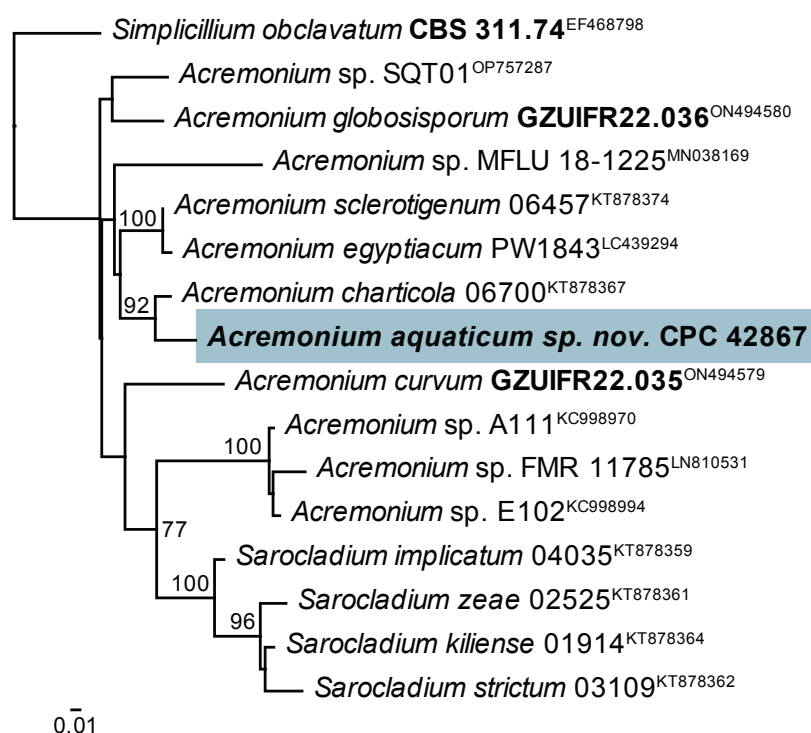


Fig. 2. Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 of the *Acremonium tef1* (second part) nucleotide alignment. Bootstrap support values (> 75 %) from 1 000 non-parametric bootstrap replicates are shown at the nodes. Culture collection or voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences derived from material with a type status are indicated with a culture or voucher number highlighted with bold face. The tree was rooted to *Simplicillium obclavatum* (culture CBS 311.74; GenBank EF468798) and the species treated here is highlighted with bold face. The scale bar indicates the expected number of changes per site.

Acrostalagmus luteoalbus (Link) Zare *et al.* [as '*luteo-albus*'], *Mycol. Res.* **108**: 581. 2004. Fig. 3.

Description and illustration: Zare *et al.* (2004).

Material examined: **South Africa**, Western Cape Province, Kirstenbosch, on leaf of *Portulacaria afra* (*Portulacaceae*), 27 Feb. 2022, P.W. Crous, HPC 3862, culture CPC 43187 = CBS 149685.

Notes: *Acrostalagmus luteoalbus* was recently reported as a major constituent of the mixed mycobiota in the wet cork liner

of a water-damaged outdoor wall, and also from indoor dust in Finland (Andersson *et al.* 2021). The present record represents a new report from South Africa, where it was isolated from a leaf of *Portulacaria afra*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to numerous sequences of *Acrostalagmus luteoalbus* (e.g. EF_332, GenBank MT528981.1; Identities = 502/502 (100 %), no gaps), and *Nectria inventa* (e.g. strain CBS 388.65, GenBank MH858627.1; Identities = 502/502 (100 %), no gaps). Closest hits using the **LSU** sequence were *Nectria*

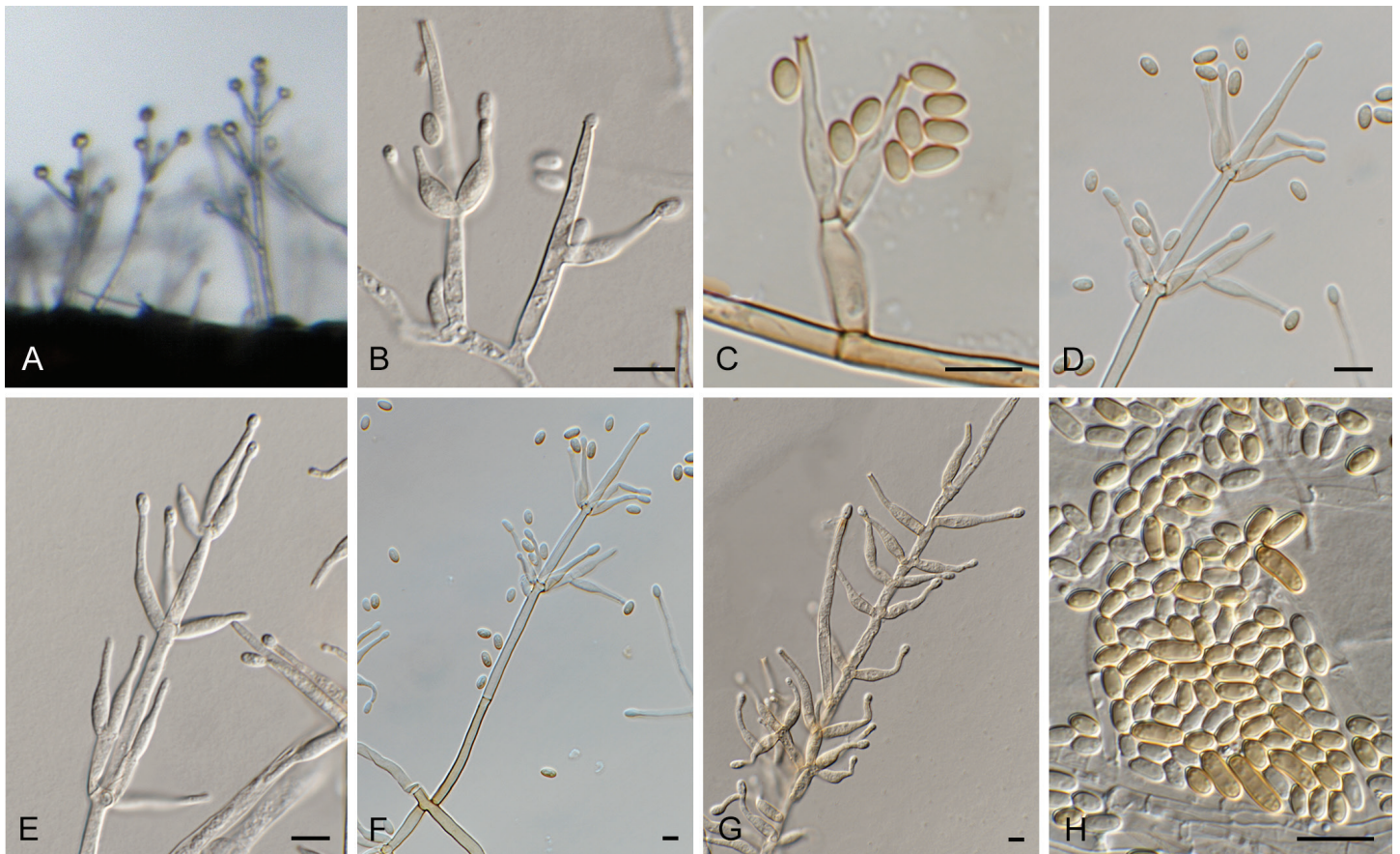


Fig. 3. *Acrostalagmus luteoalbus* (CPC 43187). A–G. Conidiophores with conidiogenous cells giving rise to conidia. H. Conidia. Scale bars = 10 µm.

inventa (strain CBS 236.55, GenBank MH869007.1; Identities = 855/855 (100 %), no gaps), *Acrostalagmus luteoalbus* (strain MUT<ITA> 4778, GenBank KP671745.1; Identities = 855/855 (100 %), no gaps), and *Acrostalagmus annulatus* (strain CBS 121213, GenBank LR025806.1; Identities = 812/812 (100 %), no gaps). Closest hits using the *rpb2* (first part) sequence had highest similarity to *Acrostalagmus luteoalbus* (strain CBS 112.16, GenBank LR026101.1; Identities = 742/743 (99 %), no gaps), and *Acrostalagmus annulatus* (strain CBS 121213, GenBank LR026108.1; Identities = 738/743 (99 %), no gaps). Closest hits using the *tef1* (second part) sequence had highest similarity to *Acrostalagmus luteoalbus* (strain CBS 388.65, GenBank LR026372.1; Identities = 787/787 (100 %), no gaps), *Acrostalagmus annulatus* (strain CBS 121213, GenBank LR026378.1; Identities = 782/786 (99 %), no gaps), and *Verticillium zaregamsianum* (strain V202, GenBank KJ443225.1; Identities = 856/904 (95 %), four gaps (0 %)).

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Appendopyricularia juncicola Crous & Osieck, *Persoonia* **48**: 265. 2022. Fig. 4.

Description and illustration: Crous et al. (2022b).

Materials examined: **Netherlands**, Overijssel Province, Reutum, Reutumerveen, 22.5 m a.s.l., 52°23'43"N, 06°49'24"E, on dead culms of *Carex elongata* (*Cyperaceae*), 20 Mar. 2022, E.R. Osieck, HPC 3952 = WI-50#4449, cultures CPC 44053 = CBS 149686, CPC 44055; Overijssel Province, Witte Veen, Haaksbergen, 39 m a.s.l., 52°08'25"N, 06°52'20"E,

on dead culms of *Juncus effusus* (*Juncaceae*), 28 Apr. 2022, E.R. Osieck, HPC 3962 = WI-55#4461, cultures CPC 44107, 44106; Utrecht Province, Nieuw-Wulven, north of Houten, 1.5 m a.s.l., 52°02'46"N, 05°10'34"E, on dead culms of *J. effusus*, 9 Dec. 2021, E.R. Osieck, HPC 3812 = WI-42#4355, culture CPC 42686.

Notes: *Appendopyricularia*, based on *A. juncicola*, was introduced as a new hyphomycete genus occurring on culms of *Juncus effusus* in the Netherlands (Crous et al. 2022b). This is the first record of this taxon also occurring on culms of *Carex elongata*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the *ITS* sequence of CPC 42686 had highest similarity to *Appendopyricularia juncicola* (strain CPC 41278, GenBank NR_182605.1; Identities = 500/501 (99 %), one gap (0 %)), *Thyridium pluriloculosum* (strain GZUIFR21.876, GenBank OK493561.1; Identities = 402/481 (84 %), 25 gaps (5 %)), and *Phialemonium dimorphosporum* (strain SLE, GenBank DQ403199.1; Identities = 412/495 (83 %), 30 gaps (6 %)). The *ITS* sequence of CPC 42686 is identical to those of CPC 44053, 44055, 44106 and 44107 (508/508, 508/508, 502/502 and 508/508 nucleotides, respectively). Closest hits using the *LSU* sequence of CPC 42686 were *Appendopyricularia juncicola* (strain CPC 41278, GenBank NG_149075.1; Identities = 808/808 (100 %), no gaps), *Paradiplococcium singulare* (strain CBS 126091, GenBank NG_066271.1; Identities = 797/839 (95 %), three gaps (0 %)), and *Barbatosphaeria varioseptata* (strain CBS 137797, GenBank NG_058674.1; Identities = 798/840 (95 %), five gaps (0 %)). The *LSU* sequence of CPC 42686 is identical to those of CPC 44053, 44055, 44106 and 44107 (792/792, 825/825, 804/804 and

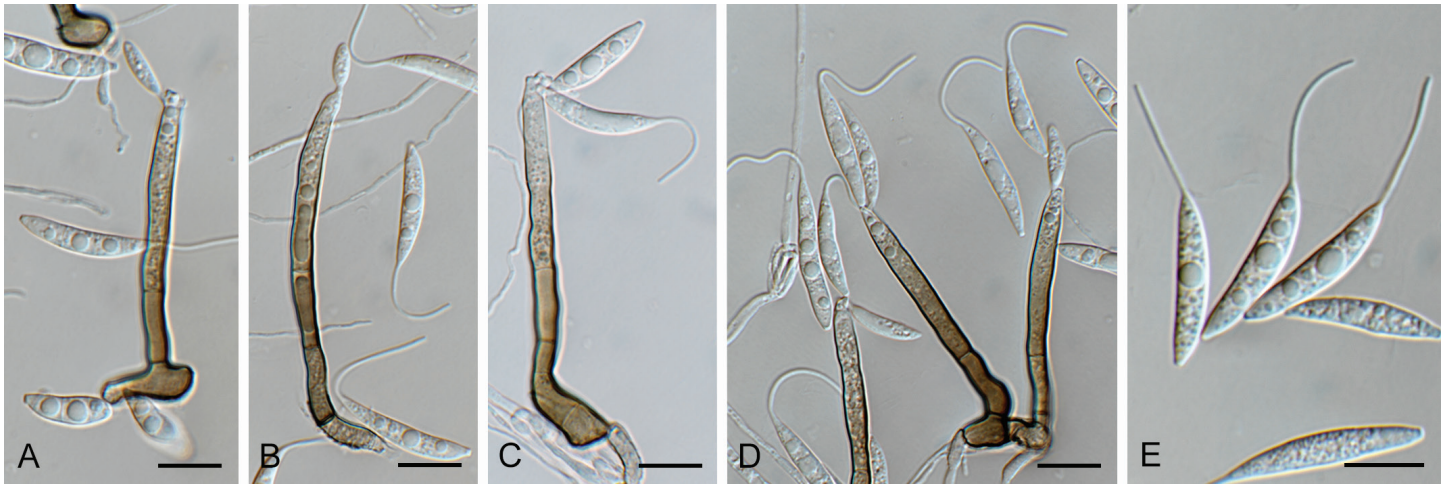


Fig. 4. *Appendopyricularia juncicola* (CPC 44053). A–D. Conidiophores with conidiogenous cells giving rise to conidia. E. Conidia. Scale bars = 10 µm.

838/838 nucleotides, respectively). Closest hits using the *tef1* (first part) sequence had highest similarity to *Appendopyricularia juncicola* (strain CPC 41278, GenBank ON605627.1; Identities = 338/345 (98 %), one gap (0 %)), *Madurella fahalii* (strain CBS 129176, GenBank MN078441.1; Identities = 141/149 (95 %), no gaps), and *Podospora comata* (strain Wa139-, GenBank CP071493.1; Identities = 151/165 (92 %), four gaps (2 %)). The *tef1* sequence of CPC 42686 is 98 % similar to those of CPC 44053, 44055 and 44106 (338/345, 337/344, and 338/345 nucleotides, respectively; all including one gap). The closest hits using the *tub2* sequence of CPC 42686 had highest similarity to *Appendopyricularia juncicola* (strain CPC 41278, GenBank ON605635.1; Identities = 671/690 (97 %), three gaps (0 %)); while the *tub2* sequence of CPC 44055 is identical to that of *Appendopyricularia juncicola* (strain CPC 41278, GenBank ON605635.1; Identities = 690/690 (100 %), no gaps). The *tub2*

sequence of CPC 42686 is 97 % similar to those of CPC 44055, 44106 and 44107 (677/696, 672/691 and 677/696, nucleotides, respectively; all three includes an indel of three nucleotides and are identical to *Appendopyricularia juncicola* strain CPC 41278, GenBank ON605635.1).

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Biscogniauxia anceps (Sacc.) J.D. Rogers *et al.*, *Mycol. Res.* **100**: 669. 1996. Fig. 5.

Description and illustration: Rogers *et al.* (1996).

Material examined: Spain, Pontevedra, O Grove, on bark of *Eucalyptus* sp. (*Myrtaceae*), 25 Mar. 2022, M.A. Delgado, HPC 3867 = RKS 1164, culture CPC 43197 = CBS 149687.

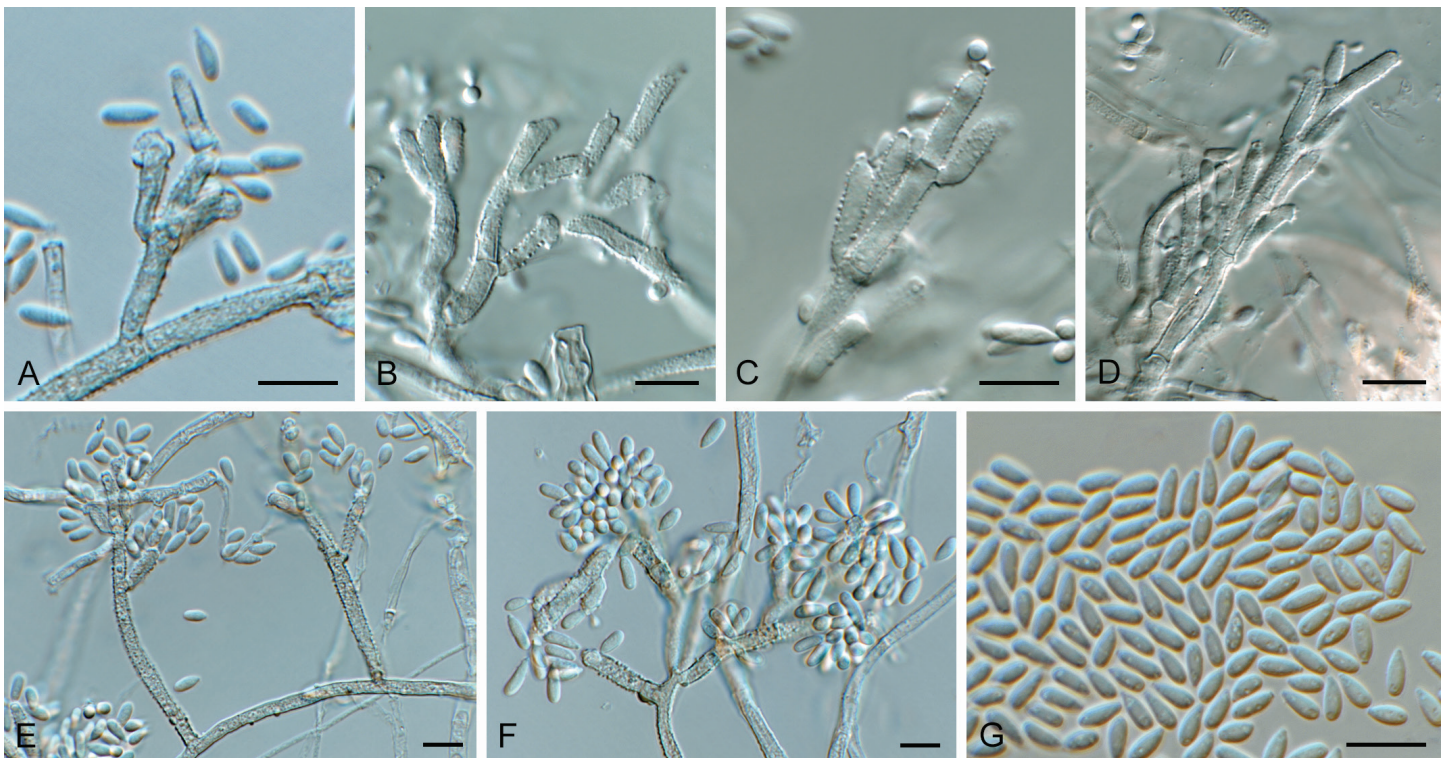


Fig. 5. *Biscogniauxia anceps* (CPC 43197). A–F. Conidiophores with conidiogenous cells giving rise to conidia. G. Conidia. Scale bars = 10 µm.

Notes: Species of *Biscogniauxia* are found as endophytes and opportunistic pathogens on old and stressed trees (Bahmani *et al.* 2021). *Biscogniauxia anceps* is known to occur on bark of various tree hosts in Europe and is reported here from *Eucalyptus* bark in Spain.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Biscogniauxia anceps* (strain 123, GenBank EF026132.1; Identities = 481/481 (100 %), no gaps), *Biscogniauxia nummularia* (strain MUCL 51395, GenBank NR_153649.1; Identities = 534/585 (91 %), 16 gaps (2 %)), and *Digitodochium amoenum* (strain LA, GenBank KC774569.1; Identities = 534/585 (91 %), 16 gaps (2 %)).

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Cephalioophora tropica Thaxt., *Bot. Gaz.* **35**: 158. 1903. Fig. 6.

Classification: Pezizomycetes, Pezizales, Ascodesmidaceae.

Description and illustration: Ruszkiewicz-Michalska *et al.* (2017).

Typus: **Lectotype** here designated, *Bot. Gaz.* **35**: 158. 1903, plate V, figs 11–16, MBT 10013412. **USA**, Louisiana, crocodile farm, pan water, 24 Nov. 2021, *Z. Jurjević* 5686 (**epitype** here designated CBS H-25171, MBT 10013411, culture ex-epitype CPC 42877 = CBS 149457).

Notes: *Cephalioophora tropica* is a pantropical and occasionally temperate species (Seifert *et al.* 2011). It is commonly isolated from dung, soil, and water (Ruszkiewicz-Michalska *et al.* 2017). Because no type was indicated in the original description, a lectotype and epitype are designated here to fix the application of the name. The genus *Cephalioophora* is considered *incertae sedis*

in MycoBank and Index Fungorum, but was shown by Hansen *et al.* (2013) and confirmed here to belong to *Ascodesmidaceae*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cephalioophora tropica* (strain CBS 133.33, GenBank MH855385.1; Identities = 529/529 (100 %), no gaps), and *Cephalioophora irregularis* (strain YG-C22, GenBank KX683420.1; Identities = 504/514 (98 %), no gaps). Closest hits using the **LSU** sequence were *Cephalioophora tropica* (strain CBS 315.66, GenBank MH870444.1; Identities = 830/830 (100%), no gaps), *Cephalioophora irregularis* (strain CBS 218.62, GenBank KC012668.1; Identities = 826/830 (99 %), no gaps), and *Ascodesmis rosicola* (voucher GUCC 190035.1, GenBank MZ221605.1; Identities = 815/830 (98 %), no gaps). Closest hits using the **SSU** sequence were *Cephalioophora tropica* (strain JCM 6019, GenBank AB001112.1; Identities = 1 000/1 000 (100 %), no gaps), *Cephalioophora irregularis* (strain IFO 6778, GenBank AB001109.2; Identities = 998/1 000 (99 %), no gaps), and *Eleutherascus lectardii* (strain CBS 626.71, GenBank NG_062685.1; Identities = 994/1 000 (99 %), no gaps). Closest hits using the **rpb1** sequence had highest similarity to *Cephalioophora tropica* (strain CBS 133.33, GenBank JX943656.1; Identities = 727/729 (99 %), no gaps), *Cephalioophora irregularis* (strain CBS 218.62, GenBank JX943655.1; Identities = 674/719 (94 %), five gaps (0 %)), and *Ascodesmis nigricans* (strain CBS 428.91, GenBank JX943653.1; Identities = 582/690 (85 %), nine gaps (1 %)). Closest hits using the **rpb2** (first part) sequence had highest similarity to *Cephalioophora tropica* (strain CBS 133.33, GenBank JX943763.1; Identities = 598/600 (99 %), no gaps), *Cephalioophora irregularis* (strain CBS 218.62, GenBank JX943762.1; Identities = 686/732 (94 %), two gaps (0 %)), and *Ascodesmis rosicola* (voucher GUCC 190204.1, GenBank MZ333140.1; Identities = 728/882 (83%), three gaps (0 %)). Closest hits using the **tef1** (second part) sequence had highest similarity to *Cephalioophora tropica* (strain CBS 133.33, GenBank KC109224.1; Identities = 901/903 (99 %),

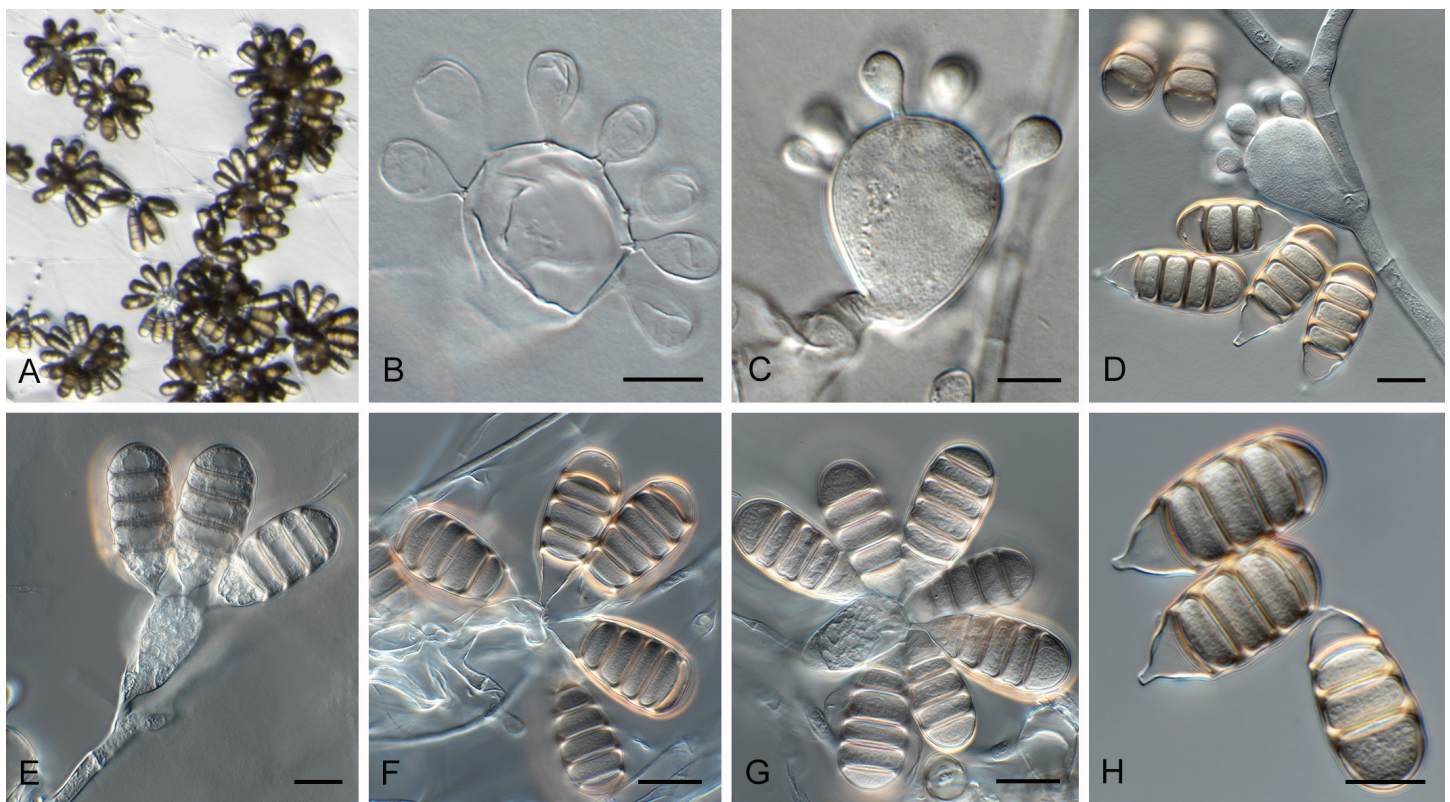


Fig. 6. *Cephalioophora tropica* (CPC 42877). **A–G.** Conidiophores with conidiogenous cells giving rise to conidia. **H.** Conidia. Scale bars = 10 µm.

no gaps), *Cephalophora irregularis* (strain CBS 218.62, GenBank KC109223.1; Identities = 899/958 (94 %), 11 gaps (1 %)), and *Ascodesmis nigricans* (strain CBS 389.68, GenBank KC109221.1; Identities = 781/887 (88 %), 24 gaps (2 %)).

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Ceratocystis ficicola Kajitani & Masuya, *Mycoscience* 52: 351. 2011. Fig. 7.

Ascomata perithecial, solitary with brown to black, globose base, 180–220 µm diam, with erect, brown neck, 1 000–1 300 µm long, becoming paler brown toward apex, 40–50 µm diam at base, 18–20 µm diam at apex. *Ostiolar hyphae* divergent, subhyaline, 130–200 µm long. *Asci* not observed. *Ascospores* hyaline, galeate, aseptate, 7–8 × 6–7 µm in top view, 4–5 µm high in side view, accumulating in creamy mucoid masses at apices of perithecia. *Thielaviopsis* asexual morph: *endoconidiophores* solitary on mycelium, pale brown to brown, smooth, tapering to truncate apex, 80–160 µm long, 5–7 µm diam at base, 1–4-septate. *Conidiogenous cells* phialidic, cylindrical, 500–75 µm long, 4–5 µm diam at base, 4 µm diam at apex. *Endoconidia* hyaline, becoming pale brown, smooth, guttulate, aseptate, subcylindrical with obtuse to truncate ends, (11–)15–17(–20) × 4–5(–6) µm, occurring in unbranched chains. *Aleuroconidia* solitary, aseptate, clavate to obovoid, hyaline, smooth, (9–) 12–14(–15) × 4–5(–6) µm, frequently forming via microcyclic conidiation from endoconidia. *Culture characteristics*: Colonies erumpent, spreading, with

moderate aerial mycelium and feathery, lobate margin, covering dish in 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, and reverse iron grey.

Materials examined: Sicily, Noto, from trunk necrosis in *Ficus carica* (*Moraceae*), 2022, G. Polizzi, CERA30 = CBS H-25213, culture CPC 44213 = CBS 149669; CERA20 = CBS H-25214, culture CPC 44214 = CBS 149670.

Notes — *Ceratocystis ficicola* causes vascular wilt of fig trees in Japan, and has also recently been reported from Greece (Tsopeles *et al.* 2021). This is the first record of the pathogen from Italy. Based on ITS alone, the present collections might represent a novel species. However, this was not supported by the secondary barcodes (see below). A closer inspection of the ITS blast alignment revealed a similarity of 577/600 nucleotides, with the 19 of the 23 mismatches being accounted for by gaps caused mainly by differences in repeat length repeats in T- or A-rich parts of the sequences.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence of CPC 44213 had highest similarity to *Ceratocystis ficicola* (strain MAFF 625119, GenBank NR_119410.1; Identities = 577/600 (96 %), 19 gaps (3 %)), *Ceratocystis cercfabiensis* (strain CMW 42512, GenBank KP727589.1; Identities = 541/598 (90 %), 20 gaps (3 %)), and *Ceratocystis uchidaei* (strain CBS 115164, GenBank NR_164012.1; Identities = 560/620 (90 %), 23 gaps (3 %)). The ITS sequences of CPC 44213 and 44214 are identical (603/603 nucleotides). Closest hits using the LSU sequence

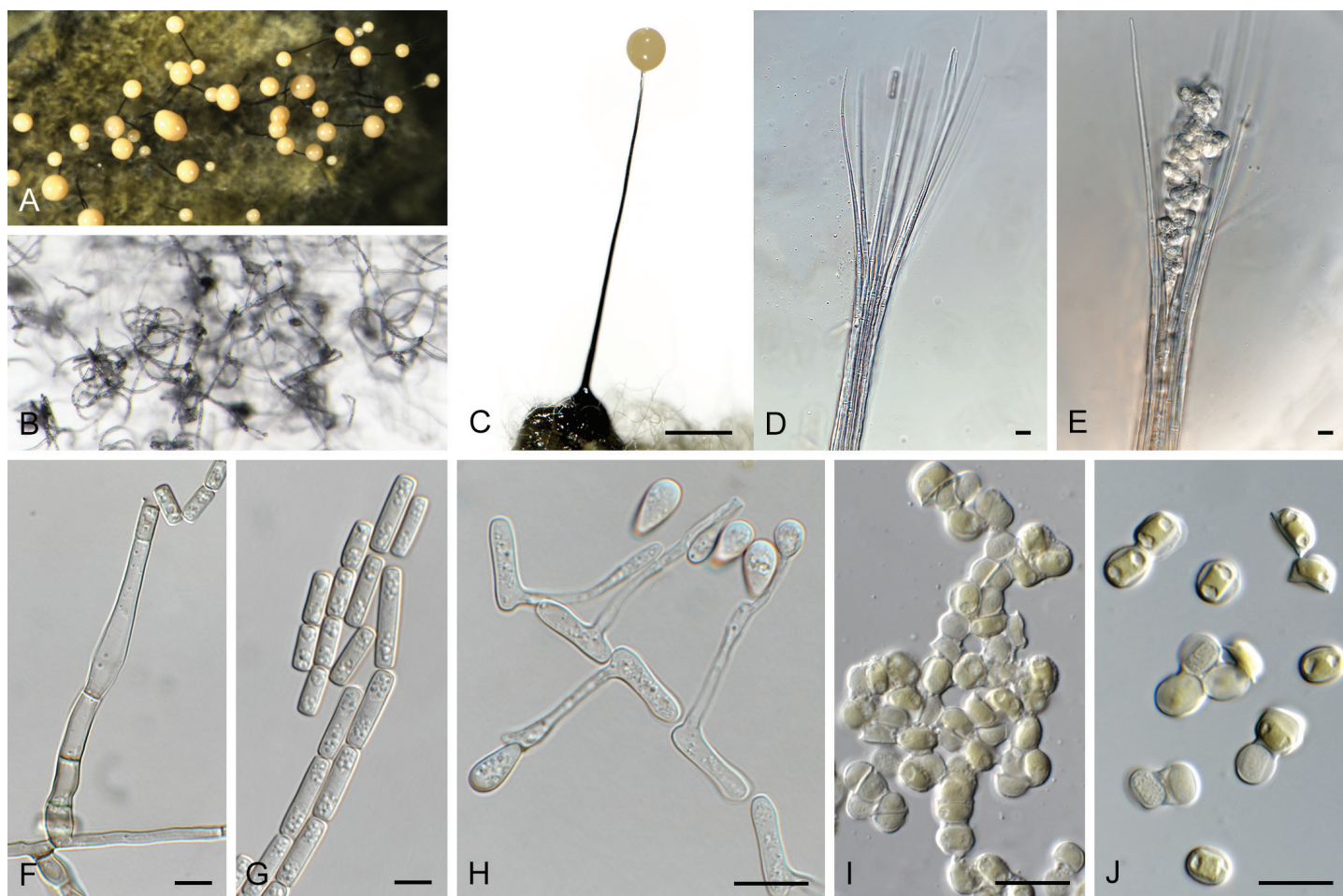


Fig. 7. *Ceratocystis ficicola* (CPC 44213). **A.** Colony on PDA. **B.** Colony on SNA. **C.** Ascoma exuding ascospores. **D, E.** Ostiolar hyphae. **F, G.** Subcylindrical endoconidia. **H.** Aleuroconidia. **I, J.** Ascospores. Scale bars: C = 300 µm, all others = 10 µm.

of CPC 44213 were *Ceratocystis ficicola* (strain CMW38543, GenBank KM495342.1; Identities = 808/809 (99 %), one gap (0 %)), *Ceratocystis polychroma* (strain CMW11424, GenBank KM495368.1; Identities = 805/808 (99 %), no gaps), and *Ceratocystis obpyriformis* (strain CBS 122511, GenBank MH874746.1; Identities = 817/821 (99 %), one gap (0 %)). Closest hits using the *rpb2* (first part) sequence had highest similarity to *Ceratocystis ficicola* (strain CMW38543, GenBank KY685082.1; Identities = 961/961 (100 %), no gaps), *Ceratocystis cercfabiensis* (strain CMW42795, GenBank KY644022.1; Identities = 902/913 (99 %), no gaps), and *Ceratocystis corymbicola* (strain CMW29120, GenBank KY644037.1; Identities = 908/920 (99 %), no gaps). Closest hits using the *tef1* (second part) sequence of CPC 44213 had highest similarity to *Ceratocystis ficicola* (strain C1355, GenBank KY316544.1; Identities = 897/897 (100 %), no gaps), *Ceratocystis fimbriata* (strain C3372, GenBank KY982682.1; Identities = 892/897 (99 %), no gaps), and *Ceratocystis uchidae* (strain C1714, GenBank KY982680.1; Identities = 892/897 (99 %), no gaps). Closest hits using the *tub2* sequence of CPC 44213 had highest similarity to *Ceratocystis huliohia* (strain B, GenBank KU043268.1; Identities = 1 241/1 327 (94 %), 27 gaps (2 %)), *Ceratocystis uchidae* (strain CBS 114720, GenBank KU043266.1; Identities = 1 241/1 327 (94 %), 27 gaps (2 %)), and *Ceratocystis populicola* (strain CBS 114725, GenBank KC589392.1; Identities = 522/621 (84 %), 35 gaps (5 %)). There was no overlap between our *tub2* sequence and the two sequences available on GenBank for *Ceratocystis ficicola* (GenBank KY685077 and KY685078).

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Chloridium caudigerum (Höhn.) S. Hughes, *Canad. J. Bot.* **36**: 748. 1958. Fig. 8.

Description and illustration: Réblová et al. (2022).

Material examined: **Netherlands**, Utrecht Province, Houten, Nieuw Wulven, 1.5 m a.s.l., 52°02'53"N, 05°09'42"E, on branch of *Ulmus laevis* (*Ulmaceae*), 28 Jan. 2022, E.R. Osieck, HPC 3827 = WI-46#4391, culture CPC 42899 = CBS 149688.

Notes: *Chloridium caudigerum* represents a common European species, found especially on decaying wood of deciduous trees. This species closely resembles *Chl. chlamydosporum* and *Chl. virescens* (Réblová et al. 2022). The sexual morph of *Chl. virescens* is also known as *Melanopsammella vermicularioides*. *Melanopsammella* is characterised by ascospores already fragmenting in the ascus. The sexual morph of *Chl. caudigerum* (also present in the collection) is similar but differs in having setose ascomata, which are glabrous in *Chl. virescens* (Réblová loc. cit.).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Chloridium caudigerum* (strain ICMP 22547, GenBank OP455384.1; Identities = 491/491 (100 %), no gaps), *Chloridium virescens* (strain CBS 127310, GenBank MH864519.1; Identities = 498/520 (96 %), one gap (0 %)), and *Chloridium jilinense* (strain NN046507, GenBank OL627659.1; Identities = 457/469 (97 %), two gaps (0 %)). Closest hits using the LSU sequence were *Chloridium caudigerum* (strain ICMP 22547, GenBank OP455491.1; Identities = 844/845 (99 %), one gap (0 %)), *Chloridium jilinense* (strain NN046507, GenBank OL655058.1; Identities = 834/840 (99 %), no gaps), and *Chloridium virescens* (strain CBS 127627, GenBank MH876080.1; Identities = 836/845

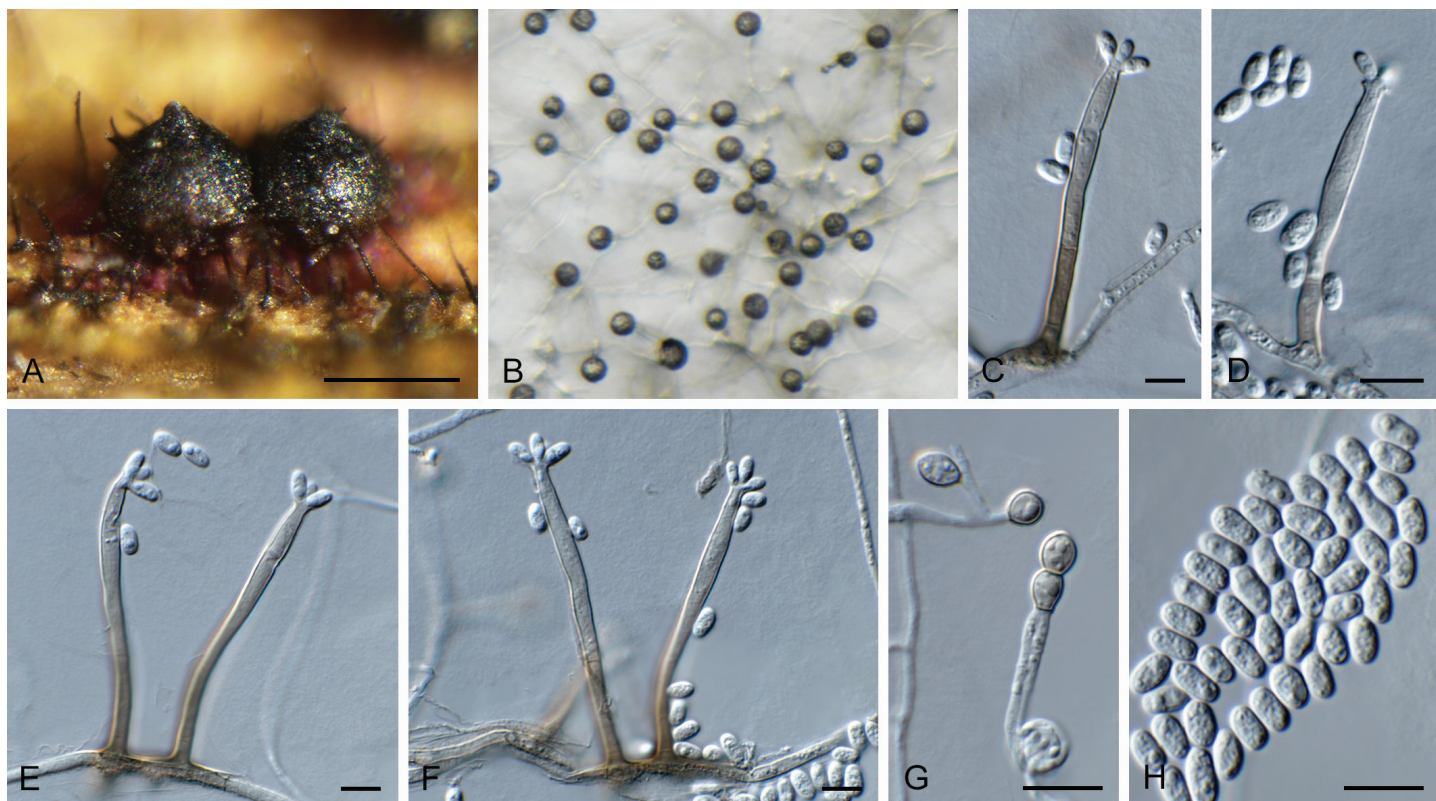


Fig. 8. *Chloridium caudigerum* (CPC 42899). **A.** Ascomata. **B–F.** Conidiophores with conidiogenous cells giving rise to conidia. **G.** Chlamydospores. **H.** Conidia. Scale bars: A = 300 μ m, all others = 10 μ m.

(99 %), one gap (0 %)). Closest hits using the *tef1* (second part) sequence had highest similarity to *Chloridium caudigerum* (strain CBS 145490, GenBank OP464953.1; Identities = 859/860 (99 %), no gaps), *Chloridium moratum* (strain FMR 11343, GenBank OP464997.1; Identities = 838/861 (97 %), two gaps (0 %)), and *Chloridium detriticola* var. *detriticola* (strain ICMP 15144, GenBank OP464977.1; Identities = 836/860 (97 %), no gaps). Closest hits using the *tub2* sequence had highest similarity to *Chloridium caudigerum* (strain FMR 12411, GenBank OP465062.1; Identities = 702/702 (100 %), no gaps), *Chloridium moratum* (strain FMR 11343, GenBank OP465102.1; Identities = 612/703 (87 %), 12 gaps (1 %)), and *Chloridium bellum* var. *luteum* (strain CBS 141.54, GenBank OP465041.1; Identities = 613/718 (85 %), 28 gaps (3 %)).

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Chloridium gamsii Réblová & Hern.-Restr., *Stud. Mycol.* **103**: 143. 2022. Fig. 9.

Description and illustration: Réblová *et al.* (2022).

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae, which become brown and verruculose adjacent to conidiophores, up to 3 µm diam. Conidiophores solitary, erect, straight, flexuous, 1–3-septate, subcylindrical, medium brown, smooth, 35–80 × 3–3.5 µm. Conidiogenous cells integrated, terminal, subcylindrical, medium brown, smooth, with flared collarette; apex incl. collarette 3–5 µm diam, 20–30 × 2–3 µm. Conidia solitary, aggregated in mucoid mass, emerging in sympodial arrangement at apex, hyaline, smooth, guttulate, ellipsoid to ovoid, aseptate, 3.5–6 × 3–3.5 µm. Chlamydospores solitary, terminal on hyphae, medium brown, smooth, thick-walled, aseptate, guttulate, ellipsoid to ovoid, 5–7 × 4–5 µm.

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

Material examined: Netherlands, Friesland Province, Terschelling, on *Cladonia portentosa* (Cladoniaceae), 7 Jun. 2021, J. Boers, HPC 3646 = CBS H-24962, culture CPC 41933 = CBS 149043.

Notes: *Chloridium gamsii* was recently described from decaying wood collected in Belgium and is reported here from a lichen in the Netherlands. Based on published data, this species appears to be common in Europe, Australasia, with a few records from Canada and the USA (Réblová *et al.* 2022).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Chloridium gamsii* (strain CBS 667.75, GenBank OP455415.1; Identities = 481/484 (99 %), no gaps), *Chloridium virescens* (strain CBS 127310, GenBank MH864519.1; Identities = 489/508 (96 %), two gaps (0 %)), and *Chloridium bifforme* (strain ICMP 23429, GenBank OP455363.1; Identities = 472/485 (97 %), two gaps (0 %)). Closest hits using the LSU sequence were *Chloridium gamsii* (strain CBS 667.75, GenBank OP455522.1; Identities = 808/809 (99 %), no gaps), *Chloridium virescens* var. *chlamydosporum* (strain CBS 126074, GenBank MH875525.1; Identities = 802/809 (99 %), no gaps), and *Chloridium peruense* (strain CBS 126074, GenBank OP455531.1; Identities = 802/809 (99 %), no gaps). Closest hits using the *tef1* (second part) sequence had highest similarity to *Chloridium gamsii* (strain CBS 667.75, GenBank OP464990.1; Identities = 814/833 (98 %), no gaps), *Chloridium bifforme* (strain ICMP 23429, GenBank OP464937.1; Identities = 813/833 (98 %), no gaps), and *Chloridium caudigerum* (strain FMR 12411, GenBank OP464956.1; Identities = 807/834 (97 %), two gaps (0 %)).

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Cladophialophora laricicola Crous & Boers, *sp. nov.* MycoBank MB 848823. Fig. 10.

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

Mycelium consisting of medium brown, smooth, septate, branched, 2.5–5 µm diam hyphae. Conidiophores erect,



Fig. 9. *Chloridium gamsii* (CPC 41933). A–D. Conidiophores with conidiogenous cells giving rise to conidia. E. Conidia. F. Chlamydospores. Scale bars = 10 µm.

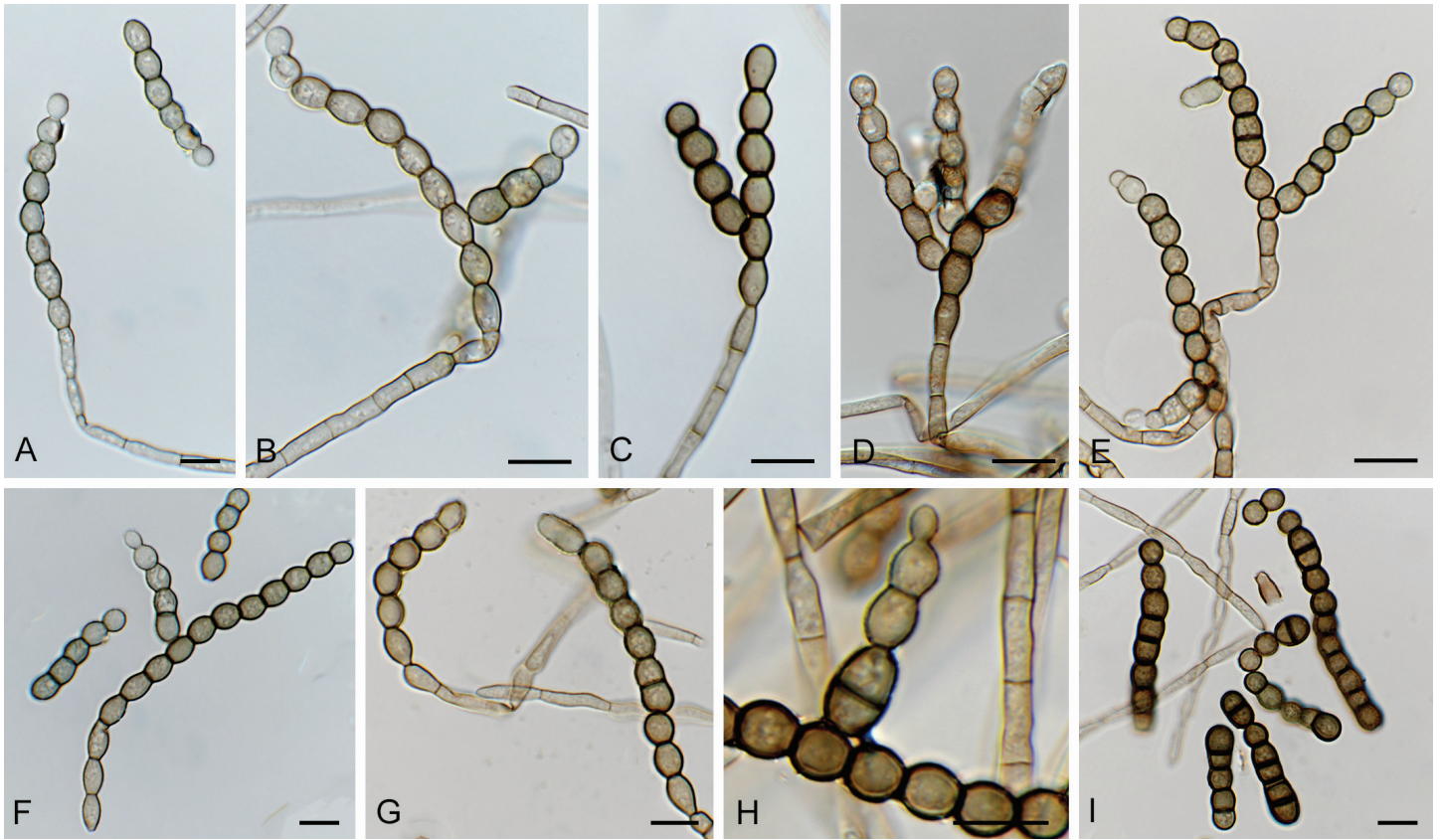


Fig. 10. *Cladophialophora laricicola* (CPC 41384). **A–E, G.** Conidiophores with conidiogenous cells giving rise to conidia. **F, H, I.** Conidia. Scale bars = 10 μm .

flexuous, subcylindrical, medium brown, smooth, with terminal and at times intercalary conidiogenous cells. *Conidiogenous cells* medium brown, subcylindrical, smooth, holoblastic, 10–15 \times 3–4 μm . *Conidia* occurring in cylindrical chains (5–12), brown, smooth to roughened, aseptate, broadly ellipsoid, guttulate, becoming thick-walled, encased in mucoid sheath, individual conidia (6–)8–9(–10) \times (4–)5(–6) μm ; at time cylindrical conidial chains form lateral chains, and in extreme cases arranged in hand-like, penicillate configuration.

Culture characteristics: Colonies erumpent, spreading, with folded surface, lobate, feathery margin, and medium aerial mycelium, reaching 10 mm diam after 2 wk at 25 $^{\circ}\text{C}$. On MEA, PDA and OA surface and reverse iron-grey.

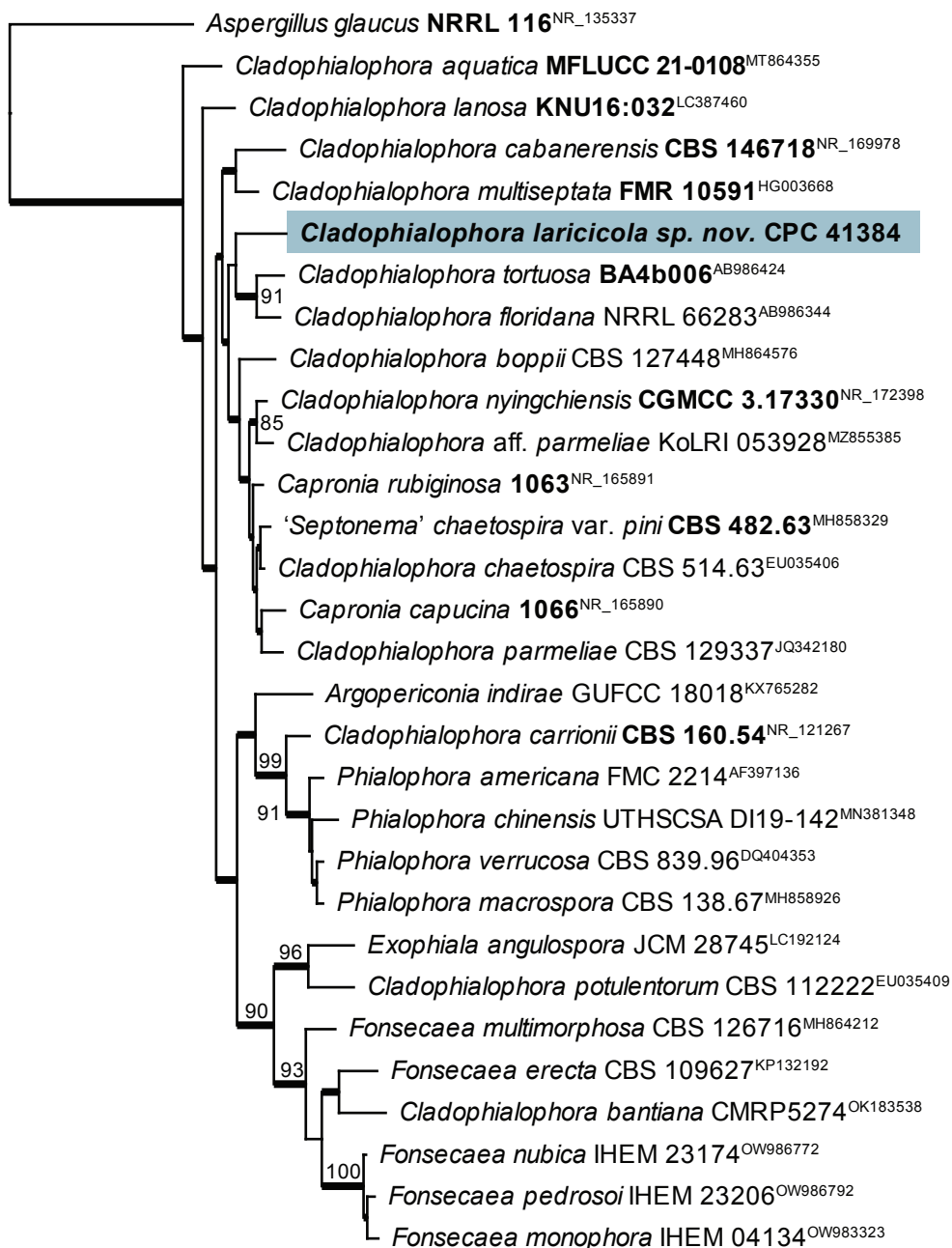
Typus: Netherlands, Drenthe Province, Dwingelderveld National Park, 52.829188, 6.432495, on dead wood of *Larix* sp. (*Pinaceae*), 16 Mar. 2021, J. Boers, HPC 3608 (**holotype** CBS H-24954 culture ex-type CPC 41384 = CBS 148944).

Notes: *Cladophialophora laricicola* is phylogenetically distinct from other species presently known from their DNA sequence data. In the maximum parsimony phylogenetic tree (Fig. 11), it clustered sister to *Cl. tortuosa* and *Cl. floridana* but with no support. A maximum likelihood analysis conducted with IQ-TREE placed it basal to all ingroup species (data not shown). All sequenced loci indicated some affinity with *Cladophialophora* but not a tight association with any other sequenced species (see below).

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

highest similarity to *Cladophialophora aff. parmeliae* (strain KoLRI_053928, GenBank MZ855385.1; Identities = 497/546 (91 %), 12 gaps (2 %)), *Cladophialophora chaetospora* (strain CBS 114747, GenBank EU035403.1; Identities = 551/607 (91 %), 14 gaps (2 %)), and *Capronia rubiginosa* (strain BBB 536, GenBank NR_165891.1; Identities = 534/589 (91 %), 17 gaps (2 %)). Closest hits using the **LSU** sequence were *Capronia semiimmersa* (strain AFTOL-ID 658, GenBank FJ358226.1; Identities = 773/782 (99 %), no gaps), *Phialophora americana* (strain MUCL 40613, GenBank AF050280.1; Identities = 773/782 (99 %), no gaps), and *Argopericonia indirae* (strain GUFCC 18018, GenBank KY977982.1; Identities = 772/782 (99 %), no gaps). Closest hits using the **tef1** (first part) sequence had highest similarity to *Cladophialophora* sp. (strain SYPF 8340, GenBank MF588932.1; Identities = 282/339 (83 %), 17 gaps (5 %)), *Exophiala bergeri* (strain RBG7236, GenBank OP066900.1; Identities = 252/303 (83 %), 15 gaps (4 %)), and *Cladophialophora carrionii* (strain CBS 114399, GenBank KJ609515.1; Identities = 228/269 (85 %), 12 gaps (4 %)). Closest hits using the **tub2** sequence had highest similarity to *Cladophialophora chaetospora* (strain CBS 114747, GenBank KF928578.1; Identities = 308/377 (82 %), ten gaps (2 %)), *Cladophialophora carrionii* (strain CBS 114393, GenBank KF928580.1; Identities = 306/382 (80 %), 21 gaps (5 %)), and *Phialophora americana* (strain CBS 221.97, GenBank KU306350.1; Identities = 283/355 (80 %), ten gaps (2 %)).

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Fig. 11. The first of four equally most parsimonious trees obtained from a '*Cladophialophora*' ITS sequence alignment. The scale bar indicates the number of changes and the numbers at the nodes represent bootstrap support values (>74 %) based on 1 000 resamplings. Branches that appear in the strict consensus tree are highlighted by thickened lines. Culture collection or voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences derived from material with a type status are indicated with a culture or voucher number highlighted with bold face. The tree was rooted to *Aspergillus glaucus* (culture NRRL 116; GenBank NR_135337) and the species treated here is highlighted with bold face.

Cylindromonium eugeniicola Crous, *Persoonia* **43**: 313. 2019.
Fig. 12.

Description and illustration: Crous *et al.* (2019c).

Material examined: **Spain**, Gran Canaria, on dead twig of *Eucalyptus* sp. (*Myrtaceae*), 1 Apr. 2022, A.L. van Iperen, HPC 3904, culture CPC 43326 = CBS 149689.

Notes: The hyphomycete genus *Cylindromonium* (based on *Cy. eugeniicola*) was described from leaf litter of *Eugenia capensis* collected in South Africa (Crous *et al.* 2019c). This is the first

record of the fungus occurring on twigs of a *Eucalyptus* sp. in Spain, which is interesting as both host genera are members of *Myrtaceae*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Cylindromonium eugeniicola* (strain CPC 37170, GenBank NR_166338.1; Identities = 563/567 (99 %), one gap (0 %)), *Cylindromonium lichenicola* (strain CBS 188.70, GenBank MH859549.1; Identities = 514/570 (90 %), 14 gaps (2 %)), and *Cylindromonium dirinariae* (strain FA0006, GenBank LC731277.1; Identities = 513/569 (90 %), 11 gaps (1 %)). Closest hits using the LSU sequence were *Cylindromonium eugeniicola*

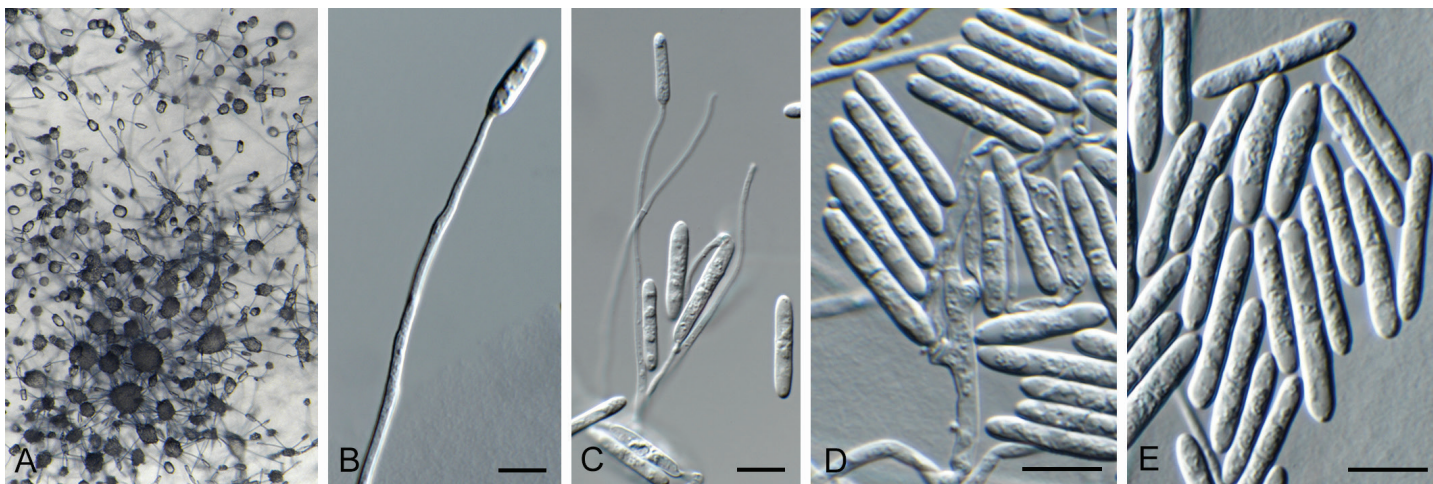


Fig. 12. *Cyldromonium eugeniicola* (CPC 43326). **A.** Colony on SNA. **B–D.** Conidiophores with conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars = 10 μm .

(strain CPC 37170, GenBank NG_068337; Identities = 828/830 (99 %), no gaps), *Trichonectria setadpressa* (voucher A.F.28886, GenBank MT154012; Identities = 819/842 (97 %), no gaps), and *Cylindrocladiella lanceolata* (strain CBS 129565, GenBank MH876849; Identities = 833/861 (97 %), no gaps).

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Cyphellophora neerlandica Crous & Boers, *sp. nov.* MycoBank MB 848821. Fig. 13.

Etymology: Name refers to the Netherlands where it was collected.

Sporulating poorly on SNA. *Mycelium* consisting of pale brown, smooth, branched, septate, 1.5–2 μm diam hyphae. *Conidiophores* reduced to conidiogenous cells aggregated in clusters, pale brown, smooth, ampulliform to ellipsoid, phialidic, 4–6 \times 3–4 μm , with cylindrical collarette, 1–2 μm long. *Conidia* solitary, pale brown, smooth, subcylindrical, straight to slightly curved, apex subobtuse, base truncate, 3-septate, (27–)30–33(–36) \times 2 μm .

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 30 mm

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

Typus: **Netherlands**, Limburg Province, Eys, brick wall, on lichen, 12 Nov. 2021, J. Boers, HPC 3805 (**holotype** CBS H-25164, culture ex-type CPC 42634 = CBS 149512); culture CPC 42641.

Cyphellophora deltoidea (Fil. March. *et al.*) Crous, *comb. nov.* MycoBank MB 848831.

Basionym: *Anthopsis deltoidea* Fil. March. *et al.*, *Canad. J. Bot.* **55**: 117. 1977.

Material examined: **Italy**, Torino, Botanical Garden, from soil, Jun. 1974, A.M. Fontana, holotype CMT 1111.74, ex-type culture CBS 263.77.

Notes: *Cyphellophora neerlandica* is related to *Cyp. clematidis* (conidia aseptate, ellipsoid, (3–)4–5(–6.5) \times (1.5–)2(–2.5) μm ; Crous *et al.* 2019b), and *Cyp. jingdongensis* (only known from its sexual morph; Yang *et al.* 2018), but is phylogenetically and morphologically distinct. In the phylogenetic tree (Fig. 14), *Cyp. neerlandica* clusters in a lineage containing sequences from the ex-type cultures of *Cyp. clematidis* and *Anthopsis deltoidea* (conidia aseptate, deltoid) as well as several unnamed species. *Anthopsis deltoidea* is the type species of the genus *Anthopsis* (Marchisio *et al.* 1977) and should be reduced to synonymy

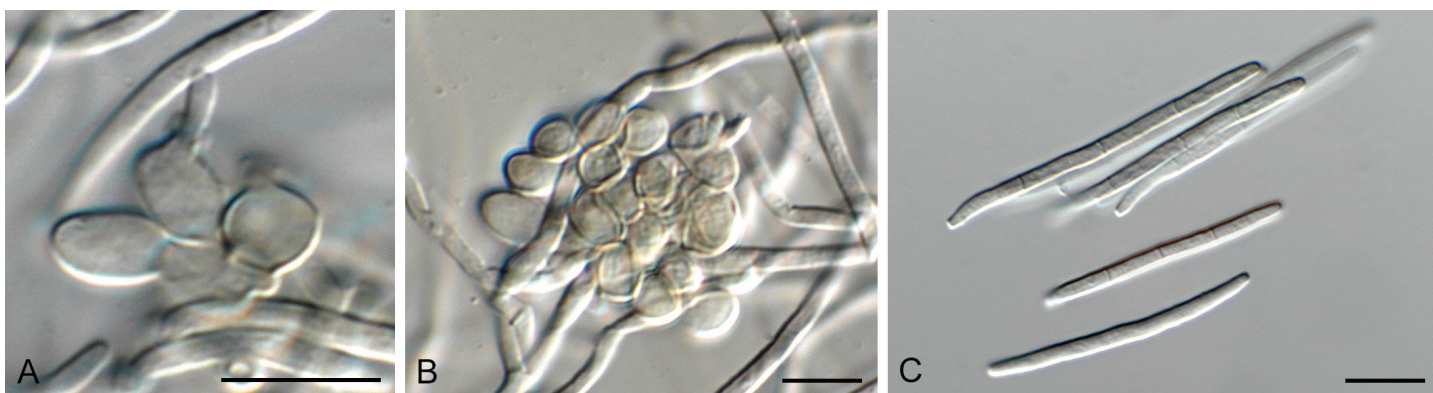


Fig. 13. *Cyphellophora neerlandica* (CPC 42634). **A, B.** Conidiogenous cells giving rise to conidia. **C.** Conidia. Scale bars = 10 μm .

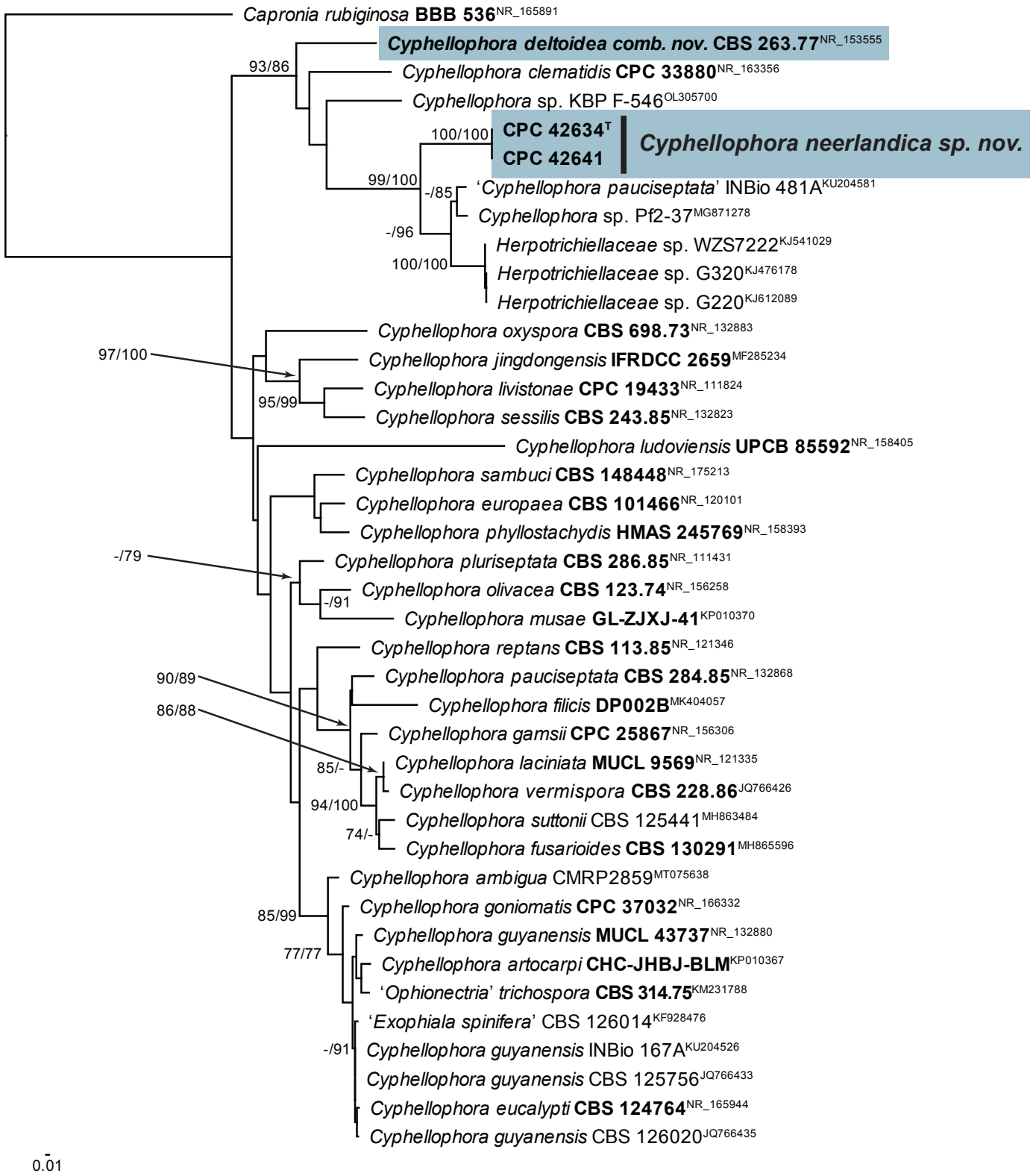


Fig. 14. Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 of the *Anthopsis* / *Cyphellophora* ITS nucleotide alignment. Maximum likelihood (> 74 %) and maximum parsimony (> 74 %) bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes. Culture collection or voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences derived from material with a type status are indicated with a culture or voucher number highlighted with bold face. The tree was rooted to *Capronia rubiginosa* (culture BBB 536; GenBank NR_165891) and the species treated here is highlighted with bold face. The scale bar indicates the expected number of changes per site.

under *Cyphellophora* (De Vries 1962), as this clade now contains species with aseptate, as well as septate conidia. *Cyphellophora clematidis* and *Cyp. deltoidea* also form a well-supported basal lineage in *Cyphellophoraceae* in the phylogeny of Quan *et al.*

(2020) (clade 2 in fig. 3). Two additional species of *Anthopsis* are known, namely *A. catenata* and *A. microspora*. Only the former is known from molecular data, and the ITS and LSU sequences of its ex-type culture (GenBank NR_159623 and MH873124)

blast distant to *Dactylospora*, indicating an association with *Dactylosporaceae* (*Sclerococcales*, *Eurotiomycetes*).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence of CPC 42634 had highest similarity to *Cyphellophora 'pauciseptata'* (voucher INBio 481A, GenBank KU204581.1; Identities = 540/601 (90 %), 16 gaps (2 %)), *Cyphellophora clematidis* (strain CBS 144983, GenBank NR_163356.1; Identities = 469/545 (86 %), 39 gaps (7 %)), and *Anthopsis deltoidea* (strain CBS 263.77, GenBank NR_153555.1; Identities = 398/452 (88 %), 22 gaps (4 %)). The ITS sequence of CPC 42634 is identical to that of CPC 42641 (591/591 nucleotides). Closest hits using the LSU sequence of CPC 42634 were *Cyphellophora clematidis* (strain CBS 144983, GenBank NG_068614.1; Identities = 818/850 (96 %), 11 gaps (1 %)), *Xenobotrytis acaducospora* (strain CBS 219.95, GenBank NG_067437.1; Identities = 816/848 (96 %), eight gaps (0 %)), and *Cyphellophora jingdongensis* (strain IFRDCC 2659, GenBank MF285236.1; Identities = 796/830 (96 %), ten gaps (1 %)). The LSU sequence of CPC 42634 differs with a single substitution from that of CPC 42641 (814/815 nucleotides). Closest hits using the *tub2* sequence of CPC 42634 had highest similarity to *Cyphellophora oxyspora* (strain CBS 698.73, GenBank KC455232.1; Identities = 309/403 (77 %), 22 gaps (5 %)), and *Cyphellophoraceae* sp. (strain not specified, GenBank MN913418.1; Identities = 269/338 (80 %), 22 gaps (6 %)). The *tub2* sequence of CPC 42634 is identical to that of CPC 42641 (495/495 nucleotides).

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Didymella brevopilosa Magaña-Dueñas et al., *J. Fungi* 7: 4. 2021. Fig. 15.

Description and illustration: Magaña-Dueñas et al. (2021).

Conidiomata pycnidial, solitary, eustromatic, brown, 200–250 µm diam, with one to several apical ostioles; wall of 3–4 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells, hyaline, smooth, ampulliform, phialidic, 4–6 × 4–5 µm. *Conidia* solitary, aseptate, fusoid-ellipsoid, apex subobtuse, base truncate, hyaline, smooth, guttulate, (4.5–)5–6(–8) × (2–)2.5–3(–3.5) µm.

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 surface amber, reverse ochreous; on PDA surface and reverse isabelline; on OA surface isabelline.

Material examined: Canada, New Brunswick, Charlotte Co., 1.5 km SW of Little Lepreau, 45.135614° -66.492269°, on buds of *Abies balsamea* (*Pinaceae*), 4 May 2021, D. Malloch, HPC 3633 = CBS H-24968, culture CPC 41600 = CBS 149049.

Notes: *Didymella brevopilosa* was recently described from submerged plant debris collected in freshwater in Spain (conidia aseptate, hyaline, smooth, bacilliform to kidney-shaped, 4–5 × 2–3 µm; Magaña-Dueñas et al. 2021). This is the first record of this fungus from Canada.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Didymella brevopilosa* (as *Didymella* sp.; strain FMR 17415, GenBank OU612373.1; Identities = 498/499 (99 %), no gaps), *Didymella americana* (strain 8907, GenBank MK646045.1; Identities = 524/531 (99 %), one gap (0 %)), *Didymella keratinophila* (strain UTHSC DI16-200, GenBank NR_158275.1; Identities = 524/531 (99 %), one gap (0 %)), and *Peyronella pomorum* (strain F115, GenBank KM979827.1; Identities = 522/529 (99 %), one gap (0 %)). Closest hits using the LSU sequence were *Didymella brevopilosa* (as *Didymella* sp.; strain FMR 17415, GenBank OU612372.1; Identities = 812/812 (100 %), no gaps), *Ascochyta medicaginicola* (strain CBS 111.53, GenBank MH868649.1; Identities = 811/812 (99 %), no gaps), *Didysimulans mezzanensis* (strain MFLUCC 15-0067, GenBank KY496733.1; Identities = 810/812 (99 %), no gaps), and *Didysimulans italica* (strain MFLUCC 15-0059, GenBank KY496730.1; Identities = 810/812 (99 %), no gaps). Closest hits using the *actA* sequence had highest similarity to are *Didymella finnmorkica* (strain CBS 145572, GenBank MK876458.1; Identities = 573/607 (94 %), no gaps), *Didymella combreti* (strain CBS 137982, GenBank KJ869228.1; Identities = 559/600 (93 %), no gaps), and *Didymella rabiei* (strain AR628, GenBank KM244530.1; Identities = 559/610 (92 %), five gaps (0 %)). Closest hits using the *rpb2* sequence had highest similarity to are *Didymella brevopilosa* (as *Didymella* sp.; strain FMR 17415, GenBank OU612359.1; Identities = 482/489 (99 %), no gaps), *Didymella aliena* (strain JZB380013, GenBank

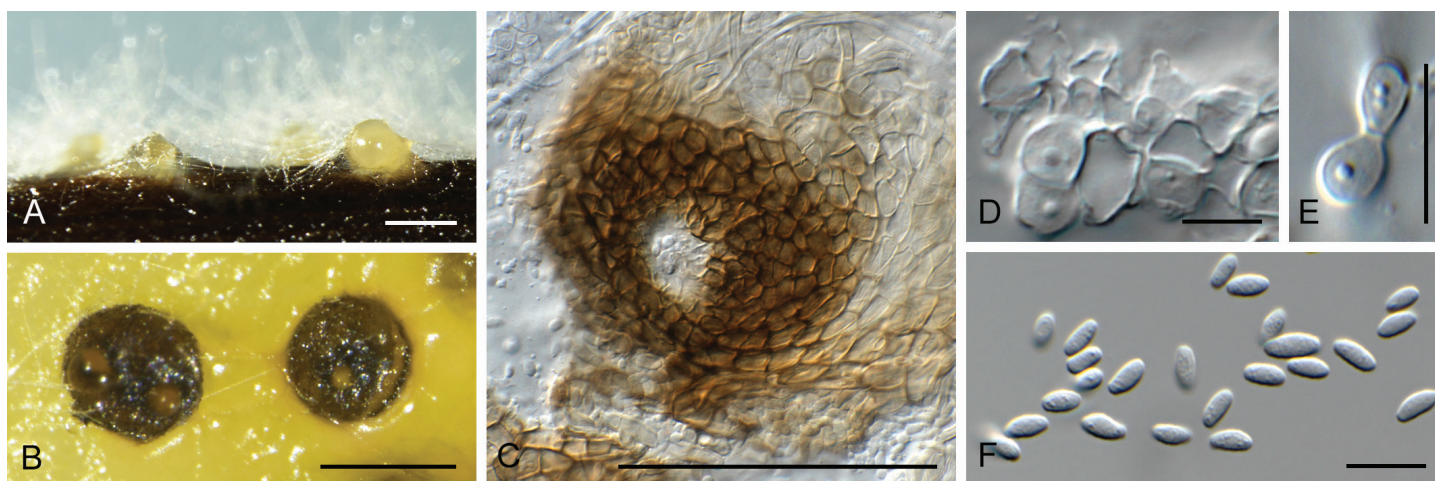


Fig. 15. *Didymella brevopilosa* (CPC 41600). A. Conidiomata on SNA. B. Conidiomata on OA. C. Conidioma with ostiole. D, E. Conidiogenous cells. F. Conidia. Scale bars = 10 µm.

MH645899.1; Identities = 524/575 (91 %), no gaps), *Didymella microchlamydospora* (strain CBS 140543, GenBank MN983514.1; Identities = 458/504 (91 %), no gaps), and *Didymella subrosea* (strain CBS 733.79, GenBank MT018174.1; Identities = 457/504 (91 %), no gaps). Closest hits using the **tub2** sequence had highest similarity to are *Didymella brevopilosa* (as *Didymella* sp.; strain FMR 17415, GenBank no gaps; Identities = 450/454 (99 %), no gaps), *Didymella glomerata* (strain ATCC MYA-2373, GenBank MZ073910.1; Identities = 447/483 (93 %), four gaps (0 %)) and *Didymella combreti* (strain CBS 137982, GenBank KJ869246.1; Identities = 448/488 (92 %), six gaps (1 %)).

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Drepanopeziza populi-albae (Kleb.) Nannf., *Nova Acta R. Soc. Scient. upsal.*, Ser. 4 8(no. 2): 170. 1932. Fig. 16.

Description and illustration: Spiers (1998), Spiers & Hopcroft (1998).

Typus: Russia, Rostov region, Shakhty, Donetsk, on *Populus alba* (*Salicaceae*), 26 Jun. 2021, T.S. Bulgakov, HPC 3708 = CBS H-25157, culture CPC 42336 = CBS 149510.

Notes: *Drepanopeziza populi-albae* is a common foliar pathogen of *Populus alba* (Spiers 1998).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Drepanopeziza populi-albae* (strain CBS 152.66, GenBank MH858754.1; Identities = 547/548 (99 %), one gap (0 %)), *Erysiphe adunca* (strain 3_23, GenBank KY660741.1; Identities = 546/548 (99 %), one gap (0 %)), and *Drepanopeziza brunnea* f. sp. '*monogermtubi*' (as *Marssonina brunnea* f. sp. '*monogermtubi*', strain RBHB1, GenBank KM246347.1;

Identities = 532/548 (97 %), one gap (0 %)). Closest hits using the **LSU** sequence were *Drepanopeziza populi-albae* (strain CBS 153.66, GenBank MH870387.1; Identities = 836/836 (100 %), no gaps), *Drepanopeziza tremulae* (strain CBS 408.64, GenBank MH870103.1; Identities = 812/824 (99 %), three gaps (0 %)), and *Mastigosporium rubricosum* (strain CBS 405.66, GenBank MH870478.1; Identities = 829/845 (98 %), no gaps).

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Endoconidioma populi Tsuneda *et al.*, *Mycologia* 96: 1129. 2004. Fig. 17.

Description and illustration: Tsuneda *et al.* (2004).

On OA forming immersed sclerotium-like structures, 70–250 μm diam, brown, ellipsoid to globose, remaining sterile. On SNA mycelium brown, covered in mucoid layer, roughened, 3–5 μm diam. *Conidiophores* reduced to solitary or aggregated conidiogenous loci on hyphae, denticulate, 2–3 μm diam, blastic, giving rise to solitary conidia. *Conidia* fusoid-ellipsoid, apex subobtuse, base truncate, 0(–1)-septate, hyaline, smooth, becoming pale brown, covered in mucoid layer, (13–)16–18(–22) \times (5–)6–6.5(–7) μm .

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

Material examined: Canada, New Brunswick, Charlotte Co., 1.5 km SW of Little Lepreau, 45.135614° –66.492269°, on buds of *Abies balsamea* (*Pinaceae*), 4 May 2021, D. Malloch, HPC 3633 = CBS H-24972, culture CPC 41602 = CBS 149070.

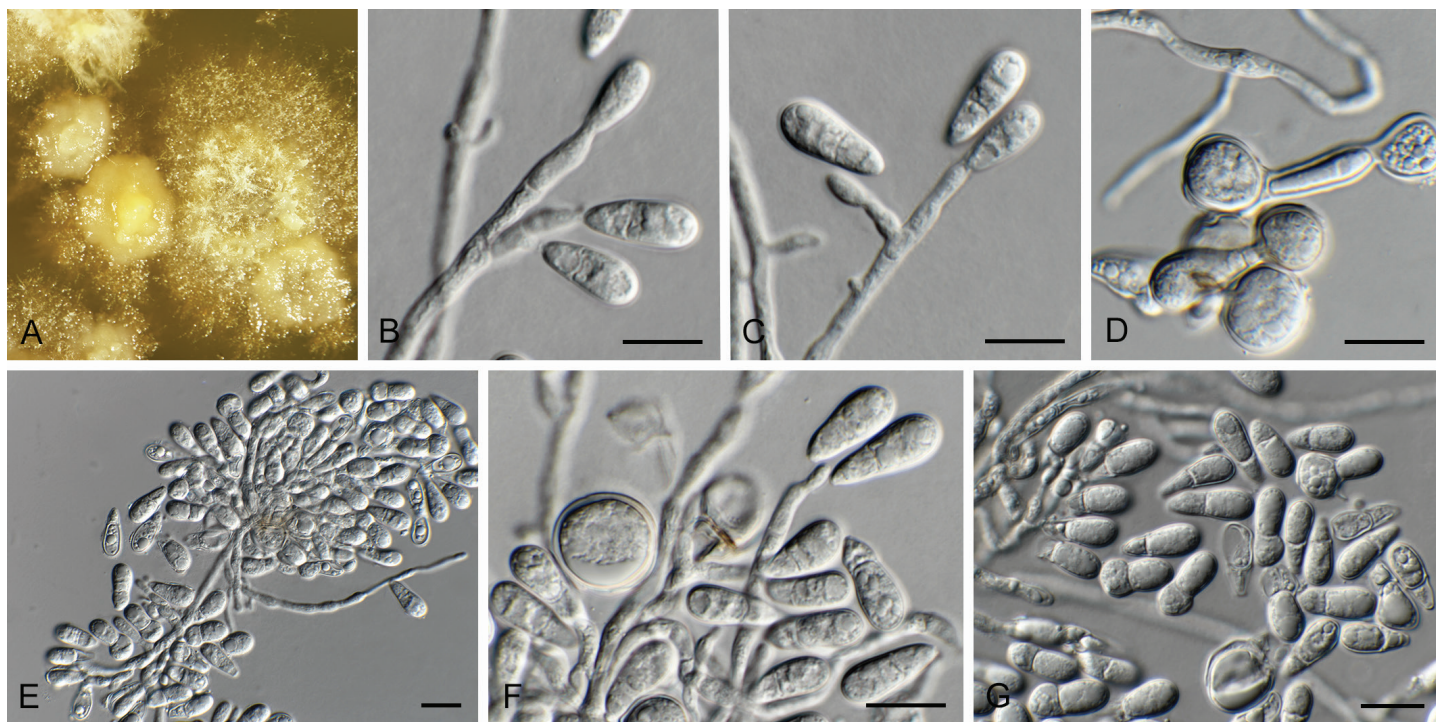


Fig. 16. *Drepanopeziza populi-albae* (CPC 42336). **A.** Colony on MEA. **B–G.** Conidiophores with conidiogenous cells giving rise to conidia (note germinating conidia in **D**). Scale bars = 10 μm .



Fig. 17. *Endoconidioma populi* (CPC 41602). A. Sclerotium-like body on SNA. B–E. Conidiogenous cells giving rise to conidia. Scale bars = 10 µm.

Notes: *Endoconidioma populi* was originally described from twigs of *Populus tremuloides* collected in Canada (Tsuneda *et al.* 2004). It produces a yeast-like morph in culture, as well as endoconidia, and a coelomycetous, coniothyrium-like morph (Crous *et al.* 2020).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to "*Hormonema carpetanum*" (strain 235J14, GenBank KU516485.1; Identities = 570/570 (100 %), no gaps), *Endoconidioma populi* (strain IRAN2350C, GenBank KX180155.1; Identities = 563/563 (100 %), no gaps), *Endoconidioma leucospermi* (as *Coniozyma leucospermi*; strain CBS 111289, GenBank EU552113.1; Identities = 578/581 (99 %), no gaps), and *Endoconidioma populi* (strain UAMH 10297, GenBank NR_121303.1; Identities = 553/556 (99 %), no gaps). Closest hits using the **LSU** sequence were "*Hormonema carpetanum*" (strain ATCC 74360, GenBank MF611880.1; Identities = 826/830 (99 %), no gaps), *Endoconidioma leucospermi* (as *Coniozyma leucospermi*; strain CBS 111289, GenBank EU552113.1; Identities = 825/830 (99 %), no gaps), *Endoconidioma euphorbiae* (strain CPC 38583, GenBank MW175391.1; Identities = 823/830 (99 %), no gaps), and *Endoconidioma populi* (strain UAMH 10297, GenBank NG_059198.1; Identities = 823/830 (99 %), no gaps).

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Fusariella atrovirens (Berk.) Sacc., *Atti dell'Istituto Veneto Scienze* 2: 463. 1884. Fig. 18.

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

Material examined: Namibia, Gobabeb Namib Research Institute, salt pan, lichenicolous on unknown lichen growing on rock, 4 Apr. 2022, P.W. Crous, HPC 3888, culture CPC 43304 = CBS 149690.

Notes: *Fusariella atrovirens* is cosmopolitan, occurring on various plant hosts, leaf litter, dung and in soil (Seifert *et al.* 2011). It is here recorded as lichenicolous, growing on an unknown lichen in Namibia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Fusariella atrovirens* (strain CBS 311.73, GenBank MH860688.1; Identities = 536/536 (100 %), no gaps), *Hydropisphaera erubescens* (strain I-10, GenBank KF813068.1; Identities = 455/456 (99 %), no gaps), and *Fusariella sinensis* (strain OUCMB110148, GenBank KP269058.1; Identities = 533/536 (99 %), no gaps). Closest hits using the **LSU** sequence were *Fusariella bizzozeriana* (strain CBS 306.73, GenBank MH878365.1; Identities = 810/810 (100 %), no gaps), *Fusariella concinna* (strain CBS 312.73, GenBank MH878376.1; Identities = 853/857 (99 %), no gaps), and *Fusariella atrovirens* (strain

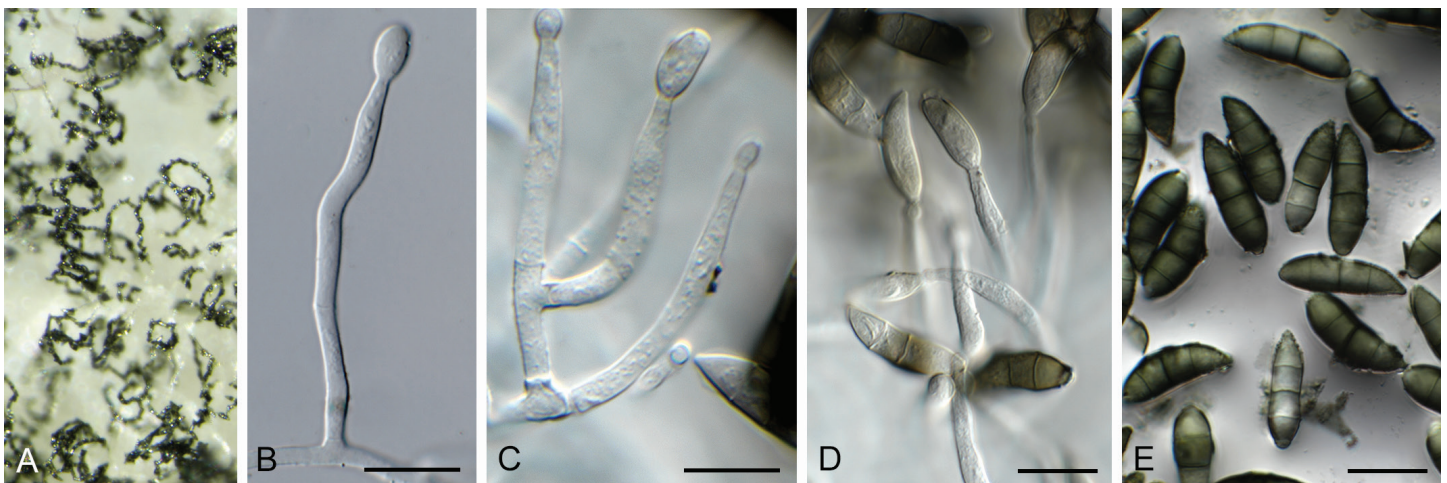


Fig. 18. *Fusariella atrovirens* (CPC 43304). A. Colony on OA. B–D. Conidiogenous cells giving rise to conidia. E. Conidia. Scale bars = 10 µm.

CBS 311.73, GenBank MH872395.1; Identities = 841/845 (99 %), two gaps (0 %)). Closest hits using the *rpb2* (first part) sequence had highest similarity to *Fusariella atrovirens* (strain AK18-21, GenBank OX335003.1; Identities = 857/868 (99 %), no gaps), *Hydropisphaera peziza* (strain CBS 102038, GenBank DQ522444.1; Identities = 716/838 (85 %), two gaps (0 %)), and *Heleococcum aurantiacum* (strain CBS 201.35, GenBank JX158463.1; Identities = 734/863 (85 %), two gaps (0 %)). Closest hits using the *tef1* (second part) sequence had highest similarity to *Fusariella* sp. (strain MFLUCC 15-0844, GenBank KX025155.1; Identities = 899/915 (98 %), no gaps), *Hydropisphaera erubescens* (strain AFTOL-ID 186, GenBank DQ518174.1; Identities = 867/916 (95 %), no gaps), and *Heleococcum japonense* (strain CBS 397.67, GenBank JX158398.1; Identities = 859/916 (94 %), no gaps). No *tef1* sequences of *Fusariella atrovirens* are available for comparison.

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

Fusariella hughesii Chab.-Frydm., *Canad. J. Bot.* **42**: 1485. 1964. Fig. 19.

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

Mycelium consisting of hyaline, smooth, branched, septate, 2.5–3 µm diam hyphae, forming hyphal swellings (up to 10 µm diam) in older hyphae on MEA and PDA. *Conidiophores* solitary or aggregated, erect, arising from superficial hyphae, subcylindrical, branched, up to 5-septate, 100 µm tall. *Conidiogenous cells* terminal and intercalary, subcylindrical with apical taper, hyaline, smooth, 20–35 × 2.5–3 µm, phialidic, giving rise to basipetal conidial chains. *Conidia* subcylindrical, 3-septate, guttulate, hyaline to pale greenish, smooth, apex obtuse, base obconically truncate, hilum 2–2.5 µm diam, straight, occurring in long, unbranched chains, (8–)16–19(–22) × (2.5–)3(–3.5) µm.

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

Material examined: **Ukraine**, Dvorichna district, Kharkiv region, Krasne Pershe village, National Park Dvorichanskyi, on overwintered stems of *Adonis vernalis* (*Ranunculaceae*), 11 Apr. 2021, A. Akulov, CWU (MYC) AS 8121 = HPC 3630 = CBS H-24976, culture CPC 41594 = CBS 149074.

Notes: *Fusariella hughesii*, which was originally isolated from seeds of *Trigonella arabica* and *Phalaris minor* in Israel (Lin *et al.* 2016), is reported here from dead stems of *Adonis vernalis* in Ukraine.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the *ITS* sequence had highest similarity to *Fusariella hughesii* (strain CBS 435.70, GenBank MH859784.1; Identities = 569/576 (99 %), no gaps), *Fusariella sinensis* (strain OUCMBI110131, GenBank KP269041.1; Identities = 545/569 (96 %), four gaps (0 %)), and *Fusariella atrovirens* (strain CBS 311.73, GenBank MH860688.1; Identities = 554/579 (96 %), four gaps (0 %)). Closest hits using the *LSU* sequence were *Fusariella hughesii* (strain CBS 435.70, GenBank MH871547.1; Identities = 722/724 (99 %), no gaps), *Hydropisphaera erubescens* (strain CBS 128364, GenBank MH876356.1; Identities = 721/724 (99 %), no gaps), and *Fusariella concinna* (strain CBS 312.73, GenBank MH878376.1; Identities = 720/724 (99 %), no gaps).

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Geonectria muralis Crous & Boers, *sp. nov.* MycoBank MB 848824. Fig. 20.

Etymology: Name refers to the phycoparasitic habit of the fungus on an old church wall.

Perithecia globose, 150–180 µm diam, orange, arising from substratal hyphae, not changing colour in KOH, with central ostiole, 15 µm diam; wall 15–18 µm thick, of 3–4 layers of *textura angularis*; outer wall smooth, with hyphal outgrowths; hyphae smooth, branched, septate, 3–4 µm diam. *Asci* 8-spored, stipitate, subcylindrical, unitunicate with apical mechanism, 40–65 × 9–11 µm. *Ascospores* bi- to triseriate, hyaline, becoming pale brown with age, smooth, guttulate, broadly ellipsoid, medianly 1-septate, constricted at septum, (12–)14–16(–17) × (5–)8–9 µm. *Asexual morph* not seen.

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

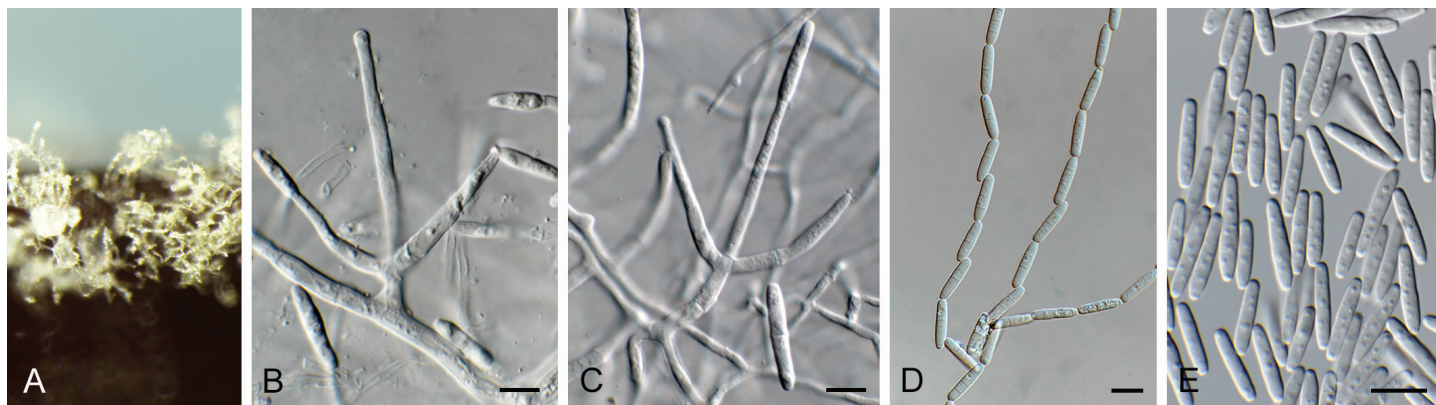


Fig. 19. *Fusariella hughesii* (CPC 41594). **A.** Sporulation on PNA. **B, C.** Conidiophores and conidiogenous cells giving rise to conidia. **D, E.** Conidia. Scale bars = 10 µm.

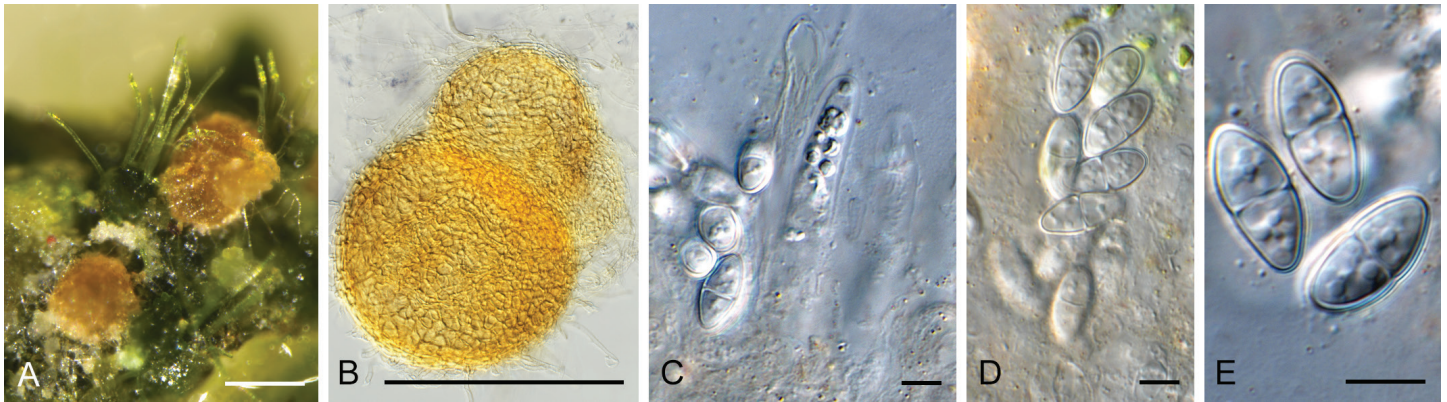


Fig. 20. *Geonectria muralis* (CPC 42404). **A.** Ascomata *in vivo*. **B.** Ascomata *in vitro*. **C, D.** Asci with ascospores. **E.** Ascospores. Scale bars: A, B = 180 μ m, all others = 10 μ m.

35 mm diam after 2 wk at 25 °C. On MEA and PDA surface and reverse sienna; on OA surface apricot. Homothallic, with perithecia also forming in culture.

Typus: Netherlands, Gelderland Province, Dodewaard, church, on algae growing on the bottom part of wall, 7 Sep. 2021, J. Boers, HPC 3749 (**holotype** CBS H-25161, culture ex-type CPC 42404 = CBS 149515); cultures CPC 42405, 42406.

Notes: *Geonectria muralis* is related to *Nectria pyrosphaera* (CBS 165.26), *Nectria zonata* (AR 1612) and *Geonectria subalpina* (CBS 143540). In the phylogenetic tree (Fig. 21), it clustered with 97 % ML bootstrap support and 93 % parsimony bootstrap support with '*Nectria zonata*', a '*Hydropisphaera* sp.' and the LSU sequence of the ex-type strain of *Geonectria subalpina*, the type species of the monotypic genus *Geonectria*. *Geonectria*, based on *G. subalpina*, was described from bare soil collected in the subalpine region, and is characterised by orange perithecia that do not change colour in 3 % KOH, striate, 1-septate, hyaline, finely striate ascospores, and an acremonium-like asexual morph (Lechat *et al.* 2018).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 42404 had highest similarity to *Hydropisphaera* sp. BGL-2019a (voucher BDNA-L-0000095, GenBank MN187059.1; Identities = 501/554 (90 %), 28 gaps (5 %)), *Nectria pyrosphaera* (strain CBS 165.26, GenBank MH854877.1; Identities = 476/569 (84 %), 41 gaps (7 %)), and *Heleococcum aurantiacum* (strain CBS 201.35, GenBank MH855645.1; Identities = 472/568 (83 %), 36 gaps (6 %)). The ITS sequence of CPC 42404 is identical to those of CPC 42405 and CPC 42406 (both 552/552 nucleotides). Closest hits using the **LSU** sequence of CPC 42404 were *Hydropisphaera* sp. BGL-2019a (voucher BDNA-L-0000095, GenBank MN181431.1; Identities = 828/842 (98 %), three gaps (0 %)), *Geonectria subalpina* (strain CBS 143540, GenBank NG_067817.1; Identities = 808/842 (96 %), four gaps (0 %)), and *Nectria zonata* (strain AR 1612, GenBank U17424.1; Identities = 809/845 (96 %), 11 gaps (1 %)). The LSU sequence of CPC 42404 differs from that of CPC 42405 at three nucleotide positions (796/799 nucleotides, all in repeat motifs).

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Harposporium illinoense Crous & Jurjević, *sp. nov.* MycoBank MB 848825. Fig. 22.

Etymology: Name refers to Illinois, the state in the USA where it was isolated.

Mycelium consisting of hyaline, smooth, branched, septate, 2–3 μ m diam hyphae, constricted at septa with age. *Conidiophores* reduced to conidiogenous cells; phialides solitary on hyphae, or in clusters, ampulliform, 5–7 \times 2.5–3 μ m, with cylindrical necks, 1.5–2 \times 1 μ m. *Conidia* solitary, aggregating in mucoid mass, hyaline, smooth, aseptate, sickle-shaped, widest in middle, apex subobtusate, base truncate, 6–10 \times 1–2 μ m.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and feathery, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA surface amber, reverse sienna; on PDA surface amber, reverse sienna; Czapek Yeast Autolysate Agar (CYA) surface amber, reverse sienna; on OA surface hazel. It also shows antibacterial properties on CYA and MEA. No growth at 37 °C, on CYA.

Typus: USA, Illinois, marijuana greenhouse, Rockwool, Oct. 2021, Z. Jurjević 5670 (**holotype** CBS H-25170, culture ex-type CPC 42872 = CBS 149456).

Notes: Species of *Harposporium* parasitise free-living nematodes and rotifers. Most species of *Harposporium* infect nematodes via ingested conidia (Glockling 1998). *Harposporium illinoense* was isolated from rockwool in a greenhouse, and was probably associated with nematodes. Phylogenetically, *H. illinoense* is quite distinct from other presently known from DNA data (Fig. 23) and also the blast results (see below) are insufficiently conclusive to provide a proper placement for this species.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Purpureocillium takamizusanense* (strain PT3, GenBank CP086360.1; Identities = 476/554 (86 %), 46 gaps (8 %)), *Harposporium helicoides* (strain CBS 944.70, GenBank MH860014.1; Identities = 490/558 (88 %), 29 gaps (5 %)), and *Drechmeria balanoides* (as *Haptocillium balanoides*, strain Harp5, GenBank EF546660.1; Identities = 475/540 (88 %), 27 gaps (5 %)). Closest hits using the **LSU** sequence were *Harposporium harposporiferum* (strain CBS 213.86, GenBank MH873635.1;

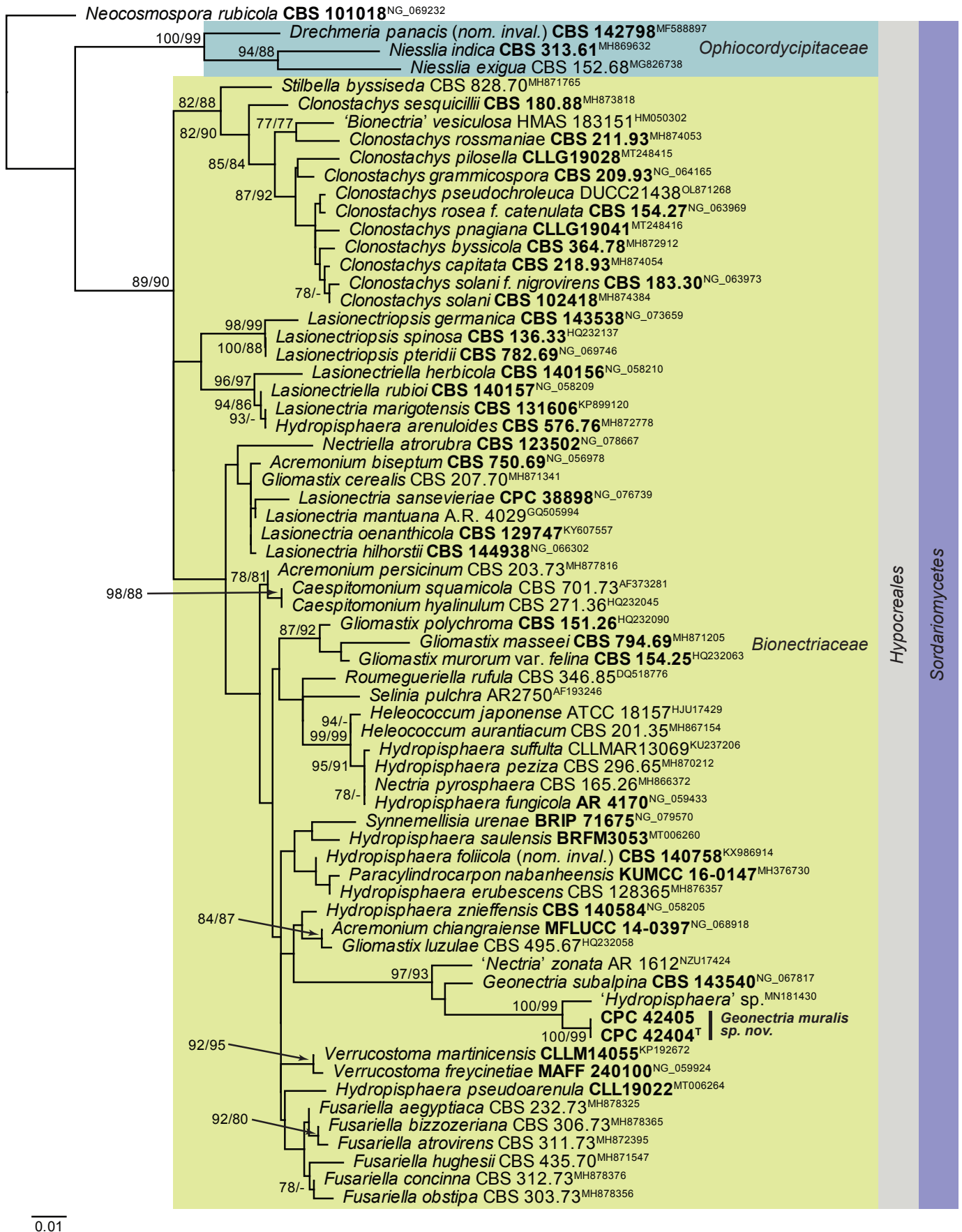


Fig. 21. Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 of the Hypocreales LSU nucleotide alignment. Maximum likelihood (> 74 %) and maximum parsimony (> 74 %) bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes. Culture collection or voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences derived from material with a type status are indicated with a culture or voucher number highlighted with bold face. The tree was rooted to *Neocosmospora rubicola* (culture CBS 101018; GenBank NG_069232) and the species treated here is highlighted with bold face. The families, order and class are shown in coloured blocks to the right of the tree. The scale bar indicates the expected number of changes per site.

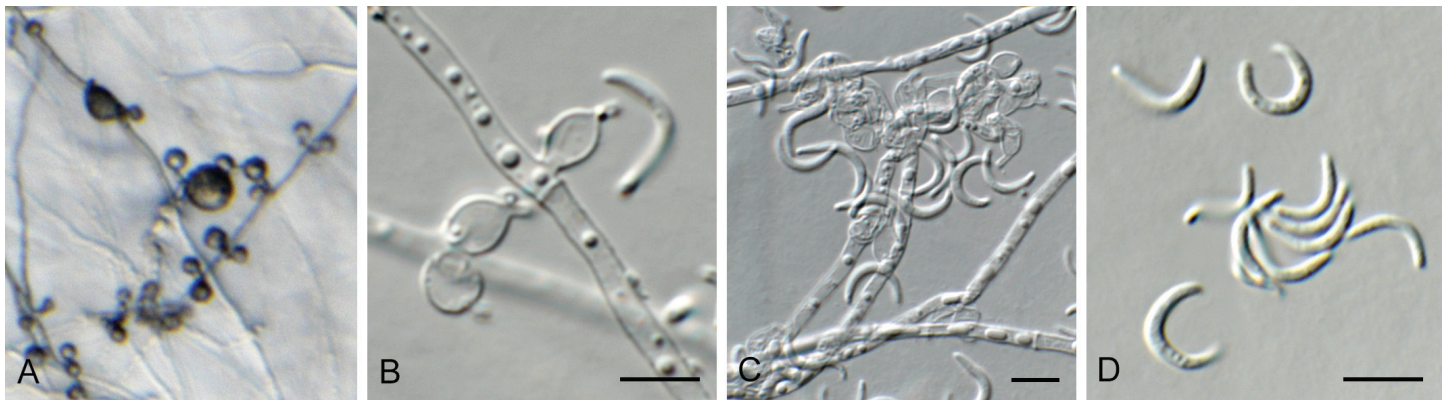


Fig. 22. *Harposporium illinoensis* (CPC 42872). A. Colony on SNA. B, C. Conidiogenous cells giving rise to conidia. D. Conidia. Scale bars = 10 µm.

Identities = 814/836 (97 %), three gaps (0 %)), *Drechmeria zeospora* (strain CBS 335.80, GenBank NG_063928.1; Identities = 787/809 (97 %), two gaps (0 %)), and *Drechmeria panacis* (*nom. inval.*) (strain SYPF 8335, GenBank MF588897.1; Identities = 810/833 (97 %), two gaps (0 %)). Closest hits using the *actA* sequence had highest similarity to *Purpureocillium lilacinum* (strain PLFJ-1, GenBank XM_018325012.1; Identities = 314/329 (95 %), no gaps), and *Purpureocillium takamizusanense* (strain PT3, GenBank XM_047986424.1; Identities = 317/338 (94 %), one gap (0 %)). Closest hits using the *rpb2* (first part) sequence had highest similarity to *Isaria takamizusanensis* (strain NHJ 3497, GenBank EU369074.1; Identities = 697/788 (88 %), no gaps), *Purpureocillium lilacinum* (strain G406, GenBank KJ443162.1; Identities = 717/813 (88 %), no gaps), and *Cordyceps gunnii* (strain OSC 76404, GenBank DQ522426.1; Identities = 674/767 (88 %), no gaps). Closest hits using the *tef1* (second part) sequence had highest similarity to *Ophiocordyceps myrmicarum* (strain CG1361, GenBank MG922555.1; Identities = 827/877 (94 %), no gaps), *Hirsutella citriformis* (voucher ARSEF 1446, GenBank KM651990.1; Identities = 840/892 (94 %), no gaps), and *Ophiocordyceps delicatula* (strain ARSEF 14442, GenBank MZ246828.1; Identities = 840/892 (94 %), no gaps). Closest hits using the *tub2* sequence had highest similarity to *Sarocladium kiliense* (strain CBS 400.52, GenBank KM232119.1; Identities = 321/418 (77 %), 25 gaps (5 %)), *Sarocladium junci* (strain CPC 41107, GenBank OK651210.1; Identities = 317/407 (78 %), 26 gaps (6 %)), and *Paecilomyces wawuensis* (strain GZU-BCECYN4-3, GenBank JQ965117.1; Identities = 317/408 (78 %), 25 gaps (6 %)).

Authors: P.W. Crous, J.Z. Groenewald & Z. Jurjević

Hysterobrevium rosae Jayasiri *et al.*, *Mycosphere* 9: 818. 2018.

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

Material examined: **Netherlands**, Utrecht Province, Nieuw Wulven, near Houten, 1.5 m a.s.l., 52°02'53"N, 05°10'09"E, on bamboo stick (used as support post, not locally grown), 11 Feb. 2022, E.R. Osieck, HPC 3837 = WI-48/ #4404, culture CPC 42948 = CBS 149699.

Notes: The genus *Hysterobrevium* is characterised by hysterothecaceous ascomata and muriform spores, which are less than 25 µm in length (Boehm *et al.* 2009). *Hysterobrevium rosae* is morphologically similar to *H. mori* (Boehm *loc. cit.*), but distinguished in having smaller hysterothecia, shorter asci and hyaline ascospores (Jayasiri *et al.* 2018).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the *ITS* sequence had highest similarity to *Hysterobrevium mori* (strain A1045A, GenBank MT230464.1; Identities = 710/710 (100 %), no gaps), *Hysterobrevium constrictum* (strain JCM 2753, GenBank NR_175063.1; Identities = 676/716 (94 %), four gaps (0 %)), and *Hysterobrevium* sp. MR-2017a (strain MFLUCC 16-2163, GenBank MZ467050.1; Identities = 393/422 (93 %), six gaps (1 %)). No *ITS* sequence of *Hysterobrevium rosae* was available for comparison. Closest hits using the *LSU* sequence were *Hysterobrevium rosae* (strain MFUCC 14-0551, GenBank MH535897.1; Identities = 844/844 (100 %), no gaps), *Hysterobrevium mori* (strain CBS 123335, GenBank FJ161202.2; Identities = 866/869 (99 %), no gaps), and *Gloniopsis praelonga* (strain SMH5280, GenBank GQ221912.2; Identities = 865/869 (99 %), no gaps). Closest hits using the *rpb2* (first part) sequence had highest similarity to *Hysterobrevium smilacis* (as *Gloniopsis smilacis*, strain CBS 114601, GenBank FJ161114.1; Identities = 833/882 (94 %), no gaps), and *Hysterobrevium constrictum* (strain HKAS 121127, GenBank OK506220.1; Identities = 808/876 (92 %), no gaps). Closest hits using the *tef1* (second part) sequence had highest similarity to *Hysterobrevium rosae* (strain MFUCC 14-0551, GenBank MH535879.1; Identities = 733/733 (100 %), no gaps), *Hysterobrevium mori* (strain EB 0315, GenBank FJ161106.1; Identities = 745/771 (97 %), no gaps), and *Hysterobrevium smilacis* (strain CBS 114601, GenBank FJ161091.1; Identities = 728/763 (95 %), no gaps).

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

Microcera physciae Crous & Boers, *Persoonia* 47: 233. 2021. Fig. 24.

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

Material examined: **Netherlands**, Limburg Province, Eys, brick wall, on lichen, 12 Nov. 2021, J. Boers, HPC 3805, culture CPC 42638.

Notes: *Microcera physciae* is a lichenicolous fungus described from *Physcia tenella* in the Netherlands (Crous *et al.* 2021b), while *M. lichenicola* was described from *Parmelia sulcata*, also in the Netherlands (Crous *et al.* 2022a).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the *ITS* sequence had highest similarity to *Microcera lichenicola* (strain CBS 149169, GenBank ON811502.1; Identities = 530/530 (100 %), no gaps), *Microcera*

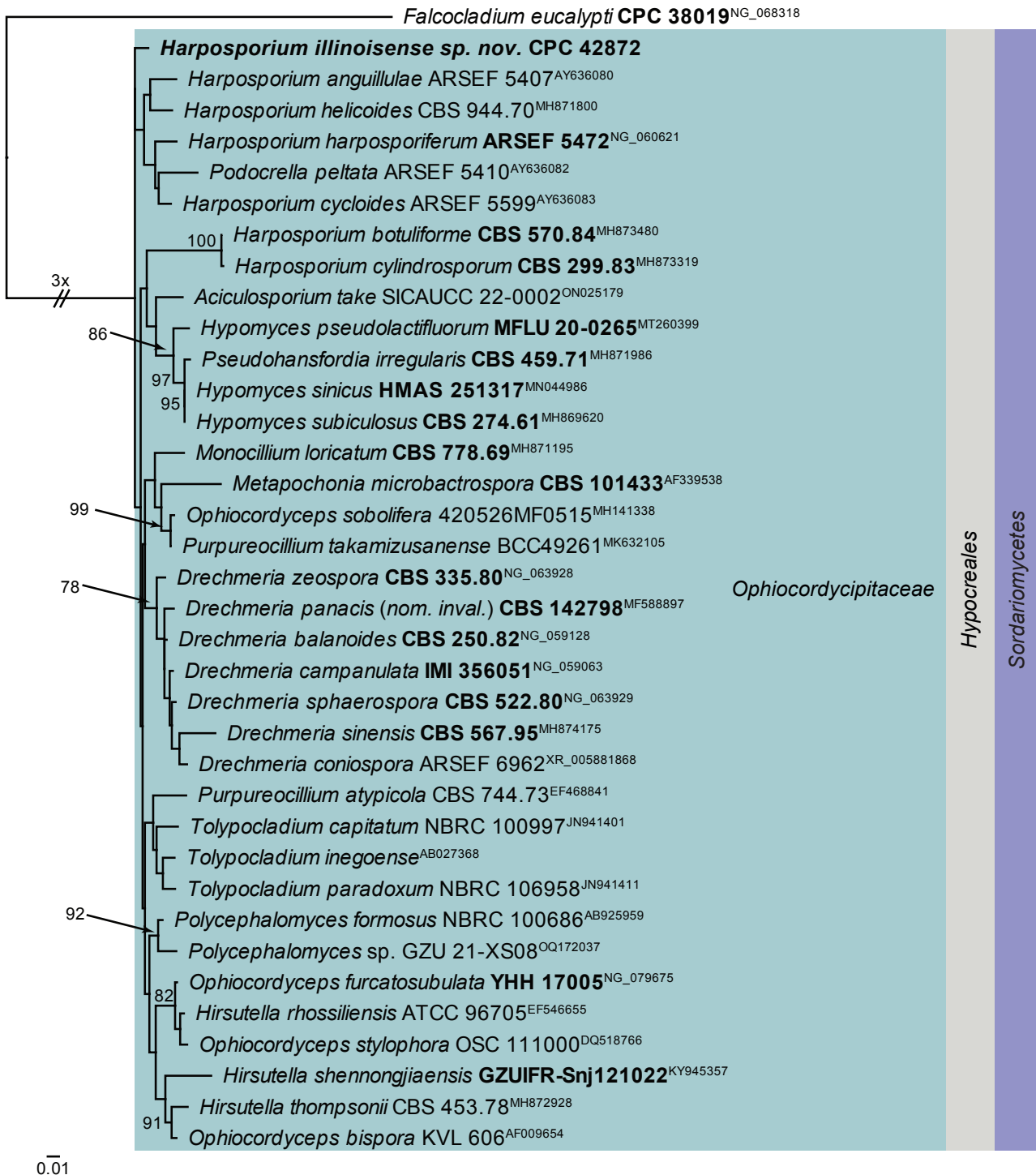


Fig. 23. Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 of the *Ophiocordycipitaceae* LSU nucleotide alignment. Bootstrap support values (> 75 %) from 1 000 non-parametric bootstrap replicates are shown at the nodes. Culture collection or voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences derived from material with a type status are indicated with a culture or voucher number highlighted with bold face. The tree was rooted to *Falcocladium eucalypti* (culture CPC 38019; GenBank NG_068318) and the species treated here is highlighted with bold face. The family, order and class are shown in coloured blocks to the right of the tree. The scale bar indicates the expected number of changes per site.

physciae (strain CBS 148283, GenBank NR_175225.1; Identities = 496/497 (99 %), no gaps), and *Microcera larvarum* (strain CBS 738.79, GenBank KM231825.1; Identities = 519/531 (98 %), three gaps (0 %)). Closest hits using the **LSU** sequence were *Microcera physciae* (strain CBS 148283, GenBank NG_081335.1; Identities = 814/814 (100 %), no gaps), *Microcera lichenicola* (strain CBS 149169, GenBank ON811561.1; Identities = 814/815 (99 %), no gaps), and *Microcera rubra* (strain CBS 638.76, GenBank

NG_058100.1; Identities = 805/816 (99 %), no gaps). Closest hits using the **rpb1** sequence had highest similarity to *Microcera physciae* (strain CPC 41284, GenBank OK651153.1; Identities = 717/720 (99 %), two gaps (0 %)), *Microcera lichenicola* (strain CBS 148313, GenBank ON803533.1; Identities = 690/720 (96 %), two gaps (0 %)), and *Microcera coccophila* (strain MAFF 241482, GenBank KC291895.1; Identities = 629/689 (91 %), two gaps (0 %)). Closest hits using the **rpb2** (first part) sequence had highest

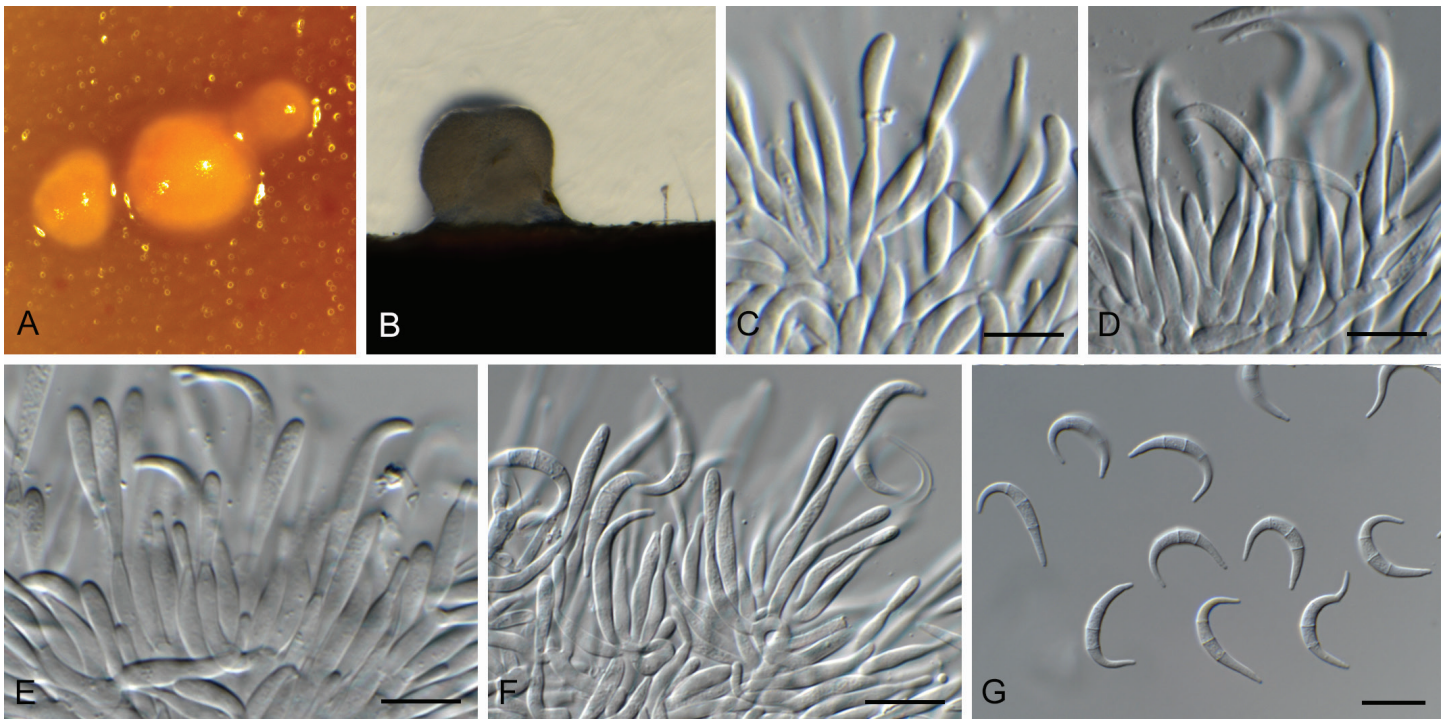


Fig. 24. *Microcera physciae* (CPC 42638). **A.** Colony sporulating on OA. **B.** Colony sporulating on PNA. **C–F.** Conidiophores and conidiogenous cells giving rise to conidia. **G.** Conidia. Scale bars = 10 μ m.

similarity to *Microcera physciae* (strain CPC 41284, GenBank OK651168.1; Identities = 871/874 (99 %), no gaps), *Microcera lichenicola* (strain CBS 148313, GenBank ON803543.1; Identities = 840/876 (96 %), one gap (0 %)), and *Microcera larvarum* (strain NRRL 20473, GenBank JX171587.1; Identities = 766/850 (90 %), one gap (0 %)). Closest hits using the *tef1* (first part) sequence had highest similarity to *Microcera physciae* (strain CPC 41284, GenBank OK651190.1; Identities = 460/470 (98 %), two gaps (0 %)), *Microcera lichenicola* (strain CBS 148313, GenBank ON803570.1; Identities = 449/483 (93 %), six gaps (1 %)), and *Microcera larvarum* (strain CBS 738.79, GenBank KM231957.1; Identities = 375/470 (80 %), 24 gaps (5 %)). Closest hits using the *tub2* sequence had highest similarity to *Microcera physciae* (strain CPC 41284, GenBank OK651208.1; Identities = 526/526 (100 %), no gaps), *Microcera lichenicola* (strain CBS 149169, GenBank ON803591.1; Identities = 524/540 (97 %), two gaps (0 %)), and *Microcera larvarum* (strain CBS 169.30, GenBank AB587032.1; Identities = 274/304 (90 %), no gaps).

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Miricatena prunicola Punith. & Spooner, *Kew Bull.* **66:** 638. 2011. Fig. 25.

Classification: *Leotiomycetes*, *Helotiales*, *incertae sedis*.

Description and illustration: Punithalingam & Spooner (2011).

The compound conidia and conidiogenesis of *M. prunicola* was discussed and fully described by Punithalingam & Spooner (2011). In this paper they comment on the terminal cells being ampulliform to lageniform to obpyriform. What they did not observe, however, is that these terminal cells become fertile, acting as conidiogenous cells, or give rise to 2–4 smaller

ampulliform phialides, 5–10 \times 3–4.5 μ m, that again give rise to solitary conidia, ellipsoid, aseptate, hyaline, smooth, guttulate, 3–4 \times 2.5–3 μ m, aggregating in a mucoid conidial mass.

Culture characteristics: Colonies erumpent, spreading, with sparse to moderate aerial mycelium and even, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On malt extract agar (MEA) surface and reverse isabelline; on potato dextrose agar (PDA) surface cinnamon, reverse isabelline; on oatmeal agar (OA) surface sienna to orange.

Typus: **Netherlands**, Gelderland Province, Ede, Kreelsche Zand, on leaves of *Prunus serotina* (*Rosaceae*), 7 Nov. 2021, *E. Sloatweg*, HPC 3800 (**epitype** designated here CBS H-25163, MBT 10013416, culture ex-epitype CPC 42627 = CBS 149448). **UK**, Surrey, Frensham, Little Pond (near), on living leaves of *Prunus serotina*, 8 Jul. 2007, *B.M. Spooner* (**holotype** K(M) 155328).

Notes: The monotypic genus *Miricatena* was introduced for *M. prunicola*, a foliar pathogen of *Prunus serotina* in the UK (Punithalingam & Spooner 2011). Due to the lack of cultures and DNA data, the phylogenetic position of *Miricatena* has remained unknown. The present record of *M. prunicola* from the Netherlands made it possible to designate an epitype for this pathogen, and also resolve its placement in the *Helotiales*, *Leotiomycetes* based on the high similarity of the ITS and LSU sequences to species of *Cadophora* and *Pyrenopeziza*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Cadophora prunicola* (voucher JKI-Cad64, GenBank MW960107.1; Identities = 490/547 (90 %), 16 gaps (2 %)), *Cadophora malorum* (strain CBS 101359, GenBank DQ404350.1; Identities = 488/548 (89 %), 17 gaps (3 %)), and *Cadophora orientoamericana* (voucher JKI-Cad62, GenBank MW804716.1;

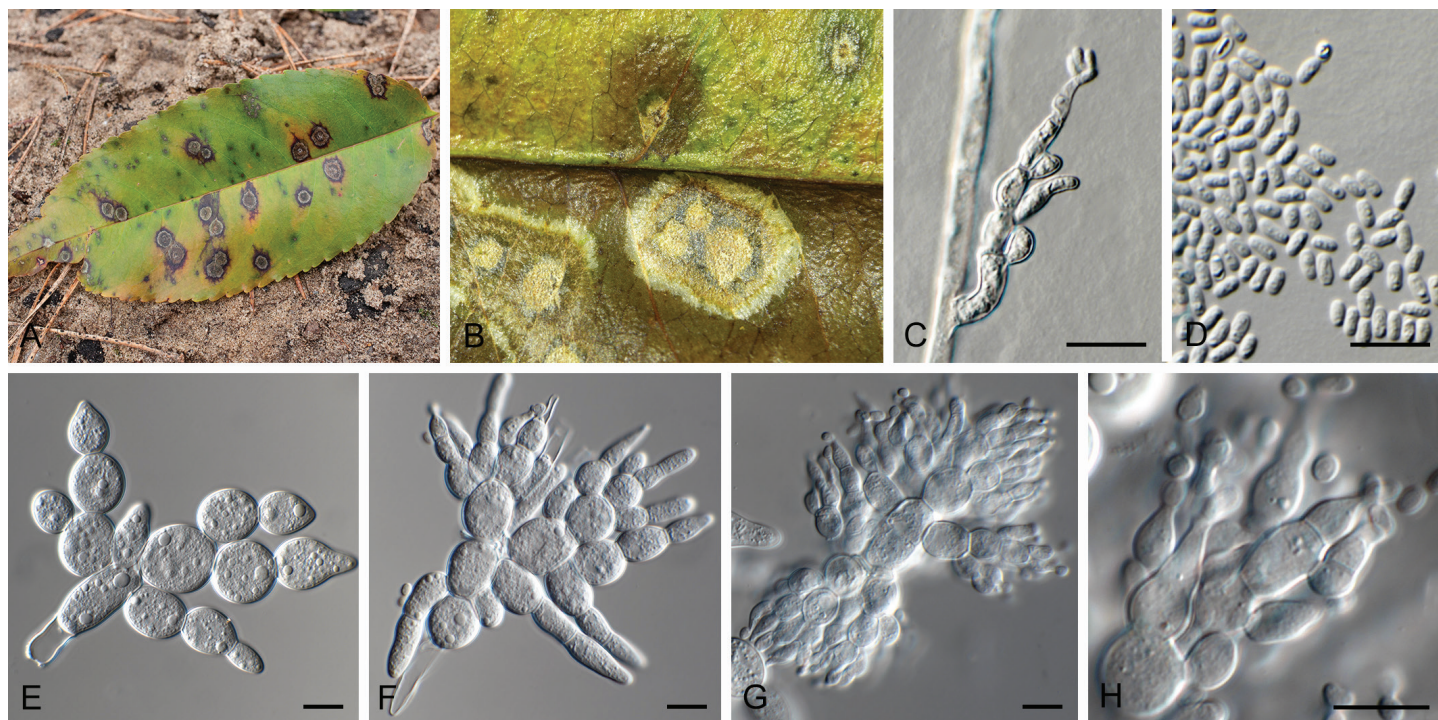


Fig. 25. *Miricatena prunicola* (CPC 42627). **A, B.** Leaf spots. **C.** Conidiogenous cells giving rise to secondary conidia. **D.** Secondary conidia. **E, F.** Primary conidia. **G, H.** Primary conidia giving rise to secondary conidia. Scale bars = 10 μ m.

Identities = 417/448 (93 %), six gaps (1 %)). Closest hits using the LSU sequence were *Cadophora luteo-olivacea* (strain CBS 128576, GenBank MH876422.1; Identities = 836/850 (98 %), no gaps), *Cadophora fastigiata* (strain CBS 872.69, GenBank MH871250.1; Identities = 836/850 (98 %), no gaps), and *Pyrenopeziza lonicerae* (strain CBS 332.58, GenBank MH869339.1; Identities = 836/850 (98 %), no gaps). No significant hits were obtained using the *tef1* (first part) sequence.

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Neoleptodontidium Crous & Jurjević, **gen. nov.** MycoBank MB 848826.

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

Classification: Sordariomycetes, Xylariomycetidae, Xylariales, incertae sedis.

Mycelium consisting of hyaline, smooth, branched, septate hyphae. **Conidiophores** solitary, erect, subcylindrical, medium brown, thick-walled, lower part finely roughened, septate, frequently rejuvenating through terminal phialide, forming a new phialide above the older phialide, where a rosette of conidia remains attached in a mucoid mass. **Conidiogenous cells** terminal, subcylindrical, medium brown, somewhat paler to the rest of the conidiophore, smooth, terminal phialidic opening with flared collarette, at times also with lateral phialidic openings on conidiogenous cell. **Conidia** solitary, hyaline, smooth, guttulate, aseptate, subcylindrical, apex obtuse, straight to slightly curved, tapering to subobtuse hilum, aggregating in mucoid mass.

Type species: *Neoleptodontidium aquaticum* Crous & Jurjević

Neoleptodontidium aquaticum Crous & Jurjević, **sp. nov.** MycoBank MB 848827. Fig. 26.

Etymology: Name refers to the fact that it was isolated from water.

Mycelium consisting of hyaline, smooth, branched, septate, 2.5–3 μ m diam hyphae. **Conidiophores** solitary, erect, subcylindrical, medium brown, thick-walled, lower part finely roughened, 1–3-septate, frequently rejuvenating through terminal phialide, forming a new phialide above the older phialide, where a rosette of conidia remains attached in a mucoid mass, 30–60 \times 2.5–3.5 μ m. **Conidiogenous cells** terminal, subcylindrical, medium brown, somewhat paler to the rest of the conidiophore, smooth, terminal phialidic opening with flared collarette, 1.5–2 μ m diam, at times also with lateral phialidic openings on conidiogenous cell, 10–30 \times 2–2.5 μ m. **Conidia** solitary, hyaline, smooth, guttulate, aseptate, subcylindrical, apex obtuse, straight to slightly curved, tapering to subobtuse hilum, 3–4 \times 1.5 μ m, aggregating in mucoid mass.

Culture characteristics: Colonies flat, spreading, with sparse to moderate aerial mycelium and feathery, lobate margin, reaching 25 mm diam after 2 wk at 25 $^{\circ}$ C. On MEA surface isabelline, reverse honey; on PDA surface and reverse honey; on OA surface olivaceous grey.

Typus: USA, North Carolina, Durham, greenhouse, hydroponic water, Oct. 2021, Z. Jurjević 5663 (**holotype** CBS H-25168, culture ex-type CPC 42868 = CBS 149455).

Additional isolate examined: USA, greenhouse, peet, Z. Jurjević 5683, culture CPC 42875.

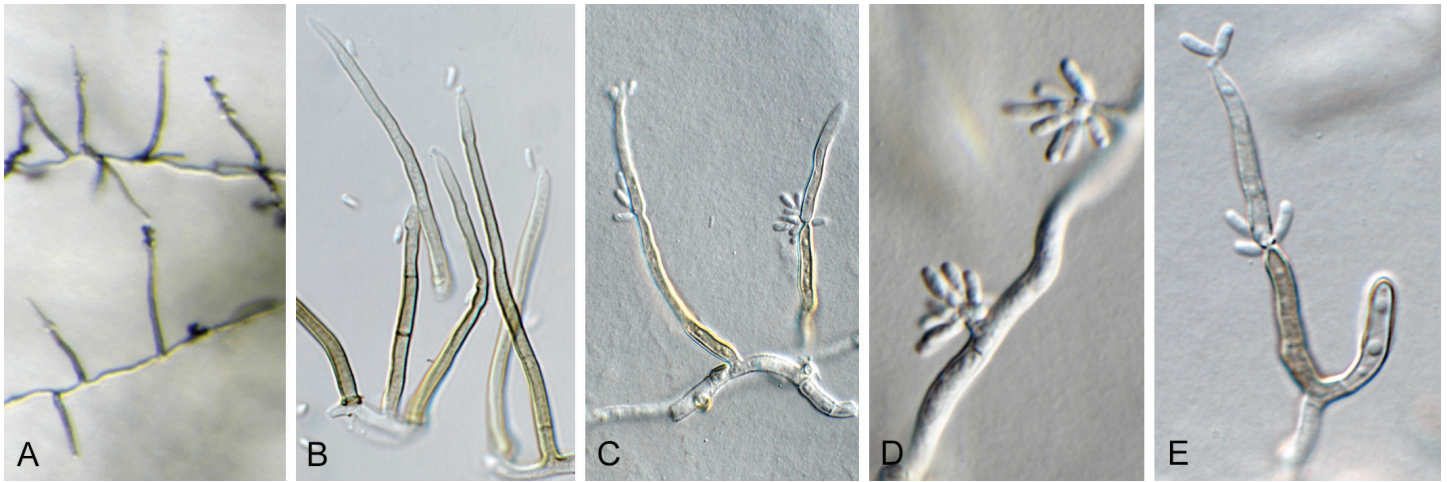


Fig. 26. *Neoleptodontidium aquaticum* (CPC 42868). **A.** Colony on SNA. **B–E.** Conidiophores and conidiogenous cells giving rise to conidia. Scale bars = 10 μ m.

Neoleptodontidium aciculare (V. Rao & de Hoog) Crous, **comb. nov.** MycoBank MB 848828.

Basionym. *Leptodontidium aciculare* V. Rao & de Hoog, *Stud. Mycol.* **28**: 37. 1986

Typus: India, Karnataka, Dt. Bidar, Maniknagar, on rotten wood, Jan. 1984, V. Rao, culture ex-type CBS 123.86.

Notes: *Neoleptodontidium* is reminiscent of the genus *Leptodontidium* (based on *L. trabinellum*), in having erect conidiophores and conidiogenous cells with a long rachis with denticles (Hernández-Restrepo *et al.* 2017). However, *Neoleptodontidium* is distinct in that it forms minute, terminal and lateral exophiala-like phialides. Phylogenetically it is allied to *Leptodontidium aciculare*, which also forms similar phialides (Rao & De Hoog 1986), and is therefore also placed in *Neoleptodontidium* (Fig. 27). *Neoleptodontidium* clusters in the *Xylariales*, but with unclear familial association; the closest families are *Oxydothidaceae*, *Castanediellaceae* and *Barrmaeliaceae*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 42868 had highest similarity to *Leptodontidium aciculare* (strain CBS 123.86, GenBank MH861931.1; Identities = 498/513 (97 %), one gap (0 %)), *Castanediella cognizarii* (strain CBS 542.96, GenBank MH862597.1; Identities = 376/418 (90 %), nine gaps (2 %)), and *Linteromyces quintinae* (strain CBS 146792, GenBank NR_171989.1; Identities = 389/433 (90 %), 11 gaps (2 %)). The ITS sequences of CPC 42868 and 42875 are identical (510/510 nucleotides). Closest hits using the **LSU** sequence of CPC 42868 were *Leptodontidium aciculare* (strain CBS 123.86, GenBank MH873620.1; Identities = 817/824 (99 %), no gaps), *Entosordaria quercina* (strain RQ, GenBank MF488994.1; Identities = 794/826 (96 %), two gaps (0 %)), and *Entosordaria perfidiosa* (strain EPE, GenBank MF488993.1; Identities = 791/826 (96 %), two gaps (0 %)). The LSU sequences of CPC 42868 and 42875 are identical (822/822 nucleotides).

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Nothoramularia Crous, J. Kruse & U. Braun, **gen. nov.** MycoBank MB 848829.

Etymology: Name refers to the fact that it resembles *Ramularia* in morphology, but is phylogenetically distinct from that genus.

Classification: *Lecanoromycetes*, *Acarosporomycetidae*, *Acarosporales*, *Acarosporaceae*.

Colonies hyperparasitic on colonies caused by the leaf-spotting *Ragnhildiana ferruginea*. **Mycelium** hyaline, composed of branched, hyaline, septate, smooth hyphae. **Conidiophores** solitary, arising from hyphae, lateral, occasionally terminal, erect, conidiophores usually aseptate, *i.e.*, reduced to conidiogenous cells, rarely with a single septum, subcylindrical to usually conical, straight to somewhat geniculate-sinuous caused by sympodial proliferation, unbranched, hyaline, thin-walled, with a single or 2–3 minute conidiogenous loci, sometimes almost denticle-like, slightly thickened and darkened, or conidia arising from minute peg-like protuberances of the hyphae, somewhat attenuated towards a truncated tip. **Conidia** solitary or usually in simple or branched acropetal chains, ellipsoid-ovoid, fusiform, subcylindrical, usually straight, 0–1-septate, thin-walled, hyaline, smooth or almost so to finely rough-walled, ends rounded to attenuated, with a single basal hilum and 1–2 hila at the apex, minute, barely thickened and darkened (adapted from Braun & Kruse 2021).

Type species: *Nothoramularia ragnhildianicola* (J. Kruse & U. Braun) Crous, J. Kruse & U. Braun

Nothoramularia ragnhildianicola (J. Kruse & U. Braun) Crous, J. Kruse & U. Braun, **comb. nov.** MB 848830. Fig. 28.

Basionym: *Ramularia ragnhildianicola* J. Kruse & U. Braun, *Schlechtendalia* **38**: 165. 2021.

Description and illustration: Braun & Kruse (2021).

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and feathery, lobate margin, reaching 6 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white, reverse luteous with patches of ochreous.

Typus: Germany, Rheinland-Pfalz, Landkreis Bad Dürkheim, Birkenheide, 1.6 km northwest of Eysersheimer Hof, meadow, 49°29'41"N, 8°15'29"E,

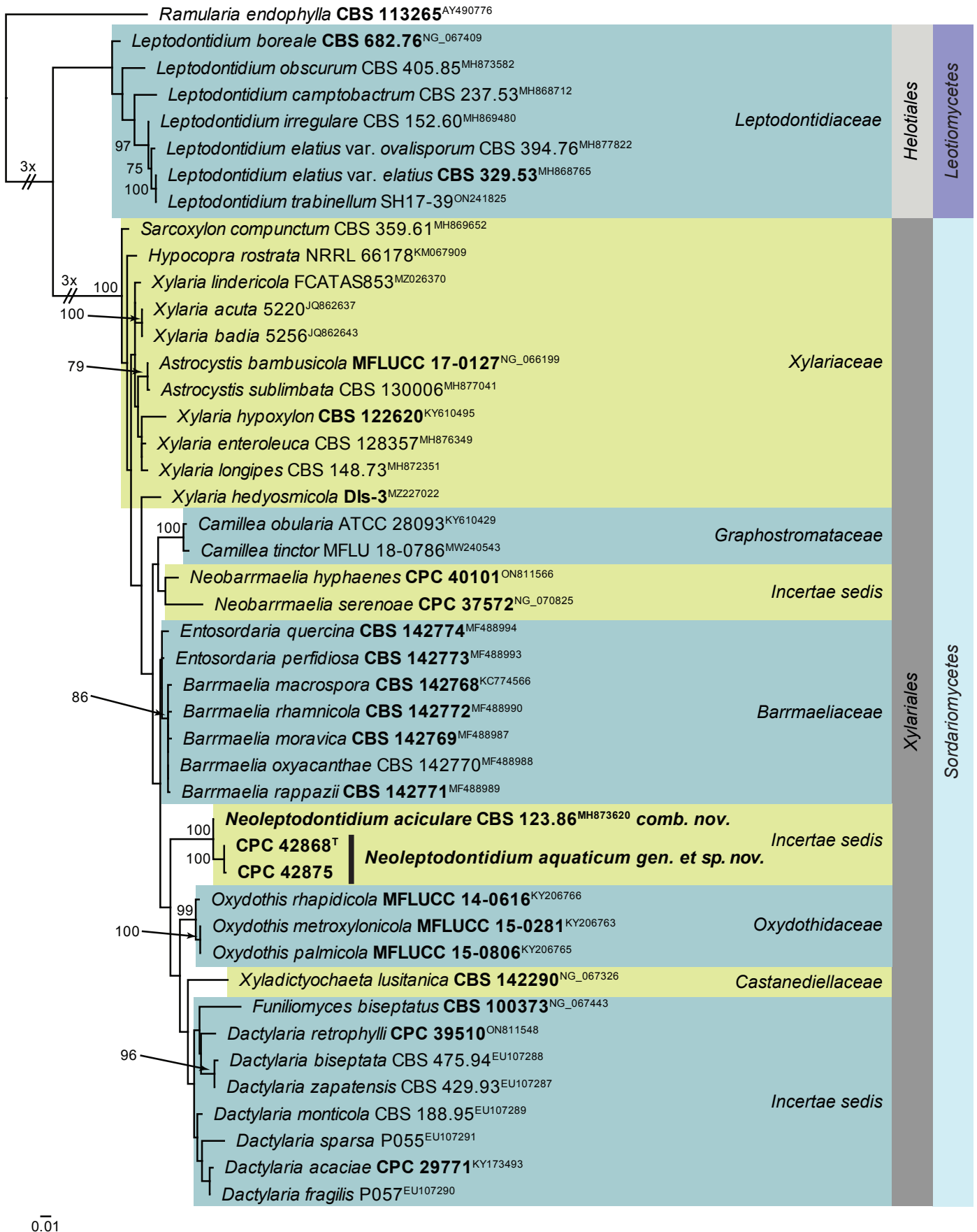


Fig. 27. Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 of the Xylariales LSU nucleotide alignment. Maximum likelihood (> 74 %) bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes. Culture collection or voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences derived from material with a type status are indicated with a culture or voucher number highlighted with bold face. The tree was rooted to *Ramularia endophylla* (culture CBS 113265; GenBank AY490776) and the species treated here are highlighted with bold face. The families, orders and classes are shown in coloured blocks to the right of the tree. The scale bar indicates the expected number of changes per site.

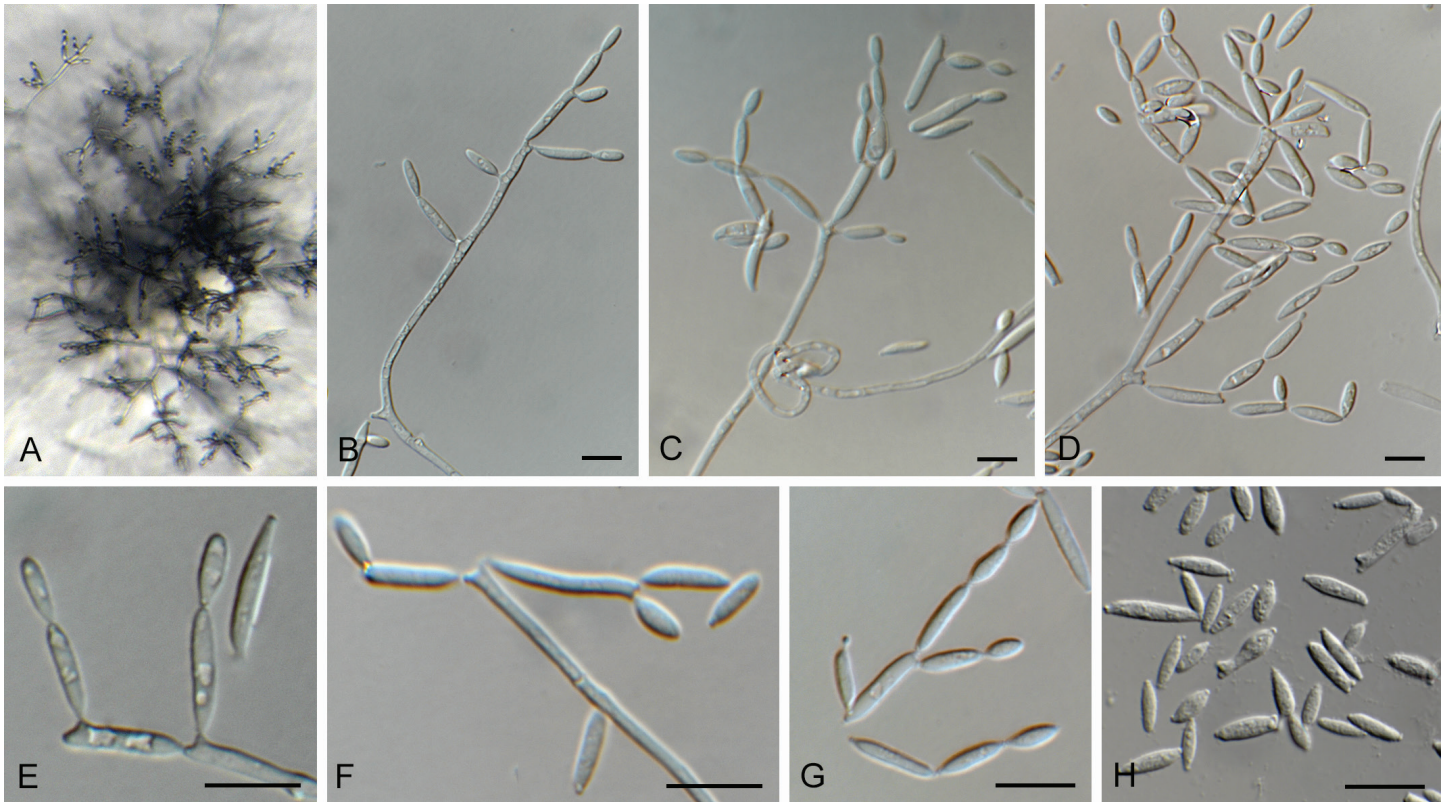


Fig. 28. *Nothoramularia ragnhildianicola* (CPC 42462). **A.** Colony on SNA. **B–D, F.** Conidiophores and conidiogenous cells giving rise to conidia. **E, G, H.** Conidia. Scale bars = 10 µm.

ca. 105 m alt, on *Ragnhildiana ferruginea* (*Mycosphaerellaceae*) parasitic on *Artemisia vulgaris* (*Asteraceae*), 8 Sep. 2020, J. Kruse (**holotype** POLL 9793), **isotype** HAL 3375 F; Rheinland-Pfalz, Landkreis Bad Dürkheim, Birkenheide, 49°29'41"N, 8°15'29"E, on *Ragnhildiana ferruginea*, parasitic on *Artemisia vulgaris*, 7 Sep. 2021, J. Kruse, POLL 9802 = HPC 3779 (**epitype** designated here CBS H-24978, MBT 10013418, culture ex-epitype CPC 42462 = CBS 149076).

Additional material examined: **Germany**, Rheinland-Pfalz, Landkreis Bad Dürkheim, Birkenheide, 49°29'41"N, 8°15'29"E, on *Ragnhildiana ferruginea*, parasitic on *Artemisia vulgaris*, 7 Sep. 2021, J. Kruse, POLL 9802 = HPC 3779, culture CPC 42463 = CBS 149075.

Notes: In culture, conidial loci are somewhat thickened, darkened, but not refractive. Ramoconidia commonly have numerous loci, giving rise to branched conidial chains. Conidiophores are erect, subcylindrical, straight, with terminal and intercalary conidiogenous cells, up to 150 µm tall, or reduced to conidiogenous loci on hyphae. Phylogenetically (Fig. 29), *No. ragnhildianicola* forms a lineage basal to *Neoacrodontiella*, *Neospermospora* and *Cytospora*, with which it clusters with moderate support (87 % maximum parsimony and 74 % maximum likelihood).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 42462 had highest similarity to *Neoacrodontiella eucalypti* (strain CBS 145561, GenBank NR_165567.1; Identities = 473/549 (86 %), 43 gaps (7 %)), *Cytospora juncicola* (strain CPC 38040, GenBank MN562153.1; Identities = 379/436 (87 %), 27 gaps (6 %)), *Vanderaaea ammophilae* (strain CBS 886.68, GenBank NR_178155.1; Identities = 465/539 (86 %), 46 gaps (8 %)), and *Corticifraga ramalinae* (voucher Pinault, GenBank ON569808.1;

Identities = 432/508 (85 %), 34 gaps (6 %)). The ITS sequence of CPC 42462 is 99 % similar to that of CPC 42463 (883/887 nucleotides, including four gaps from a single indel in an A-repeat region of the sequence). Closest hits using the **LSU** sequence of CPC 42462 were *Neoacrodontiella eucalypti* (strain CBS 145561, GenBank NG_067885.1; Identities = 622/651 (96 %), six gaps (0 %)), *Neospermospora avenae* (strain CBS 886.68, GenBank MH878416.1; Identities = 607/652 (93 %), eight gaps (1 %)), and *Cytospora juncicola* (strain CPC 38040, GenBank NG_068344.1; Identities = 597/651 (92 %), six gaps (0 %)). The LSU sequence of CPC 42462 is identical to that of CPC 42463 (739/739 nucleotides).

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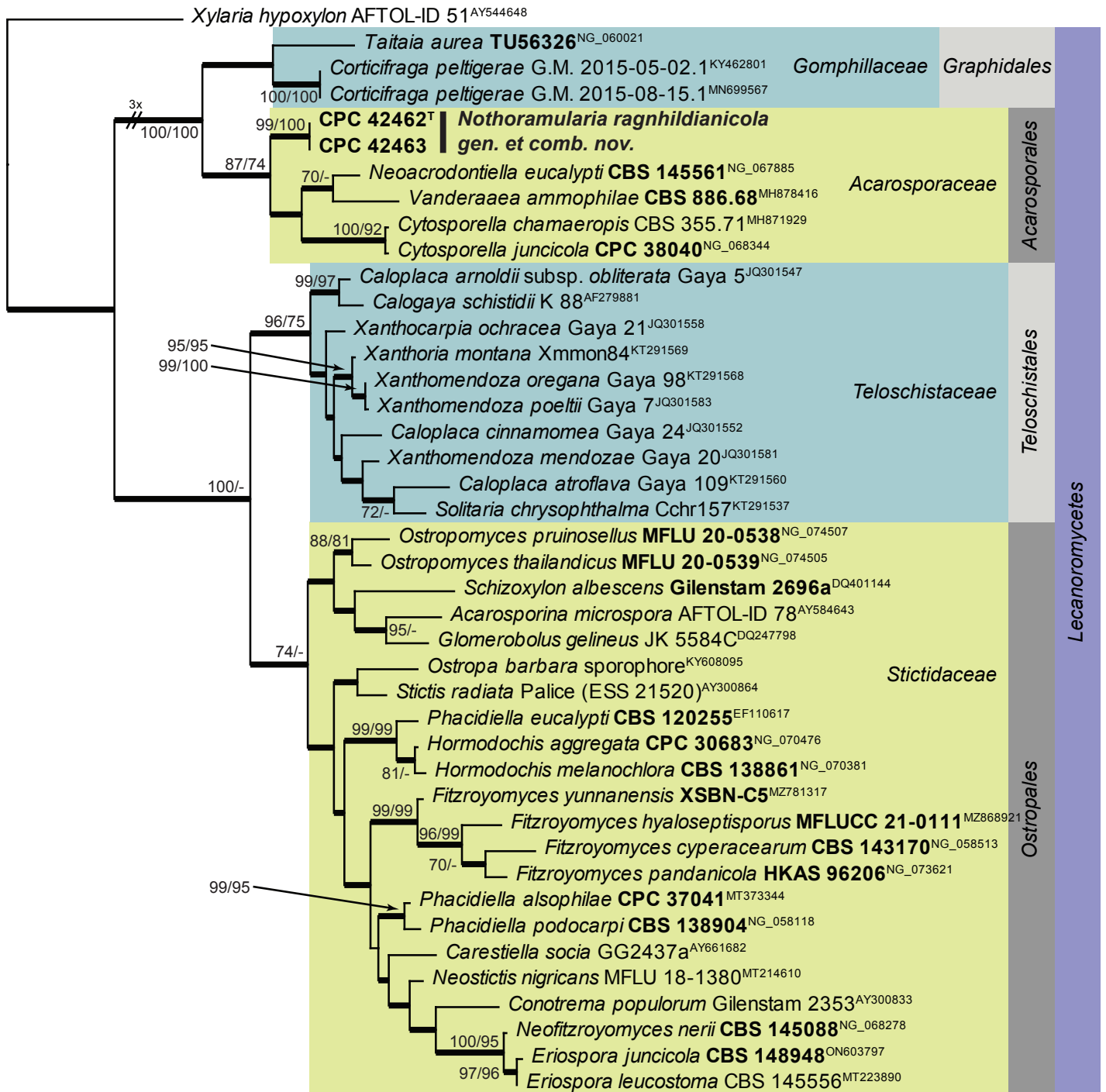
Ophiognomonia setacea (Pers.) Sogonov, *Stud. Mycol.* **62**: 64. 2008.

Description and illustration: Sogonov *et al.* (2008).

Material examined: **Spain**, Pontevedra, O Grove, on leaves of *Quercus robur* (*Fagaceae*), 21 Jan. 2022, J. Castillo, HPC 3874 = RKS 1161b, culture CPC 43206 = CBS 149691.

Notes: Known from overwintered leaves of *Fagaceae* in Canada, Europe, and the USA (Sogonov *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 *Ophiognomonia setacea* (strain CBS 859.79, GenBank AY818958.1; Identities = 534/535 (99 %), no gaps), *Ophiognomonia asiatica* (strain CBS 131351, GenBank NR_120057.1; Identities = 501/512 (98 %), five gaps (0 %)), and *Ophiognomonia sogonovii*



10

Fig. 29. The first of two equally most parsimonious trees obtained from the *Lecanoromycetes* LSU sequence alignment. The scale bar indicates the number of changes and the numbers at the nodes represent maximum parsimony (>70 %) and maximum likelihood (> 70 %) bootstrap support values from 1 000 non-parametric bootstrap replicates. Branches that appear in the strict consensus tree are highlighted by thickened lines. Culture collection or voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences derived from material with a type status are indicated with a culture or voucher number highlighted with bold face. The tree was rooted to *Xylaria hypoxylon* (AFTOL-ID 51; GenBank AY544648) and the species treated here is highlighted with bold face. The families, orders and class are shown in coloured blocks to the right of the tree.

(strain CBS 131341, GenBank NR_120053.1; Identities = 500/513 (97 %), five gaps (0 %)). Closest hits using the **LSU** sequence were *Ophiognomonium setacea* (strain CBS 859.79, GenBank AY818962.1; Identities = 830/830 (100 %), no gaps), *Gnomonia gnomon* (strain CBS 829.79, GenBank AY818964.1; Identities = 819/830 (99 %), no gaps), and *Amphiporthe hranicensis* (strain

AR3651, GenBank DQ323521.1; Identities = 817/831 (98 %), two gaps (0 %)). Closest hits using the **tef1** (first part) sequence had highest similarity to *Ophiognomonium setacea* (strain CBS 859.79, GenBank JQ414154.1; Identities = 564/564 (100 %), no gaps), *Ophiognomonium sogonovii* (strain CBS 131341, GenBank JQ414161.1; Identities = 267/278 (96 %), one gap (0 %)), and

Ophiognomonia alni-cordatae (strain CBS 131353, GenBank JQ414175.1; Identities = 226/237 (95 %), no gaps). Closest hits using the **tef1** (second part) sequence had highest similarity to *Ophiognomonia setacea* (strain CBS 859.79, GenBank JQ414154.1; Identities = 308/308 (100 %), no gaps), *Melanconis stilbostoma* (strain AFTOL-ID 936, GenBank DQ836910.1; Identities = 864/925 (93 %), two gaps (0 %)), *Cryptodiaporthe aesculi* (strain AFTOL-ID 1238, GenBank DQ836914.1; Identities = 861/924 (93 %), no gaps), and *Gnomonia gnomon* (strain AFTOL-ID 952, GenBank DQ471094.1; Identities = 859/924 (93 %), no gaps).

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Paradissoconium narthecii Crous & Boers, *Persoonia* **47**: 211. 2021. Fig. 30.

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

Material examined: **Netherlands**, Drenthe Province, Dwingeloo, on dead leaves of *Narthecium ossifragum* (*Melanthiaceae*), 26 Sep. 2021, J. Boers, HPC 3781, culture CPC 42494 = CBS 149692.

Notes: *Paradissoconium narthecii* was described from dead leaves of *Narthecium ossifragum* in the Netherlands (Crous *et al.* 2021b), for which this represents a second collection of this fungus.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Paradissoconium narthecii* (strain CBS 148449, GenBank NR_175214.1; Identities = 497/497 (100 %), no gaps), *Ramichloridium punctatum* (strain NTOU 4892, GenBank

MK448255.1; Identities = 458/502 (91 %), 14 gaps (2 %)), and *Dissoconium proteae* (strain CBS 122900, GenBank NR_156213.1; Identities = 462/507 (91 %), 17 gaps (3 %)). Closest hits using the **LSU** sequence were *Paradissoconium narthecii* (strain CBS 148449, GenBank NG_081323.1; Identities = 804/804 (100 %), no gaps), *Ramichloridium eucleae* (strain CBS 138000, GenBank NG_058086.1; Identities = 813/827 (98 %), two gaps (0 %)), and *Ramichloridium indicum* (strain CBS 171.96, GenBank EU041856.1; Identities = 795/811 (98 %), no gaps). Closest hits using the **actA** sequence had highest similarity to *Paradissoconium narthecii* (strain CPC 41970, GenBank OK651125.1; Identities = 539/539 (100 %), no gaps), *Cladosporium ramotenellum* (strain CBS 145592, GenBank MT223748.1; Identities = 382/407 (94 %), no gaps), and *Davidiellomyces australiensis* (strain CBS 142165, GenBank KY979853.1; Identities = 382/407 (94 %), no gaps). The **rpb1** sequence is identical to that of *Paradissoconium narthecii* (strain CPC 41970, GenBank OK651151.1; Identities = 518/518 (100 %), no gaps).

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Paraeutypella citricola (Speg.) L.S. Dissan. *et al.*, *Biodivers. Data J.* **9**: e63864 [14]. 2021.

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

Material examined: **Spain**, Cambrils, on bark of unknown tree, 26 Jan. 2022, J. Castillo, HPC 3869 = RKS 1158, culture CPC 43208 = CBS 149693.

Notes: *Paraeutypella citricola* was originally described (as *Eutypella citricola*) from twigs of *Citrus* in Argentina, and

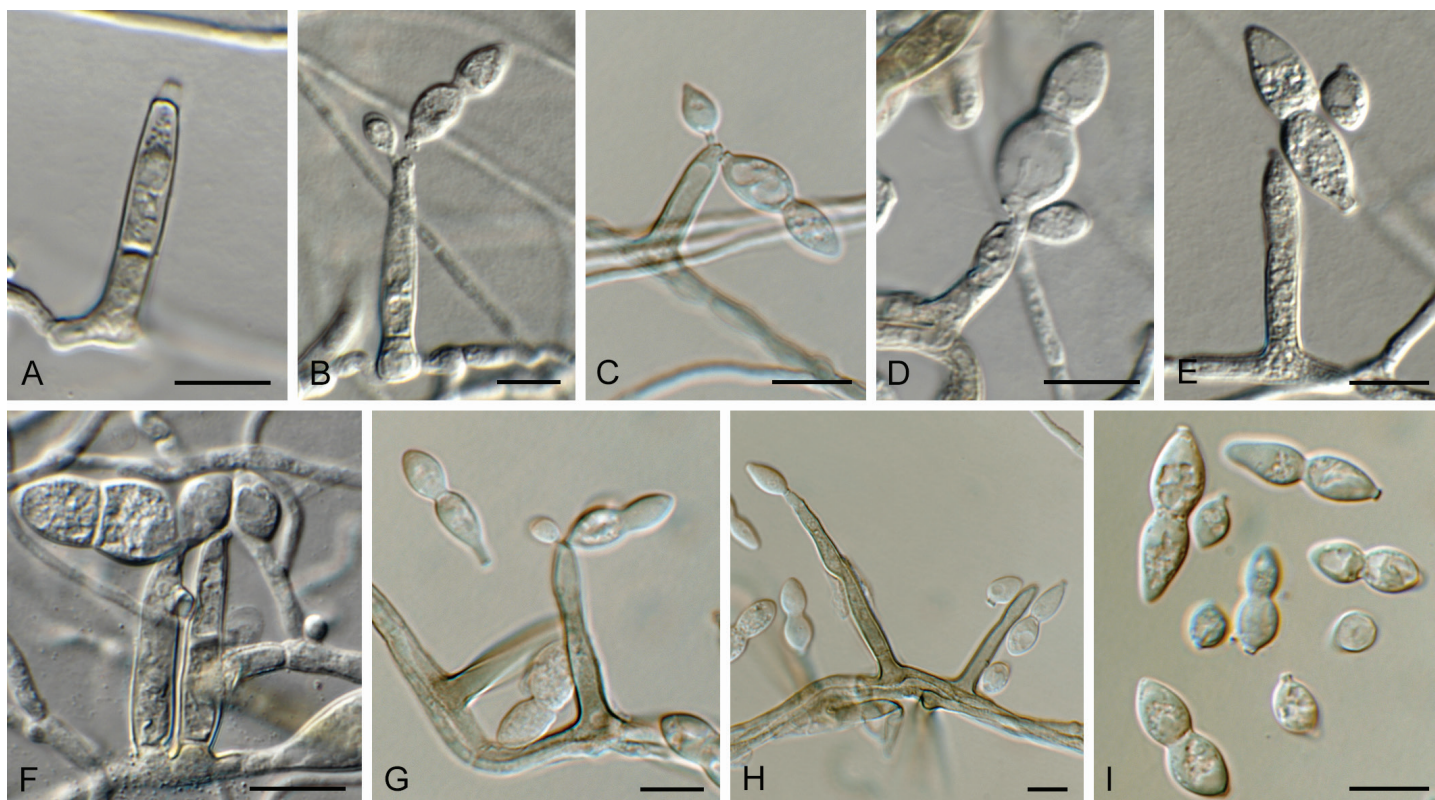


Fig. 30. *Paradissoconium narthecii* (CPC 42494). A. Conidiophore. B–H. Conidiophores and conidiogenous cells giving rise to primary and secondary conidia. I. One-septate primary and aseptate secondary conidia. Scale bars = 10 μ m.

recently reported from dead twigs of *Acer palmatum* in China (Dissanayake *et al.* 2021). It is recorded here from bark of a dead, unknown tree in Spain. This species has inoperculate asci that are distinctly amyloid (mounted in Lugol).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Paraeutypella citricola* (strain ICMP 17420, GenBank MH497577.1; Identities = 529/529 (100 %), no gaps), and *Paraeutypella vitis* (strain 59, GenBank KU320620.1; Identities = 513/530 (97 %), three gaps (0 %)). Closest hits using the **LSU** sequence were *Paraeutypella citricola* (as *Eutypella citricola*, strain CBS 128334, GenBank MH876333.1; Identities = 867/867 (100 %), no gaps), *Libertella faginea f. minor* (strain CBS 196.30, GenBank MH866558.1; Identities = 862/868 (99 %), one gap (0 %)), and *Eutypella microtheca* (strain CBS 128336, GenBank NG_064278.1; Identities = 830/837 (99 %), no gaps). Closest hits using the **rpb2** (first part) sequence had highest similarity to *Paraeutypella citricola* (strain GMBC0053, GenBank MW814898.1; Identities = 898/899 (99 %), no gaps), *Allocryptovalsa sichuanensis* (voucher HKAS 107017, GenBank MW658624.1; Identities = 770/886 (87 %), eight gaps (0 %)), and *Eutypella quaternata* (voucher MFLU 15-2605, GenBank MT432247.1; Identities = 715/860 (83 %), 14 gaps (1 %)). Closest hits using the **tub2** sequence had highest similarity to *Paraeutypella citricola* (voucher HUEFS 131041, GenBank KT175565.1; Identities = 666/671 (99 %), no gaps), *Diatrypella longiasca* (strain KUMCC 20-0021, GenBank MW239658.1; Identities = 564/663 (85 %), 26 gaps (3 %)), and *Eutypella microtheca* (strain AD53, GenBank KR822701.1; Identities = 548/667 (82 %), 39 gaps (5 %)).

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Phomatospora endopteris W. Phillips & Plowr., *Grevillea* **13**(no. 67): 76. 1885. Fig. 31.

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

Cultures derived from single ascospores shot from a perithecium onto agar, but material inadequate for description. *Ascospores* aseptate, fusoid-ellipsoid, pale brown, guttulate, longitudinally striate, ends bluntly rounded, somewhat flattened, 9–10(–11) × 3 µm. *Mycelium* consisting of hyaline, smooth, branched, septate,

1–1.5 µm diam hyphae. *Conidiophores* erect, straight to flexuous, arising from superficial hyphae, subcylindrical, 1–2-septate, or reduced to conidiogenous cells, pale brown, smooth, branched or not, 20–50 × 3–3.5 µm. *Conidiogenous cells* terminal and intercalary, pale brown, smooth, subcylindrical to obclavate, 7–20 × 3–3.5 µm, with terminal rachis of subdenticulate loci, 0.5–1 × 0.5 µm, slightly thickened and darkened. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, slightly curved, narrowly fusoid, apex subobtuse, base truncate, (11–)13–15(–18) × 1.5 µm.

Culture characteristics: Colonies erumpent, spreading, with sparse to moderate aerial mycelium and smooth, even margin, reaching 18 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse ochreous; on PDA and OA surface and reverse dirty white.

Material examined: Netherlands, Utrecht Province, Bilthoven, on stems of *Pteridium aquilinum* (*Dennstaedtiaceae*), 24 May 2021, P.W. Crous, HPC 3644 = CBS H-24975, culture CPC 41832 = CBS 149073.

Notes: *Phomatospora* species are known from marine, aquatic and terrestrial habitats, where they are usually saprobic on submerged wood or decaying twigs (Senanayake *et al.* 2016). *Phomatospora endopteris* was isolated from single ascospores that shot onto agar from decaying stems of *Pteridium aquilinum*. Although the immersed ascomata could not be located, the ascospores were fusoid-ellipsoid and longitudinally striate, which fit well with the circumscription of the genus. Ellis & Ellis (1997) list ascospores of *Phomatospora endopteris* as 10–11 × 2.5–3 µm, thus fitting with those of the present collection. *Phomatospora endopteris* is currently not known from sequence data and the blast results below confirm its association with the genus *Phomatospora*. Although the genus contains more than 100 species names, only a few are currently known from sequence data, namely *P. bellaminuta*, *P. biseriata*, *P. striatigera*, *P. uniseriata* and *P. viticola*. The lectotype species, *P. berkeleyi*, is currently not known from molecular data. See Phukhamsakda *et al.* (2020) for a recent phylogenetic treatment of the genus.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phomatospora biseriata* (strain MFLUCC 14-0832A, GenBank NR_154640.1; Identities = 478/522 (92 %), 11 gaps (2 %)), *Phomatospora* sp. (strain UBOCC-A-118152,

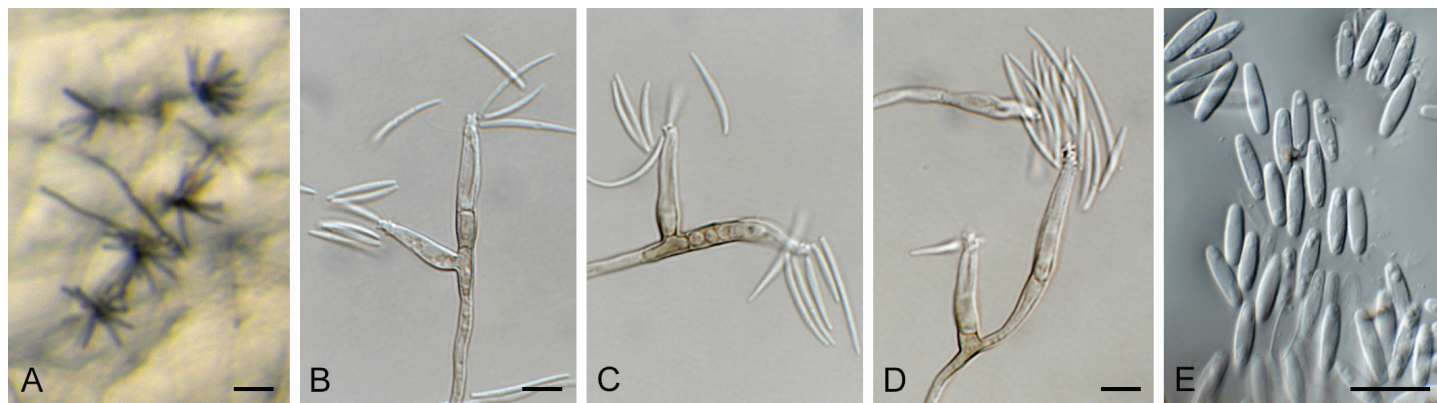


Fig. 31. *Phomatospora endopteris* (CPC 41832). **A.** Colony on SNA. **B–D.** Conidiophores and conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars = 10 µm.

GenBank MT133745.1; Identities = 523/536 (98 %), two gaps (0 %)), *Pyramidospora constricta* (strain VG116-5, GenBank OM907745.1; Identities = 537/592 (91 %), 15 gaps (2 %)), *Paramicrothyrium chinensis* (strain IA20, GenBank KM246198.1; Identities = 531/589 (90 %), 14 gaps (2 %)), and *Phomatospora striatigera* (strain CBS 133932, GenBank NR_145386.1; Identities = 536/604 (89 %), 24 gaps (3 %)). Closest hits using the **LSU** sequence were *Phomatospora* sp. from an oceanic crust in the Indian Ocean (strain UBOCC-A-118152, GenBank MT226561.1; Identities = 723/724 (99 %), no gaps), *Phomatospora uniseriata* (strain MFLUCC 17-2068, GenBank NG_073857.1; Identities = 806/826 (98 %), one gap (0 %)), and *Lanspora cylindrospora* (strain NFCCI-4427, GenBank MN168892.1; Identities = 732/753 (97 %), no gaps). Closest hits using the **SSU** sequence were *Phomatospora* sp. from an oceanic crust in the Indian Ocean (strain UBOCC-A-118152, GenBank MT226525.1; Identities = 960/963 (99 %), no gaps), *Phomatospora biseriata* (strain MFLUCC 14-0832A, GenBank NG_065654.1; Identities = 911/914 (99 %), no gaps), and *Distoseptispora aquatica* (strain MFLUCC 16-1357, GenBank MK828317.1; Identities = 852/858 (99 %), no gaps). Closest hits using the **rpb2** sequence had highest similarity to *Lanspora coronata* (strain AFTOL-ID 736, GenBank DQ470899.1; Identities = 648/840 (77 %), 15 gaps (1 %)), *Sporothrix splendens* (strain CMW23050, GenBank OM631738.1; Identities = 633/843 (75 %), 31 gaps (3 %)), and *Sporothrix fumea* (strain CMW26813, GenBank OM631721.1; Identities = 636/849 (75 %), 43 gaps (5 %)). A blast2 comparison with the two *Phomatospora rpb2* sequences on GenBank also revealed low similarity: *Phomatospora uniseriata* (strain MFLUCC 17-2068, GenBank MT394720.1; Identities = 606/817 (74 %), 28 gaps (3 %)), and *Phomatospora bellaminuta* (strain AFTOL-ID 766, GenBank FJ238345.1; Identities = 612/842 (73 %), 42 gaps (4 %)).

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Phyllosticta multicorniculata Bissett & M.E. Palm, *Canad. J. Bot.* **67**: 3382. 1989. Fig. 32.

Description and illustration: Bissett & Palm (1989).

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

Typus: **Canada**, Prince Edward Island, Milton Station, on needles of *Abies balsamea* (*Pinaceae*), 19 Jul. 1966, C.D. MacCall (**holotype** DAOM 114552); New Brunswick, Charlotte Co., 1.5 km SW of Little Lepreau, 45.135614° -66.492269°, on buds of *A. balsamea*, 4 May 2021, D. Malloch, HPC 3633 (**epitype** designated here CBS H-24979, MBT 10013419, culture ex-epitype CPC 41921 = CBS 149077).

Additional material examined. **Canada**, New Brunswick, Charlotte Co., 1.5 km SW of Little Lepreau, 45.135614° -66.492269°, on buds of *A. balsamea*, 4 May 2021, D. Malloch, HPC 3633, culture CPC 41919 = CBS 149078.

Notes: Conidia of *P. multicorniculata* are (10–)12–15(–17) × (7–)10–11(–13) µm, enclosed in a mucilaginous sheath, 1.5 µm thick, with 2–5 conoidal or cylindrical apical appendages, thus closely matching those of the holotype (Bissett & Palm 1989). Within the genus *Phyllosticta*, *P. multicorniculata* is peculiar in that it has several apical appendages, whereas most species have only a single, or no apical appendage. In the phylogenetic tree (Fig. 33), *P. multicorniculata* had a basal position in *Phyllostictaceae* (76 % / 95 % / 1). Neither the Bayesian nor the RAxML analyses resolve this species as a basal sister lineage; only in the most parsimonious trees does it take up a position as a basal sister lineage but without any support in the parsimony bootstrap consensus tree. Whether this species could represent a novel genus in the future remains to be seen as the phylogenetic trees obtained from the different analyses were inconclusive to clearly separate it from the other species in *Phyllosticta*. The similarities of the different loci seem to fit within the genetic diversity of the genus (blast results filtered for *Phyllostictaceae*): ITS (based

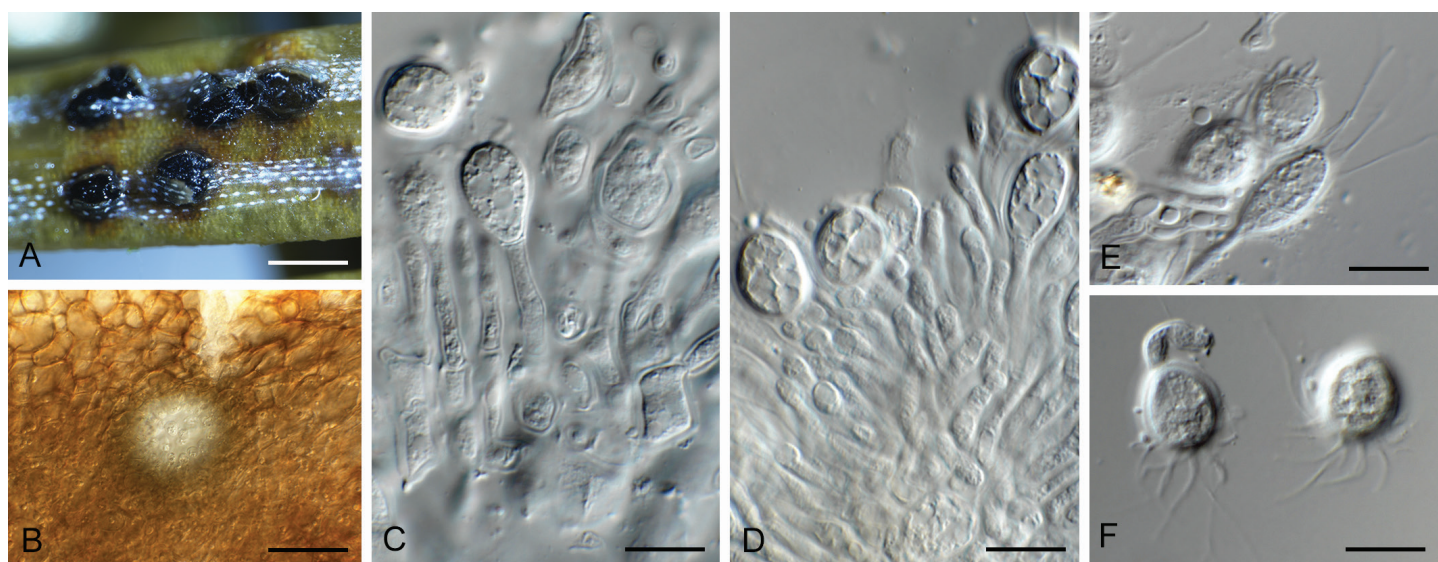


Fig. 32. *Phyllosticta multicorniculata* (CPC 41921). **A.** Erumpent conidiomata on *Abies* needle. **B.** Conidioma with central ostiole. **C, D.** Conidiogenous cells giving rise to conidia. **E, F.** Conidia with multiple apical appendages. Scale bars: A = 200 µm, all others = 10 µm.

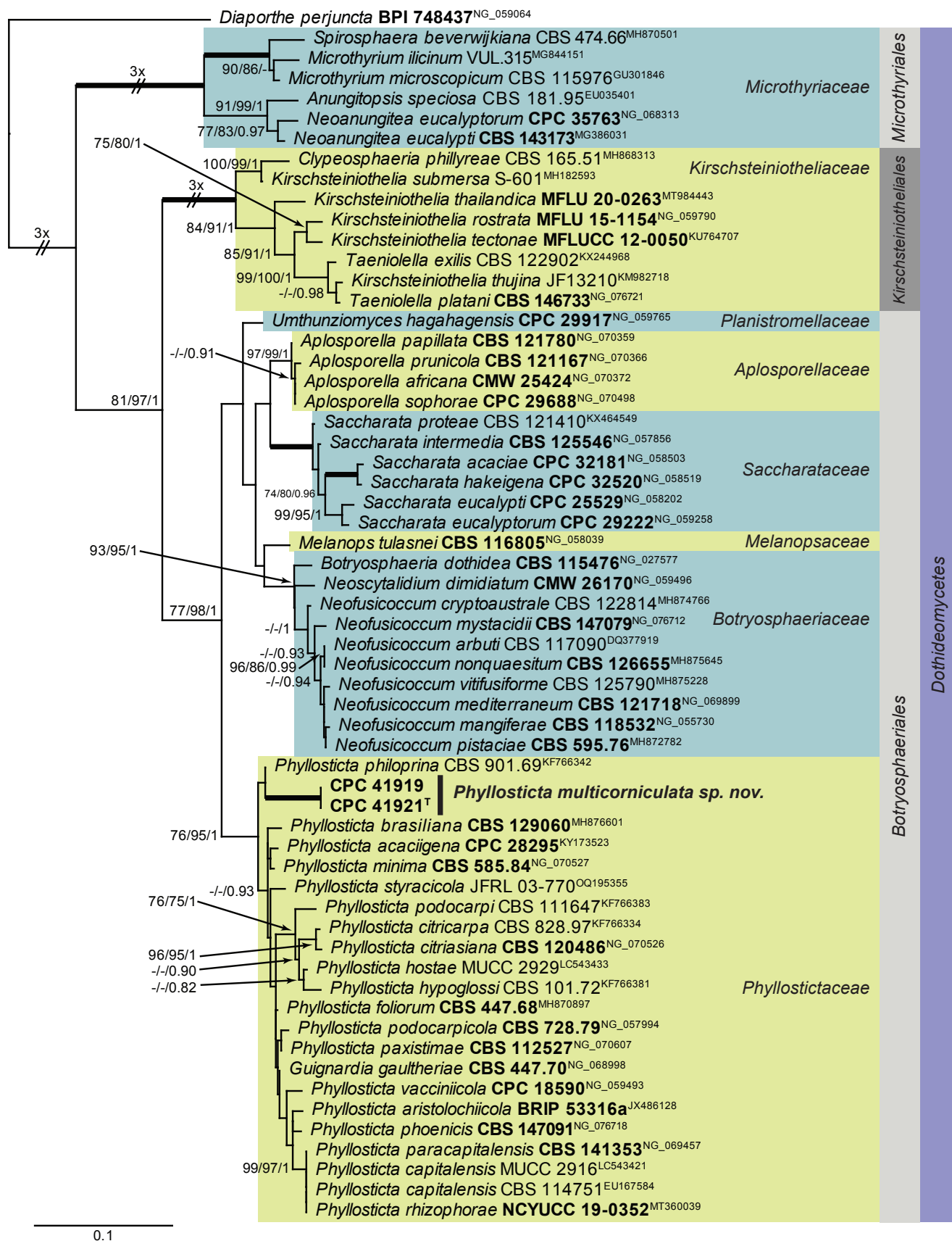


Fig. 33. Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 of the *Phyllostictaceae* and related families LSU nucleotide alignment. Maximum likelihood (> 74 %) and maximum parsimony (> 74 %) bootstrap support values from 1 000 non-parametric bootstrap replicates, and Bayesian posterior probabilities (> 0.84), are shown at the nodes. Thickened lines represent nodes which received full support (100 % / 100 % / 1) from all three analyses. Culture collection or voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences derived from material with a type status are indicated with a culture or voucher number highlighted with bold face. The tree was rooted to *Diaporthe perijuncta* (voucher BPI 748437; GenBank NG_059064) and the species treated here is highlighted with bold face. The families, orders and class are shown in coloured blocks to the right of the tree. The scale bar indicates the expected number of changes per site.

on the top 2 531 blast hits using GenBank FJ824766) = 82.08 % – 100 %; LSU (based on the top 282 blast hits using GenBank KF766342) = 90.24 % – 100 %; *actA* (based on the top 345 blast hits using the first 240 nucleotides of GenBank JX025029) = 77.13 % – 100 %; *gapdh* (based on the top 355 blast hits using GenBank MN556783) = 86.39 % – 100 %; and *tef1* (based on the top 249 blast hits using GenBank MN556818) = 79.34 % – 100 %.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 41921 had highest similarity to *Phyllosticta parthenocissi* (deposited in GenBank as *Guignardia bidwellii*; strain CBS 111645, GenBank FJ824766.1; Identities = 445/536 (83 %), 27 gaps (5 %)), *Phyllosticta foliorum* (deposited in GenBank as *Guignardia philoprina*; strain CBS 447.68, GenBank AF312014.1; Identities = 448/541 (83 %), 32 gaps (5 %)), and *Phyllosticta citricarpa* (strain PD 010 04421662, GenBank MZ416911.1; Identities = 329/367 (90 %), 15 gaps (4 %)). The ITS sequences of CPC 41921 and 41919 are identical (528/528 nucleotides). Closest hits using the **LSU** sequence of CPC 41921 were *Phyllosticta philoprina* (strain CBS 901.69, GenBank KF766342.1; Identities = 765/793 (96 %), no gaps), *Phyllosticta styracicola* (strain JFRL 03-770, GenBank OQ195355.1; Identities = 759/793 (96 %), no gaps), and *Phyllosticta minima* (strain CBS 585.84, GenBank KF766382.1; Identities = 759/793 (96 %), no gaps). The LSU sequences of CPC 41921 and 41919 are identical (793/793 nucleotides). Closest hits using the **actA** sequence of CPC 41921 had highest similarity to *Phyllosticta encephalarticola* (strain CBS 146014, GenBank MN556783.1; Identities = 462/504 (92 %), nine gaps (1 %)), *Phyllosticta austroafricana* (strain CBS 144593, GenBank MK442640.1; Identities = 445/485 (92 %), six gaps (1 %)), and *Phyllosticta hagahagaensis* (strain CBS 144592, GenBank MK442641.1; Identities = 458/504 (91 %), nine gaps (1 %)). The *actA* sequences of CPC 41921 and 41919 are identical (533/533 nucleotides). Closest hits using the **gapdh** sequence of CPC 41921 had highest similarity to *Phyllosticta hubeiensis* (strain LC1654, GenBank JX025029.1; Identities = 304/336 (90 %), no gaps), *Phyllosticta rhizophorae* (strain NCYUCC 19-0358, GenBank MT363251.1; Identities = 301/336 (90 %), no gaps), and *Phyllosticta capitalensis* (strain IPN20.1, GenBank KX280619.1; Identities = 300/335 (90 %), no gaps). The *gapdh* sequences of CPC 41921 and 41919 are identical (545/545 nucleotides). Closest hits using the **tef1** (first part) sequence of CPC 41921 had highest similarity to *Phyllosticta encephalarticola* (strain CBS 146014, GenBank MN556818.1; Identities = 290/332 (87 %), 14 gaps

(4 %)), *Phyllosticta hagahagaensis* (strain CBS 144592, GenBank MK442705.1; Identities = 290/332 (87 %), 14 gaps (4 %)), and *Phyllosticta carissicola* (strain CPC 25665, GenBank KT950879.1; Identities = 290/332 (87 %), 14 gaps (4 %)). The *tef1* sequences of CPC 41921 and 41919 are identical (409/409 nucleotides).

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Pleurotheciella aquatica Z.L. Luo *et al.*, *Mycol. Progr.* **17**: 517. 2018. Fig. 34.

Description and illustration: Huang *et al.* (2022).

Material examined: UK, England, Basingstoke, on *Allium schoenoprasum* (*Alliaceae*), May 2022, P.W. Crous, CBS H-25211, culture CPC 44105 = CBS 149694.

Notes: *Pleurotheciella aquatica* was described from submerged wood collected in China (Huang *et al.* 2022). This is the first report of this fungus from the UK.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pleurotheciella aquatica* (voucher MFLU 17-0911, GenBank NR_160591.1; Identities = 499/500 (99 %), no gaps), *Pleurotheciella fusiformis* (strain MFLUCC 16-1356, GenBank MF399235.1; Identities = 494/514 (96 %), nine gaps (1 %)), and *Pleurotheciella uniseptata* (strain KAS 4459, GenBank KT278729.1; Identities = 500/534 (94 %), 13 gaps (2 %)). Closest hits using the **LSU** sequence were *Pleurotheciella aquatica* (voucher MFLU 17-0911, GenBank NG_066193.1; Identities = 799/800 (99 %), one gap (0 %)), *Pleurotheciella fusiformis* (strain MFLUCC 17-0115, GenBank MF399249.1; Identities = 755/762 (99 %), one gap (0 %)), and *Pleurotheciella lunata* (voucher MFLU 17-0913, GenBank NG_066195.1; Identities = 790/800 (99 %), one gap (0 %)). Closest hits using the **rpb2** (first part) sequence had highest similarity to *Pleurotheciella aquatica* (strain MFLUCC 17-0464, GenBank MF401405.1; Identities = 655/655 (100 %), no gaps), *Pleurotheciella fusiformis* (strain MFLUCC 17-0113, GenBank MF401403.1; Identities = 661/699 (95 %), no gaps), and *Pleurotheciella uniseptata* (strain KUMCC 15-0407, GenBank MF401401.1; Identities = 541/599 (90 %), no gaps).

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Fig. 34. *Pleurotheciella aquatica* (CPC 44105). **A–C.** Conidiophores and conidiogenous cells giving rise to conidia. **D.** Conidia. Scale bars = 10 μ m.

Ramularia pistaciae Crous, *Persoonia* **42**: 353. 2019. Fig. 35.

Description and illustration: Crous *et al.* (2019a).

Material examined: **UK**, England, Arundale, on leaf spot on *Arbutus unedo* (*Ericaceae*), 14 May 2022, P.W. Crous & S. Denman, HPC 3955, culture CPC 44067 = CBS 149696.

Notes: *Ramularia pistaciae* was recently described from leaves of *Pistacia lentiscus* collected in Rome, Italy (Crous *et al.* 2019a). This is the first record from the UK, where it is associated with leaf spots of *Arbutus unedo*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Ramularia pistaciae* (strain CBS 145564, GenBank NR_165576.1; Identities = 491/491 (100%), no gaps), *Ramularia glennii* (strain SFI-D21, GenBank MT535837.1; Identities = 480/492 (98%), two gaps (0%)), and *Ramularia eucalypti* (strain SFI-D26, GenBank MT535835.1; Identities = 480/492 (98%), two gaps (0%)). Closest hits using the **LSU** sequence were *Ramularia alangiicola* (strain CPC 10299, GenBank KX287023.1; Identities = 825/828 (99%), no gaps), *Ramularia eucalypti* (strain CBS 120726, GenBank NG_069156.1; Identities = 812/815 (99%), no gaps), and *Ramularia rumicicola* (strain CPC 11296, GenBank KX287206.1; Identities = 824/828 (99%), no gaps (0%)). Closest hits using the **actA** sequence had highest similarity to *Ramularia pistaciae* (strain CBS 145564, GenBank MK876462.1; Identities = 571/575 (99%), no gaps), *Ramularia gaultheriae* (strain CBS 299.80, GenBank KX287693.1; Identities = 532/577 (92%), six gaps (1%)), and *Ramularia unterseheri* (strain CBS 124852, GenBank KP894376.1; Identities = 530/576

(92%), three gaps (0%)). Closest hits using the **gapdh** sequence had highest similarity to *Ramularia pistaciae* (strain CBS 145564, GenBank MK876473.1; Identities = 525/536 (98%), one gap (0%)), *Ramularia vizellae* (strain CPC 25731, GenBank KP894644.1; Identities = 417/457 (91%), seven gaps (1%)), and *Ramularia lamiigena* (strain IRAN 3985C, GenBank MW272941.1; Identities = 385/423 (91%), seven gaps (1%)). Closest hits using the **his3** sequence had highest similarity to *Ramularia tricherae* (strain CBS 108973, GenBank KP894799.1; Identities = 346/359 (96%), no gaps), *Ramularia abscondita* (strain CBS 114727, GenBank KX288753.1; Identities = 341/356 (96%), two gaps), and *Ramularia variabilis* (strain CPC 16866, GenBank KP894829.1; Identities = 345/362 (95%), no gaps). Closest hits using the **rpb2** (first part) sequence had highest similarity to *Ramularia gaultheriae* (strain CBS 299.80, GenBank KX288569.1; Identities = 620/731 (85%), no gaps), *Ramularia neodeusta* (strain CPC 13567, GenBank KX288638.1; Identities = 618/735 (84%), six gaps (0%)), and *Ramularia cyclaminicola* (strain CBS 399.51, GenBank KX288551.1; Identities = 617/736 (84%), four gaps (0%)). Closest hits using the **tef1** (first part) sequence had highest similarity to *Ramularia malicola* (strain CBS 119227, GenBank KX288036.1; Identities = 301/308 (98%), one gap (0%)), *Ramularia rumicicola* (strain CPC 11296, GenBank KX288065.1; Identities = 274/330 (83%), 17 gaps (5%)), and *Ramularia lamii* var. *lamii* (strain CBS 108971, GenBank KX288023.1; Identities = 272/313 (87%), 13 gaps (4%)).

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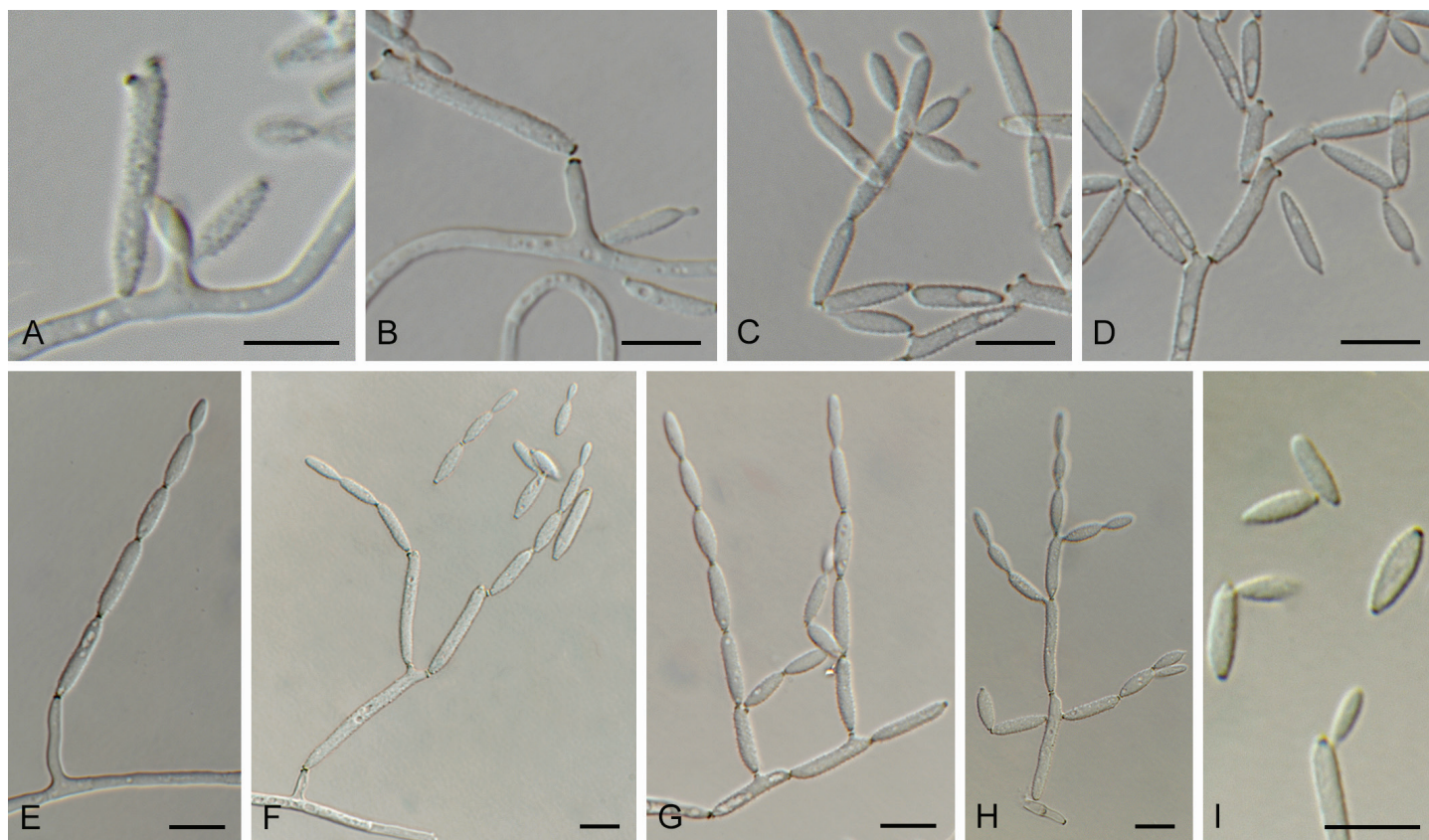


Fig. 35. *Ramularia pistaciae* (CPC 44067). **A–H.** Conidiophores and conidiogenous cells giving rise to branched conidial chains. **I.** Conidia. Scale bars = 10 μ m.

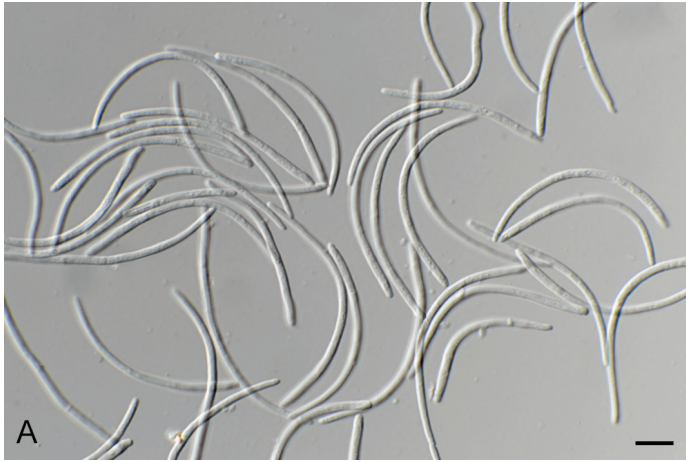


Fig. 36. *Ruptoseptoria unedonis* (CPC 44069). Conidia. Scale bar = 10 μm .

Ruptoseptoria unedonis (Roberge ex Desm.) Quaedvl. et al., *Stud. Mycol.* **75**: 357. 2013. Fig. 36.

Description and illustration: Quaedvlieg et al. (2013).

Material examined: UK, England, Arundale, on leaf spot on *Arbutus unedo* (Ericaceae), 14 May 2022, P.W. Crous & S. Denman, HPC 3956, culture CPC 44069 = CBS 149697.

Notes: *Ruptoseptoria unedonis* is known to cause prominent leaf spotting of *Arbutus unedo*, and is also known from the UK (Quaedvlieg et al. 2013).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Ruptoseptoria unedonis* (strain CBS 355.86, GenBank KF251228.1; Identities = 494/494 (100 %), no gaps), *Chuppomyces handelii* (strain CBS 113302, GenBank EU167581.1; Identities = 471/496 (95 %), four gaps (0 %)), and *Neosonderhenia eucalypti* (strain CBS 145081, GenBank NR_165602.1; Identities = 460/499 (92 %), 13 gaps (2 %)). Closest hits using the LSU sequence were *Ruptoseptoria unedonis* (strain CBS 755.70, GenBank KF251732.1; Identities = 825/826 (99 %), one gap (0 %)), *Chuppomyces handelii* (strain CBS 113302, GenBank GU214437.1; Identities = 811/828 (98 %), five gaps (0 %)), and *Pruniphilomyces circumscissus* (strain CPC 36434, GenBank MT223926.1; Identities = 795/827 (96 %), five gaps (0 %)). Closest hits using the *rpb2* (first part) sequence had highest similarity to *Ruptoseptoria unedonis* (strain CBS 755.70, GenBank MF951659.1; Identities = 768/771 (99 %), no gaps), *Chuppomyces handelii* (strain CBS 113302, GenBank MF951475.1; Identities = 677/773 (88 %), no gaps), and *Neopenidiella nectandrae* (strain ATCC 200932, GenBank MF951546.1; Identities = 580/740 (78 %), 16 gaps (2 %)).

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Schizothecium conicum (Fuckel) N. Lundq., *Symb. Bot. Upsal.* **20**(no. 1): 253 (1972) Fig. 37.

Basionym: *Cercophora conica* Fuckel, *Jahrb. Nassauischen Vereins Naturk.* **23–24**: 245. 1870 [1869–1870].

See MycoBank for synonyms.

Description and illustration: Bell & Mahoney (1995).

Material examined: Netherlands, Overijssel Province, Haaksbergen, Witte Veen, on stems of *Juncus effusus* (Juncaceae), 28 Apr. 2022, E.R. Osieck, HPC 3962 = WI-55, culture CPC 44110 = CBS 149695.

Notes: *Schizothecium conicum* is a common species occurring on dung of herbivores, and is here recorded from culms of *Juncus effusus* in the Netherlands.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Podospora conica* (strain CBS 128.94, GenBank AY515356.1; Identities = 519/521 (99 %), one gap (0 %)), *Schizothecium carpnicola* (strain CBS 228.87, GenBank NR_103589.1; Identities = 515/523 (98 %), two gaps (0 %)), and *Podospora vesticola* (strain NZ196A5, GenBank AY515365.1; Identities = 514/523 (98 %), two gaps (0 %)). Closest hits using the LSU sequence were *Schizothecium vesticola* (strain SMH3187, GenBank AY780076.1; Identities = 823/823 (100 %), no gaps), *Podospora tetraspora* (strain CBS 262.70, GenBank MH871362.1; Identities = 822/823 (99 %), no gaps), and *Podospora minicauda* (strain CBS 227.87, GenBank MH873757.1; Identities = 818/823 (99 %), no gaps). No LSU sequence of *Podospora conica* was available for comparison in GenBank.

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Sporidesmiella pini Crous, *Persoonia* **47**: 259. 2021. Fig. 38.

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

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 μm diam hyphae. **Conidiophores** solitary, erect, macronematous, straight to slightly flexuous, brown, smooth- and thick-walled, base swollen, 7–10 μm diam, 3–6-septate, 50–150 \times 3.5–4.5 μm . **Conidiogenous cells** integrated, terminal, subcylindrical, scars inconspicuous, proliferating percurrently with delayed succession, rejuvenating sympodially, pale brown, smooth, 45–65 \times 3.5–4 μm . **Conidia** solitary, dry, obovoid, medium brown, smooth, guttulate, apex obtuse, base slightly darkened, 2.5–4 μm diam, 3–4 distoseptate, with central pore in each septum, (17–)19–21(–24) \times (8–)9–10 μm .

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA and PDA surface bay with vinaceous pigment, reverse dark brick; on OA surface ochreous.

Material examined: Netherlands, Overijssel Province, Engbertsdijkvenen, near Vriezenveen, 13 m a.s.l., 52°26'53"N, 06°40'02"E, on dead culm of *Juncus effusus* (Juncaceae), 9 Mar. 2021, E.R. Osieck, HPC 3612 = WI-31/#4227 = CBS H-25196, cultures CPC 41494, 41495 = CBS 149045.

Notes: *Sporidesmiella pini* was recently described from needles of *Pinus sylvestris* collected in Utrecht Province of the Netherlands (Crous et al. 2021b). This represents a second collection from the Netherlands, namely from *Juncus effusus* culms collected in Overijssel Province. This represents the 3rd species of *Sporidesmiella* collected from *Juncus* in the Netherlands. Their conidial morphology is similar (3–4-distoseptate, obovoid) but *Sp. junci* and *Sp. juncicola* have (slightly) longer conidia: viz. (20–) 22–25(–27) \times (9–)10(–12) and (20–)28–32(–35) \times (8–)9–10 μm (Crous et al. 2021b, 2022a).

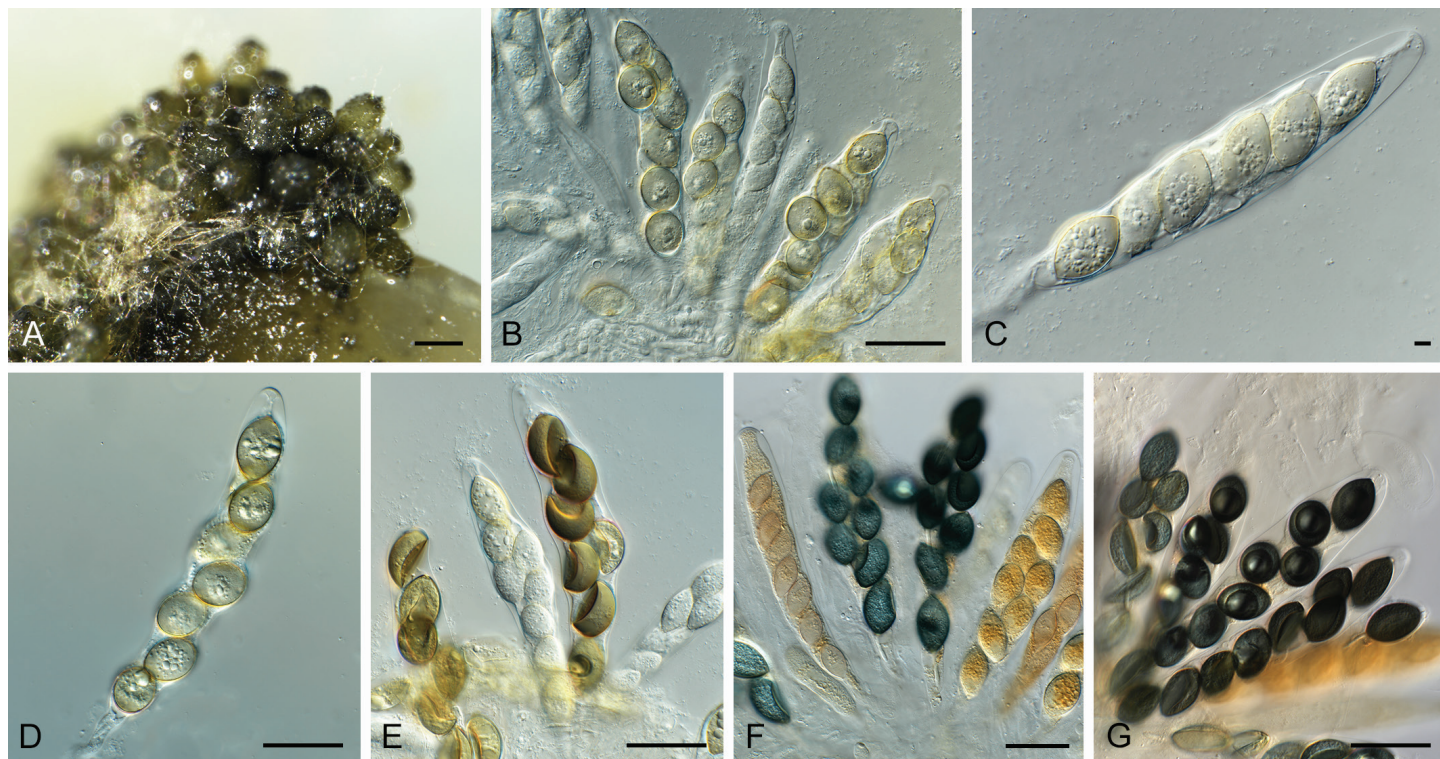


Fig. 37. *Schizothecium conica* (CPC 44110). A. Ascomata on SNA. B–G. Asci with ascospores. Scale bars: A = 180 μ m, all others = 10 μ m.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence of CPC 41494 had highest similarity to *Sporidesmiella pini* (strain CPC 40067, GenBank OK664747.1; Identities = 559/569 (98 %), five gaps (0 %; four of which involve T-repeats at three positions)), *Sporidesmiella hyalosperma* (strain CPC 37552, GenBank MT223845.1; Identities = 552/572 (97 %), ten gaps (1 %)), and *Sporidesmiella obovoidia* (strain MFLUCC 17-2372, GenBank MW286492.1; Identities = 546/570 (96 %), 15 gaps (2 %)). The ITS sequences of CPC 41494 and 41495 are 98 % identical

(551/561 nt, including five gaps all involving different numbers of T-repeats at four positions). Closest hits using the LSU sequence of CPC 41494 were *Sporidesmiella pini* (strain CPC 40067, GenBank NG_081347.1; Identities = 642/642 (100 %), no gaps), *Sporidesmiella obovoidia* (strain MFLUCC 17-2372, GenBank NG_075412.1; Identities = 639/642 (99 %), no gaps), and *Sporidesmiella hyalosperma* (strain S-1518, GenBank MK849842.1; Identities = 636/642 (99 %), no gaps). The LSU sequences of CPC 41494 and 41495 are 100 % identical (642/642 nt). Closest hits using the *rpb2* (first part) sequence



Fig. 38. *Sporidesmiella pini* (CPC 41495). A. Colony on SNA. B–E. Conidiophores and conidiogenous cells giving rise to conidia. F. Conidia. Scale bars = 10 μ m.

of CPC 41494 had highest similarity to *Sporidesmiella pini* (strain CPC 40067, GenBank OK651177.1; Identities = 746/747 (99 %), no gaps), *Sporidesmiella hyalosperma* (strain MFLUCC 18-1013, GenBank MW504070.1; Identities = 695/745 (93 %), no gaps), and *Sporidesmiella novae-zelandiae* (voucher MFLU 18-2332, GenBank MN124525.1; Identities = 656/747 (88 %), no gaps). Closest hits using the *tef1* (second part) sequence of CPC 41494 had highest similarity to *Sporidesmiella* sp. (strain JAUCC 3436, GenBank OK323223.1; Identities = 338/356 (95 %), no gaps), *Sporidesmiella hyalosperma* (voucher MFLU 18-2330, GenBank MN194033.1; Identities = 327/342 (96 %), no gaps), and *Sporidesmiella aquatica* (voucher MFLU 18-1602, GenBank MN194034.1; Identities = 323/342 (94 %), no gaps). No *tef1* sequence of *Sporidesmiella pini* is available for comparison.

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Thyronectria caraganae Voglmayr *et al.*, *Mycol. Progr.* **15**: 924. 2016. Fig. 39.

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

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. Conidiophores reduced to conidiogenous cells, 2–10 × 2–3.5 µm, forming directly on hyphae, varying from hyphal pegs to ampulliform cells, phialidic, solitary or aggregated,

giving rise to sporodochia. *Conidia* allantoid, hyaline, smooth, slightly curved, aseptate, guttulate, ends obtuse, (4–)5–8(–12) × 1.5–2(–3) µm.

Culture characteristics: Colonies flat, spreading, with sparse aerial mycelium, covering dish after 2 wk at 25 °C. On malt extract agar (MEA) surface and reverse sienna; on potato dextrose agar (PDA) surface and reverse pale luteous; on oatmeal agar (OA) surface ochreous.

Typus: Ukraine, Mykolaiv district, Berezansky area, Tashine, on *Caragana arborescens* (*Leguminosae*), 16 May 1990, L.V. Smyk (**holotype** WU 35938); Dvorichna district, Kharkiv region, Krasne Pershe village, National Park Dvorichanskyi, on twigs of *C. arborescens*, 11 Apr. 2021, A. Akulov, ex CWU (MYC) AS 8120 = HPC 3629 (**epitype** designated here CBS H-24959, MBT 10013420, culture ex-epitype CPC 41504 = CBS 148949).

Additional material examined: Ukraine, Kharkiv region, Arseniivskiyi skyt, Nnat. Park Sviati hory, on dead branch of *Caragana arborescens*, 1 Aug. 2021, A. Akulov, HPC 3729, culture CPC 42342 = CBS 149509.

Notes: When Voglmayr *et al.* (2016) described *Thyronectria caraganae*, no asexual morph was observed, and DNA was extracted directly from the specimen due to the absence of a culture. In this study, we isolated the fungus from a fresh collection, and also observed an asexual morph to develop in

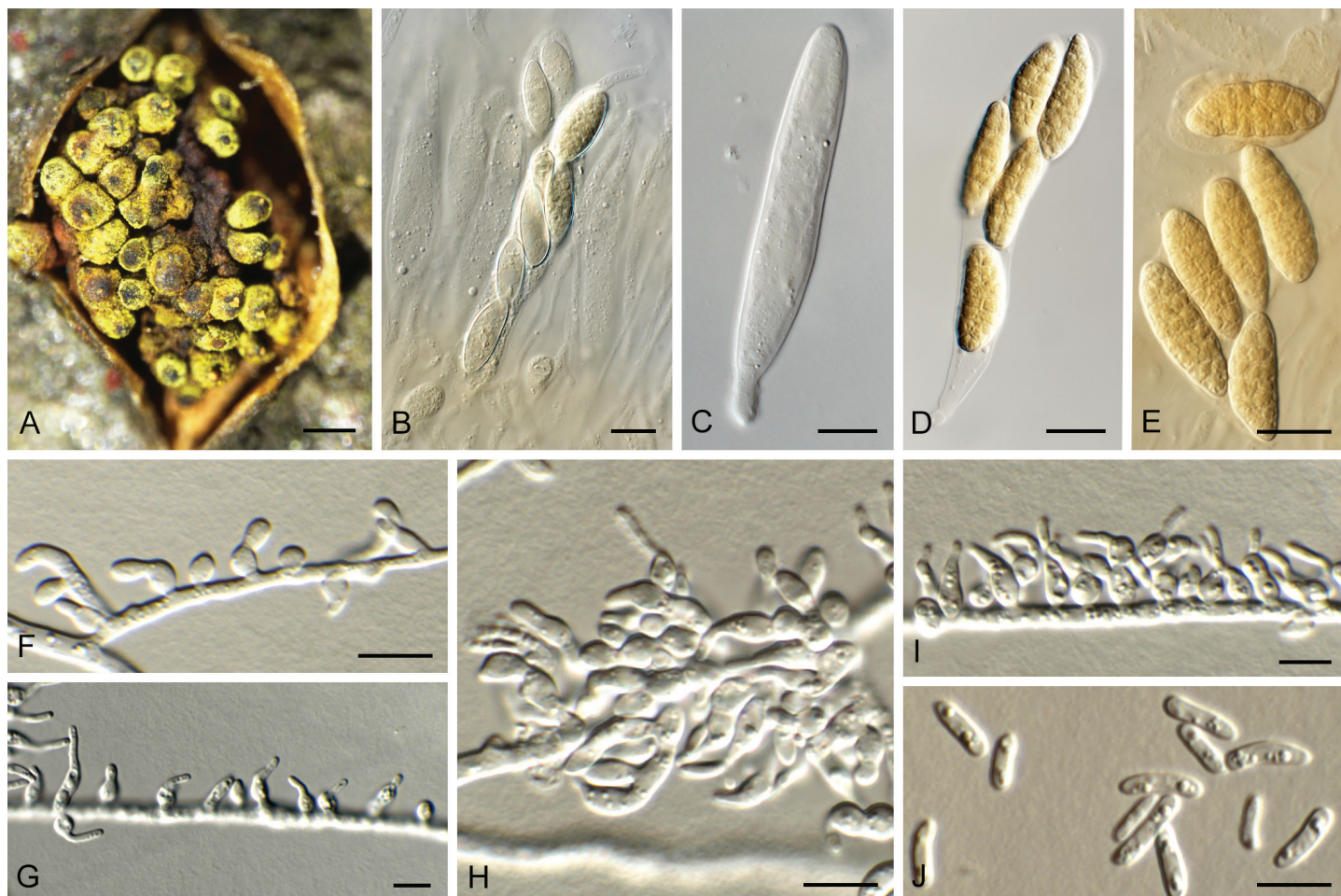


Fig. 39. *Thyronectria caraganae* (CPC 41504). A. Ascomata erumpent from host tissue. B, C. Asci. D, E. Ascospores. F–I. Conidiophores and conidiogenous cells giving rise to conidia. J. Conidia. Scale bars: A = 180 µm, all others = 10 µm.

vitro, making this an appropriate candidate for epitypification. The two cultures examined here were not genetically identical to each other. For the present, we have chosen not to introduce an additional species pending the collection of more specimens.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence of CPC 41504 had highest similarity to *Thyronectria caraganae* (voucher WU 35939, GenBank NR_155911.1; Identities = 560/560 (100 %), no gaps), *Thyronectria virens* (strain NP10, GenBank KM225684.1; Identities = 534/565 (95 %), 12 gaps (2 %)), and *Thyronectria abieticola* (strain THYA, GenBank OL439231.1; Identities = 532/563 (94 %), 12 gaps (2 %)). The ITS sequences of CPC 41504 and 42342 are 98 % identical (531/542 nt, including three gaps). Closest hits using the LSU sequence of CPC 41504 were *Thyronectria caraganae* (strain TCA1, GenBank KX514385.1; Identities = 757/757 (100 %), no gaps), *Thyronectria aurigera* (strain THAU1, GenBank OL439233.1; Identities = 738/757 (97 %), no gaps), and *Thyronectria berlinensis* (strain CBS 127382, GenBank MH875990.1; Identities = 736/756 (97 %), no gaps). The LSU sequences of CPC 41504 and 42342 are 99 % identical (752/757 nt, no gaps). A manual comparison using the *actA* sequence of CPC 41504 revealed a similarity of 91 % (224/246 nt) with *Thyronectria caraganae* (strain TCA1, GenBank KX514382.1). Closest hits using the *rpb1* sequence of CPC 41504 had highest similarity to *Thyronectria caraganae* (strain TCA1, GenBank KX514390.1; Identities = 487/488 (99 %), no gaps), *Thyronectria austroamericana* (strain GG, GenBank KJ570717.1; Identities = 414/490 (84 %), five gaps (1 %)), and *Thyronectria rhodochlora* (strain NP1, GenBank KJ570727.1; Identities = 411/490 (84 %), five gaps (1 %)). The *rpb1* sequences of CPC 41504 and 42342 are 98 % identical (479/488 nt, no gaps). Closest hits using the *rpb2* (first part) sequence of CPC 42342 had highest similarity to *Thyronectria rhodochlora* (strain NP2, GenBank KJ570751.1; Identities = 722/839 (86 %), six gaps (0 %)), *Thyronectria xanthoxyli* (strain NP12, GenBank OL440145.1; Identities = 720/837 (86 %), two gaps (0 %)), and *Thyronectria berlinensis* (strain CBS 127382, GenBank HM534883.1; Identities = 716/835 (86 %), four gaps (0 %)). Closest hits using the *tef1* (second part) sequence of CPC 42342 had highest similarity to *Thyronectria caraganae* (strain TCA1, GenBank KX514396.1; Identities = 720/728 (99 %), no gaps), *Metapochonia rubescens* (strain CBS 110436, GenBank KJ398795.1; Identities = 800/864 (93 %), no gaps), and *Metapochonia bulbillosa* (strain P6656, GenBank MT701577.1; Identities = 800/864 (93 %), no gaps). Closest hits using the *tub2* sequence of CPC 41504 had highest similarity to *Thyronectria caraganae* (strain TCA1, GenBank KX514399.1; Identities = 359/359 (100 %), no gaps), *Metapochonia bulbillosa* (strain CBS 145.70, GenBank KJ398549.1; Identities = 201/224 (90 %), eight gaps (3 %)), and *Metapochonia goniodes* (strain CBS 891.72, GenBank KJ398551.1; Identities = 202/226 (89 %), seven gaps (3 %)). The *tub2* sequences of CPC 41504 and 42342 are 97 % identical (348/359 nt, no gaps).

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Trichosphaeria pilosa (Pers.) Fuckel, *Jb. nassau. Ver. Naturk.* **23–24**: 145. 1870. [1869–1870]. Fig. 40.

Basionym: *Sphaeria pilosa* Pers., *Icon. Desc. Fung. Min. Cognit.* **2**: 41, tab. 10: 9–10. 1800: Fries, *Syst. Mycol.* **2**(2): 450. 1823.

Description and illustration: Réblová & Gams (2016).

Ascomata in densely aggregated clusters in substrate, superficial, non-stromatic, globose with papillate apex and central ostiole,

dark brown to black, 180–250 µm diam, sparsely setose; setae up to 20 µm long, 6–7 µm diam near base, dark brown, 0–1-septate, tapering to subobtusate apex. Ostiole periphysate. Paraphyses hyaline, septate, 2.5–3 µm diam, trabeculae-like. Asci 35–55 × 4–6 µm, cylindrical, short stipitate, apex obtuse, without visible discharge mechanism (in Melzer), 8-spored. Ascospores 7–8(–8.5) × (2.5–)3–3.5 µm, broadly ellipsoid, hyaline, aseptate, becoming medianly septate, guttulate, verruculose, at times with lateral pegs on some ascospores. Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. Conidiophores erect, solitary, branched below, subverticillately, or unbranched, subcylindrical, hyaline, smooth, 1–3-septate, 60–100 × 3–4 µm. Conidiogenous cells integrated, terminal and lateral, hyaline, smooth, phialidic, subcylindrical to aculeate, apex with cylindrical collarete, 1–2 µm long, 25–50 × 2.5–3 µm. Conidia aggregating in mucoid mass, hyaline, smooth, aseptate, broadly ellipsoid, guttulate, apex subobtusate, tapering to truncate hilum, 0.5 µm diam or base slightly rounded, (4.5–)5–6(–6.5) × 2.5–3 µm.

Culture characteristics: Colonies flattened, spreading, folded, with moderate aerial mycelium and smooth, lobate margin, reaching 40 mm diam after 2 wk at 25 °C. On malt extract agar (MEA), potato dextrose agar (PDA) and oatmeal agar (OA) surface and reverse olivaceous grey.

Typus: **Lectotype** designated by Clements & Shear, *Gen. fung.*, Edn 2 (Minneapolis): 261. 1931. **Germany**, Östlicher Wald, on decaying wood of *Quercus* (*Fagaceae*), spring, **neotype**, designated by Réblová & Gams (2016): Fuckel, *Fungi Rhen.* Exs. no. 946 (M-0280129). **Netherlands**, Utrecht Province, Nieuw Wulven, near Houten, 1.5 m a.s.l., 52°03'03"N, 05°09'43"E, on decayed *Salix* branch (*Salicaceae*), 28 Jan. 2022, E.R. Osieck, HPC 3824 = WI-44/#4388 (**epitype** designated here CBS H-25199, MBT 10013421, culture ex-epitype CPC 42927 = CBS 149698).

Notes: Barr (1990) circumscribed the *Trichosphaeriaceae* to include *Acanthostigma*, *Eriosphaeria*, *Rhamphoria* and *Trichosphaeria*, although Barr & Cannon (1994) agreed that the family was heterogeneous. Several taxa were subsequently relocated to *Niessliaceae*, *Lasiosphaeriaceae* and *Sordariales*. Due to these problems, Réblová & Winka (2001) suggested that no additional genera be accepted in the family, until the phylogeny of *T. pilosa* could be resolved.

Réblová & Gams (2016) examined several collections from Persoon's fungarium preserved in L under the name *S. pilosa*. However, these were shown to represent different fungi not corresponding with the protologue. Furthermore, the original illustration [Persoon 1800: tab. 10: 9–10; cited as fig. 2 in Réblová & Gams (2016)] was regarded as insufficient to serve as a nomenclatural type, and therefore a neotype was designated, which correlates well with the epitype we designate in this study.

Because of the uncertain higher-level phylogeny of *Trichosphaeria*, Réblová & Gams (2016) recommended accepting *Trichosphaeria* as the only member of the *Trichosphaeriaceae*, pending further collections of *T. pilosa*. Currently, Wijayawardene *et al.* (2022) list 11 genera as belonging to *Trichosphaeriaceae* (*Trichosphaeriales*). Based on the phylogenetic tree presented in this study (Fig. 41), *T. pilosa* is embedded within what was previously recognised as *Plectosphaerellaceae* (see for example Giraldo & Crous 2019), with *Fuscohypha expansa* as closest phylogenetic neighbour (97 % / 83 % / 1). *Trichosphaeriaceae* predates *Plectosphaerellaceae* (1885 vs 2007), and the latter is

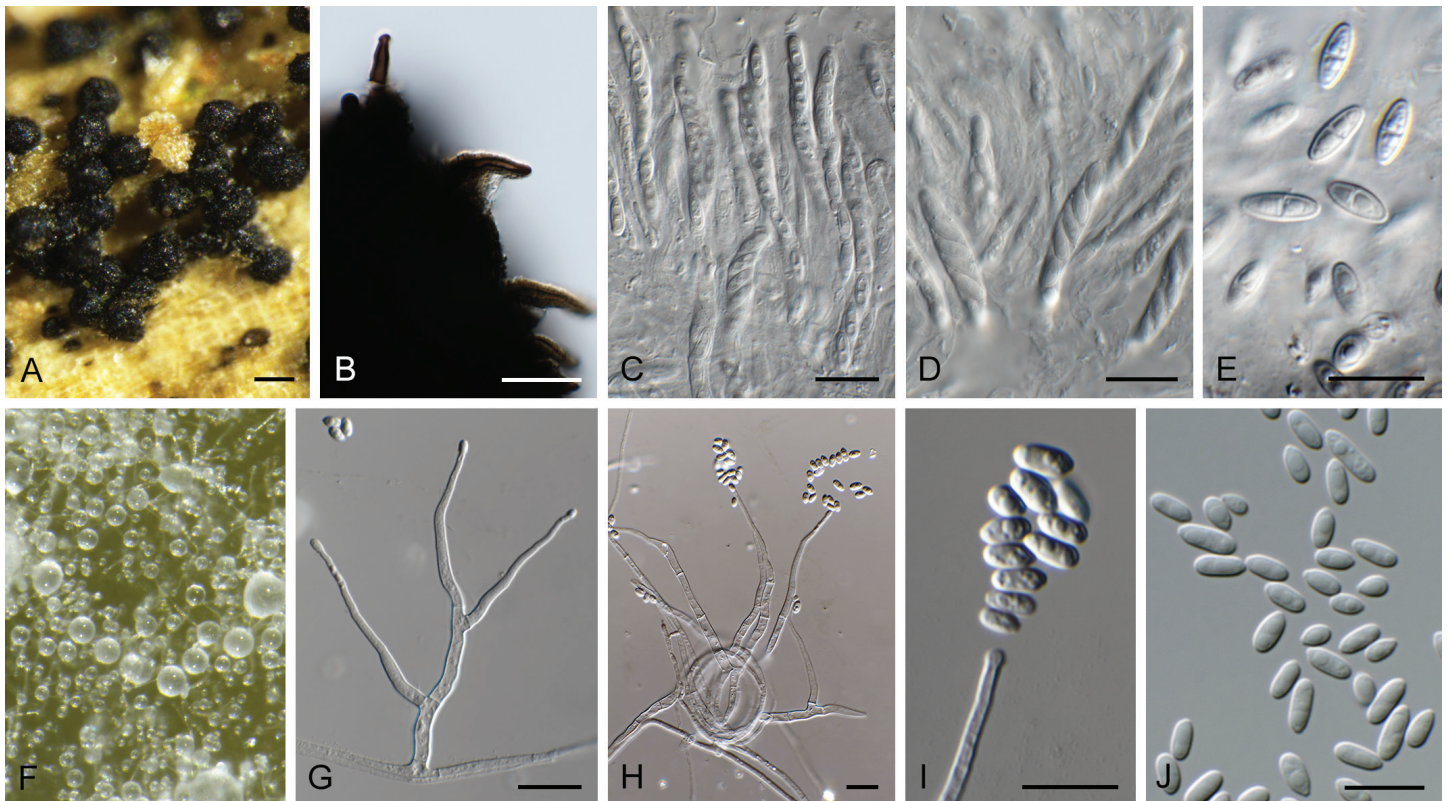


Fig. 40. *Trichosphaeria pilosa* (CPC 42927). **A.** Ascomata on host tissue. **B.** Ascomatal wall with setae. **C, D.** Asci. **E.** Ascospores. **F.** Colony on OA. **G–I.** Conidiophores and conidiogenous cells giving rise to conidia. **J.** Conidia. Scale bars: A = 180 μm , all others = 10 μm .

therefore reduced to synonym. The family clade is fully supported in all three phylogenetic analyses. On the other hand, the lineage containing *Australiascaceae*, *Glomerellaceae*, *Malaysiascaceae* and *Reticulasacaceae* had low to full support (54 % / 90 % / 1), while the node connecting these families to the *Trichosphaeriaceae* node was poorly supported in the maximum likelihood analyses (68 % and 38 %). Furthermore, this node was absent in the Bayesian phylogeny as these former families formed a sister lineage to *Falcocladiales*, *Microascales* and *Torpedosporales* with a Bayesian posterior probability value of 0.84 (data not shown). We have therefore retained the use of *Glomerellales* for those families, while resurrecting *Trichosphaeriales* for the former family *Plectosphaerellaceae*. In the phylogenetic analysis of Hyde et al. (2020), “*Trichosphaeriaceae*” (based on “*Brachysporium groenendalensis*”; see pages 357 and 364 of Hyde et al. 2020) is genetically distinct from families associated with *Glomerellales* (see pages 359 and 388 of Hyde et al. 2020). Genera previously considered to belong to *Trichosphaeriaceae* need to re-evaluated as it is clear that some of these, e.g. *Brachysporium*, need to be assigned to a different order and family.

With the designation of an epitype in this study, this matter is now resolved, although the recently introduced family *Plectosphaerellaceae* (2007) is reduced to synonymy. Based on the phylogeny of *T. pilosa*, the *Trichosphaeriaceae* presently contains 25 genera.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Verticillium albo-atrum* (strain CBS 103.95, GenBank LR026714.1; Identities = 476/496 (96 %), three gaps (0 %)), *Plectosphaerella kunmingensis* (strain KUMCC 18-0181, GenBank MK993014.1; Identities = 481/511 (94 %), 11 gaps (2 %)), and *Plectosphaerella cucumerina* (strain ZMXR22 GenBank

MT446127.1; Identities = 486/518 (94 %), ten gaps (1 %)). Closest hits using the **LSU** sequence were *Plectosphaerella kunmingensis* (voucher KUMCC 18-0181, GenBank MK993015.1; Identities = 838/848 (99%), no gaps), *Gibellulopsis nigrescens* (strain CBS179.40, GenBank MH867573.1; Identities = 836/848 (99 %), no gaps), and *Cephalosporium serrae* (strain CBS 290.30, GenBank LR025872.1; Identities = 804/816 (99 %), no gaps). No significant hits were obtained using the **actA** and **his3** sequences. Closest hits using the **rpb2** (first part) sequence had highest similarity to *Verticillium albo-atrum* (strain RgVa1, GenBank MZ710737.1; Identities = 641/694 (92 %), no gaps), *Plectosphaerella slobbergiarum* (strain NL1930002, GenBank MW890074.1; Identities = 510/557 (92 %), no gaps), and *Plectosphaerella cucumerina* (strain CBS 137.37, GenBank LR026199.1; Identities = 629/691 (91 %), no gaps). Closest hits using the **tef1** (first part) sequence had highest similarity to *Plectosphaerella ramiseptata* (strain CBS 131861, GenBank KY421317.1; Identities = 144/148 (97 %), no gaps), *Gliocladium cibotii* (strain CBS 299.70H, GenBank EF543807.1; Identities = 147/152 (97 %), no gaps), and *Plectosphaerella alismatis* (strain CBS 113362, GenBank KY421328.1; Identities = 143/148 (97 %), no gaps). Closest hits using the **tef1** (second part) sequence had highest similarity to *Plectosphaerella kunmingensis* (strain KUMCC 18-0181, GenBank MK993017.1; Identities = 834/894 (93 %), no gaps), *Plectosphaerella cucumerina* (strain CBS 144925, GenBank LR594767.1; Identities = 837/903 (93 %), no gaps), and *Plectosphaerella plurivora* (strain GZUIFR-H26.5.1, GenBank MK930456.1; Identities = 834/901 (93 %), no gaps). Closest hits using the **tub2** sequence had highest similarity to *Plectosphaerella populi* (strain CBS 139623, GenBank KY421311.1; Identities = 261/331 (79 %), 15 gaps (4 %)), and *Pleurotheciella rivularia* (strain CBS 125237, GenBank KT278760.1; Identities = 259/332 (78 %), 17 gaps (5 %)).

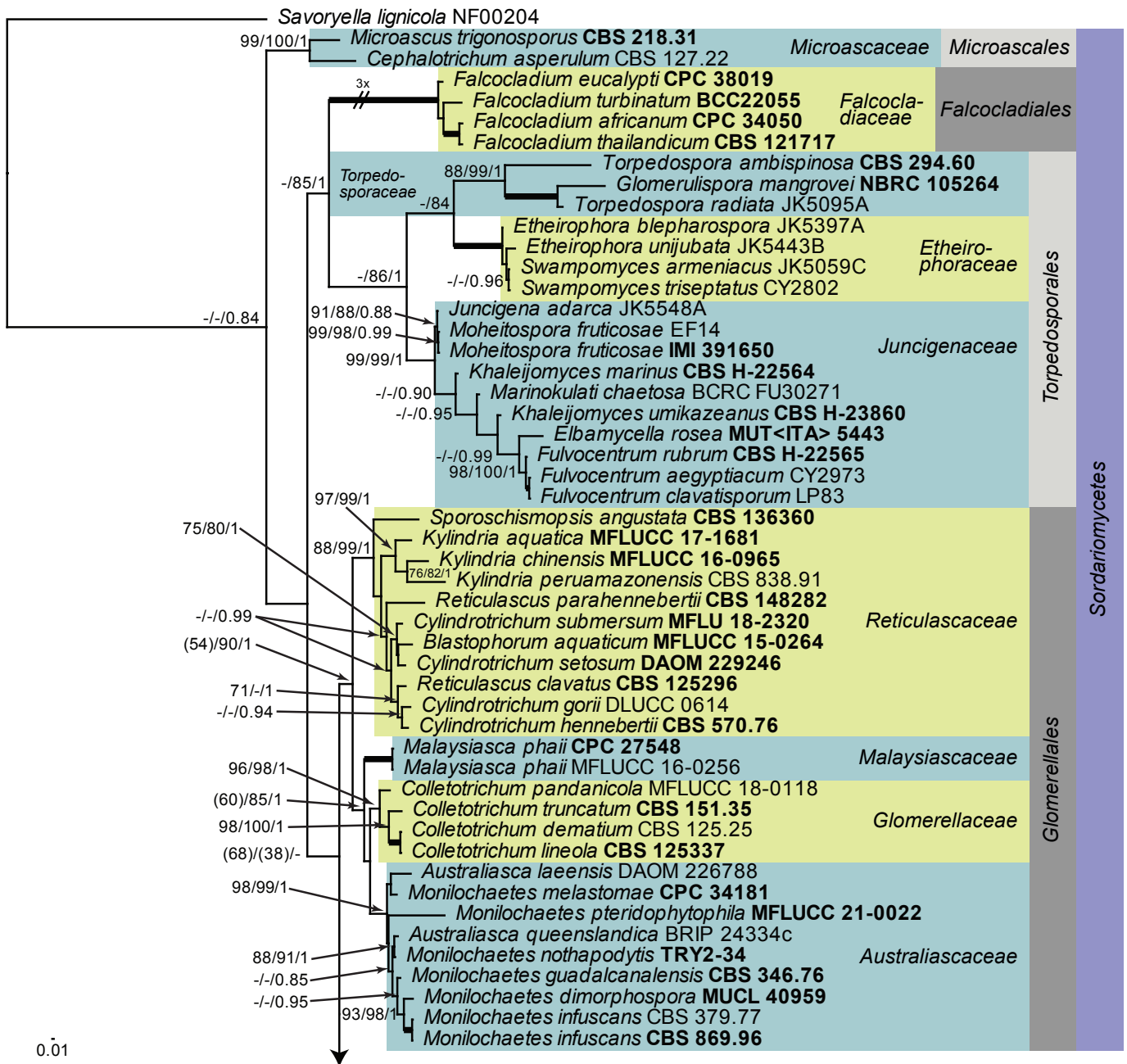


Fig. 41. Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 of the *Sordariomycetes* ITS/LSU/*tef1* nucleotide alignment. Maximum likelihood (> 74 %) and RAxML (> 74 %) bootstrap support values from 1 000 non-parametric bootstrap replicates, and Bayesian posterior probabilities (> 0.84), are shown at the nodes. Thickened lines represent nodes which received full support (100 % / 100 % / 1) from all three analyses. Culture collection or voucher numbers are indicated for all species. Sequences derived from material with a type status are indicated with a culture or voucher number highlighted with bold face. GenBank accession numbers of the sequences used in the alignment are listed in supplementary Table S2. The tree was rooted to *Savoryella lignicola* (strain NF00204) and the species treated here is highlighted with bold face. The families, orders and class are shown in coloured blocks to the right of the tree. The scale bar indicates the expected number of changes per site.

Classification: *Sordariomycetes*, *Hypocreomycetidae*, *Trichosphaeriales*, *Trichosphaeriaceae*.

Order
Trichosphaeriales M.E. Barr, *Mycologia* **75**: 11. 1983.

Family
Trichosphaeriaceae G. Winter [as '*Trichosphaerieae*'], *Rabenh. Krypt.-Fl.*, Edn 2 (Leipzig): 191. 1885.
Synonym: *Plectosphaerellaceae* W. Gams et al., *Nova Hedwigia* **85**: 476. 2007.

Currently accepted genera

Acremoniisimulans Tibpromma & K.D. Hyde, *Fungal Diversity* **93**: 88. 2018.
Acrostalagmus Corda, *Icones fungorum hucusque cognitorum* **2**: 15. 1838.
Brunneochlamydosporium Giraldo López & Crous, *Stud. Mycol.* **92**: 260. 2018.
Brunneomyces Giraldo et al., *Mycol. Progr.* **16**: 357. 2017.
Chlamydosporiella Giraldo López & Crous, *Stud. Mycol.* **92**: 270. 2018.
Chordomyces Bilanenko et al., *Fungal Diversity* **76**: 55. 2015.

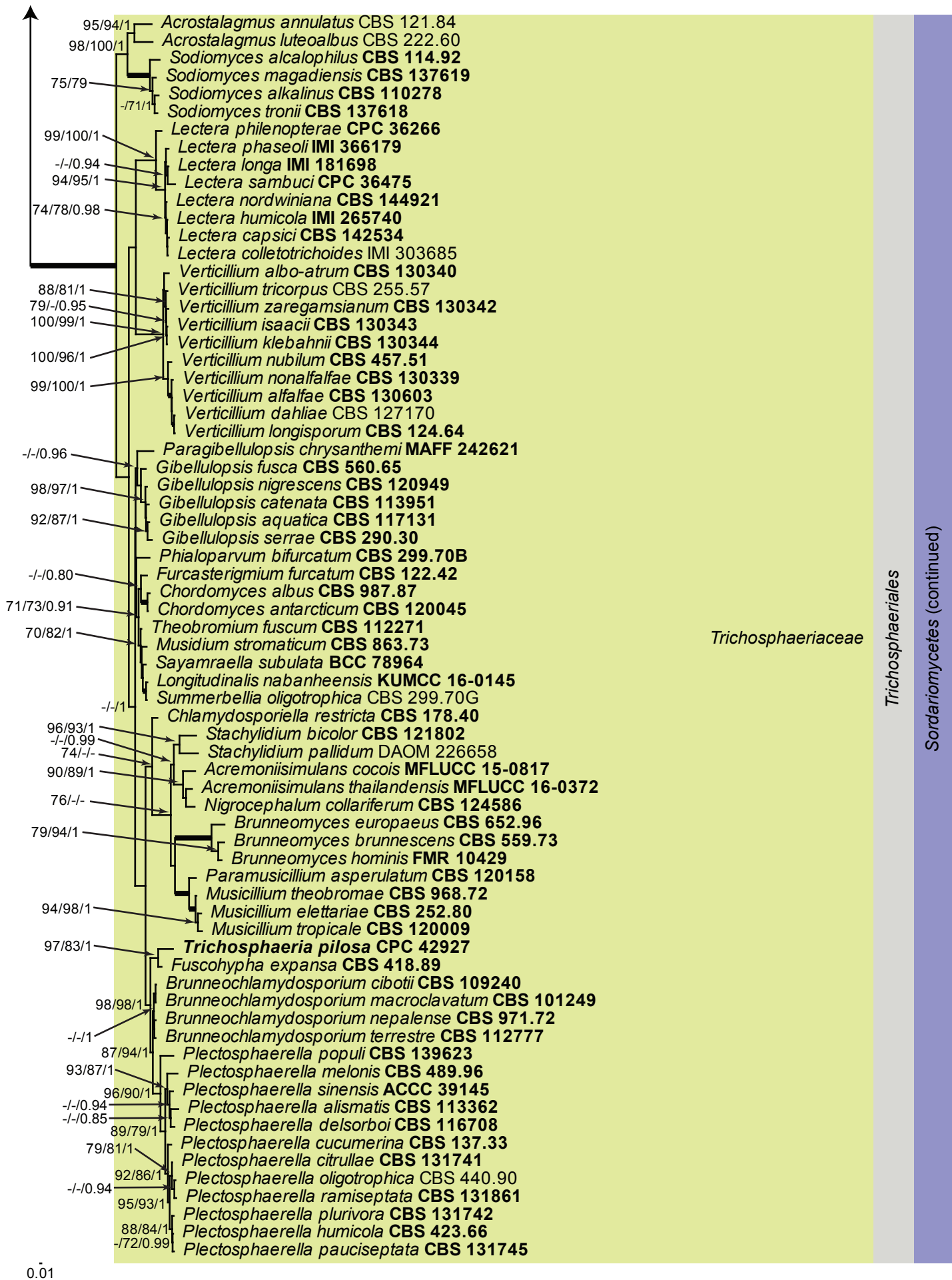


Fig. 41. (Continued).

Furcasterigmium Giraldo López, *Stud. Mycol.* **92**: 251. 2018.
Fuscohypha Giraldo López & Crous, *Stud. Mycol.* **92**: 264. 2018.
Gibellulopsis Bat. & H. Maia, *Anais Soc. Biol. Pernambuco* **16**: 153. 1959.
Lectera P.F. Cannon, *MycKeys* **3**: 28. 2012.
Longitudinalis Tibpromma & K.D. Hyde, *Fungal Diversity* **87**: 155. 2017.
Musicillium Zare & W. Gams, *Nova Hedwigia* **85**: 482. 2007.
Musidium Giraldo López & Crous, *Stud. Mycol.* **92**: 253. 2018.
Nigrocephalum Giraldo López & Crous, *Stud. Mycol.* **92**: 271. 2018.
Paragibellulopsis Giraldo López & Crous, *Stud. Mycol.* **92**: 265. 2018.
Paramusicillium Giraldo López & Crous, *Stud. Mycol.* **92**: 269. 2018.
Phialoparvum Giraldo López & Crous, *Stud. Mycol.* **92**: 265. 2018.
Plectosphaerella Kleb., *Phytopathol. Z.* **1**: 43. 1929.
Sayamraella Giraldo López & Crous, *Stud. Mycol.* **92**: 255. 2018.
Sodiomyces A.A. Grum-Grzhim. *et al.*, *Fungal Syst. Evol.* **3**: 131. 2019.
Stachylidium Link, *Mag. Neuesten Entdeck. Gesammten Naturk. Ges. Naturf. Freunde Berlin* **3**: 15. 1809.
Summerbellia Giraldo López & Crous, *Stud. Mycol.* **92**: 252. 2018.
Theobromium Giraldo López & Crous, *Stud. Mycol.* **92**: 256. 2018.
Trichosphaeria Fuckel, *Jahrb. Nassauischen Vereins Naturk.* 23–24: 144. 1870.
Verticillium Nees, *System der Pilze und Schwämme*: 56. 1817.

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Zaanenomyces versatilis Crous & Osieck, *Persoonia* **47**: 235. 2021. Fig. 42.

Mycelium consisting of pale brown, smooth, guttulate, branched, septate, 1.5–2 µm diam hyphae, forming hyphal coils. *Conidiophores* erect, solitary, arising from superficial hyphae, terminal or intercalary, pale brown, smooth, subcylindrical, 15–40 × 2–3 µm. *Conidiogenous cells* terminal, pale brown, smooth, 5–25 × 2–3 µm, developing a rachis of denticles, 1–3 × 1–2 µm, not thickened nor darkened, with truncate apices. *Conidia* solitary, dry, fusoid, widest in middle, hyaline, smooth, guttulate, apices obtuse, hilum truncate, 1–1.5 µm diam, unthickened, not darkened, 3–6(–8)-septate, (35–)50–60(–70) × (2.5–)3 µm.

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

Material examined. **Netherlands**, Utrecht Province, Nieuw Wulven, on dead stems of *Juncus effusus* (*Juncaceae*), Dec. 2021, E. Osieck, HPC 3812 = CBS H-25166, culture CPC 42831 = CBS 149453.

Notes: *Zaanenomyces* (*Tubeufiaceae*) was recently introduced for three cercosporoid-like hyphomycetes occurring on culms of *Juncus* in the Netherlands (Crous *et al.* 2021b). *Zaanenomyces versatilis* was described as having conidia that are (3–)7–10(–12)-septate, (16–)43–50(–55) × (2.5–)3(–3.5) µm). The present collection has slightly longer conidia, with less septa, but fits well based on its DNA phylogeny.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Zaanenomyces versatilis* (strain CBS 148312, GenBank NR_175227.1; Identities = 556/557 (99 %), no gaps), *Zaanenomyces moderatricis-academiae* (strain CBS 148315,

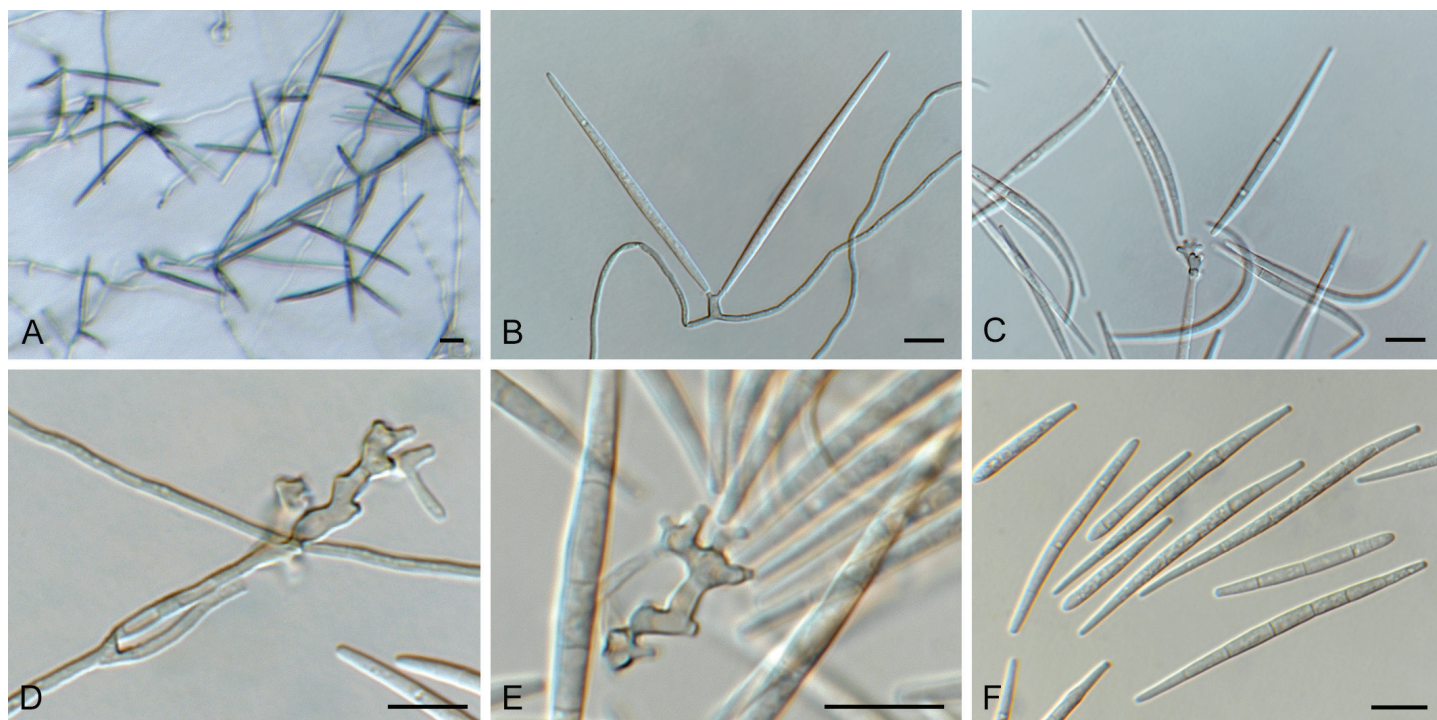


Fig. 42. *Zaanenomyces versatilis* (CPC 42831). A. Colony on SNA. B–E. Conidiophores and conidiogenous cells giving rise to conidia. F. Conidia. Scale bars = 10 µm.

GenBank NR_175222.1; Identities = 485/505 (96 %), six gaps (1 %)), and *Camporesiomyces vaccinii* (strain CBS 216.90, GenBank NR_156202.1; Identities = 490/559 (88 %), 15 gaps (2 %)). Closest hits using the **LSU** sequence were *Zaanenomyces versatilis* (strain CBS 148312, GenBank NG_081336.1; Identities = 820/820 (100 %), no gaps), *Zaanenomyces moderatricis-academicae* (strain CBS148315, GenBank NG_081331.1; Identities = 789/793 (99 %), no gaps), and *Helicosporium luteosporum* (voucher MFLU 16-2871, GenBank NG_059773.1; Identities = 811/836 (97 %), no gaps). Closest hits using the **tef1** (second part) sequence had highest similarity to *Helicosporium flavum* (strain MFLUCC 16-1230, GenBank KY873285.1; Identities = 765/825 (93 %), two gaps (0 %)), *Tubeufia cylindrothecia* (strain MFLUCC 17-1792, GenBank MH550968.1; Identities = 755/825 (92 %), two gaps (0 %)), and *Helicosporium viridisporum* (strain GZCC 22-2008, GenBank OP698087.1; Identities = 754/824 (92 %), no gaps).

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Table S1. Summary of phylogenetic information for the different analyses in this study

Table S2. GenBank accession numbers of sequences used to generate the alignment for the placement of *Trichosphaeria pilosa*.