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New and Interesting Fungi. 4

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Abstract: An order, family and genus are validated, seven new genera, 35 new species, two new combinations, two epitypes, two lectotypes, and 17 interesting new host and / or geographical records are introduced in this study. Validated order, family and genus: *Superstratomycetales* and *Superstratomycetaceae* (based on *Superstratomyces*). New genera: *Haudseptoria* (based on *Haudseptoria typhae*); *Hogelandia* (based on *Hogelandia lambearum*); *Neoscirrhia* (based on *Neoscirrhia osmundae*); *Nothoanungitopsis* (based on *Nothoanungitopsis urophyllae*); *Nothomicrosphaeropsis* (based on *Nothomicrosphaeropsis welwitschiae*); *Populomyces* (based on *Populomyces zwinianus*); *Pseudoacrospermum* (based on *Pseudoacrospermum goniomae*). New species: *Apiospora sasae* on dead culms of *Sasa veitchii* (Netherlands); *Apiospora stipae* on dead culms of *Stipa gigantea* (Spain); *Bagadiella eucalyptorum* on leaves of *Eucalyptus* sp. (Australia); *Calonectria singaporensis* from submerged leaf litter (Singapore); *Castanediella neomalaysiana* on leaves of *Eucalyptus* sp. (Malaysia); *Colletotrichum pleopeltidis* on leaves of *Pleopeltis* sp. (South Africa); *Coniochaeta deborreae* from soil (Netherlands); *Diaporthe durionigena* on branches of *Durio zibethinus* (Vietnam); *Floricola juncicola* on dead culm of *Juncus* sp. (France); *Haudseptoria typhae* on leaf sheath of *Typha* sp. (Germany); *Hogelandia lambearum* from soil (Netherlands); *Lomentospora valparaisensis* from soil (Chile); *Neofusicoccum mystacidii* on dead stems of *Mystacidium capense* (South Africa); *Neomycosphaerella guibourtiae* on leaves of *Guibourtia* sp. (Angola); *Niesslia neoexosporioides* on dead leaves of *Carex paniculata* (Germany); *Nothoanungitopsis urophyllae* on seed capsules of *Eucalyptus urophylla* (South Africa); *Nothomicrosphaeropsis welwitschiae* on dead leaves of *Welwitschia mirabilis* (Namibia); *Paracremonium bendijkiorum* from soil (Netherlands); *Paraphoma ledniceana* on dead wood of *Buxus sempervirens* (Czech Republic); *Paraphoma salicis* on leaves of *Salix*

cf. alba (Ukraine); *Parasarocladium wereldwijsianum* from soil (Netherlands); *Peziza ligni* on masonry and plastering (France); *Phyllosticta phoenicis* on leaves of *Phoenix reclinata* (South Africa); *Plectosphaerella slobbergiarum* from soil (Netherlands); *Populomyces zwinianus* from soil (Netherlands); *Pseudoacrospermum goniomae* on leaves of *Gonioma kamassi* (South Africa); *Pseudopyricularia festucae* on leaves of *Festuca californica* (USA); *Sarocladium sasijaorum* from soil (Netherlands); *Sporothrix hypoxyli* in sporocarp of *Hypoxylon petriniae* on *Fraxinus* wood (Netherlands); *Superstratomyces albomucosus* on *Pycnanthus angolensis* (Netherlands); *Superstratomyces atroviridis* on *Pinus sylvestris* (Netherlands); *Superstratomyces flavomucosus* on leaf of *Hakea multilinearis* (Australia); *Superstratomyces tardicrescens* from human eye specimen (USA); *Taeniolella platani* on twig of *Platanus hispanica* (Germany), and *Tympanis pini* on twigs of *Pinus sylvestris* (Spain).

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INTRODUCTION

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

MATERIALS AND METHODS

Isolates

Twig and leaf samples collected from around the world (see Table 1) were treated as previously detailed (Crous *et al*. 2019b), while the treatment of soil samples followed the methods of Giraldo *et al*. (2019) and Hou *et al*. (2020b). Single conidial colonies were established on Petri dishes containing 2 % malt extract agar (MEA) as described by Crous *et al.* (1991), and single ascospore cultures were established following the method described by Crous (1998). Colonies were sub-cultured on 2 % potato-dextrose agar (PDA), oatmeal agar (OA), MEA (Crous *et al*. 2019b), or autoclaved pine needles on 2 % tap water agar (PNA) (Smith *et al.* 1996), and incubated at 25 °C under continuous near-ultraviolet light to promote sporulation. Reference strains and specimens of the studied fungi are maintained in the culture collection (CBS) of the Westerdijk Fungal Biodiversity Institute (WI), Utrecht, the Netherlands.

DNA extraction, amplification (PCR) and phylogeny

Fungal mycelium (Table 1) was scraped from the surface of agar cultures with a sterile scalpel and the genomic DNA was isolated using the Wizard® Genomic DNA Purification Kit (Promega Corporation, WI, USA) following the manufacturers' protocols. All loci were amplified following previously published protocols. First, the 28S nrRNA gene (LSU) and internal transcribed spacer regions with intervening 5.8S nrRNA gene (ITS) of the nrDNA operon were sequenced for all the isolates included in this study (for amplification conditions, see Fan *et al*. 2018). Other loci were sequenced for various species or genera using primers and conditions specific for those groups of fungi. Amplification of the partial DNA-directed RNA polymerase II second largest subunit gene (*rpb2*), the partial translation elongation factor 1-alpha gene (*tef1*, first part) and the partial beta-tubulin gene (*tub2*) followed Braun *et al.* (2018), while amplification of the partial actin gene (*actA*), the partial calmodulin gene (*cmdA*), the partial glyceraldehyde-3-phosphate dehydrogenase gene (*gapdh*) and the partial histone H3 gene (*his3*) followed Videira *et al*. (2016). Amplification of the partial DNA-directed RNA polymerase II largest subunit gene (*rpb1*) followed Klaubauf *et al*. (2014), the partial translation elongation factor 1-alpha gene (*tef1*, second part) followed Réblová *et al*. (2020) and of the partial chitin synthase-1 (*chs-1*) followed Damm *et al*. (2019). 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 v. 11.1.5 (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. Phylogenetic trees were generated using Bayesian analyses performed with MrBayes v. 3.2.7a (Ronquist *et al*. 2012) for the overview trees and Maximum Parsimony analyses performed with PAUP v. 4.0b10 (Swofford 2003) as explained in Braun *et al*. (2018) for the genus and species trees. All resulting trees were printed with Geneious v. 11.1.5 and the layout of the trees was done in Adobe Illustrator v. CC 2017. Statistical measures calculated for the parsimony analyses included tree length (TL), consistency index (CI), retention index (RI) and rescaled consistency index (RC). Maximum-likelihood trees were generated with IQ-TREE v. 1.6.12 (Nguyen *et al*. 2015) and branch support values were calculated with 5 000 ultrafast

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.

Species	Culture or voucher accession number(s)[1]	Locality and Substrate	Collector(s)	GenBank accession number[2]				
				ITS	LSU	*rpb2*	*tub2*	Other loci
Alternaria chartarum	CBS 200.67 = ATCC 18044 = DAOM 59616b = IMI 124943 = MUCL 18564 = QM 8328, ex-epitype	Canada: *Populus* plywood	E.G. Simmons	MH858944.1	NG_069727.1	KC584481.1	–	*gapdh*: KC584172.1, SSU: NG_062919.1, *tef1* (first part): KC584741.1
Alternaria chartarum	CPC 38971	Namibia: Lichen hypolith under a rock	P.W. Crous	MW883400.1	MW883795.1	–	MW890118.1	*actA*: MW890017.1, *cmdA*: MW890037.1, *gapdh*: MW890046.1, *tef1* (first part): MW890080.1
Alternaria heterospora	CBS 123376, ex-type of *Ulocladium solani*	China: *Lycopersicon esculentum*, diseased leaves	Y. Wang	KC584248.1	KC584363.1	KC584488.1	–	*gapdh*: KC584176.1, SSU: KC584621.1, *tef1* (first part): KC584748.1
	CPC 38969	Namibia: Lichen hypolith under a rock	P.W. Crous	MW883401.1	MW883796.1	–	MW890119.1	*actA*: MW890018.1, *cmdA*: MW890038.1, *gapdh*: MW890047.1, *tef1* (first part): MW890081.1
Apiospora sasae, sp. nov.	CBS 146808 = CPC 38165, ex-type	Netherlands: *Sasa veitchii*, dead culms	L. van der Linde	MW883402.1	MW883797.1	MW890058.1	MW890120.1	*tef1* (second part): MW890104.1
Apiospora stipae, sp. nov.	CBS 146804 = CPC 38101, ex-type	Spain: *Stipa gigantea*, dead culm	M.A. Delgado	MW883403.1	MW883798.1	MW890059.1	MW890121.1	*tef1* (first part): MW890082.1, *tef1* (second part): MW890105.1
Bagadiella eucalyptorum, sp. nov.	CBS 147177 = CPC 39299, ex-type	Australia: *Eucalyptus* sp., leaves	A.J. Carnegie	MW883404.1	MW883799.1	–	–	–
Blastacervulus metrosideri	CBS 147006 = CPC 38759 = T19_05741C	New Zealand: *Metrosideros* sp., leaves	L. Rabbidge	MW883405.1	MW883800.1	–	–	–
	ICMP 21883, ex-type	New Zealand: *Metrosideros excelsa*, living leaves	P.R. Johnston	NR_169959.1	NG_068290.1	–	–	–
Calonectria singaporensis, sp. nov.	CBS 146712 = MUCL 048012	Singapore: Submerged leaf litter in a small stream	C. Decock	MW883406.1	MW883801.1	–	MW890122.1	*actA*: MW890019.1, *cmdA*: MW890039.1, *his3*: MW890052.1, *tef1* (first part): MW890083.1
	CBS 146713 = MUCL 048171	Singapore: Submerged leaf litter in a small stream	C. Decock	MW883407.1	MW883802.1	–	MW890123.1	*actA*: MW890020.1, *cmdA*: MW890040.1, *his3*: MW890053.1, *tef1* (first part): MW890084.1
	CBS 146714 = MUCL 048187	Singapore: Submerged leaf litter in a small stream	C. Decock	MW883408.1	MW883803.1	–	–	*actA*: MW890021.1, *cmdA*: MW890041.1, *his3*: MW890054.1, *tef1* (first part): MW890085.1
	CBS 146715 = MUCL 048320, ex-type	Singapore: Submerged leaf litter in a small stream	C. Decock	MW883409.1	MW883804.1	–	MW890124.1	*actA*: MW890022.1, *cmdA*: MW890042.1, *his3*: MW890055.1, *tef1* (first part): MW890086.1

Table 1. (Continued).

Species	Culture or voucher accession number(s)[1]	Locality and Substrate	Collector(s)	GenBank accession number[2]				
				ITS	LSU	*rpb2*	*tub2*	Other loci
Castanediella neomalaysiana, sp. nov.	CBS 147093 = CPC 39275, ex-type	Malaysia: *Eucalyptus* sp., leaves	M.J. Wingfield	MW883410.1	MW883805.1	–	–	–
Colletotrichum kinghornii	CBS 198.35, ex-type	UK: *Phormium tenax*	N.L. Alcock	NR_111751.1	NG_069631.1	–	JQ950105.1	*actA*: JQ949775.1, *chs-1*: JQ949115.1, *gapdh*: JQ948785.1, *his3*: JQ949445.1
	CPC 38766 = T19_05774B	New Zealand: *Phormium cookianum*	C. Inglis	MW883411.1	MW883806.1	–	MW890125.1	*actA*: MW890023.1, *gapdh*: MW890048.1
	CBS 147082 = CPC 39342	South Africa: *Pleopeltis* sp.	J. Roux	MW883412.1	MW883807.1	–	–	*actA*: MW890024.1, *chs-1*: MW890035.1,
Coniochaeta deborreae, sp. nov.	CBS 147215 = BE19_001008, ex-type	Netherlands: Soil	K. de Borre	MW883413.1	MW883808.1	–	–	*tef1* (first part): MW890087.1, *tef1* (second part): MW890106.1
	CBS 551.75	Norway: *Pinus sylvestris*, wood	–	MW883416.1	MW883809.1	–	–	–
Coniochaeta pulveracea	CBS 114628 = D3409 = UNI 393	Turkey: Rinsing machine in soft drinks factory	M. Stratford	MW883414.1	GQ351560.1	–	–	–
Coniochaeta rhopalochaeta	CBS 109872 = BAFC 272, ex-type	Argentina: *Bulnesia retamas*, decorticated wood	C.C. Carmarán	MW883415.1	GQ351561.1	–	–	–
Diaporthe durionigena, sp. nov.	KCSR1812.8 = VTCC 930005, ex-type	Vietnam: *Durio zibethinus*, branches	L.D. Thao	MN453530.1	–	–	MT276159.1	*tef1* (first part): MT276157.1
Endoconidioma euphorbiae	CBS 146776 = CPC 38551, ex-type	South Africa: *Euphorbia mauritanica*, leaf tip dieback	P.W. Crous	MW175350.1	MW175390.1	–	–	–
	CPC 38649	South Africa: *Euphorbia mauritanica*, tip dieback	P.W. Crous	MW883417.1	MW883810.1	MW890060.1	MW890126.1	*actA*: MW890025.1, *tef1* (second part): MW890107.1
Flammocladiella aceris	CBS 138906 = CPC 24422, ex-type	Germany: *Acer platanoides*, twigs	R.K. Schumacher	NG_058175.1	KR611901.1	MW890061.1	MW890127.1	*tef1* (first part): MW890088.1
Flammocladiella anomiae	CBS 142775 = CLL16017	Bulgaria: On stromata of *Massaria anomia*, on a thin branch of *Robinia pseudoacacia*	D. Stoykov	MN597422.1	MW883811.1	MW890062.1	MW890128.1	*tef1* (first part): MW890089.1
	CBS 144256 = JF17087, ex-type	France: On ascomata of *Massaria anomia* on a branchlet of *Robinia pseudoacacia*	J. Fournier	MN597423.1	MN597425.1	–	MW890129.1	*tef1* (first part): MW890090.1
	CBS 146685 = CPC 36302	Ukraine: On conidiomata of *Diaporthe oncostoma*, on dead branch of *Robinia pseudoacacia*	A. Akulov	MW883418.1	MW883812.1	–	MW890130.1	*tef1* (first part): MW890091.1
Floricola juncicola, sp. nov.	CBS 146811 = CPC 38197, ex-type	France: *Juncus* sp., dead culm	A. Gardiennet	MW883419.1	MW883813.1	MW890063.1	–	*tef1* (first part): MW890092.1, *tef1* (second part): MW890108.1

Table 1. (Continued).

Species	Culture or voucher accession number(s)[1]	Locality and Substrate	Collector(s)	GenBank accession number[2]				
				ITS	LSU	*rpb2*	*tub2*	Other loci
Harzia tenella	CPC 38667	South Africa: *Grielum humifusum*, stems	P.W. Crous	MW883420.1	MW883814.1	–	–	–
Haudseptoria typhae, gen. et sp. nov.	CBS 146790 = CPC 38203, ex-type	Germany: *Typha* sp., dead leaf sheath	R.K. Schumacher	MW883421.1	MW883815.1	–	MW890131.1	–
Heimiodora verticillata	CBS 147089 = CPC 39015	Namibia: *Salvadora* sp.	P.W. Crous	MW883422.1	MW883816.1	–	–	–
	CBS 201.60 = IMI 090702 = LCP 57.1589, ex-type	Thailand: Sandy coastal soil	–	MH857955.1	MH869505.1	–	–	–
Hogelandia lambearum, gen. et sp. nov.	CBS 147626 = NL19_27007, ex-type	Netherlands: Soil	L. Alssema & M. van Berkel	MW883423.1	MW883817.1	–	–	–
Lomentospora valparaisensis, sp. nov.	ChFC-164, ex-type	Chile: Soil	F. Salas	MG495075.1	–	–	MG544878.1	–
Muyocopron zamiae	CBS 146636 = CPC 37461	USA: *Zamia integrifolia*, leaves	M.J. Wingfield	MW883424.1	MW883818.1	MW890064.1	–	*tef1* (second part): MW890109.1
	CBS 202.71 = No. 070-2288	USA: *Zamia integrifolia*, leaf spot and necrotic tip	–	MW883425.1	–	–	–	–
	CBS 203.71 = No. 070-2273, ex-type	USA: *Zamia fisheri*, leaf spot and necrotic tip	–	MW883426.1	NG_066338.1	MK492731.1	–	*tef1* (second part): MK495973.1
Neocamarosporium leipoldtiae	CBS 146812 = CPC 38543, ex-type	South Africa: *Cephalophyllum pilansii*, leaves	P.W. Crous	MW883427.1	MW883819.1	–	MW890132.1	*tef1* (first part): MW890093.1
Neofusicoccum mystacidii, sp. nov.	CBS 147079 = CPC 39221, ex-type	South Africa: *Mystacidium capense*, dead stems	P.W. Crous	MW883428.1	MW883820.1	MW890065.1	MW890133.1	*gapdh*: MW890049.1, *his3*: MW890056.1, *tef1* (first part): MW890094.1
Neomycosphaerella guibourtiae, sp. nov.	CBS 147083 = CPC 39348, ex-type	Angola: *Guibourtia* sp., leaves	J. Roux	MW883429.1	MW883821.1	–	MW890134.1	*actA*: MW890026.1, *cmdA*: MW890043.1, *tef1* (first part): MW890095.1
Neoscirrhia matteucciicola, comb. nov.	CBS 259.92 = IMI 286996 = PD 91/272, ex-type	Canada: *Matteuccia struthiopteris*, affected leaf stem	–	GU237812.1	GU238100.1	–	GU237627.1	–
Neoscirrhia osmundae, gen. et comb. nov.	CBS 146803 = CPC 38085, ex-type	Netherlands: *Sasa veitchii*, culms	L. van der Linde	MW883430.1	MW883822.1	MW890066.1	MW890135.1	–
Neoscytalidium dimidiatum	CBS 146816 = CPC 38666, ex-type	South Africa: Epiphyte on stems of *Aloidendron dichotomum*	P.W. Crous	MW883431.1	MW883823.1	–	MW890136.1	*chs-1*: MW890036.1, *tef1* (first part): MW890096.1
Niesslia neoexosporioides, sp. nov.	CBS 146810 = CPC 38177, ex-type	Germany: *Carex paniculata*, dead leaves	R.K. Schumacher	MW883432.1	MW883824.1	–	MW890137.1	*actA*: MW890027.1, *tef1* (first part): MW890097.1
Nothoanungitopsis urophyllae, gen. et sp. nov.	CBS 146799 = CPC 38059, ex-type	South Africa: *Eucalyptus urophylla*, seed capsules	M.J. Wingfield	MW883433.1	MW883825.1	–	–	–
Nothomicrosphaeropsis welwitschiae gen. et sp. nov.	CBS 146829 = CPC 38879, ex-type	Namibia: *Welwitschia mirabilis*, dead leaves	P.W. Crous	MW883434.1	MW883826.1	MW890067.1	MW890138.1	–
Ophioceras leptosporum	CBS 147090 = CPC 39147	South Africa: *Syzygium cordatum*, twigs	P.W. Crous	MW883435.1	MW883827.1	–	–	*tef1* (second part): MW890110.1

Table 1. (Continued).

Species	Culture or voucher accession number(s)[1]	Locality and Substrate	Collector(s)	GenBank accession number[2]				
				ITS	LSU	*rpb2*	*tub2*	Other loci
	CBS 894.70 = ATCC 24161 = HME 2955, ex-type	UK: Dead stem of dicot plant, probably *Urtica dioica*	–	NR_111768.1	NG_057959.1	–	–	*rpb1*: JX134732.1, SSU: JX134664.1, *tef1* (second part): JX134704.1
Paracremonium bendijkiorum, sp. nov.	CBS 147228 = NL19_24005, ex-type	Netherlands: Soil	Y. Bentem & J. van Dijken	MW883436.1	MW883828.1	MW890068.1	MW890139.1	*tef1* (second part): MW890111.1
Paraphoma ledniceana, sp. nov.	CBS 146533 = MEND-F-82, ex-type	Czech Republic: Saprobe on dead wood of *Buxus sempervirens*	M. Spetik	MT371091.1	MT371396.1	MT372655.1	MT372661.1	*tef1* (first part): MT372654.1
Paraphoma salicis, sp. nov.	CBS 146797 = CPC 38651, ex-type	Ukraine: *Salix cf. alba*, leaves	A. Akulov	MW883437.1	MW883829.1	MW890069.1	MW890140.1	*actA*: MW890028.1
Parasarocladium wereldwijsianum, sp. nov.	CBS 147223 = NL19094001	Netherlands: Soil	S. Frederikze, J. Mes & S. Maghnouji	MW883438.1	–	MW890070.1	MW890141.1	–
	CBS 147224 = NL19094011	Netherlands: Soil	S. Frederikze, J. Mes & S. Maghnouji	MW883439.1	MW883830.1	MW890071.1	MW890142.1	*actA*: MW890029.1, *tef1* (second part): MW890112.1
	CBS 147226 = NL19095011, ex-type	Netherlands: Soil	S. Frederikze, J. Mes & S. Maghnouji	MW883440.1	MW883831.1	MW890072.1	MW890143.1	*actA*: MW890030.1, *tef1* (second part): MW890113.1
Peziza ligni, sp. nov.	CBS 146637 = CPC 39110 = MUCL 57889, ex-type	France: On masonry and plastering, near a wooden staircase	C. Decock	MW883441.1	MW883832.1	MW890073.1	–	–
Phyllosticta phoenicis, sp. nov.	CBS 147091 = CPC 39164, ex-type	South Africa: *Phoenix reclinata*, leaves	M.J. Wingfield	MW883442.1	MW883833.1	–	–	*actA*: MW890031.1, *gapdh*: MW890050.1, *tef1* (first part): MW890098.1
Plectosphaerella slobbergiarum, sp. nov.	CBS 147227 = NL1930002, ex-type	Netherlands: Soil	J. Slob & M. Berghuis	MW883443.1	MW883834.1	MW890074.1	–	*tef1* (second part): MW890114.1
Populomyces zwinianus, gen. et sp. nov.	CBS 147307 = NL1976004, ex-type	Netherlands: Soil	W. Vercouteren, S. Meas & R. Verhije	MW883444.1	MW883835.1	–	–	–
Porodiplodia livistonae	CBS 144428 = CPC 32154, ex-type	Australia: *Livistona australis*, leaves	P.W. Crous	NR_160355.1	NG_069575.1	–	–	*tef1* (first part): MW890099.1
Porodiplodia vitis	CBS 144634 = CPC 31642, ex-type	USA: *Vitis vinifera*, canes	E. Crenson & R.K. Schumacher	NR_163376.1	NG_070080.1	–	–	*tef1* (first part): MK442707.1
	CBS 146818 = CPC 38692	South Africa: *Virgilia oroboides*, seed pods	M.J. Wingfield	MW883445.1	MW883836.1	–	–	*tef1* (first part): MW890100.1
Pseudoacrospermum goniomae, gen. et sp. nov.	CBS 146732 = CPC 37030, ex-type	South Africa: *Gonioma kamassi*, leaves	F. Roets	MW883446.1	MW883837.1	MW890075.1	–	*tef1* (first part): MW890101.1, *tef1* (second part): MW890115.1
Pseudopyricularia festucae, sp. nov.	CBS 146629 = CPC 37915, ex-type	USA: *Festuca californica*, leaves	P.W. Crous	MW883447.1	MW883838.1	–	–	*cmdA*: MW890044.1, *rpb1*: MW890057.1
Sarocladium sasijaorum, sp. nov.	CBS 147213 = NL19100007, ex-type	Netherlands: Soil	S. Frederikze, J. Mes & S. Maghnouji	MW883448.1	MW883839.1	MW890076.1	MW890144.1	*actA*: MW890032.1, *tef1* (second part): MW890116.1
Septoria protearum	CBS 778.97 = CPC 1470 = STE-U 1470 = IMI 375230 = ATCC 201159, ex-type	South Africa: *Protea cynaroides*, leaves	L. Viljoen	KF251523.1	KF252028.1	KF252517.1	KF252992.1	*actA*: KF253827.1, *cmdA*: KF254176.1, *tef1* (first part): KF253472.1

Table 1. (Continued).

Species	Culture or voucher accession number(s)[1]	Locality and Substrate	Collector(s)	GenBank accession number[2]				
				ITS	LSU	*rpb2*	*tub2*	Other loci
	CPC 38736 = T19_05709B	New Zealand: *Kniphofia uvaria*	D. Burnt	MW883449.1	MW883840.1	–	–	*actA*: MW890033.1, *tef1* (first part): MW890102.1
Sporothrix hypoxyli, sp. nov.	CBS 141567 = CMW 47439	Netherlands: Ascomata embedded in fruiting body of *Hypoxylon petriniae* on *Fraxinus* wood	E. Osieck & W.J. Nel	MT637056.1	MW012947.1	–	MT649176.1	–
	CBS 141568 = CMW 47436	Netherlands: Ascomata embedded in fruiting body of *Hypoxylon petriniae* on *Fraxinus* wood	E. Osieck & W.J. Nel	MT637053.1	MW012946.1	–	MT649173.1	–
	CBS 141569 = CMW 47441, ex-type	Netherlands: Ascomata embedded in fruiting body of *Hypoxylon petriniae* on *Fraxinus* wood	E. Osieck & W.J. Nel	MT637058.1	MW012948.1	–	MT649178.1	–
Stemphylium eturmiunum	CBS 109845 = EGS 29.099, ex-type	New Zealand: *Lycopersicon esculentum*, fruit	E.G. Simmons	NR_154927.1	NG_069866.1	–	–	*cmdA*: KU850831.1, *gapdh*: KU850689.1
	CBS 146783 = CPC 38613, ex-type	South Africa: *Bulbinella latifolia*, leaves	P.W. Crous	MW883450.1	MW883841.1	MW890077.1	MW890145.1	*actA*: MW890034.1, *cmdA*: MW890045.1, *gapdh*: MW890051.1, *tef1* (first part): MW890103.1
Superstratomyces albomucosus, gen. et sp. nov.	CBS 140270 = DTO 277-D2, ex-type	Netherlands: Outdoor exposed *Pycnanthus angolensis* impregnated with olive oil	E.J. van Nieuwenhuijzen	NR_152544.1	KX950439.1	KX950498.1	–	*rpb1*: KX950494.1, SSU: NG_061256.1, *tef1* (second part): KX950471.1
Superstratomyces atroviridis, sp. nov.	CBS 140272 = DTO 305-E1, ex-type	Netherlands: Outdoor exposed *Pinus sylvestris* impregnated with raw linseed oil	E.J. van Nieuwenhuijzen	NR_152545.1	NG_058271.1	KX950500.1	–	*rpb1*: KX950496.1, SSU: NG_063075.1, *tef1* (second part): KX950473.1
Superstratomyces flavomucosus, sp. nov.	CBS 353.84 = DTO 305-C3, ex-type	Australia: *Hakea multilinearis*, leaf	W. Gams	NR_152543.1	KX950438.1	KX950497.1	–	*rpb1*: KX950493.1, SSU: NG_065661.1, *tef1* (second part): KX950470.1
Superstratomyces tardicrescens, sp. nov.	FMR 13786, ex-type	USA: Human eye specimen	D.A. Sutton	LR025130.1	LR025130.1	–	–	*tef1* (second part): LR025141.1
Taeniolella exilis	CBS 122902 = DAOM 14683 = MUCL 1878	Canada: *Betula papyrifera*, bark	G. Hennebert	MW883451.1	KX244968.1	–	–	–
Taeniolella platani, sp. nov.	CBS 146733 = CPC 33568, ex-type	Germany: *Platanus hispanica*, twig	R.K. Schumacher	MW883452.1	MW883842.1	–	–	*tef1* (second part): MW890117.1
Tricellula aurantiaca	CBS 146627 = CPC 36629	Russia: *Lonicera tatarica*, leaves	T.S. Bulgakov	MW883453.1	MW883843.1	–	–	–

Table 1. (Continued).

Species	Culture or voucher accession number(s)[1]	Locality and Substrate	Collector(s)	GenBank accession number[2]				
				ITS	LSU	*rpb2*	*tub2*	Other loci
	CBS 399.58 = ATCC 13128 = IMI 073024 = MUCL 28102 = PRL 1554, ex-type	Canada: Soil	–	MH857822.1	MH869354.1	–	–	–
Tryssglobulus aspergilloides	CBS 147388 = CPC 40100, ex-isoepitype	Australia: *Banksia marginata*	I.G. Pascoe & B.J. Brentwood	MW883454.1	MW883844.1	MW890078.1	–	–
	CBS 147556 = CPC 40369 = VPRI 43962, ex-epitype	Australia: *Banksia marginata*	I.G. Pascoe & B.J. Brentwood	MW883455.1	MW883845.1	MW890079.1	–	–
Tympanis pini, sp. nov.	CBS 146809 = CPC 38169, ex-type	Spain: *Pinus sylvestris*, twigs	R. Blasco	MW883456.1	MW883846.1	–	–	–
Venturia cerasi	CBS 444.54, ex-epitype	Germany: *Prunus cerasus*	H. Schweizer	NR_168750.1	MH868928.1	MK887849.1	MK926519.1	*tef1* (first part): MK888785.1
Zelosatchmopsis sacciformis	CBS 116.88 = INIFAT C87/53.1 = MW i 1640, ex-isotype	Cuba: *Guazuma ulmifolia*, fallen leaf	R.F. Castañeda	MH862122.1	MH873812.1	–	–	–

[1] ATCC: American Type Culture Collection, Virginia, USA; BAFC: Universidad de Buenos Aires, Departamento de Ciencias Biologicas; CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands; CMW: Culture Collection of the Forestry and Agricultural Biotechnology Institute (FABI) of the University of Pretoria, Pretoria, South Africa; CPC: Culture collection of Pedro Crous, housed at CBS; DAOM: Plant Research Institute, Department of Agriculture (Mycology), Ottawa, Canada; DTO: Working collection of the Indoor air and Industrial Mycology group, housed at CBS; FMR: Facultat de Medicina, Universitat Rovira i Virgili, Reus, Spain; ICMP: International Collection of Microorganisms from Plants, Landcare Research, Private Bag 92170, Auckland, New Zealand; IMI: International Mycological Institute, CABI-Bioscience, Egham, Bakeham Lane, United Kingdom; INIFAT: Alexander Humboldt Institute for Basic Research in Tropical Agriculture, Ciudad de La Habana, Cuba; LCP: Laboratory of Cryptogamy, National Museum of Natural History, Paris, France; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Rai, Thailand; MUCL: Université Catholique de Louvain, Louvain-la-Neuve, Belgium; VPRI: Victorian Department of Primary Industries, Knoxfield, Australia; VTCC: Vietnam Type Culture Collection, Center of Biotechnology, Vietnam National University, Hanoi, Vietnam.

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; LSU: large subunit (28S) of the nrRNA gene operon; *actA*: partial actin gene; *chs-1*: partial chitin synthase-1 gene; *cmdA*: partial calmodulin gene; *gapdh*: partial glyceraldehyde-3-phosphate dehydrogenase gene; *his3*: partial histone H3 gene; *rpb1*: partial DNA-directed RNA polymerase II largest subunit gene; *rpb2*: partial DNA-directed RNA polymerase II second largest subunit gene; SSU: small subunit (18S) of the nrRNA gene operon; *tef1*: partial translation elongation factor 1-alpha gene; *tub2*: partial beta-tubulin gene.

bootstrap replicates (Hoang *et al*. 2018). Best models were estimated for data partitions using ModelFinder (Kalyaanamoorthy *et al.* 2017) as implemented in IQ-TREE.

Morphology

Slide preparations were mounted in lactic acid, Shear's mounting fluid or water, from colonies sporulating on MEA, PDA, PNA or OA. Observations were made with a Nikon SMZ25 dissection-microscope, and with a Zeiss Axio Imager 2 light microscope using differential interference contrast (DIC) illumination and images recorded on a Nikon DS-Ri2 camera with associated software. Cryo Scanning Electron Microscopy methods followed Bensch *et al*. (2018). Colony characters and pigment production were noted after 2–4 wk of growth on MEA, PDA and OA (Crous *et al*. 2019b) incubated at 25 °C. Colony colours (surface and reverse) were scored using the colour charts of Rayner (1970). Sequences derived in this study were deposited in GenBank (Table 1), the alignments in TreeBASE (www.treebase.org; study number S28000), and taxonomic novelties in MycoBank (www.MycoBank.org; Crous *et al*. 2004).

RESULTS

Phylogeny

Dothideomycetes LSU phylogeny (Fig. 1, parts 1–5): The alignment contained 260 isolates and the tree was rooted to *Diaporthe perjuncta* (strain BPI 748437, GenBank NG_059064.1). The final alignment contained a total of 776 characters used for the phylogenetic analyses, including alignment gaps. The alignment contained a total of 538 unique site patterns. Based on the results of MrModelTest, dirichlet base frequencies and the GTR+I+G model was used for the Bayesian analysis. The Bayesian analyses generated 309 402 trees (saved every 100 generations) from which 232 052 were sampled after 25 % of the trees were discarded as burn-in.

Leotiomycetes LSU phylogeny (Fig. 2): The alignment contained 61 isolates and the tree was rooted to *Xylaria hypoxylon* (voucher OSC 100004, GenBank AY544648.1). The final alignment contained a total of 760 characters used for the phylogenetic analyses, including alignment gaps. The alignment contained a total of 185 unique site patterns. Based on the results of MrModelTest, dirichlet base frequencies and the GTR+I+G model was used for the Bayesian analysis. The Bayesian analyses generated 542 002 trees (saved every five generations) from which 406 502 were sampled after 25 % of the trees were discarded as burn-in.

Pezizomycetes LSU phylogeny (Fig. 3): The alignment contained 37 isolates and the tree was rooted to *Candida broadrunensis* (strain CBS 11838, GenBank KY106372.1). The final alignment

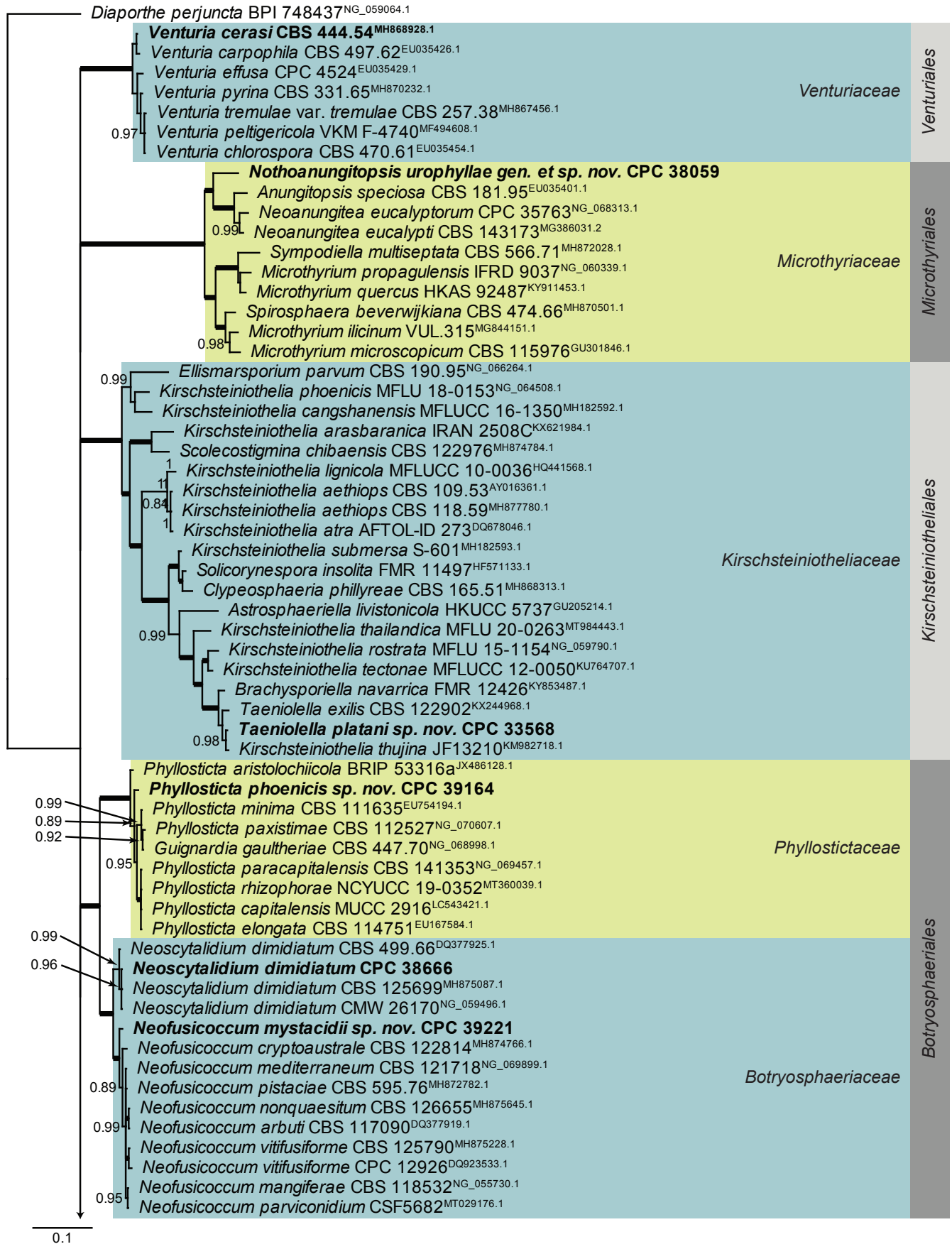

Fig. 1, parts 1–5. Consensus phylogram (50 % majority rule) resulting from a Bayesian analysis of the *Dothideomycetes* LSU nucleotide alignment. Bayesian posterior probabilities (PP) > 0.79 are shown at the nodes and the scale bar represents the expected changes per site. Thickened branches represent PP = 1. The branch leading to *Superstratomycetales* was halved to facilitate layout. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession (superscript) and / or culture collection / voucher numbers are indicated for all species. The tree was rooted to *Diaporthe perjuncta* (voucher BPI 748437, GenBank NG_059064.1) and the species treated in this study for which LSU sequence data were available are indicated in bold face.

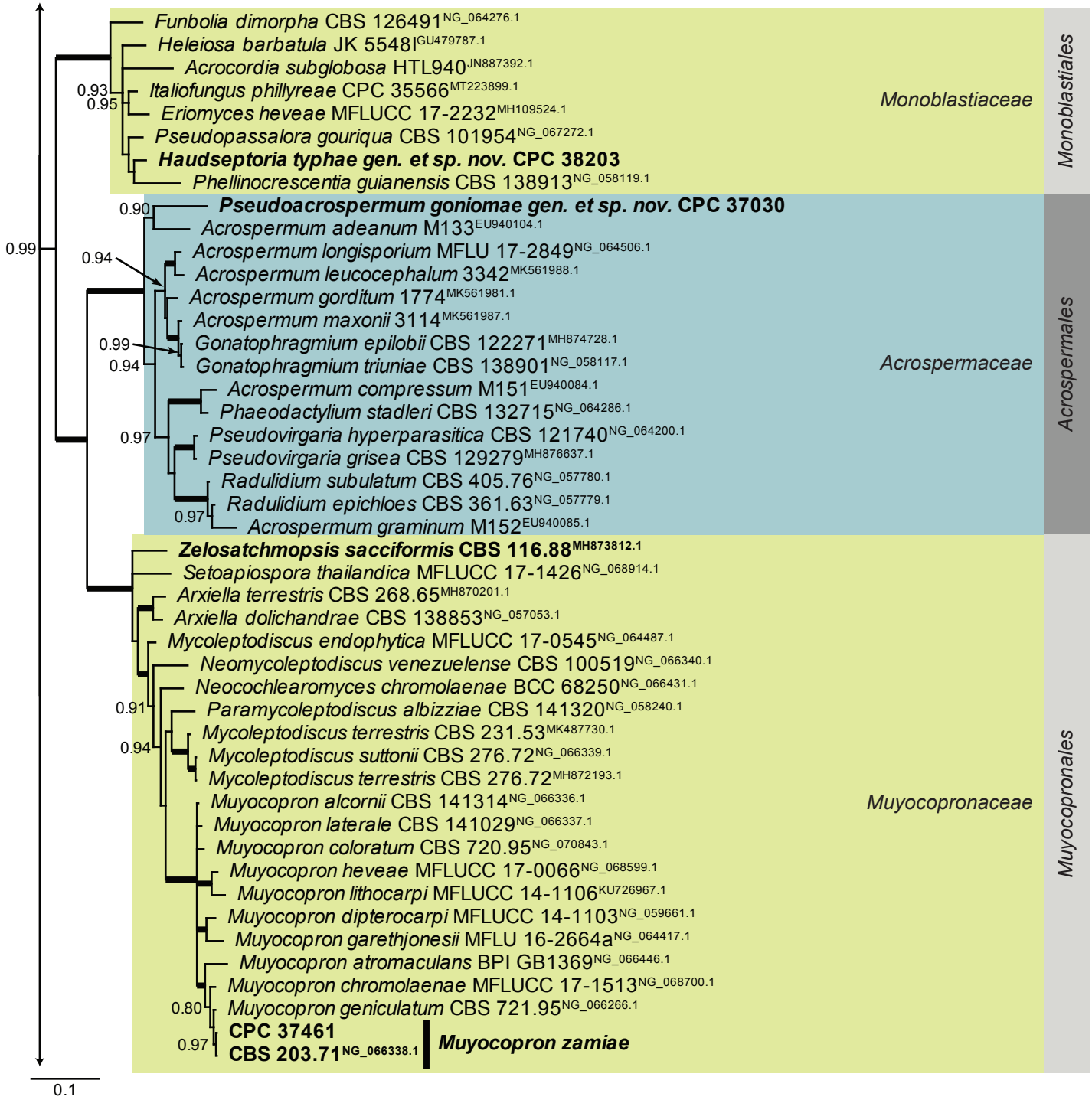

Fig. 1. (Continued).

contained a total of 739 characters used for the phylogenetic analyses, including alignment gaps. The alignment contained a total of 279 unique site patterns. Based on the results of MrModelTest, dirichlet base frequencies and the GTR+I+G model was used for the Bayesian analysis. The Bayesian analyses generated 376 002 trees (saved every five generations) from which 282 002 were sampled after 25 % of the trees were discarded as burn-in.

Sordariomycetes (*Hypocreales*) LSU phylogeny (Fig. 4): The alignment contained 70 isolates and the tree was rooted to *Ramularia endophylla* (strain CBS 113265, GenBank AY490776.1). The final alignment contained a total of 752 characters used for the phylogenetic analyses, including alignment gaps. The alignment contained a total of 199 unique site patterns. Based on the results of MrModelTest, dirichlet base frequencies and the GTR+I+G model was used for the Bayesian analysis. The Bayesian analyses generated 426 002 trees (saved every five generations) from which 319 502 were sampled after 25 % of the trees were discarded as burn-in.

Sordariomycetes (other orders) LSU phylogeny (Fig. 5, parts 1–2): The alignment contained 89 isolates and the tree was rooted to *Ramularia endophylla* (strain CBS 113265, GenBank AY490776.1). The final alignment contained a total of 796 characters used for the phylogenetic analyses, including alignment gaps. The alignment contained a total of 340 unique site patterns. Based on the results of MrModelTest, dirichlet base frequencies and the GTR+I+G model was used for the Bayesian analysis. The Bayesian analyses generated 878 002 trees (saved

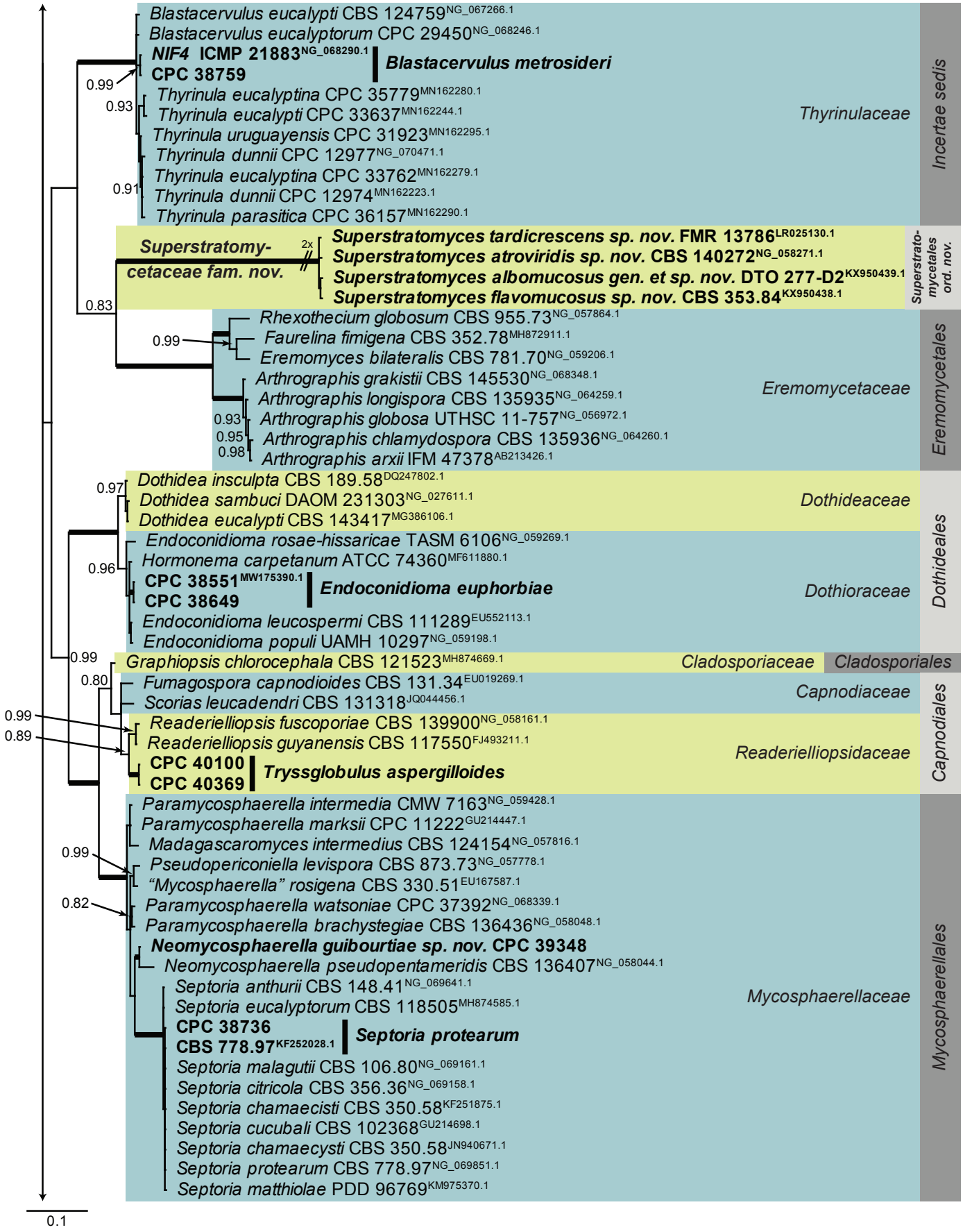

Fig. 1. (Continued).

every five generations) from which 658 502 were sampled after 25 % of the trees were discarded as burn-in.

Sordariomycetes (*Amphisphaeriales*) LSU phylogeny (Fig. 6): The alignment contained 54 isolates and the tree was rooted to *Ramularia endophylla* (strain CBS 113265, GenBank AY490776.1). The final alignment contained a total of 754 characters used

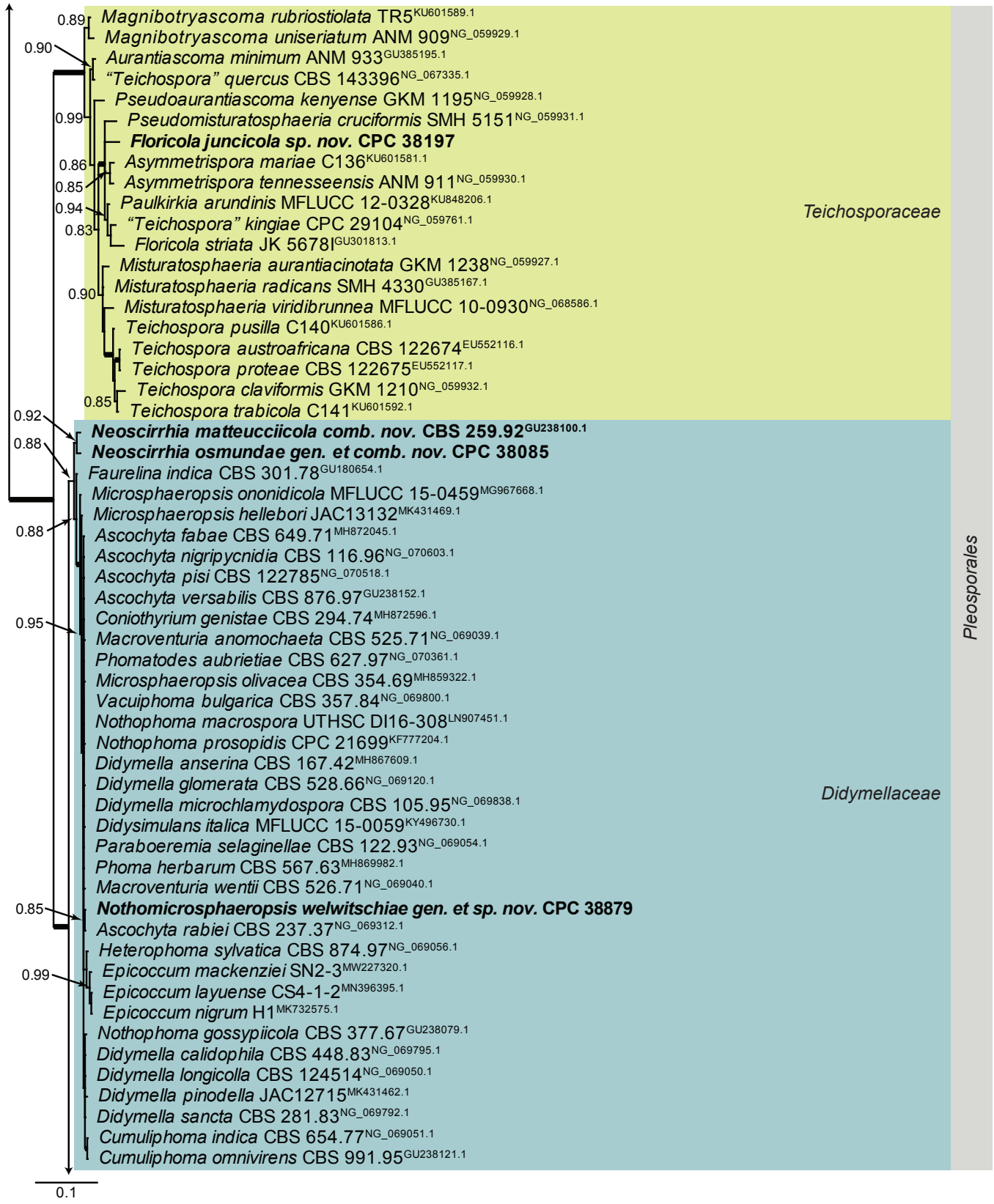

Fig. 1. (Continued).

for the phylogenetic analyses, including alignment gaps. The alignment contained a total of 194 unique site patterns. Based on the results of MrModelTest, dirichlet base frequencies and the GTR+I+G model was used for the Bayesian analysis. The Bayesian analyses generated 228 002 trees (saved every five generations) from which 171 002 were sampled after 25 % of the trees were discarded as burn-in.

Species phylogenies: Specific phylogenetic analyses were run for selected species and the resulting phylogenies are discussed in the species notes where applicable. Statistics associated with those phylogenies are provided in the figure legends. The optimal identity thresholds to discriminate filamentous fungal species followed Vu *et al*. (2019), with secondary DNA barcodes generated where necessary (Stielow *et al.* 2015).

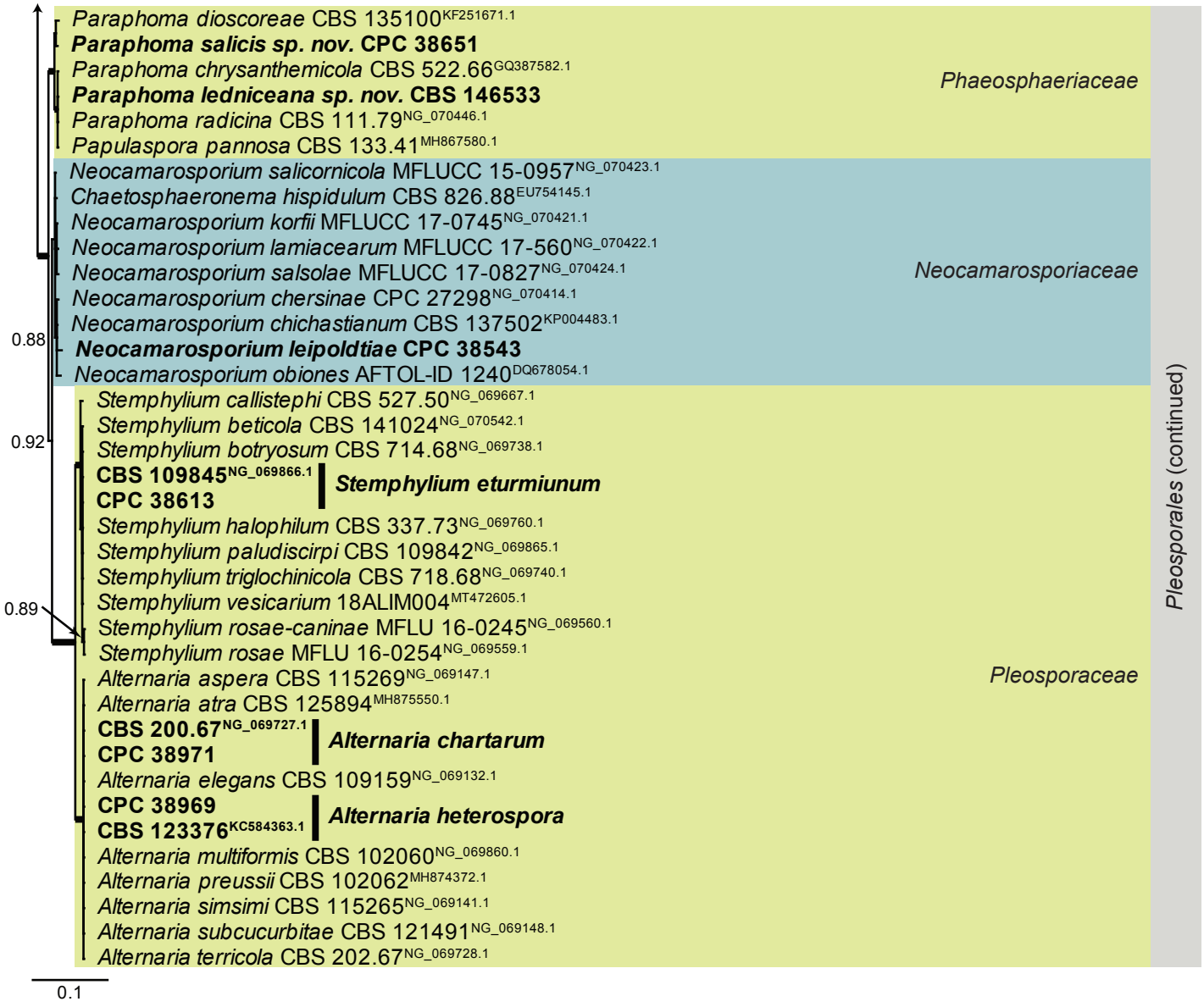

Fig. 1. (Continued).

Taxonomy

Alternaria chartarum Preuss, *Bot. Zeitung* **6**: 412. 1848. Fig. 7.

Description and illustration: Woudenberg *et al*. (2013).

Material examined: **Namibia**, Walvis Bay, from hypolithic biomass under a rock, 19 Nov. 2019, *P.W. Crous*, HPC 3101, culture CPC 38971.

Notes: *Alternaria chartarum*, which was isolated from hypolithic biomass under a rock in the Namib Desert, has previously been associated with cutaneous alternariosis in humans, and is also commonly found in indoor environments (Magina *et al*. 2000, Samson *et al*. 2019).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Alternaria alternata* (strain F13, GenBank HQ380767.1; Identities = 565/565 (100 %), no gaps), *Alternaria chartarum* (strain AC85, GenBank LC440618.1; Identities = 560/560 (100 %), no gaps), and *Alternaria aspera* (strain CBS 115269, GenBank MH862983.1; Identities = 568/569 (99 %), one gap (0 %)). Closest hits using the **LSU** sequence are *Alternaria multiformis* (strain CBS 102060, GenBank NG_069860.1; Identities = 809/809 (100 %), no gaps), *Alternaria terricola* (strain CBS 202.67, GenBank NG_069728.1; Identities = 809/809 (100 %), no gaps), and *Alternaria chartarum* (strain CBS 200.67, GenBank NG_069727.1; Identities = 809/809 (100 %), no gaps) – also see Fig. 1. Closest hits using the ***actA*** sequence had highest similarity to *Alternaria chartarum* (strain ATCC 18044, GenBank JQ671654.1; Identities = 588/589 (99 %), no gaps), *Alternaria* sp. 3 MG-2016 (strain MF-G013021, GenBank KU639836.1; Identities = 583/584 (99 %), no gaps), *Alternaria septospora* (strain CBS 109.38, GenBank JQ671655.1; Identities = 587/589 (99 %), no gaps), and *Alternaria poonensis* (strain EGS 47-138, GenBank JQ671749.1; Identities = 501/510 (98 %), no gaps). Closest hits using the ***cmdA*** sequence had highest similarity to *Alternaria* sp. 3 MG-2016 (strain MF-G242021, GenBank KU639878.1; Identities = 525/525 (100 %), no gaps), *Alternaria* sp. 1 MG-2016 (strain MF-G333011, GenBank KU639872.1; Identities = 525/525 (100 %), no gaps), *Alternaria chartarum* (strain ATCC 18044, GenBank JQ646162.1; Identities = 524/525 (99 %), no gaps), *Alternaria consortialis* (strain CBS

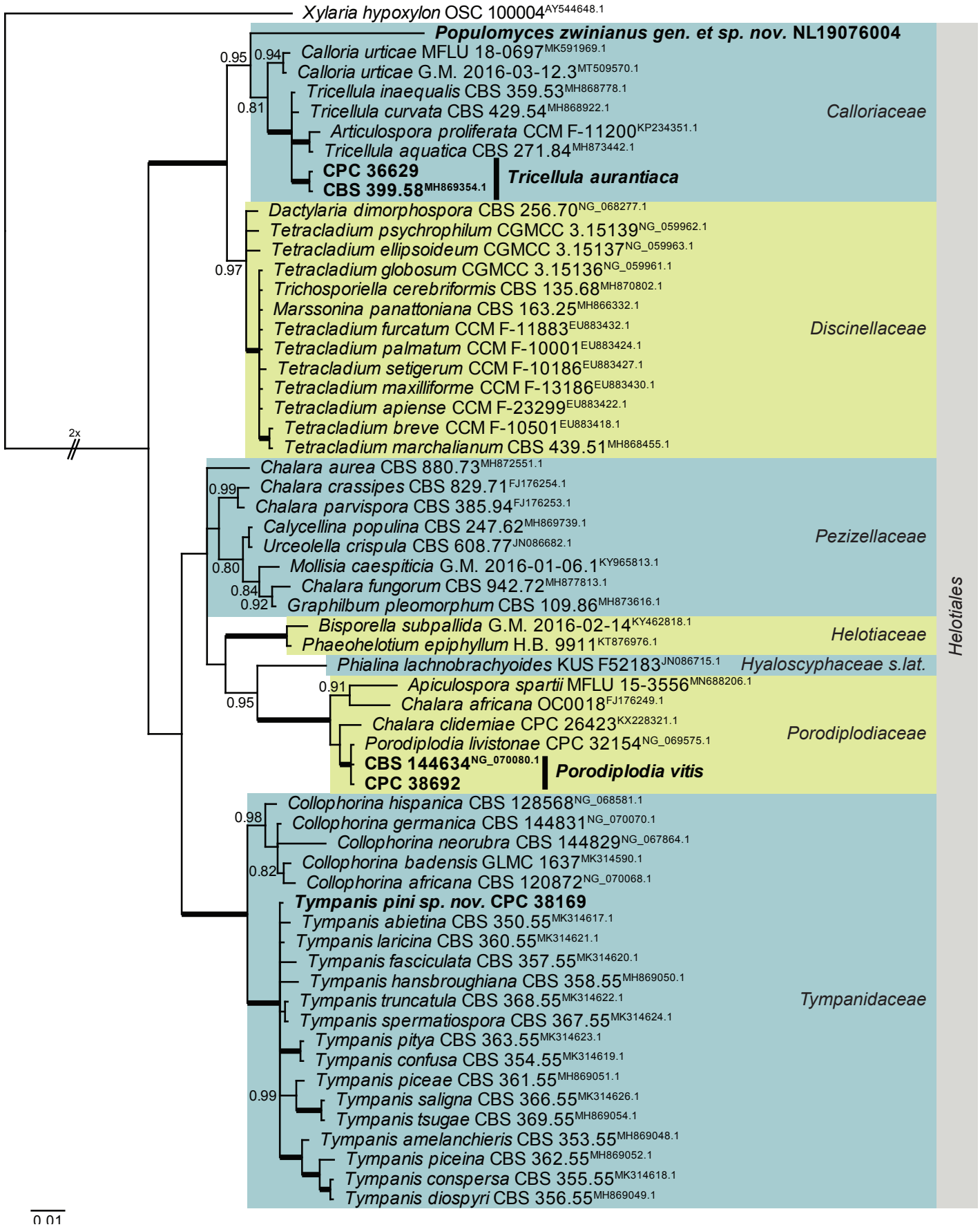

Fig. 2. Consensus phylogram (50 % majority rule) resulting from a Bayesian analysis of the *Leotiomycetes* LSU nucleotide alignment. Bayesian posterior probabilities (PP) > 0.79 are shown at the nodes and the scale bar represents the expected changes per site. Thickened branches represent PP = 1 and the most basal branch was halved to facilitate layout. Families and the order *Helotiales* are indicated with coloured blocks to the right of the tree. GenBank accession (superscript) and / or culture collection / voucher numbers are indicated for all species. The tree was rooted to *Xylaria hypoxylon* (voucher OSC 100004, GenBank AY544648.1) and the species treated in this study for which LSU sequence data were available are indicated in bold face.

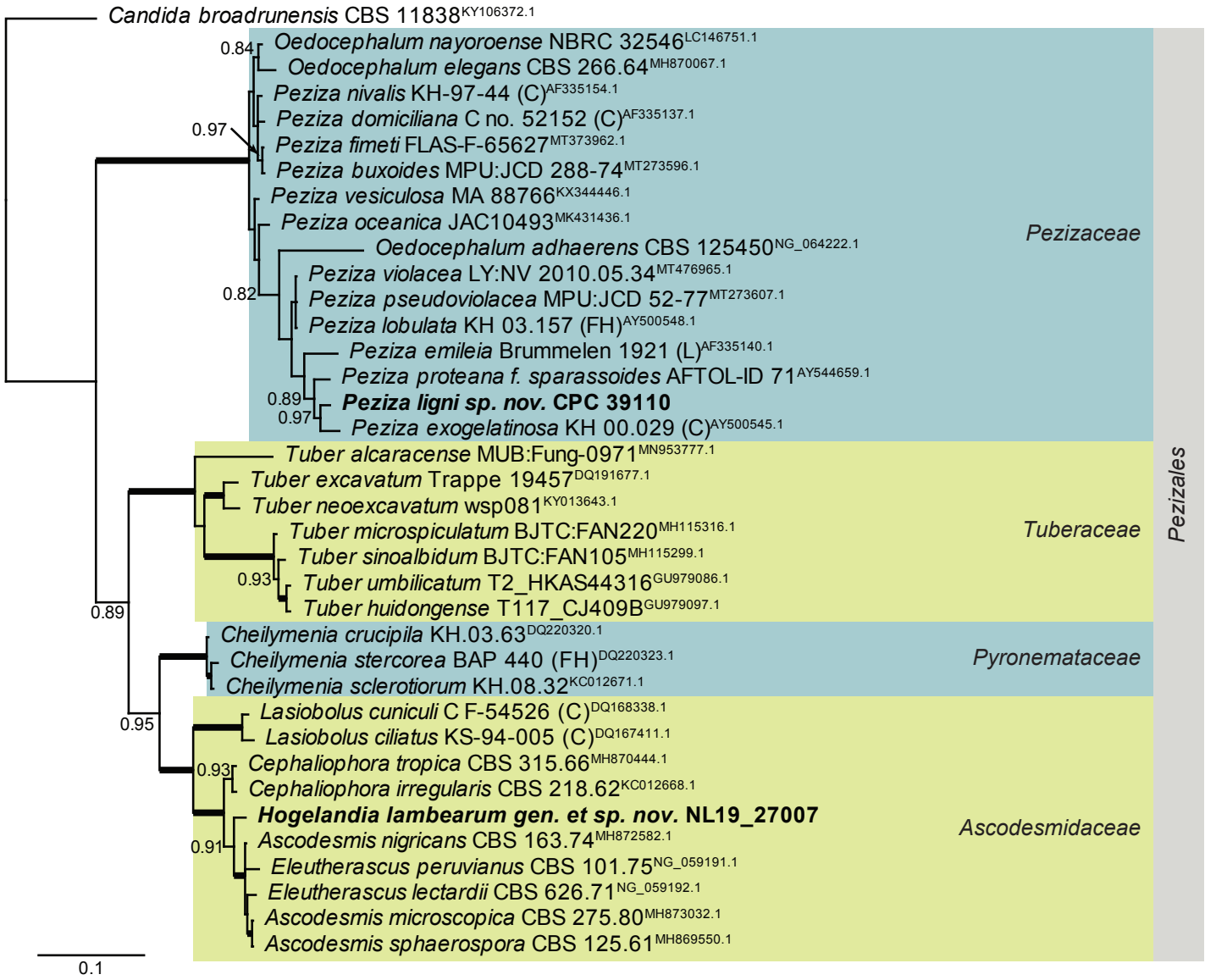

Fig. 3. Consensus phylogram (50 % majority rule) resulting from a Bayesian analysis of the *Pezizomycetes* LSU nucleotide alignment. Bayesian posterior probabilities (PP) > 0.79 are shown at the nodes and the scale bar represents the expected changes per site. Thickened branches represent PP = 1. Families and the order *Pezizales* are indicated with coloured blocks to the right of the tree. GenBank accession (superscript) and / or culture collection / voucher numbers are indicated for all species. The tree was rooted to *Candida broadrunensis* (culture CBS 11838, GenBank KY106372.1) and the species treated in this study for which LSU sequence data were available are indicated in bold face.

201.67, GenBank JQ646173.1; Identities = 506/527 (96 %), two gaps (0 %)), and *Alternaria botrytis* (strain AKC603, GenBank MT770809.1; Identities = 504/525 (96 %), no gaps). Closest hits using the ***gapdh*** sequence had highest similarity to *Alternaria chartarum* (strain AC85, GenBank LC482041.1; Identities = 408/409 (99 %), no gaps), *Alternaria aspera* (strain CBS 115269, GenBank KC584166.1; Identities = 408/409 (99 %), no gaps), and *Alternaria concatenata* (as *Ulocladium capsicum*; strain HSAUP_XF030035, GenBank AY762950.1; Identities = 408/409 (99 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Alternaria aspera* (strain CBS 115269, GenBank KC584734.1; Identities = 240/242 (99 %), no gaps), *Alternaria alternata* (strain DUCC5016, GenBank KJ638247.1; Identities = 292/311 (94 %), two gaps (0 %)), and *Alternaria japonica* (strain P400, GenBank AY375367.1; Identities = 366/395 (93 %), four gaps (1 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Alternaria chartarum* (strain ATCC 18044, GenBank JQ671994.1; Identities = 337/338 (99 %), no gaps), *Alternaria septospora* (strain CBS 109.38, GenBank JQ671995.1; Identities = 336/338 (99 %), no gaps), and *Alternaria atra* (strain ATCC 18040, GenBank JQ671998.1; Identities = 331/338 (98 %), no gaps).

Authors: P.W. Crous, D.A. Cowan, G. Maggs-Kölling, E. Marais, N. Yilmaz & M.J. Wingfield

Alternaria heterospora Woudenb. & Crous, *Stud. Mycol.* **75**: 204. 2013. Fig. 8.

Description and illustration: Woudenberg *et al*. (2013).

Material examined: **Namibia**, Walvis Bay, from hypolithic biomass under a rock, 19 Nov. 2019, *P.W. Crous*, HPC 3101, culture CPC 38969.

Notes: *Alternaria heterospora* (as *Ulocladium solani*) was described as a new species associated with leaf spots on *Lycopersicon esculentum* and *Duchesnea indica* from Hunan

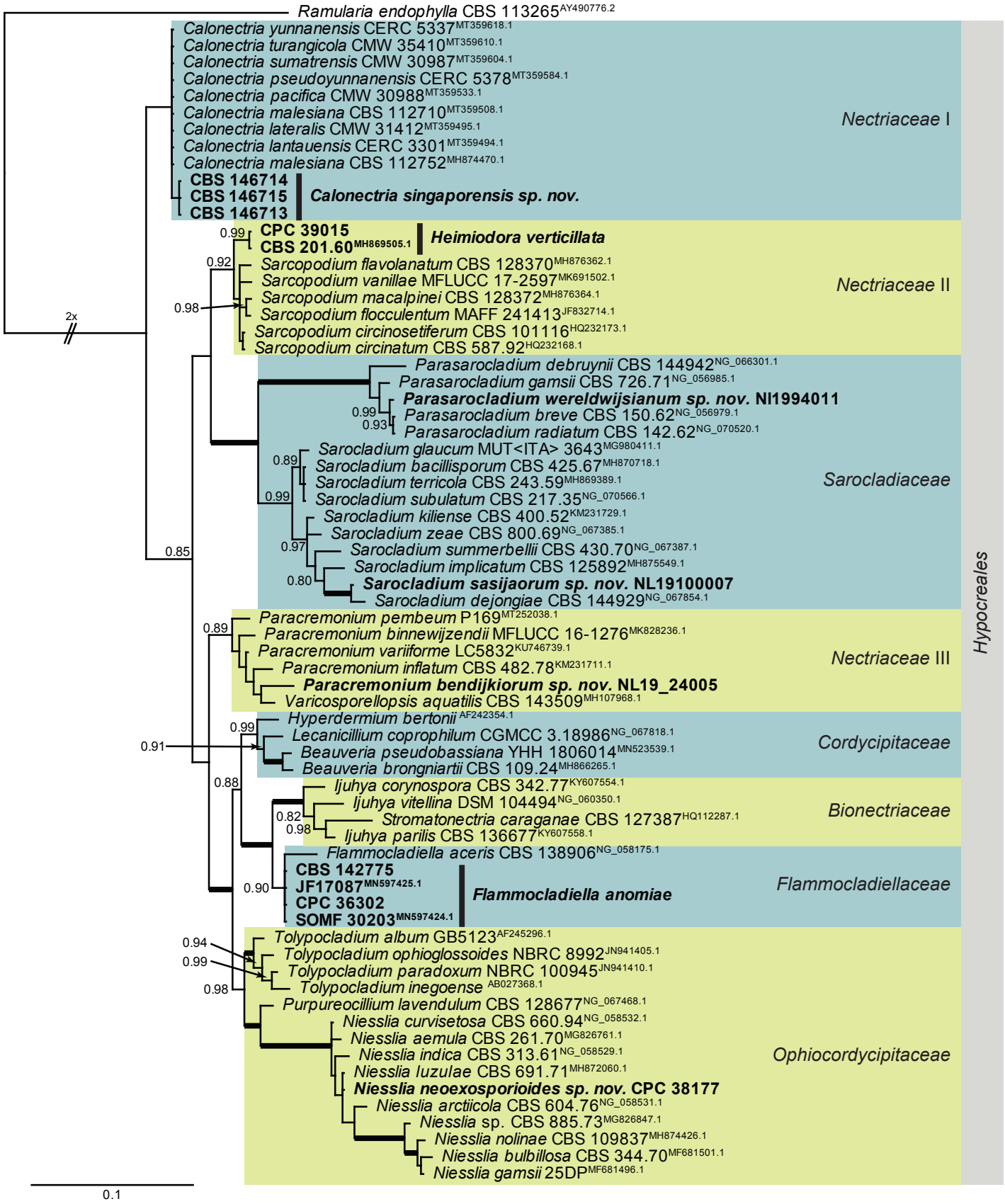

Fig. 4. Consensus phylogram (50 % majority rule) resulting from a Bayesian analysis of the *Sordariomycetes* (*Hypocreales*) LSU nucleotide alignment. Bayesian posterior probabilities (PP) > 0.79 are shown at the nodes and the scale bar represents the expected changes per site. Thickened branches represent PP = 1 and the most basal branch was halved to facilitate layout. Families and the order *Hypocreales* are indicated with coloured blocks to the right of the tree. GenBank accession (superscript) and / or culture collection / voucher numbers are indicated for all species. The tree was rooted to *Ramularia endophylla* (culture CBS 113265, GenBank AY490776.2) and the species treated in this study for which LSU sequence data were available are indicated in bold face.

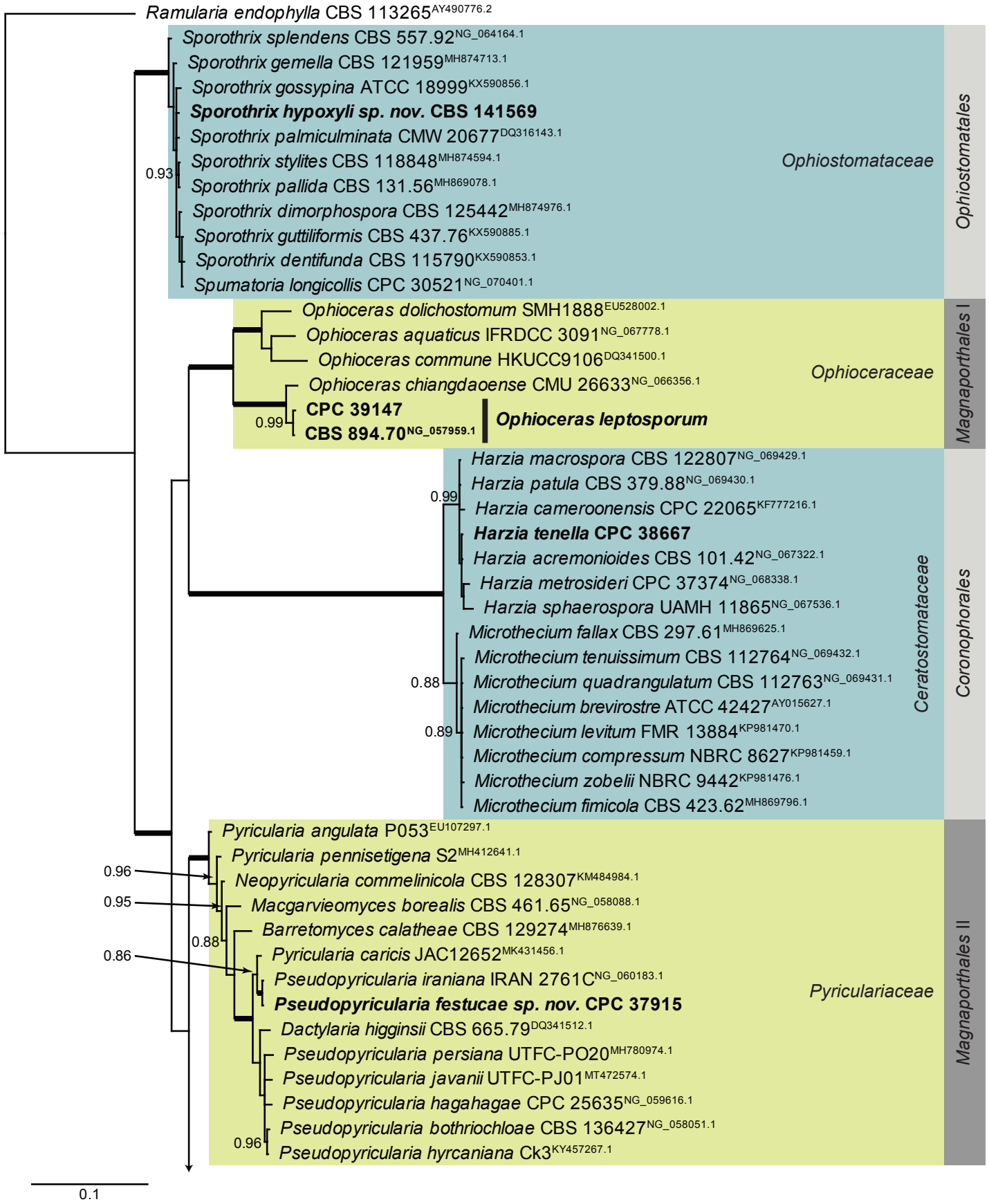

Fig. 5, parts 1–2. Consensus phylogram (50 % majority rule) resulting from a Bayesian analysis of the *Sordariomycetes* (other orders) LSU nucleotide alignment. Bayesian posterior probabilities (PP) > 0.79 are shown at the nodes and the scale bar represents the expected changes per site. Thickened branches represent PP = 1. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession (superscript) and / or culture collection / voucher numbers are indicated for all species. The tree was rooted to *Ramularia endophylla* (culture CBS 113265, GenBank AY490776.2) and the species treated in this study for which LSU sequence data were available are indicated in bold face.

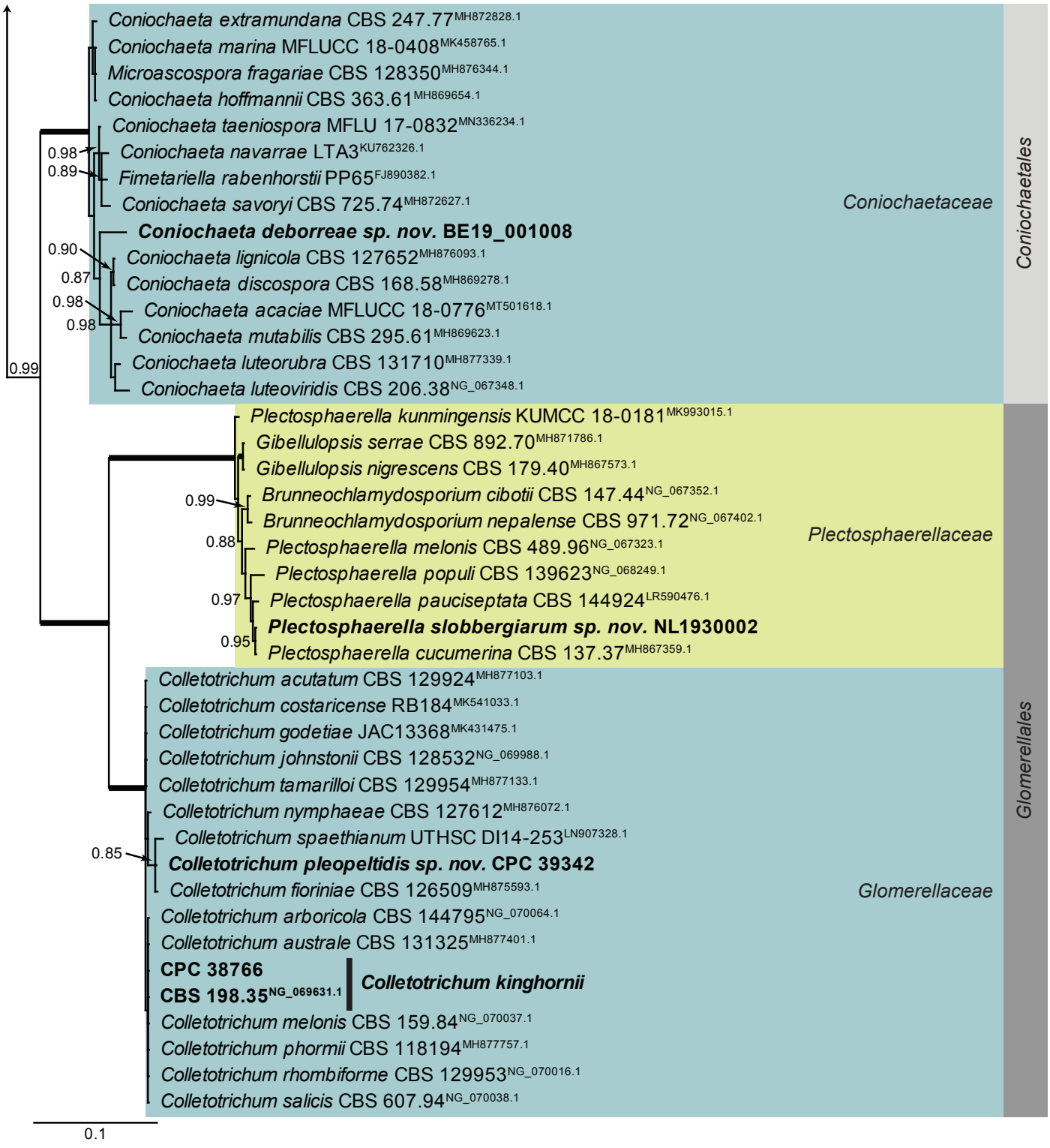

Fig. 5. (Continued).

Province in China (Wang *et al.* 2009). In the present study this species is reported from hypolithic biomass under a rock in the Namib Desert.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Alternaria atra* (strain AC90, GenBank LC440624.1; Identities = 563/563 (100 %), no gaps), *Alternaria dauci* (strain AY853, GenBank MG250469.1; Identities = 563/563 (100 %), no gaps), and *Alternaria heterospora* (strain CBS 123376, GenBank MH863292.1; Identities = 560/560 (100 %), no gaps). Closest hits using the **LSU** sequence are *Alternaria multiformis* (strain CBS 102060, GenBank NG_069860.1; Identities = 787/787 (100 %), no gaps), *Alternaria terricola* (strain CBS 202.67, GenBank NG_069728.1; Identities = 787/787 (100 %), no gaps), and *Alternaria chartarum* (strain CBS 200.67, GenBank NG_069727.1; Identities = 787/787 (100 %), no gaps) – also see Fig. 1. Closest hits using the ***actA*** sequence had highest similarity to *Alternaria atra* (strain ATCC 18040, GenBank JQ671660.1; Identities = 591/591 (100 %), no gaps), *Alternaria heterospora* (strain MF-G316021, GenBank KU639828.1; Identities = 588/588 (100 %),

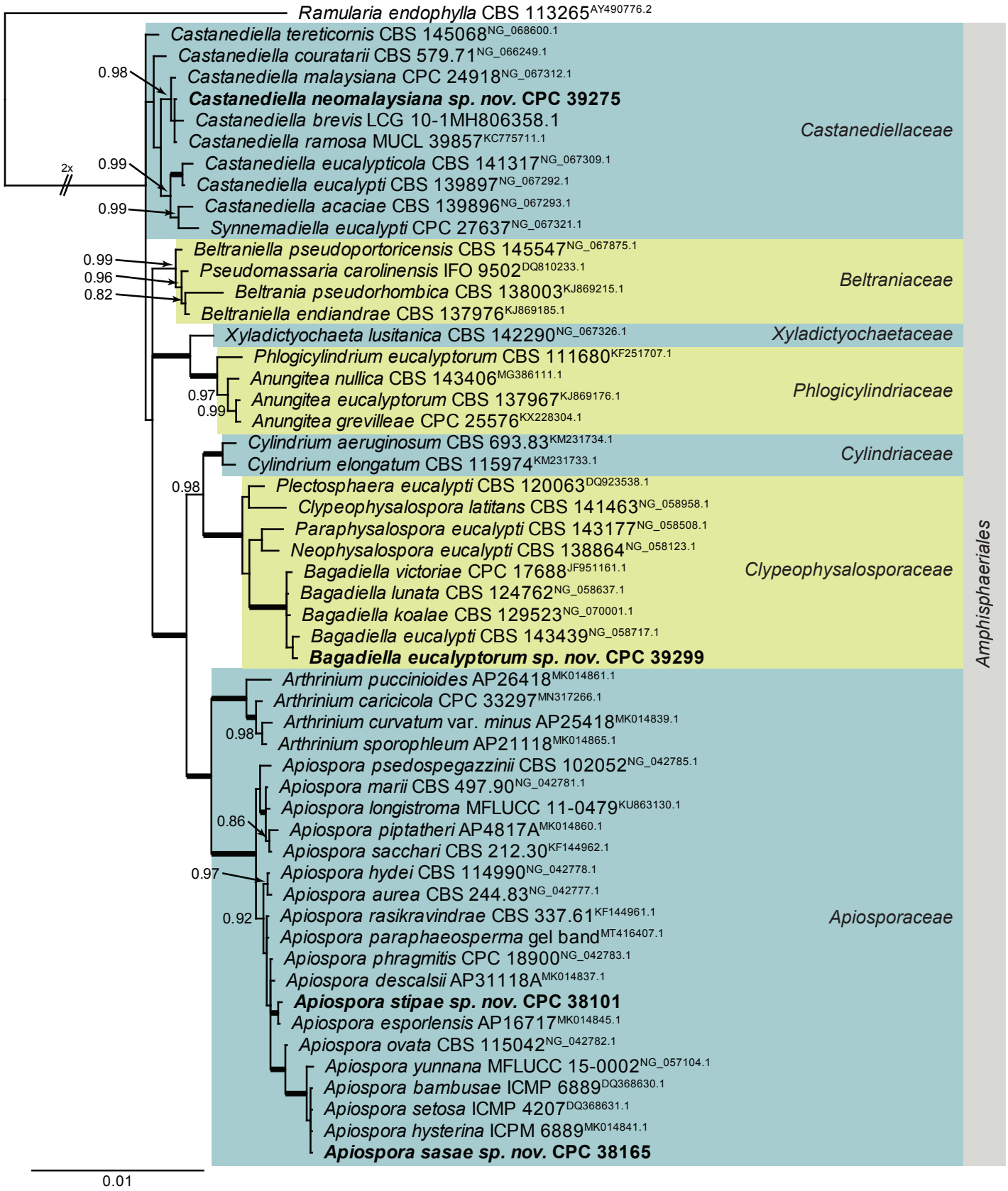

Fig. 6. Consensus phylogram (50 % majority rule) resulting from a Bayesian analysis of the *Sordariomycetes* (*Amphisphaeriales*) LSU nucleotide alignment. Bayesian posterior probabilities (PP) > 0.79 are shown at the nodes and the scale bar represents the expected changes per site. Thickened branches represent PP = 1 and the most basal branch was halved to facilitate layout. Families and the order *Amphisphaeriales* are indicated with coloured blocks to the right of the tree. GenBank accession (superscript) and / or culture collection / voucher numbers are indicated for all species. The tree was rooted to *Ramularia endophylla* (culture CBS 113265, GenBank AY490776.2) and the species treated in this study for which LSU sequence data were available are indicated in bold face.

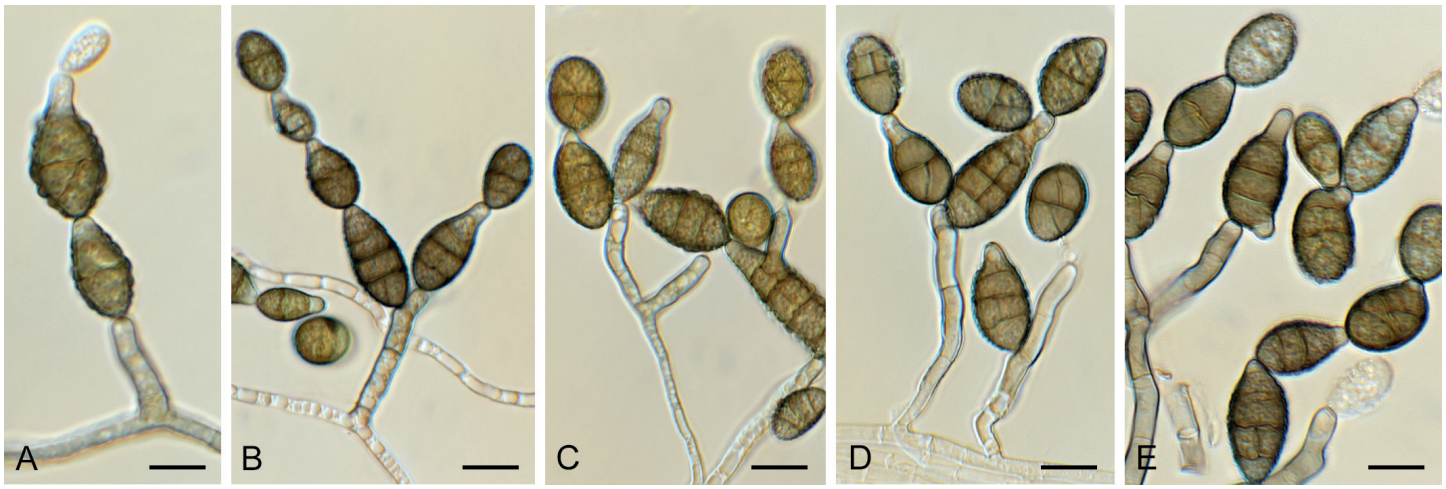

Fig. 7. *Alternaria chartarum* (CPC 38971). Conidiophores giving rise to chains of conidia. Scale bars = 10 µm.

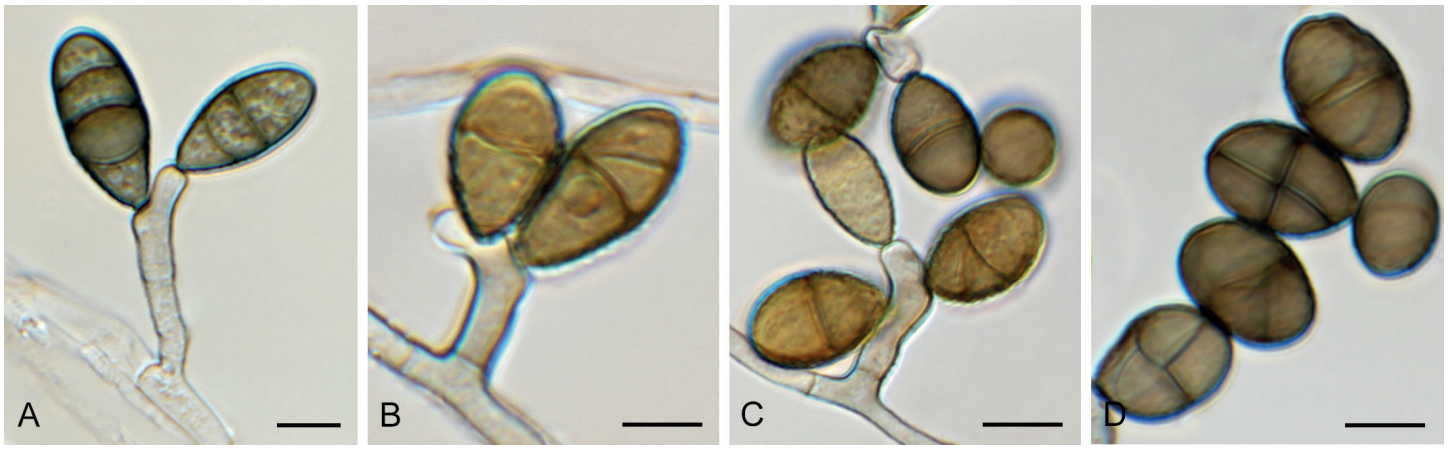

Fig. 8. *Alternaria heterospora* (CPC 38969). Conidiophores giving rise to conidia. Scale bars = 10 µm.

no gaps), and *Alternaria cucurbitae* (strain EGS 31-021, GenBank JQ671663.1; Identities = 590/591 (99 %), no gaps). Closest hits using the ***cmdA*** sequence had highest similarity to *Alternaria heterospora* (strain MF-G316021, GenBank KU639868.1; Identities = 549/549 (100 %), no gaps), *Alternaria botrytis* (strain AKC603, GenBank MT770809.1; Identities = 548/549 (99 %), no gaps), and *Alternaria obovoidea* (strain CBS 101229, GenBank JQ646172.1; Identities = 548/549 (99 %), no gaps). Closest hits using the ***gapdh*** sequence had highest similarity to *Alternaria heterospora* (strain CBS 123376, GenBank KC584176.1; Identities = 460/460 (100 %), no gaps), *Alternaria subcucurbitae* (as *Ulocladium subcucurbitae*; strain CBS 121491, GenBank EU855803.1; Identities = 460/460 (100 %), no gaps), and *Alternaria cucurbitae* (as *Ulocladium cucurbitae*; strain HSAUP_XF030282, GenBank AY762951.1; Identities = 460/460 (100 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Alternaria atra* (strain IR_Ker955, GenBank MK188501.1; Identities = 221/224 (99 %), no gaps), *Alternaria alternata* (strain MOS635, GenBank KP009004.1; Identities = 242/255 (95 %), no gaps), and *Alternaria photistica* (strain CBS 212.86, GenBank FJ214950.1; Identities = 252/267 (94 %), four gaps (1 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Alternaria atra* (strain ATCC 18040, GenBank JQ671998.1; Identities = 335/336 (99 %), no gaps), *Alternaria multiformis* (strain CBS 102060, GenBank JQ672002.1; Identities = 334/336 (99 %), no gaps), and *Alternaria cucurbitae* (strain EGS 31-021, GenBank JQ672001.1; Identities = 333/336 (99 %), no gaps).

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Apiospora sasae Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB 839279. Fig. 9.

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

Occurring on dead culms of *Sasa vetchii*. *Sporodochia* single to gregarious, initially immersed, opening via longitudinal split of epidermis, revealing black conidial mass, dry, pulvinate, 1–2 × 0.4 mm. *Paraphyses* absent. *Conidiophores* subcylindrical, rarely branched, basal and apical cell enlarged, subhyaline, thin-walled, smooth, septa red-brown, thick-walled, secession apical and lateral, lacking collarettes. *Conidiogenous cells* discrete, subcylindrical, subhyaline to pale brown, smooth to finely verruculose, holoblastic, proliferating sympodially, 5–10 × 3–4 µm. *Sterile cells* replacing normal conidia, brown, smooth, irregularly lobed, 8–25 × 7–12 µm. *Conidia* numerous, aseptate, subglobose, polygonal (6–7) to urceolate (urniform), red-brown at maturity, thick-walled, smooth, often with large central guttulate or multi-guttulate, with a lateral hyaline equatorial

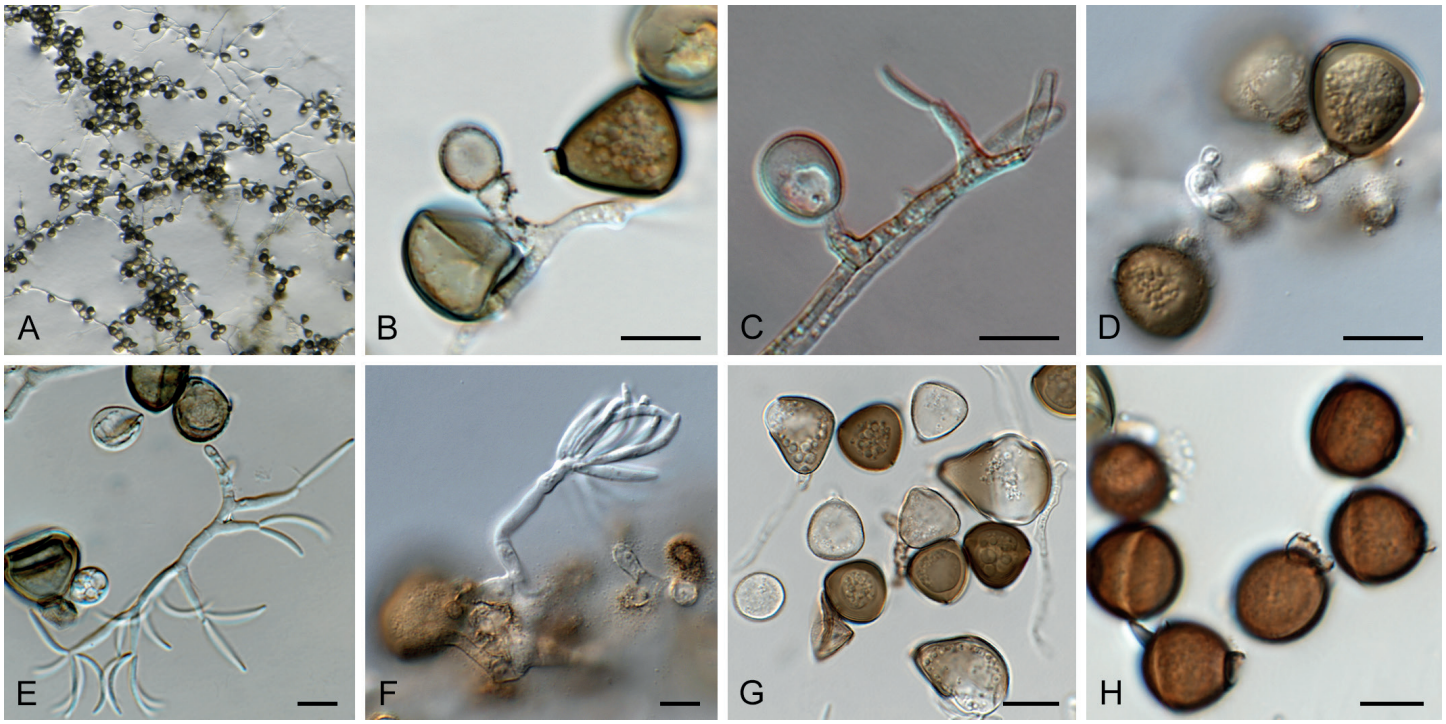

Fig. 9. *Apiospora sasae* (CPC 38165). **A.** Sporulating colony on SNA. **B.** Conidiogenous cell and conidia. **C, E.** Conidiogenous cells with both asexual morphs. **D.** Conidiogenous cells with conidia. **F.** Conidiogenous cell with conidia of synasexual morph. **G–H.** Conidia. Scale bars = 10 µm.

germ slit over entire length, often with a lateral, small protruding hilum, (16–)17–18(–20) × (15–)16–17(–19) µm. *Synasexual morph* hyaline, smooth, erect, solitary, with *conidiophores* subcylindrical, 1–2-septate, 10–20 × 3–4 µm. *Conidiogenous cells* terminal, integrated, hyaline, smooth, subcylindrical, 10–15 × 2.5–3 µm, proliferating sympodially at apex with subdenticulate loci, unthickened nor darkened. *Conidia* solitary, hyaline, aseptate, smooth, fusoid, falcate, apex subobtuse, base truncate, 10–20 × 2–2.5 µm.

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

Typus: **Netherlands**, Noord-Holland Province, Hoofddorp, on dead culms of *Sasa veitchii* (*Poaceae*), 20 May 2019, *L. van der Linde*, HPC 2959 = RKS 1101 (**holotype** CBS H-24403, culture ex-type CPC 38165 = CBS 146808).

Notes: The genus *Arthrinium* includes plant pathogens, endophytes and saprobes with a wide host range and geographic distribution (Crous & Groenewald 2013, Wang *et al.* 2018, Pintos *et al*. 2019). Although *Arthrinium* was seen as the asexual morph of *Apiospora* (Crous & Groenewald 2013), the recent epitypification of *Arthrinium* (based on *A. caricicola*; Crous *et al*. 2020b) showed this complex to represent two clades, one corresponding to *Arthrinium*, and the other to *Apiospora*. This generic complex was recently revised by Pintos *et al.* (2021), and will not be treated further here. The two taxa collected in the present study are thus best accommodated in *Apiospora*. *Apiospora sasae* is related to, but morphologically distinct from *Arthrinium yunnanum* (now *Apiospora yunnana*; conidia 10–16 µm diam; Dai *et al.* 2017) and *Arthrinium esporlense* (now *Apiospora esporlensis*; conidia 8–13 µm long; Pintos *et al.* 2019). A phylogenetic species tree is presented as Fig. 10.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Arthrinium yunnanum* (now *Apiospora yunnana*; strain JN2, GenBank MH191120.1; Identities = 646/648 (99 %), no gaps), *Arthrinium hysterinum* (now *Apiospora hysterina*; voucher AP15318, GenBank MK014873.1; Identities = 602/605 (99 %), no gaps), and *Arthrinium esporlense* (now *Apiospora esporlensis*; strain 18TJAM004, GenBank MT856406.1; Identities = 424/446 (95 %), six gaps (1 %)). Closest hits using the **LSU** sequence are *Apiospora setosa* (voucher ICMP 6888, GenBank DQ810214.1; Identities = 826/826 (100 %), no gaps), *Arthrinium hysterinum* (now *Apiospora hysterina*; voucher AP15318, GenBank MK014840.1; Identities = 817/817(100 %), no gaps), and *Apiospora tintinnabula* (voucher ICMP 6889-96, GenBank DQ810217.1; Identities = 810/812 (99 %), two gaps (0 %)) – also see Fig. 6. Closest hits using the ***rpb2*** sequence had highest similarity to *Apiospora bambusae* (strain ICMP 6889, GenBank DQ368649.1; Identities = 706/710 (99 %), no gaps), *Arthrinium yunnanum* (now *Apiospora yunnana*; voucher MFLU 18-1219, GenBank MK313857.1; Identities = 705/710 (99 %), no gaps), and *Apiospora tintinnabula* (voucher ICMP 7019-96), GenBank DQ810235.1; Identities = 705/710 (99 %), no gaps). Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Arthrinium yunnanum* (now *Apiospora yunnana*; voucher MFLU 18-1219, GenBank MK193869.1; Identities = 906/908 (99 %), no gaps), *Apiospora locuta-pollinis* (as *Arthrinium* FL-2018a; strain LC11688, GenBank MF939618.1; Identities = 856/880 (97 %), two gaps (0 %)), and *Arthrinium pseudoparenchymaticum* (now *Apiospora pseudoparenchymatica*; strain SICAUCC 18-0008, GenBank MK359205.1; Identities = 865/909 (95 %), two gaps (0 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Arthrinium hysterinum* (now *Apiospora hysterina*; voucher AP29717, GenBank MK017981.1; Identities = 387/390 (99 %),

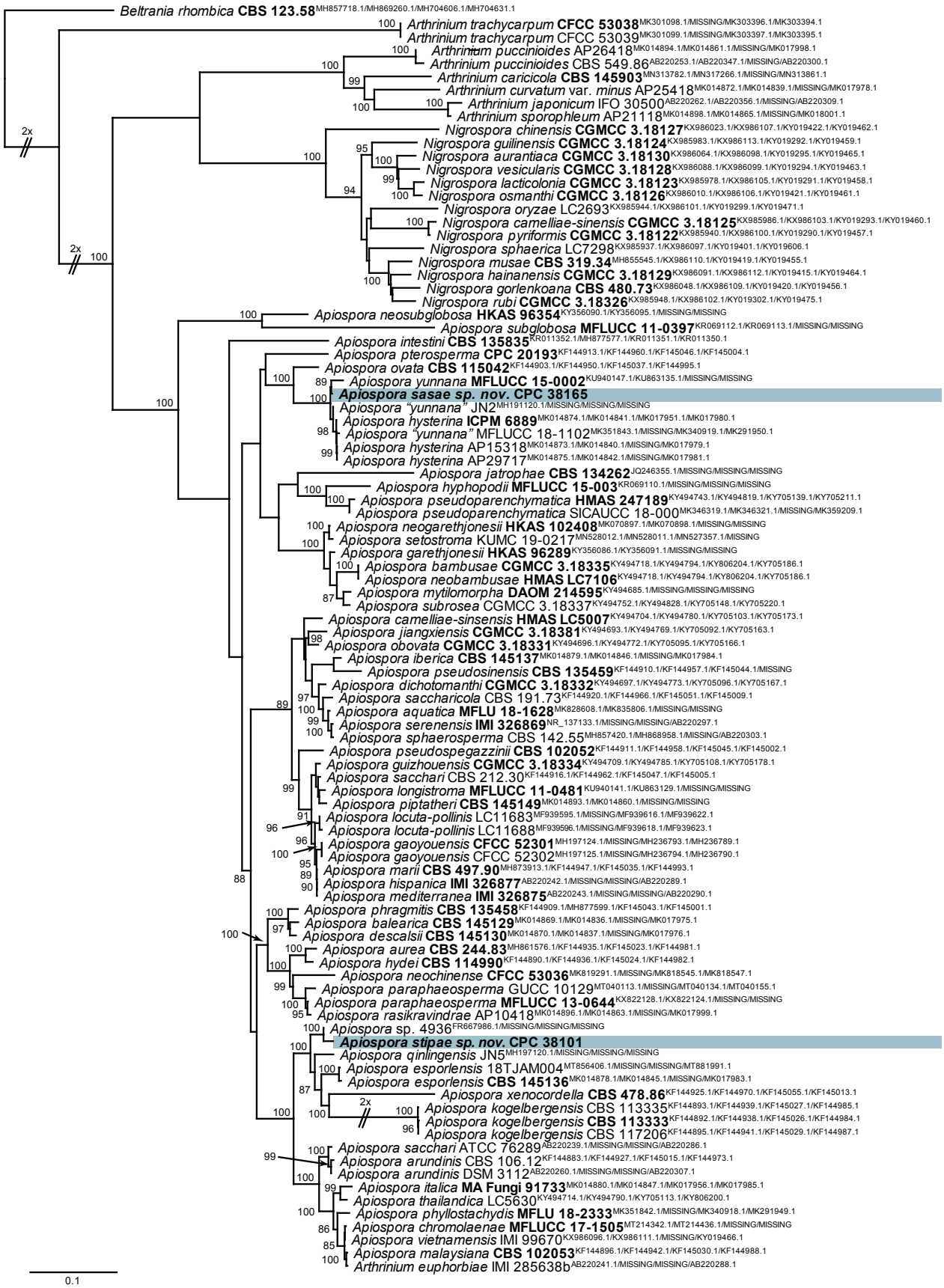

Fig. 10. Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE of the *Apiospora* multigene (ITS / LSU / *tef1* / *tub2*) nucleotide alignment of the two novel *Apiospora* species treated in this study. Some branches were halved to facilitate layout. Bootstrap support values (> 79 %) from 5 000 ultrafast bootstrap replicates are shown at the nodes. GenBank accession (superscript) and / or culture collection / voucher numbers (in bold face when having a type status) are indicated for all species. The tree was rooted to *Beltrania rhombica* (culture CBS 123.58) and the species treated in this study are highlighted with coloured blocks and bold face. Alignment statistics: 96 strains including the outgroup; 4 171 characters including alignment gaps analysed: 2 235 distinct patterns, 1 379 parsimony-informative, 365 singleton sites, 2 427 constant sites. The best models identified in IQ-TREE were: TNe+I+G4 (ITS), TIM+F+I+G4 (LSU), HKY+F+I+G4 (*tef1* and *tub2*).

no gaps), *Arthrinium yunnanum* (now *Apiospora yunnana*; strain MFLUCC 18-1102, GenBank MK291950.1; Identities = 762/774 (98 %), three gaps (0 %)), and *Arthrinium ovatum* (now *Apiospora ovata*; strain CBS 115042, GenBank KF144995.1; Identities = 697/765 (91 %), 23 gaps (3 %)).

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Apiospora stipae Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB 839280. Fig. 11.

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

Sporodochia on dead tissue, immersed, becoming erumpent, semi-superficial, single to confluent, cushion-shaped, black, dry, pulvinate. *Paraphyses* absent. *Conidiophores* cylindrical, unbranched to simple branched, hyaline, thin- and smooth-walled, septa red-brown, thick-walled, secession lateral and apical, single, lacking collarettes. *Conidia* numerous, aseptate, lens-shaped in side view, round to polygonal (6–8) in top view, olive brown to red-brown, thick-walled, smooth, eguttulate to guttulate, with lateral germ slit over entire length of conidium, often with a lateral, small, hyaline pronounced hilum, examined in water, 6.5–10.5 (length) × 6–9 (width) × 5–6 (side view) µm. Sporulating on PDA. *Mycelium* consisting of smooth, hyaline, branched, septate, 2–4 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* aggregated in clusters on hyphae, pale brown, smooth, ampulliform, 5–8 × 3–4 µm. *Conidia in vitro* (in lactic acid) brown, aseptate, smooth, granular, globose to elongated ellipsoid in surface view, (6.5–)7–8 µm diam, lenticular in side view with pale equatorial germ slit, (4.5–)5–6 µm in side view, with basal scar 1 µm diam; brown elongated cells (sterile cells?) at times intermingled among conidia.

Ascomata on host tissue (link with asexual morph unconfirmed): perithecial, on dead tissue, immersed, single, gregarious, globose, black; peridium multi-layered, consisting of *textura prismatica-epidermoidea* with thick-walled, smooth cells; inner layers hyaline, outer layers red-brown. *Paraphyses* present. *Asci* 8-spored, clavate, inoperculate, pedicel short and furcate, 87–101 × 17 µm. *Ascospores* 1-septate, hyaline, 27–30 × 8–10 µm.

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

Typus: **Spain**, Pontevedra, O Grove, on dead culm of *Stipa gigantea* (*Poaceae*), 10 Apr. 2019, *M.A. Delgado*, HPC 2973 = RKS 253 (**holotype** CBS H-24398, culture ex-type CPC 38101 = CBS 146804).

Notes: Numerous *Arthrinium* spp. occurring on diverse hosts in Europe have recently been treated (Crous & Groenewald 2013, Pintos *et al*. 2019). *Apiospora stipae* represents a new species closely related to *Arthrinium esporlense* (now *Apiospora esporlensis*; conidia (8–)9–12(–13) µm long; Pintos *et al.* 2019), from which it is morphologically distinct. A phylogenetic species tree is presented as Fig. 10.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to "*Arthrinium*" sp. (strain 4936, GenBank FR667986.1; Identities = 490/490 (100 %), no gaps), *Arthrinium esporlense* (now *Apiospora esporlensis*; strain 18TJAM004, GenBank MT856406.1; Identities = 543/560 (97 %), one gap (0 %)), and *Arthrinium qinlingense* (as *Arthrinium* sp. NJ-2018a, now *Apiospora qinlingensis*; strain JN5, GenBank MH197120.1; Identities = 553/571 (97 %), one gap (0 %)). Closest hits using the **LSU** sequence are *Arthrinium esporlense* (now *Apiospora esporlensis*; voucher AP16717, GenBank MK014845.1; Identities = 836/837 (99 %), no gaps), *Arthrinium phragmites* (now *Apiospora phragmitis*; strain CPC 18900, GenBank NG_042783.1; Identities = 896/900 (99 %), no gaps), and *Arthrinium kogelbergense* (now *Apiospora kogelbergensis*; strain CBS 113335, GenBank KF144939.1; Identities = 895/900 (99 %), no gaps) – also see Fig. 6. Closest hits using the ***rpb2*** sequence had highest similarity to *Apiospora bambusae* (strain ICMP 6889, GenBank DQ368649.1; Identities = 777/863 (90 %), no gaps), *Apiospora tintinnabula* (voucher ICMP 7019-96), GenBank DQ810235.1; Identities = 775/862 (90 %), no gaps), and *Arthrinium yunnanum* (now *Apiospora yunnana*; voucher MFLU 18-1219, GenBank MK313857.1; Identities = 773/860 (90 %), no gaps). Closest hits using the ***tef1*** sequence (first part) had highest similarity to *Arthrinium italicum* (now *Apiospora italica*; voucher AP221017, GenBank MK017956.1; Identities = 327/358 (91 %), six gaps (1 %)), *Arthrinium malaysianum* (now *Apiospora malaysiana*; strain CBS 102053, GenBank KF145030.1; Identities = 343/377 (91 %), four gaps (1 %)), and *Arthrinium thailandicum* (now *Apiospora thailandica*; strain LC5630, GenBank KY705113.1; Identities = 323/356 (91 %), four gaps (1 %)). Closest hits using

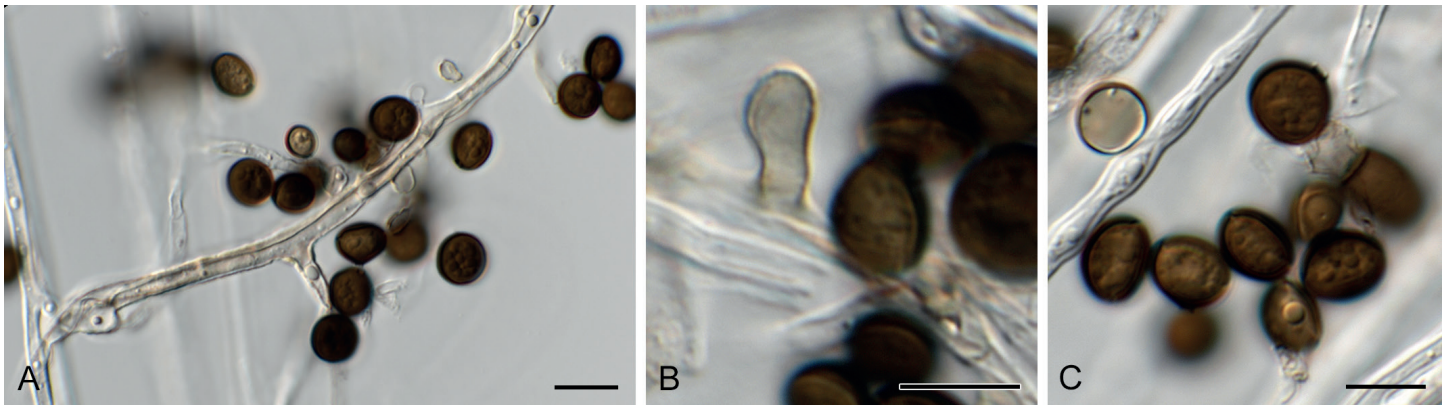

Fig. 11. *Apiospora stipae* (CPC 38101). **A.** Hyphae giving rise to conidiogenous cells with conidia. **B–C.** Conidiogenous cells and conidia. Scale bars = 10 µm.

the ***tef1*** (second part) sequence had highest similarity to *Arthrinium phyllostachium* (as *Arthrinium* sp., now *Apiospora phyllostachydis*; voucher MFLU 18-2333, GenBank MK313853.1; Identities = 893/919 (97 %), one gap (0 %)), *Arthrinium yunnanum* (now *Apiospora yunnana*; voucher MFLU 18-1219, GenBank MK193869.1; Identities = 884/920 (96 %), three gaps (0 %)), and *Nigrospora globosa* (as *Nigrospora* sp. ZZ-2018a; strain LC12441, GenBank MK336057.1; Identities = 858/907 (95 %), four gaps (0 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Arthrinium kogelbergense* (now *Apiospora kogelbergensis*; strain CBS 117206, GenBank KF144987.1; Identities = 689/776 (89 %), 30 gaps (3 %)), *Arthrinium arundinis* (now *Apiospora arundinis*; strain DSM 3112, GenBank AB220307.1; Identities = 687/781 (88 %), 27 gaps (3 %)), and *Arthrinium sacchari* (now *Apiospora sacchari*; strain ATCC 76289, GenBank AB220286.1; Identities = 684/781 (88 %), 27 gaps (3 %)).

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Bagadiella eucalyptorum Crous & Carnegie, ***sp. nov.*** MycoBank MB 839281. Fig. 12.

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

Mycelium consisting of subhyaline, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiomata* 80–100 µm diam, sporodochial, arising from an aggregated subhyaline mass of hyphal cells, that give rise to a hyaline, mucoid conidial mass. *Conidiophores* integrated, arising from a stroma or individual hyphae, smooth, branched or not, with terminal and intercalary *conidiogenous cells*, monophialidic, subcylindrical to lageniform, 10–15 × 2.5–3 µm, with minute collarettes. *Conidia* borne in mucoid heads, lunate, aseptate, curved, apex obtuse, base truncate, hyaline, (16–)17–18(–19) × 1.5(–2) µm.

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

Typus: **Australia**, New South Wales, Belanglo State Forest, Berrima, on leaves of *Eucalyptus* sp. (*Myrtaceae*), Aug. 2015, *A.J. Carnegie*, HPC 3219 (**holotype** CBS H-24560, culture ex-type CPC 39299 = CBS 147177).

Notes: Species of *Bagadiella* are commonly isolated as endophytic fungi from eucalypt leaves, but can also be associated with pale yellow leaf blotches (Cheewangkoon *et al.* 2009, Crous *et al*. 2019c). *Bagadiella eucalyptorum* is closely related to *B. eucalypti* [conidia (12–)14–17(–21) × (1.5–)2 µm; Crous *et al.* 2017] and *B. lunata* [conidia (15–)16–18(–22) × (1.3–)1.5(–1.7); Cheewangkoon *et al.* 2009]. Morphologically they are very similar, and best distinguished based on DNA sequence data. Also see the phylogenetic species tree (Fig. 13).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Bagadiella lunata* (strain CBS 124762, GenBank NR_132832.1; Identities = 587/602 (98 %), five gaps (0 %)), *Bagadiella koalae* (strain CBS 129523, GenBank NR_159638.1; Identities = 558/574 (97 %), four gaps (0 %)), and *Bagadiella victoriae* (strain CPC 20195, GenBank MN161894.1; Identities = 585/602 (97 %), one gap (0 %)). Closest hits using the **LSU** sequence are *Bagadiella eucalypti* (strain CBS 143497, GenBank MN162174.1; Identities = 842/846 (99 %), two gaps (0 %)), *Bagadiella koalae* (strain CBS 129523, GenBank NG_070001.1; Identities = 826/831 (99 %), no gaps), and *Bagadiella lunata* (strain CBS 124762, GenBank NG_058637.1; Identities = 852/858 (99 %), two gaps (0 %)) – also see Fig. 6.

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Blastacervulus metrosideri P.R. Johnst., *Fungal Syst. Evol.* **3**: 166. 2019. Fig. 14.

Description and illustration: See Johnston & Park (2019).

Material examined: **New Zealand**, Tauranga Port, on leaves of *Metrosideros* sp. (*Myrtaceae*), 22 Aug. 2019, *L. Rabbidge*, specimen CBS H-24511, culture T19_05741C = CPC 38759 = CBS 147006.

Notes: *Blastacervulus metrosideri* was described by Johnston & Park (2019) as a new foliar pathogen on *Metrosideros excelsa* in New Zealand, causing round, red-brown to black leaf spots that mostly occur on the upper leaf surface. The ITS sequence of CPC 38759 is a perfect match to that of the ex-type culture (ICMP 21883; GenBank NR_169959.1; 473/473 (100 %), no gaps) while there were three gaps present compared to the LSU sequence (GenBank NG_068290.1; 1 005/1 008 (99 %), three gaps (0 %)) – also see Fig. 1.

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

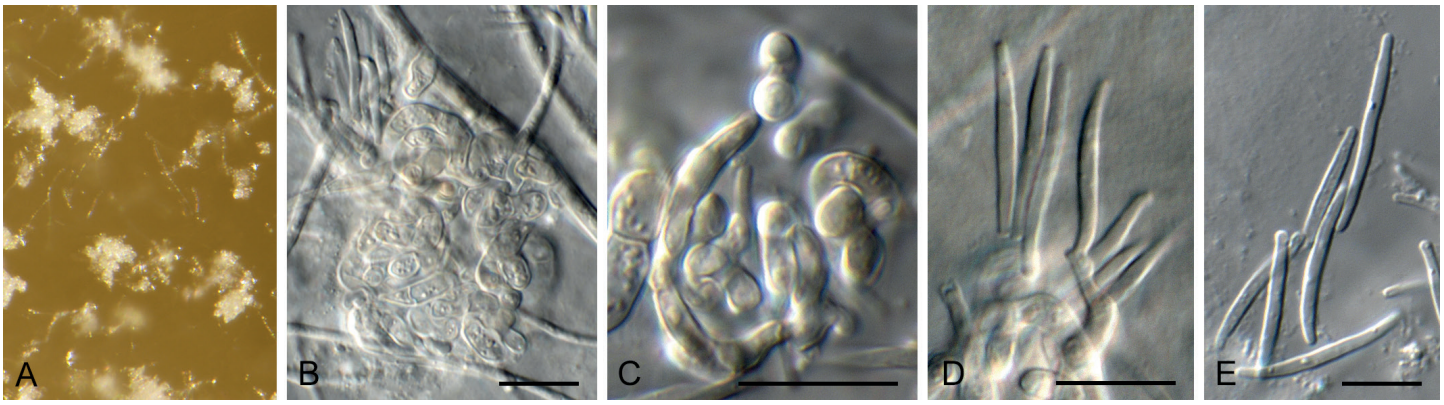

Fig. 12. *Bagadiella eucalyptorum* (CPC 39299). **A.** Colony sporulating on OA. **B–D.** Developing conidiogenous cells. **E.** Conidia. Scale bars = 10 µm.

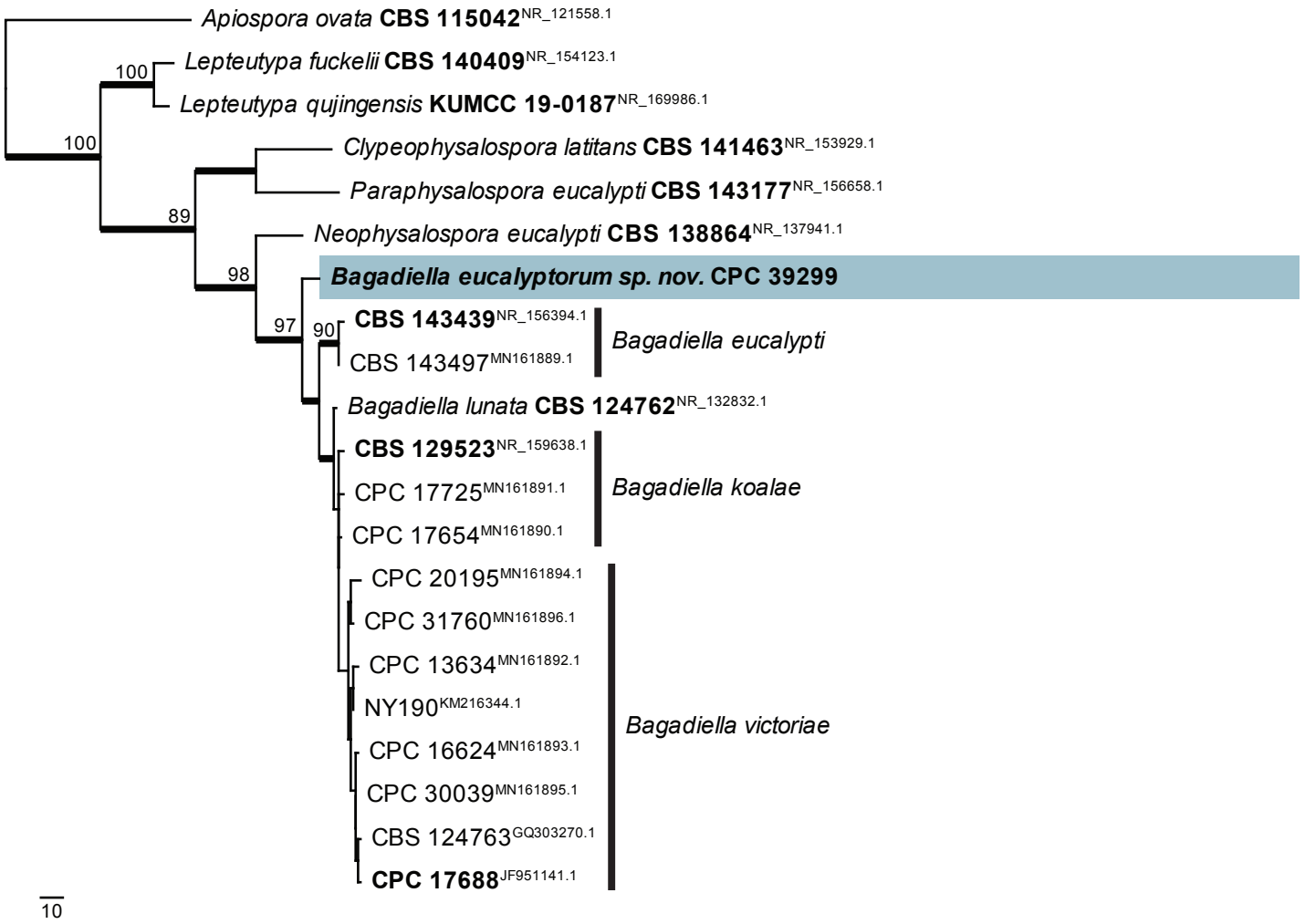

Fig. 13. The first of 519 equally most parsimonious trees obtained from a phylogenetic analysis of the *Bagadiella* ITS nucleotide alignment. The tree was rooted to *Apiospora ovata* (strain CBS 115042, GenBank NR_121558.1) and the scale bar indicates the number of changes. Parsimony bootstrap support values higher than 79 % are shown at the nodes and the treated species is highlighted with a coloured box and bold text. GenBank accession (superscript) and / or culture collection / voucher numbers (in bold face when having a type status) are indicated for all species. Branches present in the strict consensus tree are thickened. Alignment statistics: 21 strains including the outgroup; 544 characters including alignment gaps analysed: 348 constant, 71 variable and parsimony-uninformative and 125 parsimony-informative. Tree statistics: TL = 401, CI = 0.783, RI = 0.756, RC = 0.592.

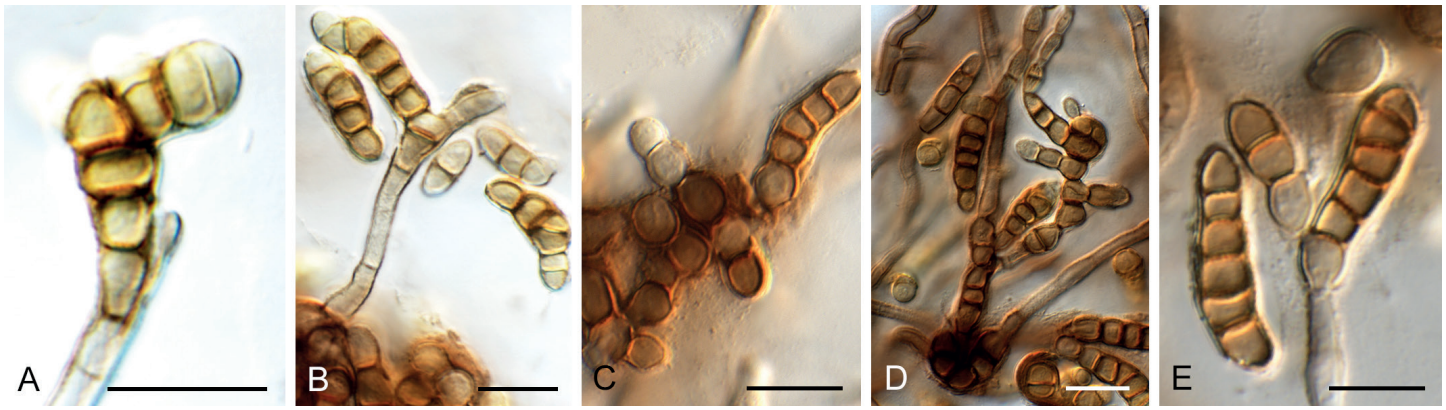

Fig. 14. *Blastacervulus metrosideri* (CPC 38759). **A–E.** Conidiogenous cells giving rise to conidia. Scale bars = 10 µm.

Calonectria singaporensis Crous & Decock, ***sp. nov.*** MycoBank MB 839282. Fig. 15.

Etymology: Name refers to Singapore, the country where this species was isolated.

Macroconidiophores comprised of a stipe, a penicillate arrangement of fertile branches, and a stipe extension ending in a terminal vesicle. Stipe septate, hyaline to pale brown at base, smooth, 50–350 µm tall. *Conidiogenous apparatus* with primary branches aseptate or 1-septate, 20–30 × 6–8 µm; secondary branches aseptate, 16–20 × 4–5 µm, and tertiary and additional

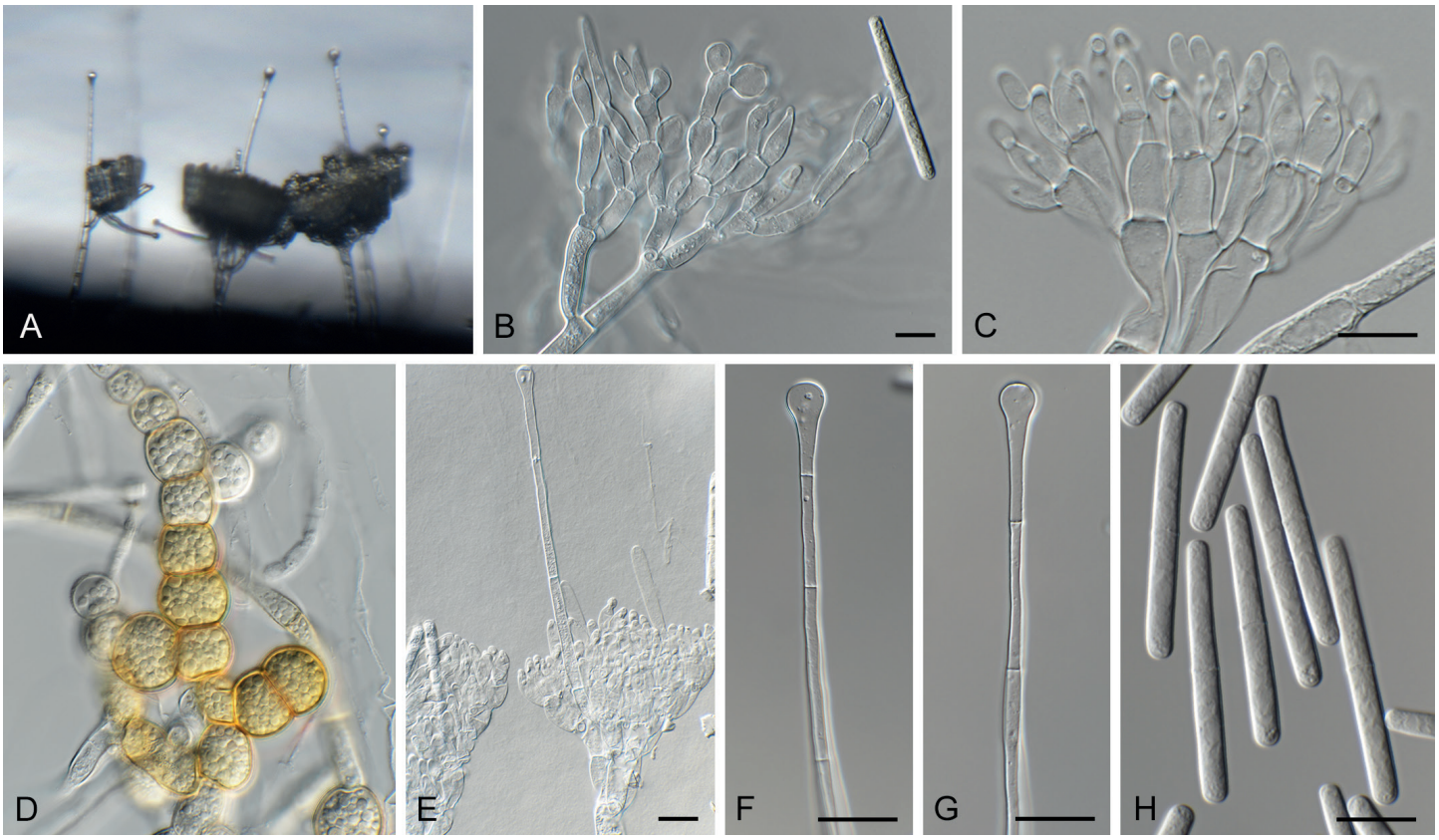

Fig. 15. *Calonectria singaporensis* (CBS 146715). **A.** Conidiophores on PNA. **B–C.** Conidiogenous apparatus. **D.** Chlamydospores. **E–G.** Conidiophores with stipe extensions and terminal vesicles. **H.** Conidia. Scale bars = 10 µm.

(–6) branches aseptate, 12–15 × 4–5 µm, each terminal branch producing 2–4 phialides; phialides doliiform to reniform, hyaline, aseptate, 9–15 × 3–5 µm, apex with minute periclinal thickening and inconspicuous collarette; stipe extensions septate, straight to flexuous, 90–200 µm long, 3–4 µm wide at apical septum, terminating in sphaeropedunculate vesicle, (4–)7–12 µm diam; lateral stipe extensions common, up to 70 µm long, terminating in small sphaeropedunculate vesicles, 4–6 µm diam. *Conidia* cylindrical, rounded at both ends, straight, (33–)37–40(–41) × (3.5–)4(–4.5) µm, 1-septate, lacking a visible abscission scar, held in cylindrical clusters by colourless slime. *Chlamydospores* dark brown, thickened, globose, 15–30 µm diam, formed in chains throughout the medium, and aggregated to form microsclerotia.

Culture characteristics: Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, even margin, covering dish after 2 wk at 25 °C. On MEA surface sienna to umber.

Typus. **Singapore**, Mac Ritchie Reservoir, South East Asian rainforest, submerged leaf litter in a small stream, Dec. 2001, *C. Decock* # SING365 (**holotype** CBS H-24749, culture ex-type MUCL 048320 = CBS 146715).

Additional materials examined: **Singapore**, Mac Ritchie Reservoir, South East Asian rainforest, submerged leaf litter in a small stream, Dec. 2001, *C. Decock* # SING365, cultures CBS 146712 = MUCL 048012, CBS 146713 = MUCL 048171, CBS 146714 = MUCL 048187.

Notes: A recent revision of the genus *Calonectria* accepted 11 species complexes, reducing the genus to 120 species (Liu *et al.* 2020). *Calonectria singaporensis* is phylogenetically distinct from all accepted species in the genus, representing a new species in the *C. kyotensis* species complex (Fig. 16). Morphologically, these taxa are all very similar, sharing sphaeropedunculate vesicles and 1-septate conidia, and are best distinguished based on their DNA sequence data.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Calonectria syzygiicola* (strain CBS 112827, GenBank KY653281.1; Identities = 530/531 (99 %), no gaps), *Calonectria ilicicola* (strain CPC 16334, GenBank GU057378.1; Identities = 530/531 (99 %), no gaps), and *Calonectria curvispora* (strain CBS 116159, GenBank GQ280568.1; Identities = 530/531 (99 %), no gaps). Closest hits using the **LSU** sequence are *Calonectria malesiana* (strain CBS 112752, GenBank MH874470.1; Identities = 861/865 (99 %), no gaps), *Calonectria ilicicola* (strain CBS 125938, GenBank MH875288.1; Identities = 858/862 (99 %), no gaps), and *Calonectria yunnanensis* (strain CERC 5337 (R), GenBank MT359618.1; Identities = 853/857 (99 %), no gaps) – also see Fig. 4. Closest hits using the ***actA*** sequence had highest similarity to *Calonectria turangicola* (now *Calonectria kyotensis*; strain CMW 35410 (R), GenBank MT335152.1; Identities = 228/246 (93 %), five gaps (2 %)), *Calonectria pseudoturangicola* (now *Calonectria kyotensis*; strain CERC 7127 (R), GenBank MT335122.1; Identities = 228/246 (93 %), five gaps (2 %)), and *Calonectria kyotensis* (strain CBS 114525 (R), GenBank MT335039.1; Identities = 228/246 (93 %), five gaps (2 %)). Closest hits using the ***cmdA*** sequence had highest similarity to *Calonectria malesiana* (strain CMW 23687 (R), GenBank MT335286.1; Identities = 646/680 (95 %), two gaps (0 %)), *Calonectria turangicola* (now *Calonectria kyotensis*; strain CMW 35410 (R), GenBank MT335389.1; Identities = 645/680 (95 %), two

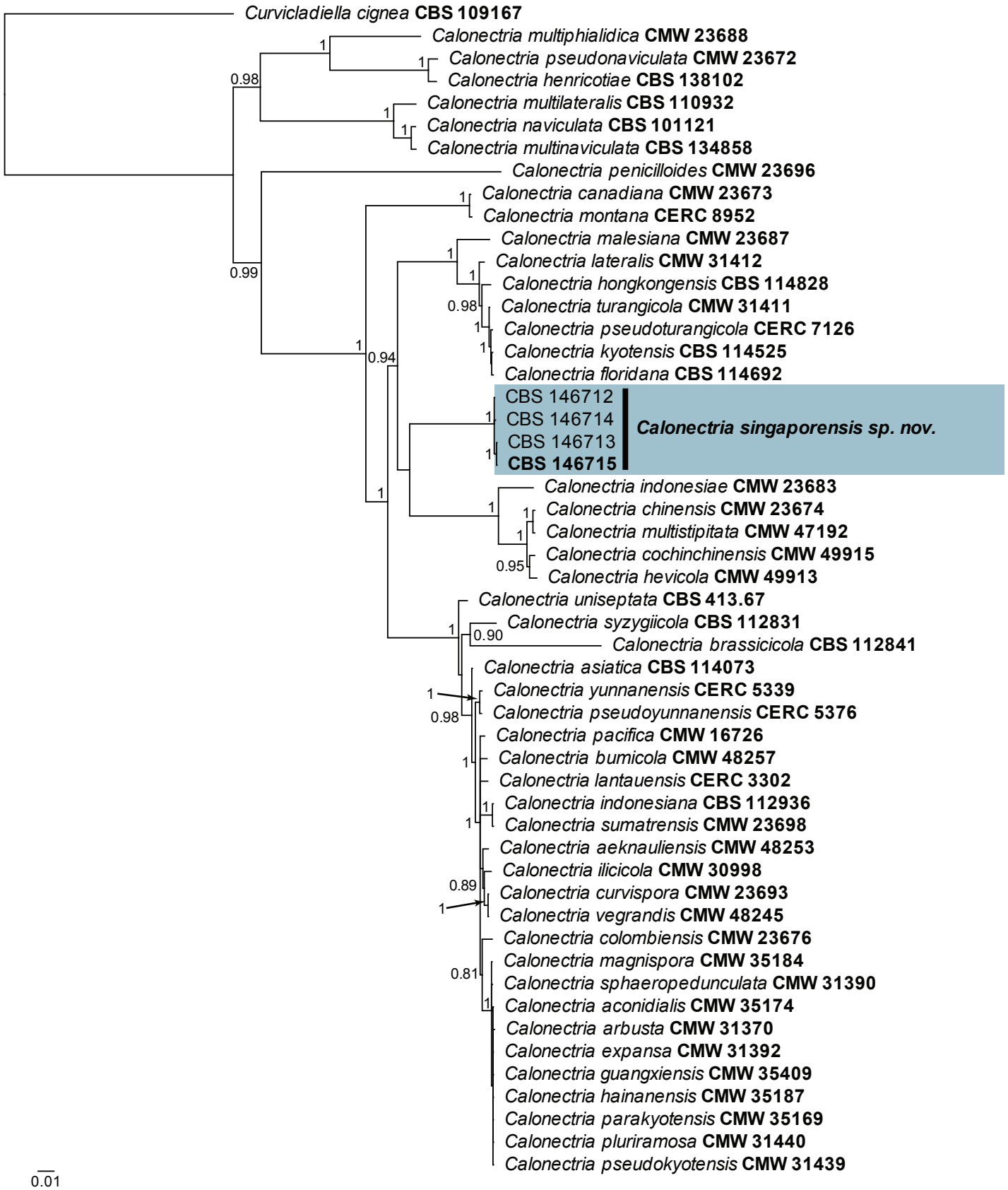

Fig. 16. Consensus phylogram (50 % majority rule) resulting from a Bayesian analysis of the *Calonectria* multigene (*actA* / *cmdA* / *his3* / ITS / LSU / *rpb2* / *tef1* / *tub2*) nucleotide alignment. The alignment is derived from the combined alignment of Liu *et al*. (2020) and GenBank accession numbers can be obtained from the same reference. Culture numbers with a type status are in bold face and the novel species is highlighted with a coloured box and bold text. Bayesian posterior probabilities (> 0.79) are shown at the nodes and the scale bar represents the expected changes per site. The tree was rooted to *Curvicladiella cignea* (culture CBS 109167). Alignment statistics: 52 strains including the outgroup; 112 / 290 / 212 / 57 / 37 / 255 / 241 / 307 unique site patterns, respectively. Tree statistics: 5 928 sampled trees from 395 000 generations.

gaps (0 %)), and *Calonectria pseudoturangicola* (now *Calonectria kyotensis*; strain CERC 7127 (R), GenBank MT335357.1; Identities = 645/680 (95 %), two gaps (0 %)). Closest hits using the ***his3*** sequence had highest similarity to *Calonectria matogrossensis* (strain GFP018, GenBank MH837652.1; Identities = 366/412 (89 %), 20 gaps (4 %)), *Calonectria pseudometrosideri* (strain CBS 134843, GenBank KM396081.1; Identities = 366/412 (89 %), 20 gaps (4 %)), and *Calonectria metrosideri* (strain CBS 133603, GenBank KC294307.1; Identities = 366/412 (89 %), 20 gaps (4 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Calonectria malesiana* (strain CSF11261, GenBank MT412818.1; Identities = 459/490 (94 %), four gaps (0 %)), *Calonectria montana* (now *Calonectria canadiana*; strain HSP65, GenBank MN356469.1; Identities = 470/502 (94 %), eight gaps (1 %)), and *Calonectria lateralis* (strain CMW 47414, GenBank MH119245.1; Identities = 467/499 (94 %), two gaps (0 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Calonectria pseudoturangicola* (now *Calonectria kyotensis*; strain CERC 7131, GenBank MF443082.1; Identities = 294/320 (92 %), seven gaps (2 %)), *Calonectria turangicola* (now *Calonectria kyotensis*; strain CSF11435, GenBank MT413127.1; Identities = 294/320 (92 %), seven gaps (2 %)), and *Calonectria kyotensis* (strain CSF16440, GenBank MT413019.1; Identities = 294/320 (92 %), seven gaps (2 %)).

Authors: P.W. Crous, J.Z. Groenewald & C. Decock

Castanediella neomalaysiana Crous, ***sp. nov.*** MycoBank MB 839283. Fig. 17.

Etymology: Name refers to the fact that it is similar to *Castanediella malaysiana*.

Mycelium consisting of smooth, brown, septate, branched, 2–3 µm diam hyphae. *Conidiophores* arising directly from superficial hyphae, subcylindrical, erect, straight, branched below or not, 0–4-septate, commonly also reduced to conidiogenous cells, pale brown, smooth, 17–60 × 2.5–3.5 µm. *Conidiogenous cells* integrated, pale brown, smooth, subcylindrical, terminal and intercalary, apex swollen with cluster of aggregated subdenticulate conidiogenous loci, 0.5 µm tall and wide, 17–22 × 2.5–3 µm. *Conidia* solitary, aseptate, fusoid, curved, widest in middle, tapering to subobtuse apices, hyaline, smooth, guttulate, (15–)17–19(–21) × 2(–3) µm.

Culture characteristics: Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, lobate margin, reaching 50 mm diam after 2 wk at 25 °C, and brown, microsclerotium-like bodies immersed in agar, but these remain sterile. On MEA and PDA surface and reverse brown vinaceous; on OA surface dark brick.

Typus: **Malaysia**, on leaves of *Eucalyptus* sp. (*Myrtaceae*), Nov. 2010, *M.J. Wingfield*, HPC 3228 (**holotype** CBS H-24547, culture ex-type CPC 39275 = CBS 147093).

Notes: *Castanediella* was established by Crous *et al*. (2015) to accommodate several species of *Amphisphaeriales*, for which Hernández-Restrepo *et al.* (2017) introduced the family *Castanediellaceae*. *Castanediella neomalaysiana* is phylogenetically closely related to *C. malaysiana* (conidia 0–1-septate, 18–30 × 2–3 µm; Hernandez-Restrepo *et al*. 2016), but differs in having shorter conidia. A phylogenetic species tree is presented in Fig. 18.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Castanediella* sp. (strain JHGB10_4A, GenBank MH267851.1; Identities = 542/558 (97 %), two gaps (0 %)), *Castanediella malaysiana* (strain CPC 24918, GenBank NR_154810.1; Identities = 545/564 (97 %), two gaps (0 %)), and *Castanediella couratarii* (strain CBS 579.71, GenBank MH860269.1; Identities = 543/565 (96 %), four gaps (0 %)). Closest hits using the **LSU** sequence are *Castanediella malaysiana* (strain CPC 24918, GenBank NG_067312.1; Identities = 846/850 (99 %), two gaps (0 %)), *Castanediella brevis* (as *Castanediella* sp.; strain LCG 10-1, GenBank MH806358.1; Identities = 755/759 (99 %), one gap (0 %)), and *Castanediella ramosa* (as *Idriella ramosa*; strain MUCL 39857, GenBank KC775711.1; Identities = 814/819 (99 %), five gaps (0 %)) – also see Fig. 6.

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

Colletotrichum kinghornii Damm *et al.*, *Stud. Mycol*. **73**: 73. 2012. Fig. 19.

Description and illustration: Damm *et al*. (2012).

Material examined: **New Zealand**, Auckland, East Tamaki, on *Phormium cookianum* (*Asphodelaceae*), 22 Aug. 2019, *C. Inglis*, culture CPC 38766 = T19_05774B.

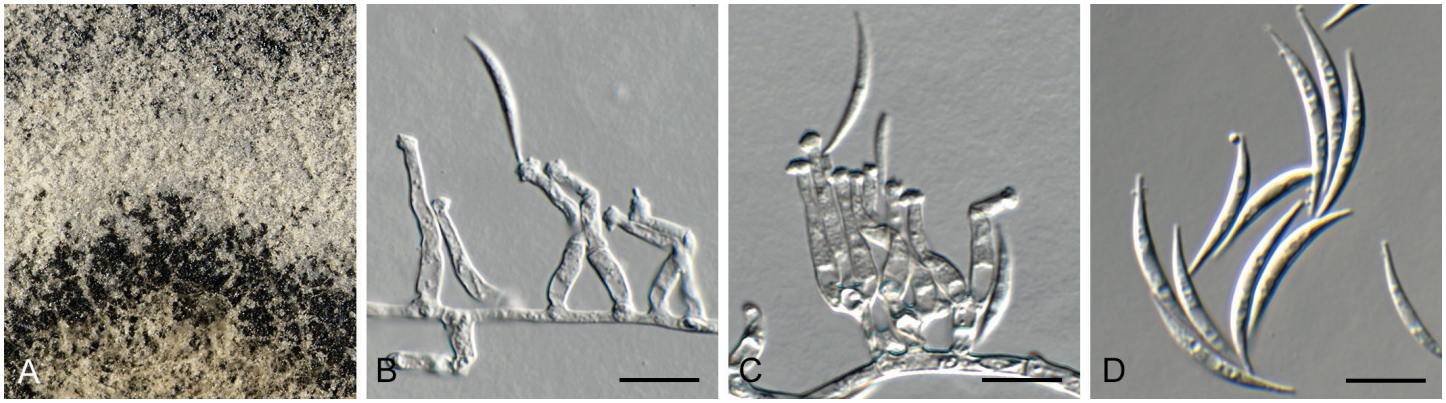

Fig. 17. *Castanediella neomalaysiana* (CPC 39275). **A.** Colony sporulating on PDA. **B–C.** Conidiogenous cells giving rise to conidia. **D.** Conidia. Scale bars = 10 µm.

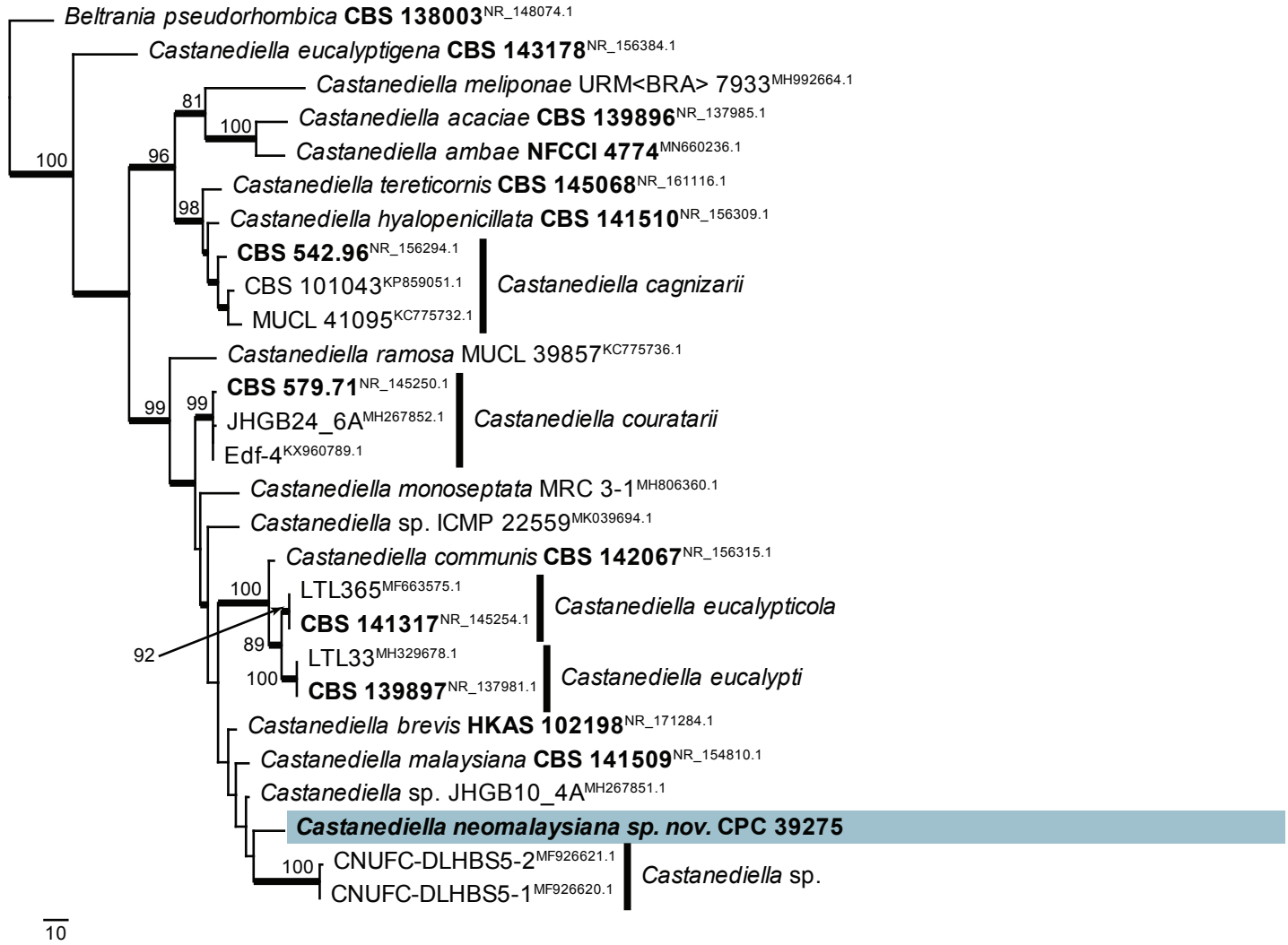

Fig. 18. The first of 11 equally most parsimonious trees obtained from a phylogenetic analysis of the *Castanediella* ITS sequence alignment. The tree was rooted to *Beltrania pseudorhombica* (strain CBS 138003, GenBank NR_148074.1) and the scale bar indicates the number of changes. Parsimony bootstrap support values higher than 79 % are shown at the nodes and the treated species is highlighted with a coloured box and bold text. GenBank accession (superscript) and / or culture collection / voucher numbers (in bold face when having a type status) are indicated for all species. Branches present in the strict consensus tree are thickened. Alignment statistics: 27 strains including the outgroup; 527 characters including alignment gaps analysed: 352 constant, 57 variable and parsimony-uninformative and 118 parsimony-informative. Tree statistics: TL = 430, CI = 0.644, RI = 0.775, RC = 0.499.

Fig. 19. *Colletotrichum kinghornii* (CPC 38766). **A.** Ascoma developing on PNA. **B–D.** Asci with ascospores. Scale bars: A = 250 µm, all others = 10 µm.

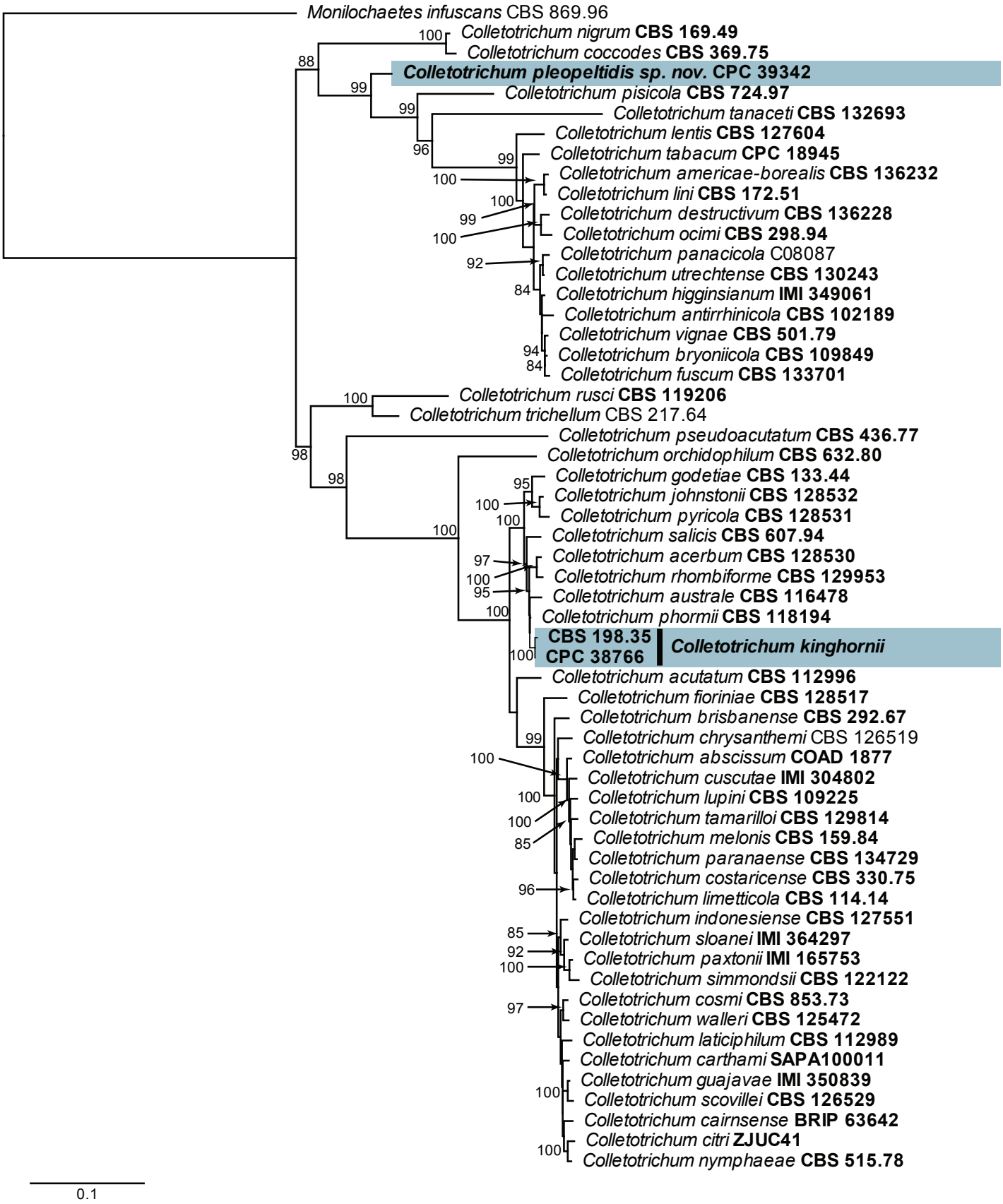

Fig. 20. Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE of the *Colletotrichum* multigene (ITS / *gapdh* / *chs-1* / *actA* / *tub2*) nucleotide alignment. Bootstrap support values (> 79 %) from 5 000 ultrafast bootstrap replicates are shown at the nodes. The alignment is derived from the combined alignment of Marin-Felix *et al.* (2017) and GenBank accession numbers can be obtained from the same reference. Culture collection / voucher numbers (in bold face when having a type status) are indicated for all species. The tree was rooted to *Monilochaetes infuscans* (culture CBS 869.96) and the species treated in this study are highlighted with coloured blocks and bold face. Alignment statistics: 58 strains including the outgroup; 1 972 characters including alignment gaps analysed: 973 distinct patterns, 596 parsimony-informative, 261 singleton sites, 1 115 constant sites. The best models identified in IQ-TREE were: TIM3e+I+G4 (ITS), K3P+I+G4 (*gapdh*), TNe+I+G4 (*chs-1*), HKY+F+G4 (*actA*), TIM2e+I+G4 (*tub2*).

Notes: *Colletotrichum kinghornii* was described based on its asexual morph from *Phormium tenax* collected in Great Britain (Damm *et al.* 2012). The present collection is the first record of its sexual morph. A phylogenetic species tree is presented as Fig. 20.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Colletotrichum kinghornii* (strain CBS 198.35, GenBank NR_111751.1; Identities = 538/538 (100 %), no gaps), *Colletotrichum phormii* (strain CBS 198.35, GenBank DQ286144.1; Identities = 571/571 (100 %), no gaps), and *Colletotrichum salicis* (strain CBS 129973, GenBank MH865705.1; Identities = 578/579 (99 %), no gaps). Closest hits using the **LSU** sequence are *Colletotrichum kinghornii* (strain CBS 198.35, GenBank NG_069631.1; Identities = 668/668 (100 %), no gaps), *Colletotrichum arboricola* (strain CBS 144795, GenBank NG_070064.1; Identities = 668/668 (100 %), no gaps), and *Colletotrichum salicis* (strain CBS 607.94, GenBank NG_070038.1; Identities = 668/668 (100 %), no gaps) – also see Fig. 5. Closest hits using the ***actA*** sequence had highest similarity to *Colletotrichum kinghornii* (strain CBS 198.35, GenBank JQ949775.1; Identities = 247/247 (100 %), no gaps), *Colletotrichum kniphofiae* (strain CBS 143496, GenBank MH107975.1; Identities = 622/641 (97 %), no gaps), and *Colletotrichum destructivum* (GenBank AY157843.1; Identities = 596/657 (91 %), 14 gaps (2 %)). Closest hits using the ***gapdh*** sequence had highest similarity to *Colletotrichum kinghornii* (strain CBS 198.35, GenBank JQ948785.1; Identities = 260/260 (100 %), no gaps), *Colletotrichum scovillei* (strain TJNH1, GenBank XM_035479122.1; Identities = 310/316 (98 %), one gap (0 %)), and *Colletotrichum orchidophilum* (strain IMI 309357, GenBank XM_022618742.1; Identities = 309/316 (98 %), one gap (0 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Colletotrichum kinghornii* (strain CBS 198.35, GenBank JQ950105.1; Identities = 485/486 (99 %), no gaps), *Colletotrichum phormii* (strain BRIP 62862, GenBank KX069820.1; Identities = 650/657 (99 %), two gaps (0 %)), and *Colletotrichum rhombiforme* (strain HYPG-1, GenBank KY581595.1; Identities = 668/683 (98 %), two gaps (0 %)).

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

Colletotrichum pleopeltidis Crous & Jol. Roux, ***sp. nov.*** MycoBank MB 839284. Fig. 21.

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

Ascomatal initials develop on media (SNA, MEA, OA, PDA), but these remain sterile. Asexual morph on SNA. Vegetative *hyphae* 3–5 µm diam, hyaline to pale brown, smooth-walled, septate, branched. *Conidiomata* acervular, up to 350 µm diam, with conidiophores and setae forming on a cushion of brown, thick-walled cells. *Setae* dark brown, smooth-walled, 3–5-septate, 90–150 µm long, base conical to cylindrical, 5–6 µm diam, tip subacutely rounded. *Conidiophores* pale to medium brown, septate, smooth, branched, up to 60 µm long. *Conidiogenous cells* pale brown, smooth, short cylindrical to ampulliform, 17–25 × 4–6 µm, with periclinal thickening and non-flaring collarette. *Conidia* hyaline, smooth, aseptate, cylindrical, apex obtuse, base rounded with prominent scar, guttulate, (15–)19–23(–25) × (5–)5.5(–6) µm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA surface olivaceous grey, reverse olivaceous grey in centre, sienna in outer region; on PDA surface pale olivaceous grey, reverse olivaceous grey in centre, ochreous in outer region; on OA surface ochreous.

Typus: **South Africa**, Limpopo Province, Louis Trichardt, Hanglip Forest Reserve, on leaves of *Pleopeltis* sp. (*Polypodiaceae*), 17 Dec. 2015, *J. Roux*, HPC 3238 (**holotype** CBS H-24550, culture ex-type CPC 39342 = CBS 147082).

Notes: *Colletotrichum pleopeltidis* belongs to the *destructivum* complex (Damm *et al.* 2014) and is closely related to *C. pisicola* [conidia fusoid, curved, (11–)15–21(–29.5) × (3–)3.5–4 µm], and *C. tanaceti* [conidia cylindrical to somewhat clavate, curved, (13–)14.5–17.5(–19) × (3–)3.5–4(–4.5) µm]. It is distinguished based on conidium morphology and phylogeny (see Fig. 20).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Colletotrichum hsienjenchang* (strain MAFF 243051, GenBank AB738855.1; Identities = 547/566 (97 %), five gaps (0 %)), *Colletotrichum fuscum* (strain DAOM216112, GenBank EU400144.1; Identities = 552/572 (97 %), 11 gaps (1 %)), and *Colletotrichum spaethianum* (strain AJ007, GenBank KT122848.1; Identities = 545/565 (96 %), five gaps (0 %)). Closest hits using the **LSU** sequence are *Colletotrichum destructivum* (strain 1212, GenBank KF181215.1; Identities = 874/878 (99 %), three gaps (0 %)), *Colletotrichum fioriniae* (strain CBS 126509, GenBank MH875593.1; Identities = 866/870 (99 %), three gaps (0 %)), and *Colletotrichum tamarilloi* (strain CBS

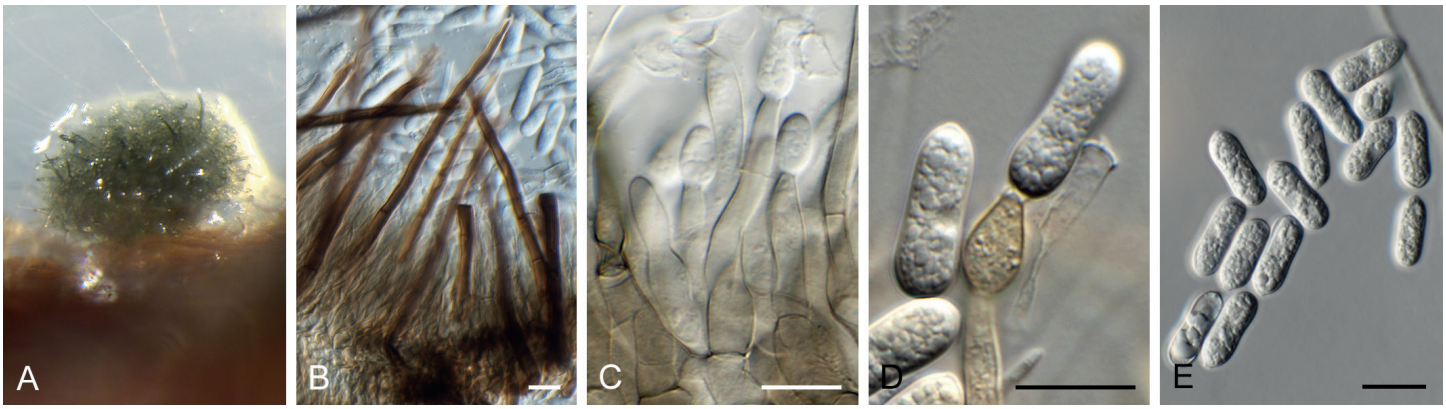

Fig. 21. *Colletotrichum pleopeltidis* (CPC 39342). **A.** Conidioma developing on PNA. **B.** Setae. **C–D.** Conidiogenous cells. **E.** Conidia. Scale bars = 10 µm.

129954, GenBank MH877133.1; Identities = 877/884 (99 %), four gaps (0 %)) – also see Fig. 5. Closest hits using the ***actA*** sequence had highest similarity to *Colletotrichum destructivum* (GenBank AY157843.1; Identities = 594/639 (93 %), nine gaps (1 %)), *Colletotrichum kniphofiae* (strain CBS 143496, GenBank MH107975.1; Identities = 573/635 (90 %), 13 gaps (2 %)), and *Colletotrichum kahawae* (strain CIFC Que2, GenBank KU579251.1; Identities = 574/642 (89 %), 19 gaps (2 %)). Closest hits using the ***chs-1*** sequence had highest similarity to *Colletotrichum panacicola* (strain YL2-2, GenBank MN894862.1; Identities = 267/283 (94 %), no gaps), *Colletotrichum lineola* (strain TYJ77301-7, GenBank MN894858.1; Identities = 267/283 (94 %), no gaps), and *Colletotrichum neorubicola* (strain CCR144, GenBank MK547526.1; Identities = 266/283 (94 %), no gaps).

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

Coniochaeta deborreae Hern.-Restr. ***sp. nov.*** MycoBank MB 838706. Fig. 22.

Etymology: Named after the collector, Kirsten de Borre, a student from the VISO Cor Mariae secondary school (Brakel, Belgium). This sample was collected during a Citizen Science project of the Westerdijk Fungal Biodiversity Institute.

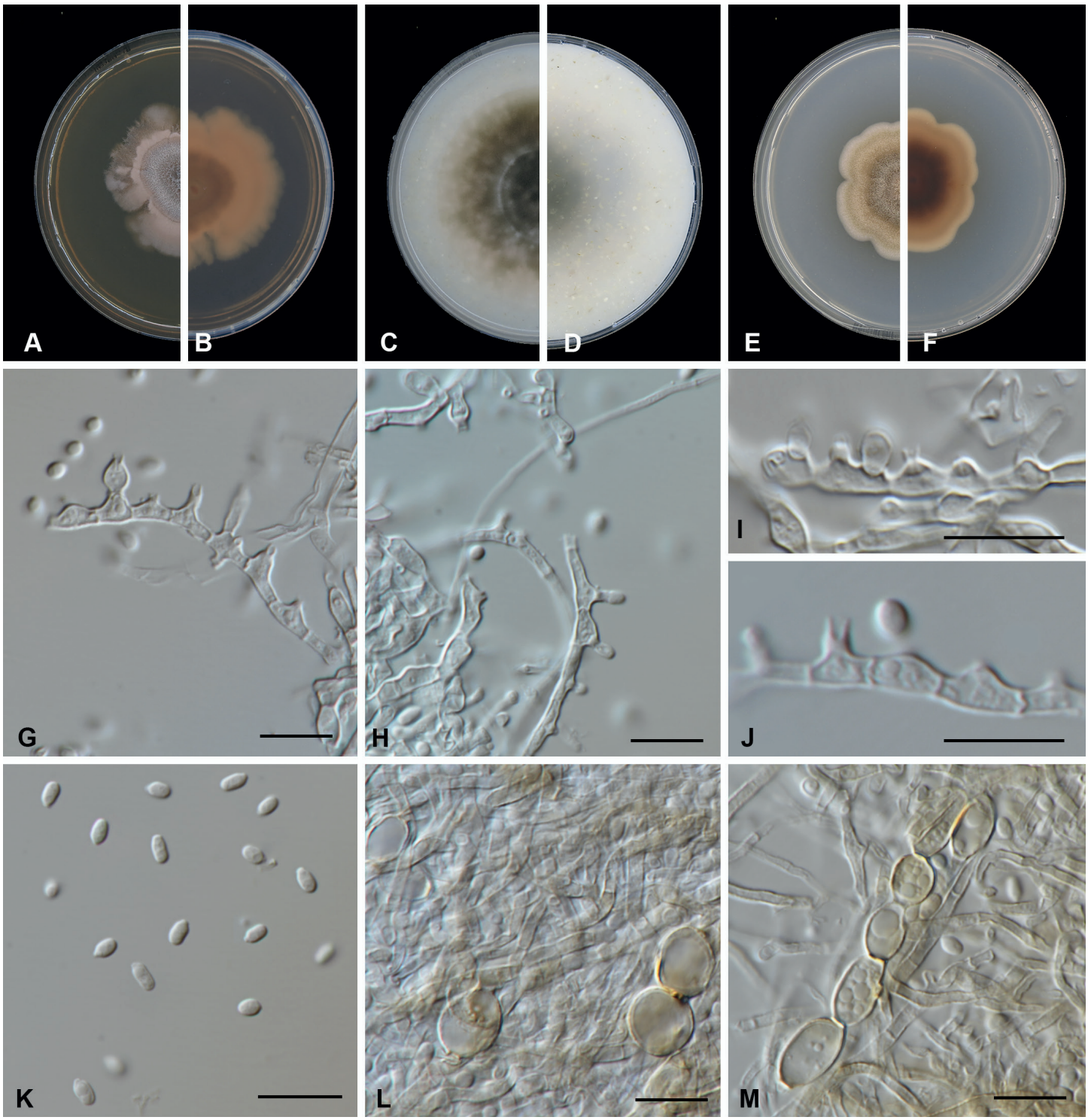

Fig. 22. *Coniochaeta deborreae* (CBS 147215). **A–B.** Colony on MEA. **C–D.** Colony on OA. **E–F.** Colony on PDA. **G–J.** Conidiogenous cells and conidia. **K.** Conidia. **L–M.** Chlamydospores. Scale bars G–M = 10 µm.

Vegetative hyphae septate, branched, hyaline to subhyaline, thin- and smooth-walled, 1–3 µm wide. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* terminal, lateral or intercalary, mono- or polyphialidic, cylindrical, ampulliform or ventricose, nearly globose, 4–11 × 2–3.5 µm, hyaline, with conspicuous periclinal thickening and distinguishable, usually cylindrical collarettes, 1–2 × 1–1.5 µm. *Conidia* aseptate, hyaline, smooth-walled, ellipsoidal to oblong, with rounded apex and truncate base, 2.5–4 × 1.5–2 µm. *Chlamydospores* solitary or in short chains, subglobose, pale brown, 6.5–13 × 5–9 µm.

Culture characteristics: Colonies after 2 wk at 25 °C on OA reaching 80 mm diam, glabrous, zonate centre vinaceous grey, olivaceous to fawn with saffron zones, margin effuse; reverse fawn to saffron. On MEA reaching 45 mm diam, velvety, zonate centre fulvous to saffron, margin irregular, lobate to fimbriate; reverse fulvous to saffron. On PDA reaching 40 mm diam, velvety, zonate, concentric circles and radial folds, umbers, cinnamon, ochreous to fulvous, margin lobate; reverse umber to fulvous; diffusible pigment ochreous.

Typus: **Belgium**, East Flanders, Brakel, from soil, 2019, *K. De Borre*, BE19_001 (**holotype** CBS H-24732, culture ex-type CBS 147215 = BE19_001008).

Additional material examined: **Norway**, Móre og Romsdal, on *Pinus sylvestris* wood, 31 Jul. 1974, *K. Venn* No. 74-55/7, culture CBS 551.75.

Notes: *Coniochaeta deborreae* is phylogenetically (Fig. 23) related to *C. boothii*, *C. pulveraceae*, *C. subcorticalis*, and *C. rhopalochaeta*. All these species were described as sexual morphs, except for *C. rhopalochaeta* that was described with both sexual and asexual morphs from decorticated wood of *Bulnesia retama* from Argentina (Romero *et al.* 1999). *Coniochaeta deborreae* differs from *C. rhopalochaeta* by having smaller conidiogenous cells (4–11 × 2–3.5 *vs*. 10–18 × 3.5–5 µm) and smaller conidia [2.5–4 × 1.5–2 µm *vs*. 5–8 × 3–5µm (Romero *et al.* 1999)]. Also see the overview phylogeny (Fig. 5).

Coniochaeta deborrae is represented by two strains respectively isolated from soil in Belgium (CBS 147215) and *Pinus sylvestris* wood in Norway (CBS 551.75). However, isolate CBS 551.75 was initially identified as *Phialophora mutabilis* (described from river water, the Netherlands). This isolate was later found to be a species of *Coniochaeta*, and identified as *C. subcorticalis* (known from *Alnus glutinosa*, Germany) as it occurred on *Pinaceae*. Morphologically, it is not possible to compare the present strain CBS 147215, nor CBS 551.75 with *C. subcorticalis*, as both species only form asexual structures, and DNA data are not available for *C. subcorticalis*.

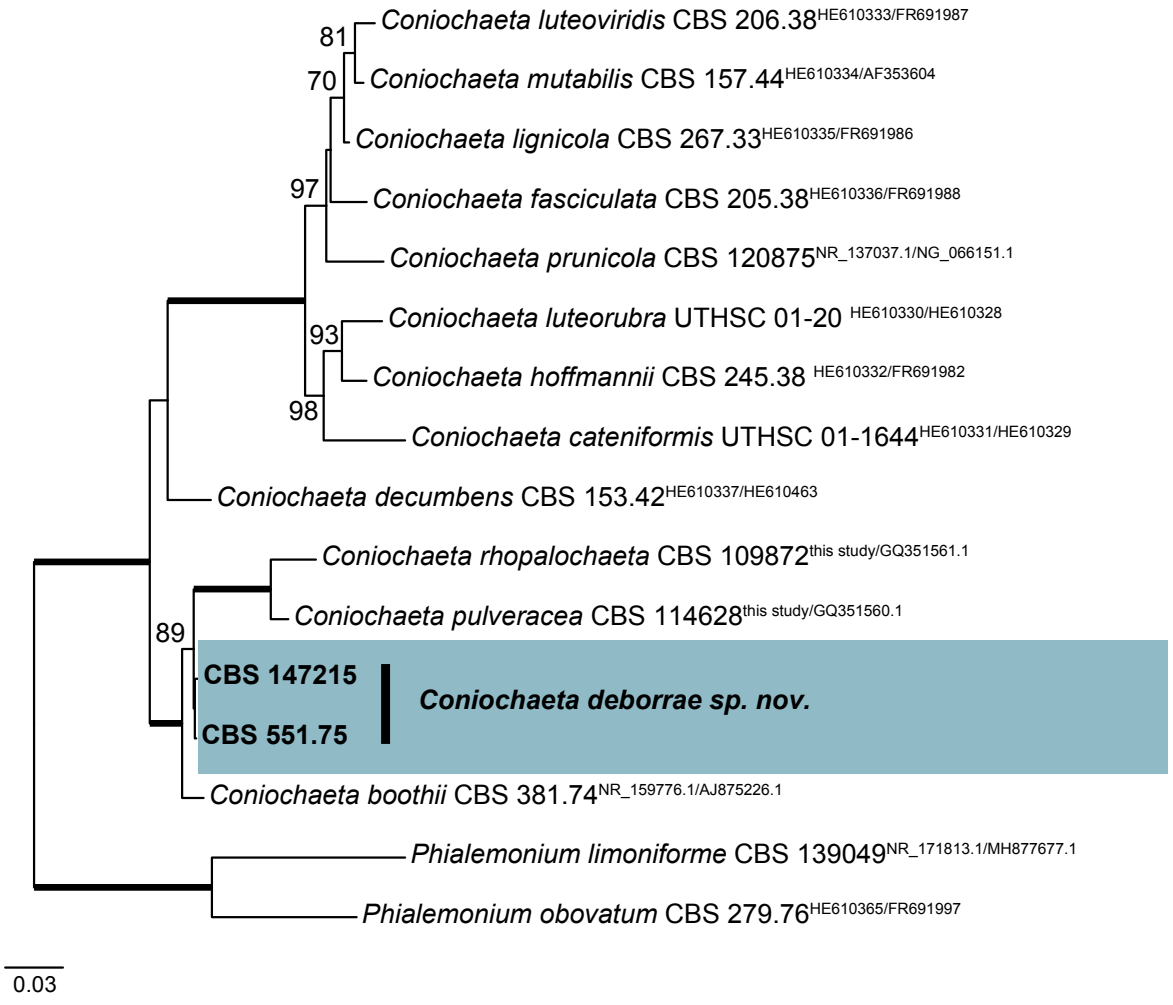

Fig. 23. Maximum composite likelihood tree obtained from the RAxML analysis of the combined ITS and LSU sequence alignment of selected *Coniochaeta* species. Bootstrap support values above 70 % are shown at the nodes. The novel species is indicated in a coloured block and bold face. The tree was rooted to *Phialemonium limoniforme* (CBS 139049) and *Ph. obovatum* (CBS 279.76). Alignment statistics: 16 strains including the outgroup; 930 characters including alignment gaps analysed (ITS: 495, LSU: 435). Model: GTR+G, alignment patterns: 400.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had the most similar identified species was *Coniochaeta boothii* (strain KoLRI_EL005219, GenBank NR_159776.1; Identities = 496/505 (98 %), two gaps (0 %)), *C. cipronana* (strain CBS 144016, GenBank NR_157478.1; Identities = 495/529 (94 %), 17 gaps (3 %)), and *C. arenariae* (strain MFLUCC 18-0409, GenBank MN047126.1; Identities = 492/526 (94 %), 14 gaps (2 %)). Closest hits using the **LSU** sequence are *Coniochaeta taeniospora* (strain LTA1, GenBank KU762325.; Identities = 792/814 (97 %), no gaps), *C. leucoplaca* (strain Jong54, GenBank FJ167399.1; Identities = 771/793 (97 %), no gaps), and *C. marina* (strain MFLUCC 18-0408, GenBank MK458765.1; Identities = 791/814 (97 %), no gaps) – also see Fig. 5. Closest hits using the ***tef1*** are *Coniochaeta rosae* (strain MFLUCC 17-0810, Genbank MG829197.1; Identities = 827/894 (93 %), three gaps (0 %)), *Coniochaeta endophytica* (strain AEA 9094, Genbank MK693159.1; Identities = 806/872 (92 %), no gaps), and *Coniochaeta baysunika* (strain MFLUCC 17-0830, Genbank MG829196.1; Identities = 826/894 (92 %), three gaps (0 %)).

Author: M. Hernández-Restrepo

Diaporthe durionigena L.D. Thao, L.T. Hien, N.V. Liem, H.M. Thanh & T.N. Khanh, ***sp. nov.*** MycoBank MB 839285.
Synonym: *Diaporthe durionigena* L.D. Thao *et al.*, *Persoonia* **44**: 385. 2020, *nom. inval*. Art. 40.8 (Shenzhen).

Diagnosis: See *Persoonia* **44**: 385. 2020 (Crous *et al.* 2020c).

Typus: **Vietnam**, Central Highlands, Dak Lak, on branches of *Durio zibethinus* (*Malvaceae*), Dec. 2018, *L.D. Thao* (**holotype** specimen VTCC 930005, preserved as metabolically inactive culture, culture ex-type KCSR1812.8 = VTCC 930005).

Note: *Diaporthe durionigena* is herewith validated, as the original description did not state that the holotype was preserved as a metabolically inactive culture.

Authors: L.D. Thao, L.T. Hien, N.V. Liem, H.M. Thanh & T.N. Khanh

Endoconidioma euphorbiae Crous, *Persoonia* **45**: 301. 2020. Fig. 24.

Description and illustration: Crous *et al.* (2020a).

Material examined: **South Africa**, Western Cape Province, Nieuwoudtville, tip dieback on *Euphorbia mauritanica* (*Euphorbiaceae*), 2018, *P.W. Crous*, HPC 3069, culture CPC 38649.

Notes: *Endoconidioma euphorbiae* is a morphologically highly variable fungus commonly associated with leaf spots and dieback on *Brunsvigia* and *Euphorbia* (Crous *et al*. 2020a), and easily confused with *E. leucospermi* on *Proteaceae* (Taylor & Crous 2001, Crous *et al*. 2013a).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Endoconidioma euphorbiae* (strain CPC 38551, GenBank MW175350.1; Identities = 590/590 (100 %), no gaps), *Endoconidioma leucospermi* (as *Coniozyma leucospermi*; strain CBS 111289, GenBank EU552113.1; Identities = 577/590 (98 %), four gaps (0 %)), and *Hormonema carpetanum* (strain 235J14, GenBank KU516485.1; Identities = 561/574 (98 %), four gaps (0 %)). Closest hits using the **LSU** sequence are *Endoconidioma euphorbiae* (strain CPC 38551, GenBank MW175390.1; Identities = 840/840 (100 %), no gaps), *Endoconidioma leucospermi* (as *Coniozyma leucospermi*; strain CBS 111289, GenBank EU552113.1; Identities = 836/841 (99 %), no gaps), and *Hormonema carpetanum* (strain ATCC 74360, GenBank MF611880.1; Identities = 835/841 (99 %), no gaps) – also see Fig. 1. Closest hits using the ***rpb2*** sequence had highest similarity to *Hormonema carpetanum* (strain ATCC 74360, GenBank MF611881.1; Identities = 830/938 (88 %), three gaps (0 %)), *Dothidea sambuci* (strain CBS 198.58, GenBank KT216559.1; Identities = 768/945 (81 %), 17 gaps (1 %)), and *Dothidea insculpta* (strain CBS 189.58, GenBank AF107800.1; Identities = 761/944 (81 %), 15 gaps (1 %)). Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Hormonema carpetanum* (strain ATCC 74360, GenBank MF611882.1; Identities = 441/468 (94 %), no gaps), *Alternaria septospora* (strain CBS 109.38, GenBank JQ672442.1; Identities = 436/469 (93 %), two gaps (0 %)), and *Alternaria smyrnii* (strain EGS 37-093, GenBank JQ672454.1; Identities = 435/469 (93 %), two gaps (0 %)). No significant hits were obtained when the ***actA*** and ***tub2*** sequences were used in blastn and megablast searches.

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

Flammocladiella anomiae Lechat & J. Fourn., Ascomycete.org **11**(6): 239. 2019. Fig. 25.

Fig. 24. *Endoconidioma euphorbiae* (CPC 38649). **A.** Colony sporulating on OA. **B–C.** Conidiogenous cells. **D.** Conidia. Scale bars = 10 µm.

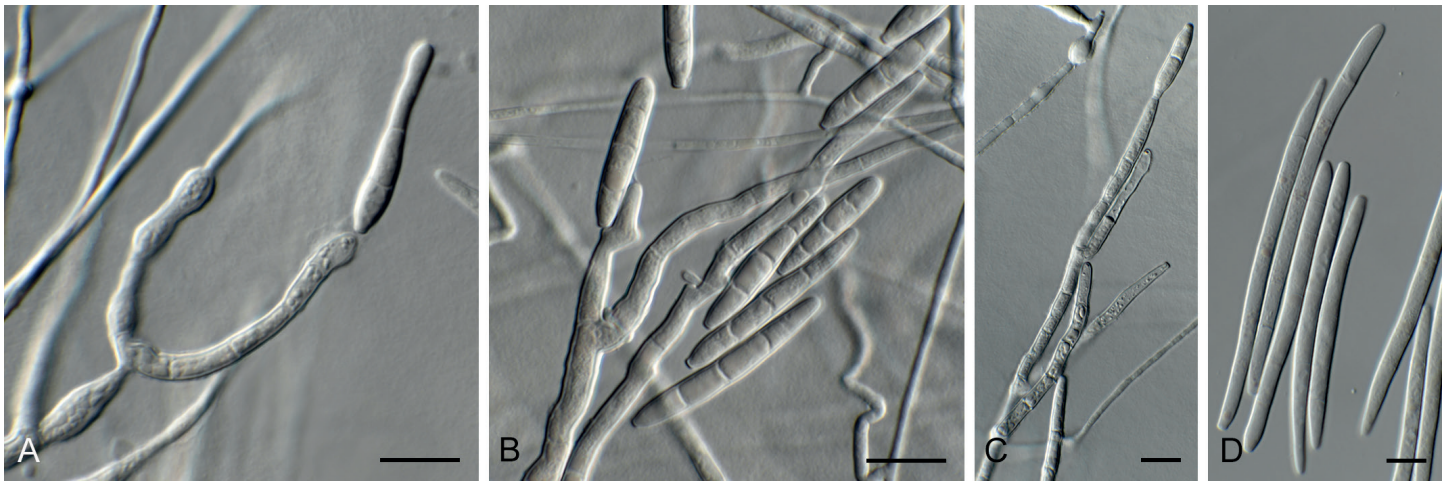

Fig. 25. *Flammocladiella anomiae* (CPC 36302). **A–C.** Conidiogenous cells giving rise to conidia. **D.** Conidia. Scale bars = 10 µm.

On SNA. *Mycelium* consisting of hyaline, smooth, branched, septate, 2.5–3 µm diam hyphae. *Conidiophores* solitary or aggregated into orange sporodochia. *Conidiophores* hyaline, smooth, multiseptate, branched, subcylindrical, 30–130 × 4–5 µm. *Conidiogenous cells* terminal and intercalary, 10–55 × 3–4 µm, proliferating sympodially, scars truncate, 2–3 µm diam. *Conidia* solitary, hyaline, smooth, granular to guttulate, straight to slightly curved, subcylindrical to narrowly obclavate, apex obtuse to subobtuse, base truncate, 1.5–2 µm diam, (1–)3-septate, (20–)30–35(–45) × (3.5–)4–5 µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 10 mm diam (on MEA and PDA), 20 mm diam on OA after 2 wk at 25 °C. On MEA surface salmon to dirty white, reverse ochreous; on PDA surface salmon, reverse saffron; on OA surface salmon.

Material examined: **Ukraine**, Okhtyrka district, NNP Hetmanskyi, Sumska Dibrova, Klymentove village, dead branch of *Robinia pseudoacacia* (*Fabaceae*), occurring on conidiomata of *Diaporthe oncostoma*, 5 Aug. 2019, *A. Akulov*, HPC 2529, CWU AS 6855 (CBS H-24358, culture CPC 36302 = CBS 146685).

Notes: According to Voglmayr & Jaklitsch (2011), *Massaria* spp. are highly host-specific, with *M. anomia* being the only species occurring on *Fabaceae* (on ascomata of *Massaria anomia* on a branchlet of *Robinia pseudoacacia*). Lechat *et al.* (2019) speculated that *F. anomiae* is host-specific on *Massaria anomia*. In this regard, collecting *M. anomiae* on conidiomata of *Diaporthe oncostoma* is unusual, although the host plant was also a dead branch of *Robinia pseudoacacia*, suggesting some association with the host. The possibility exists that ascomata of *M. anomia* were poorly developed, and therefore not seen at the time of isolation. On MEA cultures formed large orange sporodochia, with conidia becoming longer and thinner, subcylindrical, apex obtuse, base truncate, 1.5–2 µm, flexuous, up to 8-septate, (50–)65–75(–80) × 3–4 µm. Conidia of *Flammocladiella anomiae* are reported to be smaller, namely 1–3-septate, smooth, (30–) 37–45(–48) × 2–2.5 µm (Lechat *et al.* 2019).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Flammocladiella anomiae* (as *Flammocladiella* sp. CL-2019a; voucher JF17087, GenBank MN597423.1; Identities = 522/524 (99 %), no gaps), *Ijuhya vitellina* (strain DSM 104494, GenBank NR_154100.1; Identities = 522/584 (90 %), 19 gaps (3 %)), and *Ijuhya corynospora* (strain CBS 342.77, GenBank KY607539.1; Identities = 525/588 (89 %), 27 gaps (4 %)). Closest hits using the **LSU** sequence are *Flammocladiella anomiae* (as *Flammocladiella* sp. CL-2019a; voucher CLL16017, GenBank MN597426.1; Identities = 846/846 (100 %), no gaps), *Flammocladiella aceris* (strain CBS 138906, GenBank NG_058175.1; Identities = 816/830 (98 %), no gaps), and *Ijuhya parilis* (strain CBS 136677, GenBank KY607558.1; Identities = 824/846 (97 %), no gaps) – also see Fig. 4. The ***tef1*** sequence generated in this study is identical to those of *Flammocladiella anomiae* generated for CBS 144256 and CBS 142775 (464/464 and 342/342, respectively). The ***tub2*** sequence generated in this study is also identical to that of *Flammocladiella anomiae* strain CBS 144256 (526/526).

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

Floricola juncicola Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB 839286. Fig. 26.

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

Conidiomata pycnidial, separate, globose, dark brown with central ostiole, 180–200 µm diam. *Peridium* multi-layered, inner layers hyaline, outer layers brownish. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, subcylindrical to doliiform, hyaline to pale brown, smooth to finely roughened, proliferating percurrently at apex, at times bifurcate at apex, with two loci, 5–15 × 3–4 µm. *Conidia* solitary, subcylindrical, apex subobtuse, tapering in lower third to truncate, unthickened hilum, 2–3 µm diam, olive to yellow-brown, with 1-2 different sized guttules per cell, with longitudinal striations covering the length of conidial body, ornamentation partially branched, (0–)3(–5)-septate *in vitro*, 7–10-septate, with septa golden, thick-walled and constricted *in vivo*, (48–)55–65(–80) × (5–)6(–7) µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 25 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse isabelline in centre, cinnamon in outer region; on PDA

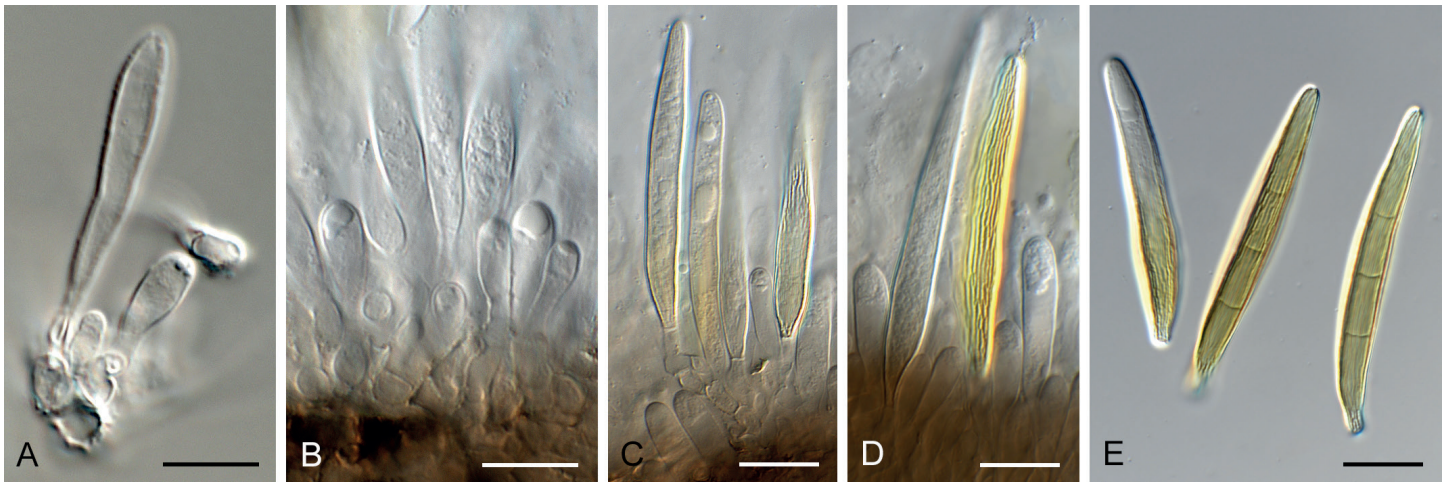

Fig. 26. *Floricola juncicola* (CPC 38197). **A–D.** Conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars = 10 µm.

surface dirty white, reverse olivaceous grey; on OA surface olivaceous grey.

Typus: **France**, La-Chaise-Dieu, on dead culm of *Juncus* sp. (*Juncaceae*), 24 Apr. 2019, *A. Gardiennet*, HPC 2970 = RKS 252 = AG19065 (**holotype** CBS H-24406, culture ex-type CPC 38197 = CBS 146811).

Notes: Jaklitsch *et al.* (2016) regarded several genera with aposphaeria-, coniothyrium-, or phoma-like asexual morphs as synonyms of *Teichospora*, presenting a new concept of a large, morphologically diverse genus representing the *Teichosporaceae*. This approach was however rejected by Boonmee *et al*. (2019), who recognised 14 genera in the family. *Floricola juncicola* clusters in the *Teichosporaceae*, being allied to *Floricola clematidis* (conidia 13–21 × 5–7 µm), from which it is distinct based on its conidial morphology. This also distinguishes it from other taxa in the genus (Phukhamsakda *et al.* 2020). A phylogenetic tree is presented as Fig. 27.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Teichospora mariae* (strain C134m, GenBank KU601580.1; Identities = 530/591 (90 %), 19 gaps (3 %)), *Floricola clematidis* (as *Teichospora* sp. CP-2020b; strain MFLUCC 17-2182, GenBank MT310638.1; Identities = 451/481 (94 %), five gaps (1 %)), and *Teichospora kingiae* (strain CPC 29104, GenBank NR_154656.1; Identities = 508/567 (90 %), 17 gaps (2 %)). Closest hits using the **LSU** sequence are *Paulkirkia arundinis* (as *Teichosporaceae* sp. DW-2016a; strain MFLUCC 12-0328, GenBank KU848206.1; Identities = 872/894 (98 %), three gaps (0 %)), *Floricola clematidis* (as *Teichospora* sp. CP-2020b; strain MFLUCC 17-2182, GenBank MT214594.1; Identities = 855/877 (97 %), two gaps (0 %)), and *Teichospora kingiae* (strain CPC 29104, GenBank NG_059761.1; Identities = 782/804 (97 %), two gaps (0 %)) – also see Fig. 1. No significant hits were obtained when the ***tef1*** (first part) sequence was used in blastn and megablast searches. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Ramusculicola thailandica* (as *Teichospora thailandica*; strain MFLUCC 17-2093, GenBank MT394653.1; Identities = 840/908 (93 %), five gaps (0 %)), *Rhytidhysteron rufulum* (voucher MFLU 18-2190, GenBank MK360087.1; Identities = 847/918 (92 %), six gaps (0 %)), and *Ramusculicola clematidis* (strain MFLUCC 17-2146, GenBank MT394652.1; Identities = 830/905 (92 %), five gaps (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Teichospora mariae* (strain C136, GenBank KU601595.1; Identities = 558/648 (86 %), two gaps (0 %)), *Teichospora striata* (strain JK 5678I, GenBank GU371758.1; Identities = 493/610 (81 %), four gaps (0 %)), and *Cenococcum geophilum* (strain OS21018, GenBank LC095396.1; Identities = 291/368 (79 %), six gaps (1 %)).

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

Harzia tenella (Berk. & M.A. Curtis) D.W. Li & N.P. Schultes, *Fung. Biol.* **121**: 900. 2017. Fig. 28.
Basionym: *Rhinotrichum tenellum* Berk. & M.A. Curtis, *Grevillea* **3** (27): 109. 1875.

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

Material examined: **South Africa**, Western Cape Province, Nieuwoudtville, on stems of *Grielum humifusum* (*Neuradaceae*), 2018, *P.W. Crous*, HPC 3043, culture CPC 38667.

Notes: In a study by Schultes *et al*. (2017), *Harzia* (1888) was shown to have priority over *Olpitrichum* (1894) and *Chlamydomyces* (1907), leading to the new combination *H. tenella*, which is here reported from *Grielum humifusum* in South Africa.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Harzia tenella* (as *Olpitrichum tenellum*; strain CBS 121.81, GenBank KY628696.1; Identities = 605/607 (99 %), no gaps), *Harzia verrucosa* (strain CBS 113456, GenBank KY628674.1; Identities = 604/607 (99 %), one gap (0 %)), and *Harzia patula* (strain CBS 379.88, GenBank NR_161009.1; Identities = 602/608 (99 %), one gap (0 %)). Closest hits using the **LSU** sequence are *Harzia macrospora* (strain CBS 343.67, GenBank MH870687.1; Identities = 841/841 (100 %), no gaps), *Harzia verrucosa* (strain CBS 113456, GenBank KY628675.1; Identities = 841/841 (100 %), no gaps), and *Harzia acremonioides* (strain CBS 101.42, GenBank NG_067322.1; Identities = 841/841 (100 %), no gaps) – also see Fig. 5.

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

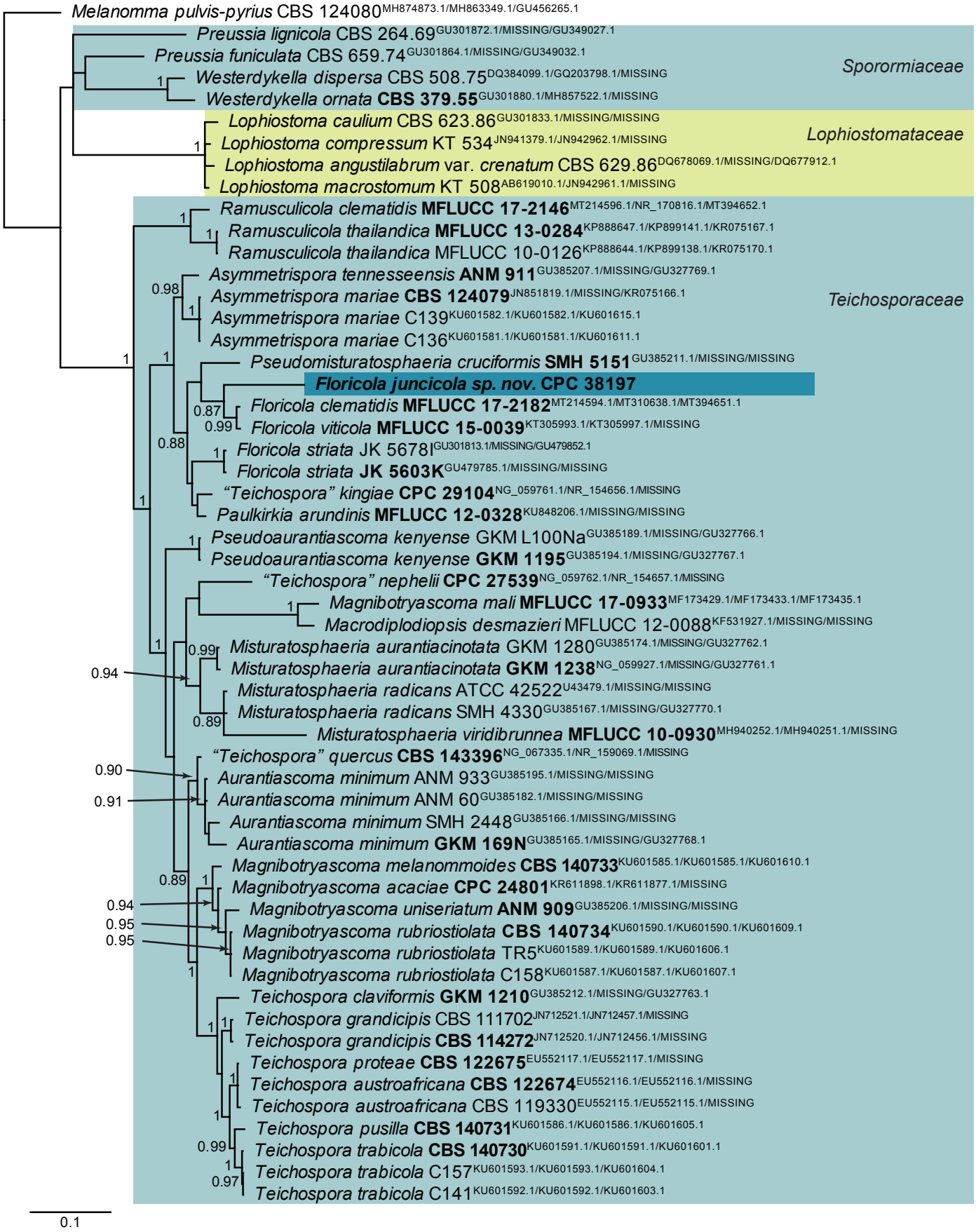

Fig. 27. Consensus phylogram (50 % majority rule) resulting from a Bayesian analysis of the *Teichosporaceae* multigene (LSU / ITS / *tef1*) nucleotide alignment. Bayesian posterior probabilities (> 0.79) are shown at the nodes and the scale bar represents the expected changes per site. Families are indicated with coloured blocks to the right of the tree. GenBank accession (superscript) and / or culture collection / voucher numbers (in bold face when having a type status) are indicated for all species. The tree was rooted to *Melanomma pulvis-pyrius* (culture CBS 124080) and the novel species treated in this study is indicated in a coloured block and bold face. Alignment statistics: 55 strains including the outgroup; 200, 315 and 359 unique site patterns, respectively. Tree statistics: 403 502 sampled trees from 1 345 000 generations.

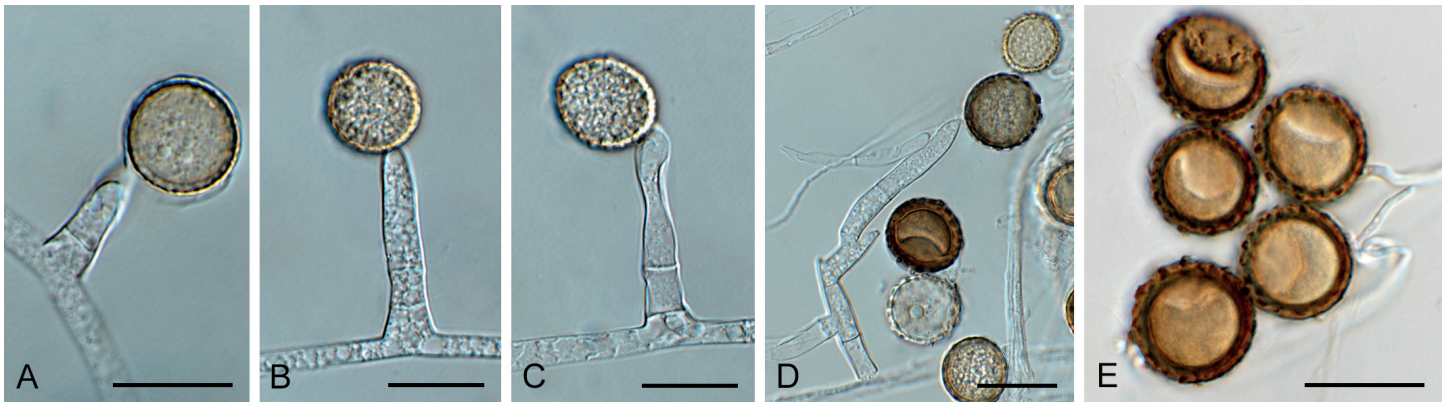

Fig. 28. *Harzia tenella* (CPC 38667). **A–D.** Conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars = 10 µm.

Haudseptoria Crous & R.K. Schumach., ***gen. nov.*** MycoBank MB 839287.

Etymology: Name refers to the fact that it is morphologically similar to *Septoria*.

Conidiomata pycnidial, erumpent to semi-superficial, dark brown, globose, with central ostiole; wall in upper region of brown *textura angularis*, in lower region of pale brown cells, concolourous with host tissue. *Conidiophores* reduced to conidiogenous cells, ampulliform to subcylindrical, smooth, proliferating sympodially at apex. *Conidia* solitary, hyaline, smooth, guttulate, subcylindrical, apex subobtuse, base truncate, transversely 1–7-septate.

Type species: *Haudseptoria typhae* Crous & R.K. Schumach.

Haudseptoria typhae Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB 839288. Fig. 29.

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

Conidiomata erumpent to semi-superficial, dark brown, globose, 100–150 µm diam with central ostiole, 10–15 µm diam; wall in upper region of brown *textura angularis*, in lower region of pale brown cells, concolourous with host tissue. *Conidiophores* reduced to conidiogenous cells, ampulliform to subcylindrical, smooth, 5–12 × 2–3 µm, proliferating sympodially at apex. *Conidia* solitary, hyaline, smooth, guttulate, subcylindrical, apex subobtuse, base truncate, filiform, straight to slightly curved, (1–)3-septate, septa thin-walled, (16–)20–23(–27) × 2(–2.5) µm *in vivo*; 35–90 × 3 µm, 3–7-septate *in vitro*.

Culture characteristics: Colonies erumpent, spreading, with sparse aerial mycelium and smooth, even margin, reaching 12 mm diam after 2 wk at 25 °C. On MEA surface buff, reverse cinnamon; on PDA surface cinnamon, reverse honey with patches of cinnamon; on OA surface buff.

Typus: **Germany**, near Berlin, moist meadow, on dead leaf sheath of *Typha* sp. (*Typhaceae*), 17 Apr. 2019, *R.K. Schumacher*, HPC 2978 = RKS 249 (**holotype** CBS H-24407, culture ex-type CPC 38203 = CBS 146790).

Notes: *Haudseptoria* represents a new septoria-like genus (Verkley *et al.* 2013) related to *Pseudopassalora gouriqua* (hyphomycete on *Protea suzannae*, South Africa; Crous *et al.* 2011), and *Phellinocrescentia guianensis* (coelomycete with aseptate conidia, on polypores in French Guiana; Crous *et al.* 2014).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Didymosphaeria futilis* (strain CMW 22186, GenBank EU552123.1; Identities = 487/521 (93 %), 13 gaps (2 %)), *Italiofungus phillyreae* (strain CPC 35566, GenBank MT223804.1; Identities = 446/499 (89 %), 16 gaps (3 %)), and *Funbolia dimorpha* (strain CPC 14170, GenBank JF951136.1;

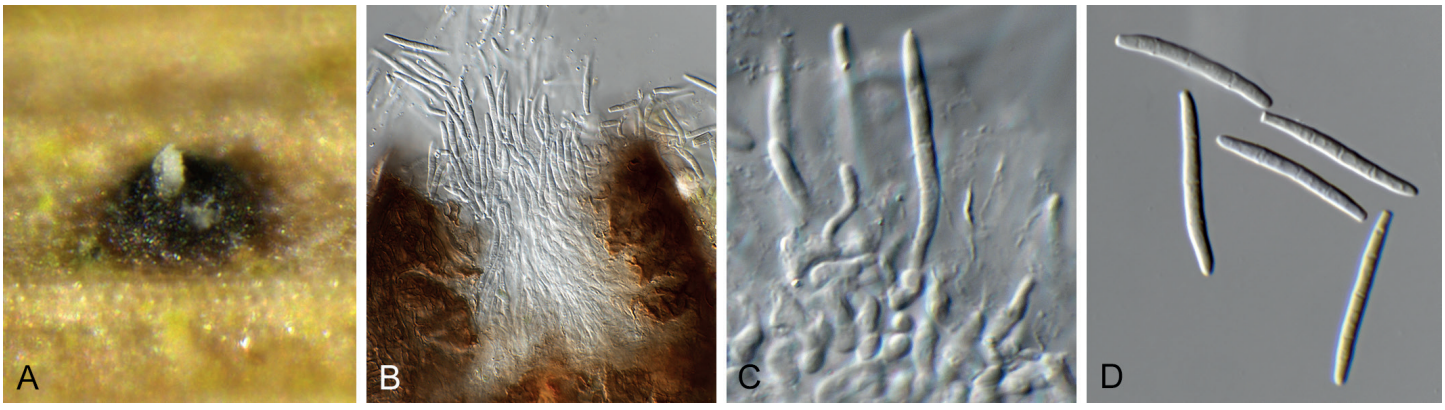

Fig. 29. *Haudseptoria typhae* (CPC 38203). **A.** Conidioma on host tissue. **B.** Conidiomatal ostiole. **C.** Conidiogenous cells giving rise to conidia. **D.** Conidia. Scale bars: A = 150 µm, all others = 10 µm.

Identities = 405/467 (87 %), 18 gaps (3 %)). Closest hits using the **LSU** sequence are *Pseudopassalora gouriqua* (strain CBS 101954, GenBank NG_067272.1; Identities = 785/808 (97 %), no gaps), *Italiofungus phillyreae* (strain CPC 35566, GenBank MT223899.1; Identities = 784/808 (97 %), no gaps), and *Eriomyces heveae* (strain MFLUCC 17-2232, GenBank MH109524.1; Identities = 779/810 (96 %), two gaps (0 %)) – also see Fig. 1. No significant hits were obtained when the ***tub2*** sequence was used in blastn and megablast searches.

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

Heimiodora verticillata Nicot, *Ann. Sci. Nat.*, Bot. Biol. Vég., sér. **12**: 384. 1960. Fig. 30.

Description and illustration: See Nicot & Parguey (1960).

Material examined: **Namibia**, Walvis Bay, on *Salvadora persica* (*Salvadoraceae*), 20 Nov. 2019, *P.W. Crous*, HPC 3120, CBS H-24533, cultures CPC 39015 = CBS 147089.

Notes: *Heimiodora verticillata* was originally isolated from sandy coastal soil in Thailand (Nicot & Parguey 1960; ex-type CBS 201.60), and its ecology has remained rather obscure. Isolating the same fungus from twig litter of a *Salvadora persica* growing on the dry desert coast in Walvis Bay, Namibia, suggests that this fungus could prefer a dry arid environment. A specimen of this fungus has also been reported from fallen leaves of a *Salvadora* sp. growing in Kasur, Pakistan (BPI 1100673). The host, *Salvadora*, is known to occur in dry environments, which could give a hint to the ecology of *H. verticillata*. The ITS and LSU sequences of CPC 39015 are a perfect match to those of the ex-type culture (CBS 201.60; GenBank MH857955.1; 554/554 (100 %), no gaps, and GenBank MH869505.1; 833/833 (100 %), no gaps, respectively) – also see Fig. 4.

Authors: P.W. Crous, D.A. Cowan, G. Maggs-Kölling, E. Marais, N. Yilmaz & M.J. Wingfield

Hogelandia Hern.-Restr., ***gen. nov.*** MycoBank MB 838707.

Etymology: Named after the school where the sample was collected, Het Hogeland College (Warffum, the Netherlands). This sample was collected during a Citizen Science project of the Westerdijk Fungal Biodiversity Institute.

Vegetative hyphae hyaline, septate, smooth. *Conidiophores* micronematous, mostly reduced to conidiogenous cells. *Conidiogenous cells* monoblastic, subcylindrical, smooth, hyaline. Secession rhexolytic. *Conidia* hyaline, smooth, thick-walled, globose to subglobose, sometimes in short chains, base with a cylindrical to cuneiform cell.

Type species: *Hogelandia lambearum* Hern.-Restr.

Hogelandia lambearum Hern.-Restr., ***sp. nov.*** MycoBank MB 838708. Fig. 31.

Etymology: Name includes the initials of the collectors Lara Alssema and Meike van Berkel, students from Het Hogeland College (Warffum, the Netherlands). This sample was collected during a Citizen Science project of the Westerdijk Fungal Biodiversity Institute.

Vegetative hyphae hyaline, septate, smooth, 1.5–4 µm. *Conidiophores* micronematous, mostly reduced to conidiogenous cells. *Conidiogenous cells* monoblastic, subcylindrical, smooth, hyaline, 5–10.5 × 2–3 µm. Secession rhexolytic. *Conidia* hyaline, smooth, thick-walled, globose to subglobose, sometimes in short chains, 8–14 µm diam, base with a cylindrical to cuneiform cell.

Culture characteristics: After 1 wk at 25 °C on OA reaching 52 mm diam, zonate, cottony, white, with moderate aerial mycelium and glabrous zones at the centre, margin entire, regular. On MEA reaching 53 mm diam, zonate, white, margin regular, reverse ochreous.

Typus: **Netherlands**, Groningen Province, Warffum, Het Hogeland College, from soil, 6 Jun. 2019, *L. Alssema & M. van Berkel*, NL19_027 (**holotype** CBS H-24733, culture ex-type CBS 147626 = NL19_27007).

Notes: *Hogelandia* is phylogenetically related to *Ascodesmis*, *Eleutherascus* and *Cephaliophora* in *Pezizomycetes* (Fig. 3). Species of these genera are also found in soil and dung samples (Guarro *et al.* 2012). Members of *Ascodesmis*, *Eleutherascus*

Fig. 30. *Heimiodora verticillata* (CPC 39015). **A.** Sporulation on SNA. **B.** Setae. **C.** Chlamydospores. **D–E.** Conidiogenous cells. **F.** Conidia. Scale bars = 10 µm.

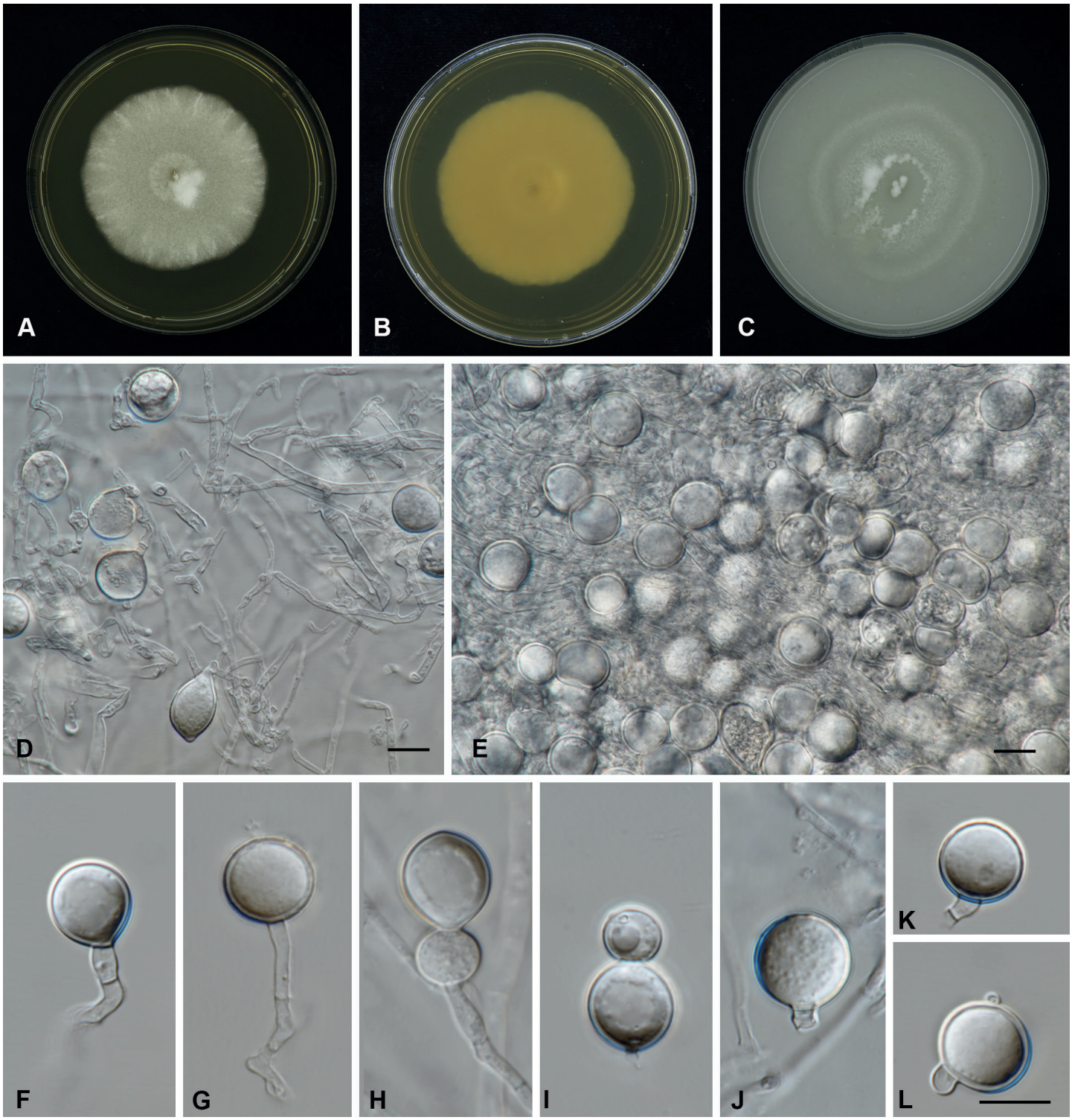

Fig. 31. *Hogelandia lambearum* (CBS 147626). **A–B.** Colony on MEA. **C.** Colony on OA. **D–E.** Mycelium and conidia. **F–H.** Conidiogenous cells and conidia. **I–L.** Conidia. Scale bars D–E, L = 10 µm. L applies to F–L.

and *Cephaliophora* are all described as sexual morphs, except for *E. tuberculata* that was described with a sporothrix- or calcarisporium-like asexual morph, characterised by erect and branched conidiophores with polyblastic conidiogenous cells that produce ellipsoidal conidia, 8.5–12.5 × 5–7.5 µm (Samson & Luiten 1975). *Hogelandia* is represented only by the asexual morph, characterised by micronematous conidiophores, monoblastic conidiogenous cells and subglobose conidia. Attempts to induce the sexual morph *in vitro* were unsuccessful.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cephaliophora* sp. (strain TD4, GenBank KY814682.1; Identities = 476/508 (94 %), five gaps (0 %)), *Cephaliophora tropica* (strain GN-HA-1-3, GenBank MG554311.1; Identities = 340/369 (92 %), six gaps (1 %)), and *Cephaliophora tropica* (strain JB-NW-1-1, GenBank MG554299.1; Identities = 333/365 (91 %), five gaps (1 %)). Closest hits using the **LSU** sequence are *Ascodesmis nigricans* (strain CBS 163.74, GenBank MH872582.1; Identities = 810/825 (98 %), no gaps), *Ascodesmis microscopica* (strain CBS 275.80, GenBank MH873032.1; Identities = 809/825 (98 %), no gaps), and *Ascodesmis sphaerospora* (strain CBS 125.61, GenBank MH869550.1; Identities = 809/825 (98 %), no gaps) – also see Fig. 3.

Author: M. Hernández-Restrepo

Lomentospora valparaisensis E. Álvarez, ***sp. nov.*** MycoBank MB 839289.
Synonym: *Lomentospora valparaisensis* E. Álvarez, *Persoonia* **40**: 299. 2018. *Nom. inval.*, Art. 40.7 (Shenzhen).

Diagnosis: See *Persoonia* **40**: 299. 2018 (Crous *et al.* 2018b).

Typus: **Chile**, Valparaiso, Italy Park, from soil, 2016, *F. Salas* (**holotype** specimen ChFC 2018164, culture ex-type ChFC-164).

Note: *Lomentospora valparaisensis* is validated here because the original description cited an incorrect acronym for the holotype specimen.

Author: E. Álvarez Duarte

Muyocopron zamiae Hern.-Restr. & Crous, *Persoonia* **42**: 219. 2019. Fig. 32.

Mycelium consisting of branched, septate, dark to pale brown, verruculose, 2–3 µm diam hyphae. *Conidiomata* sporodochium-like, superficial on agar, medium brown, consisting of a few aggregated cells to large round aggregations of conidiogenous cells. *Conidiogenous cells* globose to ampulliform, 12–20 × 9–12 µm, with distinct flared collarette, 3–6 µm diam, medium to dark brown, smooth. *Conidia* aseptate, lunate, fusoid, curved, guttulate, (17–)18–22(–25) × (4.5–)6(–6.5) µm, with a filiform, unbranched appendage at each end, (2–)7–11 µm long, hyaline, smooth. *Appressoria* and *sexual morph* not observed.

Culture characteristics: Colonies flat, spreading, with sparse to moderate aerial mycelium and feathery, lobate margin, covering dish after 2 wk at 25 °C. On MEA surface buff to honey, reverse isabelline; on PDA surface honey, reverse isabelline; on OA surface honey to isabelline.

Material examined: **USA**, Florida, Gainesville, on leaves of *Zamia integrifolia* (*Zamiaceae*), 28 Feb. 2018, *M.J. Wingfield*, HPC 2794, CBS H-24348, culture CPC 37461 = CBS 146636.

Notes: *Muyocopron zamiae* was described from leaves of *Zamia fisheri* collected in Florida, USA (Hernández-Restrepo *et al*. 2019). The collection in this study (on *Zamia integrifolia*), was also made in Florida, and represents the second known collection for this species, which seems to be common on leaves of *Zamia* spp.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Muyocopron zamiae* (strain CBS 203.71, Present study; Identities = 520/522 (99 %), no gaps), *Muyocopron coloratum* (strain CBS 720.95, GenBank NR_160197.1; Identities = 297/306 (97 %), one gap (0 %)), and *Fimetariella rabenhorstii* (strain A27_ITS-1, GenBank MN447419.1; Identities = 449/465 (97 %), two gaps (0 %)). Closest hits using the **LSU** sequence are *Muyocopron zamiae* (strain CBS 203.71, GenBank NG_066338.1; Identities = 837/837 (100 %), no gaps), *Muyocopron geniculatum* (strain CBS 721.95, GenBank NG_066266.1; Identities = 834/838 (99 %), one gap (0 %)), and *Muyocopron chromolaenae* (strain MFLUCC 17-1513, GenBank NG_068700.1; Identities = 823/834 (99 %), two gaps (0 %)) – also see Fig. 1. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Muyocopron zamiae* (strain CBS 203.71, GenBank MK495973.1; Identities = 460/460 (100 %), no gaps), *Muyocopron atromaculans* (strain MUCL 34983, GenBank MK495957.1; Identities = 441/460 (96 %), no gaps), and *Mycoleptodiscus terrestris* (strain IMI 159038, GenBank MK495977.1; Identities = 439/460 (95 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Muyocopron zamiae* (strain CBS 203.71, GenBank MK492731.1;

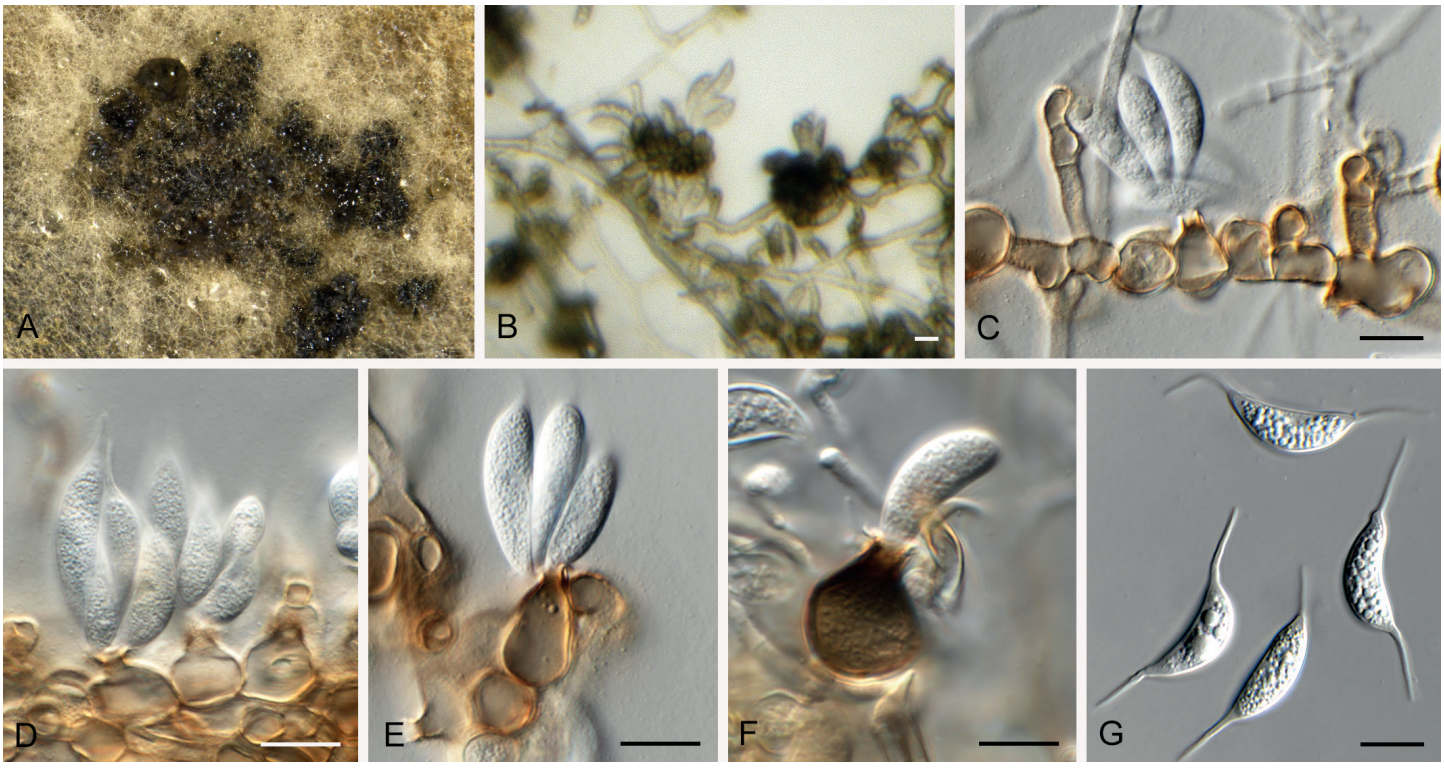

Fig. 32. *Muyocopron zamiae* (CPC 37461). **A.** Colony sporulating on OA. **B–F.** Conidiogenous cells giving rise to conidia. **G.** Conidia. Scale bars = 10 µm.

Identities = 846/846 (100 %), no gaps), *Muyocopron geniculatum* (strain CBS 721.95, GenBank MK492715.1; Identities = 761/822 (93 %), three gaps (0 %)), and *Muyocopron chromolaenae* (strain MFLUCC 17-1513, GenBank MT136761.1; Identities = 508/569 (89 %), no gaps).

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

Neocamarosporium leipoldtiae Crous, *Persoonia* **45**: 295. 2020. Fig. 33.

Conidiomata globose, brown, 200–300 µm diam, immersed, becoming erumpent with central ostiole; wall of 3–6 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* hyaline, smooth, ampulliform, proliferating percurrently at apex, 8–12 × 5–7 µm. *Conidia* solitary, medium brown, thick-walled, muriformly septate, obovoid to ellipsoid, finely roughened, thick-walled; with 3–4 horizontal septa, and 3–6 vertical or oblique septa, (13–)16–18(–20) × (9–)10–11(–12) µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, even margin, covering dish after 2 wk at 25 °C. On MEA surface and reverse sepia; on PDA surface isabelline, reverse hazel; on OA surface sepia.

Material examined: **South Africa**, Western Cape Province, Clanwilliam, Rocklands camp grounds, on leaves of *Cephalophyllum pilansii* (*Aizoaceae*), 2018, *P.W. Crous*, HPC 3055 (CBS H-24421, culture CPC 38543 = CBS 146812).

Notes: *Neocamarosporium leipoldtiae* was recently introduced for a species occurring on leaves of *Leipoldtia schultzii* in South Africa (Crous *et al.* 2020a). The collection in this study originated from the same region of the Western Cape Province, where it was isolated from leaves of *Cephalophyllum pilansii.*

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neocamarosporium* sp. (strain CF-288928, GenBank MG065823.1; Identities = 536/548 (98 %), one gap (0 %)), *Neocamarosporium salicornicola* (strain ZMCS3, GenBank MK809918.1; Identities = 512/524 (98 %), two gaps (0 %)), and *Dimorphosporicola tragani* (strain ZMCL7, GenBank MK809922.1; Identities = 510/523 (98 %), one gap (0 %)). Closest hits using the **LSU** sequence are *Neocamarosporium chichastianum* (strain IBRC-M 30126, GenBank KP004483.1; Identities = 811/815 (99 %), no gaps), *Neocamarosporium salicornicola* (strain MFLUCC 15-0957, GenBank NG_070423.1; Identities = 808/813 (99 %), no gaps), and *Neocamarosporium chersinae* (strain CPC 27298, GenBank KY929182.1; Identities = 799/804 (99 %), no gaps) – also see Fig. 1. Closest hits using the ***tef1*** sequence had highest similarity to *Dimorphosporicola tragani* (strain CBS 570.85, GenBank KU728577.1; Identities = 406/458 (89 %), ten gaps (2 %)), *Ulocladium alternariae* (strain P292, GenBank AY375370.1; Identities = 335/383 (87 %), seven gaps (1 %)), and *Alternaria japonica* (strain P400, GenBank AY375367.1; Identities = 332/384 (86 %), eight gaps (2 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Dimorphosporicola tragani* (strain CBS 570.85, GenBank KU728616.1; Identities = 305/329 (93 %), one gap (0 %)), *Dothidotthia robiniae* (as *Dothidotthia* sp. CS-2019b; strain MFLUCC 18-0692, GenBank MK933790.1; Identities = 293/331 (89 %), ten gaps (3 %)), and *Tamaricicola* sp. (strain IG114, GenBank MH001474.1; Identities = 292/331 (88 %), six gaps (1 %)).

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

Neofusicoccum mystacidii Crous, ***sp. nov.*** MycoBank MB 839290. Fig. 34.

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

On PNA. *Conidiomata* globose, erumpent, brown, pycnidial, with central ostiole, punctiform, 200–300 µm diam; wall of 6–8 layers of brown *textura angularis. Macroconidiophores* reduced to conidiogenous cells, or at times with a supporting cell, lining the inner cavity of conidioma, hyaline, smooth, subcylindrical, proliferating percurrently at apex, encased in mucoid sheath, 10–25 × 4–5 µm. *Macroconidia* aseptate, solitary, hyaline, smooth, guttulate, straight, broadly cylindrical, apex obtuse, tapering in bottom part to truncate hilum, 3–4 µm diam, with

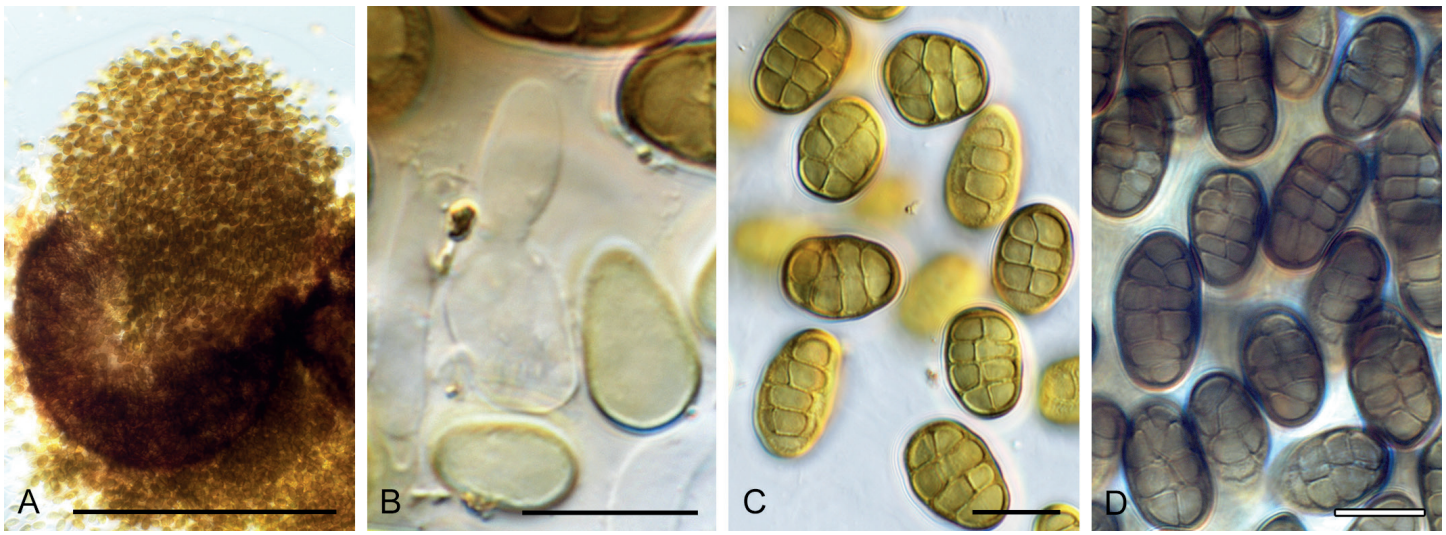

Fig. 33. *Neocamarosporium leipoldtiae* (CPC 38543). **A.** Conidioma on SNA. **B.** Conidiogenous cell giving rise to conidia. **C–D.** Conidia. Scale bars: A = 300 µm, all others = 10 µm.

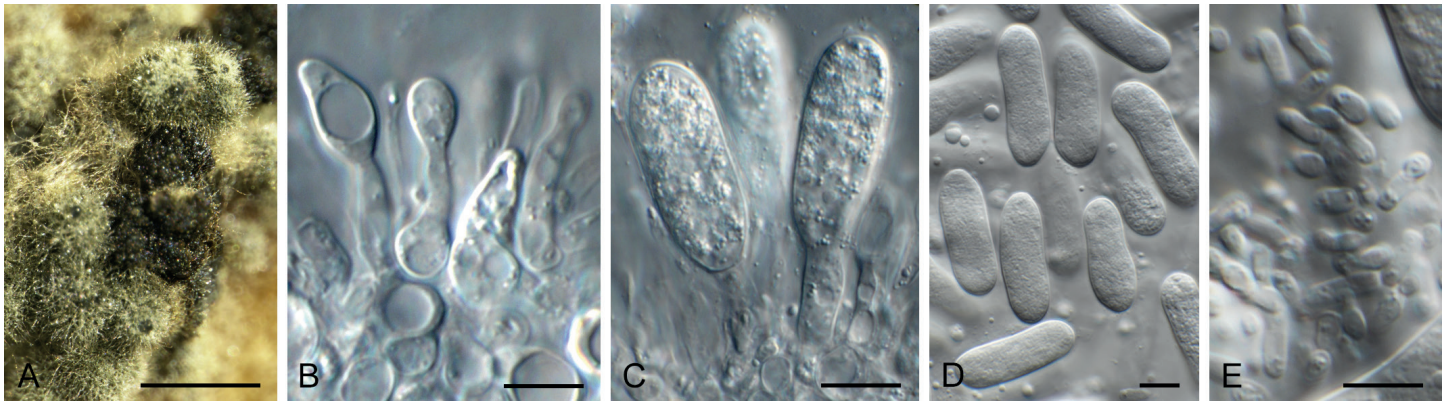

Fig. 34. *Neofusicoccum mystacidii* (CPC 39221). **A.** Sporulation on PDA. **B–C.** Conidiogenous cells. **D.** Macroconidia. **E.** Microconidia. Scale bars: A = 300 µm, all others = 10 µm.

minute marginal frill, encased in mucoid sheath, (26–)28–30(–35) × (9–)10(–11) µm. *Microconidiophores* mixed among macroconidiophores, subcylindrical, hyaline smooth, 5–12 × 3–4 µm, phialidic with periclinal thickening. *Microconidia* solitary, aseptate, subcylindrical with obtuse ends, hyaline, smooth, 3–6 × 2.5–3 µm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus: **South Africa**, Northern Province, Nelspruit, Lowveld Botanical Garden, on dead stems of *Mystacidium capense* (*Orchidaceae*), 23 Nov. 2018, *P.W. Crous*, HPC 3141 (**holotype** CBS H-24546, culture ex-type CPC 39221 = CBS 147079).

Notes: Conidiomata of *N. mystacidii* had slightly elongated necks *in vivo*, and conidia were also encased in a mucoid sheath, both characters that are not typically associated with members of *Neofusicoccum* (Phillips *et al*. 2013, Zhang *et al*. 2021a), and not observed *in vitro*. *Neofusicoccum mystacidii* is related to species such as *N. cryptoaustrale* (conidia (18–)20.5–21(–26.5) × 5–6(–6.5) µm; Crous *et al.* 2013b), *N. nonquaesitum* (conidia 17–29 × 5.5–10.5 µm; Phillips *et al.* 2013), *N. mediterraneum* (conidia (19–)22–26(–27) × (5.5–)6(–6.5) µm; Phillips *et al.* 2013) and *N. vitifusiforme* (conidia (9–)9.5–13(–14.5) × (6.5–)8–10.5(–11) µm; Phillips *et al.* 2013), species that are morphologically quite distinct. A phylogenetic species tree is presented as Fig. 35.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neofusicoccum corticosae* (now *Neofusicoccum vitifusiforme*; strain CBS 120081, GenBank MN161920.1; Identities = 542/556 (97 %), no gaps), *Neofusicoccum vitifusiforme* (strain CAP227, GenBank EF638785.1; Identities = 542/556 (97 %), no gaps), and *Neofusicoccum hellenicum* (strain CERC1959, GenBank KP217057.1; Identities = 532/547 (97 %), no gaps). Closest hits using the **LSU** sequence are *Neofusicoccum nonquaesitum* (strain CBS 126655, GenBank MH875645.1; Identities = 877/886 (99 %), no gaps), *Neofusicoccum arbuti* (strain CBS 117090, GenBank DQ377919.1; Identities = 877/886 (99 %), no gaps), and *Neofusicoccum mangiferae* (strain CBS 118532, GenBank NG_055730.1; Identities = 876/886 (99 %), no gaps) – also see Fig. 1. Closest hits using the ***gapdh*** sequence had highest similarity to *Neofusicoccum mediterraneum* (strain PD312, GenBank GU251440.1; Identities = 492/497 (99 %), no gaps), *Neofusicoccum parvum* (strain JPZZP4, GenBank KY009944.1; Identities = 512/530 (97 %), one gap (0 %)), and *Neofusicoccum australe* (strain PD253, GenBank GU251483.1; Identities = 485/497 (98 %), one gap (0 %)). Closest hits using the ***his3*** sequence had highest similarity to *Neofusicoccum mediterraneum* (strain PD311, GenBank GU251571.1; Identities = 306/309 (99 %), no gaps), *Neofusicoccum parvum* (strain PD6, GenBank GU251525.1; Identities = 303/309 (98 %), no gaps), and *Neofusicoccum australe* (strain PD253, GenBank GU251615.1; Identities = 302/309 (98 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Neofusicoccum terminaliae* (strain CBS 125263, GenBank KX464045.1; Identities = 388/391 (99 %), no gaps), *Neofusicoccum mediterraneum* (strain CBS 121718, GenBank KY855815.1; Identities = 387/391 (99 %), no gaps), and *Neofusicoccum ursorum* (strain CBS 122811, GenBank KX464047.1; Identities = 386/391 (99 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Neofusicoccum mediterraneum* (strain BAL-17, GenBank KX029198.1; Identities = 383/390 (98 %), no gaps), *Neofusicoccum vitifusiforme* (strain CMW875, GenBank HM176519.1; Identities = 385/393 (98 %), two gaps (0 %)), and *Neofusicoccum luteum* (strain CMW42482, GenBank KP860705.1; Identities = 363/373 (97 %), two gaps (0 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Neofusicoccum parvum* (strain CCF216, GenBank KC507808.1; Identities = 573/587 (98 %), no gaps), *Neofusicoccum australe* (strain CUZF10AV1, GenBank KU836639.1; Identities = 558/572 (98 %), one gap (0 %)), and *Neofusicoccum mangiferae* (strain wbhs2, GenBank KY435929.1; Identities = 567/587 (97 %), two gaps (0 %)).

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

Neomycosphaerella guibourtiae Crous & Jol. Roux, ***sp. nov.*** MycoBank MB 839291. Fig. 36.

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

Leaf spots amphigenous, irregular, brown with raised brown border, up to 10 mm diam. *Ascomata* hypophyllous, immersed, becoming erumpent, but remaining immersed under epidermis, brown, globose, 70–90 µm diam, with central ostiole, slightly papillate, up to 25 µm diam, periphysate; wall of 4–6 layers of brown *textura angularis*. *Asci* stipitate, fasciculate, obovoid, hyaline, smooth, bitunicate, 8-spored, apical chamber 1 µm diam, 32–38 × 8–10 µm. *Ascospores* tri- to multiseriate,

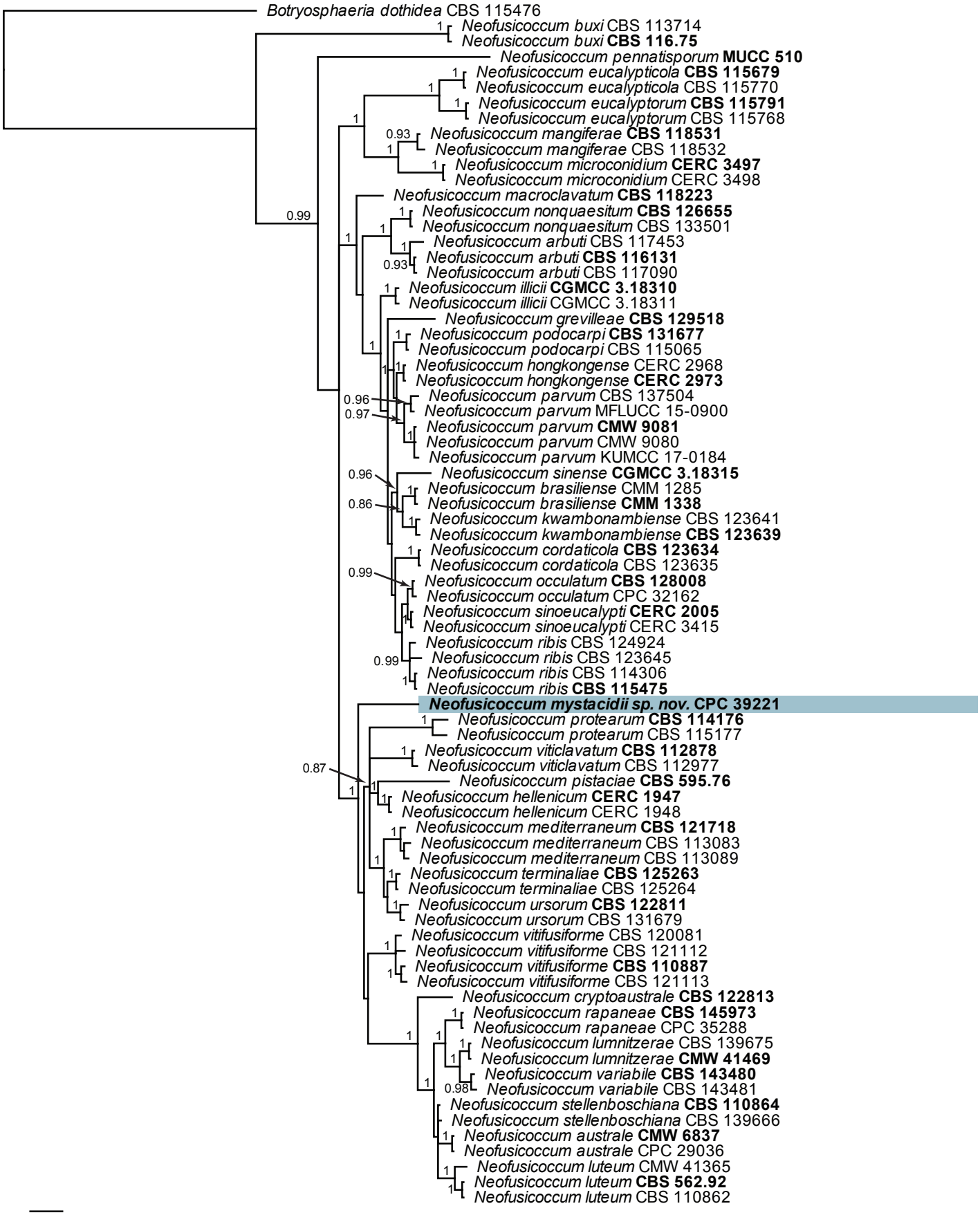

Fig. 35. Consensus phylogram (50 % majority rule) resulting from a Bayesian analysis of the *Neofusicoccum* multigene (ITS / *tef1* / *tub2* / *rpb2*) nucleotide alignment. The alignment is derived from Zhang *et al*. (2021) and GenBank accession numbers and partition models can be found in that study. Bayesian posterior probabilities (> 0.79) are shown at the nodes and the scale bar represents the expected changes per site. Culture collection numbers in bold face represent cultures with a type status. The tree was rooted to *Botryosphaeria dothidea* (culture CBS 115476) and the novel species treated in this study is indicated in a coloured block and bold face. Alignment statistics: 78 strains including the outgroup; 119 / 159 / 110 / 146 unique site patterns, respectively. Tree statistics: 49 502 sampled trees from 1 650 000 generations.

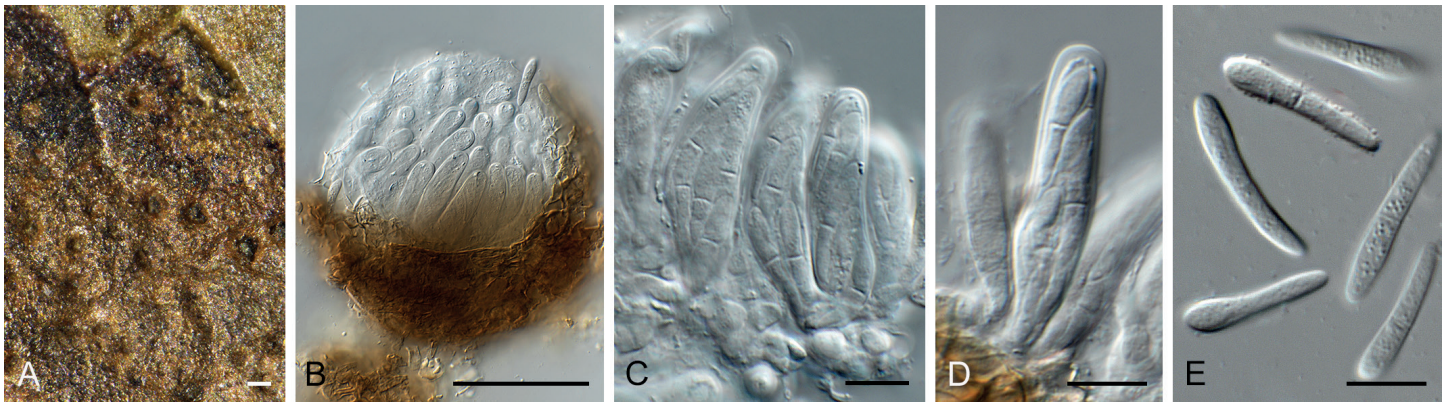

Fig. 36. *Neomycosphaerella guibourtiae* (CPC 39348). **A.** Ascomata immersed on host tissue. **B.** Ascoma. **C–D.** Asci. **E.** Ascospores. Scale bars: A–B = 90 µm, all others = 10 µm.

fusoid-ellipsoid, widest in middle of apical cell which can be asymmetrical, basal cell obtusely rounded, medianly 1-septate, not constricted at septum, guttulate to granular, (14–)16–18(–20) × (3–)3.5(–4) µm.

Culture characteristics: Colonies erumpent, spreading, surface folded, with sparse aerial mycelium and smooth, lobate margin, reaching 5–7 mm diam after 2 wk at 25 °C. On MEA and PDA surface pale olivaceous grey, reverse olivaceous grey; on OA surface ochreous in centre, pale olivaceous grey in outer region.

Typus: **Angola**, Cuanavale Source Lake, Fairy forest, on leaves of *Guibourtia* sp. (*Fabaceae*), 27 Nov. 2015, *J. Roux*, HPC 3242 (**holotype** CBS H-24551, culture ex-type CPC 39348 = CBS 147083.

Notes: *Neomycosphaerella guibourtiae* is closely related to *Neomycosphaerella pseudopentameridis* [from *Pseudopentameris macrantha* (*Poaceae*), South Africa; Crous *et al*. 2013b, Videira *et al.* 2017]. Morphologically they are quire distinct, however, in that ascospores of *N. pseudopentameridis* [(15–)16–17(–18) × (3.5–)4(–5) µm] are shorter and wider than those of *N. guibourtiae.* A phylogenetic species tree is presented as Fig. 37.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Hyalozasmidium aerohyalinosporum* (strain CBS 125011, GenBank NR_156220.1; Identities = 484/532 (91 %), 19 gaps (3 %)), *Mycosphaerella medusae* (strain BRIP 52586, GenBank NR_137044.1; Identities = 467/514 (91 %), 20 gaps (3 %)), *Madagascaromyces intermedius* (strain CBS 124154, GenBank MH863356.1; Identities = 488/538 (91 %), 20 gaps (3 %)), and *Paramycosphaerella dicranopteridis* (strain TNM 3953, GenBank NR_155639.1; Identities = 479/535 (90 %), 19 gaps (3 %)). Closest hits using the **LSU** sequence are *Paramycosphaerella brachystegiae* (strain CBS 136436, GenBank NG_058048.1; Identities = 850/860 (99 %), no gaps), *Paramycosphaerella marksii* (strain CPC 11222, GenBank GU214447.1; Identities = 850/860 (99 %), no gaps), and *Paramycosphaerella watsoniae* (strain CPC 37392, GenBank NG_068339.1; Identities = 831/841 (99 %), no gaps) – also see Fig. 1. Closest hits using the ***actA*** sequence had highest similarity to *Paramycosphaerella watsoniae* (strain CBS 146064, GenBank MN556790.1; Identities = 554/608 (91 %), 15 gaps (2 %)), *Mycosphaerella musae* (strain CIRADCOK 003, GenBank MW070786.1; Identities = 542/596 (91 %), seven gaps (1 %)), and *Hyalozasmidium aerohyalinosporum* (strain CBS 125011, GenBank KF903576.1; Identities = 497/544 (91 %), 15 gaps (2 %)). Distant hits obtained using the ***cmdA*** sequence had highest similarity to *Nowamyces piperitae* (strain CPC 32372, GenBank MN162565.1; Identities = 286/308 (93 %), no gaps), *Zasmidium pseudoparkii* (strain CBS 111049, GenBank KF902695.1; Identities = 281/301 (93 %), no gaps), and *Zasmidium corymbiae* (strain CBS 145049, GenBank MK047526.1; Identities = 281/305 (92 %), no gaps). Distant hits obtained using the ***tef1*** sequence had highest similarity to *Microcyclosporella mali* (strain CPC 16177, GenBank HM177418.1; Identities = 334/434 (77 %), 51 gaps (11 %)), *Cercospora zeae-maydis* (strain CBS 132678, GenBank JX143502.1; Identities = 208/243 (86 %), five gaps (2 %)), and *Pseudocercospora eucalyptorum* (strain CPC 35905, GenBank MN162363.1; Identities = 219/266 (82 %), 18 gaps (6 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Paramycosphaerella intermedia* (strain CBS 114356, GenBank KF902845.1; Identities = 290/342 (85 %), 12 gaps (3 %)), *Paramycosphaerella marksii* (strain CBS 110920, GenBank KF902848.1; Identities = 292/345 (85 %), 18 gaps (5 %)), and *Hyalozasmidium aerohyalinosporum* (strain CBS 125011, GenBank KF903073.1; Identities = 289/345 (84 %), 16 gaps (4 %)).

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

Neoscirrhia Crous & R.K. Schumach., ***gen. nov.*** MycoBank MB 839292.

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

Ascomata pseudothecial, gregarious, stromatic, immersed, becoming erumpent, opening by longitudinal split of epidermis, arranged parallel to the culm axis, black, thick- and smooth-walled, multi-locular, loculi in one row and one level, globose, black, soft, ostiole central, indistinct. *Peridium* multi-layered, of *textura angularis-prismatica*, inner layers hyaline, outer layers dark brown. *Pseudoparaphyses* numerous, partly evanescent, multi-celled, moniliform to cylindrical, branched, anastomosing. *Asci* 8-spored, subclavate to cylindrical, apically rounded with ocular chamber, pedicel short, broad and furcate, bitunicate, fissitunicate. *Ascospores* straight to slightly curved, cells cylindrical, ends rounded, upper cell enlarged towards median

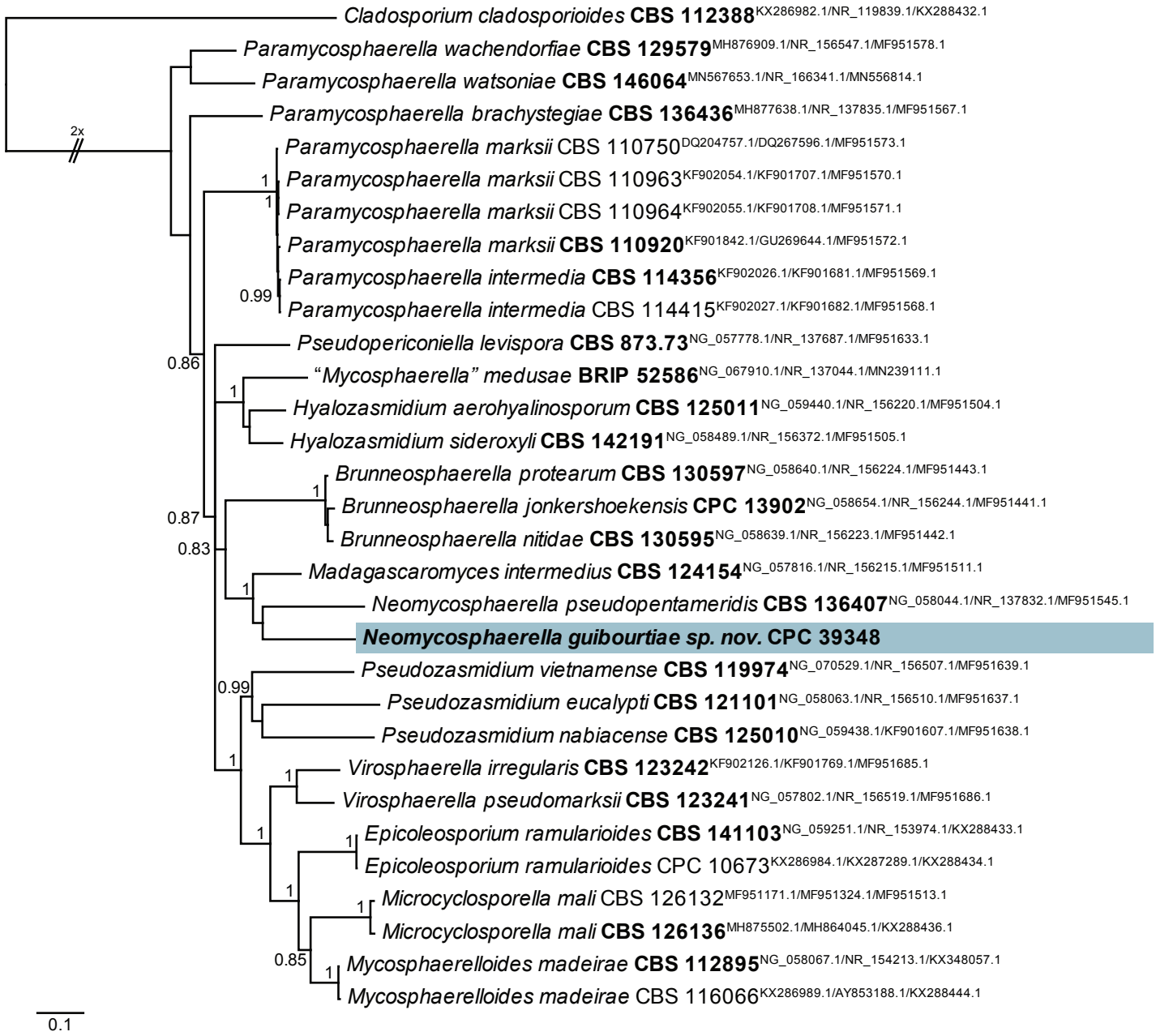

Fig. 37. Consensus phylogram (50 % majority rule) resulting from a Bayesian analysis of the *Mycosphaerellaceae* multigene (LSU / ITS / *rpb2*) nucleotide alignment. The alignment is derived from the alignment of Videira *et al*. (2017) and partition models can be found in that study. Bayesian posterior probabilities (> 0.79) are shown at the nodes and the scale bar represents the expected changes per site. The most basal branch was halved to facilitate layout. GenBank accession (superscript) and / or culture collection / voucher numbers (in bold face when having a type status) are indicated for all species. The tree was rooted to *Cladosporium cladosporioides* (culture CBS 112388) and the novel species treated in this study is indicated in a coloured block and bold face. Alignment statistics: 31 strains including the outgroup; 80 / 214 / 459 unique site patterns, respectively. Tree statistics: 192 002 sampled trees from 640 000 generations.

septum, at times with lateral swelling just above the septum hyaline, thin- and smooth-walled, constricted at septum, cytoplasm aggregated in middle region, causing ends to appear very thick-walled, apex more prominently so than basal end. *Conidiomata* pycnidial, globose, brown, with central ostiole; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining inner cavity, hyaline, smooth, doliiform to ampulliform, phialidic. *Conidia* solitary, hyaline, smooth, prominently guttulate, medianly 1-septate, subcylindrical to obovoid, ends obtuse.

Type species: *Neoscirrhia osmundae* (Peck & Clinton) Crous & R.K. Schumach.

Neoscirrhia osmundae (Peck & Clinton) Crous & R.K. Schumach., ***comb. nov.*** MycoBank MB 839293. Fig. 38.

Basionym: *Dothidea osmundae* Peck & Clinton, *Rep. (Annual) New York State Mus. Nat. Hist.* **30**: 64. 1878. (1877)

Synonyms: *Scirrhia osmundae* (Peck & Clinton) Arx, in Müller & von Arx, *Beitr. Kryptfl. Schweiz* **11**(no. 2): 382. 1962.

Metameris osmundae (Peck & Clinton) Arx & E. Müll., *Stud. Mycol.* **9**: 80. 1975.

Scirrhia osmundae (Peck & Clinton) L. Holm & K. Holm, *Bot. Notiser* **131**: 112. 1978, an isonym, see Art. 6.3 Note 2.

Ascomata pseudothecial, saprobic, gregarious, stromatic, immersed, becoming erumpent, opening by longitudinal split of epidermis,

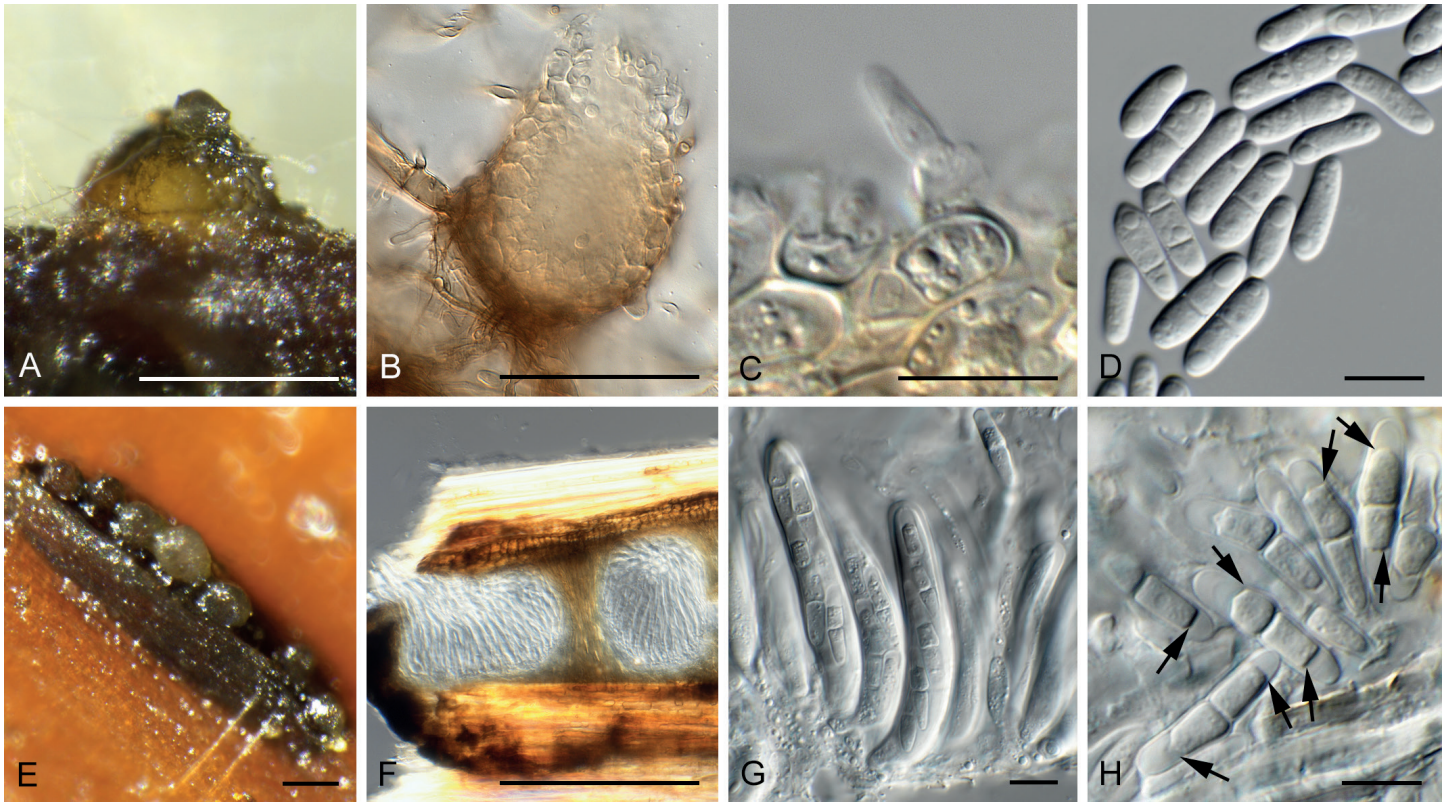

Fig. 38. *Neoscirrhia osmundae* (CPC 38085). **A.** Conidioma on PNA. **B.** Conidioma with ostiole. **C.** Conidiogenous cells. **D.** Conidia. **E–F.** Ascomata on host tissue. **G.** Asci. **H.** Ascospores (arrows indicate apical thickenings). Scale bars: A = 300 µm, B, F = 200 µm, E = 180 µm, all others = 10 µm.

arranged parallel to the culm axis, black, thick- and smooth-walled, multi-locular, loculi in one row and one level, globose, black, soft, ostiole central, indistinct, up to 180 × 200 µm. *Peridium* multi-layered, of *textura angularis-prismatica*, inner layers hyaline, outer layers dark brown. *Pseudoparaphyses* numerous, partly evanescent, multi-celled, moniliform to cylindrical, branched, anastomosing. *Asci* 8-spored, subclavate to cylindrical, apically rounded with ocular chamber, pedicel short, broad and furcate, bitunicate, fissitunicate, 71–82 × 8.5–11.5 µm, ascospores obliquely biseriate. *Ascospores* straight to slightly curved, cells cylindrical, ends rounded, upper cell enlarged towards median septum, at times with lateral swelling just above the septum hyaline, thin- and smooth-walled, constricted at septum, cytoplasm aggregated in middle region, causing ends to appear very thick-walled, apex more prominently so than basal end, enclosed in mucilaginous sheath when immature (in water), 15.5–21.5 × 4–5 µm. *Conidiomata* pycnidial, globose, 250–300 µm diam, brown, with central ostiole, 30–40 µm diam, solitary on SNA, aggregated on OA; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining inner cavity, hyaline, smooth, doliiform to ampulliform, phialidic, 5–7 × 5–6 µm. *Conidia* solitary, hyaline, smooth, prominently guttulate, medianly 1-septate, subcylindrical to obovoid, ends obtuse, (10–)12–14(–15) × (4–)4.5(–5) µm.

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

Material examined: **Netherlands**, Noord-Holland Province, Hoofddorp, on culms of *Sasa veitchii* (*Poaceae*), 18 May 2019, *L. van der Linde*, HPC 2956 = RKS 1103 (CBS H-24397, culture CPC 38085 = CBS 146803).

Notes: *Scirrhia* is based on *S. rimosa*, a species known from stems of *Phragmites australis* (*Poaceae*) collected in Europe. No culture was available so far and therefore the phylogenetic affinities were unresolved. *Scirrhia brasiliensis* is a morphologically similar species, recently described (on fronds of *Pteridium aquilinum*) in Brazil. It was shown to cluster in *Mycosphaerellaceae* (Crous *et al*. 2011), a family which type, *S. rimosa*, is expected to also belong to *Schirrhia s.str.* It is, however, quite distinct from *S. osmundae*, which has a different ascospore morphology (see below), and clusters in *Didymellaceae.*

Scirrhia osmundae was described from dead stems of *Osmunda* collected in New York, USA. Ascospores are 2-celled, but appear 3-celled due to the contraction of the protoplast in the upper cell. This phenomenon was misinterpreted by Theissen & Sydow (1915) as 3-celled ascospores. It is quite characteristic in mature ascospores, and was also observed by Holm & Holm (1978), and in the present study. Based on Holm & Holm (1978) and Obrist (1959), stromata are larger in European collections, and ascospores are 15–18 × 4 µm (15.5–21.5 × 4–5 µm in the present specimen).

Metameris japonica (from Japan) represents another possible synonym of *S. osmundae*. *Scirrhia osmundae* was first reported from Europe (Germany) by Theissen & Sydow (1915), while Obrist (1959) reported it from Switzerland, and Holm & Holm (1978) reported it from Sweden. The collection in this study appears to be the first record from the Netherlands.

Phoma matteuccicola is commonly known as a pathogen causing leaf blight and "gangrene" of fern species (De Gruyter *et al.* 2002). Because it is allied to *Neoscirrhia osmundae*, it is herewith placed in this genus.

Neoscirrhia matteucciicola (Aderkas *et al.*) Crous, ***comb. nov.*** MycoBank MB 839294.
Basionym: *Phoma matteucciicola* Aderkas *et al.*, *Canad. J. Pl. Pathol*. **14**: 227. 1992.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 38085 had highest similarity to *Microsphaeropsis olivacea* (strain CBS 432.71, GenBank MH871969.1; Identities = 526/540 (97 %), two gaps (0 %)), *Coniothyrium euonymi-japonicae* (strain CBS 302.68, GenBank MH859134.1; Identities = 526/540 (97 %), two gaps (0 %)), *Coniothyrium glomerulatum* (strain CBS 113.21, GenBank MH854688.1; Identities = 526/540 (97 %), two gaps (0 %)), and *Neoscirrhia matteucciicola* (as *Phoma matteucciicola*; strain CBS 259.92, GenBank GU237812.1; Identities = 470/484 (97 %), one gap (0 %)). Closest hits using the **LSU** sequence of CPC 38085 are *Faurelina indica* (strain CBS 301.78, GenBank GU180654.1; Identities = 903/910 (99 %), no gaps), *Microsphaeropsis ononidicola* (strain MFLUCC 15-0459, GenBank MG967668.1; Identities = 895/906 (99 %), no gaps), *Coniothyrium hellebori* (strain CBS 519.78, GenBank MH872934.1; Identities = 895/907 (99 %), no gaps), and *Neoscirrhia matteucciicola* (as *Phoma matteuciicola*; strain CBS 259.92, GenBank GU238100.1; Identities = 870/877 (99 %), no gaps) – also see Fig. 1. Closest hits using the ***rpb2*** sequence of CPC 38085 had highest similarity to *Neomicrosphaeropsis juglandis* (strain MFLUCC 18-0795, GenBank MN593307.1; Identities = 773/882 (88 %), no gaps), *Paraboeremia selaginellae* (strain CBS 122.93, GenBank LT623255.1; Identities = 783/896 (87 %), two gaps (0 %)), and *Ascochyta herbicola* (voucher MFLU 15-2126, GenBank MT432200.1; Identities = 768/879 (87 %), two gaps (0 %)). Closest hits using the ***tub2*** sequence of CPC 38085 had highest similarity to *Neoscirrhia matteucciicola* (as *Phoma matteuciicola*; strain CBS 259.92, GenBank GU237627.1; Identities = 264/289 (91 %), four gaps (1 %)), *Didymella rabiei* (strain AR628, GenBank KM244529.1; Identities = 488/547 (89 %), ten gaps (1 %)), *Epicoccum sorghinum* (strain HM19B, GenBank MN562463.1; Identities = 469/523 (90 %), nine gaps (1 %)), and *Boeremia exigua* (strain Ph.ex.001NY17, GenBank MK514090.1; Identities = 484/546 (89 %), 11 gaps (2 %)).

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

Neoscytalidium dimidiatum (Penz.) Crous & Slippers, *Stud. Mycol.* **55**: 244. 2006. Fig. 39.
Basionym: *Torula dimidiata* Penz., *Michelia* **2**(no. 8): 466. 1887.

Conidiomata pycnidial, solitary, brown, erect, globose, 250–300 µm diam, with central ostiole and slightly papillate beak; wall of 4–8 layers of brown *textura angularis. Conidiophores* subcylindrical, hyaline, smooth, lining inner cavity, 0–2-septate, unbranched, 10–22 × 3.5–4.5 µm. *Conidiogenous cells* integrated, hyaline, smooth, subcylindrical, proliferating percurrently at apex, 8–12 × 3–3.5 µm. *Conidia* solitary, aseptate, hyaline, smooth, finely guttulate, subcylindrical to fusoid-ellipsoid, apex subobtuse, base truncate, 2 µm diam, (12–)13–14(–15) × (3.5–)4(–5) µm. *Synasexual morph* forming conidia via disarticulation of hyphal fragments, pale to medium brown, smooth, subcylindrical with truncate ends, 0(–1)-septate, 5–10(–12) × 3–5 µm.

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

Material examined: **South Africa**, Western Cape Province, Nieuwoudtville, epiphyte on stems of *Aloidendron dichotomum* (*Asphodeloideae*), 2018, *P.W. Crous*, HPC 3038 (CBS H-24434, culture CPC 38666 = CBS 146816).

Notes: *Neoscytalidium dimidiatum* is associated with tree cankers (Polizzi *et al.* 2011) but also causes chronic dermatomycosis and onychomycosis in humans, mainly involving foot infections (Dionne *et al*. 2015, Zhang *et al.* 2021a). *Neoscytalidium dimidiatum* is here newly reported from *Aloidendron dichotomum* in South Africa. Zhang *et al*. (2021a) recognised *N. dimidiatum* as the only species known from molecular data in this genus and also reduced two other species (*N. novaehollandiae* and *N. orchidacearum*) to synonyms of *N. dimidiatum*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *N. novaehollandiae* (now *N. dimidiatum*; strain CBS 122071, GenBank KF766207.1; Identities = 565/565 (100 %), no gaps), *N. hyalinum* (now *N. dimidiatum*; strain CBS 125699, GenBank MH863613.1; Identities = 563/563 (100 %), no gaps), and *N. dimidiatum* (voucher INBio 30A, GenBank KU204558.1; Identities = 555/557 (99 %), no gaps). Closest hits using the **LSU** sequence are *N. novaehollandiae* (now *N. dimidiatum*; strain CMW 26170, GenBank NG_059496.1; Identities = 872/872 (100 %), no gaps), *N. hyalinum* (now *N. dimidiatum*; strain CBS 125699, GenBank MH875087.1; Identities = 881/882 (99 %), one gap (0 %)), and *N. orchidacearum* (as Neoscytalidium sp. SKH-2016, now *N. dimidiatum*; strain MFLUCC 12-0533, GenBank KU179864.1; Identities = 869/871 (99 %), no gaps) – also see Fig. 1. Closest hits using the ***chs-1*** sequence had highest similarity to *N. hyalinum* (as *Scytalidium hyalinum*, now *N. dimidiatum*; strain FMR 8342, GenBank FM211193.1; Identities = 284/284 (100 %), no gaps), *N. dimidiatum* (strain CBS 380.36, GenBank FM211196.1; Identities = 283/284 (99 %), no gaps), and *N. novaehollandiae* (now *N. dimidiatum*; strain D16GHEI, GenBank MH793720.1; Identities = 249/250 (99 %), no gaps). Closest hits using the ***tub2*** sequence had highest similarity to *N. novaehollandiae* (now *N. dimidiatum*; strain Mlty_Ma02, GenBank MT362603.1; Identities = 278/278 (100 %), no gaps), *N. dimidiatum* (strain CBS 125695, GenBank KX464764.1; Identities = 426/427 (99 %), no gaps), and *N. hyalinum* (now *N. dimidiatum*; strain IRNHM-KZN1, GenBank MG220380.1; Identities = 420/422 (99 %), no gaps).

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

Niesslia neoexosporioides Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB 839295. Fig. 40.

Etymology: Name refers to the fact that it is similar to *Niesslia exosporioides*.

Ascomata perithecial, saprobic, single, gregarious, superficial, globose with a small, flattened base, black-brown, soft, thin-walled, setose, up to 100 µm diam. *Setae* stiff, pointed, unbranched, base enlarged or simple furcate, black, red-brown under the lens, thick- and smooth-walled, lumen tight. *Peridium* few-layered, of *textura epidermoidea* with red-brown, thick-walled and smooth cells. *Paraphyses* absent. *Asci* 8-spored,

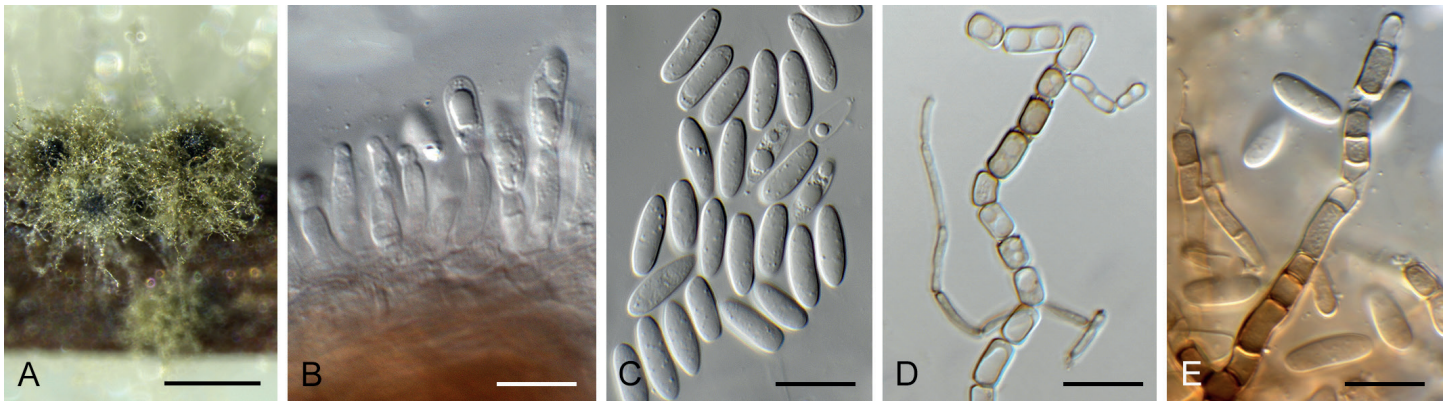

Fig. 39. *Neoscytalidium dimidiatum* (CPC 38666). **A.** Conidiomata on PNA. **B.** Conidiogenous cells. **C.** Fusicoccum-like condia. **D–E.** Phragmoconidia, with a few fusicoccum-like conidia. Scale bars = 10 µm.

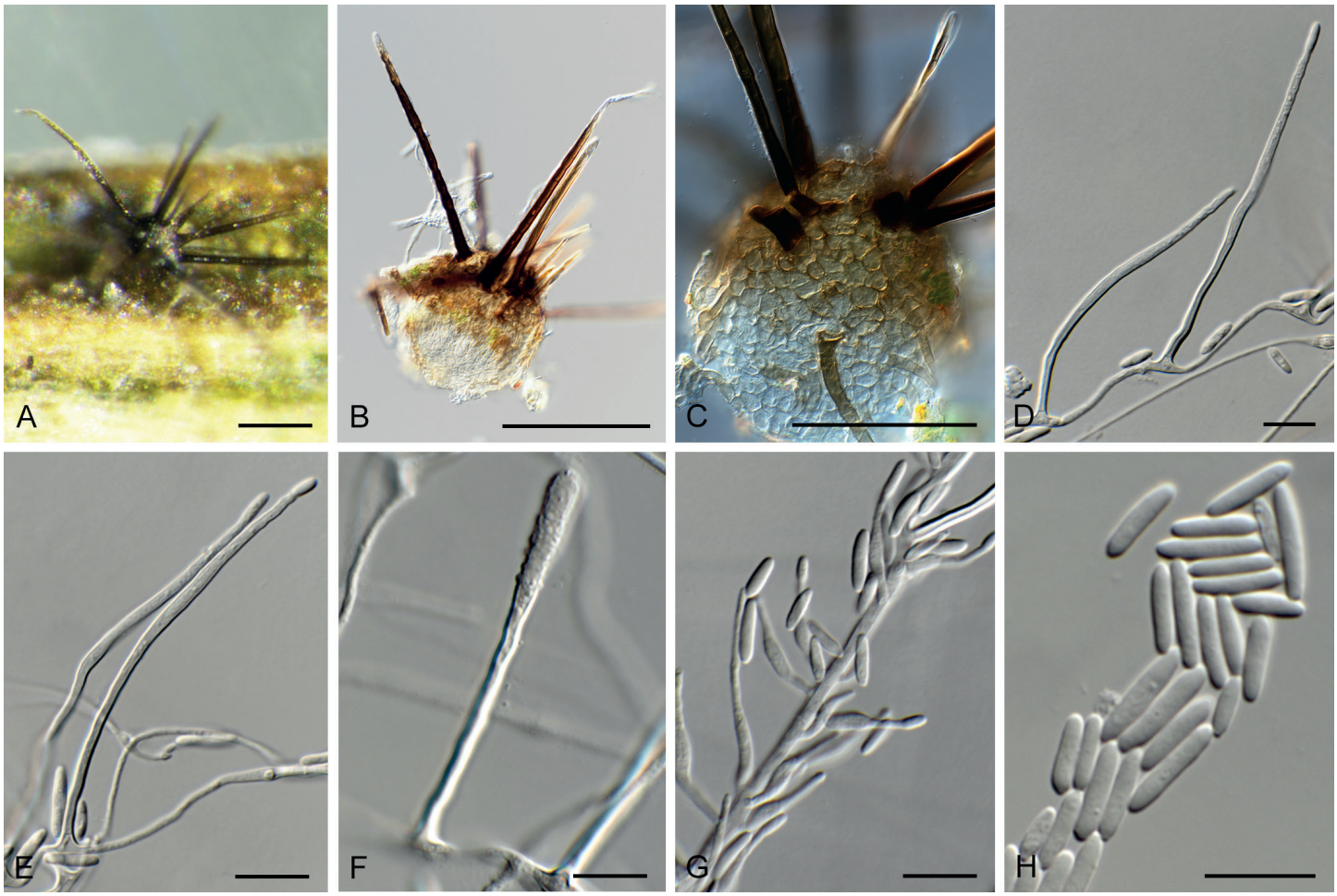

Fig. 40. *Niesslia neoexosporioides* (CPC 38177). **A.** Ascoma on host tissue. **B–C.** Ascomata with setae. **D–F.** Stipes with clavate vesicles. **G.** Conidiogenous cells. **H.** Conidia. Scale bars: A–B = 100 µm, C = 50 µm, all others = 10 µm.

cigar-shaped to clavate, inoperculate, inamyloid (water plus Lugol), ascospores obliquely biseriate, overlapping. *Ascospores* narrowly ellipsoid, straight with conical ends, hyaline, thin-walled, smooth, medianly 1-septate, thin-walled, slightly constricted, eguttulate, dimensions undetermined, specimen overmature. *Mycelium* consisting of hyaline, smooth, septate, branched, 1–2 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells, erect, flexuous, solitary to aggregated, subcylindrical, hyaline, smooth, thick-walled, 15–110 × 2–3 µm, phialidic with minute non-flared collarette, up to 1 µm long, apex 1–1.5 µm diam. *Stipes* terminating in clavate vesicles intermingled among conidiogenous cells, hyaline, smooth, with basal septum, up to 80 µm tall, vesicles 3–4 µm diam. *Conidia* solitary, aseptate, hyaline, smooth, subcylindrical, straight to slightly curved, apex subobtuse, base tapering to truncate hilum, 0.5 µm diam, (7–)8–10(–14) × 2(–2.5) µm.

Culture characteristics: Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface rosy buff, reverse cinnamon; on PDA surface buff, reverse honey; on OA surface buff.

Typus: **Germany**, near Berlin, on dead leaves of *Carex paniculata* (*Cyperaceae*), 17 Apr. 2019, *R.K. Schumacher*, HPC 2983 = RKS 250 (**holotype** CBS H-24405, culture ex-type CPC 38177 = CBS 146810).

Notes: The specimen considered in this study was initially identified as *Niesslia cf. exosporioides*, which is common on *Carex* spp. in Europe. The sexual morph was overmature resulting in the identification relying on the asexual morph that developed in culture. Conidia of *N. neoexosporioides* [(7–)8–10(–14) × 2(–2.5) µm] are larger than those of *N. exosporioides* (5–6 × 1–1.5 µm; Gams *et al*. 2019). Phylogenetically, *N. neoexosporioides* is closely related to *N. aemula* (conidia 4.5–6.5 × 1.2–2 µm; Gams *et al.* 2019), but the latter has smaller conidia. A phylogenetic species tree is presented as Fig. 41.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to "*Hypocreaceae* sp." (strain MUT<ITA> 2463, GenBank

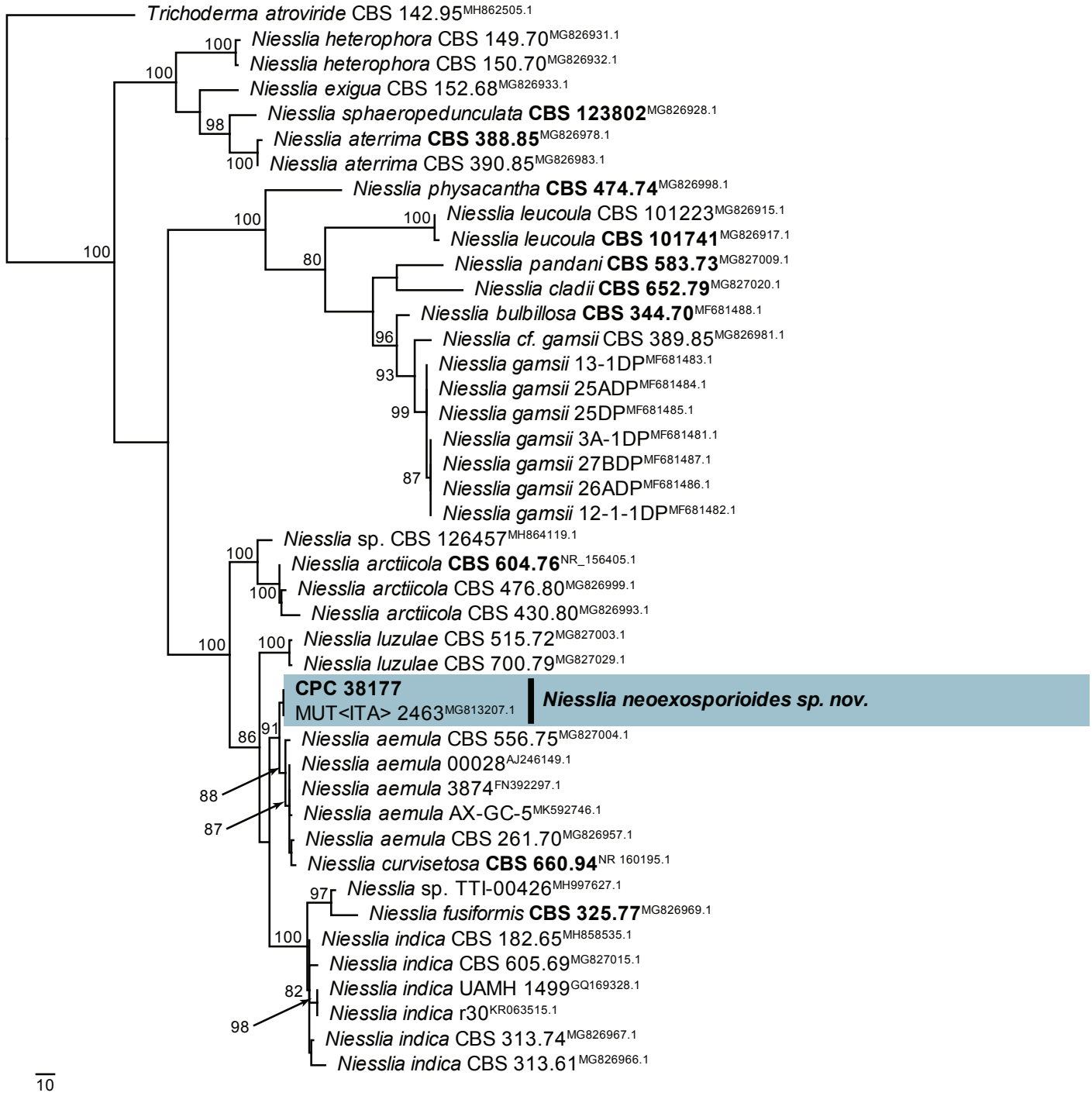

Fig. 41. The single most parsimonious tree obtained from a phylogenetic analysis of the *Niesslia* ITS nucleotide alignment. The tree was rooted to *Trichoderma atroviride* (strain CBS 142.95, GenBank MH862505.1) and the scale bar indicates the number of changes. Parsimony bootstrap support values higher than 79 % are shown at the nodes and the treated species is highlighted with a coloured box and bold text. GenBank accession (superscript) and / or culture collection / voucher numbers (in bold face when having a type status) are indicated for all species. Alignment statistics: 43 strains including the outgroup; 608 characters including alignment gaps analysed: 292 constant, 75 variable and parsimony-uninformative and 241 parsimony-informative. Tree statistics: TL = 788, CI = 0.688, RI = 0.900, RC = 0.619.

MG813207.1; Identities = 497/498 (99 %), no gaps), *Niesslia aemula* (strain AX-GC-5, GenBank MK592746.1; Identities = 561/568 (99 %), one gap (0 %)), and *Niesslia curvisetosa* (as *Monocillium curvisetosum*; strain CBS 660.94, GenBank NR_160195.1; Identities = 529/540 (98 %), three gaps (0 %)). Closest hits using the **LSU** sequence are *Niesslia luzulae* (as *Niesslia exosporioides*; strain CBS 691.71, GenBank MH872060.1; Identities = 815/816 (99 %), one gap (0 %)), "*Hypocreaceae* sp." (strain MUT<ITA> 2463, GenBank MG816499.1; Identities = 810/812 (99 %), two gaps (0 %)), and *Niesslia curvisetosa* (as *Monocillium curvisetosum*; strain CBS 660.94, GenBank MH874141.1; Identities = 888/893 (99 %), one gap (0 %)) – also see Fig. 4. No significant hits were obtained when the ***actA***, ***tef1*** and ***tub2*** sequences were used in blastn and megablast searches.

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

Nothoanungitopsis Crous, ***gen. nov.*** MycoBank MB 839296.

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

Mycelium consisting of brown, finely verruculose, septate, branched hyphae. *Conidiophores* dimorphic. *Microconidiophores* erect, flexuous, brown, thick-walled, septate. *Macroconidiophores* erect, flexuous, brown, finely verruculose, unbranched, thick-walled, base swollen, with rhizoids, multi-septate. *Conidiogenous cells* terminal, integrated, medium brown, finely verruculose, with several sympodially arranged flat-tipped denticles, scars unthickened. *Conidia* solitary or in chains of two, fusoid, 3-septate, straight, apex subobtuse, base subobtuse with truncate hilum; two central cells brown, thick-walled, finely verruculose; end cells subhyaline, smooth, thin-walled.

Type species: *Nothoanungitopsis urophyllae* Crous

Nothoanungitopsis urophyllae Crous, ***sp. nov.*** MycoBank MB 839297. Fig. 42.

Etymology: Name refers to the host species from which it was isolated, *Eucalyptus urophylla*.

Mycelium consisting of brown, finely verruculose, septate, branched, 2–3 µm diam hyphae. *Conidiophores* dimorphic. *Microconidiophores* erect, flexuous, brown, thick-walled, 50–80 × 4–6 µm, 2–3-septate. *Macroconidiophores* erect, flexuous, brown, finely verruculose, unbranched, thick-walled, base swollen, 8–12 µm diam, with rhizoids, 5–18-septate, 100–350 × 5–8 µm. *Conidiogenous cells* terminal, integrated, medium brown, finely verruculose, 15–35 × 4–5 µm, with several sympodially arranged flat-tipped denticles, scars 2–3 µm diam, unthickened. *Conidia* solitary or in chains of two, fusoid, 3-septate, straight, apex subobtuse, base subobtuse with truncate hilum, 1–1.5 µm diam; two central cells brown, thick-walled, finely verruculose; end cells subhyaline, smooth, thin-walled, (15–)16–18(–20) × (4–)5(–6) µm.

Culture characteristics: Colonies erumpent, spreading, with sparse to moderate aerial mycelium and uneven margin, reaching 5 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse isabelline.

Typus: **South Africa**, Kwazulu-Natal Province, Kwambonambi, on seed capsules of *Eucalyptus urophylla* (*Myrtaceae*), Apr. 2017, *M.J. Wingfield*, HPC 2868 (**holotype** CBS H-24395, culture ex-type CPC 38059 = CBS 146799).

Notes: *Neoanungitea* was introduced to accommodate two species occurring on eucalypt leaf litter in Australia, and characterised by having a rachis with flat-tipped sympodial loci, similar to but less conspicuous than those of *Anungitea* (Crous *et al*. 2019d). *Nothoanungitopsis* adds a third genus to this complex. Although it has unthickened conidiophore scars and conidial hila as in *Anungitopsis*, it is distinguished by lacking globose, brown swellings in its conidiophores, and having conidia that are unevenly pigmented, with two brown central cells.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Anungitopsis speciosa* (strain CBS 181.95, GenBank EU035401.1; Identities = 344/413 (83 %), 38 gaps (9 %)), *Anungitopsis lauri* (strain CBS 145067, GenBank NR_161129.1; Identities = 331/399 (83 %), 37 gaps (9 %)), and *Neoanungitea eucalypti* (strain CBS 143173, GenBank MG386031.2; Identities = 312/378 (83 %), 26 gaps (6 %)). Closest hits using the **LSU** sequence are *Neoanungitea eucalypti* (strain CBS 143173, GenBank MG386031.2; Identities = 547/588 (93 %), one gap (0 %)), *Anungitopsis speciosa* (strain CBS 181.95, GenBank EU035401.1; Identities = 542/588 (92 %), one gap (0 %)), and *Spirosphaera beverwijkiana* (strain CBS 469.66, GenBank

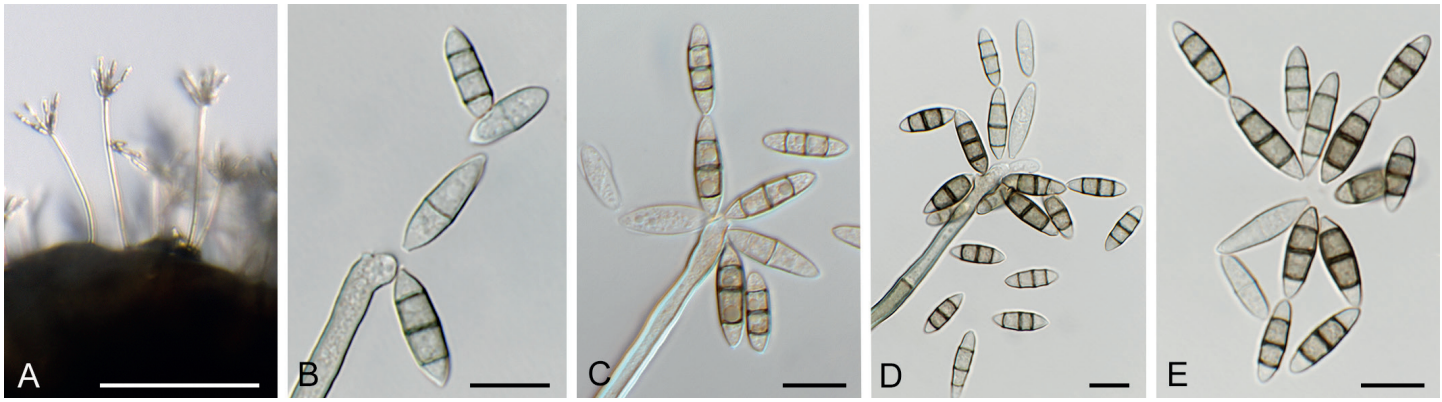

Fig. 42. *Nothoanungitopsis urophyllae* (CPC 38059). **A.** Conidiophores on PNA. **B–D.** Conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars: A = 80 µm, all others = 10 µm.

HQ696657.1; Identities = 541/588 (92 %), one gap (0 %)) – also see Fig. 1.

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

Nothomicrosphaeropsis Crous, ***gen. nov.*** MycoBank MB 839298.

Etymology: Named after its morphological similarity to *Microsphaeropsis*.

Conidiomata pycnidial, solitary, erumpent, brown, papillate with central ostiole; wall of 3–6 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity, ampulliform to doliiform, hyaline, smooth. *Conidia* solitary, hyaline, smooth, aseptate, granular, subcylindrical, apex obtuse, base bluntly rounded, straight to slightly curved, becoming pale brown with age.

Type species: *Nothomicrosphaeropsis welwitschiae* Crous

Nothomicrosphaeropsis welwitschiae Crous, ***sp. nov.*** MycoBank MB 839299. Fig. 43.

Etymology: Named after the host genus it was collected from, *Welwitschia*.

Conidiomata pycnidial, solitary, erumpent, brown, 200–250 µm diam, papillate with central ostiole; wall of 3–6 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity, ampulliform to doliiform, hyaline, smooth, 4–6 × 3–4 µm. *Conidia* solitary, hyaline, smooth, aseptate, granular, subcylindrical, apex obtuse, base bluntly rounded, straight to slightly curved, becoming pale brown with age, (4–)5–6(–7) × 2–2.5 µm.

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

Typus: **Namibia**, Hope Mine, east of Gobabeb – Namib Research Institute, on dead leaves of *Welwitschia mirabilis* (*Welwitschiaceae*), 19 Nov. 2019, *P.W. Crous*, HPC 3126 (**holotype** CBS H-24448, culture ex-type CPC 38879 = CBS 146829).

Notes: Based on ITS/LSU DNA sequence data, the present collection was initially identified as *Macroventuria wentii*, which is known from plant litter in the Nevada Death Valley, USA (van der Aa 1971). However, by incorporating more informative genes such as *rpb2* and *tub2* in the analysis (see phylogenetic tree, Fig. 44), the present isolate proved allied to *Paramicrosphaeropsis*, *Neomicrosphaeropsis* and *Microsphaeropsis*, a generic complex in *Didymellaceae* (Hou *et al*. 2020a). Genera in this complex are morphologically comparable in initially producing hyaline conidia that turn pale brown at maturity.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to "Aff. *Phoma* sp." (strain mk175, GenBank KT150686.1; Identities = 530/530 (100 %), no gaps), *Macroventuria wentii* (strain CBS 526.71, GenBank MH860250.1; Identities = 538/540 (99 %), no gaps), and *Leptosphaerulina australis* (strain CBS 234.58, GenBank MH857766.1; Identities = 538/542 (99 %), one gap (0 %)). Closest hits using the **LSU** sequence are *Ascochyta rabiei* (strain CBS 237.37, GenBank NG_069312.1; Identities = 858/858 (100 %), no gaps), *Coniothyrium genistae* (strain CBS 294.74, GenBank MH872596.1; Identities = 860/861 (99 %), no gaps), *Ascochyta fabae* (strain CBS 649.71, GenBank MH872045.1; Identities = 860/861 (99 %), no gaps), and *Macroventuria wentii* (strain CBS 526.71, GenBank NG_069040.1; Identities = 856/858 (99 %), no gaps) – also see Fig. 1. Closest hits using the ***rpb2*** sequence had highest similarity to *Neomicrosphaeropsis italica* (strain IT_24211, GenBank KU714604.1; Identities = 693/744 (93 %), no gaps), *Neomicrosphaeropsis juglandis* (strain MFLUCC 18-0795, GenBank MN593307.1; Identities = 693/744 (93 %), no gaps), and *Neomicrosphaeropsis cytisi* (strain MFLUCC 13-0396, GenBank KX572355.1; Identities = 682/742 (92 %), no gaps). A direct blast2 search against *Macroventuria rpb2* sequences on GenBank had highest similarity to *Macroventuria anomochaeta* (strain CBS 525.71, GenBank GU456346.1; Identities = 663/741 (89 %), no gaps), *Macroventuria terrestris* (strain RMF CA 12, GenBank MT018194.1; Identities = 531/596 (89 %), no gaps), and *Macroventuria wentii* (strain CBS 527.71C, GenBank MN983625.1; Identities = 530/596 (89 %), no gaps). Closest hits using the ***tub2*** sequence had highest similarity to *Paramicrosphaeropsis ellipsoidea* (strain CBS 197.97, GenBank MT005680.1; Identities = 314/333 (94 %), no gaps), *Epicoccum sorghinum* (strain FDY-5, GenBank MT799852.1; Identities = 336/364 (92 %), no gaps), *Epicoccum latusicollum* (strain HH12, GenBank MN623288.1; Identities = 337/365 (92 %), two gaps (0 %)), and *Macroventuria wentii* (strain CBS 526.71,

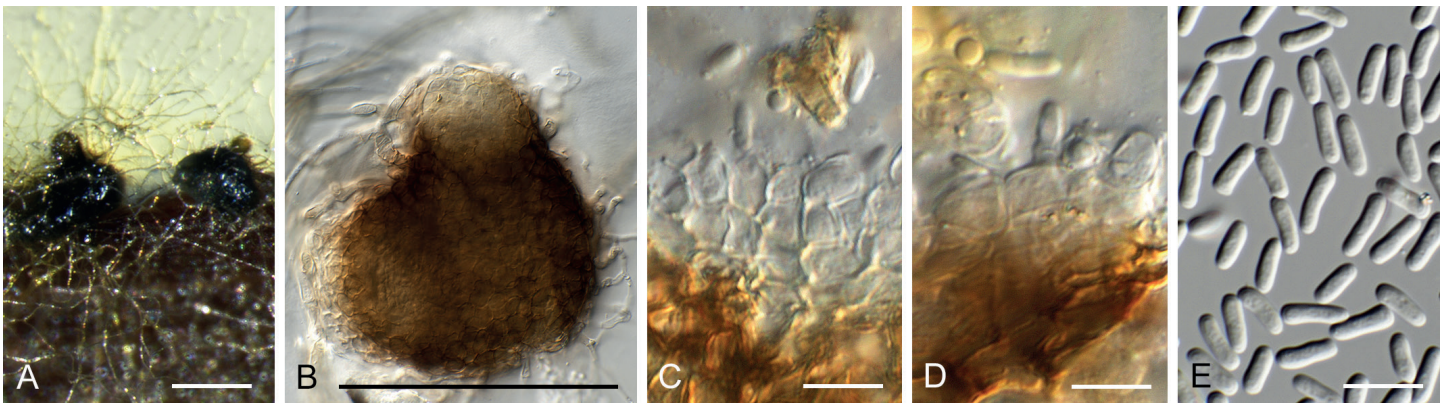

Fig. 43. *Nothomicrosphaeropsis welwitschiae* (CPC 38879). **A.** Conidiomata on PNA. **B.** Pycnidial conidioma. **C–D.** Conidiogenous cells. **E.** Conidia. Scale bars: A–B = 250 µm, all others = 10 µm.

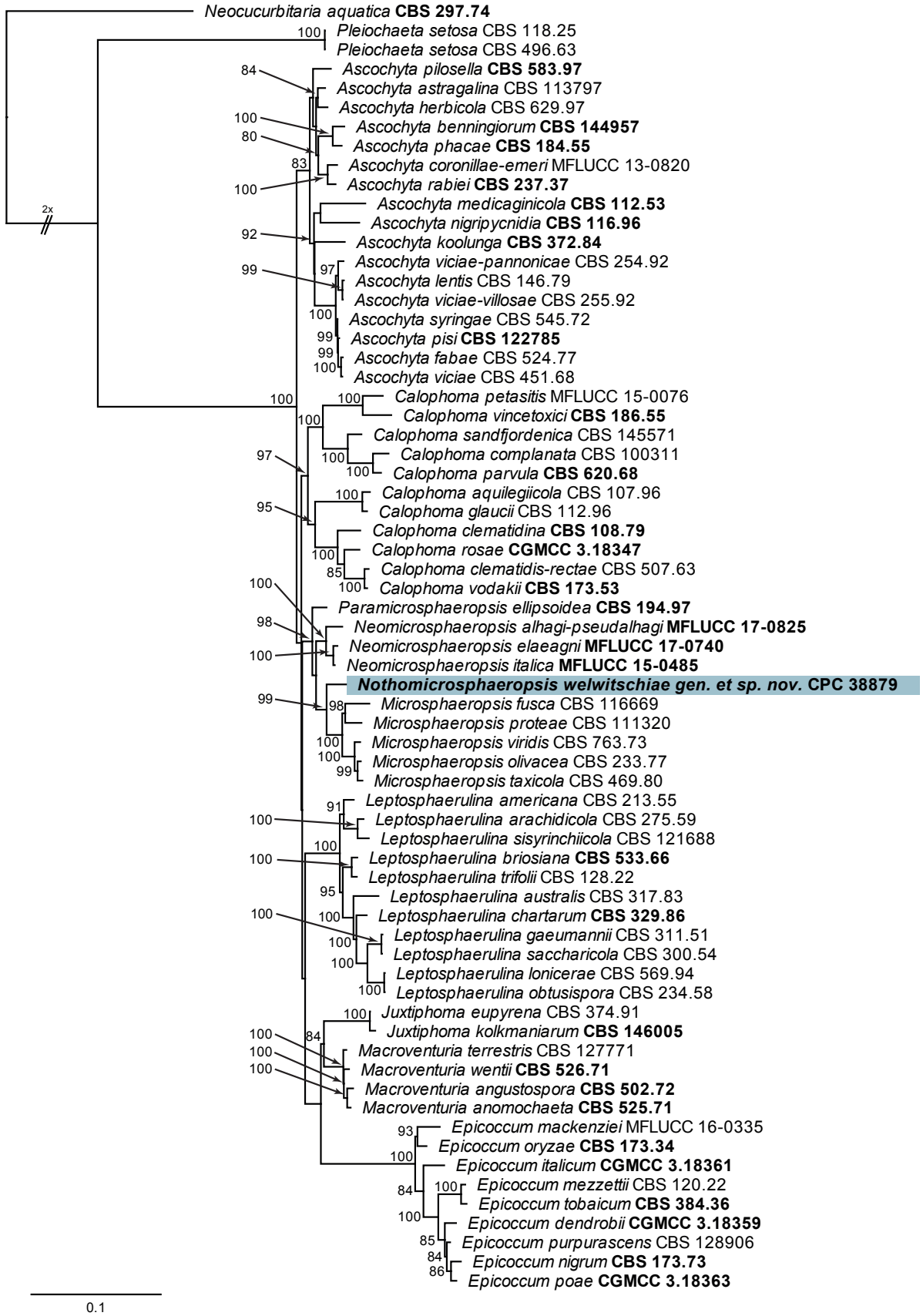

Fig. 44. Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE showing the phylogenetic position of *Nothomicrosphaeropsis welwitschiae gen. et sp. nov.* based on the multigene (ITS / LSU / *rpb2* / *tub2*) nucleotide alignment. The most basal branch was halved to facilitate layout. Bootstrap support values (> 79 %) from 5 000 ultrafast bootstrap replicates are shown at the nodes. The alignment is derived from the combined alignment of Hou *et al*. (2020a) and GenBank accession numbers can be obtained from the same reference. Culture collection / voucher numbers (in bold face when having a type status) are indicated for all species. The tree was rooted to *Neocucurbitaria aquatica* (culture CBS 297.74) and the species treated in this study is highlighted with a coloured block and bold face. Alignment statistics: 67 strains including the outgroup; 2 382 characters including alignment gaps analysed: 625 distinct patterns, 505 parsimony-informative, 94 singleton sites, 1 783 constant sites. The best models identified in IQ-TREE were: TIM2e+I+G4 (ITS), TNe+I+G4 (LSU), TNe+I+G4 (*rpb2*), TIM2e+I+G4 (*tub2*).

GenBank GU237546.1; Identities = 302/333 (91 %), no gaps). A direct blast2 search against *Macroventuria tub2* sequences on GenBank had highest similarity to *Macroventuria wentii* (strain CBS 877.70, GenBank MN984003.1; Identities = 303/333 (91 %), no gaps), *Macroventuria terrestris* (strain CBS 127771, GenBank MT005653.1; Identities = 300/331 (91 %), one gap (0 %)), and *Macroventuria anomochaeta* (strain CBS 525.71, GenBank GU237545.1; Identities = 300/333 (90 %), no gaps).

Authors: P.W. Crous, D.A. Cowan, G. Maggs-Kölling, E. Marais, N. Yilmaz & M.J. Wingfield

Ophioceras leptosporum (S.H. Iqbal) J. Walker, *Mycotaxon* **11**: 62. 1980. Fig. 45.
Basionym: *Gaeumannomyces leptosporus* S.H. Iqbal, *Trans. Brit. Mycol. Soc.* **58**: 346. 1972.

Description and illustration: See Walker (1980).

Material examined: **South Africa**, Northern Province, Nelspruit, Buffelskloof Nature Reserve, on twigs of *Syzygium cordatum* (*Myrtaceae*), Nov. 2018, *P.W. Crous*, HPC 3149, CBS H-24542, cultures CPC 39147 = CBS 147090.

Notes: Species of *Ophioceras* are commonly isolated from leaf and twig litter in freshwater habitats worldwide (Shearer *et al.* 1999). This is apparently the first record of this species from South Africa.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Ophioceras leptosporum* (strain CBS 894.70, GenBank NR_111768.1; Identities = 506/511 (99 %), no gaps), *Pestalotiopsis mangifolia* (voucher INBio 183C, GenBank KU204541.1; Identities = 499/543 (92 %), 17 gaps (3 %)), and *Myceliophthora sepedonium* (voucher INBio 571C, GenBank KU204432.1; Identities = 499/543 (92 %), 17 gaps (3 %)). Closest hits using the **LSU** sequence are *Ophioceras leptosporum* (strain CBS 894.70, GenBank NG_057959.1; Identities = 868/869 (99 %), no gaps), *Ophioceras chiangdaoense* (strain CMU 26633, GenBank NG_066356.1; Identities = 829/842 (98 %), no gaps), and *Ophioceras commune* (strain M91, GenBank JX134687.1; Identities = 816/873 (93 %), eight gaps (0 %)) – also see Fig. 5. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Ophioceras leptosporum* (strain CBS 894.70, GenBank JX134704.1; Identities = 474/475 (99 %), no gaps), *Ophioceras commune* (strain M91, GenBank JX134701.1; Identities = 434/475 (91 %), no gaps), and *Ophioceras aquaticus* (voucher S-479, GenBank MN194063.1; Identities = 404/447 (90 %), no gaps).

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

Paracremonium bendijkiorum Hern.-Restr., ***sp. nov.*** MycoBank MB838709. Fig. 46.

Etymology: Named for the collectors Yvan Bentem and Jack van Dijken students from the Het Hogeland College (Warffum, the Netherlands). This sample was collected during a Citizen Science project of the Westerdijk Fungal Biodiversity Institute.

Vegetative hyphae septate, hyaline, smooth and thin-walled, 1–4 µm wide. *Conidiophores* semi-macronematous, straight or slightly bent, simple or irregularly branched, hyaline, smooth-walled. *Conidiogenous cells* 13–33 × 1.5–3 µm, 1–1.5 µm wide at the apex, monophialidic, subcylindrical, straight or flexuous, hyaline, thin- and smooth-walled, with subcylindrical collarette. *Conidia* solitary, aseptate, subglobose, with apiculate base, 3–6 µm diam, hyaline, smooth-walled. *Chlamydospores* solitary, terminal or intercalary, hyaline, subglobose 6–7 µm diam. *Sexual morph* not observed.

Culture characteristics: Colonies after 2 wk at 25 °C on OA reaching 20 mm diam, flat, with sparse aerial mycelium, concolourous with the agar. On MEA reaching 18 mm diam, elevated, funiculose, wet, pale flesh, white, margin entire, regular. On PDA reaching 20 mm diam, elevated in the centre, funiculose to cottony, white to salmon, membranous to the periphery, margin entire.

Typus: **Netherlands**, Groningen Province, Warffum, Wibrand Geertstraat, from soil, 6 Jun. 2019, *Y. Bentem & J. van Dijken*, NL19_024 (**holotype** CBS H-24734, culture ex-type CBS 147228 = NL19_24005).

Notes: *Paracremonium* species are known from soil close to streams, caves, alkaline mud, air, beetles, and humans (Lombard

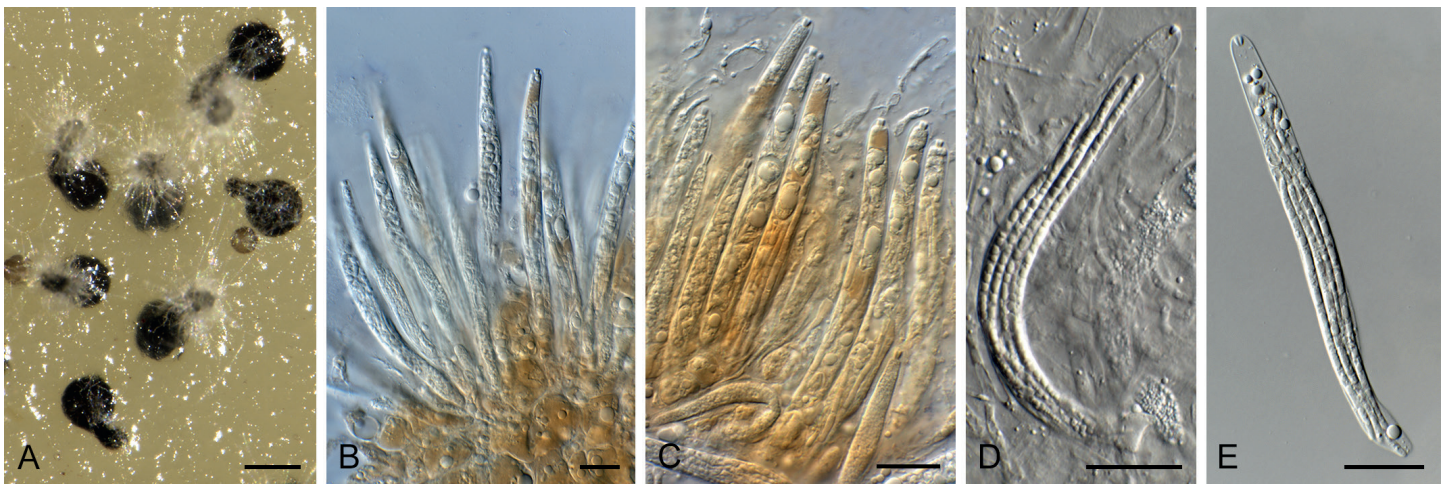

Fig. 45. *Ophioceras leptosporum* (CPC 39147). **A.** Ascomata developing on OA. **B–E.** Asci with ascospores. Scale bars: A = 250 µm, all others = 10 µm.

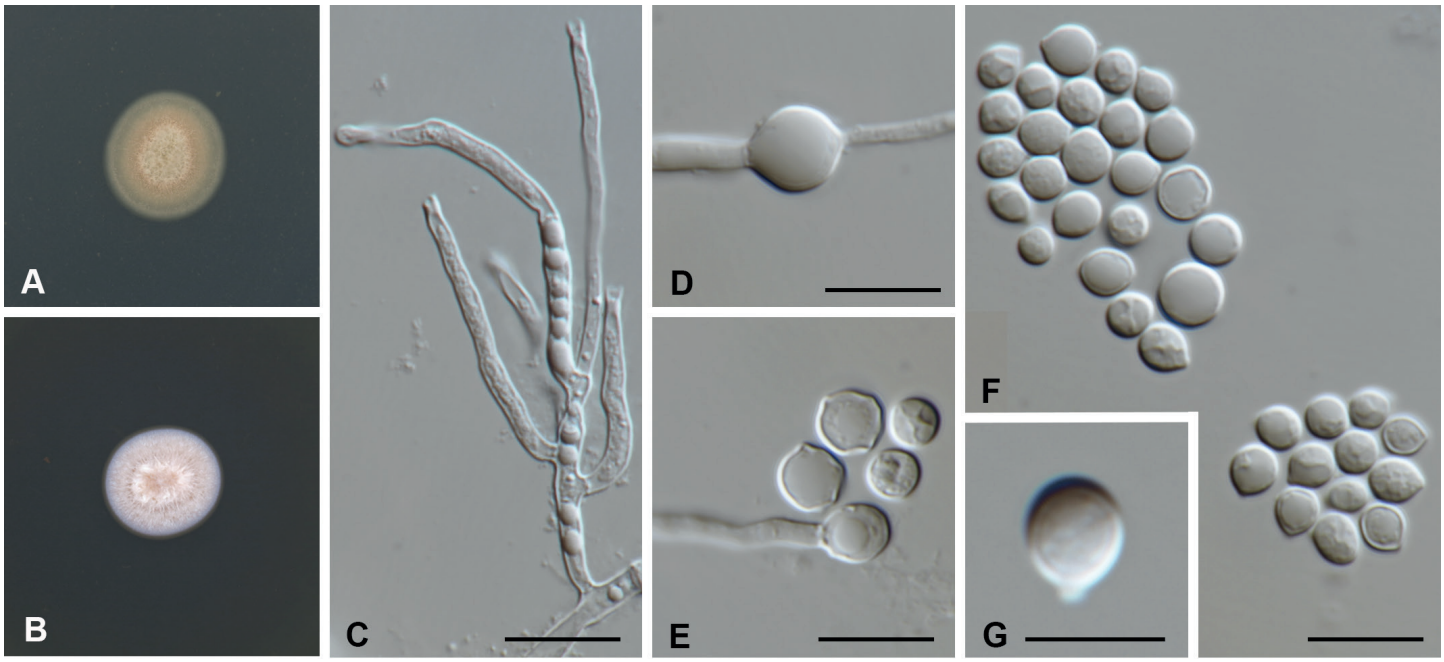

Fig. 46. *Paracremonium bendijkiorum* (CBS 147288). **A.** Colony on PDA. **B.** Colony on MEA. **C.** Conidiophores. **D.** Chlamydospore. **E.** Conidia and conidiogenous cell. **F–G.** Conidia. Scale bars C–F =10 µm, G = 5 µm.

et al. 2015, Lynch *et al.* 2016, Crous *et al.* 2017, Zhang *et al.* 2017, Al-Bedak *et al.* 2019, Zhang *et al.* 2021b). *Paracremonium bendijkiorum* is distinguished from its phylogenetically closest species, *P. inflatum,* in having subglobose conidia and chlamydospores. Another species in the genus with similar subglobose conidia is *P. apiculatum* (Zhang *et al.* 2020), which is phylogenetically distant (Fig. 47). Also see the overview phylogeny (Fig. 4).

Based on a megablast search of NCBI nucleotide database, the closest hits using the **ITS** sequence had the highest similarity to *Paracremonium inflatum* (strain CBS 485.77 GenBank NR_154312.1; Identities = 434/451 (96 %), three gaps (0 %)), *Paracremonium variiforme* strain LC5837 (GenBank KU746694.1; Identities = 426/444 (96 %), two gaps (0 %)) and *Paracremonium binnewijzendii* (strain CBS 143277, GenBank NR_157491.1; Identities = 431/454 (95 %), four gaps (0 %)). The closest hits using the **LSU** sequence had the highest similarity to *Paracremonium variiforme* (strain LC5832, GenBank KU746739.1; Identities = 825/842 (98 %), two gaps (0 %)), *Paracremonium* sp. (strain FZ2855-2, GenBank MK329029.1; Identities = 825/843 (98 %), two gaps (0 %)) and *Paracremonium* sp. (strain FZ3546-2, GenBank MK329031.1; Identities = 823/843 (98 %), two gaps (0 %)) – also see Fig. 4. The closest hits using the ***rpb2*** sequence are *Paracremonium variiforme* (strain CGMCC 3.17934 (GenBank KY883249.1; Identities = 583/654 (89 %), no gaps), *Paracremonium pembeum* (strain UCR2995, GenBank KT936355.1; Identities = 574/655 (88 %), two gaps (0 %)) and *Paracremonium contagium* (strain CBS 110348, GenBank KM232396.1; Identities = 573/655 (87 %), two gaps (0 %)). The closest hits using the ***tef1*** sequence had the highest similarity to *Paracremonium* sp. (strain LC12502, GenBank MK336059.1; Identities = 825/858 (96 %), no gaps), *Paracremonium variiforme* (strain LC5837, GenBank KX855240.1; Identities = 824/858 (96 %), no gaps) and *Paracremonium* sp. (strain LC12552, GenBank MK336061.1; Identities = 807/858 (94 %), no gaps). The closest hits using the ***tub2*** sequence had the highest similarity to *Paracremonium variiforme* (strain LC5837, GenBank KU746786.1; Identities = 232/243 (95 %), no gaps), *Paracremonium* sp. (strain LC12502 (GenBank MK336137.1; Identities = 228/239 (95 %), no gaps) and *Paracremonium* sp. (strain LC12552, GenBank MK336139.1; Identities = 225/240 (94 %), no gaps).

Author: M. Hernández-Restrepo

Paraphoma ledniceana Spetik, Eichmeier & Berraf-Tebbal, ***sp. nov.*** MycoBank MB835802. Fig. 48.

Etymology: Name refers to Lednice, where the specimen was collected.

Conidiomata pycnidial, ostiolate, uni- or bilocular, submerged, obpyriform, semi-pilose, dark brown, 250–450 µm diameter. *Conidiophores* lining the inner cavity, pale brown, smooth, densely aggregated. *Conidia* solitary, hyaline, straight, subcylindrical, apex obtuse, base truncate, (3.7–)4.5–4.9(–5.7) × (1.2–)1.5–1.7(–2.4) µm (av. 4.7 ± 0.5 × 1.6 ± 0.3 µm).

Culture characteristics: Colonies on PDA reaching 38 mm diam after 10 d at 25 °C, margin regular, floccose, erumpent, pale grey; reverse grey. On MEA reaching 27 mm diam after 10 d, margin regular, floccose, white to dirty white; reverse pale brown. On OA reaching 42 mm diam after 10 d, margin regular, floccose, white in outer ring, olivaceous grey; reverse olivaceous. No growth at 10 °C and 37 °C was observed.

Typus: **Czech Republic**, Breclav, Lednice, isolated as saprobe on dead wood of *Buxus sempervirens* (*Buxaceae*), Sep. 2018, *M. Spetik* (**holotype** BRNU 673830, isotype BRNU 673831, culture ex-type CBS 146533 = MEND-F-82).

Notes: Based on multigene (ITS, *tef1* and *tub2*) phylogenetic analyses, *P. ledniceana* differs from *P. rhaphiolepisis* by 29 nucleotides positions in the concatenated alignment, in which

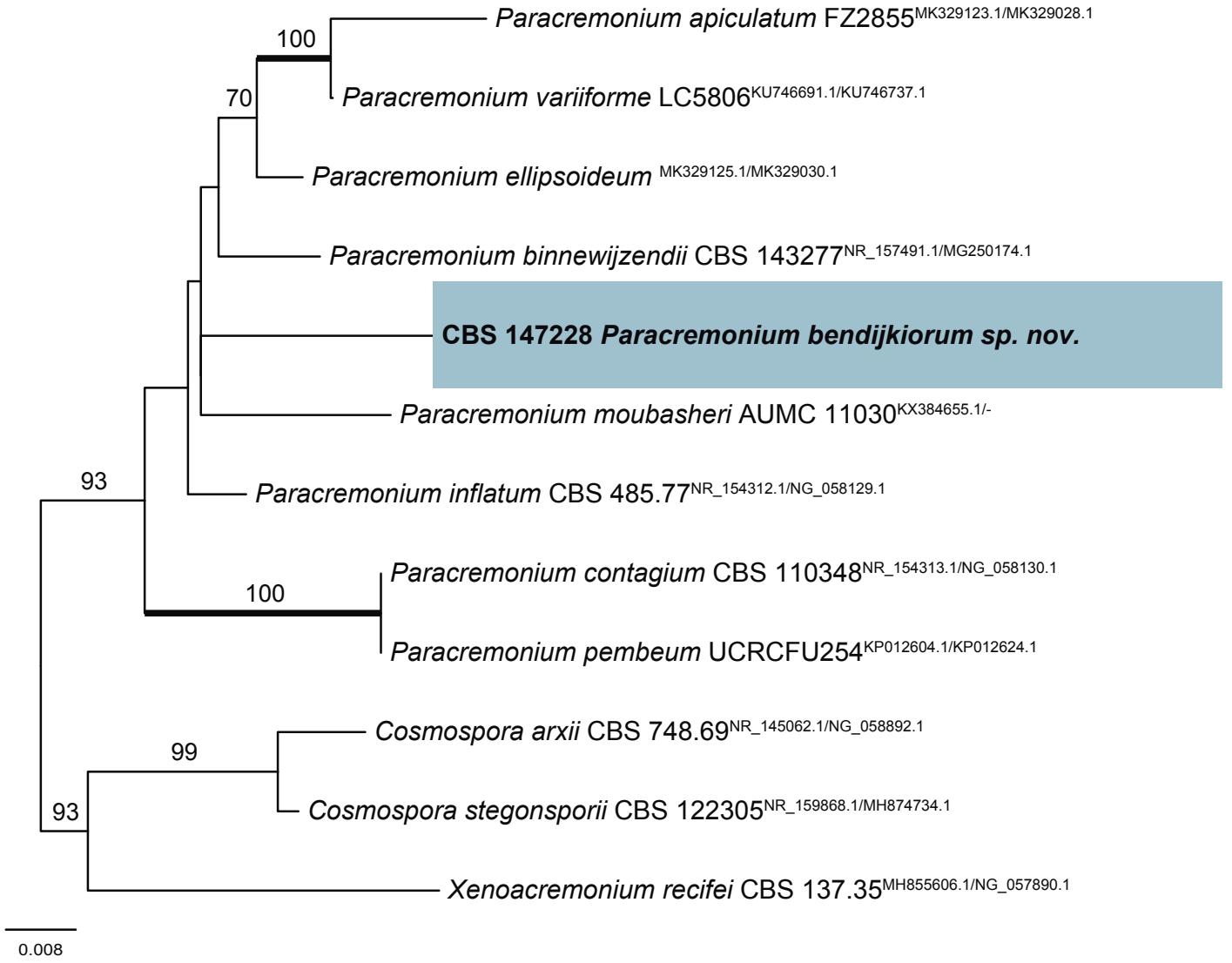

Fig. 47. Maximum composite likelihood tree obtained from the RAxML analysis of the combined ITS and LSU sequence alignment of *Paracremonium* species. Bootstrap support values above 70 % are shown at the nodes. The novel species is indicated in a coloured block and bold face. The tree was rooted to *Cosmospora arxii* (CBS 748.69), *C. stegonsporii* (CBS 122305) and *Xenoacremonium recifei* (CBS 137.35). Alignment statistics: 12 strains including the outgroup; 1 469 characters including alignment gaps analysed (ITS: 583, LSU: 886). Model: GTR+G, alignment patterns: 213.

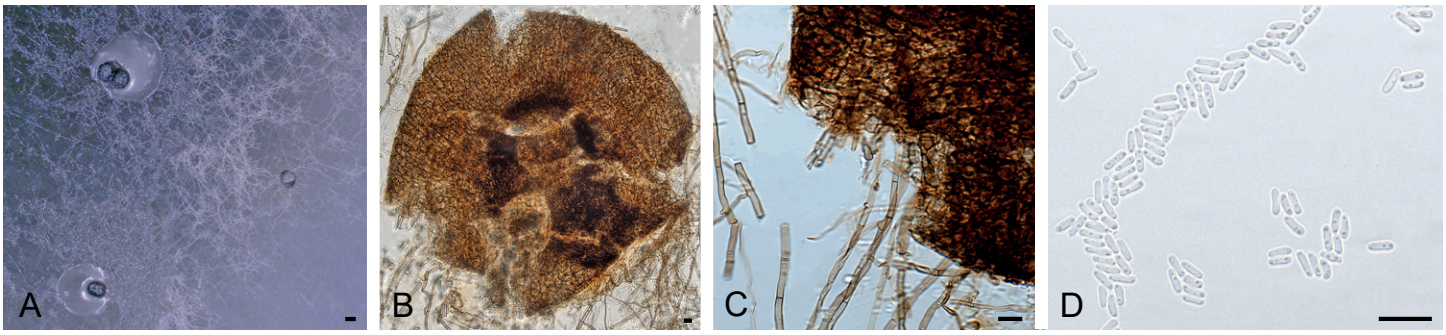

Fig. 48. *Paraphoma ledniceana* (CBS 146533). **A.** Conidiomatal pycnidia on SNA. **B–C**. Squash of conidiomata. **D.** Conidia. Scale bars: A = 100 µm, all others = 10 µm.

10 were distinct in the ITS region, six in the *tef1* region and 13 in *tub2*. Morphologically, the conidia length of *P. ledniceana* are smaller [(3.7–)4.5–4.9(–5.7) × (1.2–)1.5–1.7(–2.4) µm] compared to those of *P. rhaphiolepisis* [(4.5–)5–6(–6.5) × 2(–2.5) µm]. The obtained phylogeny (Fig. 49) placed the isolate CBS 146533 as a lineage sister to *Paraphoma rhaphiolepisis*. However, it is clearly distinct from the other known species of *Paraphoma* and it is therefore considered as a taxonomic novelty.

Based on a megablast search of NCBI nucleotide database, the closest hits using the **ITS** sequence had the highest similarity to *Paraphoma chrysanthemicola* (GenBank MK647980.1; Identities = 509/510 (99 %), one gap (0 %)), Uncultured fungus

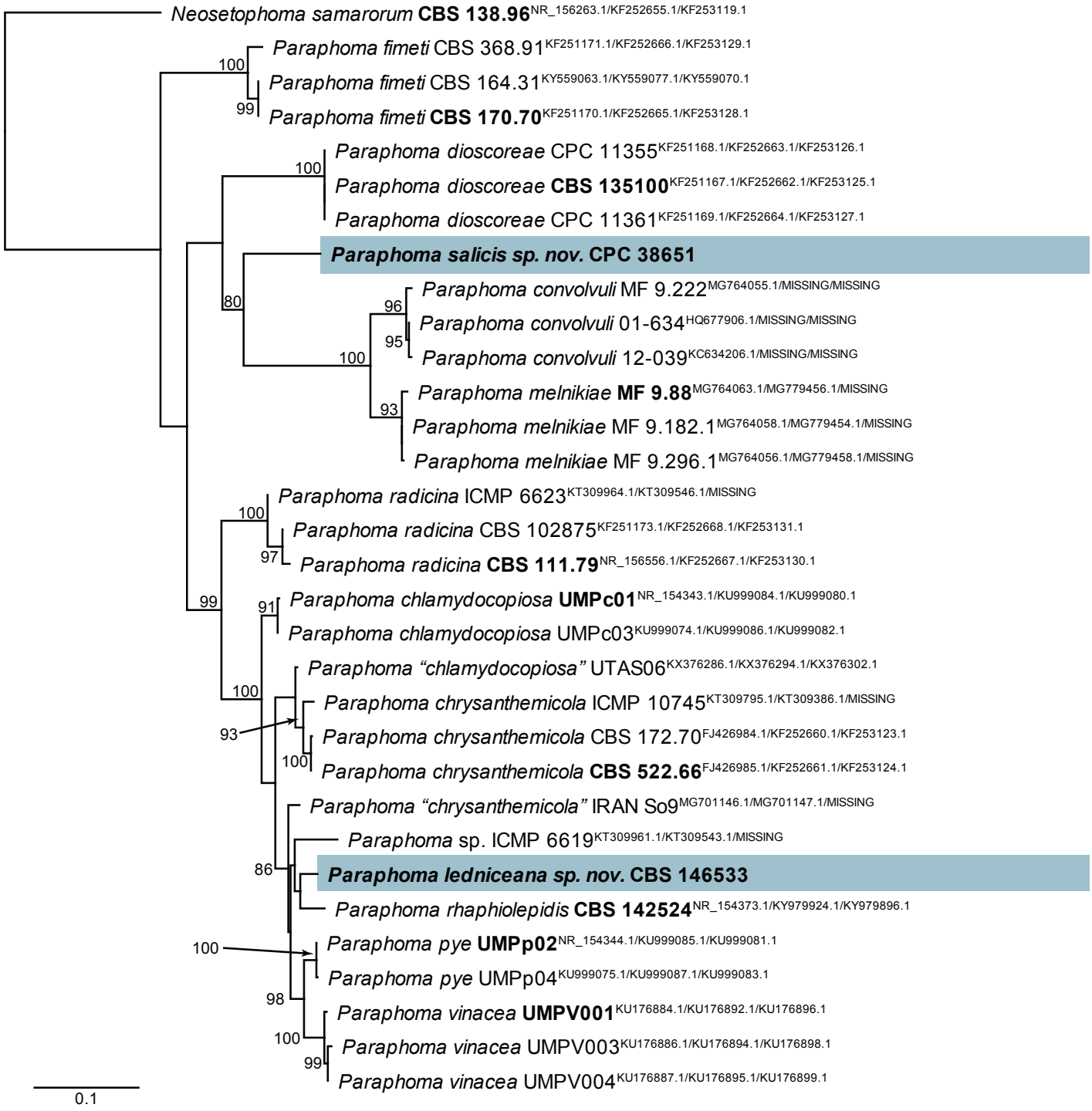

Fig. 49. Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE of the *Paraphoma* multigene (ITS / *tef1* / *tub2*) nucleotide alignment. Bootstrap support values (> 79 %) from 5 000 ultrafast bootstrap replicates are shown at the nodes. GenBank accession (superscript) and / or culture collection / voucher numbers (in bold face when having a type status) are indicated for all species. The tree was rooted to *Neosetophoma samarorum* (culture CBS 138.96) and the species treated in this study are highlighted with coloured blocks and bold face. Alignment statistics: 32 strains including the outgroup; 1 227 characters including alignment gaps analysed: 477 distinct patterns, 299 parsimony-informative, 100 singleton sites, 828 constant sites. The best models identified in IQ-TREE were: HKY+F+G4 (ITS), TNe+G4 (*tef1*), TNe+I+G4 (*tub2*).

clone (GenBank MT236451.1; Identities = 509/510 (99 %), one gap (0 %)) and *Paraphoma* sp. (GenBank MK304128.1; Identities = 506/506 (100 %), no gaps). The closest hits using the **LSU** sequence had the highest similarity to *Paraphoma* sp. (GenBank LC126021.2; Identities = 1 043/1 045 (99 %), no gaps), *Paraphoma radicina* (GenBank NG_070446.1; Identities = 1 043/1 045 (99 %), no gaps) and *Paraphoma chrysanthemicola* (GenBank GQ387582.1; Identities = 1 043/1 045 (99 %), no gaps) – also see Fig. 1; closest hits using the ***rpb2*** sequence are *Paraphoma rhaphiolepidis* (GenBank KY979851.1; Identities = 815/844 (97 %), no gaps), *Paraphoma radicina* (GenBank LT796995.1; Identities = 783/861 (91 %), no gaps) and *Paraphoma* sp. (GenBank MG779463.1; Identities = 625/733 (85 %), eight gaps (1 %)). The closest hits using the ***tef1*** sequence had the highest similarity to *Paraphoma rhaphiolepidis* (GenBank KY979896.1; Identities = 269/283 (95 %), three gaps (0 %)), *Paraphoma*

chlamydocopiosa (GenBank KX376304.1; Identities = 192/226 (85 %), no gaps) and *Paraphoma chlamydocopiosa* (GenBank KX376299.1; Identities = 192/226 (85 %), no gaps). The closest hits using the ***tub2*** sequence had the highest similarity to *Paraphoma rhaphiolepidis* (GenBank KY979924.1; Identities = 460/470 (98 %), three gaps (0 %)), *Paraphoma* sp. (GenBank MG779453.1; Identities = 433/473(99 %), no gaps) and *Paraphoma cf*. "*convolvuli*" (GenBank MG779461.1; Identities = 431/473 (91 %), three gaps (0 %)).

Authors: M. Spetik, A. Eichmeier & A. Berraf-Tebbal

Paraphoma salicis Crous & Akulov, ***sp. nov.*** MycoBank MB 839300. Fig. 50.

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

Conidiomata erumpent, solitary or aggregated, brown, globose, glabrous, 180–200 µm diam, with central ostiole, exuding creamy conidial mass. *Conidiophores* reduced to conidiogenous cells lining inner cavity, doliiform to ampulliform, hyaline, smooth, phialidic, 5–6 × 3–4 µm. *Conidia* solitary, aseptate, hyaline, smooth, ellipsoid to subcylindrical, apex obtuse, base bluntly rounded to somewhat truncate, (4–)5(–6) × (2–)2.5(–3) µm.

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

Typus: **Ukraine**, Volyn region, Liubeshiv district, Liubìaz village, on leaves of *Salix cf. alba* (*Salicaceae*), co-ocurring with *Septoria salicis* Westend., 29 Jul. 2019, *A. Akulov*, CWU AS 7121, HPC 3011 (**holotype** CBS H-24431, culture ex-type CPC 38651 = CBS 146797).

Notes: *Paraphoma* (*Phaeosphaeriaceae*) was resurrected as a distinct genus by de Gruyter *et al.* (2010), and shown to accommodate several species of saprobic, endophytic or phytopathogenic fungi affecting agricultural crops worldwide (Moslemi *et al*. 2016). *Paraphoma salicis* is phylogenetically distinct from *Paraphoma* species presently known from their DNA, and represents a new taxon occurring on leaves of *Salix* in Ukraine (Fig. 49).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Paraphoma radicina* (as *Phoma radicina*; strain VB1-2, GenBank MK764998.1; Identities = 520/587 (89 %), 23 gaps (3 %)), *Plenodomus biglobosus* (as *Leptosphaeria biglobosa*; strain CM-02, GenBank KY221834.1; Identities = 518/586 (88 %), 21 gaps (3 %)), and *Paraphoma chrysanthemicola* (strain DSM100401_C29_RLCS22, GenBank MT453289.1; Identities = 519/588 (88 %), 24 gaps (4 %)). Closest hits using the **LSU** sequence are *Paraphoma dioscoreae* (strain CBS 135100, GenBank KF251671.1; Identities = 806/809 (99 %), no gaps), *Paraphoma radicina* (strain UTHSC DI16-209, GenBank LN907352.1; Identities = 826/830 (99 %), no gaps), and *Plectosphaerella cucumerina* (strain 17chu05-05, GenBank MT102906.1; Identities = 810/814 (99 %), no gaps) – also see Fig. 1. Closest hits using the ***actA*** sequence had highest similarity to *Parastagonosporella fallopiae* (strain CBS 135981, GenBank MH460537.1; Identities = 217/241 (90 %), four gaps (1 %)), *Paraphoma chrysanthemicola* (strain ICMP 10745, GenBank KT309135.2; Identities = 206/242 (85 %), eight gaps (3 %)), and *Paraphoma radicina* (strain ICMP 6623, GenBank KT309298.2; Identities = 200/243 (82 %), ten gaps (4 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Paraphoma melnikii* (as *Paraphoma* sp. MG-2018a; voucher MF-9.240, GenBank MG779464.1; Identities = 668/735 (91 %), no gaps), *Paraphoma cf. "convolvuli"* (voucher MF-9.298.1, GenBank MG779468.1; Identities = 660/735 (90 %), no gaps), and *Paraphoma fimeti* (strain UTHSC DI16-296, GenBank LT797032.1; Identities = 817/944 (87 %), five gaps (0 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Paraphoma cf. "convolvuli"* (voucher MF-9.300.1, GenBank MG779460.1; Identities = 409/439 (93 %), no gaps), *Paraphoma melnikiae* (voucher MF-9.240, GenBank MG779453.1; Identities = 409/440 (93 %), two gaps (0 %)), and *Paraphoma rhaphiolepidis* (strain CBS 142524, GenBank KY979924.1; Identities = 413/462 (89 %), eight gaps (1 %)).

Authors: P.W. Crous & A. Akulov

Parasarocladium wereldwijsianum Hern.-Restr., ***sp. nov.*** MycoBank MB 838710. Fig. 51.

Etymology: Named after the school "Wereldwijs" (Bilthoven, the Netherlands) where the sample was collected. This sample was collected during a Citizen Science project of the Westerdijk Fungal Biodiversity Institute.

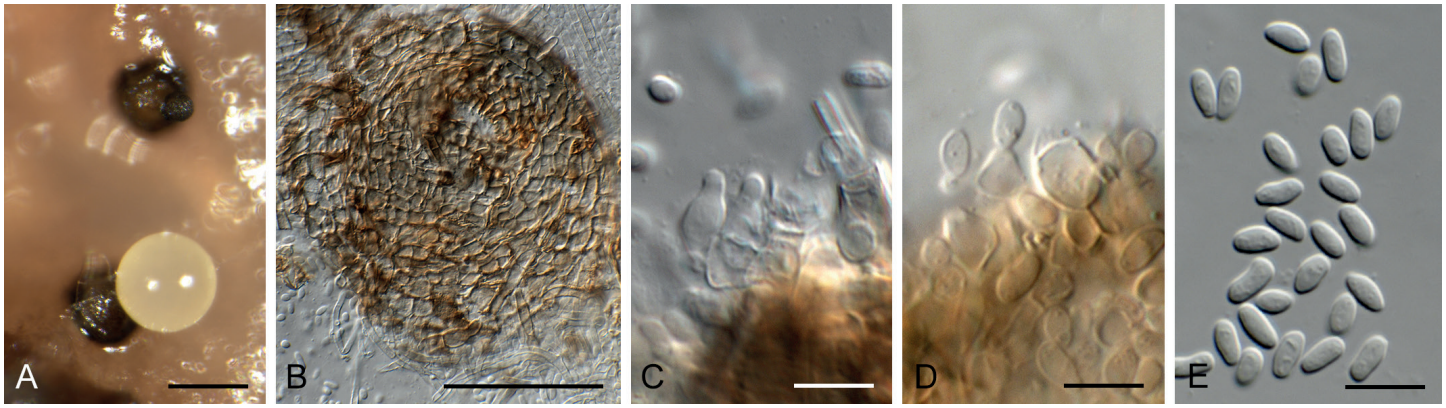

Fig. 50. *Paraphoma salicis* (CPC 38651). **A.** Conidiomata on OA. **B.** Conidioma with ostiole. **C–D.** Conidiogenous cells. **E.** Conidia. Scale bars: A–B = 200 µm, all others = 10 µm.

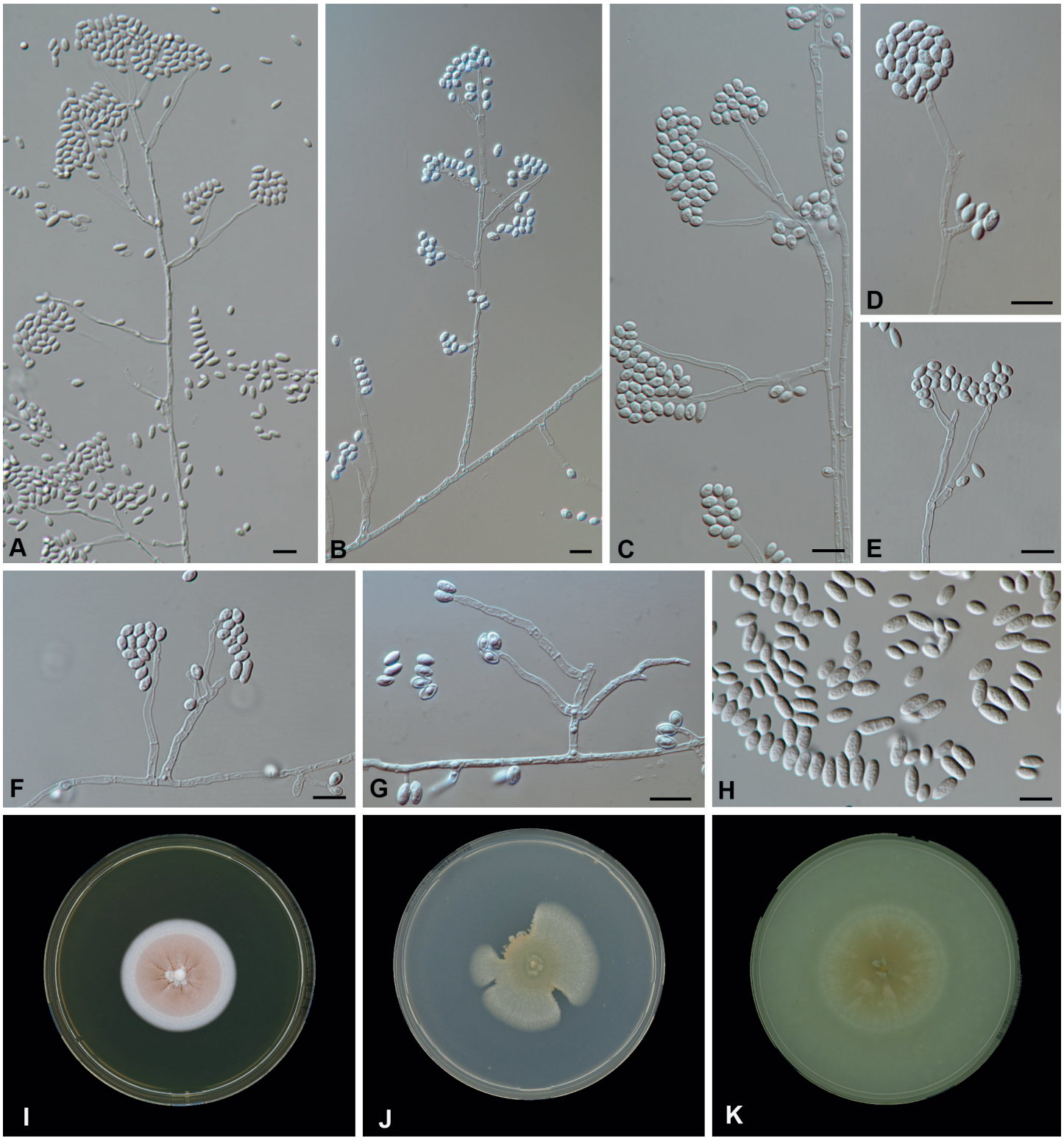

Fig. 51. *Parasarocladium wereldwijsianum* (CBS 147223). **A–G.** Conidiophores and conidia. **H.** Conidia. **I.** Colony on MEA. **J.** Colony on PDA. **K.** Colony on OA. Scale bars A–H = 10 µm.

Vegetative hyphae septate, hyaline, smooth and thin-walled, 1.5–2.5 µm wide. *Conidiophores* erect, arising directly from vegetative hyphae or ropes of hyphae, straight or slightly bent, simple or branched, sometimes verticillate, hyaline, smooth-walled. *Phialides* subulate, 11.5–45 µm long, 1.5–3.5 µm wide at the base, 1–1.5 µm wide at the apex, straight or flexuous, hyaline, thin- and smooth-walled. *Conidia* arranged in slimy heads, unicellular, ellipsoidal to obovoid, base truncated, 4–10 × 2–3 µm, hyaline, smooth-walled. *Chlamydospores* and *sexual morph* not observed.

Culture characteristics: After 7 d at 25 °C on OA attaining 30–35 mm diam, flat, sparse aerial mycelium, buff to white salmon, wet with exudate (hyaline and salmon), margin effuse; reverse no change. On MEA attaining 30 mm flat, velvety, radially folded, peach to rosy buff; reverse saffron. On PDA attaining 30–45 mm diam, flat, velvety, sparse aerial mycelium, olivaceous buff, margin irregular; reverse greenish olivaceous.

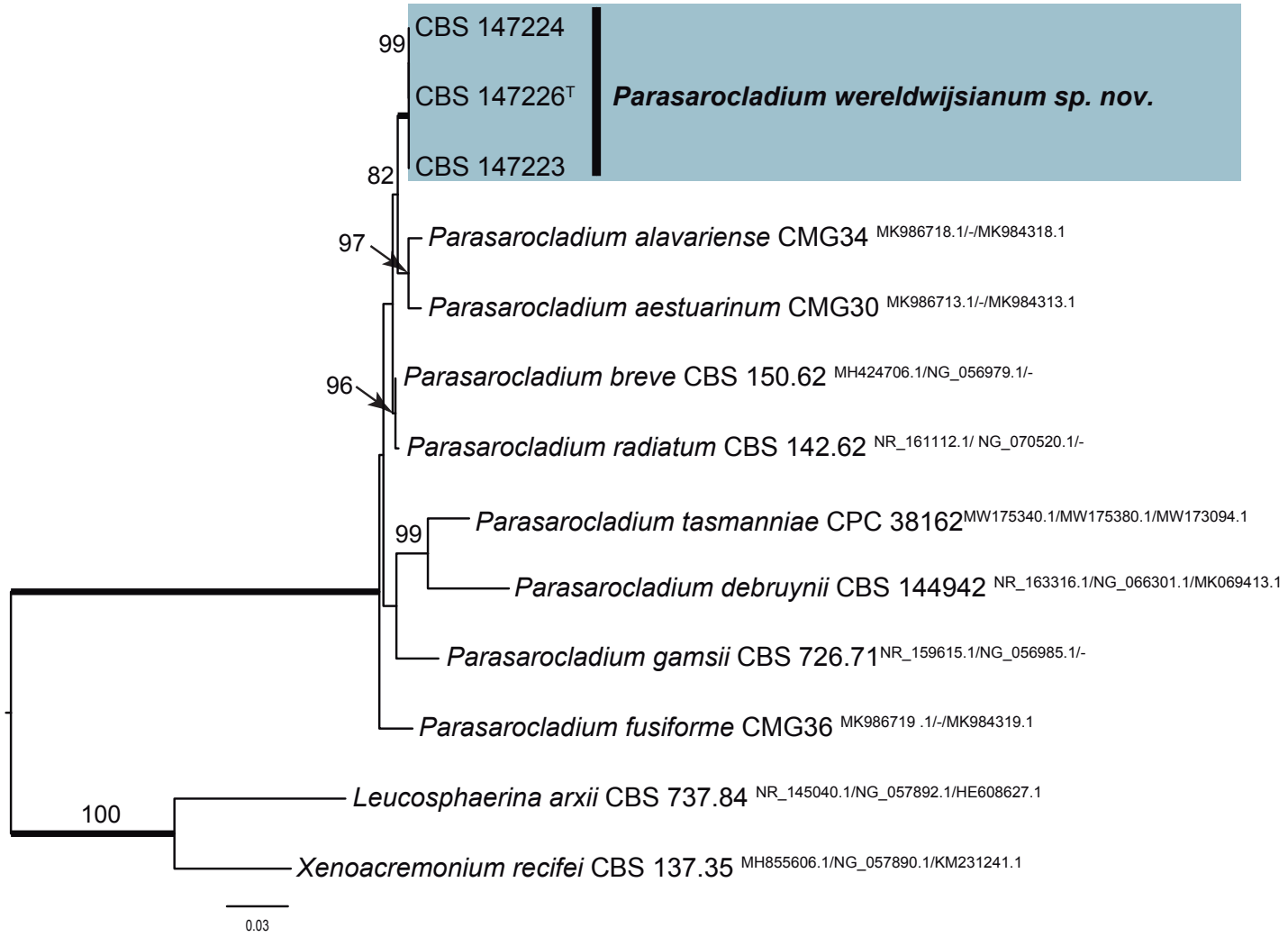

Fig. 52. Maximum composite likelihood tree obtained from the RAxML analysis of the combined ITS, LSU and actin sequence alignment of *Parasarocladium* species. Bootstrap support values above 70 % are shown at the nodes. The novel species is indicated in a coloured block and bold face. The tree was rooted to *Leucosphaerina arxii* (CBS 737.84) and *Xenoacremonium recifei* (CBS 137.35). Alignment statistics: 15 strains including the outgroup; 1 739 characters including alignment gaps analysed (ITS: 600, LSU: 851, *act*: 288). Model GTR+I+G, 395 distinct patterns.

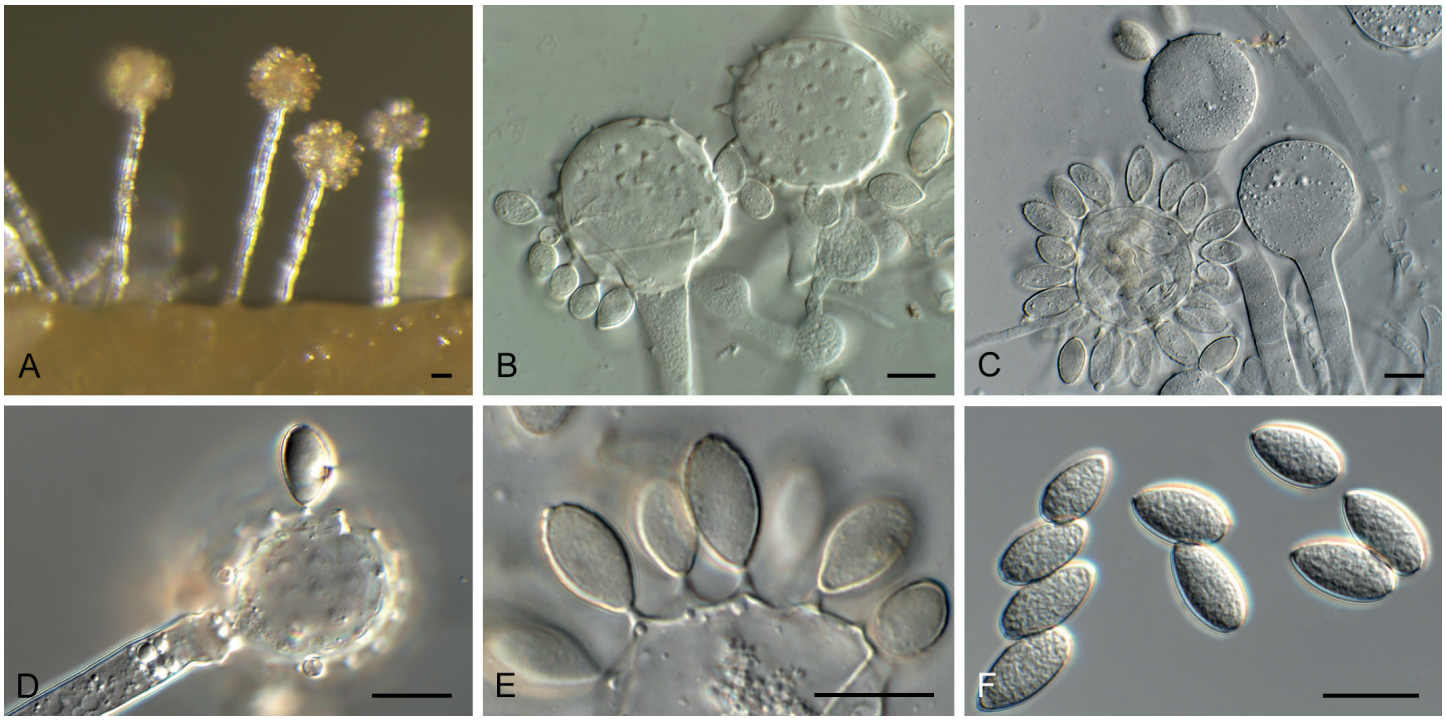

Fig. 53. *Peziza ligni* (CPC 39110). **A.** Conidiophores on OA. **B–E.** Conidiogenous cells giving rise to conidia. **F.** Conidia. Scale bars = 10 µm.

Typus: **Netherlands**, Utrecht Province, Bilthoven, from soil, 6 Jun. 2019, *S. Frederikze, J. Mes & S. Maghnouji*, NL19_095 (**holotype** CBS H-24735, culture ex-type CBS 147226 = NL19095011).

Other specimens examined: **Netherlands**, Utrecht, Bilthoven, from soil, 6 Jun. 2019, *S. Frederikze, J. Mes, & S. Maghnouji*, NL19_094 (culture CBS 147223 = NL1994001), *ibid*. (culture CBS 147224 = NL19094011).

Notes: *Parasarocladium wereldwijsianum* is represented by three strains collected in two soil samples from Bilthoven (Utrecht Province, the Netherlands). *Parasarocladium wereldwijsianum* can be distinguished from the phylogenetically closest species *P. aestuarinum* and *P. alavariense* by having olivaceous buff colonies on PDA, conidiophores that are irregularly branched, and a distinct conidial morphology [colonies buff orange, conidia globose, 3.5–4.5 × 2.5–3.5 µm in *P. aestuarinum*; colonies dark ochre yellow, conidia subglobose, 4.5–5.5 × 3–4 µm in *P. alavariense*; Gonçalves *et al.* (2019)]. Furthermore, *P. aestuarinum* and *P. alavariense* are known from marine habitats (Gonçalves *et al.* 2019) while *P. wereldwijsianum* was isolated from soil. Also see the overview phylogeny (Fig. 4) and species phylogeny (Fig. 52).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Hypocreales* sp. (strain HWJ2(1) , GenBank KM268693.1; Identities = 578/579 (99 %), no gaps), Fungal sp. (strain PH30517, GenBank KR363031.1; Identities = 496/497 (99 %), no gaps), and *Acremonium* sp. (GenBank MK651581.1; Identities = 480/481 (99 %) no gaps). Closest hits using the **LSU** sequence are *Acremonium* sp. (strain 39 OA-2013, GenBank JX535073.1; Identities = 490/490 (100 %), no gaps), *Acremonium* sp. (strain 38 OA-2013, GenBank JX535071.1; Identities = 490/490 (100 %), no gaps), and *Acremonium* sp. (strain 31 OA-2013, GenBank JX535057.1; Identities = 490/490 (100 %), no gaps) – also see Fig. 4.

Author: M. Hernández-Restrepo

Peziza ligni Crous & Decock, ***sp. nov.*** MycoBank MB 839301. Fig. 53.

Etymology: Name refers to the woody substrate (L. = *lignum*) from which it was isolated.

Mycelium consisting of hyaline, smooth, septate, branched, 4–6 µm diam. *Conidiophores* solitary, subcylindrical, erect, flexuous, hyaline, smooth, 3–5-septate, 100–200 × 7–8 µm. *Conidiogenous cells* integrated, terminal, globose to sphaeropedunculate, 22–35 µm diam, covered in numerous denticles, 1–2 × 1 µm, apex with minute marginal frill. *Conidia* solitary, aseptate, fusoid-ellipsoid, pale brown, smooth to finely roughened, apex subobtuse, base truncate, 1–2 µm diam, with marginal frill, (11–)13–14(–16) × 6(–7) µm.

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

Typus: **France**, Normandie, Seine Maritime, on masonry and plastering, near a wooden staircase, Nov. 2019, *C. Decock* (**holotype** CBS H-24559, culture ex-type MUCL 57889 = CPC 39110 = CBS 146637).

Notes: *Peziza*, the largest genus in the *Pezizales*, has been linked to *Ostracoderma* and *Oedocephalum* asexual morphs (Hanlin 1997). However, *Peziza* is paraphyletic (Hansen *et al.* 2001, 2002, 2005). The type of *Oedocephalum*, *O. elegans*, has been linked to *Peziza anthracophila*. The type of *Peziza*, *P. vesiculosa*, has however been linked to *Oedocephalum pallidum*, a species that normally occurs on dung of various animals (Stalpers 1974). *Oedocephalum* is characterised by erect, hyaline conidiophores with a terminal swelling or vesicle that gives rise to hyaline, aseptate conidia attached to the vesicle via a layer of denticles. Species of *Oedocephalum* are common on dung, wood, soil, and plant litter.

Using the key of Stalpers (1974), *P. ligni* was similar to *O. argillaceum* (decayed branch, Morocco; conidia hyaline, narrowly ellipsoidal, 12.5–15(–16) × 5.3–6.3(–6.5) µm, covered in brownish granules, distinctly larger at the ends, up to 2 µm long). *Peziza ligni* can, however, be distinguished from *O. argillaceum* by having conidia that are smooth to finely roughened, and in having smaller conidiogenous vesicles (22–35 µm diam), *vs*. 35–52 µm diam in *O. argillaceum.* A phylogenetic tree is presented as Fig. 54.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Peziza pseudoviolacea* (voucher 16504, GenBank JF908564.1; Identities = 507/561 (90 %), 11 gaps (1 %)), *Peziza emileia* (voucher L 0833270, GenBank KJ728716.1; Identities = 333/385 (86 %), 14 gaps (3 %)), and *Peziza fimeti* (voucher TAAM 171114, GenBank JQ654494.1; Identities = 327/385 (85 %), 14 gaps (3 %)). Closest hits using the **LSU** sequence are *Peziza exogelatinosa* (voucher KH 00.029 (C), GenBank AY500545.1; Identities = 874/893 (98 %), no gaps), *Peziza violacea f. terricola* (voucher MPU JCD 466-77, GenBank MT273610.1; Identities = 804/823 (98 %), no gaps), and *Peziza proteana f. sparassoides* (voucher OSC 100024, GenBank AY544659.1; Identities = 880/902 (98 %), two gaps (0 %)) – also see Fig. 3. Closest hits using the ***rpb2*** sequence had highest similarity to *Peziza exogelatinosa* (voucher KH 00.029 (C), GenBank AY500501.1; Identities = 620/681 (91 %), no gaps), *Peziza petersii* (voucher OSC 27373, GenBank MN816680.1; Identities = 556/649 (86 %), three gaps (0 %)), and *Peziza proteana f. campbellii* (voucher Wu-1937, GenBank MN816673.1; Identities = 582/683 (85 %), eight gaps (1 %)).

Authors: P.W. Crous & C. Decock

Phyllosticta phoenicis Crous, ***sp. nov.*** MycoBank MB 839302. Fig. 55.

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

Conidiomata (on PNA) pycnidial, solitary, black, erumpent, globose, exuding colourless conidial masses; pycnidia 200–300 µm diam; pycnidial wall of several layers of *textura angularis*; inner wall of hyaline *textura angularis*. *Ostiole* central, to 20 µm diam. *Conidiophores* reduced to conidiogenous cells, or with a supporting cell, that can be branched at the base; *Conidiogenous cells* subcylindrical to ampulliform, terminal, hyaline, smooth, coated in a mucoid layer, 9–15 × 3–4 µm; proliferating several times percurrently near apex. *Conidia* (9–)10–13(–15) × (7–)8(–9) µm, solitary, hyaline, aseptate, thin and smooth-walled, granular, or with a single large central guttule, fusoid-ellipsoid,

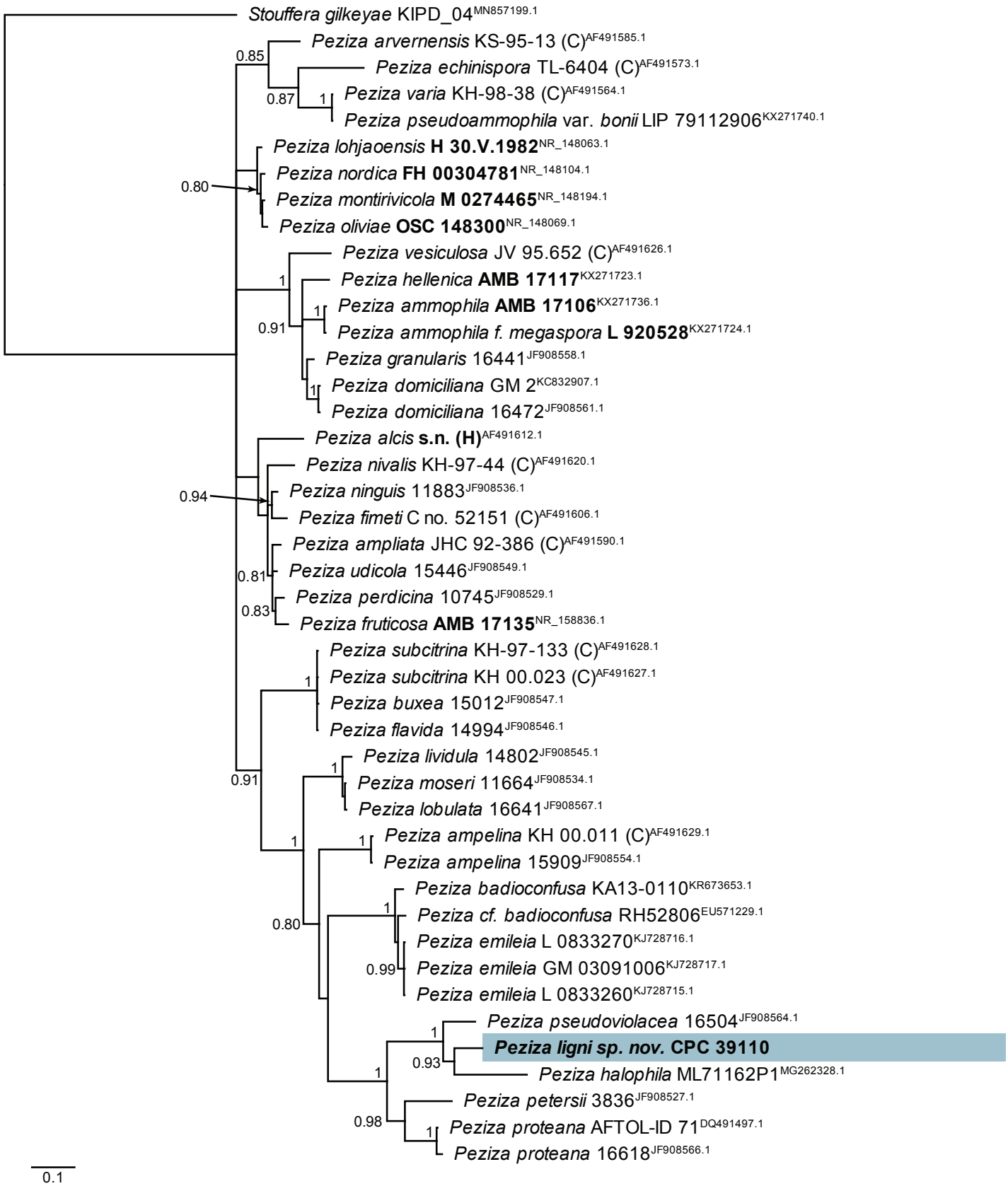

Fig. 54. Consensus phylogram (50 % majority rule) resulting from a Bayesian analysis of the *Peziza* ITS nucleotide alignment. Bayesian posterior probabilities (> 0.79) are shown at the nodes and the scale bar represents the expected changes per site. Families are indicated with coloured blocks to the right of the tree. GenBank accession (superscript) and / or culture collection / voucher numbers (in bold face when having a type status) are indicated for all species. The tree was rooted to *Stouffera gilkeyae* (voucher KIPD_04; GenBank MN857199.1) and the novel species treated in this study is indicated in a coloured block and in bold face. Alignment statistics: 44 strains including the outgroup; 486 unique site patterns. Tree statistics: 19 502 sampled trees from 65 000 generations.

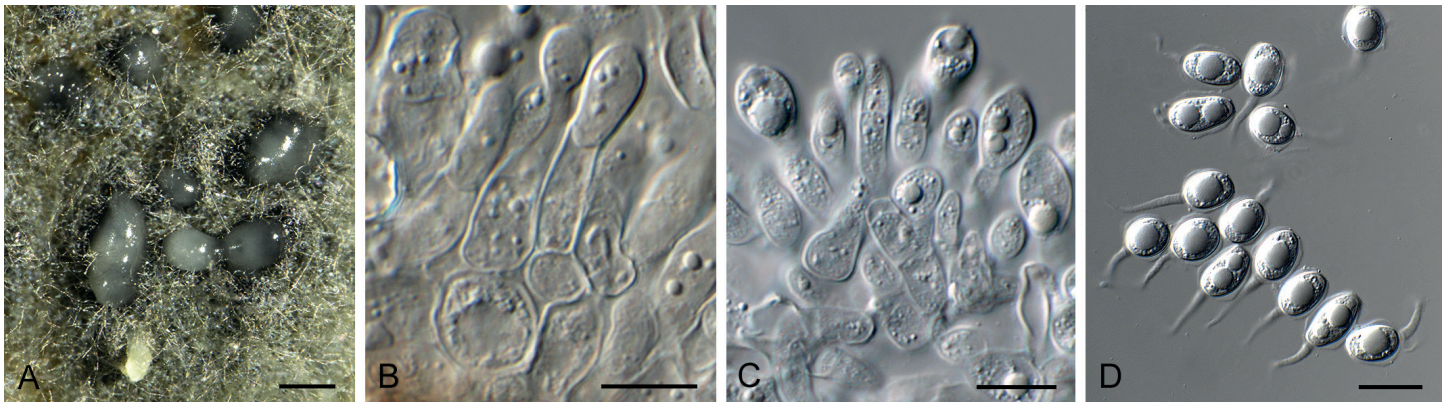

Fig. 55. *Phyllosticta phoenicis* (CPC 39164). **A.** Colony sporulating on OA. **B–C.** Conidiogenous cells. **D.** Conidia. Scale bars: A = 250 µm, all others = 10 µm.

tapering towards a narrow truncate base, 3 µm diam, enclosed in a persistent mucoid sheath, 1–2 µm thick, and bearing a hyaline, apical mucoid appendage, 10–30 µm long, 2.5–3.5 µm diam at base, flexible, unbranched, tapering towards an acutely rounded tip.

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

Typus: **South Africa**, Eastern Cape Province, Haga Haga, on leaves of *Phoenix reclinata* (*Arecaceae*), 2018, *M.J. Wingfield*, HPC 3190 (**holotype** CBS H-24544, culture ex-type CPC 39164 = CBS 147091).

Notes: Species of *Phyllosticta* are commonly encountered as endophytes, plant pathogens or saprobes (Glienke *et al.* 2011, Guarnaccia *et al.* 2017, 2019). Several species have been reported from palms. Van der Aa & Vanev (2002) refer to *P. cocoina* var. *phoenicis* as having conidia that are 8–9 × 3 µm, being more suggestive of *Phoma* or *Diaporthe*; *P. palmarum* to be representative of an undescribed ascomycetous fungus; *P. palmicola* to be a *Phoma*; *P. palmigena* to be a *Coniothyrium*, and *P. sabalicola* to be *Apiosphaeria martinii*. *Phyllosticta cocoicola* (*Guignardia cocogena*) was seen as indistinguishable from *P. arecae* (*Guignardia calami*) by Van der Aa & Vanev (2002), but there are no cultures to confirm this synonymy. Van der Aa (1973) cited conidia of *P. arecae* (on *Areca, Calamus, Caryota*) as 7–15 × 5–9 µm, thus somewhat smaller than those of *P. phoenicis*, with shorter appendages, 3–10 µm long. Punithalingam (1974) cited conidia of *P. cocoicola* (on *Cocos*) to be 10–16 × 5–6 µm, with appendages 6–9(–10) µm long, thus with narrower conidia and shorter appendages than observed in *P. phoenicis*. A phylogenetic species tree is presented as Fig. 56.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phyllosticta aristolochiicola* (strain BRIP 53316a, GenBank NR_111791.1; Identities = 569/579 (98 %), no gaps), *Phyllosticta cordylinophila* (strain MFUCC 12-0014, GenBank KC686599.1; Identities = 582/599 (97 %), five gaps (0 %)), and *Phyllosticta capitalensis* (strain MFE29, GenBank MT186150.1; Identities = 575/602 (96 %), seven gaps (2 %)). Closest hits using the **LSU** sequence are *Phyllosticta aristolochiicola* (strain BRIP 53316a, GenBank JX486128.1; Identities = 850/860 (99 %), no gaps), *Phyllosticta capitalensis* (strain MUCC 2916, GenBank LC543421.1; Identities = 825/835 (99 %), no gaps), and *Phyllosticta paracapitalensis* (strain CPC 28123, GenBank KY855805.1; Identities = 805/815 (99 %), no gaps) – also see Fig. 1. Closest hits using the ***actA*** sequence had highest similarity to *Phyllosticta lauridiae* (strain CBS 145559, GenBank MK876460.1; Identities = 582/604 (96 %), five gaps (0 %)), *Phyllosticta acaciigena* (strain CPC 28295, GenBank KY173570.1; Identities = 512/534 (96 %), one gap (0 %)), and *Phyllosticta encephalarticola* (strain CBS 146014, GenBank MN556783.1; Identities = 563/600 (94 %), one gap (0 %)). Closest hits using the ***gapdh*** sequence had highest similarity to *Phyllosticta capitalensis* (strain VIC30428, GenBank JF343743.1; Identities = 307/310 (99 %), no gaps), *Phyllosticta musarum* (strain GZAAS6.1228, GenBank KM816632.1; Identities = 458/471 (97 %), one gap (0 %)), and *Phyllosticta rhizophorae* (strain NCYUCC 19-0358, GenBank MT363251.1; Identities = 390/404 (97 %), two gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Phyllosticta capitalensis* (strain GZAAS6.1201, GenBank KM816635.1; Identities = 376/384 (98 %), no gaps), *Phyllosticta ericarum* (strain GZAAS6.1250, GenBank KR025451.1; Identities = 376/384 (98 %), no gaps), and *Phyllosticta carochlae* (strain SM52, GenBank MT118271.1; Identities = 367/384 (96 %), one gap (0 %)).

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

Plectosphaerella slobbergiarum Hern.-Restr., ***sp. nov.*** MycoBank MB 838711. Fig. 57.

Etymology: Named for the collectors Julia Slob and Maaike Berghui, students from Het Hogeland College (Warffum, the Netherlands). This sample was collected during a Citizen Science project of the Westerdijk Fungal Biodiversity Institute.

Vegetative hyphae hyaline, septate, smooth, 1.5–4 µm. *Conidiophores* semi-micronematous, hyaline, smooth, irregularly branched. *Conidiogenous cells* monophialidic, terminal or intercalary, subcylindrical to subulate, smooth, hyaline, 10–40 × 2–3 µm, with conspicuous cylindrical collarette and periclinal thickening at the conidiogenous locus, 1–3.5 × 1–2 µm. *Conidia* cylindrical to ellipsoidal with rounded apex and slightly truncate base, inequilateral, with inner plane flat and outer plane convex, guttulate, hyaline, 0–1-septate; septate conidia 6–12.5 × 2–3.5 µm; aseptate conidia 4–8.5 × 2–3 µm. *Chlamydospores* and *sexual morph* absent.

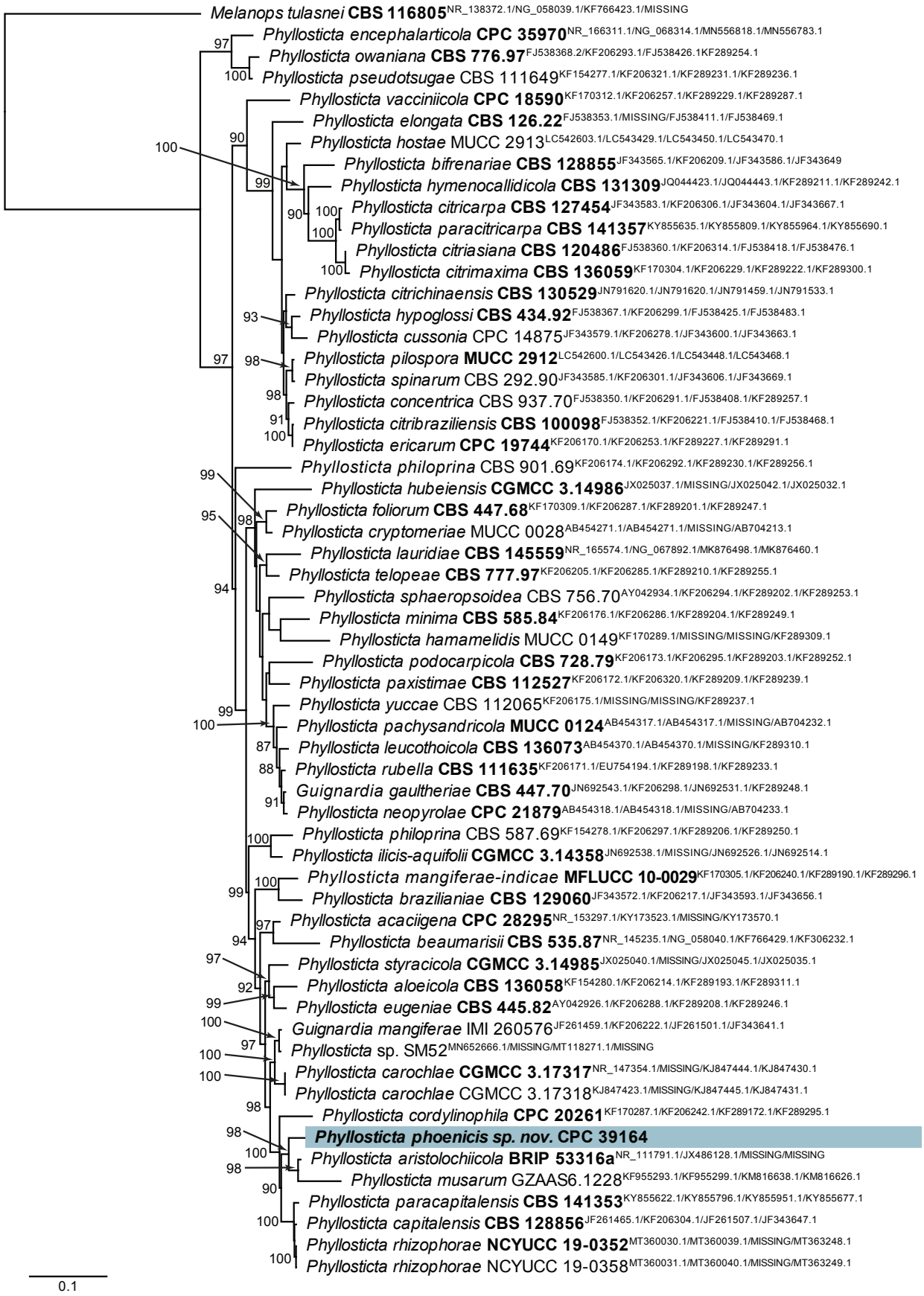

Fig. 56. Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE of the *Phyllosticta* multigene (ITS / LSU / *tef1* / *actA*) nucleotide alignment of the novel *Phyllosticta* species treated in this study. The alignment is based on Norphanphoun *et al.* (2020). Bootstrap support values (> 79 %) from 5 000 ultrafast bootstrap replicates are shown at the nodes. GenBank accession (superscript) and / or culture collection / voucher numbers (in bold face when having a type status) are indicated for all species. The tree was rooted to *Melanops tulasnei* (culture CBS 116805) and the novel species treated in this study is highlighted with a coloured block and bold face. Alignment statistics: 59 strains including the outgroup; 1 592 characters including alignment gaps analysed: 732 distinct patterns, 376 parsimony-informative, 227 singleton sites, 988 constant sites. The best models identified in IQ-TREE were: TIM2e+I+G4 (ITS), TNe+I+G4 (LSU), HKY+F+G4 (*tef1*), TPM2+F+G4 (*actA*).

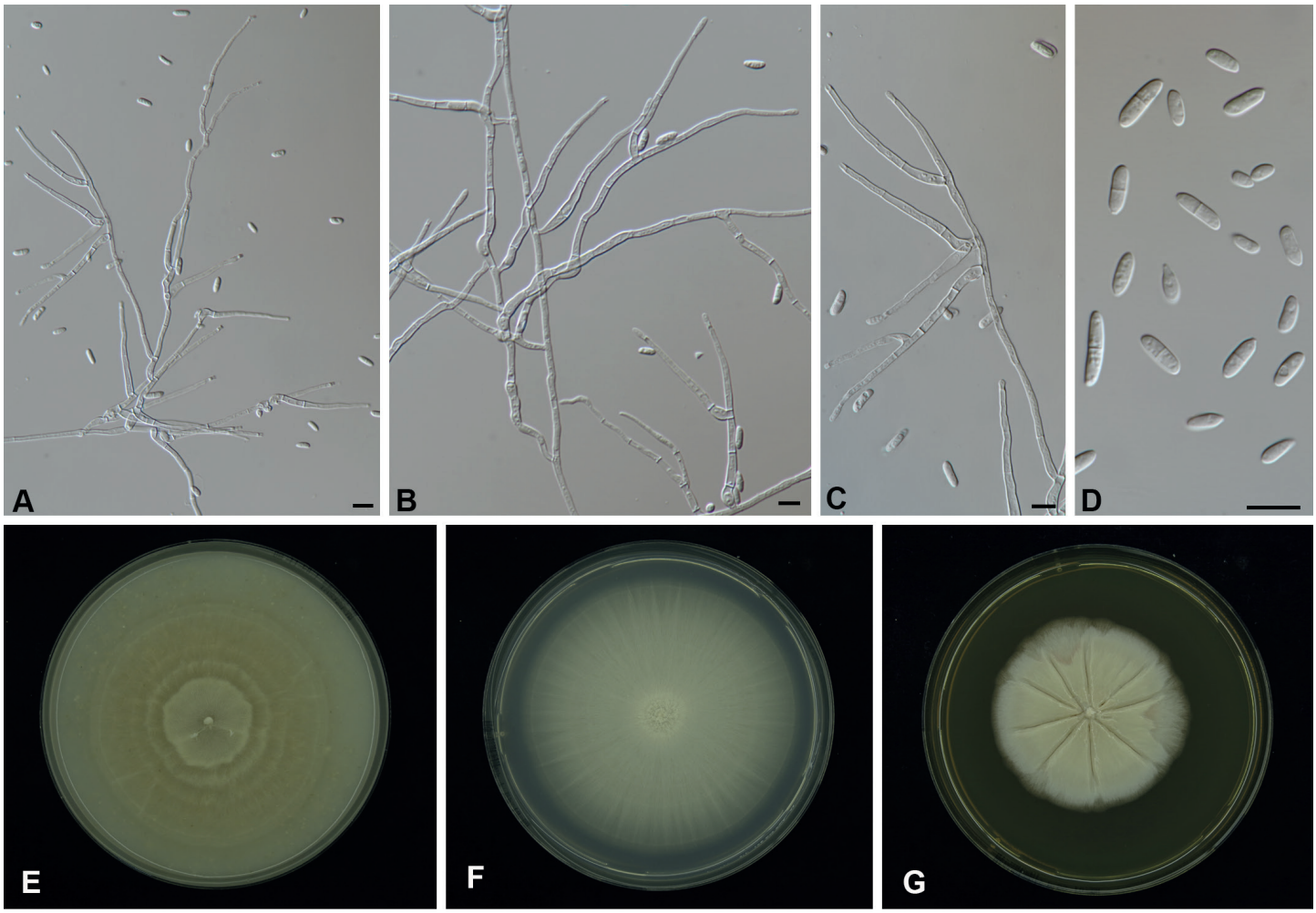

Fig. 57. *Plectosphaerella slobbergiarum* (CBS 147227). **A–C.** Conidiophores and conidia. **D.** Conidia. **E.** Colony on OA. **F.** Colony on PDA. **G.** Colony on MEA. Scale bars A–D = 10 µm.

Culture characteristics: After 2 wk at 24 °C on PDA reaching 68 mm diam, buff white, in the centre cottony, elevated, with moderate aerial mycelium, becoming less towards the periphery, fimbriate, margin regular, entire, reverse buff. On OA reaching 60 mm diam, zonate with concentric rings, buff and honey; centre with moderate aerial mycelium, glabrous towards the periphery, margin entire, regular; reverse honey buff. On MEA reaching 48 mm diam, buff, sparse aerial mycelium, wet appearance, with radial disposition of the wrinkles, margin slightly lobate; reverse ochreous with buff radial lines.

Typus: **Netherlands**, Groningen Province, Warffum, Juffer Martha street, from soil, 6 Jun. 2019, *J. Slob & M. Berghuis,* NL19_030 (**holotype** CBS H-24736, culture ex-type CBS 147227 = NL1930002).

Notes: *Plectosphaerella* comprises several plant pathogenic and soil-born species (Carlucci *et al.* 2012, Giraldo & Crous 2019, Giraldo *et al.* 2019, Zhang *et al.* 2019). *Plectosphaerella slobbergiarum* is phylogenetically distinct (Fig. 58), and distinguished from other species mainly based on *tef1* sequences.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *P. nauculispora* (strain CBS 144924 as "*pauciseptata*", GenBank LR590240.1; Identities = 545/549 (99 %), no gaps), *P. plurivora* (strain GBC-Fungus 109 as "*niemeijerarum*", GenBank MN077480.1; Identities = 541/545 (99 %), no gaps), and *P. cucumerina* (strain IIIZ1-2, GenBank MN915127.1; Identities = 544/549 (99 %), one gap (0 %)). Closest hits using the **LSU** sequence are *P. cucumerina* (strain BCC86515, GenBank MH398573.1; Identities = 817/817 (100 %), no gaps); strain CBS 137.37, GenBank MH867359.1; Identities = 817/817 (100 %), no gaps), and strain CBS 355.36, GenBank MH867324.1; Identities = 817/817 (100 %), no gaps) – also see Fig. 5. Closest hits using the ***tef1*** sequence are *P. citrulli* (strain CBS 131741 as "*citrullae*", GenBank LR026491.1; Identities = 774/787 (98 %), no gaps); strain CBS 131740, GenBank LR026490.1; Identities = 774/787 (98 %), no gaps) and *P. humicola* (strain CBS 423.66 as "*plurivora*", GenBank LR026506.1; Identities = 772/787 (98 %), no gaps).

Author: M. Hernández-Restrepo

Populomyces Hern.-Restr., ***gen. nov.*** MycoBank MB 838712.

Etymology: From Latin *Populus,* meaning civilians, and referring to the fact that the fungus was collected during a Citizen Science project of the Westerdijk Fungal Biodiversity Institute.

Vegetative hyphae hyaline, septate, smooth. *Conidiophores* micronematous, mostly reduced to conidiogenous cells.

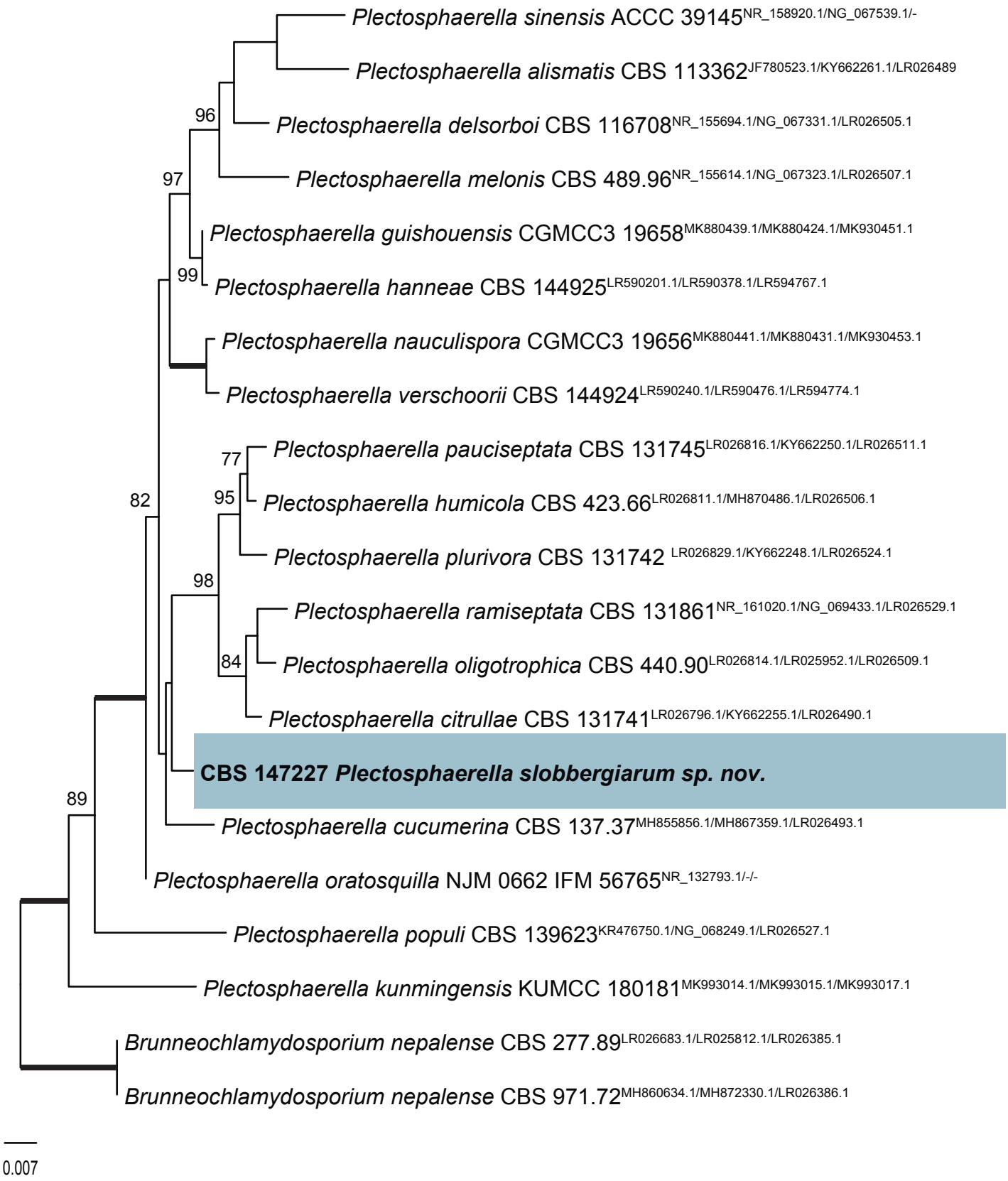

Fig. 58. Maximum composite likelihood tree obtained from the RAxML analysis of the combined ITS, LSU and *tef1* sequence alignment of *Plectosphaerella* species. Bootstrap support values above 70 % are shown at the nodes. The novel species is indicated in a coloured block and bold face. The tree was rooted to *Brunneochlamydosporium nepalense* (CBS 277.89 and CBS 971.72). Alignment statistics: 12 strains including the outgroup; 2 851 characters including alignment gaps analysed (ITS: 582, LSU: 1391, *tef1*: 878). Model: GTR+G, alignment patterns: 213.

Conidiogenous cells monophialidic, aggregated in groups, hyaline, smooth, cylindrical to lageniform. *Conidia* aseptate, cylindrical, solitary, hyaline.

Type species: *Populomyces zwinianus* Hern.-Restr.

Populomyces zwinianus Hern.-Restr., ***sp. nov.*** MycoBank MB 838713. Fig. 59.

Etymology: Name refers to the school from where the sample was collected "Zwin College" (Oostburg, the Netherlands). This sample was collected during a Citizen Science project of the Westerdijk Fungal Biodiversity Institute.

Vegetative hyphae hyaline, septate, smooth, 1–2 µm wide. *Conidiophores* micronematous, mostly reduced to conidiogenous cells. *Conidiogenous cells* monophialidic, aggregated in groups, hyaline, smooth, cylindrical to lageniform, 5–16 × 2–3.5 µm, with a cylindrical collarette, 0.5–1.5 µm deep, 1–1.5 µm wide. *Conidia* aseptate, cylindrical, solitary, hyaline, guttulate, 9–12 × 2–2.5 µm.

Culture characteristics: After 2 wk at 24 °C on OA reaching 15 mm diam, membranous, saffron; sparse aerial mycelium, margin regular; reverse pale luteous. On MEA reaching 10 mm diam, elevated, with radial disposition of the wrinkles, velvety, peach to flesh, margin slightly lobate; reverse saffron to apricot.

Typus: **Netherlands**, Zeeland Province, Yerseke, from soil, 11 Jun. 2019, *W. Vercouteren, S. Meas & R. Verhije,* NL19_076 (**holotype** CBS H-24737, ex-type strain CBS 147307 =NL1976004).

Notes: *Populomyces* is phylogenetically close to *Calloria* and *Tricellula* (Fig. 2). The cylindrical, aseptate conidia of *Populomyces* are easily distinguished from the stauroconidia of *Tricellula* (Seifert *et al.* 2011). Furthermore, *Calloria* is a polyphyletic genus with apothecial ascomata including species that are related to *Cylindrocolla* asexual morphs, characterised by polyblastic conidiogenous cells producing conidia in chains, thus distinct from the solitary conidia of *Populomyces* (Muntañola-Cvetkovic *et al.* 1997, Seifert *et al.* 2011).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Chalara* sp. (GenBank KX034388.1; Identities = 463/510 (91 %), one gap (0 %)), *Dothideomycetes* sp. (strain CK1374, GenBank MH474014.1; Identities = 444/493 (90 %), 16 gaps (3 %)), and Fungal sp. (strain LEG-103, GenBank MW201484.1; Identities = 446/496 (90 %), 15 gaps (3 %). Closest hits using the **LSU** sequence are *Calloria urticae* (strain G.M. 2016-03-12.3, GenBank MT509570.1; Identities = 630/669 (94 %), four gaps (0 %)), *Calloria urticae* (strain MFLU 18-0697, GenBank MK591969.1; Identities = 824/824 (100 %), four gaps (0 %)), and *Calloria urticae* (strain MFLU 18-0696, GenBank MK591968.1; Identities = 630/669 (94 %), four gaps (0 %)) – also see Fig. 2.

Author: M. Hernández-Restrepo

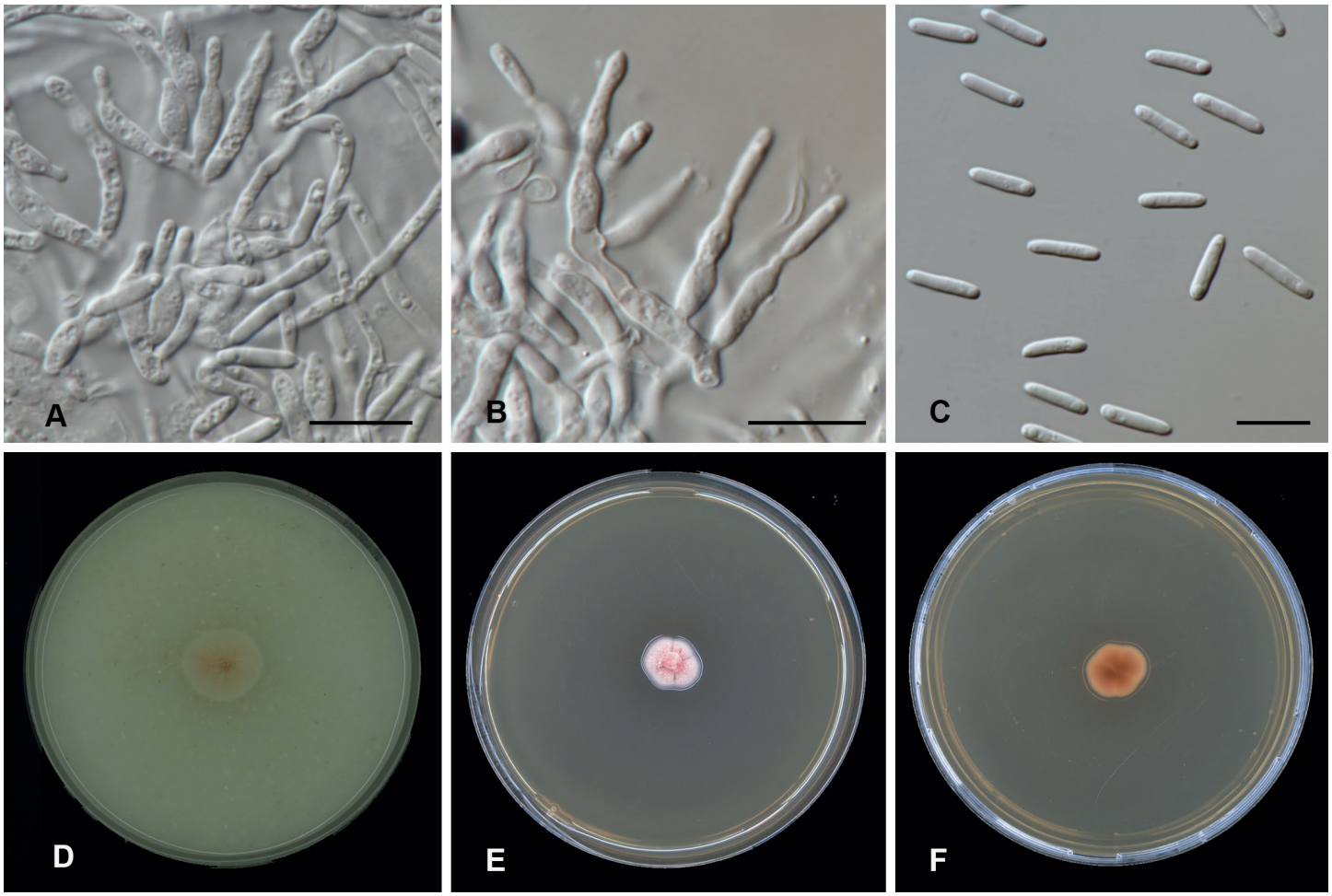

Fig. 59. *Populomyces zwinianus* (CBS 147307). **A–B.** Conidiophores and conidia. **C.** Conidia. **D.** Colony on OA. **E.** Colony on MEA. **F.** Reverse colony on MEA. Scale bars A–C = 10 µm.

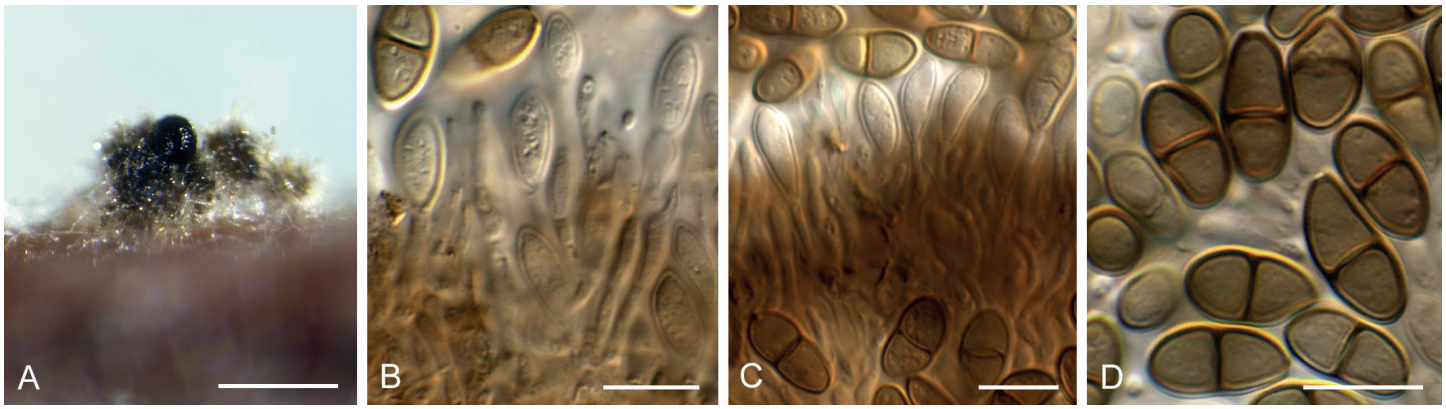

Fig. 60. *Porodiplodia vitis* (CPC 38692). **A.** Conidiomata on PNA. **B–C.** Conidiogenous cells. **D.** Conidia. Scale bars: A = 300 µm, all others = 10 µm.

Porodiplodia vitis Crous & R.K. Schumach., *Fung. Syst. Evol.* **3**: 110. 2019. Fig. 60.

Conidiomata eustromatic, uni- to multilocular, brown, globose, 150–300 µm, aggregated on PNA, ostiolate. *Conidiophores* lining inner cavity, subcylindrical, hyaline, smooth, branched, 1–3-septate, 15–20 × 2.5–4 µm, proliferating percurrently near apex. *Paraphyses* intermingled among conidiophores, hyaline, smooth, septate, subcylindrical with obtuse ends, up to 25 µm long. *Conidia* in short chains (–3), fusoid-ellipsoid to subcylindrical, medium brown, finely verruculose, guttulate, thick-walled, medianly 1-septate, apex obtuse, base truncate with central pore, (11–)12–14(–17) × (4–)6(–7) µm.

Culture characteristics: Colonies flat, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface rosy buff, reverse cinnamon; on PDA surface honey, reverse isabelline; on OA surface cinnamon.

Material examined: **South Africa**, Western Cape Province, Kirstenbosch, on seed pods of *Virgilia oroboides* (*Fabaceae*), 2018, *M.J. Wingfield*, HPC 3070 (CBS H-24436, culture CPC 38692 = CBS 146818).

Notes: *Porodiplodia* was recently established as a new genus for a species occurring on leaves of *Livistona australia* in Australia (Crous *et al.* 2018b). A second species, *P. vitis*, was described from canes of *Vitis vinifera* in the USA (Crous *et al*. 2019a).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Porodiplodia* sp. (strain EAB-24-17, GenBank MT777297.1; Identities = 459/460 (99 %), no gaps), *Porodiplodia livistonae* (strain CPC 32154, GenBank NR_160355.1; Identities = 536/538 (99 %), no gaps), and *Porodiplodia vitis* (strain CBS 144634, GenBank NR_163376.1; Identities = 543/546 (99 %), no gaps). Closest hits using the **LSU** sequence are *Porodiplodia vitis* (strain CBS 144634, GenBank NG_070080.1; Identities = 824/824 (100 %), no gaps), *Porodiplodia livistonae* (strain CPC 32154, GenBank NG_069575.1; Identities = 824/824 (100 %), no gaps), and *Chalara clidemiae* (strain CPC 26423, GenBank KX228321.1; Identities = 817/824 (99 %), no gaps) – also see Fig. 2. Closest hits using the ***tef1*** sequence had highest similarity to *Porodiplodia vitis* (strain CBS 144634, GenBank MK442707.1; Identities = 463/473 (98 %), single indel of ten nucleotides (2 % gap)), *Davidhawksworthia ilicicola* (strain CBS 261.95, GenBank KU728592.1; Identities = 205/233 (88 %), seven gaps (3 %)), and *Hymenoscyphus menthae* (strain HB_5846, GenBank KM114512.1; Identities = 204/232 (88 %), six gaps (2 %)). A comparison with the *tef1* sequence we generated of *Porodiplodia livistonae* in this study revealed a similarity of 426/439 (97 %, including a single indel of ten nucleotides (2 % gap) also present for *Porodiplodia vitis*).

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

Pseudoacrospermum Crous, ***gen. nov.*** MycoBank MB 839303.

Etymology: Name refers to the fact that it is phylogenetically closely related to *Acrospermum*.

Mycelium consisting of septate, branched, smooth, pale brown, hyphae. *Conidiophores* solitary, erect, flexuous, subcylindrical, multiseptate, unbranched with basal T-cell, arising from superficial mycelium, thick-walled, pale olivaceous, smooth, lacking rhizoids, terminating in a slightly swollen conidiogenous cell. *Conidiogenous cells* integrated, terminal, subclavate, with numerous sympodial loci aggregated in a rachis, darkened, thickened, but not refractive, pimple-like, protruding. *Conidia* solitary, smooth, pale olivaceous to granular, subclavate, curved, apex obtuse, tapering to truncate hilum, darkened, thickened, and refractive, somewhat thick-walled, transversely septate.

Type species: *Pseudoacrospermum goniomae* Crous

Pseudoacrospermum goniomae Crous, ***sp. nov.*** MycoBank MB 839304. Fig. 61.

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

Mycelium consisting of septate, branched, smooth, pale brown, 2–2.5 µm diam hyphae. *Conidiophores* solitary, erect, flexuous, subcylindrical, multiseptate, unbranched with basal T-cell, arising from superficial mycelium, thick-walled, pale olivaceous, smooth, lacking rhizoids, 100–180 × 2.5–3.5 µm, terminating in a slightly swollen conidiogenous cell. *Conidiogenous cells* integrated, terminal, subclavate, 15–20 × 4–6 µm, with numerous sympodial loci aggregated in a rachis, darkened, thickened, but not refractive, pimple-like, protruding (0.5 µm), 1–2 µm diam. *Conidia* solitary, smooth, pale olivaceous to granular, subclavate, curved, apex obtuse, tapering to truncate hilum, 2 µm diam, darkened, thickened, and refractive, somewhat thick-walled, 3(–6)-septate, (17–)21–23(–25) × (5–)6 µm.

Fig. 61. *Pseudoacrospermum goniomae* (CPC 37030). **A.** Conidiophores on SNA. **B–D.** Conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars: A = 180 µm, all others = 10 µm.

Culture characteristics: Colonies flat, spreading, surface folded, with moderate aerial mycelium and smooth, even margin, reaching 5 mm diam after 2 wk at 25 °C. On MEA surface buff to honey, reverse isabelline; on PDA surface straw in centre, outer margin buff to cinnamon, reverse cinnamon; on OA surface cinnamon.

Typus: **South Africa**, Western Cape Province, Knysna, on leaves of *Gonioma kamassi* (*Apocynaceae*), 22 Nov. 2018, *F. Roets*, HPC 2733 (**holotype** CBS H-24393, culture ex-type CPC 37030 = CBS 146732).

Notes: *Pseudoacrospermum* is phylogenetically closely related to *Acrospermum*, which is known only by a sexual morph. Based on its phylogeny, *Acrospermum* has been shown to be closely related to such as *Gonatophragmium*, *Radulidium* or *Pseudovirgaria* (Hudson *et al.* 2019), that are presently known by their asexual morphs. *Pseudoacrospermum* is distinguished based on its multiseptate conidia. There is no evidence to suggest that *Pseudoacrospermum* can be linked to *Acrospermum.* A phylogenetic tree is presented as Fig. 62.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Acrospermum maxonii* (as *Acrospermum* sp. VD-2019c; voucher 2711, GenBank MK562001.1; Identities = 344/421 (82 %), 23 gaps (5 %)), *Radulidium epichloes* (strain CBS 115704, GenBank MH862990.1; Identities = 217/236 (92 %), five gaps (2 %)), and *Acrospermum leucocephalum* (as *Acrospermum* sp. VD-2019b; voucher 764, GenBank MK562008.1; Identities = 334/413 (81 %), 22 gaps (5 %)). Closest hits using the **LSU** sequence are *Acrospermum gorditum* (as *Acrospermum* sp. VD-2019a; voucher 1774, GenBank MK561981.1; Identities = 803/867 (93 %), seven gaps (0 %)), *Acrospermum maxonii* (as *Acrospermum* sp. VD-2019c; voucher 3114, GenBank MK561987.1; Identities = 804/870 (92 %), 11 gaps (1 %)), and *Gonatophragmium triuniae* (strain CBS 138901, GenBank NG_058117.1; Identities = 764/827 (92 %), nine gaps (1 %)) – also see Fig. 1. The best hit using the ***rpb2*** sequence had highest similarity to *Pseudovirgaria hyperparasitica* (strain CBS 121739, GenBank XM_033741841.1; Identities = 573/769 (75 %), ten gaps (1 %)). Only very distant hits with taxa in *Dothideomycetes* were obtained using the ***tef1*** (first and second part) sequences. However, both these sequences were manually compared with blast2 searches against *Acrospermum tef1* sequences labelled as unverified in the GenBank nucleotide database: Closest hits using the ***tef1*** (first part) sequence had highest similarity to *Acrospermum maxonii* (strain 75017, GenBank MK604769.1; Identities = 198/234 (85 %), seven gaps (2 %)), *Acrospermum gorditum* (strain 1774, GenBank MK604778.1; Identities = 196/232 (84 %), two gaps (0 %)), and *Acrospermum leucocephalum* (strain 3342, GenBank MK604780.1; Identities = 213/256 (83 %), nine gaps (3 %)). Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Acrospermum maxonii* (strain 44, GenBank MK604767.1; Identities = 426/473 (90 %), no gaps), and *Acrospermum leucocephalum* (strain 764, GenBank MK604781.1; Identities = 412/474 (87 %), one gap (0 %)).

Authors: P.W. Crous, J.Z. Groenewald & F. Roets

Pseudopyricularia festucae Crous, ***sp. nov.*** MycoBank MB 839305. Fig. 63.

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

Mycelium consisting of branched, septate, hyaline, smooth, 2.5–3.5 µm diam hyphae. *Conidiophores* solitary, erect, subcylindrical, unbranched, flexuous, medium brown, smooth, up to 150 µm tall, 5–6 µm diam, with 1–2 basal septa. *Conidiogenous cells* terminal, integrated, medium brown, smooth, 70–100 µm tall, with a rachis of protruding denticles, 1.5–2 × 1–1.5 µm. *Conidia* solitary, pale brown, fusoid, finely roughened, 2-septate, apex subobtuse, base truncate, 1.5 µm diam, apex somewhat thickened, (25–)30–38(–40) × (6–)7 µm.

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

Typus: **USA**, California, UC Davis, on leaves of *Festuca californica* (*Poaceae*), 3 Apr. 2019, *P.W. Crous*, HPC 2915 (**holotype** CBS H-24352, culture ex-type CPC 37915 = CBS 146629).

Notes: *Pseudopyricularia* is characterised by having short, determinate, brown conidiophores with an apical rachis with flat-tipped denticles (Klaubauf *et al.* 2014, Marin-Felix *et al.* 2017). The present isolate is phylogenetically closely related to

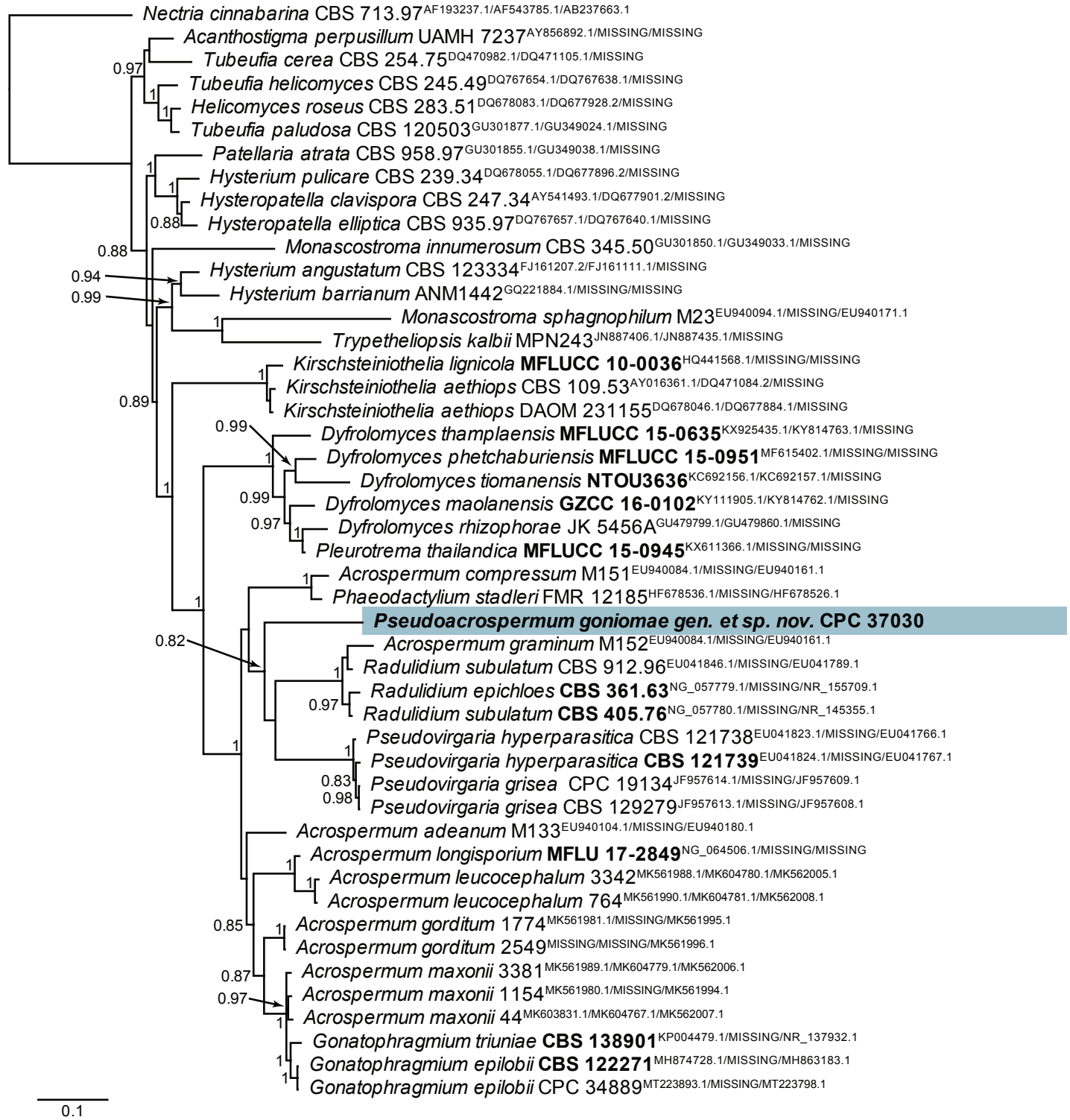

Fig. 62. Consensus phylogram (50 % majority rule) resulting from a Bayesian analysis of the *Acrospermum* and related genera multigene (LSU / *tef1* / ITS) nucleotide alignment. The alignment is derived from Hudson *et al*. (2019). Bayesian posterior probabilities (> 0.79) are shown at the nodes and the scale bar represents the expected changes per site. GenBank accession (superscript) and / or culture collection / voucher numbers (in bold face when having a type status) are indicated for all species. The tree was rooted to *Nectria cinnabarina* (culture CBS 713.97) and the novel species treated in this study is indicated in a coloured block and bold face. Alignment statistics: 47 strains including the outgroup; 595 / 418 / 284 unique site patterns, respectively. Tree statistics: 184 502 sampled trees from 1 230 000 generations.

P. iraniana (conidia (20–)22–30 × 5–8 µm, on *Juncus* sp. in Iran; Pordel *et al*. 2017) but has longer conidia, (25–)30–38(–40) × (6–)7 µm. A phylogenetic species tree is presented as Fig. 64.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pseudopyricularia iraniana* (strain IRAN 2761C, GenBank NR_158928.1; Identities = 500/504 (99 %), no gaps), *Dactylaria higginsii* (strain CBS 121934, GenBank KM009164.1; Identities = 482/509 (95 %), 7 gaps (1 %)), and *Pseudopyricularia bothriochloae* (strain CBS 136427, GenBank NR_137838.1; Identities = 519/552 (94 %), 11 gaps (1 %)). Closest hits using the **LSU** sequence are *Pseudopyricularia iraniana* (strain 17d, GenBank KY457268.1; Identities = 863/863 (100 %), no gaps), *Pyricularia caricis* (strain JAC12652, GenBank MK431456.1;

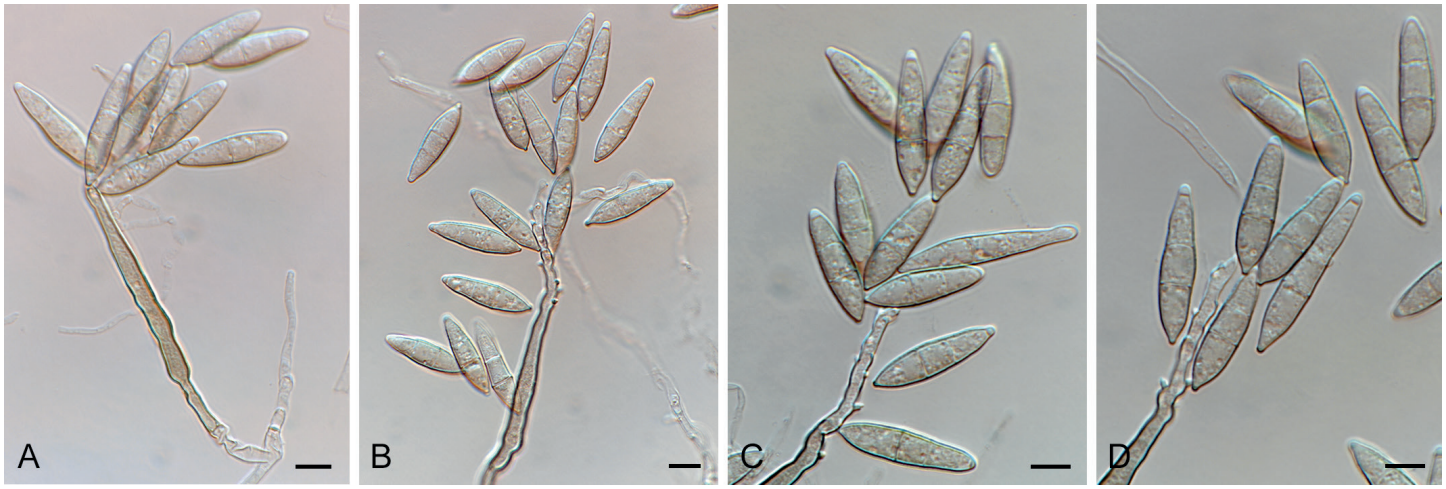

Fig. 63. *Pseudopyricularia festucae* (CPC 37915). **A–D.** Conidiophores with conidiogenous cells giving rise to conidia. Scale bars = 10 µm.

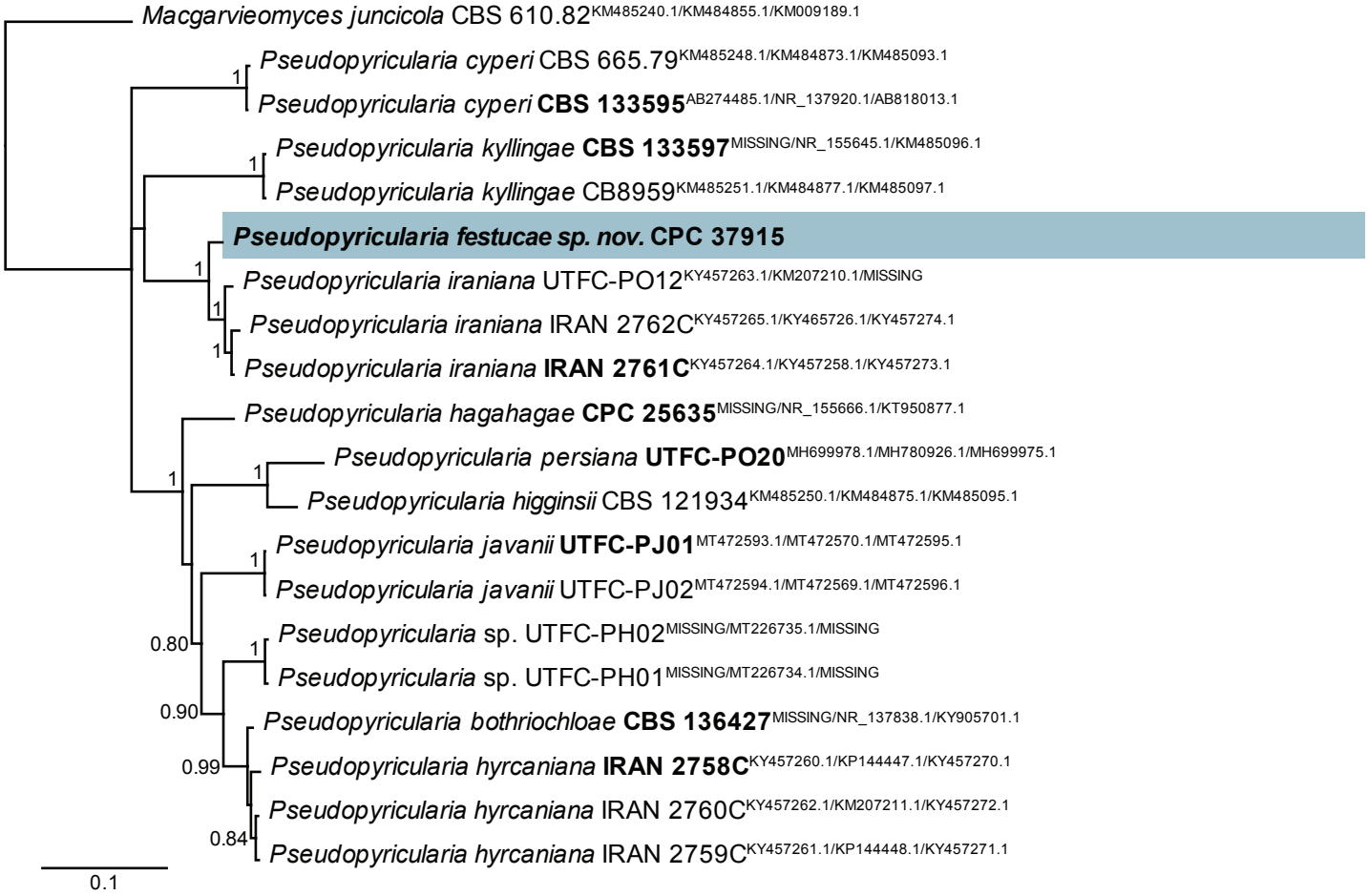

Fig. 64. Consensus phylogram (50 % majority rule) resulting from a Bayesian analysis of the *Pseudopyricularia* multigene (*cmdA* / ITS / *rpb1*) nucleotide alignment. The alignment is derived from Klaubauf *et al*. (2014). Bayesian posterior probabilities (> 0.79) are shown at the nodes and the scale bar represents the expected changes per site. GenBank accession (superscript) and / or culture collection / voucher numbers (in bold face when having a type status) are indicated for all species. The tree was rooted to *Macgarvieomyces juncicola* (culture CBS 610.82) and the novel species treated in this study is indicated in a coloured block and bold face. Alignment statistics: 20 strains including the outgroup; 248 / 123 / 254 unique site patterns, respectively. Tree statistics: 39 002 sampled trees from 130 000 generations.

Identities = 874/880 (99 %), no gaps), and *Pseudopyricularia hyrcaniana* (strain Ck3, GenBank KY457267.1; Identities = 850/863 (98 %), no gaps) – also see Fig. 5. Closest hits using the ***cmdA*** sequence had highest similarity to *Pseudopyricularia iraniana* (strain 16d, GenBank KY457263.1; Identities = 400/414 (97 %), 11 gaps (2 %)), *Pseudopyricularia kyllingae* (strain CB8959, GenBank KM485251.1; Identities = 429/511 (84 %), 17 gaps (3 %)), *Macgarvieomyces borealis* (strain CBS 461.65, GenBank KM485239.1; Identities = 156/163 (96 %), no gaps), and *Macgarvieomyces luzulae* (strain CPC 31571,

GenBank MG934521.1; Identities = 153/160 (96 %), no gaps). Closest hits using the ***rpb1*** sequence had highest similarity to *Pseudopyricularia iraniana* (strain 17d, GenBank KY457273.1; Identities = 961/981 (98 %), no gaps), *Pseudopyricularia bothriochloae* (strain CBS 136427, GenBank KY905701.1; Identities = 614/669 (92 %), no gaps), and *Pseudopyricularia hagahagae* (strain CPC 25635, GenBank KT950877.1; Identities = 926/1 013 (91 %), no gaps).

Authors: P.W. Crous, J.Z. Groenewald & L. Lombard

Sarocladium sasijaorum Hern.-Restr., ***sp. nov.*** MycoBank MB 838714. Fig. 65.

Etymology: Name reflects the names of the collectors Sami Maghnouji, Simon Frederikze, and Jason Mes, students from Wereldwijs (Bilthoven, the Netherlands). This sample was collected during a Citizen Science project of the Westerdijk Fungal Biodiversity Institute.

Vegetative hyphae septate, hyaline, smooth and thin-walled, 1–2 µm wide. *Conidiophores* erect, arising directly from vegetative hyphae or ropes of hyphae, straight or slightly bent, simple, hyaline, smooth-walled. *Phialides* subulate to acicular, 16–32 µm long, 1.5–2 µm wide at the base, 1–1.5 µm wide at the apex, straight or flexuous, hyaline, thin- and smooth-walled. *Conidia* arranged in long chains, unicellular, fusoid, with pointed ends, becoming limoniform to obovoid with age, 4–6 × 1.5–2 µm, hyaline, smooth-walled. *Chlamydospores* and *sexual morph* not observed.

Culture characteristics: After 7 d at 25 °C on OA attaining 13 mm diam, cottony, flat, with sparse aerial mycelium, buff to white, dry, margin effuse; reverse similar. On MEA attaining 14 mm diam, cottony, elevated, buff to pale luteous; reverse apricot. On PDA attaining 13 mm diam, cottony to hairy, with sparse aerial mycelium towards the periphery, olivaceous buff to white; reverse pale luteous in centre, white towards the periphery.

Typus: **Netherlands**, Utrecht Province, Bilthoven, Planetenplein, from soil, 31 Jul. 2019, *S. Frederikze, J. Mes & S. Maghnouji*, NL19_100 (**holotype** CBS H-24738, culture ex-type CBS 147213 = NL19100007).

Notes: *Sarocladium sasijaorum* is phylogenetically close to *S. dejongiae*, *S. liguanense*, and *S. clematidis* (Fig. 66). *Sarocladium clematidis* was described from Belgium on dead stems of *Clematis patens* (Phukhamsakda *et al.* 2020) and resembles *Phaeoisaria clematidis* based on morphology. *Sarocladium dejongiae* was recently described form Dutch soil (Crous *et al.*

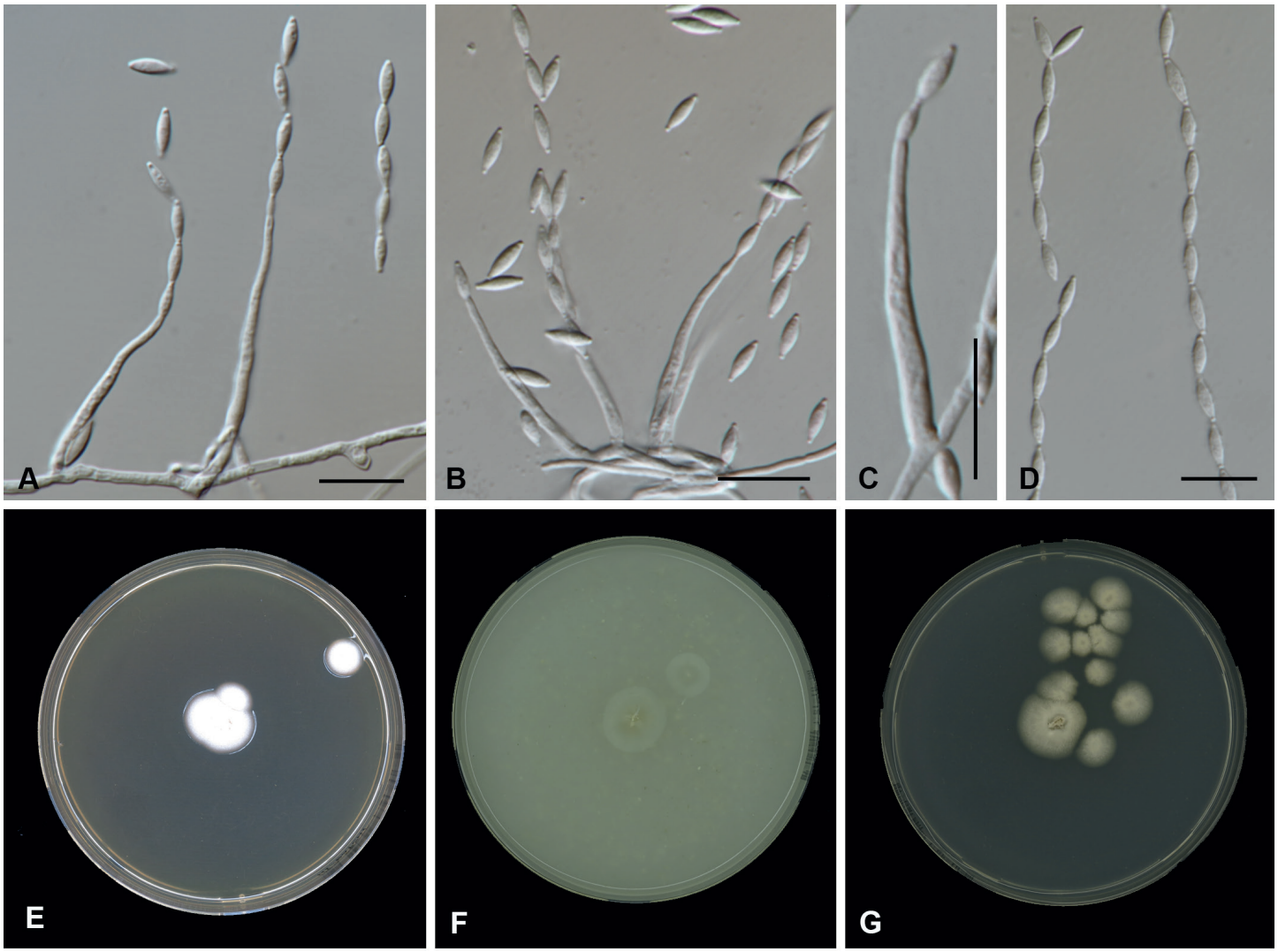

Fig. 65. *Sarocladium sasijaorum* (CBS 147213). **A–C.** Conidiophores and conidia. **D.** Conidia. **E.** Colony on MEA. **F.** Colony on OA. **G.** Colony on PDA. Scale bars A–D = 10 µm

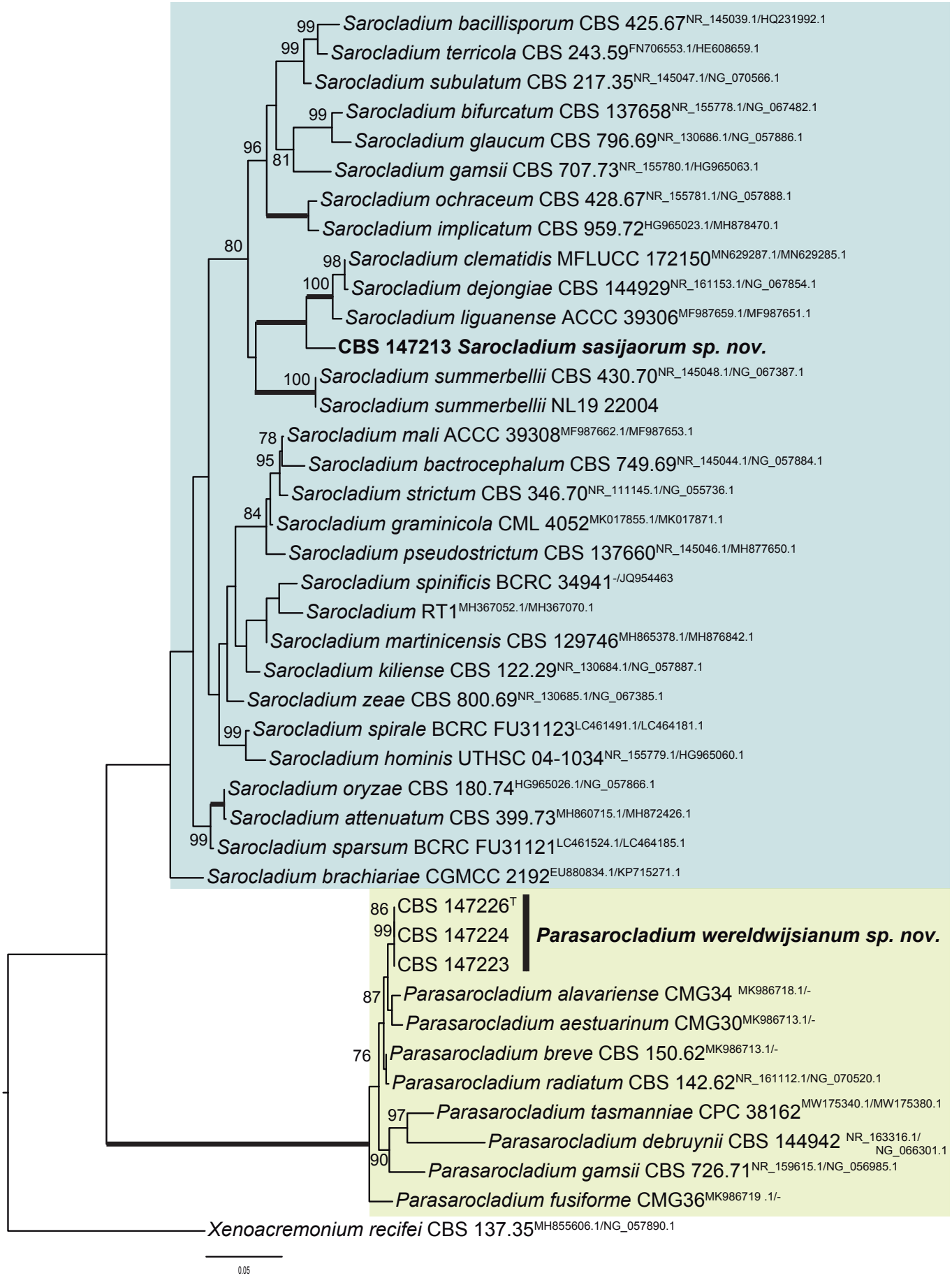

Fig. 66. Maximum composite likelihood tree obtained from the RAxML analysis of the combined ITS and LSU sequence alignment of *Sarocladiaceae* members. Bootstrap support values above 70 % are shown at the nodes. The novel species are indicated in bold face and the two genera are indicated with coloured blocks. The tree was rooted to *Xenoacremonium recifei* (CBS 137.35). Alignment statistics: 43 strains including the outgroup; 1 571 characters including alignment gaps analysed (ITS: 642, LSU: 929). Model GTR+I+G, 620 distinct patterns.

2018a) and *S. liguanense* from China on *Malus* × *domestica* (Hou *et al.* 2019). However, *S. sasijaorum* is distinguishable based on its conidial arrangement and morphology. In *S. sasijaorum* conidia are ellipsoidal with pointed ends, 4–6 × 1.5–2 µm and arranged in chains; in *S. dejongiae* conidia are ellipsoidal to cylindrical, 3–5 × 1–2 µm (av. 3 × 1.5 µm) and disposed in slimy heads (Crous *et al.* 2018a), and in *S. liguanense* conidia are ellipsoidal to cylindrical, 3–6.5 × 1.5–3 µm, and arranged in slimy heads (Hou *et al.* 2019). Furthermore, in *S. dejongiae* and *S. liguanense* chlamydospores are present (Crous *et al.* 2018a, Hou *et al.* 2019), while they were not observed in *S. sasijaorum*. Also see the overview phylogeny (Fig. 4).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Ascomycota* sp. (strain j17, GenBank EU167596.1; Identities = 488/491 (99 %), one gap (0 %)), *Hypocreales* sp. (strain f10, GenBank MN982323.1; Identities = 481/484 (99 %), one gap (0 %)), and Fungal sp (strain acwVHT103_8, GenBank JQ070513.1; Identities = 427/442 (97 %), three gaps (0 %)). Closest hits using the **LSU** sequence are *Sarocladium* sp. (strain ACCC 39306, GenBank MF987651.1; Identities = 773/779 (99 %), no gaps), *Sarocladium dejongiae* (strain CBS 144929, GenBank NG_069161.1; Identities = 773/779 (99 %), no gaps), and *Sarocladium* sp. (strain MFLUCC 17-2150, GenBank MN629285.1; Identities = 767/779 (98 %), no gaps) – also see Fig. 4. Closest hits using the ***rpb2*** sequence had highest similarity to *Sarocladium* sp. (strain MFLUCC 17-2150, GenBank MN628627.1; Identities = 683/761 (90 %), no gaps), *Acremonium* sp. DLW-2010 (strain 11665, GenBank GQ867809.1; Identities = 650/811 (80 %), four gaps (0 %)), and *Sarocladium* sp. (strain A131, GenBank KC999025.1; Identities = 650/811 (80 %), four gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Sarocladium implicatum* (strain 04035, GenBank KT878359.1; Identities = 601/630 (95 %), no gaps), *Sarocladium kiliense* (GenBank MK512750.1; Identities = 591/630 (94 %), no gaps), and *Sarocladium kiliense* (strain MB20A1, GenBank LT615314.1; Identities = 591/630 (94 %), no gaps).

Author: M. Hernández-Restrepo

Septoria protearum Viljoen & Crous, *S. African J. Bot.* **64**: 144. 1998. Fig. 67.

Description and illustration: Verkley *et al*. (2013).

Material examined: **New Zealand**, Tuaranga Port, on *Kniphofia uvaria* (*Asphodelaceae*), 22 Aug. 2019, *D. Burnt*, culture CPC 38736 = T19_05709B.

Notes: *Septoria protearum* is a plurivorous species known from various hosts in South Africa, Europe and New Zealand (Verkley *et al*. 2013). *Septoria citri* is considered to belong to the *Septoria protearum* species complex which still needs to be resolved (Verkley *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 *Septoria coprosmae* (as *Mycosphaerella coacervata*; strain CBS 113391, GenBank EU167596.1; Identities = 540/540 (100 %), no gaps), *Mycosphaerella linorum* (strain CBS 261.39, GenBank EU167590.1; Identities = 540/540 (100 %), no gaps), and *Septoria protearum* (strain CBS 778.97, GenBank NR_163551.1; Identities = 539/539 (100 %), no gaps). Closest hits using the **LSU** sequence are *Septoria protearum* (strain CBS 778.97, GenBank NG_069851.1; Identities = 751/752 (99 %), one gap (0 %)), *Septoria malagutii* (strain CBS 106.80, GenBank NG_069161.1; Identities = 751/752 (99 %), one gap (0 %)), and *Septoria citricola* (strain CBS 356.36, GenBank NG_069158.1; Identities = 751/752 (99 %), one gap (0 %)) – also see Fig. 1. Closest hits using the ***actA*** sequence had highest similarity to *Septoria protearum* (strain CBS 778.97, GenBank KF253827.1; Identities = 214/214 (100 %), no gaps), *Septoria citri* (strain CBS 315.37, GenBank JX902161.1; Identities = 543/543 (100 %), no gaps), *Septoria eucalyptorum* (strain CBS 118505, GenBank KF903501.1; Identities = 500/528 (95 %), three gaps (0 %)), and *Septoria carvi* (strain KML1860, GenBank KX822110.1; Identities = 495/531 (93 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Septoria protearum* (strain CBS 778.97, GenBank KF253472.1; Identities = 387/387 (100 %), no gaps), *Septoria citri* (strain CBS 315.37, GenBank JX901706.1; Identities 396/396 (100 %), no gaps), *Septoria chamaecisti* (strain CBS 350.58, GenBank KF253318.1; Identities = 387/387 (100 %), no gaps), and *Septoria citricola* (strain CBS 356.36, GenBank KF253329.1; Identities = 387/388 (99 %), one gap (0 %)).

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

Sporothrix hypoxyli W.J. Nel, Z.W. De Beer & T.A. Duong, ***sp. nov.*** MycoBank MB 837458. Fig. 68.

Etymology: Latin, *hypoxyli*, refers to the genus of the fungus fruiting body from which this species was isolated, *Hypoxylon*.

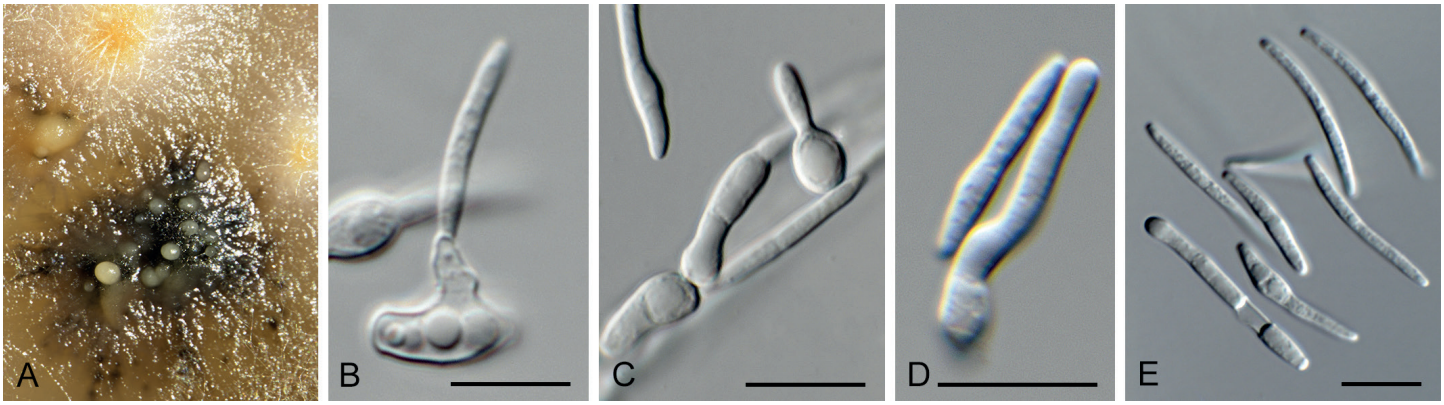

Fig. 67. *Septoria protearum* (CPC 38736). **A.** Conidiomata on OA. **B–D.** Conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars = 10 µm.

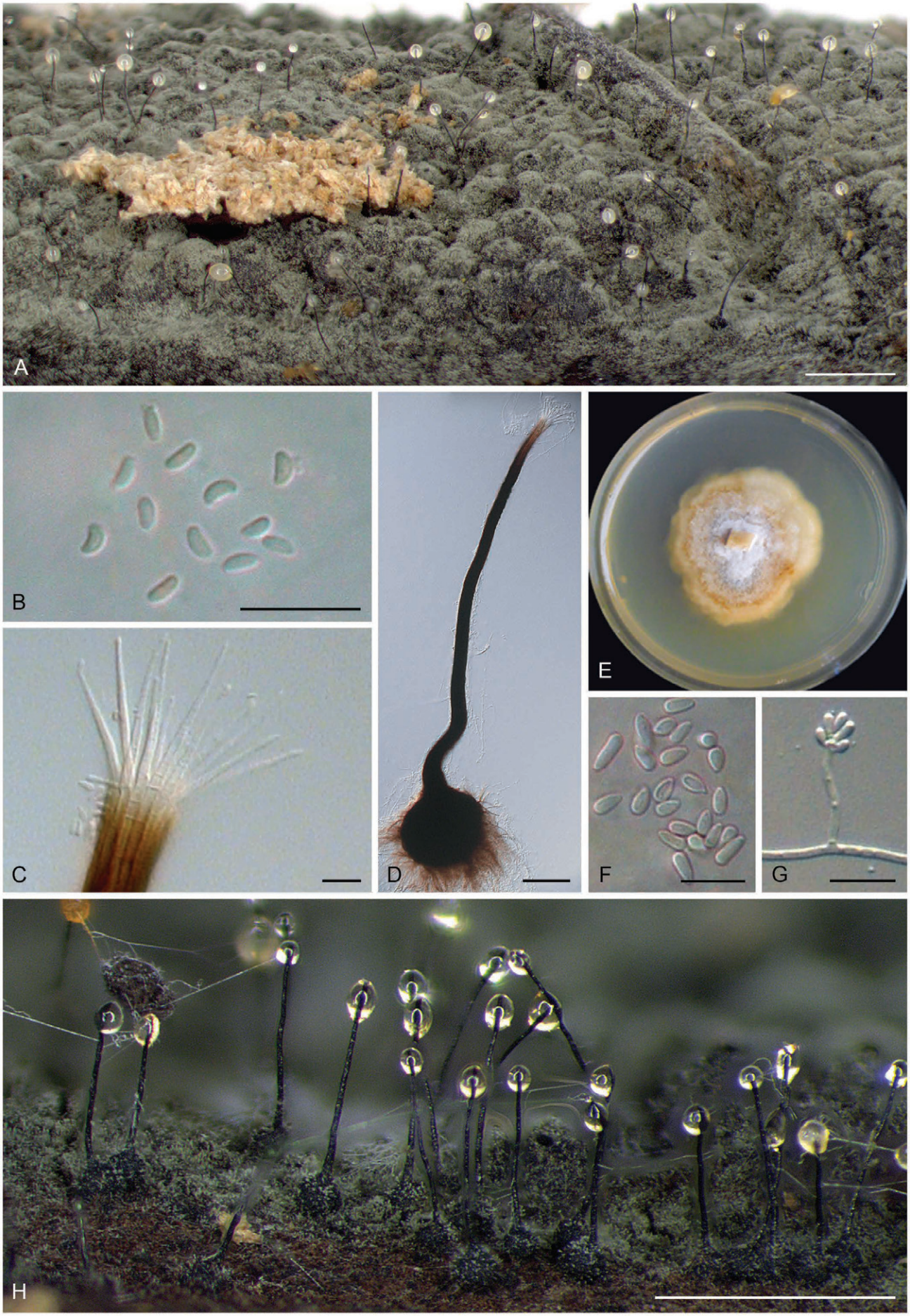

Fig. 68. *Sporothrix hypoxyli* (CBS 141569). **A, H.** Ascomata on *Fraxinus* wood embedded in fruiting body of *Hypoxylon petriniae*. **B.** Ascospores. **C.** Ostiole containing ostiolar hyphae. **D.** Ascoma. **E.** One-month-old culture on MEA. **F.** Conidia. **G.** Conidiophore. Scale bars: A, H = 1 mm, B–C, F–G = 10 µm, D = 100 µm.

Ascomatal bases black, globose, (140–)170–279(–392) µm diam, ornamented with brown hyphal hairs, (10–)18–47(–74) µm long, (1.5–)1.8–2.4(–2.6) µm diam. *Ascomatal necks*, black, mostly straight, occasionally slightly curved or kinked tapering toward apex, vary greatly in length, (429–)580–1125(–1504) µm long, (25–)35–49(–58) µm wide at base, (11–)14–23(–28) µm wide at apex. *Ostiolar hyphae* present, slightly divergent, hyaline, tapering toward tip, (24–)30–47(–59) µm long. *Asci* dehiscent. *Ascospores* produced in slimy droplet at apex of ascomatal neck, hyaline, aseptate, reniform to bean-shaped, no sheath, (2.6–)3.2–3.7(–3.8) µm long, (1.2–)1.4–1.7(–1.9) µm wide at centre. Sporothrix-like *asexual morph*. *Conidiophores* hyaline sometimes becoming light brown with age, smooth, arising singly from mycelia, micronematous, (14–)16–44(–88) µm long. *Conidiogenous cells* (4–)10–26(–40) µm long, denticulate. *Conidia* hyaline can become light brown with age, aseptate, round to obovoid, produced directly on denticles, arising either from hyphae or on conidiophores, (2.5–)3.4–4.6(–5.9) µm long, (2.2–)2.4–3(–3.5) µm wide at thickest part.

Culture characteristics (25 °C, 10 d, MEA): Colonies produce aerial mycelium initially white sometimes becoming pigmented with age, superficial mycelium in media initially white, becoming light to dark brown with age, slow growing, growing 14 mm in 10 d. Ascomata form in culture after 2–3 mo at low temperatures (5–15 °C).

Typus: **Netherlands**, Utrecht Province, Utrecht, ascomata embedded in sporocarp of *Hypoxylon petriniae* on *Fraxinus* wood, 19 Apr. 2015, *E. Osieck & W.J. Nel* (**holotype** PREM 63086, ex-type culture CMW 47441 = CBS 141569).

Additional materials examined: **Netherlands**, Utrecht Province, Utrecht, ascomata embedded in sporocarp of *Hypoxylon petriniae* on *Fraxinus* wood, 19 Apr. 2015, *E. Osieck & W.J. Nel* (PREM 63083, culture CMW 47436 = CBS 141568); Utrecht Province, Utrecht, ascomata embedded in sporocarp of *Hypoxylon petriniae* on *Fraxinus* wood, 19 Apr. 2015, *E. Osieck & W.J. Nel* (PREM 63085, culture CMW 47439 = CBS 141567).

Notes: A multigene phylogeny (Fig. 69) of combined sequences for the LSU, ITS and *tub2* gene regions resolved *Sporothrix hypoxyli* in a clade distant from all other *Sporothrix* spp. Few other species in the genus have previously been described in association with the sporocarps of other fungi (Guerrero 1971, Samuels & Müller 1979, Constantinescu & Ryman 1989). This represents the first report of a species of *Sporothrix* with ascomata embedded in the sporocarp of a *Hypoxylon* sp. Also see the overview phylogeny (Fig. 5).

Authors: W.J. Nel, Z.W. de Beer, T.A. Duong & M.J. Wingfield

Stemphylium eturmiunum E.G. Simmons, *Harvard Pap. Bot.* **6**: 204. 2001. Fig. 70.

Ascomata on PNA pseudothecial, subconical to subglobose, erumpent, brown with central ostiole, 250–350 µm diam; wall of 6–8 layers of brown *textura angularis*. *Asci* 2–8-spored, stipitate, bitunicate, fasciculate, subclavate, 120–150 × 27–35 µm, with clearly defined apical chamber, 3–5 µm diam. *Pseudoparaphyses* intermingled among asci, hyaline, smooth, hyphae-like, septate, anastomosing, 2.5–5 µm diam. *Ascospores* golden brown, smooth, ellipsoid, constricted at medium septum, ends obtuse, muriformly septate, 5–7 transverse septa, and 1–4 oblique or vertical septa per row, (28–)30–31(–34) × (10–)11–12(–13) µm. *Mycelium* consisting of medium brown, smooth, septate, branched, 3–4 µm diam hyphae. *Conidiophores* arising from superficial hyphae, subcylindrical, medium brown, smooth, straight to geniculate-sinuous, unbranched, 1–4-septate, 20–50 × 3–5 µm. *Conidiogenous cells* integrated, terminal, clavate, medium to dark brown, 7–15 × 6–7 µm, with terminal pore, 1.5–2 µm diam. *Conidia* solitary or in short chains (2–3), dark brown, verruculose, narrowly ellipsoid to subcylindrical, (14–)17–20(–22) × (8–)12–13(–14) µm, muriformly septate, at times constricted at median septum, 1–3 horizontal and 1–3 vertical or oblique septa per row.

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

Material examined: **South Africa**, Western Cape Province, Nieuwoudtville, on leaves of *Bulbinella latifolia* (*Asphodelaceae*), 2018, *P.W. Crous*, HPC 3061 (CBS H-24445, culture ex-type CPC 38613 = CBS 146783).

Notes: *Stemphylium eturmiunum* was described as a pathogen of *Allium sativum* in France and India (Woudenberg *et al.* 2017), and recently as postharvest pathogen of *Allium* in China (Fu *et al*. 2019). This is the first report of this pathogen occurring on leaves of *Bulbinella latifolia* in South Africa.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Stemphylium eturmiunum* (strain FXA6, GenBank MT898507.1; Identities = 575/575 (100 %), no gaps), *Stemphylium vesicarium* (strain UKKo1, GenBank MN328401.1; Identities = 588/589 (99 %), one gap (0 %)), and *Stemphylium botryosum* (strain CBS 714.68, GenBank NR_163547.1; Identities = 585/587 (99 %), no gaps). Closest hits using the **LSU** sequence are *Stemphylium eturmiunum* (strain CBS 109845, GenBank NG_069866.1; Identities = 826/826 (100 %), no gaps), *Stemphylium paludiscirpi* (strain CBS 109842, GenBank NG_069865.1; Identities = 826/826 (100 %), no gaps), and *Stemphylium triglochinicola* (strain CBS 718.68, GenBank NG_069740.1; Identities = 826/826 (100 %), no gaps) – also see Fig. 1. Closest hits using the ***actA*** sequence had highest similarity to *Stemphylium vesicarium* (as *Pleospora herbarum*; strain ATCC 11681, GenBank JQ671595.1; Identities = 575/585 (98 %), no gaps), *Stemphylium botryosum* (as *Pleospora tarda*; strain ATCC 42170, GenBank JQ671593.1; Identities = 575/585 (98 %), no gaps), and *Stemphylium callistephi* (strain EEB 1055, GenBank JQ671592.1; Identities = 572/585 (98 %), three gaps (0 %)). Closest hits using the ***cmdA*** sequence had highest similarity to *Stemphylium eturmiunum* (strain CBS 668.80, GenBank KU850830.1; Identities = 562/562 (100 %), no gaps), *Stemphylium botryosum* (strain M-14, GenBank MH206180.1; Identities = 553/562 (98 %), no gaps), and *Stemphylium truncatulae* (strain UMSe004, GenBank MK336838.1; Identities = 551/560 (98 %), no gaps). Closest hits using the ***gapdh*** sequence had highest similarity to *Stemphylium eturmiunum* (strain CBS 109845, GenBank KU850689.1; Identities = 581/581 (100 %), no gaps), *Stemphylium mali* (as *Stemphylium* sp. XGZ-2010b; strain CBS 124652, GenBank GQ395376.1; Identities = 554/558 (99 %), no gaps), and *Stemphylium armeriae* (strain CBS 338.73, GenBank KU850658.1; Identities = 573/581 (99 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to

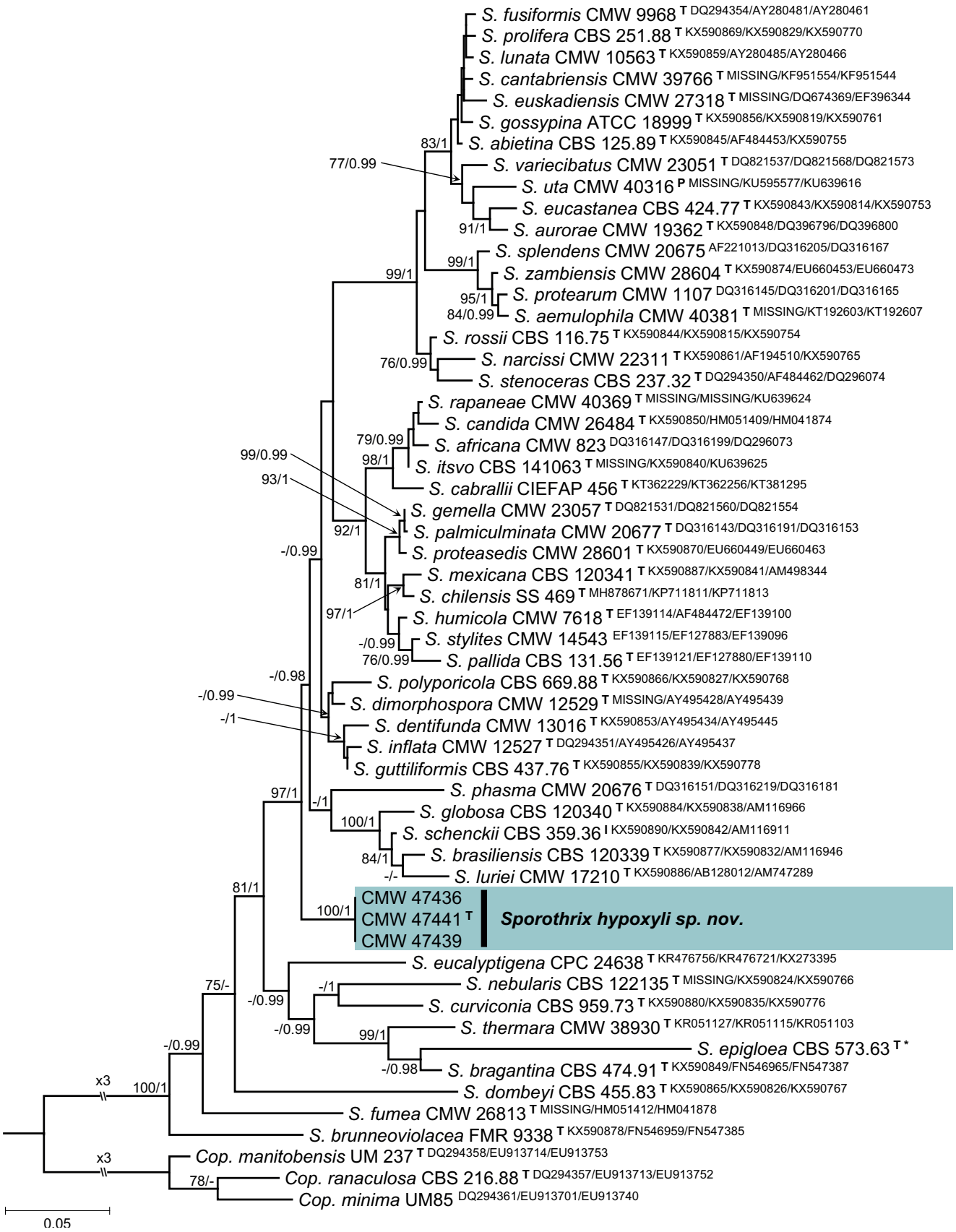

Fig. 69. Combined phylogeny of *Sporothrix* based on sequences for the LSU, ITS, and *tub2* gene regions. Datasets for the individual gene regions were prepared (MEGA v. 7) using sequences available on GenBank, aligned (MAFFT v. 7.454) and then combined manually before being analysed using Maximum Likelihood (ML; RAxML GUI v.2) and Bayesian Inference (BI; MrBayes v. 3.2.5), with the former being the tree presented. GenBank accession (superscript) and culture collection numbers are indicated for all species. The tree was rooted using isolates of the genus *Ceratocystiopsis* (*Cop*.) and basal branches were shortened to facilitate layout. Bootstrap support values (≥ 75 %; ML) and Posterior probability values (≥ 0.95; BI) are given at nodes as ML / BI. Dashes indicate low or unsupported branches. The new species is indicated in a coloured block and bold face. The scale bar indicates the number of changes. Alignment statistics: 56 strains including the outgroup taxa, 697 / 499 / 249 unique site patterns. Tree statistics: 205 738 trees sampled from 10 M generations. T = ex-type; P = Paratype; I = Isotype; * = KX590854 / KX590817 / KX590760.

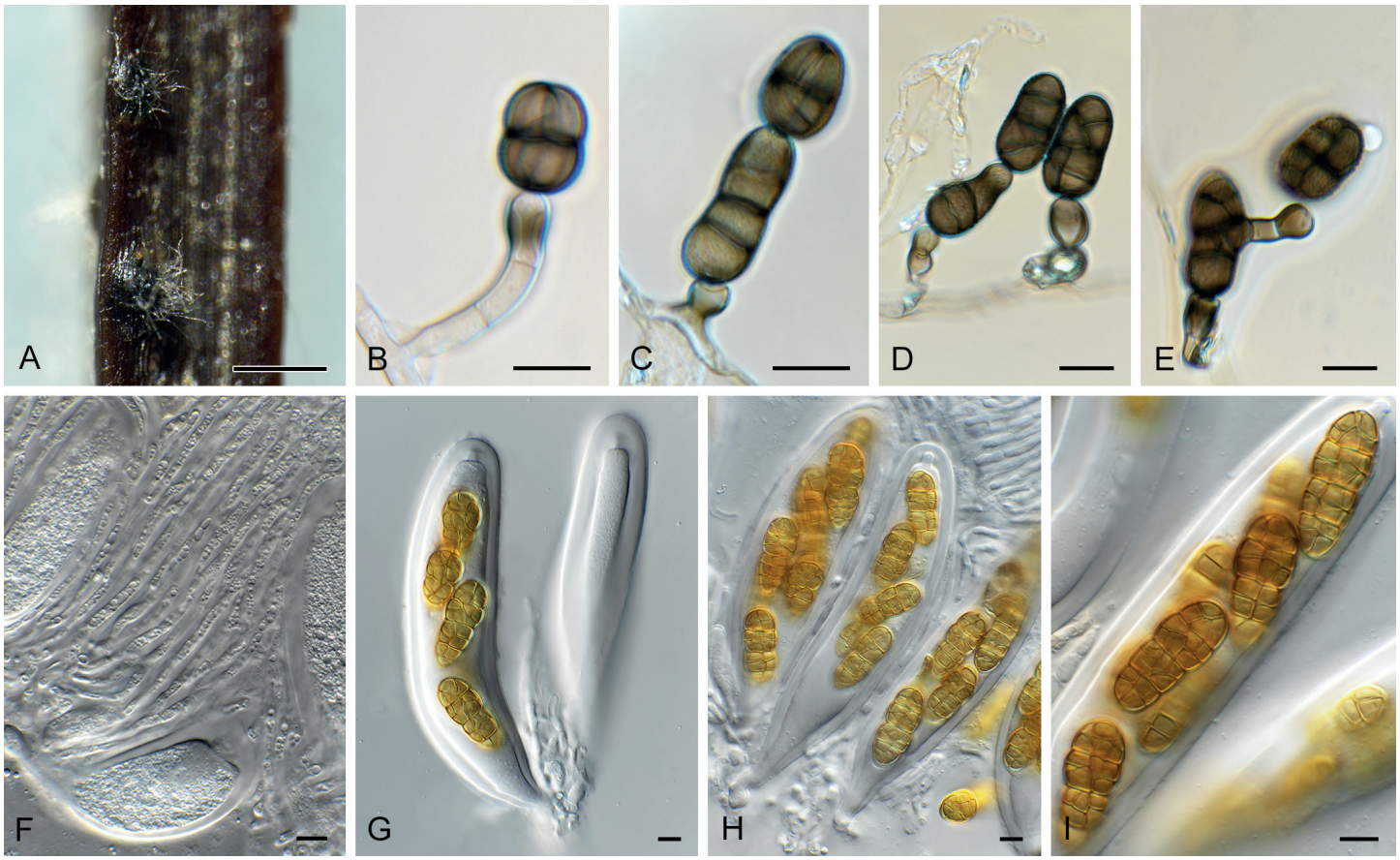

Fig. 70. *Stemphylium eturmiunum* (CPC 38613). **A.** Ascomata developing on PNA. **B–E.** Conidiophores with conidiogenous cells giving rise to conidia. **F.** Ascus and pseudoparaphyses. **G–I.** Asci and ascospores. Scale bars: A = 200 µm, all others = 10 µm.

Stemphylium vesicarium (strain BRIP 65181, GenBank KY009907.1; Identities = 800/812 (99 %), no gaps), *Stemphylium vesicarium* (as *Pleospora herbarum*; strain N131, GenBank KU738709.1; Identities = 794/806 (99 %), one gap (0 %)), and *Stemphylium botryosum* (strain ATCC 42170, GenBank JQ905202.1; Identities = 685/697 (98 %), no gaps). No *rpb2* sequences of *Stemphylium eturmiunum* are available for comparison. Closest hits using the ***tef1*** sequence had highest similarity to *Stemphylium* sp. (strain EGS48-074, GenBank AY324686.1; Identities = 421/421 (100 %), no gaps), *Stemphylium vesicarium* (strain P66, GenBank MK497791.1; Identities = 211/211 (100 %), no gaps), and *Stemphylium majusculum* (strain EGS16-068, GenBank AY324710.1; Identities = 414/421 (98 %), one gap (0 %)). No *tef1* sequences of *Stemphylium eturmiunum* are available for comparison; however, the *gapdh* sequence of strain EGS48-074 (GenBank AY316986.1) differs with only one nucleotide from sequences of *Stemphylium eturmiunum* and could therefore belong to this species.

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

Superstratomycetales van Nieuwenh., Miądl., Houbraken, Adan, Lutzoni & Samson, ***ord. nov.*** MycoBank MB 839306.
Synonym: *Superstratomycetales* van Nieuwenh. *et al.*, *Stud. Mycol.* **85**: 115. 2016. *Nom. inval.*, Arts 40.1, 40.3, see Arts 6.3, 12.1 (Shenzhen).

Etymology: From Latin "*super*" = above/on the top, and "*stratum*" = layer of material and from Greek "*myces*" = organisms, referring to fungal stains forming a top layer or covering the surface of a material.

Conidiomata pycnidial, superficial, solitary or confluent, brown to black, glabrous, globose, exuding a white mass of slimy conidia; pycnidial wall pseudoparenchymatous, of *textura angularis*, composed of 3–5 layers of pale brown to brown cells. *Setae* present or absent, erect to recurved, hyaline to subhyaline at apex and turning brown towards base, septate, verrucose to tuberculate. *Conidiophores* reduced to conidiogenous cells or branched, hyaline, smooth-walled, with terminal and intercalary conidiogenous cells. *Conidiogenous cells* phialidic, hyaline, smooth-walled, cylindrical to doliiform or ampulliform. *Conidia* hyaline, aseptate, smooth- and thin-walled, guttulate, cylindrical to navicular or ovoid.

Type genus: *Superstratomyces* van Nieuwenh., Miadl. & Samson

Superstratomycetaceae van Nieuwenh., Miądl., Houbraken, Adan, Lutzoni & Samson, ***fam. nov.*** MycoBank MB 839307.
Synonym: *Superstratomycetaceae* van Nieuwenh. *et al.*, *Stud. Mycol.* **85**: 115. 2016. *Nom. inval.*, Arts 40.1, 40.3, see Arts 6.3, 12.1 (Shenzhen).

Etymology: From Latin "*super*" = above/on the top, and "*stratum*" = layer of material and from Greek "*myces*" = organisms, referring to fungal stains forming a top layer or covering the surface of a material.

Conidiomata pycnidial, superficial, solitary or confluent, brown to black, glabrous, globose, exuding a white mass of slimy conidia; pycnidial wall pseudoparenchymatous, of *textura angularis*, composed of 3–5 layers of pale brown to brown cells.

Setae present or absent, erect to recurved, hyaline to subhyaline at apex and turning brown towards base, septate, verrucose to tuberculate. *Conidiophores* reduced to conidiogenous cells or branched, hyaline, smooth-walled, with terminal and intercalary conidiogenous cells. *Conidiogenous cells* phialidic, hyaline, smooth-walled, cylindrical to doliiform or ampulliform. *Conidia* hyaline, aseptate, smooth- and thin-walled, guttulate, cylindrical to navicular or ovoid.

Type genus: *Superstratomyces* van Nieuwenh., Miadl. & Samson

Superstratomyces van Nieuwenh., Miądl. & Samson, ***gen. nov.*** MycoBank MB 839308.
Synonym: *Superstratomyces* van Nieuwenh. *et al.*, *Stud. Mycol.* **85**: 115. 2016. *Nom. inval.,* Arts 40.1, 40.3, see Arts 6.3, 12.1 (Shenzhen).

Etymology: From Latin "*super*" = above/on the top, and "*stratum*" = layer of material and from Greek "*myces*" = organisms, referring to fungal stains forming a top layer or covering the surface of a material.

Conidiomata pycnidial, superficial, solitary or confluent, brown to black, glabrous, globose, exuding a white mass of slimy conidia; pycnidial wall pseudoparenchymatous, of *textura angularis*, composed of 3–5 layers of pale brown to brown cells. *Setae* present or absent, erect to recurved, hyaline to subhyaline at apex and turning brown towards base, septate, verrucose to tuberculate. *Conidiophores* reduced to conidiogenous cells or branched, hyaline, smooth-walled, with terminal and intercalary conidiogenous cells. *Conidiogenous cells* phialidic, hyaline, smooth-walled, cylindrical to doliiform or ampulliform. *Conidia* hyaline, aseptate, smooth- and thin-walled, guttulate, cylindrical to navicular or ovoid.

Type species: *Superstratomyces albomucosus* van Nieuwenh. & Samson

Superstratomyces albomucosus van Nieuwenh. & Samson, ***sp. nov.*** MycoBank MB 839309.
Synonym: *Superstratomyces albomucosus* van Nieuwenhuijzen & Samson, *Stud. Mycol.* **85**: 115. 2016. *Nom. inval*., Art. 35.1 (Shenzhen).

Etymology: From Latin "*albus*" = white, "*mucosus*" = slimy; referring to the conidia in white slimy masses.

Slow growing grey/olive to dark green colonies, with pycnidia forming aggregated masses (MEA and OA) and little or no slimy masses up to 5 wk (OA). On OA: 25 °C, 2–5 wk: pycnidia forming brown to black aggregated masses, individual conidiomata not present; dark pigmented hyphae; conidia smooth-walled, oval typically with blunt ends, length 2.8–6 µm, width 1.5–3 µm; aerial mycelium hyaline. On nettle stem OA, 25 °C, 4–5 wk: conidiomata brown/black, spherical to subspherical, 80–300 µm diam; conidiogenous cells phialidic.

Description and illustration: See van Nieuwenhuijzen *et al.* (2016).

Typus: **Netherlands**, Utrecht Province, Utrecht, outdoor exposed *Pycnanthus angolensis* impregnated with olive oil, *E.J. van Nieuwenhuijzen*, 9 Sep. 2013 (**holotype** CBS H-22668, culture ex-type CBS 140270 = DTO 277-D2).

Superstratomyces atroviridis van Nieuwenh. & Samson, ***sp. nov.*** MycoBank MB 839310.
Synonym: *Superstratomyces atroviridis* van Nieuwenh. & Samson, *Stud. Mycol.* **85**: 118. 2016. *Nom. inval*., Art. 35.1 (Shenzhen).

Etymology: From Latin "*ater*" = dark, black, "*viride*" = green; referring to colonies coloured dark green/ black on agar plates.

Slow growing grey/olive to dark green colonies, with pycnidia forming aggregated masses (MEA and OA) and little or no slimy masses up to 5 wk (OA). On OA, 25 °C, 2–5 wk: aggregated mass of dark brown to black pycnidia, individual conidiomata not visible; dark pigmented hyphae; conidia smooth-walled, oval typically with blunt ends, length (2 wk) 2.6–6.5 µm, width 1.6–2.8 µm; aerial mycelium hyaline. On nettle stem OA, 25 °C, 4–5 wk: individual conidiomata inconspicuous; conidiogenous cells phialidic.

Description and illustration: See van Nieuwenhuijzen *et al.* (2016).

Typus: **Netherlands**, Utrecht Province, Utrecht, outdoor exposed *Pinus sylvestris* impregnated with raw linseed oil, *E.J. van Nieuwenhuijzen*, 1 May 2014 (**holotype** CBS H-22669, culture ex-type CBS 140272).

Superstratomyces flavomucosus van Nieuwenh. & Samson, ***sp. nov.*** MycoBank MB 839311.
Synonym: *Superstratomyces flavomucosus* van Nieuwenh. & Samson, *Stud. Mycol.* **85**: 118. 2016. *Nom. inval*., Art. 35.1 (Shenzhen).

Etymology: From Latin "*flavus*" = yellow, "*mucosus*" = slimy; refers to conidia in yellow slimy masses.

Slow growing olive to grey green colonies with pycnidia forming aggregated masses and yellow-coloured slimy masses (MEA and OA). On OA, 25 °C, 2 wk: pycnidia forming yellow to dark brown aggregated masses, individual conidiomata not visible; dark pigmented hyphae; conidia smooth-walled and oval; conidia length 3.4–6.1 µm, width 2–3.4 µm; aerial mycelium hyaline. On nettle stem OA, 25 °C, 4–5 wk: pycnidia brown/yellow, spherical to subspherical, 80–170 µm diam; conidiogenous cells phialidic.

Description and illustration: See van Nieuwenhuijzen *et al.* (2016).

Typus: **Australia**, Western Australia, Perth, leaf of *Hakea multilinearis*, *W. Gams*, 1 Aug. 1983 (**holotype** CBS H-22667, culture ex-type CBS 353.84).

Authors: E.J. van Nieuwenhuijzen, J.M. Miadlikowska, J.A.M.P. Houbraken, O.C.G. Adan, F.M. Lutzoni & R.A. Samson

Superstratomyces tardicrescens Valenz.-Lopez, Rodr.-Andr., Cano, Guarro & Stchigel, ***sp. nov.*** MycoBank MB 839312.
Synonym: *Superstratomyces tardicrescens* Valenz.-Lopez *et al*., *Persoonia* **41**: 405. 2018. *Nom. inval*., Art. 35.1 (Shenzhen).

Etymology: From Latin *tarde-*, slowly, and *-crescens*, growing, due to the slow growing rates of the colonies on culture media.

Conidiomata pycnidial, superficial, solitary or confluent, brown to black, glabrous, globose, 110–125 mm diam. *Setae* erect to recurved, hyaline to subhyaline at apex and turning brown towards the base, 1–2-septate, 10–70 mm in length, 3–5 mm wide at the base, strongly verrucose to tuberculate. *Conidiophores* branched, hyaline, smooth-walled, up to 30–40 µm long, bearing lateral conidiogenous cells. *Conidiogenous cells* phialidic, hyaline, cylindrical to barrel-shaped or ampulliform, 5–8.5 × 1.5–2 µm, smooth-walled, solitary or laterally disposed on the conidiophores. *Conidia* hyaline, aseptate, smooth- and thin-walled, guttulate, cylindrical to navicular, 4–5 × 1.5–2 µm.

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

Typus: **USA**, South Carolina, from a human eye specimen, 2010, *D.A. Sutton* (**holotype** FMR H-13786, culture ex-type FMR 13786).

Notes: *Superstratomyces* was invalidly described (van Nieuwenhuijzen *et al.* 2016) as it lacked a proper description with distinguishing features. This by default invalidated all its species, the family as well as order based on the genus. These taxa are therefore validated here. See Fig. 1 for a single-locus phylogeny, and van Nieuwenhuijzen *et al.* (2016) for a multi-locus phylogenetic placement of this group of fungi.

Author: P.W. Crous

Taeniolella platani Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB 839313. Fig. 71.

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

Mycelium consisting of brown, smooth, septate, branched, 3–4 µm diam hyphae. *Conidiophores* solitary, arising from superficial hyphae, subcylindrical, dark brown, thick-walled, verruculose to warty, mostly unbranched, multiseptate, 100–250 µm tall, 8–12 µm diam. *Conidiogenous cells* integrated, terminal, holoblastic, subcylindrical, 7–15 × 8–10 µm, giving rise to chains of conidia, occasionally solitary lateral conidia. *Conidia* subcylindrical, guttulate, brown, thick-walled, 1–6-septate, septa frequently darker brown, apex obtuse, base tapering to truncate hilum, 3–5 µm diam, dark brown, 35–100 × 10–11 µm.

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

Typus: **Germany**, near Berlin, on twig of *Platanus hispanica* (*Platanaceae*), 11 Mar. 2017, *R.K. Schumacher*, HPC 2004-2 = RKS 63B (**holotype** CBS H-24378, culture ex-type CPC 33568 = CBS 146733).

Notes: The genus *Kirschsteiniothelia* has been linked to *Dendryphiopsis*, for which only an asexual morph is known, and which is common in the tropics and subtropics, and usually found on dead wood in terrestrial as well as freshwater habitats (Bao *et al*. 2018). *Taeniolella exilis*, the type of *Taeniolella*, also clusters in the *Kirschsteiniotheliaceae* (Ertz *et al.* 2016, Heuchert *et al.* 2018), although it appears distinct from *Kirschsteiniothelia* based on *K. aethiops. Taeniolella platani* represents a morphologically distinct species (see key to saprobic species in Heuchert *et al.* 2018), closely related to the sexual species *K. thujina*, which has also been reported from Europe (Zhang & Fournier 2015), suggesting that *Taeniolella* has sexual morphs that are kirschsteiniothelia-like in morphology. Both *K. thujina* and *T. platani* cluster with *T. exilis*, appearing congeneric. A phylogenetic species tree is presented as Fig. 72.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Brachysporiella navarrica* (strain CBS 142296, GenBank NR_153650.1; Identities = 429/464 (92 %), nine gaps (1 %)), *Kirschsteiniothelia thujina* (voucher JF13210, GenBank KM982716.1; Identities = 420/460 (91 %), seven gaps (1 %)), and *Kirschsteiniothelia rostrata* (voucher MFLU 15-1154, GenBank NR_156318.1; Identities = 415/462 (90 %), 11 gaps (2 %)). Closest hits using the **LSU** sequence are *Kirschsteiniothelia thujina* (voucher JF13210, GenBank KM982718.1; Identities = 803/810 (99 %), four gaps (0 %)), *Taeniolella exilis* (strain CBS 122902, GenBank KX244968.1; Identities = 840/851 (99 %), two gaps (0 %)), and *Kirschsteiniothelia rostrata* (voucher MFLU 15-1154, GenBank NG_059790.1; Identities = 847/883 (96 %), four gaps (0 %)) – also see Fig. 1. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Parafenestella parasalicum* (strain C318, GenBank MK357578.1; Identities = 434/465 (93

Fig. 71. *Taeniolella platani* (CPC 33568). **A.** Sporulation on PDA. **B–E.** Conidiogenous cells giving rise to conidia. Scale bars = 10 µm.

%), two gaps (0 %)), *Coniosporium apollinis* (strain CBS 100218, GenBank XM_007780668.1; Identities = 433/465 (93 %), no gaps), and *Parafenestella vindobonensis* (strain C302, GenBank MK357592.1; Identities = 433/465 (93 %), two gaps (0 %)).

Tricellula aurantiaca (Haskins) Arx, *The genera of fungi sporulating in pure culture*: 216. 1970. Fig. 73.
Basionym: *Volucrispora aurantiaca* Haskins, *Canad. J. Microbiol*. **4**: 278. 1958.

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

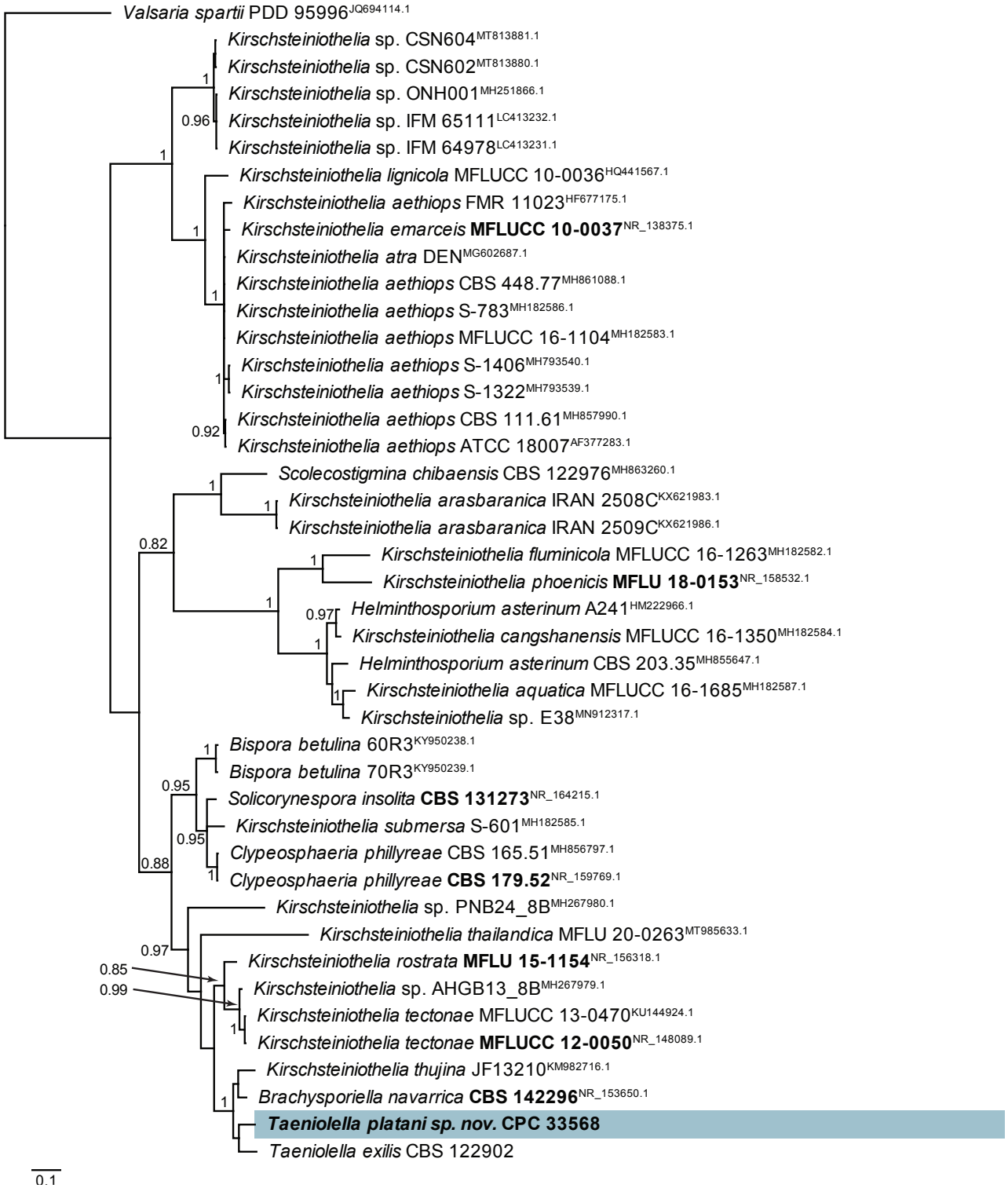

Fig. 72. Consensus phylogram (50 % majority rule) resulting from a Bayesian analysis of the *Kirschsteiniothelia s. lat.* ITS nucleotide alignment. Bayesian posterior probabilities (> 0.79) are shown at the nodes and the scale bar represents the expected changes per site. GenBank accession (superscript) and / or culture collection / voucher numbers (in bold face when having a type status) are indicated for all species. The tree was rooted to *Valsaria spartii* (voucher PDD 95996; GenBank JQ694114.1) and the novel species treated in this study is indicated in a coloured box and bold face. GTR + I + gamma and dirichlet frequencies were used as substitution model. Alignment statistics: 43 strains including the outgroup. Tree statistics: 382 unique site patterns; 4 502 sampled trees from 15 000 generations.

Mycelium consisting of hyaline, smooth, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* solitary to aggregated, up to 50 µm tall, or reduced to conidiogenous loci or a supporting cell on hyphae. *Conidiogenous cells* arising directly from hyphae, or terminal and lateral on conidiophores, hyaline, smooth, subcylindrical, 5–10 × 2–3 µm, proliferating sympodially at apex. *Conidia* hyaline, smooth, granular, Y-shaped, 3-celled, 12–18 × 7–10 µm; basal cell subcylindrical to clavate (occasionally medianly septate), 5–7 × 2–3 µm, the two upper cells separated from the basal cell by a constriction (occasionally septate), obclavate, tapering towards apex, 5–7 × 2–3 µm.

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

Material examined: **Russia**, Rostov region, Shakhty city district, shrubs near Atukhta river, on old leaves of *Lonicera tatarica* (*Caprifoliaceae*), 21 Sep. 2018 *T.S. Bulgakov*, HPC 2618 = Myc-24 (CBS H-24350, culture CPC 36629 = CBS 146627).

Notes: *Tricellula aurantiaca* was originally isolated from a water culture containing soil in Canada (Haskins 1958), and is a known aquatic hyphomycete. Isolating the same fungus from leaves of *Lonicera tatarica* in Russia, suggests that its ecology may be more complex than previously assumed.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Tricellula aurantiaca* (strain CBS 399.58, GenBank MH857822.1; Identities = 487/491 (99 %), one gap (0 %)), *Tricellula aquatica* (strain CBS 383.58, GenBank MH857818.1; Identities = 512/548 (93 %), 9 gaps (1 %)) and *Tricellula inaequalis* (strain CBS 359.53, GenBank MH857245.1; Identities = 513/550 (93 %), 13 gaps (2 %)). Closest hits using the **LSU** sequence are *Tricellula aurantiaca* (strain CBS 399.58, GenBank MH869354.1; Identities = 796/796 (100 %), no gaps), *Tricellula inaequalis* (strain CBS 359.53, GenBank MH868778.1; Identities = 878/882 (99 %), no gaps), and *Tricellula curvata* (strain CBS 429.54, GenBank MH868922.1; Identities = 853/858 (99 %), no gaps) – also see Fig. 2.

Authors: P.W. Crous, J.Z. Groenewald & T.S. Bulgakov

Tryssglobulus B. Sutton & Pascoe, *Trans. Brit. Mycol. Soc.* **88**: 44. 1987.

Saprobic. *Mycelium* superficial, brown, branched, euseptate. *Stromata* absent. *Conidiophores* arising from vegetative mycelium, mononematous, determinate or indeterminate, erect, dark brown, smooth, euseptate, producing an apical, globose, multicellular conidiogenous region, sometimes proliferating through the conidiogenous head to form an additional shorter conidiophore, each with an apical conidiogenous region. *Conidiogenous cells* integrated, restricted to and comprising the peripheral cells of the conidiogenous head, non-protuberant, brown, smooth, each with protuberant unthickened denticulate conidiogenous loci; denticles cylindrical. *Conidia* holoblastic, dry, brown, smooth, subglobose to lenticular, upper wall thicker and flatter than lower wall; denticles sometimes persisting (from Sutton & Pascoe 1987).

Type species: *Tryssglobulus aspergilloides* B. Sutton & Pascoe

Tryssglobulus aspergilloides B. Sutton & Pascoe, *Trans. Brit. Mycol. Soc.* **88**: 45. 1987. Figs 74, 75.

Colonies hypophyllous, sparse, emerging from depressions in the leaf hair layer which is associated with insect damage; rarely extending beyond such disturbed areas, consisting of 3–10 conidiophores. *Mycelium* superficial, medium to dark brown, irregularly branched, euseptate, smooth, associated with leaf hairs, 10–12 µm diam. *Stromata* absent. *Conidiophores* arising as vertical branches from vegetative mycelium, mononematous, determinate, or indeterminate, erect, straight or gently and irregularly curved, dark brown, becoming paler brown towards apices, smooth, 8–13-euseptate, (125–)300–360(–675) µm long, (6–)8–10(–12) µm wide at the base, tapering to (3–)4–6(–7) µm wide at the apex, producing a globose, multicellular, initially hyaline, but becoming brown conidiogenous region, 17–50(–80) µm diam. *Conidiophores* occasionally proliferate once or twice through the conidiogenous region to form 2–5-septate branches, 75–175 µm long at 30–90° to the main axis. Each branch terminates in a conidiogenous head. *Conidiogenous cells* integrated, restricted to the conidiogenous head, ampulliform to cuneiform, non-protuberant, pale brown, smooth, 2–4.5 × 2–4 µm, each with 1–3 protuberant, unthickened, denticulate conidiogenous loci situated on outer wall; denticles cylindrical, up to 2 × 1 µm. *Conidia* holoblastic, dry, pale brown, smooth, subglobose to almost lenticular, with upper wall slightly flattened and thicker or more melanised than lower wall, (3–)3.5–4 × (2.5–)3–3.5 µm, sometimes with part of the denticle remaining attached (from Sutton & Pascoe 1987).

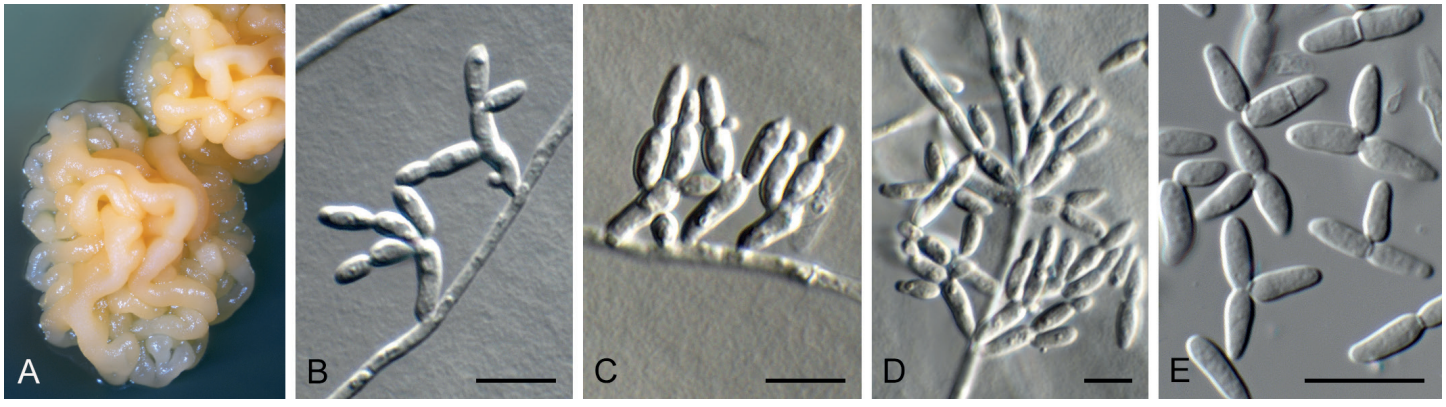

Fig. 73. *Tricellula aurantiaca* (CPC 36629). **A.** Colony on SNA. **B–D.** Conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars = 10 µm.

Typus: **Australia**, Victoria, Brisbane Ranges, 5.3 km from Switch Rd., on living leaves of *Banksia marginata*, 13 Nov. 1985, *I.G. Pascoe* (**holotype** VPRI 13072, **isotype** DAR 56184); The Gurdies, The Gurdies Nature Reserve, Lat. 38°23'-6.4", Long. 145°33'05.8", on *B. marginata*, 12 Oct. 2020, *I.G. Pascoe & B.J. Brentwood* (**epitype** designated here, dried specimen VPRI 43962 MBT 10000789, culture ex-epitype VPRI 43962 = CBS 147556 = CPC 40369); **isoepitype** CBS H-24730, culture ex-isoepitype CBS 147388 = CPC 40100).

Notes: *Tryssglobulus* is a member of *Readerielliopsidaceae* (*Capnodiales*), which includes four genera, namely *Phaeoxyphiella*, *Readerielliopsis*, *Scolecoxyphium* and *Scorias* (Abdollahzadeh *et al.* 2020).

Tryssglobulus is distinguished from morphologically similar genera in having a multicellular globose head, that gives rise to a single layer of conidiogenous cells. Sutton & Pascoe (1987) interpreted the conidiogenesis as holoblastic and solitary, mentioning that it was uncertain if the conidiogenous cells proliferated percurrently or not, as some variation was observed in the thickness of the collarettes, which could be indicative of percurrent proliferation. In the present study we were fortunate to culture this species, which made it possible to study its conidiogenesis in more detail. In doing so, we could resolve that the conidiogenous cells are holoblastic as originally reported, and do not proliferate percurrently.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 40369 had highest similarity to *Readerielliopsis fuscoporiae* (strain CBS 139900, GenBank NR_137978.1; Identities = 402/459 (88 %), 16 gaps (3 %)), *Scorias spongiosa* (voucher Ss0901, GenBank HM480490.1; Identities = 426/487 (87 %), 24 gaps (4 %)), and *Readerielliopsis guyanensis* (as *Readeriella guyanensis*; strain CBS 117550, GenBank EU707900.1; Identities = 404/462 (87 %), 15 gaps (3 %)). The ITS sequences of CPC 40369 and 40100 are identical (382/382 (100 %)). Closest hits using the **LSU** sequence of CPC 40369 are *Readerielliopsis guyanensis* (as *Readeriella guyanensis*; strain CBS 117550, GenBank FJ493211.1; Identities = 830/850 (98 %), no gaps), *Readerielliopsis fuscoporiae* (strain CBS 139900, GenBank NG_058161.1; Identities = 816/838 (97 %), no gaps), and *Fumagospora capnodioides* (strain CBS 131.34, GenBank EU019269.1; Identities = 827/856 (97 %), two gaps (0 %)). The LSU sequences of CPC 40369 and 40100 are identical (813/813 (100 %)). Distant hits obtained using the ***rpb2*** sequence of CPC 40100 had highest similarity to *Ragnhildiana gnaphaliaceae* (strain CBS 142181, GenBank MF951646.1; Identities = 373/544 (69 %), ten gaps (1 %)), *Rachicladosporium pini* (strain CPC 16770, GenBank LT799764.1; Identities = 373/548 (68 %), 22 gaps (4 %)), and *Ragnhildiana pseudotithoniae* (strain 2019-100655, GenBank MT663950.1; Identities = 375/545 (69 %), 12 gaps (2 %)). The ***rpb2*** sequences of CPC 40100 and 40369 are identical (536/536).

Authors: P.W. Crous, J.Z. Groenewald, J. Dijksterhuis & I.G. Pascoe

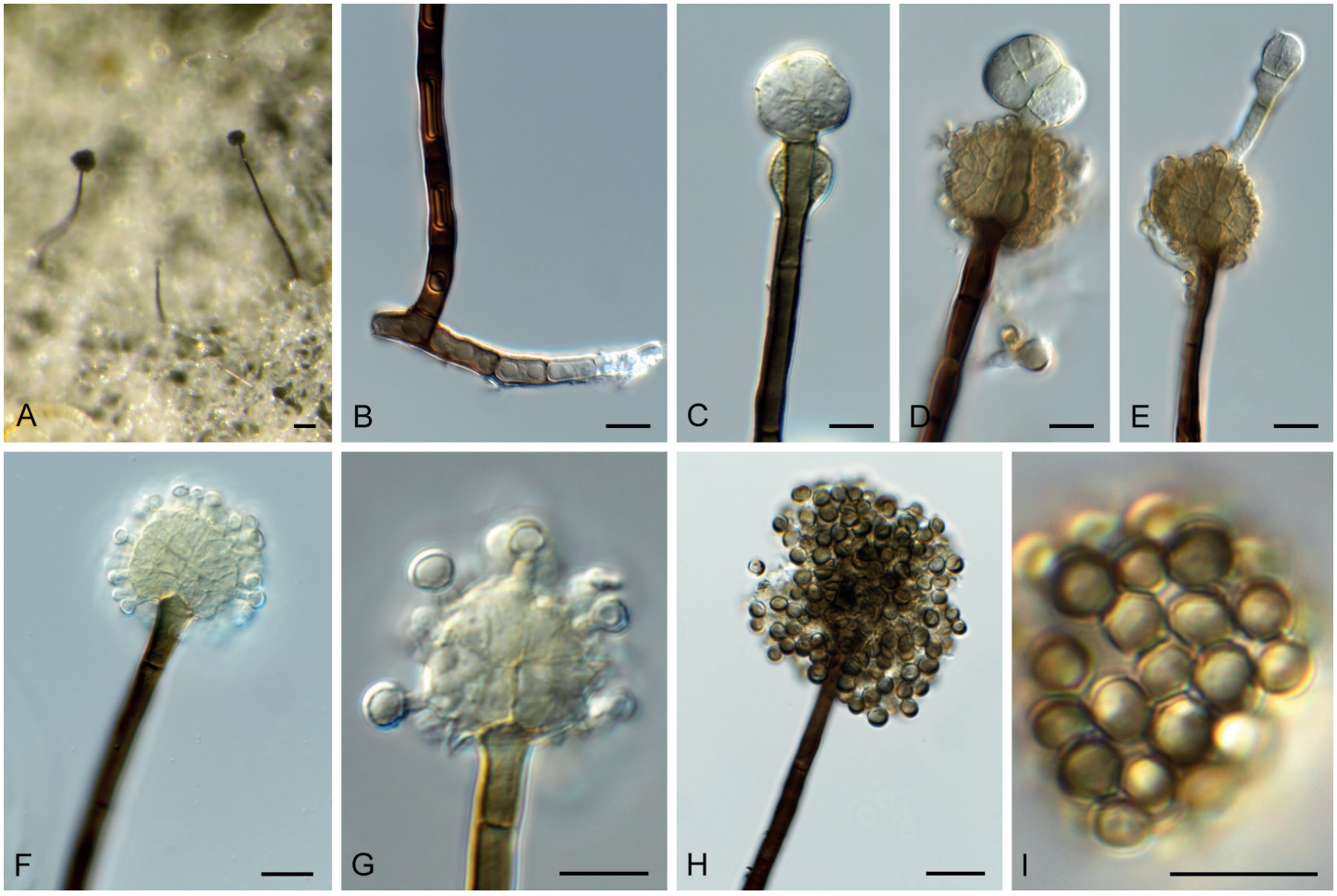

Fig. 74. *Tryssglobulus aspergilloides* (CPC 40100). **A.** Conidiophores *in vivo*. **B.** Base of conidiophore. **C–E.** Developing conidiophores with proliferation. **F, G.** Conidiogenous apparatus showing conidiogenesis. **H.** Conidiophore head with mature conidia. **I.** Conidia. Scale bars: A = 80 µm, all others = 10 µm.

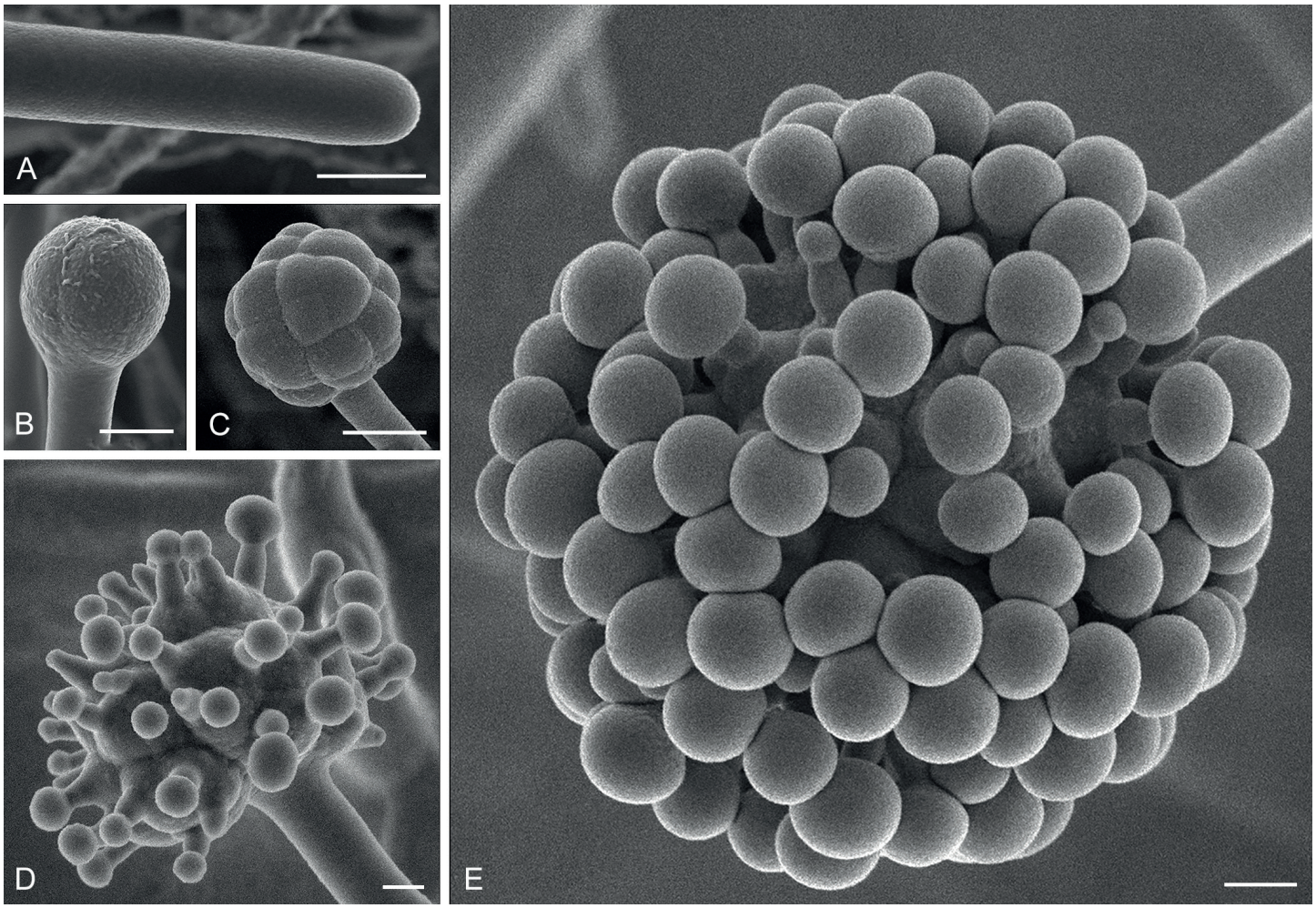

Fig. 75. *Tryssglobulus* (Cryo Scanning Electron Microscope images of CPC 40100). **A–C.** Conidiophore stalk, developing with apical conidiogenous apparatus. **D.** Conidiogenous cells giving rise to conidia. **E.** Conidiogenous cells and conidia. Scale bars: A–C = 5 µm, D, E = 2 µm.

Tympanis pini Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB 839314. Fig. 76.

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

Conidiomata superficial on OA, brown, globose, 200–250 µm diam, opening via irregular rupture, exuding creamy conidial mass; wall of 3–6 layers of brown *textura angularis. Conidiophores* lining the inner cavity, hyaline, smooth, subcylindrical, 30–80 × 2–2.5 µm, flexuous, branched below, multiseptate with conidiogenous loci distributed along the length of the conidiophore, developing as lateral phialidic nodes below septa. *Conidia* hyaline, smooth, aseptate, subcylindrical with obtuse ends, straight, 3–4 × 1–1.5 µm.

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

Typus: **Spain**, Teruel, Orihuela del Tremedal, on twigs of *Pinus sylvestris* (*Pinaceae*), 25 May 2019, *R. Blasco*, HPC 2963 = RKS 1110 (**holotype** CBS H-24404, culture ex-type CPC 38169 = CBS 146809).

Notes: Sutton & Funk (1975) concluded that *Sirodothis* was an earlier name for *Pleurophomella*, and should be used as the asexual morph of *Tympanis*. The present collection is asexual, and has a typical *Sirodothis* morphology, clustering among species of *Tympanis*, thereby supporting its description in the latter genus. Several species of *Tympanis* are known from *Pinaceae* (Ouellette & Pirozynski 1974), but as these are known only by their sexual morphs, a morphological comparison with *T. pini* is presently not possible. A phylogenetic species tree is presented as Fig. 77.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to "*Ascomycota* sp." (strain F45, GenBank GU067747.1; Identities = 487/488 (99 %), no gaps), *Tympanis truncatula* (strain CBS 368.55, GenBank MK314572.1; Identities = 466/474 (98 %), one gap (0 %)), and *Tympanis spermatiospora* (strain CBS 367.55, GenBank MK314571.1; Identities = 491/502 (98 %), three gaps (0 %)). Closest hits using the **LSU** sequence are *Tympanis truncatula* (strain CBS 368.55, GenBank MK314622.1; Identities = 853/854 (99 %), no gaps), *Tympanis spermatiospora* (strain CBS 367.55, GenBank MK314624.1; Identities = 855/857 (99 %), one gap (0 %)), and *Tympanis abietina* (strain CBS 350.55, GenBank MK314617.1; Identities = 842/845 (99 %), no gaps) – also see Fig. 2.

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

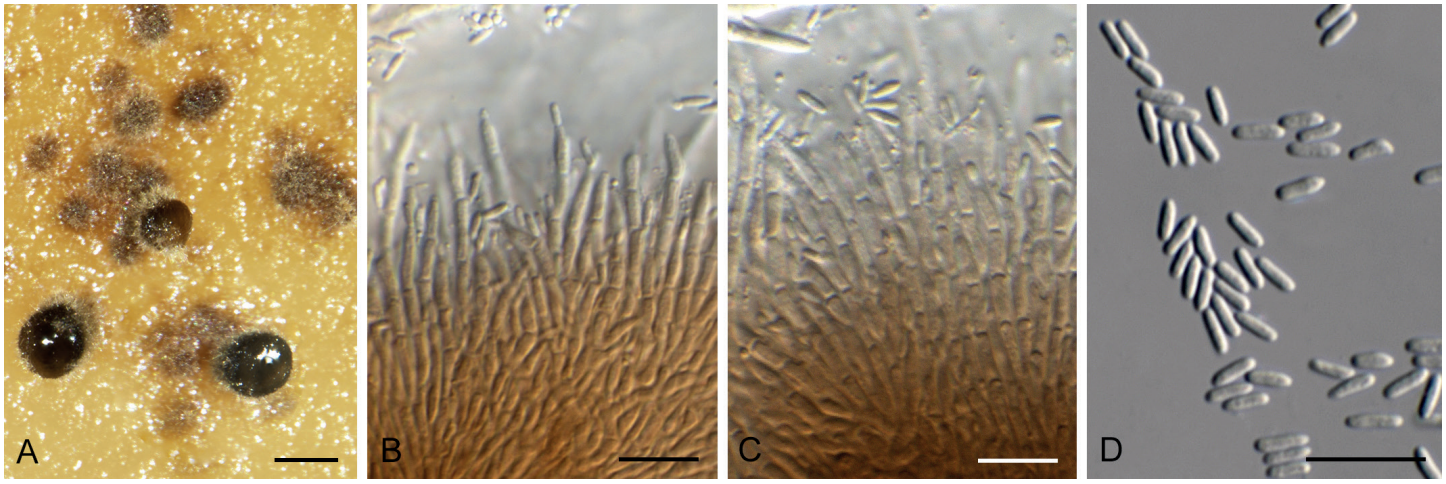

Fig. 76. *Tympanis pini* (CPC 38169). **A.** Conidiomata on OA. **B–C.** Conidiophores, conidiogenous cells and conidia. **D.** Conidia. Scale bars: A = 200 µm, all others = 10 µm.

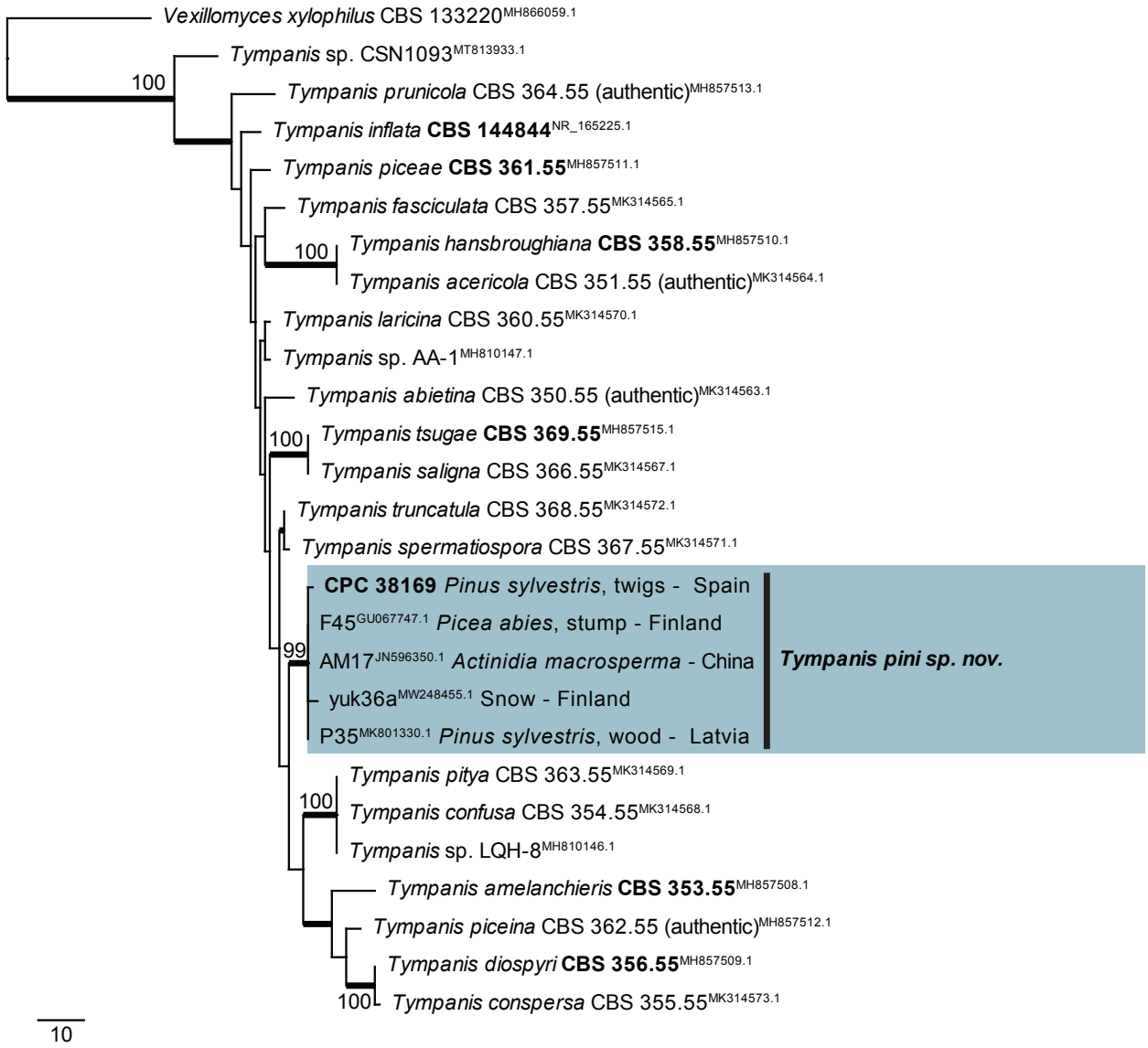

Fig. 77. The first of 46 equally most parsimonious trees obtained from a phylogenetic analysis of the *Tympanis* ITS alignment. The tree was rooted to *Vexillomyces xylophilus* (strain CBS 133220, GenBank MH866059.1) and the scale bar indicates the number of changes. Parsimony bootstrap support values higher than 79 % are shown at the nodes and the novel species is highlighted with a coloured box and bold text. GenBank accession (superscript) and / or culture collection / voucher numbers (in bold face when having a type status) are indicated for all species. Branches present in the strict consensus tree are thickened. Alignment statistics: 27 strains including the outgroup; 449 characters including alignment gaps analysed: 335 constant, 63 variable and parsimony-uninformative and 51 parsimony-informative. Tree statistics: TL = 200, CI = 0.735, RI = 0.738, RC = 0.542.

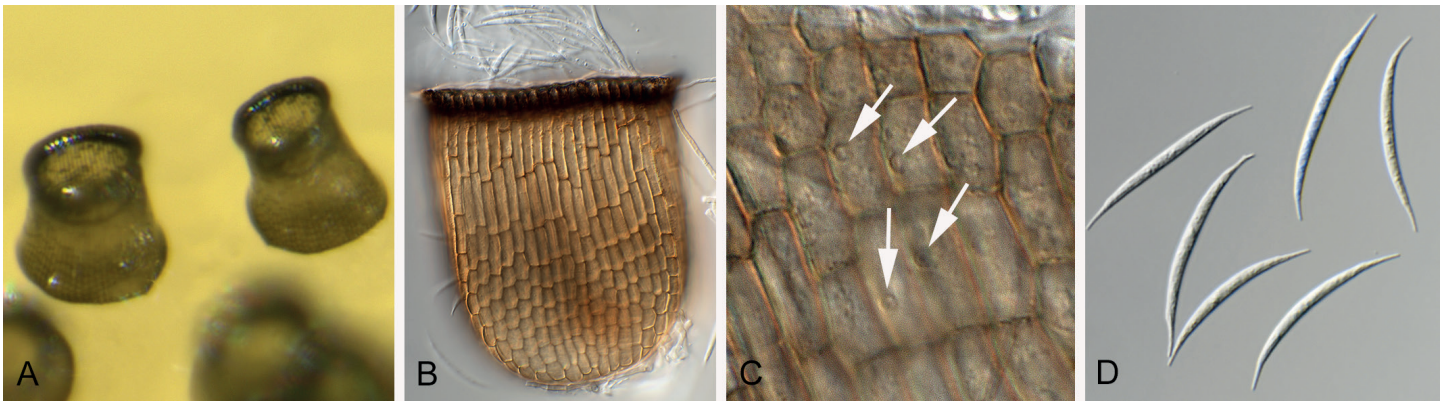

Fig. 78. *Zelosatchmopsis sacciformis* (CBS 116.88). **A–B.** Cup-shaped conidiomata. **C.** Conidiogenous loci (arrows) in conidiomatal wall. **D.** Conidia. Scale bars: A–B = 60 µm, all others = 10 µm.

Venturia cerasi Aderh., *Landw. Jahrb*. **29**: 544. 1900.
Synonyms: *Fusicladium cerasi* (Rabenh.) Erikss., Meddeland. Kongl. Lantbruksakad. Exp.-fält 1: 73. 1885.
Acrosporium cerasi Rabenh., in Braun, *Verh. Vereins Beförd. Gartenbaues Königl. Preuss. Staaten*, ser. 2, **1**: 176. 1853.

Description and illustration: Schubert *et al.* (2003), Shen *et al.* (2020).

Typus: **Germany**, Borussia, on fruits of *Prunus cerasus* (*Rosaceae*) [**lectotype** designated here, Aderhold (1900), plate 9, figs 6, 7, MTB 10000791]; Aschersleben, on *Prunus cerasus*, 17 Sep. 1954, *H. Schweizer* (**epitype** specimen designated here CBS 444.54, MBT 10000792, preserved as metabolically inactive culture, ex-epitype culture CBS 444.54).

Notes: Original fungarium material of Aderhold for *Venturia cerasi* could not be traced and is very likely not preserved. Shen *et al.* (2020) cited the lectotype designated in Schubert *et al.* (2003), but this was in error, because the lectotype pertained to *Acrosporium cerasi* Rabenh., which is the basionym of the *Fusicladium* morph. Furthermore, Schubert *et al.* (2003) cited only an "iconotype" so that this "lectotypification" has not been effected, which is introduced here:

Acrosporium cerasi Rabenh., in Braun, *Verh. Vereins Beförd. Gartenbaues Königl. Preuss. Staaten*, ser. 2, **1**: 176. 1853.

Typus: **Germany**, Borussia, on fruits of *Prunus cerasus* (*Rosaceae*) [**lectotype**, designated here, Braun (1853: plate 1, B, 1, 2), MTB 10000793].

Authors: M. Shen, J.Q. Zhang, L.L. Zhao, J.Z. Groenewald, P.W. Crous & Y. Zhang

Zelosatchmopsis sacciformis (R.F. Castañeda) Nag Raj & R.F. Castañeda, *Canad. J. Bot*. **69**: 633. 1991. Fig. 78.
Basionym: *Satchmopsis sacciformis* R.F. Castañeda, *Fungi Cubenses* **II**: 18. 1987.

Conidiomata cupulate, with dark brown border, exuding conidia in crystalline mucoid mass. Nag Raj (1993) described the basal appendage as excentric, unbranched, but did not comment on the apical cell, which also terminated in a central attenuated appendage, 3–5 µm long. In culture it also forms chains of hyaline chlamydospores. An interesting phenomenon is the conidiogenous cells that develop as phialidic pores on the inner surface of the cupulate conidiomatal wall.

Colony characteristics: Colonies erumpent, spreading, with sparse aerial mycelium on OA and PDA, moderate aerial mycelium and folded surface on MEA, margin smooth, lobate, up to 50 mm diam after 2 wk at 25 °C.
Typus: **Cuba**, Prov. Matanzas, San Miguel de los Baños, fallen leaf of *Guazuma ulmifolia*, (*Malvaceae*), 23 Jan. 1987, *R.F. Castañeda*, **isotypes** CBS H-10357, CBS H-7737, culture ex-isotype CBS 116.88 = INIFAT C87/53.1 = MW i 1640.

Notes: In the present study we resolve the higher-level phylogeny of *Zelosatchmopsis. Zelosatchmopsis* (*Muyocopronaceae*, *Dothideomycetes*) clusters apart from *Satchmopsis* (*Cochlearomycetaceae*, *Leotiomycetes*), supporting the generic differences observed by Nag Raj (1993).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Mycoleptodiscus terrestris* (strain CBS 231.53, GenBank NR_145373.1; Identities = 435/512 (85 %), 28 gaps (5 %)), *Mycoleptodiscus suttonii* (strain CBS 276.72, GenBank NR_164056.1; Identities = 403/471 (86 %), 15 gaps (3 %)), and *Mycoleptodiscus endophytica* (strain MFLUCC 17-0545, GenBank NR_158860.1; Identities = 325/358 (91%), seven gaps (1%)). Closest hits using the **LSU** sequence are *Mycoleptodiscus endophytica* (strain MFLUCC 17-0545, GenBank NG_064487.1; Identities = 790/844 (94 %), 11 gaps (1 %)), *Arxiella dolichandrae* (strain CBS 138853, GenBank MH878643.1; Identities = 730/783 (93 %), nine gaps (1 %)), and *Mycoleptodiscus suttonii* (as *Mycoleptodiscus terrestris*; strain CBS 276.72, GenBank MH872193.1; Identities = 767/824 (93 %), 14 gaps (1 %)) – also see Fig. 1.

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REFERENCES

Al-Bedak OA, Ismail MA, Mohamed RA (2019). *Paracremonium moubasheri*, a new species from an alkaline sediment of Lake Hamra in Wadi-El-Natron, Egypt with a key to the accepted species. *Studies in Fungi* **4**: 216–222.

Abdollahzadeh J, Groenewald JZ, Coetzee MPA, *et al*. 2020. Evolution of lifestyles in *Capnodiales*. *Studies in Mycology* **95**: 381–414.

Bao DF, Luo ZL, Liu JK, *et al.* (2018). Lignicolous freshwater fungi in China III: Three new species and a new record of *Kirschsteiniothelia* from northwestern Yunnan Province. *Mycosphere* **9**: 755–768.

Bensch K, Groenewald JZ, Meijer M, *et al*. (2018). *Cladosporium* species in indoor environments. *Studies in Mycology* **89**: 177–301.

Boonmee S, Wijayawardene NN, Bhat DJ, *et al.* (2019). *Misturatosphaeria viridibrunnea sp. nov*. (*Teichosporaceae, Pleosporales*) from Thailand. *Phytotaxa* **388**: 123–134.

Braun A (1853). Über einige neue oder weniger bekannte Pflanzenkrankheiten, welche durch Pilze erzeugt werden. *Verhandlungen des Vereins zur Beförderung des Gartenbaues in den Königlich Preussischen Staaten* **1**: 165–191.

Braun U, Nakashima C, Crous PW, *et al.* (2018). Phylogeny and taxonomy of the genus *Tubakia s. lat*. *Fungal Systematics and Evolution* **1**: 41–99.

Carlucci A, Raimondo ML, Santos J, *et al.* (2012). *Plectosphaerella* species associated with root and collar rots of horticultural crops in southern Italy. *Persoonia* **28**: 34–48.

Cheewangkoon R, Groenewald JZ, Summerell BA, *et al*. (2009). *Myrtaceae*, a cache of fungal biodiversity. *Persoonia* **23**: 55–85.

Constantinescu O, Ryman S (1989). New *Ophiostoma* on polypores. *Mycotaxon* **34**: 637–342.

Crous PW (1998). *Mycosphaerella* spp. and their anamorphs associated with leaf spot diseases of *Eucalyptus*. *Mycologia Memoir* **21**: 1–170. APS Press, MN, USA.

Crous PW, Cowan DA, Maggs-Kölling G, *et al.* (2020a). Fungal Planet description sheets: 1112–1181. *Persoonia* **45**: 251–409.

Crous PW, Denman S, Taylor JE, *et al*. (2013a). *Cultivation and diseases of Proteaceae: Leucadendron, Leucospermum and Protea*. 2nd edn. *CBS Biodiversity Series* **13**: 1–360. CBS-KNAW Fungal Biodiversity Centre, Utrecht, The Netherlands.

Crous PW, Gams W, Stalpers JA, *et al*. (2004). MycoBank: an online initiative to launch mycology into the 21st century. *Studies in Mycology* **50**: 19–22.

Crous PW, Groenewald JZ (2013). A phylogenetic re-evaluation of *Arthrinium*. *IMA Fungus* **4**: 133–154.

Crous PW, Luangsa-Ard JJ, Wingfield MJ, *et al.* (2018a). Fungal Planet description sheets: 785–867. *Persoonia* **41**: 238–417.

Crous PW, Minnis AM, Pereira OL, *et al*. (2011). What is *Scirrhia*? *IMA Fungus* **2**: 127–133.

Crous PW, Schumacher RK, Akulov A, *et al*. (2019a). New and Interesting Fungi. 2. *Fungal Systematics and Evolution* **3**: 57–134.

Crous PW, Schumacher RK, Wood AR, *et al.* (2020b). The Genera of Fungi – G5: *Arthrinium, Ceratosphaeria, Dimerosporiopsis, Hormodochis, Lecanostictopsis, Lembosina, Neomelanconium, Phragmotrichum, Pseudomelanconium, Rutola, and Trullula. Fungal Systematics and Evolution* **5**: 77–98.

Crous PW, Summerell BA, Swart L, *et al*. (2011). Fungal pathogens of *Proteaceae*. *Persoonia* **27**: 20–45.

Crous PW, Verkley GJM, Groenewald JZ, *et al.* (eds) (2019b). *Fungal Biodiversity*. [Westerdijk Laboratory Manual Series no.1.] Utrecht: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands.

Crous PW, Wingfield MJ, Burgess TI, *et al.* (2017). Fungal Planet description sheets: 625–715. *Persoonia* **39**: 270–467.

Crous PW, Wingfield MJ, Burgess TI, *et al.* (2018b). Fungal Planet description sheets: 716–784. *Persoonia* **40**: 240–393.

Crous PW, Wingfield MJ, Cheewangkoon R, *et al.* (2019c). Foliar pathogens of eucalypts. *Studies in Mycology* **94**: 125–298.

Crous PW, Wingfield MJ, Chooi Y-H, *et al*. (2020c). Fungal Planet description sheets: 1042–1111. *Persoonia* **44**: 301–459.

Crous PW, Wingfield MJ, Guarro J, *et al*. (2013b). Fungal Planet description sheets: 154–213. *Persoonia* **31**: 188–296.

Crous PW, Wingfield MJ, Guarro J, *et al*. (2015). Fungal Planet description sheets: 320–370. *Persoonia* **34**: 167–266.

Crous PW, Wingfield MJ, Lombard L, *et al*. (2019d). Fungal Planet description sheets: 951–1041. *Persoonia* **43**: 223–425.

Crous PW, Wingfield MJ, Park RF (1991). *Mycosphaerella nubilosa* a synonym of *M. molleriana*. *Mycological Research* **95**: 628–632.

Crous PW, Wingfield MJ, Schumacher RK, *et al*. (2014). Fungal Planet description Sheets 281–319. *Persoonia* **33**: 212–289.

Dai DQ, Phookamsak R, Wijayawardene NN, *et al*. (2017). Bambusicolous fungi. *Fungal Diversity* **82**: 1–105.

Damm U, Cannon PF, Woudenberg JHC, *et al*. (2012). The *Colletotrichum acutatum* species complex. *Studies in Mycology* **73**: 37–113.

Damm U, O'Connell RJ, Groenewald JZ, *et al*. (2014). The *Colletotrichum destructivum* species complex – hemibiotrophic pathogens of forage and field crops. *Studies in Mycology* **79**: 1–47.

Damm U, Sato T, Alizadeh A, *et al*. (2019). The *Colletotrichum dracaenophilum*, *C. magnum* and *C. orchidearum* species complexes. *Studies in Mycology* **92**: 1–46.

de Gruyter J, Woudenberg JHC, Aveskamp MM, *et al.* (2010). Systematic reappraisal of species in *Phoma* section *Paraphoma*, *Pyrenochaeta* and *Pleurophoma*. *Mycologia* **102**: 1066–1081.

Dionne B, Neff L, Lee SA, *et al*. (2015). Pulmonary fungal infection caused by *Neoscytalidium dimidiatum*. *Journal of Clinical Microbiology* **53**: 2381–2384.

Ertz D, Heuchert B, Braun U, *et al.* (2016). Contribution to the phylogeny and taxonomy of the genus *Taeniolella*, with a focus on lichenicolous taxa. *Fungal Biology* **120**: 1416–1447.

Fan XL, Bezerra JDP, Tian CM, *et al*. (2018). Families and genera of diaporthalean fungi associated with canker and dieback of tree hosts. *Persoonia* **40**: 119–134.

Fu L, Jin Y, Zhang GF, *et al*. (2019). First report of Stemphylium eturmiunum causing postharvest rot of garlic sprout in China. *Plant Disease* **103**: 1041.

Gams W, Stielow B, Gräfenhan, T. *et al.* (2019). The ascomycete genus *Niesslia* and associated monocillium-like anamorphs. *Mycological Progress* **18**: 5–76.

Giraldo A, Crous PW (2019). Inside *Plectosphaerellaceae*. *Studies in Mycology* **92**: 227–286.

Giraldo A, Hernández-Restrepo M, Crous PW (2019). New plectosphaerellaceous species from Dutch garden soil. *Mycological Progress* **18**: 1135–1154.

Glienke C, Pereira OL, Stringari D, *et al*. (2011). Endophytic and

pathogenic *Phyllosticta* species, with reference to those associated with Citrus Black Spot. *Persoonia* **26**: 47–56.

Gonçalves MFM, Vicente TFL, Esteves AC, *et al.* (2019). Novel halotolerant species of *Emericellopsis* and *Parasarocladium* associated with macroalgae in an estuarine environment. *Mycologia* **112**: 154–171.

Guarnaccia V, Gehrmann T, Silva GJ, *et al*. (2019). *Phyllosticta citricarpa* and sister species of global importance to *Citrus*. *Molecular Plant Pathology* **20**: 1619–1635.

Guarnaccia V, Groenewald JZ, Li H, *et al.* (2017). First report of *Phyllosticta citricarpa* and description of two new species, *P. paracapitalensis* and *P. paracitricarpa*, from citrus in Europe. *Studies in Mycology* **87**: 161–185.

Guarro J, Gené J, Stchigel AM, *et al.* (2012). *Atlas of Soil Ascomycetes*. CBS Biodiversity series 10. Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands.

Guerrero RT (1971). On the real nature of the 'setae' in *Tremella fuciformis*. *Mycologia* **63**: 920–924.

Hanlin RT (1997). *Illustrated Genera of Ascomycetes*. Vol. 1. St. Paul, APS Press, MN, USA.

Hansen K, Laessoe T, Pfister DH (2001). Phylogenetics of the *Pezizaceae*, with an emphasis on *Peziza*. *Mycologia* **93**: 958–990.

Hansen K, Laessoe T, Pfister DH (2002). Phylogenetic diversity in the core group of *Peziza* inferred from ITS sequences and morphology. *Mycological Research* **106**: 879–902.

Hansen K, Lobuglio KF, Pfister DH (2005). Evolutionary relationships of the cup-fungus genus *Peziza* and *Pezizaceae* inferred from multiple nuclear genes: *RPB2*, beta-tubulin and LSU rDNA. *Molecular Phylogenetics and Evolution* **36**: 1–23.

Haskins RH (1958). Hyphomycetous fungi: *Volucrispora aurantiaca n. gen., n. sp.*; *V. ornithomorpha* (Trotter) *n. comb*.; and *Tricellula curvatis n. sp.*; with the genus *Tricellula* emended. *Canadian Journal of Microbiology* **4**: 273–285.

Hernández-Restrepo M, Bezerra JDP, Tan YP, *et al.* (2019). Re-evaluation of *Mycoleptodiscus* species and morphologically similar fungi. *Persoonia* **42**: 205–227.

Hernández-Restrepo M, Gené J, Castañeda-Ruiz RF, *et al.* (2017). Phylogeny of saprobic microfungi from Southern Europe. *Studies in Mycology* **86**: 53–97.

Hernández-Restrepo M, Groenewald JZ, Lombard L, *et al.* (2016). Fungal Systematics and Evolution: FUSE 2. *Sydowia* **68**: 193–230.

Heuchert B, Braun U, Diederich P (2018). Taxonomic monograph of the genus *Taeniolella s. lat.* (*Ascomycota*). *Fungal Systematics and Evolution* **2**: 69–261.

Hoang DT, Chernomor O, von Haeseler A, *et al*. (2018). UFBoot2: Improving the ultrafast bootstrap approximation. *Molecular Biology and Evolution* **35**: 518–522.

Holm L, Holm K (1978). Some pteridicolous ascomycetes. *Botaniska Notiser* **131**: 97–115.

Hou LW, Groenewald JZ, Pfenning LH, *et al*. (2020a). The phoma-like dilemma. *Studies in Mycology* **96**: 309–396.

Hou LW, Hernández-Restrepo M, Groenewald JZ, *et al*. (2020b). Citizen science project reveals high diversity in *Didymellaceae* (*Pleosporales, Dothideomycetes*). *MycoKeys* **65**: 49–99.

Hou YM, Zhang X, Zhang NN, *et al.* (2019). Genera *Acremonium* and *Sarocladium* cause brown spot on bagged apple fruit in China. *Plant Disease* **103**: 1889–1901.

Hudson O, Buchholz M, Doyle V, *et al.* (2019). Multilocus phylogeny of *Acrospermaceae*: New epibiotic species and placement of *Gonatophragmium, Pseudovirgaria*, and *Phaeodactylium* anamorphs. *Mycologia* **111**: 1041–1055.

Jaklitsch WM, Olariaga I, Voglmayr H (2016). *Teichospora* and the *Teichosporaceae*. *Mycological Progress* **15**: 31.

Johnston PR, Park D (2019). *Blastacervulus metrosideri sp. nov*. leaf spot on *Metrosideros excelsa* in New Zealand. *Fungal Systematics and Evolution* **3**: 165–169.

Kalyaanamoorthy S, Minh BQ, Wong TKF, *et al*. (2017). ModelFinder: Fast model selection for accurate phylogenetic estimates. *Nature Methods* **14**: 587–589.

Kearse M, Moir R, Wilson A, *et al*. (2012). Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics* **28**: 1647–1649.

Klaubauf S, Tharreau D, Fournier E, *et al.* (2014). Resolving the polyphyletic nature of *Pyricularia* (*Pyriculariaceae*). *Studies in Mycology* **79**: 85–120.

Kumar S, Stecher G, Tamura K (2016). MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets. *Molecular Biology and Evolution* **33**: 1870–1874.

Lechat C, Fournier J, Stoykov D (2019). *Flammocladiella anomiae*, a new hypocrealean species from France and Bulgaria. *Ascomycete.org* **11**: 239–243.

Liu Q, Li JQ, Wingfield MJ, *et al.* (2020). Reconsideration of species boundaries and proposed DNA barcodes for *Calonectria*. *Studies in Mycology* **97**: 100106.

Lombard L, van der Merwe NA, Groenewald JZ, *et al.* (2015). Generic concepts in *Nectriaceae*. *Studies in Mycology* **80**: 189–245.

Lynch SC, Twizeyimana M, Mayorquin JS, *et al.* (2016) Identification, pathogenicity and abundance of *Paracremonium pembeum sp. nov.* and *Graphium euwallaceae sp. nov*. – two newly discovered mycangial associates of the polyphagous shot hole borer (*Euwallacea* sp.) in California. *Mycologia* **108**: 313–329.

Magina S, Lisboa C, Santos P, *et al.* (2000). Cutaneous alternariosis by *Alternaria chartarum* in a renal transplanted patient. *British Journal of Dermatology* **142**: 1261–1262.

Marin-Felix Y, Groenewald JZ, Cai L, *et al*. (2017). Genera of phytopathogenic fungi: GOPHY 1. *Studies in Mycology* **86**: 99–216.

Moslemi A, Ades PK, Groom T, *et al*. (2016). Paraphoma crown rot of pyrethrum (*Tanacetum cinerariifolium*). *Plant Disease* **100**: 2363–2369.

Muntañola-Cvetkoviç M, Hoyo P, Llimona X (1997). Fongs mitòsporics dels estatges montà, subalpí i alpí de Catalunya. *Revista Catalana de Micologia* **20**: 199–212.

Nag Raj TR (1993). *Coelomycetous anamorphs with appendage-bearing conidia*. Mycologue Publications, Waterloo, Ontario.

Nguyen L-T, Schmidt HA von Haeseler A, *et al*. (2015). IQ-TREE: A fast and effective stochastic algorithm for estimating maximum likelihood phylogenies. *Molecular Biology and Evolution* **32**: 268–274.

Nicot J, Parguey A (1960). Une moisissure nouvelle du sol en extrême-Orient: *Heimiodora verticillata nov. gen., nov. sp*. *Annales des Sciences Naturelles Botanique* **1**: 365–385.

Obrist W (1959). Untersuchungen über einige "Dothideale" Gattungen. *Phytopathologische Zeitschrift* **35**: 357–388.

Ouellette GB, Pirozynski KA (1974). Reassessment of *Tympanis* based on types of ascospore germination within asci. *Canadian Journal of Botany* **52**: 1889–1911.

Phillips AJL, Alves A, Abdollahzadeh J, *et al.* (2013). The *Botryosphaeriaceae*: genera and species known from culture. *Studies in Mycology* **76**: 51–167.

Phukhamsakda C, McKenzie EHC, Phillips AJL, *et al.* (2020). Microfungi associated with *Clematis* (*Ranunculaceae*) with an integrated approach to delimiting species boundaries. *Fungal Diversity* **102**: 1–203.

Pintos Á, Alvarado P (2021). Phylogenetic delimitation of Apiospora and Arthrinium. *Fungal Systematics and Evolution* **7**: 197–221.

Pintos Á, Alvarado P, Planas J, *et al.* (2019). Six new species of *Arthrinium*

from Europe and notes about *A. caricicola* and other species found in *Carex* spp. hosts. *MycoKeys* **49**: 15–48.

Polizzi G, Aiello D, Castello I, *et al*. (2011). Occurrence, molecular characterisation, and pathogenicity of *Neoscytalidium dimidiatum* on *Citrus* in Italy. *Acta Horticulturae* **892**: 237–243.

Pordel A, Khodaparast S, Mckenzie E, *et al*. (2017). *Two new species* of *Pseudopyricularia* from *Iran*. *Mycological Progress* **16**: 729–736.

Punithalingam E (1974). Studies on *Spheropsidales* in culture II. *Mycological Papers* **136**: 1–63.

Rayner RW (1970). *A mycological colour chart*. Commonwealth Mycological Institute and British Mycological Society. Kew, Surrey, UK.

Réblová M, Hernández-Restrepo M, Fournier J, *et al*. (2020). New insights into the systematics of *Bactrodesmium* and its allies and introducing new genera, species and morphological patterns in the *Pleurotheciales* and *Savoryellales* (*Sordariomycetes*). *Studies in Mycology* **95**: 415–466.

Romero AI, Carmarán CC, Lorenzo LE (1999). A new species of *Coniochaeta* with a key to the species known in Argentina. *Mycological Research* **6**: 689–695.

Ronquist F, Teslenko M, Van der Mark P, *et al.* (2012). MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology* **61**: 539–542.

Samson RA, Houbraken J, Thrane U, *et al*. (2019). *Food and Indoor Fungi*. [Westerdijk Laboratory Manual Series Vol. 2] Utrecht: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands.

Samson RA, Luiten B (1975). *Eleutherascus tuberculatus*, a new heat resistant ascomycete. *Transactions of the British Mycological Society* **64**: 338–340.

Samuels GJ, Müller E (1979). Life-history study of Brazilian ascomycetes 5: Two new species of *Ophiostoma* and their *Sporothrix* anamorphs. *Sydowia* **31**: 169–179.

Schubert K, Ritschel A, Braun U (2003). A monograph of *Fusicladium s. lat*. (Hyphomycetes). *Schlechtendalia* **9**: 1–132.

Schultes NP, Murtishi B, Li DW (2017). Phylogenetic relationships of *Chlamydomyces*, *Harzia*, *Olpitrichum*, and their sexual allies, *Melanospora* and *Sphaerodes*. *Fungal Biology* **121**: 890–904.

Seifert K, Morgan-Jones G, Gams W, *et al*. (2011). *The Genera of Hyphomycetes*. CBS Biodiversity Series no. 9: 1–997. Westerdijk Fungal Biodiversity Institute, Utrecht, Netherlands.

Shearer CA, Crane JL, Chen W (1999). Freshwater ascomycetes: *Ophioceras* species. *Mycologia* **91**: 145–156.

Shen M, Zhang JQ, Zhao LL, *et al.* (2020). *Venturiales*. *Studies in Mycology* **96**: 185–308.

Smith H, Wingfield MJ, Crous PW, *et al*. (1996). *Sphaeropsis sapinea* and *Botryosphaeria dothidea* endophytic in *Pinus* spp. and *Eucalyptus* spp. in South Africa. *South African Journal of Botany* **62**: 86–88.

Stalpers JA (1974). Revision of the genus *Oedocephalum* (Fungi Imperfecti). *Proceedings van de Koninklijke Nederlandse Akademie van Wetenschappen Section* C **77**: 383–401.

Stielow JB, Lévesque CA, Seifert KA, *et al.* (2015). One fungus, which genes? Development and assessment of universal primers for potential secondary fungal DNA barcodes. *Persoonia* **35**: 242–263.

Sutton BC, Funk A (1975). Conidial states of some *Pragmopora* and *Tympanis* species. *Canadian Journal of Botany* **53**: 521–526.

Sutton BC, Pascoe IG (1987). *Argopericonia* and *Tryssglobulus*, new hyphomycete genera from *Banksia* leaves. *Transactions of the British Mycological Society* **88**: 41–46.

Swofford DL (2003). *PAUP*: phylogenetic analysis using parsimony* (*and other methods). Version 4.0b10. Sinauer Associates, Sunderland.

Taylor JE, Crous PW (2001). Morphological variation and cultural characteristics of *Coniothyrium leucospermi* associated with leaf spots of *Proteaceae*. *Mycoscience* **42**: 265–271.

Theissen F, Sydow H (1915). Die Dothideales. *Annales Mycologici* **13**: 149–746.

Van der Aa HA (1971). *Macroventuria*, a new genus in the *Venturiaceae*. *Persoonia* **6**: 359–363.

Van der Aa HA, Vanev S (2002). *A revision of the species described in Phyllosticta.* Centraalbureau voor Schimmelcultures, Utrecht, The Netherlands.

Van Nieuwenhuijzen EJ, Miadlikowska JM, Houbraken JAMP, *et al*. (2016). Wood staining fungi revealed taxonomic novelties in *Pezizomycotina*: New order *Superstratomycetales* and new species *Cyanodermella oleoligni*. *Studies in Mycology* **85**: 107–124.

Verkley GJM, Quaedvlieg W, Shin HD, *et al.* (2013). A new approach to species delimitation in *Septoria. Studies in Mycology* **75**: 213–305.

Videira SIR, Groenewald JZ, Braun U, *et al*. (2016). All that glitters is not *Ramularia*. *Studies in Mycology* **83**: 49–163.

Videira SIR, Groenewald JZ, Nakashima C, *et al*. (2017). *Mycosphaerellaceae* – chaos or clarity? *Studies in Mycology* **87**: 257–421.

Voglmayr H, Jaklitsch WM (2011). Molecular data reveal high host-specificity in the phylogenetically isolated genus *Massaria* (*Ascomycota*, *Massariaceae*). *Fungal Diversity* **46**: 133–170.

Vu D, Groenewald M, de Vries M, *et al.* (2019). Large-scale generation and analysis of filamentous fungal DNA barcodes boosts coverage for kingdom fungi and reveals thresholds for fungal species and higher taxon delimitation. *Studies in Mycology* **92**: 135–154.

Walker J (1980). *Gaeumannomyces, Linocarpon, Ophiobolus* and several genera of scolecospored ascomycetes and *Phialophora* conidial states, with a note on hyphopodia. *Mycotaxon* **11**: 1–129.

Wang M, Tan XM, Liu F, *et al.* (2018). Eight new *Arthrinium* species from China. *MycoKeys* **34**: 1–24.

Wang Y, Pei YF, Zhang K, *et al.* (2009). Molecular and morphological description of a new species of *Ulocladium* from Southern China. *Mycological Progress* **8**: 207.

Woudenberg JHC, Groenewald JZ, Binder M, Crous PW (2013). *Alternaria* redefined. *Studies in Mycology* **75**: 171–212.

Woudenberg JHC, Hanse B, van Leeuwen GCM, *et al*. (2017). *Stemphylium* revisited. *Studies in Mycology* **87**: 77–103.

Zhang W, Groenewald JZ, Lombard L, *et al*. (2021a). Evaluating species in *Botryosphaeriales*. *Persoonia* **46**: 63–115.

Zhang Y, Fournier J (2015). *Kirschsteiniothelia thujina* (Peck) D. Hawksw. (*Kirschsteiniotheliaceae*), reported from Europe for the first time. *Ascomycete.org* **7**: 31–37.

Zhang Z, Schwartz S, Wagner L, *et al*. (2000). A greedy algorithm for aligning DNA sequences. *Journal of Computational Biology* **7**: 203–214.

Zhang ZF, Liu F, Zhou X, *et al.* (2017). Culturable mycobiota from Karst caves in China, with descriptions of 20 new species. *Persoonia* **39**: 1–31.

Zhang ZF, Zhou SY, Eurwilaichitr L, *et al.* (2021b). Culturable mycobiota from Karst caves in China II, with descriptions of 33 new species. *Fungal Diversity*: doi.org/10.1007/s13225-020-00453-7

Zhang ZY, Chen WH, Zou X, *et al.* (2019). Phylogeny and taxonomy of two new *Plectosphaerella* (*Plectosphaerellaceae, Glomerellales*) species from China. *MycoKeys* **57**: 47–60.