Persoonia 56, 2026: 457–547
https://www.persoonia.org

RESEARCH ARTICLE

ISSN (Online) 1878-9080
https://doi.org/10.3114/persoonia.2026.56.08

New and Interesting Fungi. 8

P.W. Crous[1,2,3*], A. Akulov[4], A.C. Alfenas[5], R.F. Alfenas[5], F. Aloi[6,7], S. Balashov[8], R.W. Barreto[5], K. Bensch[1], S.O. Cacciola[6], T. Cantillo[9], R. Castillo[10], S. Conti Taguali[6], P. Czachura[11], N.F. da Silva[5], M.A. Delgado[8], S. Denman[12], N.I. de Silva[13], R.P. de Vries[1,27], M. Figge[1], V. Guarnaccia[7,14], D.S. Guterres[5], S. Hongsanan[13], M. Horta Jung[15,16], J. Houbraken[1], T. Hülsewig[17], T. Jung[15,16], Ž. Jurjević[8], F. La Spada[6], H. Madrid[18,19], A. Mombert[20], E.R. Osieck[21], A. Pane[6], R. Parlascino[6], C.M. Pereira[5], M. Piątek[11], V. Piattino[7], M. Riolo[6], M. Sandoval-Denis[1], B. Scanu[22], M. Starink-Willemse[1], M. Stryjak-Bogacka[11], D.S. Tennakoon[13], V.A. van Ingen-Buijs[23], A.L. van Iperen[1], G.J.M. Verkley[1], S.C. Lamprecht[24], X.W. Wang[25], U. Braun[26], M.J. Wingfield[2], J.Z. Groenewald[1]

*Corresponding author: Pedro Crous, p.crous@wi.knaw.nl

Key words:
biodiversity
ITS barcodes
multi-gene phylogeny
new taxa
systematics
typification

Abstract: Eight new genera, 28 new species, four epitypes, two lectotypes, and 21 interesting new host and / or geographical records are introduced in this study. New genera include: *Amesomyces* (based on *Amesomyces atrobrunneus*), *Carteromyces* (based on *Carteromyces arctostaphyli*), *Scolecofusariella* (based on *Fusarium peltigerae*), *Nothoniesslia* (based on *Nothoniesslia solidaginis*), *Paraacanthostigma* (based on *Paraacanthostigma eucalypti*), *Paraphaeophleospora* (based on *Paraphaeophleospora tripteridis*), *Parapolyscytalum* (based on *Parapolyscytalum minutum*) and *Subverticillium* (based on *Subverticillium juncicola*). New species include: *Bisifusarium duo* (from human cornea, India), *Capronia parasitica* (on *Eutypella sorbi* on branches of *Sorbus aucuparia*, Switzerland), *Castanediella acericola* on dead leaf of *Acer* cf. *pseudoplatanus*, Germany), *Cladophialophora calamagrostidis* (on culm of *Calamagrostis arenaria*, The Netherlands), *Cladophialophora paramycetomatis* (on culms of *Elegia tectorum*, South Africa), *Cladophialophora yuccae* (on dead leaf of *Yucca* sp., Germany), *Cordana ligni* (on dead wood, Germany), *Curvularia moniliformis* (on leaves of unidentified *Poaceae*, Chile), *Davidhawksworthia rubi* (on *Rubus* stems, Germany), *Exophiala ligni* (on dead wood, Germany), *Fusarium aloetica* (on symptomatic leaves of *Aloe ferox*, South Africa), *Harzia cupressicola* (on needles of *Cupressus* sp., The Netherlands), *Hoehneliella falsiundulosetulata* (on bark of woody host, Germany), *Mjuua pseudoclavispora* (in association with *Fusarium paeoniae* and a bacterium, on dead fruit of *Alnus glutinosa*, Germany), *Monilinia yunnanensis* (on fruit of *Prunus persica*, China), *Niesslia goniomae* (on leaf of *Gonioma kamassi*, South Africa), *Nothoniesslia solidaginis* (on dead stems of *Solidago* sp., Germany), *Paraacanthostigma eucalypti* (on bark of *Eucalyptus globulus*, Australia), *Phaeococcomyces mesembryanthemi* (on *Mesembryanthemum schultzii*, South Africa), *Phialemonium parasulfureum* (on algae, Germany), *Phytophthora caput-medusae* (from rhizosphere soil of *Citrus* × *aurantium*, Italy), *Pleurophragmium fallopiae* (on dead leaf *Fallopia* sp., Germany), *Rhinotrichella carpini* (on dead branches of *Carpinus betulus*, Ukraine), *Stagonosporopsis citri* (on peel of living fruit of *Citrus latifolia*, quarantine interception), *Subverticillium juncicola* (on culms of *Juncus effusus*, Netherlands), *Veronaea parabrunnea* (on *Eutypella prunastri* on twigs of *Prunus spinosa*, France), *Veronaea parasiticola* (on *Euonymus europaeus*, Germany), *Verrucocladosporium mesembryanthemi* (on *Mesembryanthemum schultzii*, South Africa). New combinations include: *Amesomyces atrobrunneus* (based on *Chaetomium atrobrunneum*), *Amesomyces cymbiformis* (based on *Chaetomium cymbiforme*), *Amesomyces dreyfussii* (based on *Chaetomium dreyfussii*), *Amesomyces gelasinosporus* (based on *Chaetomium gelasinosporum*), *Amesomyces hispanicus* (based on *Amesia hispanica*), *Amesomyces khuzestanicus* (based on *Amesia khuzestanica*), *Amesomyces nigricolor* (based on *Chaetomium nigricolor*), *Amesomyces raii* (based on *Chaetomium raii*), *Carteromyces arctostaphyli* (based on *Carteria arctostaphyli*), *Carteromyces canariensis* (based on *Carteria canariensis*), *Capronia americana* (based on *Cadophora americana*), *Didymella conyzaphthora* (based on *Phoma conyzaphthora*), *Heterotruncatella watsoniae* (based on *Pestalotia watsoniae*), *Hoehneliella undulosetulata* (based on *Paramenisporopsis undulosetulata*), *Microascus stellatus* (based on *Humicola stellata*), *Neoceratosperma marasasii* (based on

Citation: Crous PW, Akulov A, Alfenas AC, Alfenas RF, Aloi F, Balashov S, Barreto RW, Bensch K, Cacciola SO, Cantillo T, Castillo R, Conti Taguali S, Czachura P, da Silva NF, Delgado MA, Denman S, de Silva NI, de Vries RP, Figge M, Guarnaccia V, Guterres DS, Hongsanan S, Horta Jung M, Houbraken JA, Hülsewig T, Jung T, Jurjević Ž, La Spada F, Madrid H, Mombert A, Osieck ER, Pane A, Parlascino R, Pereira CM, Piątek M, Piattino V, Riolo M, Sandoval-Denis M, Scanu B, Starink-Willemse M, Stryjak-Bogacka M, Tennakoon DS, van Ingen-Buijs VA, van Iperen AL, Verkley GJM, Lamprecht SC, Wang XW, Braun U, Wingfield MJ, Groenewald JZ (2026). New and Interesting Fungi. 8. *Persoonia* **56**: 457–547. doi: 10.3114/persoonia.2026.56.08
Received: 20 March 2026; **Accepted:** 24 April 2026; **Effectively published online:** 29 May 2026
Corresponding editor: C.M. Visagie

Abstract: *Mycosphaerella marasasii*), *Paraphaeophleospora tripteridis* (based on *Septoria tripteridis*), *Parapolyscytalum minutum* (based on *Infundichalara minuta*), *Scolecofusariella peltigerae* (based on *Fusarium peltigerae*) and *Veronaea brunnea* (based on *Exophiala brunnea*). *Zygophiala* is reduced to synonymy under *Schizothyrium*, *Paramenisporopsis* and *Klebahnopycnis* under *Hoehneliella*, and the descriptions of the order *Comminutisporales* and family *Comminutisporaceae* are emended.

[1]Westerdijk Fungal Biodiversity Institute, Uppsalalaan 8, 3584 CT Utrecht, The Netherlands
[2]Department of Genetics, Biochemistry and Microbiology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, 0002, South Africa
[3]Microbiology, Department of Biology, Utrecht University, Padualaan 8, Utrecht, 3584 CH, The Netherlands
[4]Department of Mycology and Plant Resistance, V. N. Karazin Kharkiv National University, Maidan Svobody 4, 61022 Kharkiv, Ukraine
[5]Departamento de Fitopatologia, Universidade Federal de Viçosa, 36570-900, Viçosa, MG, Brazil
[6]Department of Agriculture, Food and Environment (Di3A), University of Catania, Via Santa Sofia 100, 95123, Catania, Italy
[7]Department of Agricultural, Forest and Food Sciences (DISAFA), University of Torino, Largo Braccini 2, 10095 Grugliasco, Italy
[8]EMSL Analytical, Inc., 200 Route 130 North, Cinnaminson, NJ 08077 USA
[9]Postgraduate Program in Earth Modeling and Environmental Sciences PPGM, State University of Feira de Santana, Av. Transnordestina, s/n, Novo Horizonte, Feira de Santana 44036-900, BA, Brazil
[10]Escuela de Tecnología Médica, Facultad de Medicina y Ciencias de la Salud, Universidad Mayor, Camino La Pirámide 5750, 8580745 Huechuraba, Santiago, Chile
[11]W. Szafer Institute of Botany, Polish Academy of Sciences, Lubicz 46, PL-31-512 Kraków, Poland
[12]Forest Research, Alice Holt Lodge, Farnham, Surrey, UK
[13]Shenzhen Key Laboratory of Microbial Genetic Engineering, College of Life Science and Oceanography, Shenzhen University, Shenzhen 518060, P.R. China
[14]Interdepartmental Centre for Innovation in the Agro-Environmental Sector, AGROINNOVA, University of Torino, Largo Braccini 2, 10095 Grugliasco (TO), Italy
[15]Department of Forest Protection and Wildlife Management, Phytophthora Research Centre, Faculty of Forestry and Wood Technology, Mendel University in Brno, Zemědělská 3, 61300 Brno, Czech Republic
[16]Phytophthora Research and Consultancy, Am Rain 9, 83131 Nussdorf, Germany
[17]Brink 9, 58452 Witten, Germany
[18]Escuela de Tecnología Médica, Facultad de Medicina y Ciencias de la Salud, Universidad Mayor, Av. Alemania 281, 4801043 Temuco, Chile
[19]Centro para la Resilencia, Adaptación y Mitigación (CReAM), Universidad Mayor, Av. Alemania 281, 4801043 Temuco, Chile
[20]Conservatoire botanique national de Franche-Comté - Observatoire régional des Invertébrés | 9 rue Jacquard - BP 61738 - 25043 Besançon Cedex, France
[21]Jkvr. C.M. van Asch van Wijcklaan 19, 3972 ST Driebergen-Rijsenburg, Netherlands
[22]Department of Agricultural Sciences, University of Sassari, Viale Italia 39A, 07100, Sassari, Italy
[23]Netherlands Institute for Vectors, Invasive plants and Plant Health (NIVIP), National Plant Protection Organization (NPPO), Netherlands Food and Consumer Product Safety Authority (NVWA), Geertjesweg 15, 6706 EA, Wageningen, the Netherlands
[24]Department of Plant Pathology, Stellenbosch University, Private Bag X1, Matieland, 7602, South Africa
[25]State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, No. 3, 1st Beichen West Road, Chaoyang District, Beijing 100101, China
[26]Martin Luther University Halle-Wittenberg, Institute of Biology, Geobotany and Botanical Garden, Herbarium, Am Kirchtor 3, 06099 Halle (Saale), Germany
[27]Fungal Biotechnology, Luxembourg Institute of Science and Technology, 5 Rue Bommel, 4940 Hautcharage, Luxembourg

INTRODUCTION

Recent estimates for the number of fungi on earth range from 2.2 to 3.8 million species (Hawksworth & Lücking 2017, Niskanen *et al.* 2023). It is consequently of concern that based on current estimates, only around 200 000 taxa have been described (Crous *et al.* 2025). This emphasises an urgent need to accelerate the discovery, description and importantly, the preservation of new fungal species. Unfortunately, based on current taxonomic practises, only 2000–2500 fungal species are described annually (Cheek *et al.* 2020). The New and Interesting Fungi (NIF) series is published annually, and aims to facilitate the description of novel species, while also reporting new host or geographical records, and new sexual-asexual connections.

MATERIALS AND METHODS

Isolates

Samples of taxa presented in this paper were treated as previously described by Crous *et al.* (2019c). Single conidial colonies were established on Petri dishes containing 2 % malt extract agar (MEA) following the methods of Crous *et al.* (1991), single ascospore cultures were established as described by Crous (1998), and single hyphal tip colonies of *Phytophthora caput-medusae sp. nov.* were established according to Conti Taguali *et al.* (2025). Colonies were sub-cultured on different media, including 2 % potato dextrose agar (PDA), oatmeal agar (OA), MEA (Crous *et al.* 2019c), V8 agar (V8A) (Jung *et al.* 2017), corn meal agar (CMA), carrot

agar (CA) (Jung *et al.* 2017), or autoclaved pine needles on 2 % tap water agar (PNA) (Smith *et al.* 1996). Cultures were incubated at 25 °C under continuous near-ultraviolet light to promote sporulation, except for *Phytophthora caput-medusae sp. nov.*, for which sporulation was promoted by following the procedure described by Aloi *et al.* (2021). Reference strains and specimens of the studied fungi are maintained in the culture collection and fungarium (CBS) of the Westerdijk Fungal Biodiversity Institute (WI), Utrecht, the Netherlands.

DNA extraction, amplification (PCR), sequencing and phylogeny

Genomic DNA was extracted from fungal strains using standard procedures. Fifteen gene regions were amplified with PCR and then Sanger sequenced in both directions, including the nrDNA internal transcribed spacer region ITS1-5.8S-ITS2 (ITS), the nrDNA large and small subunits (LSU and SSU), the partial actin gene (*actA*), the partial β-tubulin gene (*BenA* = *tub2*), the partial calmodulin gene (*CaM* = *cmdA*), the mitochondrial gene cytochrome oxidase subunits I and II (*cox1* and *cox2*), the partial glyceraldehyde-3-phosphate dehydrogenase gene (*gapdh*), the partial heat shock protein 90 gene (*hsp90*), the partial ribosomal protein L10 gene (L10), the partial dehydrogenase subunit 1 gene (*nadh1*), the partial DNA-directed RNA polymerase II largest subunit gene (*rpb1*), the partial DNA-directed RNA polymerase II second largest subunit gene (*rpb2*), two regions of the translation elongation factor 1-alpha gene (*tef1*), and a putative ribosome biogenesis protein gene (*Tsr1*). Sequences were deposited in NCBI's GenBank nucleotide database (https://www.ncbi.nlm.nih.gov/genbank/) and accession numbers are listed under the materials examined.

Each newly generated sequence was subjected to a BLAST search against the NCBI database (https://blast.ncbi.nlm.nih.gov/Blast.cgi) to identify closely related sequences that guided subsequent phylogenetic analyses. The phylogenetics approaches used are provided in the figure legends.

Morphology

Slide preparations were mounted in lactic acid, Shear's mounting fluid, Melzer's solution, or water, from colonies sporulating on MEA, PDA, PNA or OA. Observations were made with a Nikon SMZ25 dissection microscope, and with a Zeiss Axio Imager 2 light microscope using differential interference contrast (DIC) illumination and images recorded on a Nikon DS-Ri2 camera with associated software. Colony characters and pigment production were noted after 2–4 wk of growth on MEA, PDA and OA (Crous *et al.* 2019c) incubated at 25 °C. Colony colours (surface and reverse) were scored using the colour charts of Rayner (1970). Taxonomic novelties were submitted to MycoBank (www.MycoBank.org; Crous *et al.* 2004).

RESULTS AND DISCUSSION

Taxonomy

Replacement names for *Amesia* and *Carteria*

According to Article 53.1 of the *International Code of Nomenclature for algae, fungi, and plants* (ICNafp), a name published later that is spelled exactly like an earlier name based on a different type is a later homonym and is illegitimate.

The generic name *Amesia* has previously been used for a plant genus in the family *Orchidaceae*, rendering our fungal genus *Amesia* illegitimate (Wang *et al.* 2016). Similarly, the fungal genus *Carteria* (Wang *et al.* 2019a) proved to be a later homonym of the algae genus *Carteria* Diesing (1866) and also of the plant genus *Carteria* Small (1910) (*Orchidaceae*). Therefore, we propose replacement names for both genera and recombine the species originally described under *Amesia* and *Carteria*:

Amesomyces X.Wei Wang & Houbraken, ***nom. nov.*** MB 863490.
Replaced synonym: *Amesia* X.Wei Wang, Samson & Crous, *Stud. Mycol*. **84**: 156. 2016. nom. illeg., non *Amesia* A. Nelson & J.F. Macbr. 1913 (*Orchidaceae*)

Type species: *Amesomyces atrobrunneus* (L.M. Ames) X.Wei Wang & Houbraken

Amesomyces atrobrunneus (L.M. Ames) X.Wei Wang & Houbraken, ***comb. nov***. MB 863491.
Basionym: *Chaetomium atrobrunneum* L.M. Ames, *Mycologia* **41**(6): 641. 1949.

Amesomyces cymbiformis (Lodha) X.Wei Wang & Houbraken, ***comb. nov***. MB 863492.
Basionym: *Chaetomium cymbiforme* Lodha, *J. Indian Bot. Soc*. **43**: 129. 1964.

Amesomyces dreyfussii (Arx) X.Wei Wang & Houbraken, ***comb. nov.*** MB 863493.
Basionym: *Chaetomium dreyfussii* Arx, *Beih. Nova Hedwigia* **84**: 6. 1986.

Amesomyces gelasinosporus (Aue & E. Müll.) X.Wei Wang & Houbraken, ***comb. nov***. MB 863494.
Basionym: *Chaetomium gelasinosporum* Aue & E. Müll., *Ber. Schweiz. Bot. Ges*. **77**: 193. 1967.

Amesomyces hispanicus (Y. Marín & Stchigel) X.Wei Wang & Houbraken, ***comb. nov.*** MB 863495.
Basionym: *Amesia hispanica* Y. Marín & Stchigel, *J. Fungi* **9** (4, no. 463): 7. 2023.

Amesomyces khuzestanicus (M. Mehrabi *et al.*) X.Wei Wang & Houbraken, ***comb. nov.*** MB 863496.
Basionym: *Amesia khuzestanica* M. Mehrabi *et al.*, *Mycol. Progr*. **19** (9): 939. 2020.

Amesomyces nigricolor (L.M. Ames) X.Wei Wang & Houbraken, ***comb. nov.*** MB 863497.
Basionym: *Chaetomium nigricolor* L.M. Ames, *Mycologia* **42** (5): 645. 1950.

Amesomyces raii (G. Malhotra & Mukerji) X.Wei Wang & Houbraken, ***comb. nov***. MB 863498.
Basionym: *Chaetomium raii* G. Malhotra & Mukerji, *Rev. Mycol. (Paris)* **40** (2): 182. 1976.

Carteromyces X.Wei Wang & Houbraken, ***nom. nov.*** MB 863499.
Replaced synonym: *Carteria* X.Wei Wang & Houbraken, *Stud. Mycol*. **93**: 194 (2019), nom. illeg., non *Carteria* Diesing (1866) [algae], nec *Carteria* Small (1910) [*Orchidaceae*]

Type species: *Carteromyces arctostaphyli* (X.Wei Wang & Houbraken) X.Wei Wang & Houbraken

Carteromyces arctostaphyli (X.Wei Wang & Houbraken) X.Wei Wang & Houbraken, ***comb. nov.*** MB 863500.
Basionym: *Carteria arctostaphyli* X.Wei Wang & Houbraken, *Stud. Mycol.* **93**: 194 (2019).

Carteromyces canariensis (Sastoque *et al.*) X.Wei Wang & Houbraken, ***comb. nov.*** MB 863501.
Basionym: *Carteria canariensis* Sastoque *et al.*, *Persoonia* **54**: 99. 2025.

Authors: X.W. Wang & J. Houbraken

Anthostoma decipiens (DC.) Nitschke, *Pyrenomyc. Germ.* **1**: 111. 1867.
Basionym: *Sphaeria decipiens* DC., *Fl. Franç. Ed. 3* **2**: 285. 1805, nom. sanct.
Synonyms: *Botryosphaeria decipiens* (DC.) Cooke, *Grevillea* **13**(68): 108. 1885.
Lopadostoma decipiens (DC.) P.M.D. Martin, *S. African J. Bot.* **35**: 399. 1969.
Lopadostoma decipiens (DC.) P.M.D. Martin*, S. African J. Bot.* **42**(1): 75. 1976.
Cryptosphaeria decipiens (DC.) Læssøe & Spooner*, Kew Bull.* **49**(1): 56. 1994.
Eutypella decipiens (DC.) Dissan. *et al., Fungal Diversity* **134**: 564. 2025, nom. inval.
Cytospora corylicola Sacc., *Syll. Fung.* **2**: 328. 1883.

Description: Rocchi *et al.* (2010).

Material examined: **Unknown**, *Corylus avellana* (fruit), Jun. 1951, *G. Goidánich*, culture CBS 231.51. GenBank sequence ITS: PZ110978.

Notes: *Cytospora corylicola* has been widely reported as the causal agent of 'mal dello stacco' of hazelnut, also known as Cytospora canker (Trotter, 1933, 1946, Servazzi 1950, Salerno 1961). However, recent studies conducted in Italy identified *Anthostoma decipiens* as the causal agent of that disease using a polyphasic approach combining morphological and molecular identification and pathogenicity tests (Linaldeddu *et al.* 2016, Martino *et al.* 2024). Notably, no *Cytospora* species were detected in these investigations. Given the inconsistency in the pathogen identification associated with the "mal dello stacco", DNA sequence comparisons were conducted on the strain CBS 231.51, originally reported as *C. corylicola* and isolated from *Corylus avellana*. Phylogenetic analysis based on the ITS sequence identified the strain as *A. decipiens* (Fig. 1). Morphologically, several *Cytospora* species are almost indistinguishable from *A. decipiens,* which likely accounts for the confusion regarding this species. Additionally, *C. decipiens* was reported as the asexual morph of *A. decipiens* (Saracchi *et al.* 2008, Rocchi *et al.* 2010). However, the phylogenetic tree produced in this study shows that *A. decipiens* strains, including CBS 231.51, form a clade distinct from *Cytospora* spp. Consequently, based on the currently available evidence, historical records of *C. corylicola* likely refer to *A. decipiens*.

Authors: V. Guarnaccia & V. Piattino

Bisifusarium duo Crous, ***sp. nov.*** MB 863241. Fig. 2.

Etymology: Described as *Bisifusarium* 2 (*duo*) by Zhang *et al.* (2025).

Description and illustration: Zhang *et al.* (2025).

Typus: **India**, Gijarat, Ahmedabad, from human cornea, collection date and *collector* unknown (**holotype** CBS H-25452, culture ex-type CBS 135686). GenBank sequences ITS: PV158444; *rpb2* (first part): PV167639.

Additional material examined: **USA**, Pennsylvania, Malvern, non-potable water, Dec. 2023, *Z. Jurjević*, 5894, culture CPC 48135 = CBS 151628. GenBank sequences ITS: PZ221265; LSU: PZ221333; *cmdA*: PZ228597; *rpb1*: PZ228623; *rpb2* (first part): PZ228742; *tef1* (first part): PZ228648; *tub2*: PZ228702.

Notes: *Bisifusarium* sp. 2 is phylogenetically closely related to but distinct from *B. dimerum* (Fig. 2). Zhang *et al.* (2025) refrained from officially naming this species, as its relationship with *B. dimerum* was unclear. The collection of a new isolate from the USA (CBS 151628), showed that it represents a complex of several closely related strains, of which CBS 151628 represent a third species. We have thus provided a name for *Bisifusarium* sp. 2.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 48135 had highest similarity to *Bisifusarium delphinoides* [as *Fusarium delphinoides*; strain FMB-SS1-TA(S), GenBank MG020724.1; Identities = 524/529 (99 %), three gaps (0 %)], *Bisifusarium nectrioides* [as *Fusarium nectrioides*; strain CBS 176.31, GenBank EU926245.1; Identities = 520/528 (98 %), two gaps (0 %)], and *Bisifusarium penzigii* [as *Fusarium penzigii*; strain CBS 317.34, GenBank NR_137707.1; Identities = 518/528 (98 %), two gaps (0 %)]. Closest hits using the **LSU** sequence of CPC 48135 are *Bisifusarium dimerum* [as *Fusarium dimerum*; strain NRRL 20691, GenBank PP336539.1; Identities = 879/881 (99 %), no gaps], *Bisifusarium nectrioides* [as *Fusarium nectrioides*; strain CBS 176.31, GenBank KM231659.1; Identities = 824/830 (99 %), no gaps], and *Bisifusarium penzigii* [as *Fusarium penzigii*; strain CBS 317.34, GenBank

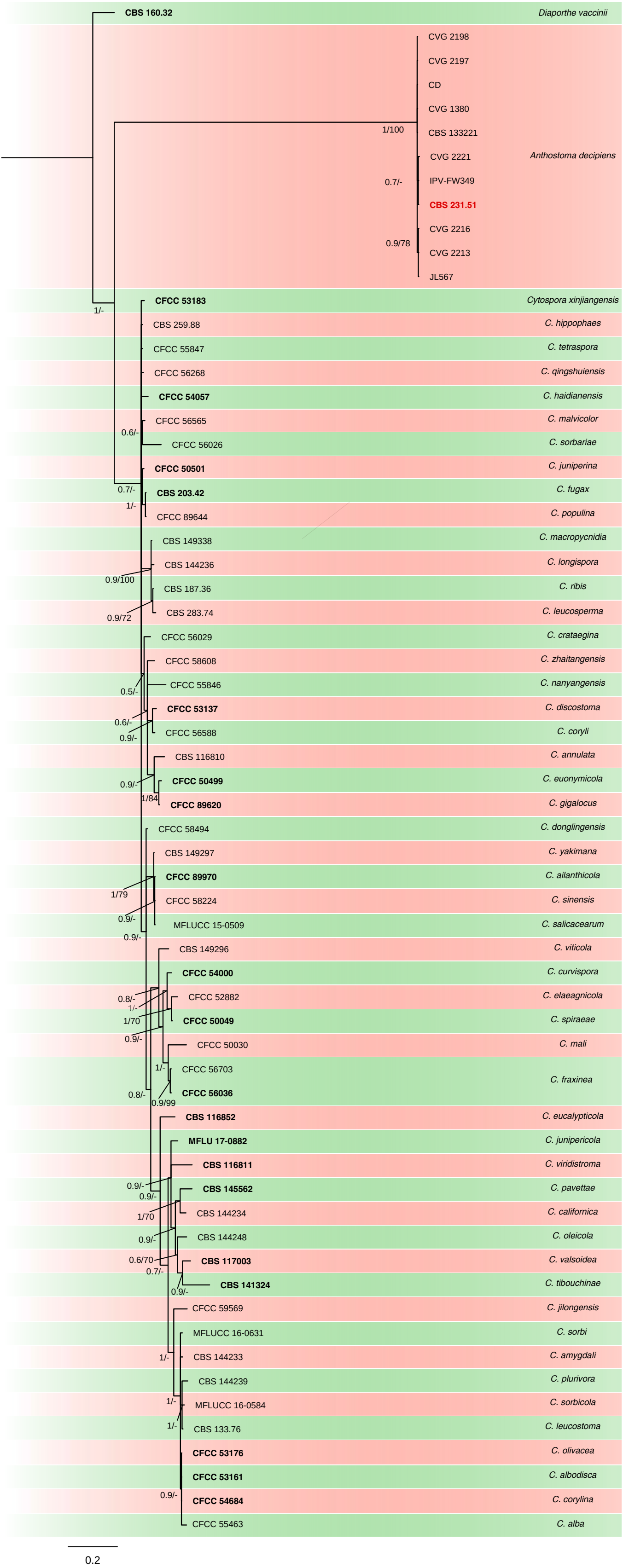

Fig 1. The phylogenetic tree of *Anthostoma decipiens* resulting from a Bayesian analysis of the ITS sequences. Bayesian posterior probabilities and Maximum likelihood bootstrap support values are indicated at the nodes. Ex-type strains are reported in Bold font and the strain CBS 231.51 from the current study are reported in red. The tree was rooted to *Diaporthe vaccinii* (CBS 160.32).

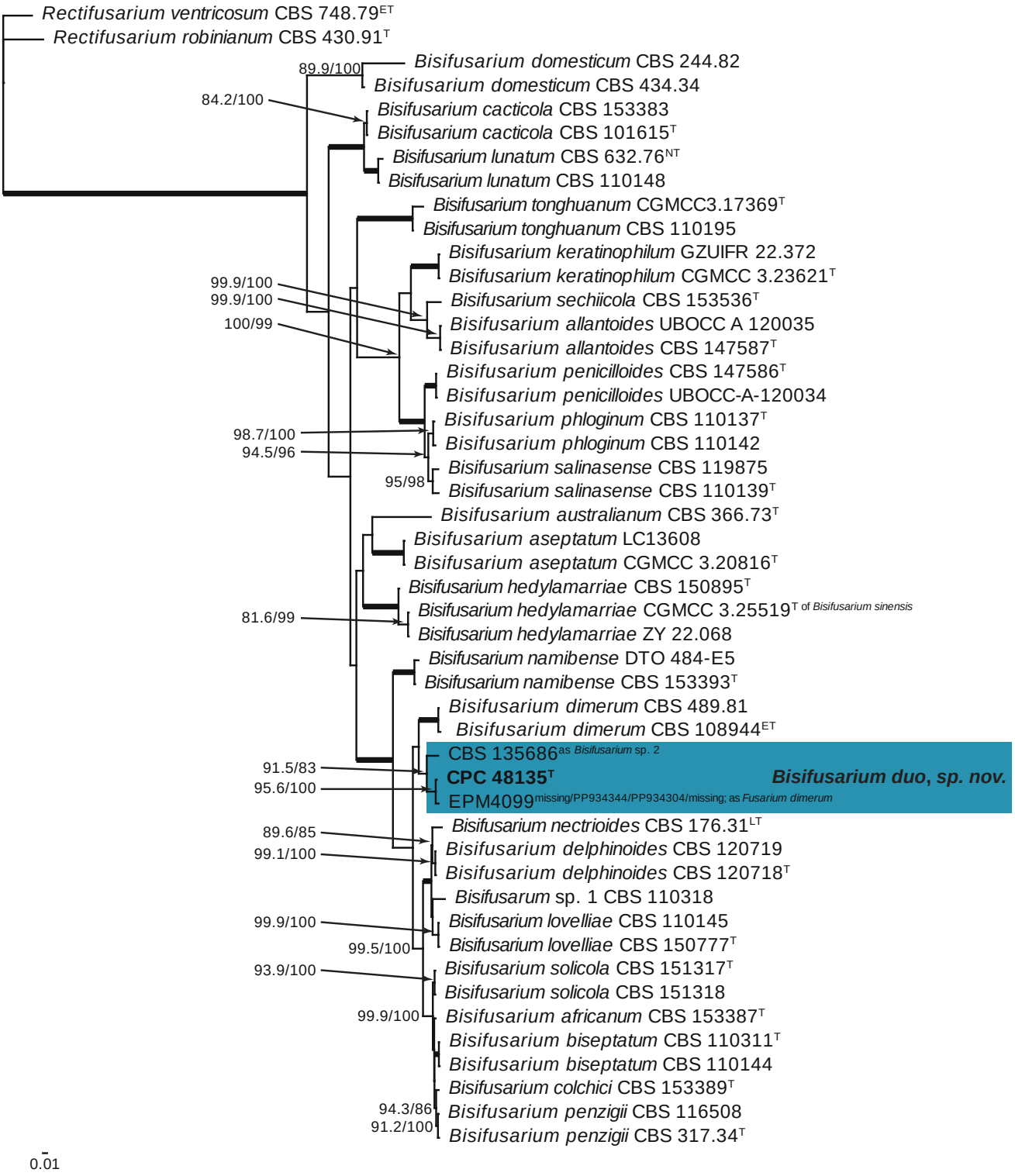

Fig. 2. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Bisifusarium* ITS-*rpb2*-*tef1*-*tub2* nucleotide alignment from Zhang *et al.* (2025). Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Thickened branches resprest a SH-aLRT test value of 100 and a bootstrap support value of 100 %. Culture collection or specimen voucher numbers are indicated for all species; see Zhang *et al.* (2025) for GenBank accession numbers. Strains from material with a type status are indicated with superscript letters (T: ex-type; ET: ex-epitype; LT: ex-lectotype; NT: ex-neotype). The tree was rooted to *Rectifusarium ventricosum* (CBS 748.79) and *Rectifusarium robinianum* (CBS 430.91) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 48 strains including the outgroup; 2513 characters including alignment gaps analysed: 1130 distinct patterns, 830 parsimony-informative, 167 singleton sites, 1516 constant sites. The best-fit models identified for the entire alignment in IQ-TREE using the TESTNEW option were: ITS (1–473): TPM2+R2; *rpb2* (474–1237): TIM3e+G4; *tef1* (1238–2010): TIM2e+I+G4; *tub2* (2011–2513): TPM3+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

KM231661.1; Identities = 824/830 (99 %), no gaps]. Closest hits using the ***cmdA*** sequence of CPC 48135 had highest similarity to *Bisifusarium dimerum* [as *Fusarium dimerum*; strain CBS 108944, GenBank KM231365.1; Identities = 605/657 (92 %), three gaps (0 %)], *Bisifusarium penzigii* [as *Fusarium penzigii*; strain CBS 317.34, GenBank KM231364.1; Identities = 598/658 (91 %), five gaps (0 %)], and *Bisifusarium biseptatum* [as *Fusarium biseptatum*; strain CBS 110311, GenBank MW811028.1; Identities = 524/579 (91 %), seven gaps (1 %)]. Closest hits using the ***rpb1*** sequence of CPC 48135 had highest similarity to *Bisifusarium biseptatum* [as *Fusarium biseptatum*; strain CBS 110311, GenBank MW811053.1; Identities = 643/673 (96 %), no gaps], *Bisifusarium penzigii* [as *Fusarium penzigii*; strain CBS 317.34, GenBank KM232211.1; Identities = 680/721 (94 %), three gaps (0 %)], and *Bisifusarium dimerum* [as *Fusarium dimerum*; strain CBS 108944, GenBank KM232212.1; Identities = 670/716 (94 %), four gaps (0 %)]. Closest hits using the ***rpb2*** (first part) sequence of CPC 48135 had highest similarity to *Bisifusarium dimerum* [as *Fusarium dimerum*; strain EPM4099, GenBank PP934344.1; Identities = 856/861 (99 %), no gaps], *Bisifusarium dimerum* [as *Fusarium dimerum*; strain FRC E-328, GenBank KR674024.1; Identities = 561/581 (97 %), no gaps], *Bisifusarium solicola* [strain CPC 47715, GenBank PP620558.1; Identities = 725/754 (96 %), no gaps], and *Bisifusarium* 2 [as *Fusarium* sp.; strain CBS 135686, GenBank PV167639.1; Identities = 723/754 (96 %), no gaps (0 %)]. Closest hits using the ***tef1*** (first part) sequence of CPC 48135 had highest similarity to *Bisifusarium dimerum* [as *Fusarium dimerum*; strain EPM4099, GenBank PP934304.1; Identities = 423/429 (99 %), three gaps (0 %)], *Bisifusarium dimerum* [as *Fusarium dimerum*;strain FRC E-328, GenBank KR673916.1; Identities = 376/398 (94 %), six gaps (1 %)], and *Bisifusarium delphinoides* [as *Fusarium delphinoides*; strain SZMC 11492, GenBank HF569904.1; Identities = 426/457 (93 %), eight gaps (1 %)]. No significant hits were obtained when the ***tub2*** sequence was used in blastn and megablast searches.

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

Capronia helvetica Crous & Mombert, ***sp. nov.*** MB 863242. Fig. 3.

Etymology: Name refers to the place it was collected, Switzerland.

Mycelium of pale brown, smooth, branched, septate, 2.5–3 µm diam. hyphae. *Conidiophores* erect, solitary, pale brown, smooth, subcylindrical, 0–2-septate, up to 20 µm tall. *Conidiogenous cells* integrated, terminal and intercalary, pale brown, smooth, 4–6 × 2–3 µm, with peg-like phialidic opening, 0.5–2 × 0.5–1 µm. *Conidia* solitary, aggregating in mucoid mass, pale brown, smooth, aseptate, guttulate, subcylindrical with obtuse ends, 3–5 × 1.5–2 µm.

Culture characteristics: Colonies erumpent, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 5 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse iron grey.

Typus: **Switzerland**, canton of Bern, Kandersteg, Gasteretal, 1425 m.a.s.l., 46.453337°N, 7.707952°E, 9 Aug. 2024, on *Eutypella sorbi* on branches of *Sorbus aucuparia* (*Rosaceae*), *E. Stöckli & A. Mombert*, Herb. Pers. AM2408091 (**holotype** CBS H-25746, culture ex-type CPC 49173 = CBS 153461); ditto, culture CPC 49174. GenBank sequences of CPC 49173 and CPC 49174 ITS: PZ221266, PZ221267; LSU: PZ221334, PZ221335.

Notes: *Capronia helvetica* grows as a typical black yeast in culture, and is related (Fig. 4) to *Capronia capensis* (described from dead twigs, South Africa; Crous *et al.* 2024c), and *Cadophora americana* (from wood pulp, USA), which is presently treated as a species of *Phialophora* (Li *et al.* 2017), but also has several *Capronia* synonyms (Untereiner *et al.* 2008). A new combination is, therefore proposed below in *Capronia* to accommodate the oldest basionym for this species.

Capronia americana (Nannf.) Crous & Mombert, ***comb. nov.*** MB 863243.
Basionym: *Cadophora americana* Nannf., *Svenska Skogsvårdsforen. Tidskr*. **3–4**: 412. 1934.
Synonyms: *Phialophora americana* (Nannf.) S. Hughes, *Canad. J. Bot*. **36**: 795. 1958.
Dictyotrichiella semiimmersa Cand. & Sulmont, *Rev. Mycol. (Paris)* **36**: 242. 1972.
Capronia semiimmersa (Cand. & Sulmont) Unter. & F.A. Naveau, *Mycologia* **91**: 73. 1999.
Capronia svrcekiana Réblová, *Czech Mycol*. **49**: 82. 1996.

Typus: **USA**, Wisconsin, woodpulp, *A. Richards*, holotype slide 6320-2 (UPS). Living strain deposited as UAMH 10875 = CDC 10. GenBank sequences ITS-LSU: EU514696; *tub2*: EU514712.

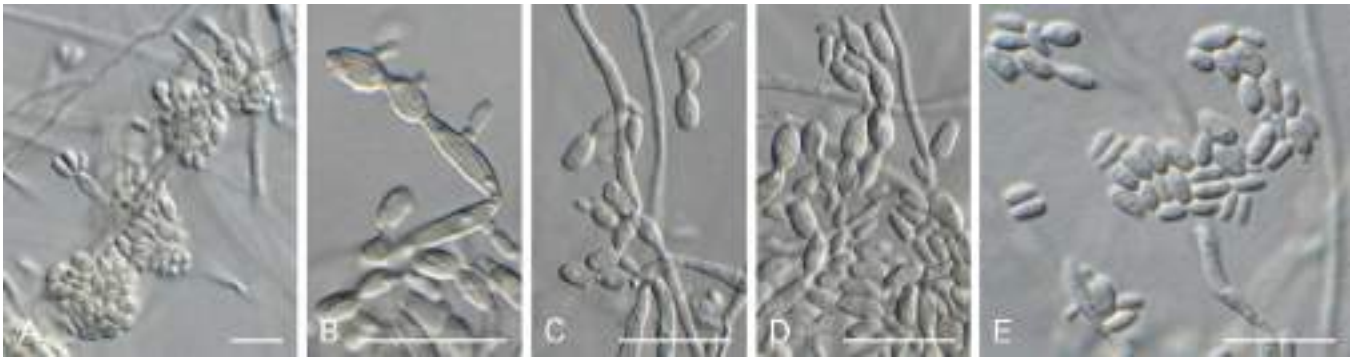

Fig. 3. *Capronia helvetica* (CPC 49173). **A–E.** Conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

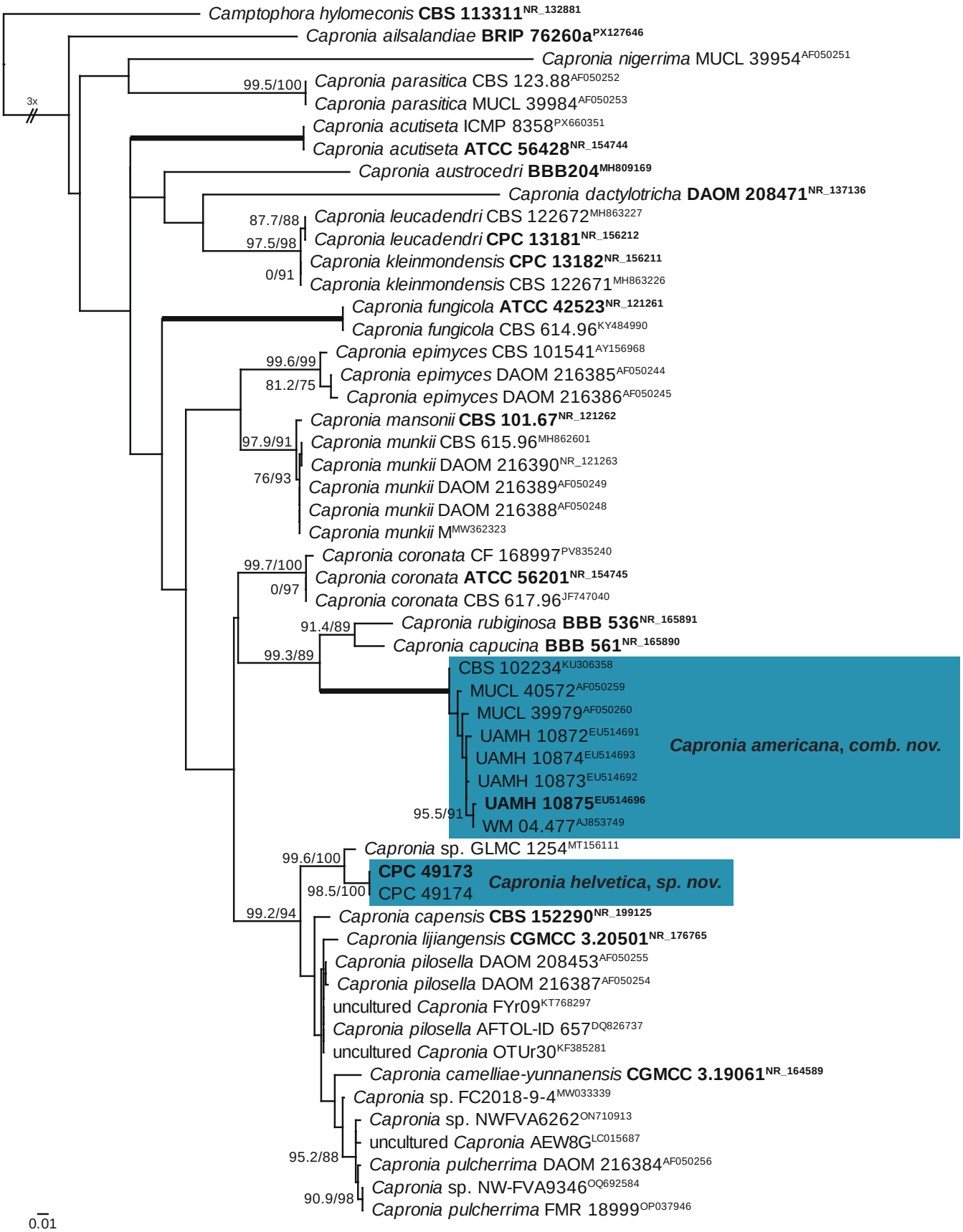

Fig. 4. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Capronia* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Thickened branches resprest a SH-aLRT test value of 100 and a bootstrap support value of 100 %. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Camptophora hylomeconis* (CBS 113311; GenBank NR_132881) and the novelties described here are highlighted with coloured blocks and **bold** font. The root branch was shortened to facilitate layout. Alignment statistics: 54 strains including the outgroup; 652 characters including alignment gaps analysed: 368 distinct patterns, 246 parsimony-informative, 62 singleton sites, 343 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

Notes: Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 49173 had highest similarity to *Capronia camelliae-yunnanensis* [strain CGMCC 3.19061, GenBank NR_164589.1; Identities = 484/511 (95 %), five gaps (0 %)], *Capronia lijiangensis* [strain CGMCC 3.20501, GenBank NR_176765.1; Identities = 525/560 (94 %), nine gaps (1 %)], and *Capronia pilosella* [strain AFTOL-ID 657, GenBank DQ826737.1; Identities = 561/599 (94 %), 10 gaps (1 %)]. The ITS sequences of CPC 49173 and CPC 49174 are identical (590/590 nt). Closest hits using the **LSU** sequence are *Capronia capensis* [strain CPC 47666, GenBank PQ499001.1; Identities = 769/773 (99 %), no gaps], *Capronia lijiangensis* [strain CGMCC 3.20501, GenBank NG_081534.1; Identities = 808/813 (99 %), one gap (0 %)], and *Capronia pilosella* [strain AFTOL-ID 657, GenBank DQ823099.1; Identities = 806/812 (99 %), no gaps]. The LSU sequences of CPC 49173 and CPC 49174 are identical (812/812 nt).

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

Castanediella acericola Crous & Hülsewig, ***sp. nov.*** MB 863244. Fig. 5.

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

Mycelium consisting of hyaline, smooth, branched, septate, 2–3 µm diam. hyphae, forming chains of globose to ellipsoid, brown chlamydospores, 6–9 µm diam. *Conidiophores* mostly reduced to conidiogenous cells or with a supporting cell, branched or not, hyaline to pale brown, smooth. *Conidiogenous cells* solitary or in clusters on hyphae, hyaline to pale brown, smooth, subuliform to ellipsoid to subcylindrical, 4–23 × 2–4 µm, with several flat-tipped apical denticles, 0.5–2 × 1 µm, proliferating sympodially, polyblastic. *Conidia* hyaline, smooth, aseptate, falcate, sides parallel but tapering prominently at ends, which are curved, beak-like, apical end longer than basal end, (11–)15–18(–23) × (2–)3(–4) µm.

Culture characteristics: Colonies flat, spreading, with sparse aerial mycelium, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse leaden black.

Typus: **Germany**, North Rhine-Westphalia, Witten, Recreation area Hohenstein, on dead leaf *Acer* cf. *pseudoplatanus* (*Sapindaceae*), 23 Jul. 2023, *T. Hülsewig*, HPC 4250, Thorben 1099 (**holotype** CBS H-25498, culture ex-type CPC 46555 = CBS 152299). GenBank sequences ITS: PZ221268; LSU: PZ221336.

Notes: Species of *Castanediella* are characterized by having branched, hyaline to pale brown conidiophores, holoblastic, sympodial conidiogenous cells and falcate, cylindrical or fusiform, 0–3-sepate, hyaline conidia (Crous *et al.* 2015). *Castanediella acericola* is similar phylogenetically (Fig. 6) and morphologically to *C. couratarii* (conidia 9.5–19 × 2–3 µm; Hernandez-Restrepo *et al.* 2016), but has larger conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Menispora cobaltina* [strain MUOB 376303, GenBank OK376751.1; Identities = 542/553 (98 %), one gap (0 %)], *Castanediella couratarii* [strain CBS 579.71, GenBank NR_145250.1; Identities = 523/538 (97 %), two gaps (0 %)], and *Castanediella malaysiana* [strain CPC 24918, GenBank NR_154810.1; Identities = 531/554 (96 %), two gaps (0 %)]. *Menispora cobaltina* is currently only known from ITS sequences. Closest hits using the **LSU** sequence are *Castanediella neomalaysiana* [strain CPC 39275, GenBank MW883805.1; Identities = 799/812 (98 %), one gap (0 %)], *Castanediella malaysiana* [strain CPC 24918, GenBank NG_067312.1; Identities = 799/812 (98 %), one gap (0 %)], and *Castanediella eucalypticola* [strain CBS 141317,

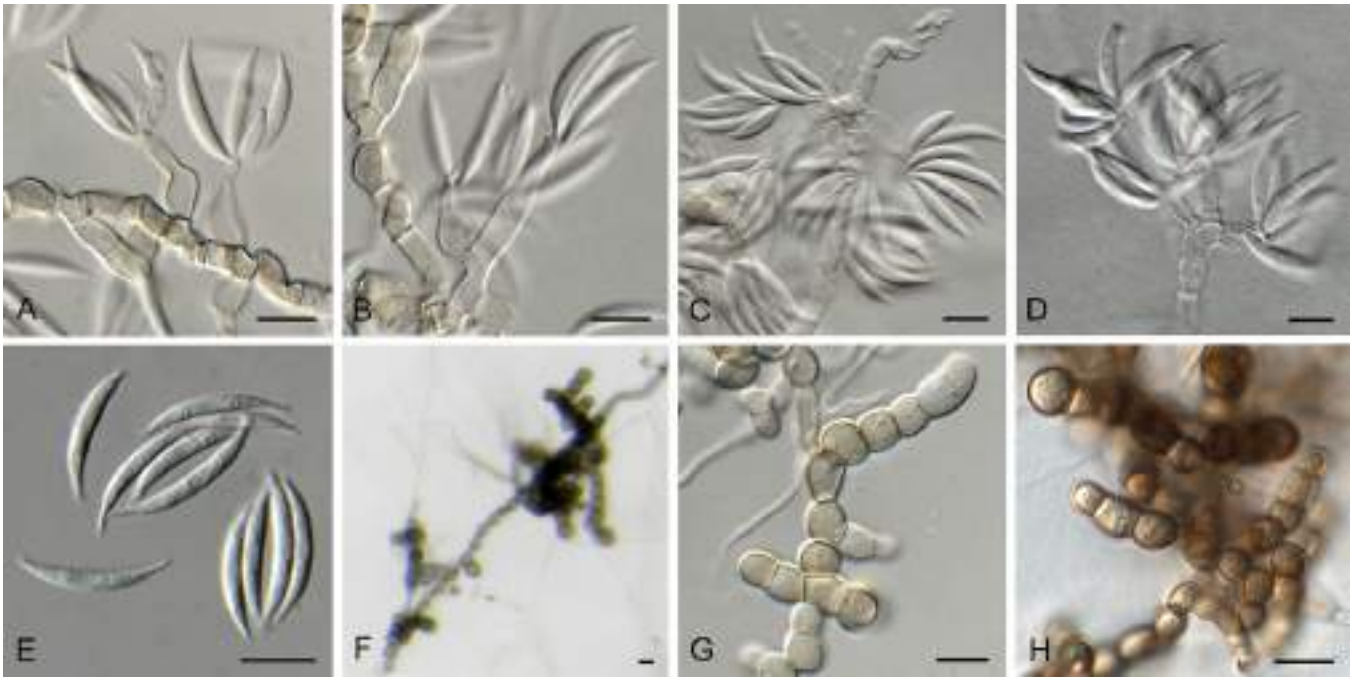

Fig. 5. *Castanediella acericola* (CPC 46555). **A–E.** Conidiophores, conidiogenous cells and conidia. **F–H.** Chlamydospore-like structures. Scale bars = 10 µm.

Fig. 6. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Castanediella* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Diaporthe eres* (CBS 138594; GenBank NR_144923) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 45 strains including the outgroup; 561 characters including alignment gaps analysed: 296 distinct patterns, 192 parsimony-informative, 60 singleton sites, 309 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: SYM+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

GenBank NG_067309.1; Identities = 798/812 (98 %), one gap (0 %)].

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

Cladophialophora calamagrostidis Crous & Osieck, ***sp. nov.*** MB 863245. Fig. 7.

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

Mycelium consisting of brown, smooth, branched, septate, 2–2.5 µm diam. hyphae. *Conidiogenous cells* integrated, terminal and intercalary, developing as hyphal pegs or hyphal cells, rarely as ellipsoid conidiogenous cells on hyphae, 4–6 × 3–4 µm, developing to form a cluster of polyphialides. *Conidia* solitary, in a mucoid mass, brown, smooth, guttulate, ellipsoid, apex subobtuse, base truncate, 1 µm diam., widest in middle of cell, (4–)5–6(–7) × (2–)2.5(–3) µm.

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

Typus: **The Netherlands**, Texel, De Slufter, on culm of *Calamagrostis arenaria* (*Poaceae*), 10 Jan. 2024, *E.R. Osieck*, HPC 4363 = WI-88, coll. 4780 (**holotype** CBS H-25510, culture ex-type CPC 47750 = CBS 152387); ditto, cultures CPC 47751–47755. GenBank sequences of CPC 47750 and CPC 47752 = CBS 153524, ITS: PZ221269, PZ221270; LSU: PZ221337, PZ221338; *tub2*: PZ228703, PZ228704.

Notes: *Cladophialophora calamagrostidis* is related to *C. boppii,* which is mainly associated with chronic cutaneous and subcutaneous infections such as chromoblastomycosis (Brasch *et al.* 2011). The two species are phylogenetically (Fig. 8) and morphologically quite distinct, as *C. calamagrostidis* has conidia produced in a mucoid mass, not forming conidial chains as found in *C. boppii.*

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 47750 had highest similarity to *Cladophialophora chaetospira* [voucher CC 14-28, GenBank KF359558.1; Identities = 525/594 (88 %), 27 gaps (4 %)], *Xylohypha curta* [strain CBS 239.89, GenBank MH862169.1; Identities = 518/590 (88 %), 18 gaps (3 %)], and "*Septonema*" *chaetospira* var. *pini* [strain CBS 482.63, GenBank MH858329.1; Identities = 520/594 (88 %), 28 gaps (4 %)]. The ITS sequences of CPC 47750 and CPC 47752 are 100 % (581/581 nt) identical. Closest hits using the **LSU** sequence of CPC 47750 are *Matsushimaea fertilis* [strain CBS 437.93, GenBank MH874079.1; Identities = 808/830 (97 %), two gaps (0 %)], *Cladophialophora boppii* [strain CBS 126.86, GenBank NG_058762.1; Identities = 808/830 (97 %), two gaps (0 %)], and *Cladophialophora arxii* [strain IFM 52022, GenBank LT883516.1; Identities = 837/867 (97 %), five gaps (0 %)]. The LSU sequences of CPC 47750 and CPC 47752 are 100 % (1165/1165 nt) identical. Closest hits using a blastn search with the ***tub2*** sequence of CPC 47750 had highest similarity to *Cladophialophora* sp. [strain SYPF 8340, GenBank MF614145.1; Identities = 378/513 (74 %), 35 gaps (6 %)], *Cladophialophora guttulata* [strain CX104B2, GenBank OP857259.1; Identities = 264/336 (79 %), 17 gaps (5 %)], and *Cladophialophora chaetospira* [strain CBS 114747, GenBank KF928578.1; Identities = 295/387 (76 %), 21 gaps (5 %)]. The *tub2* sequences of CPC 47750 and CPC 47752 are 100 % (565/565 nt) identical.

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

Cladophialophora paramycetomatis Crous, ***sp. nov.*** MB 863246. Fig. 9.

Etymology: Name refers to its similarity to *Cladophialophora mycetomatis.*

Conidiophores dimorphic. *Microconidiophores* arising from superficial mycelium, erect, pale brown, up to 100 µm tall, with stipe consisting of 1–3 subcylindrical cells, 20–25 × 2–3 µm, that give rise to primary and secondary ramoconidia that form a similar conidiogenous apparatus than macroconidiophores. *Macroconidiophores* solitary, erect, subcylindrical, dark brown, straight to flexuous, 100–200 × 3–4 µm, 4–16-septate, thick-walled, guttulate, smooth, branching apically or not. *Conidiogenous cells* subcylindrical, medium brown, smooth, 20–25 × 3–3.5 µm, loci 2–2.5 µm diam. *Primary branches* 0–1-septate, medium brown, smooth, 17–25 × 3–3.5 µm. *Primary ramoconidia* subcylindrical, aseptate, medium brown,

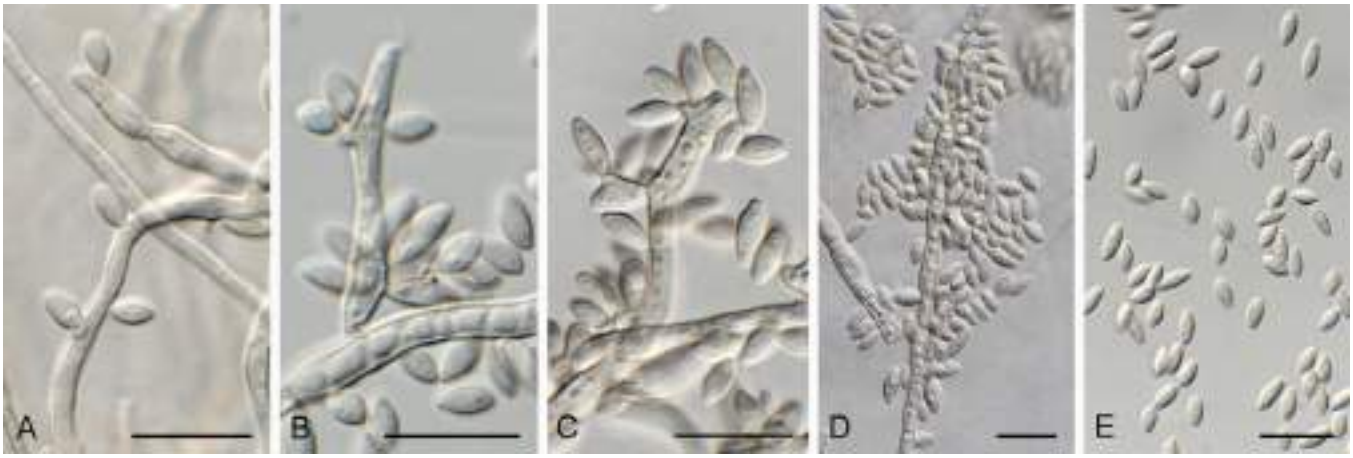

Fig. 7. *Cladophialophora calamagrostidis* (CPC 47750). **A–C.** Conidiogenous cells. **D, E.** Conidia. Scale bars = 10 µm.

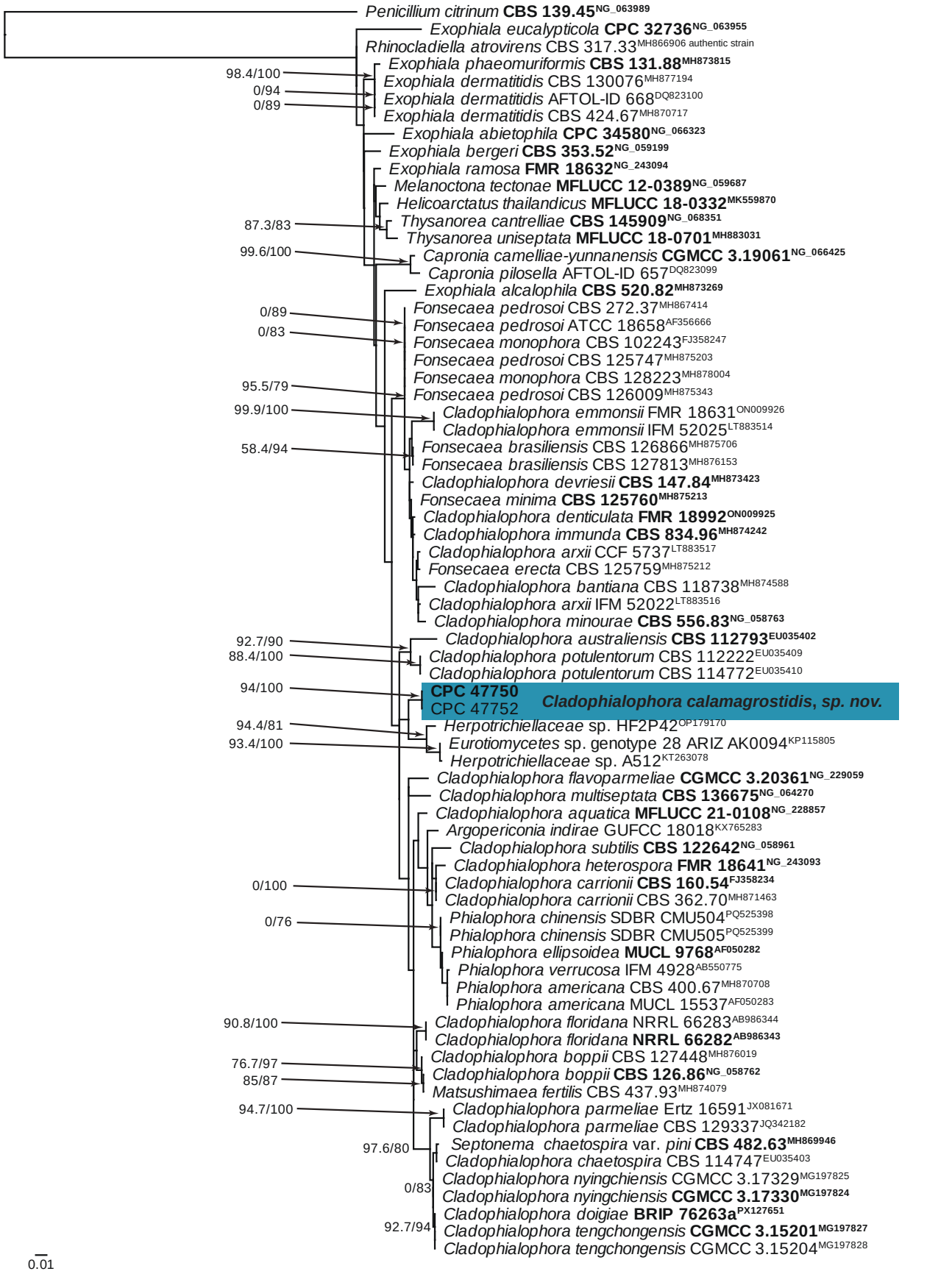

Fig. 8. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Herpotrichiellaceae* LSU nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Penicillium citrinum* (CBS 139.45; GenBank NG_063989) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 72 strains including the outgroup; 876 characters including alignment gaps analysed: 193 distinct patterns, 94 parsimony-informative, 96 singleton sites, 686 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TNe+I+R3. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

7–20 × 3–3.5 µm; *secondary ramoconidia* medium brown, aseptate, smooth, 12–15 × 3 µm; hila flattened, somewhat darkened, not thickened, 1–1.5 µm diam. *Intermediary conidia* pale brown, smooth, fusoid-ellipsoid, aseptate, 7–9 × 2–2.5 µm; *terminal conidia* pale brown, smooth, aseptate, fusoid-ellipsoid, 5–7 × 2–2.5 µm; hila 0.5–1 µm diam.

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

Material examined: **South Africa**, Western Cape Province, Cape Town, Kirstenbosch, on culms of *Elegia tectorum* (*Restionaceae*), 13 Apr. 2023, *P.W. Crous*, HPC 4165 (**holotype** CBS H-25458; culture ex-type CPC 46080 = CBS 152211). GenBank sequences ITS: PZ221271; LSU: PZ221339.

Notes: *Cladophialophora mycetomatis* (CBS 122637) was described from a Mexican patient with mycetoma (ramoconidia cylindrical to fusiform, 2.5–4.0 × 2.5–3.0 µm; conidia holoblastic, fusiform, produced in long chains; 2.5–3 × 2–3 µm, subhyaline to pale olivaceous; Badali *et al.* 2008). *Cladophialophora paramycetomatis* was isolated from culms of *Elegia tectorum* collected in South Africa, and has larger ramoconidia and conidia. The two species are phylogenetically distinct (Fig. 10).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cladophialophora* "*mycetomatis*" [voucher MEL 7333, GenBank OP437822.1; Identities = 527/535 (99 %), two gaps (0 %)], *Cladophialophora tumulicola* [strain JCM 28763, GenBank LC192095.1; Identities = 564/618 (91 %), 19 gaps (3 %)], and *Cladophialophora aquatica* [strain JAUCC2324, GenBank MH844808.1; Identities = 517/562 (92 %), 13 gaps (2 %)], with the ex-type of *Cladophialophora mycetomatis* being 91 % similar [CBS 122637, GenBank NR_111364.1; Identities = 495/544 (91 %), 22 gaps (4 %)]. Closest hits using the **LSU** sequence are *Cladophialophora mycetomatis* [strain CBS 122637, GenBank NG_058960.1; Identities = 769/783 (98 %), no gaps], *Cladophialophora chaetospira* [strain SD08A02, GenBank PP381326.1; Identities = 803/834 (96 %), three gaps (0 %)], and *Cladophialophora tengchongensis* [strain CGMCC 3.15201, GenBank MG197827.1; Identities = 794/825 (96 %), three gaps (0 %)].

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

Cladophialophora yuccae Crous & Hülsewig, ***sp. nov.*** MB 863247. Fig. 11.

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

Mycelium consisting of pale brown, smooth, branched, septate, 2–2.5 µm diam. hyphae. *Conidiophores* pale brown to brown, smooth, subcylindrical, mostly unbranched to geniculous-sinuous, 1–3-septate, 15–50 × 3–4 µm. *Conidiogenous cells* integrated, terminal, subcylindrical, pale brown, smooth, 10–20 × 2.5–3 µm, proliferating sympodially at apex; loci flat, truncate, 1.5–2 µm diam. *Ramoconidia* 0–1-septate, pale brown, smooth, guttulate, 11–20 × 3–4 µm; hila flattened, not thickened nor darkened, 1–2 µm diam. *Conidia* fusoid-ellipsoid, smooth, pale brown, guttulate, in branched chains, 0–1-septate, (8–)9–11(–13) × 2–2.5 µm; hila flattened, not thickened not darkened, 0.5–1.5 µm diam.

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

Typus: **Germany**, North Rhine-Westphalia, Witten, Recreation area Hohenstein, on dead leaf *Yucca* sp. (*Asparagaceae*), 29 Jul. 2023, *T. Hülsewig*, HPC 4268, Thorben 1125 (**holotype** CBS H-25474, culture ex-type CPC 46802 = CBS 152217). GenBank sequences ITS: PZ221272; LSU: PZ221340; *tef1* (first part): PZ228649; *tub2*: PZ228705.

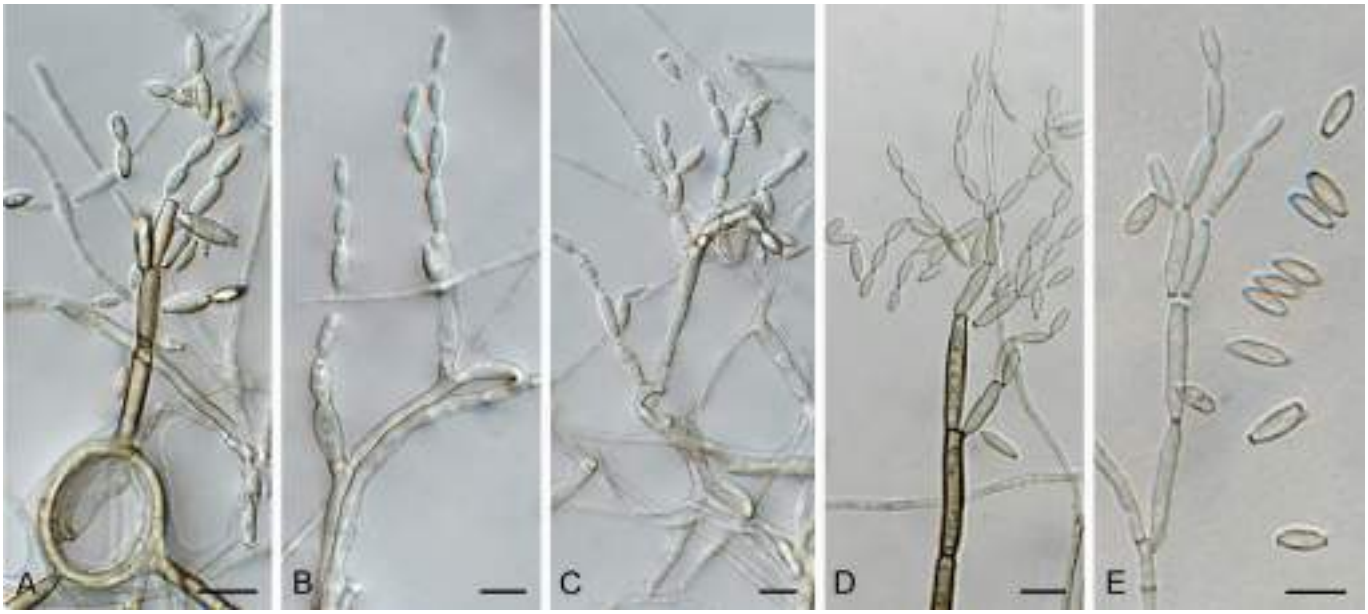

Fig. 9. *Cladophialophora paramycetomatis* (CPC 46080). **A–E.** Conidiophores and conidiogenous cells giving rise to conidia. Scale bars = 10 µm.

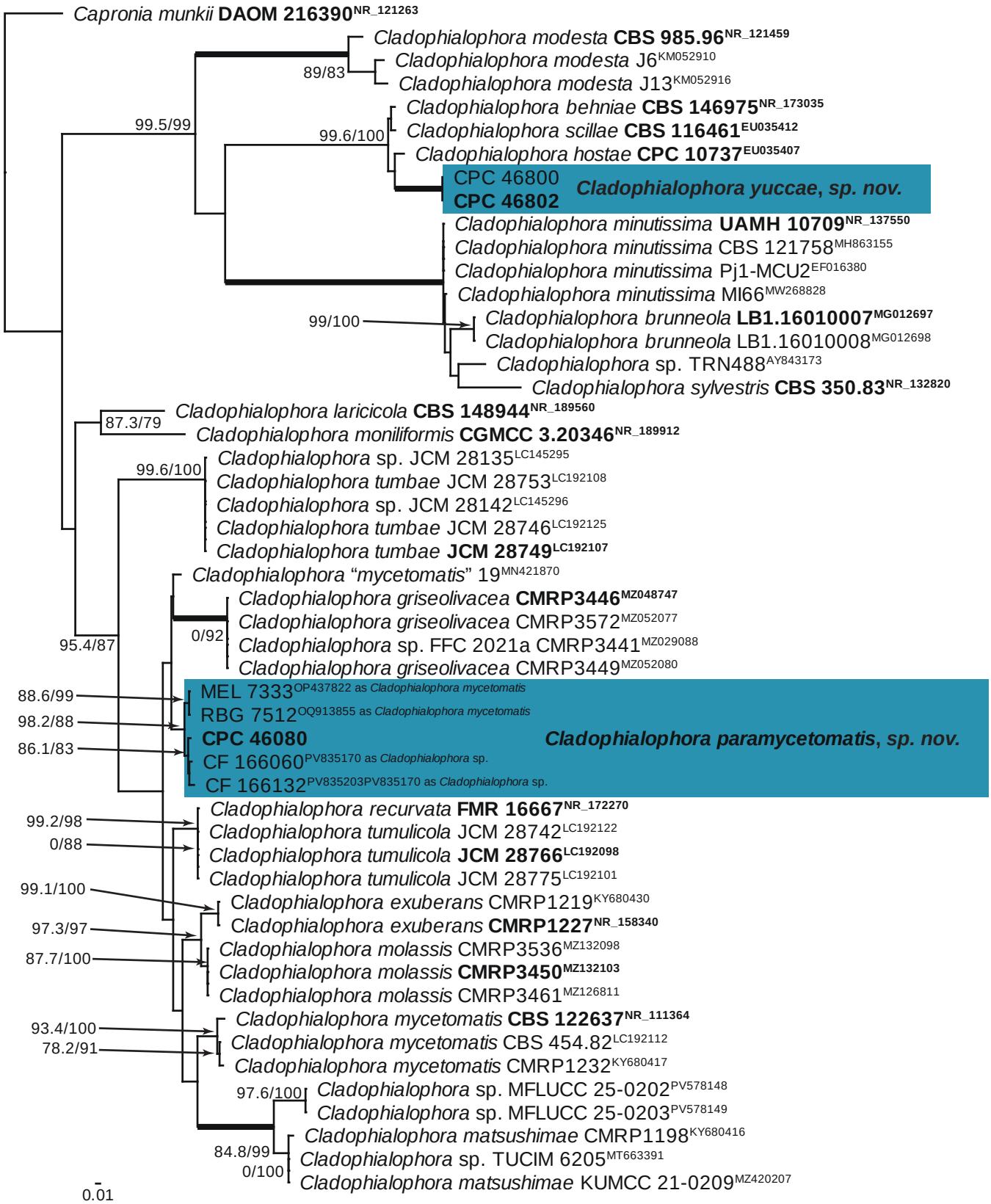

Fig. 10. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Cladophialophora* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Thickened branches resprest a SH-aLRT test value of 100 and a bootstrap support value of 100 %. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Capronia munkii* (DAOM 216390; GenBank NR_121263) and the novelties described here are highlighted with coloured blocks and **bold** font. Alignment statistics: 51 strains including the outgroup; 630 characters including alignment gaps analysed: 365 distinct patterns, 255 parsimony-informative, 36 singleton sites, 339 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

Additional material examined: **Germany**, North Rhine-Westphalia, Witten, Recreation area Hohenstein, on dead leaf *Yucca* sp. (*Asparagaceae*), 18 Aug. 2023, *T. Hülsewig*, HPC 4266, Thorben 1124, CBS H-25700, culture CPC 46800 = CBS 153454. GenBank sequences ITS: PZ221273; LSU: PZ221341.

Notes: *Cladophialophora yuccae*, which occurs on *Yucca* leaves, is related to *Cladophialophora hostae*, described from leaves of *Hosta* in Korea [conidia in long chains (–60), simple or branched, subcylindrical, or narrowly ellipsoid, smooth, pale olivaceous, 0–1-septate, (7–)10–15(–20) × (1.5–)2(–2.5) µm; Crous *et al.* 2007], but the two species are morphologically and phylogenetically distinct (Fig. 10).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 46802 had highest similarity to *Cladophialophora hostae* [strain CPC 10737, GenBank EU035407.1; Identities = 521/553 (94 %), seven gaps (1 %)], *Cladophialophora behniae* [strain CBS 146975, GenBank NR_173035.1; Identities = 461/491 (94 %), four gaps (0 %)], and *Cladophialophora scillae* [strain CBS 116461, GenBank EU035412.1; Identities = 517/552 (94 %), six gaps (1 %)]. The ITS sequences of CPC 46800 and 46802 are identical (563/563 nt). Closest hits using the **LSU** sequence are *Cladophialophora hostae* [strain CPC 10737, GenBank EU035407.1; Identities = 877/894 (98 %), no gaps], *Cladophialophora scillae* [strain CBS 116461, GenBank EU035412.1; Identities = 876/894 (98 %), no gaps], and *Cladophialophora behniae* [strain CBS 146975, GenBank NG_076728.1; Identities = 853/871 (98 %), no gaps]. The LSU sequences of CPC 46800 and 46802 are identical (826/826 nt). Closest hit using the ***tef1*** (first part) sequence of CPC 46802 had distant similarity to *Cladophialophora behniae* [strain CPC 38914, GenBank MZ078222.1; Identities = 187/217 (86 %), two gaps (0 %)]. No significant hits were obtained when the ***tub2*** sequence of CPC 46802 was used in blastn and megablast searches.

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

Comminutisporales Abdollahz. & Crous, *Stud. Mycol.* **95**: 390. 2020, **emend.** Piątek, Stryjak-Bog., Czachura & Crous

Saprobic. *Ascomata* pseudothecial, immersed, uniloculate, separate. *Asci* bitunicate, 8-spored. *Pseudoparaphyses* absent, hamathecial tissue abundant, ostiolar canal periphysate. *Ascospores* muriformly septate, forming secondary ascospores within the ascus. *Hyphae* hyaline, becoming olivaceous, forming hyaline, aseptate endoconidia. ***Conidiomata*** **pycnidial, aggregated in a brown stroma.** ***Conidiogenous cells*** **brown, cylindrical, giving rise to a conidium.** ***Conidia*** **hyaline, becoming brown, muriformly septate, forming endoconidia, both encased in mucoid sheath** (adapted from Ramaley 1996, Abdollahzadeh *et al.* 2020, Crous *et al.* 2021b).

Comminutisporaceae Abdollahz. & Crous, *Stud. Mycol.* **95**: 390. 2020, **emend.** Piątek, Stryjak-Bog., Czachura & Crous

Saprobic. *Ascomata* pseudothecial, immersed, uniloculate, separate. *Asci* bitunicate, 8-spored. *Pseudoparaphyses* absent, hamathecial tissue abundant, ostiolar canal periphysate. *Ascospores* muriformly septate, forming secondary ascospores within the ascus. *Hyphae* hyaline, becoming olivaceous, forming hyaline, aseptate endoconidia. ***Conidiomata*** **pycnidial, aggregated in a brown stroma.** ***Conidiogenous cells*** **brown, cylindrical, giving rise to a conidium.** ***Conidia*** **hyaline, becoming brown, muriformly septate, forming endoconidia, both encased in mucoid sheath** (adapted from Ramaley 1996, Abdollahzadeh *et al.* 2020, Crous *et al.* 2021b).

Type genus: *Comminutispora* A.W. Ramaley

Cippumomyces Crous *et al.*, *Persoonia* **47**: 269. 2021.

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

Type species: *Cippumomyces mortalis* Crous *et al.*

Cippumomyces mortalis Crous *et al.*, *Persoonia* **47**: 269. 2021.

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

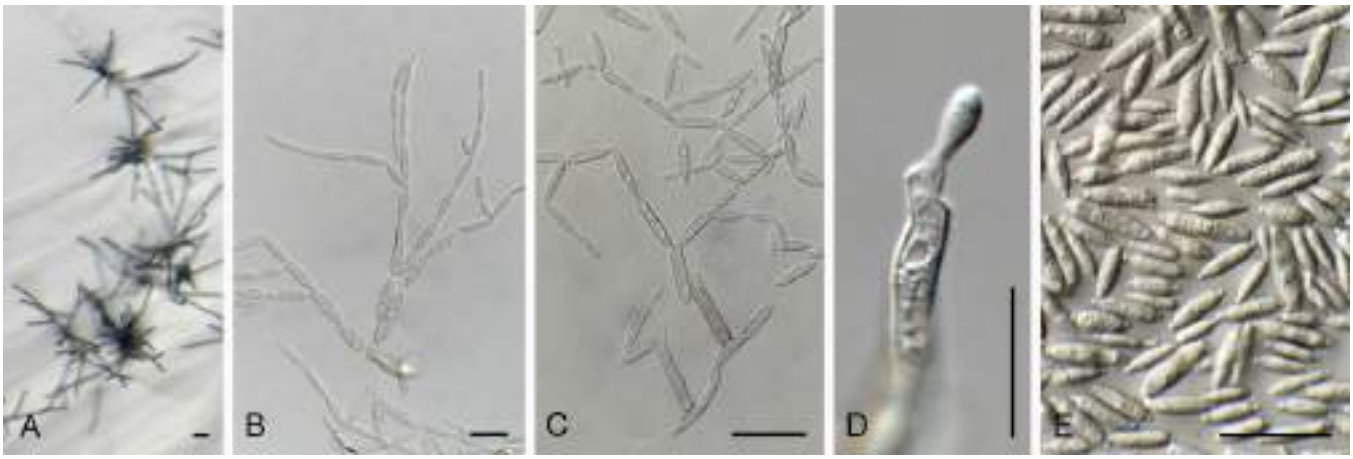

Fig. 11. *Cladophialophora yuccae* (CPC 46802). **A.** Conidiophores on SNA. **B, C.** Conidia in chains. **D.** Conidiogenous loci. **E.** Conidia. Scale bars: A = 20 µm, all others = 10 µm.

Typus: **USA**, Clinton County Pennsylvania, on tombstone, adjacent to Lock Haven University Campus, 14 Oct. 2020, *G.M. Ricci* (**holotype** CBS H-24893, culture ex-type CPC 41588 = CBS 148452). GenBank sequences ITS: OK664755; LSU: OK663794; *rpb2*: OK651180.

Cippumomyces romamitchelliae Y.P. Tan, *Index of Australian Fungi* **19**: 1. 2023.

Diagnosis: See Tan & Shivas (2023).

Typus: **Australia**, Queensland, Petford, from soil, 19 Apr. 2021, *Y.P. Tan* (**holotype** BRIP 72497a permanently preserved in a metabolically inactive state). GenBank sequences ITS: OR673887; LSU: OR673896.

Ramimonilia Stielow & Quaedvl., *Fungal Syst. Evol.* **3**: 130. 2019.
Synonym: *Ramimonilia* Stielow & Quaedvl., *Fungal Diversity* **65**: 155. 2014. Nom. inval., Art. 40.7 (Shenzhen).

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

Type species: *Ramimonilia apicalis* Stielow & Quaedvl.

Ramimonilia apicalis Stielow & Quaedvl., *Fungal Syst. Evol.* **3**: 131. 2019.
Synonym: *Ramimonilia apicalis* Stielow & Quaedvl., *Fungal Diversity* **65**: 155. 2014. Nom. inval., Art. 40.7 (Shenzhen).

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

Typus: **Spain**, Patones, from rock (**holotype** CBS 118327, culture and specimen preserved as metabolically inactive, culture ex type TRN437). GenBank sequences ITS: NR_144959; LSU: GU323984; SSU: AY843263.

Notes: The genus *Cippumomyces* was described by Crous *et al.* (2021b) to accommodate the slow-growing, rock-inhabiting fungus *Cippumomyces mortalis* isolated from a tombstone in the USA. It forms pycnidial conidiomata embedded in a brown stroma, brown conidiogenous cells with hyaline to brown, muriformly septate conidia that produce endoconidia both of which are encased in mucoid sheath (Crous *et al.* 2021b). The second known species of *Cippumomyces* – *C. romamitchelliae* – was isolated from soil in Australia and described based only on DNA sequence data. Its morphological features remain unknown (Tan & Shivas 2023). The genus *Ramimonilia* contains one species *Ramimonilia apicalis* isolated from rock in Spain (Egidi *et al.* 2014, Crous *et al.* 2019b). It forms only pale to dark brown, branched hyphae consisting of chained cells with apical germination (Egidi *et al.* 2014).

The initial multigene (LSU-*tef1*-ITS-*rpb2*) phylogenetic analyses, with dataset including members of the order *Capnodiales* s. str. only, placed *Cippumomyces* in the family *Neoantennariellaceae* as relative to genera *Fumiglobus*, *Neoantennariella* and *Neoasbolisia*, although without support and on the long branch (Crous *et al.* 2021b). The lifestyle of *Cippumomyces* is however not typical for the *Capnodiales* s. str., which contains almost exclusively sooty moulds, with only a few exceptions (Abdollahzadeh *et al.* 2020, Czachura *et al.* 2025). Previous single-gene (ITS or LSU) phylogenetic analyses, with datasets including representatives of *Dothideomycetes*, positioned *Ramimonilia* as a separate and distant lineage to remaining sampled species, with *Neophaeotheca triangularis* (syn. *Phaeotheca triangularis*) as the most closely related species (Ruibal *et al.* 2008, Egidi *et al.* 2014). The phylogenetic and systematic placement of *Ramimonilia* within *Capnodiales* s. lat. remains unresolved (Hyde *et al.* 2024). The preliminary megablast search of NCBI's GenBank nucleotide database showed that *Cippumomyces* and *Ramimonilia* are closely related.

We reanalysed the phylogenetic positions of *Cippumomyces* and *Ramimonilia* with the larger multigene (ITS-LSU-SSU-*rpb2*-*tef1*) dataset used by Piątek *et al.* (2024) containing representatives of all orders currently recognized within previous paraphyletic order *Capnodiales* s. lat. In our analyses, *Cippumomyces mortalis* and *C. romamitchelliae* formed a well-supported lineage (MLB = 73, BPP = 0.96) that was resolved as a fully supported sister group to moderately supported lineage (MLB = 65, BPP = 0.94) formed by *Comminutispora agavacearum* and *Ramimonilia apicalis* (Fig. 12). Therefore, the genus *Cippumomyces* belongs in the *Comminutisporales* rather than the *Capnodiales* s. str. This phylogenetic placement is also supported by morphological traits such as the muriformly septate ascospores (in *Comminutispora*) or conidia (in *Cippumomyces*) and formation of endoconidia that are known both in *Cippumomyces* and *Comminutispora* but not in representatives of the *Capnodiales* s. str. (Ramaley 1996, Abdollahzadeh *et al.* 2020, Crous *et al.* 2021b). The genus *Ramimonilia* also resides in the *Comminutisporales* and this phylogenetic placement is shown for the first time here. Due to its sterile nature, it cannot be compared with other genera in this order. The descriptions of the order *Comminutisporales* and family *Comminutisporaceae* are emended by characters given in bold.

Authors: M. Piątek, M. Stryjak-Bogacka, P. Czachura & P.W. Crous

Cordana ligni Crous & Hülsewig, ***sp. nov.*** MB 863248. Fig. 13.

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

Conidiophores erect, subcylindrical, flexuous, medium brown, smooth, thin-walled, multiseptate, up to 300 µm tall, unbranched, 4–5 µm wide at base, which develops rhizoids with age; tapering towards apex, with apical cell subhyaline, giving rise to a rosette of 4–6 *conidiogenous cells*, subuliform, 15–25 × 3–4 µm, hyaline, smooth, granular, apex swollen, 3–4 µm diam., with cluster of denticles, 1–2 × 1 µm, cicatrized. *Conidia* solitary, ellipsoid, brown, smooth, guttulate, medianly 1-septate, constricted at septum or not, apex obtuse, tapering from septum to truncate hilum, 0.5 µm diam., 7–8(–9) × (3.5–)4 µm.

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

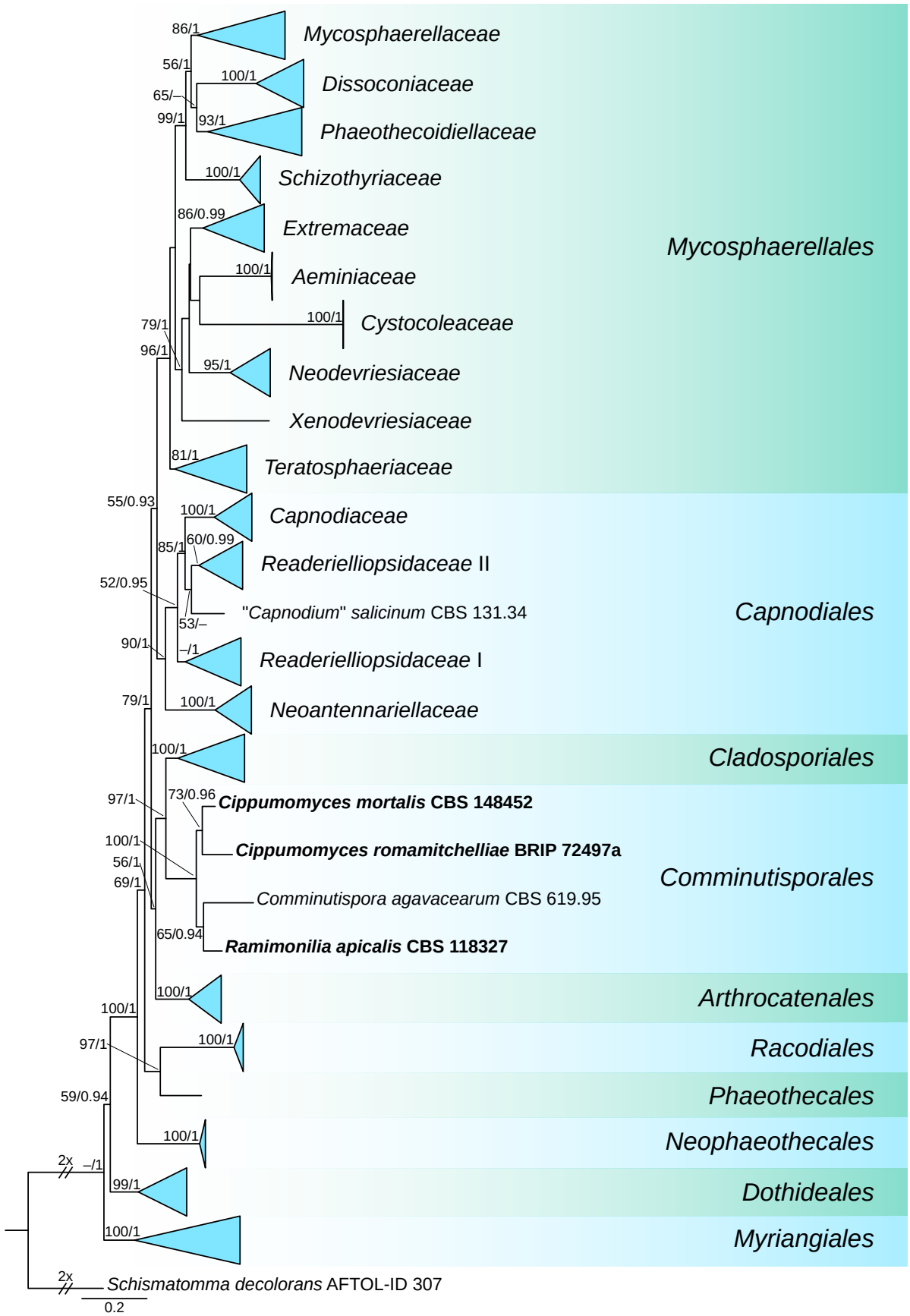

Fig. 12. Phylogenetic tree of the *Capnodiales* s. lat., *Dothideales* and *Myriangiales* obtained from a maximum likelihood analysis of the combined multi-locus alignment (4740 characters, including gaps: ITS: 828, LSU: 746, SSU: 950, *rpb2*: 1103, *tef1*: 1113). The dataset included sequences used by Piątek *et al.* (2024), with slight modifications (see table deposited at figshare.com – doi: https://doi.org/10.6084/m9.figshare.31898359). Maximum likelihood and Bayesian Inference analyses were conducted using RAxML-NG v. 1.1.0 (Kozlov *et al.* 2019) and MrBayes v. 3.2.6 (Ronquist *et al.* 2012), respectively. Main clades are collapsed, except for the clade representing the order *Comminutisporales*. The positions of *Cippumomyces mortalis*, *C. romamitchelliae* and *Ramimonilia apicalis* are indicated in **bold**. Maximum likelihood bootstrap (MLB) support values > 50 % and Bayesian posterior probabilities (BPP) > 0.9 are shown at the nodes. The tree is rooted with *Schismatomma decolorans*. The scale bar represents the expected number of changes per site. The table, alignment, and uncollapsed phylogenetic tree were deposited at figshare.com (table – doi: https://doi.org/10.6084/m9.figshare.31898359; alignment and uncollapsed phylogenetic tree – doi: https://doi.org/10.6084/m9.figshare.31898497; in the uncollapsed tree, all MLB/BPP values are given at the nodes).

Typus: **Germany**, North Rhine-Westphalia, Witten, Recreation area Hohenstein, on dead wood, 24 Aug. 2024, *T. Hülsewig*, HPC 4525, Thorben 1297 (**holotype** CBS H-25744, culture ex-type CPC 49130 = CBS 153462). GenBank sequences ITS: PZ221274; LSU: PZ221342.

Notes: The present collection is a typical species of "*Pseudobotrytis*", having pigmented, erect, solitary conidiophores that terminate in a whorl of conidiogenous cells, each with a terminal cluster of denticles that give rise to pigmented, ellipsoid, 0–1-septate conidia (Ellis 1971). However, *Pseudobotrytis* has been shown to be a synonym of *Cordana* (Hernańdez-Restrepo *et al.* 2014). *Cordana ligni* is related (Fig. 14) to *C. bisbyi* [conidia ovoid, aseptate, (5–)7.2(–9) × 2.5–3.6 µm; Timonin 1961], but has slightly wider, 1-septate conidia. It is also very similar to *C. terrestris* (conidia 1-septate, 6–11 × 3–4 µm; Hernańdez-Restrepo *et al.* 2014), but phylogenetically distinct.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cordana bisbyi* [strain CBS 213.65, GenBank NR_154786.1; Identities = 503/526 (96 %), five gaps (0 %)], *Cordana terrestris* [strain CBS 401.52, GenBank MH857096.1; Identities = 496/526 (94 %), 11 gaps (2 %)], and *Cordana pauciseptata* [strain KUNCC 23-13512, GenBank PQ845797.1; Identities = 445/482 (92 %), 10 gaps (2 %)]. Closest hits using the **LSU** sequence are *Porosphaerella borinquensis* [strain CBS 126246, GenBank MH875449.1; Identities = 810/816 (99 %), no gaps], *Cordana terrestris* [as *Pseudobotrytis terrestris*; strain FMR 11157, GenBank KF771875.1; Identities = 856/865 (99 %), no gaps], and *Cordana yunnanensis* [voucher YMF 1.6947, GenBank NG_241940.1; Identities = 790/802 (99 %), no gaps].

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

Curvularia moniliformis Madrid, Cantillo & R. Castillo, ***sp. nov.*** MB 858310. Fig. 15.

Etymology: The name refers to the abundant moniliform hyphae produced by this fungus in culture.

Vegetative hyphae septate, branched, light olivaceous to mid olivaceous brown, thin- to thick-walled, smooth, mostly 1–8 µm wide, with moniliform segments composed of swollen melanized cells up to 15 µm wide, anastomosing. *Conidiophores* macronematous, mononematous, solitary, septate, simple, straight to flexuous, strongly geniculate at the fertile part, light olivaceous brown to dark brown, often paler at the apex, smooth to verruculose, with cell walls often thicker than those of the supporting vegetative hyphae, 70–230 × 5–8 µm. *Conidiogenous cells* integrated, terminal and intercalary, subcylindrical to irregularly shaped, mono to polytretic, proliferating sympodially, 4–12 µm long. *Conidia* mostly subcylindrical to narrowly ellipsoid, straight, light olivaceous brown to mid golden brown, with a small pale area at each pole, finely verruculose, 21–32(–36) × 9–14 µm, constantly 3–distoseptate, with rounded to subtruncate poles. Hilum more or less thick and dark.

Culture characteristics: Colonies on water agar with sterilized corn leaves at 25 °C fast-growing, hairy, grey to olivaceous brown; reverse dark brown.

Typus: **Chile**, Cordillera Province, Río Carrillo National Park, on leaves of unidentified *Poaceae*, 26 Aug. 2016, *H. Madrid & L. Linaje* (**holotype** SGO 168421, culture ex-type HM 100). GenBank sequences ITS: PV245936; *gapdh*: PV236017.

Notes: BLAST searches with sequences of this fungus showed that *Curvularia buchloes* CBS 246.49 (ex-type strain), residing in the *spicifera*-clade of *Curvularia* (Madrid *et al.* 2014) is the most closely related species. The sequence identities were 100 % for the ITS region (GenBank MH856511) and 99.55 % for the *gapdh* locus (GenBank KM061789). Despite their genetic similarity, *C. buchloes* and *C. moniliformis* are morphologically distinct with the

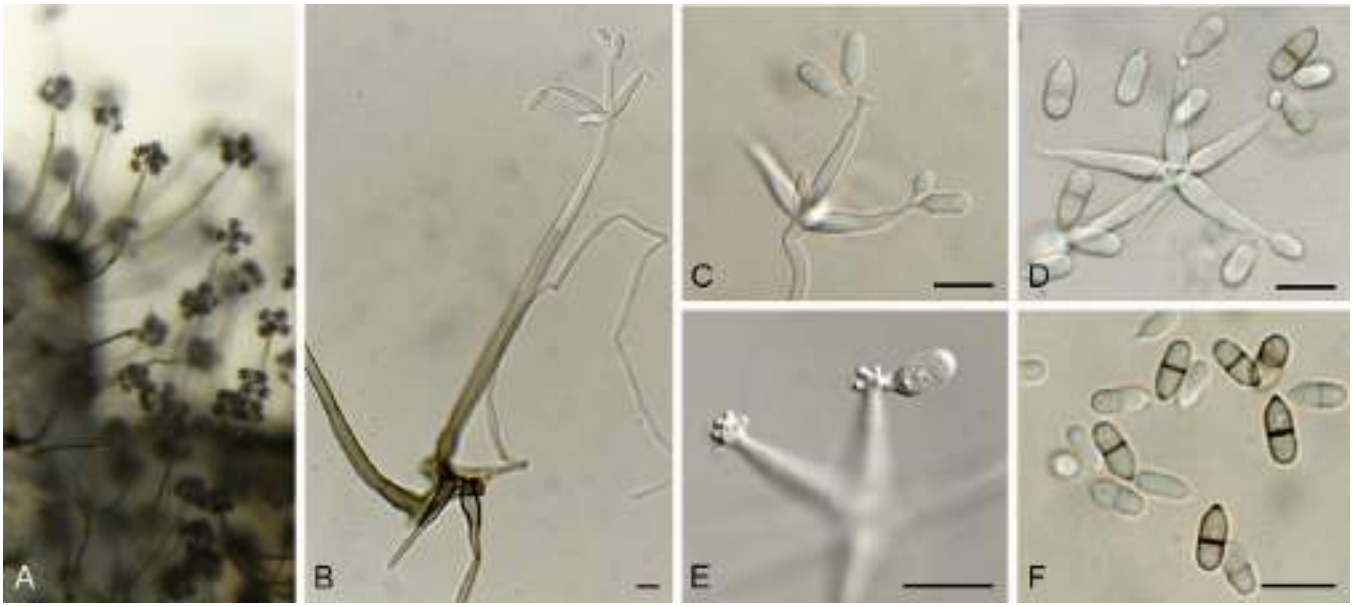

Fig. 13. *Cordana ligni* (CPC 49130). **A.** Colony in culture. **B–E.** Conidiophores and conidiogenous cells giving rise to conidia. **F.** Conidia. Scale bars = 10 µm.

Fig. 14. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Cordana* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Fusarium ipomoeae* (CGMCC 3.19496; GenBank NR_164596) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 72 strains including the outgroup; 598 characters including alignment gaps analysed: 341 distinct patterns, 201 parsimony-informative, 84 singleton sites, 313 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: SYM+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

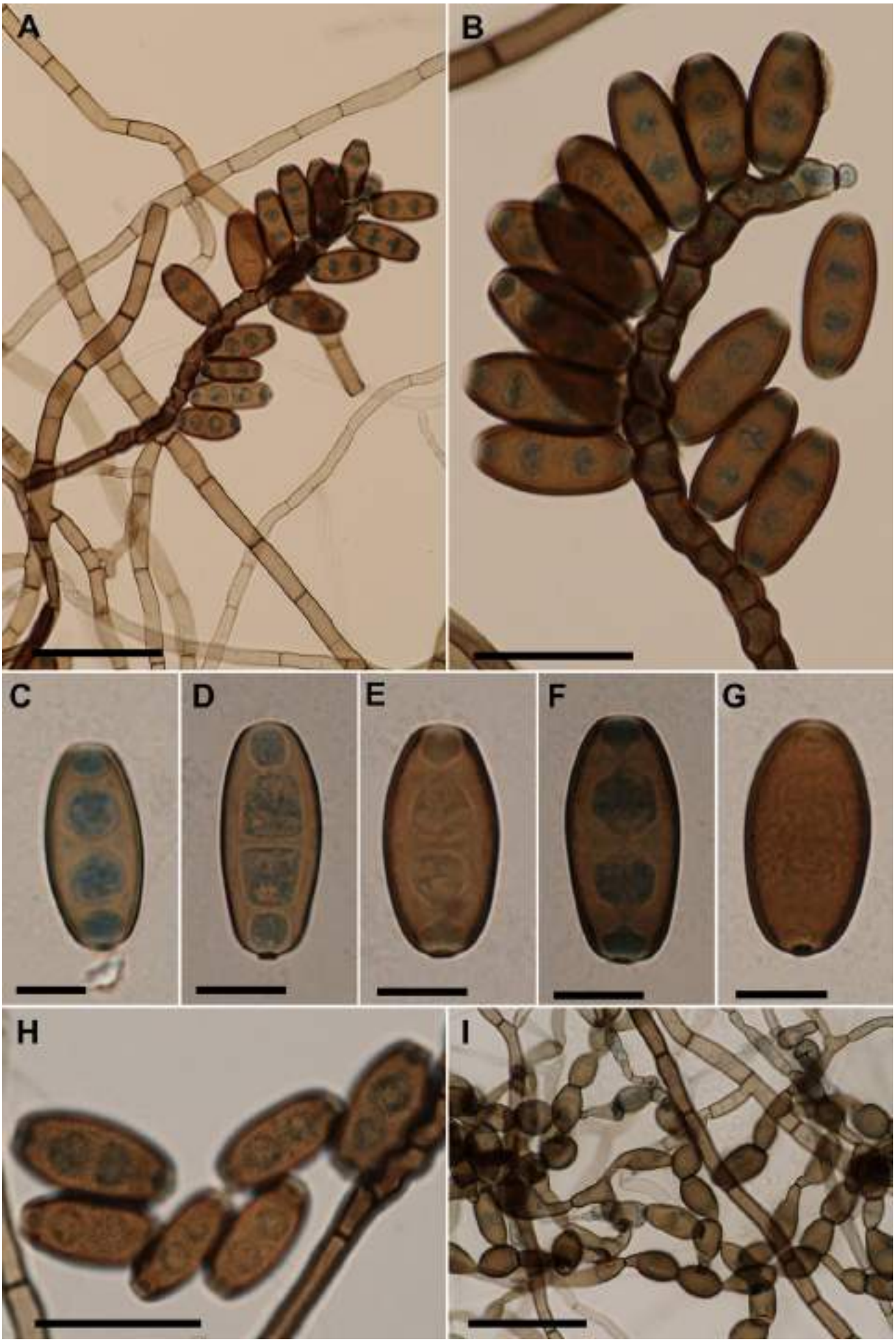

Fig. 15. *Curvularia moniliformis* (SGO 168421). **A, B.** Conidiophores and conidia. **C–H.** Conidia (G and H focusing on the finely verruculose conidial wall ornamentation). **I.** Moniliform hyphae. Scale bars: A, I = 40 µm; B, H = 30 µm; C–G = 10 µm. Scale bars = 10 µm.

former species having longer and narrower conidia (27–86 × 8–11 µm) which often appear distinctly curved and have up to nine distosepta (Sivanesan 1987, Manamgoda *et al.* 2014). Another species closely related to *C. moniliformis* was *C. rouhanii* CBS 144674 (ex-type strain) with 100 % identity for the ITS region (GenBank KX139030) and 99.32 % identity for *gapdh* (GenBank MG428694). The conidia of this fungus are shorter and narrower, i.e., 15–30.5 × 5.3–10 µm (Mehrabi-Koushki *et al.* 2018) than those of *C. moniliformis*. In a phylogenetic reconstruction based on ITS + *gapdh* sequences, *C. buchloes*, *C. rouhanii* and *C. moniliformis* formed a distinct clade with 81 % bootstrap support, clearly separated from other members of the *spicifera*-clade (Fig. 16).

Authors: H. Madrid, T. Cantillo & R. Castillo

Cyphellophora capiguarae (Attili-Angelis *et al.*) Iturr.-Gonz. *et al.*, *Persoonia* **45**: 345. 2020. Fig. 17.
Basionym: *Phialophora capiguarae* Attili-Angelis *et al.*, *Fungal Diversity* **65**: 70. 2014.

Mycelium consisting of hyaline to pale brown, branched, septate, 1.5–2 µm diam. hyphae. *Conidiophores* solitary, erect, flexuous, subcylindrical, medium brown, smooth, multiseptate, up to 400 µm tall, 3–3.5 µm wide at base. *Conidiogenous apparatus* penicillate, frequently branching at apex, forming a series of primary and secondary branches that give rise to *conidiogenous cells*, terminal and intercalary, narrowly ampulliform to subuliform, phialidic, brown, smooth, with long neck, slightly flared at apex, 1.5–2 µm diam., 15–20 × 3.5–4 µm. *Conidia* in long, unbranched chains, subcylindrical, 0–1-septate, pale brown, smooth, tapering at truncate ends that appear slightly darkened, (6.5–)8–10(–11) × 2(–2.5) µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 8 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

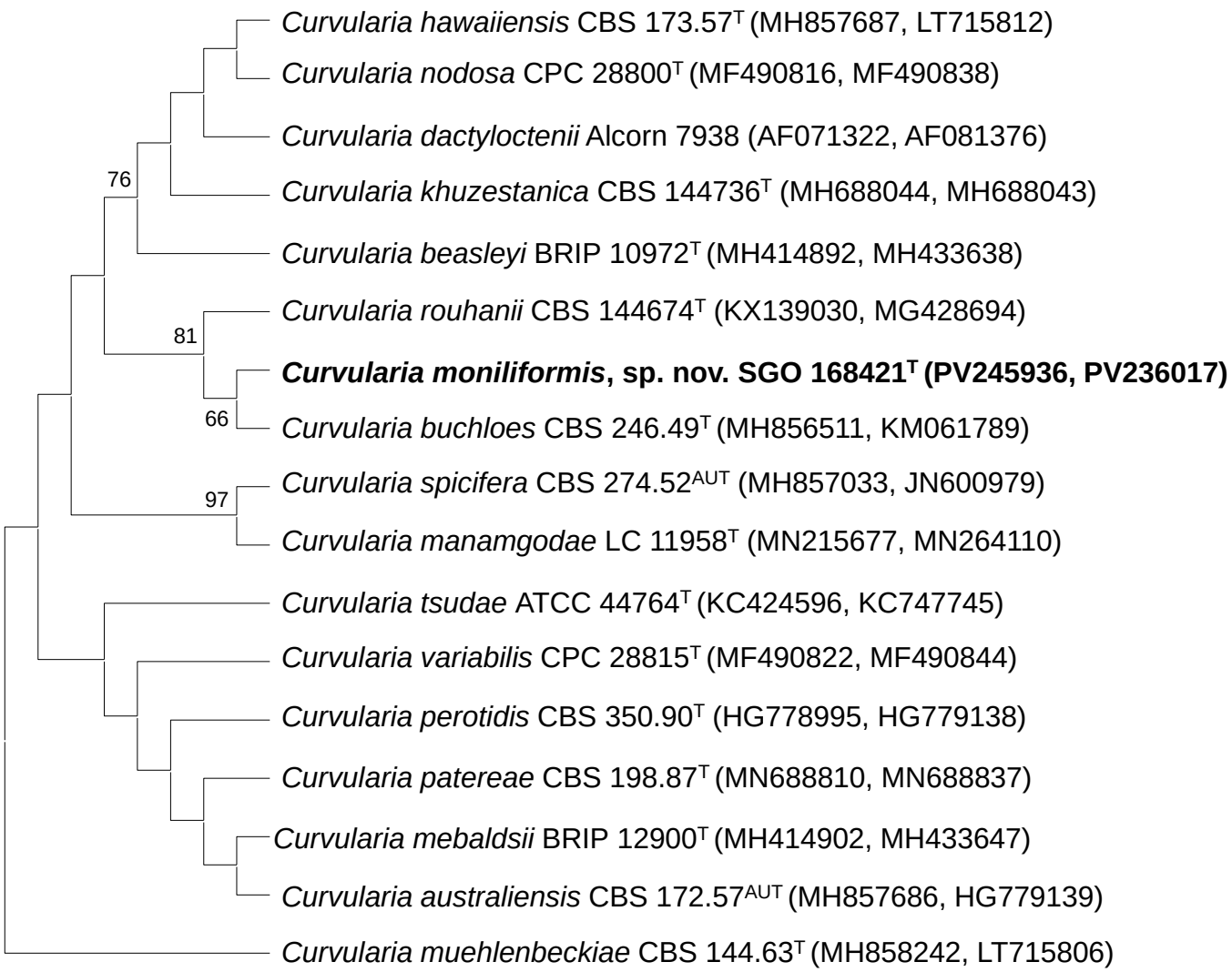

Fig. 16. Maximum likelihood phylogeny reconstruction based on an ITS + *gapdh* concatenated alignment (total length: 891 char.). The phylogenetic analysis was carried out with the MEGA XI software (Tamura *et al.* 2021). The ingroup included 16 species allied to the *spicifera*-clade of *Curvularia* as revealed in Madrid *et al.* (2014), Mehrabi-Koushki *et al.* (2018) and Iturrieta-González *et al.* (2020). *Curvularia muehlenbeckiae*, a member of the *hominis*-clade (Madrid *et al.* 2014), was used as outgroup. GenBank accession numbers of ITS and *gapdh*, respectively, are given in parentheses after each isolate number. Bootstrap values ≥ 50 % are shown near the internodes. |

Material examined: **Brazil**, Minas Gerais, Viçosa experimental farm, from stalks of *Agapanthus praecox* (*Amaryllidaceae*), Feb. 2024, *P.W. Crous*, HPC 4392, CBS H-25711, culture COAD 3996 = CPC 47898 = CBS 153570. GenBank sequences ITS: PZ221275; LSU: PZ221343; *rpb1*: PZ228624; *tub2*: PZ228706.

Notes: *Cyphellophora capiguarae* was initially described as *Phialophora capiguarae* from leaf-cutting ants in São Paulo, Brazil (Attili-Angelis *et al.* 2014, Crous *et al.* 2020a), and the present isolate adds a further collection, but from stems of *Agapanthus praecox* in Viçosa, Minas Gerais.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cyphellophora capiguarae* [as *Phialophora* sp. JBS-2014a; strain CBS 132767, GenBank KF928464.1; Identities = 574/577 (99 %), one gap (0 %)], *Cyphellophora oxyspora* [strain CBS 698.73, GenBank NR_132883.1; Identities = 468/525 (89 %), 23 gaps (4 %)], and *Cyphellophora sessilis* [strain SP12_386Ca, GenBank MN065481.1; Identities = 533/624 (85 %), 35 gaps (5 %)]. Closest hits using the **LSU** sequence are *Cyphellophora capiguarae* [as *Phialophora* sp. JBS-2014a; strain CBS 131954, GenBank KF928529.1; Identities = 718/718 (100 %), no gaps], *Scolecobasidium fusarioideum* [strain CBS 210.95, GenBank KF156154.1; Identities = 781/794 (98 %), one gap (0 %)], and *Cyphellophora oxyspora* [strain CBS 416.89, GenBank MH873869.1; Identities = 819/833 (98 %), two gaps (0 %)]. Closest hits using the ***rpb1*** sequence had distant similarity to *Cyphellophora europaea* [strain CBS 129.96, GenBank FJ358380.1; Identities = 532/732 (73 %), 21 gaps (2 %)], *Cyphellophora oxyspora* [as *Phialophora oxyspora*; strain CBS 698.73, GenBank JQ766402.1; Identities = 508/698 (73 %), nine gaps (1 %)], and *Cyphellophora phyllostachydis* [strain HLHNZWYZZ08, GenBank KP122924.1; Identities = 505/703 (72 %), 27 gaps (3 %)]. No *rpb1* sequences of *Cyphellophora capiguarae* are available for comparison. Closest hits using the ***tub2*** sequence had highest similarity to *Cyphellophora capiguarae* [as *Phialophora* sp. JBS-2014a; strain CBS 131954, GenBank KF928593.1; Identities = 368/380 (97 %), no gaps], *Cyphellophora* sp. 1 II-2020 [strain FMR 17714, GenBank LR814116.1; Identities = 336/357 (94 %), no gaps], and *Cyphellophora panamaensis* [strain CPC 46528, GenBank PQ497778.1; Identities = 329/429 (77 %), 19 gaps (4 %)].

Authors: P.W. Crous, J.Z. Groenewald, R.W. Barreto, R.F. Alfenas & A.C. Alfenas

Davidhawksworthia rubi Crous & Hülsewig, ***sp. nov.*** MB 863249. Fig. 18.

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

Isolated from green synnemata in vivo, and although synnemata formed in vitro, they remained sterile. *Conidiomata* sporodochial, up to 300 µm diam., pale green to crystalline, consisting of densely aggregated conidiophores, branched, septate, subcylindrical, hyaline, smooth. *Conidiogenous cells* terminal and intercalary, hyaline, smooth, monophialidic, straight to curved, solitary or in whorls of up to 4, 12–25 × 2.5–3.5 µm; apical collarette prominent, not flared. *Conidia* solitary, hyaline, smooth, guttulate, ellipsoid to subcylindrical, aseptate, apex obtuse, tapering to truncate hilum, 1.5 µm diam., (8.5–)10–12(–13) × (4–)5 µm.

Culture characteristics: Colonies erumpent, spreading, surface folded with moderate aerial mycelium and smooth, lobate margin, reaching 20 mm diam. after 2 wk at 25 °C. On MEA surface and reverse pale luteous with patches of bluish green; on PDA surface and reverse bluish green to dark bluish green; OA surface bluish green.

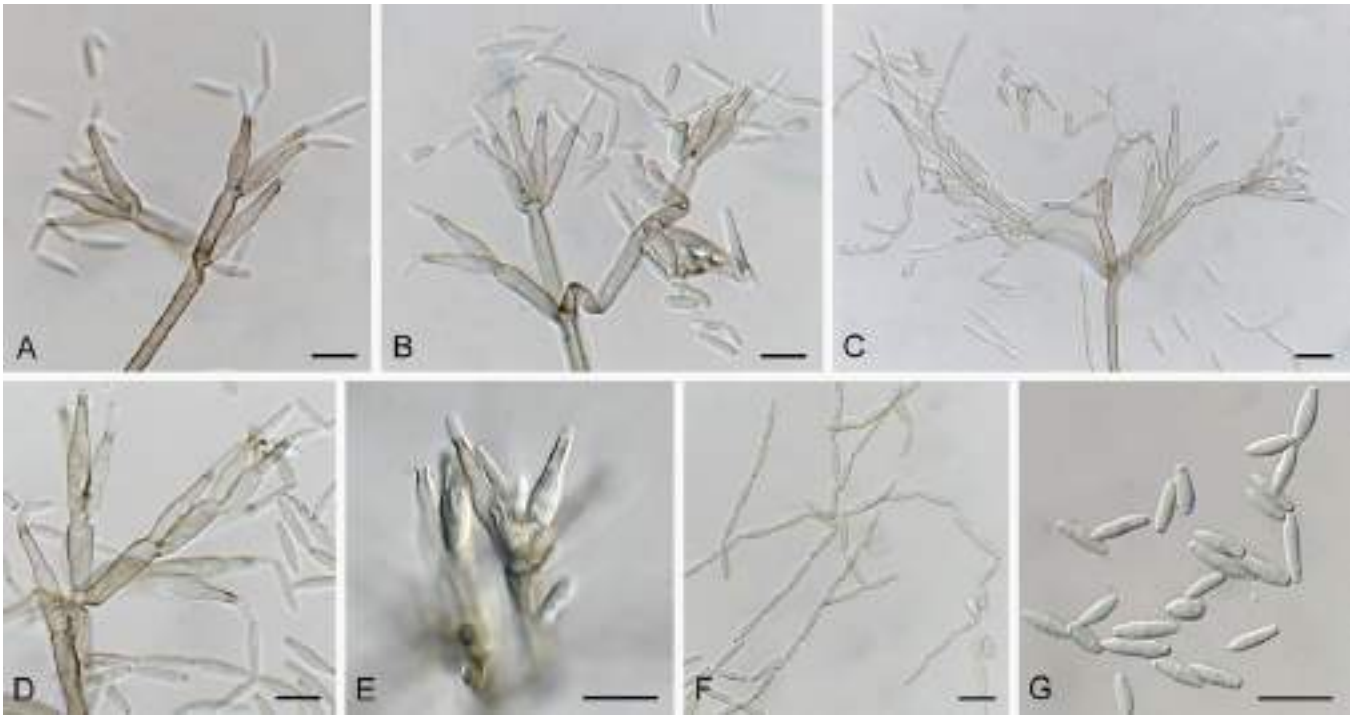

Fig. 17. *Cyphellophora capiguarae* (CPC 47898). **A–E.** Conidiophores and conidiogenous cells giving rise to conidia. **F, G.** Conidia. Scale bars = 10 µm.

Typus: **Germany**, North Rhine-Westphalia, Witten, Recreation area Hohenstein, on *Rubus* stems (*Rosaceae*), 25 May 2024, *T. Hülsewig*, HPC 4494, Thorben 1275 (**holotype** CBS H-25738, culture ex-type CPC 48394 = CBS 153522). GenBank sequences ITS: PZ221276; LSU: PZ221344; *tef1* (first part): PZ228650.

Notes: *Davidhawksworthia* is known to form sporodochia or solitary phialidic conidiophores giving rise to aseptate, subcylindrical conidia (Crous & Groenewald 2016). Conidia of *D. rubi* were isolated from blue-green synnemata. Although such synnemata developed in culture, they remained sterile. *Davidhawksworthia rubi* is morphologically and phylogenetically distinct from the other two species known in the genus (Fig. 19).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Davidhawksworthia ilicicola* [strain CBS 734.94, GenBank NR_154008.1; Identities = 473/519 (91 %), eight gaps (1 %)], *Neofabraea brunneipila* [voucher MFLU 15-0231, GenBank MK584984.1; Identities = 472/519 (91 %), eight gaps (1 %)], and *Pseudofabraea citricarpa* [strain HB-2-D-Co, GenBank MK942863.1; Identities = 470/519 (91 %), seven gaps (1 %)]. Closest hits using the **LSU** sequence are *Davidhawksworthia ilicicola* [strain CBS 734.94, GenBank NG_067307.1; Identities = 850/870 (98 %), no gaps], *Davidhawksworthia quintiniae* [strain CBS 146963, GenBank NG_074481.1; Identities = 844/870 (97 %), no gaps], and *Pezicula eucalyptigena* [strain CBS 144637, GenBank NG_068615.1; Identities = 841/870 (97 %), no gaps]. Closest hits using a blastn search with the ***tef1*** (first part) sequence had highest similarity to *Davidhawksworthia ilicicola* [strain CBS 734.94, GenBank KU728593.1; Identities = 387/515 (75 %), 44 gaps (8 %)], *Neofabraea kienholzii* [strain CBS 355.72, GenBank KX982716.1; Identities = 352/472 (75 %), 44 gaps (9 %)], and *Neofabraea perennans* [strain CBS 139.41, GenBank KX982710.1; Identities = 361/503 (72 %), 60 gaps (11 %)].

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

Dialonectria quaternatae Lechat & J. Fourn., *Ascomycete. org* **11**: 9. 2019. Fig. 20.

Ascomata perithecial, superficial, seated on a pseudoparenchymatous basal stroma in groups of 10–20, obpyriform to subglobose, 250–350 µm high, 250–300 µm diam. (homothallic, up to 120 µm diam. in culture), collapsing laterally or not when dry, red, red orange in lactic acid, and ark purple in 3 % KOH; surface finely roughened; apex obtuse to discoidal, concolourous with palisade or cylindrical cells. *Basal stroma* orange to saffron; wall 12–15 µm thick, composed of two regions. *Asci* cylindrical, 65–85 × 6.5–10 µm, 8-spored, uniseriate to biseriate in upper part, with apical mechanism; paraphyses evanescent at maturity. *Ascospores* (11–)12–13(–15) × (5–)6(–7) µm, ellipsoid, ends subobtuse, medianly 1-septate, guttulate, hyaline, becoming yellow and verruculose at maturity. *Mycelium* of hyaline, smooth, branched, septate, 2–3 µm diam. hyphae. *Microconidiophores* reduced to conidiogenous cells or branched once at base, 0–2-septate. *Microconidiogenous cells* hyaline, smooth. erect, subcylindrical, 55–80 × 2.5–3 µm; apex phialidic with minutely flared collarette, with conidia aggregating in mucoid mass. *Microconidia* hyaline, smooth, granular, 0(–1)-septate, curved, fusoid-ellipsoid to irregularly subclavate, apex subobtuse, base truncate, (8–)12–14(–22) × (2.5–)3–3.5 µm. *Sporodochia* orange, formed abundantly on OA and SNA. *Conidiophores* up to 120 µm tall, densely aggregated, irregularly branched up to three times, bearing 1–3 *monophialides*, subcylindrical, 20–60 × 2–2.5 µm, smooth, hyaline, thin-walled with periclinal thickening and inconspicuous collarette. *Sporodochial macroconidia* falcate,

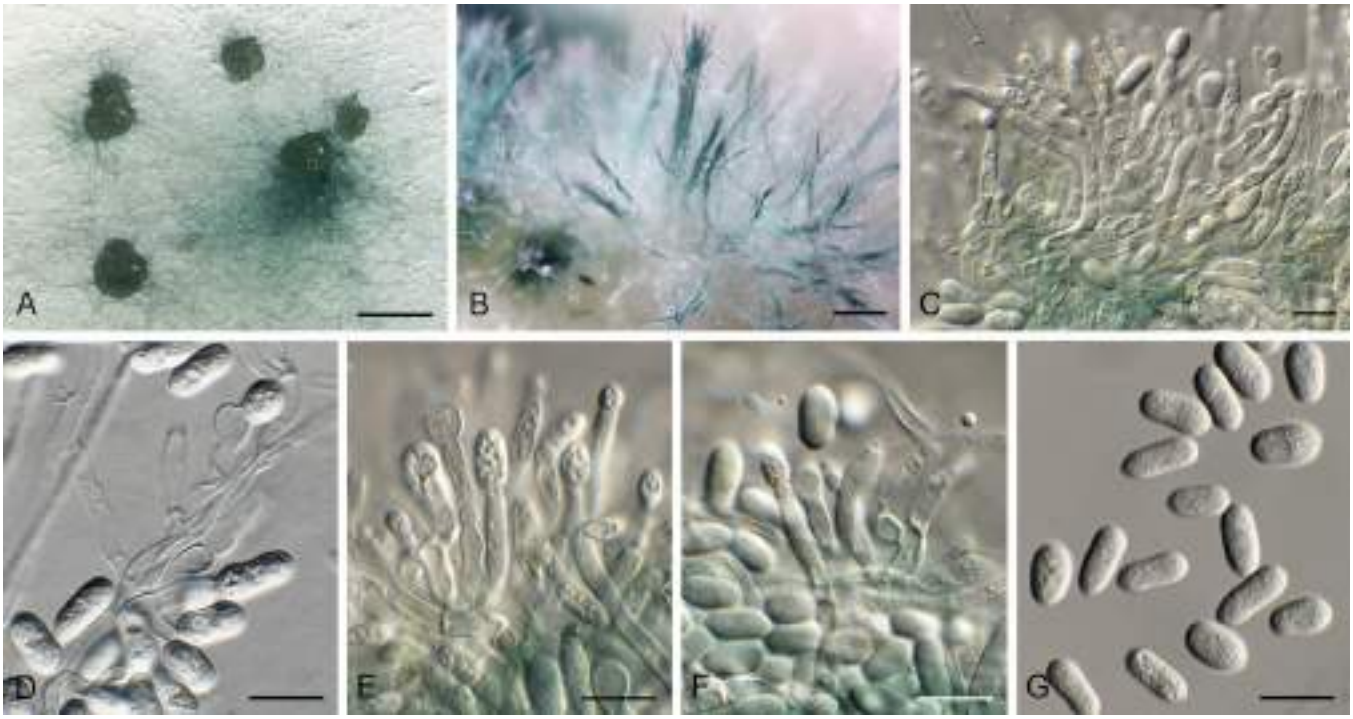

Fig. 18. *Davidhawksworthia rubi* (CPC 48394). **A, B.** Synnemata in culture. **C–F.** Conidiogenous cells. **G.** Conidia. Scale bars: A = 300 µm, B = 150 µm, all others = 10 µm.

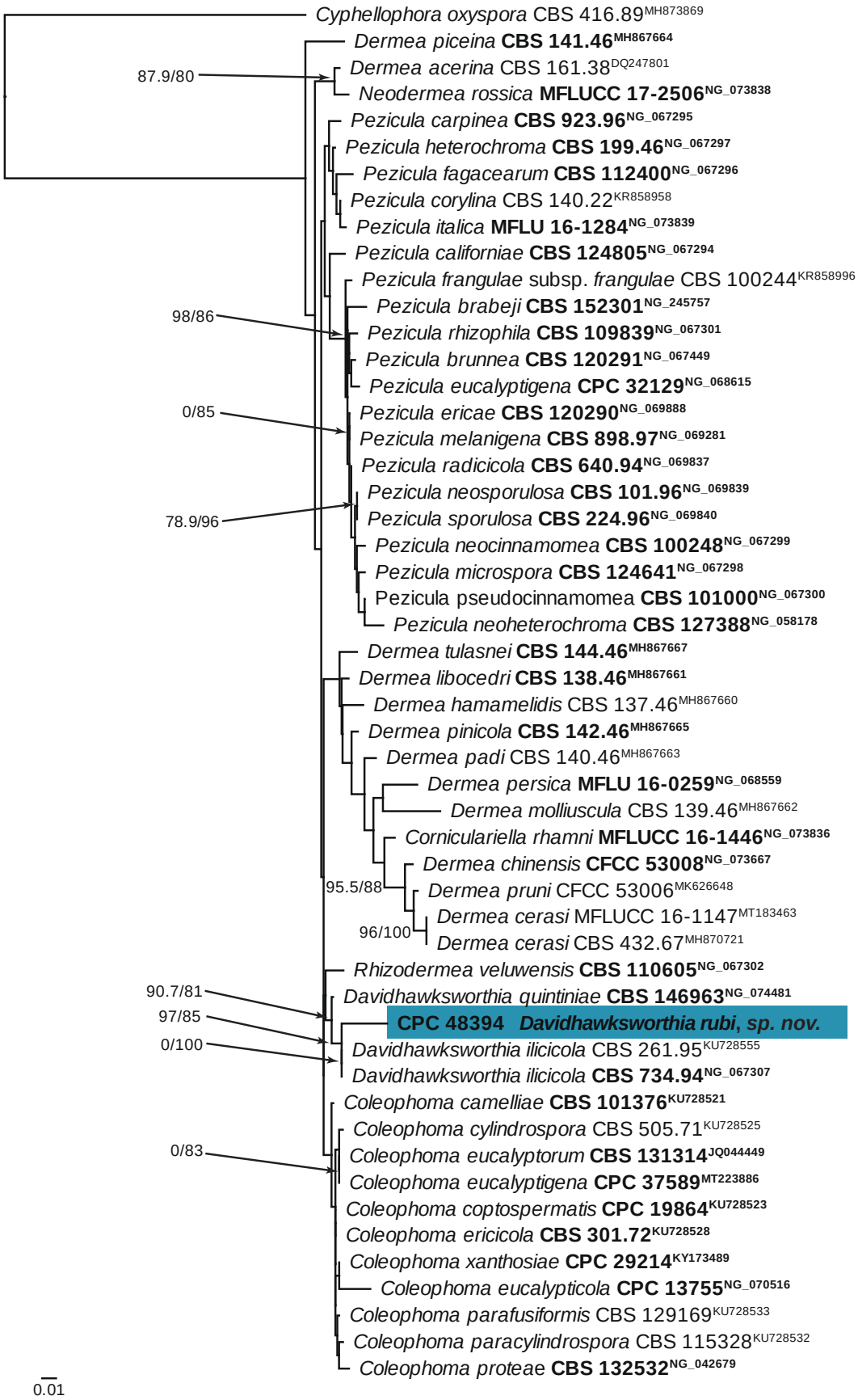

Fig. 19. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Dermeaceae* LSU nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Cyphellophora oxyspora* (CBS 416.89; GenBank MH873869) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 52 strains including the outgroup; 811 characters including alignment gaps analysed: 144 distinct patterns, 88 parsimony-informative, 91 singleton sites, 632 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM3e+I+R2. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

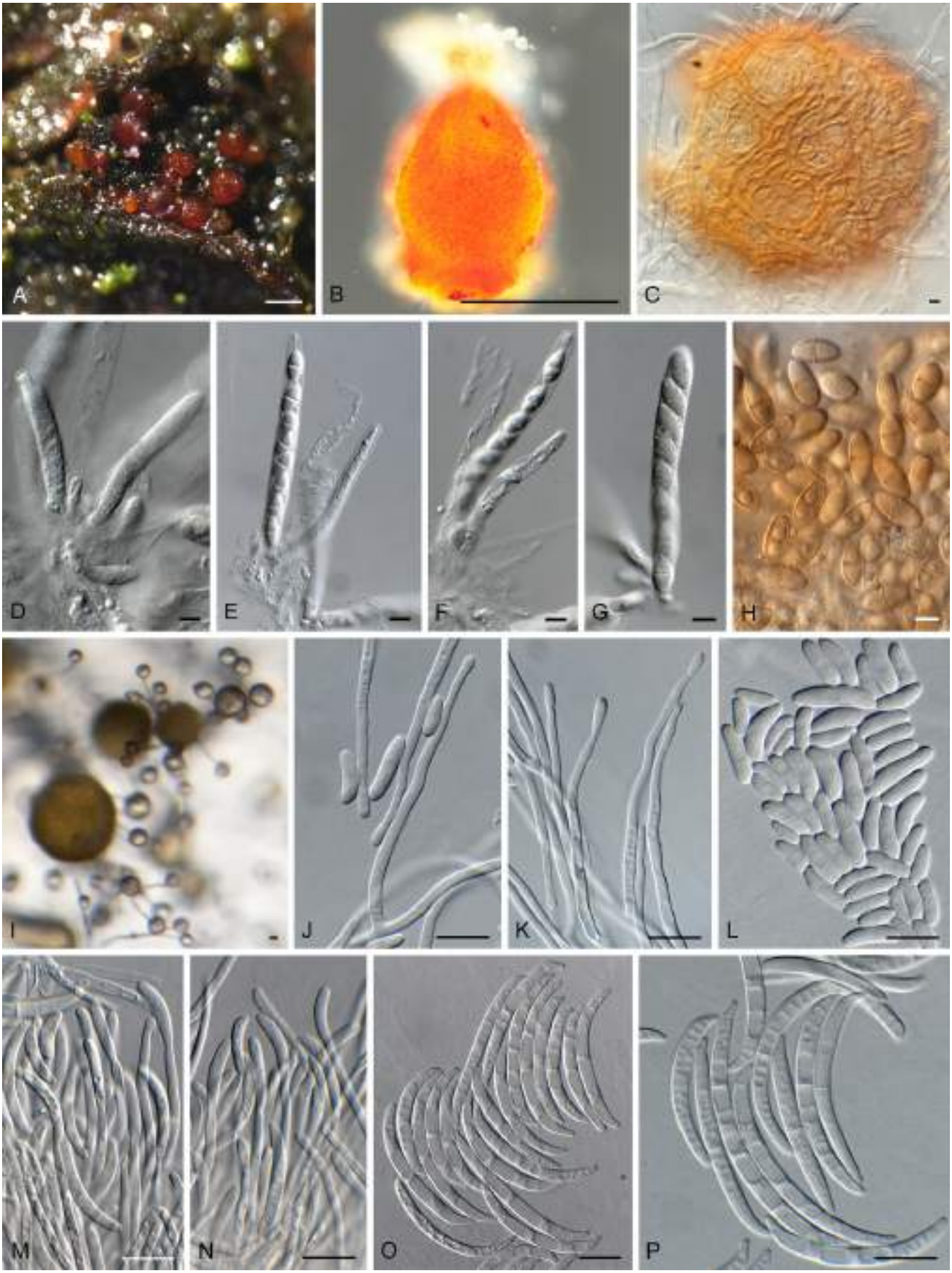

Fig. 20. *Dialonectria quaternatae* (CPC 47736). **A.** Perithecia on host. **B.** Perithecium exuding ascospores. **C.** Surface view of perithecial wall. **D–G.** Asci. **H.** Ascospores. **I.** Sporulation on SNA. **J, K.** Conidiogenous cells giving rise to aerial microconidia. **L.** Microconidia. **M.** Sporodochial conidiogenous cells giving rise to macroconidia. **N, O.** Macroconidia. Scale bars: A, B = 300 µm, all others = 10 µm.

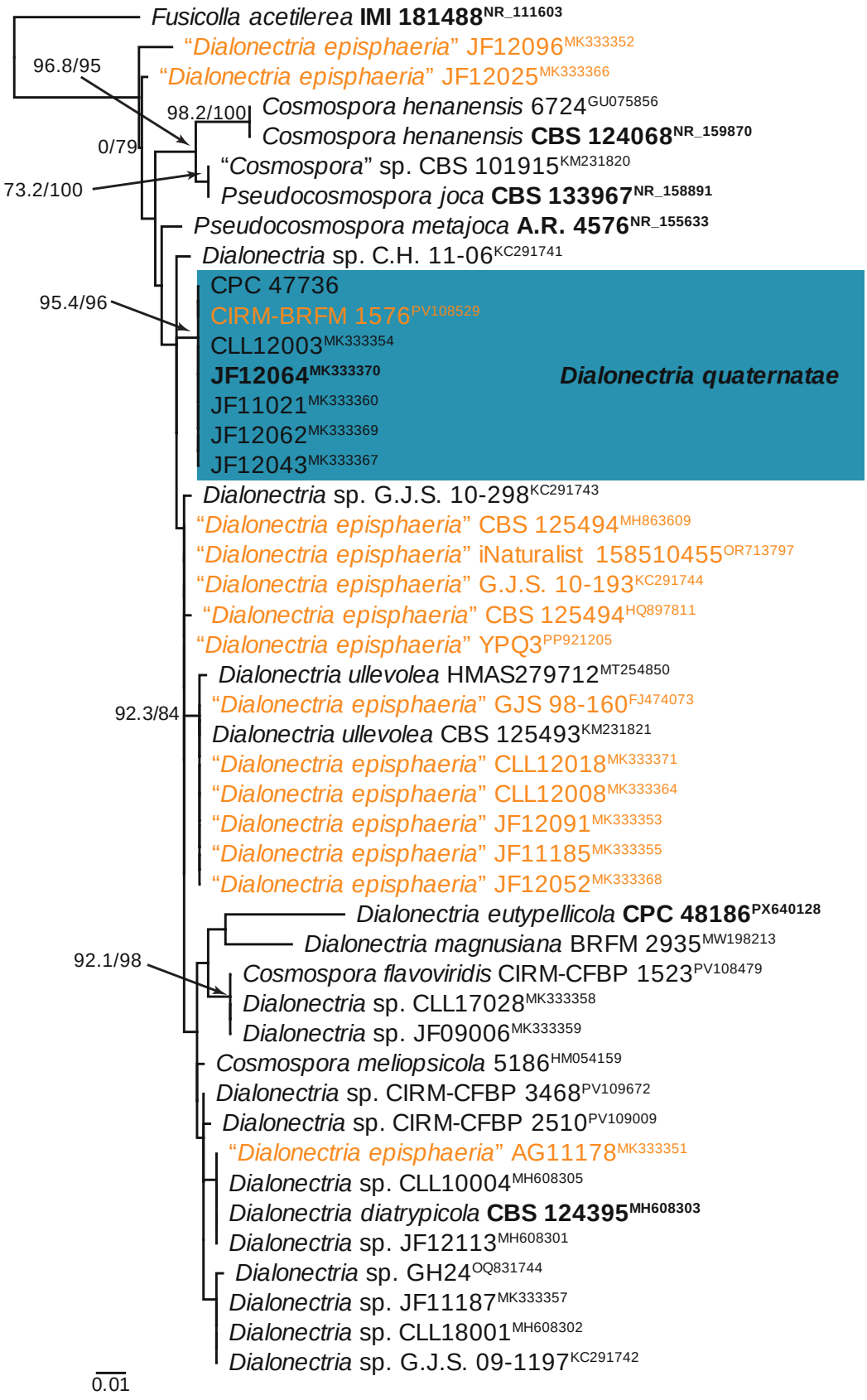

Fig. 21. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Dialonectria* ITS nucleotide alignment. Sequences labelled on GenBank as "*Dialonectria episphaeria*" are indicated with an orange colour. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Fusicolla acetilerea* (IMI 181488; GenBank NR_111603) and the species treated here is highlighted with a coloured block and **bold** font. Alignment statistics: 46 strains including the outgroup; 505 characters including alignment gaps analysed: 107 distinct patterns, 39 parsimony-informative, 38 singleton sites, 428 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TNe+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

guttulate, hyaline, smooth, tapering toward both ends, moderately curved, apex curved to hooked, base with poorly developed foot cell, 1(–3)-septate, (32–)38–45(–55) × (3–)3.5(–4) µm.

Culture characteristics: Colonies flat, spreading with sparse aerial mycelium and even, lobate margin, reaching 30 mm diam. after 2 wk at 25 °C; on OA and MEA surface and reverse orange.

Material examined: **France**, Doubs, les taureaux, 727 m.a.s.l., 47.286924°N, 6.706102°E, on branch of *Fagus sylvatica*, 28 Jan. 2024, *A. Mombert*, AM2401281, HPC 4364 (CBS H-25790, culture CPC 47736 = CBS 155204). GenBank sequences ITS: PZ221277; LSU: PZ221345.

Notes: *Dialonectria episphaeria*, the type species of *Dialonectria*, was long applied to most red nectriaceous fungi occurring in temperate regions on *Diatrypaceae*, making its definition confusing. This species needs to be epitypified based on newly collected material on *Diatrype* on *Crataegus* from northern Germany (Gräfenhan *et al.* 2011). According to Booth (1959), who revised the type specimen of *Diatrype stigma, D. episphaeria* has smaller ascomata (125–140 µm), always laterally pinched when dry, and smaller ascospores (7–11 × 3.5–5 µm). In culture, it differs from *D. quaternatae* by having macroconidia with 2–5 transverse septa and an obtuse apex, as well as smaller microconidia (6–9 × 2–3) µm.

The present culture, CPC 47736, is phylogenetically distinct from *D. episphaeria* (Gräfenhan *et al.* 2011), and identical to *D. quaternatae* (Lechat *et al.* 2019) (Fig. 21), even though it has larger ascospores and longer conidia. *Dialonectria quaternatae* appears to be a common species on ascomycetes occurring on branches of *Fagus sylvatica* in France.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Dialonectria episphaeria* [strain CIRM-BRFM 1576, GenBank PV108529.1; Identities = 508/508 (100 %), no gaps], *Dialonectria magnusiana* [strain BRFM 1591, GenBank MW198212.1; Identities = 501/511 (98 %), three gaps (0 %)], and *Neonectria lugdunensis* [strain HSE 14.1, GenBank OR900527.1; Identities = 611/647 (94 %), nine gaps (1 %)]. However, significant variation exists between ITS sequences deposited under *Dialonectria episphaeria* in GenBank, with the most distant seuence being 95 % similar to our isolate (also see Fig. 21). Although identical in blast2 comparisons, our ITS sequence did not receive any hits with those of *D. quaternatae* in the megablast search, most likely due to sequence length differences. Closest hits using the **LSU** sequence are *Cosmospora elegans* [as *Cosmospora* sp. PC-2024a; strain CBS 152410, GenBank PQ484126.1; Identities = 851/860 (99 %), no gaps], *Cosmospora lavitskiae* [strain CBS 501.81, GenBank PX232797.1; Identities = 863/873 (99 %), no gaps], and *Cosmospora berkeleyana* [strain CBS 382.70C, GenBank MH871500.1; Identities = 863/873 (99 %), no gaps].

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

Didymella conyzaphthora (L.L. Duarte & R.W. Barreto) C.M. Pereira, N.F. Silva & R.W. Barreto, ***comb. nov.*** MB 861975. Figs 22, 23.

Basionym: *Phoma conyzaphthora* L.L. Duarte & R.W. Barreto, *Fungal Biol*. **120**: 9. 2016.

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

Emended description (based on *in vitro* colonies on parboiled rice): *Mycelium* 4–10 µm diam., composed of filamentous, pale brown, smooth, sparingly branched, septate hyphae and torulose, thicker-walled hyphae constricted at septa. *Chlamydospores* either intercalary or terminal, mostly forming long chains, dark brown, smooth, thick-walled, globose, ellipsoid or somewhat distorted, 8.5–20 × 5.5–14 µm. *Sclerotia* composed of a mixture of pigmented hyphae and chlamydospores, dark brown to black, irregular, somewhat fan-shaped, occasionally globose, 37–80 µm diam. while immature, coalescing to form large sclerotial mats over the substrate. *Alpha conidia* solitary, hyaline, smooth, thick-walled, globose, 1.5–4.5 × 1–4 µm. *Beta conidia* solitary, hyaline, smooth, thin-walled, bacilliform to cylindrical, straight, occasionally flexuous, 0–1-septate, 3–11 × 0.5–1.5 µm. *Spermatia* solitary, hyaline, smooth, thin-walled, globose, 1–2 × 1–2 µm.

Typus: **Brazil**, state of Minas Gerais, Caldas, on living stems of *Conyza sumatrensis* (*Asteraceae*), 21 Apr. 2010, *E. Guatimosim*, EG 27 (**holotype** VIC 31607, culture ex-type COAD 1066). GenBank sequences ITS: PX860095; LSU: KJ194473; *rpb2*: PX863911; *tub2*: PX863915.

Additional material examined: **Brazil**, state of Minas Gerais, Caldas, on *C. sumatrensis*, 20 Mar. 2022, *R.W. Barreto*, RWB 2380c (culture COAD 3491); ibid., on stems of *C. sumatrensis*, 20 Mar. 2022, *R.W. Barreto*, RWB 2383a (culture COAD 3508); ibid., on leaves of *C. sumatrensis*, 20 Mar. 2022, *R.W. Barreto*, RWB 2380c (culture COAD 3579). GenBank sequences COAD 3491: ITS: PX860096; LSU: PX860099; *rpb2*: PX863912; *tub2*: PX863916. GenBank sequences COAD 3508: ITS: PX860097; LSU: PX860100; *rpb2*: PX863913; *tub2*: PX863917. GenBank sequences COAD 3579: ITS: PX860098; LSU: PX860101; *rpb2*: PX863914; *tub2*: PX863918.

Notes: The species formerly named *Phoma conyzaphthora* – species epithet meaning destroyer of horseweed (*Conyza* spp.) – was found once on *C. sumatrensis* – horseweed (erroneously identified as *C. canadensis*), and described, along with other members of the mycobiota of that weed (Duarte *et al.* 2016). *Phoma conyzaphthora* was based on a single isolate (COAD 1066). At that time, the combination of a molecular evaluation (involving only LSU sequences) and morphological data led the authors to recognize it as a new species of *Phoma*. A renewed search for additional material was conducted in 2022 and resulted in three additional isolates of this species. Here, through a multi-locus analysis, including ITS, LSU, *rpb2*, and *tub2* gene fragments, we concluded that this species has been misplaced in *Phoma.* It is thus transferred to the genus *Didymella* under the new combination *D. conyzapthora*.

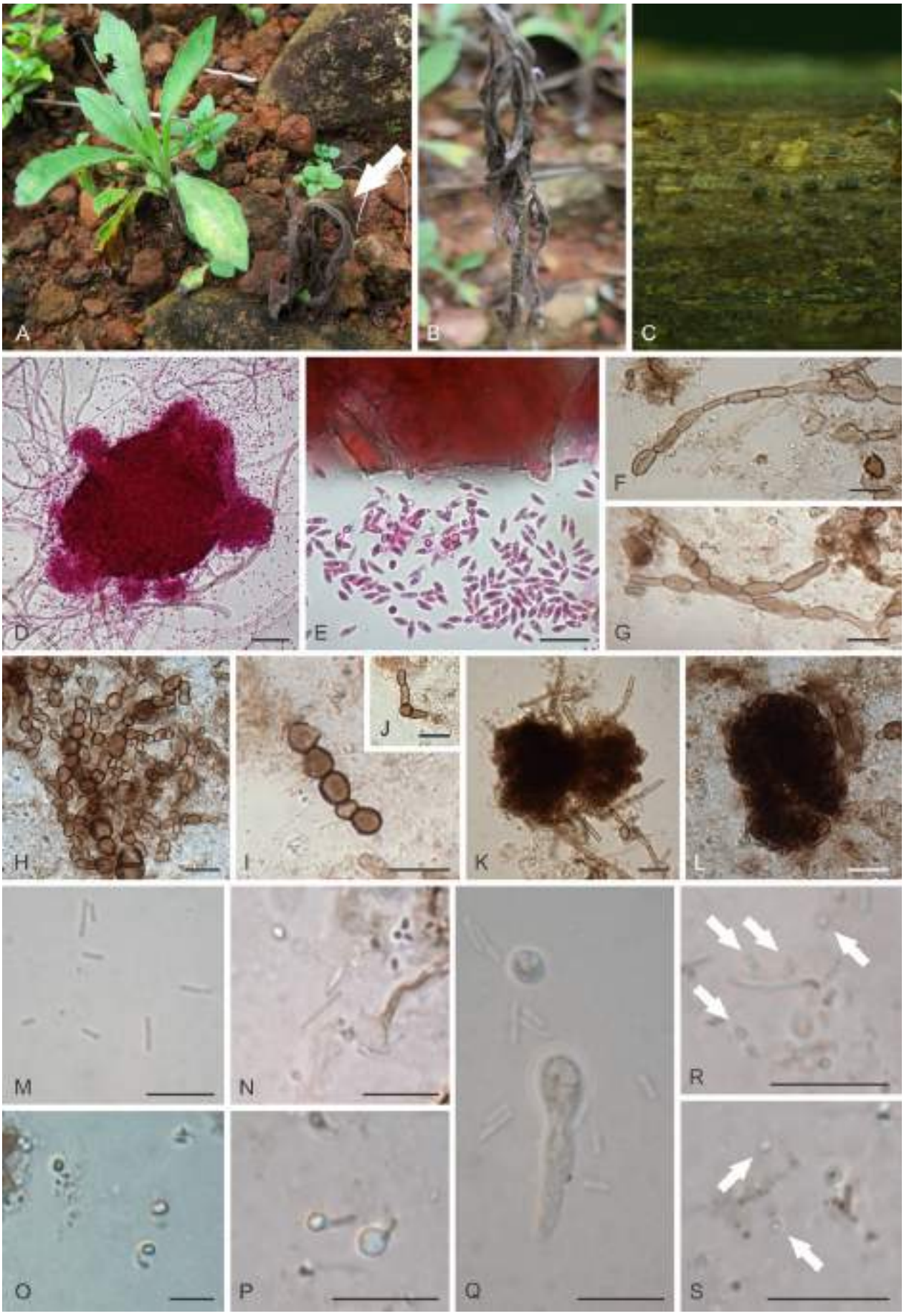

Fig. 22. *Didymella conyzaphthora* (COAD 1066). **A.** Healthy (left) and diseased (right, indicated by a white arrow) *Conyza sumatrensis* plants. **B.** Symptoms caused by *Didymella conyzapthora* on *C. sumatrensis*. **C.** Pycnidial conidiomata formed on the stem of *C. sumatrensis*. **D.** Pycnidium (squashed) surrounded by filamentous hyphae and liberating abundant conidia. **E.** Close-up of conidia liberated from pycnidium. **F, G.** Torulose hyphae. **H–J.** Chlamydospore chains. **K, L.** Sclerotial primordia. **M, N.** *β* conidia. **O, P.** *α* conidia. **Q.** One germinating *α* sporidium and one non-germinated *α* sporidium (above) together with several cylindrical non-germinated *β* conidia. **R, S.** Spermatia (indicated with white arrows). Scale bars: D = 50 µm; E–L = 20 µm; M–S = 10 µm.

A more detailed examination of this fungus including in vitro observations, expanded the original description to include features that had not been included in the original description. Conidia were the only spore form observed and described by Duarte *et al.* (2016). Nevertheless, several additional spore forms were observed and described here. It is acknowledged that their function and names are, mostly tentative. Conidia are the evident spores produced in pycnidia on the natural substrate (diseased *C. sumatrensis* in the field) and also in vitro. Strangely, experimental evidence (unpubl. results) indicated that, although conidia germinate readily, conidial suspensions appear to not infect horseweed. Their function remains uncertain. Chlamydospores and sclerotia are easily recognized and provided the infective inoculum, used in experiments on horseweed. These are clearly survival structures for *D. conyzapthora* and may germinate to infect horseweed or produce spores that are infective. The minute structures we called alpha and beta conidia (terminology borrowed from that used for conidia of *Phomopsis* spp.) are abundantly produced in inoculum suspensions of all of the isolates of *D. conyzapthora* and whereas alpha conidia were commonly seen forming germ tubes, beta conidia (as for beta conidia in *Phomopsis* spp.) were never seen germinating. Their function remains uncertain. In the case alpha conidia our conjecture is that they may represent the main functionally infective structures of *D. conyzapthora*. This, nevertheless, requires confirmation and is technically difficult to achieve. The smallest structures are spheroidal and provisionally treated as spermatia due to their size and failure to germinate. (Supplementary material, Figshare https://doi.org/10.6084/m9.figshare.31842517).

Authors: C.M. Pereira, N. F. da Silva, D. S. Guterres & R.W. Barreto

Exophiala ligni Crous & Hülsewig, ***sp. nov.*** MB 863251. Fig. 24.

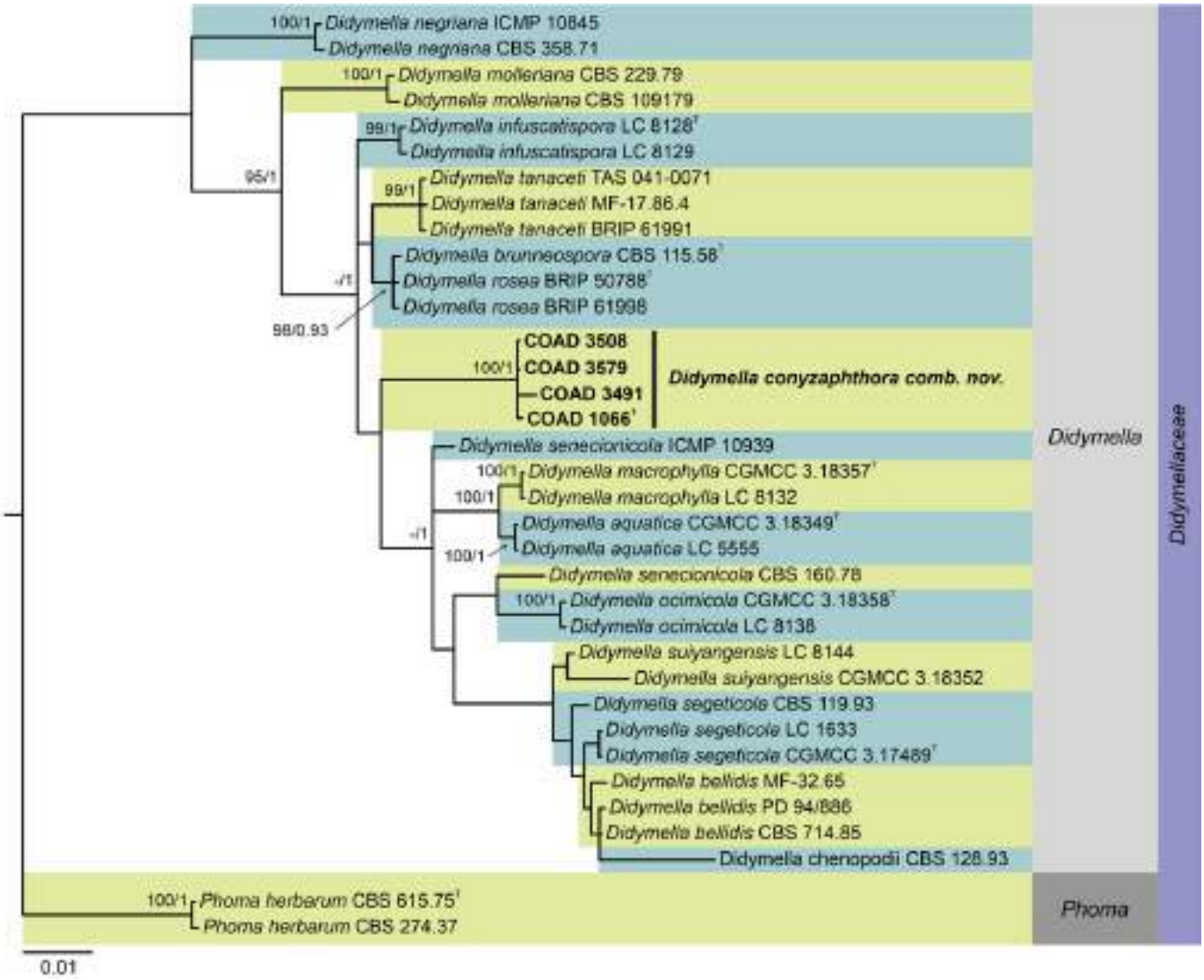

Fig. 23. Multigene phylogeny of *Didymella* based on ITS, LSU, *rpb2*, and *tub2* sequences. Individual datasets were aligned using the MUSCLE algorithm implemented in MEGA X v. 10.2.2 (Kumar *et al.* 2018), and concatenated using SequenceMatrix v. 1.8 (Vaidya *et al.*, 2011). Phylogenetic analyses were conducted within the CIPRES portal (Miller *et al.*, 2010). Maximum Likelihood (ML) was carried out with RAxML-HPC ver. 8.2.12 (Stamatakis, 2014). The best-fit nucleotide substitution models were selected using ModelTest2 v. 2.1.6 tool (Darriba *et al.*, 2012) and applied in the Bayesian Inference (BI) analysis conducted with MrBayes v. 3.2.1 tool (Ronquist *et al.*, 2012). The tree was rooted with *Phoma herbarum* CBS 615.75 and CBS 274.37. Values at nodes indicate ML Bootstrap support values (BS ≥ 70 %) and Bayesian posterior probabilities (PP ≥ 0.90). The taxon studied is highlighted in bold (^{T} = ex-type). The alignment and tree were deposited in TreeBASE / Zenodo / Figshare under doi https://doi.org/10.6084/m9.figshare.31842517.

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

Mycelium consisting of smooth, pale brown, branched, septate, 1.5–2 µm diam. hyphae. *Conidiophores* reduced to conidiogenous cells or with a supporting cell. *Conidiogenous cells* integrated, intercalary on hyphae, with lateral phialidic pegs, 0.5–1 × 0.5 µm. *Conidia* solitary, aggregating in mucoid mass, aseptate, subhyaline, smooth, subcylindrical to ellipsoid, straight to curved with obtuse ends, 3–4 × 1.5–2 µm.

Culture characteristics: Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 7 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse dark mouse grey.

Typus: **Germany**, North Rhine-Westphalia, Witten, Recreation area Hohenstein, on dead wood, 30 Jul. 2024, *T. Hülsewig*, HPC 4509, Thorben 1282 (**holotype** CBS H-25742, culture ex-type CPC 49106 = CBS 153460). GenBank sequences ITS: PZ221278; LSU: PZ221346; *tef1* (first part): PZ228651; *tub2*: PZ228707.

Notes: *Exophiala lignii* is similar to *Exophiala moniliae* (from branch of *Quercus* in Northwest European Russia, but also associated with phaeohyphomycosis, conidia 2.5–4 × 1.5–2.5 µm; de Hoog & Hermanides-Nijhof 1977), and the two species are phylogenetically distinct (Fig. 25).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Herpotrichiellaceae* sp. [strain wF5, GenBank KT265803.1; Identities = 519/519 (100 %), no gaps], *Exophiala moniliae* [strain KoLRI49754, GenBank MT586950.1; Identities = 504/520 (97 %), four gaps (0 %)], and *Exophiala quercina* [strain CPC 33408, GenBank NR_170053.1; Identities = 560/582 (96 %), seven gaps (1 %)]. Closest hits using the **LSU** sequence are *Exophiala quercina* [strain CPC 33408, GenBank NG_073874.1; Identities = 847/853 (99 %), no gaps], *Exophiala moniliae* [strain CBS 520.76, GenBank MH872772.1; Identities = 847/854 (99 %), one gap (0 %)], and *Exophiala spinifera* [strain L22F, GenBank OR143832.1; Identities = 842/854 (99 %), four gaps (0 %)]. Closest hits using the ***tef1*** (first part) sequence had highest similarity to *Exophiala quercina* [strain CBS 146024, GenBank MT223713.1; Identities = 270/288 (94 %), three gaps (1 %)], *Exophiala bergeri* [strain RBG7236, GenBank OP066900.1; Identities = 234/287 (82 %), 14 gaps (4 %)], and *Exophiala eucalyptigena* [strain CBS 148273, GenBank ON803564.1; Identities = 228/275 (83 %), seven gaps (2 %)]. Closest hits using a blastn search with the ***tub2*** sequence had highest similarity to *Phaeoannellomyces elegans* [strain CBS 101597, GenBank KF928571.1; Identities = 295/383 (77 %), 22 gaps (5 %)], *Exophiala eucalyptigena* [strain CBS 148273, GenBank ON803590.1; Identities = 299/389 (77 %), 19 gaps (4 %)], and *Exophiala xenobiotica* [strain CBS 117674, GenBank DQ182573.1; Identities = 291/380 (77 %), 14 gaps (3 %)].

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

Fusarium agapanthi O'Donnell *et al.*, *Mycologia* **108**: 987. 2016.

Materials examined: **South Africa**, Western Cape Province, Cape Town, Kirstenbosch, soil surrounding *Agapanthus praecox*, Apr. 2023, *P.W. Crous*, cultures CBS 151448 = CPC 47716, CBS 151449 = CPC 47719, CBS 151450 = CPC 47720, CBS 151451 = CPC 47721, CPC 47705, CPC 47708; Western Cape Province, Cape Town, Kirstenbosch, on stalks of *Agapanthus* sp., 13 Apr. 2023, *P.W. Crous*, HPC 4160, cultures CPC 45896, CPC 45898, CPC 47293; Western Cape Province, Cape Town, Kirstenbosch, on *Agapanthus*, leaf, 22 Nov. 2023, *P.W. Crous*, HPC 4323, cultures CPC 47345, CPC 47351; Western Cape Province, Cape Town, Kirstenbosch, on stalks of *Agapanthus*, 22 Nov. 2023, *P.W. Crous*, HPC 4320, culture CPC 47348; Western Cape Province, Cape Town, Kirstenbosch, on stalks of *Agapanthus praecox* subspec. *minimus*, 22 Nov. 2023, *P.W. Crous*, HPC 4322, culture CPC 47349; Gauteng Province, Pretoria, Future Africa campus, on stems of *Agapanthus* sp., 7 Apr. 2024, *P.W. Crous*, HPC 4435, cultures CPC 47875, 47876 (associated bacteria include *Alsobacter metallidurans*, *Chryseobacterium* sp., *Klebsiella pasteuri, Klebsiella* sp., *Microbacterium imperiale, Pseudomonas punonensis, Pseudomonas straminae, Pseudomonas straminae, Sphingobium sionense* and *Staphylococcus* sp.). **UK**, England, Cornwell, St. Ives, on stems of *Agapanthus* sp., May 2024, *P.W. Crous*, HPC 4475, cultures CPC 48156, CPC 48158. GenBank sequences ITS: PZ221279–PZ221282; *cmdA*: PZ228598, PZ228599; *rpb2* (first part): PZ228743; *tef1* (first part): PZ228652–PZ228662; *tub2*: PZ228708, PZ228709.

Notes: Crous *et al.* (2024a) reported *Fusarium agapanthi* from the Western Cape of South Africa. It is herewith reported from Gauteng Province of South Africa, with a further new

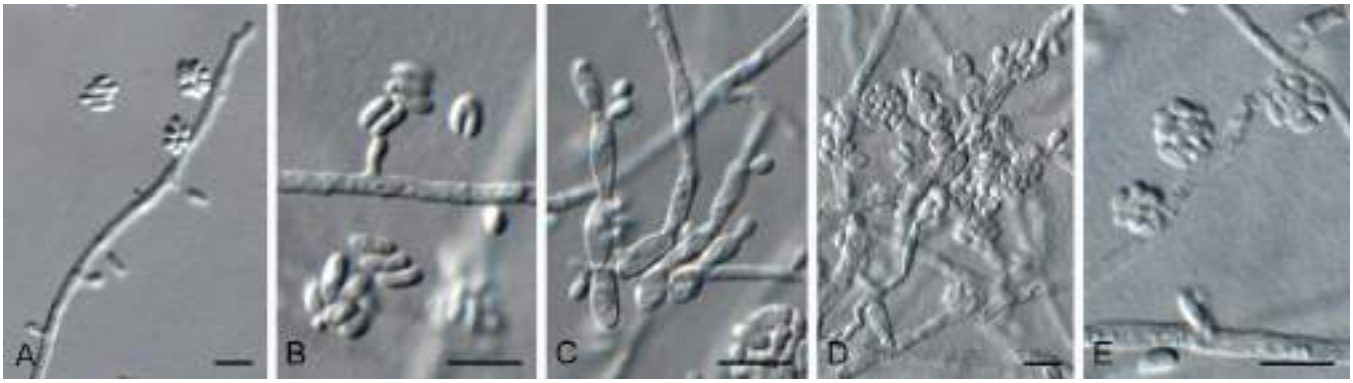

Fig. 24. *Exophiala ligni* (CPC 49106). **A–E.** Conidiogenous cells and conidia. Scale bars = 10 µm.

report on *Agapanthus praecox* subsp. *minimus* from Cornwall in the UK.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 48156 had highest similarity to *Fusarium agapanthi* [strain CPC 27741, GenBank LS422777.1; Identities = 525/525 (100 %), no gaps], *Fusarium circinatum* [strain SF48, GenBank KX276637.1; Identities = 524/525 (99 %), no gaps], and *Fusarium subglutinans* [strain IHEM 03820, GenBank OW983244.1; Identities = 524/525 (99 %), no gaps]. The ITS sequence of CPC 48156 is identical to those of CPC 47875 (521/521 nt), CPC 47876 (509/509 nt) and CPC 48158 (523/523 nt). Closest hits using the ***cmdA*** sequence of CPC 48156 had highest similarity to *Fusarium agapanthi* [strain NRRL 54463, GenBank KU900611.1; Identities = 408/408 (100 %), no gaps], *Fusarium dendrobii* [strain KACC 47733,

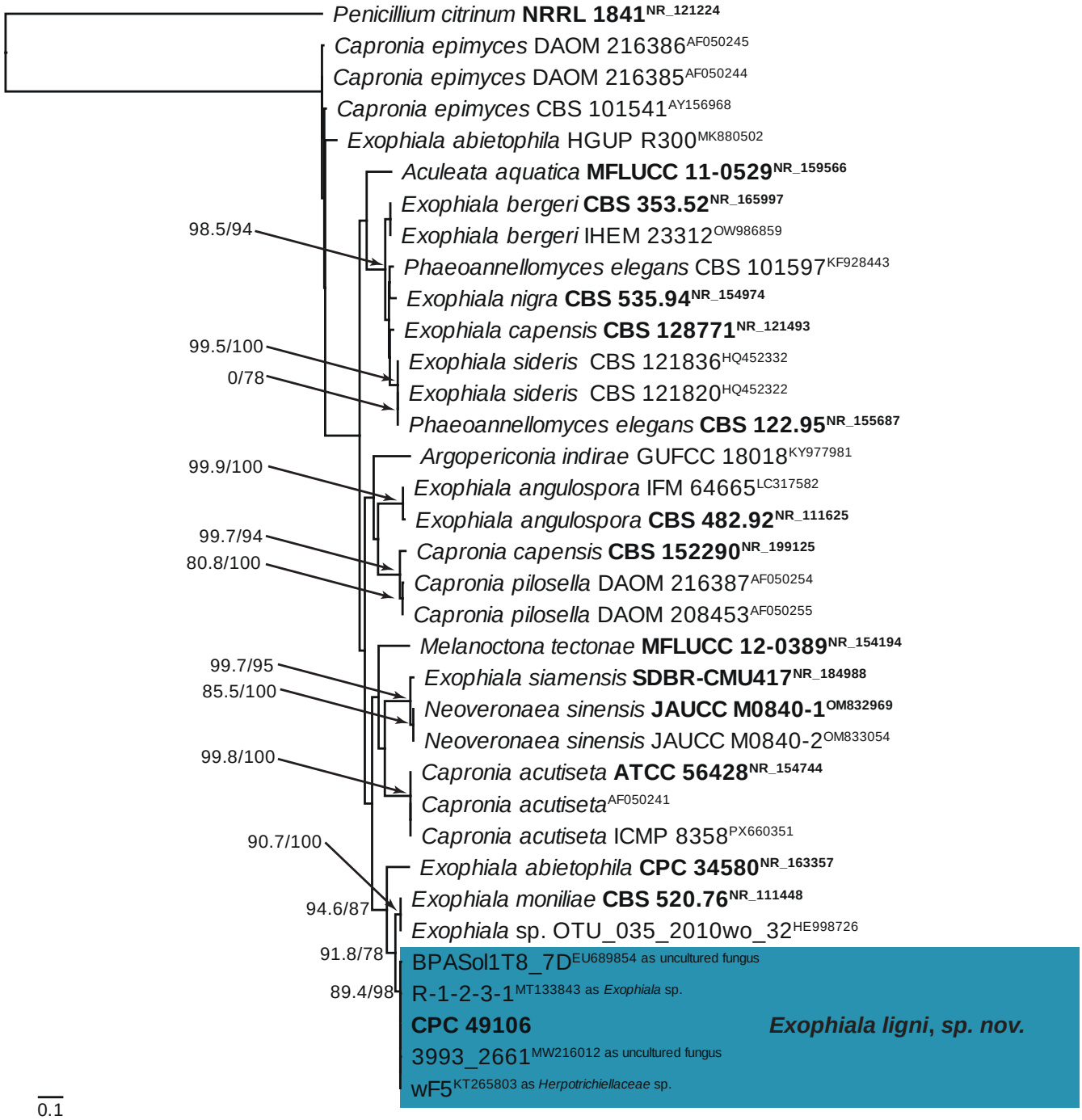

Fig. 25. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Exophiala* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Penicillium citrinum* (NRRL 1841; GenBank NR_121224) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 35 strains including the outgroup; 644 characters including alignment gaps analysed: 317 distinct patterns, 179 parsimony-informative, 96 singleton sites, 369 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

GenBank PV755441.1; Identities = 405/408 (99 %), no gaps], and *Fusarium anthophilum* [strain CBS 119859, GenBank MN534164.1; Identities = 404/408 (99 %), no gaps]. The *cmdA* sequences of of CPC 48156 and of CPC 48158 are identical (408/408 nt). Closest hits using the ***rpb2*** (first part) sequence of CPC 48156 had highest similarity to *Fusarium agapanthi* [strain NRRL 54464, GenBank MN193884.1; Identities = 909/909 (100 %), no gaps], *Fusarium ananatum* [strain CCF 6808, GenBank PV189496.1; Identities = 884/910 (97 %), one gap (0 %)], and *Fusarium guttiforme* [strain NRRL 2294, GenBank MN193889.1; Identities = 884/910 (97 %), one gap (0 %)]. Closest hits using the ***tef1*** (first part) sequence of CPC 48156 had highest similarity to *Fusarium agapanthi* [strain NRRL 54464, GenBank MN193856.1; Identities = 666/666 (100 %), no gaps], *Fusarium guttiforme* [strain CBS 409.97, GenBank MT010999.1; Identities = 644/666 (97 %), three gaps (0 %)], and *Fusarium mexicanum* [strain MXMIC-715.1, GenBank MH287748.1; Identities = 644/666 (97 %), four gaps (0 %)]. The *tef1* sequence of of CPC 48156 differ with one indel from CPC 48158 and CPC 47348 (662/663 and 656/657 nt, respectively), while CPC 48156 is identical to CPC 45896 (661/661 nt), CPC 45898 (666/666 nt), CPC 47293 (664/664 nt), and CPC 47345 (666/666 nt). Closest hits using the ***tub2*** sequence of CPC 48156 had highest similarity to *Fusarium agapanthi* [strain NRRL 31653, GenBank KU900634.1; Identities = 497/497 (100 %), no gaps], *Fusarium guttiforme* [strain CBS 409.97, GenBank MT011048.1; Identities = 505/516 (98 %), no gaps], and *Fusarium cymbidii* [strain ZHKUCC 23-0916, GenBank PQ031154.1; Identities = 504/516 (98 %), no gaps]. The *tub2* sequences of of CPC 48156 and of CPC 48158 are identical (513/513 nt).

Authors: P.W. Crous, J.Z. Groenewald, S. Denman, M. Sandoval-Denis

Fusarium aloetica Crous & Lampr*.,* ***sp. nov*****.** MB 863252. Fig. 26.

Etymology: Named after the host genus, *Aloe*.

Conidiophores on SNA abundant on aerial mycelium, straight or geniculous-flexuous, erect, smooth- and thin-walled, commonly irregularly branched, up to 120 µm tall or reduced to conidiogenous cells borne laterally on hyphae; *conidiogenous cells* mono- and polyphialidic, subulate, to subcylindrical, smooth- and thin-walled, proliferating sympodially, or in clusters, 10–25 × 3–4 µm, with periclinal thickening at apex; *microconidia* formed abundantly, hyaline, smooth- and thin-walled, ellipsoid to obovoid, 0(–1)-septate, (7–)9–12(–16) × 3–3.5(–4) µm, clustering in discrete false heads at the tip of phialides. *Sporodochia* on CLA white to pale yellow or orange. *Sporodochial conidiophores* densely aggregated, irregularly branched, typically producing dense whorls of 2–4 phialides; *sporodochial conidiogenous cells* monophialidic, subulate to doliiform, 12–20 × (3–)3.5–4(–4.5) µm, smooth- and thin-walled, with periclinal thickening and an inconspicuous apical collarette. *Sporodochial conidia* with parallel walls, straight to distinctly curved (almost circle-shaped), tapering toward the basal part; apical cell curved and papillate; basal cell foot-shaped, notch poorly developed, (3–)5(–6)-septate, hyaline, thin- and smooth-walled; 3-septate conidia: (28–)32–42(–52) × 3.5–4 µm; 4-septate conidia: (42–)45–48(–55) × 3.5–4(–4.5) µm; 5-septate conidia: (50–)55–57(–67) × (3–)3.5–4 µm; 6-septate conidia 60–67 × 3.5–4 µm. *Chlamydospores* absent.

Culture characteristics: Colonies erumpent, spreading, with abundant aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA surface saffron, reverse peach; on PDA surface peach to red, reverse vinaceous, and on OA surface saffron.

Typus: **South Africa**, Western Cape Province, Albertinia, on symptomatic leaves of *Aloe ferox* (*Asphodelaceae*), 31 Jul. 2020, *S.C. Lamprecht* (**holotype** CBS H-25947, culture ex-type PPRI 29873 = CPC 40400 = CBS 154462). GenBank sequences ITS: PZ221283; *cmdA*: PZ228600; *rpb1*: PZ228625; *rpb2* (first and second part): PZ228744; *tef1* (first part): PZ228663; *tub2*: PZ228710.

Additional materials examined: **South Africa**, Western Cape Province, Albertinia, on symptomatic of *Aloe ferox*, 31 Jul. 2020, *S.C. Lamprecht*, PPRI 29880 = CPC 40399 = CBS 154461; PPRI 29896 = CPC 40409 = CBS 154463; PPRI 29886 = CPC 40395; PPRI 29882 = CPC 40396; PPRI 29872 = CPC 40397; PPRI 29874 = CPC 40398; PPRI 29890 = CPC 40401; PPRI 29895 = CPC 40402; PPRI 29891 = CPC 40403; PPRI 29888 = CPC 40404; PPRI 29875 = CPC 40405; PPRI 29893 = CPC 40406; PPRI 29889 = CPC 40407; PPRI 29884 = CPC 40408; PPRI 29877 = CPC 40410; PPRI 29883 = CPC 40411; PPRI 29881 = CPC 40412; PPRI 29887 = CPC 40413; PPRI 29906 = CPC 40414; PPRI 29897 = CPC 40415. GenBank sequences ITS: PZ221284– PZ221302; *cmdA*: PZ228601– PZ228619; *rpb1*: PZ228626– PZ228644; *rpb2* (first and second part): PZ228745– PZ228764; *tef1* (first part): PZ228664– PZ228683; *tub2*: PZ228711– PZ228729.

Notes: Pathogenicity tests on healthy leaves wounded with colonized toothpicks of *Fusarium aloetica* confirmed that it can cause leaf lesions, while control inoculations with sterile toothpicks did not induce any lesions. Lesions were large and necrotic with yellow to orange halos. The lower leaves were also highly susceptible, with lesions developing more rapidly than on the younger, upper leaves. Since *F. aloetica* was also isolated from *Aloe* roots, there is a possibility that the fungus can grow systemically within the plant. Phylogenetically, it is related to *F. phyllophilum* (Fig. 27).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 40400 had highest similarity to *Fusarium proliferatum* [strain F43, GenBank MW995637.1; Identities = 538/538 (100 %), no gaps], *Fusarium oxysporum* [strain F64, GenBank MW995658.1; Identities = 538/538 (100 %), no gaps], and *Fusarium mundagurra* [strain IHEM 05390, GenBank OW983784.1; Identities = 536/536 (100 %), no gaps]. Sequences of the examined strains included for this species were identical to, or differed by up to three nucleotides, to the sequence from the ex-type strain CPC 40400. Closest hits using the ***cmdA*** sequence of CPC 40400 had highest similarity to *Fusarium* sp. LL-2022a [strain LLC1198, GenBank OP485930.1; Identities = 572/575 (99 %), no gaps], *Fusarium udum* [strain CBS 747.79, GenBank MN534154.1; Identities = 571/575 (99 %), no gaps], and *Fusarium*

Fig. 26. *Fusarium aloetica* (CPC 40400). **A, B.** Sporodochia. **C, D.** Aerial conidia. **E–H.** Mono- and polyphialidus with microconidia. **I.** Microconidia. **J, K.** Sporodochial conidiogenous cells. **L.** Sporodochial conidia. Scale bars = 10 µm.

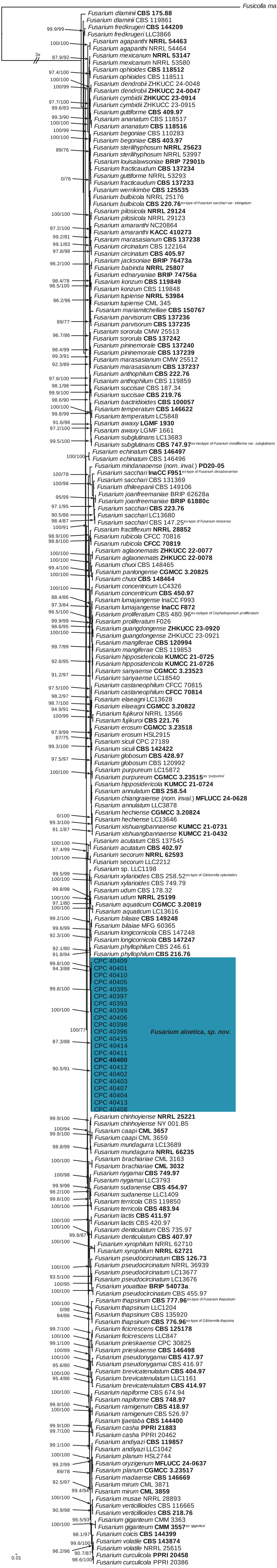

Fig. 27. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Fusarium fujikuroi* species complex *tef1-rpb2-rpb1-CaM-tub2* nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers are indicated for all species. GenBank accession numbers can be retrieved from fusarium.org. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Fusicolla matuoi* (CBS 581.78) and the novelty described here is highlighted with a coloured block and **bold** font. The root branch was shortened to facilitate layout. Alignment statistics: 221 strains including the outgroup; 5196 characters including alignment gaps analysed: 2443 distinct patterns, 1359 parsimony-informative, 764 singleton sites, 3073 constant sites. The best-fit model sidentified in IQ-TREE using the TESTNEW option were: *tef1* (1–725): TIM2e+G4; *rpb2* (726–2467): TNe+I+R3; *rpb1* (2468–3986): TIM3e+R2; *CaM* (3987–4624): TNe+G4; *tub2* (4625–5196): TNe+G4;. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

xylarioides [strain CBS 749.79, GenBank MN534213.1; Identities = 560/564 (99 %), no gaps]. Sequences of the examined strains included for this species were identical to, or differed by one nucleotide, to the sequence from the ex-type strain CPC 40400. Closest hits using the ***rpb1*** sequence of CPC 40400 had highest similarity to *Fusarium xylarioides* [strain NRRL 25486, GenBank MN193930.1; Identities = 1670/1675 (99 %), no gaps], *Fusarium phyllophilum* [strain NRRL 13617, GenBank MN193920.1; Identities = 1667/1675 (99 %), no gaps)], and *Fusarium udum* [strain NRRL 25194, GenBank MN193928.1; Identities = 1667/1675 (99 %), no gaps]. Sequences of the examined strains included for this species were identical to, or differed by up to six nucleotides, to the sequence from the ex-type strain CPC 40400. Closest hits using the ***rpb2*** (first part) sequence of CPC 40400 had highest similarity to *Fusarium phyllophilum* [strain CBS 187.34, GenBank KU604300.1; Identities = 715/718 (99 %), no gaps], *Fusarium annulatum* [strain PUF023, GenBank HQ423217.1; Identities = 715/718 (99 %), no gaps], and *Fusarium bilaiae* [strain MFG 60364, GenBank MW286116.1; Identities = 711/718 (99 %), no gaps]. Sequences of the examined strains included for this species were identical to, or differed by up to two nucleotides, to the sequence from the ex-type strain CPC 40400. Closest hits using the ***rpb2*** (second part) sequence of CPC 40400 had highest similarity to *Fusarium phyllophilum* [strain NRRL 13617, GenBank MN193892.1; Identities = 791/800 (99 %), no gaps], *Fusarium xylarioides* [strain NRRL 25486, GenBank MN193902.1; Identities = 788/800 (99 %), no gaps], and *Fusarium tupiense* [strain UMAF_0917, GenBank KP753443.1; Identities = 778/800(97 %), no gaps]. Sequences of the examined strains included for this species were identical to, or differed by up to four nucleotides, to the sequence from the ex-type strain CPC 40400. Closest hits using the ***tef1*** (first part) sequence of CPC 40400 had highest similarity to *Fusarium udum* [strain LLC2177, GenBank OP487080.1; Identities = 651/670 (97 %), six gaps (0 %)], *Fusarium phyllophilum* [strain NRRL 13617, GenBank MN193864.1; Identities = 652/672 (97 %), eight gaps (1 %)], and *Fusarium* sp. LL-2022a [strain LLC1198, GenBank OP487046.1; Identities = 645/668 (97 %), seven gaps (1 %)]. Sequences of the examined strains included for this species were identical to, or differed by up to 17 nucleotides, to the sequence from the ex-type strain CPC 40400. Closest hits using the ***tub2*** sequence of CPC 40400 had highest similarity to *Fusarium phyllophilum* [strain CBS 246.61, GenBank MW402316.1; Identities = 523/529 (99 %), no gaps], *Fusarium longicornicola* [strain NRRL 52706, GenBank MW402360.1; Identities = 523/529 (99 %), no gaps], and *Fusarium xylarioides* [as *Gibberella xylarioides*; strain NRRL 25486, GenBank AY707118.1; Identities = 522/529 (99 %), no gaps]. Sequences of the examined strains included for this species were identical to, or differed by up to seven nucleotides, to the sequence from the ex-type strain CPC 40400.

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

Fusicolla melogrammatis (as '*melogrammae*') Lechat & Aplin, *Persoonia* **37**: 281. 2016. Fig. 28.

Perithecia solitary or in groups of 2–3, subglobose papillate, pale yellow, 180–220 µm diam., outer surface covered in crustose hyphae, forming a hyphal collar around the short neck; hyphal setae thick-walled, 4–5 µm diam. *Asci* sessile, subcylindrical, hyaline, smooth, apex flattened, with visible apical mechanism (slight reaction in Melzer), 8-spored, unitunicate, 55–70 × 5–6 µm. *Ascospores* broadly ellipsoid, guttulate, ends obtuse, not to slightly constricted at median septum, finely verruculose, hyaline to pale brown, 9–10(–11) × 4(–4.5) µm. *Asexual morph* fusarioid. Sporodochial *conidia* curved with equal walls, apex curved, basal cell poorly developed, foot-shaped, guttulate, 3-septate, (35–)40–44(–50) × (4.5–)5 µm.

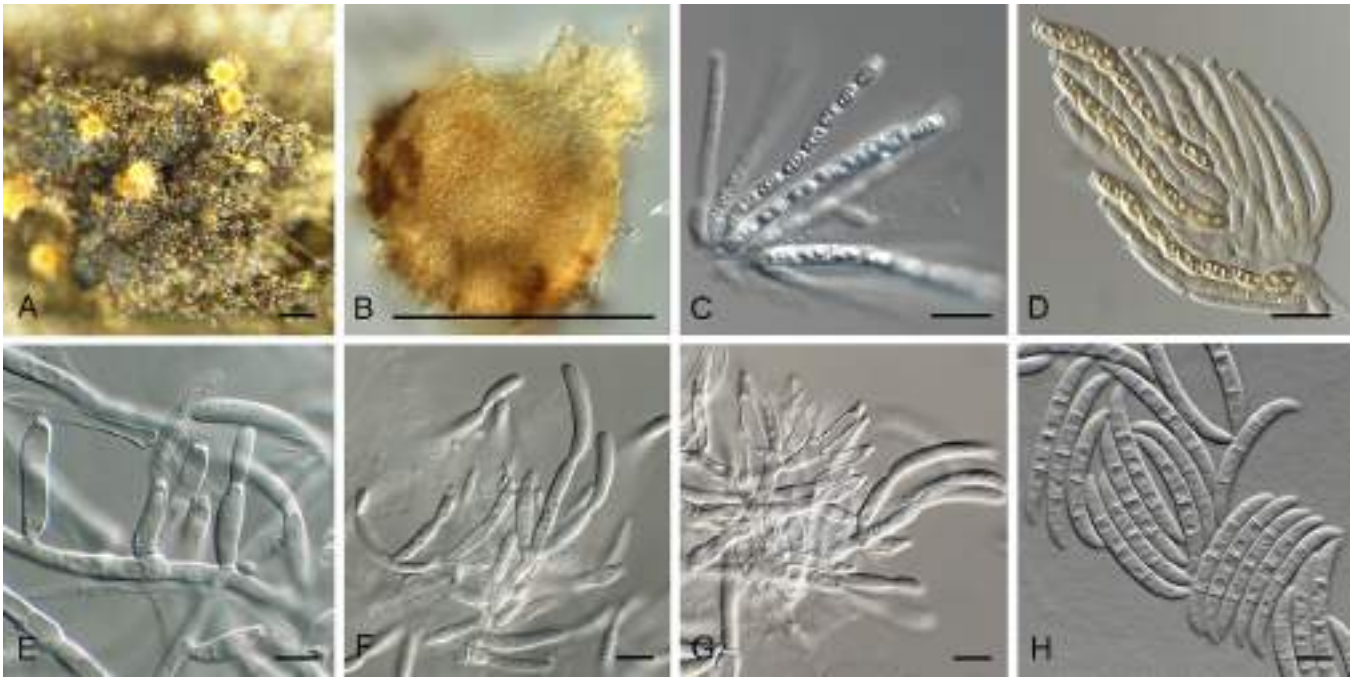

Fig. 28. *Fusicolla melogrammatis* (CPC 45227). **A, B.** Perithecia. **C, D.** Asci and ascospores. **E–G.** Conidiogenous cells, **H.** Conidia. Scale bars: A, B = 220 µm, all others = 10 µm.

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

Material examined: **Ukraine**, Ternopil region, Zalischyky district, National Nature Park, Dniester Canyon, forest near Dzhuryn waterfall, on the stromata of *Melogramma campulosporum* (*Melogrammataceae*), on dead branches of *Carpinus betulus* (*Betulaceae*), 13 Aug. 2022, *A. Akulov*, HPC 4043 = CWU (Myc) AS 8430 (CBS H-25518; culture CPC 45227 = CBS 150778). GenBank sequences ITS: PZ221303; LSU: PZ221347; *rpb1*: PZ228645; *rpb2* (first part): PZ228765; *tub2*: PZ228730.

Notes: *Fusicolla melogrammatis* was described on on dead stromata of *Melogramma campylosporum* on bark of *Carpinus betulus* collected in the UK (Crous *et al.* 2016), and this is the first report from Ukraine.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Fusicolla violacea* [strain CBS 634.76, GenBank MH861015.1; Identities = 539/540 (99 %), one gap (0 %)], *Fusicolla melogrammatis* [strain CBS 141092, GenBank NR_155096.1; Identities = 526/528 (99 %), two gaps (0 %)], and *Fusicolla gigantispora* [voucher MFLU 17-2620, GenBank MN047105.1; Identities = 507/521 (97 %), six gaps (1 %)]. Closest hits using the **LSU** sequence are *Fusicolla melogrammatis* [strain CBS 141092, GenBank NG_058275.1; Identities = 859/860 (99 %), no gaps], *Fusicolla violacea* [strain CBS 634.76, GenBank NG_058099.1; Identities = 825/829 (99 %), no gaps], and *Fusicolla quarantenae* [strain CGMCC 3.20777, GenBank OL897054.1; Identities = 848/858 (99 %), no gaps]. Closest hits using the ***rpb1*** sequence had distant similarity to *Fusicolla* sp. [strain NRRL 22136, GenBank JX171491.1; Identities = 677/792 (85 %), two gaps (0 %)], *Fusarium burgessii* [strain RBG5319, GenBank KJ716217.1; Identities = 493/619 (80 %), two gaps (0 %)], and *Fusarium devonianum* [strain NRRL 22134, GenBank JX171490.1; Identities = 629/797 (79 %), 22 gaps (2 %)]. No *rpb1* sequence of *Fusicolla melogrammatis* is available for comparison. Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Fusicolla violacea* [strain CBS 634.76, GenBank HQ897696.1; Identities = 558/593 (94 %), no gaps], *Fusicolla guangxiensis* [strain 12537, GenBank OQ134114.1; Identities = 419/468 (90 %), no gaps], and *Fusicolla quarantenae* [strain 111JB, GenBank MW556626.1; Identities = 476/542 (88 %), two gaps (0 %)]. No *rpb2* sequence of *Fusicolla melogrammatis* is available for comparison. Closest hits using the ***tub2*** sequence had highest similarity to *Fusicolla melogrammatis* [strain CBS 141092, GenBank MW834305.1; Identities = 467/467 (100 %), no gaps], *Fusicolla violacea* [strain CBS 634.76, GenBank KM232095.1; Identities = 499/540 (92 %), 13 gaps (2 %)], and *Fusicolla sporellula* [strain CBS 110191, GenBank MW834308.1; Identities = 423/473 (89 %), 11 gaps (2 %)].

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

Harzia cupressicola Crous, ***sp. nov.*** MB 863253. Fig. 29.

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

Mycelium consisting of hyaline, smooth, branched, septate, 4–5 µm diam. hyphae. *Conidiophores* dimorphic. *Microconidiophores* erect, cylindrical, straight to curved, hyaline, smooth, 1–3-septate, 100–130 × 5–6 µm. *Microconidiogenous cells* terminal and intercalary, having swollen vesicles that are aspergillus-like, globose, hyaline, smooth, 10–12 µm diam., covered in ampulliform, hyaline phialides, 7–10 × 3–5 µm. *Microconidia* hyaline, smooth, aseptate, ellipsoid to clavate with truncate hilum, 3–3.5 × 2

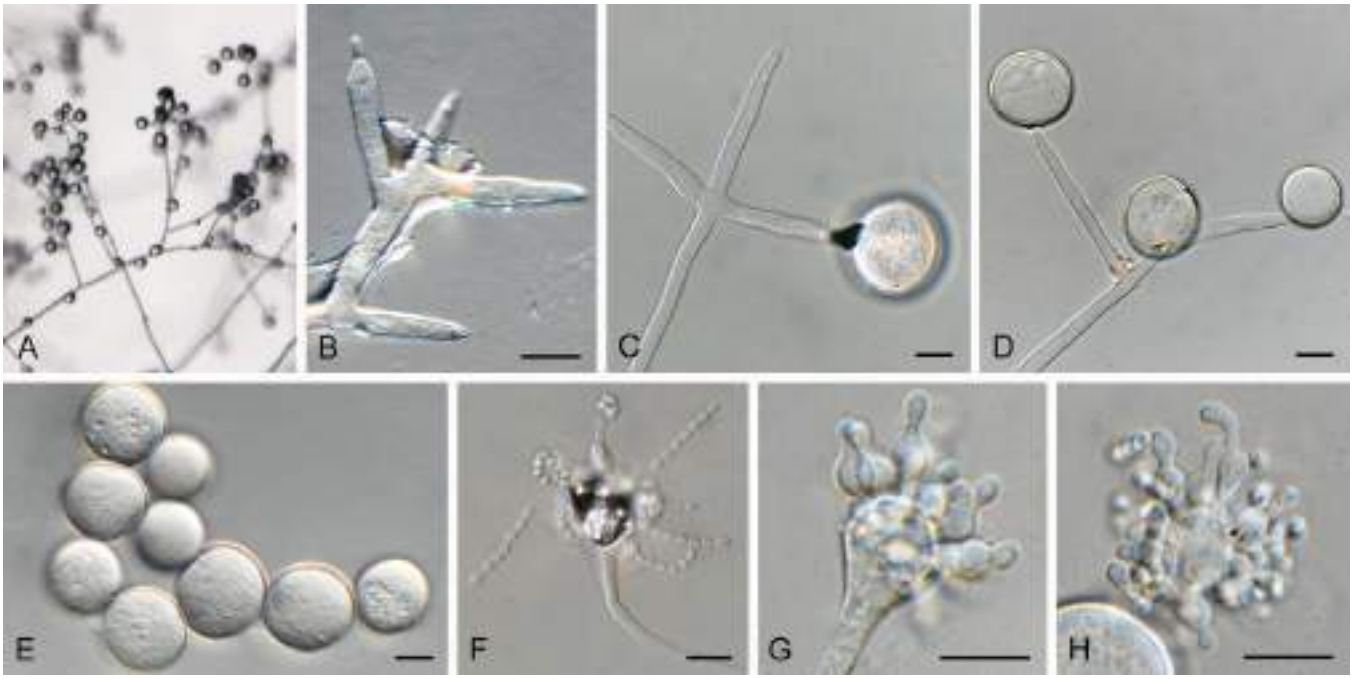

Fig. 29. *Harzia cupressicola* (CPC 47852). **A.** Colony on SNA. **B–D.** Conidiogenous cells and macroconidia. **E.** Macroconidia. **F–H.** Swollen vescicles with chains of microconidia. Scale bars = 10 µm.

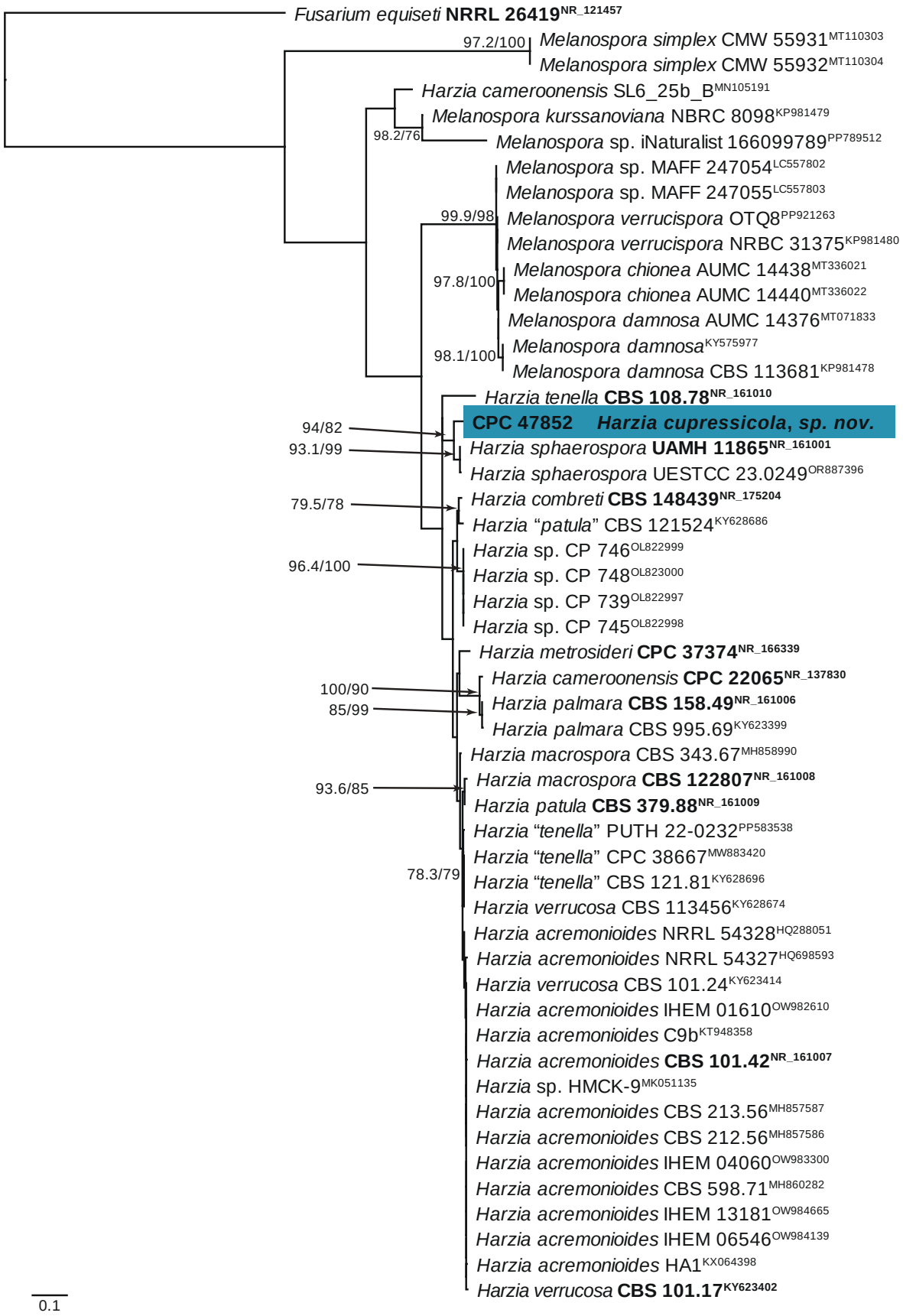

Fig. 30. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Harzia* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Fusarium equiseti* (NRRL 26419; GenBank NR_121457) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 51 strains including the outgroup; 667 characters including alignment gaps analysed: 334 distinct patterns, 242 parsimony-informative, 89 singleton sites, 336 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2+F+I+R2. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

µm, occurring in unbranched chains. *Macroconidiophores* terminal and intercalary on hyphae, multiseptate, branched or not, subcylindrical, hyaline, smooth, up to 600 µm tall, 4–5 µm wide. *Macroconidiogenous cells* hyaline, smooth, terminal and intercalary, subcylindrical with apical taper, 35–45 × 4–5 µm, with terminal separating cell. *Macroconidia* solitary, globose, guttulate, pale brown, smooth- and thick-walled, (22–)24–25(–27) µm diam.

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

Typus: **Netherlands**, Gelderland Province, Wageningen, on needles of *Cupressus* sp., (*Cupressaceae*), 12 Feb. 2024, *R. Smits*, HPC 4372 (**holotype** CBS H-25705, culture ex-type CPC 47852 = CBS 153456). GenBank sequences ITS: PZ221304; LSU: PZ221348.

Notes: *Harzia cupressicola* clusters (Fig. 30) sister to *Harzia sphaerospora* [macroconidia (18–)19–23(–25) × (15–)18–22(–25) µm, microconidia 2–4 × 1.5–3 µm; Li *et al.* 2016], although it has slightly larger macroconidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Harzia sphaerospora* [strain UAMH 11865, GenBank NR_161001.1; Identities = 560/584 (96 %), 12 gaps (2 %)], *Olpitrichum patulum* [strain CBS 121524, GenBank KY628686.1; Identities = 592/635 (93 %), 21 gaps (3 %)], and *Harzia combreti* [strain CBS 148439, GenBank NR_175204.1; Identities = 591/634 (93 %), 21 gaps (3 %)]. Closest hits using the **LSU** sequence are *Harzia sphaerospora* [strain ZGS54_1, GenBank OR887107.1; Identities = 849/853 (99 %), no gaps], *Harzia macrospora* [strain CBS 343.67, GenBank MH870687.1; Identities = 876/881 (99 %), no gaps], and *Harzia tenella* [strain PUTH 22-0232, GenBank PP583560.1; Identities = 876/881 (99 %), no gaps].

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

Heterotruncatella watsoniae (Verwoerd & Dippenaar) Crous, ***comb. nov.*** MB 863254. Fig. 31.

Basionym: *Pestalotia watsoniae* Verwoerd & Dippenaar, *S. African J. Sci.* **27**: 327. 1930.

Conidiomata stromatic, pycnidial to acervular, semi-immersed to erumpent, black, up to 350 µm diam. *Conidiophores* lining the cavity, hyaline, smooth, septate, branched, up to 40 µm tall, 3–4 µm wide. *Conidiogenous cells* integrated, subcylindrical, smooth, hyaline, terminal and intercalary, proliferating percurrently, 10–20 × 2.5–3 µm. *Conidia* fusoid, 3-euseptate, (18–)19–20(–21) × (6–)7(–8) µm, straight to slightly constructed at septa, basal cell obconic with truncate base, median cells doliiform, thick-walled, verruculose, brown; apical cell conic, thin-walled, hyaline, smooth, giving rise to 3–5 apical appendages at different levels on apical cell, unbranched, or branched, tubular, attenuated, flexuous, 15–30 µm long. Basal appendage usually absent, but when present tubular, filiform, unbranched, centric.

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

Typus: **South Africa**, Western Cape Province, Stellenbosch Botanical Garden, on leaves of *Watsonia rosea* var. *alba*, 1926, *L. Verwoerd* (**holotype** PREM 34586); Knysna, on leaf of *Watsonia* sp. (*Iridaceae*), 6 Dec. 2023, *P.W. Crous*, HPC 4332 (**epitype** designated here CBS H-25484, MBT 10032554, culture ex-type CPC 47335 = CBS 152282). GenBank sequences ITS: PZ221305; LSU: PZ221349; *rpb2* (first part): PZ228766; *tef1* (first part): PZ228684.

Notes: *Pestalotia watsoniae* was described as having conidia with two median cells, 12.5–16 × 7.5–9 µm, basal cell 2.5–4 µm long, apical cell conical, appendages 4–5, occasionally 3, sometimes branched (Verwoerd & Dippenaar 1930). The present collection, also on *Watsonia* from the Western Cape

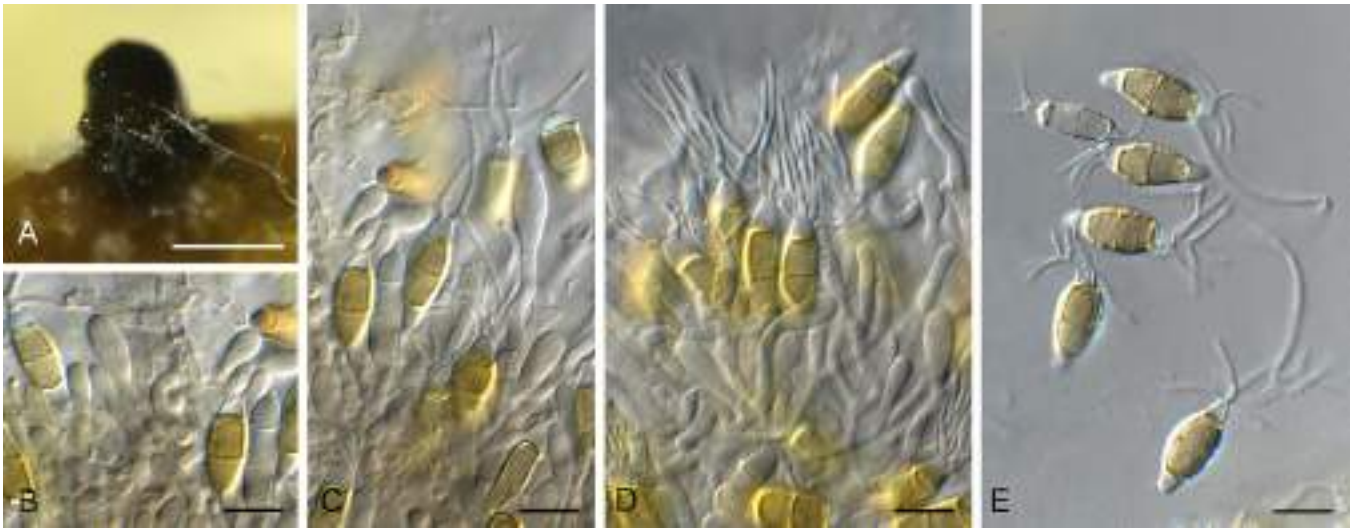

Fig. 31. *Heterotruncatella watsoniae* (CPC 47335). **A.** Conidioma with oozing conidia. **B–D.** Conidiogenous cells. **E.** Conidia. Scale bars: A = 300 µm, all others = 10 µm.

Province, is morphologically similar to the holotype, and represents appropriate material for epitypification.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Heterotruncatella proteicola* [strain CBS 123029, GenBank MH553993.1; Identities = 507/515 (98 %), one gap (0 %)], *Heterotruncatella singularis* [strain CBS 144031, GenBank MH554161.1; Identities = 505/516 (98 %), two gaps (0 %)], *Heterotruncatella breviappendiculata* [strain CPC 17239, GenBank NR_161096.1; Identities = 503/517 (97 %), three gaps (0 %)], and *Heterotruncatella longissima* [strain CBS 144137, GenBank MH554101.1; Identities = 502/515 (97 %), one gap (0 %)]. Closest hits using the **LSU** sequence are *Heterotruncatella restionacearum* [strain CBS 118150, GenBank MH554203.1; Identities = 791/795 (99 %), no gaps], *Heterotruncatella spartii* [strain CBS 143894, GenBank MH554336.1; Identities = 791/795 (99 %), no gaps], and *Heterotruncatella synapheae* [strain CBS 143909, GenBank MH554360.1; Identities = 789/795 (99 %), no gaps]. Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Heterotruncatella proteicola* [strain CBS 144020, GenBank MH554989.1; Identities = 553/566 (98 %), no gaps], *Heterotruncatella spartii* [strain CPC 17945, GenBank MH555014.1; Identities = 221/233 (95 %), no gaps], and *Heterotruncatella restionacearum* [strain CBS 119210, GenBank MH554892.1; Identities = 534/566 (94 %), no gaps]. Closest hits using a blastn search with the ***tef1*** (first part) sequence had highest similarity to *Heterotruncatella proteicola* [strain CBS 123029, GenBank MH554419.1; Identities = 462/523 (88 %), 15 gaps (2 %)], *Heterotruncatella diversa* [strain CBS 143908, GenBank MH554595.1; Identities = 354/402 (88 %), nine gaps (2 %)], and *Heterotruncatella avellanea* [strain CBS 143896, GenBank MH554571.1; Identities = 372/434 (86 %), 12 gaps (2 %)].

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

Hoehneliella Bres. & Sacc., in Strasser, *Verh. K. K. Zool.-Bot. Ges. Wien* **52**: 437. 1902.
Synonyms: *Klebahnopycnis* Kirschst., *Ann. Mycol.* **37**(1/2): 120. 1939.
Paramenisporopsis Matsush., *Matsushima Mycol. Mem*. **10**: 26. [2001] 2003.

Type species: *Hoehneliella perplexa* Bres. & Sacc.

Hoehneliella falsiundulosetulata Crous & Hülsewig, ***sp. nov.*** MB 863255. Fig. 32.

Etymology: Referring to its similarity to *Paramenisporopsis undulosetulata.*

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam. hyphae. Conidiomata separate, erumpent, cupulate, unilocular, setose, dark brown. *Conidiophores* subcylindrical, flexuous, hyaline to subhyaline, smooth, multiseptate, up to 300 µm tall (in vitro). *Setae* associated with conidiophores, subcylindrical, straight to flexuous, thick-walled, dark brown, smooth (base verruculose), apex subacute, sterile or fertile, up to 200 µm tall, and up to 8-septate, 4–5 µm diam. at base. *Conidiogenous cells* integrated, terminal or intercalary on conidiophore branches, hyaline, smooth, subcylindrical, phialidic, 3–20 ×

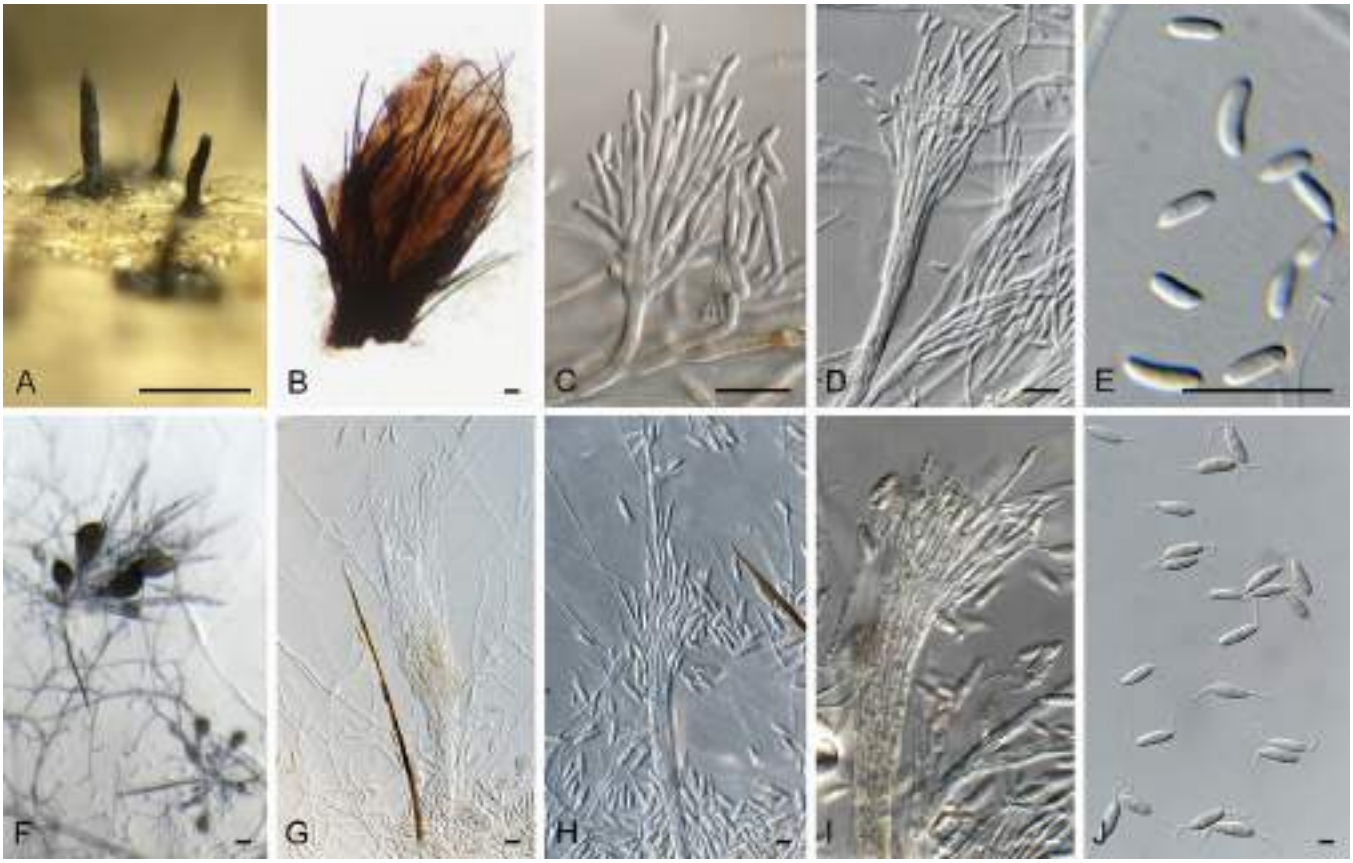

Fig. 32. *Hoehneliella falsiundulosetulata* (CPC 47996). **A, B.** Synnemata on host tissue. **C, D.** Conidiophores and conidiogenous cells giving rise to microconidia. **E.** Microconidia. **F–I.** Conidiophores and setae in culture, with macroconidia. **J.** Macroconidia. Scale bars = 10 µm.

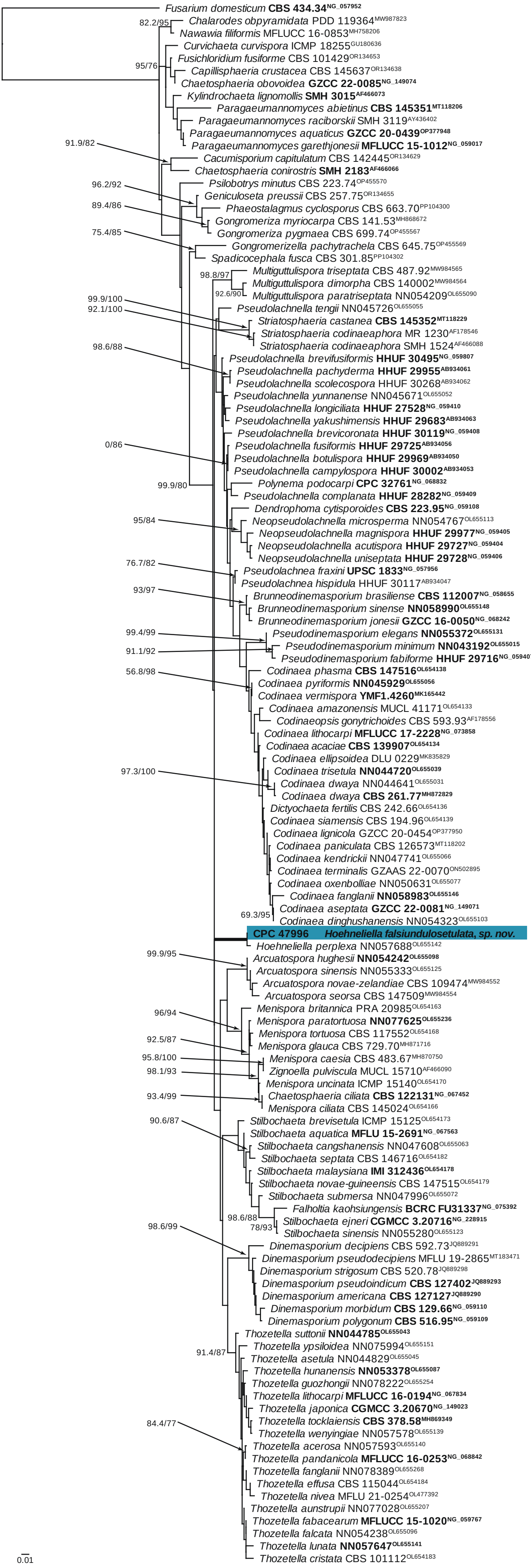

Fig. 33. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Chaetosphaeriaceae* LSU nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Thickened branches resprest a SH-aLRT test value of 100 and a bootstrap support value of 100 %. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Fusarium domesticum* (CBS 434.34; GenBank NG_057952) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 125 strains including the outgroup; 854 characters including alignment gaps analysed: 253 distinct patterns, 170 parsimony-informative, 80 singleton sites, 604 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2+F+I+R4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

2–2.5 µm. *Conidia* dimorphic. *Microconidia* subcylindrical, apex subobtuse, hilum truncate, smooth, pale brown, 5–7 × 1.5–2 µm. *Macroconidia* fusoid to subcylindrical, pale to medium brown, guttulate, smooth, medianly 1-septate, apex subobtuse, hilum truncate, with hair-like appendages, central at apex, and excentric at hilum; appendages straight, irregularly waved, 5–8 µm long (mostly only one per end, but two also observed), (9–)10–12 × 3 µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 10 mm diam. after 2 wk at 25 °C. On MEA surface dirty white, reverse buff; on PDA surface ochreous, with diffuse red pigment, reverse umber; on OA surface olivaceous grey.

Typus: **Germany**, North Rhine-Westphalia, Witten, Recreation area Hohenstein, mycoparasitic on bark of woody host, 27 Feb. 2024, *T. Hülsewig*, HPC 4374, Thorben 1197 (**holotype** CBS H-25714, culture ex-type CPC 47996 = CBS 153529). GenBank sequences ITS: PZ221306; LSU: PZ221350.

Hoehneliella undulosetulata (Matsush.) Crous & Hülsewig, ***comb. nov*.** MB 863504.
Basionym: Paramenisporopsis undulosetulata Matsush*., Matsush. Mycol. Mem*. **10**: 26. 2003. (2001).

Notes: While studying *Paramenisporopsis*, we observed that although in culture conidiophores are aggregated in synnemata with adjacent brown setae (as illustrated by Matsushima 2003), with time (and in vivo) they form cupulate conidiomata, resembling the genus *Hoehneliella* (see Nag Raj 1993). We thus regard these two genera as synonyms, with *Hoehneliella* being the older name. *Hoehneliella perplexa* has macroconidia that are 9–15 × 2.5–3.5 µm (av. 12.2 × 3 µm; Nag Raj 1993), while a Chinese collection produced slightly smaller conidia 7–11 × 2–2.5 µm (Wu & Diao 2022), and conidia of *Klebahnopycnis clematidis* were cited as 8–12 × 2–3 µm (Kirschstein 1939). Further studies incorporating multigene data would therefore be required to resolve the species boundaries in *Hoehneliella.*

Paramenisporopsis is known from a single species, *P. undulosetulosa* (on decaying twig, Japan). The present collection from Germany corresponds well in general morphology with the morphology of the type but has shorter conidiogenous cells (3–20 × 2–2.5 µm vs 16–30 × 2.5–3 µm), wider setae (4–5 µm diam at base vs 2.5–3 µm diam), shorter conidial appendages [5–8 µm long vs 2.5–10(–15) µm long; Matsushima 2003]. The most significant difference is however, that the German collection is dimorphic (on host and in culture), with the microconidia being much smaller, and lacking appendages. The present study finally resolves the phylogeny of the genus, showing it to belong to *Sordariomycetes* (*Sordariomycetidae*; *Chaetosphaeriales*; *Chaetosphaeriaceae*; Fig. 33).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pseudolachnella* sp. GCR-2022a [strain HKAS 122737, GenBank OQ158963.1; Identities = 457/521 (88 %), 28 gaps (5 %)], *Pseudolachnella scolecospora* [strain CC.LJC.S1, GenBank PP407840.1; Identities = 455/521 (87 %), 28 gaps (5 %)], and *Pseudolachnea hispidula* [voucher G.M. 2015-05-30.4, GenBank MN700937.1; Identities = 456/526 (87 %), 27 gaps (5 %)].Closest hits using the **LSU** sequence are *Hoehneliella perplexa* [strain NN057688, GenBank OL655142.1; Identities = 840/843 (99 %), no gaps], *Stilbochaeta brevisetula* [strain ICMP 22548, GenBank OL654174.1; Identities = 850/880 (97 %), two gaps (0 %)], *Pseudolachnella yakushimensis* [voucher HHUF 29996, GenBank AB934064.1; Identities = 819/846 (97 %), four gaps (0 %)], and *Pseudolachnella fusiformis* [voucher HHUF 29725, GenBank AB934056.1; Identities = 817/845 (97 %), 3 gaps (0 %)].

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

Microascus stellatus (Bunce) Houbraken, Verkley, R.P. de Vries & J.Z. Groenew., ***comb. nov.*** MB 863256. Fig. 34.
Basionym: *Humicola stellata* Bunce [as '*stellatus*'], *Trans. Brit. Mycol. Soc.* **44**(3): 372. 1961.
Synonym: *Thermomyces stellatus* (Bunce) Apinis, *Nova Hedwigia* **5**: 75. 1963.

Description: Adapted from Bunce (1961) and Ellis (1971) – *Conidiophores* on long aerial hyphae, solitary, 1–15 µm × 1.5–3 µm, occasionally branched and/or separated from the basal cell by a septum. *Conidia* singly, terminally on conidiophores; subglobose and hyaline when young, stellate and mid brown to greyish brown when mature, smooth, 4–6(–8) projections, 5–10 × 5–9 µm. *Sexual morph* not observed.

Typus: **UK**, England, Hertshire, Harpenden, Rothamsted, from mouldy hay, Aug. 1961, *M. Bunce* (**holotype** IMI 077024, **isotypes** CBS H-7844, CBS H-7845, culture ex-type CBS 272.61 = ATCC 22113 = IMI 077024). GenBank sequences ITS: MH858051; LSU: MH869618; *tef1* (second part): PZ228685; *tub2*: PZ228731.

Additional material examined: **Germany**, from pleural fluid of man, *H.P.R. Seeliger*, CBS H-18807, culture CBS 241.64 = ATCC 22717 = MUCL 8434.

Notes: Six species have been described in *Thermomyces*: *T. dupontii*, *T. ibadanensis*, *T. lanuginosus*, *T. stellatus*, *T. thermophilus* and *T. verrucosus*. Of these, only *T. dupontii* and *T. lanuginosus* are currently accepted within *Thermomyces* (*Trichocomaceae*, *Eurotiales*) (Houbraken *et al.* 2020), with *T. ibadanensis* being a synonym of *T. lanuginosus* and *T. thermophilus* a synonym of *T. dupontii* (Houbraken *et al.* 2014, 2020). *Thermomyces verrucosus* is classified in *Chaetomiaceae* (*Sordariales*) and was combined in *Botryotrichum* (as *B. verrucosum*) (Wang *et al.* 2019b). Previous phylogenetic studies showed that *T. stellatus* belongs to the *Microascaeae* (*Microascales*) (Houbraken *et al.* 2014, Steindorf *et al.* 2024). This study evaluated the phylogenetic relationship and placed the species in *Microascus*, with *M. senegalensis* being its closest phylogenetic relative (Fig. 35). Molecular taxonomic studies of *Microascus* have shown that the genus includes both sexually and asexually reproducing species. *Microascus* species typically produce dark-colored colonies and have annellidic conidiogenous cells, which are borne singly on aerial hyphae or in groups of 2–5 on short, simple, or sparsely branched conidiophores. Conidia are formed in basipetal dry chains (Sandoval-Denis *et al.* 2016). The position of *Thermomyces stellatus* in *Microascus*

was unexpected based on morphology and physiology, as this species is thermotolerant, with an optimum growth temperature of 40 °C (Bunce 1961, Morgenstern *et al. 2012*), whereas other species in the genus typically grow optimally between 20 °C and 30 °C (Jagielski *et al.* 2016, Sandoval-Denis *et al.* 2016). Additionally, *M. stellatus* produces stellate-shaped conidia singly, two features not observed in other *Microascus* species.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Microascus senegalensis* [strain CBS 277.74, GenBank NR_132949.2; Identities = 593/638 (93 %), 22 gaps (3 %)], *Microascus pyramidus* [strain CBS 668.71, GenBank LN850779.1; Identities = 579/634 (91 %), 29 gaps (4 %)], and *Microascus levis* [strain CGMCC 3.19308, GenBank NR_172834.1; Identities = 563/617 (91 %), 24 gaps (3 %)]. Closest hits using the **LSU** sequence are *Microascus cinereus* [strain DUCC15381, GenBank OP604180.1; Identities = 884/902 (98 %), six gaps (0 %)], *Microascus gracilis* [strain CBS 300.61, GenBank MH869627.1; Identities = 884/902 (98 %), six gaps (0 %)], and *Microascus trigonosporus* [strain CBS 494.70, GenBank LN850806.1; Identities = 884/902 (98 %), six gaps (0 %)]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Microascus senegalensis* [strain CBS 594.78, GenBank LN850926.1; Identities = 846/879 (96 %), no gaps], *Microascus appendiculatus* [strain CBS 594.78, GenBank KX924055.1; Identities = 846/879 (96 %), no gaps], and *Microascus alveolaris* [strain CBS 150.64, GenBank KX924052.1; Identities = 843/879 (96 %), no gaps]. Closest hits using the ***tub2*** sequence had highest similarity to *Microascus trigonosporus* [strain CBS 601.67, GenBank LN850880.1; Identities = 330/366 (90 %), 17 gaps (4 %)], *Microascus terreus* [strain CBS 807.73, GenBank KX924373.1; Identities = 330/366 (90 %), 17 gaps (4 %)], and *Microascus gracilis* [strain CBS 126.14, GenBank KX924295.1; Identities = 335/372 (90 %), 16 gaps (4 %)].

Authors: R.P. de Vries, J.A. Houbraken, G.J.M. Verkley, J.Z. Groenewald

Mjuua agapanthi Crous & Sand.-Den., *Fungal Syst. Evol.* **13**: 157. 2024.

Materials examined: **South Africa**, Western Cape Province, Cape Town, Kirstenbosch, on dead flower stalks of *Agapanthus praecox* (*Amaryllidaceae*), Apr. 2023, *P.W. Crous* (**holotype** CBS H-25357, culture ex-type CPC 46094 = CBS 151304) (ex-holotype culture includes *F. agapanthi*, which is essential to allow *M. agapanthi* to grow, and a bacterium); Gauteng Province, Pretoria, Future Africa campus, on stems of *Agapanthus* sp., 7 Apr. 2024, *P.W. Crous*, HPC 4435, cultures CPC 47072, 47073 (GenBank ITS: PX139302, LSU: PX139299, SSU: PX139305).

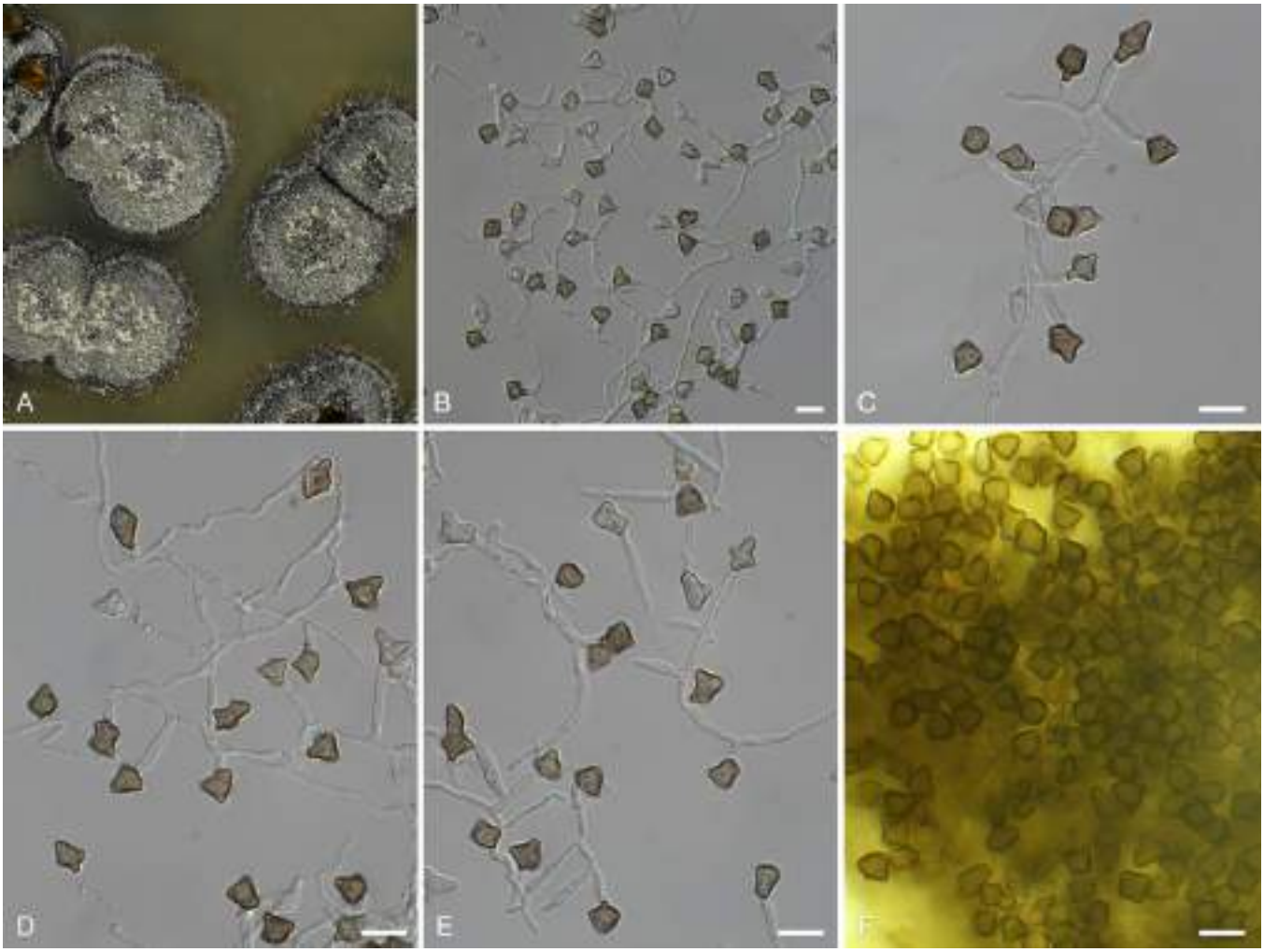

Fig. 34. *Microascus stellatus* (CBS 272.61). **A.** Detail of colony on MEA. **B–E.** Conidiophores and conidia. **F.** Conidia. Scale bar = 10 µm.

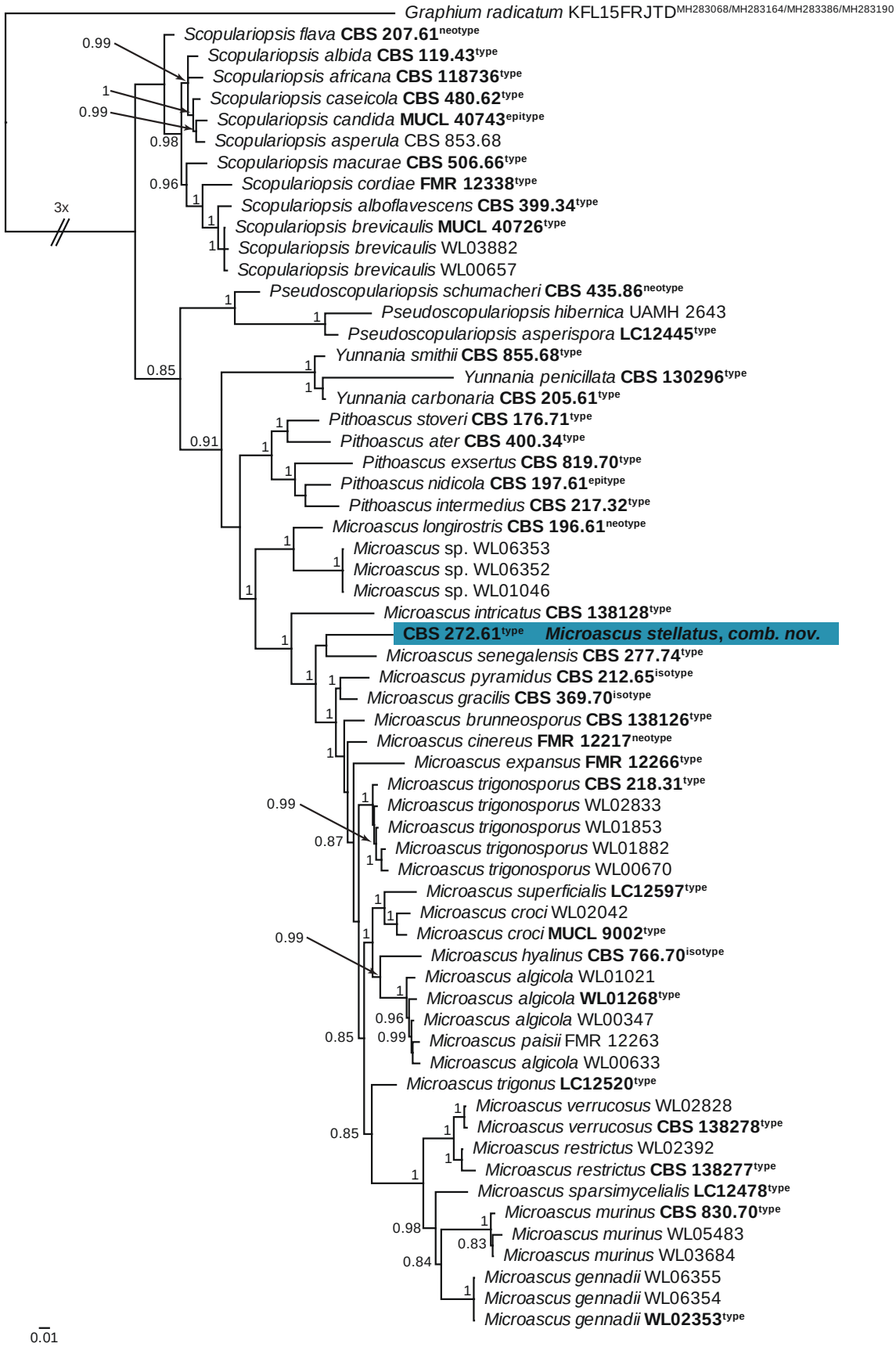

Fig. 35. Consensus phylogram (50 % majority rule) of 9602 trees resulting from a Bayesian analysis of the *Microascaceae* ITS-LSU-*tef1*-*tub2* nucleotide alignment (63 sequences including outgroup; 3054 (ITS: 1–660 ; LSU: 661–1519l; *tef1*: 1520–2434; *tub2*: 2435–3054) aligned positions; 1171 (408 + 176 + 299 + 288) unique site patterns; 320000 generations with trees sampled every 50 generations) using MrBayes v. 3.2.7a (Ronquist *et al.* 2012). Bayesian posterior probabilities (PP) >0.84 are shown at the nodes. Culture collection or specimen voucher numbers are indicated for all species. GenBank numbers and analysis conditions can be found in Wang *et al.* (2024); the alignment is also a reduced dataset based on the alignment of Wang *et al.* (2024). Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Graphium radicatum* (KFL15FRJTD; GenBank MH283068/MH283164/MH283386/MH283190) and the the novelty described here is highlighted with a coloured block and **bold** font. The root branch was shortened to facilitate layout. The scale bar represents the expected changes per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

Notes: In addition to reporting *Mjuua agapanthi* in association with *Fusarium agapanthi* on *Agapanthus* stalks in the Western Cape (Crous *et al.* 2024a), the mycophilic association is herewith also reported from Gauteng Provice in South Africa, showing the association between these two fungi to be well established on *Agapanthus* spp.

Authors: P.W. Crous, J.Z. Groenewald & M. Sandoval-Denis

Mjuua pseudoclavispora Crous, Hülsewig & Sand.-Den., ***sp. nov.*** MB 863257. Figs 36, 37.

Etymology: Named refers to its similarity to *Stilbella clavispora*.

Synnemata erect, arising from submerged hyphae, hyaline, smooth, straight, up to 60 µm diam., 600 µm tall, consisting of numerous tightly aggregated conidiophores. *Conidiogenous cells* terminal on septate, cylindrical, hyaline, smooth conidiophores, with each terminal cell giving rise to 1–3 conidiogenous cells, subcylindrical, hyaline, smooth, phialidic, with distinct collarette, and percurrent proliferation, 20–35 × 2–3 µm. *Conidia* hyaline, smooth, aseptate, globose to clavate, apex obtuse, base truncate with minute marginal frill, solitary, aggregating in mucoid mass, (5–)6–8 × (3.5–)4(–5) µm. *Microconidiophores* arising from submerged hyphae or sides of synnemata, reduced to conidiogenous cells or short conidiophores, hyaline, smooth, subcylindrical, 0–2-septate, giving rise to 1–3 conidiogenous cells, subcylindrical to

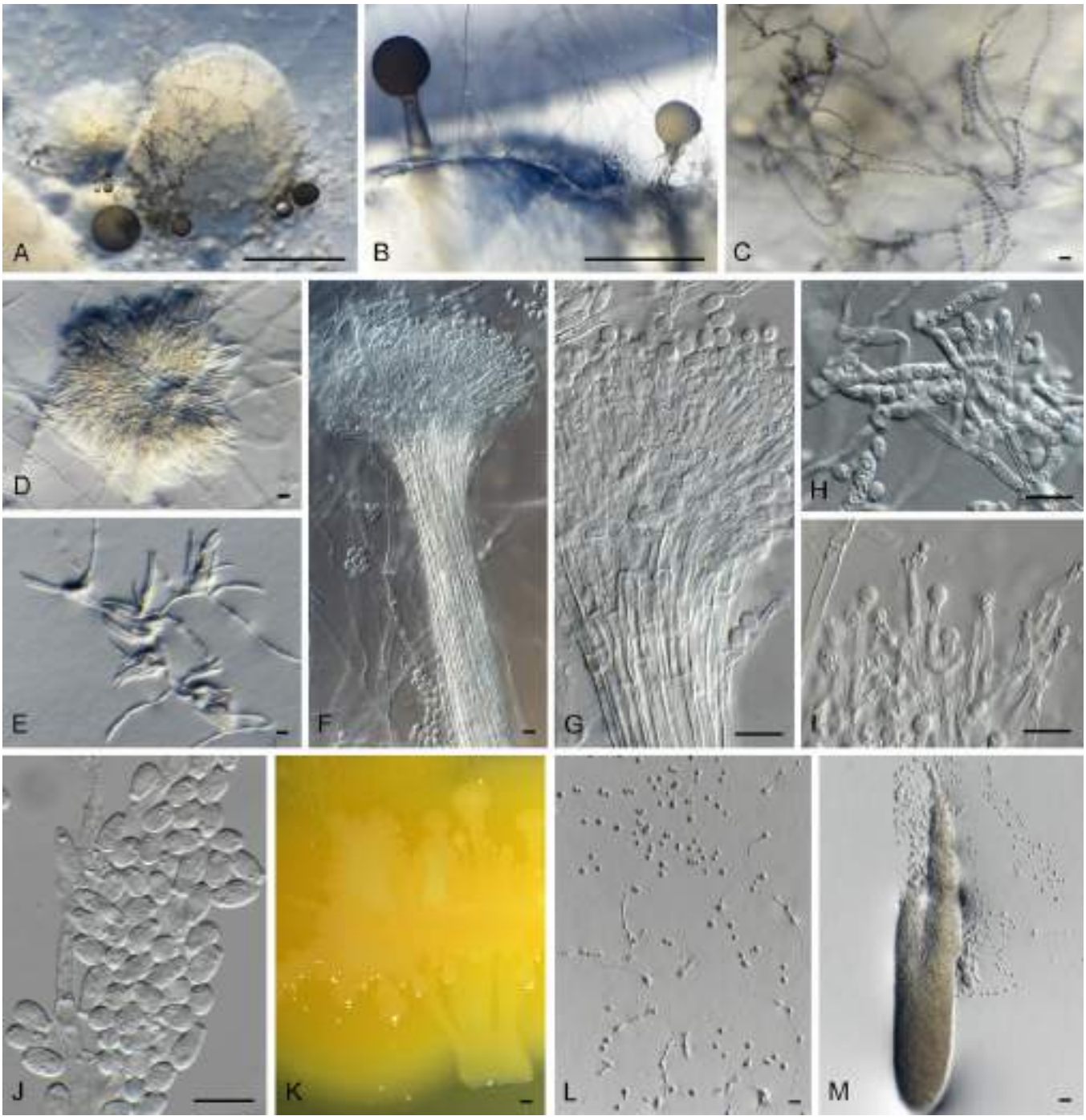

Fig. 36. *Mjuua pseudoclavispora* (CPC 47843). **A, B.** Synnemata and bacteria. **C.** Chains of microconidia. **D, E.** Sporodochial *Fusarium* conidia. **F, G.** Synnemata. **H.** Anastomosis between *Fusarium* and *Mjuua* conidia. **I.** Synnematal conidiogenous cells. **J.** Synnematal conidia. **K.** Bacteria. **L, M.** Synnematal conidia starting to germinate, but not growing without *Fusarium*. Scale bars: A, B = 600 µm, C, D, M = 20 µm, all others = 10 µm.

subulate, hyaline, smooth, 20–30 × 3–4 µm, phialidic, giving rise to long unbranched chains of conidia. *Microconidia* aseptate, hyaline, smooth, fusoid with subtruncate ends, apex slightly more tapered than base, (8–)10–11(–12) × (2.5–)3 µm.

Typus: **Germany**, North Rhine-Westphalia, Witten, Recreation area Hohenstein, Floodplain forest, on *Alnus glutinosa*, dead fruit, 29 Feb. 2024, *T. Hülsewig*, HPC 4418 = Thorben 1200 (**holotype** CBS H-25782 (microscope slide), culture ex-type CPC 47843 = CBS 154063), in association with *Fusarium paeoniae*, which is essential to allow *M. pseudoclavispora* to grow, and a bacterium. GenBank sequences ITS: PX139304; LSU: PX139301; SSU: PX139307. The bacterium isolated from HPC 4418 (NCCB 101036) was identified as a *Rahnella* sp., partial 16S 99.4 % similarity to the type strain of *Rahnella victoriana*.

Additional material examined: **Germany**, North Rhine-Westphalia, Witten, Recreation area Hohenstein, mixture forest (*Alnus/Larix*), on twigs of *Alnus glutinosa* (*Betulaceae*), 4 Mar. 2024, *T. Hülsewig*, HPC 4417 = Thorben 1201, culture CPC 47841 = CBS 154064 (in association with *Cylindrodendrum hubeiense*, which is essential to allow *M. pseudoclavispora* to grow, and a bacterium); ditto, CPC 47842 (GenBank ITS: PX139303, LSU: PX139300, SSU: PX139306); North Rhine-Westphalia, Witten, Recreation area Hohenstein, mixture forest (*Alnus/Larix*), on twigs of *Alnus glutinosa*, 4 Mar. 2024, *T. Hülsewig*, HPC 4417 = Thorben 1201, culture CPC 47874 = CBS 154065 (in association with *Fusarium annulatum*, which is essential to allow *M. pseudoclavispora* to grow, and a bacterium); North Rhine-Westphalia, Witten, Recreation area Hohenstein, Floodplain forest, on *Alnus glutinosa*, dead fruit, 29 Feb. 2024, *T. Hülsewig*, HPC 4418 = Thorben 1200, culture CPC 47844 = CBS 154066 (in association with *Fusarium paeoniae*, which is essential to allow *M. pseudoclavispora* to grow, and a bacterium).

Notes: Seifert (1985) described *Stilbella clavispora* from rotting wood of *Alnus glutinosa* collected in Sweden (Sweden, Gästrikland, Gavle, Lovudden, 24 Aug. 1950, J.A. Nannfeldt no. 11135, UPS). Diagnostic characters noted were the white synnemata, and large, clavate, aseptate conidia. An unusual feature was the occurrence of amorphous crystalline material on the upper half of the synnemata. Synnemata were noted to be 300–500 µm tall, 25–75 µm wide, with conidiogenous cells phialidic, in whorls of three, 21–31 µm long, 1.5–2 µm wide, conidia clavate, 7.5–12 × 3–4.5 µm, with slightly thickened walls. In this study we report on two collections from *Alnus glutinosa* from Germany (on twigs, and on dead fruit), where the fungus was found to be mycophilic in association with *Fusarium* spp., and *Cylindrodendrum hubeiense*, and always in association with different bacteria, some of which are endohyphal, and accumulate at the apex of the synnemata. It is possible that the "amorphous crystalline material" observed by Seifert (1985) are the result of these bacteria. Although we originally assumed the German collections to represent *S. clavispora*, the phialides are narrower, and the conidia longer, suggesting that *S. clavispora* possibly represents a third species of *Mjuua*. Unfortunately, when the "mixed" cultures were plated out after having been peserved at -80 °C for a year, the bacteria could no longer be seen on SNA, and only microconidial chains of *Mjuua pseudoclavispora* developed. We have since recollected *Mjuua pseudoclavispora* on dead fruit of *Alnus glutinosa*, and the fungus seems common in this nische.

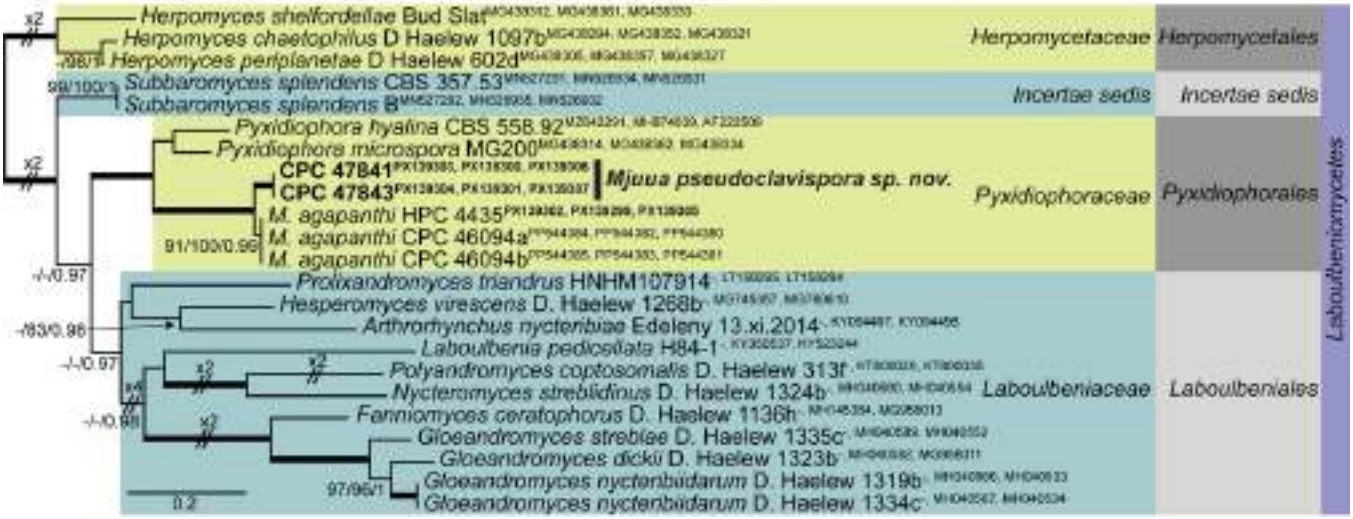

Fig. 37. *Mjuua pseudoclavispora.* Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Laboulbeniomycetes* ITS-LSU-SSU nucleotide alignment. Bootstrap support values (BS) > 74 % from 1000 ultrafast bootstrap replicates are shown at the nodes, followed by BS from 1000 non-parametric replicates on raxmlGUI 2.0 (Stamatakis (2014), Edler *et al.* (2021)), and bayesian posterior probability values > 0.84 obtained using MrBayes v. 3.2.7a (Ronquist *et al.* 2012). Thickened branches indicate full support (BS = 100 and PP = 1. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript ITS, LSU and SSU, respectively) are indicated for all species. The tree was rooted to the *Herpomycetales* (*Herpomyces chaetophilus* D Haelew 1097b, *H. periplanetae* D Haelew 602d and *H. shelfordellae* Bud Slat) and the novelty described here is indicated in bold font. Alignment statistics: 23 strains including the outgroup; 2654 characters including alignment gaps analysed: 922 parsimony-informative, 1414 constant sites. The best-fit models identified in IQ-TREE using the TESTNEW option and MrModelTest (Posada & Crandall 1998) were, respectively: ITS (1727–2654): HKY+F+I+G4, GTR+I+G; LSU (1–936): TIM3+F+I+G4, GTR+I+G; SSU (937–1726): TIM3+F+G4, GTR+I+G. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

Authors: P.W. Crous, T. Hülsewig, M. Sandoval-Denis & M. Figge

Monilinia yunnanensis Sand.-Den. & Crous, ***sp. nov.*** MB 863258.
Synonyms: *Monilia yunnanensis* M.J. Hu & C.X. Luo, *PLoS ONE* **6**: e24990. 2011. Nom. inval., Art. 39.1, Art. 40.1, see Arts 8.4, 40.3 Note 3 and 40.6 (Melbourne).
Monilinia yunnanensis M.J. Hu & C.X. Luo ex Sand.-Den. & Crous, *Stud. Mycol.* **86**: 164. 2017. Nom. inval., Art. 40.1, see Arts 8.4, 40.3 Note 3 and 40.6 (Melbourne).

Description and illustration: Hu *et al.* (2011).

Typus: **China**, Yunnan Province, Anning City, isolated from fruit of *Prunus persica* (*Rosaceae*), 5 Aug. 2010, *M.J. Hu & C.X. Luo* (**holotype** AF2011002 (in CCTCC), preserved as metabolically inactive culture, culture ex-type YKG10-61c), China Center for Type Culture Collection (CCTCC) at Wuhan University, Wuhan City, Hubei Province, China. GenBank sequences *gapdh*: HQ908783; *tub2*: HQ908773.

Notes: Monilia yunnanensis was invalidly described (Hu *et al.* 2011), as it was published without a Latin description (which was still required in 2011). A holotype was also not assigned (Marin-Felix *et al.* 2017), with only a living culture mentioned. The name is validated here.

Authors: M. Sandoval-Denis & P.W. Crous

Niesslia goniomae Crous & M.J. Wingf., ***sp. nov.*** MB 863259. Fig. 38.

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

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam. hyphae. *Conidiophores* reduced to conidiogenous cells, solitary, erect, flexuous, hyaline, smooth, 20–50 × 2–2.5 µm; walls slightly thickened at basal part, apex phialidic, 1 µm diam., collarette inconspicuous. *Conidia* solitary, aggregating in mucoid mass, hyaline, smooth, subcylindrical to fusoid, tapering to subobtuse ends with truncate hilum, 0.5 µm diam., aseptate, guttulate, (5–)8–10(–12) × 1.5–2 µm.

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

Typus: **South Africa**, Western Cape Province, Knysna, Groenkloof Forest, on leaf of *Gonioma kamassi* (*Apocynaceae*), Oct. 2023, *M.J. Wingfield*, HPC 4305 (**holotype** CBS H-25483, culture ex-type CPC 47308 = CBS 152281). GenBank sequences ITS: PZ221307; LSU: PZ221351; *rpb2* (first part): PZ228767; *tef1* (first and second part): PZ228686; *tub2*: PZ228732.

Notes: *Niesslia goniomae* is related (Fig. 39) to *Niesslia stellenboschiana* [on leaves of *Eucalyptus* sp., South Africa, conidia (6–)6.5–7(–8) × (1.5–)2 µm; Crous *et al.* 2019a], but the two species are phylogenetically and morphologically distinct.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 47308 had highest similarity to *Niesslia tenuis* [strain CBS 197.70, GenBank MG826942.1; Identities = 542/561 (97 %), 12 gaps (2 %)], *Cephalosporium ballagii* [strain CBS 134.33, GenBank OQ429516.1; Identities = 497/518 (96 %), 11 gaps (2 %)], and *Niesslia stellenboschiana* [strain CBS 145531, GenBank NR_165230.1; Identities = 525/552 (95 %), eight gaps (1 %)]. The ITS sequences of CPC 47308 and 47296 are 99 % (546/546 nt, including one gap) similar. Closest hits using the **LSU** sequence of CPC 47308 are *Niesslia tenuis* [strain CBS 113275, GenBank OQ055646.1; Identities = 777/778 (99 %), no gaps], *Niesslia barbula* [as *Niesslia exilis*; strain CBS 560.74, GenBank AY489720.1; Identities = 801/803 (99 %), no gaps], and *Cephalosporium ballagii* [strain CBS 134.33, GenBank OQ055427.1; Identities = 776/778 (99 %), no gaps]. The LSU sequences of CPC 47308 and 47296 are identical (799/799 nt). Closest hits using the ***rpb2*** (first part) sequence of CPC 47308 had highest similarity to *Niesslia tenuis* [strain CBS 432.66, GenBank OQ560702.1; Identities = 615/656 (94 %), no gaps], *Cephalosporium ballagii* [strain CBS 134.33, GenBank OQ453903.1; Identities = 690/738 (93 %), no gaps], *Niesslia marinisedimenta* [strain SFC20171120-M03, GenBank PQ355477.1; Identities = 701/757 (93 %), no gaps], and *Nothoeucasphaeria buffelskloofina* [strain CPC 45066, GenBank OR683725.1; Identities = 688/756 (91 %), no gaps].

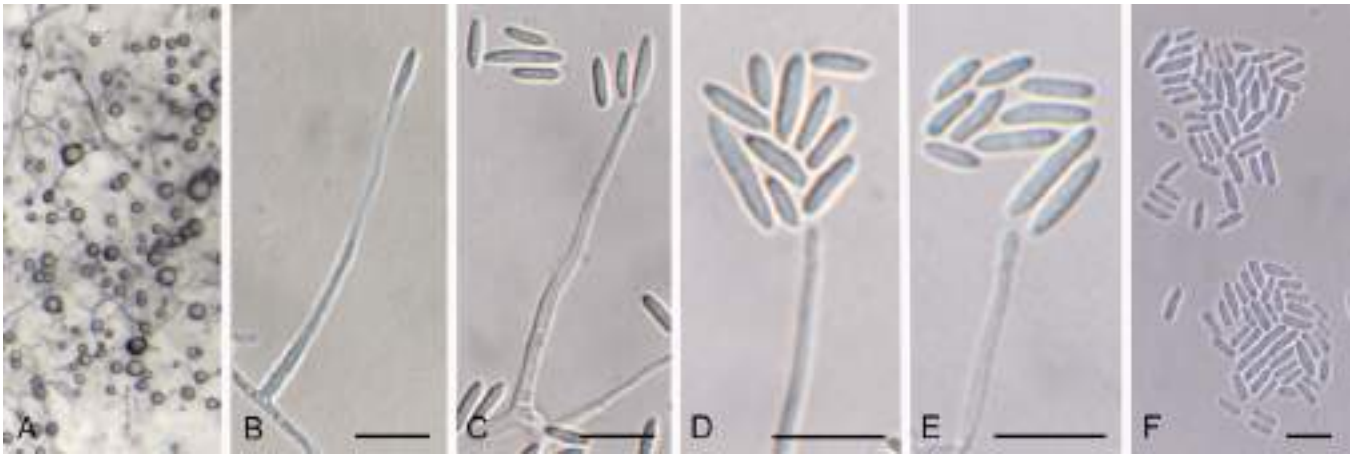

Fig. 38. *Niesslia goniomae* (CPC 47308). **A.** Colony on SNA. **B–E.** Conidiogenous cells giving rise to conidia. **F.** Conidia. Scale bars = 10 µm.

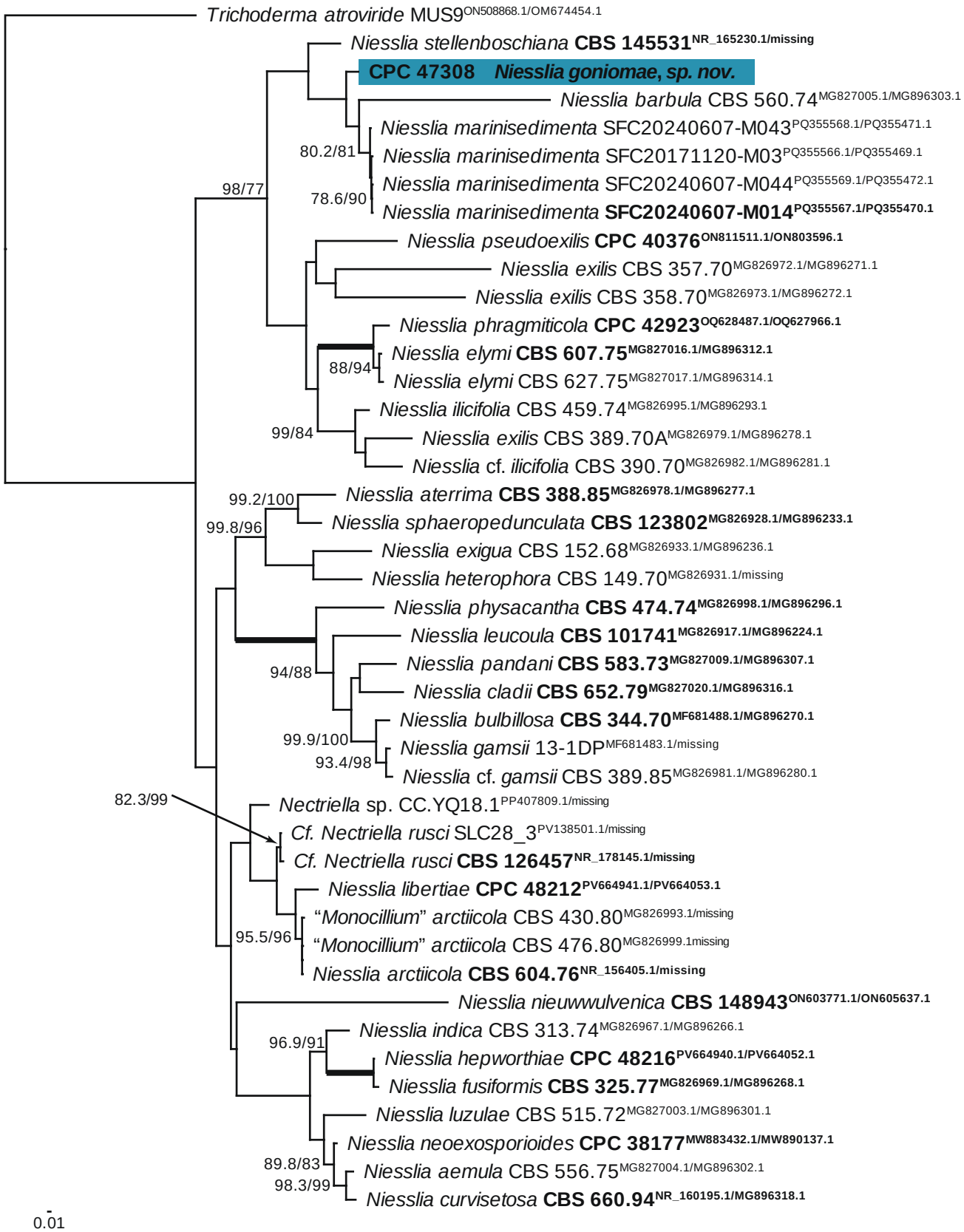

Fig. 39. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Niesslia* ITS-*tub2* nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Thickened branches resprest a SH-aLRT test value of 100 and a bootstrap support value of 100 %. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Trichoderma atroviride* (MUS9; GenBank ON508868.1/OM674454.1) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 43 strains including the outgroup; 1131 characters including alignment gaps analysed: 700 distinct patterns, 453 parsimony-informative, 130 singleton sites, 548 constant sites. The best-fit models identified in IQ-TREE using the TESTNEW option were: ITS (1–651): TIM2+F+I+G4; *tub2* (652–1131): TIM3+F+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

The *rpb2* sequences of CPC 47308 and 47296 are 97 % (738/757 nt) similar. No significant hits were obtained using the ***tef1*** (first part) sequence of CPC 47308 in megablast and blastn searches. The *tef1* (first part) sequences of CPC 47308 and 47296 are 95 % (498/526 nt, including five gaps) similar. Closest hits using the ***tef1*** (second part) sequence of CPC 47308 had highest similarity to *Niesslia tenuis* [strain CBS 202.70, GenBank PV414538.1; Identities = 683/697 (98 %), no gaps], *Niesslia marinisedimenta* [strain SFC20240607-M044, GenBank PQ355492.1; Identities = 872/890 (98 %), no gaps], and *Niesslia barbula* [as *Niesslia exilis*; strain CBS 560.74, GenBank AY489614.1; Identities = 871/890 (98 %), no gaps]. The *tef1* (second part) sequences of CPC 47308 and 47296 are 99 % (881/890 nt) similar. Closest hits using the ***tub2*** sequence of CPC 47308 had highest similarity to *Nothoeucasphaeria buffelskloofina* [strain CPC 45066, GenBank OR683718.1; Identities = 459/562 (82 %), 42 gaps (7 %)], *Niesslia marinisedimenta* [strain SFC20240607-M043, GenBank PQ355471.1; Identities = 340/373 (91 %), 12 gaps (3 %)], *Niesslia pseudoexilis* [strain CBS 148333, GenBank ON803596.1; Identities = 361/429 (84 %), 27 gaps (6 %)], and *Niesslia phragmiticola* [strain CPC 42923, GenBank OQ627966.1; Identities = 348/434 (80 %), 28 gaps (6 %)].

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

Neoceratosperma marasasii (Crous & M.J. Wingf.), Crous & M.J. Wingf., ***comb. nov.*** MB 863260.
Basionym: *Mycosphaerella marasasii* Crous & M.J. Wingf., *Mycol. Res.* **95**(9): 1111. 1991.
Synonyms: *Pseudocercospora marasasii* Crous & M.J. Wingf., *Mycol. Res.* **95**(9): 1111. 1991.
Stenella marasasii (Crous & M.J. Wingf.) B. Sutton & Crous, *Mycol. Res.* **101**(2): 219. 1997.
Zasmidium marasasii (Crous & M.J. Wingf.) Crous & U. Braun, *Schlechtendalia* **20**: 102. 2010.

Description and illustration: Crous & Wingfield (1991).

Typus: **South Africa**, Limpopo Province, Tzaneen, on leaves of *Syzygium cordatum* (*Myrtaceae*), 26 Sep. 1989, *M.J. Wingfield* (**holotype** PREM 50635, culture ex-type CPC 186 = CBS 153700). GenBank sequences ITS: PZ221308; LSU: PZ221352; *cmdA*: PZ228620; *rpb2* (first part): PZ228768; *tub2*: PZ228733.

Notes: *Mycosphaerella marasasii* (asexual morph *Pseudocercospora marasasii*) was described as a foliar pathogen of *Syzygium cordatum* collected in the Limpopo Province of South Africa (Crous & Wingfield 1991). Because conidia and hyphae were later observed to be verruculose, the asexual morph was first placed in *Stenella*, and subsequently in *Zasmidium*. More recently, the ex-type culture of this fungus was revived, which facilitated a phylogenetic comparison (Fig. 40), showing that it belongs in *Neoceratosperma*, which has zasmidium-like asexual morphs (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 *Neoceratosperma yunnanense* [strain CBS 119975, GenBank NR_155461.1; Identities = 480/482 (99 %), no gaps], *Neoceratosperma alsophilae* [strain CPC 24694, GenBank NR_155472.1; Identities = 473/482 (98 %), one gap (0 %)], and *Passalora helicteris-viscidae* [strain P47, GenBank KC677894.1; Identities = 432/440 (98 %), no gaps]. Closest hits using the **LSU** sequence are *Mycosphaerella marasasii* [strain CPC 348, GenBank GU214445.1; Identities = 855/855(100 %), no gaps], *Passalora helicteris-viscidae* [strain P47, GenBank KC677926.1; Identities = 851/853 (99 %), no gaps], and *Xenosonderhenia eucalypti* [strain CBS 138858, GenBank NG_058120.1; Identities = 804/823 (98 %), no gaps]. Closest hits using the ***cmdA*** sequence had highest similarity to *Neoceratosperma yunnanense* [strain CBS 119975, GenBank KF902787.1; Identities = 347/362 (96 %), one gap (0 %)], *Paramycosphaerella marksii* [strain CBS 110963, GenBank KF902583.1; Identities = 270/289 (93 %), no gaps], and *Zasmidium corymbiae* [strain CBS 145047, GenBank MK047524.1; Identities = 274/294 (93 %), no gaps]. Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Neoceratosperma yunnanense* [strain CBS 119975, GenBank MF951534.1; Identities = 800/854 (94 %), no gaps], *Neoceratosperma legnephoricola* [strain CBS 142189, GenBank MF951532.1; Identities = 808/913 (88 %), no gaps], and *Neoceratosperma haldinae* [strain CBS 142190, GenBank MF951533.1; Identities = 770/915 (84 %), no gaps]. Closest hits using the ***tub2*** sequence had highest similarity to *Neoceratosperma yunnanense* [strain CBS 119975, GenBank KF903072.1; Identities = 321/331 (97 %), no gaps], *Pseudocercospora nelumbonicola* [strain RK4111, GenBank LC200982.1; Identities = 312/381 (82 %), 16 gaps (4 %)], and *Phaeophleospora stramenti* [strain CBS 118909, GenBank KF902871.1; Identities = 279/342 (82 %), 14 gaps (4 %)].

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

Nothoniesslia Crous & Hülsewig, ***gen. nov.*** MB 863271.

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

Mycelium consisting of hyaline, smooth, septate, branched hyphae. *Conidiophores* solitary, erect, arising from superficial hyphae, reduced to *conidiogenous cells*, straight to flexuous, subulate, with basal half thick-walled, apical part thin-walled, with minute collarette, not flared. *Conidia* aggregating in mucoid mass, hyaline, smooth, guttulate, subcylindrical to fusoid-ellipsoid, aseptate, ends obtuse. *Ascomata* perithecial, solitary, dark brown, globose, collapsing at maturity, covered in black spines.

Type species: *Nothoniesslia solidaginis* Crous & Hülsewig

Nothoniesslia solidaginis Crous & Hülsewig, ***sp. nov.*** MB 863272. Fig. 41.

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

Mycelium consisting of hyaline, smooth, septate, branched, 2–3 µm diam. hyphae. *Conidiophores* solitary, erect, arising from superficial hyphae, reduced to *conidiogenous cells*, straight to flexuous, subulate, with basal half thick-walled, apical part thin-walled, 1–1.5 µm diam., with minute

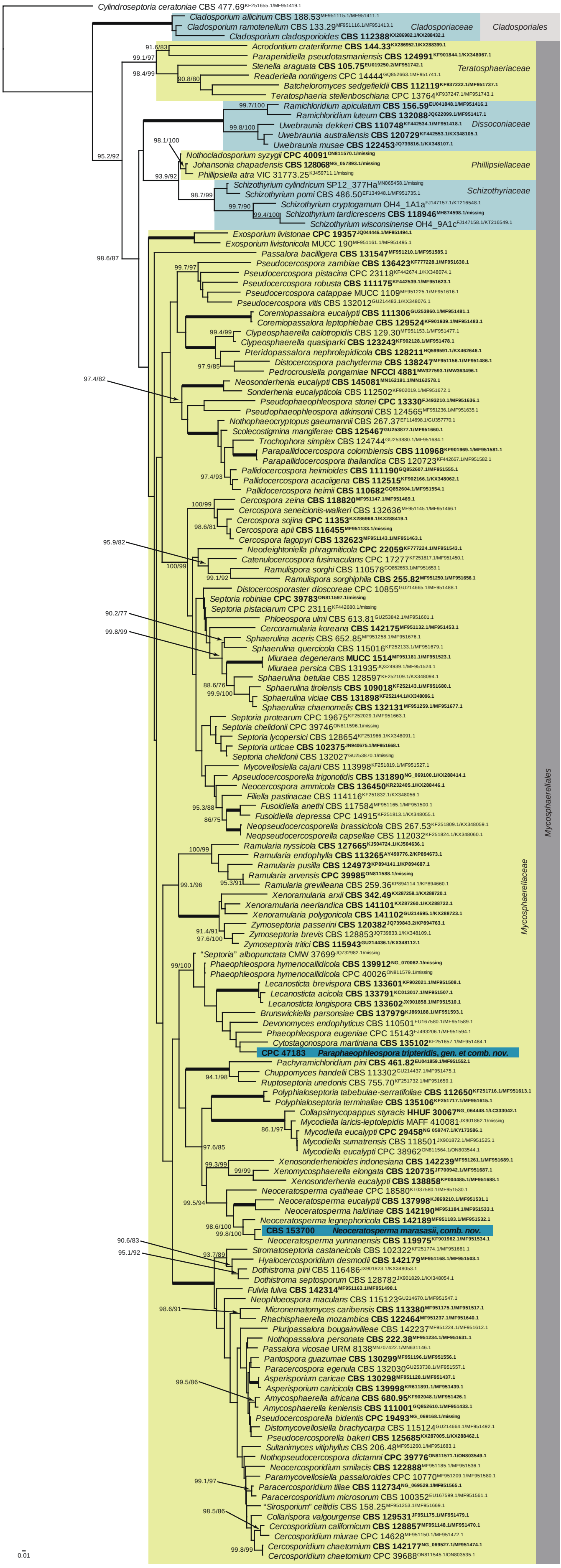

Fig. 40. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Mycosphaerellales* LSU-*rpb2* nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Thickened branches resprest a SH-aLRT test value of 100 and a bootstrap support value of 100 %. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Cylindroseptoria ceratoniae* (CBS 477.69; GenBank KF251655.1/MF951419.1) and the novelties described here are highlighted with a coloured blocks and **bold** font. Families and orders are shown to the right of the tree in coloured blocks. Alignment statistics: 158 strains including the outgroup; 1461 characters including alignment gaps analysed: 778 distinct patterns, 631 parsimony-informative, 81 singleton sites, 748 constant sites. The best-fit models identified in IQ-TREE using the TESTNEW option were: LSU (1–748): GTR+F+I+R4; *rpb2* (749–1461): GTR+F+I+R6. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

collarette, not flared. *Conidia* aggregating in mucoid mass, hyaline, smooth, guttulate, subcylindrical to fusoid-ellipsoid, aseptate, ends obtuse, 3.5–5 × 1.5–2 µm. *Ascomata* perithecial, solitary, dark brown, globose, 100–180 µm diam., collapsing at maturity, covered in black spines, 50–80 × 8–11 µm. Sample overmature.

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

Typus: **Germany**, North Rhine-Westphalia, Witten, on dead stems of *Solidago* sp. (*Asteraceae*), 12 Nov. 2022, *T. Hülsewig*, HPC 4090, herbar.nr. 1057 (**holotype** CBS H-25315, culture ex-type CPC 45496 = CBS 150798). GenBank sequences ITS: PZ221318; LSU: PZ221362; *tef1* (first part): PZ228693; *tub2*: PZ228736.

Notes: In their treatment of *Niesslia*, Gams *et al.* (2019) recognised sexual morphs by their small, superficial, mostly dark brown, shiny and typically spine-covered ascomata. Asexual morphs were formerly accommodated in the genus *Monocillium*, characterised in having phialides that are usually partly or entirely thick-walled, tapering to a conidiiferous neck, or a non-sporulating vesicle. Several older names need to be compared with *Pothoniesslia*, namely *Neoniesslia* (Crous *et al.* 2024b), *Collarina*, *Hyaloseta*, *Monocillium*, *Nitschkia, Nitschkiopsis* and *Pseudoniesslia*, with which it only shares 77–84 % ITS sequence similarity with species deposited in GenBank, thus being phylogenetically quite distinct (Fig. 42).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Niesslia exilis* [strain CBS 389.70A, GenBank MG826979.1; Identities = 487/554 (88 %), 22 gaps (3 %)], *Monocillium nordinii* [strain CBS 147.70, GenBank MG826930.1; Identities = 487/555 (88 %), 20 gaps (3 %)], and *Niesslia rhizomorpharum* [as *Niesslia tenuis*; strain CBS 642.85, GenBank MG827019.1; Identities = 465/535 (87 %), 23 gaps (4 %)]. Closest hits using the **LSU** sequence are *Harposporium illinoisense* [strain CBS 149456, GenBank OQ990063.1; Identities = 803/833 (96 %), three gaps (0 %)], *Polycephalomyces formosus* [strain CGMCC 5.2204, GenBank MN586840.1; Identities = 819/850 (96 %), seven gaps (0 %)], and *Monocillium loricatum* [strain CBS 778.69, GenBank MH871195.1; Identities = 813/844 (96 %), one gap (0 %)]. Closest hits using the ***tef1*** (first part) sequence with a blastn search had distant similarity to *Niesslia phragmiticola* [strain CPC 42923, GenBank OQ627954.1; Identities = 322/415 (78 %), 24 gaps (5 %)], *Brevistachys ossiformis* [strain CBS 112792, GenBank KU846091.1; Identities = 193/225 (86 %), eight gaps (3 %)], and *Synhelminthosporium synnematoferum* [strain CGMCC 3.23574, GenBank ON600599.1; Identities = 190/224 (85 %), four gaps (1 %)]. Closest hits using the ***tub2*** sequence with a blastn search had distant similarity to *Niesslia pseudoexilis* [strain CBS 148333, GenBank ON803596.1; Identities = 419/525 (80 %), 37 gaps (7 %)], *Niesslia phragmiticola* [strain CPC 42923, GenBank OQ627966.1; Identities = 332/400 (83 %), 13 gaps (3 %)], and *Myrtacremonium eucalypti* [strain CBS 142161, GenBank KY979912.1; Identities = 339/40 5(84 %), 22 gaps (5 %)].

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

Paraacanthostigma Crous, ***gen. nov.*** MB 863261.

Etymology: Name reflects its similarity to the genus *Acanthostigma*.

Ascomata superficial, separate to aggregated, globose, 200–250 µm diam., shiny black with dark brown setae, aseptate, thick-walled, with acute apices, 50–100 µm long,

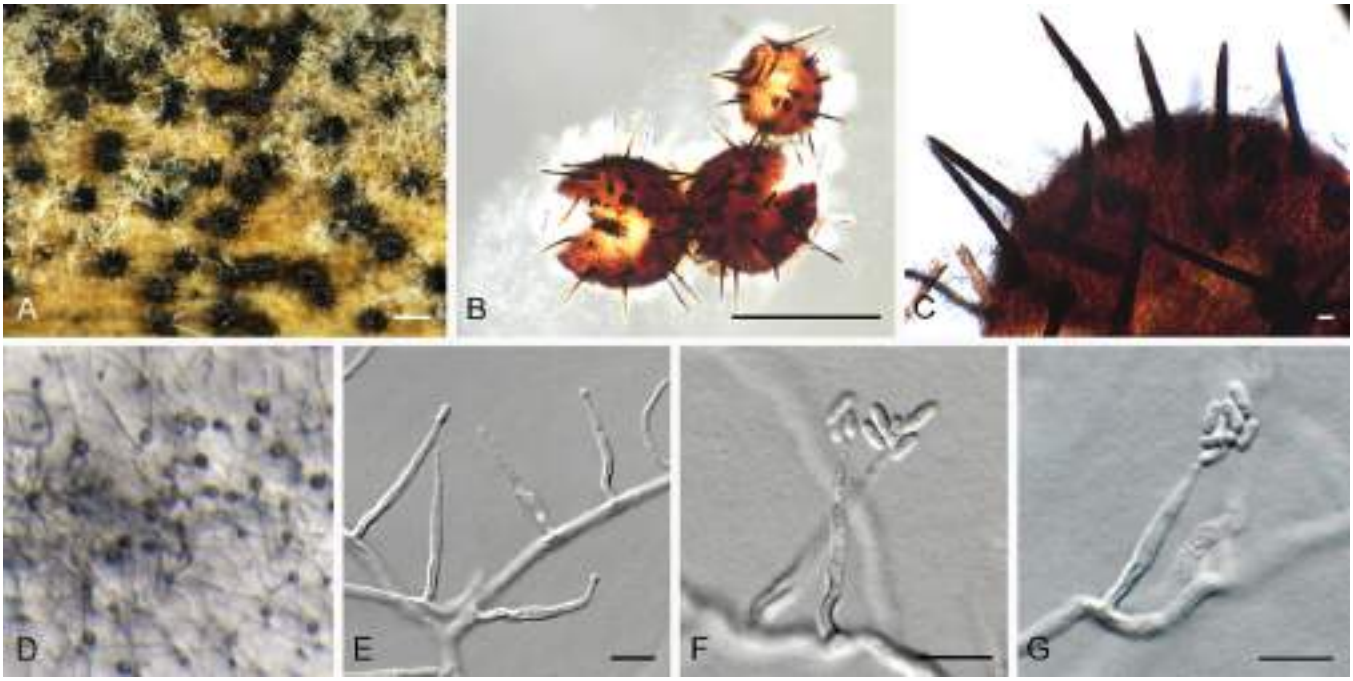

Fig. 41. *Nothoniesslia solidaginis* (CPC 45496). **A–C.** Ascomata on host tissue. **D.** Colony on SNA. **E–G.** Conidiogenous cells giving rise to conidia. Scale bars: A, B = 180 µm, all others = 10 µm.

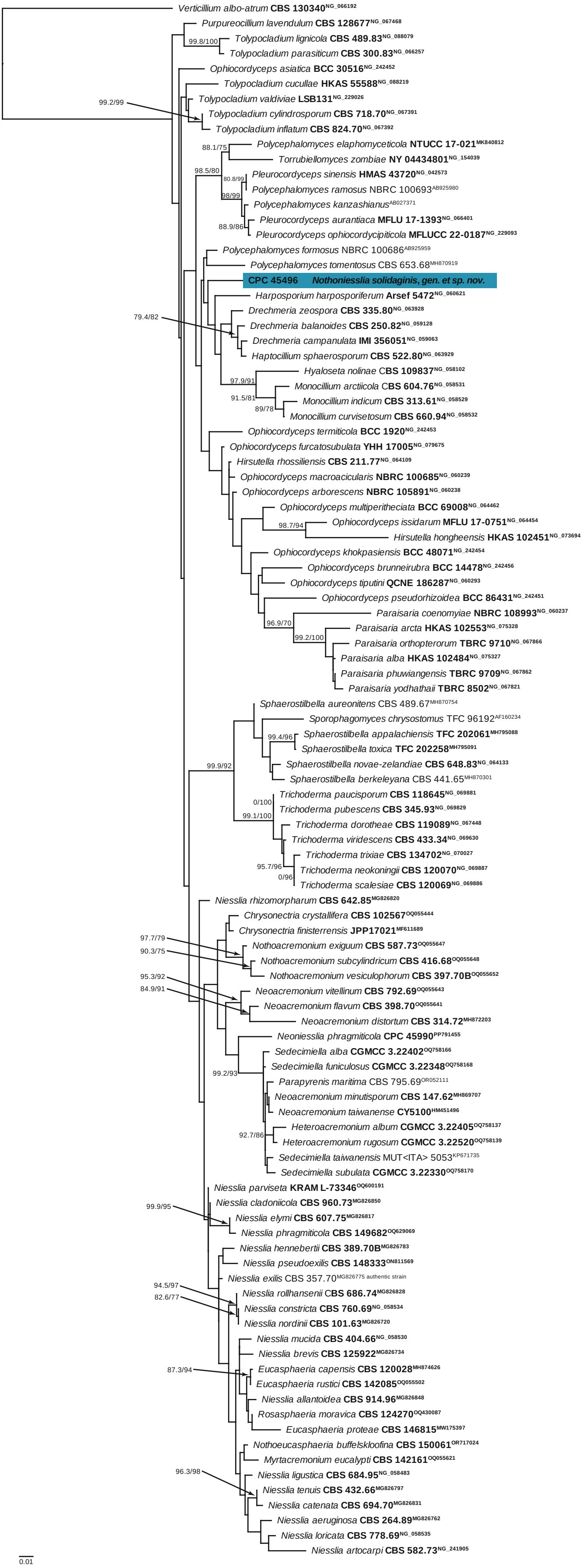

Fig. 42. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Hypocreales* LSU nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Verticillium albo-atrum* (CBS 130340; GenBank NG_066192) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 103 strains including the outgroup; 826 characters including alignment gaps analysed: 316 distinct patterns, 197 parsimony-informative, 82 singleton sites, 547constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TN+F+R4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

5–7 µm diam. at base; ascomatal wall of 3–6 layers of brown textura angularis. *Pseudoparaphyses* hyaline, smooth, anastomosing, 2–3 µm diam. *Asci* bitunicate, cylindrical-clavate, apex obtuse, stipitate, 8-spored, 70–90 × 12–14 µm. *Ascospores* fusoid, straight to slightly curved, tapering towards both ends, hyaline, smooth, guttulate, widest in mid region, 7–9(–10)-septate, constricted at septa, (45–)48–50(–60) × 5(–6) µm. *Conidiophores* solitary or arising from ascomatal wall, unbranched, multiseptate, thick-walled, dark brown, 60–150 × 8–10 µm. *Conidiogenous cells* integrated, 10–20 × 6–7 µm, terminal, brown, smooth, with several sympodial denticles, 1–2 × 2 µm. *Conidia* solitary, subcylindrical, once coiled, pale brown, smooth, guttulate, apex subobtuse, hilum truncate, 5–8 µm diam, whole conidia 12–25 µm long, 3–8-septate, in culture 1–2 times coiled, filaments 3–5 µm diam, multiseptate, 25–35 µm diam.

Type species: *Paraacanthostigma eucalypti* Crous

Paraacanthostigma eucalypti Crous, ***sp. nov.*** MB 863262. Fig. 43.

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

Ascomata superficial, separate to aggregated, globose, 200–250 µm diam., shiny black with dark brown setae, aseptate, thick-walled, with acute apices, 50–100 µm long, 5–7 µm diam. at base; ascomatal wall of 3–6 layers of brown textura angularis. *Pseudoparaphyses* hyaline, smooth, anastomosing, 2–3 µm diam. *Asci* bitunicate, cylindrical-clavate, apex obtuse, stipitate, 8-spored, 70–90 × 12–14 µm. *Ascospores* fusoid, straight to slightly curved, tapering towards both ends, hyaline, smooth, guttulate, widest in mid region, 7–9(–10)-septate, constricted at septa, (45–)48–50(–60) × 5(–6) µm. *Conidiophores* solitary or arising from ascomatal wall, unbranched, multiseptate, thick-walled, dark brown, 60–150 × 8–10 µm *Conidiogenous cells* integrated, 10–20 × 6–7 µm, terminal, brown, smooth, with several sympodial denticles, 1–2 × 2 µm. *Conidia* solitary, subcylindrical, once coiled, pale brown, smooth, guttulate, apex subobtuse, hilum truncate, 5–8 µm diam, whole conidia 12–25 µm long, 3–8-septate, in culture 1–2 times coiled, filaments 3–5 µm diam, multiseptate, 25–35 µm diam.

Fig. 43. *Paraacanthostigma eucalypti* (CPC 48196). **A–E.** Asexual morph in culture, with conidiophores, conidia and setae. **F, G.** Ascomata on host, with setae. **H.** Hyphae on host. **I–L.** Asci and ascospores. Scale bars = 10 µm, except F, G = 250 µm.

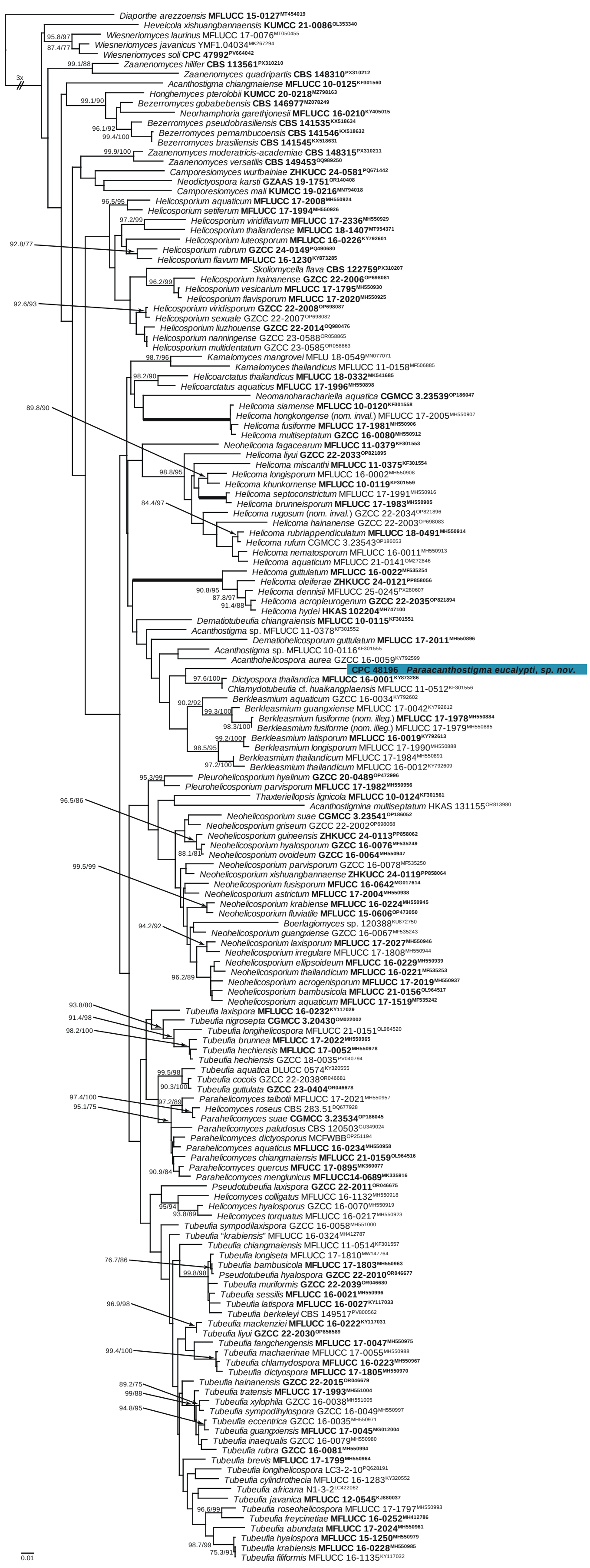

Fig. 44. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Tubeufiales tef1* nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Thickened branches resprest a SH-aLRT test value of 100 and a bootstrap support value of 100 %. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Diaporthe arezzoensis* (MFLUCC 15-0127; GenBank MT454019) and the novelty described here is highlighted with a coloured block and **bold** font. The root branch was shortened to facilitate layout. Alignment statistics: 159 strains including the outgroup; 891 characters including alignment gaps analysed: 426 distinct patterns, 304 parsimony-informative, 54 singleton sites, 533 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM+F+R5. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

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

Typus: **Australia**, Victoria, Rhyll, on underside of bark of *Eucalyptus globulus* (*Myrtaceae*), Jan. 2014, *I. Pascoe*, HPC 4457 (**holotype** CBS H-25732, culture ex-type CPC 48196 = CBS 153527). GenBank sequences ITS: PZ221309; LSU: PZ221353; *rpb2* (first part): PZ228769; *tef1* (second part): PZ228687.

Notes: In their revision of the *Tubeufiales*, Bonmee *et al.* (2014) showed that ascomata with setae have evolved on more than one occasion in the *Tubeufiaceae*, and that it is not a reliable character to define genera in this family. Species accommodated in *Acanthostigma*, for example, show that the genus is polyphyletic (Fig. 44). Because *Acanthostigma* lacks a known asexual morph and is polyphyletic, similar genera with helicosporous asexual morphs have been described such as *Acanthohelicospora* (macronematous conidiophores), and *Neoacanthostigma* (micronematous conidiophores). *Paraacanthostigma* is distinguished from these genera by having micronematous conidiophores, and pigmented, brown setae that develop directly on the agar surface, without the sexual morph.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neohelicosporium hyalosporum* [strain GZCC 16-0076, GenBank MF467923.1; Identities = 815/948 (86 %), 42 gaps (4 %)], *Neohelicosporium guangxiense* [strain GZCC 16-0089, GenBank MF467919.1; Identities = 451/520 (87 %), 24 gaps (4 %)], and *Acanthohelicospora aurea* [strain GZCC 16-0060, GenBank KY321323.1; Identities = 483/562 (86 %), 29 gaps (5 %)]. The ITS sequences of *Acanthostigmina* on GenBank are less than 90 % similar to that of CPC 48196. Closest hits using the **LSU** sequence are *Acanthostigmina scopula* [strain GZCC 23-0114, GenBank PP639388.1; Identities = 820/836 (98 %), three gaps (0 %)], *Acanthostigmina multiseptatum* [strain GZCC 23-0544, GenBank PP639393.1; Identities = 819/836 (98 %), three gaps (0 %)], and *Neohelicosporium aquaticum* [strain GZCC 23-0342, GenBank PP639461.1; Identities = 813/830 (98 %), three gaps (0 %)]. Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Acanthohelicospora aurea* [strain GZCC 16-0060, GenBank MF589911.1; Identities = 726/858 (85 %), no gaps], *Helicoma septoconstrictum* [strain MFLUCC 17-2001, GenBank MH551042.1; Identities = 715/859 (83 %), two gaps (0 %)], and *Neohelicosporium krabiense* [strain MFLUCC 16-0224, GenBank MH551077.1; Identities = 715/860 (83 %), two gaps (0 %)]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Dictyospora thailandica* [strain MFLUCC 18-0641, GenBank MH550897.1; Identities = 778/862 (90 %), no gaps], *Berkleasmium thailandicum* [strain MFLUCC 17-1984, GenBank MH550891.1; Identities = 777/863 (90 %), two gaps (0 %)], and *Chlamydotubeufia* cf. *huaikangplaensis* [strain MFLUCC 11-0512, GenBank KF301556.1; Identities = 783/870 (90 %), no gaps].

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

Paraphaeophleospora Crous, ***gen. nov.*** MB 863263.

Etymology: Name refers to its similarity to *Phaeophleospora*.

Leaf spots amphigenous, subcircular, pale brown with raised dark brown margin. *Conidiomata* amphigenous, brown, immersed, pycnidial, globose; wall of 3–4 layers of dark brown textura angularis. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, subcylindrical to ampulliform, proliferating sympodially. *Conidia* solitary, hyaline, smooth, guttulate and granular, subcylindrical, flexuous, apex subobtuse, base truncate, (1–)3-septate.

Type species: *Paraphaeophleospora tripteridis* (Cejp) Crous

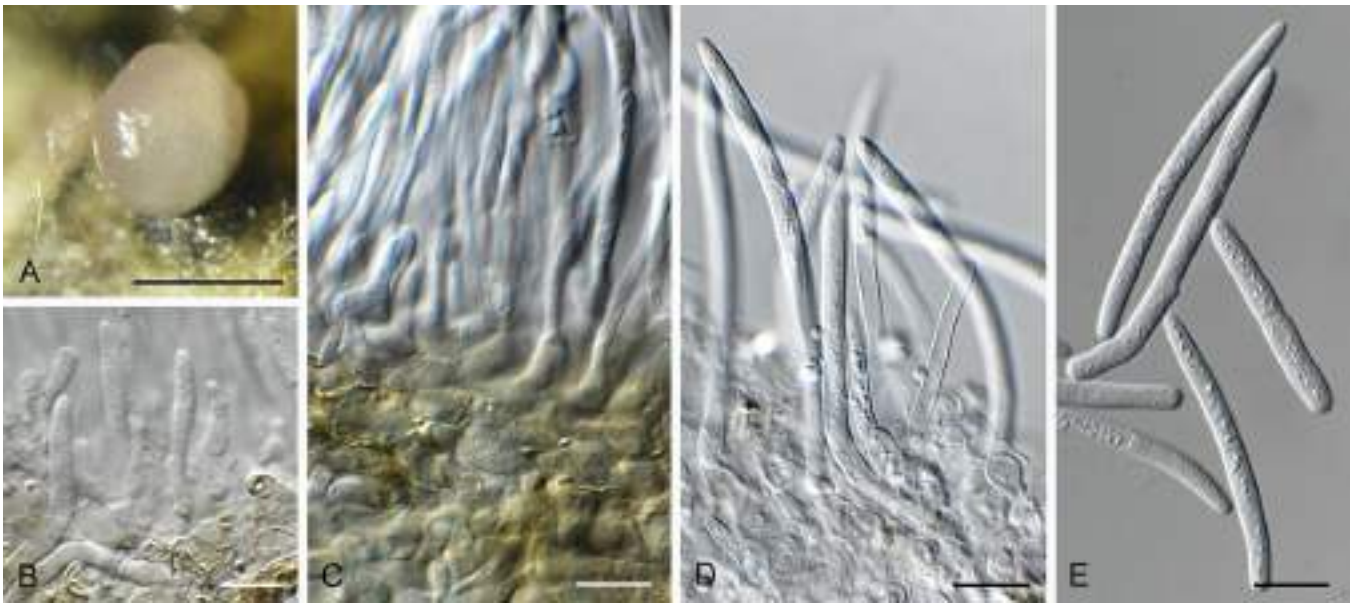

Fig. 45. *Paraphaeophleospora tripteridis* (CPC 47183). **A.** Conidioma in culture. **B–D.** Conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars = 10 µm.

Paraphaeophleospora tripteridis (Cejp) Crous, ***comb. nov.*** MB 863264. Fig. 45.
Basionym: *Septoria tripteridis* Cejp, *Bothalia* **10**: 345. 1971.

Leaf spots amphigenous, subcircular, 2–5 mm diam., pale brown with raised dark brown margin. *Conidiomata* amphigenous, brown, immersed, pycnidial, globose, 150–200 µm diam.; wall of 3–4 layers of dark brown textura angularis. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, subcylindrical to ampulliform, proliferating sympodially, 5–15 × 5–7 µm. *Conidia* solitary, hyaline, smooth, guttulate and granular, subcylindrical, flexuous, apex subobtuse, base truncate, (1–)3-septate, (45–)50–65(–70) × (3–)4(–5) µm.

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

Typus: **South Africa**, Orange Free State Province, Fauresmith Municipality, on *Osteospermum* sp. (=*Tripteris* sp.), Apr. 1939, *L.C.C. Liebenberg* (**holotype** PREM 41849); Western Cape Province, Cederberg, Cederberg City Hall, on leaf of *Osteospermum moniliferum* (*Asteraceae*), Sep. 2023, *M.J. Wingfield*, HPC 4279 (**epitype** designated here CBS H-25482, MBT 10032561, culture ex-epitype CPC 47183 = CBS 152222). GenBank sequences ITS: PZ221310; LSU: PZ221354; *actA*: PZ228595; *rpb2* (first part): PZ228770; *tef1* (first part): PZ228688.

Notes: *Septoria tripteridis* was described by Cejp (1971) from leaves of *Tripteris* sp. collected in the Orange Free State Province of South Africa. Conidia were recorded as 55–70 × 2.5–3(–3.5) µm in vivo, oblong cylindrical, indistinctly septate, and pale green in mass. Although the present collection matches the type, it is not a true *Septoria* (Quaedvlieg *et al.* 2013). Phylogenetically (Fig. 40), it is related to *Phaeophleospora* (pigmented conidia, and pigmented, percurrent proliferating conidiogenous cells), and *Cytostagonospora* (conidia hyaline, sparcely septated, conidiogenous cells hyaline, polyphialides), thus neither being a good fit for the present collection. A new genus is thus introduced to accommodate it.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Septoria albopunctata* [strain SaHbuUSA-6, GenBank MN544298.1; Identities = 469/486 (97 %), three gaps (0 %)], *Phaeophleospora pteridivora* [strain COAD 1182, GenBank NR_155664.1; Identities = 466/485 (96 %), four gaps (0 %)], and *Phaeophleospora eugeniae* [strain CPC 15143, GenBank FJ493188.1; Identities = 444/466 (95 %), eight gaps (1 %)]. Closest hits using the **LSU** sequence are *Phaeophleospora eugeniicola* [strain CPC 2557, GenBank FJ493208.2; Identities = 800/805 (99 %), no gaps], *Phaeophleospora eugeniae* [strain CPC 15143, GenBank FJ493206.1; Identities = 800/805 (99 %), no gaps], and *Septoria albopunctata* [strain CMW 37699, GenBank JQ732982.1; Identities = 799/804 (99 %), no gaps]. Closest hits using the ***actA*** sequence in a blastn search had highest similarity to *Devonomyces endophyticus* [as *Mycosphaerella endophytica*; strain CBS 114662, GenBank JX902107.1; Identities = 494/538 (92 %), six gaps (1 %)], *Phaeophleospora gregaria* [strain CBS 110501, GenBank KF903396.1; Identities = 479/522 (92 %), six gaps (1 %)], and *Phaeophleospora scytalidii* [strain CBS 118493, GenBank KF903493.1; Identities = 477/522 (91 %), six gaps (1 %)].

Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Cytostagonospora martiniana* [strain CBS 135102, GenBank MF951484.1; Identities = 772/902 (86 %), no gaps], *Phaeophleospora eugeniae* [strain CBS 142184, GenBank MF951594.1; Identities = 704/828 (85 %), no gaps], and *Devonomyces endophyticus* [strain CBS 114709, GenBank MF951591.1; Identities = 757/902 (84 %), no gaps]. Closest hits using the ***tef1*** (first part) sequence in a blastn search had highest similarity to *Cytostagonospora martiniana* [strain CBS 135102, GenBank KF253113.1; Identities = 289/342 (85 %), 11 gaps (3 %)], *Devonomyces endophyticus* [as *Mycosphaerella endophytica*; strain CBS 114662, GenBank JX901654.1; Identities = 238/292 (82 %), 15 gaps (5 %)], and *Phaeophleospora gregaria* [strain CBS 110501, GenBank KF903161.1; Identities = 238/292 (82 %), 15 gaps (5 %)].

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

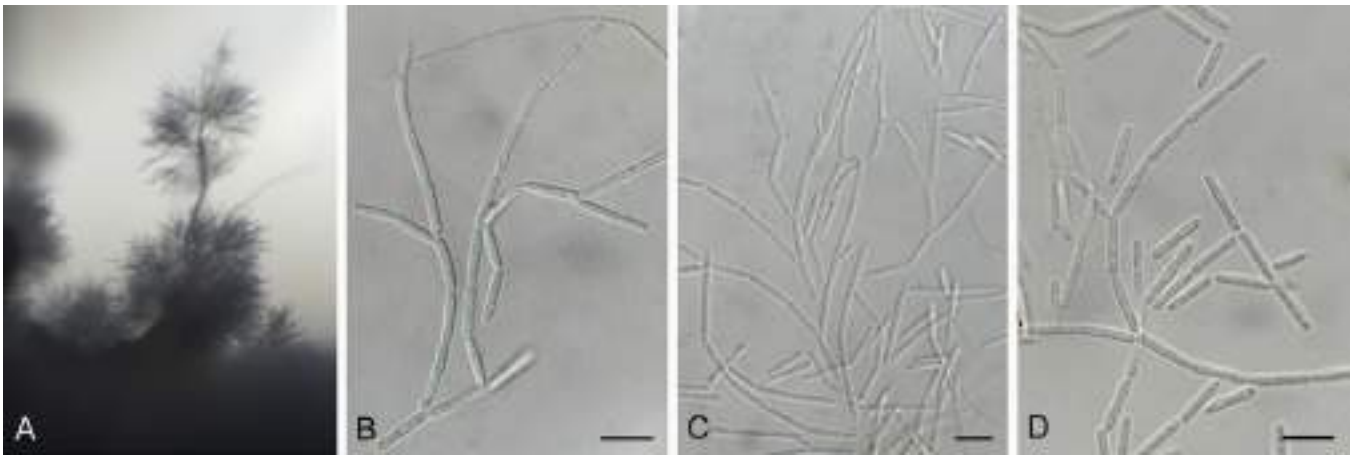

Fig. 46. *Parapolyscytalum minimum* (CPC 48458). **A.** Colony on SNA. **B–D.** Conidiophores and conidiogenous cells giving rise to conidia. Scale bars = 10 µm.

Parapolyscytalum Crous, ***gen. nov.*** MB 863265.

Etymology: Name refers to its similarity to *Polyscytalum* and *Xenopolyscytalum*.

Mycelium of smooth, hyaline, branched, septate hyphae. Dimorphic. *Penicillate conidiophores* erect, with white tufts of catenulate conidia; conidiophores cylindrical, erect, hyaline, smooth, 1–3-septate, base lacking rhizoids. *Conidiogenous cells* apical, integrated, hyaline, smooth, apex swollen, proliferating sympodially, giving rise to 1–2 ramoconidia. *Ramoconidia* hyaline, smooth, aseptate, subcylindrical. *Conidia* subcylindrical, hyaline, smooth, aseptate, in branched chains; hila with slightly thickened loci. *Chalara-like conidiophores* rare, erect, cylindrical, unbranched, pale brown, smooth. *Conidiogenous cells* phialidic, hyaline to pale brown, terminally or intercalary, subconical to lageniform, collarette mostly funnel-shaped, rarely cylindrical. *Conidia*

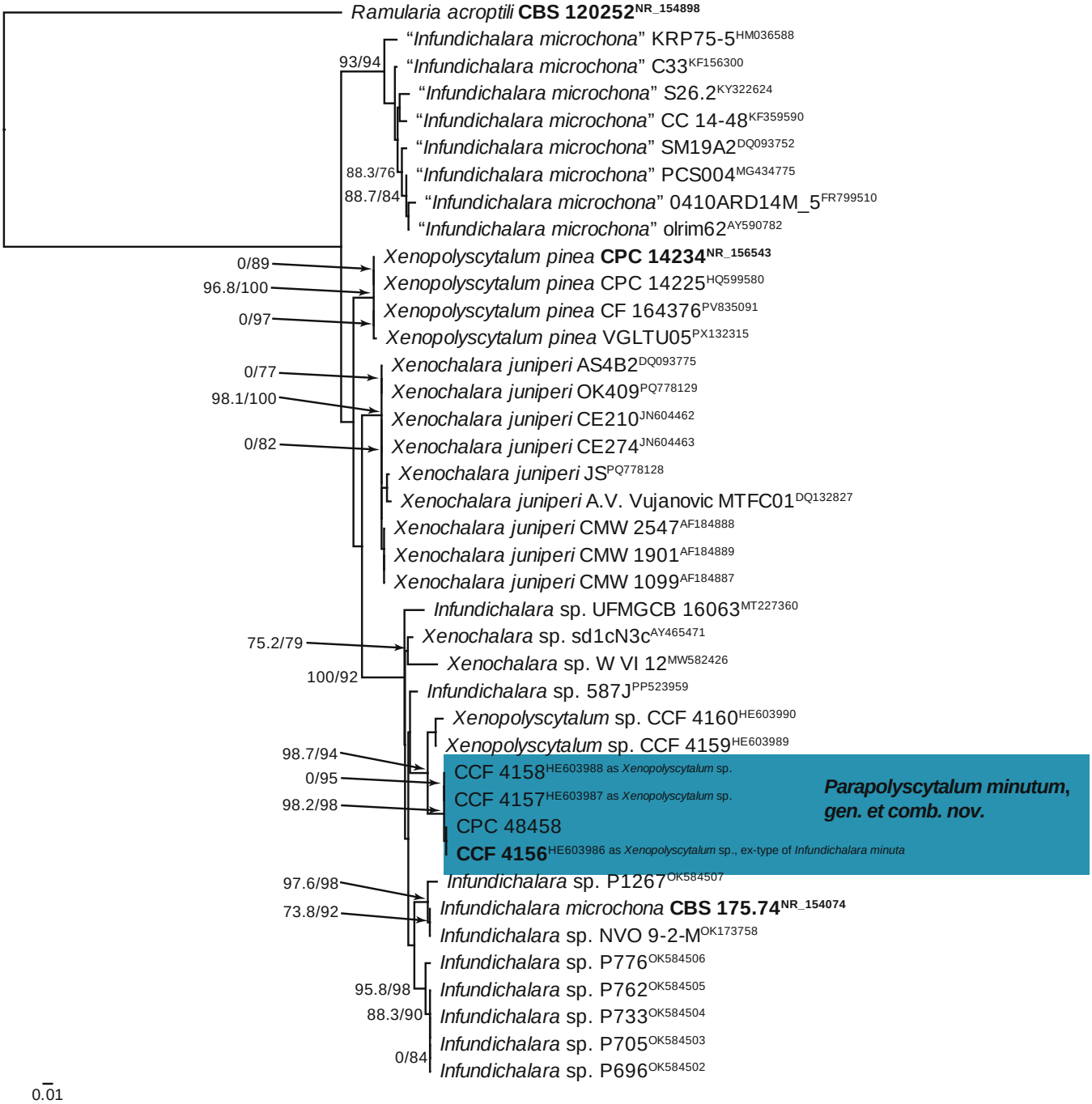

Fig. 47. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the ITS nucleotide alignment including *Parapolyscytalum minutum*. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Ramularia acroptili* (CBS 120252; GenBank NR_154898) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 40 strains including the outgroup; 520 characters including alignment gaps analysed: 202 distinct patterns, 78 parsimony-informative, 120 singleton sites, 322 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TNe+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

wedge-shaped with truncate base, hyaline, smooth, forming either short chains or clusters (adapted from Koukol 2012).

Type species: *Parapolyscytalum minutum* (Koukol) Crous

Parapolyscytalum minutum (Koukol) Crous, ***comb. nov.*** MB 863266. Fig. 46.
Basionym: *Infundichalara minuta* Koukol, *Mycotaxon* **120**: 346. 2012.

Chalara-like morph not observed (CPC 48458): *Mycelium* of smooth, hyaline, branched, septate, 1.5–2 µm diam. hyphae. *Conidiophores* penicillate, erect, with white tufts of catenulate conidia; conidiophores cylindrical, erect, hyaline, smooth, 1–3-septate, up to 35 µm tall, 2–3(–4) µm wide, base lacking rhizoids. *Conidiogenous cells* apical, integrated, hyaline, smooth, 10–20 × 2–3 µm, apex swollen, proliferating sympodially, giving rise to 1–2 ramoconidia. *Ramoconidia* hyaline, smooth, aseptate, subcylindrical, 9–12 × 1.5–2 µm. *Conidia* subcylindrical, hyaline, smooth, aseptate, in branched chains, (7–)9–11 × 1.5–2 µm; hila with slightly thickened loci.

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

Material examined: **Netherlands**, Limburg Province, *Pinus nigra* needles (*Pinaceae*), Feb. 2023, *P. Copini*, culture CPC 48458 = CBS 155312. GenBank sequences ITS: PZ221311; LSU: PZ221355; *tub2*: PZ228734.

Notes: *Parapolyscytalum* is superficially similar to *Xenopolyscatalum*, except that the latter lacks a chalara-like morph (Koukol 2012). Phylogenetically (Fig. 47), *Parapolyscytalum* is distinct from *Xenopolyscatalum,* and clusters basal in a clade identified by Koukol & Seifertová (2026) as *Infundichalara* (based on *I. microchona*) and *Ciliolarina*. Given its distinct morphology and phylogeny, a new genus is introduced here to accommodate it.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Infundichalara minuta* [as *Xenopolyscytalum* sp.; strain CCF 4156, GenBank HE603986.1; Identities = 456/457 (99 %), one gap (0 %)], *Ciliolarina ligniseda* [voucher SBRH847, GenBank MH221525.1; Identities = 473/498 (95 %), one gap (0 %)], and *Infundichalara microchona* [strain CBS 175.74, GenBank NR_154074.1; Identities = 480/506 (95 %), two gaps (0 %)]. Closest hits using the **LSU** sequence are *Constrictochalara constricta* [as *Chalara constricta*; strain CBS 248.76, GenBank FJ176256.1; Identities = 842/853 (99 %), no gaps], *Tricladium caudatum* [strain CCM F-13498, GenBank GQ477318.1; Identities = 839/850 (99 %), no gaps], and *Constrictochalara clavatospora* [strain NN078179, GenBank OP173652.1; Identities = 860/872 (99 %), no gaps]. Closest hits using the ***tub2*** sequence had distant partial similarity to *Neolauriomyces eucalypti* [strain CPC 32623, GenBank MH327890.1; Identities = 257/323 (80 %), 21 gaps (6 %)].

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

Phaeococcomyces mesembryanthemi Crous, ***sp. nov.*** MB 863267. Fig. 48.

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

Mycelium absent. *Conidia* aggregating in mucoid mass, dark brown, thick-walled, verruculose, globose, 5–7 µm diam., budding, giving rise to subhyaline, smooth, thick-walled, guttulate, globose conidia, 4–5 µm diam.

Culture characteristics: Colonies erumpent, reaching 3 mm diam. after 2 wk at 25 °C (lacking aerial mycelium). On MEA, PDA and OA surface and reverse iron grey.

Typus: **South Africa**, Western Cape Province, Cederberg, on *Mesembryanthemum schultzei* (*Aizoaceae*), Aug. 2024, *M.J. Wingfield*, HPC 4552 (**holotype** CBS 153534, preserved as a metabolically inactive culture, culture ex-type CPC 49172B = CBS 153534). GenBank sequences ITS: PZ221312; LSU: PZ221356.

Notes: *Phaeococcomyces mesembryanthemi* was isolated from dead leaves of *Mesembryanthemum schultzei* and is a presumed saprobe. Phylogenetically (Fig. 49), it is related to but distinct from *P. mexicanus*, which is morphologically similar (conidia ellipsoid to globose, hyaline, thick-walled, finely verruculose, 4–6 × 3–6 µm; Moreno-Rico *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 *Phaeococcomyces mexicanus* [strain CBS 137164, GenBank NR_132074.1; Identities = 485/512 (95 %), seven gaps (1 %)], *Phaeococcomyces nigricans*

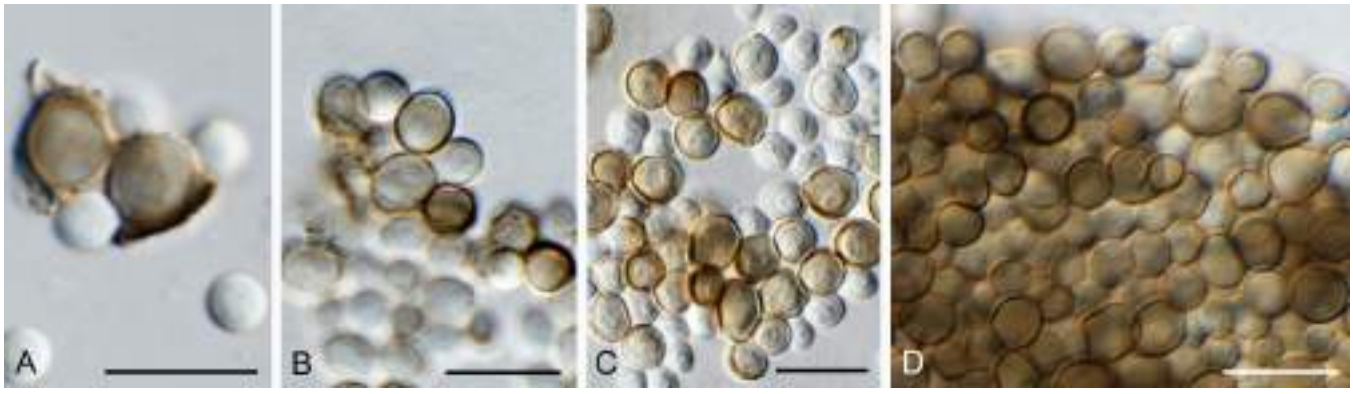

Fig. 48. *Phaeococcomyces mesembryanthemi* (CPC 49172). **A–D.** Conidia budding in culture. Scale bars = 10 µm.

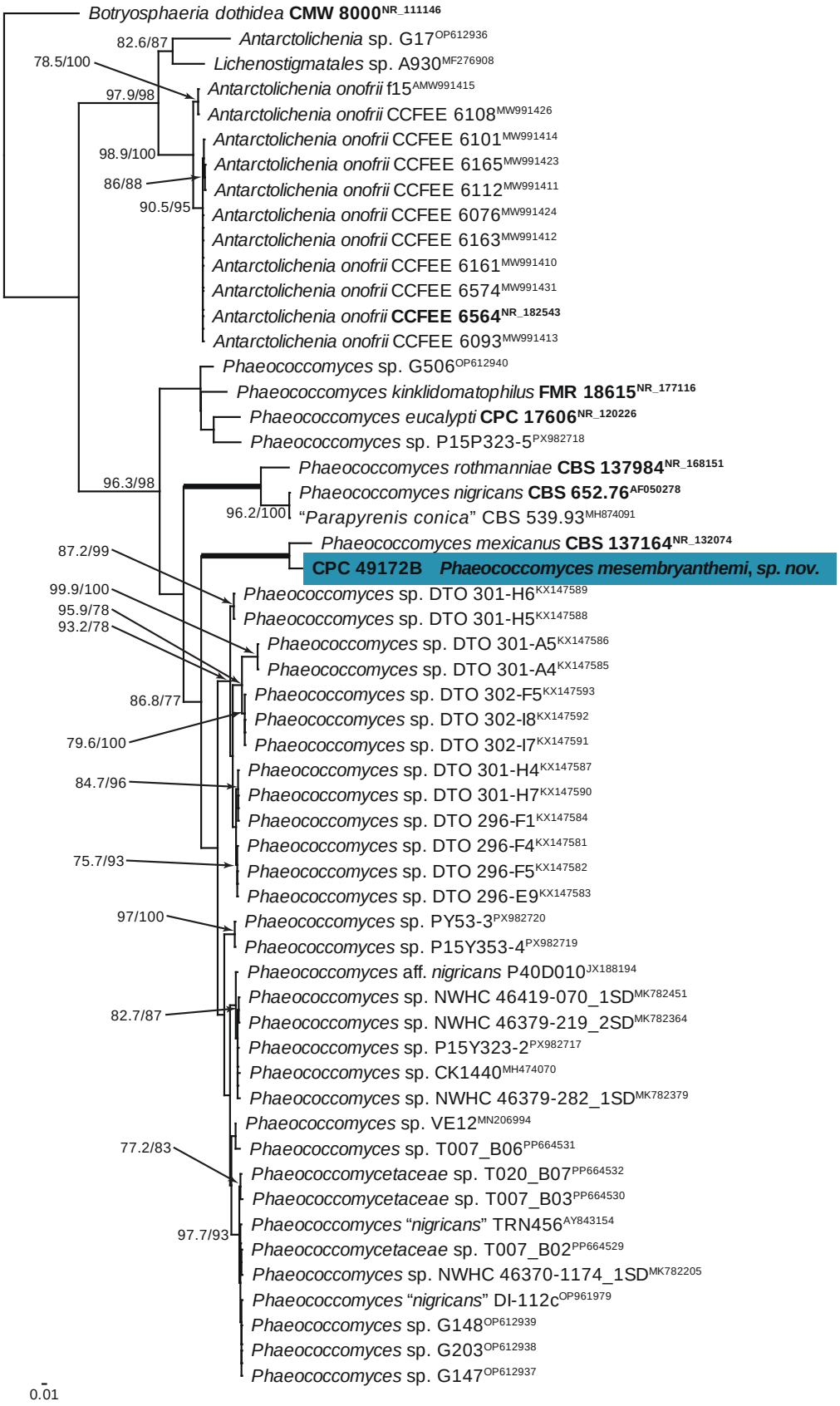

Fig. 49. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Phaeococcomyces* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Thickened branches resprest a SH-aLRT test value of 100 and a bootstrap support value of 100 %. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Botryosphaeria dothidea* (CMW 8000; GenBank NR_111146) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 55 strains including the outgroup; 581 characters including alignment gaps analysed: 315 distinct patterns, 205 parsimony-informative, 50 singleton sites, 326 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+R3. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

[strain DI-112c, GenBank OP961979.1; Identities = 342/397 (86 %), 16 gaps (4 %)], and *Phaeococcomyces rothmanniae* [strain CBS 137984, GenBank NR_168151.1; Identities = 437/536 (82 %), 33 gaps (6 %)]. Closest hits using the **LSU** sequence are *Phaeococcomyces mexicanus* [strain CBS 137164, GenBank NG_058078.1; Identities = 831/840 (99 %), no gaps], *Phaeococcomyces nigricans* [strain CBS 553.90, GenBank MH873917.1; Identities = 802/822 (98 %), four gaps (0 %)], and *Phaeococcomyces rothmanniae* [strain CBS 137984, GenBank NG_068752.1; Identities = 767/799 (96 %), six gaps (0 %)].

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

Phialemonium parasulfureum Crous & Hülsewig, ***sp. nov.*** MB 863268. Fig. 50.

Etymology: Name refers to its similarity to *Cephalotheca sulfurea.*

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2.5 µm diam. hyphae, frequently forming hyphal ropes. *Conidiophores* erect, solitary, frequently reduced to conidiogenous cells directly on hyphae, or with a supporting cell, giving rise to 1–3 phialidic *conidiogenous cells*, hyaline, smooth, ampulliform, phialidic, 8–12 × 3–4 µm, with long cylindrical neck, 4–5 µm long, with minute percurrent proliferations. *Conidia* occurring in long, unbranched chains, limoniform thick-walled, with truncate ends, aseptate, smooth, hyaline, granular, remaining attached to one another until mature, hila 1–1.5 µm diam., conidia (4–)5–6 × (3–)4 µm.

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

Typus: **Germany**, North Rhine-Westphalia, Witten, Recreation area Hohenstein, on algae, 28 Apr. 2024, *T. Hülsewig*, HPC 4466, Thorben 1253 (**holotype** CBS H-25733, culture ex-type CPC 48200 = CBS 153459). GenBank sequences ITS: PZ221313; LSU: PZ221357; *cmdA*: PZ228621; *rpb1*: PZ228646; *rpb2* (first part): PZ228771; *tef1* (second part): PZ228689; *tub2*: PZ228735.

Notes: Species of *Phialemonium* are commonly isolated from environmental sources, which is also true for *P. parasulfurea*, isolated from algae in Germany. *Phialemonium parasulfureum* is phylogentically (Fig. 51) related to but morphologically distinct from *P. inflatum* (conidia 4–5 × 2–3 µm; Perdomo *et al.* 2013) and *P. limoniforme* (conidia 3–4 × 2–2.5 µm; Crous *et al.* 2015).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cephalotheca* sp. [strain IHEM 28260, GenBank OU989303.1; Identities = 517/518 (99 %), no gaps], *Phialemonium inflatum* [strain CBS 259.39, GenBank NR_165996.1; Identities = 502/519 (97 %), two gaps (0 %)], and *Cephalotheca sulfurea* [strain FPFCF64PS-3, GenBank OR405029.1; Identities = 481/498 (97 %), two gaps (0 %)]. Closest hits using the **LSU** sequence are *Cephalotheca sulfurea* [strain AH1001_3A, GenBank KC311468.1; Identities = 832/835 (99 %), no gaps], *Phialemonium inflatum* [strain CBS 250.33, GenBank MH866878.1; Identities = 830/835 (99 %), no gaps], and *Phialemonium guarroi* [strain FMR 17080, GenBank NG_067802.1; Identities = 804/819 (98 %), no gaps]. Closest hits using the ***cmdA*** sequence had highest similarity to *Cephalotheca sulfurea* [strain CBS 135.34, GenBank LT634023.1; Identities = 591/654 (90 %), four gaps (0 %)], *Phialemonium inflatum* [strain CBS 183.65, GenBank LT633977.1; Identities = 588/665 (88 %), 14 gaps (2 %)], and *Sagenomella oligospora* [strain CCF 1552, GenBank LT634018.1; Identities = 511/671 (76 %), 25 gaps (3 %)]. Closest hits using the ***rpb1*** sequence had highest similarity to *Cephalotheca* sp. 1 VH-2016 [strain CCF 1459, GenBank LT634069.1; Identities = 667/702 (95 %), three gaps (0 %)], *Cephalotheca sulfurea* [strain CBS 135.34, GenBank LT634024.1; Identities = 672/711 (95 %), no gaps],

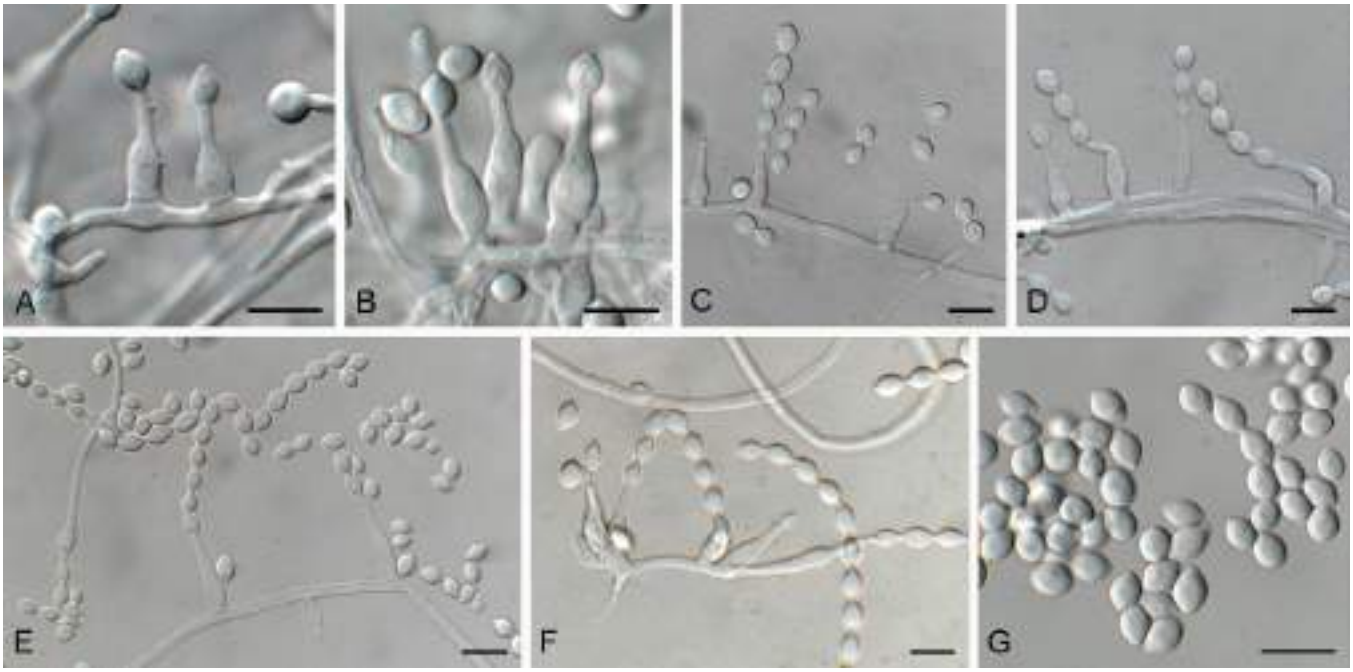

Fig. 50. *Phialemonium parasulfureum* (CPC 48200). **A–F.** Conidiogenous cells giving rise to conidia. **G.** Conidia. Scale bars = 10 µm.

and *Phialemonium inflatum* [strain CCF 4135, GenBank LT633997.1; Identities = 655/697 (94 %), three gaps (0 %)]. Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Phialemonium inflatum* [strain CBS 259.39, GenBank LT633974.1; Identities = 805/857 (94 %), no gaps], *Cephalotheca sulfurea* [strain CBS 135.34, GenBank LT634025.1; Identities = 797/854 (93 %), no gaps], and *Phialemonium globosum* [strain CBS 131713, GenBank LT633969.1; Identities = 691/816 (85 %), eight gaps (0 %)]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Phialemonium inflatum* [strain CCF 4135, GenBank LT633995.1; Identities = 875/909 (96 %), one gap (0 %)], *Cephalotheca sulfurea* [strain CCF 5135, GenBank LT634030.1; Identities = 889/924 (96 %), two gaps (0 %)], and *Phialemonium limoniforme* [strain CBS 139049, GenBank LT634000.1; Identities = 861/924 (93 %), two gaps (0 %)]. Closest hits using the ***tub2*** sequence in a blastn search had highest similarity to *Cephalotheca* sp. [strain

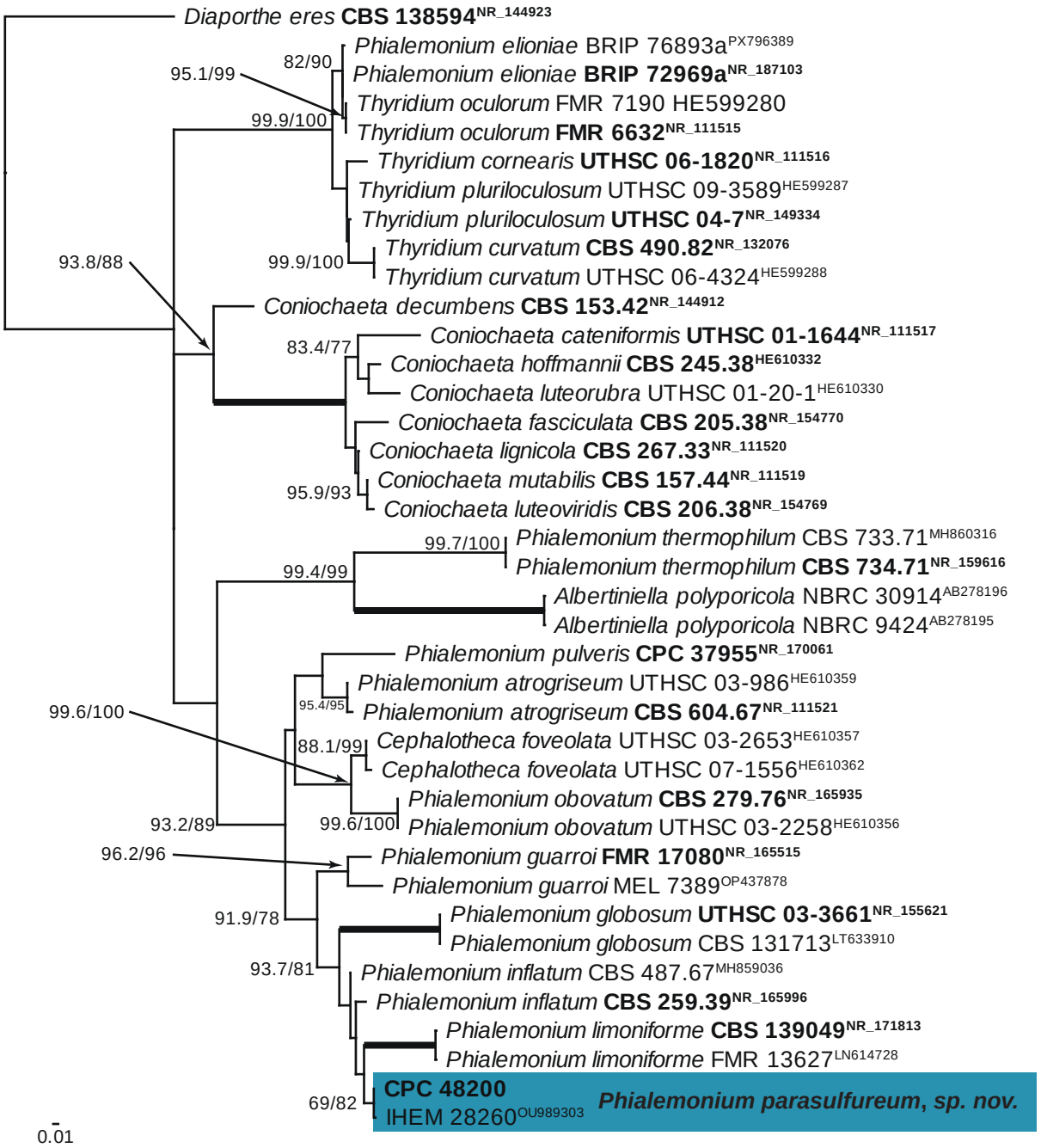

Fig. 51. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Phialemonium* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Thickened branches respresent a SH-aLRT test value of 100 and a bootstrap support value of 100 %. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Diaporthe eres* (CBS 138594; GenBank NR_144923) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 39 strains including the outgroup; 626 characters including alignment gaps analysed: 356 distinct patterns, 289 parsimony-informative, 32 singleton sites, 305 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TNe+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

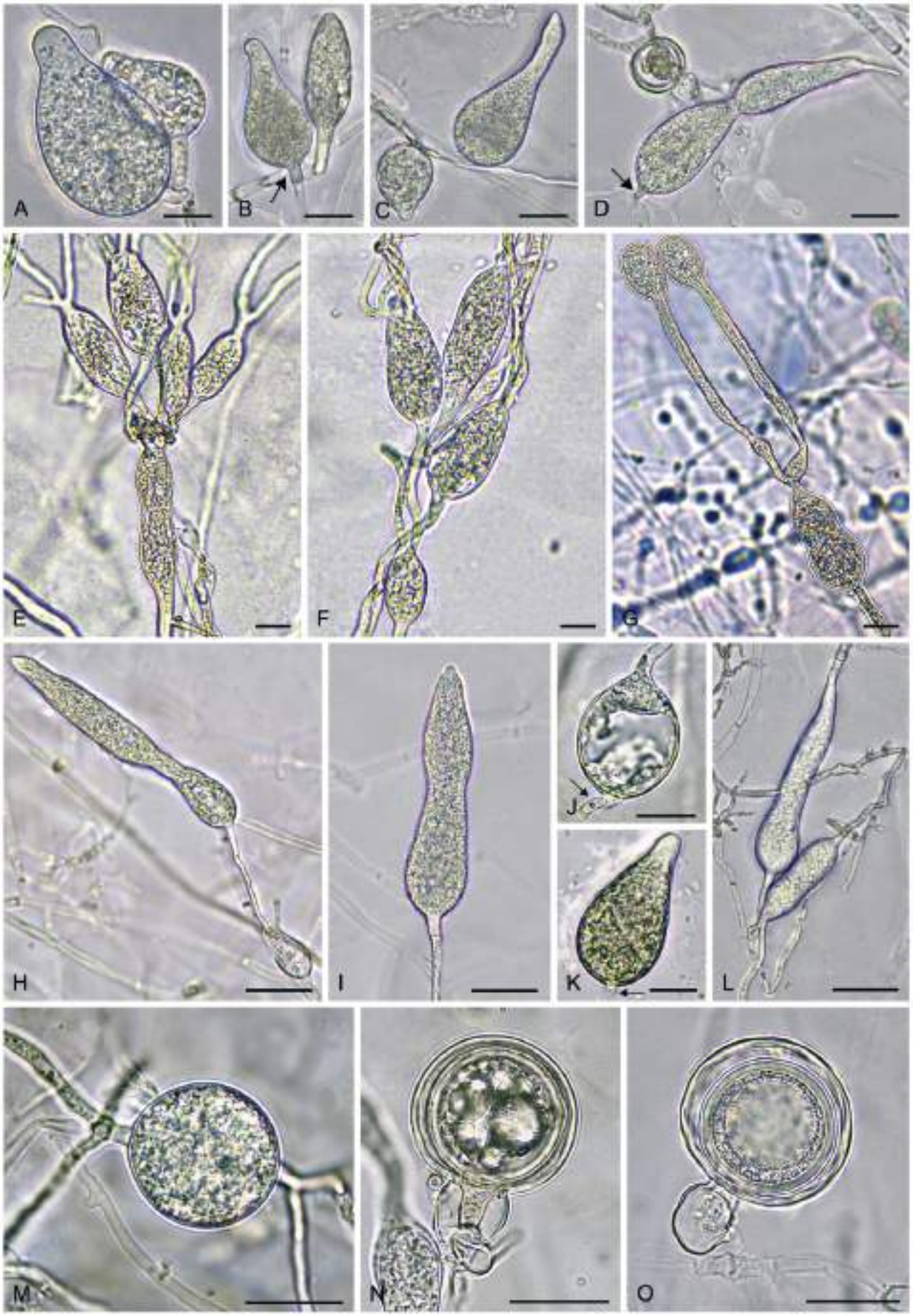

Fig. 52. *Phytophthora caput-medusae.* **A–K.** Sporangia produced in non-sterile soil extract. **A–C.** Mature nonpapillate, obpyriform, fusiform or ovoid sporangia (in B the arrow indicates the pedicel). **D.** Sub-ellipsoid sporangium with pedicel (arrow) germinating through the apex forming a new fusiform sporangium. **E–G.** Sporangia showing direct germination through the apex, developing in chains that tangle with each other along the sporangiophores. **H, I.** Distorted fusiform sporangia. **J.** Ovoid to subglobose detached sporangium with pedicel (arrow). **K.** Obpyriform detached sporangium with pedicel (arrow). **L.** Elongated hyphal swellings. **M.** Terminal chlamydospore. **N.** Oogonium with plerotic aborted oospore and amphigynous antheridium. **O.** Oogonium with slightly aplerotic mature oospore and paragynous antheridium. Scale bars: 25 µm.

IHEM 27904, GenBank OU641334.1; Identities = 411/454 (91 %), eight gaps (1 %)], *Phialemonium inflatum* [strain CCF 4135, GenBank LT633994.1; Identities = 396/442 (90 %), eight gaps (1 %)], and *Cephalotheca sulfurea* [strain CCF 5135, GenBank LT634029.1; Identities = 392/440 (89 %), seven gaps (1 %)].

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

Phytophthora caput-medusae La Spada, Cacciola & Aloi, ***sp. nov.*** MB 856844. Figs 52–54.

Etymology: Named refers to the shape and distinctive spatial arrangement of mature sporangia and hyphal swellings, which resemble the intertwined, snake-like hair of Medusa, the mythical Gorgon of Greek mythology.

Sporangia are abundantly produced on V8A and CA after 4 d of flooding with non-sterile soil extract (Jung *et al.* 1996, Aloi *et al.* 2021). They are occasionally caducous with medium-length pedicels of 5–20 µm (av. 10.0 ± 3.3 µm), ovoid/obovoid, pyriform/obpyriform, ellipsoid, fusiform or allantoid, and nonpapillate (average size 86.4 ± 16.9 ×

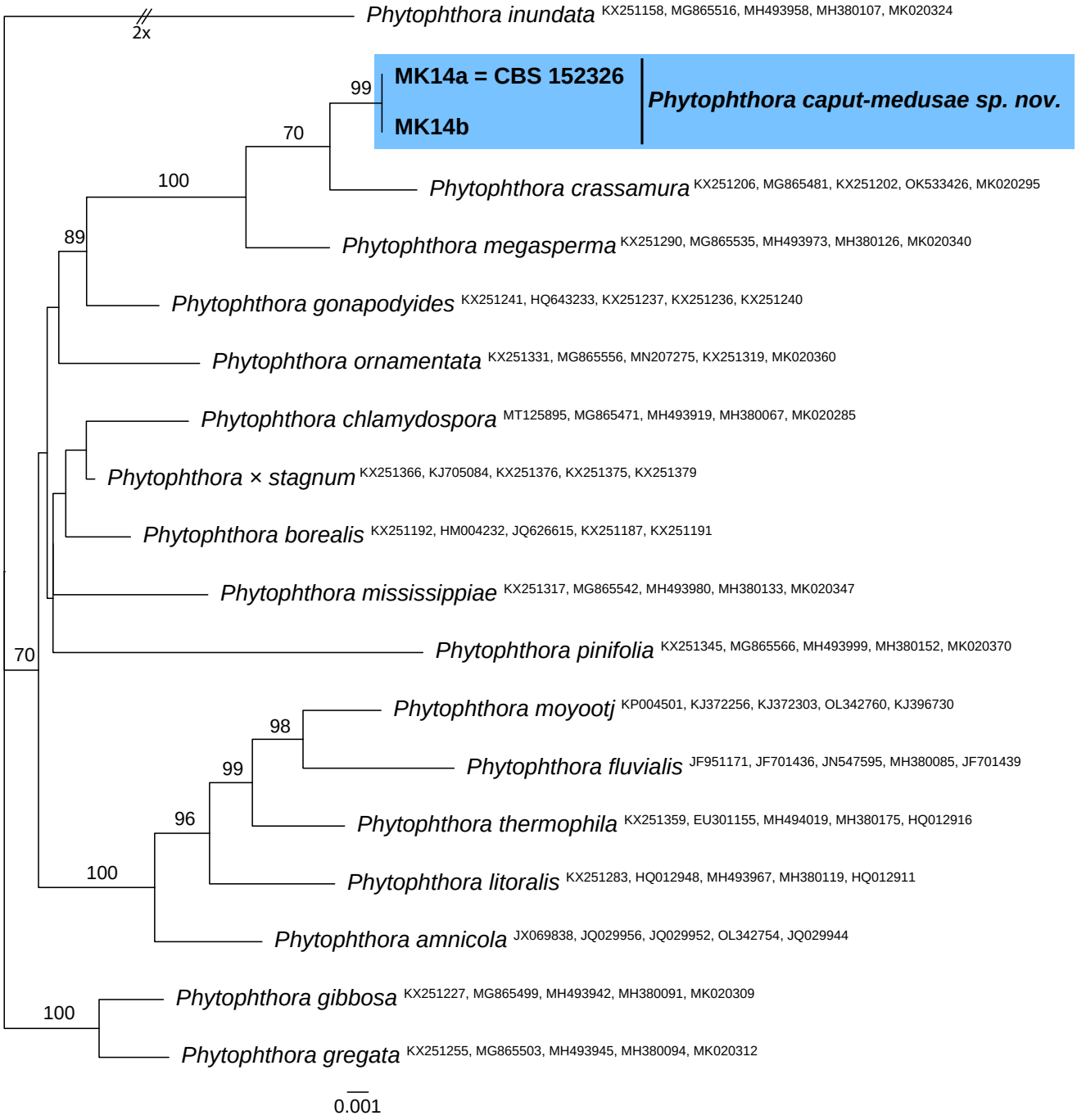

Fig. 53. Consensus phylogram (50 % majority rule) of *Phytophthora* Clade 6, subclade 6b obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 of the nuclear five loci (LSU, ITS, *tub2*, *L10* and *hsp90*) sequence alignment. Bootstrap support values (> 70 %) from 1000 non-parametric bootstrap replicates are shown at the nodes. GenBank accession numbers (superscript) of LSU, ITS, *tub2*, *L10* and *hsp90* sequences from the selected culture collection ex-types are indicated for all species. The tree was rooted to *Phytophthora inundata* (GenBank KX251158, MG865516, MH493958, MH380107 and MK020324). The scale bar indicates the expected number of changes per site. The alignment and tree were deposited in Figshare under doi 10.6084/m9.figshare.29400644.

47.3 ± 6.6 µm; overall range 53.8–104.1 × 40.5–61.6 µm; mean length/breadth ratio of 1.8 ± 0.4) (Fig. 52A–K). Most sporangia germinate directly through the apex, with one or often multiple sporangiophores evolving in chains that tangle with each other (Fig. 52D–H, J, L). *Zoospores* are rarely observed. Elongated hyphal swellings and subglobose thin-walled chlamydospores (mean diameter 23.8 ± 2.8 µm) are formed in non-sterile soil extract (Fig. 52L, M). *Phytophthora caput-medusae* is a homothallic species producing abundant gametangia in single culture on V8A at 25 °C (Fig. 52N, O). *Oogonia* are globose to subglobose and born laterally (mean diameter 47.9 ± 1.3 µm). *Oospores* with large lipid globule are plerotic or aplerotic (mean diameter 40.9 ± 2.7 µm; plerotic index = 85 %) and have an abortion rate of 12 % (Fig. 52D, N). Oospore wall thickness and index average 3.9 ± 0.4 µm and 0.47 ± 0.02, respectively. *Antheridia* are globose and amphigynous (43 %; Fig. 52N) or paragynous (57 %; Fig. 52O), averaging 17.1 ± 1.7 × 15.2 ± 0.6 µm.

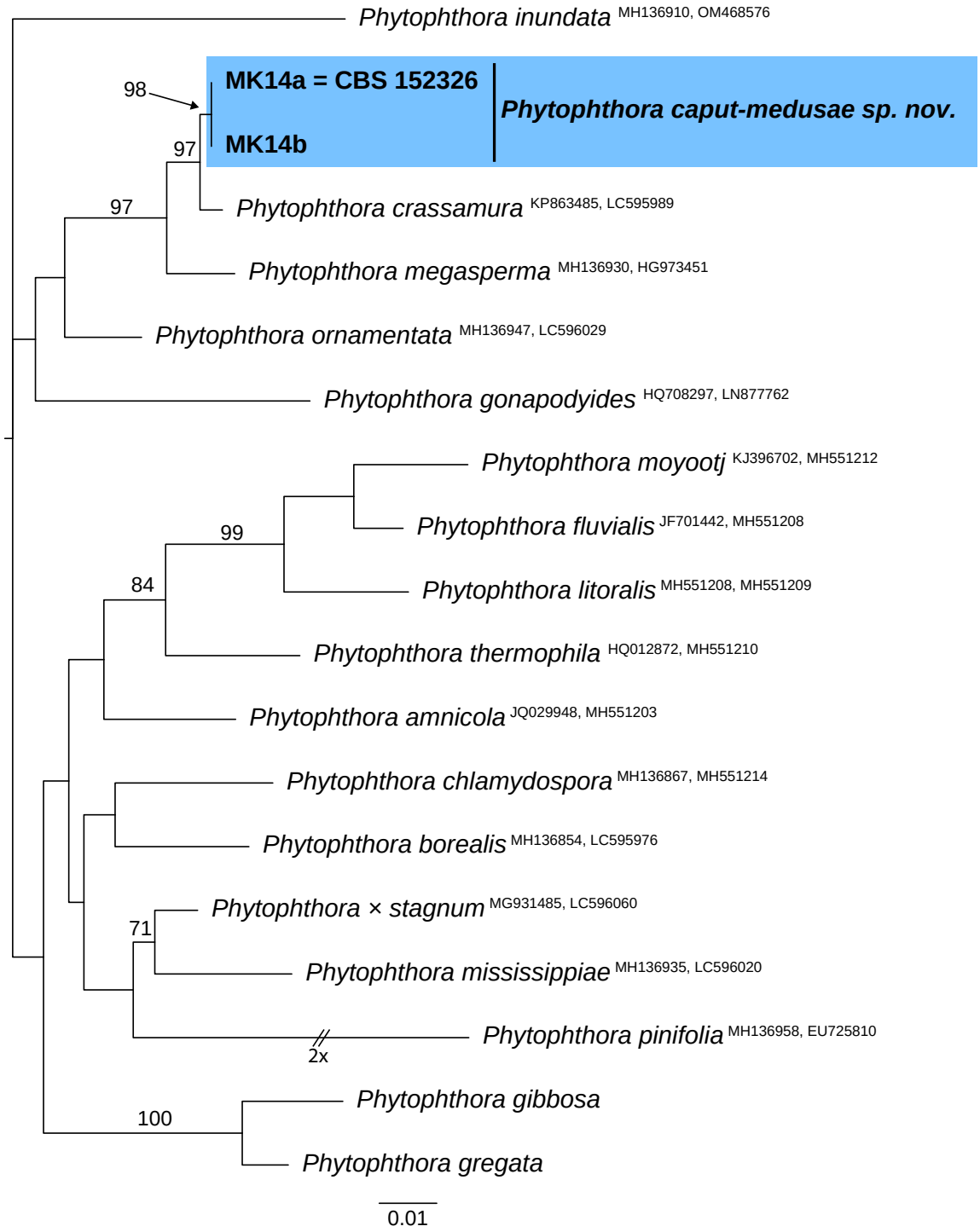

Fig. 54. Consensus phylogram (50 % majority rule) of *Phytophthora* Clade 6, subclade 6b obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 of the mitochondrial loci *cox2* and *cox1* sequence alignment. Bootstrap support values (> 70 %) from 1000 non-parametric bootstrap replicates are shown at the nodes. GenBank accession numbers (superscript) of *cox2* and *cox1* sequences from the selected culture collection ex-types are indicated for all species. The tree was rooted to *Phytophthora inundata* (GenBank MH136910 and OM468576). The scale bar indicates the expected number of changes per site. The alignment and tree were deposited in Figshare under doi 10.6084/m9.figshare.29400644.

Culture characteristics: Colonies are faintly radiate and appressed to submerged on V8A, faintly petaloid and woolly on PDA, uniform, appressed to submerged with limited aerial mycelium on CMA, and faintly petaloid and submerged to appressed on CA.

Cardinal temperatures: Minimum, optimum and maximum for growth in V8A are 3 °C, 25 °C and 30 °C, respectively. Radial growth rate at 25 °C on V8A in the dark is 5.8 ± 0.1 mm/d.

Typus: **Italy**, Siracusa Province, Lentini, isolated from rhizosphere soil of *Citrus* × *aurantium* (*Rutaceae*), May 2021, *F. Aloi & S. Conti Taguali* (**holotype** CBS H-25495, culture ex-type CBS 152326 = MK14a); ditto, culture MK14b. GenBank sequences of CBS 152326 (= MK14a) are ITS: PV820440; LSU: PV820438; *L10*: PV805053; *cox1*: PV805059; *cox2*: PV816357; *tub2*: PV805051; *hsp90*: PV805055; *nadh1*: PV805057. GenBank sequences of MK14b are ITS: PV820441; LSU: PV820439; *L10*: PV805054; *cox1*: PV805060; *cox2*: PV816358; *tub2*: PV805052; *hsp90*: PV805056; *nadh1*: PV805058.

Notes: *Phytophthora caput-medusae* is related to *Phytophthora crassamura* (CBS 140357) and *Phytophthora megasperma* (CBS 402.72), from which it is distinguished based on a combination of morphological, morphometric and physiological features. Among these, the presence of chlamydospores in *P. caput-medusae* stands out, as they are absent in both *P. crassamura* and *P. megasperma* (Scanu *et al.* 2015). Other distinguishing features include the occurrence of caducity of sporangia and their mean length/breadth ratio (1.8 ± 0.2 in *P. caput-medusae*, 1.6 ± 0.1 in *P. crassamura*, and 2.3 ± 0.2 in *P. megasperma*), the oospore wall index (0.47 ± 0.02 in *P. caput-medusae*, 0.57 ± 0.04 in *P. crassamura*, and 0.41 ± 0.08 in *P. megasperma*). Finally, the maximum temperature for growth (30 °C in *P. caput-medusae*, 32-35 °C for *P. crassamura*, and 27–32.5 °C for *P. megasperma*) (Erwin & Ribeiro 1996, Scanu *et al.* 2015).

Phytophthora caput-medusae resides in both the nuclear phylogeny, derived from a concatenated alignment of five loci (LSU, ITS, *tub2*, *L10*, and *hsp90*), and the mitochondrial *cox1-cox2* phylogeny within subclade 6b of *Phytophthora* Clade 6 (Abad *et al.* 2023), forming an independent lineage in sister position to *P. crassamura* with bootstrap support of 70 and 97 %, respectively (Figs 53, 54). *Phytophthora megasperma* resides in a basal position to this cluster. The consistent placement in both nuclear and mitochondrial phylogenies confirms the status of *P. caput-medusae* as a distinct phylogenetic species.

Authors: F. La Spada, F. Aloi, R. Parlascino, S. Conti Taguali, M. Riolo, B. Scanu, M. Horta Jung, A. Pane, T. Jung & S.O. Cacciola

Pleurophragmium fallopiae Crous & Hülsewig, ***sp. nov.*** MB 863269. Fig. 55.

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

Mycelium consisting of hyaline, branched, septate, 3–4 µm diam. hyphae. *Conidiophores* solitary, erect, medium brown, smooth, subcylindrical, straight to flexuous, 1–2-septate, mostly unbranched, arising from superficial hyphae, 30–60 × 4–6 µm with slightly swollen base. *Conidiogenous cells* subcylindrical, pale brown, smooth, integrated, terminal, 25–50 × 4–5 µm, with apical rachis having numerous pimple-like denticles, 1 × 1 µm, cicatrized, darkened, slightly thickened. *Conidia* solitary, pale brown, smooth, guttulate, 3-septate, subclavate, widest at apical septum, with flared sheath around middle of conidium, (13–)16–18(–20) × 5(–6) µm; hilum slightly darkened and thickened, 1–1.5 µm diam.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and feathery margin, reaching 8 mm diam. after 2 wk at 25 °C. On MEA surface and reverse

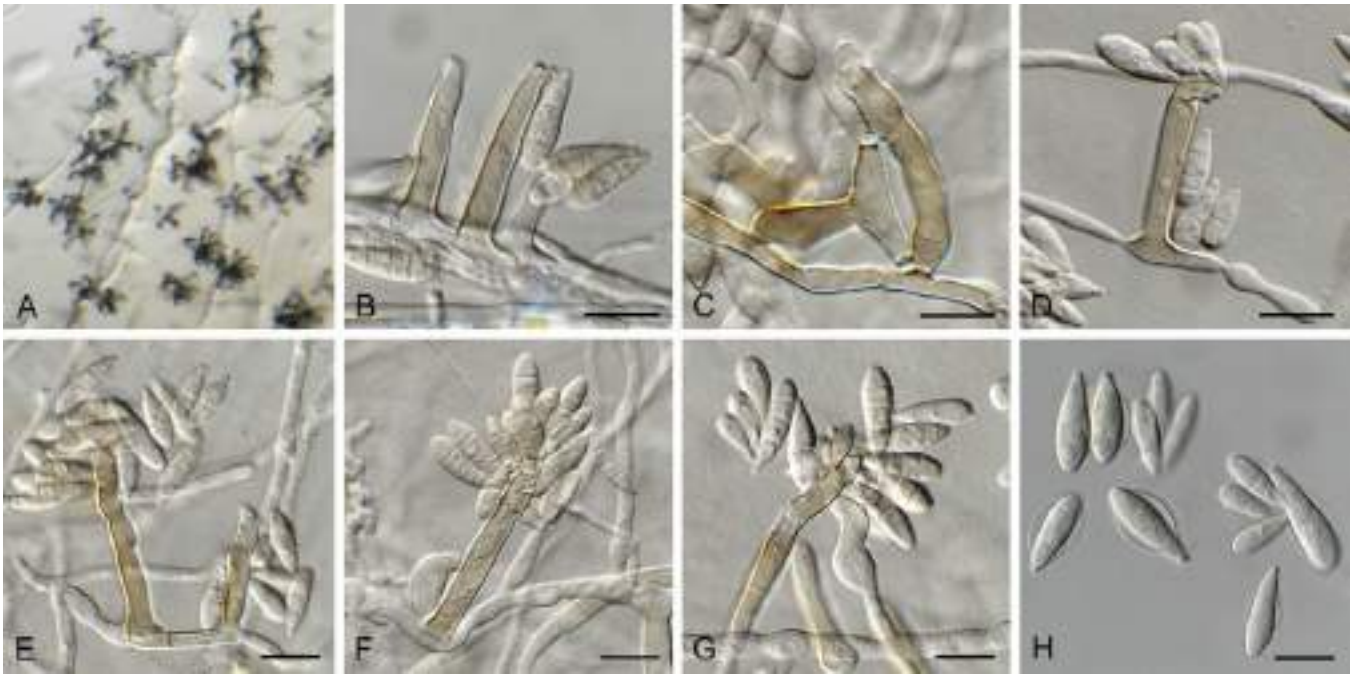

Fig. 55. *Pleurophragmium fallopiae* (CPC 48053). **A.** Colony on SNA. **B–G.** Conidiogenous cells giving rise to conidia. **H.** Conidia. Scale bars = 10 µm.

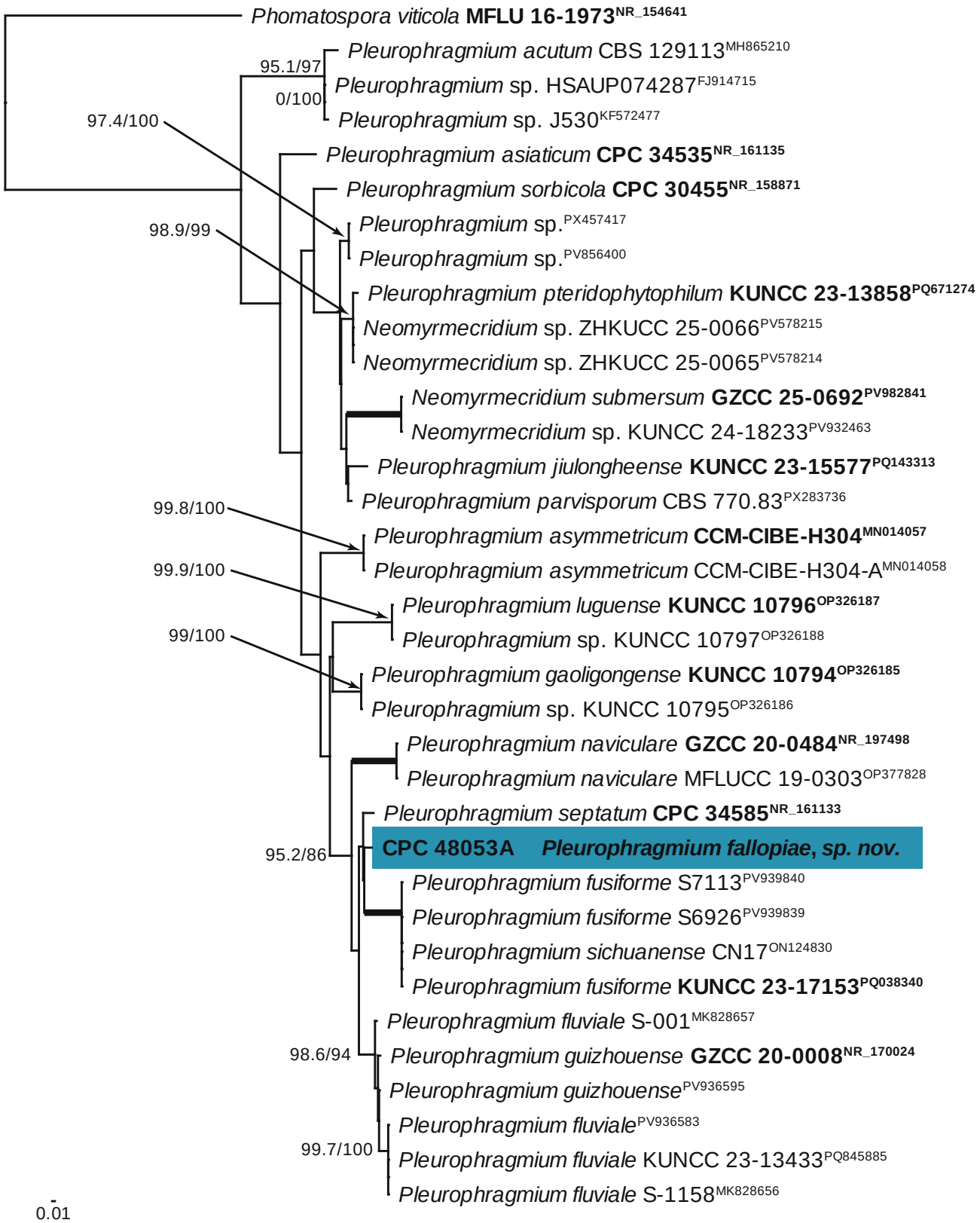

Fig. 56. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Pleurophragmium* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Thickened branches resprest a SH-aLRT test value of 100 and a bootstrap support value of 100 %. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Phomatospora viticola* (MFLU 16-1973; GenBank NR_154641) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 35 strains including the outgroup; 553 characters including alignment gaps analysed: 235 distinct patterns, 164 parsimony-informative, 47 singleton sites, 342 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

honey; on PDA surface and reverse buff, and OA surface isabelline.

Typus: **Germany**, North Rhine-Westphalia, Witten, Recreation area Hohenstein, on dead leaf *Fallopia* sp. (*Polygonaceae*), 28 Mar. 2024, *T. Hülsewig*, HPC 4447 = Thorben 1241 (**holotype** CBS H-25724, culture ex-type CPC 48053A = CBS 153457). GenBank sequences ITS: PZ221314; LSU: PZ221358; *rpb2* (first part): PZ228772; *tef1* (second part): PZ228690.

Notes: *Pleurophragmium* (as *Neomyrmecridium*) has solitary, unbranched conidiophores, polyblastic, denticulate conidiogenous cells, and fusoid-ellipsoid, septate conidia encased in a mucoid sheath (Crous *et al.* 2018). *Pleurophragmium fallopiae* is phylogenetically distinct (Fig. 56) from other species in the genus (Réblová *et al.* 2025)

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pleurophragmium septatum* [strain CBS 145073, GenBank NR_161133.1; Identities = 509/527 (97 %), four gaps (0 %)], ***Pleurophragmium fluviale*** [strain S-001, GenBank MK828657.1; Identities = 471/495 (95 %), seven gaps (1 %)], *Pleurophragmiumguizhouense* [strain GZCC 20-0008, GenBank NR_170024.1; Identities = 490/516 (95 %), seven gaps (1 %)], and *Pleurophragmiumnaviculare* [strain GZCC 20-0484, GenBank NR_197498.1; Identities = 480/519 (92 %), 11 gaps (2 %)]. Closest hits using the **LSU** sequence are *Pleurophragmium fluviale* [strain MFLUCC 15-0366, GenBank NG_068652.1; Identities = 807/811 (99 %), no gaps], *Pleurophragmium guizhouense* [strain GZCC 20-0008, GenBank PX560239.1; Identities = 823/828 (99 %), no gaps], and *Pleurophragmium septatum* [strain CBS 145073, GenBank NG_066289.1; Identities = 852/858 (99 %), no gaps]. Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Pleurophragmium guizhouense* [strain GZCC 20-0008, GenBank MT023016.1; Identities = 687/741 (93 %), no gaps], *Pleurophragmium fluviale* [strain S-1158, GenBank MN124540.1; Identities = 685/741 (92 %), no gaps], and *Pleurophragmium naviculare* [as *Neomyrmecridium* sp. JY-2022a; strain GZCC 20-0484, GenBank OP473095.1; Identities = 682/741 (92 %), no gaps]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Pleurophragmium fluviale* [voucher S-1158, GenBank MN194061.1; Identities = 871/895 (97 %), no gaps], *Pleurophragmium guizhouense* [strain GZCC 20-0008, GenBank MT023013.1; Identities = 883/912 (97 %), no gaps], and *Pleurophragmium naviculare* [as *Neomyrmecridium* sp. JY-2022a; strain GZCC 20-0484, GenBank OP473007.1; Identities = 876/907 (97 %), no gaps].

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

Polyscytalum vaccinii Crous, *Persoonia* **47**: 205. 2021. Fig. 57.

Material examined: **The Netherlands**, Gelderland Province, Wageningen, on *Vaccinium myrtillus* (*Ericaceae*), 2024, *P.W. Crous*, HPC 4376, culture CPC 47888 = CBS 153573. GenBank sequences ITS: PZ221315; LSU: PZ221359.

Notes: *Polyscytalum vaccinii* was recently described from *Vaccinium myrtillus* in the Netherlands (Limburg Province; Crous *et al.* 2021b), and the present collection represents a second isolate from the Netherlands, but from Gelderland.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Polyscytalum vaccinii* [strain CBS 148446, GenBank NR_175211.1; Identities = 398/404 (99 %), one gap (0 %)], *Anungitea eucalyptigena* [strain CPC 28762, GenBank NR_164411.1; Identities = 519/542 (96 %), four gaps (0 %)], and *Subulispora rectilineata* [strain CBS 568.71, GenBank MH860266.1; Identities = 371/388 (96 %), two gaps (0 %)]. Closest hits using the **LSU** sequence are *Polyscytalum vaccinii* [strain CPC 39935, GenBank OK663748.1; Identities = 806/810 (99 %), two gaps (0 %)], *Polyscytalum neofecundissimum* [strain CBS 143390, GenBank NG_066207.1; Identities = 914/924 (99 %), two gaps (0 %)], and *Anungitea eucalyptigena* [strain CPC 28762, GenBank NG_057129.1; Identities = 812/823 (99 %), two gaps (0 %)].

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

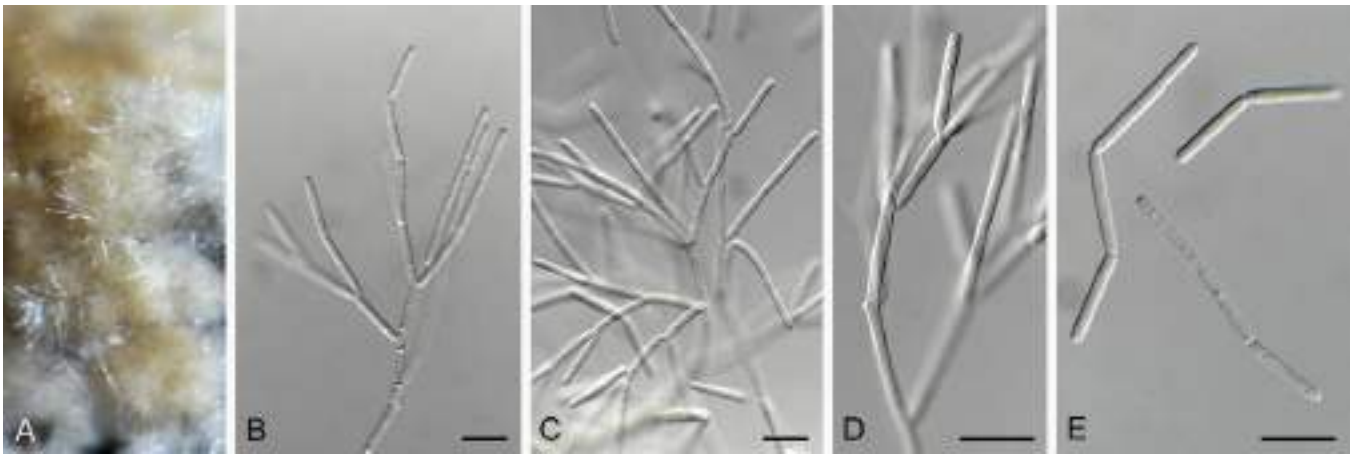

Fig. 57. *Polyscytalum vaccinii* (CPC 47888). **A.** Colony in culture. **B–D.** Conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars = 10 µm.

Pseudoberkleasmium chiangmaiense Y.Z. Lu & K.D. Hyde, *Fungal Diversity* **96**: 62. 2019. Figs 58, 59.

Description: See Hyde *et al.* (2019).

Material examined: **China**, Yunnan Province, on dead stem of *Citrus maxima* (*Rutaceae*), 18 Mar. 2019, *D.S. Tennakoon*, SZU25-031. GenBank sequences ITS: PV845193; LSU: PV845188; SSU: PV839840; *tef1*: PV853878.

Notes: *Pseudoberkleasmium chiangmaiense* introduced by Hyde *et al.* (2019) was collected from decaying wood of an unknown plant in Thailand. Subsequently, it was reported from decayed wood in freshwater habitats (Bao *et al.* 2021) and decaying culms of *Zea mays* (Tian *et al.* 2022). *Pseudoberkleasmium chiangmaiense* is hyphomycetous, dictyosporous and has compact, scattered, irregular, dark brown to black, glistening sporodochia. Conidia are acrogenous, solitary, broadly ellipsoidal to obovoid, flattened, muriform, guttulate, smooth-walled (Hyde *et al.* 2019, Bao *et al.* 2021, Tian *et al.* 2022).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **LSU** sequence had highest similarity to *Pseudoberkleasmium chiangmaiense* [strain MFLUCC 17-2088, GenBank MT214585.1; Identities = 860/861 (99 %), no gaps], *P. chiangmaiense* [strain MFLU 17-1118, GenBank NG_067861.1; Identities = 845/845 (100 %), no gaps], and *P. chiangmaiense* [strain MFLU 21-0290, GenBank OM065940.1; Identities = 842/842 (100 %), no gaps]. The closest hits using the **SSU** sequence are *P. chiangmaiense* [strain MFLU 21-0290, GenBank OM065948.1; Identities = 1018/1029 (99 %), one gap (0 %)], and *P. chiangraiense* [strain MFLUCC 21-0161, GenBank OL606409.1; Identities = 1014/1015 (99 %), one gap (0 %)]. The closest hits using the **ITS** sequence are *P. chiangmaiense* [strain MFLU 21-0290, GenBank OM066271.1; Identities = 878/884 (99 %), no gaps], and *P. chiangmaiense* [strain MFLUCC 17-2088, GenBank MT310630.1; Identities = 487/493 (99 %), no gaps]. The closest hits using the ***tef1*** sequence are *P. chiangmaiense* [strain MFLUCC 17-1809, GenBank MK131261.1; Identities = 911/914 (99 %), no gaps], and *P. chiangmaiense* [strain MFLU 21-0290, GenBank OM102996.1; Identities = 899/901 (99 %), no gaps].

According to the phylogeny results, our collection (SZU25-031) groups with *P. chiangmaiense* isolates (MFLU 21-0290, MFLUCC 17-1809 and MFLUCC 17-2088) in a well-supported clade.

Author: D.S. Tennakoon & S. Hongsanan

Pseudodactylaria yunnanensis Y.R. Sun *et al.*, *Phytotaxa* **701**: 192. 2025. Fig. 60.

Mycelium consisting of hyaline, smooth, branched, septate, 2–3 µm diam. hyphae. *Conidiophores* solitary, erect, subcylindrical, hyaline, smooth, 1–2-septate, unbranched, 15–40 × 3.5–5 µm. *Conidiogenous cells* terminal, integrated, hyaline, smooth, subcylindrical, 15–30 × 3.5–5 µm; apical part forming a rachis with numerous sympodial denticles, 1–2 × 1–2 µm; cicatrized, not darkened, slightly thickened. *Conidia* solitary, hyaline, smooth, guttulate, fusoid, tapering to subobtuse apex, truncate hilum, 1.5 µm diam., medianly 1-septate, (17–)20–23(–25) × (3.5–)4 µm.

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

Materials examined: **Germany**, North Rhine-Westphalia, Witten, Recreation area Hohenstein, on dead leaf of *Fallopia* sp. (*Polygonaceae*), 28 Mar. 2024, *T. Hülsewig*, HPC 4447, Thorben 1241, CBS H-25725, culture CPC 48053B = CBS 153458; North Rhine-Westphalia, Brüggen, Brachter

Fig. 58. *Pseudoberkleasmium chiangmaiense* (SZU25-031). **A.** Colonies on substrate. **B.** Close-up of colonies. **C.** Conidia attached to the host surface. **D–H.** Conidia. Scale bars = 20 µm.

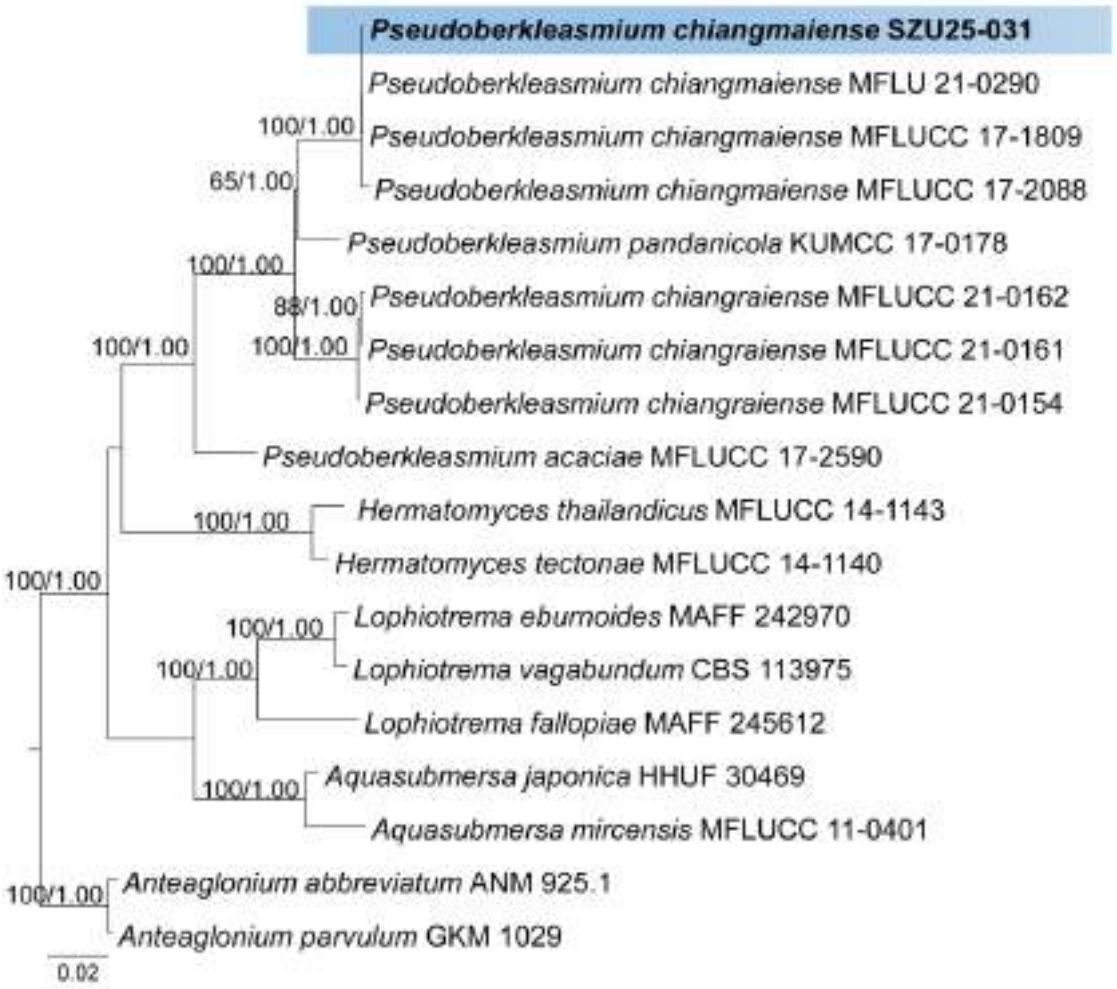

Fig. 59. Phylogenetic analysis for *Pseudoberkleasmium chiangmaiense* inferred from a maximum likelihood analysis of LSU/SSU/ITS/*tef1*/*rpb2* sequences (see Suppl. Table DOI: 10.6084/m9.figshare.31938288). The analysis was performed with RAxML v. 8.2.12 (Stamatakis 2014) using the rapid bootstrapping and search algorithm, with GTR+GAMMA nucleotide substitution model, and 1 000 bootstrap replicates. Maximum likelihood support values > 65 % are indicated on the branches. The tree is rooted with *Anteaglonium abbreviatum* (ANM 925.1) and *A. parvulum* (GKM 1029). The species treated here is highlighted with Bold face and indicated in a blue box. Scale bar on the tree indicates the expected number of changes per site. The matrix and the resulting tree have been submitted at figshare (DOI: 10.6084/m9.figshare.31932492).

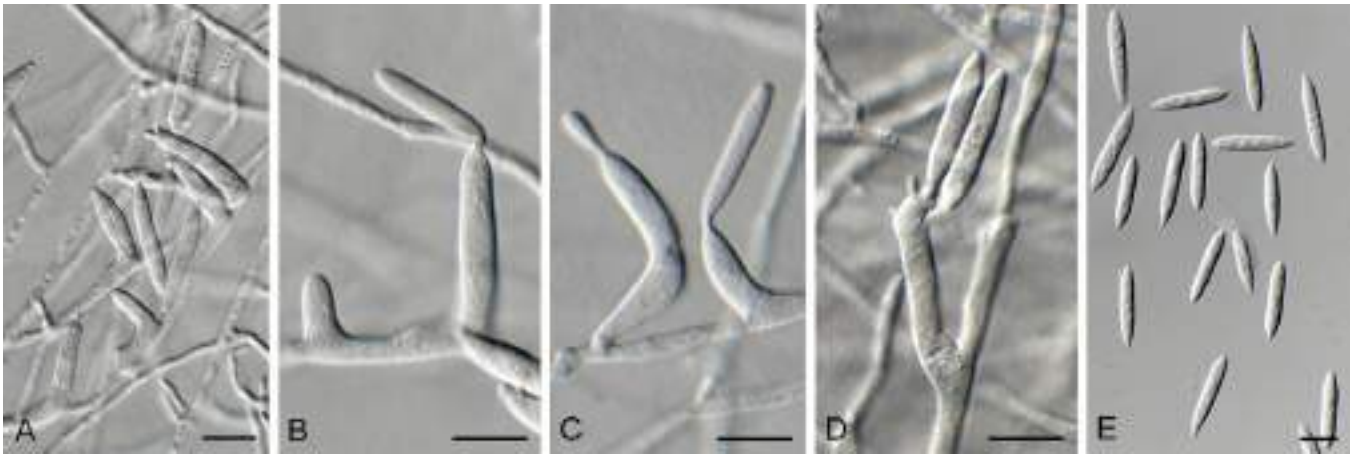

Fig. 60. *Pseudodactylaria yunnanensis* (CPC 48053B). **A–D.** Conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars = 10 µm.

Wald (Depot), on *Betula* sp. (*Betulaceae*), 14 Apr. 2024, *T. Hülsewig*, HPC 4450, Thorben 1238, CBS H-25726, culture CPC 48054 = CBS 153533. GenBank sequences ITS: PZ221316, PZ221317; LSU: PZ221360, PZ221361; *rpb2* (first part): PZ228773, PZ228774; *tef1* (second part): PZ228691, PZ228692.

Notes: *Pseudodactylaria* has solitary, hyaline, unbranched, septate conidiophores, with integrated, polyblastic, denticulate conidiogenous cells and solitary, fusoid-ellipsoid, hyaline conidia (Crous *et al.* 2017). *Pseudodactylaria yunnanensis* is known from China, where it was isolated from decaying wood in a freshwater river, having conidia 16.5–25 × 3–5 µm (Sun *et al.* 2025), thus closely matching the present collections from Germany.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 48053 had highest similarity to *Pseudodactylaria yunnanensis* [as *Pseudodactylaria* sp. YRS-2025a; strain KUNCC 23-14364, GenBank PV351335.1; Identities = 469/471 (99 %), no gaps], *Pseudodactylaria* sp. [voucher MO314567, GenBank ON176013.1; Identities = 525/529 (99 %), no gaps], *Pseudodactylaria* sp. JM-2023a [strain KUNCC 23-14329, GenBank PQ845930.1; Identities 4= 477/492 (97 %), four gaps (0 %)], and *Pseudodactylaria fusiformis* [voucher MFLU 20-0204, GenBank NR_171965.1; Identities = 491/512 (96 %), three gaps (0 %)]. The ITS sequences of CPC 48053 and CPC 48054 differ at 1 nt position (523/524 nt identical). Closest hits using the **LSU** sequence of CPC 48053 are *Pseudodactylaria yunnanensis* [as *Pseudodactylaria* sp. YRS-2025a; voucher HKAS 131650, GenBank PV475202.1; Identities = 810/810 (100 %), no gaps], *Pseudodactylaria fusiformis* [strain MFLUCC 20-0085, GenBank NG_073841.1; Identities = 825/831 (99 %), no gaps], *Pseudodactylaria camporesiana* [strain MFLUCC 18-1410, GenBank MN796326.1; Identities = 821/830 (99 %), one gap (0 %)], and *Pseudodactylaria albicolonia* [strain MFLUCC 21-0095, GenBank MZ493341.1; Identities = 813/835 (97 %), three gaps (0 %)]. The LSU sequences of CPC 48053 and CPC 48054 are 100 % identical (830/830 nt). Closest hits using the ***rpb2*** (first part) sequence of CPC 48053 had highest similarity to *Pseudodactylaria* sp. NGL-2025a [strain KUNCC 23-14329, GenBank PX233790.1; Identities = 719/768 (94 %), no gaps], *Pseudodactylaria fusiformis* [strain MFLUCC 20-0085, GenBank MT188555.1; Identities = 718/779 (92 %), no gaps], *Thermothelomyces hinnuleus* [strain CBS 539.82, GenBank HQ871808.1; Identities = 325/402 (81 %), two gaps (0 %)], and *Myceliophthora guttulata* [strain CGMCC 3.15185, GenBank KC352949.1; Identities = 293/363 (81 %), two gaps (0 %)]. The *rpb2* sequences of CPC 48053 and CPC 48054 are 99 % similar (813/822 nt identical). Closest hits using the ***tef1*** (second part) sequence of CPC 48053 had highest similarity to *Pseudodactylaria yunnanensis* [as *Pseudodactylaria* sp. YRS-2025a; voucher HKAS 131650, GenBank PV491868.1; Identities = 874/884 (99 %), no gaps], *Pseudodactylaria fusiformis* [strain MFLUCC 20-0085, GenBank MT188556.1; Identities = 848/901 (94 %), two gaps (0 %)], *Chloridium fuscum* [strain CBS 148531, GenBank OP464985.1; Identities = 842/927 (91 %), four gaps (0 %)], and *Stilbochaeta novae-guineensis* [strain CBS 147517, GenBank OL654061.1; Identities = 840/927 (91 %), four gaps (0 %)]. The *tef1* sequences of CPC 48053 and CPC 48054 are 100 % identical (900/900 nt).

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

Pseudothyridariella aquilariae T.Y. Du *et al.*, *J. Syst. Evol.* **63**: 453. 2024. Fig. 61.

Description: See Du *et al.* (2024).

Material examined: **China**, Yunnan Province, dead twigs of *Magnolia* sp. (*Magnoliaceae*), 25 Aug. 2019, *N.I. de Silva*,

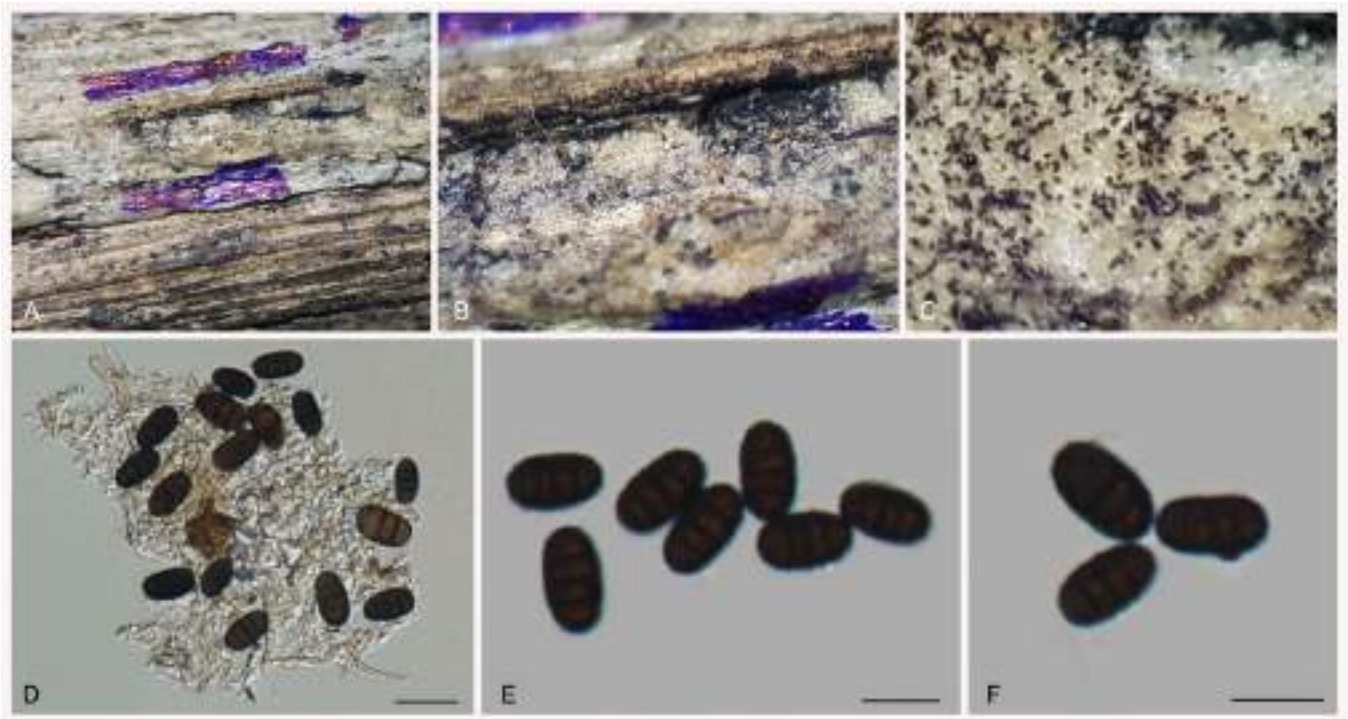

Fig. 61. *Pseudothyridariella aquilariae* (SZU 25-034). **A, B.** Plant substrate. **C.** Scattered conidia on plant substrate. **D–F.** Conidia. Scale bars: D–F = 10 µm.

SZU 25-034. GenBank sequences ITS: PV915286; LSU: PV915328; SSU: PV915329; *rpb2*: PV931733; *tef1-α*: PV931734.

Notes: *Pseudothyridariella* was introduced by Mapook *et al.* (2020) with the type *P. chromolaenae*. Currently, four saprobic species are known in *Pseudothyridariella*. *Pseudothyridariella aquilariae* was introduced by Du *et al.* (2024). The phylogenetic analyses indicated that the new strain (SZU 25-034) clustered with the ex-type of *P. aquilariae* (ZHKUCC 23-0044) (Fig. 62). *Pseudothyridariella aquilariae* is coelomycetous and characterized by having solitary or scattered pycnidia holoblastic, discrete, phialidic, ampulliform conidiogenous cells. Conidia are hyaline when immature and become brown to dark brown with age, oblong to ellipsoidal in shape, guttulate, rough-walled, with three transverse septa (Du *et al.* 2024). The holotype MHZU 23-0025 was identified on dead branch of *Aquilaria sinensis* (*Thymelaeaceae*) in Guangdong Province, China. The new collection (SZU 25-034) was saprobic on dead twigs of *Magnolia* species (*Magnoliaceae*) Yunnan Province, China. In the present study, we recognize the new collection (SZU 25-034) as the

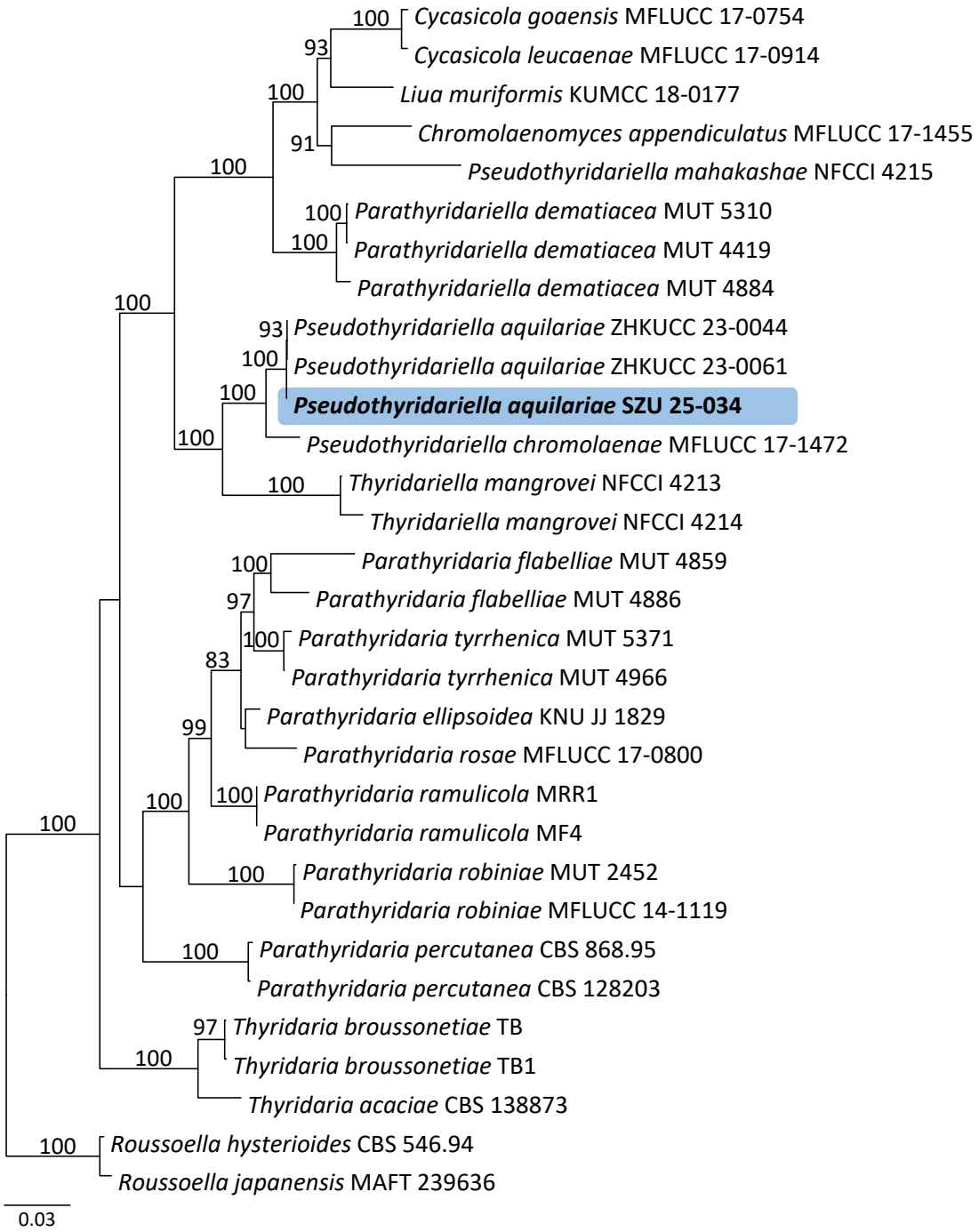

Fig. 62. Phylogenetic analysis for *Pseudothyridariella aquilariae* inferred from a maximum likelihood analysis of LSU/SSU/ITS/*tef1*/*rpb2* sequences (see Suppl. Table DOI: 10.6084/m9.figshare.31938366). The analysis was performed with RAxML v. 8.2.12 (Stamatakis 2014) using the rapid bootstrapping and search algorithm, with GTR+GAMMA nucleotide substitution model, and 1000 bootstrap replicates. Maximum likelihood support values > 75 % are indicated on the branches. The tree is rooted with *Roussoella hysterioides* (CBS 546.94) and *R. japanensis* (MAFT 239636). The species treated here is highlighted with Bold face and indicated in a blue box. Scale bar on the tree indicates the expected number of changes per site. The matrix and the resulting tree have been deposited at TreeBASE (study ID: S32558). The matrix and the resulting tree have been submitted at figshare (DOI: 10.6084/m9.figshare.31938372).

first record of *P. aquilariae* from *Magnolia*. Further collections of *Pseudothyridariella* species will be useful for understanding their geographical distribution.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **LSU** sequence had highest similarity to *Pseudothyridariella* sp. [strain AK07, GenBank OR580989.1; Identities = 809/809 (100 %), no gaps], *P. aquilariae* [strain ZHKUCC 23-0044, GenBank PP809728.1; Identities = 809/809 (100 %), no gaps], and *P. idesiae* [strain UESTCC 23.0423, GenBank PQ184702.1; Identities = 807/809 (99 %), no gaps]. The closest hits using the **SSU** sequence are *Pseudothyridariella* sp. [strain AK07, GenBank OR580990.1; Identities = 1028/1029 (99 %), no gaps], *P. aquilariae* [strain ZHKUCC 23-0044, GenBank NG_244195.1; Identities = 1028/1029 (99 %), no gaps], and *Aquilariomyces* sp. TD-2024a [strain ZHKUCC 23-0041, GenBank PQ604625.1; Identities = 1024/1027 (99 %), one gap (0 %)]. The closest hits using the **ITS** sequence are *Pseudothyridariella* sp. [strain AK07, GenBank OR580988.1; Identities = 499/500 (99 %), no gaps], *P. aquilariae* [strain ZHKUCC 23-0044, GenBank OR825376.1; Identities = 499/500 (99 %), no gaps], and *P. idesiae* [strain UESTCC 23.0423, GenBank NR_190270.1; Identities = 474/502 (94 %), eight gaps (1 %)]. The closest hits using the ***tef1-α*** sequence are *P. idesiae* [strain UESTCC 23.0423, GenBank PQ346495.1; Identities = 886/900 (98 %), one gap (0 %)], *Pseudothyridariella* sp. RL-2023a [strain 522, GenBank OR251154.1; Identities = 880/894 (98 %), one gap (0 %)], and *P. chromolaenae* [strain MFLUCC 17-1472, GenBank MT235771.1; Identities = 876/889 (99 %), one gap (0 %)]. The closest hits using the ***rpb2*** sequence are *Pseudothyridariella* sp. [strain AK07, GenBank OR576779.1; Identities = 888/888 (98 %), no gaps], *Pseudothyridariella* sp. [strain HKAS 127179, GenBank OR253762.1; Identities = 885/916 (97 %), no gaps], and *P. chromolaenae* [strain MFLUCC 17-1472, GenBank MT235807.1; Identities = 700/726 (96 %), one gap (0 %)].

Rhinotrichella carpini Crous & Akulov, ***sp. nov.*** MB 863273. Fig. 63.

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

Mycelium consisting of hyaline, septate, branched, 3–4 µm diam. hyphae. *Conidiophores* dimorphic. *Microconidiophores* erect, subcylindrical, branched, septate, hyaline with terminal conidiogenous cells, 20–100 × 3–4 µm. *Microconidiogenous cells* hyaline, smooth, 10–40 × 3–4 µm, subcylindrical to fusoid, phialidic. *Microconidia* hyaline, smooth, clavate with truncate hilum, 1.5–2 µm diam., aseptate, guttulate, forming in long disarticulating chains that eventually form clusters, (6–)7–8(–10) × (5–)6–7 µm. *Macroconidiophores* erect, flexuous, branched below, medium brown, smooth, septate, thick-walled, up to 500 µm tall, 4–5 µm diam. *Macroconidiogenous cells* integrated, terminal and intercalary, up to 120 µm long, with several erect, sympodial denticles, 2–3 × 1–1.5 µm, rhexolytic. *Macroconidia* solitary, globose to subglobose, aseptate, medium brown, finely verruculose, (7–)8–10(–11) × (7–)8–9(–10) µm, with basal marginal frill, 1–2 × 1.5–2 µm.

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

Typus: **Ukraine**, Ternopil region, Zalischyky district, National Nature Park, Dniester Canyon, forest near Dzhuryn waterfall, on stromata of *Melogramma campylosporum* (*Melogrammataceae*), on dead branches of *Carpinus betulus* (*Betulaceae*), 13 Aug. 2022, *A. Akulov*, HPC 4044 = CWU(Myc) AS 8431 (**holotype** CBS H-25285, culture ex-type CPC 45245 = CBS 150072). GenBank sequences ITS: PZ221319; LSU: PZ221363; SSU: PZ205450; *actA*: PZ228596; *tef1* (second part): PZ228694.

Authors: N.I. de Silva & S. Hongsanan

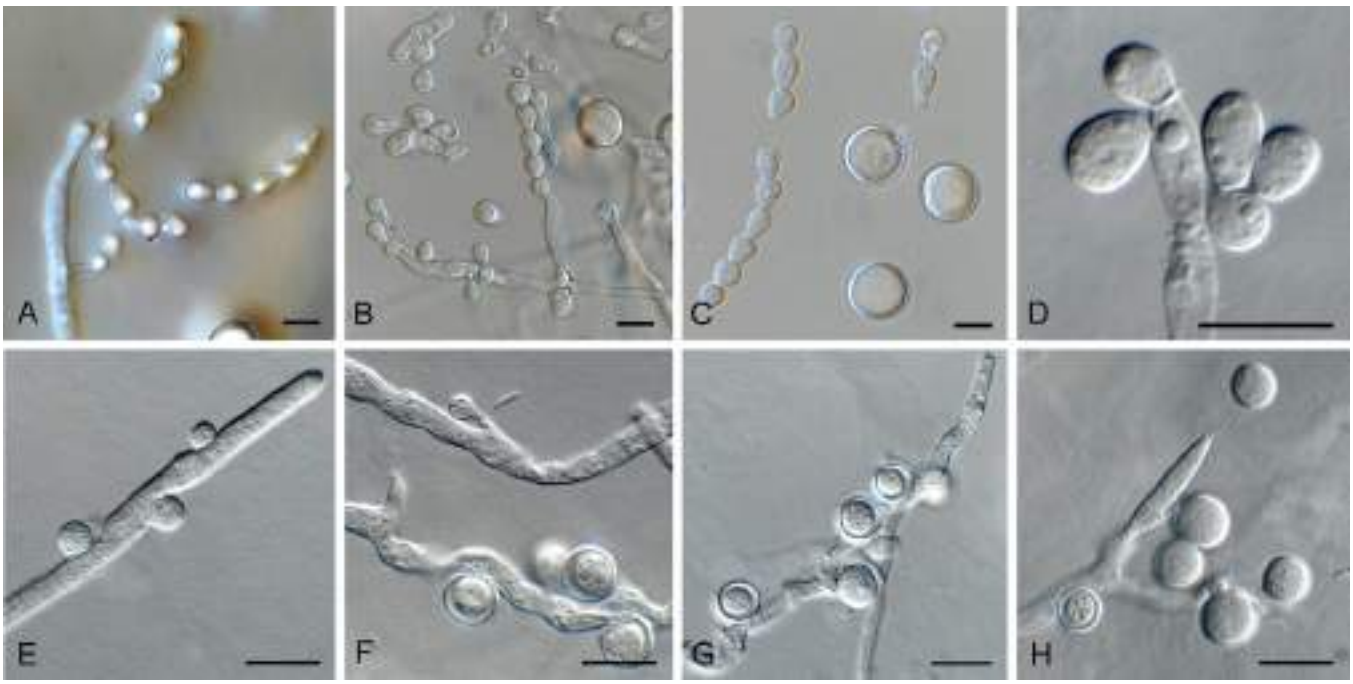

Fig. 63. *Rhinotrichella carpini* (CPC 45245). **A–H.** Conidiophores and conidiogenous cells giving rise to chains of conidia. Scale bars = 10 µm.

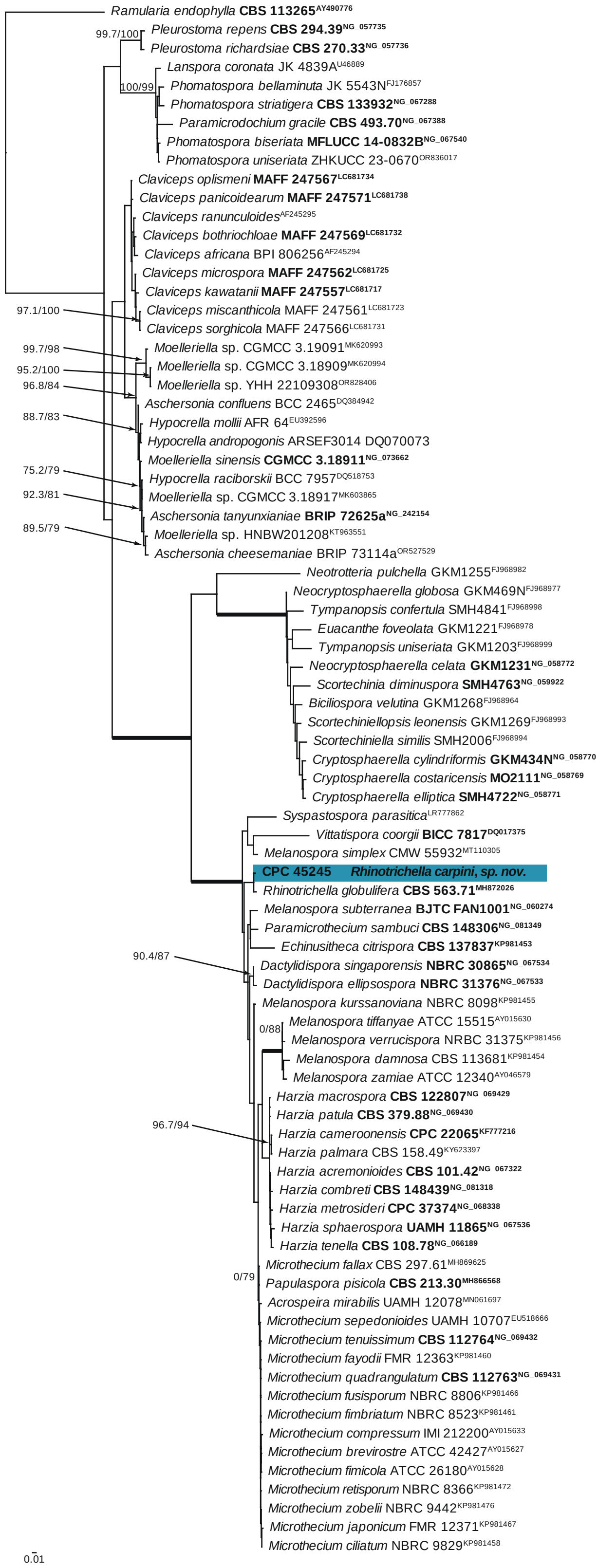

Fig. 64. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Rhinotrichella* and allied genera LSU nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Thickened branches resprest a SH-aLRT test value of 100 and a bootstrap support value of 100 %. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Ramularia endophylla* (CBS 113265; GenBank AY490776) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 83 strains including the outgroup; 878 characters including alignment gaps analysed: 388 distinct patterns, 302 parsimony-informative, 86 singleton sites, 490 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: GTR+F+I+R3. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

Notes: *Rhinotrichella carpini* is related (Fig. 64) to *Rhinotrichella globulifera* (isolated from *Ganoderma tsugae*, Japan, conidia globose, smooth to finely verruculose, 9–12 µm diam.; de Hoog & Hermanides-Nijhof 1977). *Rhinotrichella globulifera* is distinct in that it lacks the long disarticulating chains of microconidia, and also has smaller pimple-shaped denticles, 1–1.5 µm long, and more globose macroconidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Melanospora kurssanoviana* [strain NBRC 8098, GenBank KP981479.1; Identities = 438/493 (89 %), 34 gaps (6 %)], *Dactylidispora singaporensis* [strain NBRC 30865, GenBank LC146748.1; Identities = 432/494 (87 %), 26 gaps (5 %)], and *Dactylidispora singaporensis* [strain NBRC 30865, GenBank NR_161014.1; Identities = 432/494 (87 %), 26 gaps (5 %)]. The genus *Rhinotrichella* is at present only represented by a single LSU sequence in the nucleotide database of NCBI Genbank. Closest hits using the **LSU** sequence are *Rhinotrichella globulifera* [strain CBS 563.71, GenBank MH872026.1; Identities = 883/892 (99 %), one gap (0 %)], *Dactylidispora singaporensis* [strain NBRC 30865, GenBank NG_067534.1; Identities = 837/865 (97 %), 12 gaps (1 %)], and *Microthecium quadrangulatum* [strain CBS 112763, GenBank KY628700.1; Identities = 864/893 (97 %), 12 gaps (1 %)]. Closest hits using the **SSU** sequence are *Melanospora kurssanoviana* [strain NBRC 8098, GenBank KP981500.1; Identities = 1009/1026 (98 %), two gaps (0 %)], *Microthecium fusisporum* [as *Microthecium* sp. YM-2015d; strain NBRC 8806, GenBank KP981511.1; Identities = 1006/1025 (98 %), one gap (0 %)], and *Microthecium tenuissimum* [strain CBS 112764, GenBank KR055813.1; Identities = 1006/1025 (98 %), one gap (0 %)]. No significant hits were obtained when the ***actA*** sequence was used in blastn and megablast searches. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Microthecium fimicola* [as *Microthecium* sp. YM-2015c; strain FMR 13148, GenBank KP981593.1; Identities = 753/910 (83 %), two gaps (0 %)], *Microthecium levitum* [strain FMR 13884, GenBank KP981598.1; Identities = 753/910 (83 %), two gaps (0 %)], and *Melanospora kurssanoviana* [strain NBRC 8098, GenBank KP981583.1; Identities = 740/896 (83 %), two gaps (0 %)].

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

Schizothyrium Desm., *Ann. Sci. Nat.*, Bot., sér. 3 **11**(2): 360. 1849.
Synonym: *Zygophiala* E.W. Mason, *Mycol. Pap.* **13**: 3. 1945.

Schizothyrium pomi (Mont. & Fr.) Arx, *Proc. Kon. Ned. Akad. Wetensch.*, Ser. C, **62**: 336. 1959. Fig. 65.

Material examined: **Netherlands**, Bilthoven, Sweelincklaan 87, on fruit of *Malus* sp. (*Rosaceae*), Nov. 2023, *P.W. Crous*, HPC 4298, isolated from thyrothecia, culture CPC 47290 = CBS 152279. GenBank sequences ITS: PZ221320; LSU: PZ221364; *rpb2* (first part): PZ228775; *tef1* (first part): PZ228695.

Notes: Single ascospore isolates of *Schizothyrium pomi* produced a *Zygophiala* morph in culture, confirming the generic synonymy of *Zygophiala* under *Schizothyrium*, as suggested by Batzer *et al.* (2008).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Schizothyrium pomi* [strain CBS 406.61, GenBank EF134949.1; Identities = 521/521 (100 %), no gaps], *Schizothyrium qianense* [as *Zygophiala qianensis*; strain LWH-LNLZ-14, GenBank KF806030.1; Identities = 510/518 (98 %), one gap (0 %)], and *Schizothyrium cryptogamum* [as *Zygophiala cryptogama*; strain LHYTB43, GenBank FJ941847.1; Identities = 449/457 (98 %), no gaps]. Closest hits using the **LSU** sequence are *Schizothyrium pomi* [strain CBS 486.50, GenBank EF134948.1; Identities = 812/812 (100 %), no gaps], *Schizothyrium cylindricum* [strain SP12_377Ha, GenBank MN065458.1; Identities = 809/812 (99 %), no gaps], and *Schizothyrium cryptogamum* [strain CBS 118949, GenBank MH874599.1; Identities = 807/812 (99 %), no gaps]. Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Schizothyrium pomi* [strain CBS 486.50, GenBank MF951735.1; Identities = 768/770 (99 %), no gaps], *Schizothyrium cryptogamum* [strain OH4_1A1a, GenBank KT216548.1; Identities = 646/785 (82 %), nine gaps (1 %)], and *Schizothyrium wisconsinense* [strain OH4_9A1c, GenBank KT216549.1; Identities = 635/783 (81 %), eight gaps (1 %)]. The best hit using the ***tef1*** (first part) sequence was identical to *Schizothyrium pomi* [strain CPC 16179, GenBank HM177431.1; Identities = 359/359 (100 %), no gaps].

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

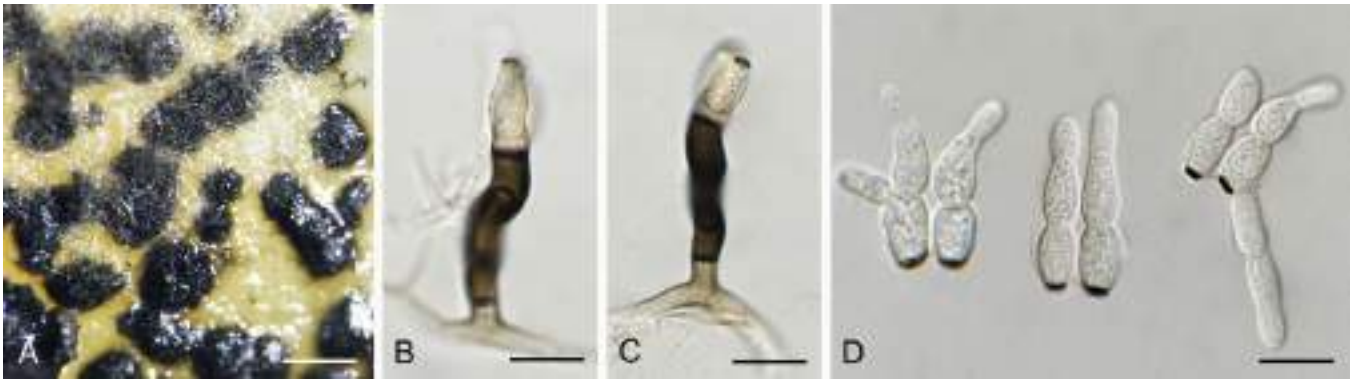

Fig. 65. *Schizothyrium pomi* (CPC 47290). **A.** Ascomata on host tissue. **B, C.** Conidiophores, **D.** Conidia. Scale bars: A = 400 µm, all others = 10 µm.

Spegazzinia tessarthra (Berk. & M.A. Curtis) Sacc., *Syll. Fung.* **4**: 758. 1886. Fig. 66.

Sporodochia dark brown, 1–5 mm diam. *Conidiophores* up to 60 µm tall, 1.5–2 µm wide, erect, flexuous, brown, smooth to verruculose, unbranched. *Conidiogenous cells* verruculose, brown, subcylindrical, 5–15 × 2–3 µm. *Conidia* dimorphic. *Alpha conidia* stellate, 8–15 µm diam., globose, 4–6-celled, prominently constricted at septa, spinulose, with numerous spines, each spine 2–10 µm long. *Beta conidia* 10–15 µm diam., globose, pale to dark brown, 4-celled, smooth, constricted at septa.

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 and reverse luteous; on PDA surface and reverse saffron; on OA surface buff.

Material examined: **Spain**, Pontevedra, O Grove, on dead leaves of *Zea mays* (*Poaceae*), 30 Jan. 2024, *M.A. Delgado*, HPC 4452, RKS 1186, CBS H-25727, culture CPC 48084 = CBS 153467. GenBank sequences ITS: PZ221321; LSU: PZ221365; *tef1* (second part): PZ228696.

Notes: The present collection from Spain correlates well with the original description, which was made from balsa wood collected in Japan (Tanaka *et al.* 2015).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Spegazzinia tessarthra* [strain MFLUCC 18-1624, GenBank ON117290.1; Identities = 503/503 (100 %), no gaps], *Spegazzinia radermacherae* [strain MFLUCC 17-2285, GenBank NR_163331.1; Identities = 451/453 (99 %), one gap (0 %)], and *Spegazzinia musae* [voucher MFLU 19-2823, GenBank MW063160.1; Identities = 418/441 (95 %), nine gaps (2 %)]. Closest hits using the **LSU** sequence are *Spegazzinia tessarthra* [strain MFLUCC 18-1624, GenBank ON117308.1; Identities = 845/845 (100 %), no gaps], *Rhytidhysteron neorufulum* [strain MFLU2350, GenBank OR663922.1; Identities = 839/840 (99 %), no gaps], and *Spegazzinia radermacherae* [voucher MFLU 20-0469, GenBank MW084354.1; Identities = 819/820 (99 %), no gaps]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Spegazzinia tessarthra* [strain SH 287, GenBank AB808560.2; Identities = 910/913 (99 %), no gaps], *Teichospora thailandica* [strain MFLUCC 17-0909, GenBank MK360089.1; Identities = 895/910 (98 %), no gaps], and *Pseudosetoseptoria oryzae* [voucher MFLU 23-0176, GenBank OR500315.1; Identities = 884/897 (99 %), no gaps].

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

Staheliella nodosa Emden, *Acta Bot. Neerl.* **23**(3): 251. 1974. Fig. 67.

Conidiophores erect, solitary, subcylindrical, flexuous, brown, smooth, base bulbous, lacking rhizoids, 2–6-septate, stipe rejuvenating percurrently, thick-walled, 10–15 µm wide, up to 500 µm tall. *Conidiogenous cells* integrated, terminal, subcylindrical, 150–200 × 9–10 µm; apex somewhat swollen with inconspicuous loci at apex, 2.5–3 µm diam., not thickened nor darkened. *Conidia* occurring in branched chains of arthroconidia that branch at basal cell. Basal cell triangular, base truncate, 3–4 µm diam., giving rise to two apical chains, lateral apical loci 3–4 µm diam., forming chains of arthroconidia 7–8 long, brown, smooth, cylindrical with truncate ends, except for apical conidia with rounded apex; conidial segments aseptate, 3–5 × 4.5–5 µm.

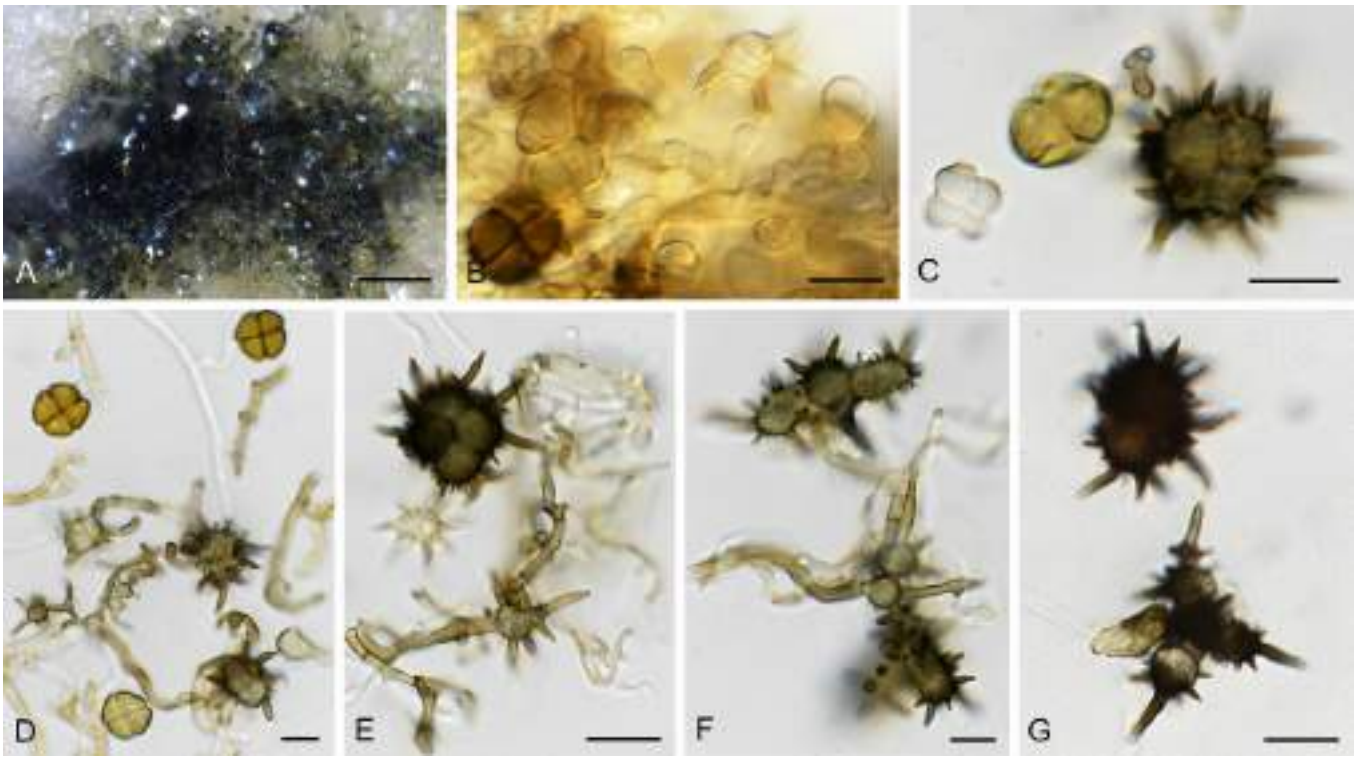

Fig. 66. *Spegazzinia tessarthra* (CPC 48084). **A.** Colony on OA. **B–G.** Conidiophores, conidiogenous cells giving rise to alpha and beta conidia. Scale bars: A = 1 mm, all others = 10 µm.

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

Material examined: **Brazil**, Minas Gerais, Caraça, on plant debris, Feb. 2024, *P.W. Crous*, HPC 4403 = CBS H-25707, culture COAD 3986 = CPC 47862. GenBank sequences ITS: PZ221322; LSU: PZ221366.

Notes: *Staheliella nodosa* was initially described from soil collected from a tropical location, Surinam (van Emden 1974). Finding the same fungus on plant debris in Brazil, fits with its presumed ecology. Genetically, and morphologically the Brazilian isolate matches well with the ex-type culture from Surinam.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Staheliella nodosa* [strain CBS 589.73, GenBank MH860777.1; Identities = 481/488 (99 %), one gap (0 %)], *Neometulocladosporiella eucalypti* [strain CPC 31787, GenBank NR_160350.1; Identities = 500/546 (92 %), 12 gaps (2 %)], and *Rutstroemia punicae* [strain KL497, GenBank MK501758.1; Identities = 500/551 (91 %), 17 gaps (3 %)]. Closest hits using the **LSU** sequence are *Staheliella nodosa* [strain CBS 589.73, GenBank MH872508.1; Identities = 847/850 (99 %), no gaps], *Lanzia allantospora* [strain CBS 124334, in GenBank as CBS 1243.34, GenBank AB926154.1; Identities = 828/851 (97 %), two gaps (0 %)], and *Neometulocladosporiella* [strain CPC 31787, GenBank NG_064541.1; Identities = 826/851 (97 %), two gaps (0 %)].

Authors: P.W. Crous, J.Z. Groenewald, R.W. Barreto, R.F. Alfenas & A.C. Alfenas

Stachylidium chayuense Chao Ma *et al.*, *Phytotaxa* **694**: 80. 2025. Fig. 68.

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam. hyphae. *Conidiophores* solitary to aggregated, erect, flexuous, subcylindrical, up to 400 µm tall, 4–5 µm wide, brown, finely verruculose, up to 18-septate, becoming pale brown towards apex, verticillate with 8–10 whorls of phialides (2–4) in the upper two thirds of conidiophores. *Conidiogenous cells* fusoid-ellipsoid, brown, verruculose, monophialidic, 11–14 × 3–4 µm. *Conidia* solitary, aggregated in mucoid mass, subcylindrical with obtuse ends, aseptate, brown, smooth, (5–)6–7 × (2–)2.5 µm.

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

Material examined: **Brazil**, Minas Gerais, Inhotim, unidentified lily, Mar. 2024, *P.W. Crous*, HPC 4409 = CBS H-25723; culture COAD 3987 = CPC 48046. GenBank sequences ITS: PZ221323; LSU: PZ221367; *rpb2* (first part): PZ228776; *tef1* (second part): PZ228697.

Notes: The Brazilian collection correlates well morphologically with the description of *Stachylidium chayuense* from China (Ma *et al.* 2025). The two strains are also genetically nearly identical based on the loci included here.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Stachylidium chayuense* [as *Stachylidium* sp. CM-2024a; strain HKAS 134942, GenBank PQ323341.1; Identities = 518/519 (99 %), one gap (0 %)], *Stachylidium bicolor* [strain CBS 292.72,

Fig. 67. *Staheliella nodosa* (CPC 47862). **A.** Conidiophores. **B–G.** Conidiophores and conidiogenous cells giving rise to chains of conidia. **H.** Conidia. Scale bars: A = 20 µm, all others = 10 µm.

GenBank MF803167.1; Identities = 484/524 (92 %), 10 gaps (1 %)], and *Chlamydosporiella restricta* [strain IHEM 03704, GenBank OW983195.1; Identities = 499/551 (91 %), 20 gaps (3 %)]. Closest hits using the **LSU** sequence are *Stachylidium chayuense* [as *Stachylidium* sp. CM-2024a; strain HKAS 134942, GenBank PQ323343.1; Identities = 866/867 (99 %), no gaps], *Stachylidium bicolor* [strain DAOM 226658, GenBank GU180651.1; Identities = 855/862 (99 %), no gaps], and *Acremoniisimulans thailandensis* [strain MFLUCC 16-0372, GenBank NG_228789.1; Identities = 806/819 (98 %), one gap (0 %)]. Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Stachylidium chayuense* [as *Stachylidium* sp. CM-2024a; strain HKAS 134942, GenBank PQ563349.1; Identities = 873/884 (99 %), no gaps], *Nigrocephalum collariferum* [as *Acremonium collariferum*; strain CBS 124585, GenBank LR026192.1; Identities = 627/743 (84 %), no gaps], and *Stachylidium bicolor* [strain DAOMC 226658, GenBank LR026228.1; Identities = 625/745 (84 %), four gaps (0 %)]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Stachylidium chayuense* [as *Stachylidium* sp. CM-2024a; strain HKAS 134941, GenBank PQ563352.1; Identities = 768/781 (98 %), two gaps (0 %)], *Stachylidium bicolor* [strain DAOMC 226658, GenBank LR026534.1; Identities = 716/762 (94 %), two gaps (0 %)], *Nigrocephalum paracollariferum* [strain FMR 20069, GenBank PP392591.1; Identities = 726/780 (93 %), two gaps (0 %)], and *Nigrocephalum paracollariferum* [strain FMR 20174, GenBank PP392592.1; Identities = 724/780 (9 3 %), two gaps (0 %)].

Authors: P.W. Crous, J.Z. Groenewald, R.W. Barreto, R.F. Alfenas & A.C. Alfenas

Stagonospora schoeni Keissl., *Krypt. Exs.* Cent. **26**: no. 2523. 1923. Fig. 69.

Conidiomata erumpent, globose, solitary to aggregated in agar, dark brown, 200–350 µm diam., with central, dark brown ostiole; wall of 3–6 layers of brown textura angularis. *Conidiophores* reduced to conidiogenous cells, hyaline, smooth, ampulliform, proliferating percurrently, 5–12 × 3–5 µm. *Paraphyses* intermingled among conidiogenous cells, hyaline, smooth, septate, 3–5 µm diam., extending above conidiogenous cells. *Conidia* hyaline, smooth, guttulate, subcylindrical with obtuse ends, 4-septate, not constricted at septa, apex obtuse, hilum truncate, 3–4 µm diam., (28–)33–38(–40) × (7–)8(–9) 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 pale olivaceous grey to olivaceous grey, reverse olivaceous grey.

Material examined: **UK**, England, Cornwall, St. Ives, on living leaf of *Schoenus nigricans* (*Cyperaceae*), 8 May 2024, *P.W. Crous*, HPC 4469 (CBS H-25734; culture CPC 48204 = CBS 153532). GenBank sequences ITS: PZ221324; LSU: PZ221368; *rpb2* (first part): PZ228777.

Notes: *Stagonospora* is characterised by pycnidial conidiomata, percurrently proliferating phialides, and 1–multiseptate, hyaline, cylindrical or fusoid-ellipsoidal conidia (Quaedvlieg *et al.* 2013). *Stagonospora schoeni* is genetically distinct from other species of *Stagonospora* known from culture based on the loci studied here. Morphologically, it correlates well with the description of *S. schoeni* (type from Austria, conidia 30–40 × 10 µm), which was previously reported from the UK (conidia 4-septate, 30–36 × 7–8 µm) by Dennis (1986, 1988).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Stagonospora bicolor* [voucher EK16-3, GenBank MH300022.1; Identities = 466/479 (97 %), one gap (0 %)], *Stagonospora trichophoricola* [strain CBS 136764, GenBank NR_156586.1; Identities = 500/516 (97 %), one gap (0 %)], and *Stagonospora pseudoperfecta* [voucher HHUF 29087, GenBank NR_155768.1; Identities = 479/498 (96 %), two gaps (0 %)]. Closest hits using the **LSU** sequence are *Stagonospora pseudoperfecta* [strain HHUF 29087, GenBank NG_059399.1; Identities = 834/839 (99 %), no gaps], *Stagonospora trichophoricola* [strain 12-B-5, GenBank OR244351.1; Identities = 834/840 (99 %), no gaps], and *Stagonospora imperaticola* [voucher MFLU 16-2788, GenBank NG_059793.1; Identities = 851/858 (99 %), no gaps]. Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Stagonospora trichophoricola* [strain TF2F21, GenBank LC907017.1; Identities = 676/738 (92 %),

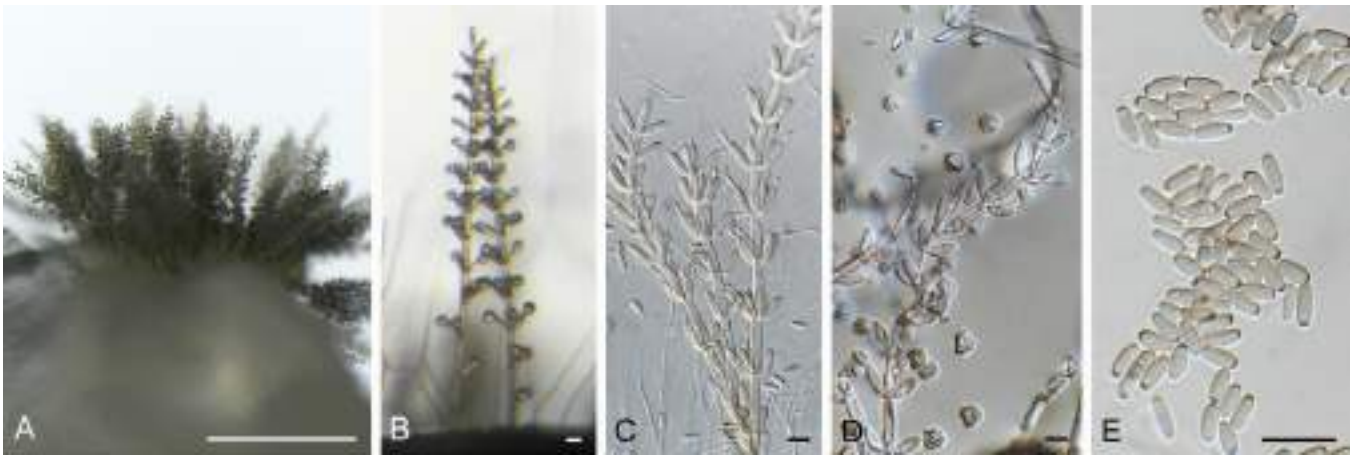

Fig. 68. *Stachylidium chayuense* (CPC 48046). **A.** Colony on SNA. **B–D.** Conidiophores and conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars = 10 µm.

no gaps], *Stagonospora lomandrae* [strain CBS 143447, GenBank MG386147.1; Identities = 761/848 (90 %), no gaps], *Neottiosporina paspali* [strain CBS 331.37, GenBank GU371779.1; Identities = 803/895 (90 %), one gap (0 %)], and *Stagonospora tauntonensis* [as *Stagonospora* sp. TVS-2020a; strain BRIP 70684, GenBank OM390189.1; Identities = 712/802 (89 %), two gaps (0 %)].

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

Stagonosporopsis citri Crous, ***sp. nov.*** MB 863274. Fig. 70.

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

Conidiomata pycnidial, brown, subglobose, 200–300 µm diam., erumpent, solitary to aggregated with central papillate ostiole; wall of 3–6 layers of brown textura angularis. *Conidiophores* reduced to *conidiogenous cells* lining the inner cavity, hyaline, smooth, ampulliform, monophialidic, 5–8 × 5–7 µm. *Conidia* solitary, hyaline (brown in conidial mass oozing from pycnidium), smooth, guttulate, aseptate, straight, ends obtuse, subcylindrical, 5–7 × 2 µm. *Mycelium* becomes brown, verruculose, 3–5 µm diam., forming intercalary brown, ellipsoid chlamydospores, up to 12 µm diam.

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 pale olivaceous grey, reverse umber; on PDA surface ochreous, reverse ochreous to umber, and OA surface ochreous.

Typus: **The Netherlands**, quarantine border interception, on peel of living fruit of *Citrus latifolia* (*Rutaceae*), 2024, isol. *P.W. Crous*, HPC 4483 (**holotype** CBS H-25737, culture ex-type CPC 48236 = CBS 153516). GenBank sequences ITS: PZ221325; LSU: PZ221369; *rpb2* (first part): PZ228778; *tub2*: PZ228737.

Notes: *Stagonosporopsis* includes approximately 40 species, the majority of which are known from DNA data. Species occur on wide host ranges and cause diseases ranging from stunting of plants, seedling damping-off, leaf spots, dieback, crown rot, stem canker, flower blight, and fruit rot (Marin-Felix *et al.* 2019). *Stagonosporopsis citri* is the first species described from Rutaceae, where it was associated with lesions on peels of *Citrus latifolia.* Phylogenetically (Fig. 71), it is quite distinct from other species in the genus.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Ectophoma multirostrata* [strain M1407, GenBank OQ793629.1; Identities = 488/504 (97 %), six gaps (1 %)], *Epicoccum keratinophilum* [strain VJP12, GenBank OM945845.1; Identities = 488/504 (97 %), six gaps (1 %)], and *Stagonosporopsis ajacis* [strain Yubari5, GenBank LC905400.1; Identities = 487/503 (97 %), three gaps (0 %)]. Closest hits using the **LSU** sequence are *Stagonosporopsis pogostemonis* [strain TYJ-SP2, GenBank OR533527.1; Identities = 887/888 (99 %), no gaps], *Sphaeronaema indicum* [strain CBS 273.60, GenBank MH869535.1; Identities = 887/889 (99 %), one gap (0 %)], and *Allophoma tropica* [strain MFLUCC 23-0050, GenBank OR711078.1; Identities = 886/888 (99 %), no gaps]. Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Anthodidymella ranunculacearum* (nom. inval.) [strain MFLUCC 17-2184, GenBank MT394681.1; Identities = 766/861 (89 %), no gaps], *Remotididymella capsici* [strain MFLUCC 24-0031, GenBank PQ412488.1; Identities = 785/886 (89 %), four gaps (0 %)], and *Ectophoma multirostrata* [voucher HGUP

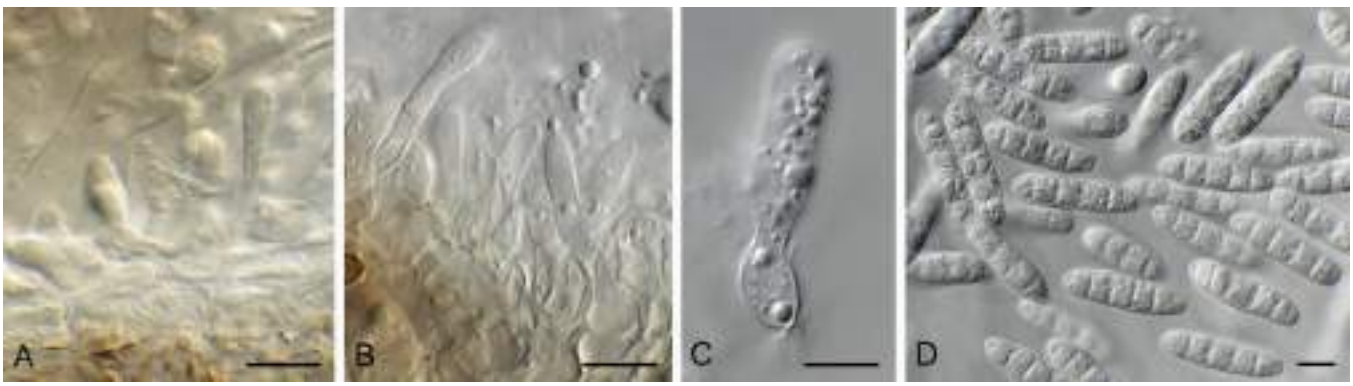

Fig. 69. *Stagonospora schoeni* (CPC 48204). **A–C.** Conidiogenous cells giving rise to conidia. **D.** Conidia. Scale bars = 10 µm.

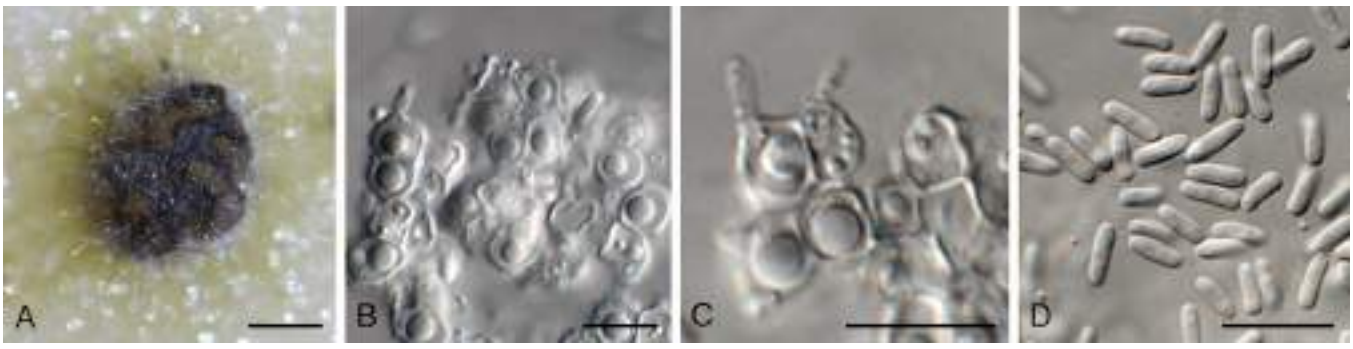

Fig. 70. *Stagonosporopsis citri* (CPC 48236). **A.** Conidiomata. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars = 10 µm.

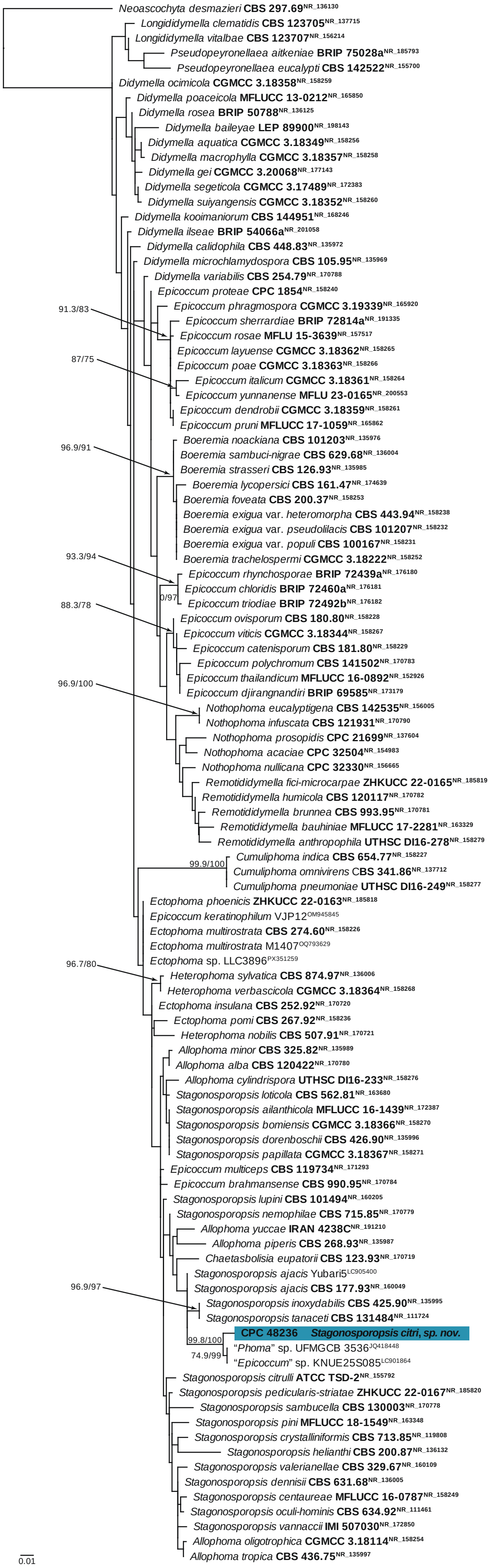

Fig. 71. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Didymellaceae* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Neoascochyta desmazieri* (CBS 297.69; GenBank NR_136130) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 105 strains including the outgroup; 500 characters including alignment gaps analysed: 170 distinct patterns, 76 parsimony-informative, 47 singleton sites, 377constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+I+R3. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

R623, GenBank MN560152.1; Identities = 787/891 (88 %), no gaps]. Closest hits using the ***tub2*** sequence had highest similarity to *Ectophoma multirostrata* [strain M1417, GenBank OQ791163.1; Identities = 440/474 (93 %), seven gaps (1 %)], *Boeremia exigua* [strain Ph.ex.001NY17, GenBank MK514090.1; Identities = 438/473 (93 %), three gaps (0 %)], and *Stagonosporopsis chrysanthemi* [strain CBS 500.63, GenBank MW815129.1; Identities = 436/473 (92 %), five gaps (1 %)].

Authors: P.W. Crous, J.Z. Groenewald & V.A. van Ingen-Buijs

Subverticillium Crous & Osieck, ***gen. nov.*** MB 863275.

Etymology: Name refers to its verticillium-like morphology.

Mycelium consisting of hyaline, smooth, branched, septate hyphae. *Conidiophores* solitary, erect, hyaline, smooth, subcylindrical, straight to flexuous, unbranched, multi-septate. *Conidiogenous cells* monophialides, hyaline, smooth, subuliform, penicillate or arranged in verticillate whorls of 4–6, direct on stipe or on a short lateral branch; phialides with periclinal thickening and minute collarette. *Conidia* solitary, aggregating in mucoid mass, hyaline, smooth, aseptate, obovoid.

Type species: *Subverticillium juncicola* Crous & Osieck

Subverticillium juncicola Crous & Osieck, ***sp. nov.*** MB 863276. Figs 72.

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

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam. hyphae. *Conidiophores* solitary, erect, hyaline, smooth, subcylindrical, straight to flexuous, unbranched, up to 180 µm tall, 3–4 µm wide at base, 3–8-septate. *Conidiogenous cells* monophialides, hyaline, smooth, subuliform, penicillate or arranged in verticillate whorls of 4–6, direct on stipe or on a short lateral branch, 4–6 × 3–4 µm; phialides 12–20 × 2.5–3 µm, with periclinal thickening and minute collarette. *Conidia* solitary, aggregating in mucoid mass, hyaline, smooth, aseptate, obovoid, 2.5–3 µm diam.

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

Typus: **The Netherlands**, North Holland Province, Texel, Binnen Muy, on culms of *Juncus effusus* (*Juncaceae*), 6 Dec. 2022, *E.R. Osieck*, HPC 4068 = WI-66/#4597 (**holotype** CBS H-25305, culture ex-type CPC 45367 = CBS 150779). GenBank sequences ITS: PZ221326; LSU: PZ221370; *rpb1*: PZ228647; *rpb2* (first part): PZ228779; *tef1* (second part): PZ228698; *tub2*: PZ228738.

Notes: *Subverticillium juncicola* represents a single lineage in *Nectriaceae* that is phylogenetically (Fig. 73) related to *Thyronectria* but has a distinct asexual morph (Voglmayr *et al.* 2022). *Subverticillium* is thus introduced as a new genus to accommodate this fungus that has a verticillium-like morphology.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Thyronectria cucurbitula* [strain CBS 12549, GenBank MH863662.1; Identities = 491/536 (92 %), 14 gaps (2 %)], *Thyronectria abieticola* [strain THYA, GenBank OL439231.1; Identities = 491/536 (92 %), 14 gaps (2 %)], and *Cosmospora khandalensis* [strain IMI 112791, GenBank NR_145058.1; Identities = 491/537 (91 %), 16 gaps (2 %)]. Closest hits using the **LSU** sequence are *Tolypocladium* sp. [strain RKAG 373, GenBank KU183703.1; Identities = 847/876 (97 %), five gaps (0 %)], *Pseudodiploospora longispora* [strain 60319, GenBank KY765315.1; Identities = 846/877 (96 %), seven gaps (0 %)], *Cordyceps sinensis* [strain SHANGHAI, GenBank AB067710.1; Identities = 845/876

Fig. 72. *Subverticillium juncicola* (CPC 45367). **A.** Colony on SNA. **B–E.** Conidiophores and conidiogenous cells giving rise to conidia. **F.** Conidia. Scale bars = 10 µm.

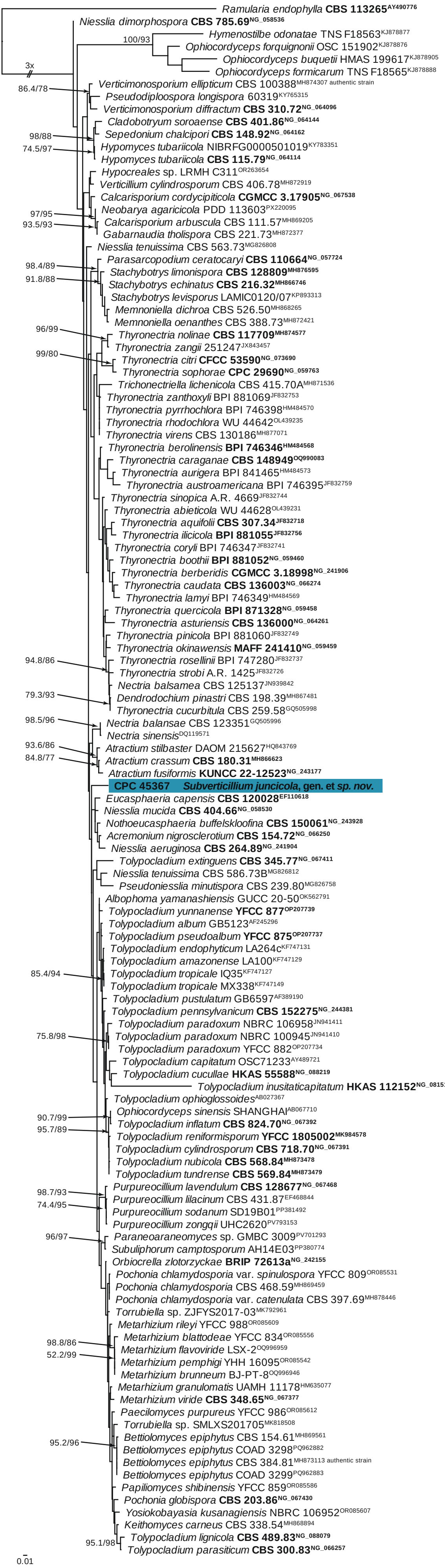

Fig. 73. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Hypocreales* LSU nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Ramularia endophylla* (CBS 113265; GenBank AY490776) and the novelty described here is highlighted with a coloured block and **bold** font. The root branch was shortened to facilitate layout. Alignment statistics: 124 strains including the outgroup; 888 characters including alignment gaps analysed: 330 distinct patterns, 184 parsimony-informative, 123 singleton sites, 581constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM3e+I+R3. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

(96 %), five gaps (0 %)], and *Thyronectria xanthoxyli* [strain NP11, GenBank OL439242.1; Identities = 840/874 (96 %), three gaps (0 %)]. Closest hits using the ***rpb1*** sequence had highest similarity to *Allantonectria miltina* [strain CBS 125499, GenBank KM232270.1; Identities = 581/736 (79 %), 18 gaps (2 %)], *Tilachlidium brachiatum* [strain CBS 505.67, GenBank KM232272.1; Identities = 580/738 (79 %), 22 gaps (2 %)], and *Thyronectria virens* [strain NP10, GenBank KM225689.1; Identities = 563/719 (78 %), 27 gaps (3 %)]. No significant hits were obtained when the ***rpb2*** sequence was used in blastn and megablast searches. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Tolypocladium paradoxum* [strain YFCC 882, GenBank OP223148.1; Identities = 860/945 (91 %), six gaps (0 %)], *Tolypocladium japonicum* [strain NBRC 9647, GenBank OP223146.1; Identities = 857/943 (91 %), two gaps (0 %)], and *Tolypocladium bacillisporum* [strain C53, GenBank LC684526.1; Identities = 856/943 (91 %), two gaps (0 %)]. A blast2 comparison against all *tef1* sequences of *Thyronectria* in GenBank had highest similarity to *Thyronectria okinawensis* [as *Pleonectria okinawensis*; strain MAFF 241410, GenBank JF832585.1; Identities = 364/401 (91 %), two gaps (0 %)], *Thyronectria orientalis* [strain 8912, GenBank KX372535.1; Identities = 364/401 (91 %), two gaps (0 %)], and *Thyronectria virens* [as *Pleonectria virens*; strain Y.H. 08-11, GenBank JF832589.1; Identities = 363/401 (91 %), two gaps (0 %)]. Closest hits using the ***tub2*** sequence had highest similarity to *Thyronectria coryli* [strain NeCo1, GenBank KJ570644.1; Identities = 299/363 (82 %), 19 gaps (5 %)], *Thyronectria boothii* [as *Pleonectria boothii*; strain A.R. 4481, GenBank JF832871.1; Identities = 316/388 (81 %), 22 gaps (5 %)], and *Thyronectria ilicicola* [as *Pleonectria ilicicola*; strain A.R. 4497, GenBank JF832843.1; Identities = 311/381 (82 %), 22 gaps (5 %)].

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

Teratosphaeria agapanthi (Kalchbr. & Cooke) Crous, *IMA Fungus* **2**(1): 61. 2011.

Description and illustration: Crous *et al.* (2011).

Material examined: **Brazil**, Minas Gerais, Viçosa University campus, from leaves of *Agapanthus praecox* (*Amaryllidaceae*), Feb. 2024, *P.W. Crous*, HPC 4391, culture CPC 47790. **UK**, England, Cornwall, St. Ives, on living leaves of *A. praecox*, 8 May 2024, *P.W. Crous*, HPC 4475, culture CPC 48222 = CBS 153572. GenBank sequences ITS: PZ221327, PZ221328; LSU: PZ221371, PZ221372; *tub2*: PZ228739.

Notes: *Teratosphaeria agapanthi* is a foliar pathogen of *Agapanthus* spp., originating from South Africa, where this host is native (Crous *et al.* 2011, 2020b). The present collections represent new records for this plant pathogen from Brazil and the UK. It is relevant that single ascospore isolates from the UK were homothallic in culture, a feature not previously observed for this species.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 47790 had highest similarity to *Teratosphaeria agapanthi* [strain CPC 32077, GenBank MT223862.1; Identities = 503/503 (100 %), no gaps], *Teratosphaeria combreti* [strain CBS 146985, GenBank NR_173053.1; Identities = 482/503 (96 %), one gap (0 %)], and *Teratosphaeria hortaea* [strain CBS 124156, GenBank NR_156520.1; Identities = 470/506 (93 %), six gaps (1 %)]. The ITS sequences of CPC 47790 and CPC 48222 are 100 % (501/501 nt) identical. Closest hits using the **LSU** sequence of CPC 47790 are *Teratosphaeria agapanthi* [strain CBS 129064, GenBank JF770469.1; Identities = 870/870 (100 %), no gaps], *Teratosphaeria combreti* [strain CBS 146985, GenBank NG_076742.1; Identities = 867/870 (99 %), no gaps], and *Teratosphaeria cryptica* [strain CPC 936, GenBank GU214505.1; Identities = 861/870 (99 %), no gaps]. The LSU sequences of CPC 47790 and CPC 48222 are 100 % (870/870 nt) identical. Closest hits using the ***tub2*** sequence of CPC 48222 had highest similarity to *Teratosphaeria combreti* [strain CPC 38958, GenBank MZ078270.1; Identities = 448/527 (85 %), three gaps (0 %)], *Teratosphaeria majorizuluensis* [strain CBS 120040, GenBank KF442473.1; Identities = 288/344 (84 %), 23 gaps (6 %)], and *Teratosphaeria considenianae* [strain CBS 120087, GenBank FJ952510.1; Identities = 286/342 (84 %), 21 gaps (6 %)].

Authors: P.W. Crous, J.Z. Groenewald, S. Denman, R.W. Barreto, R.F. Alfenas & A.C. Alfenas

Veronaea parabrunnea Crous & Mombert, ***sp. nov.*** MB 863277. Fig. 74.

Etymology: Name refers to its similarity to *Exophiala brunnea*.

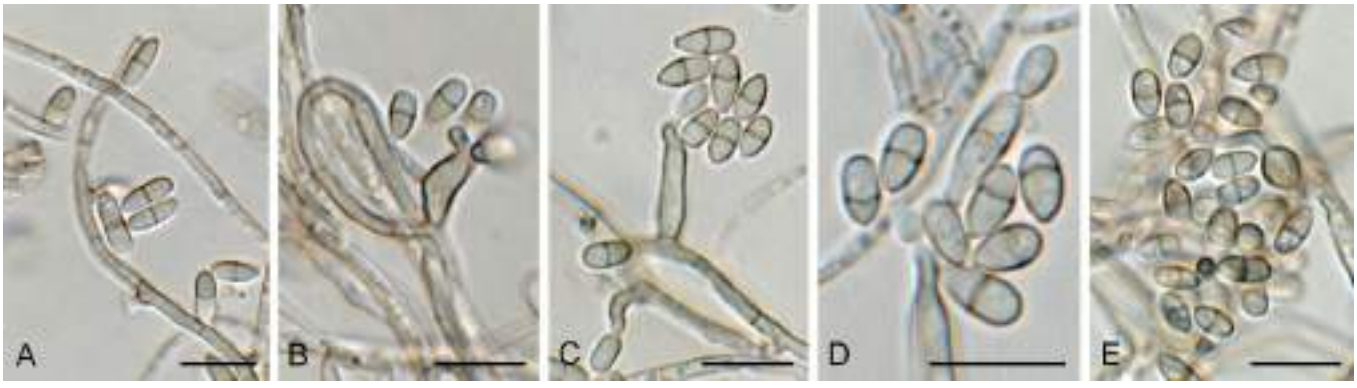

Fig. 74. *Veronaea parabrunnea* (CPC 48188). **A–E.** Conidiogenous cells and conidia. Scale bars = 10 µm.

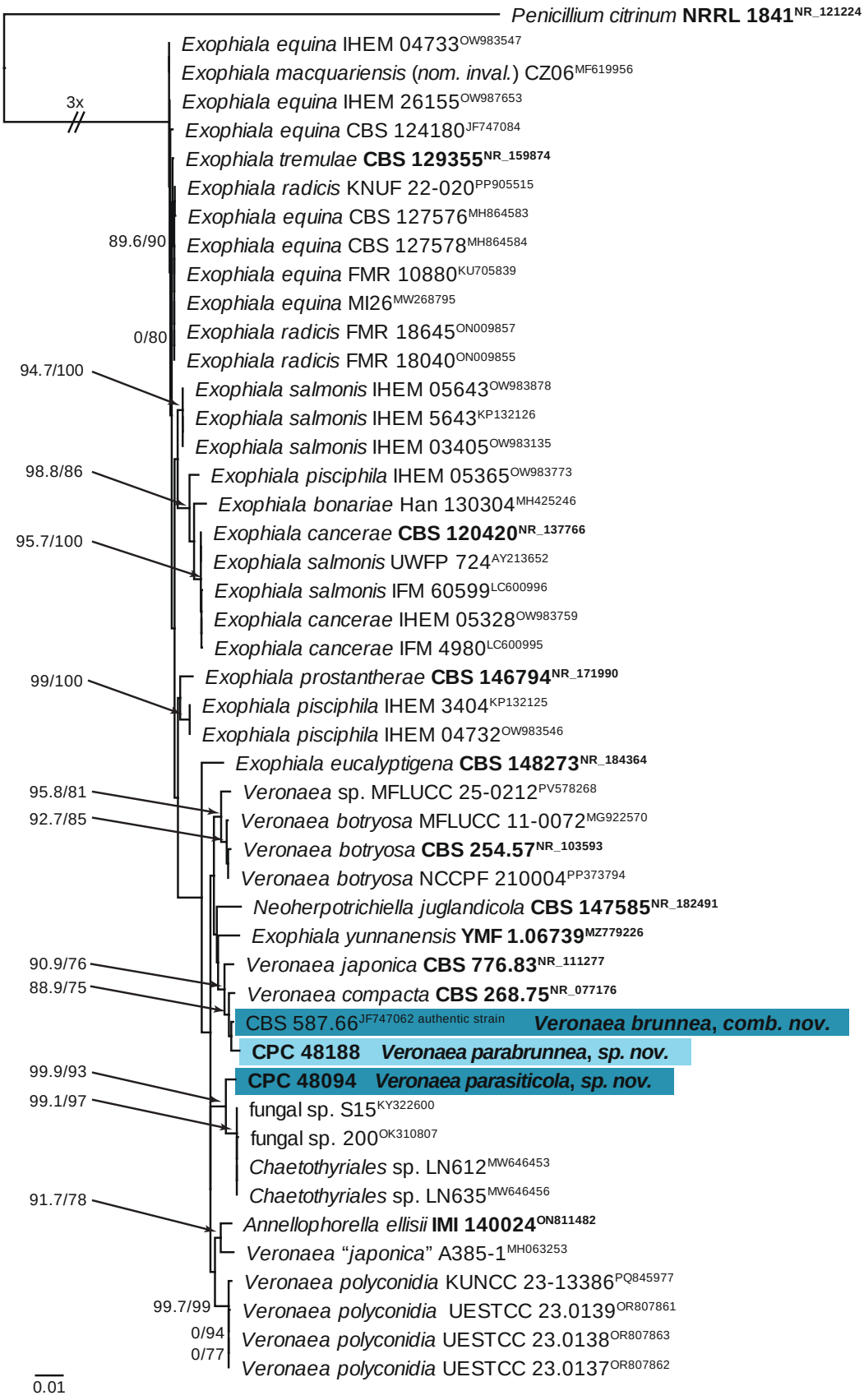

Fig. 75. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Exophiala* and *Veronaea* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Penicillium citrinum* (NRRL 1841; GenBank NR_121224) and the novelties described here are highlighted with coloured blocks and **bold** font. The root branch was shortened to facilitate layout. Alignment statistics: 48 strains including the outgroup; 613 characters including alignment gaps analysed: 258 distinct patterns, 143 parsimony-informative, 106 singleton sites, 364 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: SYM+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

Mycelium of brown, smooth, septate, branched, 1.5–2 µm diam. hyphae. *Conidiophores* subcylindrical, brown, smooth, branched or not, 0–2-septate, up to 50 µm tall, 3–3.5 µm wide. *Conidiogenous cells* brown, smooth, reduced to hyphal pegs, or ampulliform to fusoid-ellipsoid, 5–20 × 2–3.5 µm, monophialidic with apical collarette. *Conidia* solitary, brown, smooth, subcylindrical to ellipsoid to subclavate, (0–)1-septate, apex obtuse, tapering from septum to truncate hilum, 0.5 µm diam., (5–)6–7(–10) × (2.5–)3 µm.

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

Typus: **France**, Côte d'Or, Marcilly-sur-Tille, étang de Marcilly, 269 m.a.s.l., 47.51659°N, 5.14340°E, on *Eutypella prunastri* on twigs of *Prunus spinosa* (*Rosaceae*), 19 Mar. 2024, *A. Mombert*, Herb. pers. CBNM0083, HPC 4439 (**holotype** CBS H-25731, culture ex-type CPC 48188 = CBS 153520). GenBank sequences ITS: PZ221329; LSU: PZ221373; *tef1* (first part): PZ228699; *tub2*: PZ228740.

Notes: *Veronaea brunnea* (as *Exophiala brunnea*; new combination introduced below) has flask-shaped conidiogenous cells, 6–20 × 2–4 µm, and ellipsoid to ovoid, occasionally 1-septate conidia, 4.5–10 × 2–3 µm (de Hoog *et al.* 2011), and is thus morphologically similar, but phylogenetically (Fig. 75) distinct from *V. parabrunnea*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Exophiala brunnea* [strain CBS 587.66, GenBank JF747062.1; Identities = 544/560 (97 %), three gaps (0 %)], *Veronaea compacta* [strain CBS 268.75, GenBank NR_077176.1; Identities = 568/593 (96 %), four gaps (0 %)], and *Veronaea japonica* [strain CBS 776.83, GenBank NR_111277.1; Identities = 569/596 (95 %), six gaps (1 %)]. Closest hits using the **LSU** sequence are *Veronaea compacta* [strain CBS 268.75, GenBank NG_057790.1; Identities = 850/857 (99 %), one gap (0 %)], *Exophiala brunnea* [strain CBS 587.66, GenBank MH870554.1; Identities = 894/903 (99 %), one gap (0 %)], and *Veronaea japonica* [strain CBS 776.83, GenBank MH873402.1; Identities = 892/908 (98 %), three gaps (0 %)]. Closest hits using a blastn search with the ***tef1*** (first part) sequence had highest similarity to *Exophiala eucalyptigena* [strain CBS 148273, GenBank ON803564.1; Identities = 247/280 (88 %), six gaps (2 %)], *Exophiala salmonis* [strain AFTOL-ID 671, GenBank EF413612.1; Identities = 245/281 (87 %), six gaps (2 %)], and *Exophiala bergeri* [strain RBG7236, GenBank OP066900.1; Identities = 247/293 (84 %), 11 gaps (3 %)]. Closest hits using a blastn search with the ***tub2*** sequence had highest similarity to *Exophiala brunnea* [strain CBS 587.66, GenBank JN112442.1; Identities = 282/320 (88 %), 13 gaps (4 %)], *Veronaea aquatica* [strain JAUCC2549, GenBank MW248394.1; Identities = 501/569 (88 %), 12 gaps (2 %)], and *Exophiala nagquensis* [strain CGMCC 3.17284, GenBank KP347922.1; Identities = 273/317 (86 %), 13 gaps (4 %)].

Veronaea brunnea (Papendorf) Crous & Mombert, ***comb. nov.*** MB 863278.
Basionym: *Exophiala brunnea* Papendorf, *Trans. Brit. Mycol. Soc*. **52**: 487. 1969.

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

Veronaea parasiticola Crous & Hülsewig, ***sp. nov.*** MB 863279. Fig. 76.

Etymology: Name refers to its mycophilic lifestyle.

Mycelium of pale brown, smooth, brown, septate, 2–3.5 µm diam. hyphae. *Conidiophores* solitary to aggregated on hyphae, brown, smooth, subcylindrical, branched or not, 1–3-septate, 5–30 × 2.5–3 µm. *Conidiogenous cells* reduced to hyphal pegs or subcylindrical to ellipsoid, brown, smooth, terminal and intercalary, 5–15 × 2–2.5 µm, phialidic, 1–1.5 µm diam., with non-flared collarette. *Conidia* solitary, brown, smooth, guttulate, aseptate, ellipsoid, apex obtuse, tapering to truncate hilum, 0.5–1 µm diam., (4–)5(–6) × (2–)2.5(–3) µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 10 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, reverse iron grey.

Typus: **Germany**, North Rhine-Westphalia, Witten, Recreation area Hohenstein, mycoparasitic on *Dactylonectria* sp. on *Euonymus europaeus* (*Celastraceae*), 14 Mar. 2024, *T. Hülsewig*, HPC 4442, Thorben 1212 (**holotype** CBS H-25728, culture ex-type CPC 48094 = CBS 153523). GenBank sequences ITS: PZ221330; LSU: PZ221374; *tub2*: PZ228741.

Fig. 76. *Veronaea parasiticola* (CPC 48094). **A–C.** Conidiophores, conidiogenous cells and conidia. **D, E.** Conidia. Scale bars = 10 µm.

Notes: *Veronaea parasiticola* is related to *V. brunnea* and *V. parabrunnea* (described elsewhere in this study), but is phylogenetically distinct (Fig. 75), and has smaller, aseptate conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Veronaea polyconidia* [strain UESTCC 23.0138, GenBank OR807863.1; Identities = 561/608 (92 %), 13 gaps (2 %)], *Exophiala brunnea* [strain CBS 587.66, GenBank MH858890.1; Identities = 553/609 (91 %), 19 gaps (3 %)], and *Veronaea japonica* [strain CBS 776.83, GenBank MH861692.1; Identities = 553/610 (91 %), 19 gaps (3 %)]. Closest hits using the **LSU** sequence are *Helicoarctatus thailandicus* [strain MFLUCC 18-0332, GenBank MK559870.1; Identities = 847/858 (99 %), one gap (0 %)], *Exophiala pisciphila* [strain AFTOL-ID 669, GenBank DQ823101.1; Identities = 882/894 (99 %), one gap (0 %)], and *Fonsecaea pedrosoi* [strain CBS 271.37, GenBank AF050276.1; Identities = 869/881 (99 %), one gap (0 %)]. Closest hits using a blastn search with the ***tub2*** sequence had highest similarity to *Veronaea polyconidia* [strain BY110.1, GenBank OR817661.1; Identities = 302/368 (82 %), 10 gaps (2 %)], *Neoherpotrichiella juglandicola* [strain CBS 147585, GenBank ON181438.1; Identities = 367/480 (76 %), 30 gaps (6 %)], and *Veronaea botryosa* [strain DI15-135, GenBank MN477327.1; Identities = 363/476 (76 %), 20 gaps (4 %)].

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

Verrucocladosporium mesembryanthemi Crous, ***sp. nov.*** MB 863280. Fig. 77.

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

Mycelium consisting of hyaline, smooth, branched, septate, 4–6 µm diam. hyphae. *Conidiophores* arising from superficial hyphae, separate, subcylindrical, straight to geniculate-sinuous, branched below or not, becoming thick-walled, verruculose, brown, constricted or swollen at some septa, 3–12-septate, 30–150 × 6–7 µm. *Conidiogenous cells* terminal and intercalary, brown, verruculose, thick-walled, subcylindrical, 15–30 × 5–7 µm, with several thickened, darkened, coronate scars, 2–3 µm diam. *Primary ramoconidia* brown, verruculose to warty, thick-walled, subcylindrical, 25–60 × 5–7 µm; *secondary ramoconidia* fusoid-ellipsoid, 0–3-septate, 25–35 × 6–8 µm; *conidia* in branched chains, fusoid-ellipsoid, 0–1-septate, (17–)20–25(–27) × (6–)7–8 µm; all conidia brown, thick-walled, verruculose to warty, with hila thickened, darkened and refractive, 2–3 µm diam., cladosporium-like with outer rim and inner dome.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and feathery margin, reaching 10 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse umber.

Typus: **South Africa**, Western Cape Province, Cederberg, on *Mesembryanthemum schultzei* (*Aizoaceae*), Aug. 2024, *M.J. Wingfield*, HPC 4552 (**holotype** CBS H-25745, culture ex-type CPC 49172-A = CBS 153464). GenBank sequences ITS: PZ221331; LSU: PZ221375; *rpb2* (first part): PZ228780; *tef1* (first part): PZ228700.

Notes: *Verrucocladosporium mesembryanthemi* is closely related (Fig. 78) to *V. carpobroti* [on *Carpobrotus quadrifidus*, South Africa, conidia (10–)12–14(–16) × (4–)5–6 µm; Crous *et al.* 2020a], *V. visseri* [on *Carpobrotus eduli*, South Africa, conidia (8–)9–10(–11) × (3.5–)4(–4.5) µm; Crous *et al.* 2019d], and *V. dirinae* [on the lichen *Dirina massiliensis*, UK, conidia 4–18(–23) × (2-)2.5–3.5 µm; Crous *et al.* 2007]. Three of these species originate from hosts growing in the dry, extremophilic west coast of South Africa, while *V. dirinae* occurs on a lichen in the UK, suggesting that members of the genus are common in extreme environments under poor nutrient conditions.

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

Fig. 77. *Verrucocladosporium mesembryanthemi* (CPC 49172-A). **A.** Colony sporulating on SNA. **B, C.** Conidiophores. **D–F.** Conidiogenous cells giving rise to conidia. **G.** Conidia in chains. Scale bars = 10 µm.

had highest similarity to *Verrucocladosporium visseri* [strain CPC 36317, GenBank NR_166320.1; Identities = 477/487 (98 %), one gap (0 %)], *Verrucocladosporium dirinae* [strain CBS 112794, GenBank NR_152317.1; Identities = 479/490 (98 %), no gaps], and *Verrucocladosporium carpobroti* [strain CBS 146784, GenBank NR_171765.1; Identities = 605/624 (97 %), four gaps (0 %)]. Closest hits using the **LSU** sequence are *Verrucocladosporium carpobroti* [strain CBS 146784, GenBank NG_074493.1; Identities = 853/857 (99 %), no gaps], *Verrucocladosporium visseri* [strain CPC 36317, GenBank NG_068322.1; Identities = 852/858 (99 %), no gaps], and *Graphiopsis chlorocephala* [strain CPC 11969, GenBank EU009458.2; Identities = 857/865 (99 %), no gaps]. No significant hits were obtained when the ***rpb2*** and ***tef1*** sequences were used in blastn and megablast searches as only ITS and LSU sequences are available for *Verrucocladosporium* on NCBI GenBank.

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

Volutella ciliata (Alb. & Schwein.) Fr., *Syst. Mycol.* **3**(2): 467. 1832. nom. sanct. Fig. 79.

Basionym: *Tubercularia ciliata* Alb. & Schwein., *Consp. Fung. Lusat*.: 68. 1805.

Synonyms: *Atractium ciliatum* (Alb. & Schwein.) Link, *Mag. Neuesten Entdeck. Gesammten Naturk. Ges. Naturf. Freunde Berlin* **7**: 32. 1816.

Scolecofusarium ciliatum (Alb. & Schwein.) L. Lombard *et al.*, *Stud. Mycol.* **98** (no. 100116): 74. 2021. nom. inval., Art. 41.5.

Conidiomata separate, erumpent, cupulate, up to 350 µm diam., with densely aggregated central conidiophore mass, surrounded by slightly curved setae. *Setae* smooth, pale brown, thick-walled, multiseptate, apex subobtuse, thin-walled, 200–350 × 6–9 µm. *Conidiophores* hyaline, smooth, 3–6-septate, subcylindrical, extensively branched, 50–70 µm tall, 3–4 µm wide, terminating in penicillate cluster of conidiogenous cells. *Conidiogenous cells* hyaline, smooth, subcylindrical to fusoid, with elongated, curved apical part,

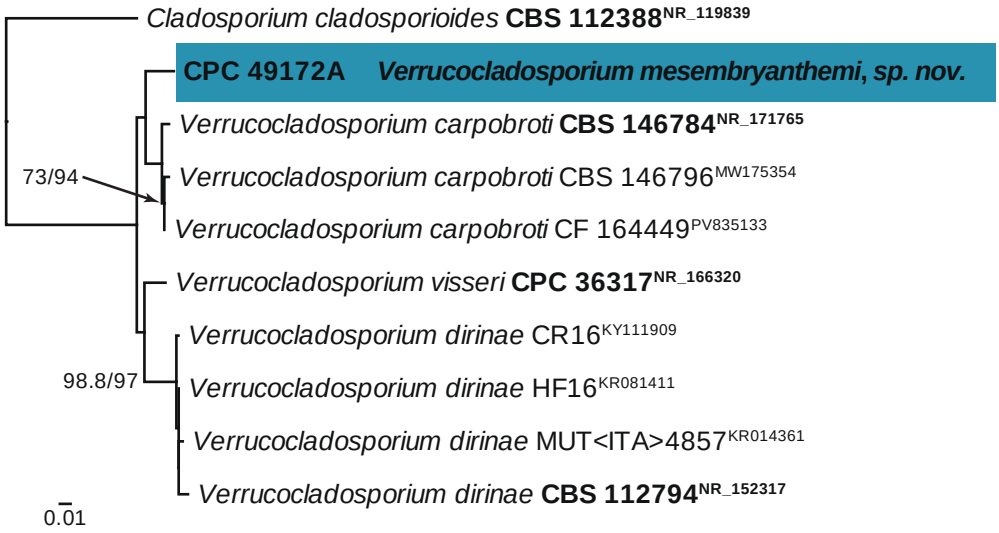

Fig. 78. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Verrucocladosporium* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Cladosporium cladosporioides* (CBS 112388; GenBank NR_119839) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 10 strains including the outgroup; 681 characters including alignment gaps analysed: 109 distinct patterns, 29 parsimony-informative, 71 singleton sites, 581 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TNe+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

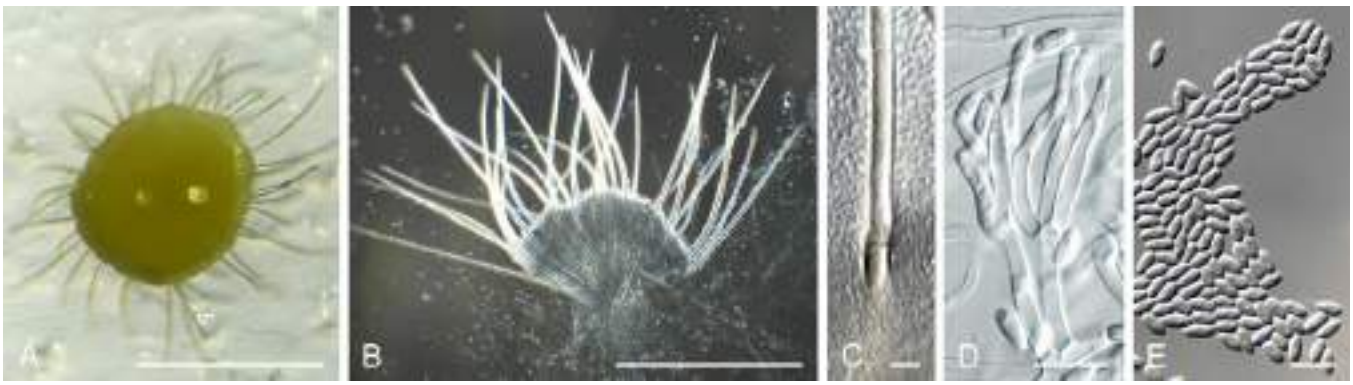

Fig. 79. *Volutella ciliata* (CPC 47881). **A, B.** Cupulate conidiomata with setae. **C.** Seta among among conidiophores. **D.** Conidiophores and conidiogenous cells giving rise to conidia. **E.** Conidia. Scale bars: A, B = 350 µm, all others = 10 µm.

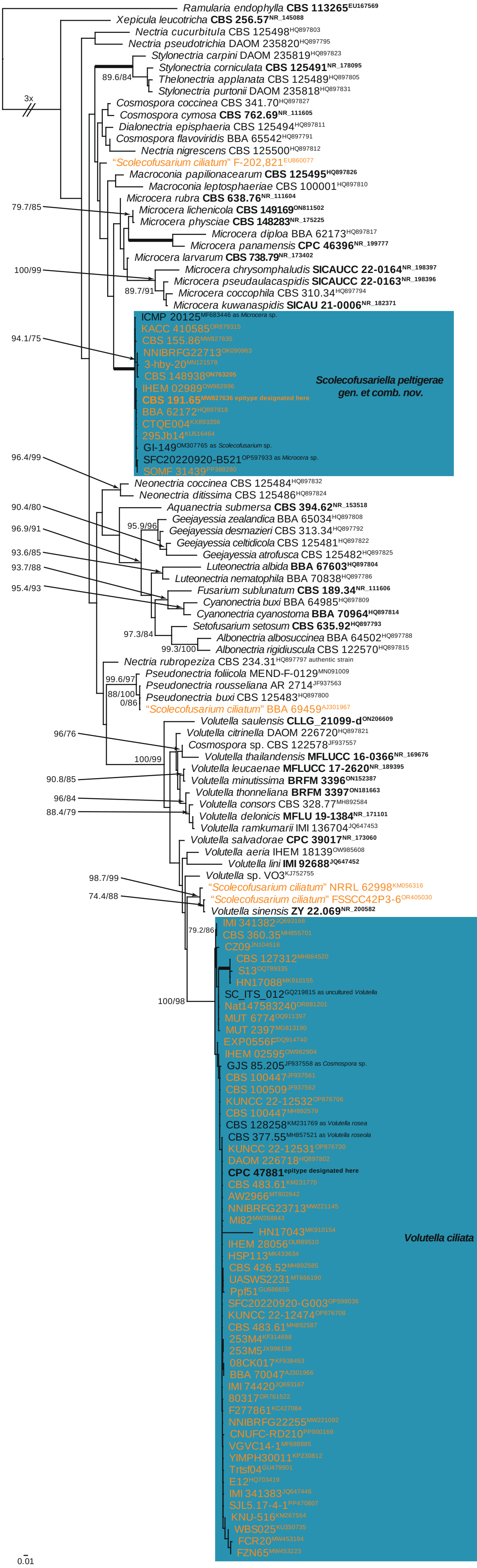

Fig. 80. Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the "*Scolecofusarium ciliatum*" ITS nucleotide alignment. Sequences labelled on GenBank as "*Scolecofusarium ciliatum*" are indicated with an orange colour. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Thickened branches resprest a SH-aLRT test value of 100 and a bootstrap support value of 100 %. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Ramularia endophylla* (CBS 113265; GenBank EU167569) and the species treated here are highlighted with coloured blocks and **bold** font. The root branch was shortened to facilitate layout. Alignment statistics: 131 strains including the outgroup; 644 characters including alignment gaps analysed: 427 distinct patterns, 225 parsimony-informative, 108 singleton sites, 311 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.31353595).

with apical collarette slightly flared, up to 3 µm long, 1–1.5 µm wide, 12–20 × 3–3.5 µm. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, ellipsoid, apex subobtuse, hilum truncate, (5–)6(–7) × 2.5–3 µm.

Culture characteristics: Colonies flat, spreading, with sparse to moderate aerial mycelium and even lobate margins, reaching 60 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface pale luteous, and reverse luteous.

Typus: **Germany**, Lausitz, MEL 2332148 (**lectotype** designated here, MBT 10032796) (see Karakehian *et al.* 2025). **France**, Côte d'Or, Boussenois, combe du jeune Sagne, 369 m.a.s.l., 47.63629°N, 5.20964°E, on *Hypoxylon perforatum* on wood of *Fraxinus* (*Oleaceae*), 3 Sep. 2024, *A. Mombert*, Herb. pers. CBNM0082, HPC 4438 (**epitype** designated here CBS H-25798, MBT 10032797, culture ex-type CPC 47881 = CBS 154453). GenBank sequences ITS: PZ221332; *cmdA*: PZ228622; *tef1* (first part): PZ228701.

Notes: "*Scolecofusarium*" is monotypic, and has fusoid, long, flexuous, multiseptate conidia (Crous *et al.* 2021a). Cultures commonly referred to in literature as *Volutella ciliata*, have aseptate conidia, and represent a distinct genus and species. However, as shown here, the name "*Scolecofusarium ciliatum*" is a synonym of *Volutella ciliata*, as it is based on the same basionym, *Tubercularia ciliata*, thus being unavailable for this species. From the phylogenetic tree (Fig. 80) it is clear that sequences labelled as "*Scolecofusarium ciliatum*" in NCBI GenBank are not all conspecific, with a large group forming a sister clade to *Microcera* (*Scolecofusariella*, see below) and a second larger group clusters with *Volutella* s. str. and represent *Volutella ciliata*.

Scolecofusariella Sand.-Den. & Crous, ***gen. nov.*** MB 863521.
Misapplied name: *Scolecofusarium* L. Lombard *et al.* (Crous *et al.* 2021: 74), nom. inval. (Art. 6.2, 40.3).

Type species: *Fusarium peltigerae* Westend.

Description: Crous *et al.* (2021: 74, under *Scolecofusarium*), adapted from Samuels *et al.* (1991) & Gerlach & Nirenberg (1982).

Scolecofusariella peltigerae (Westend.) Sand.-Den. & Crous, ***comb. nov.*** MB 863522.
Basionym: *Fusarium peltigerae* Westend., *Herb. Crypt. Belg*. **9**: no. 414. 1849.
Misapplied name: as *Scolecofusarium ciliatum* "(Link)" L. Lombard *et al.* (Crous *et al.* 2021: 74), nom. inval. (Art. 41.5).

Typus: **Belgium**, aux environs de Courtrai (Kortrijk), Oct., on thalli of *Peltigera rufescens* [Westend., Herb. Crypt. Belg. 414] (BR5020140796491, **lectotype** designated here, MBT 10032798). **Germany**, on branch canker of *Fagus sylvatica*, 1961, *W. Gerlach* (**epitype** designated here, CBS H-12687, MBT 10032799), culture ex-epitype CBS 191.65 = ATCC 16068 = ATCC 24137 = BBA 9661 = DSM 62172 = IMI 112499 = NRRL 20431).

Description: See Crous *et al.* (2021a: 74, under *Scolecofusarium*).

Notes: The names *Scolecofusarium* and *Scolecofusarium ciliatum* are invalid, caused by previous confusions around the epithet "*ciliatum*", such as in the case of *Atractium* and *Fusarium ciliatum*. These names were previously assigned to Link (e.g., Gerlach & Nirenberg 1982), although they are combinations based on *Tubercularia ciliata* Alb. & Schwein. The confused nomenclature of these names requires the introduction of new unequivocal names for the genus and its type species. The originally intended "type species" of *Scolecofusarium*, *Atractium ciliatum* (Alb. & Schwein.) Link (≡ *Tubercularia ciliata* Alb. & Schwein.), pertains to *Volutella* (nom. cons. et nom. sanct.), and is the type species of the latter genus, i.e., this species name is not applicable as type for *Scolecofusariella*. *Fusarium peltigerae* is the next available name (see Gerlach & Nirenberg 1982: 87). Hawksworth (1979) had examined type material of *F. peltigerae* deposited in herb. Kew [K(M) 408838, slide ex-type IMI 223542]. Crous *et al.* (2021a) listed *Sphaeria agnina* Desm. [≡ *Calonectria agnina* (Desm.) Sacc.] as synonym of *Scolecofusarium ciliatum*, and Gerlach & Nirenberg (1982) cited *Calonectria decora* (Wallr.) Sacc. as sexual morph of "*Fusarium ciliatum* Link" which goes back to Wollenweber (1943). However, these assumptions were not based on examinations of designated types and are not applicable. *Sphaeria decora* Wallr., the basionym of *Calonectria decora*, was neotypified by Rossman (1983), and Lechat & Fournier (2018) re-allocated this species to *Flammocladiella*, including synonymy of *Flammocladiella aceris* Crous *et al.*, *Sphaeria agnina*, and *Nectria massariae* Pass., which was also listed as synonym of *Scolecofusarium ciliatum* by Crous *et al.* (2021a).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Scolecofusarium ciliatum* [strain CBS 483.61, GenBank MH892587.1; Identities = 545/545 (100 %), no gaps], *Volutella roseola* [strain CBS 377.55, GenBank MH857521.1; Identities = 545/546 (99 %), one gap (0 %)], and *Volutella salvadorae* [strain CBS 147070, GenBank NR_173060.1; Identities = 515/546 (94 %), three gaps (0 %)]. Closest hits using the ***cmdA*** sequence in a blastn search had highest similarity to *Scolecofusarium ciliatum* [strain CBS 426.52, GenBank MH936836.1; Identities = 425/437 (97 %), three gaps (0 %)], and *Volutella rosea* [strain CBS 128258, GenBank KM231335.1; Identities = 624/648 (96 %), five gaps (0 %)]. Closest hits using the ***tef1*** (first part) sequence in a blastn search had distant similarity to *Volutella rosea* [strain CBS 128258, GenBank KM231900.1; Identities = 491/524 (94 %), 11 gaps (2 %)], *Volutella leucaenae* [voucher MFLU 19-0977, GenBank ON892551.1; Identities = 414/524 (79 %), 40 gaps (7 %)], and *Volutella consors* [strain CBS 139.79, GenBank KM231899.1; Identities = 424/539 (79 %), 39 gaps (7 %)].

Authors: P.W. Crous, J.Z. Groenewald, K. Bensch, U. Braun & A. Mombert

ACKNOWLEDGEMENTS

This research of H. Madrid and colleagues was funded by Comisión Nacional de Investigación Científica y Tecnológica (CONICYT), Fondo Nacional de Desarrollo Científico y Tecnológico (FONDECYT), Chile, project no. 11140562. The work of P.W. Crous and colleagues benefitted from funding by the European Union's Horizon 2020 research and innovation program (RISE) under the Marie Skłodowska-Curie grant agreement No. 101008129, project acronym "Mycobiomics", and the Dutch NWO Roadmap grant agreement No. 2020/ENW/00901156, project "Netherlands Infrastructure for Ecosystem and Biodiversity Analysis – Authoritative and Rapid Identification System for Essential biodiversity information" (acronym NIEBA-ARISE). The study of M. Piątek, M. Stryjak-Bogacka and P. Czachura was supported by the statutory funds of the W. Szafer Institute of Botany, Polish Academy of Sciences, Kraków (Poland).

Declaration on conflict of interest The authors include members of the Editorial Board of Persoonia. They were not involved in the journal's review of, or decisions related to, this manuscript.

REFERENCES

Abad ZG, Burgess TI, Bourret T, *et al.* (2023). *Phytophthora*: taxonomic and phylogenetic revision of the genus. *Studies in Mycology* **106**: 259–348. https://doi.org/10.3114/sim.2023.106.05

Abdollahzadeh J, Groenewald JZ, Coetzee MPA, *et al.* (2020). Evolution of lifestyles in *Capnodiales*. *Studies in Mycology* **95**: 381–414. https://doi.org/10.1016/j.simyco.2020.02.004

Aloi F, Zamora-Ballesteros C, Martín-García J, *et al.* (2021). Co-infections by *Fusarium circinatum* and *Phytophthora* spp. on *Pinus radiata*: complex phenotypic and molecular Interactions. *Plants* **10**: 1976. https://doi.org/10.3390/plants10101976

Attili-Angelis D, Duarte APM, Pagnocca FC, *et al.* (2014). Novel *Phialophora* species from leaf-cutting ants (tribe *Attini*). *Fungal Diversity* **65**: 65–75. https://doi.org/10.1007/s13225-013-0275-0

Badali H, Gueidan C, Najafzadeh MJ, *et al.* (2008). Biodiversity of the genus *Cladophialophora*. *Studies in Mycology* **61**: 175–191. https://doi.org/10.3114/sim.2008.61.18.

Bao DF, Hyde KD, McKenzie EHC, *et al.* (2021). Biodiversity of lignicolous freshwater hyphomycetes from China and Thailand and description of sixteen species. *Journal of Fungi* **7**: 669. https://doi.org/10.3390/jof7080669

Batzer JC, Mercedes Diaz Arias M, Harrington TC, *et al.* (2008). Four species of *Zygophiala* (*Schizothyriaceae, Capnodiales*) are associated with the sooty blotch and flyspeck complex on apple. *Mycologia* **100**: 246–258. https://doi.org/10.1080/15572536.2008.11832480

Boonmee S, Rossman AY, Liu JK, *et al.* (2014). *Tubeufiales*, *ord. nov*., integrating sexual and asexual generic names. *Fungal Diversity* **68**: 239–298. https://doi.org/10.1007/s13225-014-0304-7

Booth C (1959). Studies of pyrenomycetes IV. *Nectria* (part 1). *Mycological Papers* **73**: 1–115.

Brasch J, Dressel S, Müller-Wening K, *et al.* (2011). Toenail infection by *Cladophialophora boppii*. *Medical Mycology* **49**: 190–193. https://doi.org/10.3109/13693786.2010.516458

Bunce ME (1961). *Humicola stellatus sp. nov*., a thermophylic mould from hay. *Transactions of the British Mycological Society* **44**: 372–376.

Cejp K (1971). Some Members of the *Sphaeropsidales* from South Africa. *Bothalia* **10**: 341–346. https://doi.org/10.4102/abc.v10i2.1528

Cheek M, Lughadha EC, Kirk P, *et al.* (2020). New scientific discoveries: Plants and fungi. *Plants, People and Planet* **2**: 371–388. https://doi.org/10.1002/ppp3.10148

Conti Taguali S, La Spada F, Pane A, *et al.* (2025). Are environmental factors correlated with the diversity of *Phytophthora* in organically and conventionally managed citrus orchards in Sicily? Insights from metabarcoding and baiting. *Mycological Progress* **24**: 76. https://doi.org/10.1007/s11557-025-02091-2.

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, Braun U, Schubert K, *et al.* (2007). Delimiting *Cladosporium* from morphologically similar genera. *Studies in Mycology* **58**: 33–56. https://doi.org/10.3114/sim.2007.58.02.

Crous PW, Carnegie AJ, Wingfield MJ, *et al.* (2019a). Fungal Planet description sheets: 868–950. *Persoonia* **42**: 291–473. https://doi.org/10.3767/persoonia.2019.42.11.

Crous PW, Cowan DA, Maggs-Kölling G, *et al.* (2020a). Fungal Planet description sheets: 1112–1181. *Persoonia* **45**: 251–409. https://doi.org/10.3767/persoonia.2020.45.10.

Crous PW, Dijksterhuis J, Figge M, *et al.* (2024a). *Mjuua agapanthi gen. et sp. nov*., a biotrophic mycoparasite of *Fusarium* spp. *Fungal Systematics and Evolution* **13**: 153–161. https://doi.org/10.3114/fuse.2024.13.09

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 (2016). They seldom occur alone. *Fungal Biology* **120**: 1392–1415. https://doi.org/10.1016/j.funbio.2016.05.009.

Crous PW, Groenewald JZ, Bensch K, *et al.* (2025). Genera of phytopathogenic fungi known from culture: 1–379. *Studies in Mycology* **112**: 261–633. https://doi.org/10.3114/sim.2025.112.05

Crous PW, Jurjević Z, Balashov S, *et al.* (2024b). Fungal Planet description sheets: 1614–1696. *Fungal Systematics and Evolution* **13**: 183–440. https://doi.org/10.3114/fuse.2024.13.11

Crous PW, Lombard L, Sandoval-Denis M, *et al.* (2021a). *Fusarium*: more than a node or a foot-shaped basal cell. *Studies in Mycology* **98**: 100116. https://doi.org/10.1016/j.simyco.2021.100116.

Crous PW, Luangsa-Ard JJ, Wingfield MJ, *et al.* (2018). Fungal Planet description sheets: 785–867. Persoonia 41: 238–417. https://doi.org/10.3767/persoonia.2018.41.12

Crous PW, Osieck ER, Jurjević Ž, *et al.* (2021b). Fungal Planet description sheets: 1284–1382. *Persoonia* **47**: 178–374. https://doi.org/10.3767/persoonia.2021.47.06

Crous PW, Schubert K, Braun U, *et al.* (2007). Opportunistic, human-pathogenic species in the *Herpotrichiellaceae* are phenotypically similar to saprobic or phytopathogenic species in the *Venturiaceae. Studies in Mycology* **58**: 185–217. https://doi.org/10.3114/sim.2007.58.07

Crous PW, Schumacher RK, Akulov A, *et al.* (2019b). New and interesting fungi. 2. *Fungal Systematics and Evolution* **3**: 57–134. https://doi.org/10.3114/fuse.2019.03.06

Crous PW, Shivas RG, Quaedvlieg W, *et al.* (2014). Fungal Planet description sheets: 214–280. *Persoonia* **32**: 184–306. https://doi.org/10.3767/003158514X682395

Crous PW, Tanaka K, Summerell BA, *et al.* (2011). Additions to the *Mycosphaerella* complex. *IMA Fungus* **2**: 49–64. https://doi.

org/10.5598/imafungus.2011.02.01.08

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

Crous PW, Wingfield MJ (1991). *Mycosphaerella marasasii sp. nov*. and its *Pseudocercospora* anamorph on leaves of *Syzygium cordatum*. *Mycological Research* **95**: 1108–1102.

Crous PW, Wingfield MJ, Burgess TI, *et al.* (2017). Fungal Planet description sheets: 625–715. *Persoonia* **39**: 270–467. https://doi.org/10.3767/persoonia.2017.39.11

Crous PW, Wingfield MJ, Guarro J, *et al.* (2015). Fungal Planet description sheets: 320–370. *Persoonia* **34**: 167–266. https://doi.org/10.3767/003158515x688433

Crous PW, Wingfield MJ, Jurjević Ž, *et al.* (2024c). Fungal Planet description sheets: 1697–1780. *Fungal Systematics and Evolution* **14**: 325–577. https://doi.org/10.3114/fuse.2024.14.19.

Crous PW, Wingfield MJ, Lombard L, *et al.* (2019d). Fungal Planet description sheets: 951–1041. *Persoonia* **43**: 223–425. https://doi.org/10.3767/persoonia.2019.43.06.

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.* (2020b). New and Interesting Fungi 3. *Fungal Systematics and Evolution* **6**: 157–231. https://doi.org/10.3114/fuse.2020.06.09

Czachura P, Janik P, Piątek M (2025). *Chaetocapnodium magnum* and *Chaetocapnodium polonicum* from conifer resins disclose an unknown lifestyle in the *Capnodiales* (*Dothideomycetes*). *MycoKeys* **119**: 315–333. https://doi.org/10.3897/mycokeys.119.159094

Darriba D, Taboada GL, Doallo R, *et al.* (2012). jModelTest 2: more models, new heuristics and parallel computing. *Nature Methods* **9**: 772–772. https://doi.org/10.1038/nmeth.2109

de Hoog GS, Hermanides-Nijhof EJ (1977). The black yeasts and allied Hyphomycetes. *Studies in Mycology* **15**: 1–222.

de Hoog GS, Vicente VA, Najafzadeh MJ, *et al.* (2011). Waterborne *Exophiala* species causing disease in cold-blooded animals. *Persoonia* **27**: 46–72. https://doi.org/10.3767/003158511X614258.

Dennis RWG (1986). *Fungi of the Hebrides.* Royal Botanic Gardens, Kew, UK.

Dennis RWG (1988). Some overlooked fungi on British *Cyperaceae*. *Transactions of the Botanical Society of Edinburgh* **45**: 213–216.

Du TY, Tibpromma S, Hyde KD, *et al.* (2024). The polyphasic approach reveals ten novel and one known *Ascomycota* taxa from terrestrial agarwood-producing trees. *Journal of Systematics and Evolution* **63**: 431–468. https://doi.org/10.1111/jse.13128

Duarte LL, Santos FMC, Barreto RW (2016). Mycobiota of the weed *Conyza canadensis* (*Asteraceae*) in Brazil. *Fungal Biology* **120**: 1118-1134. doi: 10.1016/j.funbio.2016.05.015

Edler D, Klein J, Antonelli A, *et al.* (2021). raxmlGUI 2.0: A graphical interface and toolkit for phylogenetic analyses using RAxML. *Methods in Ecology and Evolution* **12**: 373–377. https://doi.org/10.1111/2041-210X.13512

Egidi E, de Hoog GS, Isola D, *et al.* (2014). Phylogeny and taxonomy of meristematic rock-inhabiting black fungi in the *Dothideomycetes* based on multi-locus phylogenies. *Fungal Diversity* **65**: 127–165. https://doi.org/10.1007/s13225-013-0277-y

Ellis MB (1971). *Dematiaceous Hyphomycetes*. Commonwealth Mycological Institute, Kew, Surrey, England.

Erwin DC, Ribeiro OK (1996). *Phytophthora diseases worldwide*. American Phytopathological Society (APS Press), St. Paul, Minnesota, USA. https://doi.org/10.1046/j.1365-3059.1998.0179a.x

Gams W, Stielow B, Gräfenhan T, *et al.* (2019). The ascomycete genus *Niesslia* and associated monocillium-like anamorphs. *Mycological Progress* **18**: 5–76. https://doi.org/10.1007/s11557-018-1459-5

Gerlach W, Nirenberg H (1982). The genus *Fusarium* – a pictorial atlas. *Mitteilungen aus der Biologischen Bundesanstalt für Land- und Forstwirtschaft Berlin-Dahlem* **209**: 1–406.

Gräfenhan T, Schroers H-J, Nirenberg HI, *et al.* (2011). An overview of the taxonomy, phylogeny, and typification of nectriaceous fungi in *Cosmospora, Acremonium, Fusarium, Stilbella*, and *Volutella*. *Studies in Mycology* **68**: 79–113. https://doi.org/10.3114/sim.2011.68.04.

Hawksworth DL (1979). The lichenicolous Hyphomycetes. *Bulletin of the British Museum (Natural History), Botany* **6**: 183–300.

Hawksworth DL, Lücking R (2017). Fungal diversity revisited: 2.2 to 3.8 million species. *Microbiology Spectrum* **5**: FUNK-0052-2016. https://doi.org/10.1128/microbiolspec.funk-0052-2016

Hernández-Restrepo M, Gené J, Mena-Portales J, *et al.* (2014) New species of *Cordana* and epitypification of the genus. *Mycologia* **106**: 723–734. http://dx.doi.org/10.3852/13-122

Hernández-Restrepo M, Groenewald JZ, Crous PW (2016). Taxonomic and phylogenetic re-evaluation of *Microdochium*, *Monographella* and *Idriella*. *Persoonia* **36**: 57–82. https://doi.org/10.3767/003158516X688676

Hou LW, Giraldo A, Groenewald JZ, *et al.* (2023). Redisposition of acremonium-like fungi in *Hypocreales*. *Studies in Mycology* **105**: 23–203. https://doi.org/10.3114/sim.2023.105.02.

Houbraken J, de Vries RP, Samson RA (2014). Modern taxonomy of biotechnologically important *Aspergillus* and *Penicillium* species. *Advances in Applied Microbiology* **86**: 199–249. https://doi.org/10.1016/B978-0-12-800262-9.00004-4

Houbraken J, Kocsubé S, Visagie CM, *et al.* (2020). Classification of *Aspergillus*, *Penicillium*, *Talaromyces* and related genera (*Eurotiales*): An overview of families, genera, subgenera, sections, series and species. *Studies in Mycology* **95**: 5–169. https://doi.org/10.1016/j.simyco.2020.05.002

Hu MJ, Cox KD, Schnabel G, *et al.* (2011). *Monilinia* species causing brown rot of peach in China. *PLoS ONE* **6**: e24990. https://doi.org/10.1371/journal.pone.0024990.

Hyde KD, Noorabadi MT, Thiyagaraja V, *et al.* (2024). The 2024 Outline of *Fungi* and fungus-like taxa. *Mycosphere* **15**: 5146–6239. https://doi.org/10.5943/mycosphere/15/1/25

Hyde KD, Tennakoon DS, Jeewon R, *et al.* (2019). Fungal diversity notes 1036–1150: taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity* **96**: 1–242. https://doi.org/10.1007/s13225-019-00429-2

Iturrieta-González I, Gené J, Wiederhold N, *et al.* (2020). Three new *Curvularia* species from clinical and environmental sources. *MycoKeys* **68**: 1–21. https://doi.org/10.3897/mycokeys.68.51667

Jagielski T, Sandoval-Denis M, Yu J, *et al.* (2016). Molecular taxonomy of scopulariopsis-like fungi with description of new clinical and environmental species. *Fungal Biology* **120**: 586–602. doi: 10.1016/j.funbio.2016.01.014

Jung T, Blaschke H, Neumann P (1996). Isolation, identification and pathogenicity of *Phytophthora* species from declining oak stands. *European Journal of Forest Pathology* **26**: 253–272. https://doi.org/10.1111/j.1439-0329.1996.tb00846.x

Jung T, Horta Jung M, Cacciola SO, *et al.* (2017). Multiple new cryptic pathogenic *Phytophthora* species from *Fagaceae* forests in Austria, Italy and Portugal. *IMA Fungus* **8**: 219–244. https://doi.org/10.5598/imafungus.2017.08.02.02.

Kalyaanamoorthy S, Minh BQ, Wong TKF, *et al.* (2017). ModelFinder: Fast model selection for accurate phylogenetic estimates. *Nature Methods* **14**: 587–589. https://doi.org/10.1038/nmeth.4285

Karakehian JM, Rödel T, Damm U, *et al.* (2025). Specimens in the National Herbarium of Victoria, Australia (MEL) and in Naturalis Biodiversity Center of Leiden, Netherlands (L) associated with Albertini and Schweinitz's Conspectus fungorum in Lusatiae superioris. *TAXON* **74**: 174–190. https://doi.org/10.1002/tax.13239

Kirschstein W (1939). Über neue, seltene und kritische Ascomyceten und Fungi imperfecti. II. *Annales Mycologici* **37**: 88–140.

Koukol O (2012). A new species of *Infundichalara* from pine litter. *Mycotaxon* **120**: 343–352. https://doi.org/10.5248/120.343

Koukol O, Seifertová P (2026). Unravelling anamorph-teleomorph connections allows proper classification of chalara-like anamorphs of *Helotiales* and *Chaetosphaeriales*. *Mycologia* **118**: 163–189. https://doi.org/10.1080/00275514.2025.2562791.

Kozlov AM, Darriba D, Flouri T, *et al.* (2019). RAxML-NG: a fast, scalable and user-friendly tool for maximum likelihood phylogenetic inference. *Bioinformatics* **35**: 4453–4455. https://doi.org/10.1093/bioinformatics/btz305

Kumar S, Stecher G, Li M, *et al.* (2018). MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. *Molecular Biology and Evolution* **35**: 1547–1549. https://doi.org/10.1093/molbev/msy096

Lechat C, Fournier J (2018). *Flammocladiella decora*, a new combination to accommodate the hypocrealean fungus *Nectria decora*. *Ascomycete.org* **10**(1): 48–54. https://doi.org/10.25664/ART-0227

Lechat C, Fournier J, Gardiennet A (2019). Three new species of *Dialonectria* (*Nectriaceae*) from France. *Ascomycete.org* **11**: 5–11. https://doi.org/10.25664/art-0251

Li DW, Schultes N, Vossbrinck C (2016). *Olpitrichum sphaerosporum*: a new USA record and phylogenetic placement. *Mycotaxon* **131**: 123–133.

Li Y, Xiao J, de Hoog GS, *et al.* (2017). Biodiversity and human-pathogenicity of *Phialophora verrucosa* and relatives in *Chaetothyriales*. *Persoonia* **38**: 1–19. https://doi.org/10.3767/003158517X692779.

Linaldeddu BT, Deidda A, Scanu B *et al.* (2016). Phylogeny, morphology and pathogenicity of *Botryosphaeriaceae*, *Diatrypaceae* and *Gnomoniaceae* associated with branch diseases of hazelnut in Sardinia (Italy). *European Journal of Plant Pathology* **146***:* 259–279. https://doi.org/10.1007/s10658-016-0912-z

Ma C, He S-C, Cai T, *et al.* (2025). A new species of *Stachylidium* (*Trichosphaeriaceae*) from Xizang, China. *Phytotaxa* **694**: 77–85. https://doi.org/10.11646/phytotaxa.694.1.6

Madrid H, da Cunha KC, Gené J, *et al.* (2014). Novel *Curvularia* species from clinical specimens. *Persoonia* **33**: 48–60. 10.3767/003158514X683538

Manamgoda DS, Rossman AY, Castlebury LA, *et al.* (2014) The genus *Bipolaris*. *Studies in Mycology* **79**: 221–288. https://doi.org/10.1016/j.simyco.2014.10.002

Mapook A, Hyde KD, McKenzie EHC, *et al.* (2020). Taxonomic and phylogenetic contributions to fungi associated with the invasive weed *Chromolaena odorata* (Siam weed). *Fungal Diversity* **101**: 1–175. https://doi.org/10.1007/s13225-020-00444-8

Marin-Felix Y, Groenewald JZ, Cai L, *et al.* (2017). Genera of phytopathogenic fungi: GOPHY1. *Studies in Mycology* **86**: 99–216. https://doi.org/10.1016/j.simyco.2017.04.002

Marin-Felix Y, Hernández-Restrepo M, Iturrieta-González I, *et al.* (2019). Genera of phytopathogenic fungi: GOPHY 3. *Studies in Mycology* **94**: 1–124. https://doi.org/10.1016/j.simyco.2019.05.001

Martino I, Monchiero M, Gullino ML, *et al.* (2024). Characterization and pathogenicity of fungal species associated with hazelnut trunk diseases in North-western Italy. *Journal of Plant Pathology* **107**: 87–105. https://doi.org/10.1007/s42161-024-01595-2

Matsushima T (2003). Matsushima Mycological Memoirs 10. *Matsushima Mycological Memoirs* **10**: 1–214.

Mehrabi-Koushki M, Pooladi P, Eisvand P, *et al.* (2018) *Curvularia ahvazensis* and *C. rouhanii* spp. nov. from Iran. *Mycosphere* **9**: 1173–1186. https://doi.org/10.5943/mycosphere/9/6/7

Miller MA, Pfeiffer W, Schwartz T (2010). Creating the CIPRES Science Gateway for inference of large phylogenetic trees. In: *Proceedings of the Gateway Computing Environments Workshop (GCE)*, 14 Nov. 2010. New Orleans, Louisiana: 1–8. https://doi.org/10.1109/GCE.2010.5676129

Minh BQ, Schmidt HA, Chernomor O, *et al.* (2020). IQ-TREE 2: New models and efficient methods for phylogenetic inference in the genomic era. *Molecular Biology and Evolution* **37**: 1530–1534. https://doi.org/10.1093/molbev/msaa015

Mo YK, Lanfear R, Hahn MW, *et al.* (2023). Updated site concordance factors minimize effects of homoplasy and taxon sampling. *Bioinformatics* **39**: btac741. https://doi.org/10.1093/bioinformatics/btac741

Moreno-Rico O, Groenewald JZ, Crous PW (2014). Foliicolous fungi from *Arctostaphylos pungens* in Mexico. *IMA Fungus* **5**: 7–15. https://doi.org/10.5598/imafungus.2014.05.01.02.

Morgenstern I, Powlowski J, Ishmael N, *et al.* (2012). A molecular phylogeny of thermophilic fungi. *Fungal Biology* **116**: 489–502. https://doi.org/10.1016/j.funbio.2012.01.010

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

Niskanen T, Lücking R, Dahlberg A, *et al.* (2023). Pushing the frontiers of biodiversity research: Unveiling the global diversity, distribution, and conservation of fungi. *Annual Review of Environment and Resources* **48**: 149–176. https://doi.org/10.1146/annurev-environ-112621-090937

Perdomo H, García D, Gené J, *et al.* (2013). *Phialemoniopsis*, a new genus of *Sordariomycetes*, and new species of *Phialemonium* and *Lecythophora*. *Mycologia* **105**: 398–421. https://doi.org/10.3852/12-137.

Piątek M, Stryjak-Bogacka M, Czachura P (2024). *Arthrocatenales*, a new order of extremophilic fungi in the *Dothideomycetes*. *MycoKeys* **108**: 47–74. https://doi.org/10.3897/mycokeys.108.128033

Posada D, Crandall KA (1998). MODELTEST: testing the model of DNA substitution. *Bioinformatics* **14**: 817–818. https://doi.org/10.1093/bioinformatics/14.9.817

Quaedvlieg W, Verkley GJ, Shin HD, *et al.* (2013). Sizing up *Septoria*. *Studies in Mycology* **75**: 307–390. https://doi.org/10.3114/sim0017.

Ramaley AW (1996). *Comminutispora gen. nov*. and its *Hyphospora gen. nov*. anamorph. *Mycologia* **88**: 132–136. https://doi.org/10.1080/00275514.1996.12026633

Rayner RW (1970). *A Mycological Colour Chart*. Commonwealth Mycological Institute, UK.

Réblová M, Nekvindová J, Bauchová L, *et al.* (2025). *Pleurophragmium parvisporum* (*Ascomycota*): One name, seven stories – a case highlighting the need for verification of strains from public culture collections. *IMA Fungus* **16**: e173033. https://doi.org/10.3897/imafungus.16.173033

Rocchi F, Quaroni S, Sardi P, *et al.* (2010). Studies on *Anthostoma decipiens* involved in *Carpinus betulus* decline. *Journal of Plant*

Pathology **92**: 637–644.

Ronquist F, Huelsenbeck JP (2003). MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* **19**: 1572–1574. https://doi.org/10.1093/bioinformatics/btg180

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. https://doi.org/10.1093/sysbio/sys029

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. https://doi.org/10.1093/sysbio/sys029

Rossman AY (1983). The phragmosporous species of *Nectria* and related genera. *Mycological Papers* **150**: 1–164.

Ruibal C, Platas G, Bills GF (2008). High diversity and morphological convergence among melanised fungi from rock formations in the Central Mountain System of Spain. *Persoonia* **21**: 93–110. https://doi.org/10.3767/003158508X371379

Salerno M (1961). *Cytospora corylicola* Sacc. e patogenesi del «Mal dello stacco» del nocciolo (*Corylus avellana* L.) in Sicilia. *Rivista di Patologia Vegetale* **38***:* 38–64.

Sandoval-Denis M, Gené J, Sutton DA, *et al.* (2016). Redefining *Microascus*, *Scopulariopsis* and allied genera. *Persoonia* **36**: 1–36. https://doi.org/10.3767/003158516X688027

Saracchi M, Rocchi F, Quaroni S (2008). Further studies on the etiological agents of *Carpinus betulus* decline. *Journal of Plant Pathology* **90**: 453–453.

Scanu B, Linaldeddu BT, Deidda A, *et al.* (2015). Diversity of *Phytophthora* species from declining Mediterranean maquis vegetation, including two new species, *Phytophthora crassamura* and *P. ornamentata* sp. nov. *PLoS ONE* **10**: e0143234. https://doi.org/10.1371/journal.pone.0143234

Seifert KA (1985). A monograph of *Stilbella* and some allied Hyphomycetes. *Studies in Mycology* **27**: 1–235.

Servazzi O (1950). Brevi notizie sulla “Moria” o “Seccume” del Nocciolo gentile delle Langhe. *Nuovo Giornale Botanico Italiano* **57**: 679–682.

Sivanesan A (1987). Graminicolous species of *Bipolaris*, *Curvularia*, *Drechslera*, *Exserohilum* and their teleomorphs. *Mycological Papers* **158**: 154–185.

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.

Stamatakis A (2014). RAxML version 8: A tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics* (Oxford, England) **30**: 1312–1313. https://doi.org/10.1093/bioinformatics/btu033

Steindorff AS, Aguilar-Pontes MV, Robinson AJ, *et al.* (2024). Comparative genomic analysis of thermophilic fungi reveals convergent evolutionary adaptations and gene losses. *Communications Biology* **7**: 1124. https://doi.org/10.1038/s42003-024-06681-w

Sun Y-R, Shen H-W, Liu N-G, *et al.* (2025) *Pseudodactylaria yunnanensis sp. nov.* (*Pseudodactylariaceae*) from China. *Phytotaxa* **701**: 189–198. https://doi.org/10.11646/phytotaxa.701.2.5

Tamura K, Stecher G, Kumar S (2021). MEGA11: Molecular Evolutionary Genetics Analysis version 11. *Molecular Biology and Evolution* **38**: 3022–3027. https://doi.org/10.1093/molbev/msab120

Tan YP, Shivas RG (2023). Index of Australian Fungi no. 19. Zenodo. https://doi.org/10.5281/zenodo.10005579

Tanaka K, Hirayama K, Yonezawa H, *et al.* (2015). Revision of the *Massarineae* (*Pleosporales, Dothideomycetes*). *Studies in Mycology* **82**: 75–136. https://doi.org/10.1016/j.simyco.2015.10.002

Tian X, Tibpromma S, Karunarathna SC, *et al.* (2022). A new species and a new host record of *Pseudoberkleasmium* (*Pseudoberkleasmiaceae, Dothideomycetes*) from *Cocos nucifera* and *Zea mays* in northern Thailand. *Phytotaxa* **547**: 232–242. https://doi.org/10.11646/phytotaxa.547.3.2

Timonin MI (1961). New species of the genus *Pseudobotrytis*. *Ceiba* **9**: 27–29.

Trotter A (1933). Contributi alla patologia del Nocciolo. I - Il seccume dei fusti da *Cytospora*. *Ricerche, osservazioni e divulgazione fitopatologica per la Campania e il Mezzogiorno* **2**: 17–27.

Trotter A (1946). Rassegna delle consultazioni e delle attività della Sez. di Patologia vegetale dell’Osservatorio di Portici. *Ricerche, Osservazioni e Divulgazione Fitopatologica per la Campania e il Mezzogiorno* **10**: 1–64.

Untereiner WA, Angus A, Réblová M, *et al.* (2008). Systematics of the *Phialophora verrucosa* complex: new insights from analyses of β-tubulin, large subunit nuclear rDNA and ITS sequences. *Botany* **86**: 742–750.

Vaidya G, Lohman DJ, Meier R (2011). SequenceMatrix: concatenation software for the fast assembly of multi-gene datasets with character set and codon information. *Cladistics* **27**: 171–180. https://doi.org/10.1111/j.1755-0998.2010.02965.x

Van Emden JH (1974). *Staheliella*, a new genus of hyphomycetes from tropical soil. *Acta Botanica Neerlandica* **23**: 251–256.

Verwoerd L, Dippenaar BJ (1930). Descriptions of some new species of South African fungi and of species not previously recorded from South Africa. *South African Journal of Science* **27**: 326–330.

Voglmayr H, Polhorský A, Halasů V. *et al.* (2022). New species, combinations and records of *Thyronectria*, with a key to species. *Mycological Progress* **21**: 257–278. https://doi.org/10.1007/s11557-021-01763-z

Wang M-M, Yang S-Y, Li Q, *et al.* (2024). *Microascaceae* from the marine environment, with descriptions of six new species. *Journal of Fungi* **10**: 45. https://doi.org/10.3390/jof10010045

Wang XW, Bai FY, Bensch K, *et al.* (2019a). Phylogenetic re-evaluation of *Thielavia* with the introduction of a new family *Podosporaceae*. *Studies in Mycology* **93**: 155–252. https://doi.org/10.1016/j.simyco.2019.08.002.

Wang XW, Houbraken J, Groenewald JZ, *et al.* (2016). Diversity and taxonomy of *Chaetomium* and chaetomium-like fungi from indoor environments. *Studies in Mycology* **84**: 145–224. https://doi.org/10.1016/j.simyco.2016.11.005.

Wang XW, Yang FY, Meijer M, *et al.* (2019b). Redefining *Humicola* sensu stricto and related genera in the *Chaetomiaceae*. *Studies in Mycology* **93**: 65–153. https://doi.org/10.1016/j.simyco.2018.07.001

Wollenweber HW (1943). *Fusarium*-Monographie. II. Fungi parasitici et saprophytici. *Zentralblatt für Bakteriologie Abt. 2* **106**: 104–135.

Wu W, Diao Y (2022). Anamorphic chaetosphaeriaceous fungi from China. *Fungal Diversity* **116**: 1–546 (2022). https://doi.org/10.1007/s13225-022-00509-w

Zhang K, Sandoval-Denis M, Kandemir H, *et al.* (2025). Taxonomic revision of *Bisifusarium* (*Nectriaceae*). *Persoonia* **54**: 197–223. https://doi.org/10.3114/persoonia.2025.54.06

