FUSE

Fungal Systematics and Evolution

VOLUME 1
JUNE 2018
PAGES 169–215

doi.org/10.3114/fuse.2018.01.08

New and Interesting Fungi. 1

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

Abstract: This study introduces two new families, one new genus, 22 new species, 10 new combinations, four epitypes, and 16 interesting new host and / or geographical records. *Cylindriaceae* (based on *Cylindrium elongatum*) is introduced as new family, with three new combinations. *Xyladictyochaetaceae* (based on *Xyladictyochaeta lusitanica*) is introduced to accommodate *Xyladictyochaeta. Pseudoanungitea* gen. nov. (based on *P. syzygii*) is described on stems of *Vaccinium myrtillus* (Germany). New species include: *Exophiala eucalypticola* on *Eucalyptus obliqua* leaf litter, *Phyllosticta hakeicola* on leaves of *Hakea* sp., *Setophaeosphaeria citricola* on leaves of *Citrus australasica,* and *Sirastachys cyperacearum* on leaves of *Cyperaceae* (Australia); *Polyscytalum chilense* on leaves of *Eucalyptus urophylla* (Chile); *Pseudoanungitea vaccinii* on *Vaccinium myrtillus* (Germany); *Teichospora quercus* on branch tissue of *Quercus* sp. (France); *Fusiconidium lycopodiellae* on stems of *Lycopodiella inundata, Monochaetia junipericola* on twig of *Juniperus communis, Myrmecridium sorbicola* on branch tissues of *Sorbus aucuparia, Parathyridaria philadelphi* on twigs of *Philadelphus coronarius,* and *Wettsteinina philadelphi* on twigs of *Philadelphus coronarius* (Germany); *Zygosporium pseudogibbum* on leaves of *Eucalyptus pellita* (Malaysia); *Pseudoanungitea variabilis* on dead wood (Spain); *Alfaria acaciae* on leaves of *Acacia propinqua, Dictyochaeta mimusopis* on leaves of *Mimusops caffra,* and *Pseudocercospora breonadiae* on leaves of *Breonadia microcephala* (South Africa); *Colletotrichum kniphofiae* on leaves of *Kniphofia uvaria, Subplenodomus iridicola* on *Iris* sp., and *Trochila viburnicola* on twig cankers on *Viburnum* sp. (UK); *Polyscytalum neofecundissimum* on *Quercus robur* leaf litter, and *Roussoella euonymi* on fallen branches of *Euonymus europaeus* (Ukraine). New combinations include: *Cylindrium algarvense* on leaves of *Eucalyptus* sp. (Portugal), *Cylindrium purgamentum* on leaf litter (USA), *Cylindrium syzygii* on leaves of *Syzygium* sp. (Australia), *Microdochium musae* on leaves of *Musa* sp. (Malaysia), *Polyscytalum eucalyptigenum* on *Eucalyptus grandis* × *pellita* (Malaysia), *P. eucalyptorum* on leaves of *Eucalyptus* (Australia), *P. grevilleae* on leaves of *Grevillea* (Australia), *P. nullicananum* on leaves of *Eucalyptus* (Australia), *Pseudoanungitea syzygii* on *Syzygium cordatum* leaf litter (South Africa), and *Setophaeosphaeria sidae* on leaves of *Sida* sp. (Brazil). New records include: *Sphaerellopsis paraphysata* on leaves of *Phragmites* sp., *Vermiculariopsiella dichapetali* on leaves of *Melaleuca* sp. and *Eucalyptus regnans*, and *Xyladictyochaeta lusitanica* on leaf litter of *Eucalyptus* sp. (Australia); *Camarosporidiella mackenziei* on twigs of *Caragana* sp. (Finland); *Cyclothyriella rubronotata* on twigs of *Ailanthus altissima*, *Rhinocladiella quercus* on *Sorbus aucuparia* branches (Germany); *Cytospora viticola* on stems of *Vitis vinifera* (Hungary); *Echinocatena arthrinioides* on leaves of *Acacia crassicarpa* (Malaysia); *Varicosporellopsis aquatilis* from garden soil (Netherlands); *Pestalotiopsis hollandica* on needles of *Cupressus sempervirens* (Spain), *Pseudocamarosporium africanum* on twigs of *Erica* sp. (South Africa), *Pseudocamarosporium brabeji* on branch of *Platanus* sp. (Switzerland); *Neocucurbitaria cava* on leaves of *Quercus ilex* (UK); *Chaetosphaeria myriocarpa* on decaying wood of *Carpinus betulus, Haplographium delicatum* on decaying *Carpinus betulus* wood (Ukraine). Epitypes are designated for: *Elsinoë mimosae* on leaves of *Mimosa diplotricha* (Brazil), *Neohendersonia kickxii* on *Fagus sylvatica* twig bark (Italy), *Caliciopsis maxima* on fronds of *Niphidium crassifolium* (Brazil), *Dictyochaeta septata* on leaves of *Eucalyptus grandis* × *urophylla* (Chile), and *Microdochium musae* on leaves of *Musa* sp. (Malaysia).

Published online: 18 April 2018.

Dedicated to Vadim Alexandrovich Mel'nik (*16 March 1937, †10 April 2017).

INTRODUCTION

New and Interesting Fungi (NIF) is introduced as a new series of papers that will supplement other series focussed on expanding existing knowledge of fungal biodiversity and fungal conservation. Another similar series such as the Fungal Planet (www.fungalplanet.org) aims to provide a rapid and simplified outlet for researchers to describe new fungal species as well as to highlight the environments where these fungi were isolated. The Fungal Planet series established in 2006 emphasises a holistic conservation of all life on the planet including not only plants and animals but also fungi (Crous *et al*. 2017a, b).

This new series of papers focusses not only on new fungal taxa but also on those that are generally interesting and that deserve notice. Like other series including the already mentioned Fungal Planet, the Genera of Fungi (GoF) series (Crous & Groenewald 2017, Giraldo *et al.* 2017), the Genera of Phytopathogenic Fungi (GOPHY) series (Marin-Felix *et al.* 2017), and the Fungal Systematics and Evolution series (Crous *et al.* 2015a, Hernandez-Restrepo *et al.* 2016, Krisai-Greilhuber *et al.* 2017) it has become evident that there are many undescribed species of fungi and new host or geographical records for which a scientific repository is lacking. Most of these could easily never be described or catalogued, and thus being lost to science. This justified the decision to launch the new series New and Interesting Fungi (NIF). It is hoped that this series will provide an attractive vehicle for mycologists to publish single new species or to highlight the relevance of important fungi.

Many known fungal species need to be recollected and epi- or neotypified in order to secure the application of old names already in use and resolve their DNA phylogeny. Subsequent to the end of the long-standing dual nomenclature for fungi (Hawksworth *et al*. 2011, Wingfield *et al*. 2012) and the connection of different morphs to a single name (Rossman *et al*. 2015, Réblová *et al.* 2016), it became clear that a vehicle was required to ensure that these data could be easily and effectively published. This would be comparable to "data release papers" published in other fields of science and biology (Miller et al. 2013, Vu *et al.* 2016). The New and Interesting Fungi series will link not only asexual and sexual morphs of species, but also provide opportunities to merge morphological observations with DNA sequence data, providing a means for rapid and accurate identification. New and Interesting Fungi will appear twice each year (June and December) in the journal Fungal Systematics and Evolution (www.FUSE-journal.org). Mycologists and other researchers wishing to contribute to future issues in this series are encouraged to contact Pedro Crous (p.crous@westerdijkinstitute.nl) before submission to ensure that potential conflicts with activities arising from other research groups can be avoided.

MATERIALS AND METHODS

Isolates

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

DNA extraction, amplification (PCR) and phylogeny

Fungal mycelium (Supplementary Table 1) was scraped from the agar surface of cultures with a sterile scalpel and the genomic DNA was isolated using the Wizard® Genomic DNA Purification Kit (Promega Corporation, WI, USA) following the manufacturers' protocols. The 28S nrRNA gene (LSU) and internal transcribed spacer regions with intervening 5.8S nrRNA gene (ITS) of the nrDNA operon were sequenced for all the isolates included in this study. Other loci were sequenced for various species or genera using primers and conditions specific for those groups of fungi (see references for details). The resulting fragments were sequenced in both directions using the respective PCR primers and the BigDye Terminator Cycle Sequencing Kit v. 3.1 (Applied Biosystems Life Technologies, Carlsbad, CA, USA); DNA sequencing amplicons were purified through Sephadex G-50 Superfine columns (Sigma-Aldrich, St. Louis, MO) in MultiScreen HV plates (Millipore, Billerica, MA). Purified sequence reactions were analysed on an Applied Biosystems 3730xl DNA Analyzer (Life Technologies, Carlsbad, CA, USA). The DNA sequences were analysed and consensus sequences were computed using SeqMan Pro v. 13 (DNASTAR, Madison, WI, USA).

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

included tree length (TL), consistency index (CI), retention index (RI) and rescaled consistency index (RC).

Morphology

Slide preparations were mounted in lactic acid, Shear's mounting fluid or water, from colonies sporulating on MEA, PDA, PNA, BLA or OA. Sections through conidiomata were made by hand. Observations were made with a Nikon SMZ25 dissection-microscope, and with a Zeiss Axio Imager 2 light microscope using differential interference contrast (DIC) illumination and images recorded on a Nikon DS-Ri2 camera with associated software. Colony characters and pigment production were noted after 2–4 wk of growth on MEA, PDA and OA (Crous *et al*. 2009b) incubated at 25 °C. Colony colours (surface and reverse) were scored using the colour charts of Rayner (1970). Sequences derived in this study were deposited in GenBank (Supplementary Table 1), the alignment in TreeBASE (www.treebase.org; study number S22442), and taxonomic novelties in MycoBank (www.MycoBank.org; Crous *et al*. 2004).

RESULTS

Phylogeny

Dothideomycetes LSU phylogeny: The alignment contained 125 isolates and *Candida broadrunensis* (CBS 11838, GenBank KY106372.1) was used as outgroup. The final alignment contained a total of 808 characters used for the phylogenetic analyses, including alignment gaps. Based on the results of MrModelTest, dirichlet base frequencies and the GTR+I+G model was used for the Bayesian analysis. The Bayesian analyses generated 38 302 trees from which 28 728 were sampled after 25 % of the trees were discarded as burn-in. The posterior probability values (PP) were calculated from the 28 728 trees (Fig. 1 overview *Dothideomycetes*; PP >0.74 shown). The alignment contained a total of 345 unique site patterns.

Eurotiomycetes and *Leotiomycetes* LSU phylogeny: The alignment contained 44 isolates and *Orbilia vinosa* (GenBank DQ470952.1) was used as outgroup. The final alignment contained a total of 813 characters used for the phylogenetic analyses, including alignment gaps. Based on the results of MrModelTest, dirichlet base frequencies and the GTR+I+G model was used for the Bayesian analyses. The Bayesian analyses generated 9 702 trees from which 7 278 were sampled after 25 % of the trees were discarded as burn-in. The posterior probability values (PP) were calculated from the 7 278 trees (Fig. 2 overview *Eurotiomycetes*; PP >0.74 shown). The alignment contained a total of 253 unique site patterns.

Sordariomycetes LSU phylogeny: The alignment contained 148 isolates and *Candida broadrunensis* (CBS 11838, GenBank KY106372.1) was used as outgroup. The final alignment contained a total of 761 characters used for the phylogenetic analyses, including alignment gaps. Based on the results of MrModelTest, dirichlet base frequencies and the GTR+I+G model was used for the Bayesian analysis. The Bayesian analyses generated 34 702 trees from which 26 028 were sampled after 25 % of the trees were discarded as burn-in. The posterior probability values (PP) were calculated from the 26 028 trees (Fig. 3 overview *Sordariomycetes*; first value: PP >0.74 shown). The alignment contained a total of 361 unique site patterns.

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

Taxonomy

Alfaria acaciae Crous & M.J. Wingf., ***sp. nov.*** MycoBank MB824766. Fig. 4.

Etymology: Name refers to *Acacia,* the genus of the substrate from which this fungus was collected.

Conidiomata sporodochial, surrounded by setae, black with dark green to black slimy conidial masses, 80–250 µm diam. *Setae* flexuous, unbranched, thick-walled, apex obtuse, dark brown, verruculose, 3–6-septate, 100–150 × 5–7 µm. *Conidiophores* densely aggregated, arising from hyaline basal stroma, becoming pigmented and verruculose towards conidiogenous region, subcylindrical, 3–5-septate, branched, 30–55 × 2–2.5 µm. *Conidiogenous cells* integrated, terminal and intercalary, subcylindrical, becoming pigmented and verruculose at upper region, phialidic with periclinal thickening and flared collarette, 10–20 × 2–2.5 µm. *Conidia* solitary, fusoid-ellipsoid, straight, apex subobtuse, base truncate, 1.5–2 µm diam, aseptate, guttulate, granular, medium brown, smooth, (6–)8–10(–12) × (2.5–)3 µm.

Culture characteristics: Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margins, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface dirty white to pale luteous, reverse luteous. On PDA surface dirty white, reverse pale luteous. On OA surface pale luteous.

Specimens examined: **South Africa**, Western Cape Province, Stellenbosch, Helshoogte Pass, on leaves of *Acacia propinqua* (*Fabaceae*), Jul. 2012, *M.J. Wingfield* (holotype CBS H-23428, culture ex-type CPC 31882 = CBS 143504); *ibid.*, CPC 31940.

Notes: *Alfaria cyperi-esculenti* was originally described from *Cyperus esculentus* in Spain, where it causes a serious foliar disease (Crous *et al.* 2014). This species is currently known only from its sexual morph, which complicates a morphological comparison with the present, asexual isolate from South Africa. Although phylogenetically closely related (Fig. 5), we regard them as two distinct species (see bp differences below). Furthermore, culture characteristics also differ between the two species, with cultures of *A. acaciae* growing faster, and paler in colour than the ochreous / apricot cultures of *A. cyperi-esculenti* (Crous *et al.* 2014).

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *A. cyperi-esculenti* (GenBank KJ869143; Identities 567 / 577 (98 %), 5 gaps (0 %)), *Myrothecium leucotrichum* (GenBank AJ301992; Identities 566 / 578 (98 %), 7 gaps (1 %)) and *A. thymi* (GenBank KU845990; Identities 559 / 572 (98 %), 8 gaps (1 %)). The ITS sequences of CPC 31882 and 31940 are identical. The highest similarities using the LSU sequence were *A. cyperi-esculenti* (GenBank KJ869200; Identities 803 / 804 (99 %), no gaps), *A. thymi* (GenBank KU845999; Identities 824 / 828 (99 %), 1 gap (0 %)) and *A. caricicola* (GenBank KU845992; Identities 822 / 828 (99 %), 1 gap (0 %)). The highest similarities using the *cmdA*

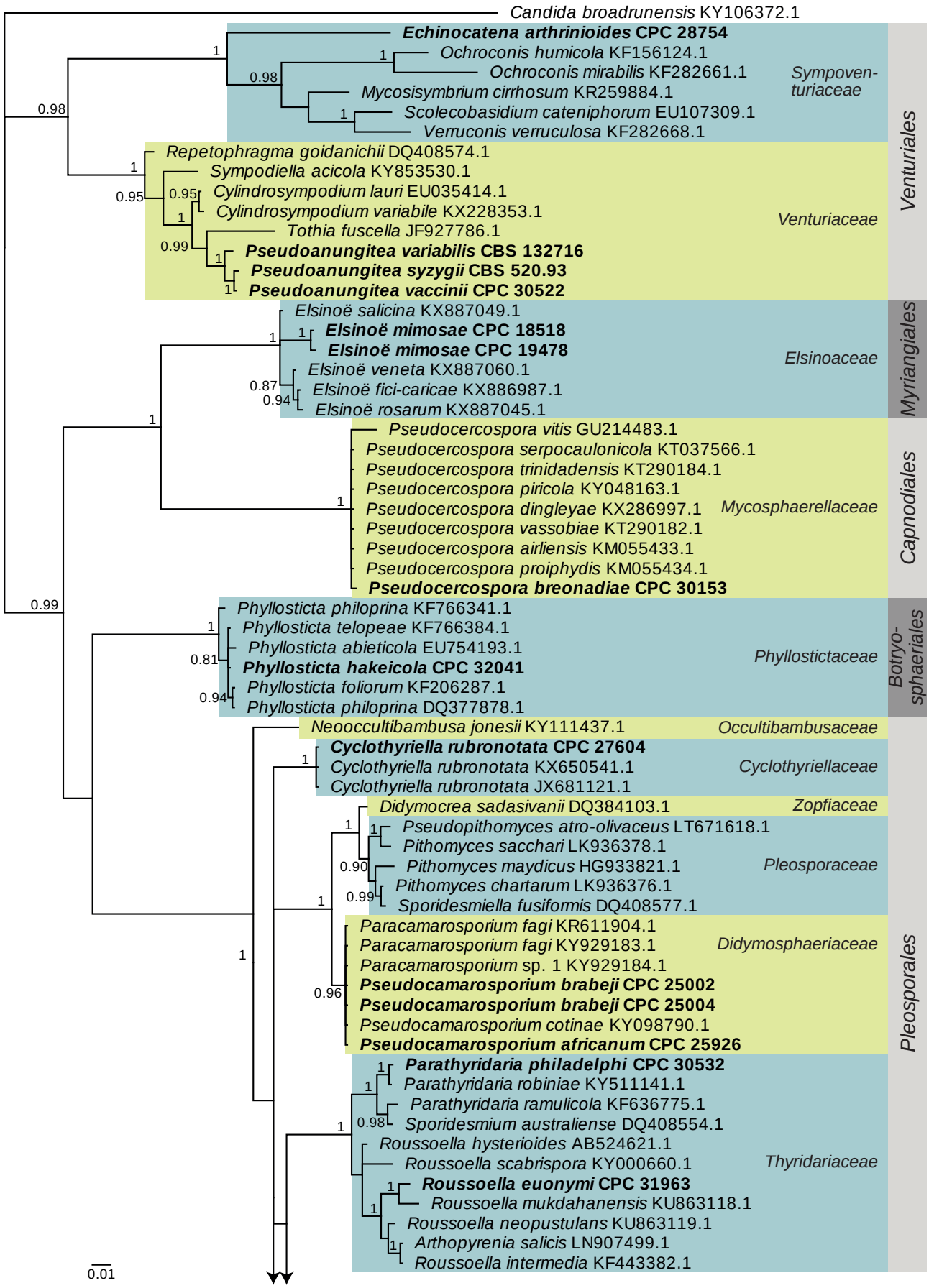

Fig. 1. Consensus phylogram (50 % majority rule) resulting from a Bayesian analysis of the *Dothideomycetes* LSU sequence alignment. Bayesian posterior probabilities (PP) > 0.74 are shown at the nodes and the scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession or culture collection numbers are indicated behind the species names. The tree was rooted to *Candida broadrunensis* (GenBank KY106372.1) and the novelties treated in this study for which LSU sequence data were available are indicated in bold face.

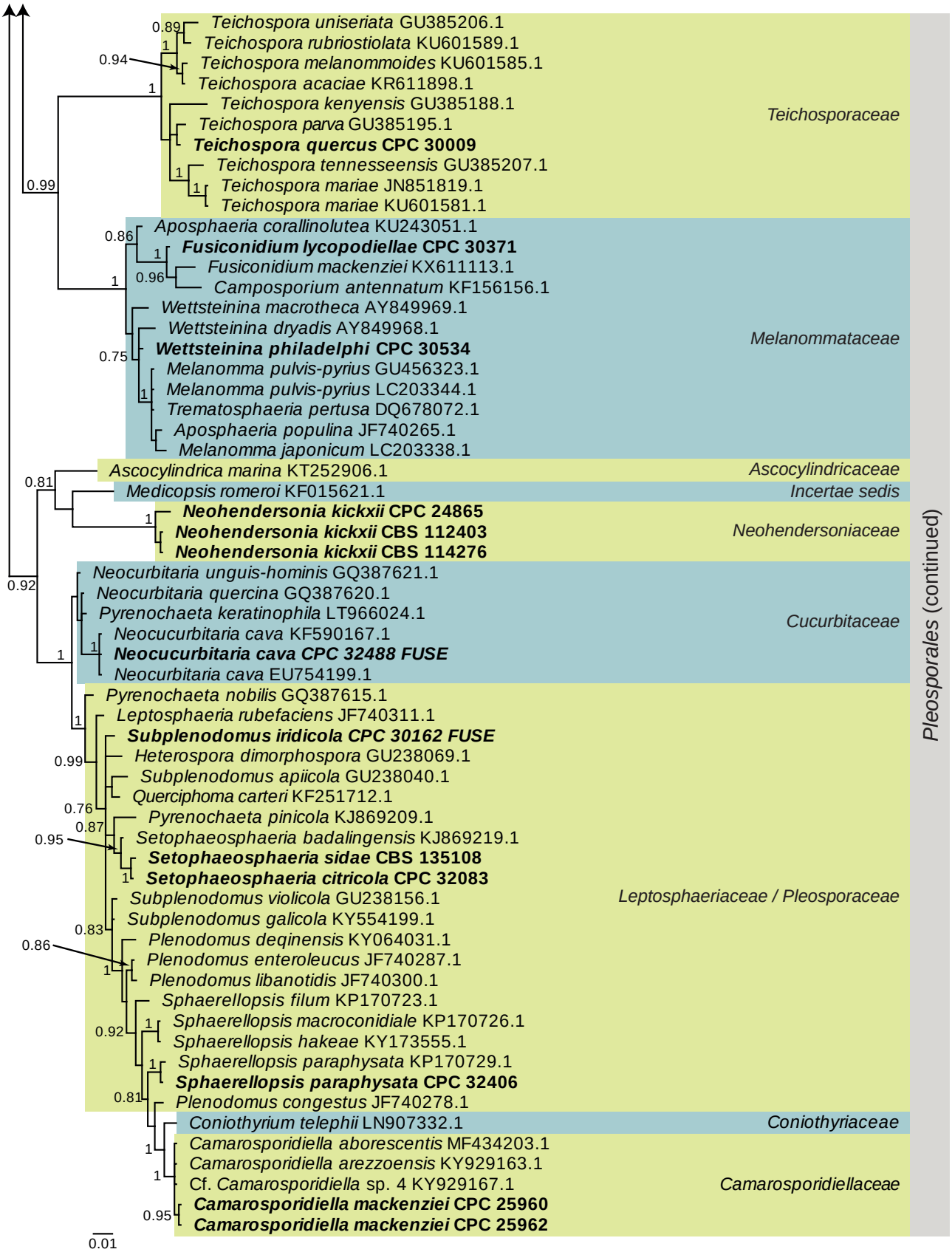

Fig. 1. (Continued).

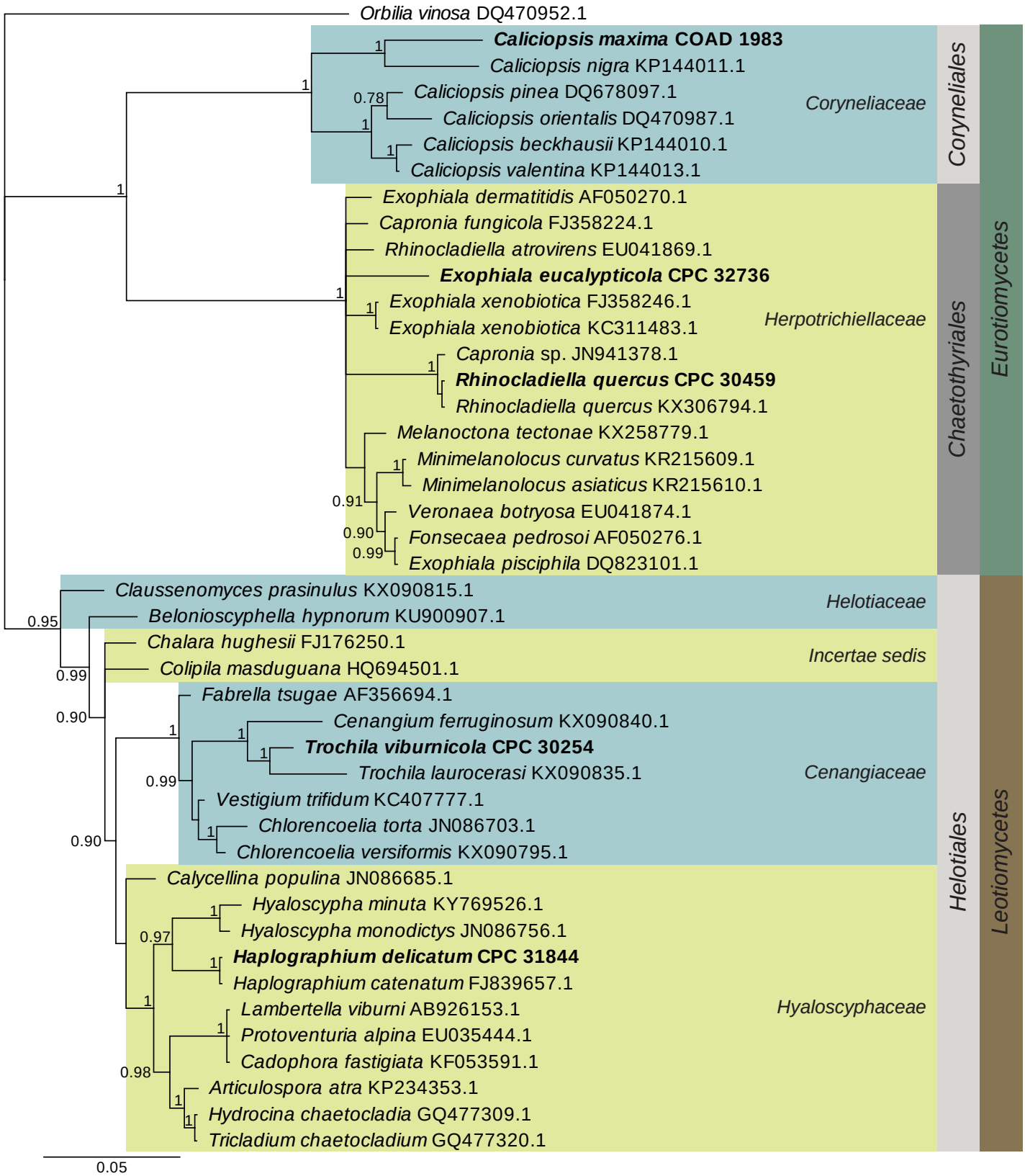

Fig. 2. Consensus phylogram (50 % majority rule) resulting from a Bayesian analysis of the *Eurotiomycetes* and *Leotiomycetes* LSU sequence alignment. Bayesian posterior probabilities (PP) > 0.74 are shown at the nodes and the scale bar represents the expected changes per site. Families, orders and classes are indicated with coloured blocks to the right of the tree. GenBank accession or culture collection numbers are indicated behind the species names. The tree was rooted to *Orbilia vinosa* (GenBank DQ470952.1) and the novelties treated in this study for which LSU sequence data were available are indicated in bold face.

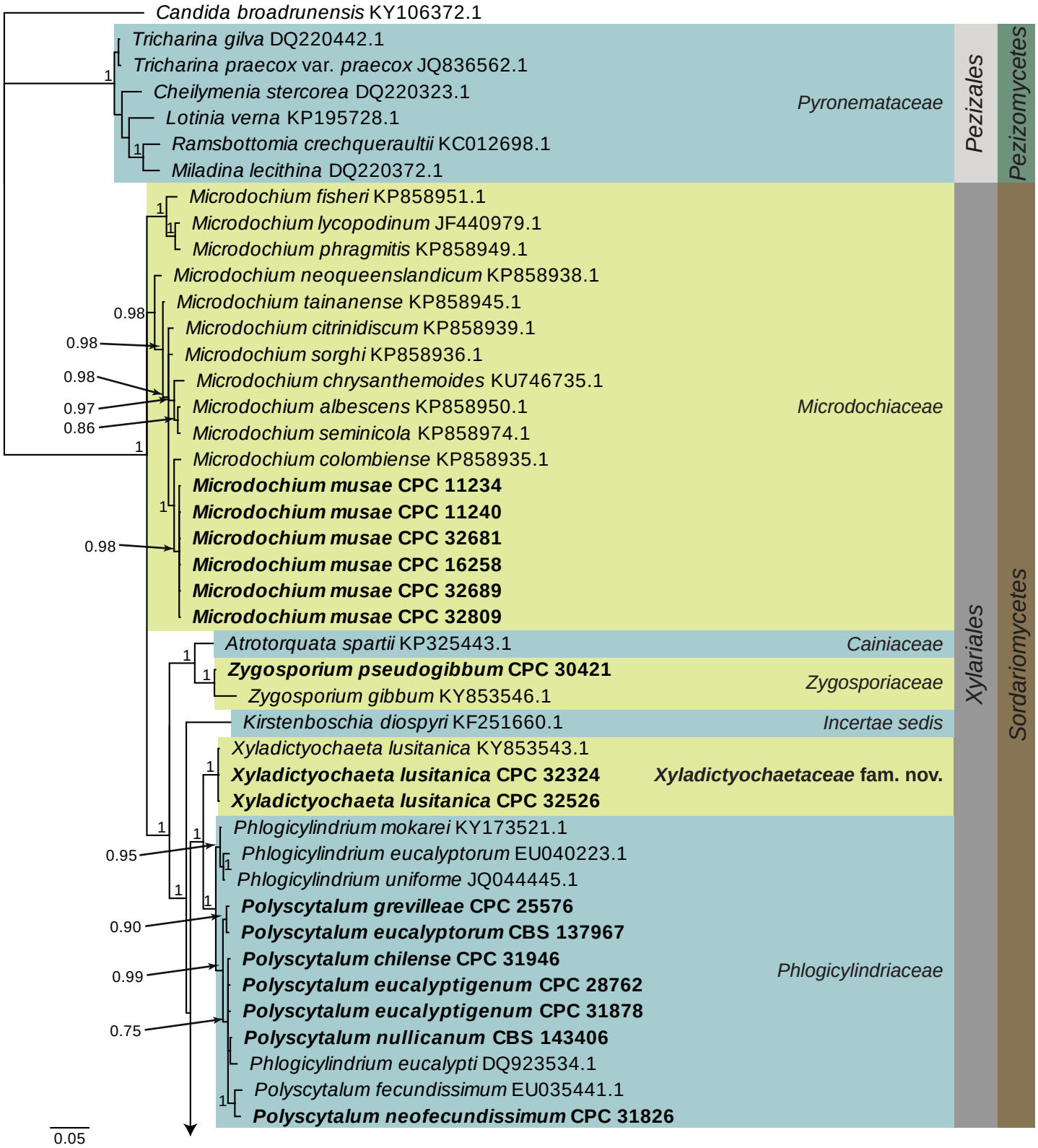

Fig. 3. Consensus phylogram (50 % majority rule) resulting from a Bayesian analysis of the *Pezizomycetes* and *Sordariomycetes* LSU sequence alignment. Bayesian posterior probabilities (PP) > 0.74 are shown at the nodes and the scale bar represents the expected changes per site. Families, orders and classes are indicated with coloured blocks to the right of the tree. GenBank accession or culture collection numbers are indicated behind the species names. The tree was rooted to *Candida broadrunensis* (GenBank KY106372.1) and the novelties treated in this study for which LSU sequence data were available are indicated in bold face.

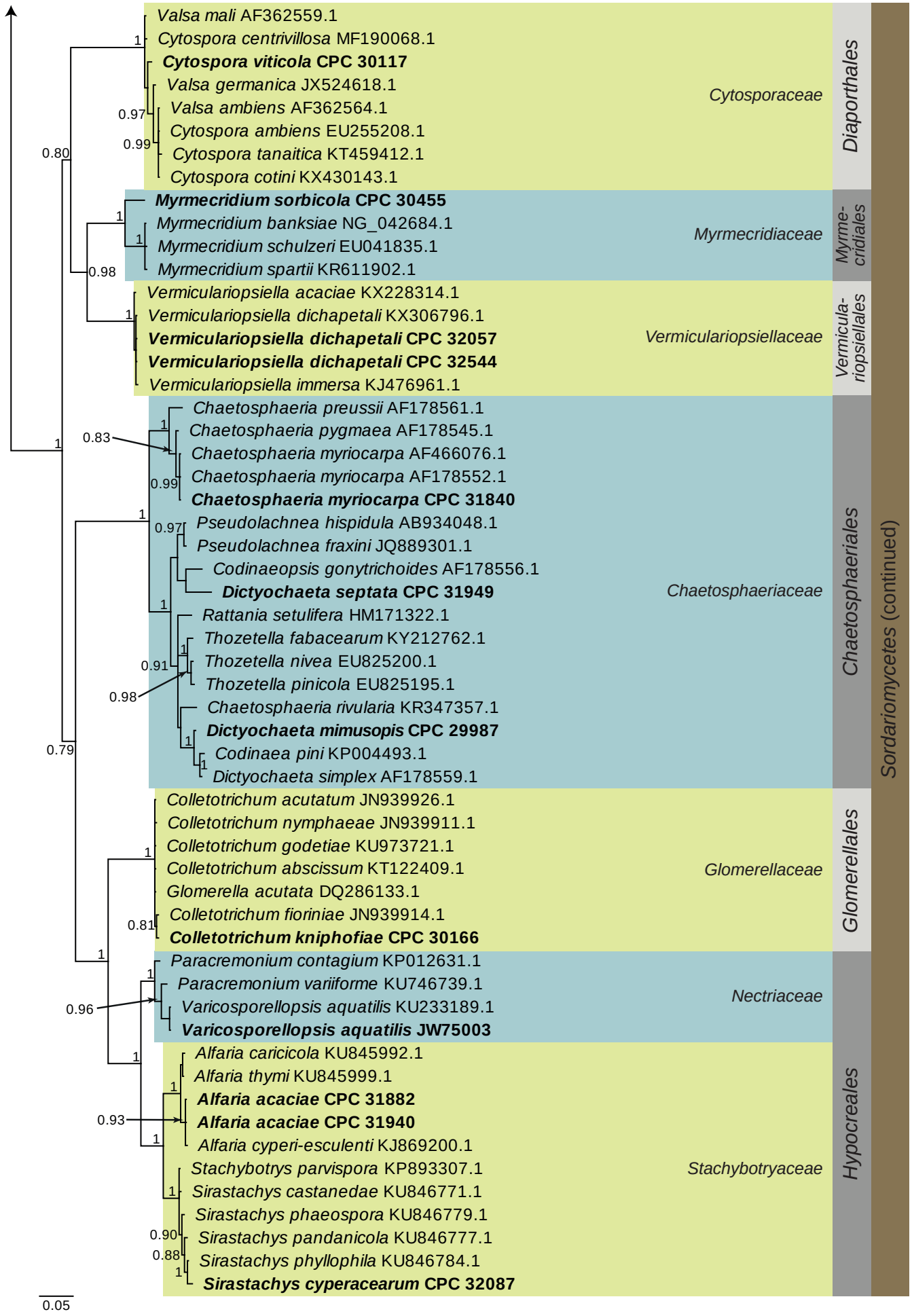

Fig. 3. (Continued).

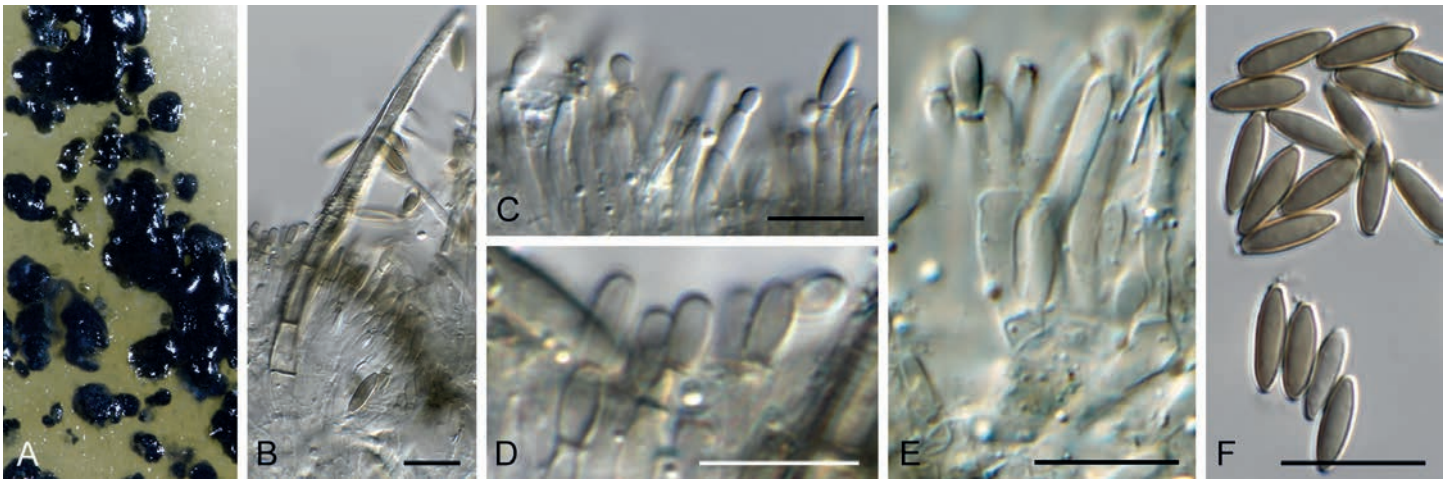

Fig. 4. *Alfaria acaciae* (CBS 143504). **A.** Colony on OA. **B.** Conidioma with seta. **C–E.** Conidiogenous cells. **F.** Conidia. Scale bars = 10 μm.

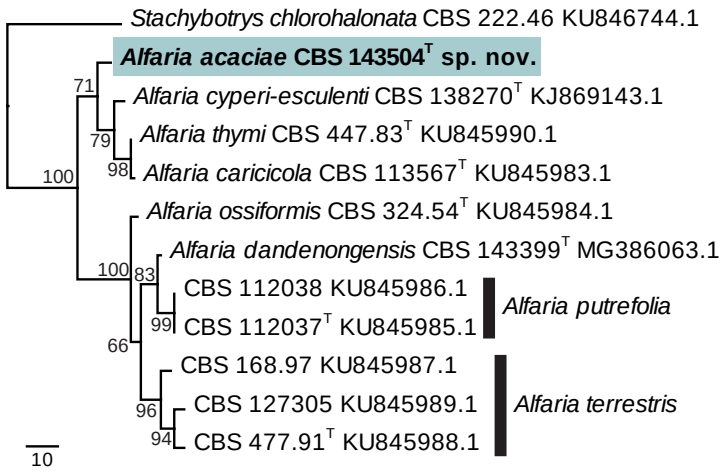

Fig. 5. Single most parsimonious tree obtained from a phylogenetic analysis of the *Alfaria* ITS alignment (12 strains including the outgroup; 538 characters analysed: 306 constant, 46 variable and parsimony-uninformative and 186 parsimony-informative). The tree was rooted to *Stachybotrys chlorohalonata* (GenBank KU846744.1) and the scale bar indicates the number of changes. Bootstrap support values higher than 49 % are shown at the nodes and novelties are highlighted with a coloured box and bold text. Species names are indicated to the right of the tree, or before the culture collection and GenBank accession numbers. A superscript T denotes strains with a type status. Tree statistics: TL = 130, CI = 0.900, RI = 0.892, RC = 0.803.

sequence of CPC 31882 were *A. terrestris* (GenBank KU845979; Identities 479 / 544 (88 %), 7 gaps (1 %)), *Gregatothecium humicola* (GenBank KU846285; Identities 475 / 544 (87 %), 7 gaps (1 %)) and *A. ossiformis* (GenBank KU845977; Identities 461 / 545 (85 %), 10 gaps (1 %)). The highest similarities using the *rpb2* sequence of CPC 31882 were *A. putrefolia* (GenBank KU846003; Identities 624 / 704 (89 %), 3 gaps (0 %)), *A. ossiformis* (GenBank KU846002; Identities 620 / 710 (87 %), 3 gaps (0 %)) and *A. caricicola* (GenBank KU846001; Identities 536 / 597 (90 %), no gaps). The *rpb2* sequences of CPC 31882 and 31940 were identical. The highest similarities using the *tef1* sequence of CPC 31882 were *A. terrestris* (GenBank KU846010; Identities 321 / 378 (85 %), 26 gaps (6 %)), *A. caricicola* (GenBank KU846008; Identities 370 / 441 (84 %), 20 gaps (4 %)) and *A. ossiformis* (GenBank KU846009; Identities 313 / 373 (84 %), 27 gaps (7 %)). The *tef1* sequences of CPC 31882 and 31940 were identical. The highest similarities using the *tub2* sequence of CPC 31882 were *A. terrestris* (GenBank KU846019; Identities 331 / 348 (95 %), 3 gaps (0 %)), *A. putrefolia* (GenBank KU846017; Identities 330 / 347 (95 %), 1 gap (0 %)) and *A. ossiformis* (GenBank KU846015; Identities 328 / 348 (94 %), 3 gaps (0 %)).

Caliciopsis maxima (Berk. & M.A. Curtis) Höhn., *Sitzungsber Akad. Wiss. Wien, Math.-Naturwiss. Kl., Abt. 1*, **128**: 84. 1919. Fig. 6.
Basionym: *Capnodium maximum* Berk. & M.A. Curtis, *J. Linn. Soc., Bot*. **10**(46): 391. 1868 (1869).

Stromata mostly abaxial, limited to sporangial sori of ferns, hidden from view beneath the host sporangia until black ascigerous, bristle-like stromatic columnar tubes push up and protrude from the sori, or otherwise are produced on wounded tissues, sometimes bordering entire pinnules; not associated with discoloration or necrosis of the opposite surface of the frond; rarely adaxial; starting as minute, erumpent cushions, increasing in diameter and thickness after emergence. *Ascigerous columns* long-stalked, prominently beaked, undergoing repeated apical proliferation; additional stromatic column material is formed in a renewed vegetative growth phase at the funnel-shaped apex of each stalk; the process is repeated as many as five times; primary column usually longer, reaching up to 1.7 mm long, all columns formed later, not exceeding 700 μm in length; stalk long, slender, flexuous,

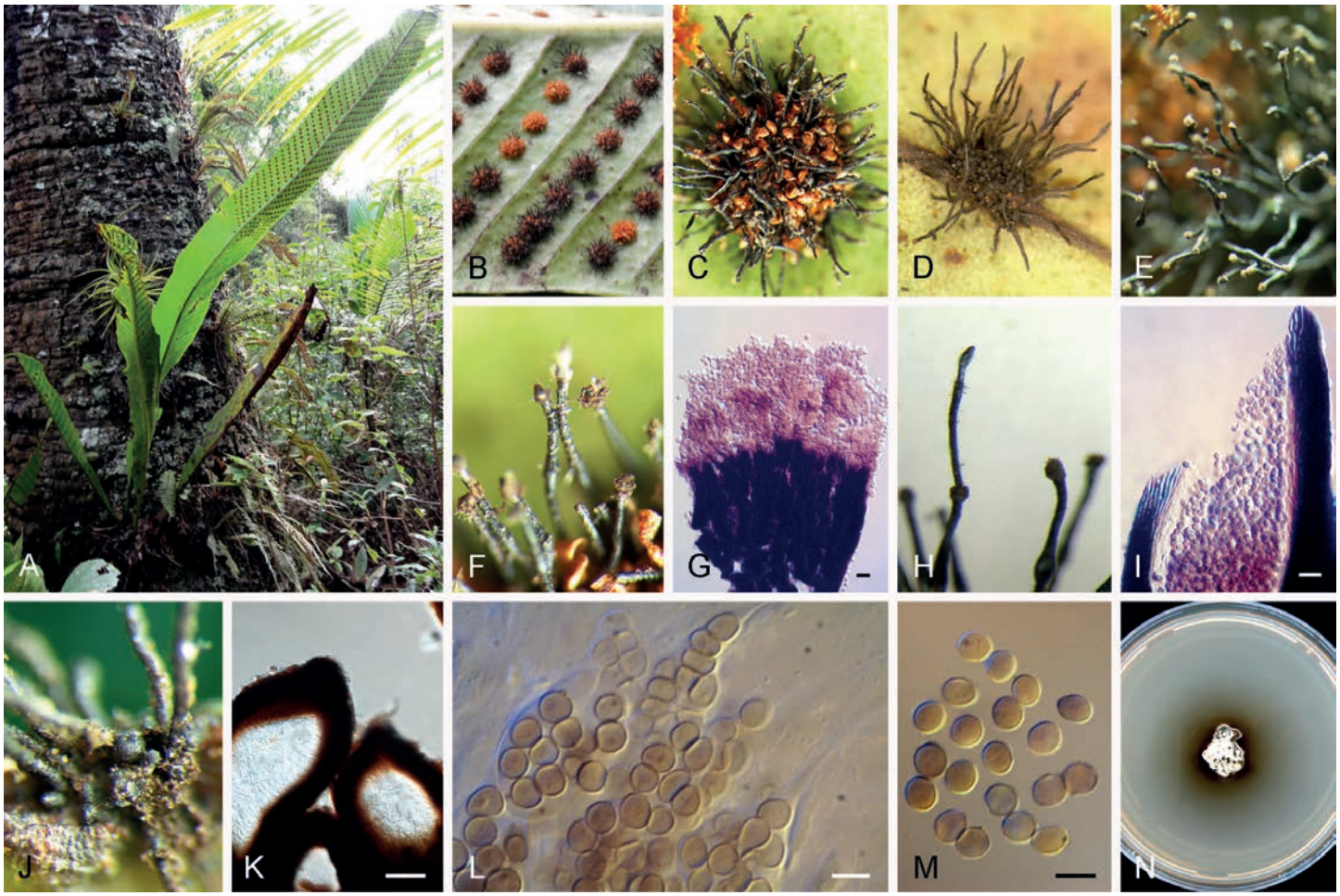

Fig. 6. *Caliciopsis maxima* (CPC 24674, VIC 42568). **A.** Habitat where the fungus and host (*Niphidium crassifolium*) was found – note growth of fern as an epiphyte on trunk of araucaria. **B–D.** Detail of fern sporangia colonized by the fungus. **E–F.** Detail of the ascospores aggregate formed by ascospores release. **G**. Squashed terminal portion of the ascomata, note the pulvurulent reddish-brown mass of ascospores. **H.** Detail of the percurrent proliferation of the ascoma. **I.** Vertical section of the upper portion of an ascoma. **J.** Spermogonium at the base of columnar ascomata. **K.** Vertical section of spermogonium, containing spermatia. **L.** Asci. **M.** Ascospores. **N.** Culture on PCA. Scale bars: G, I = 5 µm, K–M = 10 µm.

35–50 µm diam, covered with brown hyphae. *Ascigenous swelling* (locules) subterminal, ellipsoid, 125–150 µm diam, 200–350 µm in length, apical dehiscence, forming a reddish brown pulverulent of terminally aggregated ascospores. *Asci* bitunicate, evanescent, obclavate, pedicellate, straight or slightly curved, 15–17 × 8–10 µm, 8-spored, aparaphysate, hyaline, smooth. *Ascospores* inordinate, overlapping, globose or subglobose, 3–4 µm diam, aseptate, eguttulate, yellowish brown, thin-walled, smooth. *Spermogonium* subglobose, sessile or short stipitate, papillate, often covered in pale brown hyphae, aggregated below ascomatal tubes, black, smooth. *Spermatia* unicellular, narrowly fusiform, 11–24 × 3–4 µm, hyaline, smooth.

Culture characteristics: Colonies on PCA slow-growing, 15–20 mm diam after 1 mo; irregular, convex with papillate surface, edges entire, aerial mycelium sparse to absent, composed of black hyphal tufts, vinaceous buff towards periphery, pigmenting the medium with cinnamon taint; sepia in reverse; colonies sterile.

Specimens examined: **Cuba**, on fronds of *Niphidium* sp. (*Polypodiaceae*) (originally identified as *Polypodium* sp.), 1941, *Wright* (holotype CUP-029913). **Brazil**, Rio de Janeiro, Nova Friburgo, on fronds of *Niphidium crassifolium* (*Polypodiaceae*), 5 Nov. 2011, *R.W. Barreto* (epitype designated here VIC 42568, MBT373013, culture ex-epitype COAD 1983 = CPC 24674); *ibid,* on fronds of *Microgramma squamulosa* (*Polypodiaceae*), 10 Oct. 2013, *R.W. Barreto* (VIC 42602).

Notes: The epitype specimen of *Caliciopsis maxima* (*Coryneliaceae*) proposed here closely matches the morphology of the holotype and several additional collections studied by Fitzpatrick (1942), including one recorded on the same host and location in Brazil (NY-02928724). On all materials, stromata were produced on sori of sporangia, or on wounded tissues, not associated with discoloration or tissue necrosis of the opposite surface of the frond. Ascigerous columns had a tendency to undergo repeated apical proliferation, a feature that differs from all other known species; ascospores are typically globose or subglobose, yellowish brown, 3–4 µm diam (Fitzpatrick 1942). Based on phylogenetic evidence, the genus resides in the *Coryneliaceae*, within the *Eurotiomycetes*, as recently demonstrated through molecular analysis (Prieto *et al.* 2013, Garrido-Benavent & Pérez-Ortega 2015, Wood *et al.* 2016). In the combined ITS-LSU analysis (Fig. 7), *C. maxima* clustered in a basal position, suggesting that the fungal species associated with ferns are evolutionarily basal to the evolution of their relatives, as previously demonstrated for the cercosporoid and mycosphaerella-like species occurring on ferns (Guatimosim *et al.* 2016).

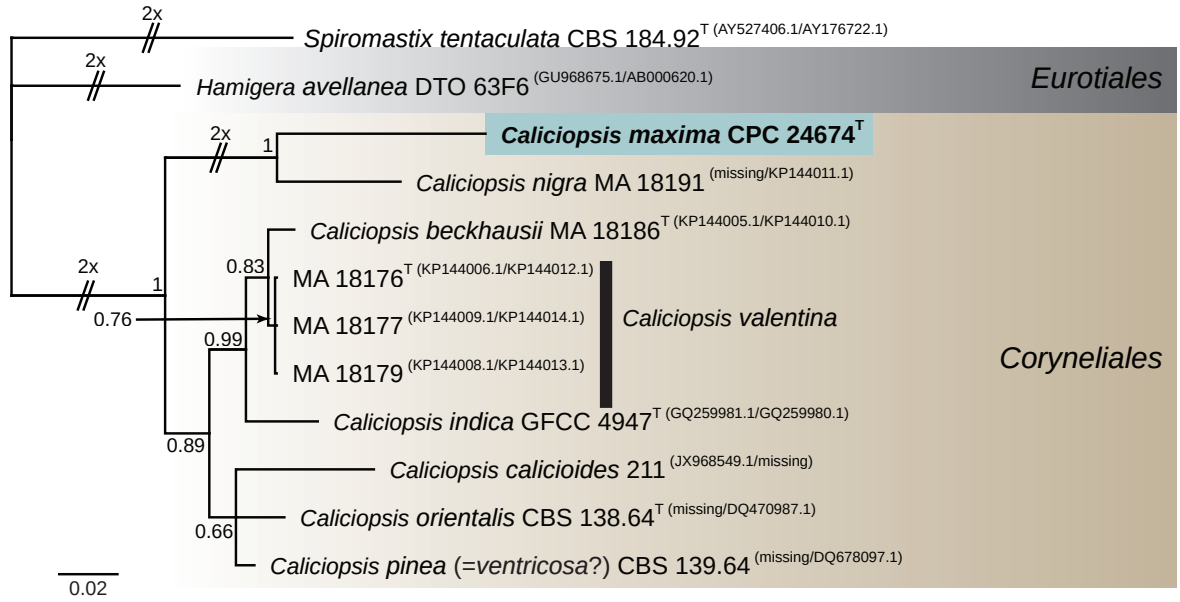

Fig. 7. Consensus phylogram (50 % majority rule) resulting from a Bayesian analysis of the combined ITS and LSU alignment of *Caliciopsis* species. Bayesian posterior probabilities are indicated at the nodes and the scale bar represents the expected changes per site. The tree was rooted to *Spiromastix tentaculata* (culture CBS 184.92) and the novelty treated in this study is highlighted with a coloured box and bold text. A superscript T denotes strains with a type status. GenBank accession and/or culture collection numbers are indicated behind the species names. Orders are indicated to the very right of the tree. The more basal branches were halved to facilitate easier layout. The ITS partition had 198 unique site patterns and the LSU partition had 139 unique site patterns out of the included 548 and 853 characters respectively.

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Corynelia uberata* (GenBank KU204606; Identities 474 / 544 (87 %), 21 gaps (3 %)), *Caliciopsis pinea* (GenBank KY099604; Identities 323 / 361 (89 %), 6 gaps (1 %)) and *C. beckhausii* (GenBank NR_132090; Identities 330 / 370 (89 %), 11 gaps (2 %)). The highest similarities using the LSU sequence were *C. nigra* (GenBank KP144011; Identities 771 / 825 (93 %), 5 gaps (0 %)), *C. pinea* (GenBank DQ678097; Identities 779 / 839 (93 %), 6 gaps (0 %)) and *C. valentina* (GenBank KP144013; Identities 780 / 842 (93 %), 6 gaps (0 %)).

Camarosporidiella mackenziei Wanas*. et al*., *Stud. Mycol*. **87**: 236. 2017. Fig. 8.

Conidiomata separate, pycnidial, globose, 150–200 µm diam, with central ostiole; wall of 2–3 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* tightly aggregated, lining the inner cavity, hyaline, smooth, subcylindrical to ampulliform or doliiform, proliferating percurrently at apex, 5–8 × 3–4 µm. *Conidia* solitary, hyaline, smooth, guttulate to granular, subcylindrical to ellipsoid, apex obtusely rounded, base truncate, (3–)4–5(–6) × (2–)2.5(–3) µm. *Ascomata* pseudothecial, intra- to subcorticolous, singly to densely crowded, tufted if fully developed, erumpent, subglobose with flattened base, later somewhat fusing at the base, ostiole central and indistinct, black, finely rough, thick, soft, basally with a few red brown, thick-walled, smooth and gnarled hyphae, 0.5–0.75 mm diam. *Peridium* multi-layered, consisting of a *textura angularis* with red brown, thick-walled and smooth cells, inner layer hyaline, cells 10–17 µm diam. *Pseudoparaphyses* numerous, longer than the asci, basally moniliform otherwise cylindrical and filiform, short celled, multi-celled, branched, with a few anastomoses, hyaline, thin-walled, smooth, septa in the upper part smooth and thin-walled, eguttulate, 3–4 µm in diam. *Asci* 8-spored, cylindrical, bitunicate, fissitunicate, thick-walled, apically roundish, pedicel short and furcate, inamyloid (water plus Lugol), 131–210 × 15–16 µm, ascospores oblique uniseriate. *Ascospores* 8(–10)-celled, muriform, ellipsoid, mostly straight, both parts of the spore approx. equal in size, end cells conical or roundish, wall golden brownish, thick and always smooth, median septum constricted, otherwise smooth to faintly constricted, thick-walled and reddish, one longitudinal septum per cell, end cells aseptate, plasma eguttulate, without a gelatinous sheath and appendages, examined in water, living and mature, 30–35(–44) × 10–12.5 µm (av. 31.4 × 11.5).

Culture characteristics: Colonies spreading, with fluffy, moderate to abundant aerial mycelium. On MEA, PDA and OA surface and reverse dark mouse grey.

Specimens examined: **Finland**, Outokumpu, on twig of *Caragana* sp. (*Fabaceae*), 31 Dec. 2014, *M. Pennanen*, specimen CBS H-23430, culture CPC 25960 = CBS 144200; *ibid.*, CPC 25962.

Notes: Isolates CPC 25960 and CPC 25962 were treated as "*Camarosporium* sp. 2" in Crous & Groenewald (2017). The species was subsequently placed in the genus *Camarosporidiella* by Wanasinghe *et al.* (2017), clustering within the *C. mackenziei* clade. The latter taxon was described from twigs of *Caragana arborescens* collected in Russia. Although the present collection produced only the microconidial morph in culture, the sexual morph was observed on host tissue, which is a new observation for this species.

Based on a megablast search using the ITS sequence of CPC 25960, the closest matches in NCBI's GenBank nucleotide database were *C. mackenziei* (GenBank MF434159; Identities 542 / 543 (99 %), 1 gap (0 %)), *C. melnikii* (GenBank MF434162; Identities 540 / 544 (99 %), 1 gap (0 %)) and *C. caraganicola* (GenBank MF434124; Identities 540 / 544 (99 %), 1 gap (0 %)). The highest similarities using the LSU sequence of CPC 25960,

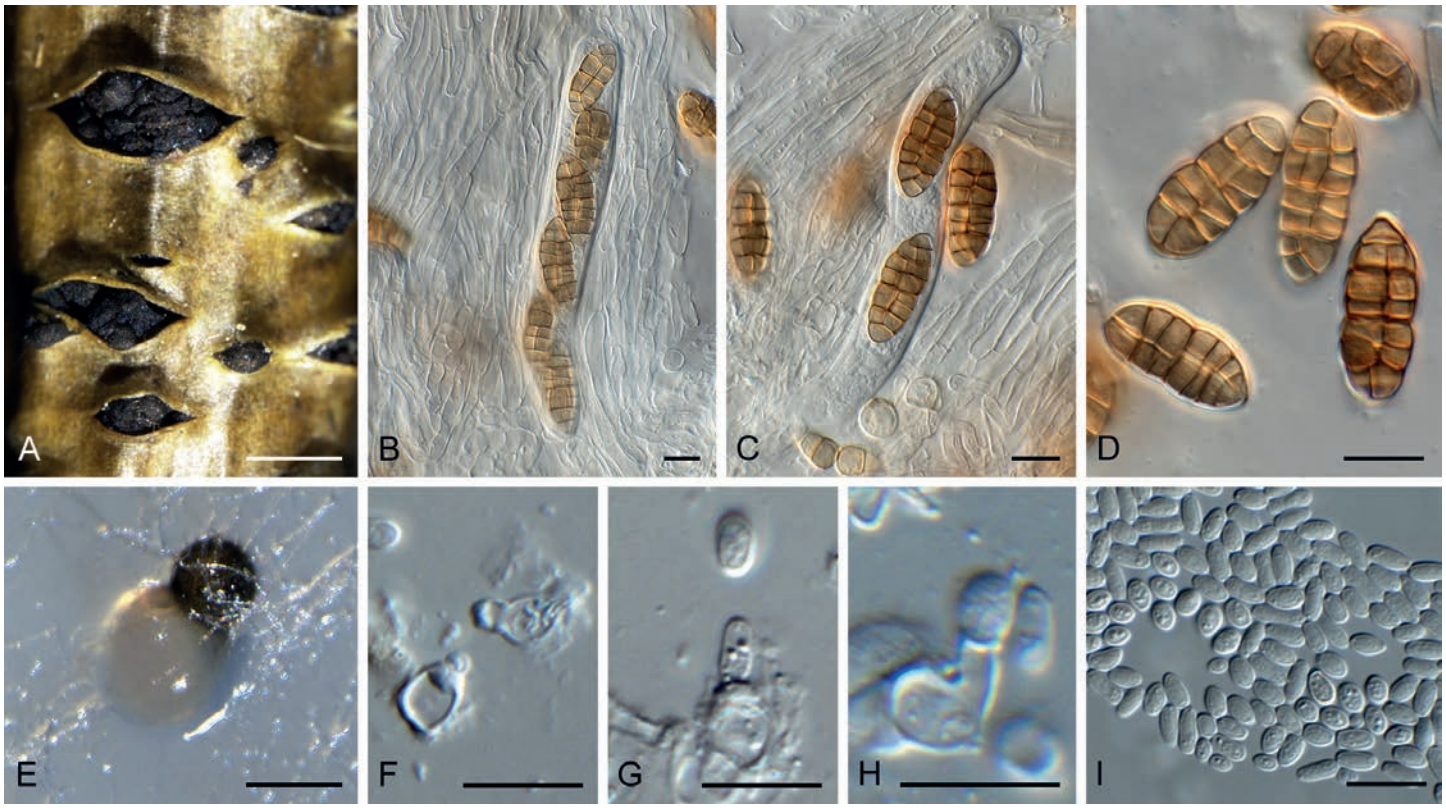

Fig. 8. *Camarosporidiella mackenziei* (CPC 25960). **A.** Ascomata on host tissue. **B, C.** Asci. **D.** Ascospores. **E.** Conidioma. **F–H.** Conidiogenous cells. **I.** Conidia. Scale bars: A = 0.75 mm, E = 200 μm, all others = 10 μm.

the closest matches in NCBI's GenBank nucleotide database were *C. aborescentis* (GenBank MF434203; Identities 821 / 822 (99 %), no gaps), "*Cf. Camarosporium* sp. 4" (GenBank KY929167; Identities 821 / 822 (99 %), no gaps) and *C. arezzoensis* (GenBank KY929163; Identities 821 / 822 (99 %), no gaps). The highest similarities using the *tef1* sequence of CPC 25960, the closest matches in NCBI's GenBank nucleotide database were *C. mackenziei* (GenBank MF434423; Identities 904 / 907 (99 %), no gaps), *C. italica* (GenBank MF434415; Identities 899 / 907 (99 %), no gaps) and *C. arborescentis* (GenBank MF434380; Identities 899 / 907 (99 %), no gaps).

Chaetosphaeria myriocarpa (Fr.) C. Booth, *Mycol. Pap*. **68**: 5. 1957. Fig. 9.
Basionym: *Sphaeria myriocarpa* Fr., *Kongl. Vetensk. Acad. Hand.* **267**. 1817.
Synonym: *Sphaeria myriocarpa* Fr., *Syst. mycol*. **2**(2): 459. 1823.

Mycelium consisting of medium brown, verruculose, branched, septate, 2–3 μm diam hyphae. *Conidiophores* solitary, erect, subcylindrical, flexuous, unbranched, at times rejuvenating percurrently in apical part, 1–5-septate, dark brown, thick-walled, roughened in lower region, 35–100 × 2.5–3 μm. *Conidiogenous cells* integrated, terminal, medium brown, smooth, subcylindrical to obovoid, 25–30 × 2.5–3 μm; apex with flared collarette, 2–3 μm diam. *Conidia* occurring in chains, aggregating in mucoid mass, hyaline, smooth, apex obtuse, abruptly tapering to a truncate base, creating triangular conidia, 2.5–3 × 2.5 μm.

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

Specimen examined: **Ukraine**, Ternopil region, Zalischyky district, Dniester Canyon, on decaying wood of *Carpinus betulus* (*Betulaceae*), 5 Oct. 2016, *A. Akulov*, specimen ex CWU (MYC) AS 6049 (dried culture CBS H-23426, culture CPC 31840 = CBS 143389).

Notes: *Chaetosphaeria myriocarpa* is commonly isolated from dead woody substrates in Europe, and represents a new record for Ukraine. Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Ch. myriocarpa* (GenBank JF340253; Identities 483 / 490 (99 %), 1 gap (0 %)), *Ch. pygmaea* (GenBank AF178545; Identities 473 / 496 (95 %), 3 gaps (0 %)) and *Phialophora phaeophora* (GenBank AF083191; Identities 503 / 533 (94 %), 2 gaps (0 %)). The highest similarities using the LSU sequence were *Ch. myriocarpa* (GenBank AF178552; Identities 841 / 841 (100 %), no gaps), *Ch. pygmaea* (GenBank AF178545; Identities 837 / 843 (99 %), 2 gaps (0 %)) and *Ch. preussii* (GenBank AF178561; Identities 816 / 835 (98 %), no gaps). Only distant matches were obtained with the *tub2* sequence, e.g. with *Chaetomium jodhpurense* (GenBank KP336854; Identities 292 / 361 (81 %), 19 gaps (5 %)).

Colletotrichum kniphofiae Crous & Denman, ***sp. nov.*** MycoBank MB824769. Fig. 10.

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

Asexual morph on OA (sterile on other media). *Conidiomata* acervular, conidiophores formed on a cushion of pale brown, angular cells, 6–15 μm diam. *Setae* rarely observed in culture, brown, flexuous, verruculose, tapering to subobtuse apices, 5–8-septate, up to 100 μm long. *Conidiophores* hyaline, septate, branched, smooth-walled, up to 60 μm long. *Conidiogenous*

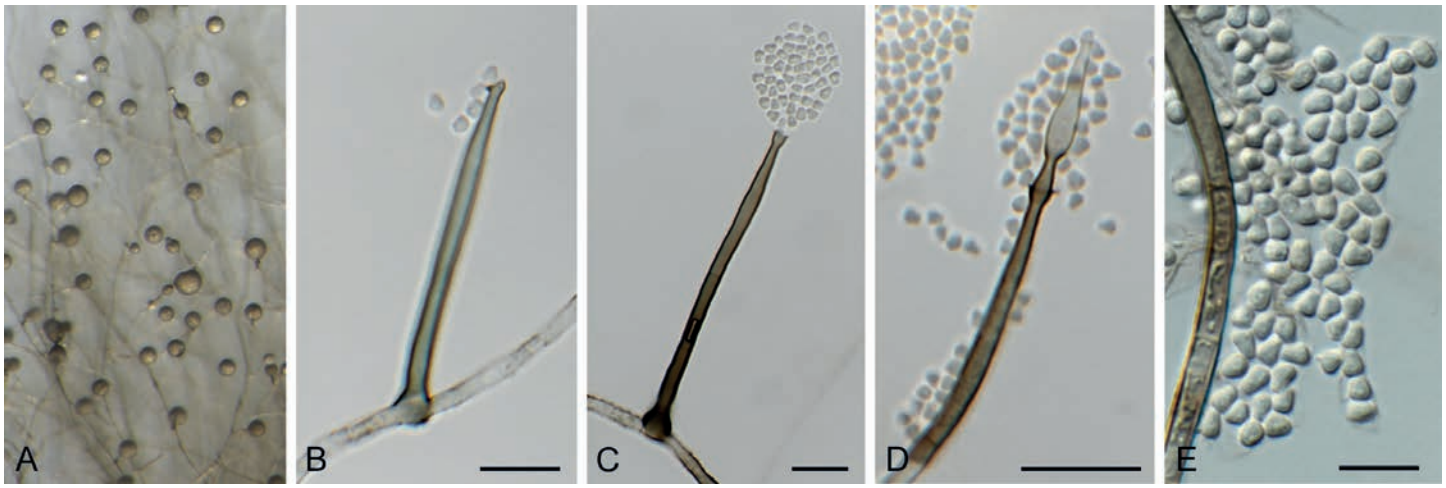

Fig. 9. *Chaetosphaeria myriocarpa* (CBS 143389). **A.** Conidiophores on SNA. **B–D.** Conidiophores. **E.** Conidia. Scale bars = 10 μm.

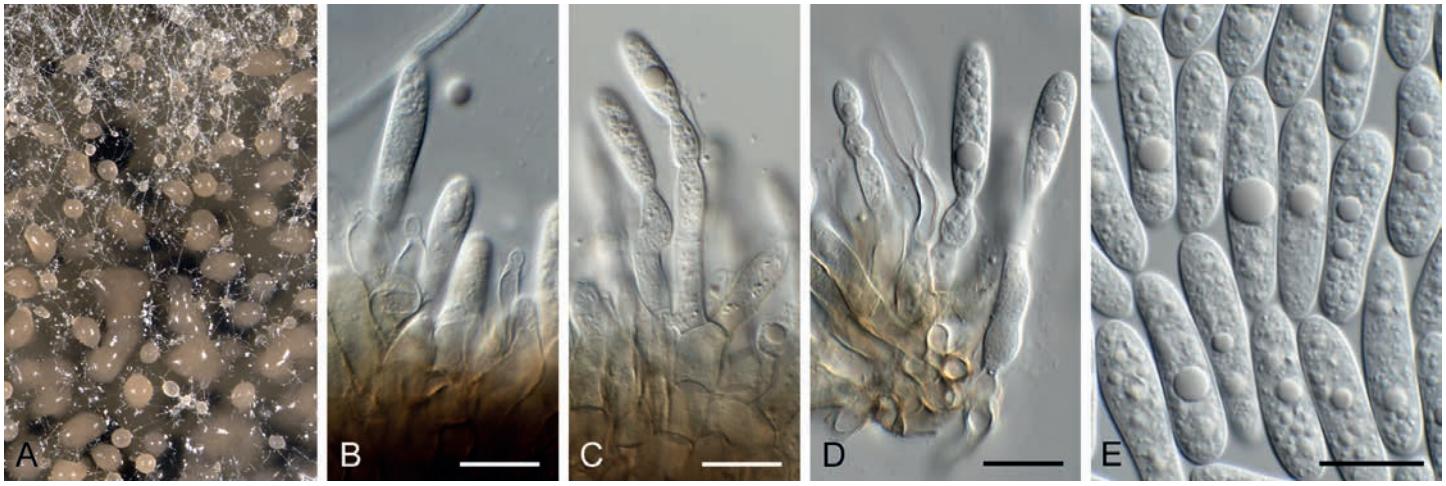

Fig. 10. *Colletotrichum kniphofiae* (CBS 143496). **A.** Colony on OA. **B–D.** Conidiogenous cells. **E.** Conidia. Scale bars = 10 μm.

cells hyaline, smooth, cylindrical, 12–20 × 4–7 μm, phialidic with periclinal thickening. *Conidia* hyaline, smooth-walled, aseptate, straight, rarely curved, prominently multi-guttulate, fusoid to subcylindrical, apex obtuse, tapering at base to truncate hilum, 2 μm diam, (17–)25–28(–37) × (5–)6(–7) μm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and even, lobate margins, covering dish after 2 wk at 25 °C. On MEA surface dirty white with patches of olivaceous grey, reverse amber with patches of olivaceous grey. On PDA surface and reverse olivaceous grey with patches of smoke grey. On OA surface olivaceous grey.

Specimen examined: **UK**, England, Upton Grey, on leaves of *Kniphofia uvaria* (*Xanthorrhoeaceae*), 28 Mar. 2016, *P.W. Crous* (holotype CBS H-23432, culture ex-type CPC 30166 = CBS 143496); *ibid*., CPC 30168.

Notes: Sexual morph not observed, but ascospores harvested from plant material, indicating that a sexual morph exists. *Colletotrichum kniphofiae* was isolated from dead leaves of *Kniphofia*, and nothing is known regarding its ecology, and no species of *Colletotrichum* have been described from this host. Supported by its distinct DNA phylogeny (Fig. 11), we believe this collection represents a distinct species.

Based on a megablast search using the ITS sequence of CPC 30166, the closest matches in NCBI's GenBank nucleotide database were *Co. godetiae* (GenBank KX756147; Identities 567 / 575 (99 %), 2 gaps (0 %)), *Co. pyricola* (GenBank KU963516; Identities 565 / 575 (95 %), 2 gaps (0 %)) and *Co. salicis* (GenBank KU498278; Identities 565 / 575 (95 %), 2 gaps (0 %)). The ITS sequences of CPC 30166 and CPC 30168 are identical. The highest similarities using the LSU sequence of CPC 30166 were *Co. godetiae* (GenBank KU973721; Identities 837 / 839 (99 %), no gaps), *Co. acutatum* (GenBank JN939926; Identities 837 / 839 (99 %), no gaps) and *Co. fioriniae* (GenBank JN939914; Identities 837 / 839 (99 %), no gaps). The highest similarities using the *actA* sequence were *Co. destructivum* (GenBank AY157843; Identities 596 / 657 (91 %), 16 gaps (2 %)), *Co. kahawae* (GenBank KU579251; Identities 595 / 659 (90 %), 26 gaps (3 %)) and *Co. orbiculare* (GenBank AB778553; Identities 584 / 654 (89 %), 22 gaps (3 %)). The highest similarities using the *chs1* sequence were *Co. salicis* (GenBank JQ949131; Identities 245 / 252 (97 %), no gaps), *Co. godetiae* (GenBank KY171916; Identities 244 / 252 (97 %), no gaps) and *Co. rhombiforme* (GenBank JQ949118; Identities 243 / 252 (97 %), no gaps). The highest similarities using the *gapdh* sequence were *Co. pyricola* (GenBank KU221341; Identities 560 / 604 (93 %), 4 gaps (0 %)), *Co. nymphaeae* (GenBank KP339289; Identities 556 / 602 (92 %), 2 gaps (0 %)) and *Co. fioriniae* (GenBank KF944354; Identities 542 / 589 (92 %), 9 gaps (1 %)). The highest similarities using the *tub2* sequence were with *Co. phormii* (GenBank KX069820.1; Identities 386 / 413 (93 %), 7 gaps (1 %)), *Co. australe* (GenBank JQ950106.1; Identities 385 /

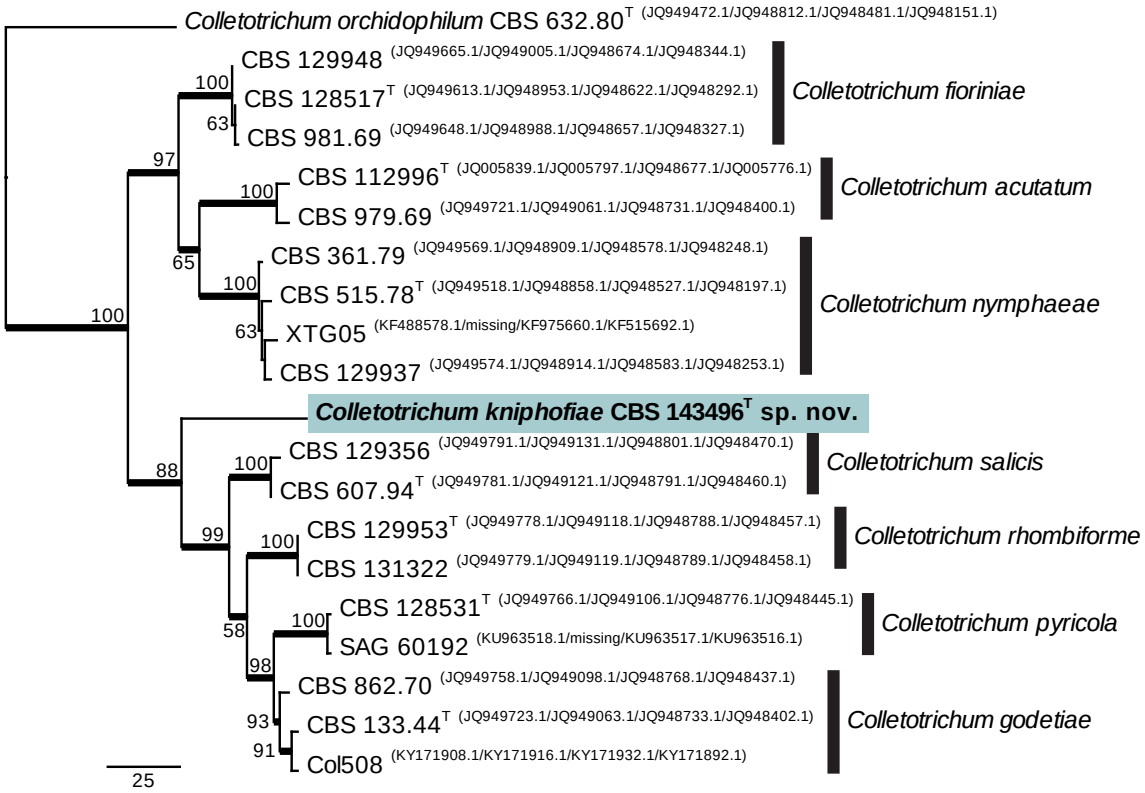

Fig. 11. The first of three equally most parsimonious trees obtained from a phylogenetic analysis of the combined *actA*, *chs-1*, *gapdh* and ITS alignment representing *Colletotrichum* species (20 strains including the outgroup; 1 301 characters analysed: 1 038 constant, 106 variable and parsimony-uninformative and 157 parsimony-informative). The tree was rooted to *Colletotrichum orchidophilum* (culture CBS 632.80) and the scale bar indicates the number of changes. Bootstrap support values higher than 49 % are shown at the nodes and novelties are highlighted with a coloured box and bold text. Species names are indicated to the right of the tree and GenBank accession numbers are indicated behind the culture collection numbers. A superscript T denotes strains with a type status and branches present in the strict consensus tree are thickened. Tree statistics: TL = 366, CI = 0.839, RI = 0.904, RC = 0.758.

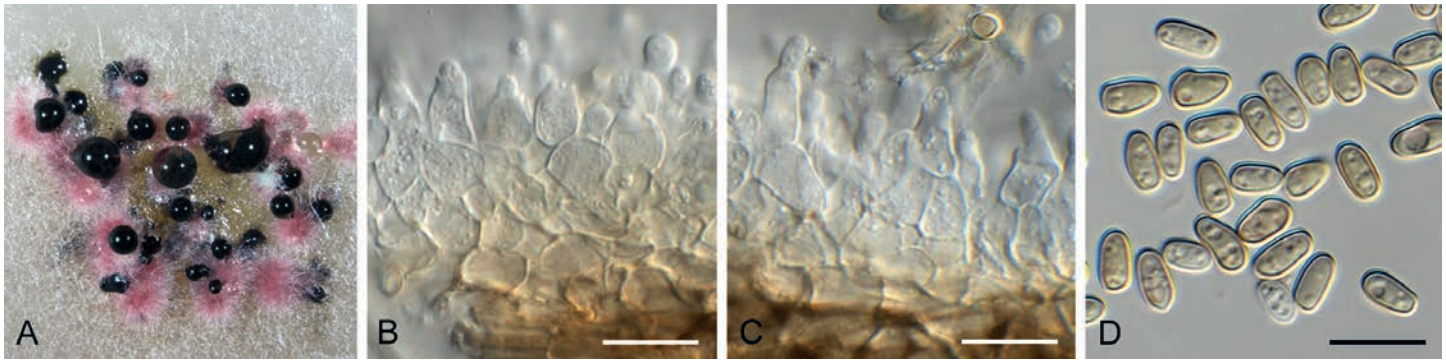

Fig. 12. *Cyclothyriella rubronotata* (CPC 27604). **A.** Colony on OA. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars = 10 µm.

413 (93 %), 7 gaps (1 %)) and *Co. scovillei* (GenBank KY475561.1; Identities 384 / 414 (93 %), 8 gaps (1 %)).

Cyclothyriella rubronotata (Berk. & Broome) Jaklitsch & Voglmayr, *Stud. Mycol*. **85**: 41. 2016. Fig. 12.
Basionym: *Melogramma rubronotatum* Berk. & Broome, *Ann. Mag. nat. Hist. Ser.* 3, **3**: 375. 1859.

Conidiomata erumpent, globose, 200–250 µm diam, with central ostiole; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* lining the inner cavity, reduced to conidiogenous cells or with a single supporting cell. *Conidiogenous cells* hyaline, smooth, subcylindrical to ampulliform, 6–12 × 3–5 µm; apex with prominent periclinal thickening, rarely with percurrent proliferation. *Conidia* solitary, brown, smooth, thin-walled, guttulate, subcylindrical, mostly straight, apex obtuse, base truncate, (4.5–)5(–6) × (2.5–)3 µm.

Culture characteristics: Colonies spreading, flat on OA, erumpent on MEA and PDA, with moderate aerial mycelium and feathery margins, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse apricot, on OA surface pale violet, on PDA surface coral with flesh in outer region, reverse sienna with patches of umber.

Specimen examined: **Germany**, near Berlin, on twig of *Ailanthus altissima* (*Simaroubaceae*), 4 Jun. 2015, *R.K. Schumacher* (specimen CBS H-23423, culture CPC 27604 = CBS 144201).

Notes: The genus *Cyclothyriella* was recently introduced by Jaklitsch & Voglmayr (2016), who also treated the taxonomic history of this genus in detail. The asexual morph isolated in this study closely resembles that described and illustrated by Jaklitsch & Voglmayr (2016), who reported conidia as (2–)4.5–6(–6.5) × (2–) 2.7–3.5(–4) µm, first hyaline, becoming medium brown with age. This fungus is common in Europe, and here we present a culture from Germany to supplement the Austrian material studied by Jaklitsch & Voglmayr (2016).

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Cyclothyriella rubronotata* (GenBank NR_147651; Identities 564 / 564 (100 %), no gaps), *Melanomma pulvis-pyrius* (GenBank KY189979; Identities 400 / 476 (84 %), 20 gaps (4 %)) and *Ascochyta medicaginicola* (GenBank KX381183; Identities 359 / 419 (86 %), 10 gaps (2 %)). The highest similarities using the LSU sequence were *Cy. rubronotata* (GenBank KX650541; Identities 833 / 833 (100 %), no gaps), *Thyridaria rubronotata* (GenBank JX681121; Identities 833 / 833 (100 %), no gaps) and *Neooccultibambusa jonesii* (GenBank KY111437; Identities 781 / 812 (96 %), 2 gaps (0 %)).

Cylindriaceae Crous & L. Lombard, ***fam. nov.*** MycoBank MB824770.

Mycelium consisting of hyaline, smooth, septate, branched, hyphae. *Conidiophores* aggregated in sporodochia, or solitary, erect; hyphae and basal part of conidiophores becoming pale brown, smooth, subcylindrical, erect, septate, branched. *Conidiogenous cells* terminal and intercalary, subcylindrical, hyaline, smooth, with several sympodial flat-tipped loci, unthickened, not darkened. *Ramoconidia* hyaline, smooth, guttulate, subcylindrical. *Conidia* aseptate, hyaline, smooth, arranged in long, branched chains, scars unthickened, slightly refractive.

Type genus: Cylindrium Bonord.

Note: The genus *Cylindrium*, based on *C. elongatum*, was regarded by Lombard *et al*. (2015) as *incertae sedis*, and thus *Cylindriaceae* is herewith introduced to accommodate this genus.

Cylindrium algarvense (Cheew. & Crous) Crous, ***comb. nov.*** MycoBank MB824771.
Basionym: *Polyscytalum algarvense* Cheew. & Crous, *Persoonia* **23**: 73. 2009.

Description and illustration: Cheewangkoon *et al*. (2009).

Specimen examined: **Portugal**, Faro, Algarve, on *Eucalyptus* sp. (*Myrtaceae*), 24 Jan. 2007, *P.W. Crous* (holotype CBS H-20289, culture ex-type CPC 14936 = CBS 124770); *ibid*. (CPC 14937, CPC 14938).

Note: See discussion under *Polyscytalum* and Fig. 13.

Cylindrium purgamentum (Crous) Crous, ***comb. nov.*** MycoBank MB824772.
Basionym: *Polyscytalum purgamentum* Crous, *Persoonia* **37**: 363. 2016.

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

Specimen examined: **USA**, Texas, Austin, on leaf litter, Aug. 2013, *P.W. Crous* (holotype CBS H-22899, culture ex-type CPC 29580 = CBS 142114).

Note: See discussion under *Polyscytalum* and Fig. 13.

Cylindrium syzygii (Crous & R.G. Shivas) Crous, ***comb. nov.*** MycoBank MB824773.
Basionym: *Pseudoidriella syzygii* Crous & R.G. Shivas, *Persoonia* **27**: 135. 2011.

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

Specimen examined: **Australia**, Queensland, Mackay, Eungella National Park, on leaves of *Syzygium* sp. (*Myrtaceae*), 14 Jul. 2009, *P.W. Crous & K.L. Crous*, (holotype CBS H-20758, cultures ex-type CPC 17233 = CBS 131307).

Note: See discussion under *Polyscytalum* and Fig. 13. By placing *Pseudoidriella syzygii* in *Cylindrium,* the genus *Pseudoidriella* is also reduced to synonymy with *Cylindrium*. This suggests that the conidiomata of *Cylindrium* could be reduced to solitary conidiophores, as well as sporodochia, as observed in this species. Interestingly enough, an LSU sequence attributed to *Tristratiperidium microsporum* also clustered in this clade (Fig. 3), which completely disagrees with the morphology of this fungus. This suggests that this sequence (MFLUCC) should be reconsidered. The ITS sequence from the same culture placed *Tristratiperidium microsporum* with *Kirstenboschia diospyri* (Fig. 13).

Cytospora viticola D.P. Lawr. *et al.*, *Pl. Pathol.* **66**: 718. 2017. Fig. 14.

Conidiomata (on PDA) with stromata up to 500 µm diam, rosette cytosporoid, subdivided by invaginations, up to four radially arranged. *Conidiophores* hyaline, smooth, branched, 1–3-septate, 15–20 × 2–3 µm, immersed in a mucilaginous layer. *Conidiogenous cells* phialidic with periclinal thickening and apical taper, 10–15 × 1.5–2 µm. *Conidia* hyaline, smooth, guttulate, allantoid, aseptate, (5–)6–7(–7.5) × 1(–1.5) µm.

Culture characteristics: Colonies spreading, with sparse aerial mycelium and smooth, lobate margins, covering dish after 1 mo at 25 °C. On MEA surface isabelline, reverse brown vinaceous. On PDA surface and reverse. On OA surface sepia.

Specimen examined: **Hungary**, Pécs wine region, on stems of *Vitis vinifera* (*Vitaceae*), 5 Nov. 2014, *K.Z. Váczy* (specimen CBS H-23278, culture T15 / 464 = CPC 30117 = CBS 143162).

Notes: Species of *Cytospora* are commonly known from woody plants and generally have wide host ranges. Two *Cytospora* species, *C. vinacea* and *C. viticola,* causing dieback and cankers of grapevines in the USA were recently described (Lawrence *et al*. 2017). Other species known from *Vitis* include *C. ceratosperma* (CBS 397.36), as well as the European taxa *C. vitis* and *Valsa vitis*, which are insufficiently known, and for which we could not trace type material. The isolate described here was associated with cankers on grapevines in Hungary, and is similar to *C. viticola*.

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were

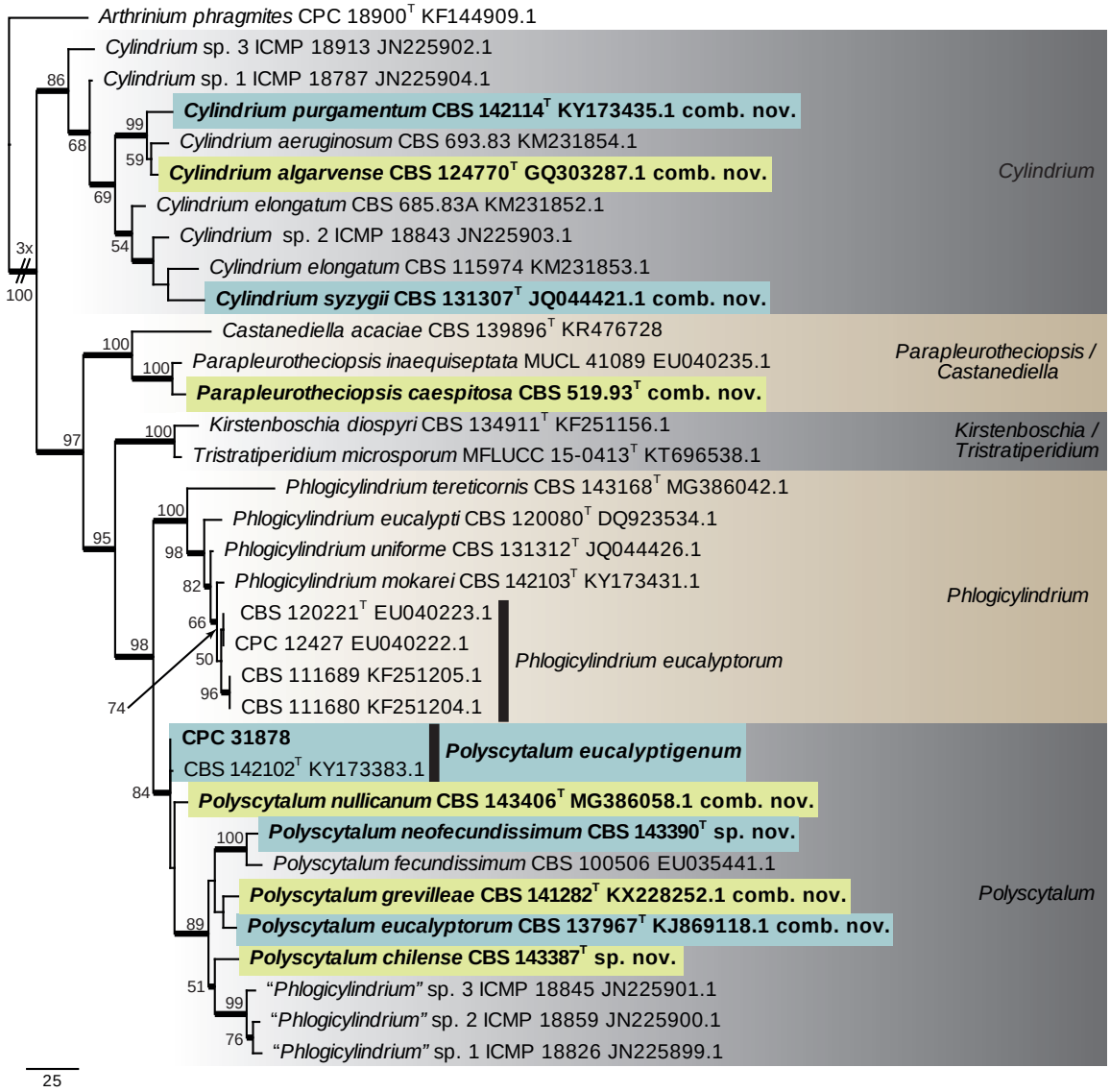

Fig. 13. The first of 72 equally most parsimonious trees obtained from a phylogenetic analysis of the ITS alignment representing the genera *Cylindrium*, *Parapleurotheciopsis*, *Phlogicylindrium* and *Polyscytalum* (34 strains including the outgroup; 538 characters analysed: 309 constant, 49 variable and parsimony-uninformative and 180 parsimony-informative). The tree was rooted to *Arthrinium phragmites* (GenBank KF144909.1) and the scale bar indicates the number of changes. Bootstrap support values higher than 49 % are shown at the nodes and novelties are highlighted with a coloured box and bold text. Species names are indicated to the right of the tree, or before the culture collection and GenBank accession numbers. Genera are indicated to the very right of the tree. A superscript T denotes strains with a type status and branches present in the strict consensus tree are thickened. The most basal branch was shortened three times to facilitate easier layout. Tree statistics: TL = 634, CI = 0.565, RI = 0.777, RC = 0.439.

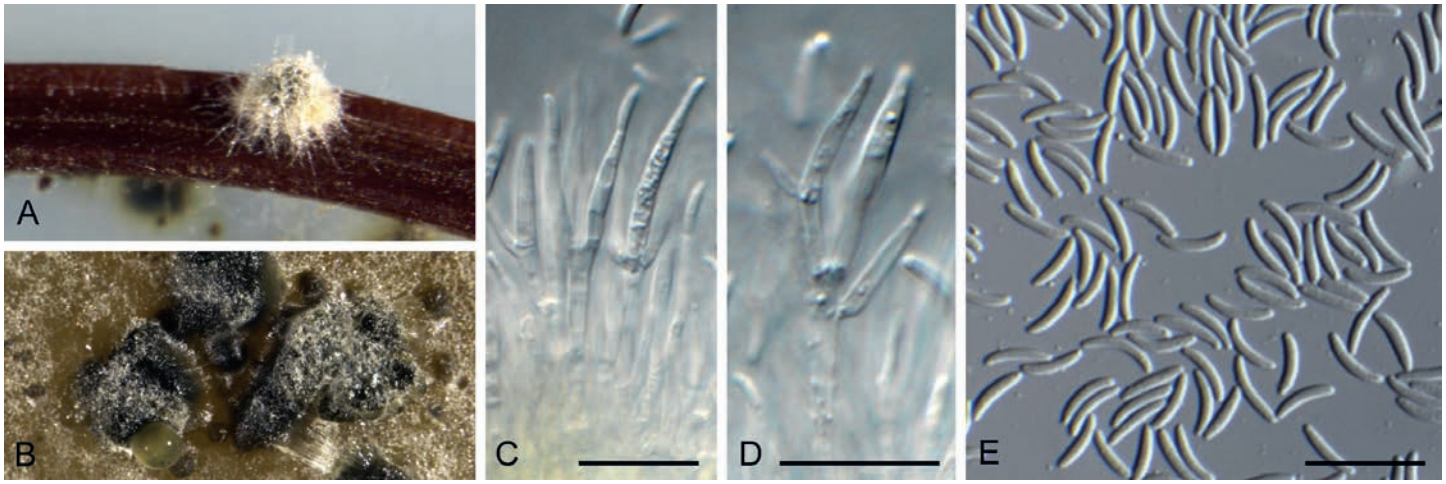

Fig. 14. *Cytospora viticola* (CBS 143162). **A.** Colony on PNA. **B.** Colony on OA. **C, D.** Conidiogenous cells. **E.** Conidia. Scale bars = 10 μm.

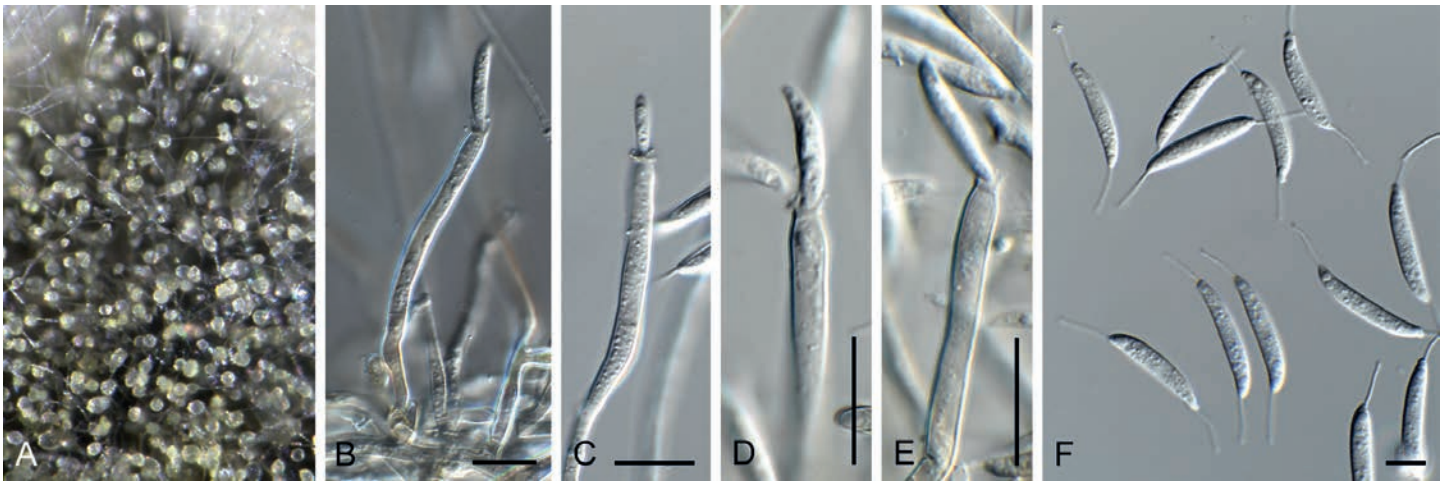

Fig. 15. *Dictyochaeta mimusopsis* (CBS 143435). **A.** Colony on OA. **B–E.** Conidiophores. **F.** Conidia. Scale bars = 10 µm.

Cy. sibiraeae (GenBank KR045651; Identities 566 / 591 (96 %), 8 gaps (1 %)), *Cy. chrysosperma* (GenBank KT692596; Identities 568 / 594 (96 %), 7 gaps (1 %)) and *Cy. germanica* (GenBank KX168596; Identities 563 / 590 (95 %), 7 gaps (1 %)). Our ITS sequence is identical to *Cy. viticola* (GenBank KX256239; Identities 423 / 423 (100 %), no gaps), but was not a result in the megablast search as roughly half of the first internal spacer region sequence is missing for the deposited sequences of that species. The highest similarities using the LSU sequence were *Valsa mali* (GenBank AF362559; Identities 837 / 842 (99 %), 1 gap (0 %)), *Cy. centrivillosa* (GenBank MF190068; Identities 830 / 837 (99 %), 1 gap (0 %)) and *Cy. ambiens* (GenBank EU255208; Identities 772 / 779 (99 %), no gaps). The highest similarities using the *actA* sequence were *Cy. salicicola* (GenBank KU982637; Identities 163 / 180 (91 %), 6 gaps (3 %)), *Cy. parasitica* (GenBank KT459410; Identities 190 / 212 (90 %), 10 gaps (4 %)) and *Cy. cincta* (GenBank KU710994; Identities 223 / 250 (89 %), 13 gaps (5 %)). The highest similarities using the *rpb2* sequence were *Cy. berberidis* (GenBank KU710948; Identities 658 / 727 (91 %), no gaps), *Cy. schulzeri* (GenBank KU710980; Identities 656 / 727 (90 %), no gaps) and *Cy. rostrata* (GenBank KU710974; Identities 656 / 727 (90 %), no gaps). The highest similarities using the *tef1* sequence were *Cy. viticola* (GenBank KX256274; Identities 253 / 253 (100 %), no gaps), *Cy. mali* (GenBank KU710928; Identities 359 / 422 (85 %), 24 gaps (5 %)) and *Cy. sophorae* (GenBank KU710941; Identities 422 / 517 (82 %), 26 gaps (5 %)). The highest similarities using the *tub2* sequence were *V. malicola* (GenBank KT934374; Identities 363 / 413 (88 %), 18 gaps (4 %)), *V. sordida* (GenBank KT428034; Identities 346 / 396 (87 %), 14 gaps (3 %)) and *Cy. carbonacea* (GenBank KP310825; Identities 343 / 395 (87 %), 16 gaps (4 %)).

Dictyochaeta mimusopis Crous & M.J. Wingf., ***sp. nov.*** MycoBank MB824774. Fig. 15.

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

Mycelium consisting of branched, septate, hyaline, 3–4 µm diam hyphae. *Conidiophores* solitary, erect, pale brown, smooth, subcylindrical, unbranched, straight to flexuous, 1–6-septate, 40–150 × 3–4 µm. *Conidiogenous cells* monophialidic, integrated, terminal, pale brown, smooth, subcylindrical, 30–55 × 3(–3.5) µm; with flared apical collarette, 3–4 µm diam. *Conidia* solitary, aseptate, hyaline, smooth, guttulate to granular, inequilateral, fusoid, outer plane convex, apex subacute, base truncate, 1–1.5 µm diam, (11–)16–18(–20) × 2.5–3(–3.5) µm, with a single unbranched, flexuous appendage at each end, (6–)7(–8) µm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margins, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface hazel with cinnamon pigment, reverse sepia. On PDA surface cinnamon, reverse amber. On OA surface sienna with patches of olivaceous grey.

Specimen examined: **South Africa**, Eastern Cape Province, Haga Haga, on leaves of *Mimusops caffra* (*Sapotaceae*), Dec. 2010, *M.J. Wingfield* (holotype CBS H-23412, culture ex-type CPC 29987 = CBS 143435).

Notes: *Dictyochaeta mimusopis* is closely allied to isolates in the *Di. simplex* complex (conidia 14–19 × 2.1–2.7 µm; Hughes & Kendrick 1968).

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Di. simplex* (GenBank EF029193; Identities 482 / 503 (96 %), 1 gap (0 %)), *Di. fertilis* (GenBank AF178540; Identities 469 / 491 (96 %), 5 gaps (1 %)) and *Codinaea pini* (GenBank NR_137943; Identities 485 / 521 (93 %), 22 gaps (4 %)). The highest similarities using the LSU sequence were *Di. simplex* (GenBank AF178559; Identities 830 / 836 (99 %), no gaps), *Codinaea pini* (GenBank KP004493; Identities 829 / 838 (99 %), 1 gap (0 %)) and *Rattania setulifera* (GenBank HM171322; Identities 815 / 835 (98 %), no gaps).

Dictyochaeta septata (B. Sutton & Hodges) Whitton *et al.*, *Fungal Diversity* **4**: 148. 2000. Fig. 16.
Basionym: *Codinaea septata* B. Sutton & Hodges, *Nova Hedwigia* **26**(2–3): 520. 1975.
Synonym: *Dictyochaeta septata* (B. Sutton & Hodges) Aramb. & Cabello, *Mycotaxon* **34**(2): 682 (1989) (nom. inval. Art 41.5, Melbourne).

Mycelium consisting of hyaline, septate, branched, smooth, 2–3 µm diam hyphae. *Conidiophores* solitary, erect, brown, smooth, subcylindrical, straight to flexuous, 1–3-septate, 30–120 × 4–6 µm. *Conidiogenous cells* terminal, integrated, pale brown, smooth, mono-, rarely polyphialidic, 10–30 × 4–5 µm; collarette flared, 3–4 µm diam. *Conidia* solitary, hyaline, smooth, guttulate, granular, subcylindrical, falcate, ends subobtuse, (14–)15–19(–

Fig. 16. *Dictyochaeta septata* (CBS 143386). **A.** Colony on SNA. **B–D.** Conidiophores. **E.** Conidia. Scale bars = 10 μm.

20) × 2.5(–3) μm, medianly 1-septate, with a single unbranched, flexuous appendage at each end, 5–7 μm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margins, reaching 45 mm diam after 2 wk at 25 °C. On MEA surface hazel with cinnamon pigment, reverse sepia. On PDA surface cinnamon, reverse amber. On OA surface sienna with patches of olivaceous grey.

Specimens examined: **Brazil**, Espirito Santo, Vania, on *Eucalyptus* sp. (*Myrtaceae*), 11 Dec. 1973, *C.S. Hodges* (holotype K(M) IMI 181532f). **Chile**, on leaves of *Eucalyptus grandis* × *urophylla* (*Myrtaceae*), Jun. 2010, *M.J. Wingfield* (epitype of *Codinaea septata* designated here CBS H-23427, MBT381137, culture ex-epitype CPC 31949 = CBS 143386).

Notes: This collection closely resembles *Codinaea septata*, described from *Eucalyptus* leaves in Brazil with its conidia being 1(–2)-septate, (14.5–)17.5–23 × 2 μm, and conidiophores 30–105 × 4–6 μm (Sutton & Hodges 1975). Although we have in recent papers treated the genera *Codinaea* (setulate conidia) as distinct from *Dictyochaeta* (asetulate conidia) (Crous *et al*. 2015b), it appears that they could very well represent a single genus, with preference given to the older name, *Dictyochaeta*.

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Pseudolachnella guaviyunis* (GenBank KJ834524; Identities 480 / 542 (89 %), 13 gaps (2 %)), *Di. simplex* (GenBank EF029193; Identities 462 / 519 (89 %), 9 gaps (1 %)) and *Thozetella fabacearum* (GenBank KY212754; Identities 478 / 544 (88 %), 27 gaps (4 %)). The highest similarities using the LSU sequence were *T. pinicola* (GenBank EU825195; Identities 810 / 837 (97 %), 2 gaps (0 %)), *T. nivea* (GenBank EU825200; Identities 807 / 837 (96 %), 2 gaps (0 %)) and *P. fraxini* (GenBank JQ889301; Identities 806 / 836 (96 %), 1 gap (0 %)). No close hits were obtained when the *tef1* sequence was used in a megablast search.

Echinocatena arthrinioides R. Campb. & B. Sutton, *Trans. Brit. Mycol. Soc*. **69**: 130. 1977. Fig. 17.

Mycelium consisting of branched, septate, pale brown, smooth, 1.5–2 μm diam hyphae. *Conidiophores* erect, solitary, 20–50 × 3–4 μm, unbranched, straight to flexuous, pale brown, smooth, 3–7-septate. *Conidiogenous cells* in simple or branched acropetal chains, 5–7 × 3–4 μm, separated by thick, dark brown, refractive septa, appearing like a separating cell, pale brown, echinulate, doliiform to cylindrical, constricted at septa, polyblastic,

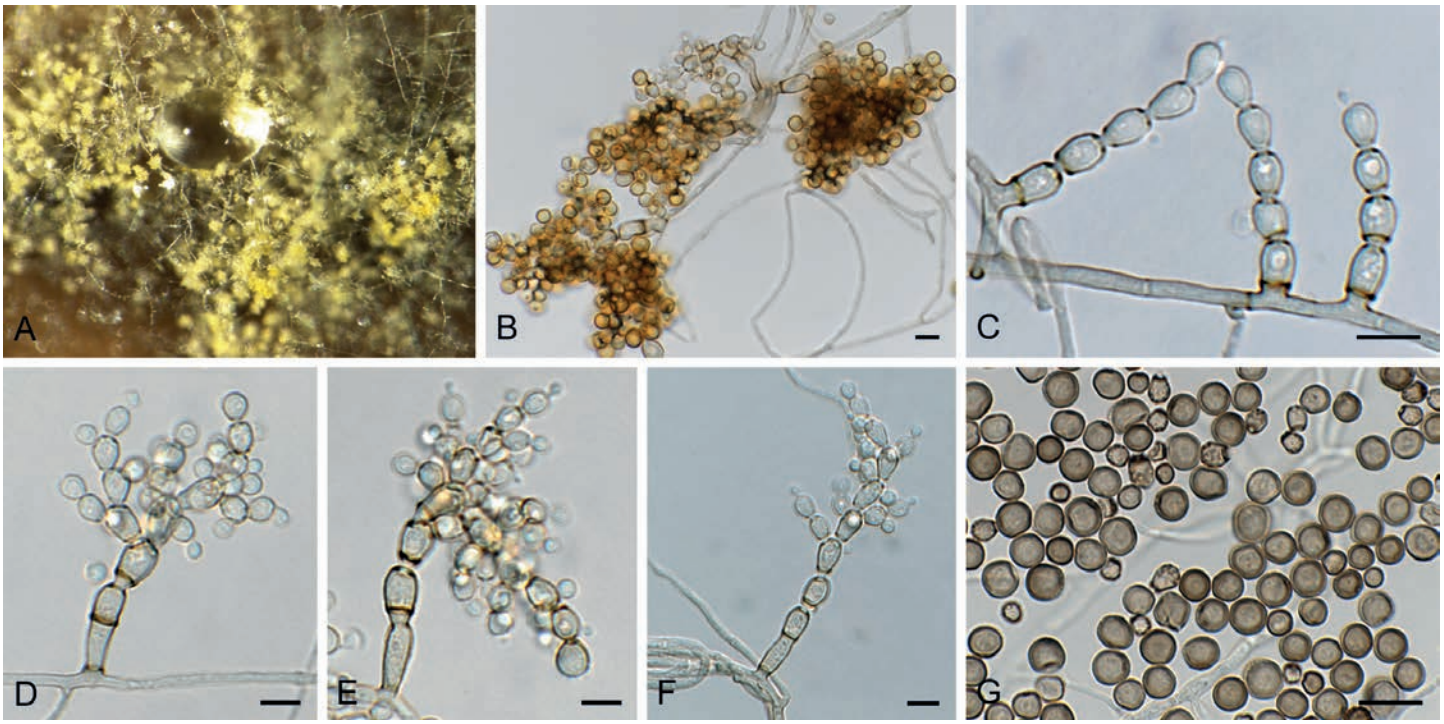

Fig. 17. *Echinocatena arthrinioides* (CPC 28754). **A.** Colony on MEA. **B–F.** Conidiophores. **G.** Conidia. Scale bars = 10 μm.

integrated with 5–7 conidiogenous loci. *Conidia* (4–)5–6(–7) µm diam, solitary, spherical, orange-brown, thick-walled, aseptate, echinulate.

Specimen examined: **Malaysia**, on leaves of *Acacia crassicarpa* (*Fabaceae*), 1 Jul. 2015, *M.J. Wingfield* (specimen CBS H-23424, culture CPC 28754 = CBS 144202).

Notes: *Echinocatena arthrinioides* was originally described from leaf litter collected in India. This collection has conidia that are slightly larger those observed for the type collection (3.5–4.5 µm; Campbell & Sutton 1977), and DNA data would be required to fully resolve if this strain is conspecific with the type (IMI 199279).

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were "*Fusicladium* sp." from marine sponges in Panama (GenBank JN837045; Identities 524 / 530 (99 %), no gaps) and "*Sympoventuriaceae* sp." from a human nail in Hong Kong (GenBank LC158598; Identities 448 / 452 (99 %), no gaps); the remaining matches were with the 5.8S nrRNA genes of *Fusicladium* species. The highest similarities using the LSU sequence were *Mycosisymbrium cirrhosum* (GenBank KR259884; Identities 758 / 828 (92 %), 9 gaps (1 %)), *Scolecobasidium cateniphorum* (GenBank EU107309; Identities 758 / 829 (91 %), 11 gaps (1 %)) and *Verruconis verruculosa* (GenBank KF282668; Identities 757 / 829 (91 %), 11 gaps (1 %)).

Elsinoë mimosae Viégas, *Bragantia* **4**: 13. 1944.

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

Specimens examined: **Brazil**, São Paulo, Campinas, on *Mimosa* sp. (*Leguminosae*), 31 Mar. 1931, *H.P. Krug & O. Zagatto* (holotype IAC No. 2836); **Brazil**, Rio de Janeiro, Itaguaí, Mazomba, on *Mimosa diplotricha* (= *Mimosa invisa*), Mar. 1999, *R.W. Barreto* (epitype designated here MBT381423, preserved in metabolically inactive state, ex-epitype culture CBS 141878) = CPC 19478 = RWB 154. **Ecuador**, Coca, on *Mimosa diplotricha*, Nov. 2000, *R.W. Barreto*, specimen CBS H-22804, culture CPC 18518 = RWB 224 = CBS 141943.

Notes: The epitype was designated in Fan *et al*. (2017), but that epitypification was not effected since the holotype was not "explicitly" cited (Art 9.8, Melbourne Code). We correct this situation by citing the holotype as "IAC No. 2836".

Exophiala eucalypticola Crous & T.I. Burgess, ***sp. nov.*** MycoBank MB824775. Fig. 18.

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

Mycelium consisting of pale brown, smooth, septate, branched, 2–2.5 µm diam hyphae. *Conidiophores* arising as lateral ends of hyphae, or reduced to conidiogenous cells, integrated on hyphae, erect, medium brown, smooth, subcylindrical, 3–15 × 2–3 µm; scars thickened and darkened, 1 µm diam. *Conidia* occurring in branched chains, pale brown, smooth, 0–1-septate, fusoid-ellipsoidal, with hila that are thickened and darkened, 1 µm diam, (7–)10–13(–15) × (2.5–)3(–4) µm. Synasexual morph: *Conidiogenous cells* integrated as phialidic loci on creeping hyphae, 1–2 × 1 µm. *Conidia* dimorphic, with exophiala-like conidia pale brown, smooth, aseptate, ellipsoid, 4–7 × 2–3 µm.

Culture characteristics: Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, lobate margins, reaching 10 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface slimy, chestnut to black.

Specimen examined: **Australia**, Victoria, Melbourne, Dandenong Ranges, Silvan Reservoir Park, leaf litter of *Eucalyptus obliqua* (*Myrtaceae*), 1 Dec. 2016, *P.W. Crous* (holotype CBS H-23305, cultures ex-type CPC 32736 = CBS 143412).

Notes: The genera *Exophiala* and *Rhinocladiella* contain several clinically relevant species (de Hoog 1977). Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *R. aquaspersa* (GenBank AB091214; Identities 458 / 519 (88 %), 18 gaps (3 %)), *E. phaeomuriformis* (GenBank KP761151; Identities 485 / 555 (87 %), 27 gaps (4 %)) and *R. coryli* (GenBank KX306768; Identities 518 / 594 (87 %), 25 gaps (4 %)). The highest similarities using the LSU sequence were *E. xenobiotica* (GenBank KC311483; Identities 831 / 862 (96 %), 7 gaps (0 %)), *E. xenobiotica* (GenBank FJ358246; Identities 826 / 857 (96 %), 7 gaps (0 %)) and *Melanoctona tectonae* (GenBank KX258779; Identities

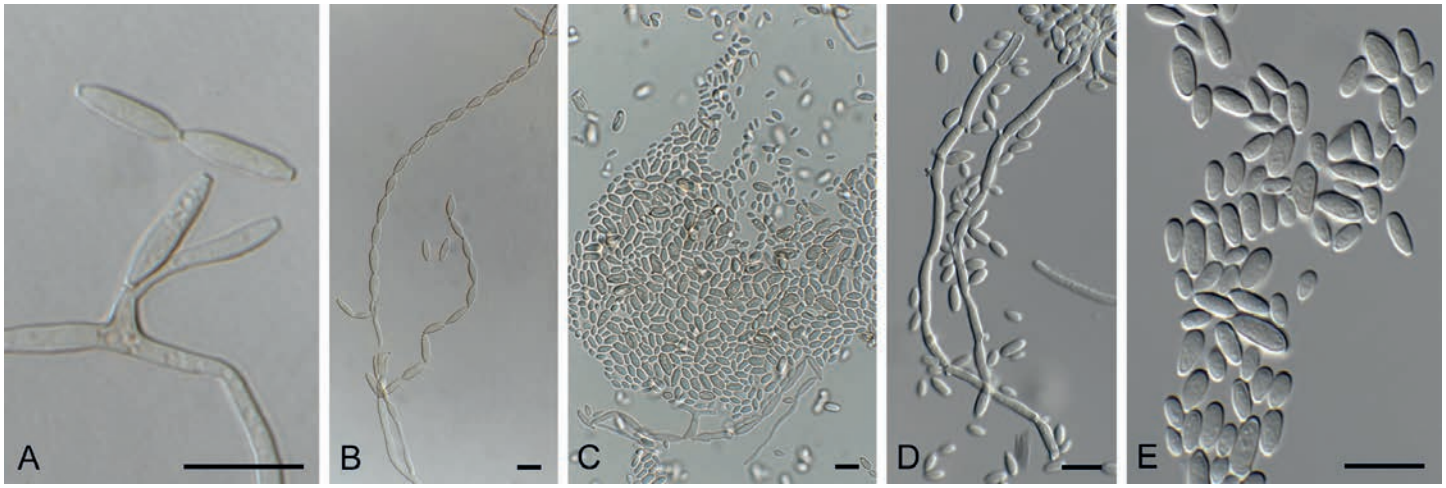

Fig. 18. *Exophiala eucalypticola* (CBS 143412). **A.** Conidiogenous cell. **B.** Conidial chain. **C, D.** Typical *Exophiala* morph with conidiogenous cells reduced to phialides. **E.** Conidia. Scale bars = 10 µm.

828 / 860 (96 %), 6 gaps (0 %)). The present collection is best allocated to this generic complex, and until better resolved it is best placed in *Exophiala*. No significant hits were obtained when the *tef1* and *tub2* sequences were used in a megablast search.

Fusiconidium lycopodiellae Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB824776. Fig. 19.

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

Mycelium consisting of hyaline, smooth, branched, septate, 2.5–4 µm diam hyphae. *Hyphopodia* absent. *Conidiophores* solitary, erect, subcylindrical, geniculate-sinuous, brown, smooth, 1–2-septate, 20–50 × 3–5 µm. *Conidiogenous cells* terminal, subcylindrical, brown, smooth, 10–17 × 3–4 µm, proliferating sympodially, holoblastically; scars unthickened, undarkened, 2–3 µm diam. *Conidia* solitary, brown, smooth, granular, subcylindrical, apex obtuse, tapering in lower cell to truncate hilum, 2–3 µm diam, (7–)8–9(–11)-septate, (65–)75–85(–100) × (7–)8(–9) µm.

Culture characteristics: Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margins, covering dish after 1 mo at 25 °C. On MEA surface ochreous, reverse amber. On PDA surface and reverse amber. On OA surface luteous.

Specimen examined: **Germany**, near Berlin, on stems of *Lycopodiella inundata* (*Lycopodiaceae*), 25 Feb. 2016, *R.K. Schumacher* (holotype CBS H-23407, culture ex-type CPC 30371 = CBS 143437).

Notes: The present collection is reminiscent of *Clasterosporium*, except that it lacks hyphopodia (Ellis 1971). Based on LSU sequence data it is allied to *Fusiconidium* (Li *et al*. 2017), except that it lacks percurrent proliferation of the conidiogenous cells, and fusoid to ellipsoid conidia, and probably represents a new genus in this complex. However, due to the poor sporulation of the culture, we have tentatively named it in *Fusiconidium*.

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Camposporium cambrense* (GenBank KY853428; Identities 481 / 502 (96 %), 3 gaps (0 %)), *Phragmocephala atra* (GenBank KP698721; Identities 495 / 523 (95 %), 4 gaps (0 %)) and *Phragmocephala garethjonesii* (GenBank NR_147636; Identities 493 / 523 (94 %), 3 gaps (0 %)). The highest similarities using the LSU sequence were *Fusiconidium mackenziei* (GenBank KX611113; Identities 806 / 815 (99 %), no gaps), *Paradendryphiella salina* (GenBank KF156156; Identities 780 / 791 (99 %), no gaps) and *Aposphaeria corallinolutea* (GenBank KU243051; Identities 804 / 817 (98 %), no gaps).

Haplographium delicatum Berk. & Broome, *Ann. Mag. Nat. Hist., Ser*. 3, **3**(17): 361. 1859. Fig. 20.

Conidiophores erect, subcylindrical, straight to flexuous, brown, thick-walled, verruculose, base with T-cell, lacking rhizoids, 70–160 × 5–6 µm, 5–10-septate. Conidiophores with swollen apical cell, pale brown, giving rise to 3–6 apical conidiogenous cells or primary branches; primary branches subcylindrical, straight to allantoid, hyaline, smooth, 5–10 × 2.5–3 µm. *Conidiogenous cells* hyaline, smooth, subcylindrical, straight to slightly curved, 6–12 × 2–2.5 µm, proliferating sympodially at apex. *Conidia* aggregating in mucoid mass, hyaline, smooth, guttulate, subcylindrical, straight, apex slightly swollen, obtuse, base truncate, (3–)5–6(–7.5) × 2(–2.5) µm.

Culture characteristics: Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margins, reaching 13 mm diam after 2 wk at 25 °C. On MEA surface and reverse pale luteous. On PDA surface pale olivaceous grey, reverse ochreous. On OA surface umber, with diffuse sienna pigment.

Specimen examined: **Ukraine**, Ternopil region, Zalischyky district, Dniester Canyon, on decaying wood of *Carpinus betulus* (*Betulaceae*), 5 Oct. 2016, *A. Akulov*, specimen ex CWU (MYC) AS 6049 (dried culture CBS H-23417, culture CPC 31844 = CBS 143493).

Notes: The genus *Haplographium* is based on *H. delicatum* described from wood collected in Britain. The present collection is phylogenetically similar to strains identified as *H. catenatum* and *H. delicatum* (Crous *et al.* 2009a). Because the genus *Haplographium* lacks a type and the species concepts are still in flux, we have identified the present collection as *H. delicatum.* Species of *Haplographium* have been linked to *Dematioscypha* sexual morphs (Raitviir 2001), but this relationship also requires further study.

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *H.*

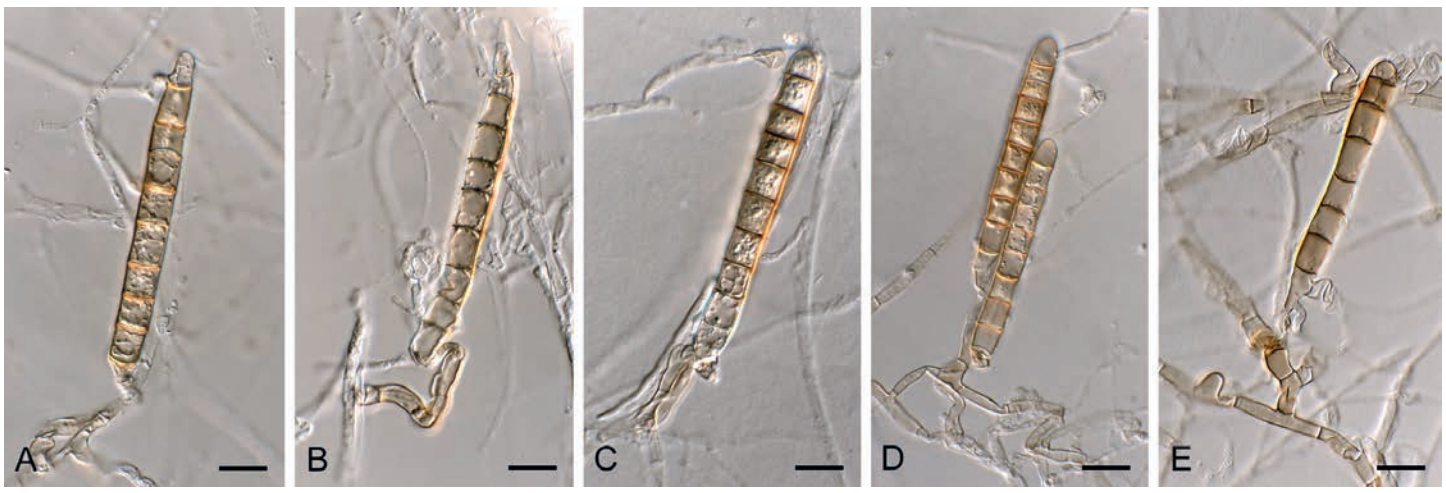

Fig. 19. *Fusiconidium lycopodiellae* (CBS 143437). **A–E.** Conidiophores giving rise to multiseptate conidia. Scale bars = 10 µm.

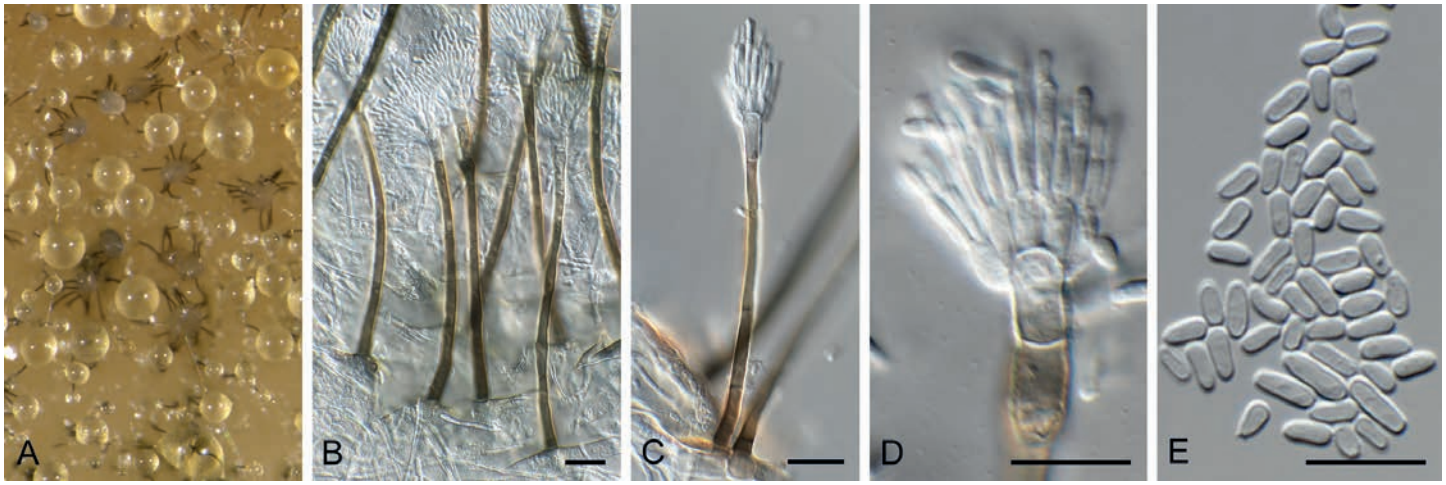

Fig. 20. *Haplographium delicatum* (CBS 143493). **A.** Colony on OA. **B–C.** Conidiophores. **D.** Conidiogenous cells. **E.** Conidia. Scale bars = 10 μm.

catenatum (GenBank FJ839620; Identities 528 / 533 (99 %), 1 gap (0 %)), *H. delicatum* (GenBank HF677177; Identities 495 / 500 (99 %), 1 gap (0 %)) and *Ciliciopodium brevipes* (GenBank KM231856; Identities 401 / 451 (89 %), 10 gaps (2 %)). The highest similarities using the LSU sequence were *H. catenatum* (GenBank FJ839657; Identities 855 / 855 (100 %), no gaps), *Hyaloscypha minuta* (GenBank KY769526; Identities 832 / 857 (97 %), 3 gaps (0 %)) and *Hy. monodictys* (GenBank JN086756; Identities 808 / 833 (97 %), 3 gaps (0 %)).

Microdochium musae (T.Y. Lin & J.M. Yen) Crous, ***comb. nov.*** MycoBank MB824777. Fig. 21.
Basionym: *Sphaerulina musae* T.Y. Lin & J.M. Yen, *Rev. Mycol.* (Paris) **35**: 326. 1971.

Ascomata (on OA) solitary, immersed on leaf tissue (superficial to immersed on banana leaf agar), globose, semi-papillate with central ostiole, pale brown, 200–250 μm diam; wall of 6–8 layers of pale brown *textura angularis*. *Paraphyses* intermingled among asci, hyaline smooth, septate, unbranched, constricted at septa, hyphae-like, 4–5 μm diam, with obtuse ends. *Asci* fasciculate, hyaline, unitunicate, apical mechanism staining blue in Meltzer's, broadly ellipsoid, straight to curved, 8-spored, stipitate, 80–100 × 17–22 μm. *Ascospores* bi- to triseriate, hyaline to faintly pinkish, smooth, guttulate, obovoid, apex obtuse, tapering from middle to base, straight to curved, 3–6-septate, at times with mucoid sheath, frequently constricted at median septum, (30–) 32–33(–35) × (6–)7(–8) μm.

Culture characteristics: Colonies flat, spreading, with sparse aerial mycelium, radially folded, and even margins, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface and reverse saffron. On PDA surface and reverse salmon. On OA surface salmon.

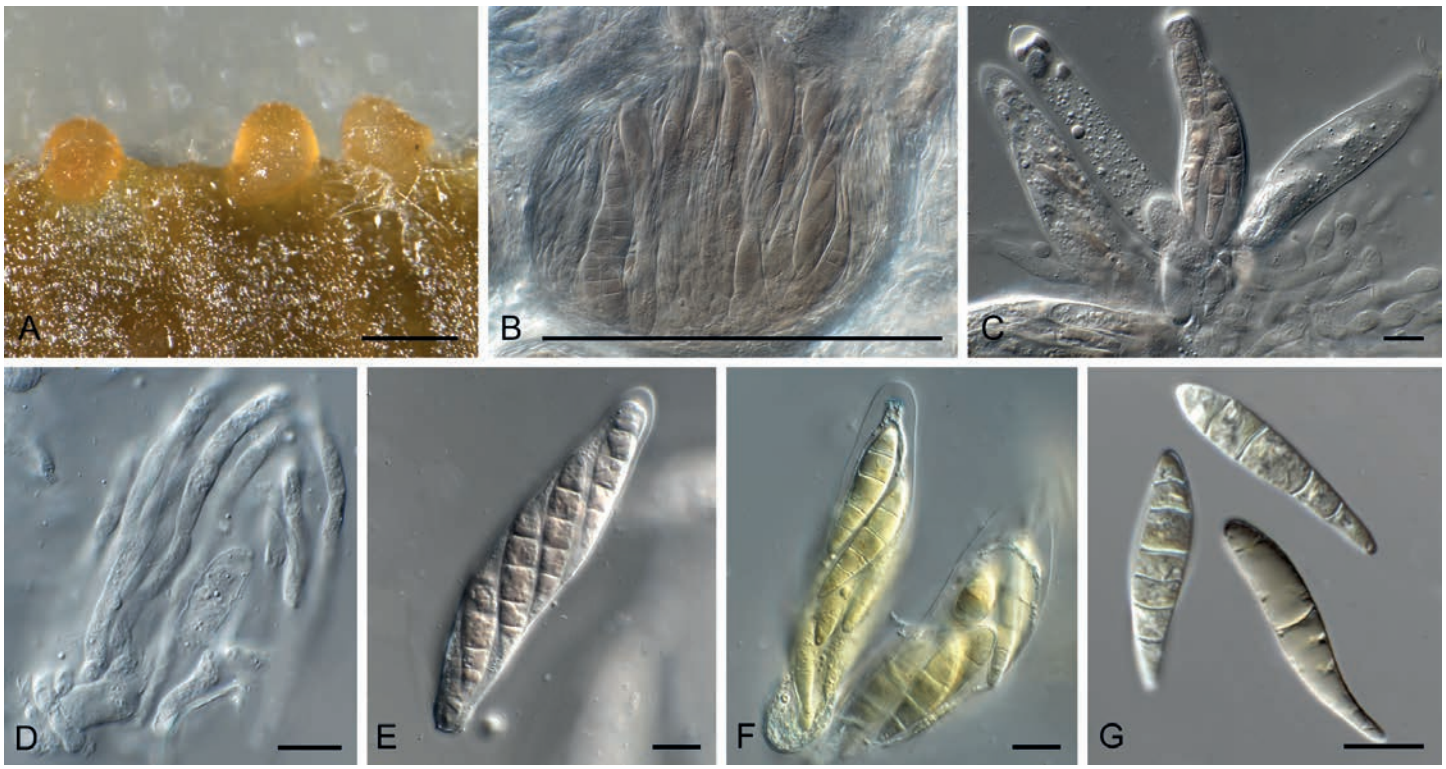

Fig. 21. *Microdochium musae* (CBS 143500). **A.** Ascomata on banana leaf. **B.** Vertical section through ascoma. **C.** Asci. **D.** Paraphyses. **E.** Subhyaline ascospores. **F.** Ascus in Meltzer's reagent. **G.** Ascospores. Scale bars: A, B = 250 μm, all others = 10 μm.

Specimens examined. **Republic of China** (Taiwan), on leaves of *Musa* sp. (*Musaceae*), 1970, *T. Wang*, holotype missing, lectotype designated here, MBT381229 (Lin & Yen 1971, fig. 2 D–F). **Malaysia**, Sabah, on leaves of *Musa* sp., 2016, *P.W. Crous* (epitype designated here, CBS H-23431, MBT381140, culture ex-epitype CPC 32689 = CBS 143500).

Additional cultures examined: **Costa Rica**, on *Musa* cv. Cavendish, May 2002, *P.W. Crous* (CBS 111018 = CPC 5380). **Malaysia**, on *Musa* leaves, 2010, *P.W. Crous* (CPC 32681), *ibid.* (CPC 32809). **Mauritius**, on *Musa* leaves, Jan. 2004, *Y. Jaufeerally-Fakim* (CPC 11234), *ibid.* (CPC 11240). **Mexico**, Chiapas, on *Musa* leaves, 16 Dec. 2008, *M. de J. Yanez Morales* (CPC 16258).

Notes: The genus *Sphaerulina* was treated by Quaedvlieg *et al.* (2013), and represents a genus in the *Mycosphaerellaceae*, to which *S. musae* (Lin & Yen 1971) is not related. "*Sphaerulina" musae* clusters among species of *Microdochium*, which have sexual morphs that are morphologically similar (Hernández-Restrepo *et al.* 2016), justifying this new combination.

Microdochium musae is commonly associated with brown necrotic areas on banana leaves, appears to be globally distributed along with its host, and is assumed to be weakly pathogenic (unpubl. data). Because the holotype could not be traced in Taiwan or Paris, the original illustration is proposed as lectotype and a neotype is designated. Colonies initially have a yeast-like appearance in culture, and single ascospores give rise to the sexual morph, suggesting that the species is homothallic.

Based on a megablast search using the ITS sequence of CPC 32689, the closest matches in NCBI's GenBank nucleotide database were *Sphaerulina musae* (GenBank AY293061; Identities 477 / 477 (100 %), no gaps), *Mi. stoveri* (GenBank FJ430601; Identities 537 / 540 (99 %), no gaps) and *Mi. colombiense* (GenBank KP858999; Identities 499 / 516 (97 %), 3 gaps (0 %)). The highest similarities using the LSU sequence of CPC 32689, the closest matches in NCBI's GenBank nucleotide database were *Mi. colombiense* (GenBank KP858935; Identities 834 / 842 (99 %), no gaps), *Mi. citrinidiscum* (GenBank KP858939; Identities 831 / 842 (99 %), no gaps) and *Mi. sorghi* (GenBank KP858936; Identities 831 / 842 (99 %), no gaps). The highest similarities using the *actA* sequence of CPC 16258 were *Chaetopsina fulva* (GenBank KM231165; Identities 404 / 422 (96 %), no gaps), *Fusarium phaseoli* (GenBank KM231203; Identities 400 / 419 (95 %), no gaps) and *Ch. acutispora* (GenBank KM231164; Identities 401 / 421 (95 %), no gaps). The *actA* sequences of CPC 11234, 11240, 16258, 32681 and 32809 are identical, but differ with two nucleotides from CPC 32689. No significant hits were obtained when the *cmdA* sequences were used in a megablast search. The *cmdA* sequences of CPC 11234, 11240, 16258, 32689 and 32809 are identical, but differ one nucleotide from CPC 32681. The highest similarities using the *rpb2* sequence of CPC 32689 were *Mi. colombiense* (GenBank KP859108; Identities 740 / 782 (95 %), no gaps), *Mi. majus* (GenBank KP859110; Identities 675 / 780 (87 %), 4 gaps (0 %)) and *M. nivale* (GenBank KP859117; Identities 679 / 785 (86 %), 6 gaps (0 %)). No significant hits were obtained when the *tef1* and *tub2* sequences of CPC 32681 were used in a megablast search. The *tef1* sequences of CPC 11234, 11240, 16258 and 32689 are identical. The *tub2* sequences of CPC 11234, 11240, 32689 and 32809 are identical, but differ one nucleotide from CPC 16258.

Monochaetia junipericola Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB824778. Fig. 22.

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

Conidiomata pycnidioid, separate to gregarious, erumpent, ovoid, 150–250 µm diam. *Conidiophores* arising from central stroma, hyaline, smooth, 3–6-septate, branched, subcylindrical, 40–100 × 3–4 µm. *Conidiogenous cells* terminal and intercalary, hyaline, smooth, subcylindrical, 10–30 × 2.5–3 µm, proliferating percurrently at apex. *Conidia* fusoid-ellipsoid, 4-septate, not constricted at septa, medium brown, finely verruculose, end cells hyaline, (22–)25–27(–28) × (5–)6(–7) µm, apical cell terminating in a single, unbranched, filiform, flexuous appendage, 10–20 µm long; basal cell with single, unbranched, flexuous, excentric appendage, 2–15 µm long. *Conidiomata* with *beta conidia* developing on OA, beta conidia hyaline, smooth, filiform, curved, apex obtuse, base truncate, 12–22 × 1.5–2 µm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and feathery, lobate margins, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface pale luteous, reverse luteous. On PDA surface smoke grey with patches of isabelline, reverse pale luteous. On OA surface pale luteous with patches of amber.

Specimen examined: **Germany**, near Berlin, on twig of *Juniperus communis* (*Cypressaceae*), 20 Apr. 2016, *R.K. Schumacher* (holotype CBS H-23408, culture ex-type CPC 30561 = CBS 143391).

Fig. 22. *Monochaetia junipericola* (CBS 143391). **A.** Conidiomata on PDA. **B, C.** Conidiophores giving rise to conidia. **D.** Conidia. **E.** Beta conidia. Scale bars = 10 µm.

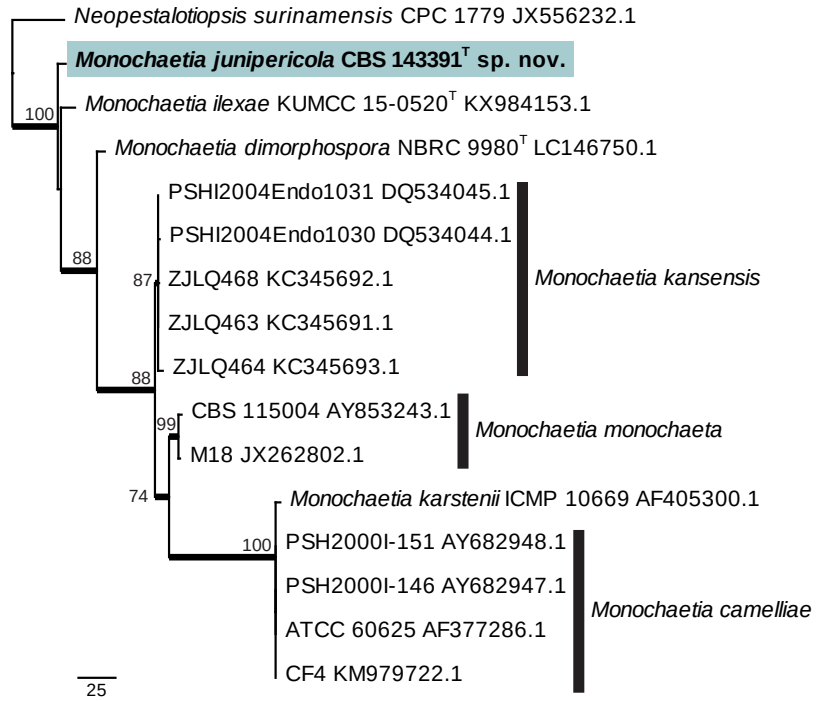

Fig. 23. The first of eight equally most parsimonious trees obtained from a phylogenetic analysis of the *Monochaetia* ITS alignment (16 strains including the outgroup; 524 characters analysed: 373 constant, 29 variable and parsimony-uninformative and 122 parsimony-informative). The tree was rooted to *Neopestalotiopsis surinamensis* (GenBank JX556232.1) and the scale bar indicates the number of changes. Bootstrap support values higher than 49 % are shown at the nodes and novelties are highlighted with a coloured box and bold text. Species names are indicated to the right of the tree, or before the culture collection and GenBank accession numbers. A superscript T denotes strains with a type status and branches present in the strict consensus tree are thickened. Tree statistics: TL = 238, CI = 0.782, RI = 0.899, RC = 0.702.

Notes: Nag Raj (1993) defined the genus *Monochaetia* to accommodate taxa with acervular conidiomata and fusiform, brown, transversely septate conidia with a single cellular apical, and single cellular basal appendage (when present). Nag Raj (1993) also regarded *Mo. juniperi* as synonym of *Sarcostroma foliicola*, occurring on needles of *Juniperus communis*. Morphologically *S. foliicola* has fusiform, 5-septate conidia, 18–22.5 × 7–8(–9) µm, apical appendage 3–8(–9) µm, and basal appendage excentric, 3–11 µm, thus smaller than those of *M. junipericola*. Phylogenetically, *M. junipericola* is basal to the other *Monochaetia* species known from ITS sequences (Fig. 23).

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Mo. ilexae* (GenBank NR_148179; Identities 497 / 516 (96 %), 7 gaps (1 %)), *Mo. dimorphospora* (GenBank LC146750; Identities 498 / 527 (94 %), 20 gaps (3 %)) and *Synnemadiella eucalypti* (GenBank KY173467; Identities 497 / 538 (92 %), 10 gaps (1 %)). The highest similarities using the LSU sequence were *Mo. ilexae* (GenBank KX984152; Identities 846 / 847 (99 %), no gaps), *Mo. kansensis* (GenBank DQ534035; Identities 832 / 833 (99 %), no gaps) and *Mo. monochaeta* (GenBank KF590148; Identities 828 / 829 (99 %), no gaps). Only distant hits were obtained using the *rpb2* sequence; some of these were *Pestalotiopsis versicolor* (GenBank DQ368654; Identities 662 / 803 (82 %), 4 gaps (0 %)), *P. fici* (GenBank XM_007830789; Identities 657 / 800 (82 %), no gaps) and *Discosia brasiliensis* (GenBank KF827475; Identities 658 / 805 (82 %), 4 gaps (0 %)). No significant hits were obtained when the *tef1* sequence was used in a megablast search. The best hit using the *tub2* sequence was with *Mo. kansensis* (GenBank DQ534049; Identities 356 / 407 (87 %), 3 gaps (0 %)).

Myrmecridium sorbicola Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB824779. Fig. 24.

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

On OA (only medium with sporulation). *Mycelium* consisting of hyaline, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* solitary, erect, flexuous, unbranched, brown, subcylindrical, smooth, 1–18-septate, 50–200 × 4–7 µm. *Conidiogenous cells* integrated, terminal and intercalary, 20–65 × 3–4 µm, with a rachis of pimple-like denticles, 0.5–1 × 0.5 µm. *Conidia* solitary, obovoid, initially hyaline, but pale brown with age, apex obtuse, hilum 1 µm diam, (0–)1(–3) septate, with mucoid sheath surrounding conidium in median region, 1–2 µm diam, (7–)8–10(–15) × 4(–5) µm.

Culture characteristics: Colonies flat, spreading, with sparse aerial mycelium and even, lobate margins, reaching 12 mm diam after 2 wk at 25 °C. On MEA surface and reverse luteous. On PDA surface and reverse pale luteous. On OA surface pale luteous.

Specimen examined: **Germany**, near Berlin, on branch of *Sorbus aucuparia* (*Rosaceae*), 17 Feb. 2016, *R.K. Schumacher* (holotype CBS H-23405, culture ex-type CPC 30455 = CBS 143433).

Notes: *Myrmecridium* was introduced by Arzanlou *et al.* (2007) for ramichloridium-like taxa having hyaline mycelium, and relatively unpigmented, pimple-like denticles, and obovoid to fusoid conidia with a wing-like gelatinous sheath. *Myrmecridium sorbicola* is distinct from known species based on its conidial morphology, with conidia being (0–)1(–3)-septate, (7–)8–10(–15) × 4(–5) µm.

Fig. 24. *Myrmecridium sorbicola* (CBS 143433). **A–E.** Conidiophores. **F.** Conidia with wing-like appendages. Scale bars = 10 µm.

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *My. schulzeri* (GenBank KF986544; Identities 447 / 513 (87 %), 14 gaps (2 %)), *My. phragmitis* (GenBank NR_137782; Identities 494 / 567 (87 %), 18 gaps (3 %)) and *My. fluviae* (GenBank KX839679; Identities 419 / 481 (87 %), 15 gaps (3 %)). The highest similarities using the LSU sequence were *My. banksiae* (GenBank NG_042684; Identities 813 / 842 (97 %), 2 gaps (0 %)), *My. schulzeri* (GenBank EU041835; Identities 812 / 842 (96 %), 2 gaps (0 %)) and *My. spartii* (GenBank KR611902; Identities 812 / 843 (96 %), 3 gaps (0 %)).

Nematogonum ferrugineum (Pers.) S. Hughes, *Canad. J. Bot.* **36**: 789. 1958. Fig. 25.
Basionym: *Monilinia ferruginea* Pers., *Mycol. eur.* (Erlanga) **1**: 30. 1822.

Mycelium consisting of hyaline, smooth, branched, septate, 3–4 µm diam hyphae. *Conidiophores* dimorphic. *Microconidiophores* reduced to conidiogenous cells on hyphae, erect, golden-brown, smooth, cylindrical, 20–40 × 6–8 µm. *Macroconidiophores* erect, flexuous, subcylindrical, smooth, golden-brown, flexuous, up to 400 µm tall, 8–10 µm diam, 2–7-septate, unbranched, terminal conidiogenous cell clavate, but at times also intercalary (appears to be linked to rejuvenating conidiophore), 25–100 × 11–15 µm; loci sympodial, thickened, somewhat darkened, 1–2 µm diam. *Conidia* occurring in branched chains, obovoid to ellipsoid, thick-walled, golden-brown, smooth, granular, apex obtuse, tapering to a truncate hilum, thickened and somewhat darkened, 1–2 µm diam, attached via a narrow isthmus, aseptate; primary conidia 15–21 × 12–14 µm; secondary conidia 11–15 × 8–9 µm; tertiary conidia 7–10 × 6–7 µm.

Culture characteristics: Colonies not growing on MEA, PDA or SNA. Colonies on OA pale luteous, flat, spreading, with sparse aerial mycelium and feathery, lobate margins, reaching 40 mm diam after 2 wk at 25 °C.

Specimen examined: **Ukraine**, Ternopil region, Zalischyky district, Dniester Canyon, on ascomata of *Melogramma campylosporum* on trunk of fallen *Carpinus betulus* (*Betulaceae*), 7 Oct. 2016, *A. Akulov,* specimen ex CWU (MYC) AS 6079 (dried culture CBS H-23418, culture CPC 31872 = CBS 144203).

Notes: Matsushima (1975) firstly reported an aspergillus-like synasexual morph for *Nematogonum highlei* (a synonym of *N. ferrugineum*). His description and illustrations correspond well with the conidiophores we observed in this study. Walker & Minter (1981) studied the conidiogenesis of *N. ferrugineum* and cited conidia to be ellipsoid, 4–24 × 3–15 µm, which become progressively smaller towards the tips of the chains. However, no distinction was made between primary, secondary or tertiary

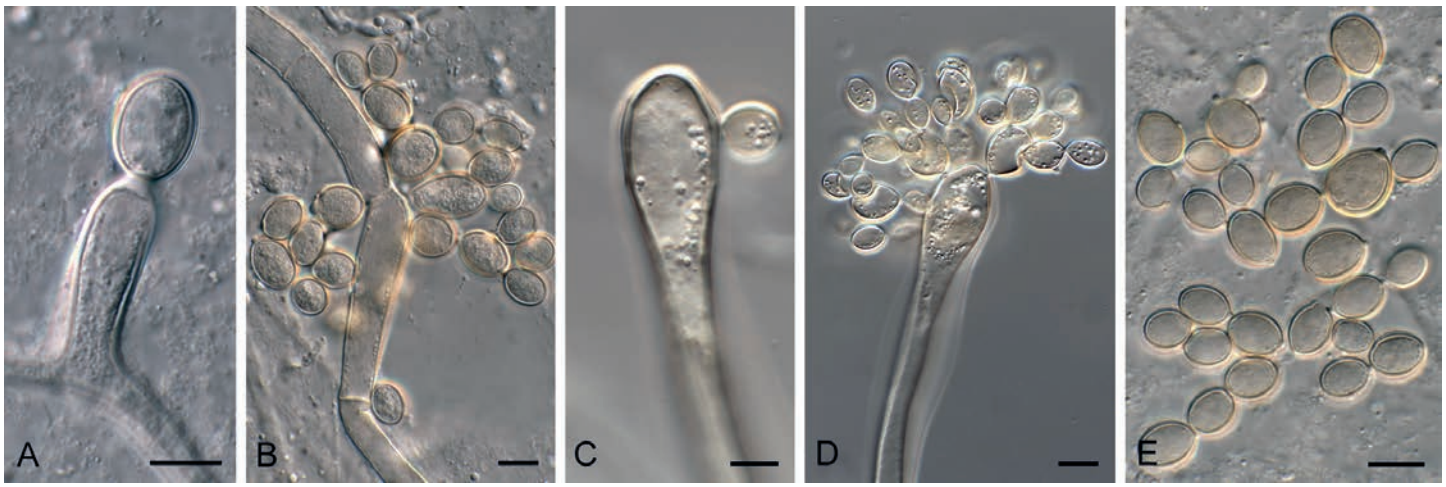

Fig. 25. *Nematogonum ferrugineum* (CPC 31872). **A.** Microconidiophore. **B–D.** Conidiophores with conidiogenous cells. **E.** Conidia. Scale bars = 10 µm.

conidia. The general conidium dimensions observed here, 7–21 × 6–15 µm, in the collection are different from the original species description, but correspond well with those provided by Matsushima (1975), 7–22 × 6.5–15 µm.

Nematogonum is not known from any sequence data that we were able to locate, and is listed as "*incertae sedis*" in MycoBank and Index Fungorum. In the present study, we were unable to generate an LSU sequence. However, based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Melanospora* spp. (*Melanosporales, Hypocreomycetidae, Sordariomycetes*), of which most members are also fungicolous. *Nematogonum ferrugineum* is known as an obligate fungicolous fungus on species of *Neonectria,* but has also been found on *Chaetomella, Cladosporium, Graphium, Melogramma, Tritirachium* and *Verticillium* representatives (Walker & Minter 1981, Gams *et al.* 2004, Akulov 2011).

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Melanospora kurssanoviana* (GenBank KP981479; Identities 500 / 549 (91 %), 12 gaps (2 %)), *Me. singaporensis* (GenBank LC146748; Identities 519 / 582 (89 %), 20 gaps (3 %)) and *Papulaspora funabasensis* (GenBank LC228646; Identities 508 / 569 (89 %), 17 gaps (2 %)). The highest similarities using the *tef1* sequence were *My. banksiae* (GenBank NG_042684; Identities 813 / 842 (97 %), 2 gaps (0 %)), *My. schulzeri* (GenBank EU041835; Identities 812 / 842 (96 %), 2 gaps (0 %)) and *My. spartii* (GenBank KR611902; Identities 812 / 843 (96 %), 3 gaps (0 %)). No significant hits were obtained when the *tef1* sequence was used in a megablast search. All attempts to generate an LSU sequence for this culture failed, irrespective of using fresh DNA or different primer sets.

Neocucurbitaria cava (Schulzer) Valenzuela-Lopez *et al*., *Stud. Mycol*. **90**: 46. 2018. Fig. 26.
Basionym: *Phoma cava* Schulzer, *Verh. K. K. Zool.-Bot. Ges. Wien* **21**: 1248. 1871.

Conidiomata pycnidial, solitary, dark brown with 1–2 papillate ostioles, 150–250 µm diam; wall of 2–3 layers of brown *textura angularis. Conidiophores* lining the inner cavity, hyaline, smooth, subcylindrical, branched, 1–4-septate, 7–20 × 2–3 µm. *Conidiogenous cells* phialidic, with periclinal thickening, hyaline, smooth, subcylindrical, apical and intercalary, 4–7 × 2–3 µm. *Conidia* solitary, hyaline, smooth, aseptate, subcylindrical, guttulate, with bluntly rounded ends, (3–)3.5(–4) × 1.5 µm.
Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margins, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface pale mouse grey, reverse mouse grey. On PDA surface olivaceous grey, reverse iron-grey. On OA surface iron-grey.

Specimen examined: **UK**, England, Bournmouth, on leaves of *Quercus ilex* (*Fagaceae*), 30 Dec. 2016, *P.W. Crous* (specimen CBS H-23414, culture CPC 32488 = CBS 143400).

Notes: The present collection is morphologically similar to that of the epitype, which was described from soil collected in Germany and has conidia that are aseptate, hyaline, smooth- and thin-walled, mostly cylindrical to slightly allantoid, 2.5–3.5 × 1–1.5 µm, guttulate (Valenzuela-Lopez *et al*. 2018). The present study adds a new culture of *N. cava* from the UK.

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *N. cava* (GenBank JF440610; Identities 475 / 480 (99 %), 2 gaps (0 %)), *N. hakeae* (GenBank KY173436; Identities 512 / 533 (96 %), 3 gaps (0 %)) and *Ochrocladosporium frigidarii* (GenBank FJ755255; Identities 439 / 463 (95 %), no gaps). The highest similarities using the LSU sequence were *Ne. cava* (GenBank EU754199; Identities 855 / 855 (100 %), no gaps), *Ne. quercina* (GenBank GQ387620; Identities 848 / 855 (99 %), 1 gap (0 %)) and *Ne. unguis-hominis* (GenBank GQ387621; Identities 847 / 855 (99 %), 1 gap (0 %)). The highest similarities using the *actA* sequence were *Parastagonospora nodorum* (GenBank CP022855; Identities 469 / 508 (92 %), 2 gaps (0 %)), *Alternaria hordeicola* (GenBank JQ671637; Identities 478 / 520 (92 %), 2 gaps (0 %)) and *Al. triticimaculans* (GenBank JQ671631; Identities 478 / 520 (92 %), 2 gaps (0 %)). The highest similarities using the *rpb2* sequence were *Ne. populi* (GenBank MF795816; Identities 1035 / 1059 (98 %), no gaps), *Ne. juglandicola* (GenBank MF795815; Identities 1027 / 1059 (97 %), no gaps) and *Ne. cisticola* (GenBank MF795814; Identities 995 / 1058 (94 %), no gaps). The highest similarities using the *tub2* sequence were *Ne. populi* (GenBank MF795902; Identities 500 / 515 (97 %), 2 gaps (0 %)), *Ne. juglandicola* (GenBank MF795901; Identities 498 / 516 (97 %), 3 gaps (0 %)) and *Pyrenochaeta hakeae* (GenBank KY173613; Identities 500 / 534 (94 %), 10 gaps (1 %)).

Neohendersonia kickxii (Westend.) Sutton & Pollack, *Mycopathol. Mycol. Appl*. **52**: 334. 1974.
Basionym: *Stilbospora kickxii* Westend., *Bull. Séances Cl. Sci. Acad. Roy. Belgique* **18**: 409. 1851.

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

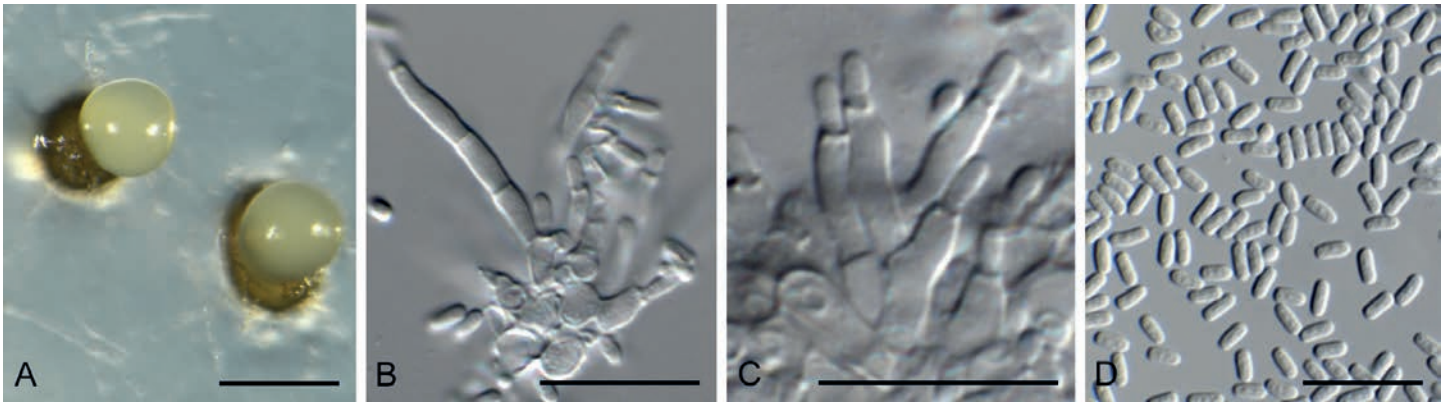

Fig. 26. *Neocucurbitaria cava* (CBS 143400). **A.** Conidiomata on SNA. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars: A = 200 µm, all others = 10 µm.

Specimens examined: **Belgium**, Courtrai, Parc Saint-George, on branch of *Fagus sylvatica* (*Fagaceae*) (substrate originally determined as *Betula pubescens* and later corrected with *Fagus sylvatica*), *G.D. Westendorp* (holotype BR5020162018281). **Italy**, Pian di Novello, on bark of twigs from *Fagus sylvatica*, 8 May 1996, *R. Danti* (epitype designated here of *Stilbospora kickxii* MycoBank MBT381143, preserved in metabolically inactive state, ex-epitype culture CBS 112403).

Notes: The epitype was originally designated in Giraldo *et al*. (2017), but a culture without any specimen was cited. This situation is herewith corrected, by stating that the culture is preserved as "metabolically inactive".

Parapleurotheciopsis caespitosa (Crous *et al*.) Crous, ***comb. nov.*** MycoBank MB824780.
Basionym: *Anungitea caespitosa* Crous *et al*., *Canad. J. Bot.* **73**(2): 225. 1995.

Description and illustration: Crous *et al*. (1995).

Specimen examined: **South Africa**, Mpumalanga, Sabie, on leaf litter of *Syzygium cordatum* (*Myrtaceae*), Nov. 1992, *M.J. Wingfield* (holotype PREM 51686, culture ex-type CPC 565 = CBS 519.93).

Note: See discussion under *Polyscytalum* and Fig. 13.

Parathyridaria philadelphi Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB824781. Fig. 27.

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

Conidiomata (on OA) separate, pycnidial, brown, globose, erumpent, 250–300 µm diam, with central ostiole; wall of 6–8 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, ampulliform, proliferating percurrently near phialidic apex, 4–7 × 3–4 µm. *Conidia* aseptate, solitary, subcylindrical, apex obtuse, base bluntly rounded, brown, smooth, at times slightly granular, (4–)5(–6) × 2 µm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and even, lobate margins, reaching 45 mm diam after 2 wk at 25 °C. On MEA surface pale olivaceous grey with patches of ochreous, reverse amber. On PDA surface amber, reverse chestnut. On OA surface amber with patches of sienna and vinaceous buff.

Specimen examined: **Germany**, near Berlin, on twigs of *Philadelphus coronarius* (*Hydrangeaceae*), 2 Apr. 2016, *R.K. Schumacher* (holotype CBS H-23409, culture ex-type CPC 30532 = CBS 143432).

Notes: The genus *Parathyridaria* was recently introduced by Jaklitsch & Voglmayr (2016). Phylogenetically (Fig. 28), *Pa. philadelphi* is allied to *Pa. robiniae*, a sexual species recently described from Italy on *Robinia pseudoacacia* (Tibpromma *et al*. 2017).

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Pa. robiniae* (GenBank KY511142; Identities 709 / 715 (99 %), no gaps), *Roussoella mukdahanensis* (GenBank KU940129; Identities 602 / 718 (84 %), 20 gaps (2 %)) and *Pa. ramulicola* (GenBank NR_147657; Identities 406 / 429 (95 %), 3 gaps (0 %)). The highest similarities using the LSU sequence were *Pa. robiniae* (GenBank KY511141; Identities 854 / 855 (95 %), no gaps), *Sporidesmium australiense* (GenBank DQ408554; Identities 835 / 846 (99 %), 1 gap (0 %)) and *Pa. ramulicola* (GenBank KF636775; Identities 846 / 859 (98 %), no gaps). The highest similarity using the *tef1* sequence was with *Pa. ramulicola* (GenBank KX650536; Identities 314 / 352 (89 %), 7 gaps (1 %)).

Pestalotiopsis hollandica Maharachch. *et al*., *Stud. Mycol.* **79**: 164. 2014. Fig. 29.

Conidiomata pycnidial, globose, separate, immersed to erumpent on banana leaf agar, dark brown to black, 120–350 µm diam, exuding a globose, dark brown conidial mass. *Conidiophores* subcylindrical, branched, hyaline, smooth, 1–2-septate, 15–30 × 3–5 µm. *Conidiogenous cells* terminal and intercalary, subcylindrical, hyaline, smooth, 8–15 × 2.5–3.5 µm; proliferating percurrently at apex. *Conidia* solitary, fusoid-ellipsoid, 4-septate, versicoloured, central three cells brown, of which the median cell is dark brown, guttulate, verruculose, apical and basal cells hyaline, conidia (22–)24–26(–27) × (7–)8(–9) µm, apical cell 3–4 µm long, basal cell 3–5 µm long, apical cell with three flexuous appendages, unbranched, attachment apical, 17–25 µm long, basal cell with central unbranched appendage, 3–9 µm long.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and feathery, lobate margins, covering dish after 2 wk at 25 °C. On MEA surface dirty white, reverse luteous. On PDA surface pale luteous to luteous, reverse amber. On OA surface pale luteous.

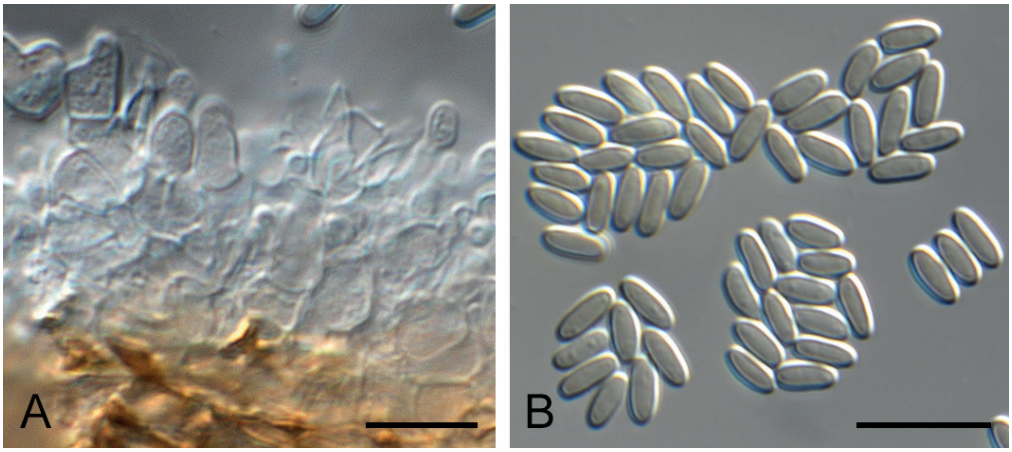

Fig. 27. *Parathyridaria philadelphi* (CBS 143432). **A.** Conidiogenous cells. **B.** Conidia. Scale bars = 10 µm.

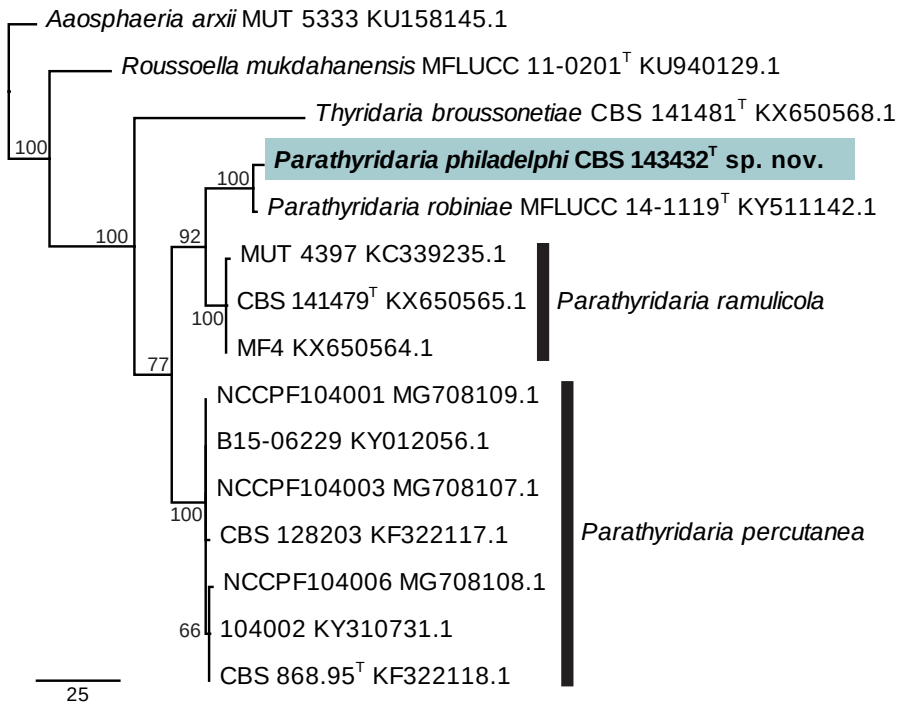

Fig. 28. Single most parsimonious tree obtained from a phylogenetic analysis of the *Parathyridaria* ITS alignment (15 strains including the outgroup; 412 characters analysed: 297 constant, 51 variable and parsimony-uninformative and 64 parsimony-informative). The tree was rooted to *Aaosphaeria arxii* (GenBank KU158145.1) and the scale bar indicates the number of changes. Bootstrap support values higher than 49 % are shown at the nodes and novelties are highlighted with a coloured box and bold text. Species names are indicated to the right of the tree, or before the culture collection and GenBank accession numbers. A superscript T denotes strains with a type status. Tree statistics: TL = 172, CI = 0.866, RI = 0.861, RC = 0.746.

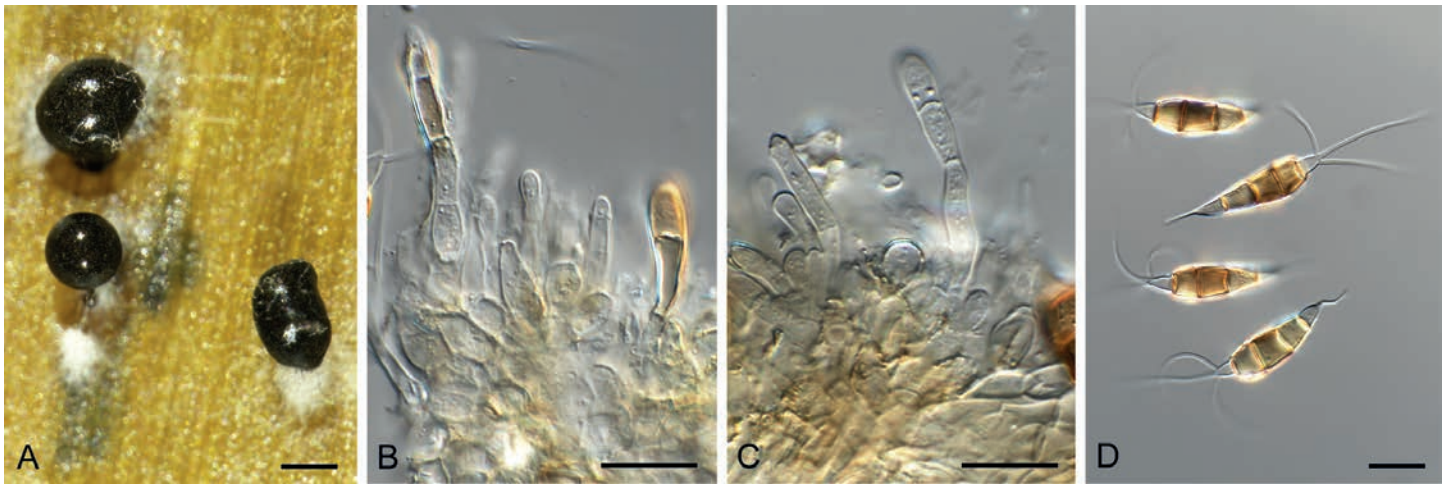

Fig. 29. *Pestalotiopsis hollandica* (CBS 143436). **A.** Conidiomata on BLA. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars: A = 300 μm, all others = 10 μm.

Specimen examined: **Spain**, Zaragoza, Carretera el Frago, on needles of *Cupressus sempervirens* (*Cupressaceae*), 7 Jan. 2016, *R. Blasco*, culture CPC 30399 = CBS 143436.

Notes: Phylogenetically the present collection is identical (based on ITS and LSU, and almost identical based on *tub2*) to *Pe. hollandica* (Maharachchikumbura *et al*. 2014). Morphologically, however, they are quite distinct, with *Pe. hollandica* having conidia that are larger, (25–)25.5–33(–34) × 8.5–10(–10.5) μm, with 1–4 tubular apical appendages, 20–40 μm long. Based on a megablast search using the ITS sequence in NCBI's GenBank nucleotide database, the ITS sequence is identical to *Pe. hollandica* (CBS 265.33; GenBank NR_147555), *Pe. monochaeta* (CBS 144.97; GenBank NR_147554) and *Pe. funerea* (ML4DY; GenBank EF055197). The highest similarities using the LSU sequence in NCBI's GenBank nucleotide database, the LSU sequence is identical to *Pe. monochaeta* (CBS 144.97; GenBank KM116229), *Pe. hollandica* (CBS 265.33; GenBank KM116228) and *Pe. hangzhouensis* (PSHI2002Endo390; GenBank DQ657865). The highest similarities using the *tef1* sequence were *Pe. verruculosa* (GenBank JX399061; Identities 298 / 299 (99 %), no gaps), *Pe. hollandica* (GenBank KM199481; Identities 281 / 286 (98 %), no gaps) and *Pe. brassicae* (GenBank KM199558; Identities 268 / 273 (98 %), no gaps). The highest similarities using the *tub2* sequence were *Pe. hollandica* (GenBank KM199388; Identities 446 / 447 (99 %), no gaps), *Pe. italiana* (GenBank KP781882; Identities 442 / 445 (99 %), 2 gaps (0 %)) and *Pe. monochaeta* (GenBank KX642435; Identities 448 / 452 (99 %), 2 gaps (0 %)).

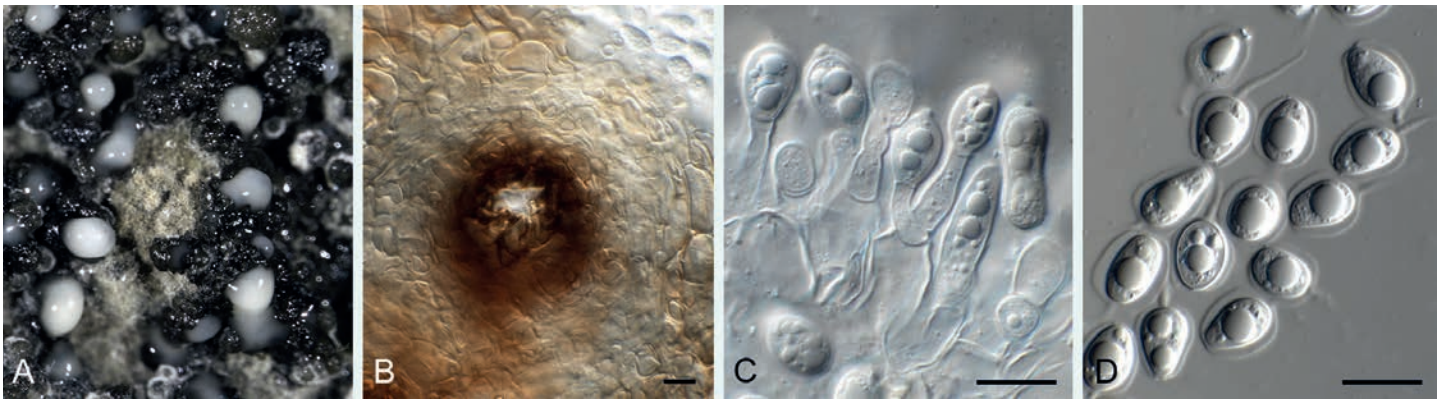

Fig. 30. *Phyllosticta hakeicola* (CBS 143492). **A.** Colony on PDA. **B.** Conidiomatal ostiole. **C.** Conidiogenous cells. **D.** Conidia. Scale bars = 10 μm.

Phyllosticta hakeicola Crous & T.I. Burgess, ***sp. nov.*** MycoBank MB824782. Fig. 30.

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

Conidiomata pycnidial, solitary, globose, dark brown, 150–250 μm diam, with central ostiole, 25–40 μm diam; wall of 3–8 layers of brown *textura angularis. Conidiophores* lining the inner cavity, 1–2-septate, subcylindrical, hyaline, smooth, branched below, 20–30 × 6–10 μm. *Conidiogenous cells* terminal and intercalary, subcylindrical, hyaline, smooth, 8–15 × 3–5 μm, proliferating percurrently at apex. *Conidia* solitary, ellipsoid to obovoid, aseptate, smooth, hyaline, guttulate, granular, (9–)10–13(–15) × (6.5–)7 μm; conidia encased in a persistent mucoid sheath, 2–3 μm diam, but with a single apical mucoid appendage, 5–12 × 1.5–2 μm, tapering to subacutely rounded apex.

Culture characteristics: Colonies flat to erumpent, spreading, with sparse to moderate aerial mycelium and feathery, lobate margins, reaching 55 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse iron-grey.

Specimen examined: **Australia**, New South Wales, Fitzroy Falls, on leaves of *Hakea* sp. (*Proteaceae*), 26 Nov. 2016, *P.W. Crous* (holotype CBS H-23315, culture ex-type CPC 32041 = CBS 143492).

Notes: Van der Aa & Vanev (2002) placed *Phyllosticta hakeae* in the genus *Microsphaeropsis*, and presently no species of *Phyllosticta* are known from *Hakea*. Phylogenetically (Fig. 31),

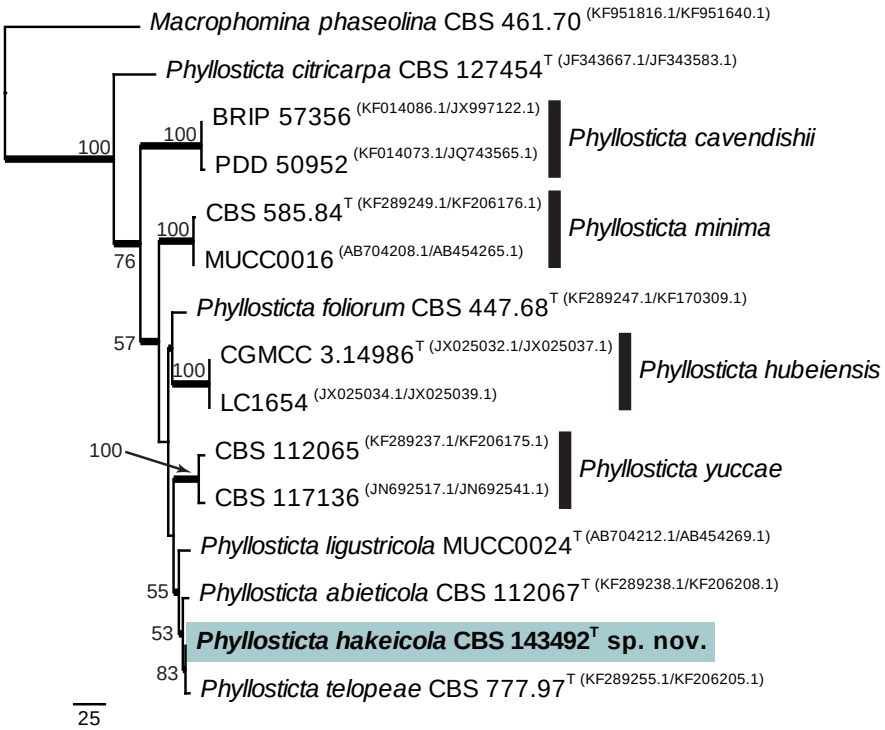

Fig. 31. The first of three equally most parsimonious trees obtained from a phylogenetic analysis of the combined *actA* and ITS alignment representing *Phyllosticta* species (15 strains including the outgroup; 659 characters analysed: 387 constant, 140 variable and parsimony-uninformative and 132 parsimony-informative). The tree was rooted to *Macrophomina phaseolina* (culture CBS 461.70) and the scale bar indicates the number of changes. Bootstrap support values higher than 49 % are shown at the nodes and novelties are highlighted with a coloured box and bold text. Species names are indicated to the right of the tree, or before the culture collection and GenBank accession numbers. A superscript T denotes strains with a type status and branches present in the strict consensus tree are thickened. Tree statistics: TL = 426, CI = 0.826, RI = 0.739, RC = 0.611.

Ph. hakeicola is closely related to *Ph. telopeae* (also *Proteaceae*; Crous *et al*. 2000), but can be distinguished by its larger conidia, (12–)13–16(–18) × (7–)8–9 μm (Swart *et al*. 1998).

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Ph. telopeae* (GenBank KF206205; Identities 568 / 570 (99 %), no gaps), *Ph. abieticola* (GenBank NR_147344; Identities 562 / 570 (99 %), 2 gaps (0 %)) and *Ph. ligustricola* (GenBank NR_136951; Identities 609 / 626 (97 %), 4 gaps (0 %)). The highest similarities using the LSU sequence were *Ph. telopeae* (GenBank KF766384; Identities 841 / 841 (100 %), no gaps), *Ph. abieticola* (GenBank EU754193; Identities 852 / 854 (99 %), no gaps) and *Ph. philoprina* (GenBank DQ377878; Identities 852 / 854 (99 %), no gaps). The highest similarities using the *actA* sequence were *Ph. abieticola* (GenBank KF289238; Identities 225 / 225 (100 %), no gaps), *Ph. telopeae* (GenBank KF289255; Identities 222 / 225 (99 %), no gaps) and *Ph. foliorum* (GenBank KF289247; Identities 221 / 225 (98 %), no gaps). The highest similarities using the *gapdh* sequence were *Ph. hubeiensis* (GenBank JX025029; Identities 339 / 351 (97 %), 1 gap (0 %)), *Ph. cavendishii* (GenBank KU716083; Identities 324 / 337 (96 %), no gaps) and *Ph. citricarpa* (GenBank KX280614; Identities 323 / 336 (96 %), no gaps). The highest similarities using the *tef1* sequence were *Ph. telopeae* (GenBank KF766435; Identities 303 / 308 (98 %), no gaps), *Ph. yuccae* (GenBank JX227948; Identities 371 / 396 (94 %), 5 gaps (1 %)) and *Ph. minima* (GenBank KF766432; Identities 287 / 309 (93 %), 6 gaps (1 %)).

Polyscytalum chilense Crous & M.J. Wingf., ***sp. nov.*** MycoBank MB824783. Fig. 32.

Etymology: Name refers to Chile, the country where this fungus was collected.

Mycelium consisting of branched, septate, brown, smooth, 2–3 μm diam hyphae. *Conidiophores* solitary, erect, 1–3-septate, subcylindrical, brown, smooth, straight to geniculous-sinuous, 30–60 × 3–4 μm. *Conidiogenous cells* terminal and intercalary, subcylindrical to clavate, 7–12 × 3–4 μm; scars arranged in a rachis, prominent, thickened, darkened and refractive, 1–1.5 μm diam. *Conidia* cylindrical, pale brown, smooth, prominently guttulate, 1-septate, apex obtuse, base truncate, 1–1.5 μm diam, somewhat darkened and refractive, in very long, unbranched chains, (13–)15–18(–20) × (2–)2.5 μm.

Culture characteristics: Colonies erumpent, spreading, with sparse aerial mycelium and feathery, lobate margins, reaching 15 mm diam after 2 wk at 25 °C. On MEA surface ochreous, reverse chestnut. On PDA surface and reverse amber. On OA surface iron-grey.

Specimen examined: **Chile**, on leaves of *Eucalyptus urophylla* (*Myrtaceae*), Jun. 2010, *M.J. Wingfield* (holotype CBS H-23403, culture ex-type CPC 31946 = CBS 143387).

Notes: Sutton (1973) established the genus *Anungitea* for a genus of hyphomycetes with dark, solitary conidiophores, bearing a head of denticles with flattened conidiogenous scars that are neither thickened nor darkened, and chains of cylindrical, 1-septate subhyaline conidia. Since its introduction, several taxa have been added to the genus, and because the type *A. fragilis* remains phylogenetically undefined, the generic concept has widened. As seen in the present study, several of these "*Anungitea*" species cluster with *Po. fecundissimum*, the type species of *Polyscytalum*. It has become clear that the generic concepts of these two genera overlap and that several species would be better accommodated in *Polyscytalum* than in *Anungitea*. *Polyscytalum* has cylindrical conidia that vary from being 0–1-septate, hyaline to pale brown, smooth, with truncate ends (those in *Anungitea* have obtuse ends), and the scars can be somewhat darkened and refractive, but unthickened in both genera (see *Pseudoanungitea* with thickened hila elsewhere in this manuscript).

Phylogenetically (Fig. 13), *Po. chilense* is distinct from all species known from *Eucalyptus* (Crous *et al.* 2017a) and is most similar to *Po. grevilleae*, which has setae, and smaller conidia, (10–)13–16(–22) × (2–)2.5–3 μm (Crous *et al.* 2016b).

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Po. grevilleae* (GenBank KX228252; Identities 537 / 560 (96 %), no gaps), *Po. eucalyptorum* (GenBank NR_132904; Identities 534 / 560 (95 %), 1 gap (0 %)) and *Po. fecundissimum* (GenBank EU035441; Identities 371 / 391 (95 %), 2 gaps (0 %)). The highest similarities using the LSU sequence were *Po. eucalyptigena* (GenBank KY173477; Identities 818 / 821 (99 %), no gaps), *Phlogicylindrium eucalypti* (GenBank DQ923534; Identities 888 / 896 (99 %), 1 gap (0 %)) and *Po. eucalyptorum* (GenBank KJ869176; Identities 878 / 886 (99 %), no gaps).

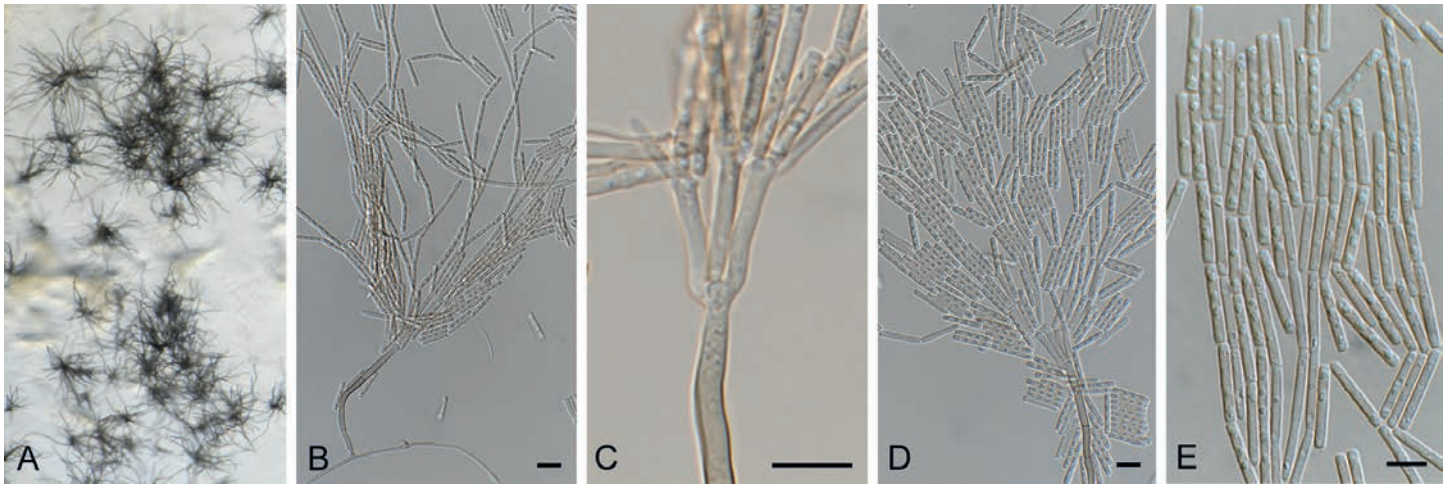

Fig. 32. *Polyscytalum chilense* (CBS 143387). **A.** Colony on SNA. **B–D.** Conidiophores giving rise to conidial chains. **E.** Conidia. Scale bars = 10 μm.

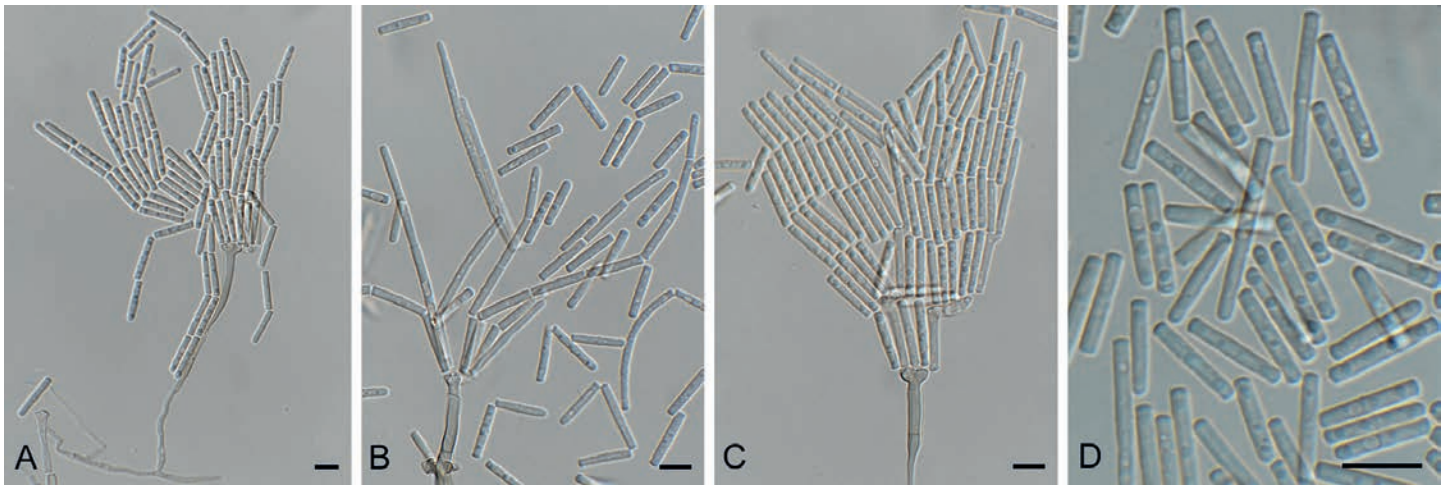

Fig. 33. *Polyscytalum eucalyptigenum* (CBS 143388). **A–C.** Conidiophores giving rise to conidial chains. **D.** Conidia. Scale bars = 10 µm.

Polyscytalum eucalyptigenum (Crous & M.J. Wingf.) Crous & M.J. Wingf., ***comb. nov.*** MycoBank MB824784. Fig. 33.
Basionym: *Anungitea eucalyptigena* Crous & M.J. Wingf., *Persoonia* **37**: 339. 2016.

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

Mycelium consisting of brown, smooth, septate, 2–3 µm diam hyphae. *Conidiophores* erect, solitary, subcylindrical, unbranched, brown, smooth, flexuous, 1–3-septate, 20–100 × 3–4 µm. *Conidiogenous cells* integrated, terminal, 7–15 × 3–4 µm, apex swollen with several sympodial loci, denticulate, flat-tipped, 1–2 × 2–2.5 µm, not thickened nor darkened. *Ramoconidia* subcylindrical, pale brown, smooth, 0–1-septate, 12–20 × 2.5–3 µm. *Conidia* occurring in long, unbranched chains, cylindrical with truncate ends, hyaline, smooth, guttulate, medianly 1-septate, (11–)13–17(–20) × (2–)2.5 µm.

Culture characteristics: Colonies flat, spreading, with sparse aerial mycelium and feathery, lobate margins, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface ochreous, reverse iron-grey. On PDA surface amber, reverse brown vinaceous. On OA surface olivaceous grey.

Specimens examined: **Chile**, on leaves of *Eucalyptus grandis* × *uromycoides* (*Myrtaceae*), Jun. 2010, *M.J. Wingfield* (specimen CBS H-23421, culture CPC 31878 = CBS 143388). **Malaysia**, Kota Kinabalu, on leaf spots of *Eucalyptus grandis* × *pellita* (*Myrtaceae*), 30 May 2015, *M.J. Wingfield* (holotype CBS H-22888, culture ex-type CPC 28762 = CBS 142102).

Notes: The present collection from Chile is morphologically and phylogenetically (Fig. 13) similar to the ex-type strain of *Po. eucalyptigenum* from Malaysia (ramoconidia 16–20 × 2.5–3 µm, conidia (11–)14–16(–18) × (2–)2.5(–3) µm; Crous *et al*. 2016a). Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Po. eucalyptigena* (GenBank KY173383; Identities 570 / 571 (99 %), no gaps), *Po. grevilleae* (GenBank KX228252; Identities 548 / 571 (96 %), 11 gaps (1 %)) and *Po. eucalyptorum* (GenBank NR_132904; Identities 545 / 571 (95 %), 12 gaps (2 %)). The highest similarities using the LSU sequence were *Po. eucalyptorum* (GenBank KY173477; Identities 819 / 821 (99 %), no gaps), *Po. grevilleae* (GenBank KX228304; Identities 824 / 831 (99 %), no gaps) and *Phlogicylindrium eucalypti* (GenBank DQ923534; Identities 835 / 844 (99 %), 1 gaps (0 %)).

Polyscytalum eucalyptorum (Crous & R.G. Shivas) Crous, ***comb. nov.*** MycoBank MB824785.
Basionym: *Anungitea eucalyptorum* Crous & R.G. Shivas, *Persoonia* **32**: 199. 2014.

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

Specimen examined: **Australia**, Queensland, Dave's Creek, S28°12'13.7" E153°12'9.5", on *Eucalyptus* (*Myrtaceae*) leaf litter, 11 Jul. 2009, *P.W. Crous & R.G. Shivas,* (holotype CBS H-21678, culture ex-type CPC 17207 = CBS 137967).

Polyscytalum grevilleae (Crous & Jacq. Edwards) Crous, ***comb. nov.*** MycoBank MB824786.
Basionym: *Anungitea grevilleae* Crous & Jacq. Edwards, *Persoonia* **36**: 327. 2016.

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

Specimen examined: **Australia**, Victoria, Royal Botanic Gardens Cranbourne, S38°7' 49.6" E145°16'9", on leaves of *Grevillea* sp. (*Proteaceae*), 7 Nov. 2014, *P.W. Crous & J. Edwards* (holotype CBS H-22591, culture ex-type CPC 25576 = CBS 141282).

Polyscytalum neofecundissimum Crous & Akulov, ***sp. nov.*** MycoBank MB824787. Fig. 34.

Etymology: Name refers to its morphological similarity to *Polyscytalum fecundissimum*.

Conidiophores reduced to conidiogenous cells or erect, flexuous, subcylindrical, branched, up to 100 µm tall, pale brown, smooth. *Conidiogenous cells* terminal and intercalary, subcylindrical, pale brown, smooth, 20–25 × 3–4 µm, proliferating sympodially at apex, scars unthickened, 2–2.5 µm diam. *Conidia* occurring in chains, cylindrical with obtuse ends, hyaline, smooth, medianly 1-septate, guttulate, (12–)14–17(–20) × 2(–3) µm.

Culture characteristics: Colonies erumpent, spreading, surface folded, with moderate aerial mycelium and smooth, lobate

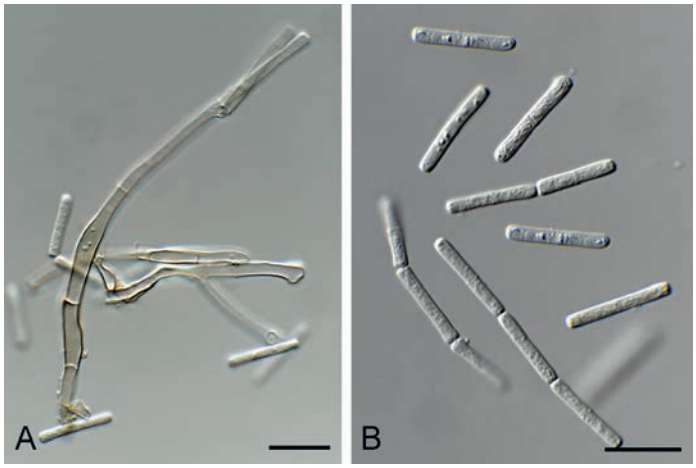

Fig. 34. *Polyscytalum neofecundissimum* (CBS 143390). **A.** Conidiophore. **B.** Conidial chains. Scale bars = 10 μm.

margins, reaching 20 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, reverse iron-grey.

Specimen examined: **Ukraine**, Ternopil region, Zalischyky district, Dniester Canyon, on leaf litter of *Quercus robur* (*Fagaceae*), associated with the mycelium of *Cladosporium* sp., 7 Oct. 2016, *A. Akulov,* specimen ex CWU (MYC) AS 6073 isotype (holotype CBS H-23419, culture ex-type CPC 31826 = CBS 143390).

Notes: *Polyscytalum neofecundissimum* is morphologically and phylogenetically (Fig. 13) similar to *Po. fecundissimum* (conidia 13–18 × 2 μm; Ellis 1971), except that it has larger conidia. Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Po. fecundissimum* (GenBank EU035441; Identities 562 / 578 (97 %), no gaps), *Subulispora britannica* (GenBank EF029198; Identities 535 / 571 (94 %), 2 gaps (0 %)) and *Pseudophloeospora eucalyptorum* (GenBank NR_145406; Identities 436 / 494 (88 %), 18 gaps (3 %)). The highest similarities using the LSU sequence were *Po. fecundissimum* (GenBank EU035441; Identities 800 / 809 (99 %), no gaps), *Po. eucalyptigena* (GenBank KY173477; Identities 812 / 823 (99 %), 2 gaps (0 %)) and *Po. eucalyptorum* (GenBank KJ869176; Identities 831 / 843 (99 %), 2 gaps (0 %)).

Polyscytalum nullicananum (Crous) Crous, ***comb. nov.*** MycoBank MB824788.
Basionym: *Anungitea nullicana* Crous, *Persoonia* **39**: 411. 2017.

Description and illustration: Crous *et al*. (2017b).

Specimen examined: **Australia**, New South Wales, Nullica State Forest, on leaf litter of *Eucalyptus* sp. (*Myrtaceae*), 29 Nov. 2016, *P.W. Crous* (holotype CBS H-23297, culture ex-type CPC 32528 = CBS 143406).

Pseudoanungitea Crous, ***gen. nov.*** MycoBank MB824789.

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

Mycelium consisting of branched, septate, brown, smooth, 2–3 μm diam hyphae. *Conidiophores* solitary, erect, septate, subcylindrical, brown, smooth, straight to flexuous. *Conidiogenous cells* terminal and intercalary, subcylindrical to clavate; scars arranged in a rachis, prominent, thickened, darkened and refractive. *Conidia* fusoid-ellipsoid, pale brown, smooth, prominently guttulate, 0–1-septate, hila somewhat darkened and refractive, in short (1–2) unbranched chains.

Type species: *Pseudoanungitea syzygii* (Crous *et al.*) Crous.

Pseudoanungitea syzygii (Crous *et al*.) Crous, ***comb. nov.*** MycoBank MB824790.
Basionym: *Anungitea syzygii* Crous *et al*., *Canad. J. Bot*. **73**(2): 225. 1995.

Description and illustration: Crous *et al.* (1995).

Specimen examined: **South Africa**, Mpumalanga, Sabie, on leaf litter of *Syzygium chordatum* (*Myrtaceae*), Mar. 1993, *W.J. Swart* (holotype PREM 51687, culture ex-type CPC 578 = CBS 520.93).

Notes: *Anungitea* includes species with dark, solitary conidiophores, bearing a head of denticles with flattened conidiogenous scars that are unthickened and not darkened, and chains of cylindrical, 1-septate subhyaline conidia, with apical and basal scars (Sutton 1973). *Anungitopsis* is similar but includes taxa with indistinguishable scars arranged in a rachis. *Neoanungitea* is somewhat intermediate between these two genera, having a rachis, but with flat-tipped loci (Crous *et al.* 2017b).

Because the type species of *Anungitea* (*A. fragilis*) is not presently known from culture and needs to be recollected (leaves of *Abies balsamea*, Manitoba, Canada), the phylogeny of *Anungitea* remains unresolved, and several unrelated taxa have been described in the genus. The two species treated here cluster apart from the generic clade assumed to be *Anungitea s. str*. They differ from *Anungitea* in having terminal and intercalary conidiogenous cells, and refractive, thickened scars that give rise to short conidial chains with somewhat darkened and refractive hila.

Pseudoanungitea vaccinii Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB824791. Fig. 35.

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

Mycelium consisting of branched, septate, brown, smooth, 2–3 μm diam hyphae. *Conidiophores* solitary, erect, 0–3-septate, subcylindrical, brown, smooth, straight to flexuous, 8–40 × 3–5 μm. *Conidiogenous cells* terminal and intercalary, subcylindrical to clavate, 5–20 × 3–5 μm; scars arranged in a rachis, prominent, thickened, darkened and refractive, 1–1.5 μm diam. *Conidia* fusoid-ellipsoid, pale brown, smooth, prominently guttulate, 0–1-septate, apex obtuse, base truncate, 1–1.5 μm diam, somewhat darkened and refractive, in short (1–2) unbranched chains, (8–)10–12(–13) × (2–)3(–4) μm.

Culture characteristics: Colonies erumpent, spreading, with sparse aerial mycelium and smooth, lobate margins, reaching 7 mm diam after 1 mo at 25 °C. On MEA, PDA and OA surface and reverse brown vinaceous.

Specimen examined: **Germany**, near Berlin, on stem of *Vaccinium myrtillus* (*Ericaceae*), 16 Jan. 2016, *R.K. Schumacher* (holotype CBS H-23422, culture ex-type CPC 30522 = CBS 143164).

Fig. 35. *Pseudoanungitea vaccinii* (CBS 143164). **A–E.** Conidiophores. **F.** Conidia. Scale bars = 10 μm.

Notes: Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Anungitea syzygii* (GenBank KY853424; Identities 499 / 526 (95 %), 4 gaps (0 %)), *Tothia fuscella* (GenBank JF927786; Identities 504 / 561 (90 %), 11 gaps (1 %)) and *T. spartii* (GenBank NR_132917; Identities 430 / 487 (88 %), 15 gaps (3 %)). The highest similarities using the LSU sequence were *Cylindrosympodium lauri* (GenBank EU035414; Identities 840 / 855 (98 %), no gaps), *Cy. variabile* (GenBank KX228353; Identities 836 / 852 (98 %), no gaps) and *An. syzygii* (GenBank KY853484; Identities 802 / 823 (98 %), 6 gaps (0 %)).

Pseudoanungitea variabilis Hern.-Restr., ***sp. nov.*** MycoBank MB824792. Fig. 36.

Etymology: Name refers to the variable conidial morphology.

Mycelium consisting of branched, septate, pale brown to brown, smooth, 1–2 μm diam hyphae. *Conidiophores* solitary, erect, simple, rarely branched, subcylindrical, straight to flexuous, 0–7-septate, brown paler to the apex, smooth, 18–100 × 2–3 μm. *Conidiogenous cells* terminal and intercalary, sympodial, denticulate, subcylindrical, 8.5–23.5 × 2.5–4 μm; denticles prominent, sometimes darkened, 1–1.5 μm diam. *Conidia* in short chains (1–2(–4)), two shapes *a*. fusoid-ellipsoid, hyaline, smooth, sometimes guttulate, 0–1-septate, apex obtuse or truncate, base truncate, 1–1.5 μm diam, somewhat darkened and refractive, 8–14 × 2–2.5(–3) μm; *b*. globose, subglobose to pyriform, hyaline, smooth, aseptate, apex obtuse, base truncated, 1–1.5 μm diam, 4–8.5 × 2–4 μm.

Culture characteristics: Colonies after 1 mo at 25 °C, on OA reaching 6 mm, velvety, brown vinaceous, entire to lobate margin; reverse brown vinaceous. On MEA and PDA reaching 6–12 mm, effuse becoming raised, aerial mycelium pale mouse grey, submerged mycelium black, lobate margin; reverse black.

Specimen examined: **Spain**, Castilla la Mancha, Hayedo de la Tejera Negra Natural Park, on dead wood, May 2011, *M. Hernández-Restrepo, J. Mena & J. Guarro* (holotype CBS H-23494, culture ex-type CBS 132716).

Notes: *Pseudoanungitea variabilis* is distinct from other species in the genus due to its having two conidial shapes. Some conidia are fusoid-ellipsoid resembling those of *Ps. syzygii* and *Ps. vaccini* (Crous *et al.* 1995, this study). However, *Ps. variabilis* can be distinguished by the presence of globose conidia.

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Sympodiella acicola* (GenBank KY853468; Identities 370 / 412 (90 %), 17 gaps (4 %)), *Tothia fuscella* (GenBank JF927786; Identities 469 / 528 (89 %), 13 gaps (2 %)) and *T. spartii* (GenBank NR_132917; Identities 399 / 448 (89 %), 10 gaps (2 %)). The highest similarities using the LSU sequence were *Cylindrosympodium lauri* (GenBank EU035414; Identities 820 / 849 (97 %), 6 gaps (0%)), *Cyl. variabile* (GenBank KX228353; Identities 819 / 849 (96 %), 6 gaps (0%)) and *Repetophragma goidanichii* (GenBank DQ408574; Identities 802 / 836 (96 %), 9 gaps (1 %)).

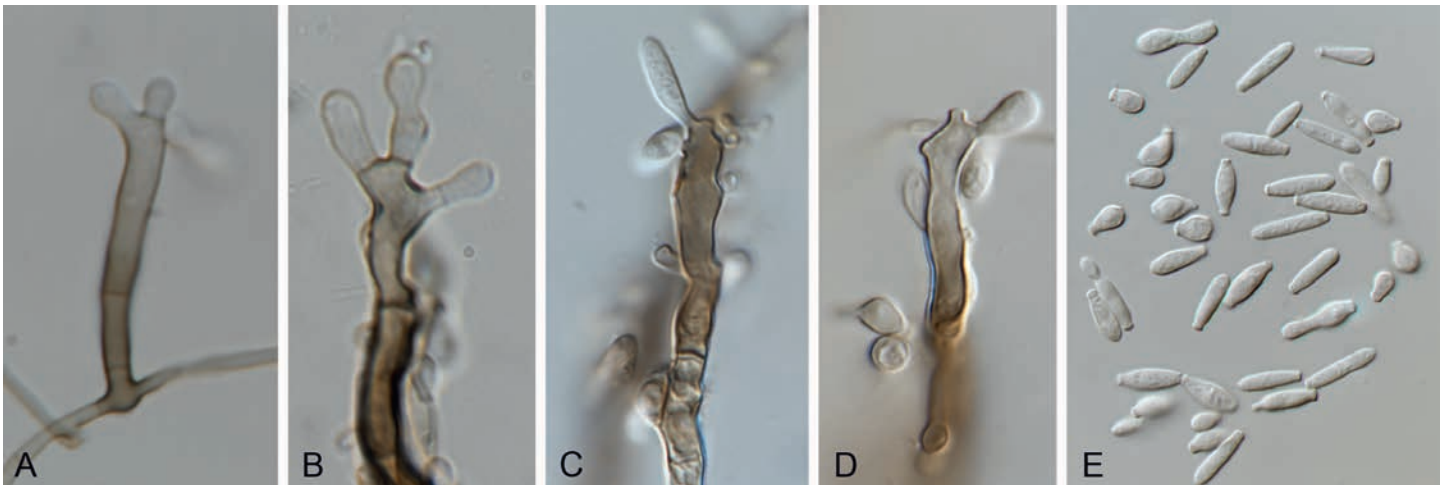

Fig. 36. *Pseudoanungitea variabilis* (CBS 132716). **A.** Conidiophores. **B–D.** Conidiogenous cells. **E.** Conidia. Scale bars = 10 μm.

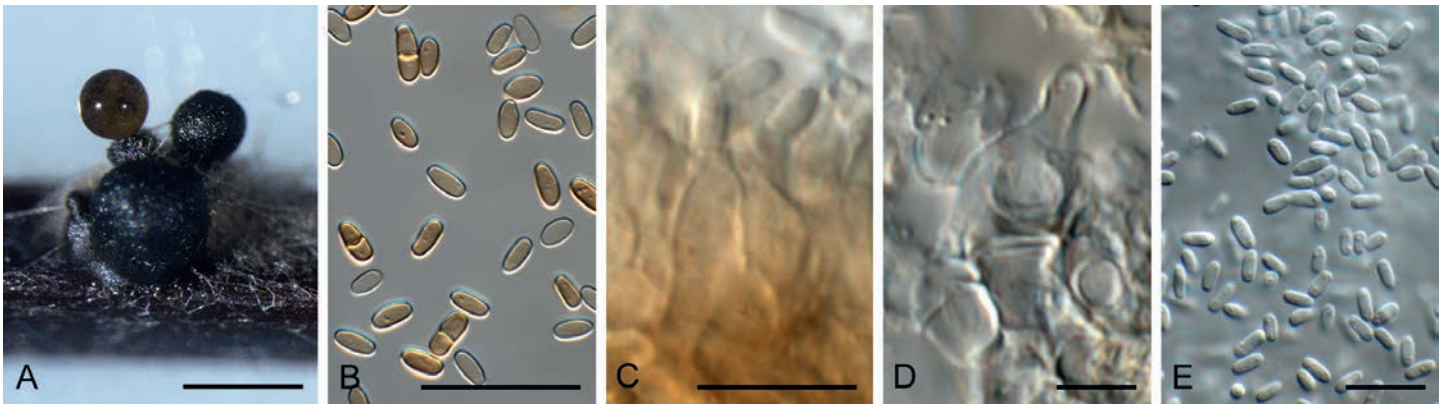

Fig. 37. *Pseudocamarosporium africanum* (CPC 25926). **A.** Conidioma on PNA. **B.** Pigmented macroconidia. **C, D.** Conidiogeous cells. **E.** Microconidia. Scale bars: A = 200 μm, all others = 10 μm.

Pseudocamarosporium africanum (Damm *et al.*) Crous, *Sydowia* **67**: 110. 2015. Fig. 37.
Basionym: *Paraconiothyrium africanum* Damm *et al.*, *Persoonia* **20**: 15. 2008.

Conidiomata separate, pycnidial, brown, erumpent, globose, 150–200 μm diam, with 1–2 ostioles, exuding a brown conidial mass; wall of 3–4 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, doliiform with periclinal thickening at apex, 4–9 × 3–6 μm. *Conidia* solitary, hyaline, smooth, becoming brown, finely roughened, subcylindrical, apex obtuse, at times slightly clavate, base truncate to bluntly rounded, 0–1-septate, (6–)7–8(–9) × (2.5–)3–3.5(–4) μm. *Spermatogonia* separate or in same conidioma as conidia, globose, brown, up to 150 μm diam, with central ostiole; wall of 3–4 layers of brown *textura angularis*. *Spermatophores* reduced to conidiogenous cells. *Spermatogenous cells* lining the inner cavity, ampulliform to doliiform, hyaline, smooth, 4–6 × 3–4 μm, apex with visible periclinal thickening and minute collarette. *Spermatia* solitary, smooth, hyaline, subcylindrical, straight to slightly curved, apex obtuse, base truncate, 3–5 × 1.5 μm.

Culture characteristics: Colonies spreading, with sparse to moderate aerial mycelium. On MEA surface pale mouse grey, reverse greyish sepia; on PDA surface and reverse fuscous black; on OA surface mouse grey.

Specimen examined: **South Africa**, Western Cape Province, Franschhoek pass, twigs of *Erica* sp. (*Ericaceae*), Nov. 2014, *M.J. Wingfield* (specimen CBS H-23425, culture CPC 25926 = CBS 144204).

Notes: The present collection is phylogenetically identical to *Pseudocamarosporium africanum*. The latter taxon was originally described from branches of *Prunus persica* in South Africa. Morphologically, the two collections are also similar in that conidia of the ex-type strain of *Ps. africana* are 1-septate, rarely 3- or 4-celled, brown and thick-walled, verruculose, (4–) 6.5–9.5(–12) × (2.5–)3–4(–5) μm (Damm *et al*. 2008).

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Ps. africanum* (GenBank EU295650; Identities 457 / 457 (100 %), no gaps), *Ps. cotinae* (GenBank KY098789; Identities 475 / 477 (99 %), no gaps) and *Pseudocamarosporium* "sp. 2" (GenBank KY929162; Identities 475 / 477 (99 %), no gaps). The highest similarities using the LSU sequence were *Ps. cotinae* (GenBank KY098790; Identities 835 / 835 (100 %), no gaps), *Pseudocamarosporium* "sp. 2" (GenBank KY929187; Identities 835 / 835 (100 %), no gaps) and *Paracamarosporium* "sp. 1" (GenBank KY929184; Identities 835 / 835 (100 %), no gaps).

Pseudocamarosporium brabeji (Marinc. *et al.*) Crous, *Sydowia* **67**: 110. 2015. Fig. 38.
Basionym: *Camarosporium brabeji* Marinc. *et al*., in Marincowitz *et al.*, *CBS Diversity Ser.* (Utrecht) **7**: 90. 2008.

Conidiomata pycnidial, superficial on PNA, solitary, globose, brown, 200–250 μm diam, with central papillate ostiole up to 100 μm diam. *Peridium* of 3–6 layers of brown *textura angularis*, thick-walled, dark brown. *Conidiophores* reduced to

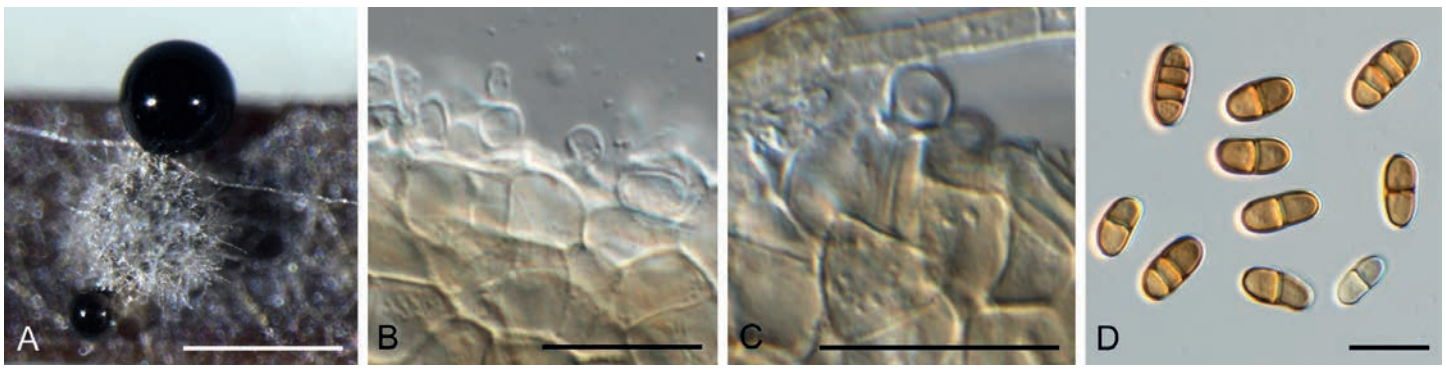

Fig. 38. *Pseudocamarosporium brabeji* (CPC 25002). **A.** Conidioma on PNA. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars: A = 250 μm, all others = 10 μm.

conidiogenous cells. *Conidiogenous cells* hyaline, smooth, 5–8 × 4–5 µm, ampulliform to doliiform with periclinal thickening at apex. *Conidia* brown, ellipsoid or subcylindrical, (9–)10–12(–13) × (4–)5(–6) µm, 1–3-transversely septate, straight or oblique, smooth to finely roughened, thick-walled.

Culture characteristics: Colonies flat, spreading with moderate aerial mycelium. On MEA surface pale mouse grey, reverse greyish sepia; on PDA surface and reverse fuscous black; on OA surface honey.

Specimens examined: **Switzerland**, on branch of *Platanus* sp. (*Platanaceae*), 24 Jun. 2014, *O. Holdenrieder* (specimen CBS H-23429, culture CPC 25002 = CBS 144205); *ibid*. (CPC 25004, 25843, 27400, 30973, 31482).

Notes: *Pseudocamarosporium* and *Paracamarosporium* were recently introduced to accommodate camarosporium-like taxa that reside in *Didymosphaeriaceae* (Wijayawardene *et al*. 2014). Both genera were also shown to include species with a coniothyrium-like morphology (Crous *et al.* 2015a). *Pseudocamarosporium brabeji* was treated as *Pseudocamarosporium* sp. 2. in Crous & Groenewald (2017).

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Ps. tilicola* (GenBank KJ747050; Identities 555 / 555 (100 %), no gaps), *Ps. brabeji* (GenBank EU552105; Identities 578 / 579 (99 %), 1 gap (0 %)), and *Ps. lonicerae* (GenBank KJ747047; Identities 571 / 572 (99 %), 1 gap (0 %)). The highest similarities using the LSU sequence were *Ps. cotinae* (GenBank KY098790; Identities 882 / 882 (100 %), no gaps), *Paracamarosporium* "sp. 1" (GenBank KY929184; Identities 882 / 882 (100 %), no gaps) and *Pa. fagi* (GenBank KY929183; Identities 882 / 882 (100 %), no gaps).

Pseudocercospora breonadiae Crous & Jol. Roux, ***sp. nov.*** MycoBank MB824793. Fig. 39.

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

Sporulation on the underside of leaves; lesions indistinct, pale to medium brown zones, containing several fungi, with *Pseudocercospora breonadiae* being intermixed with a *Zasmidium* sp., with superficial brown verruculose hyphae, and dark brown, verruculose, solitary, erect to flexuous conidiophores, giving rise to dark brown, verruculose obclavate conidia with thickened, darkened hila. *Mycelium* superficial on host surface, pale brown, smooth, branched, septate, 3–4 µm diam. *Conidiophores* solitary, arising from superficial hyphae, pale brown, smooth, erect, geniculate-sinuous, subcylindrical, 0–3-septate, 10–30 × 3–4 µm. *Conidiogenous cells* integrated, terminal, pale brown, smooth, subcylindrical with several terminal sympodial loci, flat-tipped, not thickened nor darkened, 1–1.5 µm diam, 7–12 × 3–4 µm. *Conidia* solitary, pale brown, smooth, guttulate, mostly gently curved, narrowly obclavate, apex subobtuse, base obconically truncate, 1–2 µm diam, 5–6(–8)-septate, (30–)50–80(–100) × (2.5–)3(–3.5) µm.

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

Specimen examined: **South Africa**, Limpopo Province, Wolkberg, on leaves of *Breonadia microcephala* (*Rubiaceae*), Jan. 2010, *J. Roux* (holotype CBS H-23413, culture ex-type CPC 30153 = CBS 143489).

Notes: No species of *Pseudocercospora* have been described from *Breonadia microcephala*. The closest allied species to *Ps. breonadiae* was *Ps. planaltinensis*, which was described from leaves of a *Chamaecrista* sp. in Brazil (Fig. 40). However, it is morphologically distinct, having cylindrical to obclavate conidia, 1–8-septate, 49–129 × 3–5 µm (Silva *et al*. 2016).

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Ps. planaltinensis* (GenBank KT290137; Identities 503 / 505 (99 %), no gaps), *Ps. fuligena* (GenBank GU214675; Identities 539 / 543 (99 %), 1 gap (0 %)) and *Ps. chengtuensis* (GenBank GU214672; Identities 539 / 543 (99 %), 1 gap (0 %)). The highest similarities using the LSU sequence were *Ps. dingleyae* (GenBank KX286997; Identities 840 / 841 (99 %), no gaps), *Ps. proiphydis* (GenBank KM055434; Identities 840 / 841 (99 %), no gaps) and *Ps. airliensis* (GenBank KM055433; Identities 840 / 841 (99 %), no gaps). The highest similarities using the *actA* sequence were *Ps. paraguayensis* (GenBank KF903444; Identities 507 / 521 (97 %), no gaps), *Ps. piricola* (GenBank KY048162; Identities 562 / 578 (97 %), no gaps) and *Ps. flavomarginata* (GenBank JX902134; Identities 522 / 537 (97 %), no gaps). The highest similarities using the *rpb2* sequence were *Ps. neriicola* (GenBank KX462647; Identities 681 / 686 (99 %), no gaps), *Ps. crispans* (GenBank KX462623; Identities 674 / 686 (98 %), no gaps) and *Ps. fukuokaensis* (GenBank KX462632; Identities 672 / 686 (98 %), no gaps). The highest similarities using the *tef1* sequence were *Ps. basiramifera* (GenBank DQ211677; Identities 464 / 518 (90 %), 13 gaps (2 %)), *Ps. parapseudarthriae* (GenBank

Fig. 39. *Pseudocercospora breonadiae* (CBS 143489). **A–C.** Conidiophores. **D.** Conidia. Scale bars = 10 µm.

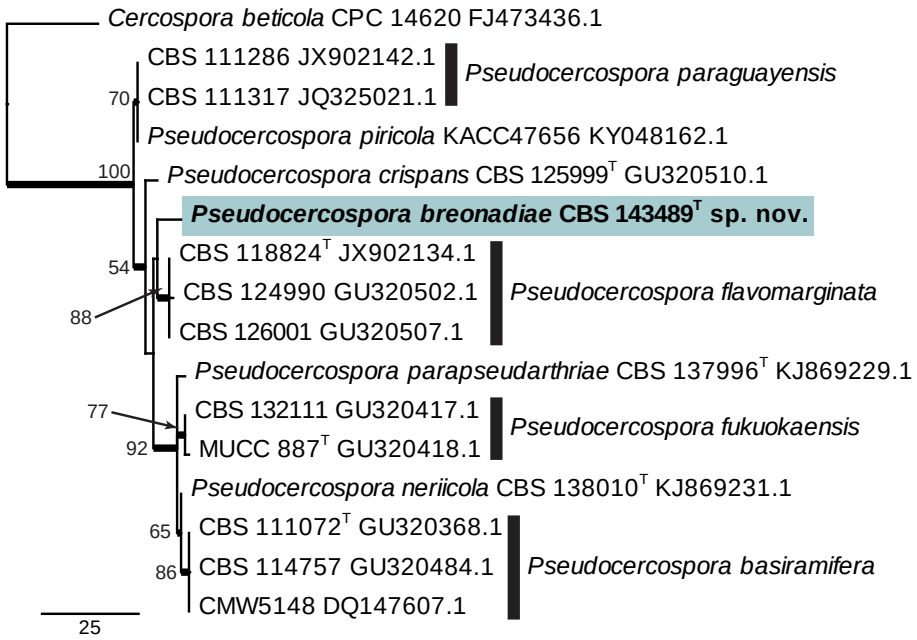

Fig. 40. The first of six equally most parsimonious trees obtained from a phylogenetic analysis of the combined *Pseudocercospora actA* alignment (16 strains including the outgroup; 191 characters analysed: 120 constant, 51 variable and parsimony-uninformative and 20 parsimony-informative). The tree was rooted to *Cercospora beticola* (GenBank FJ473436.1) and the scale bar indicates the number of changes. Bootstrap support values higher than 49 % are shown at the nodes and novelties are highlighted with a coloured box and bold text. Species names are indicated to the right of the tree, or before the culture collection and GenBank accession numbers. A superscript T denotes strains with a type status and branches present in the strict consensus tree are thickened. Tree statistics: TL = 89, CI = 0.899, RI = 0.870, RC = 0.782.

KJ869238; Identities 457 / 511 (89 %), 6 gaps (1 %)) and *Ps. jahnii* (GenBank KM393284; Identities 449 / 509 (88 %), 8 gaps (1 %)).

Rhinocladiella quercus Crous & R.K. Schumach., *Sydowia* **68**: 219. 2016. Fig. 41.

Mycelium consisting of pale brown, smooth, branched, septate, 2–3 μm diam hyphae. *Conidiophores* trimorphic. *Microconidiophores* exophiala-like, reduced to conidiogenous loci on hyphae, phialidic hyphal pegs solitary, 1–2 × 1 μm, giving rise to a mucoid conidial mass. *Macroconidiophores* ramichloridium-like, cylindrical, erect, medium brown, smooth, 1–2-septate, unbranched, straight, 20–30 × 2–3 μm. *Conidiogenous cells* terminal, medium brown, smooth, developing a rachis of pimple-like denticles, 0.5 μm diam, refractive, 11–25 × 2–3 μm. *Conidia* solitary, hyaline, smooth, ellipsoid to cylindrical, straight to slightly curved, (3–)4(–5) × 1.5–2 μm. Cladophialophora-like morph developing at hyphal ends, with cells becoming swollen, ellipsoid, aseptate, and prominently constricted at septa, in branched chains, 4–7 × 3–4 μm.

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

Specimen examined: **Germany**, near Berlin, on branch of *Sorbus aucuparia* (*Rosaceae*), 17 Feb. 2016, *R.K. Schumacher* (specimen CBS H-23406, culture CPC 30459 = CBS 143495).

Notes: *Rhinocladiella quercus* was recently described from twigs of *Quercus robur* collected near Berlin in Germany (Hernández-

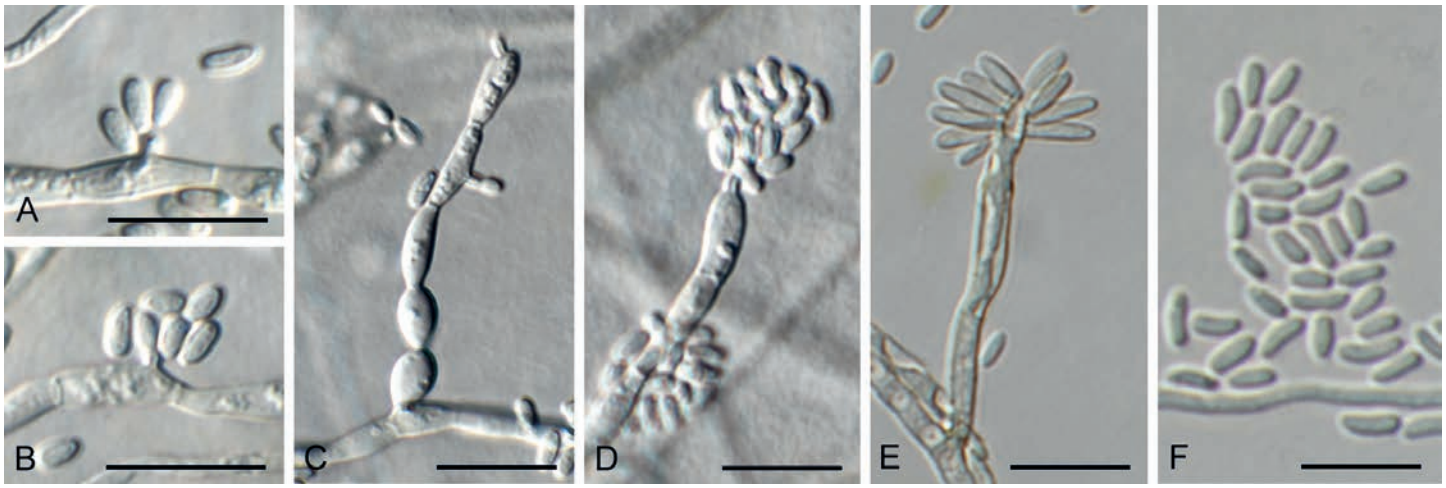

Fig. 41. *Rhinocladiella quercus* (CBS 143495). **A, B.** Conidiogenous loci. **C–E.** Conidiophores. **F.** Conidia. Scale bars = 10 μm.

Restrepo *et al.* 2016). The morphology of the present collection on *Sorbus aucuparia* closely matches that of the type.

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *R. quercus* (GenBank KX306769; Identities 633 / 642 (99 %), 1 gap (0 %)), *Capronia* sp. (GenBank AF050240; Identities 613 / 617 (99 %), 1 gap (0 %)) and *Cladophialophora* sp. (GenBank JX494354; Identities 621 / 634 (98 %), 3 gaps (0 %)). The highest similarities using the LSU sequence were *R. quercus* (GenBank KX306794; Identities 792 / 792 (100 %), no gaps), *Capronia* sp. (GenBank JN941378; Identities 799 / 801 (99 %), no gaps) and *Ca. fungicola* (GenBank FJ358224; Identities 768 / 801 (96 %), 3 gaps (0 %)). No significant hits were obtained when the *tef1* and *tub2* sequences were used in a megablast search.

Roussoella euonymi Crous & Akulov, ***sp. nov.*** MycoBank MB824794. Fig. 42.

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

Conidiomata erumpent, globose, brown, pycnidial, 150–300 µm diam, with central ostiole, exuding a black conidial mass. *Conidiophores* reduced to conidiogenous cells, lining the inner cavity, hyaline, smooth, ampulliform to doliiform, proliferating percurrently at apex, 5–12 × 5–7 µm. *Conidia* solitary, ellipsoid, guttulate, aseptate, apex obtuse, base 2 µm diam, bluntly rounded, thick-walled, becoming warty, golden-brown to red-brown, (6–)7(–8) × (4–)5–6 µm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and even, lobate margins, reaching 60 mm diam after 2 wk at 25 °C. On MEA surface olivaceous grey with patches of pale olivaceous grey, reverse pale olivaceous grey. On PDA surface olivaceous grey, reverse iron-grey. On OA surface iron-grey.

Specimen examined: **Ukraine**, Ternopil region, Zalischyky district, Dniester Canyon, on fallen branches of *Euonymus europaeus* (*Celastraceae*), 14 Oct. 2016, *A. Akulov*, specimen ex CWU (MYC) AS 6061 isotype (holotype CBS H-23420, culture ex-type CPC 31963 = CBS 143426).

Notes: Based on the LSU sequence, *Roussoella euonymi* is accommodated in the *Roussoellaceae*, being similar to other asexual species such as *Ro. solani* and *Ro. mexicana* (Crous *et al.* 2015b, c). Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were numerous unidentified "*Pleosporales* sp." sequences (e.g. GenBank HM116753; Identities 542 / 561 (97 %), 1 gap (0 %)), with the closest known species being *Ro. neopustulans* (GenBank KJ474833; Identities 441 / 474 (93 %), 5 gaps (1 %)) and *Ro. pustulans* (GenBank KJ474830; Identities 442 / 478 (92 %), 4 gaps (0 %)). The highest similarities using the LSU sequence were *Ro. mukdahanensis* (GenBank KU863118; Identities 837 / 847 (99 %), no gaps), *Arthopyrenia salicis* (GenBank LN907499; Identities 843 / 854 (99 %), no gaps) and *Ro. neopustulans* (GenBank KU863119; Identities 839 / 850 (99 %), no gaps). Only distant hits were obtained using the *actA* sequence; some of these were *Stagonosporopsis cucurbitacearum* (GenBank KX246908; Identities 459 / 509 (90 %), 10 gaps (1 %)), *S. citrulli* (GenBank KX246907; Identities 459 / 509 (90 %), 10 gaps (1 %)) and *S. caricae* (GenBank KX246909; Identities 458 / 509 (90 %), 10 gaps (1 %)). Only distant hits were obtained using the *rpb2* sequence; for example with *Torula herbarum* (GenBank KF443393; Identities 582 / 735 (79 %), 6 gaps (0 %)). No significant hits were obtained with the *tub2* sequence.

Setophaeosphaeria citricola Crous & M.J. Wingf., ***sp. nov.*** MycoBank MB824795. Fig. 43.

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

Ascomata on twigs immersed, black, 150–250 µm diam, globose, opening via a central ostiole that could with age become an irregular rupture in ascomatal wall; wall of 2–3 layers of brown *textura angularis. Asci* bitunicate, sessile, subcylindrical to narrowly ellipsoid, apical chamber 1–2 µm diam, stipitate, 50–70 × 11–15 µm. *Ascospores* multiseriate, hyaline, thin-walled, smooth, aseptate, fusoid-ellipsoidal, widest in upper third, apex subobtusely rounded, base obtuse, (16–)19–20(–22) × (4.5–)5(–6) µm. *Conidiomata* pycnidial, 150–250 µm diam, aggregated, globose, pale brown with dark brown central ostiole, 20–30 µm diam, ostiole surrounded by brown, thick-walled, verruculose, septate hyphae, up to 100 µm long, 4–5 µm diam at base, apex obtuse. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, ampulliform to doliiform, 5–7 × 5–6 µm, phialidic with prominent periclinal thickening. *Conidia* solitary, hyaline, smooth, aseptate, multiguttulate and granular, fusoid-ellipsoid, straight to irregularly twisted, apex obtuse, base truncate, 2 µm diam, (10–)12–14(–17) × 3–3.5(–4) µm.

Culture characteristics: Colonies flat, spreading, with sparse aerial mycelium and even, lobate margins, reaching 45 mm diam after 2 wk at 25 °C. On MEA surface pale mouse grey to mouse grey, reverse mouse grey. On PDA surface olivaceous grey, reverse mouse grey. On OA surface olivaceous grey.

Specimen examined: **Australia**, New South Wales, Mount Annan Botanical Garden, on leaves of *Citrus australasica* (*Rutaceae*), 25 Nov. 2016, *P.W. Crous* (holotype CBS H-23271, culture ex-type CPC 32083 = CBS 143179).

Notes: *Coniothyrium sidae* was recently described from a *Sida* sp. collected in Brazil (Quaedvlieg *et al*. 2013). Although the ITS is identical (Fig. 44), the morphology is very different, with the sexual morph having hyaline, aseptate ascospores, those of *Con. sidae* being brown, (3–)5-septate, (18–)20–24(–26) × (4–)5(–5.5) µm, and conidia being smaller, fusoid-ellipsoidal, straight to slightly curved, (9–)10–12(–13) × (2.5–)3 µm. Conidia of *S. citri*, described from *Citrus* in Italy, are smaller than those of *S. citricola*, 3.5–5 × 2–3 µm (Crous *et al.* 2017b).

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Con. sidae* (GenBank KF251149; Identities 518 / 520 (99 %), no gaps), *Phaeosphaeria setosa* (GenBank AF439500; Identities 472 / 476 (99 %), no gaps) and *S. hemerocallidis* (GenBank KJ869161; Identities 503 / 521 (97 %), 10 gaps (1 %)). The highest similarities using the LSU sequence were *Con. sidae* (GenBank KF251653; Identities 835 / 836 (99 %), no gaps), *S. badalingensis* (GenBank KJ869219; Identities 828 / 832 (99 %), no gaps) and *Leptosphaeria rubefaciens* (GenBank JF740311; Identities 843 / 854 (99 %), no gaps). The highest similarities

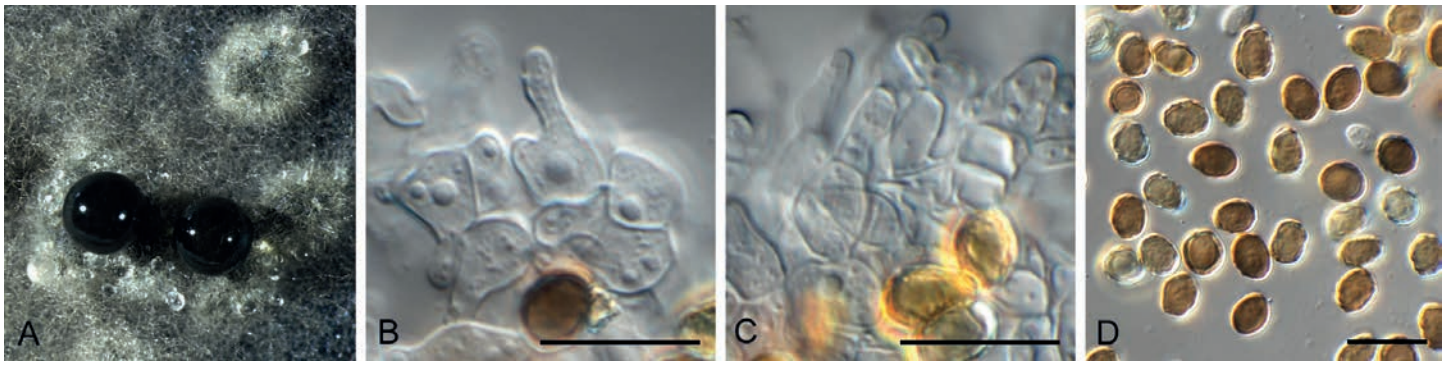

Fig. 42. *Roussoella euonymi* (CBS 143426). **A.** Conidiomata on PDA. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars = 10 μm.

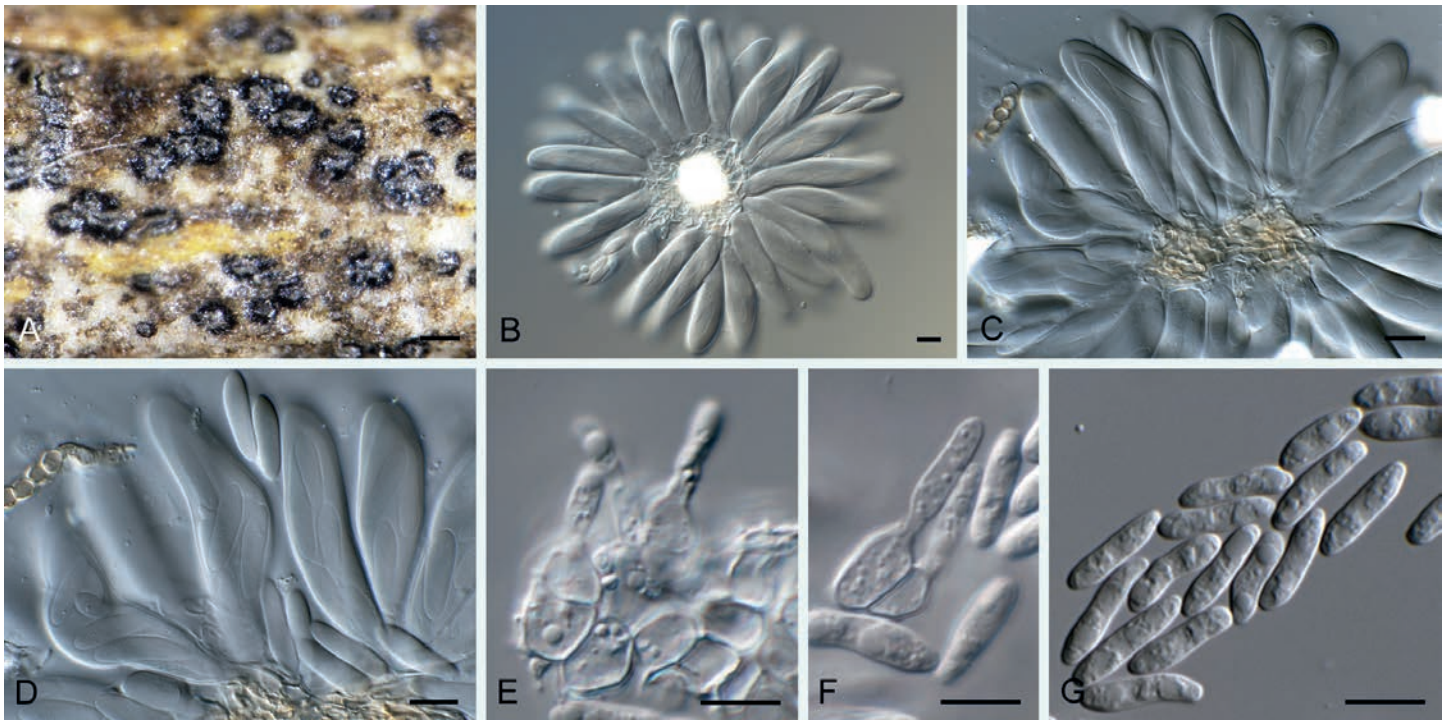

Fig. 43. *Setophaeosphaeria citricola* (CBS 143179). **A.** Ascomata submerged in host tissue. **B–D.** Asci and ascospores. **E, F.** Conidiogenous cells. **G.** Conidia. Scale bars: A = 250 μm, all others = 10 μm.

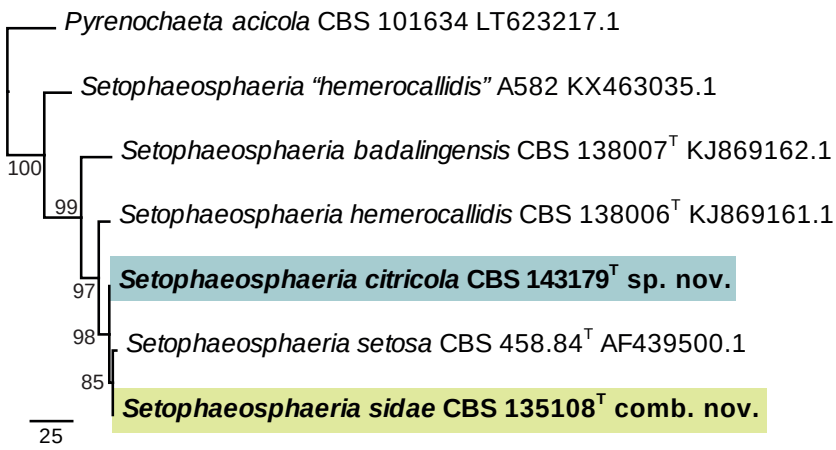

Fig. 44. Single most parsimonious tree obtained from a phylogenetic analysis of the *Setophaeosphaeria* ITS alignment (Seven strains including the outgroup; 487 characters analysed: 389 constant, 64 variable and parsimony-uninformative and 34 parsimony-informative). The tree was rooted to *Pyrenochaeta acicola* (GenBank LT623217.1) and the scale bar indicates the number of changes. Bootstrap support values higher than 49 % are shown at the nodes and novelties are highlighted with a coloured box and bold text. A superscript T denotes strains with a type status. GenBank accession and/or culture collection numbers are indicated behind the species names. Tree statistics: TL = 127, CI = 0.937, RI = 0.830, RC = 0.778.

using the *rpb2* sequence were *Pyrenochaeta unguis-hominis* (GenBank LT717682; Identities 715 / 847 (84 %), no gaps), *Py. cava* (GenBank LT717681; Identities 705 / 847 (83 %), no gaps) and *Py. hakeae* (GenBank KY173593; Identities 705 / 847 (83 %), no gaps). The best hit with the *tef1* sequence was with *Con. sidae* (GenBank KF253109; Identities 439 / 500 (88 %), 21 gaps (4 %)) while the *tub2* sequence was less than 87 % identical to species of *Pyrenochaeta*, *Neocucurbitaria* and *Cucurbitaria*.

Setophaeosphaeria sidae (Quaedvl. *et al.*) Crous, ***comb. nov.*** MycoBank MB824796.
Basionym: *Coniothyrium sidae* Quaedvl. *et al.*, *Stud. Mycol.* **75**: 374. 2013.

Specimen examined: **Brazil**, Rio de Janeiro, Nova Friburgo, Riograndina, along roadside on *Sida* sp. (*Malvaceae*), 24 Feb. 2008, *R.W. Barreto* (holotype CBS H-21315, culture ex-type CPC 19602 = RWB 866 = CBS 135108).

Sirastachys cyperacearum Crous & T.I. Burgess, ***sp. nov.*** MycoBank MB824797. Fig. 45.

Etymology: Name refers to *Cyperaceae*, the substrate from which this fungus was collected.

Conidiophores macro- and mononematous, single or in groups of 2–3, thin-walled, smooth, unbranched, erect, straight to flexuous, 3–4-septate, stipe 70–90 × 3–5 µm, bearing 5–10 conidiogenous cells. *Conidiogenous cells* phialidic, clavate to subclavate, hyaline (to faintly greenish), smooth, 10–12 × 3–5 µm, with collarettes. *Conidia* solitary, aseptate, ellipsoid, thick-walled, dark brown, guttulate, verrucose, (5–)6–7(–8) × (2.5–)3 µm, with rounded ends.

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

Specimen examined: **Australia**, New South Wales, Fitzroy Falls, on leaves of *Cyperaceae*, 26 Nov. 2016, *P.W. Crous* (holotype CBS H-23308, culture ex-type CPC 32087 = CBS 143444).

Notes: The genus *Sirastachys*, based on *Si. phaeospora*, was recently established by Lombard *et al*. (2016). Phylogenetically the present collection is closely related to *Si*. *phaeospora,* but distinct in that the latter has smaller conidia, 4–5 × 2–3 µm, and shorter conidiophores (40–65 µm long) (Lombard *et al*. 2016).

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Si. phaeospora* (GenBank KU846667; Identities 581 / 588 (99 %), 2 gaps (0 %)), *Si. pandanicola* (GenBank KU846664; Identities 555 / 563 (99 %), 3 gaps (0 %)) and *Stachybotrys parvispora* (GenBank JN093263; Identities 543 / 552 (98 %), 2 gaps (0 %)). The highest similarities using the LSU sequence were *Si. phyllophila* (GenBank KU846784; Identities 822 / 827 (99 %), 1 gap (0 %)), *Si. pandanicola* (GenBank KU846777; Identities 820 / 827 (99 %), 1 gap (0 %)) and *Si. phaeospora* (GenBank KU846779; Identities 817 / 827 (99 %), 1 gap (0 %)).

Sphaerellopsis paraphysata Crous & Alfenas, *IMA Fungus* **5**: 411. 2014. Fig. 46.

Conidiomata eustromatic, pycnidioid, 200–300 µm diam, immersed to erumpent, dark brown, multilocular, ostiolate, ostioles 30–40 µm diam; wall of 4–6 layers of medium brown *textura angularis. Conidiophores* reduced to conidiogenous cells, or 1–2-septate, hyaline, smooth, ampulliform to subcylindrical, unbranched, 7–20 × 3–5 µm. *Conidiogenous cells* hyaline, smooth, subcylindrical to ampulliform with percurrent proliferation at apex, 7–13 × 3–5 µm. *Conidia* solitary, hyaline, smooth, guttulate, medianly 1-septate, constricted or not, ellipsoid with mucoid polar appendages, (12–)14–17(–18) × (4–)4.5–5.5(–6) µm.

Culture characteristics: Colonies flat, spreading, with sparse aerial mycelium and feathery margin, reaching 15 mm diam after 2 wk. On MEA, PDA and OA surface and reverse olivaceous grey.

Specimen examined: **Australia**, New South Wales, Sussex Inlet, on leaves of *Phragmites* sp. (*Poaceae*), 27 Nov. 2016, *P.W. Crous*, CBS 143579 = CPC 32406.

Notes: *Sphaerellopsis paraphysata* was recently described on a rust on *Pennisetum* sp. collected in Brazil (Trakunyingcharoen *et al.* 2014), and this is the first record of this hyperparasite from Australia.

Fig. 45. *Sirastachys cyperacearum* (CBS 143444). **A.** Conidiophores on SNA. **B–D.** Conidiophores. **E.** Conidia. Scale bars = 10 µm.

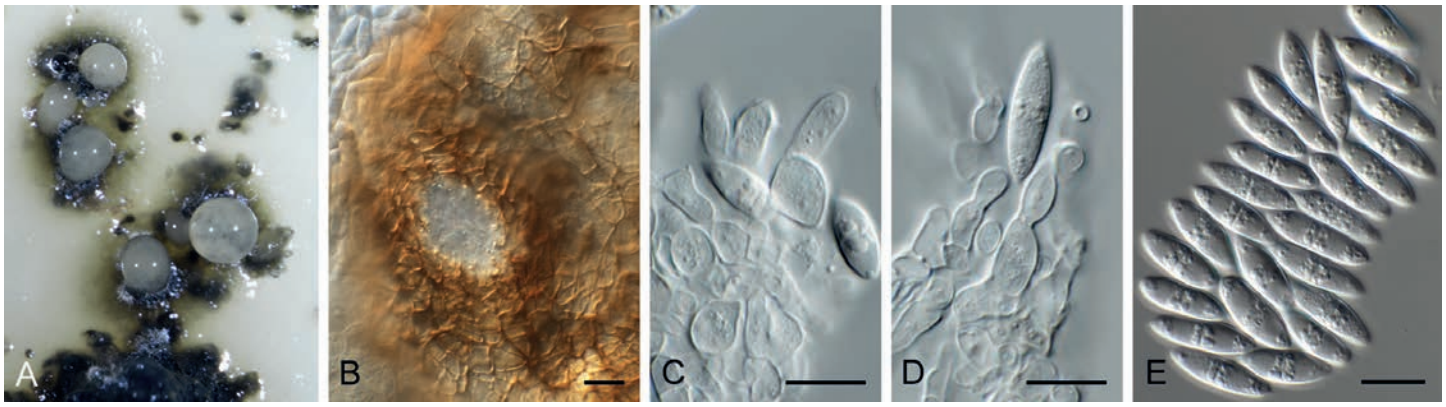

Fig. 46. *Sphaerellopsis paraphysata* (CPC 32406). **A.** Conidiomata on OA. **B.** Ostiolar region of conidioma. **C, D.** Conidiogenous cells. **E.** Conidia. Scale bars = 10 μm.

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Sphaerellopsis paraphysata* (GenBank NR_137956; Identities 554 / 561 (99 %), no gaps), *Eudarluca caricis* (GenBank KP170655; Identities 426 / 475 (90 %), 7 gaps (1 %)) and *Subplenodomus drobnjacensis* (GenBank MG131867; Identities 426 / 481 (89 %), 14 gaps (2 %)). The highest similarities using the LSU sequence were *Sphaerellopsis paraphysata* (GenBank KP170729; Identities 840 / 841 (99 %), no gaps), *Plenodomus congestus* (GenBank JF740278; Identities 846 / 855 (99 %), 1 gap (0 %)) and *Con. telephii* (GenBank LN907332; Identities 847 / 857 (99 %), 1 gap (0 %)). The highest similarities using the *rpb2* sequence were *Leptosphaeria biglobosa* (GenBank FO905662; Identities 680 / 868 (78 %), 4 gaps (0 %)), *Curvularia affinis* (GenBank HG779159; Identities 674 / 871 (77 %), 15 gaps (1 %)) and *Plenodomus enteroleucus* (GenBank KY064042; Identities 603 / 770 (78 %), 8 gaps (1 %)). The highest similarity using the *tef1* sequence was *Sp. paraphysata* (GenBank KP170685; Identities 496 / 505 (98 %), 4 gaps (0 %)). The highest similarity using the *tub2* sequence was *Sp. paraphysata* (GenBank KP170710; Identities 300 / 304 (99 %), no gaps).

Subplenodomus iridicola Crous & Denman, ***sp. nov.*** MycoBank MB824798. Fig. 47.

Etymology: Name refers to the fact that the fungus is found on *Iris*.

Fig. 47. *Subplenodomus iridicola* (CBS 143395). **A.** Ascomata on BLA. **B.** Conidioma on SNA. **C–E.** Asci with ascospores. **F.** Paraphyses. **G, H.** Germinating ascospores. **I.** Conidia. Scale bars: A, B = 200 μm, all others = 10 μm.

Leaf spots pale brown with blackish margins, amphigenous, elongated, subcircular, 4–7 mm diam, up to 4 cm long. *Ascomata* immersed, globose, dark brown, 150–250 µm diam, with central ostiole, 20–30 µm diam; wall of 4–6 layers of brown *textura angularis*. *Pseudoparaphyses* intermingled among asci, subcylindrical, hyaline, smooth, hyphae-like, 2–3 µm diam. *Asci* 8-spored, fasciculate, stipitate, bitunicate, narrowly ellipsoid, ocular chamber 1.5–2 µm diam, 80–100 × 10–15 µm. *Ascospores* multiseriate, fusoid-ellipsoid, pale brown, guttulate, finely roughened, constricted at median septum, developing 1(–4) additional septa in both cells, at times first cell above median septum slightly swollen, (19–)21–25(–27) × (5–)6(–7) µm. Germinating ascospores become distorted, up to 8 µm diam, with germ tubes via terminal or intercalary cells. *Conidiomata* pycnidial, globose, pale brown, 100–200 µm diam, with central papillate ostiole, 20–30 µm diam; wall of 4–6 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining inner cavity, doliiform, hyaline, smooth, phialidic with periclinal thickening, 4–7 × 4–6 µm. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, subcylindrical to narrowly ellipsoid, apex obtuse, base truncate, (4–)5–6(–7) × (2.5–)3 µm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margins, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface ochreous, reverse amber. On PDA surface and reverse isabelline. On OA surface rosy buff with patches of isabelline and cinnamon.

Specimen examined: **UK**, England, Upton Grey, on *Iris* sp. (*Iridaceae*), 28 Mar. 2016, *P.W. Crous* (holotype CBS H-23415, culture ex-type CPC 30162 = CBS 143395).

Notes: *Subplenodomus* was established by de Gruyter *et al.* (2013) for *Su. violicola*. Phylogenetically *Su. iridicola* is closely related to *Su. galicola*, but distinct in that the latter (described from a dead stem of *Galium* sp. collected in Italy) has larger ascospores [30–40 × 6–9 µm, (3–)4-septate] and asci (66–120 × 12–17 µm) (Tibpromma *et al*. 2017).

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Alloleptosphaeria italica* (GenBank KT454722; Identities 428 / 458 (93 %), 6 gaps (1 %)), *Subplenodomus galicola* (GenBank KY554204; Identities 505 / 576 (88 %), 23 gaps (3 %)) and *Leptosphaeria rubefaciens* (GenBank KT804116; Identities 448 / 495 (91 %), 12 gaps (2 %)). The highest similarities using the LSU sequence were *Su. galicola* (GenBank KY554199; Identities 848 / 854 (99 %), no gaps), *Su. violicola* (GenBank GU238156; Identities XXX / 848 / 854 (99 %), no gaps) and *Plenodomus deqinensis* (GenBank KY064031; Identities 843 / 849 (99 %), no gaps).

Teichospora quercus Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB824799. Fig. 48.

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

Ascomata solitary to gregarious, semi-immersed, becoming erumpent, dark brown, uniloculate, globose with papillate ostiole, 200–350 µm diam; peridium thick-walled, multi-layered, of *textura angularis*, brown, becoming hyaline inwards. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical-clavate, short-stipitate, rounded at apex, with ocular chamber, 60–110 × 10–15 µm. *Ascospores* tri- to multiseriate, hyaline, fusiform or ellipsoid-fusoid, straight, widest just above median septum, (1–)3-septate, but becoming golden brown, with mucoid sheath (up to 2.5 µm diam), (19–)20–22(–25) × (4–)5(–6) µm. *Pseudoparaphyses* longer than asci, filiform, cells cylindrical, branched, hyaline, thin-walled, smooth, 2–2.5 µm diam. *Conidiomata* globose to subglobose, 150–300 µm diam, with central ostiole, sessile on foot of brown stroma; wall of 6–8 layers of pale brown *textura angularis*, becoming hyaline towards inside. *Conidiophores*

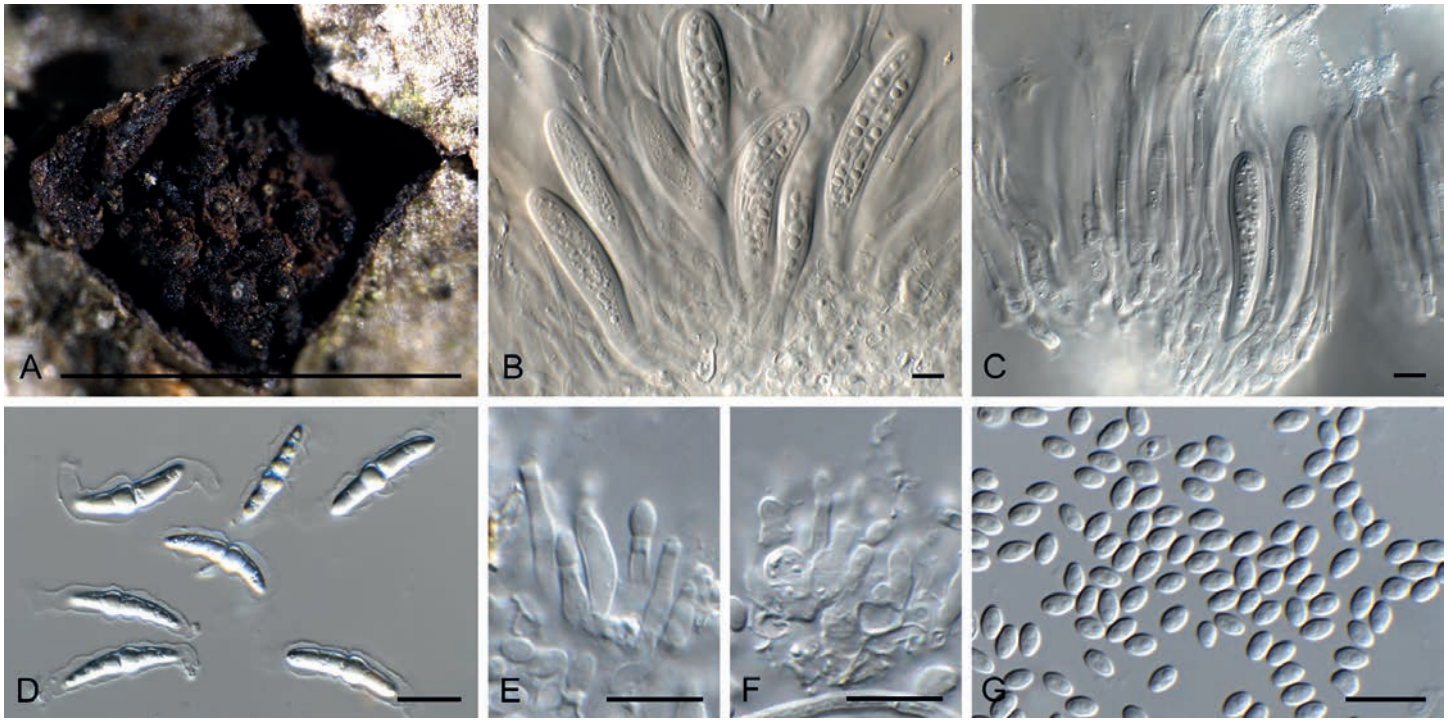

Fig. 48. *Teichospora quercus* (CBS 143396). **A.** Ascoma on host tissue. **B, C.** Asci and pseudoparaphyses. **D.** Ascospores. **E, F.** Conidiogenous cells. **G.** Conidia. Scale bars: A = 350 µm, all others = 10 µm.

subcylindrical, hyaline, smooth, branched at base, 10–20 × 3–5 µm. *Conidiogenous cells* terminal and intercalary, hyaline, smooth, subcylindrical, phialidic with prominent percurrent proliferation, 5–10 × 2–4 µm. *Conidia* solitary, ellipsoid, hyaline, smooth, guttulate, apex obtuse, base truncate, 1.5–2 µm diam, (4–)5(–6) × (2.5–)3 µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margins, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface smoke grey in centre, olivaceous grey in outer zone, reverse olivaceous grey. On PDA surface pale olivaceous grey, reverse smoke grey with diffuse sienna pigment. On OA surface pale olivaceous grey.

Specimen examined: **France**, Cléron, on stroma of pyrenomycete, on branch of *Quercus* sp. (*Fagaceae*), 15 Nov. 2015, *G. Moyne* (holotype CBS H-23404, culture ex-type CPC 30009 = CBS 143396).

Notes: The genus *Teichospora* was treated in detail by Jaklitsch & Voglmayr (2016) and includes several generic synonyms. Although the present collection was initially assumed to represent a new genus, it clusters phylogenetically with other species of *Teichospora*. It is, however, morphologically distinct, in that the ascospores remain hyaline, and are surrounded by a mucoid sheath, and are only 1(–3) transversely septate. The asexual morph, however, is phoma-like, which again resembles those of *Teichospora*. Nevertheless, if additional gene loci eventually show this clade to represent more than one genus, *T. quercus* will most likely be placed in a separate genus.

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *T. rubriostiolata* (GenBank KU601590; Identities 562 / 589 (95 %), 4 gaps (0 %)), *T. melanommoides* (GenBank KU601585; Identities 561 / 590 (95 %), 7 gaps (1 %)) and *T. acaciae* (GenBank NR_138410; Identities 559 / 591 (95 %), 8 gaps (1 %)). The highest similarities using the LSU sequence were *T. parva* (GenBank GU385195; Identities 851 / 854 (99 %), no gaps), *T. acaciae* (GenBank KR611898; Identities 800 / 810 (99 %), no gaps) and *T. melanommoides* (GenBank KU601585; Identities 841 / 852 (99 %), no gaps). The highest similarities using the *rpb2* sequence were *T. rubriostiolata* (GenBank KU601596; Identities 745 / 829 (90 %), no gaps), *T. trabicola* (GenBank KU601600; Identities 732 / 830 (88 %), no gaps) and *Melanomma radicans* (GenBank AY485625; Identities 701 / 826 (85 %), no gaps). The highest similarities using the *tef1* sequence were *T. trabicola* (GenBank KU601603; Identities 410 / 477 (86 %), 25 gaps (5 %)), *T. rubriostiolata* (GenBank KU601608; Identities 404 / 471 (86 %), 16 gaps (3 %)) and *T. melanommoides* (GenBank KU601610; Identities 399 / 466 (86 %), 9 gaps (1 %)).

Trochila viburnicola Crous & Denman, ***sp. nov.*** MycoBank MB824800. Fig. 49.

Etymology: Name refers to the fact that the fungus occurs (*icola* = dweller) on stems of *Viburnum*.

Conidiomata pale brown, globose, somewhat flattened, 120–250 µm diam, opening by irregular rupture, becoming acervular; wall of 3–6 layers of pale brown *textura angularis*. *Macroconidiophores* lining inner cavity, hyaline, smooth, subcylindrical, branched, 1–7-septate, 10–40 × 4–6 µm. *Macroconidiogenous cells* integrated, terminal and intercalary, hyaline, smooth, subcylindrical to doliiform, 5–13 × 4–5 µm, with semi-flared collarette, 1–3 µm tall, proliferating percurrently. *Macroconidia* solitary, hyaline, smooth, guttulate, aseptate, subcylindrical, straight, apex obtuse, base truncate, 3–4 µm diam with prominent marginal frill, (5–)6–7 × (3–)4 µm. *Microconidiophores* similar in morphology to *macroconidiophores*, 8–20 × 3–4 µm. *Microconidiogenous cells* terminal and intercalary, subcylindrical to ampulliform, 4–7 × 2.5–3 µm, proliferating percurrently. *Microconidia* similar to macroconidia but smaller, 3–4 × 2–2.5 µm, with minute marginal frill.

Culture characteristics: Colonies flat, spreading, surface folded, with sparse aerial mycelium and smooth, lobate margins, reaching 50 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface pale luteous to ochreous, reverse ochreous.

Specimen examined: **UK**, England, Upton Grey, on twig cankers of *Viburnum* sp. (*Adoxaceae*), 28 Mar. 2016, *P.W. Crous* (holotype CBS H-23416, culture ex-type CPC 30254 = CBS 144206).

Notes: The genus *Sirophoma* is known from *Viburnum*, but is distinct from the present collection in that it has pycnidial conidiomata with central ostioles, long flexuous conidiophores,

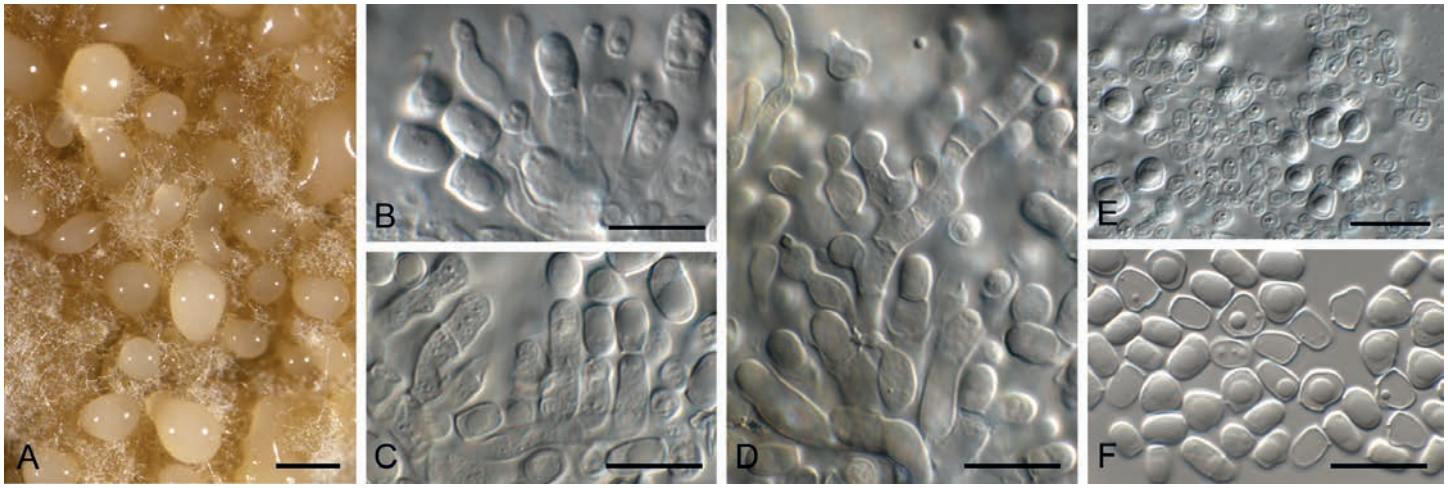

Fig. 49. *Trochila viburnicola* (CPC 30254). **A.** Conidiomata on OA. **B–D.** Conidiogenous cells. **E, F.** Micro- and macroconidia. Scale bars: A = 200 µm, all others = 10 µm.

and globose to pyriform conidia. Based on DNA sequence similarity, the present asexual collection is similar to sequences of the sexual morph *Trochila* (*Dermateaceae*). *Trochila* has been linked to cryptocline-like asexual morphs, and hence it is tentatively placed in this genus. A species of *Trochila* known from *Viburnum* is *T. tini*, but as this species is not known from culture and only the sexual morph is known, a comparison is impossible.

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Crumenulopsis sororia* (GenBank KY941133; Identities 437 / 487 (90 %), 7 gaps (1 %)), *Cenangiopsis quercicola* (GenBank LT158425; Identities 506 / 552 (92 %), 4 gaps (0 %)) and *Vestigium trifidum* (GenBank NR_121556; Identities 502 / 551 (91 %), 3 gaps (0 %)). The highest similarities using the LSU sequence were *Vestigium trifidum* (GenBank KC407777; Identities 833 / 860 (97 %), 3 gaps (0 %)), *Fabrella tsugae* (GenBank AF356694; Identities 798 / 824 (97 %), 2 gaps (0 %)) and *Trochila laurocerasi* (GenBank KX090835; Identities 812 / 839 (97 %), no gaps). The highest similarities using the *rpb2* sequence were *Hyalopeziza nectrioides* (GenBank JN086836; Identities 551 / 689 (80 %), 6 gaps (0 %)), *Chlorencoelia torta* (GenBank JN086854; Identities 618 / 777 (80 %), 6 gaps (0 %)) and *Loramyces macrosporus* (GenBank JN086838; Identities 533 / 671 (79 %), 7 gaps (1 %)). Only distant hits to *Cucurbitaria* and *Trichoderma* were obtained when the *tef1* sequence was used in a megablast search.

Varicosporellopsis aquatilis Lechat & J. Fourn., *Ascomycete.org* **8**(3): 87. 2016. Fig. 50.

On SNA: *Mycelium* consisting of hyaline, branched, septate, smooth, 3–5 μm diam hyphae, lacking chlamydospores, and frequently forming hyphal coils. *Conidiophores* solitary, erect, branched at base, 0–2-septate, or reduced to conidiogenous cells; branched conidiophores consist of a basal stipe, 15–30 × 3–5 μm, giving rise to 1–3 lateral branches, 0–1-septate, or conidiogenous cells, 40–100 × 3–5 μm. *Conidiogenous cells* subcylindrical with slight apical taper, hyaline, smooth, 35–60 × 3–4 μm, apex phialidic with minute cylindrical collarette, 1–2 μm tall, giving rise to clusters of slimy conidia. *Conidia* solitary, hyaline, smooth, granular to guttulate, ellipsoid, aseptate, straight to curved, apex subobtuse, base tapered to a truncate hilum, 1–1.5 μm diam, (6–)11–13(–15) × (3–)4(–4.5) μm.

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

Specimen examined: **The Netherlands**, Culemborg, from garden soil, Feb. 2017, *H. van Warenburg*, culture JW75003 = CBS 143509.

Notes: Morphologically *Varicosporellopsis aquatilis* resembles *Acremonium curvulum* in having curved, fusoid-ellipsoid conidia with truncate hila. However, it can be distinguished in that it lacks chlamydospores, and has much larger conidia than *A. curvulum* (4–6.7 × 1.4–2.1 μm; Gams 1971), from which it is also phylogenetically distinct. Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *V. aquatilis* (GenBank KU233187; Identities 524 / 530 (99 %), 2 gaps (0 %)), *Fusarium merismoides* var. *violaceum* (GenBank EU860060; Identities 842 / 906 (93 %), 27 gaps (2 %)) and *Thyronectria asturiensis* (GenBank KJ570690; Identities 854 / 919 (93 %), 25 gaps (2 %)). The highest similarities using the LSU sequence were *V. aquatilis* (GenBank KU233189; Identities 835 / 836 (99 %), no gaps), *Paracremonium variiforme* (GenBank KU746739; Identities 823 / 836 (98 %), no gaps) and *Pa. contagium* (GenBank KP012631; Identities 790 / 804 (98 %), no gaps). Only distant hits were obtained using the *actA* sequence; some of these were *Verticillium dahliae* (GenBank CP010981; Identities 874 / 973 (90 %), 15 gaps (1 %)), *Fusarium oxysporum* f. sp. *dianthi* (GenBank LT841228; Identities 870 / 977 (89 %), 17 gaps (1 %)) and *Fusarium graminearum* (GenBank HG970335; Identities 872 / 979 (89 %), 21 gaps (2 %)). The highest similarities using the *tub2* sequence were *Pa. inflatum* (GenBank KM232101; Identities 528 / 583 (91 %), 9 gaps (1 %)), *Pa. contagium* (GenBank KM232103; Identities 532 / 599 (89 %), 9 gaps (1 %)) and *Pa. pembeum* (GenBank KU053055; Identities 438 / 500 (88 %), 9 gaps (1 %)).

Varicosporellopsis aquatilis was recently described from submerged wood collected in freshwater in southwestern France. The acremonium-like asexual morph is morphologically similar, but its conidia are somewhat smaller, 6–11 × 2.8–3.2 μm (Lechat & Fournier 2016).

Vermiculariopsiella dichapetali Crous, *Persoonia* **32**: 213. 2014. Fig. 51.

Conidiomata sporodochial, on SNA erumpent, crystalline, up to 500 μm diam, with brown, erect setae distributed throughout conidioma, thick-walled, flexuous, finely roughened, 180–500 × 4–10 μm, 6–20-septate, with obtuse ends. *Conidiophores* aggregated in stroma, subcylindrical, 2–4-septate, branched below, 35–70 × 3–4 μm. *Conidiogenous cells* phialidic, terminal, cylindrical with curved apex, pale brown, smooth to finely roughened, 12–26 × 2.5–3 μm, apex 1.5–2 μm diam. *Conidia* solitary, hyaline, smooth, guttulate, aseptate, straight to slightly curved, inequilateral, outer plane convex, apex subobtusely rounded, with truncate hilum, excentric, 1 μm diam, (14–)16–19(–21) × 2.5(–3) μm.

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

Specimens examined: **Australia**, New South Wales, Barron Grounds Nature Reserve, on leaves of *Melaleuca* sp. (*Myrtaceae*), 26 Nov. 2016, *P.W. Crous* (culture CPC 32057 = CBS 143424); Victoria, La Trobe State Forest, on leaves of *Eucalyptus regnans* (*Myrtaceae*), 30 Nov. 2016, *P.W. Crous* (CBS H-23312, culture CPC 32544 = CBS 143440).

Notes: *Vermiculariopsiella dichapetali* was described from leaves of *Dichapetalum rhodesicum* collected in Botswana (Crous *et al*. 2014), and these are the first records from Australia. Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Ve. dichapetali* (GenBank KX306771; Identities 532 / 534 (99 %), no gaps), *Ve.immersa* (GenBank KY853476; Identities 532 / 534 (99 %), 2 gaps (0 %)) and *Ve. acaciae* (GenBank NR_145253; Identities 520 / 536 (97 %), 7 gaps (1 %)). The highest similarities using the LSU sequence were *Ve. dichapetali* (GenBank KX306796; Identities 716 / 716 (100 %), no gaps), *Ve. acaciae* (GenBank KX228314; Identities 837 / 839 (99 %), no gaps) and *Ve. immersa* (GenBank KJ476961; Identities 822 / 827 (99 %), 4 gaps (0 %)). Only distant

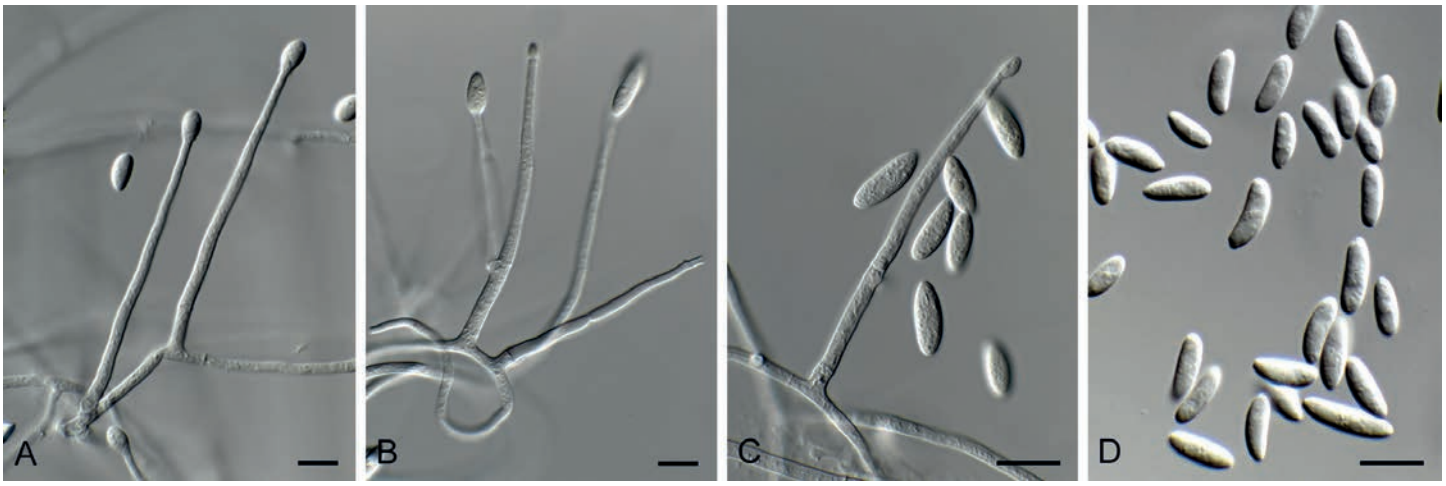

Fig. 50. *Varicosporellopsis aquatilis* (CBS 143509). **A–C.** Conidiophores. **D.** Conidia. Scale bars = 10 µm.

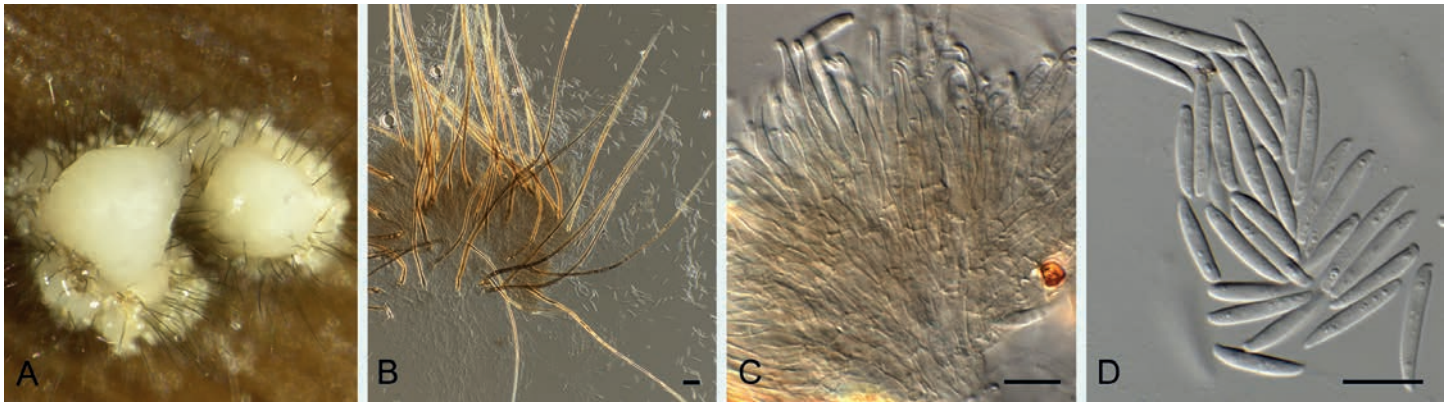

Fig. 51. *Vermiculariopsiella dichapetali* (CPC 32057). **A.** Conidiomata on BLA. **B.** Conidioma with setae on SNA. **C.** Conidiophores. **D.** Conidia. Scale bars = 10 µm.

hits were obtained using the *actA* sequence of CPC 32544; some of these were *Xenogliocladiopsis eucalyptorum* (GenBank KM231140; Identities 390 / 418 (93 %), no gaps), *Allantonectria miltina* (GenBank KM231247; Identities 388 / 418 (93 %), no gaps) and *X. cypellocarpa* (GenBank KM231141; Identities 388 / 418 (93 %), no gaps).

Wettsteinina philadelphi Crous & R.K. Schumach., ***sp. nov.*** MycoBank MB824801. Fig. 52.

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

Conidiomata pycnidial, solitary to aggregated, globose, 250–350 µm diam, with central ostiole; wall of 6–8 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining inner cavity, hyaline, smooth, subcylindrical to ampulliform, 10–15 × 3–5 µm, with numerous, prominent percurrent proliferations in apical region. *Conidia* solitary, medium brown, finely roughened, guttulate, fusoid-ellipsoid, apex obtuse, tapering prominently in lower third to truncate hilum, 1–1.5 µm diam; with (2–)3(–5) transverse eusepta, and 1–3 muriform or vertical septa, (11–)15–20(–23) × (5–)6–7(–8) µm.

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

Specimen examined: **Germany**, near Berlin, on twigs of *Philadelphus coronarius* (*Hydrangeaceae*), 2 Apr. 2016, *R.K. Schumacher* (holotype CBS H-23410, culture ex-type CPC 30534 = CBS 143392).

Notes: The present camarosporium-like collection is described in the genus *Wettsteinina*, although this genus is primarily known from its sexual morphs (Zhang *et al.* 2012), with one reference to a possible stagonospora-like asexual morph (Farr & Rossman 2018).

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Alpinaria rhododendri* (GenBank NR_147686; Identities 505 / 534 (95 %), 10 gaps (1 %)), *Herpotrichia juniperi* (GenBank JX981496; Identities 443 / 472 (94 %), 7 gaps (1 %)) and *He. pinetorum* (GenBank KP966102; Identities 442 / 471 (94 %), 8 gaps (1 %)). The highest similarities using the LSU sequence were *Melanomma pulvis-pyrius* (GenBank LC203344; Identities 847 / 853 (99 %), no gaps), *Trematosphaeria pertusa* (GenBank DQ678072; Identities 847 / 853 (99 %), no gaps) and *Wettsteinina macrotheca* (GenBank AY849969; Identities 838 / 844 (99 %), no gaps). Only distant similarity to *He. juniperi* sequences were obtained with the *tef1* sequence.

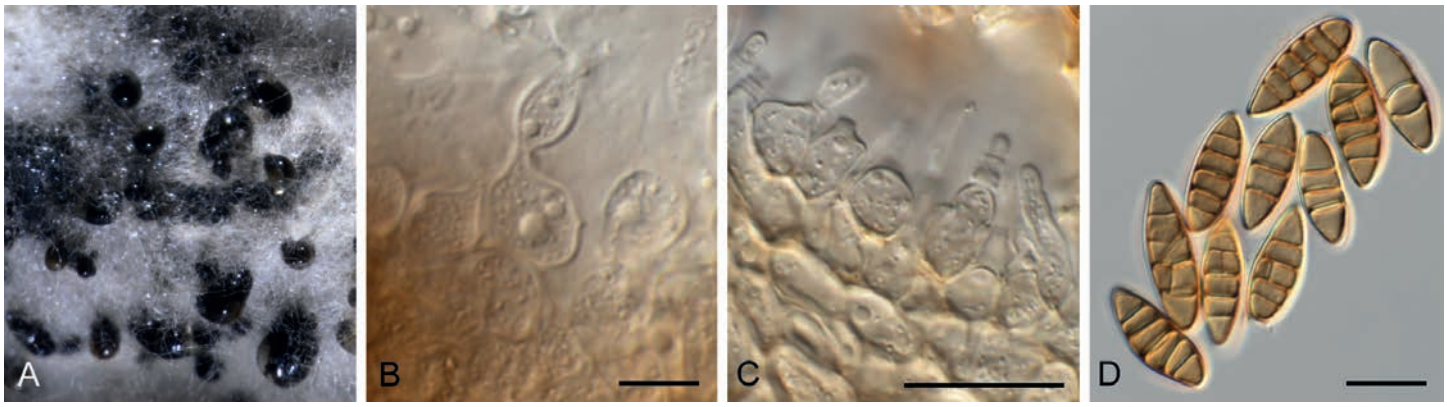

Fig. 52. *Wettsteinina philadelphi* (CPC 30534). **A.** Conidiomata on PDA. **B, C.** Conidiogenous cells. **D.** Conidia. Scale bars = 10 μm.

Xyladictyochaetaceae Crous & Hern.-Restr., ***fam. nov.*** MycoBank MB824802.

Mycelium consisting of medium brown, smooth, septate, branched, hyphae, forming globose, intercalary, brown, smooth, chlamydospore-like structures. *Conidiophores* erect, brown, smooth, subcylindrical, flexuous, multiseptate. *Conidiogenous cells* terminal and intercalary, polyphialidic; phialidic opening lacking flared collarettes. *Conidia* solitary, aggregating in slimy mass, hyaline, smooth, fusoid-ellipsoid, slightly curved, apex subacute, base truncate, medianly 1-septate; each end with flexuous, unbranched appendage.

Type genus: *Xyladictyochaeta* Hern.-Restr. *et al.*

Xyladictyochaeta lusitanica Hern.-Restr. *et al.*, *Stud. Mycol.* **86**: 94. 2017. Fig. 53.

Mycelium consisting of medium brown, smooth, septate, branched, 3–4 μm diam hyphae, that form globose, intercalary, brown, smooth, chlamydospore-like structures, 5–6 μm diam. *Conidiophores* erect, brown, smooth, subcylindrical, flexuous, multiseptate, 60–150 × 3–5 μm. *Conidiogenous cells* terminal and intercalary, polyphialidic, 2–6 × 2–2.5 μm; phialidic opening 1 μm diam, lacking flared collarettes. *Conidia* solitary, aggregating in slimy mass, hyaline, smooth, fusoid-ellipsoid, slightly curved, apex subacute, base truncate, 1 μm diam, medianly 1-septate, (10–) 11–12(–13) × (2.5–)3 μm; each end with flexuous, unbranched appendage, apex central, base excentric, 3–7 μm diam.

Culture characteristics: Colonies flat, spreading, surface folded, with sparse to moderate aerial mycelium and feathery, lobate margins, reaching 20 mm diam after 2 wk at 25 °C. On MEA and PDA surface and reverse amber. On OA surface olivaceous grey.

Specimens examined: **Australia**, New South Wales, Nullica State Forest, on *Eucalyptus* sp. (*Myrtaceae*) leaf litter, 29 Nov. 2016, *P.W. Crous*, (CBS H-23291, culture CPC 32324 = CBS 143502); *ibid*. (CPC 32526).

Notes: The genus *Xyladictyochaeta*, based on *Xy. lusitanica*, was recently described from *Eucalyptus* leaves collected in Portugal (Hernández-Restrepo *et al*. 2017), and this is the first record of this fungus from Australia. *Xyladictyochaeta* represents an undescribed family in *Xylariales*, and *Xyladictyochaetaceae* is introduced to accommodate it. Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Xy. lusitanica* (GenBank KY853479; Identities 571 / 573 (99 %), no gaps), *Anungitea eucalyptigena* (GenBank KY173383; Identities 517 / 578 (89 %), 16 gaps (2 %)) and *Beltraniopsis neolitseae* (GenBank NR_148072; Identities 521 / 583 (89 %), 19 gaps (3 %)). The ITS sequences of CPC 32324 and 32526 differs with three nucleotides (morphologically they are similar, except for prominent differences in conidiophore length). The highest similarities using the LSU sequence were *Xy. lusitanica* (GenBank KY853543; Identities 801 / 801 (100 %), no gaps), *Phlogicylindrium eucalypti* (GenBank DQ923534; Identities 822 / 844 (97 %), no gaps) and *Phl. mokarei* (GenBank KY173521; Identities 796 / 818 (97 %), no gaps). The LSU sequences of CPC 32324 and CPC 32526 are identical. No

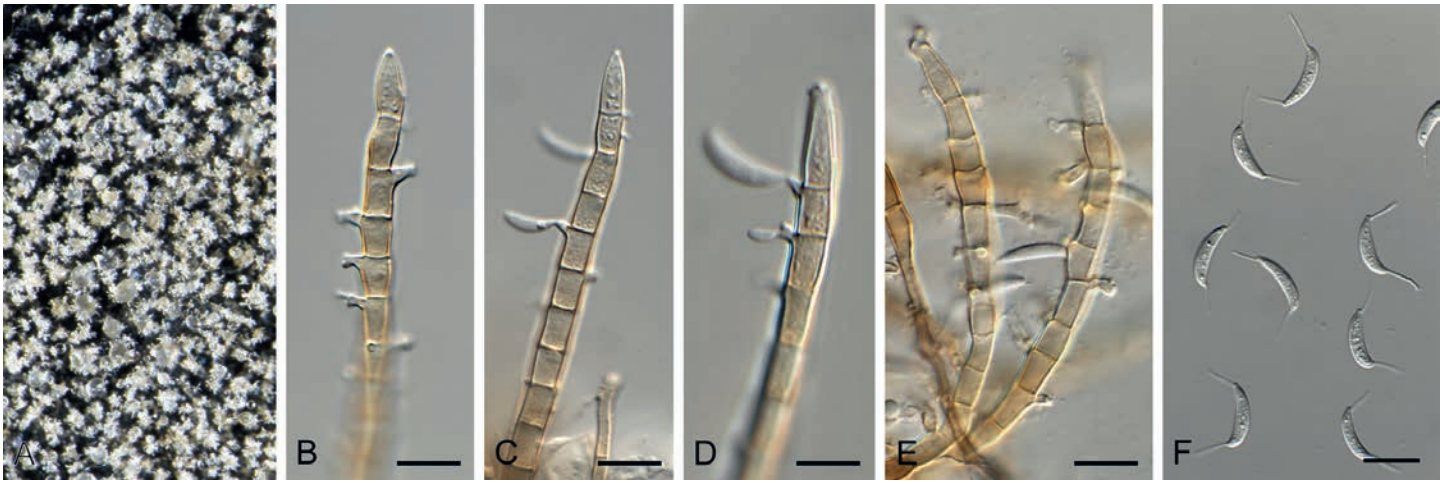

Fig. 53. *Xyladictyochaeta lusitanica* (CPC 32324). **A.** Conidiophores on PDA. **B–E.** Conidiophores on SNA. **F.** Conidia. Scale bars = 10 μm.

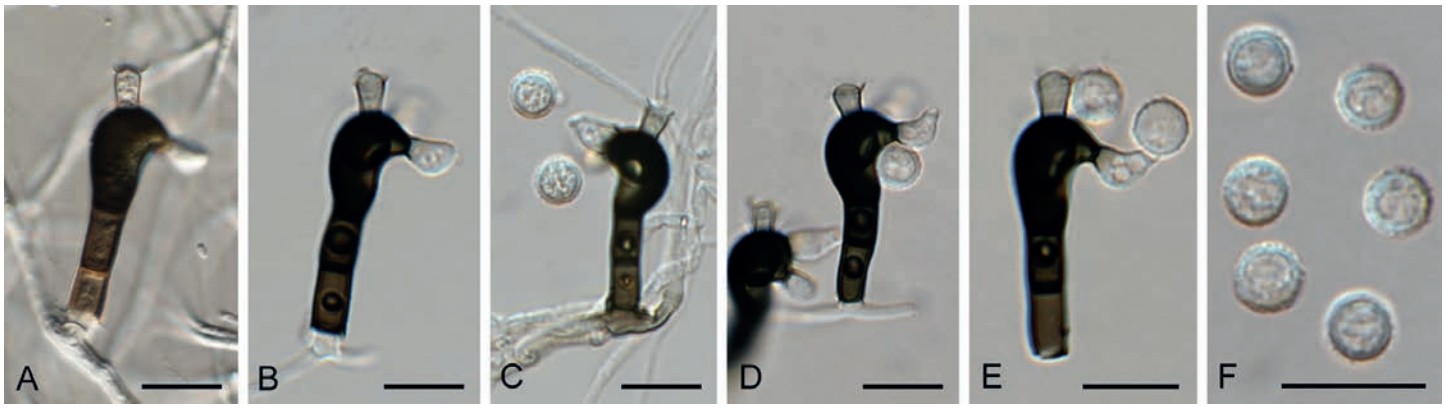

Fig. 54. *Zygosporium pseudogibbum* (CPC 30421). **A–E.** Conidiophores with conidiogenous cells. **F.** Conidia. Scale bars = 10 μm.

significant matches were obtained using the *tef1* sequences and the *tef1* sequences of CPC 32324 and CPC 32526 differ with one nucleotide and a single CA-repeat. No significant matches were obtained using the *tub2* sequence and the *tub2* sequences of CPC 32324 and CPC 32526 are 99 % identical (806 / 813, 1 gap).

Zygosporium pseudogibbum Crous, ***sp. nov.*** MycoBank MB824803. Fig. 54.

Etymology: Name refers to its morphological similarity to *Zygosporium gibbum.*

Conidiophores solitary, erect, consisting of 1–2 pale brown basal cells forming a stipe, 7–15 × 3–4 μm, giving rise to a curved, dark brown terminal vesicle, 11–12 × 6–8 μm. *Conidiogenous cells* arranged in a whorl of 3–4 on a terminal vesicle, hyaline, smooth, reniform, 4–6 × 3–4 μm. *Vesicle* with single apical cell, 4–5 × 3–4 μm, pale brown, cylindrical, with obtuse apex and prominent collarette. *Conidia* solitary, globose, verruculose, faintly olivaceous, 6(–7) μm diam.

Culture characteristics: Colonies flat, spreading, surface folded, with sparse to moderate aerial mycelium and smooth, lobate margins, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface buff to dirty white, reverse luteous. On PDA surface buff to dirty white, reverse saffron. On OA surface buff to dirty white.

Specimen examined: **Malaysia**, Sabah, on leaves of *Eucalyptus pellita* (*Myrtaceae*), Mar. 2016, *M.J. Wingfield* (holotype CBS H-23411, culture ex-type CPC 30421 = CBS 143503).

Notes: Morphologically, the present collection matches the description of *Z. gibbum*, a European taxon (reference isolate, FMR 13130 = CBS 137306; leaf litter Canary Islands; Hernandez-Restrepo *et al*. 2017), which has a wide host range and wide geographical distribution (Ellis 1971). Phylogenetically, however, it clusters sister to this species, and thus a new taxon is introduced to accommodate it. The vesicle gives rise to a single apical cell that appears to be a conidiogenous cell, but could play a different role entirely (moisture droplet, insect dispersal). Active spore dispersal was observed on host tissue, and it could be that conidia on this cell can actively discharge.

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Z. gibbum* (GenBank KY853482; Identities 481 / 504 (95 %), 1 gap (0 %)), *Podosordaria muli* (GenBank JX156377; Identities 462 / 499 (93 %), 14 gaps (2 %)) and *Poronia australiensis* (GenBank KP012826; Identities 384 / 434 (88 %), 21 gaps (4 %)). The highest similarities using the LSU sequence were *Z. gibbum* (GenBank KY853546; Identities 739 / 757 (98 %), 6 gaps (0 %)), *Atrotorquata spartii* (GenBank KP325443; Identities 818 / 846 (97 %), 2 gaps (0 %)) and *Circinotrichum cycadis* (GenBank KJ869178; Identities 804 / 849 (95 %), 6 gaps (0 %)). Only distant hits were obtained using the *actA* sequence; some of these were *Penicillifer pulcher* (GenBank KM231107; Identities 390 / 418 (93 %), no gaps), *Neonectria neomacrospora* (GenBank KM231143; Identities 389 / 418 (93 %), no gaps) and *Cylindrodendrum album* (GenBank KM231152; Identities 387 / 418 (93 %), no gaps). No significant hits were obtained when the *tub2* sequence was used.

ACKNOWLEDGEMENTS

This work was partially funded by the Szechenyi 2020 programme, the European Regional Development Fund and the Hungarian Government (GINOP-2.3.2-15-2016-00061). We are grateful to Arien van Iperen (cultures), Mieke Starink-Willemse (DNA isolation, amplification, and sequencing), and Marjan Vermaas (photographic plates) for their technical assistance.

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Supplementary Table 1. Collection details and GenBank accession numbers of isolates belonging to species treated in this study.

Species name	Culture accession number(s)[1]	Country	Substrate (including host)	Collector and Collection date	GenBank accession number[2]										
					ITS	LSU	*actA*	*chs-1*	*cmdA*	*gapdh*	*rpb1*	*rpb2*	SSU	*tef1*	*tub2*
Alfaria acaciae	CBS 143504^{T} = CPC 31882	South Africa	*Acacia propinqua*, leaves	M.J. Wingfield, Jul. 2012	MH107881.1	MH107929.1	–	–	MH107991.1	–	–	MH108000.1	–	MH108012.1	MH108035.1
	CPC 31940	South Africa	*Acacia propinqua*, leaves	M.J. Wingfield, Jul. 2012	MH107882.1	MH107930.1	–	–	–	–	–	MH108001.1	–	MH108013.1	–
Caliciopsis maxima	COAD 1983^{ET} = CPC 24674	Brazil	*Niphidium crassifolium*, fronds	R.W. Barreto, 5 Nov. 2011	KX891229.1	KX891228.1	–	–	–	–	–	–	–	–	–
Camarosporidiella mackenziei	CBS 144200 = CPC 25960	Finland	*Caragana* sp., twig	M. Pennanen, 31 Dec. 2014	KY929129.1	KY929164.1	–	–	–	–	–	–	–	KY929198.1	–
	CPC 25962	Finland	*Caragana* sp., twig	M. Pennanen, 31 Dec. 2014	KY929130.1	KY929165.1	–	–	–	–	–	–	–	KY929199.1	–
Chaetosphaeria myriocarpa	CBS 143389 = CPC 31840	Ukraine	*Carpinus betulus*, decaying wood	A. Akulov, 5 Oct. 2016	MH107883.1	MH107931.1	–	–	–	–	–	–	–	–	MH108036.1
Colletotrichum kniphofiae	CBS 143496^{T} = CPC 30166	UK	*Kniphofia uvaria*, leaves	P.W. Crous, 28 Mar. 2016	MH107884.1	MH107932.1	MH107975.1	MH107990.1	–	MH107998.1	–	–	–	–	MH108037.1
	CPC 30168	UK	*Kniphofia uvaria*, leaves	P.W. Crous, 28 Mar. 2016	MH107885.1	–	–	–	–	–	–	–	–	–	–
Cyclothyriella rubronotata	CBS 144201 = CPC 27604	Germany	*Ailanthus altissima*, twig	R.K. Schumacher, 4 Jun. 2015	MH107886.1	MH107933.1	–	–	–	–	–	–	–	–	–
Cylindrium algarvense	CBS 124770^{T} = CPC 14936	Portugal	*Eucalyptus* sp.	P.W. Crous, 24 Jan. 2007	GQ303287.1	GQ303318.2	–	–	–	–	–	–	–	–	–
Cylindrium purgamentum	CBS 142114^{T} = CPC 29580	USA	Leaf litter	P.W. Crous, Aug. 2013	KY173435.1	KY173525.1	–	–	–	–	–	–	–	–	–
Cylindrium syzygii	CBS 131307^{T} = CPC 17233	Australia	*Syzygium* sp., leaves	P.W. Crous & K.L. Crous, 14 Jul. 2009	JQ044421.1	JQ044441.1	–	–	–	–	–	–	–	–	–
Cytospora viticola	CBS 143162 = CPC 30117 = T15/464	Hungary	*Vitis vinifera*, stems	V.K. Zoltán, 5 Nov. 2014	MH107887.1	MH107934.1	MH107976.1	–	–	–	–	MH108002.1	–	MH108014.1	MH108038.1
Dictyochaeta mimusopis	CBS 143435^{T} = CPC 29987	South Africa	*Mimusops caffra*, leaves	M.J. Wingfield, Dec. 2010	MH107888.1	MH107935.1	–	–	–	–	–	–	–	–	–
Dictyochaeta septata	CBS 143386^{ET} = CPC 31949	Chile	*Eucalyptus grandis* × *urophylla*, leaves	M.J. Wingfield, Jun. 2010	MH107889.1	MH107936.1	–	–	–	–	–	–	–	MH108015.1	–
Echinocatena arthrinioides	CBS 144202 = CPC 28754	Malaysia	*Acacia crassicarpa*, leaves	M.J. Wingfield, 1 Jul. 2015	MH107890.1	MH107937.1	–	–	–	–	–	–	–	–	–
Elsinoë mimosae	CBS 141878^{ET} = CPC 19478 = RWB 154	Brazil	*Mimosa diplotricha*	R.W. Barreto, Mar. 1999	KX887255.1	KX887018.1	–	–	–	–	–	KX887136.1	–	KX886900.1	–
	CBS 141943 = CPC 18518 = RWB 224	Ecuador	*Mimosa diplotricha*	R.W. Barreto, Nov. 2000	KX887254.1	KX887017.1	–	–	–	–	JN992635.1	KX887135.1	JN940564.1	KX886899.1	–
Exophiala eucalypticola	CBS 143412^{T} = CPC 32736	Australia	*Eucalyptus obliqua*, leaf litter	P.W. Crous, 1 Dec. 2016	MH107891.1	MH107938.1	–	–	–	–	–	–	–	MH108016.1	MH108039.1
Fusiconidium lycopodiellae	CBS 143437^{T} = CPC 30371	Germany	*Lycopodiella inundata*, stems	R.K. Schumacher, 25 Feb. 2016	MH107892.1	MH107939.1	–	–	–	–	–	–	–	–	–
Haplographium delicatum	CBS 143493 = CPC 31844	Ukraine	*Carpinus betulus*, decaying wood	A. Akulov, 5 Oct. 2016	MH107893.1	MH107940.1	–	–	–	–	–	–	–	–	–
Microdochium musae	CBS 111018 = CPC 5380	Costa Rica	*Musa* cv. Cavendish	P.W. Crous, May 2002	AY293061.1	–	–	–	–	–	–	–	–	–	–
	CBS 143499 = CPC 32809	Malaysia	*Musa* sp., leaves	P.W. Crous, 2010	MH107894.1	MH107941.1	MH107977.1	–	MH107992.1	–	–	–	–	–	MH108040.1
	CBS 143500^{NT} = CPC 32689	Malaysia	*Musa* sp., leaves	P.W. Crous, 2016	MH107895.1	MH107942.1	MH107978.1	–	MH107993.1	–	–	MH108003.1	–	MH108017.1	MH108041.1
	CPC 11234	Mauritius	*Musa* sp., leaves	Y. Jaufeerally-Fakim, Jan. 2004	MH107896.1	MH107943.1	MH107979.1	–	MH107994.1	–	–	–	–	MH108018.1	MH108042.1
	CPC 11240	Mauritius	*Musa* sp., leaves	Y. Jaufeerally-Fakim, Jan. 2004	MH107897.1	MH107944.1	MH107980.1	–	MH107995.1	–	–	–	–	MH108019.1	MH108043.1
	CPC 16258	Mexico	*Musa* sp., leaves	M. de J. Yanez Morales, 16 Dec. 2008	MH107898.1	MH107945.1	MH107981.1	–	MH107996.1	–	–	–	–	MH108020.1	MH108044.1
	CPC 32681	Malaysia	*Musa* sp., leaves	P.W. Crous, 2010	MH107899.1	MH107946.1	MH107982.1	–	MH107997.1	–	–	–	–	–	–
Monochaetia junipericola	CBS 143391^{T} = CPC 30561	Germany	*Juniperus communis*, twig	R.K. Schumacher, 20 Apr. 2016	MH107900.1	MH107947.1	–	–	–	–	–	MH108004.1	–	MH108021.1	MH108045.1
Myrmecridium sorbicola	CBS 143433^{T} = CPC 30455	Germany	*Sorbus aucuparia*, branch	R.K. Schumacher, 17 Feb. 2016	MH107901.1	MH107948.1	–	–	–	–	–	–	–	–	–
Nematogonum pseudoferrugineum	CBS 144203^{T} = CPC 31872	Ukraine	*Carpinus betulus*, trunk of fallen plant	A. Akulov, 7 Oct. 2016	MH107902.1	–	–	–	–	–	–	–	–	MH108022.1	–
Neocucurbitaria cava	CBS 143400 = CPC 32488	UK	*Quercus ilex*, leaves	P.W. Crous, 30 Dec. 2016	MH107903.1	MH107949.1	MH107983.1	–	–	–	–	MH108005.1	–	–	MH108046.1
Neohendersonia kickxii	CBS 112403^{ET}	Italy	*Fagus sylvatica*, bark of twigs	R. Danti, 8 May 1996	KX820255.1	KX820266.1	–	–	–	–	–	–	–	–	–
Parapleurotheciopsis caespitosa	CBS 519.93^{T} = CPC 565	South Africa	*Syzygium chordatum*, leaf litter	M.J. Wingfield, Nov. 1992	MH107904.1	MH107950.1	–	–	–	–	–	–	–	–	–
Parathyridaria philadelphi	CBS 143432^{T} = CPC 30532	Germany	*Philadelphus coronarius*, twigs	R.K. Schumacher, 2 Apr. 2016	MH107905.1	MH107951.1	–	–	–	–	–	–	–	MH108023.1	–
Pestalotiopsis hollandica	CBS 143436 = CPC 30399	Spain	*Cupressus sempervirens*, needles	R. Blasco, 7 Jan. 2016	MH107906.1	MH107952.1	–	–	–	–	–	–	–	MH108024.1	MH108047.1
Phyllosticta hakeicola	CBS 143492^{T} = CPC 32041	Australia	*Hakea* sp., leaves	P.W. Crous, 26 Nov. 2016	MH107907.1	MH107953.1	MH107984.1	–	–	MH107999.1	–	–	–	MH108025.1	–
Polyscytalum chilense	CBS 143387^{T} = CPC 31946	Chile	*Eucalyptus urophylla*, leaves	M.J. Wingfield, Jun. 2010	MH107908.1	MH107954.1	–	–	–	–	–	–	–	–	–
Polyscytalum eucalyptigenum	CBS 143388 = CPC 31878	Chile	*Eucalyptus grandis* × *uromycoides*, leaves	M.J. Wingfield, Jun. 2010	MH107909.1	MH107955.1	–	–	–	–	–	–	–	–	–
Polyscytalum eucalyptorum	CBS 137967^{T} = CPC 17207	Australia	*Eucalyptus*, leaf litter	P.W. Crous & R.G. Shivas, 11 Jul. 2009	KJ869118.1	KJ869176.1	–	–	–	–	–	–	–	KJ869234.1	–
Polyscytalum grevilleae	CBS 141282^{T} = CPC 25576	Australia	*Grevillea* sp., leaves	P.W. Crous & J. Edwards, 7 Nov. 2014	KX228252.1	KX228304.1	–	–	–	–	–	–	–	–	–
Polyscytalum neofecundissimum	CBS 143390^{T} = CPC 31826	Ukraine	*Quercus robur*, leaf litter	A. Akulov, 7 Oct. 2016	MH107910.1	MH107956.1	–	–	–	–	–	–	–	–	–
Polyscytalum nullicanum	CBS 143406^{T} = CPC 32528	Australia	*Eucalyptus*, leaf litter	P.W. Crous, 29 Nov. 2016	MG386058.1	MG386111.1	–	–	–	–	–	–	–	–	–
Pseudoanungitea syzygii	CBS 520.93^{T} = CPC 578	South Africa	*Syzygium cordatum*, leaf litter	W.J. Swart, Mar. 1993	MH107911.1	MH107957.1	–	–	–	–	–	–	–	–	–
Pseudoanungitea vaccinii	CBS 143164^{T} = CPC 30522	Germany	*Vaccinium myrtillus*, stem	R.K. Schumacher, 16 Jan. 2016	MH107912.1	MH107958.1	–	–	–	–	–	–	–	–	–
Pseudoanungitea variabilis	CBS 132716^{T} = FMR 11934	Spain	Dead wood	M. Hernández-Restrepo, J. Mena & J. Guarro, May 2011	KY853424.1	KY853484.1	–	–	–	–	–	–	–	–	–
Pseudocamarosporium africanum	CBS 144204 = CPC 25926	South Africa	*Erica* sp., twigs	M.J. Wingfield, Nov. 2014	KY929156.1	KY929185.1	–	–	–	–	–	–	–	–	–
Pseudocamarosporium brabeji	CBS 144205 = CPC 25002	Switzerland	*Platanus* sp., branch	O. Holdenrieder, 24 Jun. 2014	KY929157.1	KY929186.1	–	–	–	–	–	–	–	–	–
Pseudocercospora breonadiae	CBS 143489^{T} = CPC 30153	South Africa	*Breonadia microcephala*, leaves	J. Roux, Jan. 2010	MH107913.1	MH107959.1	MH107985.1	–	–	–	–	MH108006.1	–	MH108026.1	–
Rhinocladiella quercus	CBS 143495 = CPC 30459	Germany	*Sorbus aucuparia*, branch	R.K. Schumacher, 17 Feb. 2016	MH107914.1	MH107960.1	–	–	–	–	–	–	–	MH108027.1	MH108048.1
Roussoella euonymi	CBS 143426^{T} = CPC 31963	Ukraine	*Euonymus europaeus*, fallen branches	A. Akulov, 14 Oct. 2016	MH107915.1	MH107961.1	MH107986.1	–	–	–	–	MH108007.1	–	–	MH108049.1
Setophaeosphaeria citricola	CBS 143179^{T} = CPC 32083	Australia	*Citrus australasica*, leaves	P.W. Crous, 25 Nov. 2016	MH107916.1	MH107962.1	–	–	–	–	–	MH108008.1	–	MH108028.1	MH108050.1
Setophaeosphaeria sidae	CBS 135108^{T} = CPC 19602 = RWB 866	Brazil	*Sida* sp.	R.W. Barreto, 24 Feb. 2008	KF251149.1	KF251653.1	–	–	–	–	–	KF252158.1	–	KF253109.1	KF252648.1
Sirastachys cyperacearum	CBS 143444^{T} = CPC 32087	Australia	*Cyperaceae*, leaves	P.W. Crous, 26 Nov. 2016	MH107917.1	MH107963.1	–	–	–	–	–	–	–	–	–
Sphaerellopsis paraphysata	CBS 143579 = CPC 32406	Australia	*Phragmites* sp., leaves	P.W. Crous, 27 Nov. 2016	MH107918.1	MH107964.1	–	–	–	–	–	MH108009.1	–	MH108029.1	MH108051.1
Subplenodomus iridicola	CBS 143395^{T} = CPC 30162	UK	*Iris* sp.	P.W. Crous, 28 Mar. 2016	MH107919.1	MH107965.1	–	–	–	–	–	–	–	–	–
Teichospora quercus	CBS 143396^{T} = CPC 30009	France	*Quercus* sp., branch	G. Moyne, 15 Nov. 2015	MH107920.1	MH107966.1	–	–	–	–	–	MH108010.1	–	MH108030.1	–
Trochila viburnicola	CBS 144206^{T} = CPC 30254	UK	*Viburnum* sp., twig cankers	P.W. Crous, 28 Mar. 2016	MH107921.1	MH107967.1	–	–	–	–	–	MH108011.1	–	MH108031.1	–
Varicosporellopsis aquatilis	CBS 143509 = JW75003	The Netherlands	Garden soil	H. van Warenburg, Feb. 2017	MH107922.1	MH107968.1	MH107987.1	–	–	–	–	–	–	–	MH108052.1
Vermiculariopsiella dichapetali	CBS 143424 = CPC 32057	Australia	*Melaleuca* sp., leaves	P.W. Crous, 26 Nov. 2016	MH107923.1	MH107969.1	–	–	–	–	–	–	–	–	–
	CBS 143440 = CPC 32544	Australia	*Eucalyptus regnans*, leaves	P.W. Crous, 30 Nov. 2016	MH107924.1	MH107970.1	MH107988.1	–	–	–	–	–	–	–	–
Wettsteinina philadelphi	CBS 143392^{T} = CPC 30534	Germany	*Philadelphus coronarius*, twigs	R.K. Schumacher, 2 Apr. 2016	MH107925.1	MH107971.1	–	–	–	–	–	–	–	MH108032.1	–
Xyladictyochaeta lusitanica	CBS 143502 = CPC 32324	Australia	*Eucalyptus* sp., leaf litter	P.W. Crous, 29 Nov. 2016	MH107926.1	MH107972.1	–	–	–	–	–	–	–	MH108033.1	MH108053.1
	CPC 32526	Australia	*Eucalyptus* sp., leaf litter	P.W. Crous, 29 Nov. 2016	MH107927.1	MH107973.1	–	–	–	–	–	–	–	MH108034.1	MH108054.1
Zygosporium pseudogibbum	CBS 143503^{T} = CPC 30421	Malaysia	*Eucalyptus pellita*, leaves	M.J. Wingfield, Mar. 2016	MH107928.1	MH107974.1	MH107989.1	–	–	–	–	–	–	–	MH108055.1

[1] CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands; COAD: Coleção Octávio de Almeida Drumond (COAD), housed at the Universidade Federal de Viçosa, Viçosa, Brazil; CPC: Culture collection of Pedro Crous, housed at CBS; RWB: Personal collection of Robert Barreto, Departmento de Fitopatologia, Universidade Federal de Viçosa,

[2] ITS: internal transcribed spacers and intervening 5.8S nrDNA; LSU: large subunit (28S) of the nrRNA gene operon; *actA*: partial actin gene; *chs-1*: partial chitin synthase-1 gene; *cmdA*: partial calmodulin gene; *gapdh*: partial glyceraldehyde-3-phosphate dehydrogenase gene; *rpb1*: partial DNA-directed RNA polymerase II largest subunit gene; *rpb2*: