Persoonia 50, 2023: 158–310
www.ingentaconnect.com/content/nhn/pimj

RESEARCH ARTICLE

ISSN (Online) 1878-9080
https://doi.org/10.3767/persoonia.2023.50.05

Fungal Planet description sheets: 1478–1549

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Key words

ITS nrDNA barcodes
LSU
new taxa
systematics

Abstract Novel species of fungi described in this study include those from various countries as follows: **Australia**, *Aschersonia mackerrasiae* on whitefly, *Cladosporium corticola* on bark of *Melaleuca quinquenervia*, *Penicillium nudgee* from soil under *Melaleuca quinquenervia*, *Pseudocercospora blackwoodiae* on leaf spot of *Persoonia falcata*, and *Pseudocercospora dalyelliae* on leaf spot of *Senna alata*. **Bolivia**, *Aspicilia lutzoniana* on fully submersed siliceous schist in high-mountain streams, and *Niesslia parviseta* on the lower part and apothecial discs of *Erioderma barbellatum* on a twig. **Brazil**, *Cyathus bonsai* on decaying wood, *Geastrum albofibrosum* from moist soil with leaf litter, *Laetiporus pratigiensis* on a trunk of a living unknown hardwood tree species, and *Scytalidium synnematicum* on dead twigs of unidentified plant. **Bulgaria**, *Amanita abscondita* on sandy soil in a plantation of *Quercus suber*. **Canada**, *Penicillium acericola* on dead bark of *Acer saccharum*, and *Penicillium corticola* on dead bark of *Acer saccharum*. **China**, *Colletotrichum qingyuanense* on fruit lesion of *Capsicum annuum*. **Denmark**, *Helminthosphaeria leptospora* on corticioid *Neohypochnicium cremicolor*. **Ecuador (Galapagos)**, *Phaeosphaeria scalesiae* on *Scalesia* sp. **Finland**, *Inocybe jacobssonii* on calcareous soils in dry forests and park habitats. **France**, *Cortinarius rufomyrrheus* on sandy soil under *Pinus pinaster*, and *Periconia neominutissima* on leaves of *Poaceae*. **India**, *Coprinopsis fragilis* on decaying bark of logs, *Filoboletus keralensis* on unidentified woody substrate, *Penicillium sankaranii* from soil, *Physisporinus tamilnaduensis* on the trunk of *Azadirachta indica*, and *Poronia nagaraholensis* on elephant

Citation: Crous PW, Osieck ER, Shivas RG, et al. 2023. Fungal Planet description sheets: 1478–1549. Persoonia 50: 158–310. https://doi.org/10.3767/persoonia.2023.50.05.
Effectively published online: 29 June 2023 [Received: 1 April 2023; Accepted: 10 May 2023].

dung. **Iran**, *Neosetophoma fici* on infected leaves of *Ficus elastica*. **Israel**, *Cnidariophoma eilatica* (incl. *Cnidariophoma* gen. nov.) from *Stylophora pistillata*. **Italy**, *Lyophyllum obscurum* on acidic soil. **Namibia**, *Aureobasidium faidherbiae* on dead leaf of *Faidherbia albida*, and *Aureobasidium welwitschiae* on dead leaves of *Welwitschia mirabilis*. **Netherlands**, *Gaeumannomycella caricigena* on dead culms of *Carex elongata*, *Houtenomyces caricicola* (incl. *Houtenomyces* gen. nov.) on culms of *Carex disticha*, *Neodacampia ulmea* (incl. *Neodacampia* gen. nov.) on branch of *Ulmus laevis*, *Niesslia phragmiticola* on dead standing culms of *Phragmites australis*, *Pseudopyricularia caricicola* on culms of *Carex disticha*, and *Rhodoveronaea nieuwwulvenica* on dead bamboo sticks. **Norway**, *Arrhenia similis* half-buried and moss-covered pieces of rotting wood in grass-grown path. **Pakistan**, *Mallocybe ahmadii* on soil. **Poland**, *Beskidomyces laricis* (incl. *Beskidomyces* gen. nov.) from resin of *Larix decidua* ssp. *polonica*, *Lapidomyces epipinicola* from sooty mould community on *Pinus nigra*, and *Leptographium granulatum* from a gallery of *Dendroctonus micans* on *Picea abies*. **Portugal**, *Geoglossum azoricum* on mossy areas of laurel forest areas planted with *Cryptomeria japonica*, and *Lunasporangiospora lusitanica* from a biofilm covering a biodeteriorated limestone wall. **Qatar**, *Alternaria halotolerans* from hypersaline sea water, and *Alternaria qatarensis* from water sample collected from hypersaline lagoon. **South Africa**, *Alfaria thamnochorti* on culm of *Thamnochortus fraternus*, *Knufia aloeicola* on *Aloe gariepensis*, *Muriseptatomyces restionacearum* (incl. *Muriseptatomyces* gen. nov.) on culms of *Restionaceae*, *Neocladosporium arctotis* on nest of cases of bag worm moths (*Lepidoptera, Psychidae*) on *Arctotis auriculata*, *Neodevriesia scadoxi* on leaves of *Scadoxus puniceus*, *Paraloratospora schoenoplecti* on stems of *Schoenoplectus lacustris*, *Tulasnella epidendrea* from the roots of *Epidendrum* × *obrienianum*, and *Xenoidriella cinnamomi* (incl. *Xenoidriella* gen. nov.) on leaf of *Cinnamomum camphora*. **South Korea**, *Lemonniera fraxinea* on decaying leaves of *Fraxinus* sp. from pond. **Spain**, *Atheniella lauri* on the bark of fallen trees of *Laurus nobilis*, *Halocryptovalsa endophytica* from surface-sterilised, asymptomatic roots of *Salicornia patula*, *Inocybe amygdaliolens* on soil in mixed forest, *Inocybe pityusarum* on calcareous soil in mixed forest, *Inocybe roseobulbipes* on acidic soils, *Neonectria borealis* from roots of *Vitis berlandieri* × *Vitis rupestris*, *Sympoventuria eucalyptorum* on leaves of *Eucalyptus* sp., and *Tuber conchae* from soil. **Sweden**, *Inocybe bidumensis* on calcareous soil. **Thailand**, *Cordyceps sandindaengensis* on *Lepidoptera* pupa, buried in soil, *Ophiocordyceps kuchinaraiensis* on *Coleoptera* larva, buried in soil, and *Samsoniella winandae* on *Lepidoptera* pupa, buried in soil. **Taiwan region (China)**, *Neophaeosphaeria livistonae* on dead leaf of *Livistona rotundifolia*. **Türkiye**, *Melanogaster anatolicus* on clay loamy soils. **UK**, *Basingstokeomyces allii* (incl. *Basingstokeomyces* gen. nov.) on leaves of *Allium schoenoprasum*. **Ukraine**, *Xenosphaeropsis corni* on recently dead stem of *Cornus alba*. **USA**, *Nothotrichosporon aquaticum* (incl. *Nothotrichosporon* gen. nov.) from water, and *Periconia philadelphiana* from swab of coil surface. Morphological and culture characteristics for these new taxa are supported by DNA barcodes.

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Acknowledgements The work of P.W. Crous and colleagues benefitted from funding by the European Union's Horizon 2020 research and innovation program (RISE) under the Marie Skłodowska-Curie grant agreement No. 101008129, project acronym 'Mycobiomics', and the Dutch NWO Roadmap grant agreement No. 2020/ENW/00901156, project 'Netherlands Infrastructure for Ecosystem and Biodiversity Analysis – Authoritative and Rapid Identification System for Essential biodiversity information' (acronym NIEBA-ARISE). G. Gulden, B. Rian and I. Saar thank K. Bendiksen at the fungarium and G. Marthinsen at NorBol, both Natural History Museum, University of Oslo for valuable help with the collections, and the sequencing of our finds of *A. similis* from 2022. Sincere thanks to A. Voitk for assistance with the colour plate and review of the manuscript. I. Saar was supported by the Estonian Research Council (grant PRG1170). P. Rodriguez-Flakus and co-authors are greatly indebted to their colleagues and all staff of the Herbario Nacional de Bolivia, Instituto de Ecología, Universidad Mayor de San Andrés, La Paz, for their generous long-term cooperation. Their research was financially supported by the National Science Centre (NCN) in Poland (grants numbers 2018/02/X/NZ8/02362 and 2021/43/B/NZ8/02902). Y.P. Tan and colleagues thank M.K. Schutze (Department of Agriculture and Fisheries, Queensland, Australia) for determining the identity of the insect hosts for *Aschersonia mackerrasiae*. The Australian Biological Resources Study funded the project that led to the discovery of *Aschersonia mackerrasiae*. K.G.G. Ganga acknowledges support from the University Grants Commission (UGC), India, in the form of a UGC research fellowship (Ref No. 20/12/2015(ii) EU-V), and the authorities of the University of Calicut for providing facilities to conduct this study. S. Mahadevakumar acknowledges the Director, KSCSTE - Kerala Forest Research Institute and Head of Office, Botanical Survey of India, Andaman and Nicobar Regional Centre, Port Blair for the necessary support and M. Madappa, Department of Studies in Botany, University of Mysore for technical assistance. A.R. Podile thanks the Department of Science and Technology, Govt. of India for the JC Bose Fellowship (Grant No. JCB/2017/000053) & MoE and IOE-Directorate-UOH for project (Grant No.UOH-IOE-RC3-21-065). Financial support was provided to R. de L. Oliveira and K.D. Barbosa by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brazil (CAPES) – Finance code 001, and to I.G. Baseia and M.P. Martín by the National Council for Scientific and Technological Development (CNPq) under CNPq-Universal 2016 (409960/2016-0) and CNPq-visiting researcher (407474/2013-7). E. Larsson acknowledges the Swedish Taxonomy Initiative, SLU Artdatabanken, Uppsala, Sweden. H.Y. Mun and J. Goh were supported by a grant from the Nakdonggang National Institute of Biological Resources (NNIBR), funded by the Ministry of Environment (MOE) of the Republic of Korea (NNIBR202301106). J. Trovão and colleagues were financed by FEDER - Fundo Europeu de Desenvolvimento Regional funds through the COMPETE 2020 - Operational Programme for Competitiveness and Internationalisation (POCI), and by Portuguese funds through FCT- Fundação para a Ciência e a Tecnologia in the framework of the project POCI-01-0145-FEDER-PTDC/EPH-PAT/3345/ 2014. Their research was carried out at the R & D Unit Centre for Functional Ecology – Science for People and the Planet (CFE), with reference UIDB/04004/2020, financed by FCT/MCTES through national funds (PIDDAC). João Trovão was supported by POCH - Programa Operacional Capital Humano (co-funding by the European Social Fund and national funding by MCTES), through a 'FCT- Fundação para a Ciência e Tecnologia' PhD research grant (SFRH/BD/132523/2017). O. Kaygusuz and colleagues thank the Research Fund of the Isparta University of Applied Sciences for their financial support under the project number 2021-ILK1-0155. They also thank N. Sánchez Biezma of the Department of Drawing and Scientific Photography at the Alcalá University for his help in the digital preparation of the photographs. The research of M. Spetik and co-authors was supported by project No. IGA-ZF/2021-SI1003. V. Darmostuk and colleagues acknowledge our colleagues and all staff of the Herbario Nacional de Bolivia, Instituto de Ecología, Universidad Mayor de San Andrés, La Paz, for their generous long-term cooperation. They would also like to thank the SERNAP (http://sernap.gob.bo), and all protected areas staff, for providing permits for scientific studies, as well as their assistance and logistical support during the field works. This research was financially supported by the National Science Centre (NCN) in Poland (grant number DEC-2013/11/D/NZ8/ 03274). M. Kaliyaperumal and co-authors thank the Centre of Advanced Studies in Botany, University of Madras for the laboratory facilities. M. Kaliyaperumal thanks the Extramural Research-SERB, DST (EMR/2016/003078), Government of India, for financial assistance. M. Kaliyaperumal and K. Kezo thanks RUSA 2.0 (Theme-1, Group-1/2021/49) for providing a grant. M. Shivannegowda and colleagues thank C.R. Santhosh, Department of Studies in Microbiology, University of Mysore, Manasagangotri, Mysuru for technical support. They also thank K.R. Sridhar, Mangalore University, Karnataka, India and S.S.N. Maharachchikumbura, University of Electronic Science and Technology of China, Chengdu for their support and helping with technical inputs. The study of G.G. Barreto and co-authors was financed in part by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brazil (CAPES - Finance Code 001), and the Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq - Proc. 131503/2019-7; Proc. 312984/2018-9); the authors also thank to Programa de Pós-Graduação em Botânica – PPGBOT. L.F.P. Gusmão thanks to Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) for a research grant. T. Nkomo and colleagues thank the National Research Foundation of South Africa for funding this study, with additional funding from the Forestry and Agricultural Biotechnology Institute and the University of Pretoria. G. Delgado is grateful to W. Colbert and S. Ward (Eurofins Built Environment) for continual encouragement and provision of laboratory facilities. J.G. Maciá-Vicente acknowledges support from the Landes-Offensive zur Entwicklung Wissenschaftlich-ökonomischer Exzellenz (LOEWE) of the state of Hesse within the framework of the Cluster for Integrative Fungal Research (IPF) of Goethe University Frankfurt. F. Esteve-Raventós and colleagues acknowledge P. Juste and J.C. Campos for the loan of some collections for study and N. Subervielle and L. Hugot (Conservatoire Botanique National de Corse, Office de l'Environnement de la Corse, Corti) for their assistance. They also acknowledge the Balearic Mycology Group (FCB) for their permanent help in the search for collections in the Balearic Islands, and Y. Turégano for obtaining some of the sequences presented here, and L. Parra for his suggestions and help on nomenclatural issues. S. Mongkolsamrit and colleagues were financially supported by the Platform Technology Management Section, National Centre for Genetic Engineering and Biotechnology (BIOTEC), Project Grant No. P19-50231. S. De la Peña-Lastra and colleagues thank the Atlantic Islands National Maritime-Terrestrial Park authorities and guards. A. Mateos and co-authors would like to thank Secretaria Regional do Ambiente e Alterações Climáticas Açores for the permission granted for the sampling (Licença nº 16/2021/DRAAC). To the ECOTOX group for co-funding the trip. J. Mack & D.P. Overy were funded by Agriculture & Agri-Food Canada (Project ID#002272: Fungal and Bacterial Biosystematics-bridging taxonomy and "omics" technology in agricultural research and regulation) and are grateful for molecular sequencing support from the Molecular Technologies Laboratory (MTL) at the Ottawa Research & Development Centre of Agriculture & Agri-Food Canada. The study of P. Czachura was funded by the National Science Centre, Poland, under the project 2019/35/N/NZ9/04173. The study of M. Piątek and co-authors was funded by the National Science Centre, Poland, under the project 2017/27/B/NZ9/02902. O. Yarden and L. Granit were funded by the Israel Science Foundation (grant number 888/19). H. Taşkın and colleagues received support from the Bulgarian Academy of Sciences and the Scientific and Technological Research Council of Türkiye (Bilateral grant agreement between BAS and TÜBİTAK, project number 118Z640). The authors would also like to thank S. Şahin (İzmir, Türkiye) for conveying one of the localities of *A. abscondita*. Andrew Miller would like to thank the Roy J. Carver Biotechnology Center at the University of Illinois for Sanger sequencing. E.R. Osieck thanks Staatsbosbeheer for permission to collect fungi in Nieuw Wulven, in the Netherlands. P. van 't Hof and co-authors thank the Galapagos Genetic Barcode project supported by UK Research and Innovation, Global Challenges Research Fund, Newton Fund, University of Exeter, Galapagos Science Center, Universidad San Francisco de Quito, Galapagos Conservation Trust, and Biosecurity Agency of Galapagos (ABG).


Rhodoveronaea nieuwwulvenica

Fungal Planet 1478 – 29 June 2023

Rhodoveronaea nieuwwulvenica Crous & Osieck, *sp. nov.*

Etymology. Name refers to the location where it was collected, Nieuw Wulven.

Classification — *Rhamphoriaceae*, *Rhamphoriales*, *Sordariomycetes*.

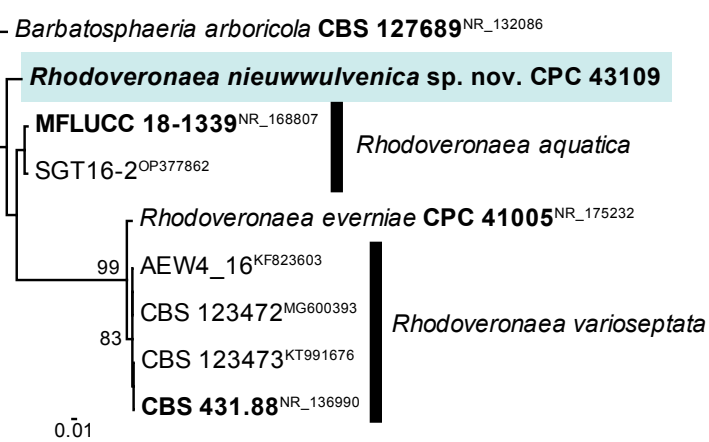
Mycelium consisting of hyaline to pale brown, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* solitary, erect, subcylindrical, flexuous, arising from superficial hyphae, 20–60 × 4–5 µm, thick-walled, red-brown, 2–3-septate, finely roughened. *Conidiogenous cells* terminal, integrated, subcylindrical, 20–50 × 4–5 µm, medium brown, finely verruculose, forming a rachis with subdenticulate loci, 0.5 µm diam, not darkened, slightly thickened. *Conidia* solitary, subcylindrical to narrowly fusoid-ellipsoid, apex subobtuse, base bluntly rounded, hilum 0.5–1 µm diam, medium brown, guttulate, smooth-walled, 3-septate, (8–)11–13(–14) × (3–)4(–4.5) µm.

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

Typus. Netherlands, Utrecht Province, Nieuw Wulven, near Houten, 1.5 m a.s.l., N52°03' E05°10', on dead bamboo stick, 11 Feb. 2022, *E.R. Osieck*, HPC 3837 = WI-48/#4404 (holotype CBS H-25172; culture ex-type CPC 43109 = CBS 149447; ITS, LSU, *rpb2* (first part) and *tef1* (second part) sequences GenBank OQ628466.1, OQ629048.1, OQ627935.1 and OQ627955.1; MycoBank MB 848053).

Notes — *Rhodoveronaea* was introduced by Arzanlou et al. (2007) for *R. varioseptata (*conidia 0–2(–3)-septate, (8–)11–13(–15) × (2–)3–4(–6) µm), which was later linked to a sexual morph by Réblová (2009). Although *R. nieuwwulvenica* has conidia of similar dimensions, they tend to be primarily 3-septate. *Rhodoveronaea aquatica* has larger conidia (1–3-septate, 23–27 × 9–11 µm; Lou et al. 2019), while *R. everniae* (conidia 0–3-septate, (6.5–)9–11(–12) × (3–)4(–4.5) µm; Crous et al. 2021c) again has smaller conidia. Phylogenetically, *R. nieuwwulvenica* is distinct from all presently known species.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 43109 had highest similarity to *Rhodoveronaea aquatica* (voucher MFLU 18-1593, GenBank NR_168807.1; Identities = 451/476 (95 %), four gaps (0 %)), *Rhodoveronaea varioseptata* (strain CBS 123473, GenBank KT991676.1; Identities = 401/451 (89 %), nine gaps (1 %)) and *Rhodoveronaea everniae* (strain CBS 148309, GenBank NR_175232.1; Identities = 449/512 (88 %), 12 gaps (2 %)). Closest hits using the **LSU** sequence of CPC 43109 are *Rhodoveronaea aquatica* (strain MFLUCC 18-1339, GenBank NG_068647.1; Identities = 778/783 (99 %), no gaps), *Rhodoveronaea varioseptata* (strain CBS 431.88, GenBank NG_057786.1; Identities = 792/819 (97 %), no gaps) and *Rhodoveronaea everniae* (strain CPC 41005, GenBank OK663776.1; Identities = 754/781 (97 %), no gaps). Closest hits using the ***rpb2*** (first part) sequence of CPC 43109 had highest similarity to *Rhodoveronaea aquatica* (strain GZCC 20-0447, GenBank OP473107.1; Identities = 809/865 (94 %), no gaps), *Rhodoveronaea varioseptata* (strain CBS 123472, GenBank JX066701.1; Identities = 726/886 (82 %), eight gaps (0 %)) and *Barbatosphaeria arboricola* (strain CBS 114120, GenBank KM492900.1; Identities = 717/889 (81 %), ten gaps (1 %)). Closest hits using the ***tef1*** (second part) sequence of CPC 43109 had highest similarity to *Rhodoveronaea aquatica* (strain GZCC 20-0447, GenBank OP473041.1; Identities = 829/865 (96 %), no gaps), *Xylolentia* sp. JY-2022a (strain GZCC 20-0426, GenBank OP473039.1; Identities = 806/867 (93 %), four gaps (0 %)) and *Stilbochaeta novae-guineensis* (strain CBS 147515, GenBank OL654060.1; Identities = 814/882 (92 %), four gaps (0 %)).



Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy et al. 2017, Minh et al. 2020) of the *Rhodoveronaea* ITS nucleotide alignment. Bootstrap support values (> 74 % are shown) from 1000 non-parametric bootstrap replicates are shown at the nodes. Culture collection numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Barbatosphaeria arboricola* (CBS 127689; GenBank NR_132086) and the novelty described here is highlighted with a coloured block and **bold** font. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 9 strains including the outgroup; 526 characters including alignment gaps analysed: 103 distinct patterns, 63 parsimony-informative, 62 singleton sites, 401 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.22249690).

Colour illustrations. Nieuw Wulven, near Houten in Utrecht Province, the Netherlands. Conidiophores and conidiogenous cells giving rise to conidia on SNA; conidia. Scale bars = 10 µm.

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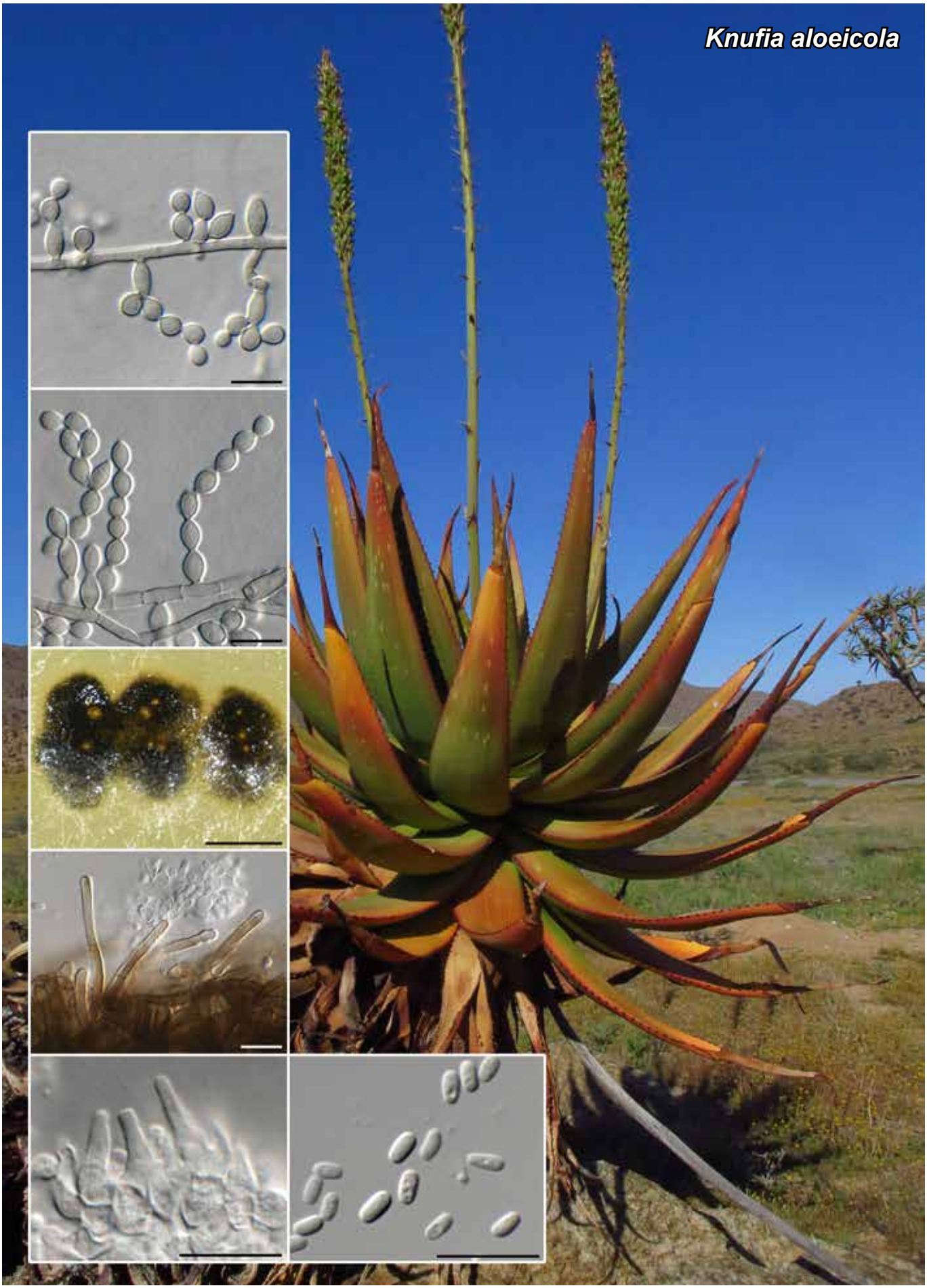
Knufia aloeicola

Fungal Planet 1479 – 29 June 2023

Knufia aloeicola Crous, *sp. nov.*

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

Classification — *Trichomeriaceae*, *Chaetothyriales*, *Chaetothyriomycetidae*, *Eurotiomycetes*.

Mycelium consisting of medium brown, smooth, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* solitary, erect, medium brown, smooth, subcylindrical, 1–2-septate, 10–20 × 2.5–3.5 µm, giving rise to conidial chains or reduced to a conidiogenous cell with 1–2 sympodial loci, giving rise to branched or unbranched conidial chains. *Conidiogenous cells* medium brown, fusoid-ellipsoid, smooth, 5–10 × 3–4 µm. *Conidia* guttulate, in branched or unbranched chains, broadly ellipsoid to subglobose, aseptate, medium brown, smooth, 3.5–6 × 3–3.5 µm, with median apical and basal locus, 1 µm diam, not thickened; conidia remaining attached in chains, breaking into shorter chains with age. *Synasexual morph* coelomycetous: *conidiomata* developing in concentric circles, eustromatic, pycnidial, immersed on OA, subglobose with one to several ostioles oozing a pale creamy conidial mass; conidiomata surrounded by brown setae up to 20 µm tall, 2.5–3 µm diam with obtuse ends. *Conidiophores* lining the inner cavity, hyaline, smooth, reduced to conidiogenous cells or a supporting cell, subcylindrical. *Conidiogenous cells* hyaline, smooth, ampulliform to subcylindrical, phialidic with periclinal thickening, 5–7 × 4–5 µm. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, subcylindrical to ellipsoid with obtusely rounded ends, 4–6 × 2–2.5 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 15–30 mm diam after 2 wk at 25 °C. On malt extract agar (MEA) surface sienna, reverse sienna to umber; on potato dextrose agar (PDA) surface and reverse olivaceous grey; on oatmeal agar (OA) surface olivaceous grey in centre, pale luteous in outer region.

Typus. South Africa, Northern Cape Province, Springbok, on *Aloe gariepensis* (*Aloaceae*), 28 Aug. 2021, *M.J. Wingfield*, HPC 3769 (holotype CBS H-24971; culture ex-type CPC 42456 = CBS 149069; ITS and LSU sequences GenBank OQ628467.1 and OQ629049.1; MycoBank MB 848054).

Additional isolate examined. South Africa, Northern Cape Province, Springbok, on leaves of *A. gariepensis*, Nov. 2018, *M.J. Wingfield*, HPC 3769 = CBS H-24963, culture CPC 42454 = CBS 149044, ITS and LSU sequences GenBank OQ628468.1 and OQ629050.1.

Colour illustrations. *Aloe gariepensis* growing near Springbok, South Africa. Branched conidial chains of hyphomycetous morph; coelomycetous synasexual morph; setae; conidiogenous cells giving rise to conidia; conidia. Scale bars = 250 µm (conidiomata), 10 µm (all others).

Notes — *Knufia* includes melanised ascomycetes that are commonly found in extreme environments, ranging from rock-inhabiting, lichenicolous fungi, opportunistic human pathogens, insect associates and plant pathogens (Isola et al. 2022). *Knufia aloeicola* is related to '*Phialocephala' fluminis* and *Knufia hypolithi* (Crous et al. 2021a), but is phylogenetically and morphologically distinct. Furthermore, '*Phialocephala' fluminis* is better accommodated in *Knufia* (also see Tanney & Seifert 2020), and hence a new combination is proposed below.

Knufia fluminis (Shearer et al.) Crous, *comb. nov.* — MycoBank MB 848055

Basionym. *Phialocephala fluminis* Shearer et al., Mycologia 68: 186. 1976.

Material examined. USA, Illinois, Macon County, Decatur, Sangamon River, submerged balsa wood, 15 Apr. 1975, *C.A. Shearer & J.L. Crane* (holotype ILLS 36160, culture ex-type ATCC 32105 = CBS 351.85).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 42454 had highest similarity to *Phialocephala fluminis* (strain CBS 351.85, GenBank MH861889.1; Identities = 549/559 (98 %), one gap (0 %)), *Knufia hypolithi* (strain CBS 146991, GenBank NR_173045.1; Identities = 545/568 (96 %), ten gaps (1 %)) and *Knufia tsunedae* (strain FMR 10621, GenBank NR_132842.1; Identities = 483/518 (93 %), 14 gaps (2 %)). The ITS sequence of CPC 42454 is identical to that of CPC 42456 (558/558 nucleotides). Closest hits using the **LSU** sequence of CPC 42454 are *Phialocephala fluminis* (strain CBS 351.85, GenBank MH873578.1; Identities = 749/754 (99 %), two gaps (0 %)), *Knufia hypolithi* (strain CBS 146991, GenBank NG_076736.1; Identities = 743/754 (99 %), no gaps) and *Knufia karalitana* (strain CCFEE 5656, GenBank NG_067535.1; Identities = 742/755 (98 %), two gaps (0 %)). The LSU sequence of CPC 42454 is identical to that of CPC 42456 (752/752 nucleotides).

Supplementary material

FP1479 Phylogenetic tree.

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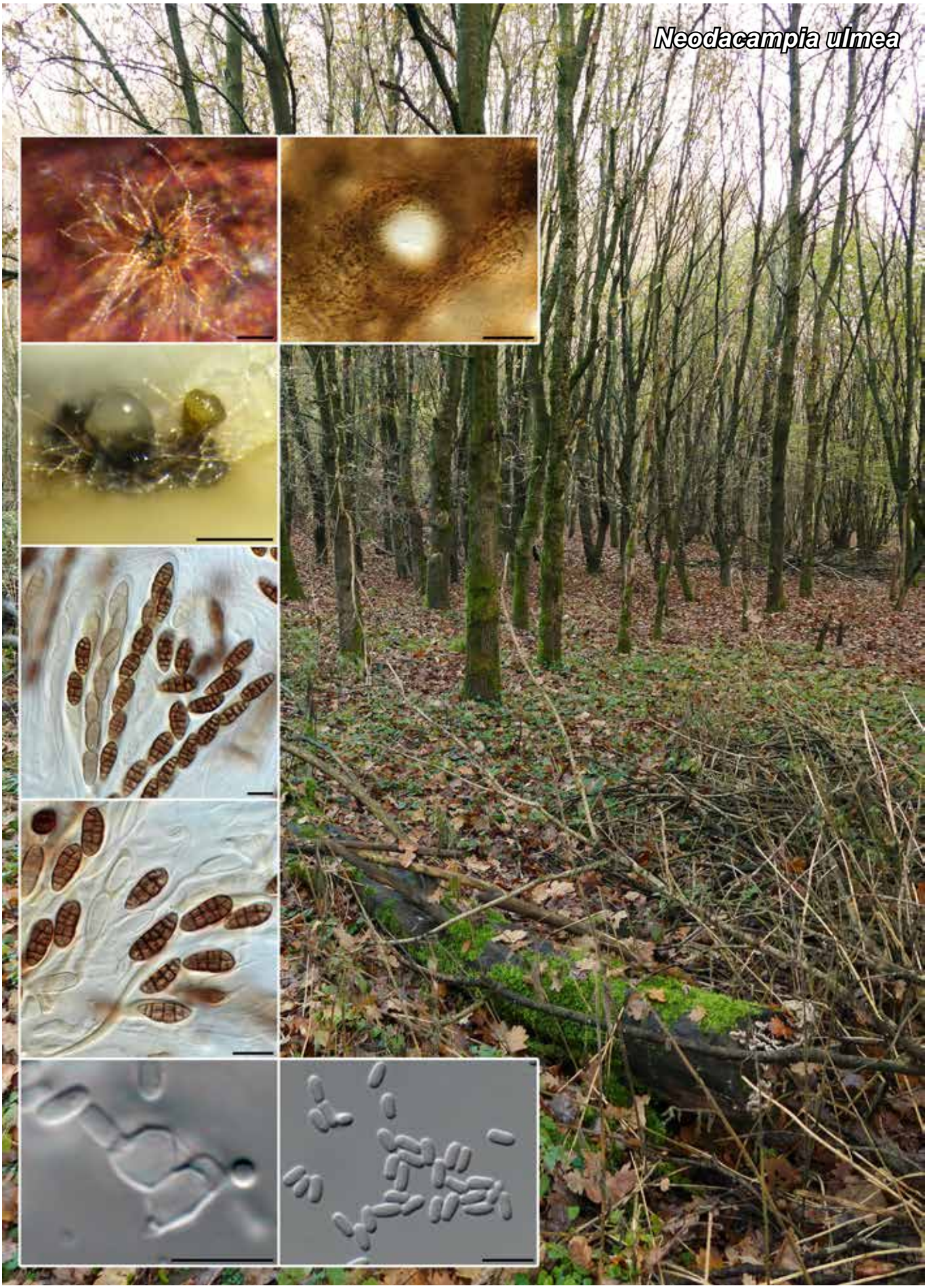
Neodacampia ulmea

Fungal Planet 1480 – 29 June 2023

Neodacampia Crous & Osieck, *gen. nov.*

Etymology. Name refers to its morphological similarity to *Dacampia*.

Classification — *Phaeosphaeriaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*.

Pseudothecia immersed, becoming erumpent, papillate, associated with red discolouration of wood, globose, brown; wall of 6–10 layers of brown *textura angularis*. *Pseudoparaphyses* hyphae-like, hyaline, smooth, branched, septate, intermingled among asci. *Asci* subcylindrical, bitunicate with apical chamber, 8-septate, stipitate with basal stalk. *Ascospores* overlapping, biseriate, fusoid-ellipsoid, brown, guttulate, smooth, muriformly septate, 3(–6) horizontal septa, constricted at primary median septum, with numerous vertical or oblique septa; mucoid sheath absent.

Type species. *Neodacampia ulmea* Crous & Osieck
MycoBank MB 848056

Neodacampia ulmea Crous & Osieck, *sp. nov.*

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

Pseudothecia immersed in host tissue, becoming erumpent, papillate, associated with red discolouration of wood, globose, brown, 300–350 µm diam; wall of 6–10 layers of brown *textura angularis*. *Pseudoparaphyses* hyphae-like, hyaline, smooth, branched, septate, 2–2.5 µm diam, intermingled among asci. *Asci* subcylindrical, bitunicate with apical chamber, 8-septate, stipitate with basal stalk, 100–140 × 10–13 µm. *Ascospores* overlapping, biseriate, fusoid-ellipsoid, brown, guttulate, smooth, muriformly septate, 3(–6) horizontal septa, constricted at primary median septum, less at secondary septa, with 0–2 vertical or oblique septa (also occurring in end cells), 2nd cell often enlarged, end cells obtuse; mucoid sheath absent, (14–)15–17(–18) × (6.5–)7(–7.5) µm. In culture forming spermatogonia similar to ascomata in anatomy; *spermatia* hyaline, smooth, aseptate, guttulate, 3.5–5 × 2 µm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, lobate margin, reaching 40–45 mm diam after 2 wk at 25 °C. On malt extract agar (MEA) surface olivaceous grey, reverse smoke grey in centre, olivaceous grey in outer region; on potato dextrose agar (PDA) surface and reverse amber in centre, red in outer region; on oatmeal agar (OA) surface umber.

Typus. Netherlands, Utrecht Province, Nieuw Wulven, near Houten, 1.5 m a.s.l., N52°02'56" E05°09'58", on branch of *Ulmus laevis* (*Ulmaceae*), 31 Dec. 2021, *E.R. Osieck*, HPC 3813 = WI-43/#4367 (XVIII-26) (holotype CBS H-25165; culture ex-type CPC 42680 = CBS 149452; ITS, LSU, SSU, *rpb2* (first part) and *tef1* (second part) sequences GenBank OQ628469.1, OQ629051.1, OQ628447.1, OQ627936.1 and OQ627956.1; MycoBank MB 848057).

Notes — *Neodacampia* resembles the lichenicolous *Dacampia* (*Dacampiaceae*; Ertz et al. 2015), but is more closely related to the asexual *Banksiophoma* (*Phaeosphaeriaceae*; Crous et al. 2017a). *Neodacampia,* which is monotypic based on *N. ulmea*, is associated with a red discolouration of wood on which solitary pseudothecia occur, characterised by pseudoparaphyses, and muriformly septate ascospores that lack a sheath, and for which no asexual morph was observed in culture. The asexual morph, if found, would likely be phoma-like, given its close association to *Banksiophoma*. The taxonomic placement of this wood saprobe in *Phaeosphaeriaceae* was quite unexpected since members of this family occur mostly on monocotyledons (Jaklitsch et al. 2016).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to '*Phaeosphaeria*' sp. (strain G330, GenBank KR094442.1; Identities = 495/503 (98 %), no gaps), *Septoriella hibernica* (strain CBS 145371, GenBank NR_164460.1; Identities = 415/455 (91 %), 12 gaps (2 %)) and *Septoriella allojunci* (strain MFLUCC 15-0701, GenBank KU058718.1; Identities = 415/454 (91 %), 15 gaps (3 %)). Closest hits using the **LSU** sequence are *Didymocyrtis brachylaenae* (strain CPC 32651, GenBank NG_067827.1; Identities = 826/836 (99 %), one gap (0 %)), *Diederichomyces cladoniicola* (strain UTHSC DI16-313, GenBank LN907456.1; Identities = 825/836 (99 %), one gap (0 %)) and *Neosulcatispora agaves* (strain CPC 26407, GenBank KT950867.1; Identities = 824/836 (99 %), one gap (0 %)). Closest hits using the **SSU** sequence are *Coniothyrium concentricum* (strain CBS 589.79, GenBank EU754053.1; Identities = 1006/1006 (100 %), no gaps), *Parastagonospora uniseptata* (strain MFLUCC 13-0387, GenBank NG_063666.1; Identities = 1007/1008 (99 %), one gap (0 %)) and *Wojnowicia dactylidicola* (strain MFLUCC 13-0738, GenBank NG_063564.1; Identities = 1007/1008 (99 %), one gap (0 %)). Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Banksiophoma australiensis* (strain CBS 142163, GenBank KY979846.1; Identities = 668/794 (84 %), no gaps), *Brunneomurispora lonicerae* (strain KUMCC 18-0157, GenBank MK359079.1; Identities = 714/856 (83 %), four gaps (0 %)) and *Septoriella callistemonis* (strain CPC 38761, GenBank MZ078194.1; Identities = 721/874 (82 %), 14 gaps (1 %)). Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Didymocyrtis cladoniicola* (strain UTHSC DI16-313, GenBank LT797117.1; Identities = 787/819 (96 %), no gaps), *Phaeosphaeria sinensis* (strain MFLUCC 18-1552, GenBank MK360072.1; Identities = 778/810 (96 %), no gaps) and *Paraphoma radicina* (strain 17chuncheon01-04, GenBank MT946675.1; Identities = 765/798 (96 %), no gaps).

Colour illustrations. *Ulmus laevis* at Nieuw Wulven, near Houten in Utrecht Province, the Netherlands. Ascoma on wood, with red discolouration; ostiole; conidiomata in culture; asci and ascospores; conidiogenous cells giving rise to conidia; conidia. Scale bars = 300 µm (ascomata and conidiomata), 10 µm (all others).

Supplementary material

FP1480 Phylogenetic tree.

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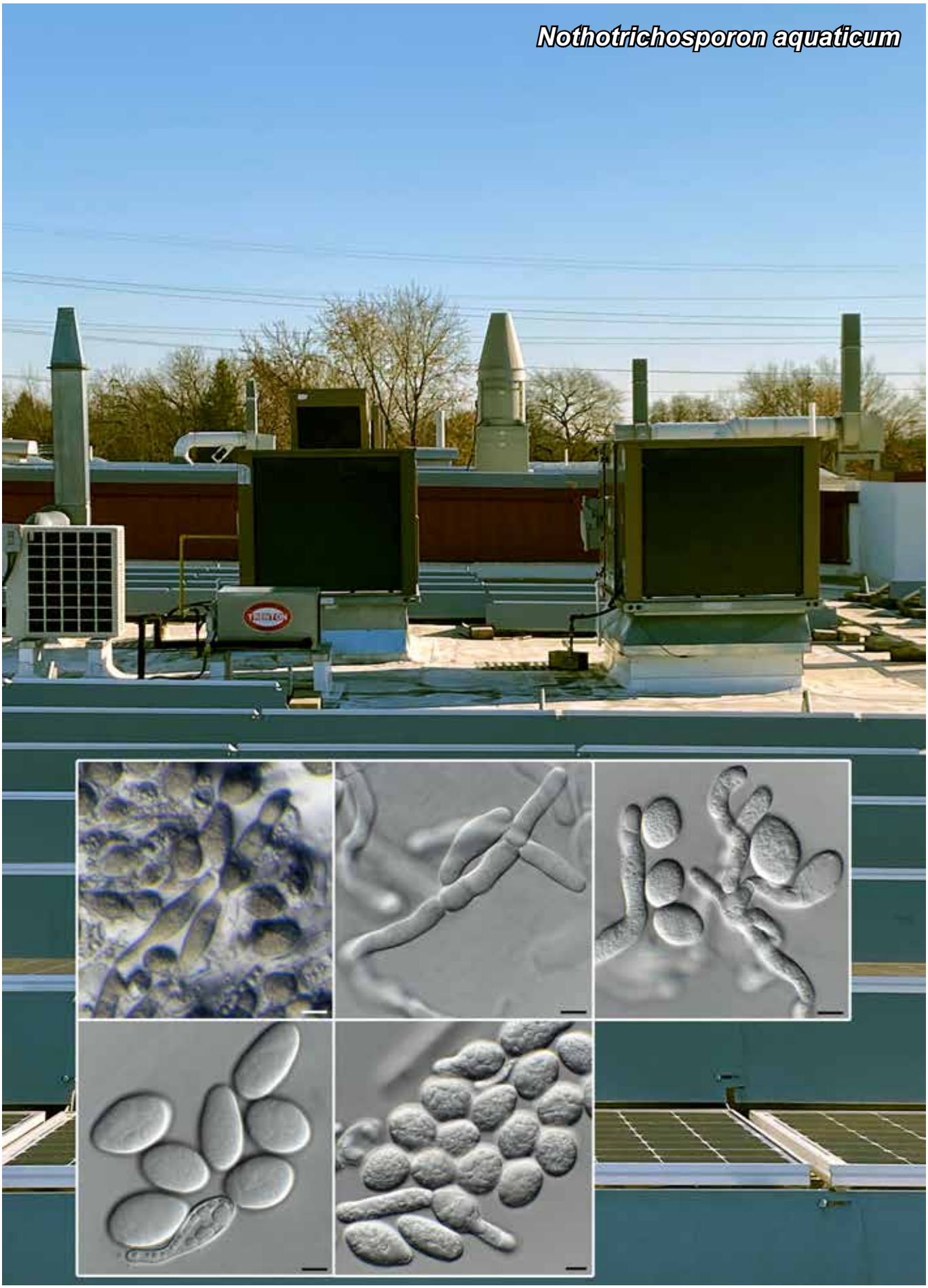
Nothotrichosporon aquaticum

Fungal Planet 1481 – 29 June 2023

Nothotrichosporon Crous, M. Groenew. & Jurjević, *gen. nov.*

Etymology. Name refers to the fact that it is distinct from *Trichosporon*.

Classification — *Trichosporonaceae*, *Trichosporonales*, *Tremellomycetes*.

Mycelium consisting of hyaline, smooth, thin-walled, sparsely septate, rarely branched hyphae, disarticulating into subcylindrical arthroconidia, and budding to form ellipsoid conidia. *Arthroconidia* hyaline, smooth, guttulate, thin-walled, subcylindrical, ends become obtuse. *Secondary conidia* hyaline, smooth, guttulate, thin-walled, ellipsoid.

Type species. *Nothotrichosporon aquaticum* Crous, M. Groenew. & Jurjević
MycoBank MB 848058

Nothotrichosporon aquaticum Crous, M. Groenew. & Jurjević, *sp. nov.*

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

Mycelium consisting of hyaline, smooth, thin-walled, sparsely septate, rarely branched hyphae, 4–8 µm diam, disarticulating into subcylindrical arthroconidia, and budding to form ellipsoid conidia. *Arthroconidia* hyaline, smooth, guttulate, thin-walled, subcylindrical, ends become obtuse, 35–55 × 12–17 µm. *Secondary conidia* hyaline, smooth, guttulate, thin-walled, ellipsoid, (22–)28–32(–35) × (17–)19–20(–22) µm.

All physiological growth tests were done at 24 °C for a period of 10 d. Assimilation tests were performed using the ID 32 C identification system for yeasts (bioMérieux SA).

Fermentation — Glucose is fermented.

Carbon assimilation — D-glucose, D-galactose (w), cycloheximide, sucrose, lactic acid, D-cellobiose, D-maltose, D-trehalose, 2-keto-D-gluconate, a-methyl-D-glucoside (delayed), D-mannitol, myo-inositol, D-sorbitol, D-xylose, D-ribose, glycerol, meso-erythritol, sodium glucoronate, D-melezitose, potassium gluconate, L-sorbose (delayed), are assimilated. N-acetyl-glucosamine, L-arabinose, D-raffinose, D-lactose, L-rhamnose, D-melibiose, D-glucosamine, are not assimilated.

Nitrogen assimilation — ethylamine, L-lysine, cadaverine are assimilated. Nitrate, nitrite, D-glucosamine HCl, tryptophane, pepton are not assimilated.

Other tests — Growth in 0.01 % cycloheximide is positive. Growth at 15 °C, 24 °C, 30 °C is positive. Growth at 37 °C is negative. Growth in 50 % glucose is negative.

Culture characteristics — Colonies flat, spreading, sectoring, folded, with sparse aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On malt extract agar (MEA), potato dextrose agar (PDA) and oatmeal agar (OA) surface and reverse dirty white.

Typus. USA, Louisiana, Abbeville, pen water, Oct. 2021, *Ž. Jurjević* 5667 (holotype CBS H- 25224; culture ex-type CPC 42870 = CBS 18113; ITS and LSU sequences GenBank OQ628470.1 and OQ629052.1; MycoBank MB 848059).

Notes — *Effuseotrichosporon* was described for a single-species lineage formed by *Trichosporon vanderwaltii* in *Trichosporonaceae*, and characterised by true hyphae that disarticulate into arthroconidia. The present collection is related to *Effuseotrichosporon* based on ITS blast searches, although phylogenetically distinct, and therefore accommodated in the new genus, *Nothotrichosporon.*

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Effuseotrichosporon vanderwaltii* (strain CBS 12124, GenBank NR_153975.1; Identities = 459/485 (95 %), 12 gaps (2 %)), *Prillingera fragicola* (strain JCM 1530, GenBank NR_136945.1; Identities = 423/450 (94 %), 11 gaps (2 %)) and *Apiotrichum gamsii* (strain CBS 8245, GenBank NR_073247.1; Identities = 452/483 (94 %), six gaps (1 %)). Closest hits using the **LSU** sequence are *Vanrija humicola* (strain CBS 571, GenBank KY110010.1; Identities = 824/858 (96 %), six gaps (0 %)), *Apiotrichum scarabaeorum* (strain CBS 5601, GenBank NG_057009.1; Identities = 810/845 (96 %), one gap (0 %)) and *Aegeritella tuberculata* (strain WA51216, GenBank KT380846.1; Identities = 772/802 (96 %), three gaps (0 %)).

Colour illustrations. Collection site near Abbeville, Louisiana, USA. Colony on synthetic nutrient-poor agar; hyphae giving rise to arthroconidia and secondary conidia. Scale bars = 10 µm.

Supplementary material

FP1481 Phylogenetic tree.

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Xenoidriella cinnamomi

Fungal Planet 1482 – 29 June 2023

Xenoidriella Crous, *gen. nov.*

Etymology. Name refers to its morphological similarity to *Idriella*.

Classification — *Microdochiaceae*, *Xylariales*, *Xylariomycetidae*, *Sordariomycetes*.

Mycelium consisting of pale brown, smooth, branched, septate hyphae. *Conidiophores* solitary, arising from superficial hyphae, medium brown, thick-walled, smooth, subcylindrical, flexuous, 1–6-septate. *Conidiogenous cells* terminal, integrated, brown, smooth, forming a rachis of denticulate loci, not thickened nor darkened. *Conidia* solitary, hyaline, smooth, guttulate, fusoid, medianly 1-septate, tapering towards subacutely rounded apex and truncate hilum.

Type species. *Xenoidriella cinnamomi* Crous
MycoBank MB 848060.

Xenoidriella cinnamomi Crous, *sp. nov.*

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

Mycelium consisting of pale brown, smooth, branched, septate, 2–3.5 µm diam hyphae. *Conidiophores* solitary, arising from superficial hyphae, medium brown, thick-walled, smooth, subcylindrical, flexuous, 1–6-septate, 40–120 × 4–6 µm. *Conidiogenous cells* terminal, integrated, 20–40 × 3–4 µm, brown, smooth, forming a rachis of denticulate loci, 0.5–1 × 1 µm, not thickened nor darkened. *Conidia* solitary, hyaline, smooth, guttulate, fusoid, medianly 1-septate, tapering towards subacutely rounded apex and truncate hilum, 1 µm diam, (20–)23–27(–30) × (2.5–)3 µm.

Culture characteristics — Colonies erumpent, spreading, with sparse to moderate aerial mycelium and smooth, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On malt extract agar (MEA), potato dextrose agar (PDA) and oatmeal agar (OA) surface and reverse umber.

Typus. South Africa, Western Cape Province, Cape Town, on leaf of *Cinnamomum camphora* (*Lauraceae*), 27 Feb. 2022, *P.W. Crous*, HPC 3839 (holotype CBS H-25173; culture ex-type CPC 43130 = CBS 149458; ITS, LSU, SSU, *rpb2* (first part) and *tef1* (second part) sequences GenBank OQ628471.1, OQ629053.1, OQ628448.1, OQ627937.1 and OQ627957.1; MycoBank MB 848061).

Notes — *Xenoidriella cinnamomi* is related to *Neoidriella desertorum* CBS 985.72 (Hernández-Restrepo et al. 2016a), *Guayaquilia cubensis* and the appendaged coelomycete *Ciliosporella italica*. Morphologically *X. cinnamomi* is distinct from *N. desertorum* in having 1-septate conidia, and lacking chlamydospores. Furthermore, it is distinct from *Guayaquilia*, which is characterised by having macronematous, tree-like conidiophores, (0–)1-septate navicular conidia, and thick-walled, 1-septate, brown chlamydospores (Magdama et al. 2020).

Closest hits using the **ITS** sequence of CPC 43130 are *Monographella* sp. (strain HGGJ-16, GenBank KR708990.1; Identities = 365/400 (91 %), seven gaps (1 %)), *Guayaquilia cubensis* (strain SG1001, GenBank OP380877.1; Identities = 378/420 (90 %), 13 gaps (3 %)) and *Ciliosporella italica* (strain MFLUCC 16-1146, GenBank NR_169717.1; Identities = 465/519 (90 %), 26 gaps (5 %)). Closest hits using the **LSU** sequence of CPC 43130 are *Ciliosporella italica* (strain MFLUCC 16-1146, GenBank NG_073833.1; Identities = 763/789 (97 %), three gaps (0 %)), *Selenodriella fertilis* (strain CBS 148328, GenBank ON400824.1; Identities = 758/786 (96 %), one gap (0 %)) and *Idriella cubensis* (strain MUCL 39017, GenBank KC775708.1; Identities = 758/790 (96 %), five gaps (0 %)). Closest hits using the **SSU** sequence of CPC 43130 are *Pirozynskiomyces sinensis* (no strain number supplied, GenBank KY994108.1; Identities = 932/956 (97 %), no gaps), *Arthrinium japonicum* (strain IFO 30500, GenBank AB220211.1; Identities = 932/956 (97 %), no gaps) and *Xenoanthostomella calami* (as *Xenoanthostomella* sp. SK-2022a, strain MFLUCC 14-0617B, GenBank ON650709.1; Identities = 932/957 (97 %), two gaps (0 %)). Closest hits using the ***rpb2*** (first part) sequence of CPC 43130 had highest similarity to *Biscogniauxia arima* (voucher 122, GenBank GQ304736.1; Identities = 641/818 (78 %), six gaps (0 %)), *Peroneutypa scoparia* (strain MFLUCC 11-0478, GenBank KU940179.1; Identities = 641/823 (78 %), 19 gaps (2 %)) and *Kretzschmaria pavimentosa* (voucher 109, GenBank GQ844787.1; Identities = 641/827 (78 %), ten gaps (1 %)). Distant hits obtained using the ***tef1*** (second part) sequence of CPC 43130 had highest similarity to *Microdochium trichocladiopsis* (strain MPI-CAGE-CH-0230, GenBank XM_046152772.1; Identities = 736/802 (92 %), no gaps), *Microdochium chrysanthemoides* (strain LC5466, GenBank KX855236.1; Identities = 731/802 (91 %), no gaps) and *Xenoanthostomella chromolaenae* (strain MFLUCC 17-1484, GenBank MN648732.1; Identities = 701/773 (91 %), no gaps).

Colour illustrations. *Cinnamomum camphora* growing near Cape Town, South Africa. Conidiophores and conidiogenous cells giving rise to conidia on pine needle agar; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Supplementary material

FP1482 Phylogenetic tree.

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Paraloratospora schoenoplecti

Fungal Planet 1483 – 29 June 2023

Paraloratospora schoenoplecti Crous, *sp. nov.*

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

Classification — *Phaeosphaeriaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*.

Ascomata immersed in bleached white areas on culms, becoming erumpent, globose, brown, 200–300 µm diam with central ostiole, 15–20 µm diam; wall of 3–5 layers of brown *textura angularis. Pseudoparaphyses* intermingled among asci, hyphae-like, hyaline, smooth, branched, septate, 2.5–3 µm diam. *Asci* fusoid-ellipsoid, bitunicate, 8-spored with ocular chamber, stipitate, fasciculate, 70–80 × 11–13 µm. *Ascospores* tri- to multiseriate, fusoid, medium brown, smooth, guttulate, 3-septate, slightly constricted at septa, second cell from the apex slightly swollen, (22–)25–28(–30) × (3–)3.5(–5) µm. Ascospores shot onto agar brown, germinating from multiple cells, in irregular direction, constricted at septa, 4–5 µm diam. Cultures homothallic, also forming sexual morph in culture.

Culture characteristics — Colonies flat to erumpent, spreading, with moderate aerial mycelium and feathery, lobate margin, reaching 40 mm diam after 2 wk at 25 °C. On malt extract agar (MEA) surface and reverse olivaceous grey; on potato dextrose agar (PDA) surface pale olivaceous grey, reverse olivaceous grey; on oatmeal agar (OA) surface saffron to pale luteous.

Typus. South Africa, Western Cape Province, Cape Town, on stems of *Schoenoplectus lacustris* (*Cyperaceae*), 6 Mar. 2022, *P.W. Crous*, HPC 3844 (holotype CBS H-25175; culture ex-type CPC 43149 = CBS 149459; ITS, LSU, *rpb2* (first part), *tef1* (first part) and *tub2* sequences GenBank OQ628472.1, OQ629054.1, OQ627938.1, OQ627947.1 and OQ627960.1; MycoBank MB 848062).

Notes — *Paraloratospora schoenoplecti* clusters with *Pa. gahniae,* but has longer ascospores, and is phylogenetically distinct. *Paraloratospora*, based on *Pa. camporesii*, is characterised as being phaeosphaeria-like and having hyaline to pale brown, fusoid to ellipsoidal, septate ascospores, the second cell from the apex swollen, smooth-walled, with or without a mucilaginous sheath (Hyde et al. 2020). *Paraloratospora* is presently known to accommodate two species, *Pa. camporesii* (ascospores 3-septate, 20–24 × 3–5 µm) and *Pa. gahniae* (ascospores 3(–4)-septate, (18–)20–22(–25) × (4.5–)5 µm; Crous et al. 2017b). *Paraloratospora* represents a distinct clade in the *Phaeosphaeriaceae*, and several other taxa accommodated in *Phaeosphaeria* will have to be allocated to it.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Paraloratospora gahniae* (strain CPC 32454, GenBank NR_156675.1; Identities = 545/562 (97 %), four gaps (0 %)), *Phaeosphaeria norfolcia* (strain CBS 593.86, GenBank MH861997.1; Identities = 487/527 (92 %), two gaps (0 %)) and *Phaeosphaeria caricicola* (strain CBS 603.86, GenBank KF251182.1; Identities = 515/566 (91 %), 11 gaps (1 %)). Closest hits using the **LSU** sequence are *Paraloratospora gahniae* (strain CPC 32454, GenBank NG_059852.1; Identities = 806/806 (100 %), no gaps), *Phaeosphaeria caricicola* (strain CBS 133078, GenBank MH877523.1; Identities = 804/806 (99 %), no gaps) and *Phaeosphaeria glyceriae-plicatae* (strain CBS 101261, GenBank MH874330.1; Identities = 804/806 (99 %), no gaps). Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Paraloratospora gahniae* (strain CPC 32454, GenBank MG386148.1; Identities = 739/768 (96 %), no gaps), *Septoriella callistemonis* (strain CPC 38761, GenBank MZ078194.1; Identities = 653/820 (80 %), eight gaps (0 %)) and *Paraphoma fimeti* (strain UTHSC DI16-296, GenBank LT797032.1; Identities = 653/821 (80 %), eight gaps (0 %)). The best hit using the ***tef1*** (first part) sequence had highest similarity to *Paraloratospora gahniae* (strain CPC 32454 (GenBank MG386157.1; Identities = 245/290 (84 %), three gaps (1 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Paraloratospora gahniae* (strain CPC 32454, GenBank MG386170.1; Identities = 286/298 (96 %), one gap (0 %)), *Dothidotthia robiniae* (strain MFLUCC 16-1185, GenBank MK933788.1; Identities = 266/301 (88 %), 14 gaps (4 %)) and *Phaeosphaeria caricicola* (strain CBS 603.86, GenBank KF252676.1; Identities = 264/300 (88 %), five gaps (1 %)).

Colour illustrations. *Schoenoplectus lacustris* growing near Cape Town, South Africa. Ascomata forming on pine needle agar; ascoma with ostiole; asci with ascospores and pseudoparaphyses; germinating ascospores. Scale bars = 150 µm (ascoma), 10 µm (all others).

Supplementary material

See the supplementary material FP1480 for a phylogenetic tree containing this novel species.

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Alfaria thamnochorti

Fungal Planet 1484 – 29 June 2023

Alfaria thamnochorti Crous, *sp. nov.*

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

Classification — *Stachybotryaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*.

Conidiomata sporodochial, globose, brown, 80–100 µm diam; wall of 3–4 layers of pale brown *textura intricata* to *angularis*. *Conidiogenous cells* lining inner cavity, subcylindrical, pale brown, smooth, 10–25 × 2–3 µm, proliferating inconspicuously percurrently at apex. *Conidia* cylindrical, guttulate, straight to flexuous, smooth, pale to dark brown (depending on agar medium), apex obtuse, base truncate, aseptate, (25–)30–45(–50) × 2(–3) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and feathery, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On malt extract agar (MEA) surface saffron, reverse sienna; on potato dextrose agar (PDA) surface saffron, reverse ochreous; on oatmeal agar (OA) surface saffron.

Typus. South Africa, Western Cape Province, Cape Town, on culm of *Thamnochortus fraternus* (*Restionaceae*), 6 Mar. 2022, *P.W. Crous*, HPC 3848 (holotype CBS H-25176; culture ex-type CPC 43155 = CBS 149460; ITS, LSU, *rpb2* (first part), *tef1* (first part) and *tub2* sequences GenBank OQ628473.1, OQ629055.1, OQ627939.1, OQ627948.1 and OQ627961.1; MycoBank MB 848063).

Notes — *Alfaria* was introduced by Crous et al. (2014) for a sexual genus associated with leaf apical necrosis of *Cyperus esculentus*, and later shown to have microthyrium-like asexual morphs. *Alfaria thamnochorti* is placed basal to a lineage containing amongst others *A. terrestris* (conidia fusoid, 6–8 × 2–3 µm), *A. ossiformis* (conidia ossiform to ellipsoid, (5–)6–7 × 2–3 µm; Lombard et al. 2016), and *A. junci* (conidia subcylindrical, (10–)11–12(–13) × 2(–2.5) µm; Crous et al. 2021c), but is distinct in having much larger conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Alfaria terrestris* (strain F9(NSA3&NLC2), GenBank MW301193.1; Identities = 505/519 (97 %), six gaps (1 %)), *Alfaria ossiformis* (strain CBS 324.54, GenBank NR_145068.1; Identities = 502/516 (97 %), two gaps (0 %)) and *Myrothecium gramineum* (strain CBS 324.54, GenBank AY254151.1; Identities = 502/516 (97 %), two gaps (0 %)). Closest hits using the **LSU** sequence are *Alfaria terrestris* (strain CBS 168.97, GenBank KU845996.1; Identities = 811/813 (99 %), no gaps), *Alfaria dandenongensis* (strain CBS 143399, GenBank NG_069537.1; Identities = 810/813 (99 %), no gaps) and *Amerosporium atrum* (strain CBS 151.69, GenBank MH877704.1; Identities = 810/813 (99 %), no gaps). Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Alfaria dandenongensis* (strain CBS 143399, GenBank MG386146.1; Identities = 771/818 (94 %), no gaps), *Alfaria ossiformis* (strain CBS 324.54, GenBank KU846002.1; Identities = 677/724 (94 %), no gaps) and *Alfaria humicola* (strain ZSY10, GenBank MH818829.1; Identities = 673/724 (93 %), no gaps). Closest hits using the ***tef1*** (first part) sequence had highest similarity to *Alfaria terrestris* (strain CBS 127305, GenBank KU846012.1; Identities = 298/345 (86 %), 12 gaps (3 %)), *Alfaria ossiformis* (strain CBS 324.54, GenBank KU846009.1; Identities = 333/396 (84 %), 16 gaps (4 %)) and *Alfaria acaciae* (strain CBS 143504, GenBank MH108012.1; Identities = 322/387 (83 %), 31 gaps (8 %)). The best hit using the ***tub2*** sequence had highest similarity to *Alfaria tabebuiae* (strain CBS 145066, GenBank MK047579.1; Identities = 471/551 (85 %), 25 gaps (4 %)).

Colour illustrations. Culm of *Thamnochortus fraternus* growing in Cape Town, South Africa. Conidiomata forming on oatmeal agar; conidiogenous cells giving rise to conidia; conidia. Scale bars = 50 µm (conidiomata), 10 µm (all others).

Supplementary material

FP1484 Phylogenetic tree.

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Neodevriesia scadoxi

Fungal Planet 1485 – 29 June 2023

Neodevriesia scadoxi Crous, *sp. nov.*

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

Classification — *Neodevriesiaceae*, *Mycosphaerellales*, *Dothideomycetidae*, *Dothideomycetes*.

Conidiomata pycnidial, solitary or gregarious, globose, 30–90 µm diam with central ostiole; wall of 2–3 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining inner cavity, ampulliform, hyaline, smooth, phialidic, 4–5 × 3–4 µm. *Conidia* solitary, hyaline, smooth, subcylindrical with obtuse ends, aseptate, rarely 1-septate in older conidia, 3–5 × 1.5–2 µm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with sparse aerial mycelium and smooth, lobate margin, reaching 6 mm diam after 2 wk at 25 °C. On malt extract agar (MEA), potato dextrose agar (PDA) and oatmeal agar (OA) surface and reverse fuscous black.

Typus. South Africa, Western Cape Province, Cape Town, on leaves of *Scadoxus puniceus* (*Amaryllidaceae*), 27 Feb. 2022, *P.W. Crous*, HPC 3851 (holotype CBS H-25177; culture ex-type CPC 43161 = CBS 149461; ITS, LSU, *rpb2* (first part) and *tub2* sequences GenBank OQ628474.1, OQ629056.1, OQ627940.1 and OQ627962.1; MycoBank MB 848064).

Notes — *Neodevriesia* is a cladosporium-like genus including species that are foliicolous, saprobic or plant pathogenic (Quaedvlieg et al. 2014). *Neodevriesia scadoxi* is allied to other species of *Neodevriesia*, and probably represents a synasexual morph, given the fact that it has a phoma-like morphology.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Recurvomyces* sp. (strain CR18, GenBank KY111910.1; Identities = 473/476 (99 %), one gap (0 %)), *Neodevriesia bulbillosa* (strain CBS 118285, GenBank NR_144953.1; Identities = 484/500 (97 %), seven gaps (1 %)) and *Neodevriesia lagerstroemiae* (strain CBS 125422, GenBank MH863701.1; Identities = 480/522 (92 %), 18 gaps (3 %)). Closest hits using the **LSU** sequence are *Neodevriesia bulbillosa* (strain CBS 118285, GenBank KF310029.1; Identities = 742/747 (99 %), one gap (0 %)), *Neodevriesia strelitziicola* (strain CPC 37387, GenBank MN567651.1; Identities = 788/807 (98 %), four gaps (0 %)) and *Neodevriesia kalakoutskii* (strain VKM F-4872, GenBank MZ025963.1; Identities = 800/820 (98 %), four gaps (0 %)). The best hit using the ***rpb2*** (first part) sequence had highest similarity to *Capnodiales* sp. (strain CBS 118346, GenBank GU371752.1; Identities = 665/738 (90 %), no gaps). Closest hits using the ***tub2*** sequence had highest similarity to *Neodevriesia bulbillosa* (strain TRN81, GenBank KF546782.1; Identities = 388/398 (97 %), two gaps (0 %)), *Petrophila incerta* (strain TRN139b, GenBank KF546769.1; Identities = 300/371 (81 %), 16 gaps (4 %)) and *Teratosphaeria ohnowa* (strain CBS 112896, GenBank KF442464.1; Identities = 284/352 (81 %), 20 gaps (5 %)).

Colour illustrations. *Scadoxus puniceus* growing at Cape Town, South Africa. Conidiomata forming on synthetic-nutrient-poor agar; conidiogenous cells giving rise to conidia; conidia. Scale bars = 90 µm (conidiomata), 10 µm (all others).

Supplementary material

FP1485 Phylogenetic tree.

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Neocladosporium arctotis

Fungal Planet 1486 – 29 June 2023

Neocladosporium arctotis Crous, *sp. nov.*

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

Classification — *Cladosporiaceae*, *Cladosporiales*, *Dothideomycetidae*, *Dothideomycetes*.

Ascomata (in vivo) pseudothecial, brown, erumpent, globose, slightly papillate, 60–90 µm diam with central ostiole, 10–15 µm diam; wall of 3–4 layers of brown *textura angularis*. *Pseudothecia* linked via a network of superficial brown hyphae on host tissue. *Asci* fasciculate, stipitate, 8-spored, bitunicate, broadly ellipsoid, with ocular chamber, 37–45 × 13–17 µm. *Ascospores* multiseriate, guttulate with angular inclusions, hyaline, smooth, thick-walled, with thin sheath covering spore, not constricted at submedian septum (apical cell 1 µm longer than basal cell), (13–)15–16 × 5(–6) µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On malt extract agar (MEA) surface olivaceous grey, reverse iron grey; on potato dextrose agar (PDA) surface and reverse olivaceous grey; on oatmeal agar (OA) surface pale olivaceous grey (cultures sterile).

Typus. South Africa, Northern Cape Province, Springbok, on nest of cases of bag worm moths (*Lepidoptera, Psychidae*) on *Arctotis auriculata* (*Asteraceae*), 2 Sept. 2021, *M.J. Wingfield*, HPC 3750 (holotype CBS H-25162; culture ex-type CPC 42433 = CBS 149508; ITS and LSU sequences GenBank OQ628475.1 and OQ629057.1; MycoBank MB 848065).

Notes — The mycosphaerella-like morphology, and ascospores with angular inclusions, directly point to the *Davidiella* sexual morphs of cladosporium-like taxa (Aptroot 2006, Bensch et al. 2012). This is the first sexual morph reported for a species of *Neocladosporium*, being closely related to the asexual species *N. syringae* and *N. osteospermi* (Crous et al. 2020a, b).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neocladosporium syringae* (strain CPC 35750, GenBank NR_170057.1; Identities = 520/540 (96 %), two gaps (0 %)), *Neocladosporium osteospermi* (strain CBS 146813, GenBank NR_171766.1; Identities = 525/551 (95 %), 12 gaps (2 %)) and *Davidiellomyces australiensis* (strain CBS 142165, GenBank NR_154036.1; Identities = 501/543 (92 %), 16 gaps (2 %)). Closest hits using the **LSU** sequence are *Neocladosporium syringae* (strain CPC 35750, GenBank NG_074421.1; Identities = 813/817 (99 %), one gap (0 %)), *Neocladosporium osteospermi* (strain CBS 146813, GenBank NG_074494.1; Identities = 800/805 (99 %), no gaps) and *Neocladosporium leucadendri* (strain CBS 131317, GenBank NG_057949.1; Identities = 836/844 (99 %), no gaps).

Colour illustrations. *Arctotis auriculata* growing at Springbok, South Africa. Ascomata in host tissue; ascoma; asci and ascospores; ascospores with angular inclusions. Scale bars = 90 µm (ascomata), 45 µm (ascoma), 10 µm (all others).

Supplementary material

FP1486 Phylogenetic tree.

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Xenosphaeropsis corni

Fungal Planet 1487 – 29 June 2023

Xenosphaeropsis corni Crous & Akulov, *sp. nov.*

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

Classification — *Phacidiaceae*, *Phacidiales*, *Leotiomycetes*.

Conidiomata on dead stems immersed, subepidermal, dark brown, pycnidial, globose, 250–300 µm diam with central ostiole; wall of 6–8 layers of brown *textura angularis*. Description on OA: *Conidiophores* subcylindrical, hyaline, smooth, branched at base or reduced to conidiogenous cells, 15–22 × 5–8 µm. *Conidiogenous cells* ampulliform to subcylindrical, hyaline, smooth, proliferating percurrently at apex, 10–17 × 5–8 µm. *Conidia* solitary, aseptate, median to golden brown, finely roughened, prominently thick-walled, ellipsoid, apex subobtuse, base truncate, 2 µm diam, at times with marginal frill, (10–)12–13(–15) × 7–8(–9) µm.

Culture characteristics — Colonies flat, spreading, growing in concentric circles, with moderate aerial mycelium and smooth, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On malt extract agar (MEA) surface and reverse saffron; on potato dextrose agar (PDA) surface ochreous, reverse umber; on oatmeal agar (OA) surface saffron.

Typus. Ukraine, Kharkiv region, artificial decorative growth near the main building of V.N. Karazin National University of Kharkiv, on recently dead stem of *Cornus alba* (*Cornaceae*), 22 Aug. 2021, *A. Akulov*, HPC 3747, CWU (Myc) AS 8240 (holotype CBS H-25160; culture ex-type CPC 42402 = CBS 149511; ITS, LSU, *rpb2* (first part), *tef1* (first part) and *tub2* sequences GenBank OQ628476.1, OQ629058.1, OQ627941.1, OQ627949.1 and OQ627963.1; MycoBank MB 848066).

Colour illustrations. The photo depicts the main building of V.N. Karazin National University of Kharkiv, near which the type specimen was collected. Conidiomata on host tissue; conidiomata on oatmeal agar; conidiogenous cells giving rise to conidia; conidia. Scale bars: conidiomata = 300 µm, all others = 10 µm.

Notes — *Xenosphaeropsis corni* is related to *X. pyriputrescens* (*Phacidiaceae*), the causal agent of stem-end rot, calyx-end rot and wound-associated rot on *Pyrus communis* fruit in the USA (Xiao & Rogers 2004). It is distinct in that *X. pyriputrescens* has larger conidia that are clavate, ovoid, subglobose to ellipsoidal, 10–19.5 × 7.5–13.5 µm (Zhao et al. 2021).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Allantophomopsis cytisporea* (strain A_DA_21_15, GenBank MK790134.1; Identities = 471/480 (98 %), one gap (0 %)), *Allantophomopsis* sp. 1(strain CBS 322.36, GenBank KJ663839.2; Identities = 490/501 (98 %), two gaps (0 %)) and *Allantophomopsis lunata* (strain CBS 137781, GenBank NR_132922.1; Identities = 489/501 (98 %), two gaps (0 %)). Closest hits using the **LSU** sequence are *Allantophomopsis* sp. 2 (strain CPC 24280, GenBank KR873265.1; Identities = 826/833 (99 %), no gaps), *Bacilliformis hyalinus* (voucher MFLU 18-2671, GenBank NG_068618.1; Identities = 840/848 (99 %), one gap (0 %)) and *Allantophomopsiella pseudotsugae* (strain CBS 437.71, GenBank MH871973.1; Identities = 839/847 (99 %), no gaps). Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Xenosphaeropsis pyriputrescens* (strain CBS 115176, GenBank MW735656.1; Identities = 813/848 (96 %), one gap (0 %)), *Allantophomopsis* sp. 1(strain CBS 322.36, GenBank KY676741.1; Identities = 602/668 (90 %), no gaps) and *Allantophomopsis cytisporea* (strain ATCC 66955, GenBank CP103035.1; Identities = 747/831 (90 %), one gap (0 %)). Closest hits using the ***tef1*** (first part) sequence had highest similarity to *Xenosphaeropsis pyriputrescens* (strain CBS 115176, GenBank MZ073952.1; Identities = 209/221 (95 %), three gaps (1 %)), *Allantophomopsis cytisporea* (strain ATCC 66955, GenBank CP103023.1; Identities = 182/188 (97 %), two gaps (1 %)) and *Dothiora oleae* (strain SAG 68856-SF, GenBank KY613610.1; Identities = 174/187 (93 %), one gap (0 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Xenosphaeropsis pyriputrescens* (strain CBS 115176, GenBank MZ073942.1; Identities = 492/527 (93 %), three gaps (0 %)), *Allantophomopsis cytisporea* (strain ATCC 66955, GenBank CP103031.1; Identities = 453/526 (86 %), ten gaps (1 %)), and *Allantophomopsis lycopodina* (strain ATCC 66958, GenBank CP103007.1; Identities = 448/513 (87 %), four gaps (0 %)).

Supplementary material

FP1487 Phylogenetic tree.

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Muriseptatomyces restionacearum

Fungal Planet 1488 – 29 June 2023

Muriseptatomyces Crous, *gen. nov.*

Etymology. Name refers to its muriformly septate ascospores.

Classification — *Lindgomycetaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*.

Ascomata immersed, becoming erumpent, subglobose, brown with long neck, and central ostiole, surrounded by brown, septate setae; wall of 3–6 layers of brown *textura angularis. Hamathecium* composed of numerous filiform, septate, branched, hyphae-like pseudoparaphyses. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical-clavate, pedicellate. *Ascospores* 1–2-seriate, fusoid with subobtuse ends, golden brown, muriformly septate, constricted at septa, third cell from the apex swollen, straight to slightly curved, verruculose, guttulate, thick-walled, surrounded by a gelatinous sheath.

Type species. *Muriseptatomyces restionacearum* Crous MycoBank MB 848067.

Muriseptatomyces restionacearum Crous, *sp. nov.*

Etymology. Name refers to the *Restionaceae*.

Saprobic on dead culms. *Ascomata* immersed, 200–250 µm diam, becoming erumpent, subglobose, brown with long neck up to 300 µm long, and central ostiole, surrounded by brown, septate setae; wall of 3–6 layers of brown *textura angularis. Hamathecium* composed of numerous filiform, septate, branched, hyphae-like pseudoparaphyses, 2–3 µm diam. *Asci* 115–160 × 21–25 µm, 8-spored, bitunicate, fissitunicate, cylindrical-clavate, pedicellate. *Ascospores* (32–)34–36(–40) × (7–)9–10 µm, 1–2-seriate, fusoid with subobtuse ends, golden brown, 5–7(–8)-septate, with several oblique septa, constricted at septa, third cell from the apex swollen, straight to slightly curved, verruculose, guttulate, thick-walled, surrounded by a gelatinous sheath.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On malt extract agar (MEA), potato dextrose agar (PDA) and oatmeal agar (OA) surface and reverse olivaceous grey.

Typus. South Africa, Western Cape Province, Cape Town, Green Point Park, on culms of *Restionaceae*, 6 Mar. 2022, *P.W. Crous*, HPC 3843 (holotype CBS H-25174; culture ex-type CPC 43141 = CBS 149513; ITS, LSU, SSU and *tef1* (second part) sequences GenBank OQ628477.1, OQ629059.1, OQ628449.1 and OQ627958.1; MycoBank MB 848068).

Notes — *Muriseptatomyces restionacearum* is related to species of *Hongkongmyces* (based on *H. pedis*; *Lindgomycetaceae*), characterised by pseudothecia with bitunicate asci, and overlapping biseriate ascospores, broad-fusiform, sometimes tapering towards the ends, hyaline, 1-septate, surrounded with mucilaginous sheath (Dong et al. 2020), and the hyphomycete *Mycofalcella iqbalii* (CBS 400.93). However, *Mycofalcella* is based on *M. calcarata* (*Tricladiaceae*), so the culture CBS 400.93 appears to represent a different genus, allied to the *M. restionacearum*. *Muriseptatomyces* is characterised by having pseudothecia with long necks surrounded by setae, hyphae-like pseudoparaphyses, and muriformly septate ascospores, third cell from the apex swollen, ascospores surrounded by a sheath.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Hongkongmyces kokensis* (strain LR4, GenBank MZ538507.1; Identities = 351/377 (93 %), nine gaps (2 %)), *Hongkongmyces thailandica* (voucher MFLU 17-0004, GenBank NR_156319.1; Identities = 427/461 (93 %), eight gaps (1 %)) and *Clohesyomyces aquaticus* (strain MFLUCC 18-1037, GenBank MT627725.1; Identities = 324/352 (92 %), ten gaps (2 %)). Closest hits using the **LSU** sequence are *Hongkongmyces brunneosporus* (strain DLUCC 1425, GenBank MW004644.1; Identities = 838/846 (99 %), no gaps), *Clohesyomyces symbioticus* (voucher ARIZ DM0177, GenBank OK135171.1; Identities = 824/833 (99 %), one gap (0 %)) and *Hongkongmyces aquaticus* (strain MFLUCC 18-1150, GenBank MN913694.1; Identities = 835/846 (99 %), no gaps). Closest hits using the **SSU** sequence are *Lepidosphaeria nicotiae* (strain SRS-172-F-2019, GenBank MT328170.1; Identities = 994/995 (99 %), no gaps), *Lindgomyces angustiascus* (strain ILL A640-1a, GenBank NG_065002.1; Identities = 994/995 (99 %), no gaps), and *Lindgomyces lemonweirensis* (strain ILL 40793, GenBank NG_064975.1; Identities = 994/995 (99 %), no gaps). Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Hongkongmyces brunneosporus* (as *Hongkongmyces* sp. DB-2020a, strain MFLUCC 17-1317, GenBank MW018839.1; Identities = 896/928 (97 %), no gaps), *Aquimassariosphaeria kunmingensis* (strain KUMCC 18-1019, GenBank MT954409.1; Identities = 799/837 (95 %), two gaps (0 %)) and *Hongkongmyces thailandica* (strain MFLUCC 16-0406, GenBank KY771327.1; Identities = 862/904 (95 %), one gap (0 %)).

Colour illustrations. Culms of *Restionaceae* growing near Cape Town, South Africa. Ascomata developing in culture; asci and ascospores; ascospores with mucoid sheath. Scale bars: ascomata = 250 µm, all others = 10 µm.

Supplementary material

FP1488 Phylogenetic tree.

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Periconia neominutissima

Fungal Planet 1489 – 29 June 2023

Periconia neominutissima Crous, *sp. nov.*

Etymology. Name refers to its morphological similarity to *Periconia minutissima*.

Classification — *Periconiaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*.

Conidiophores arising from superficial to immersed mycelium, subcylindrical, flexuous, solitary or in clusters of 2–3, base swollen, 12–15 µm diam, with brown rhizoids; stalk up to 700 µm tall, thick-walled, medium to dark brown, smooth, up to 18-septate, 7–12 µm diam above basal cell, 5–8 µm diam below apical conidiogenous region; lateral branches: primary branches subcylindrical, 0–3-septate, 14–40 × 6–7 µm; secondary branches subcylindrical, 0–1-septate, 12–25 × 6–7 µm. *Conidiogenous cells* in whorls of 1–3, ampulliform to obovoid, pale to red brown, 6–8 × 4–5 µm. *Conidia* in short, branched, compact chains, spherical, medium to red brown, verruculose, thick-walled, (4–)5(–6) µm diam.

Culture characteristics — Colonies erumpent, spreading, with moderate to abundant aerial mycelium, covering dish after 2 wk at 25 °C. On malt extract agar (MEA) surface smoke grey, reverse luteous; on potato dextrose agar (PDA) surface and reverse olivaceous grey; on oatmeal agar (OA) surface smoke grey.

Typus. France, Normandy, Sinte Marguerite sur mer, on *Poaceae*, 24 Aug. 2021, *P.W. Crous*, HPC 3745 (holotype CBS H-25159; culture ex-type CPC 42368 = CBS 149514; ITS, LSU and *tef1* (first part) sequences GenBank OQ628478.1, OQ629060.1 and OQ627950.1; MycoBank MB 848069).

Notes — *Periconia neominutissima* is morphologically similar to *P. minutissima* in having spherical, verruculose conidia, 4–6(–7) µm diam (Ellis 1971). However, conidia are medium to red-brown, thus different to the straw-coloured to pale brown conidia of *P. minutissima*, and distinct from the reference strain of *P. minutissima* (MUT 2887; Yang et al. 2022).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Periconia* sp. (strain 10b, GenBank KX394553.1; Identities = 485/486 (99 %), no gaps), *Periconia minutissima* (strain MUT<ITA> 2887, GenBank MG813227.1; Identities = 443/453 (98 %), no gaps) and *Periconia macrospinosa* (strain UFMG PEZ8, GenBank KY364630.1; Identities = 472/486 (97 %), no gaps). Closest hits using the **LSU** sequence are *Periconia thysanolaenae* (strain KUMCC 20-0262, GenBank NG_081511.1; Identities = 840/844 (99 %), one gap (0 %)), *Periconia neobrittanica* (strain CPC 37903, GenBank NG_068342.1; Identities = 834/843 (99 %), no gaps) and *Periconia banksiae* (strain CBS 129526, GenBank NG_064279.1; Identities = 834/843 (99 %), no gaps). Closest hits using the ***tef1*** (first part) sequence had highest similarity to *Periconia macrospinosa* (voucher CRB-JD A126, GenBank MT793777.1; Identities = 123/130 (95 %), no gaps) and *Periconia cyperacearum* (strain CPC 32138, GenBank MH327882.1; Identities = 239/297 (80 %), 26 gaps (8 %)).

Colour illustrations. Collection site at Sinte Marguerite sur mer, Normandy, France. Conidiophores; conidiophores and conidiogenous cells giving rise to conidia on synthetic nutrient-poor agar; conidiophores with rhizoids; conidia. Scale bars = 20 µm (conidiophores), 10 µm (all others).

Supplementary material

FP1489 Phylogenetic tree.

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Basingstokeomyces allii

Fungal Planet 1490 – 29 June 2023

Basingstokeomyces Crous & Denman, *gen. nov.*

Etymology. Name refers to Basingstoke, UK where it was isolated.

Classification — *Vandijckellaceae*, *Helotiales*, *Leotiomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate, hyphae. *Conidiophores* erect, penicillate, flame-like, hyaline, becoming bright yellow on synthetic nutrient-poor agar; conidiophores in clusters, subcylindrical, septate, with terminal clusters of 2–4 cylindrical, smooth, hyaline, aseptate primary branches with several flat-tipped apical loci that give rise to secondary and tertiary cylindrical branches. *Conidiogenous cells* terminal, subcylindrical, with several flat-tipped apical loci, unthickened and not darkened. *Conidia* occurring in branched chains, subcylindrical, aseptate, hyaline, smooth, guttulate, ends obtuse, aggregated in mucoid packets.

Type species. Basingstokeomyces allii Crous & Denman
MycoBank MB 848070

Basingstokeomyces allii Crous & Denman, *sp. nov.*

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

Mycelium consisting of hyaline, smooth, branched, septate, 2–2.5 µm diam hyphae. *Conidiophores* erect, penicillate, flame-like, hyaline, becoming bright yellow on synthetic nutrient-poor agar; conidiophores in clusters, subcylindrical, 1–3-septate, 30–50 × 3–3.5 µm, with terminal clusters of 2–4 cylindrical, smooth, hyaline, aseptate primary branches with several flat-tipped apical loci that give rise to secondary and tertiary cylindrical branches, 5–6 × 1.5–2 µm. *Conidiogenous cells* terminal, subcylindrical, 18–30 × 2.5–3 µm, with several flat-tipped apical loci, unthickened and not darkened, 1–1.5 µm diam. *Conidia* occurring in branched chains, subcylindrical, aseptate, hyaline, smooth, guttulate, ends obtuse, (4–)5–6(–8) × 1.5–2 µm, aggregated in mucoid packets.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and feathery, lobate margin, reaching 15 mm diam after 2 wk at 25 °C. On malt extract agar (MEA) surface and reverse ochreous; on potato dextrose agar (PDA) surface and reverse dirty white; on oatmeal agar (OA) surface dirty white.

Typus. UK, England, Basingstoke, on *Allium schoenoprasum* (*Amaryllidaceae*), May 2022, *P.W. Crous* (holotype CBS H-25210; culture ex-type CPC 44071 = CBS 149671; ITS, LSU and *rpb2* (first part) sequences GenBank OQ628479.1, OQ629061.1 and OQ627942.1; MycoBank MB 848071).

Notes — *Basingstokeomyces* is related to *Vandijckella johannae*, a hyphomycete isolated from soil in the Netherlands, characterised by simple conidiophores, mostly reduced to monophialides borne singly and laterally on aerial hyphae, and chains of aseptate conidia (Crous et al. 2017b). *Basingstokeomyces* is distinct in that it has penicillate conidiophores, and conidiogenous cells with flat-tipped apical loci, unthickened and not darkened, giving rise to chains of aseptate conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Vandijckella johannae* (strain CBS 143182, GenBank NR_172156.1; Identities = 477/485 (98 %), one gap (0 %)) and *Mycoarthris corallina* (no strain number listed, GenBank AH009124.2; Identities = 442/450 (98 %), one gap (0 %)). Closest hits using the **LSU** sequence are *Vandijckella johannae* (strain CBS 143182, GenBank NG_075222.1; Identities = 836/840 (99 %), no gaps), *Polyphilus sieberi* (strain DSM 106515, GenBank NG_067556.1; Identities = 833/840 (99 %), no gaps) and *Polyphilus frankenii* (strain DSM 106520, GenBank NG_067557.1; Identities = 831/840 (99 %), no gaps). No significant hits were obtained using the ***rpb2*** (first part) sequence.

Colour illustrations. Allium schoenoprasum growing at Basingstoke, England, UK. Conidiophores and conidiogenous cells giving rise to conidia on synthetic nutrient-poor agar; penicillate conidiophores with branched apical apparatus; catenulate conidia. Scale bars = 10 µm.

Supplementary material

FP1490 Phylogenetic tree.

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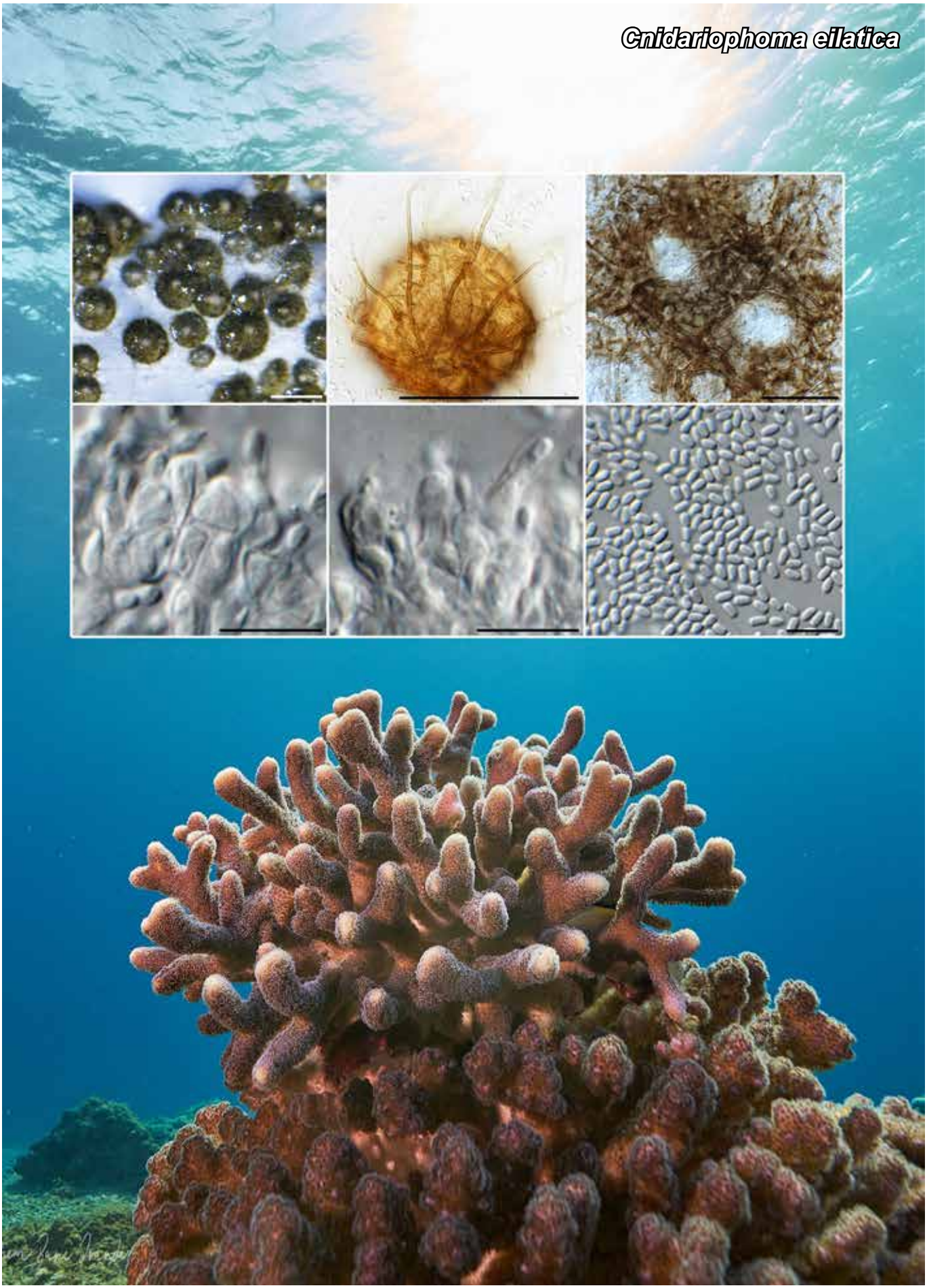
Cnidariophoma eilatica

Fungal Planet 1491 – 29 June 2023

Cnidariophoma Crous & Yarden, *gen. nov.*

Etymology. Name refers to the coral phylum *Cnidaria*, a substrate from which it was isolated and its phoma-like morphology.

Classification — *Pleosporaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*.

Conidiomata pycnidial, eustromatic, pale to medium brown, covered in brown setae, with one to several ostioles; wall of 3–4 layers of *textura prismatica* to *angularis. Conidiophores* lining inner cavity, hyaline, smooth, reduced to conidiogenous cells with supporting cell, ampulliform, phialidic with periclinal thickening prominent cylindrical collarette, extending past conidia in some cases. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, subcylindrical with obtuse ends.

Type species. Cnidariophoma eilatica Crous & Yarden
MycoBank MB 848072

Cnidariophoma eilatica Crous & Yarden, *sp. nov.*

Etymology. Name refers to Eilat, the location where it was collected.

Conidiomata pycnidial, eustromatic, pale to medium brown, 70–150 µm diam, covered in brown setae, with one to several ostioles, 20–30 µm diam; wall of 3–4 layers of *textura prismatica* to *angularis. Conidiophores* lining inner cavity, hyaline, smooth, reduced to conidiogenous cells with supporting cell, ampulliform, phialidic with periclinal thickening prominent cylindrical collarette, 1–5 µm tall, extending past conidia in some cases, 5–10 × 3–4 µm. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, subcylindrical with obtuse ends, (3–)4–5 × 2–3 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 20–25 mm diam after 2 wk at 25 °C. On malt extract agar (MEA) surface olivaceous grey, reverse iron grey; on potato dextrose agar (PDA) surface and reverse iron grey; on oatmeal agar (OA) surface olivaceous grey.

Typus. Israel, Eilat, N29.5° E34.9°, from *Stylophora pistillata* (*Pocilloporidae*), a coral in the Red Sea, May 2022, *O. Yarden* (holotype CBS H-25212; culture ex-type CPC 44117 = CBS 149672; ITS, LSU, *actA*, *rpb2* (first part) and *tub2* sequences GenBank OQ628480.1, OQ629062.1, OQ627931.1, OQ627943.1 and OQ627964.1; MycoBank MB 848073).

Notes — Many members of the phylum *Cnidaria* have been shown to harbour a diverse variety of fungi (Yarden 2014). *Cnidariophoma eilatica* is related to *Decorospora gaudefroyi*, a marine ascomycete characterised by having ascospores that are surrounded by a mucoid sheath, and occurring in temperate waters of Europe, North America and Argentina on driftwood, pilings and a variety of marsh plants (Inderbitzin et al. 2002, Haridas et al. 2020). Phylogenetically and morphologically, it appears to represent a distinct phoma-like genus. Of interest is that an additional new species, *Microascus rothbergiorum*, was recently described from the same coral species (Crous et al. 2022b).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Dendryphion penicillatum* (strain 48/3.6.1, GenBank DQ865101.1; Identities = 521/582 (90 %), 19 gaps (3 %)), *Tamaricicola muriformis* (strain IT_9172, GenBank KU900317.1; Identities = 513/581 (88 %), 17 gaps (2 %)) and *Comoclathris spartii* (strain TGF26-MRL, GenBank KU714703.1; Identities = 429/472 (91 %), 10 gaps (2 %)). Closest hits using the **LSU** sequence are *Sphaerellopsis macroconidiale* (strain CBS 233.51, GenBank KP170726.1; Identities = 789/805 (98 %), no gaps), *Tamaricicola muriformis* (strain IT_9175, GenBank KU729856.1; Identities = 800/818 (98 %), three gaps (0 %)) and *Alloleptosphaeria clematidis* (strain MFLUCC 17-2071, GenBank MT214557.1; Identities = 791/810 (98 %), no gaps). Distant hits using the ***actA*** sequence had highest similarity to *Exserohilum longirostratum* (strain CBS 128055, GenBank LT837620.1; Identities = 569/635 (90 %), 14 gaps (2 %)), *Setosphaeria rostrata* (strain CBS 128062, GenBank LT837683.1; Identities = 567/633 (90 %), 12 gaps (1 %)) and *Setosphaeria holmii* (strain BRIP 10724, GenBank LT837654.1; Identities = 567/634 (89 %), 13 gaps (2 %)). Distant hits using the ***rpb2*** (first part) sequence had highest similarity to *Comoclathris incompta* (strain CBS 467.76, GenBank KC584504.1; Identities = 716/813 (88 %), four gaps (0 %)), *Comoclathris lonicerae* (voucher MFLU 18-1236, GenBank OL771441.1; Identities = 689/811 (85 %), no gaps) and *Clathrospora elynae* (strain CBS 161.51, GenBank KC584495.1; Identities = 691/814 (85 %), six gaps (0 %)). Distant hits using the ***tub2*** sequence had highest similarity to *Libertasomyces platani* (strain CPC 29609, GenBank KY173604.1; Identities = 387/466 (83 %), 23 gaps (4 %)), *Libertasomyces quercus* (strain CBS 134.97, GenBank KY929212.1; Identities = 385/466 (83 %), 23 gaps (4 %)) and *Fenestella crataegi* (strain C314, GenBank MK357599.1; Identities = 388/470 (83 %), 28 gaps (5 %)).

Colour illustrations. The coral *Stylophora pistillata* from the Red Sea.. Conidiomata forming on synthetic-nutrient-poor agar; conidioma with setate; ostioles; conidiogenous cells giving rise to conidia; conidia. Scale bars = 150 µm (conidiomata), 20 µm (ostioles), 10 µm (all others).

Supplementary material

FP1491 Phylogenetic tree.

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Sympoventuria eucalyptorum

Fungal Planet 1492 – 29 June 2023

Sympoventuria eucalyptorum Crous, *sp. nov.*

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

Classification — *Sympoventuriaceae*, *Venturiales*, *Pleosporomycetidae*, *Dothideomycetes*.

Mycelium consisting of pale olivaceous, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* solitary, arising from superficial hyphae, reduced to conidiogenous cells, forming branched, sympodially proliferating chains of conidia. *Conidiogenous cells* subcylindrical, pale brown, smooth, 3–10 × 2–3 µm, proliferating sympodially at apex, with unthickened, not darkened, flat-tipped apical loci. *Conidia* in branched chains, subcylindrical, smooth, pale brown, (1–)3-septate; 1-septate conidia 16–17 × 2.5–3 µm, 3-septate conidia (18–)22–24(–28) × 3(–3.5) µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 15 mm diam after 2 wk at 25 °C. On malt extract agar (MEA) surface isabelline, reverse brown vinaceous; on potato dextrose agar (PDA) surface and reverse umber; on oatmeal agar (OA) surface sienna.

Typus. Spain, Gran Canaria, Caldera, on leaves of *Eucalyptus* sp. (*Myrtaceae*), Apr. 2022, *A.L. van Iperen*, HPC 3902 (holotype CBS H-25205; culture ex-type CPC 43332 = CBS 149673; ITS, LSU and *tef1* (first part) sequences GenBank OQ628481.1, OQ629063.1 and OQ627951.1; MycoBank MB 848074).

Notes — *Sympoventuria* is presently known from four species occurring on *Myrtaceae* leaf litter, three of which occur on *Eucalyptus* (Wei et al. 2022). *Sympoventuria eucalyptorum* is closely related to *S. capensis* (conidia (1–)3(–5)-septate; 10–65 × 2.5–5 µm; Crous et al. 2007), but distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Sympoventuria capensis* (strain CBS 120136, GenBank NR_121323.1; Identities = 519/535 (97 %), two gaps (0 %)), *Sympoventuria melaleucae* (strain CBS 143407, GenBank NR_156668.1; Identities = 496/540 (92 %), 10 gaps (1 %)) and *Helicoma olivaceum* (strain CBS 728.83, GenBank DQ351725.1; Identities = 498/548 (91 %), 17 gaps (3 %)). Closest hits using the **LSU** sequence are *Sympoventuria capensis* (strain CBS 120136, GenBank NG_057984.1; Identities = 785/785 (100 %), no gaps), *Sympoventuria melaleucae* (strain CBS 143407, GenBank NG_058520.1; Identities = 817/822 (99 %), no gaps) and *Sympoventuria africana* (strain CBS 121639, GenBank NG_073684.1; Identities = 773/780 (99 %), no gaps). No significant hits were obtained using the ***tef1*** (first part) sequence.

Colour illustrations. *Eucalyptus* sp. growing at Gran Canaria, Spain. Conidiophores and conidiogenous cells giving rise to conidia on synthetic nutrient-poor agar; catenulate conidia. Scale bars = 10 µm

Supplementary material

FP1492 Phylogenetic tree.

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Pseudopyricularia caricicola

Fungal Planet 1493 – 29 June 2023

Pseudopyricularia caricicola Crous & Osieck, *sp. nov.*

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

Classification — *Pyriculariaceae*, *Magnaporthales*, *Sordariomycetidae*, *Sordariomycetes*.

Conidiophores solitary, erect, straight or slightly curved, unbranched, medium brown, smooth, 1–2-septate, 120–180 × 6–7 µm. *Conidiogenous cells* integrated, terminal, medium brown, smooth, 90–120 × 6–7 µm, forming a rachis with several protruding denticles, 1–2 × 1 µm. *Conidia* solitary, obclavate, pale brown, finely roughened, guttulate, 2-septate, hila truncate, 2 µm diam, slightly protruding, unthickened, not darkened, (33–)38–42 × (8–)9(–10) µm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium and feathery, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On malt extract agar (MEA), potato dextrose agar (PDA) and oatmeal agar (OA) surface and reverse saffron, with patches of umber.

Typus. Netherlands, Utrecht Province, Nieuw Wulven, near Houten, 1.5 m a.s.l., N52°02'47" E05°10'34", on culms of *Carex disticha* (*Cyperaceae*), 26 Apr. 2022, *E.R. Osieck*, HPC 3954 = WI-52/#4464 (XVIII-58) (holotype CBS H-25209; culture ex-type CPC 44063 = CBS 149674; ITS, LSU and *actA* sequences GenBank OQ628482.1, OQ629064.1 and OQ627932.1; MycoBank MB 848075).

Notes — *Pseudopyricularia caricicola* is closely related to *P. festucae* (conidia (25–)30–38(–40) × (6–)7 µm), on *Festuca californica* in California; Crous et al. 2021b) and *P. iraniana* (conidia (20–)22–30 × 5–8 µm, on *Juncus* sp. in Iran; Pordel et al. 2017), but has larger conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pseudopyricularia festucae* (strain CPC 37915, GenBank MW883447.1; Identities = 498/511 (97 %), two gaps (0 %)), *Pseudopyricularia iraniana* (strain IRAN 2761C, GenBank NR_158928.1; Identities = 486/501 (97 %), two gaps (0 %)) and *Pseudopyricularia higginsii* (as *Dactylaria higginsii*, strain CBS 121934, GenBank KM009164.1; Identities = 476/503 (95 %), five gaps (0 %)). Closest hits using the **LSU** sequence are *Pseudopyricularia festucae* (strain CPC 37915, GenBank MW883838.1; Identities = 853/858 (99 %), no gaps), *Pyricularia caricis* (strain JAC12652, GenBank MK431456.1; Identities = 852/858 (99 %), no gaps) and *Pseudopyricularia iraniana* (strain IRAN 2761C, GenBank NG_060183.1; Identities = 848/854 (99 %), one gap (0 %)). Closest hits using the ***actA*** sequence had highest similarity to *Pseudopyricularia bothriochloae* (strain CBS 136427, GenBank KY905700.1; Identities = 639/688 (93 %), eight gaps (1 %)), *Pyricularia oryzae* (strain LpKY97, GenBank CP050925.1; Identities = 583/697 (84 %), 27 gaps (3 %)) and *Xenopyricularia junci* (strain CPC 40968, GenBank OK651127.1; Identities = 494/556 (89 %), 14 gaps (2 %)).

Colour illustrations. *Carex disticha* growing at Nieuw Wulven, near Houten in Utrecht Province, the Netherlands. Conidiophores and conidiogenous cells giving rise to conidia on synthetic nutrient-poor agar; denticulate conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Supplementary material

FP1493 Phylogenetic tree.

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Houtenomyces caricicola

Fungal Planet 1494 – 29 June 2023

Houtenomyces Crous & Osieck, *gen. nov.*

Etymology. Name refers to Houten, the town close to where it was collected.

Classification — *Plectosphaerellaceae*, *Glomerellales*, *Hypocreomycetidae*, *Sordariomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate hyphae. *Conidiophores* solitary, unbranched, erect, septate, subcylindrical, hyaline, smooth. *Conidiogenous cells* integrated, terminal, hyaline, smooth, phialidic with periclinal thickening. *Conidia* solitary, aggregating in mucoid mass, hyaline, smooth, guttulate, 1-septate, subcylindrical, tapering at ends, apex subobtuse, hilum protruding, truncate.

Type species. *Houtenomyces caricicola* Crous & Osieck
MycoBank MB 848076

Houtenomyces caricicola Crous & Osieck, *sp. nov.*

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

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* solitary, unbranched, erect, 1–3-septate, subcylindrical, hyaline, smooth, 60–100 × 3–5 µm. *Conidiogenous cells* integrated, terminal, hyaline, smooth, phialidic with periclinal thickening, 30–70 × 3–5 µm. *Conidia* solitary, aggregating in mucoid mass, hyaline, smooth, guttulate, 1-septate, subcylindrical, tapering at ends, apex subobtuse, hilum protruding, truncate, 1–1.5 µm diam, (18–)25–28(–32) × (3.5–)4–5(–6) µm.

Culture characteristics — Colonies erumpent, spreading, folded, with moderate aerial mycelium and feathery, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On malt extract agar (MEA), potato dextrose agar (PDA) and oatmeal agar (OA) surface dirty white, reverse luteous to honey.

Typus. Netherlands, Utrecht Province, Nieuw Wulven, near Houten, 1.5 m a.s.l., N52°02'47" E05°10'34", on culms of *Carex disticha* (*Cyperaceae*), 26 Apr. 2022, *E.R. Osieck*, HPC 3954 = WI-52/#4464 (XVIII-58) (holotype CBS H-25208; culture ex-type CPC 44030 = CBS 149675; ITS, LSU and *rpb2* (first part) sequences GenBank OQ628483.1, OQ629065.1 and OQ627944.1; MycoBank MB 848077).

Notes — *Houtenomyces* adds another hyphomycetous genus to the *Acremonium* complex. Phylogenetically it is allied to *Plectosphaerella* and *Verticillium* (Giraldo & Crous 2019), sharing features such as solitary, septate conidiophores with phialidic conidiogenous cells that give rise to 1-septate conidia that aggregate in a mucoid mass. Phylogenetically, it is distinct from other genera in this complex. Although morphologically similar to taxa in *Plectosphaerellaceae*, its large, 1-septate, subcylindrical conidia are characteristic.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Gibellulopsis nigrescens* (strain C3, GenBank MK361141.1; Identities = 482/532 (91 %), 15 gaps (2 %)), *Gibellulopsis serrae* (as *Cephalosporium serrae*, strain JW 38004, GenBank LR590188.1; Identities = 482/532 (91 %), 15 gaps (2 %)) and *Gibellulopsis catenata* (strain IHEM 06573, GenBank OW984155.1; Identities = 482/532 (91 %), 15 gaps (2 %)). Closest hits using the **LSU** sequence are *Musicillium theobromae* (strain MFLUCC 18-0109, GenBank MH260305.1; Identities = 821/840 (98 %), no gaps), *Stachylidium bicolor* (strain DAOM 226658, GenBank GU180651.1; Identities = 835/855 (98 %), no gaps) and *Brunneochlamydosporium nepalense* (strain CBS 971.72, GenBank NG_067402.1; Identities = 820/840 (98 %), three gaps (0 %)). Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Gibellulopsis nigrescens* (strain CBS 100829, GenBank LR026144.1; Identities = 509/602 (85 %), no gaps), *Chordomyces antarcticum* (strain A140, GenBank KJ443153.1; Identities = 738/883 (84 %), two gaps (0 %)) and *Plectosphaerella plurivora* (strain JW 255003, GenBank LR594800.1; Identities = 666/798 (83 %), five gaps (0 %)).

Colour illustrations. *Carex disticha* growing at Nieuw Wulven, near Houten in Utrecht Province, the Netherlands. Conidiophores and conidiogenous cells giving rise to conidia on synthetic nutrient-poor agar; conidia. Scale bars = 10 µm.

Supplementary material

FP1494 Phylogenetic tree.

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Aureobasidium welwitschiae

Fungal Planet 1495 – 29 June 2023

Aureobasidium welwitschiae Crous, *sp. nov.*

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

Classification — *Saccotheciaceae*, *Dothideales*, *Dothideomycetidae*, *Dothideomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate hyphae that become dark brown, thick-walled, verruculose, covered in mucilage, 7–9 µm diam, forming solitary or clusters of globose *chlamydospores*, 12–25 µm diam. *Conidiogenous cells* reduced to conidiogenous loci which are inconspicuous phialidic openings on hyphae, giving rise to conidia that aggregate in a mucoid mass. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, fusoid-ellipsoid, straight to slightly curved, apex obtuse, base tapered, hilum subobtuse, (6–)8–12(–13) × (3.5–)4(–4.5) µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On malt extract agar (MEA), potato dextrose agar (PDA) surface and reverse dark mouse grey; on oatmeal agar (OA) surface umber in centre, pale luteous in outer region.

Typus. Namibia, Gobabeb-Namib Research Institute, Gorob Mine, Namib-Naukluft National Park, on dead leaf tips of *Welwitschia mirabilis* (*Welwitschiaceae*), 4 Apr. 2022, *P.W. Crous*, HPC 3885 (holotype CBS H-25203; culture ex-type CPC 43222 = CBS 149676; ITS, LSU, *actA*, *tef1* (second part) and *tub2* sequences GenBank OQ628484.1, OQ629066.1, OQ627933.1, OQ627959.1 and OQ627965.1; MycoBank MB 848078).

Notes — *Aureobasidium welwitschiae* resembles *A. iranianum* (conidia (5–)7–9(–14) × 3–6 µm; hyaline to dark brown, smooth, aseptate, thin-walled, ellipsoidal to spherical to ovoid; Arzanlou & Khodaei 2012) and *A. thailandense* (conidia 3–10 × 5–12 µm; subglobose, ovoid, or pyriform; Petersen et al. 2013), but from which it is phylogenetically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Aureobasidium iranianum* (strain QCC M016/17, GenBank KY781746.1; Identities = 540/552 (98 %), three gaps (0 %)), *Aureobasidium thailandense* (strain PBUAP70, GenBank KP965483.1; Identities = 539/551 (98 %), three gaps (0 %)) and *Kabatiella bupleuri* (strain G3 IBMiP, GenBank MW450864.1; Identities = 539/551 (98 %), three gaps (0 %)). Closest hits using the **LSU** sequence are *Selenophoma mahoniae* (strain CBS 388.92, GenBank EU754213.1; Identities = 849/861 (98 %), no gaps), *Kabatiella microsticta* (strain CBS 114.64, GenBank MH870008.1; Identities = 854/869 (98 %), one gap (0 %)) and *Aureobasidium tremulum* (strain UN_1, GenBank MK503660.1; Identities = 853/869 (98 %), four gaps (0 %)). Closest hits using the ***actA*** sequence had highest similarity to *Aureobasidium subglaciale* (strain EXF-2481, GenBank XM_013491737.1; Identities = 393/406 (97 %), no gaps), *Aureobasidium melanogenum* (strain CBS 110374, GenBank XM_041025991.1; Identities = 393/406 (97 %), no gaps) and *Aureobasidium pullulans* (strain EXF-150, GenBank XM_029905906.1; Identities = 391/406 (96 %), no gaps). Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Aureobasidium melanogenum* (strain CBS 110374, GenBank XM_041024707.1; Identities = 877/914 (96 %), one gap (0 %)), *Aureobasidium namibiae* (strain CBS 147.97, GenBank XM_013574385.1; Identities = 871/914 (95 %), one gap (0 %)) and *Aureobasidium pullulans* (strain R106, GenBank U19723.1; Identities = 867/914 (95 %), one gap (0 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Aureobasidium pullulans* (strain EXF-1702B, GenBank FJ157861.1; Identities = 312/364 (86 %), 21 gaps (5 %)), *Aureobasidium melanogenum* (strain GXZ-6, GenBank MT114425.1; Identities = 303/357 (85 %), 16 gaps (4 %)) and *Aureobasidium namibiae* (strain CBS 147.97, GenBank FJ157863.1; Identities = 308/363 (85 %), 20 gaps (5 %)).

Colour illustrations. *Welwitschia mirabilis* growing in the Namib Desert, Namibia. Hypha with conidiogenous locus giving rise to conidium; colony on synthetic nutrient-poor agar; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Supplementary material

FP1495 Phylogenetic tree.

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Aureobasidium faidherbiae

Fungal Planet 1496 – 29 June 2023

Aureobasidium faidherbiae Crous, *sp. nov.*

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

Classification — *Saccotheciaceae*, *Dothideales*, *Dothideomycetidae*, *Dothideomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate hyphae, 4–6 µm diam, frequently with nodulose swellings; hyphae turn dark brown with age, becoming thick-walled, verruculose, covered in mucilage, constricted at septa, 10–12 µm diam. *Conidiogenous cells* reduced to inconspicuous phialidic loci on hyphae, 1–1.5 µm diam. *Conidia* hyaline, smooth, aseptate, guttulate, fusoid-ellipsoid, curved to hooked, widest in middle, apex subobtuse, tapering to truncate hilum, 1–1.5 µm diam; primary conidia 15–20 × 4–5 µm, forming several flat-tipped denticulate apical loci that give rise to clusters of secondary conidia, (10–)12–15(–17) × (3–)3.5(–4) µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On malt extract agar (MEA), potato dextrose agar (PDA) and oatmeal agar (OA) surface and reverse leaden black.

Typus. Namibia, Gobabeb-Namib Research Institute, Kuiseb River, on dead leaf of *Faidherbia albida* (*Fabaceae*), 5 Apr. 2022, *P.W. Crous*, HPC 3883 (holotype CBS H-25204; culture ex-type CPC 43294 = CBS 149677; ITS, LSU, *rpb2* (first part) and *tef1* (first part) sequences GenBank OQ628485.1, OQ629067.1, OQ627945.1 and OQ627952.1; MycoBank MB 848079).

Notes — *Aureobasidium faidherbiae* is related to *A. thailandense* (conidia 3–10 × 5–12 µm; subglobose, ovoid, or pyriform; Petersen et al. 2013), *A. bupleuri* (conidia 10–20 × 4–8 µm; ellipsoid, reniform or lunate, hyaline to olivaceous black; Bills et al. 2012), and *A. welwitschiae* (conidia (6–)8–12(–13) × (3.5–)4(–4.5) µm fusoid-ellipsoid; see elsewhere in this paper), but is phylogenetically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Kabatiella* sp. from soil in a dam in an arid region of Oman (strain SQU-KH09, GenBank KU945836.1; Identities = 527/527 (100 %), no gaps), *Aureobasidium thailandense* (strain PBUAP70, GenBank KP965483.1; Identities = 538/550 (98 %), two gaps (0 %)) and *Aureobasidium bupleuri* (strain G3 IBMiP, GenBank MW450864.1; Identities = 538/550 (98 %), two gaps (0 %)). Closest hits using the **LSU** sequence are *Kabatiella microsticta* (strain CBS 114.64, GenBank MH870008.1; Identities = 814/827 (98 %), three gaps (0 %)), *Aureobasidium pullulans* (strain RGA003, GenBank JX188092.1; Identities = 810/825 (98 %), no gaps) and *Aureobasidium tremulum* (strain UN_1, GenBank MK503660.1; Identities = 810/825 (98 %), one gap (0 %)). Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Aureobasidium melanogenum* (strain P16, GenBank CP061917.1; Identities = 718/836 (86 %), two gaps (0 %)), *Aureobasidium pullulans* (strain EXF-150, GenBank XM_029907989.1; Identities = 712/837 (85 %), two gaps (0 %)) and *Kabatiella microsticta* (strain KUC3002, GenBank KX893330.1; Identities = 693/813 (85 %), three gaps (0 %)). No significant hits were obtained when the ***tef1*** sequence was used in blastn and megablast searches.

Colour illustrations. *Faidherbia albida* growing along Kuiseb River in Namibia. Colonies on synthetic nutrient-poor agar; hyphae with conidiogenous loci giving rise to primary and secondary conidia; conidia become thick-walled, septate and pigmented with age. Scale bars = 10 µm.

Supplementary material

See the supplementary material FP1495 for a phylogenetic tree containing this novel species.

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Periconia philadelphiana

Fungal Planet 1497 – 29 June 2023

Periconia philadelphiana Crous & Jurjević, *sp. nov.*

Etymology. Name refers to the location where it was collected, Philadelphia.

Classification — *Periconiaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*.

Conidiophores arising from superficial and immersed mycelium, subcylindrical, flexuous, solitary, stalk up to 500 µm tall, thick-walled, dark brown, smooth, up to 20-septate, 4–6 µm diam above basal septum, 4–5 µm diam below apical conidiogenous region. *Conidiogenous cells* integrated, terminal, in whorls of up to three, clavate to obovoid, pale brown, verruculose, 8–14 × 4–6 µm. *Conidia* in short, branched, compact chains, spherical, pale to dark brown, verruculose to warty, thick-walled, (6–)8–9(–11) µm diam; mature conidia with hilum appearing as subhyaline germ pore, 1 µm diam.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On malt extract agar (MEA) surface ochreous, reverse sienna; on potato dextrose agar (PDA) surface pale luteous, reverse umber in middle, pale luteous in outer region; on oatmeal agar (OA) surface umber in middle, pale luteous in outer region. No growth at 37 °C.

Typus. USA, PA, Philadelphia, HVAC coil, swab, Oct. 2020, *Ž. Jurjević* 5568 (holotype CBS H-25197; culture ex-type CPC 42854 = CBS 149681; ITS, LSU and *tef1* (first part) sequences GenBank OQ628486.1, OQ629068.1 and OQ627953.1; MycoBank MB 848080).

Notes — *Periconia philadelphiana* is closely related, but morphologically and phylogenetically distinct from *P. chimonanthi* (conidia 7–8 × 6–7 µm, catenate, globose, initially hyaline greenish brown, becoming yellowish brown to brown at maturity, verruculose; Yang et al. 2022), *P. homothallica*, a sexual species (Tanaka et al. 2015), *P. minutissima* (conidia spherical, verruculose conidia, 4–6(–7) µm diam; Ellis 1971), and *P. neominutissima* (conidia spherical, medium to red brown, verruculose, thick-walled, (4–)5(–6) µm diam; see FP1489).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Periconia* sp. from a *Cyphomyrmex wheeleri* nest in the USA (strain CY191, GenBank HQ608021.1; Identities = 525/529 (99 %), no gaps), *Periconia chimonanthi* (strain KUMCC 20-0266, GenBank NR_176752.1; Identities = 502/529 (95 %), four gaps (0 %)) and *Periconia homothallica* (voucher HHUF 29105, GenBank NR_153446.1; Identities = 494/518 (95 %), five gaps (0 %)). Closest hits using the **LSU** sequence are *Periconia banksiae* (strain CBS 129526, GenBank NG_064279.1; Identities = 852/856 (99 %), no gaps), *Periconia neobrittanica* (strain CPC 37903, GenBank NG_068342.1; Identities = 848/856 (99 %), no gaps) and *Periconia homothallica* (voucher HHUF 29105, GenBank NG_059397.1; Identities = 841/849 (99 %), no gaps). No significant hits were obtained using the ***tef1*** (first part) sequence.

Colour illustrations. Collection site at Philadelphia, USA. Conidiophores and conidiogenous cells giving rise to conidia on synthetic nutrient-poor agar; conidiogenous cells and conidia; conidia. Scale bars = 10 µm.

Supplementary material

See the supplementary material FP1489 for a phylogenetic tree containing this novel species.

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Niesslia phragmiticola

Fungal Planet 1498 – 29 June 2023

Niesslia phragmiticola Crous & Osieck, *sp. nov.*

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

Classification — *Niessliaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells, arising singly from superficial hyphae, erect, flexuous, subcylindrical to subulate, with apical taper, thick-walled in lower region, phialidic with cylindrical collarette, 1–2 µm long, 20–40 × 2–3 µm. *Conidia* solitary, aggregating in mucoid mass, subcylindrical with subobtuse apices, aseptate, hyaline, smooth, guttulate, (3.5–)5–6(–9) × 1.5(–2) µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 10 mm diam after 2 wk at 25 °C. On malt extract agar (MEA), potato dextrose agar (PDA) and oatmeal agar (OA) surface and reverse saffron.

Typus. Netherlands, Utrecht Province, Nieuw Wulven, near Houten, 1.5 m a.s.l., N52°03'05" E05°09'47", on dead standing culms of *Phragmites australis* (*Poaceae*), 28 Jan. 2022, *E.R. Osieck*, HPC 3825 = WI-45/#4384 (holotype CBS H-25198; culture ex-type CPC 42923 = CBS 149682; ITS, LSU, *actA*, *tef1* (first part) and *tub2* sequences GenBank OQ628487.1, OQ629069.1, OQ627934.1, OQ627954.1 and OQ627966.1; MycoBank MB 848081).

Notes — *Niesslia phragmiticola* is related to *N. elymi* (Scotland, on *Elymus arenarius*; sporodochia common; phialides 25–38 µm long; conidia subcylindrical, 4–6 × 1.2–1.5 µm; Gams et al. 2019). *Niesslia phragmiticola* lacks sporodochia, and has somewhat larger conidia than *N. elymi*, but the two species are best separated based on their DNA phylogeny. This represents the second *Niesslia* species on *Phragmites* culms at this collection site (1st *N. neoexosporoides*; type of this species on *Carex*, Crous et al. 2022a). Interestingly, the genus has been rarely reported from this substrate (Van Ryckegem 2005 did not find any during intensive sampling of this substrate in Flanders, Belgium).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Niesslia elymi* (as *Niesslia exosporioides*, strain CBS 607.75, GenBank MG827016.1; Identities = 485/494 (98 %), two gaps (0 %)), *Niesslia ilicifolia* (strain CBS 459.74, GenBank MG826995.1; Identities = 459/509 (90 %), 17 gaps (3 %)) and *Niesslia stellenboschiana* (strain CBS 145531, GenBank NR_165230.1; Identities = 455/509 (89 %), 20 gaps (3 %)). Closest hits using the **LSU** sequence are *Niesslia elymi* (as *Niesslia exosporioides*, strain CBS 607.75, GenBank MG826817.1; Identities = 835/838 (99 %), no gaps), *Niesslia cladoniicola* (strain CBS 960.73, GenBank MG826850.1; Identities = 825/838 (98 %), no gaps) and *Niesslia ilicifolia* (strain CBS 459.74, GenBank MG826798.1; Identities = 822/838 (98 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Niesslia pseudoexilis* (strain CBS 148333, GenBank ON803514.1; Identities = 574/641 (90 %), 16 gaps (2 %)), *Xenocylindrocladium serpens* (strain CBS 128439, GenBank KM231125.1; Identities = 382/412 (93 %), no gaps) and *Gliocephalotrichum longibrachium* (strain CBS 126571, GenBank KM231117.1; Identities = 395/424 (93 %), one gap (0 %)). Distant hits obtained using the ***tef1*** (first part) sequence had highest similarity to *Memnoniella echinata* (strain CBS 344.39, GenBank KU846225.1; Identities = 202/231 (87 %), 12 gaps (5 %)), *Memnoniella pseudonilagirica* (strain CBS 136405, GenBank KU846237.1; Identities = 199/229 (87 %), 12 gaps (5 %)) and *Memnoniella brunneoconidiophora* (strain CBS 109477, GenBank KU846218.1; Identities = 197/227 (87 %), seven gaps (3 %)). The best hit obtained using the ***tub2*** sequence had highest similarity to *Niesslia pseudoexilis* (strain CBS 148333, GenBank ON803596.1; Identities = 406/503 (81 %), 30 gaps (5 %)).

Colour illustrations. *Phragmites australis* growing at Nieuw Wulven, near Houten in Utrecht Province, the Netherlands. Conidiophores on synthetic nutrient-poor agar; conidiogenous cells giving rise to conidia; conidia; conidiogenous cells and conidia. Scale bars = 10 µm.

Supplementary material

FP1498 Phylogenetic tree.

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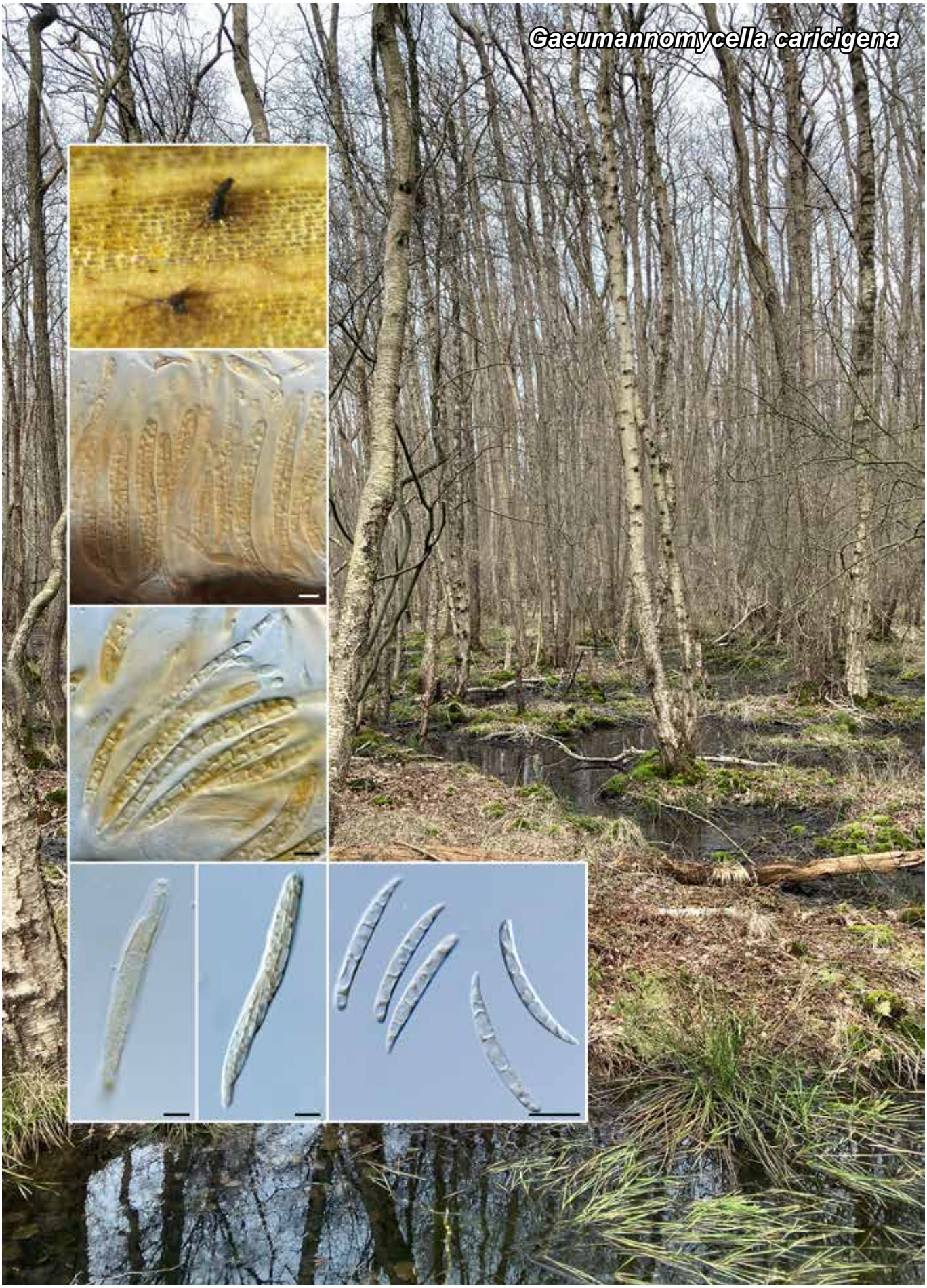
Gaeumannomycella caricigena

Fungal Planet 1499 – 29 June 2023

Gaeumannomycella caricigena Crous & Osieck, *sp. nov.*

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

Classification — *Magnaporthaceae*, *Magnaporthales*, *Sordariomycetidae*, *Sordariomycetes*.

Perithecia immersed in host tissue, solitary, black, with somewhat irregular, cylindrical, black periphysate neck, up to 600 µm long, up to 80 µm diam, and globose base, 250–300 µm diam; wall of 3–6 layers of brown *textura angularis*. *Paraphyses* hyaline, septate, unbranched, 2.5–3 µm diam. *Asci* unitunicate, 8-spored, subclavate to subcylindrical, with basal taper and foot cell, curved with non-amyloid apical mechanism (in Melzer), 80–100 × 9–11 µm. *Ascospores* hyaline, smooth, guttulate, 3-septate, apex obtuse, base tapered, subobtuse, (35–)38–40(–42) × (3.5–)4 µm. *Cultures* sterile.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, even margin, reaching 50 mm diam after 2 wk at 25 °C. On malt extract agar (MEA), potato dextrose agar (PDA) and oatmeal agar (OA) surface and reverse olivaceous grey

Typus. Netherlands, Overijssel Province, Reutumerveen near Reutum, N52°23'43" E06°49'24", on dead culms of *Carex elongata* (*Cyperaceae*), 20 Mar. 2022, *E.R. Osieck*, HPC 3952 = WI-50/#4449 (holotype CBS H-25207; culture ex-type CPC 44028 = CBS 149683; ITS and LSU sequences GenBank OQ628488.1 and OQ629070.1; MycoBank MB 848082).

Notes — *Gaeumannomycella* was introduced by Hernández-Restrepo et al. (2016) for species occurring on *Cyperaceae*, namely *G. caricis* (*asexual, conidia* lunate or cylindrical, hyaline, 6.5–9.5 × 1–2 µm; Hernández-Restrepo et al. 2016) and *G. caricicola* (sexual, ascomatal necks up to 167 µm long, asci 73–210 × 9–18 µm, ascospores 0–3-septate, 32–45 × 3–3.5 µm; Crous et al. 2019a). *Gaeumannomycella caricigena* is phylogenetically distinct from both species, but also morphologically distinct in that it has perithecia with necks up to 600 µm long, and shorter asci (80–100 × 9–11 µm). *Gaeumannomycella* (confined to *Cyperaceae, Carex*) is close to *Gaeumannomyces* (mainly on *Poaceae*, grasses) but has much shorter ascospores.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Gaeumannomycella caricicola* (strain CBS 145041, GenBank NR_163360.1; Identities = 505/518 (97 %), three gaps (0 %)), *Gaeumannomycella caricis* (strain CBS 388.81, GenBank NR_146245.1; Identities = 476/504 (94 %), seven gaps (1 %)) and *Nakataea oryzae* (voucher DAR71531, GenBank MH516052.1; Identities = 485/523 (93 %), eight gaps (1 %)). Closest hits using the **LSU** sequence are *Gaeumannomycella caricis* (strain CBS 388.81, GenBank NG_058109.1; Identities = 737/748 (99 %), no gaps), *Gaeumannomyces tritici* (strain CBS 450.77, GenBank MH872854.1; Identities = 752/764 (98 %), no gaps) and *Slopeiomyces cylindrosporus* (strain CBS 610.75, GenBank NG_057751.1; Identities = 752/764 (98 %), no gaps).

Colour illustrations. *Carex elongata* growing at Reutumerveen near Reutum in Overijssel Province, the Netherlands. Perithecial necks protruding from host tissue; asci with ascospores; ascospores. Scale bars = 10 µm.

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Phaeosphaeria scalesiae

Fungal Planet 1500 – 29 June 2023

Phaeosphaeria scalesiae Crous, *sp. nov.*

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

Classification — *Phaeosphaeriaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*.

Conidiomata pycnidial, solitary, immersed to erumpent, globose, brown, with central ostiole, 150–300 µm diam; wall of 3–6 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining inner cavity. *Conidiogenous cells* subhyaline, smooth, ampulliform to doliiform, 4–6 × 4–5 µm; proliferating inconspicuously at apex. *Conidia* solitary, pale brown, smooth, guttulate, subcylindrical, straight to curved, apex obtuse, base obclavate to subcylindrical, hilum truncate, 1.5–2 µm diam, (1–)3(–5)-septate, (18–)24–26(–32) × 2.5(–3) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On malt extract agar (MEA), potato dextrose agar (PDA) and oatmeal agar (OA) surface smoke grey, reverse sienna to smoke grey.

Typus. Ecuador, Galapagos Islands, San Cristobal Island, on *Scalesia* sp. (*Asteraceae*), 20 May 2021, *D.A. Ortiz*, HPC 3921 = S13-AZ1 (holotype CBS H-25206; culture ex-type CPC 44012 = CBS 149684; ITS, LSU and *rpb2* (first part) sequences GenBank OQ628489.1, OQ629071.1 and OQ627946.1; MycoBank MB 848083).

Notes — *Phaeosphaeria scalesiae* is related to *P. phoenicicola* (conidia 1–3-septate, (8–)12–14(–16) × (2–)2.5(–3) µm; Crous et al. 2016) based on a blast search using its ITS sequence, but morphologically distinct as it has larger conidia, and is the first species of *Phaeosphaeria* reported on *Scalesia.*

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phaeosphaeria phoenicicola* (strain CPC 28711, GenBank NR_156608.1; Identities = 484/497 (97 %), no gaps), *Hendersonia culmiseda* (strain CBS 100.72, GenBank MH860403.1; Identities = 484/498 (97 %), two gaps (0 %)) and *Phaeosphaeria oryzae* (strain MUT<ITA> 2928, GenBank MG813229.1; Identities = 474/488 (97 %), one gap (0 %)). Closest hits using the **LSU** sequence are *Phaeosphaeria acaciae* (voucher MFLU 17-0496, GenBank NG_069453.1; Identities = 819/819 (100 %), no gaps), *Phaeosphaeria lunariae* (strain CPC 26679, GenBank KX306791.1; Identities = 814/814 (100 %), no gaps) and *Phaeosphaeria cycadis* (strain KUMCC 18-0161, GenBank NG_070078.1; Identities = 810/810 (100 %), no gaps). Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Phaeosphaeria acaciae* (strain KUMCC 20-0214, GenBank MW192765.1; Identities = 737/809 (91 %), two gaps (0 %)), *Phaeosphaeria oryzae* (strain MFLUCC 11-0170, GenBank KM434306.1; Identities = 580/638 (91 %), no gaps) and *Phaeosphaeria musae* (strain MFLUCC 11-0133, GenBank KM434304.1; Identities = 579/638 (91 %), no gaps).

Colour illustrations. *Scalesia* sp. on San Cristobal Island (Photo credit G.F. Rivas-Torres). Conidioma on pine needle agar; broken conidioma with conidia; conidiogenous cells; conidia. Scale bars = 300 µm (conidiomata), 10 µm (all others).

Supplementary material

See the supplementary material FP1480 for a phylogenetic tree containing this novel species.

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Arrhenia similis

Fungal Planet 1501 – 29 June 2023

Arrhenia similis Gulden, Rian & I. Saar, *sp. nov*.

Etymology. From Latin *simile* = likeness, referring to the similarity to other species of the complex.

Classification — *Hygrophoraceae*, *Agaricales*, *Agaricomycetes.*

Basidioma dimidiate, fan-shaped, laterally stipitate. *Pileus* 0.5–2.8 cm, young almost plane to faintly convex, gradually becoming wavy and slightly depressed towards stipe, surface smooth with faint concentric ridges, opaque, hygrophanous, margin turned in at first, even and smooth, becoming straight, crenulate, sometimes slightly ribbed, grey brown (M51, N51, P51, S75, R 75; Cailleux 1981), drying to beige (L91, M91). *Lamellae* adnexed to adnate, close, occasionally forked, thin, approximately 2 mm high, lamellulae from pileus margin, grey (N91, P91) almost concolourous with the pileus. *Stipe* 0.4–0.6 × 0.1–0.3 cm, lateral, solid, concolourous with the pileus, more or less white strigose to pubescent from base upwards. *Context* thin, concolourous with pileus, without noticeable smell and taste. *Spore print* white. Dry basidioma with a conspicuously white stipe well contrasting lamellae and pileus. *Basidiospores* 5.5–7.5(–7.9) × 4.0–6.2 µm, av. 6.4 × 5.0 µm, Q = 1.1–1.5, $Q_{av.}$ = 1.3, n = 190, ellipsoid to pip-shaped to broadly ellipsoid-subglobose with prominent apiculus, smooth, hyaline, inamyloid, acyanophilic. Spores of holotype measured in Congo red from spore print: (5.5–)5.8–7.0(–7.5) × 4.5–5.4 µm, av. 6.4 × 5.1 µm, Q = 1.2–1.4, $Q_{av.}$ = 1.3, n = 25. *Basidia* 25–32 × 6–7 µm, 4-spored, clavate, hyaline, not siderophilous. *Cystidia* absent. *Hymenophoral trama* of ± parallel 4–10 µm wide hyphae with segments of medium length, pale brown from membranal pigment, in some parts darker brown. *Pileipellis* of ± parallel, 5–10 µm wide hyphae with segments of medium length, brown from membranal pigment, occasionally zebra-incrusted. *Stipitipellis* of similar hyphae; strigosity at base of stipe of hyaline, 3–4.5 µm wide, long-celled hyphae. All hyphae thin-walled. *Clamp connections* at base of basidia and abundant in all tissues.

Habitat & Distribution — Solitary or in small groups, growing on half-buried pieces of rotting wood (e.g., *Picea*), old lichen fragments (*Peltigera*), grass turf, on and among bryophytes, often in or along paths, in dry grassland and woodland. Known in Europe (Norway, Russian North Karelia) and western North America (Canada: BC; USA: AL, WA).

Typus. Norway, Buskerud, Ringerike, near Grunntjern, N60°09'09" E10°20'06", in grass-grown path, on and around a wooden chip overgrown with grass turf (*Deschampsia flexuosa*) and bryophytes, in a hemiboreal, mixed spruce and pine forest with occasional *Betula*, *Salix* etc., on calcareous ground (Cambro-Silurian rocks), 12 Oct. 2021, *B. Rian, G. Gulden & G. Strømsøe*, GG 8/21 (holotype O-F-203792, isotype TUF117928; ITS sequence GenBank OQ161625; MycoBank MB 847742).

Additional materials examined. Norway, Akershus, Nannestad, Nordmokorset, among moss and *Salix herbacea*, on dead wood of *Picea abies*, 15 Sept. 1997, *L. Ryvarden* (O-F-63232, ITS sequence GenBank MT967299); Hedmark, Kongsvinger, Berger, among moss and *Salix herbacea*, 26 Aug. 2005, *H. Eriksen, A.B. Stærnes, T. Solem, M. Gjestland & H. Karlsen* (O-F-67900, ITS sequence GenBank MT967301). Five more collections were sampled in the type locality, growing in the same path: O-F-203791 (TUF117870, ITS sequence GenBank OQ161621) from 3 Oct. 2020, O-F-203795 (ITS sequence GenBank OQ161622), from 12 Oct. 2021, and O-F-204285, O-F-204286, O-F-204287 from 4 Oct. 2022. Basidiome size, shape, colours etc. of these were within the range of the type collection, but some specimens were almost sessile. Substrates: a leaf sheath of living grass (*Deschampsia flexuosa*), tiny sticks of wood, and bryophytes.

Notes — *Arrhenia similis* matches the taxon named AC-1 in the phylogeny of Voitk et al. (2020). Macroscopically it resembles *A. subglobisemen* most closely, but we have not found reliable macroscopic distinguishing characters to separate it consistently from several species in the *A. acerosa* complex. Intraspecific spore size variation within the complex is wide, but some species, like *A. similis,* with relatively short and broad spores are more consistent. On an average, the spores of *A. similis* are narrower and slightly shorter than those of the sister species *A. subglobisemen* and they are both shorter and wider than those of *A. acerosa s. str.* Interestingly, basidioma of *A. acerosa* (O-F-203793, O-F-203794/ TUF117939; sequences GenBank OQ161623 and OQ161624) occurred in two places in the same path in between the *A. similis* sites, all within a stretch of 30 m.

Voitk et al. (2020) concluded that the *A. acerosa* complex demonstrated a preference for woody or dead herbaceous substrates. The occurrence of one specimen of *A. similis* on a leaf sheet of a living *Deschampsia* may not contradict this; the actual sheet appeared dry, without living tissue. Notably, the occurrence of *A. similis* on *Peltigera* in Russia and Canada does not imply any close relationship with *Arrhenia peltigerina*, see Diedrich et al. (2022).

Based on a blast search of the UNITE database, the closest hits of ITS sequence from the isotype are *Arrhenia subglobisemen* (GenBank MT967351; Identities = 599/604 (98 %), 13 gaps (2 %)) and *A. latispora* (GenBank MT967324; Identities = 602/610 (92 %), 51 gaps (8 %)).

Colour illustrations. Collection site of the holotype of *Arrhenia similis*, Norway. Lower inserts show holotype in situ; basidia and spores in Congo Red (spores rest on a common black baseline, apiculus upwards; the distance between the lower black line and upper white line is 5 µm). Scale bars = 10 mm (basidiomata), 10 µm (basidia).

Supplementary material

FP1501 Phylogenetic tree.

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Aspicilia lutzoniana

Fungal Planet 1502 – 29 June 2023

Aspicilia lutzoniana Rodr. Flakus, Szczepańska & Flakus, *sp. nov.*

Etymology. Named in honour of François Lutzoni (Durham, USA), our friend and the prominent Canadian-born lichenologist, for his magnificent contribution to knowledge on the phylogenetics and evolution of lichen symbioses, including freshwater lichens.

Classification — *Megasporaceae*, *Pertusariales*, *Lecanoromycetes*.

Thallus lichenised, crustose, areolate to rimose, 0.1–0.9 mm thick, smooth, matt to indistinctly shiny, whitish grey to dark grey or olive brown, encrusted with crystals; photobiont *Trebouxia* clade I15 (acc. Kosecka et al. 2022), cells 5–17 µm diam. *Prothallus* usually present, pale grey to blackish, sometimes with a greenish tinge, faintly fimbriate. *Areoles* flat to slightly convex, angular, smooth, vanishing at the thallus margin, 0.2–1 mm diam. *Cortex* 10–30 µm thick, composed of several layers of thick-walled cells, cells 5–9 × 2–8 µm, the uppermost part brownish grey, sometimes covered with a thin epinecral layer. *Apothecia* aspicilioid, abundant (0.2–)0.4–0.8(–1.2) mm diam and 180–300 µm high, immersed, 1–3(–4) per areole, round to irregular (when more than one per areole). *Disc* dark grey to black, concave to rarely flat, epruinose. *Proper margin* indistinct. *Thalline margin* apparent, thin, slightly elevated, much darker than the thallus, greyish black, rarely with a thin white rim on the inside edge. *Epihymenium* greyish green to olive brown, 5–15 µm high, N+ caerulescens green, K+ orange brown (Caesiocinerea green pigment). *Hymenium* colourless, 100–200 µm tall, K/I+ dark blue. *Paraphyses* septate, 1–2 µm wide, anastomosing, submoniliform with 1–3 globose apical cells, 2–6 µm wide at the top. *Hypothecium* colourless, 50–100 µm high, I+ blue. *Exciple* paraplectenchymatous, I+ blue, composed of thick-walled cells, 2–9 × 2–7 µm, hyaline and 7–15 µm wide in the lower part, grey-pigmented and up to 50–60 µm wide in the upper part. *Asci* 8-spored, cylindrical to clavate, 85–140 × 30–45 µm, the outer coat K/I+ blue, the wall and apical dome K/I-. *Ascospores* hyaline, simple, ellipsoid, (16–)18–24(–25) × 12–16(–17) µm (n = 40). *Pycnidia* immersed, 100–130 × 80–100 µm, ostiolar region black, upper part in section with greyish pigment, N+ caerulescens green, K+ orange brown. *Conidiogenous cells* hyaline, 7–13 × 1.5–2 µm. *Conidia* hyaline, filiform, straight, (7–)8–12(–13) × 1–1.5 µm. *Spot tests*: thallus K-, C-, KC-, P-, I-. *Secondary metabolites*: unknown terpenoid detected by TLC.

Habit, Habitat & Distribution — *Aspicilia lutzoniana* is known from two localities where its abundant populations are growing on fully submersed siliceous schist in high-mountain streams in open Páramo Yungueño vegetation between 3734 and 3914 m a.s.l. in Bolivian Andes.

Typus. Bolivia, La Paz Department, Nor Yungas Province, Choquetanka stream, near Pongo village, close to the road Coroico-La Paz, S16°19'20.48" W67°57'19.15", 3914 m a.s.l., Páramo Yungueño, on siliceous schists in a stream, 14 Feb. 2019, leg. *P. Rodriguez de Flakus* 4025, *A. Flakus & S. Gallegos* (holotype KRAM L-73347, isotype LPB; ITS, LSU, and mtSSU sequences GenBank OQ586176, OQ586169 and OQ586385; MycoBank MB 847865).

Additional materials examined. Bolivia, La Paz Department, Nor Yungas Province, ibid., S16°19'27.89" W67°57'22.68", 3824 m a.s.l., 26 Nov. 2011, *A. Flakus*, 23323-2 (KRAM, LPB; ITS, LSU and mtSSU sequences GenBank OQ586177, OQ586165 and OQ586381); ibid., S16°19'20.48" W67°57'19.15", 3914 m a.s.l., 14 Feb. 2019, *P. Rodriguez-Flakus* 4021, *A. Flakus* & *S. Gallegos* (KRAM, LPB; ITS, LSU and mtSSU sequences GenBank OQ586178, OQ586167, OQ586182, OQ586385 and OQ586383), *P. Rodriguez-Flakus* 4024, *A. Flakus* & *S. Gallegos* (KRAM, LPB; ITS, LSU and mtSSU sequences GenBank OQ586175, OQ586168 and OQ586384); PNANMI Cotapata, Jinchumuruni stream, below Pongo village, road Coroico-La Paz, S16°19'15.72" W67°56'32.89", 3734 m a.s.l., Páramo Yungueño, on siliceous schist in a stream with crystalline water, 9 Dec. 2016, *leg. P. Rodriguez-Flakus* 3779 & *A. Flakus* (KRAM, LPB; ITS, LSU and mtSSU sequences GenBank OQ586174, OQ586166 and OQ586382).

Notes — *Aspicilia* is one of the eight genera established within *Megasporaceae* (Nordin et al. 2010, Sohrabi et al. 2013, Haji Moniri et al. 2017, Zakeri et al. 2017). Although cosmopolitan, the family is poorly studied in South America where it is represented by seven species (Galloway & Quilhot 1998, Calvelo & Liberatore 2002, Rodriguez-Flakus et al. 2016, Fryday et al. 2021). From Bolivia, only three of them, *Aspicilia cinerea*, *Circinaria contorta* and *Megaspora verrucosa*, were reported so far (Nylander 1861, Feuerer et al. 1998, Flakus et al. 2013). The newly introduced species, *Aspicilia lutzoniana*, is quite distinctive and differs from the other freshwater members of *Megasporaceae* by having a unique combination of ascospore (16–25 × 12–17 µm) and conidial (7–13 µm long) sizes, absence of secondary metabolites (except terpenoids), mainly rounded apothecia with much darker than the thallus margin (greyish black) and a separate phylogenetic position. In our phylogenetic analyses, *A. lutzoniana* is shown to be the most closely related to *A. knudsenii* known from the Sonora Desert, USA. Nevertheless, the latter species has a different, brown to olive brown thallus, larger ascospores ((18–)20–27(–30) × (10–)12–17(–18) µm) and conidia (5–12(–22) µm long), and also contains stictic and norstictic acids or rarely hyposalazinic acid instead of nostictic acid (Owe-Larsson et al. 2007). There are several species known from freshwater or humid habitats which are similar to *A. lutzoniana* in their morphology (e.g., *A. aquatica*, *A. calcitrapa*, *A. cyanescens*, *A. humida*, *A. laevata A. malvinae*, *Circinaria caesiocinerea*, and *Oxneriaria supertegens*). Within them, *A. aquatica*, *A. laevata* and *O. supertegens*, are known as the most typical aquatic species, and can be separated from *A. lutzoniana* in having the following characteristics: i) larger ascospores (22–35 × 13–20 µm) and conidia (12–16 µm long), ii) smaller ascospores (13–23 × 9–13 µm), larger conidia (18–25 µm long) and presence of stictic and norstictic acids, and iii) whitish thallus, larger irregular apothecia with thick white margin and larger conidia (31–37 µm long) (Thomson 1984, Fletcher et al. 2009, Thüs & Schultz 2009).

(Notes continued on Supplementary page)

Colour illustrations. The Choquetanka stream near Pongo village in high-mountain Páramo Yungueño vegetation, La Paz department, Bolivia (photo credit A. Flakus). A habit of thallus with ascomata; cross-section of the apothecial margin (mounted in LPCB); ascus (mounted in Lugol's iodine solution pre-treated by KOH); ascospores (left) and conidia (right) (mounted in water). Scale bars = 500 µm (a habit), 10 µm (all others).

Supplementary material

FP1502-1 Phylogenetic tree.

FP1502-2 Table. GenBank and voucher accession numbers of sequences included in the phylogenetic analyses.

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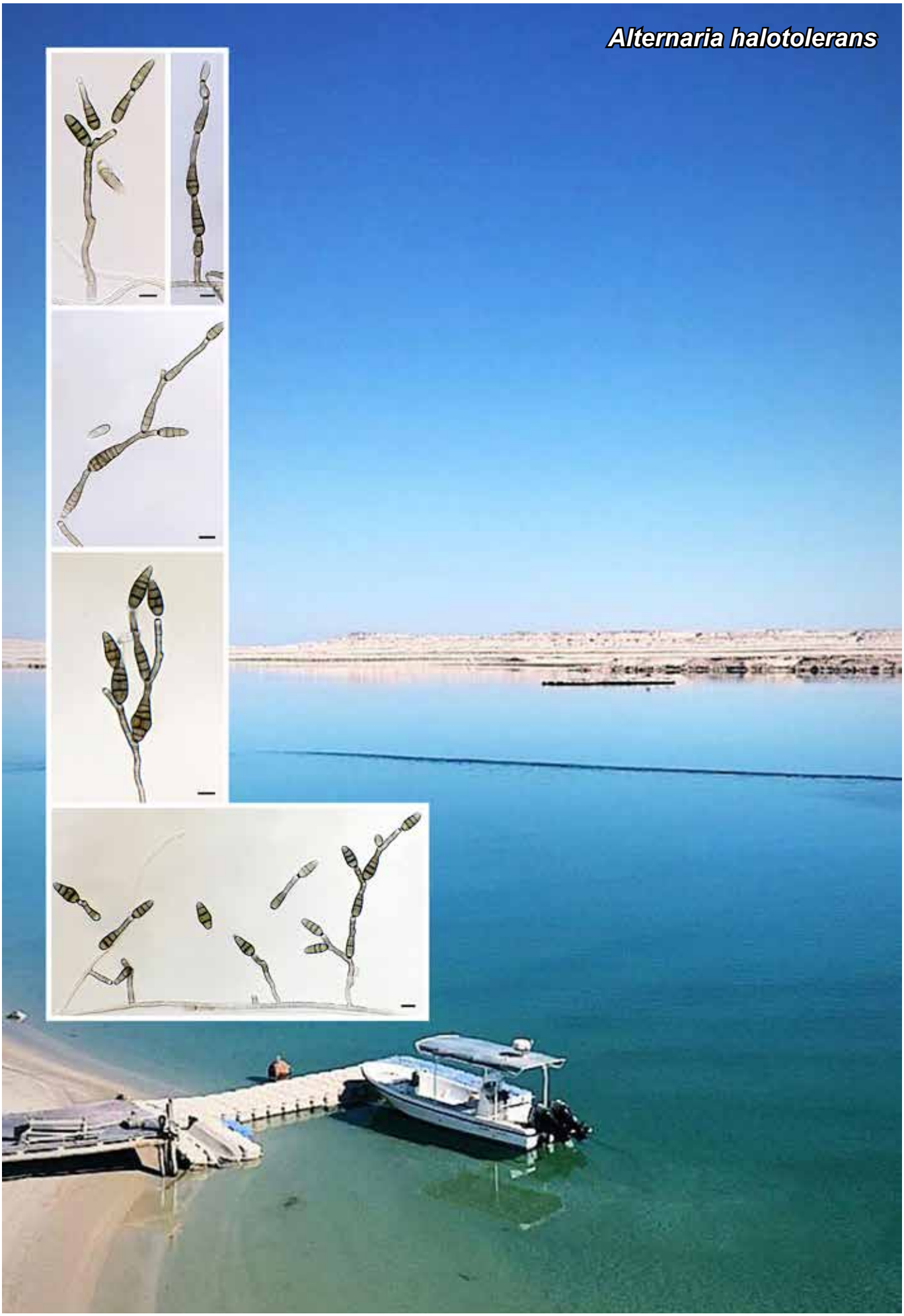
Alternaria halotolerans

Fungal Planet 1503 – 29 June 2023

Alternaria halotolerans R. Fotedar, M. Sand.-Den., A. Kolecka & T. Boekhout, *sp. nov.*

Etymology. Named after its ability to grow in hypersaline sea water with high salinity.

Classification — *Pleosporaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*.

On Potato carrot agar (PCA), *mycelium* consisting of pale brown, septate, smooth, straight to slightly curved hyphae. *Primary conidiophores* solitary, occasionally branched, smooth, straight to slightly curved, septate, pale brown with a hyaline tip, (12–)20.5–49(–70) × 2.5–3.5 µm, bearing up to four geniculate conidiogenous extensions with darkened conidiogenous loci. *Conidia* solitary or in short chains, simple or branched, pale olive brown, (narrowly) ovoid to obpyriform, primary conidia (19.5–)27–46(–65) × (5–)5.5–9(–11.5) µm, with 4–6 transverse septa and 0–3 oblique or longitudinal septa, rough-walled at the lower sections and smooth-walled at the top sections. The conidial body sometimes constricted near thickened and darkened transverse septa. Conidia can form an apical secondary conidiophore which can again form a geniculate conidiogenous extension. *Sexual morph* not observed.

Culture characteristics — Colonies after 7 d at 25 °C. On PCA, reaching 68 mm diam, flat, margin entire, colourless with olivaceous rings; with patches of felty, white aerial mycelium. On Synthetic nutrient poor agar (SNA), reaching 60 mm diam, flat, margin fimbriate; with colourless, woolly, white aerial mycelium at centre.

Typus. Qatar, Doha, Inland Sea, Khor Al- Adaid, E51.3325 N24.55226, from hypersaline sea water at 2.5 m depth, 20 Sept. 2014, *R. Fotedar* (holotype CBS H-24902 (dried culture); culture ex-type 2M108 = QCC M0010/16 = CBS 146348; ITS, LSU, *gapdh* and *tef1* sequences GenBank KY387606, KY781812, KY387604 and KY387608; MycoBank MB 844257).

Notes — *Alternaria halotolerans* was isolated from seawater with a salinity of 57–58 PSU (Practical Salinity Units) and a temperature of 32–33 °C from a pelagic site located at the entrance of the 10 km long channel that allows exchange of sea water from the Arabian Gulf to the Inland Sea (Fotedar et al. 2018).

Phylogenies inferred from the combined *gapdh*, ITS, LSU and *tef1* sequences placed *Alternaria halotolerans* within *Alternaria* section *Infectoriae*, representing a novel lineage related but phylogenetically distinct from *Alternaria cesenica* and *A. pseudoventricosa*, two recently described species known from *Bellevalia romana* (*Asparagaceae*) in Italy, and horse dung in Spain, respectively (Liu et al. 2015, Marin-Felix et al. 2019). *Alternaria halotolerans* differs from the two above-mentioned species most notably in its isolation substrate and geographic origin; however, being also distinguished from *A. pseudoventricosa* by its ovoid, and slightly slender conidia, on which longitudinal septa occur much more frequently. Conversely, *A. cesenica* is only known from its sexual morph (Liu et al. 2015), a morph not observed for *A. halotolerans*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Alternaria ventricosa* (strain CBS 121546, GenBank MH863116.1; Identities = 544/544 (100 %), no gaps) and *Alternaria quercicola* (strain ISK1_7, GenBank MK460940.1; Identities = 544/544 (100 %), no gaps). Closest hits using the **LSU** sequence are *Alternaria slovaca* (strain CBS 567.66, GenBank NG_069726.1; Identities = 837/837 (100 %), no gaps), and *A. quercicola* (strain CPC 26165, GenBank KX228348.1; Identities = 837/837 (100 %), no gaps). Closest hits using the ***gapdh*** sequence had highest similarity to *Alternaria caespitosa* (strain CBS 177.80, GenBank KC584178.1; Identities = 521/525 (99 %), no gaps) and *Alternaria peglionii* (strain CBS 103.26, GenBank JQ646286.1; Identities = 514/522 (98 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *A. slovaca* (strain CBS 567.66, GenBank KC584702.1; Identities = 231/238 (97 %), no gaps) and *Alternaria hordeicola* (strain CBS 121458, GenBank LR134371.1; Identities = 229/238 (96 %), no gaps).

Colour illustrations. Khor Al- Adaid, Qatar. Conidiophores; conidiogenous cells; conidia. Scale bars = 10 µm.

Supplementary material

FP1503 & 1504 Phylogenetic tree.

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Alternaria qatarensis

Fungal Planet 1504 – 29 June 2023

Alternaria qatarensis R. Fotedar, M. Sand.-Den., Jack W. Fell, A. Kolecka & T. Boekhout, *sp. nov*.

Etymology. Name refers to the country of origin, Qatar, from where the fungus was collected.

Classification — *Pleosporaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*.

On Potato carrot agar (PCA), *primary conidiophores* solitary, smooth, straight to slightly curved, septate, pale brown with a hyaline tip, (17.5–)26.5–48.5(–58) × 3–3.5 µm, bearing 0–2 geniculate conidiogenous extensions with darkened conidiogenous loci. *Conidia* in chains, simple or branched, pale olive-brown, (narrowly) ovoid to obpyriform, primary conidia (27–)32.5–42.5(–47.5) × (5–)6–9.5(–12) µm, with 6–8 transverse septa and 0–3 oblique or longitudinal septa, smooth-walled. Conidia can form apical and lateral secondary conidiophores which can again form a geniculate conidiogenous extension. *Sexual morph* not observed.

Culture characteristics — Colonies after 7 d at 25 °C. On PCA, reaching 56–61 mm diam, flat, margin entire, white with woolly olivaceous grey aerial mycelium at centre, sparse aerial mycelium at the margin. On synthetic nutrient poor agar (SNA) reaching 53–55 mm diam, flat, margin fimbriate, colourless, aerial mycelium sparse.

Typus. Qatar, Doha, Inland Sea, Khor Al-Adaid, from water sample collected from hypersaline lagoon, E51.2884 N24.6706, depth 0.5 m, 11 Dec. 2013, *R. Fotedar* & *J.W. Fell* (holotype CBS 146387 preserved in a metabolically inactive state; culture ex-type INM7 = QCC M009 = CBS 146387 = MUCL 57539; ITS, LSU, *gapdh*, and *tef1* sequences GenBank KY387605, KY781811, KY387603, and KY387607; MycoBank MB 819521).

Additional material examined. Qatar, Doha, Al- Khor, from water sample collected from hypersaline marine water, E51.52821 N25.68958, depth 2.5 m, 13 Feb. 2015, *R. Fotedar*, culture CBS 146346 = 3M142; ITS, LSU, *gapdh* and *tef1* sequences GenBank MK480720, MK480721, OL964366, and OL989030.

Notes — *Alternaria qatarensis* was collected during a survey of mycobiota of the coastal marine water surrounding Qatar (Fotedar et al. 2018). Strains assigned to *A. qatarensis* cluster as a novel lineage, not directly related to any of the species currently known based on molecular data within the section *Chalastospora* of *Alternaria*.

Phylogenetically, the closest species to *A. qatarensis* in section *Chalastospora* is the recently described *Alternaria pobletensis* (Marin-Felix et al. 2019). *Alternaria qatarensis* differs from *A. pobletensis* not only in its biogeographic and ecological association (sea water in Qatar *vs* animal dung in Europe for *A. pobletensis*), but also morphologically by its shorter conidiophores (up to 58 µm vs up to 82 µm in *A. pobletensis*) and slender conidia (5–12 µm wide vs 5–20 µm in *A. pobletensis*). Conversely, relatively abundant longitudinal septa are observed in conidia of both *A. pobletensis* and *A. qatarensis*, an uncommon feature in species of section *Chalastospora* (Woudenberg et al. 2013, Marin-Felix et al. 2019).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *A. pobletensis* (strain FMR 16448, GenBank NR_166226.1; Identities = 527/529 (99 %), two gaps), and *Alternaria cetera* (strain AW3013, GenBank MT802499.1; Identities = 523/524 (99 %), one gap). Closest hits using the **LSU** sequence are *Alternaria malorum* (strain CBS 126589, GenBank MH875629.1; Identities = 881/883 (99 %), no gaps) and *Alternaria obclavata* (strain CBS 124120, GenBank MH874877; Identities = 881/883 (99 %), no gaps). Closest hits using the ***gapdh*** sequence had highest similarity to *Alternaria armoraciae* (strain CBS 118702, GenBank KC584099.1; Identities = 492/501 (98 %), no gaps) and *Alternaria breviramosa* (strain CBS 121331, GenBank KC584148.1; Identities = 487/501 (97 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *A. obclavata* (strain CBS 124120, GenBank KC584701.1; Identities = 225/240 (94 %), four gaps) and *A. armoraciae* (strain CBS 118702, GenBank KC584638.1; Identities = 221/235 (94 %), eight gaps).

Colour illustrations. Khor Al-Adaid Inland sea and desert, Qatar (Wikimedia commons, photo by Flashpacker Travelguide, licensed under the Creative Commons Attribution-Share Alike 2.0 generic license). Conidiophores; conidiogenous cells; conidia. Scale bars = 10 µm.

Supplementary material

FP1503 & 1504 Phylogenetic tree.

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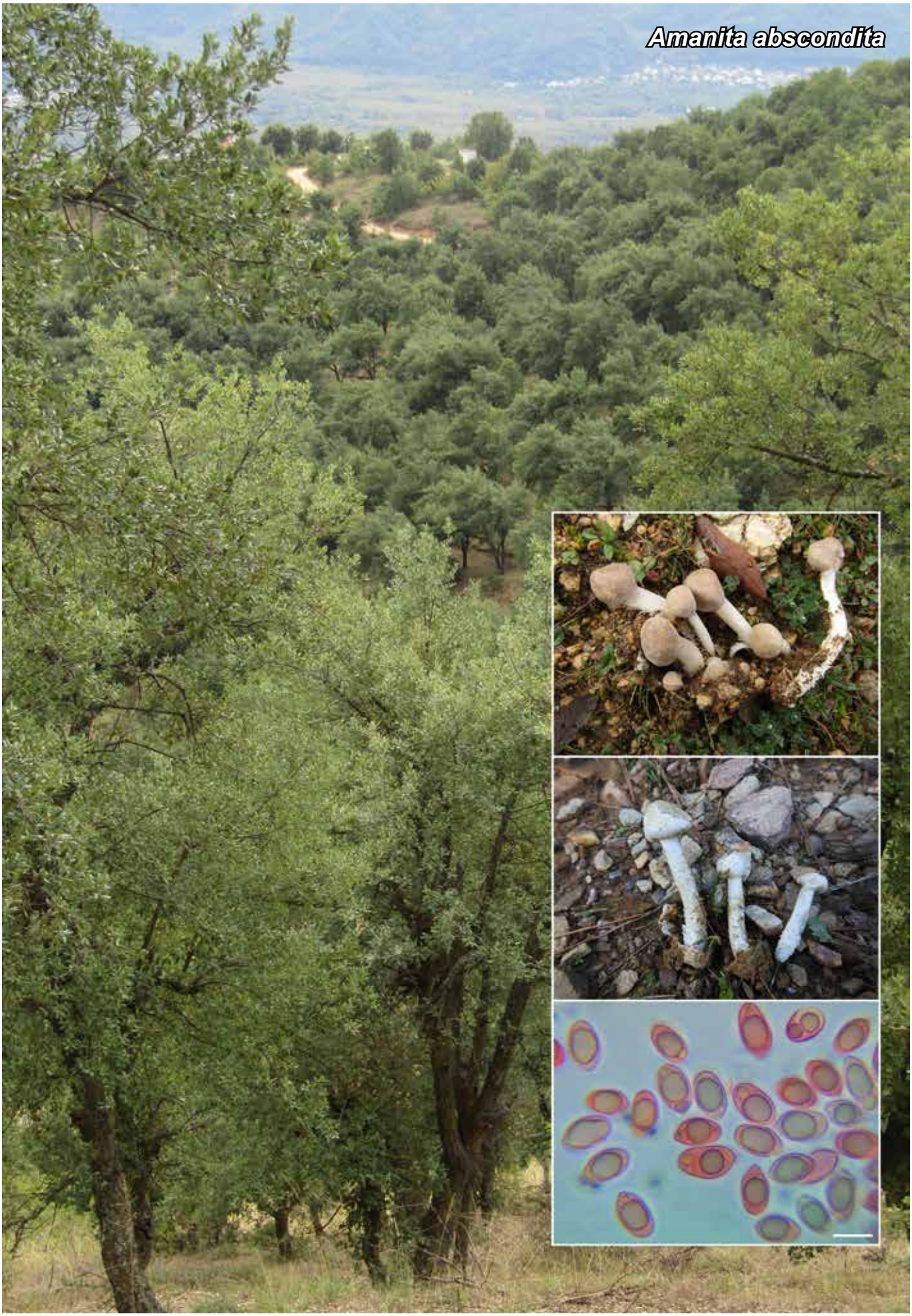
Amanita abscondita

Fungal Planet 1505 – 29 June 2023

Amanita abscondita Assyov, Bozok, Taşkın & Yarar, *sp. nov.*

Etymology. Latin, *absconditus* = hidden, concealed – with reference to both the recent recognition of the species and to its secotioid habit.

Classification — *Amanitaceae*, *Agaricales*, *Agaricomycotina*.

Basidiomata secotioid, scattered or clustered in groups of up to 10. *Pileus* almost spherical, ovoid or somewhat irregular, up to 2.5 cm across; margin strongly enrolled, sometimes slightly appendiculate, forming a narrow opening through which the stipe attaches to the pileal interior; surface pruinose, in very young basidiomata whitish, soon greyish, often with adhering irregular, whitish patches of general veil. *Stipe* cylindrical or subcylindrical, straight or more or less curved, up to 7 × 0.8 cm, extremely fragile, whitish, smooth or somewhat fibrillose, often cracking into large scales, with remnants of general veil as cup-shaped, whitish, crumbly volva at the base. *Hymenium* secotioid, in surface view with irregularly poroid appearance, whitish, in section loculate; chambers rounded or polyhedral, rarely elongated, up to 2 mm across. *Basidiospores* smooth, hyaline, inamyloid and non-dextrinoid, usually with a single, large, central guttule in KOH and NH_4OH, 8.6–15.2 × 5.2–9 µm, Q = 1.45–1.96; Lav = 10.4–12.9 µm, Wav = 6.2–7.6 µm, Qav = 1.66–1.71 (n = 120, incl. apiculi), oblong or ellipsoid, occasionally pruniform; apiculus prominent, 1–1.5 µm long. *Basidia* broadly clavate to clavate, thin-walled, hyaline, 1–4-spored. *Hymenial trama and subhymenium* subcellular, composed of rounded, polygonal or irregular, thin-walled elements up to 23 × 16 µm. *General veil* on stipe base (volva), internal layer: sphaerocysts abundant, 31.8–91.7 × 26.9–75.7 µm, other inflated elements present but rare, undifferentiated hyphae 3–8 µm wide; on stipe base, external layer: compact, sphaerocysts present, but not abundant, undifferentiated hyphae sometimes in bundles; clamp connections present; tromboplerous hyphae not seen in either layer; on pileal surface: as on stipe base. *Pileipellis* up to 250 µm thick, composed of neatly packed spherical, ovoid, pyriform or cystidioid inflated elements, 9.3–27.7 × 7.7–25.8 µm, intermixed with scarce undifferentiated hyphae, 1–3 µm broad; in places bundles of inflated elements protruding through the main surface (corresponding to pileal pruinosity). *Stipe context* longitudinally acrophysalidic, undifferentiated hyphae 1.5–4 µm wide, hyaline, thin-walled acrophysalides narrowly clavate, 65–118.8 × 9.1–17.8 µm, hyaline, thin-walled, in ammoniacal Congo red with characteristic, fine, zebroid, epiparietal pigments; clamp connections occasionally seen; tromboplerous hyphae not encountered. *Microchemical reactions* K-K reaction negative in all parts.

Habit, Habitat & Distribution — Known from Bulgaria and Türkiye, where it appears scattered or in groups between November and December in stands with Mediterranean evergreen oaks.

Typus. Bulgaria, Blagoevgrad Province, Petrich Municipality, Ograzhden Mt, in the vicinity of Parvomay village, N41°25'03.8" E23°07'47.3", elev. c. 255 m a.s.l., in a plantation of *Quercus suber*, 12 Dec. 2021, *B. Assyov* (holotype in SOMF: SOMF 30424; isotype in Fungarium of Osmaniye Korkut Ata University: FBozok 1172; ITS sequence GenBank ON705264; MycoBank MB 845175).

Additional materials examined. Türkiye, İzmir Province, Karacadağ, N38°04'29.1" E27°07'51.1", elev. c. 315 m a.s.l., in sandy soil in a mixed forest of *Pinus* sp., *Cistus* sp., and *Quercus* cf. *coccifera,* 24 Nov. 2019, *F. Bozok, H. Taşkın & M. Yarar* (paratype in Fungarium of Osmaniye Korkut Ata University: FBozok 1010; ITS sequence GenBank ON705265).

Notes — *Amanita abscondita* is the second secotioid member of the genus in Europe, next to *A. torrendii* (Bresadola 1902, Miller & Horak 1992, Neville & Poumarat 2004, Justo et al. 2010), with which the new species is phylogenetically related and shares an obvious morphological similarity. The two species could be distinguished on account of their gross morphology, the colour of pilei in particular. In *A. abscondita* pilei tend to quickly turn greyish in age, while in *A. torrendii* they are white to yellowish or ochraceous tinted (Miller & Horak 1992, Neville & Poumarat 2004). Microscopically the new species is easily identified on account of its basidiospores, which are shorter, up to 15.2 µm long (vs up to 20 µm in *A. torrendii*, Neville & Poumarat 2004; up to 16 µm in Portuguese material, collected by Camille Torrend; Miller & Horak 1992) and on average considerably broader, 6.2–7.6 µm (vs 5.95 µm in *A. torrendii*; Neville & Poumarat 2004), with very different average quotient ratio, 1.66–1.71 (vs 2.06–2.38 in *A. torrendii*, apiculi included; Miller & Horak 1992, Neville & Poumarat 2004). Further on, *A. abscondita* is separated by the architecture of the general veil, which has an outer stratum composed predominantly of undifferentiated filamentous hyphae and few inflated elements, and an inner stratum of abundant sphaerocysts interspersed with undifferentiated hyphae. The volva of *A. torrendii* is reported to contain numerous sphaerocysts in all parts and may have a very thin filamentous outer stratum only by exception (Neville & Poumarat 2004). The phylogenetic analysis places the sequences of *A. abscondita* in a well-supported clade, sister to the clade of *A. torrendii*, the latter encompassing three Spanish sequences, as well as one accession from Cyprus. The Bulgarian and the Turkish sequences are almost identical to each other in pairwise comparison (99.81 %) and differ by a single indel. The sequences of *A. abscondita* differ considerably from those of *A. torrendii* by 11 to 14 substitutions and/or indels, resulting in 96.31 % to 97.00 % similarity. The mycorrhizal partner of *A. abscondita* is presently unknown, but evergreen species of oaks and representatives of the *Cistaceae* family were present in both localities where specimens of *A. abscondita* were collected.

(Notes continued on Supplementary page)

Colour illustrations. Holotype collection area at Ograzhden Mt., Bulgaria. Holotype collection SOMF 30424 (top); paratype collection FBozok 1010 (middle); basidiospores in Congo red (bottom; from holotype). Scale bar = 10 µm.

Supplementary material

FP1505-1 Phylogenetic tree.
FP1505-2 Line drawing of microscopic characters.

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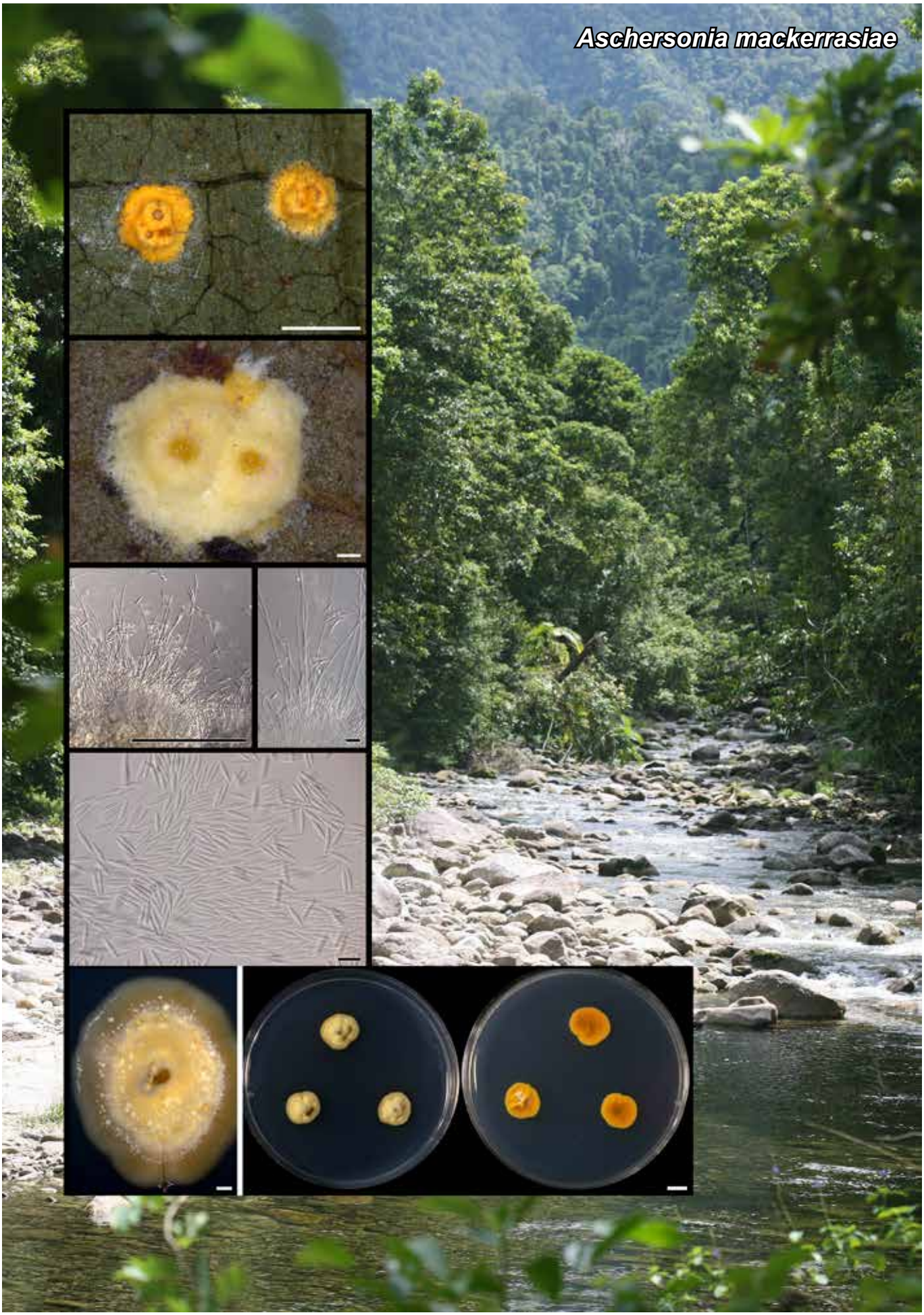
Aschersonia mackerrasiae

Fungal Planet 1506 – 29 June 2023

Aschersonia mackerrasiae Y.P. Tan, R.G. Shivas, Abell, Hywel-Jones & Marney, *sp. nov.*

Etymology. Named after Mabel Josephine (Jo) Mackerras (née Bancroft) (1896–1971), an Australian zoologist, entomologist and parasitologist. Jo Mackerras studied fly-borne diseases in cattle and fatal epizootics in fresh-water fish; led pioneering research into malaria control; and made major contributions to the study of parasites in Australian marsupials. In her retirement, Jo Mackerras began a detailed study of Australian cockroaches, and helped establish the Marine Research Station on Heron Island.

Classification — *Clavicipitaceae*, *Hypocreales*, *Sordariomycetes*.

Hosts are whiteflies (*Hemiptera*: *Aleyrodidae*) attached to lower leaf surfaces in tropical and sub-tropical rainforests. *Mycelium* covers host, yellow to orange, with a membranous, fibrillose white to yellow hypothallus. *Stromata* less than 1 mm diam. *Conidiomata* scattered in stroma, cavities or convolutions in stroma, ostiolate, exude pale yellow conidial masses. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* phialides, cylindrical, 15–20 × 1–1.5 µm, narrowed at the apex, densely crowed on the hymenium. *Paraphyses* abundant, scattered throughout the hymenium, cylindrical to filiform, up to 120 × 1–2 µm. *Conidia* fusiform, 10–12.5 × 1.5–2 µm, straight, smooth-walled, hyaline.

Culture characteristics (25 °C, 7 d, in darkness) — On potato dextrose agar (PDA) 4–5 mm diam; after 4 wk colonies up to 1.5 cm diam and 2 mm high, compact, flat to pulvinate, straw-coloured with a flat pale luteous margin 2 mm wide; reverse sienna at the centre becoming paler towards the margin. Conidial masses produced in culture near the colony margin.

Typus. Australia, Queensland, Lacey Creek, on whitefly, 7 June 2015, *S.E. Abell, T.S. Marney, M.D.E. & R.G. Shivas* (holotype BRIP 62731a, includes ex-type culture; LSU, *rpb2* and *tef1α* sequences GenBank OP793808, OP797905 and OP797910; MycoBank MB 846892).

Additional materials examined. See Supplementary page.

Notes — *Aschersonia* species are entomopathogens of whiteflies (*Aleyrodidae*, *Hemiptera*) and scale insects (*Coccidae*, *Hemiptera*) that have been understudied and often overlooked. The most recent species to have been described was *A. narathiwatensis* from Thailand (Mongkolsamrit et al. 2014). The generic names *Aschersonia* and *Hypocrella* are synonyms (Rossman et al. 2016).

Aschersonia mackerrasiae was collected several times from parasitised whiteflies on leaves in tropical and sub-tropical rainforests across eastern Queensland. *Aschersonia mackerrasiae* differs from *Hypocrella siamensis* (strain BCC 8105) by sequence comparison of the *rpb2* (GenBank DQ522411; Identities 798/826 (97 %); unique nucleotide at positions 17(C), 26(G), 29(G), 50(T), 65(C), 77(A), 80(C), 137(C), 167(T), 290(G), 293(T), 302(T), 329(C), 378(T), 431(T), 491(T), 527(G), 596(C), 638(C), 644(A), 677(T), 695(C), 720(A), 728(C), 737(T), 746(T), 755(C), 770(C)), and *tef1* (GenBank DQ522317; Identities 837/915 (91 %), 19 gaps; unique nucleotide at positions 6(C), 36(A), 39(T), 69(T), 82(C), 93(T), 105(T), 108(A), 162(C), 180(A), 268(C), 276(T), 288(A), 303(C), 324(T), 335(G), 345(C), 348(G), 372(G), 384(T), 402(T), 478(C), 504(C), 522(T), 537(C), 562(A), 570(T), 612(T), 624(C), 627(T), 633(T), 645(A), 648(C), 660(C), 663(C), 675(C), 678(C), 693(A), 699(C), 723(T), 726(C), 729(T), 741(T), 745(C), 750(T), 759(T), 765(C), 780(T), 795(G), 810(T), 819(A), 822(C), 825(C), 834(G), 840(G), 858(T), 879(T), 882(A), 900(C)).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest relevant hits using the **LSU** sequence are *H. siamensis* (strain BCC 8105, GenBank KC713635, Identities 825/825 (100 %)), *A. luteola* (strain SM00098.03, GenBank JN940907, Identities 833/834 (99 %)), *H. discoidea* (strain BCC 7865, GenBank DQ384946, Identities 833/834 (99 %)) and *A. calendulina* (strain SM00186.01, GenBank JN940909, Identities 832/836 (99 %), two gaps). The closest relevant hits using the ***rpb2*** sequence are *H. discoidea* (strain BCC 9481, GenBank DQ452462, Identities 770/788 (98 %)), *H. siamensis* (strain BCC 8105, GenBank DQ522411, Identities 798/826 (97 %)) and *A. paraphysata* (strain BCC 1467, GenBank DQ452463, Identities 597/639 (93 %)). The closest relevant hits using the ***tef1α*** sequence are *H. discoidea* (strain BCC 7865, GenBank DQ384975, Identities 874/929 (94 %)), *H. luteola* (strain BCC 19360, GenBank GU552147, Identities 839/893 (94 %), one gap); and *H. siamensis* (strain BCC 8105, GenBank KC713630, Identities 813/875 (94 %)).

Colour illustrations. *Aschersonia mackerrasiae*. Stromata (BRIP 62731a); stroma (BRIP 62329a); paraphyses and conidia (BRIP 62329a, left and right); conidia (BRIP 62731a); colony on PDA after 4 wk (BRIP 62731a); upper surface of colonies (BRIP 62731a); lower surface of colonies (BRIP 62731a). Scale bars = 1 mm, 100 µm, 100 µm, 10 µm, 10 µm, 1 mm, 1 cm, respectively.

Supplementary material

FP1506 Phylogenetic tree.

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Cladosporium corticola

Fungal Planet 1507 – 29 June 2023

Cladosporium corticola Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

Etymology. From the Latin *cortex* meaning bark, from which the fungus was isolated. The bark was collected by Year 8 students at St Joseph's Nudgee College as part of a mycology project organised by their science teacher Belinda Drury. The students were Nick Cheney, Jordan Cordingley, Finn Curran, Jackson Dalton, Henry Dennis, Oliver Douyere, Joshua Eckersall, Xander Eyles, Eric Fitzgerald, Toby Gall, William Gibson, Angus Glyde, Hayden Hamilton, Toby Harvey, Mark Hili, Samuel Howard, Lucas Jebreen, Dean Keys, Lachlan Mills, Paddy Williams, Lincoln Wright and Nicholas Zeitoun.

Classification — *Cladosporiaceae*, *Cladosporiales*, *Dothideomycetes*.

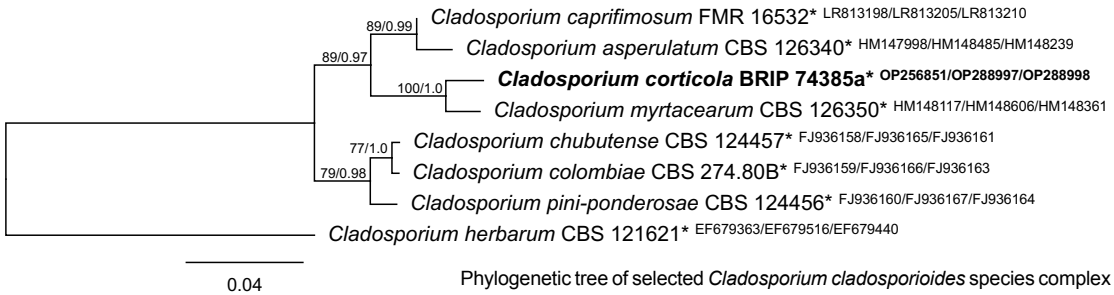
On synthetic nutrient agar (SNA): *Mycelium* comprised of pale brown to brown, finely verruculose or smooth, branched, septate, 2.5–4 µm diam hyphae. *Conidiophores* macronematous or sometimes micronematous, erect, straight or flexuous, terminal or lateral, cylindrical, often geniculate towards apex, unbranched, subcylindrical, 50–450 × 3–4 µm, not swollen or slightly swollen at the apex, septate, brown to dark brown; walls smooth or finely verrucose, thickened to 1 µm diam. *Conidiogenous cells* integrated, terminal and lateral, cylindrical, often geniculate, 5–35 × 3–4.5 µm, pale brown to brown, smooth; conidiogenous loci thickened, darkened and refractive. *Ramoconidia* subcylindrical and often geniculate, mid-brown, 10–35 × 3.5–6 µm, 0–1-septate, smooth; conidiogenous loci thickened, darkened, refractive, 1.5–2 µm diam. *Conidia* in branched chains of up to eight, narrowly ellipsoidal, 4–11 × 3–5 µm, aseptate, pale yellowish brown to brown, smooth.

Culture characteristics (25 °C, 7 d, in darkness) — Colonies on potato dextrose agar (PDA) olivaceous black, velutinous, 15–20 mm diam; reverse greenish black. On oatmeal agar (OA) olivaceous black, velutinous, 15 mm diam, reverse greenish black. On SNA olivaceous black, velutinous, 5 mm diam, reverse greenish black.

Typus. Australia, Queensland, Brisbane, from bark of *Melaleuca quinquenervia* (*Myrtaceae*), 2 Nov. 2021, *B. Drury* & Year 8 science students at St Joseph's Nudgee College (holotype preserved as metabolically inactive culture BRIP 74385a; culture ex-type BRIP 74385a; ITS, *actA* and *tefla* sequences GenBank OP256851, OP288997 and OP288998; MycoBank MB 845973).

Notes — In the phylogenetic analysis, *C. corticola* is sister to *C. myrtacearum*, which has been isolated from *Corymbia* and *Eucalyptus* spp. (*Myrtaceae*) in Australia and from *Indigofera* sp. in South Africa (Braun et al. 2005, Bensch et al. 2015). *Cladosporium corticola* shares similar morphology with *C. myrtacearum* but has longer and slender conidiophores (cf. 14–96 × 3–7(–9.5) µm, swollen at the base). *Cladosporium corticola* is distinguished from *C. myrtacearum* (ex-type strain CBS 126350) by sequence comparison of *actA* (GenBank HM148606; Identities 196/204 (96 %), one gap; unique nucleotide at positions 65(C), 78(C), 79(C), 89(A), 144(A), 156(G), 175(C)), and *tef1α* (GenBank HM148361; Identities 404/431 (94 %), seven gaps (1 %); unique nucleotide at positions 13(T), 23(T), 29(C), 31(T), 52(T), 135(G), 137(A), 138(A), 165(T), 167(A), 168(C), 169(A), 173(T), 174(T), 177(T), 179(G), 193(C), 324(C), 326(T), 341(G)).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest relevant hits with the **ITS** region are *C. perangustum* (strain CPC 22375, GenBank MF473177, Identities 685/685 (100 %)), *C. angustisporum* (strain CBS 125983, GenBank MH863862, Identities 684/684 (100 %)) and *C. asperulatum* (strain CPC 22364, GenBank MF472934, Identities 683/683 (100 %)). The closest relevant hits with the ***actA*** sequence are *C. myrtacearum* (strain Clad 4, GenBank OK001228, Identities 152/152 (100 %)), *C. myrtacearum* (strain CBS 126349, GenBank HM148605, Identities 203/204 (99 %), no gap) and *C. asperulatum* (strain CPC 15614, GenBank KT600576, Identities 192/205 (94 %), two gaps). The closest relevant hits with the ***tef1α*** sequence are *C. myrtacearum* (strain CBS 126349, GenBank HM148360, Identities 301/317 (95 %), no gap), *C. ruguloflabelliforme* (strain CBS 140494, GenBank KT600557, Identities 298/318 (94 %), two gaps) and *C. tenuissimum* (strain DTO:324-A3, GenBank MF473723, Identities 382/431 (89 %), eight gaps (1 %)).



Phylogenetic tree of selected *Cladosporium cladosporioides* species complex based on a maximum likelihood analysis of the ITS, *actA* and *tef1α* gene regions. Analyses were performed on the Geneious Prime ® 2022 platform (Biomatters Ltd.) using RAxML v. 8.2.11 (Stamatakis 2014) and MrBayes v. 3.2.6 (Huelsenbeck & Ronquist 2001), both based on the GTR substitution model with gamma-distribution rate variation. RAxML bootstrap (bs) support values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). GenBank accession numbers are indicated (superscript ITS/*actA*/*tef1α*). *Cladosporium herbarium* ex-type strain CBS 121621 was used as outgroup. Novel taxon is indicated in **bold**. Ex-type strains indicated with an asterisk (*). The alignment and trees are publicly available in 10.5281/zenodo.7714511.

Colour illustrations. Bark of *Melaleuca quinquenervia* growing in Brisbane, Australia (photo credit Belinda Drury). Colony on PDA, OA, and SNA; conidiophores on colony surface; ramoconidia and conidia; conidia. Scale bars = 1 cm (colony), 1 mm (conidiophores on colony surface), 10 µm (ramoconidia and conidia).

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Colletotrichum qingyuanense

Fungal Planet 1508 – 29 June 2023

Colletotrichum qingyuanense N. Zhang, P. Wong, W. Yang, S. Luo & Y. Zhu, *sp. nov.*

Etymology. Named after the location, Qingyuan, where the fungus was collected.

Classification — *Glomerellaceae*, *Glomerellales*, *Sordariomycetes*.

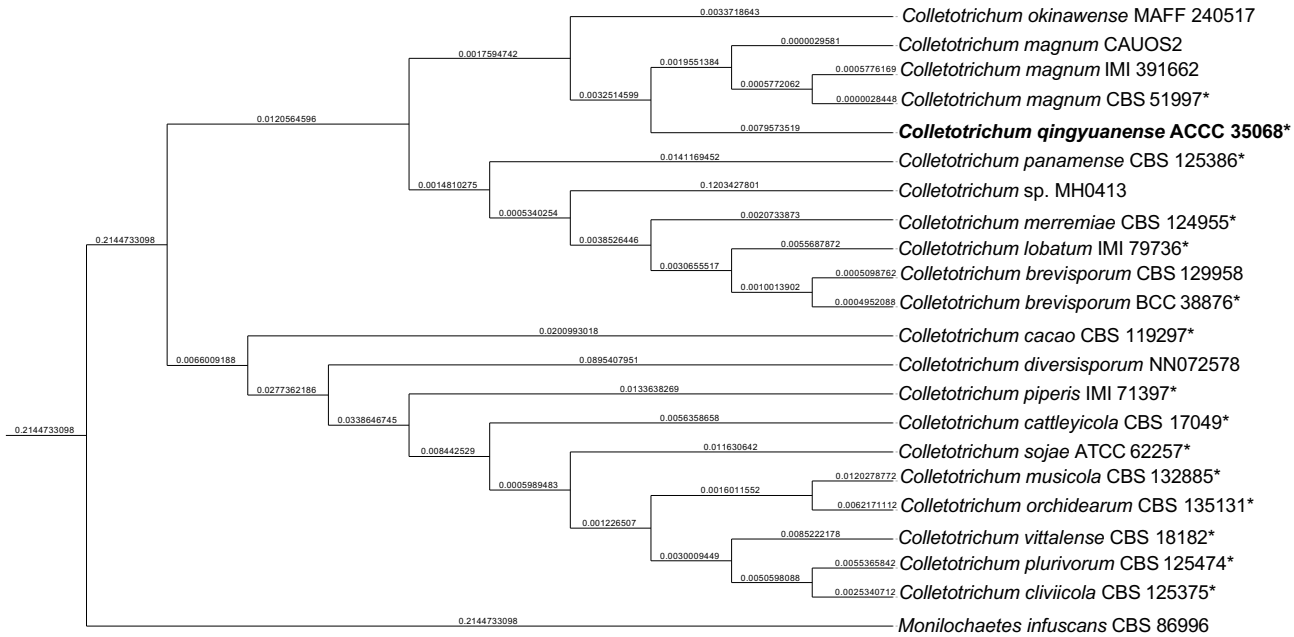
Sexual morph not observed. *Asexual morph* on potato dextrose agar (PDA). *Hyphae* 1–4 µm diam, hyaline, darkening with age, smooth-walled, septate, branched. *Mycelium* hyaline, forming grey or dark grey radial streaks with age from production of conidiomata. *Conidiomata* black, single or in clusters, 100–300 µm, superficial or embedded, irregular in outline, consisting of conidiophores and setae. *Conidiogenous cells* formed on conidiomata, cylindrical to ampulliform, straight to curved, hyaline to pale brown, 10.5–18 × 3.5–7 µm. *Conidia* hyaline, smooth-walled, aseptate, straight, sometimes slightly curved, cylindrical, apex rounded, base rounded to slightly tapering, 12.5–18 × 3.5–5.5 µm, mean ± SD = 14.15 ± 1.22 × 4.58 ± 0.41 µm, L/W ratio = 3.09, a few conidia turn pale brown with age, or are 1-septate. *Setae* straight to curved, smooth-walled or with small verruca, brown or dark brown, lighter towards apex, 33–79 µm in length, 2–5 µm diam, base cylindrical, some slightly inflated. *Appressoria* ellipsoidal, pyriform or irregular in outline, smooth-walled, pale to dark brown, 7.5–12.5 × 5.5–7.5 µm. *Chlamydospores* not observed.

Cultural characteristics — Colonies on PDA flat with entire margin, reaching 3.3–3.5 cm diam in 7 d at 25 °C; sparse aerial mycelium, forming grey to dark grey radial streaks with age from production of conidiomata.

Typus. China, Hebei Province, Qingyuan, from fruit lesion of *Capsicum annuum* (*Solanaceae*), 12 Sept. 2020, *N. Zhang* (holotype preserved as metabolically inactive culture ACCC 35068; ex-type culture ACCC 35068; *act, chs-1, gapdh, his3,* ITS, and *tub2* sequences GenBank ON804307, ON804308, ON804309, ON804310, ON804311, and ON804312; MycoBank MB 845568).

Notes — Brown spots were observed on the fruit of chili pepper (*Capsicum annuum*) in a field in Qingyuan, Hebei Province, China. The necrotic fruit lesions were suborbicular, sunken, with acervuli arranged in the middle of the lesions (see photo plate). The fruit spots were 5–10 mm diam, discrete, sometimes in clusters and coalescing. Severe infections could destroy whole fruit. This pathogen has not been previously recorded from China (Liu et al. 2022), and is here described as new.

Phylogenetic analyses show that it is closest to *C. magnum* (Fig. 1) but differs in mycelial growth rate (3.3–3.5 cm vs < 3.0 cm), septation (0–1 vs 1–3) and conidiogenous cell formation (formed in conidiomata vs directly from hyphae). It has a 97 % identity (244/252 bp) for the partial *act* gene sequence and 76 % identity (177/233 bp, with 45 bp gap) for the partial *gapdh* gene sequence of the ex-type strain of *C. magnum*, CBS 519.97. Phylogenetic analysis based on sequence data from six loci (*act*, *chs-1*, *gapdh*, *his3*, ITS and *tub2*) places the fungus in the Kahawae clade of the *C. magnum* complex (Damm et al. 2019, Liu et al. 2022), with a bootstrap support value of 99 %.



Multilocus phylogenetic tree inferred from the combined *act*, *chs-1*, *gapdh*, *his3*, *tub2* and ITS sequence alignment. The evolutionary analyses were conducted in IQ-TREE v. 2.1.3 (Nguyen et al. 2015) using the Maximum Likelihood method. The tree was rooted to *Monilochaetes infuscans* CBS 869.96. Ex-type strains are marked with an asterisk (*). TreeBASE number: S29731.

Colour illustrations. A field of chilies (*Capsicum annuum*) in Hebei Province, China. Disease symptoms on chili fruit; colony of *C. qingyuanense* on PDA; seta; appressoria; conidia. Scale bars = 1 cm (disease symptoms and culture plate), 10 µm (all others).

Supplementary material

FP1508 Phylogenetic tree.

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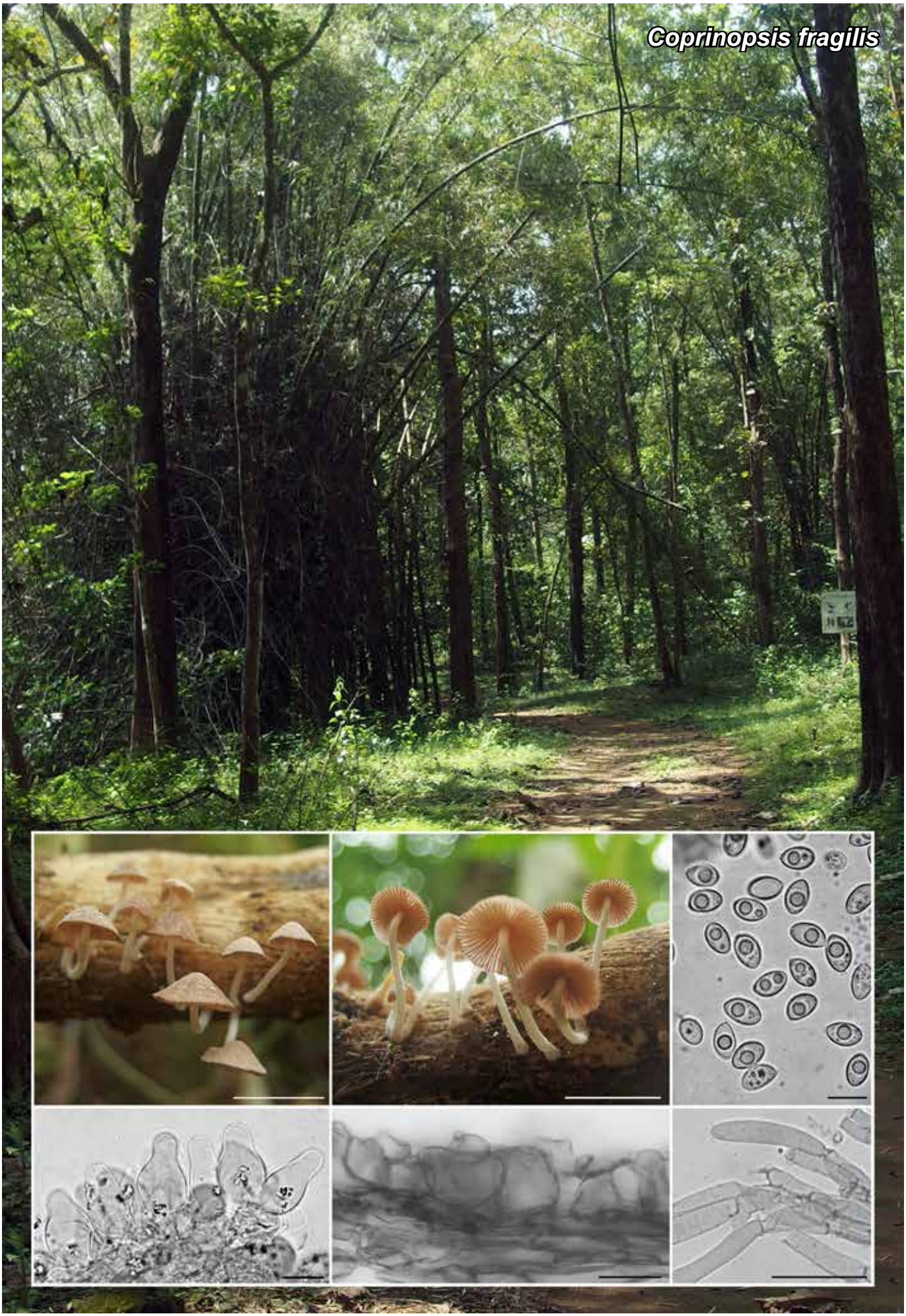
Coprinopsis fragilis

Fungal Planet 1509 – 29 June 2023

Coprinopsis fragilis K.G.G. Ganga, Manim. & K.P.D. Latha, *sp. nov.*

Etymology. Name refers to its fragile basidiocarps.

Classification — *Psathyrellaceae*, *Agaricales*, *Agaricomycetes*.

Basidiocarps small, fragile, psathyrelloid. *Pileus* 3–10 × 2–4 mm at maturity, initially convex, becoming broadly conical with age; surface white when young, becoming white on velar remnants and brownish grey (6C3 Kornerup & Wanscher 1978) elsewhere with age, hygrophanous and becoming paler, initially completely covered with a fibrillose veil that later splits into finely fibrillose patches, more so on and around the centre, translucent-striate towards the margin; margin straight, crenate. *Lamellae* adnexed, crowded, initially white, becoming brownish orange (6C4) to light brown (6D4) at maturity, with lamellulae in two tiers; edge finely torn under a lens, concolourous with the sides. *Stipe* 9–25 × 1 mm, central, terete, equal, hollow; surface white all over, smooth to finely floccose; base slightly enlarged to subbulbous with short strigose hairs, often connate, inserted. *Odour* and *taste* not distinctive. *Basidiospores* 8–10(–11) × 5–6 × 5–6 µm, av. 9.32 × 5.75 × 5.4 µm, Q_1 = 1.5–2.0, Q_{1avg} = 1.63, Q_2 = 1.5–2.0, Q_{2avg} = 1.73, lenticular, ovoid in face view, somewhat phaseoliform to subamygdaliform in side view, pale brown to almost hyaline, slightly thick-walled, with an indistinct germ-pore. *Basidia* 19–23 × 10–11 µm, clavate or pedicellate-clavate, hyaline, thin-walled, 4-spored; sterigmata up to 5 µm long. *Pleurocystidia* absent. Lamella-edge sterile. *Cheilocystidia* 20–28 × 9–12 µm, abundant, utriform to subutriform or rarely clavate, often with amorphous contents that dissolve partially in 3 % aqueous KOH, hyaline, slightly thick-walled. *Lamellar trama* subregular with inflated hyphae; hyphae 5–12 µm wide, hyaline, thin-walled. *Pileipellis* a cutis overlaid with a suprapellis composed of globose to subglobose elements intermixed with scattered velar hyphae; hyphae 5–10 µm wide, pale brown, thin-walled; suprapellis elements 30–47 × 20–33 µm, hyaline to pale brown, thin-walled; velar hyphae 3–9 µm wide, short, cylindrical, branched, often with a clavate terminal cell, hyaline, thin-walled. *Stipitipellis* a cutis overlaid by velar hyphae; hyphae 3–8 µm, hyaline, slightly thick-walled; velar hyphae 5–10 µm wide, similar to those on the pileipellis. *Clamp connections* observed only at the base of cheilocystidia and on velar hyphae on the pileipellis.

Habit, Habitat & Distribution — In large groups, on decaying bark of logs. Known from two different localities in Kerala State, India.

Typus. India, Kerala State, Ernakulam District, Thattekad Forest, N10°07'44.8" E76°41'12.3", 23 Oct. 2018, *K.G. Greeshma Ganga* (holotype G286 (CALI); ITS and LSU sequences GenBank OP852345 and OP852344; MycoBank MB 846455).

Additional materials examined. India, Kerala State, Malappuram District, Calicut University Botanical Garden, N11°08'02.0" E75°53'29.0", 26 July 2016, *K.G. Greeshma Ganga* G45; ibid., 28 July 2016, *K.G. Greeshma Ganga* G46.

Colour illustrations. India, Kerala State, Ernakulam District, Thattekad Forest, type locality. The upper insets show basidiocarps, basidiocarps showing lamellae, basidiospores, lower insets show cheilocystidia, pileipellis, velar hyphae on pileipellis. Scale bars = 5 mm (basidiocarps), 10 µm (basidiospores and cheilocystidia), 50 µm (all others).

Notes — *Coprinopsis fragilis* is characterised by a brownish grey pileus with scattered patches of velar remnants; adnexed and crowded lamellae; a stipe with short strigose hairs at the base; ovoid and almost hyaline basidiospores with an indistinct germ-pore; a hymenium devoid of pleurocystidia; utriform to lageniform or clavate cheilocystidia with amorphous contents and a cutis-type pileipellis overlaid with a suprapellis composed of globose to subglobose elements intermixed with velar elements. This species shows a pileus that lacks radial sulcations, non-deliquescent lamellae, ovoid basidiospores and the absence of pleurocystidia and hence belongs to *Coprinopsis* section *Quartoconatae* (Wächter & Melzer 2020).

Coprinopsis musae, a species originally described from Denmark (Örstadius et al. 2015), seems to be close to *C. fragilis* in having smaller basidiocarps, hyaline to very pale brown basidiospores, the absence of pleurocystidia, a pileipellis with a suprapellis composed of narrow horizontal hyphae followed by globose to ellipsoid elements and a lignicolous habitat. *Coprinopsis musae,* however, has a pileus without visible velar remnants, a stipe which is devoid of short strigose hairs at the base and versiform cheilocystidia devoid of amorphous materials. *Coprinopsis marcescibilis*, a species reported from the British Isles, France and the Netherlands (Van Waveren 1985), has a pileipellis with a suprapellis composed of horizontal hyphae and a hymenium devoid of pleurocystidia. However, the macro- and microscopic characters of *C. marcescibilis,* such as a larger (15–35 mm diam), reddish brown pileus with an appendiculate margin, dark reddish brown basidiospores and cheilocystidia lacking amorphous materials, make it different from *C. fragilis.*

Coprinopsis pseudomarcescibilis, a Spanish species (Crous et al. 2017a), resembles *C. fragilis* in having white velar remnants on the pileus, the absence of pleurocystidia and a lamella-edge with cheilocystidia of almost similar morphology. However, *C. pseudomarcicibilis* can be distinguished from *C. fragilis* in having larger basidiocarps, an umbonate pileus with an appendiculate margin, a stipe base without strigose hairs, reddish brown and larger basidiospores (11–16.5(–17) × 6–8 µm), cheilocystidia lacking amorphous materials and a terrestrial habitat. In the ITS phylogram, *C. fragilis* nested within a clade representing the section *Quartoconatae* of the genus *Coprinopsis,* alongside the species so far treated under the section, *C. musae, C. pseudomarcescibilis* and *C. marcescibilis,* with maximum bootstrap (BS) support (100 % BS). Within this clade, *C. fragilis* is closely related to, but appeared as a lineage distinct from *C. musae,* with full bootstrap support (100 % BS).

Supplementary material

FP1509 Phylogenetic tree.

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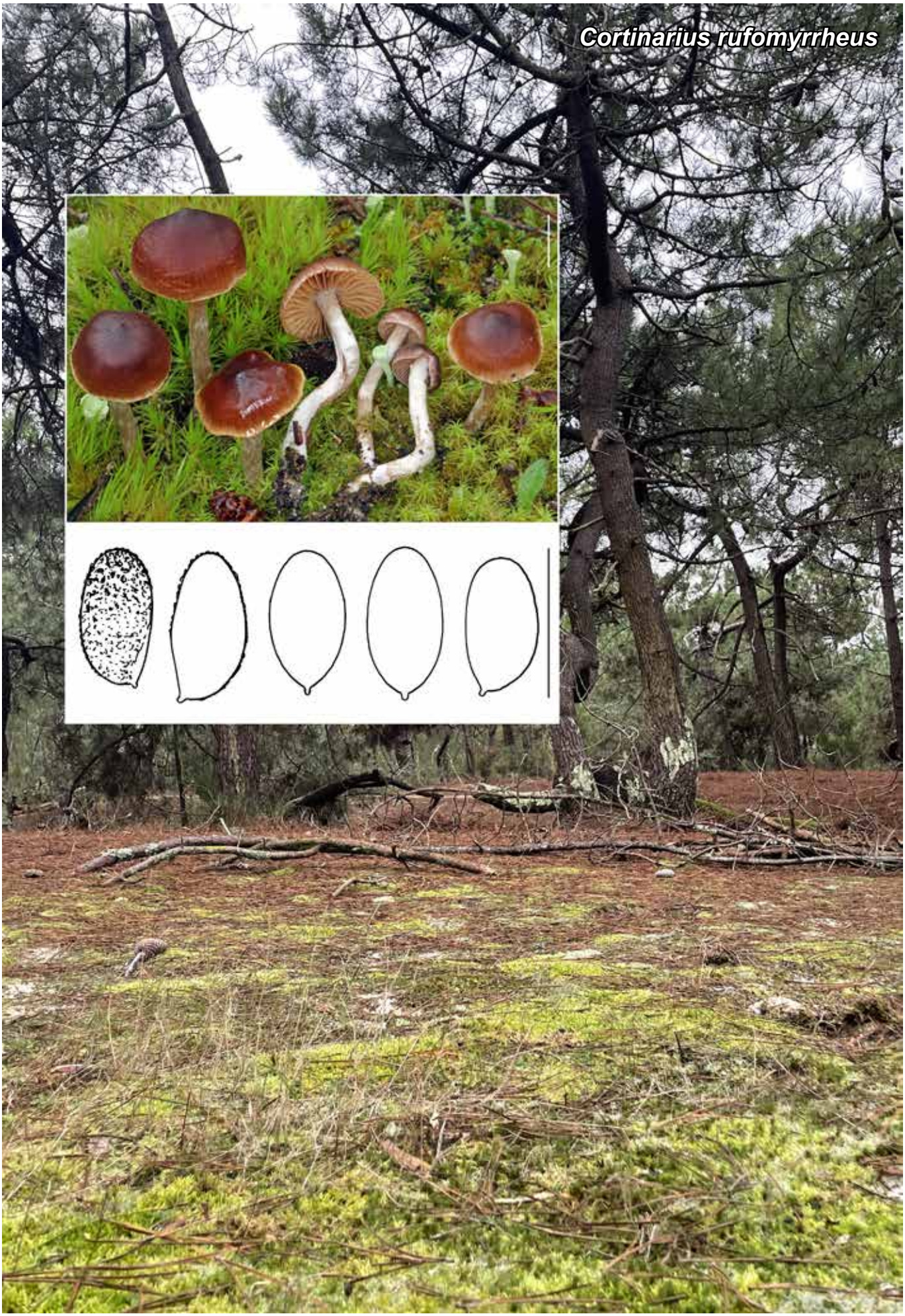
Cortinarius rufomyrrheus

Fungal Planet 1510 – 29 June 2023

Cortinarius rufomyrrheus Eyssart., Sleiman & Bellanger, *sp. nov.*

Etymology. Named after the general colour of the cap, from the Latin adjectives *rufus*, 'reddish', and *myrrheus*, 'chestnut brown'.

Classification — *Cortinariaceae*, *Agaricales*, *Agaricomycetes*.

Cap 9–20 mm diam, convex with a small and obtuse umbo, hygrophanous, of a beautiful reddish chestnut brown or reddish fawn colour, abruptly faded at the margin, which is creamy clay, striated translucent on about half of the radius, delicately covered in young specimens by a tenuous and fibrillose whitish veil, especially at the margin, deciduous, quickly vanishing when the cap opens up. *Gills* emarginate, light brown-beige in young specimens then ochraceous-beige, paler at the edge. *Stipe* 35–60 × 2–3.5 mm, cylindrical or almost so, pearly white, pruinose at the top, covered by a whitish universal veil forming fine girdles on the whole length except above the whitish and little developed cortina. *Flesh* thin, pinkish ochraceous, whitish in the cortex; *smell* sweet but rather weak, evoking burnt meat and reminiscent of that of *Entoloma nausiosme*. *Spores* (holotype) measuring on spore-print (6.6–)7.7–8.2–8.6(–8.9) × (4.4–)4.6–5–5.3(–5.5) µm, Q = (1.3–)1.5–1.6–1.8(–1.9), n = 60, and on hymenium (7.6–)8.2–8.8–9.3(–9.6) × (4.6–)4.7–5.0–5.2(–5.4) µm, Q = (1.5–)1.6–1.8–1.9(–2.1), n = 51, yellowish brown under the microscope, not or very slightly and slowly dextrinoid, regularly ellipsoid, sometimes also ellipsoid-elongated to almost subcylindrical especially on hymenium, lowly ornamented with medium to low and irregular warts, sometimes appearing almost smooth, more developed at the top on some spores. Additional material: FR2019054, on hymenium, (7.2–)7.7–8.3–8.9(–9.3) × (4.2–)4.3–4.7–5.2(–5.4) µm, Q = (1.5–)1.7–1.8–2, n = 31. FR2019055, on stipe, (8.0–)8.4–9.0–9.7(–10.3) × (4.6–)5.0–5.5–5.8(–6.2) µm, Q = (1.4–)1.5–1.6–1.8(–1.9), n = 52. FR2019057, on stipe, (7.7–)7.9–8.5–9.3(–9.8) × (4.8–)5.1–5.5–5.9(–6.1) µm, Q = (1.4–)1.5–1.6(–1.7), n = 45. *Basidia* tetrasporic, clavate, 25–35 × 8–9 µm. *Cystidia* absent. *Pileipellis* a cutis of repent hyphae 5–10 µm wide, up to 15(–20) µm in the subcutis, coloured by a smooth epiparietal yellowish brown pigment. *Clamp-connections* present in all parts.

Typus. France, Loire-Atlantique, La Baule-Escoublac, Escoublac forest, on sandy soil under *Pinus pinaster*, 10 Nov. 2016, *G. Eyssartier*, GE 16.023 (holotype PC0714854, isotype in herb. GE; GenBank sequences ITS, LSU and *RPB2* OM519318, OQ255806 and OM584297; Index Fungorum IF 559460).

Additional materials examined. Lebanon, Qamouaa, limestone soil under *Abies cilicica*, 1608 m a.s.l., 2 Dec. 2018, *S. Sleiman*, Q1-10 (GenBank sequences ITS and *RPB2* MZ088103 and OM584294); ibid., Q1-11 (GenBank sequences ITS and *RPB2* MZ088104 and OM584295); ibid., Q1-13 (GenBank sequences ITS and *RPB2* MZ088106 and OM584296).

Colour illustrations. France, Loire-Atlantique, La Baule-Escoublac, Escoublac forest, on sandy soil under *Pinus pinaster* (typus). Basiodiomata at type location; spores from holotype. Scale bars = 1 cm (basidiomata), 10 µm (spores).

Notes — *Cortinarius rufomyrrheus* belongs to the diversified and still incompletely described section *Castanei* (= *C. decipiens* sensu Suárez-Santiago et al. 2009), in which it constitutes a moderately-supported clade in the ITS phylogeny, as well as a strongly-supported clade in the *RPB2* phylogeny (not shown), close to, e.g., *C. decipiens* s.str., *C. falsosus*, *C. pulchripes* and *C. castaneus* (see Supplementary material). In the field, these species are still difficult to distinguish from each other, sharing brown to brownish black cap, a stipe often tinged with blue at the top and a lack of any obvious smell. Conversely, the numerous synonymies unveiled by the recent molecular revision of this lineage by Liimatainen et al. (2020) ignore divergent morphological characters between some synonymised taxa. This paradoxical situation may reflect the real evolutionary history of sect. *Castanei*, which would display both crypticism within species complexes and phenotypic homoplasy among other taxa. However, this might also result from the recent diversification of the lineage, which would not have allowed enough time for mutations to accumulate and polymorphisms to be fixed (incomplete lineage sorting) at the ITS locus of genetically isolated species to unambiguously distinguish them. We tend to favour the latter hypothesis because some species complexes not resolved in ITS phylogenies, are deciphered by the use of the *RPB2* phylogenetic marker (Kokkonen 2020). It seems thus that in sect. *Castanei* – and probably other sections in subgen. *Telamonia* –, the ITS locus alone is not sufficiently discriminating and needs to be complemented by the analysis of another marker like *RPB2*. The taxonomic status of *C. subodoratus* for instance, treated as a late synonym of *C. castaneus* by Liimatainen *et al.* (2020) in spite of morphological and organoleptic differences, deserves closer inspection because the ITS sequence of the two species differs from each other by only two evolutionary events at this locus. The requirement for a second DNA barcode in *Basidiomycota* is in no means restricted to *Cortinarius*, as in the genus *Hebeloma* for instance, the use of mtSSU, *RPB2* and *Tef1a* sequences is necessary to distinguish several species that were not resolved by the sole use of ITS (Beker et al. 2016).

Morphologically, *C. rufomyrrheus* is closest to *Cortinarius subturibulosus* (syn. *C. subcoronatus*, *C. urdaibaiensis*, *C. salicinus*, *C. helianthemorum*), which belongs to section *Bombycini* (Liimatainen et al. 2020, Bellanger et al. 2021). This ubiquitous species can co-occur with *C. rufomyrrheus* in the same habitat, raising risks of confusion. Fortunately, the two species can be distinguished by spores which are at least for some of them clearly dextrinoid, covered with dark, well-marked warts and on average of bigger size in *C. subturibulosus*: 9–11 × 5–5.5(–6) µm in the original description (Kizlik & Trescol 1991), 'reaching 9 µm and up to 11 µm' in Bellanger et al. (2021), and (7.5–)8.1–8.8–9.4(–10.7) × (4.7–)5–5.4–5.7(–6.0) µm, n = 50, in collection GE 16.022 (this study). In addition, although not constant in all collections, *C. subturibulosus* has been described with a clear smell of cedarwood, orange blossom or rosemary flower.

Supplementary material

FP1510 Phylogenetic tree.

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Cyathus bonsai

Fungal Planet 1511 – 29 June 2023

Cyathus bonsai J.S. Góis, R. Cruz, P. Marinho & Baseia, *sp. nov.*

Etymology. Named in reference to the substrate where the species was growing, on plant debris in a bonsai pot.

Classification — *Nidulariaceae*, *Agaricales*, *Agaricomycetes.*

Peridium infundibuliform, 5.6–8.54 × 4.57–6.61 mm, not expanded at the mouth or tapering abruptly at the base. *Emplacement* 2.17–4.20 mm, conspicuous, dark brown (7F6–7F7 Kornerup & Wanscher 1978). *Exoperidium* woolly to hirsute, dark brown (6F7), with 0.38–0.68 mm tomentum, arranged in irregular and flexible tufts. *External wall* conspicuously plicated, 0.33–0.68 mm between the folds. *Mouth* slightly fimbriated in a continuous pattern, 0.22–0.31 mm in height, dark brown (7F7). *Endoperidium* grey (5D1–6D1), conspicuously plicated, 0.44–0.60 mm between the folds. *Perceptible* bright, contrasting with the exterior. *Stipe* 0.80–1.46 mm, brown. *Epiphragm* absent. *Peridioles* 2.47–3.01 × 1.93–2.24 mm diam, brownish grey (7F2–8E2), 6–10 per basidioma, angular to elliptical in shape at borders, smooth surface. *Tunic* present, hyaline. Double-layered cortex: exocortex and endocortex black in colour and mesocortex greyish white. *Mesocortex* powdery with loose hyphae. *Basidiospores* smooth, hyaline, 13.35–20.67 × 7.03–12.98 µm (L = 15.00 µm; W = 9.92 µm; n = 30), slightly elliptical to elongated (Q = 1.15–1.66 µm), elliptical in average (Qm = 1.35 µm). Apicule present in some spores and basidiospore wall 2.10–3.63 µm

Typus. Brazil, Natal, Rio Grande do Norte, on decaying wood, July 2014, *I.G. Baseia* (holotype UFRN-Fungos 3452; ITS sequence GenBank OP718804; MycoBank MB 846284).

Notes — According to Brodie's (1975) morphological classification, *Cyathus bonsai* can be inserted in group VII (*striatus*), and in the molecular clades by Zhao et al. (2007) this species belongs to the *striatum* clade. Morphologically, this species resembles *Cyathus montagnei* and *C. striatus*. However, *C. bonsai* can be distinguished from those species by its larger peridioles, darker basidiomes, and the double-layered cortex, while the other two species have a single-layered cortex, a feature that is enough to separate the species (Tulasne & Tulasne 1844, Brodie 1975). In the ITS phylogeny, *C. bonsai* groups with *C. amazonicus, C. parvocinereus* and *C. pyristriatus*. The similarities with *C. amazonicus* are due to the presence of a fimbriated mouth, double-layered cortex, and peridium tomentum over 0.5 mm, but *C. amazonicus* differs from *C. bonsai* by the larger peridium tomentum (up to 1.25 mm), smaller peridioles, darker mesocortex hyphae and by having an expanded mouth (Trierveiler-Pereira et al. 2009, Góis et al. 2021). In addition to the differences cited above, it is essential to highlight that the phylogenetic branch of *C. bonsai* supports a genetic distance from *C. amazonicus*, showing a greater divergence in base pairs (86 % of similarity) when compared to the other species of the clade. *Cyathus parvocinereus* has a similar basidiospore size and double-layered cortex but differs in having smaller peridioles (1.5–2 mm), basidiospores globose to slightly ellipsoidal in shape, smaller basidiomata (up to 7 mm), and an inconspicuous peridium wall (Cruz & Baseia 2014). Regarding *Cyathus pyristriatus,* this species differs by larger peridioles (3–3.5 mm), smaller basidiospores (up to 17 µm), clavate basidiomata and woolly peridium, with lighter colours (Hyde et al. 2016).

Colour illustrations. Urban environment near to the locality where the type species was collected in Natal, Rio Grande do Norte, Brazil. Peridium; upper view of peridioles; cross-section of the peridiole showing the double-layered cortex; basidiospores. All images from the holotype, UFRN-Fungos 3452. Scale bars = 2 mm (peridium and peridioles), 1 mm (double-layered cortex), 10 µm (basidiospores).

Supplementary material

FP1511 Phylogenetic tree.

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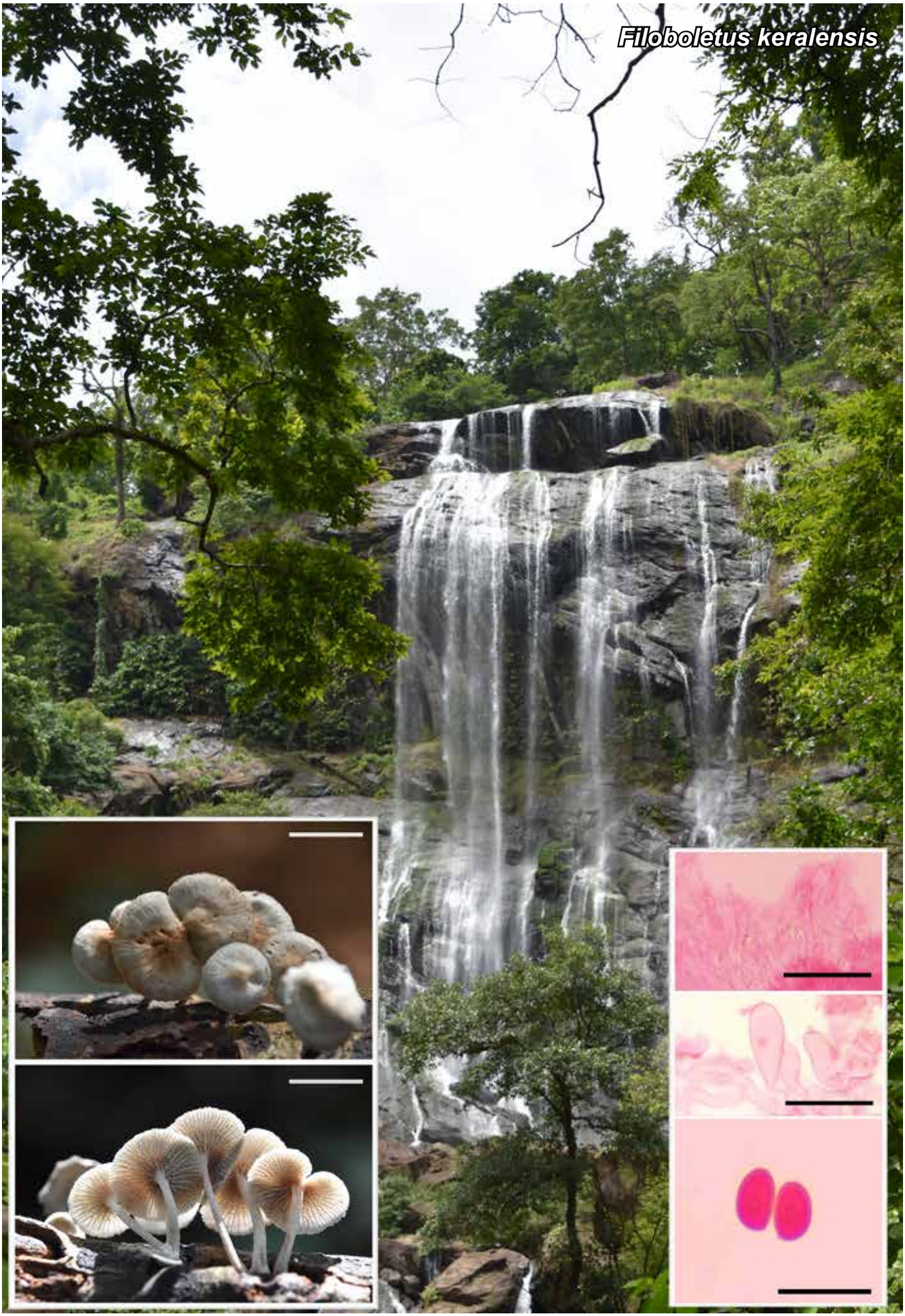

Filoboletus keralensis

Fungal Planet 1512 – 29 June 2023

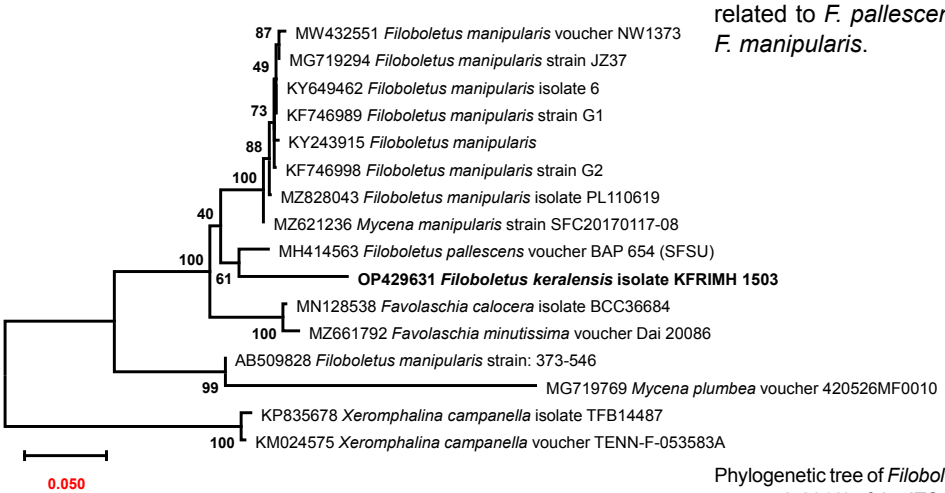
Filoboletus keralensis Mahadevak., K.T. Mufeeda, Sh. Kumar., Chandran. & K.R. Sridhar, *sp. nov.*

Etymology. The name *keralensis* refers to the Kerala state, India, from which this species was collected.

Classification — *Tricholomataceae*, *Agaricales*, *Agaricomycitidae*, *Agaricomycetes*.

Pileus 1.5–3.8 cm diam, conico-companulate to convex with conical umbo, hygrophanous, translucently reticulate, finely white pruinose, pale whitish to greyish; during moist conditions it turns hyaline. *Hymenophore* tubular and adnate. *Tubes* 1.2–3.1 mm long, arranged in radial rows with angular-round pores, 0.3–0.9 mm wide. *Stipe* (35–)58 × (0.4–)2.3 mm, cylindrical, thickened in the base, white to hyaline and completely white pruinose. *Odour* indistinct. *Edibility* not known. *Basidiospores* (6.8–)7.6 × (4.1–)5.3 µm, white, smooth and ellipsoid to broadly ellipsoid. *Basidia* (14.5–)19.4 × (5.9–)6.8 µm, clamped, clavate with sterigmata reaching up to 5.5 µm long. *Cheilocystidia* (48.4–)67.2 × (7.1–)13.2 µm, forming a sterile lamellae edge, lageniform, subcylindrical or sub-clavate, largely diverticulate and or sometimes irregularly branched in the apex. *Pleurocystidia* not observed. *Hyphae* of pileipellis 4–12 µm wide, clamped and diverticulate terminal cells. *Pileocystidia* (23.9–)29.8 × (7.4–)11.2 µm, abundant and irregularly shaped.

Typus. India, Kerala, Thrissur, Peechi-Vazhani Wildlife Sanctuary, basidiomata growing in groups on unidentified woody substrate, 31 May 2022, *S. Mahadevakumar, S. Kumar & K.T. Mufeeda* (holotype KFRIMH1503; GenBank sequences ITS and LSU OP429631 and OP429632; MycoBank MB 845633).



Phylogenetic tree of *Filoboletus keralensis* constructed using MEGA v. X (Kumar et al. 2018) of the ITS-rDNA sequence alignment by Neighbour-Joining Method (Saitou & Nei 1987). Thepercentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1 000 replicates) are shown next to the branches (Felsenstein 1985). The evolutionary distances were computed using the Kimura 2-parameter method (Kimura 1980) and are in the units of the number of base substitutions per site. This analysis involved 16 nucleotide sequences and a total of 937 positions in the final dataset. The phylogenetic position of *Filoboletus keralensis* is indicated in **bold**. The alignment and trees are publicly available in 10.6084/m9.figshare.22255477.

Colour illustrations. Peechi-Vazhani Wildlife Sanctuary with waterfalls from where the *Filoboletus keralensis* was collected. Sporocarps of *F. keralensis* showing typical morphology (front view and reverse (left panel), details of basidia and basidiospores of *F. keralensis*. Scale bars = 3 cm (left panel), 20 µm (pileipellis and basidia), 10 µm (basidiospores).

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of KFRIMH1503 had highest similarity to *Filoboletus pallescens* (voucher DED8303, GenBank MH414562; Identities = 587/611 (91.40 %), six gaps (0 %)), *Filoboletus pallescens* (voucher BAP654, GenBank MH414563; Identities = 579/610 (91.39 %), five gaps (0 %)) and the type of *Mycena manipularis* (strain FSI6090902, GenBank MZ621236; Identities = 569/615 (89.15 %), ten gaps (1 %)), *Favolaschia calocera* (BCC36684, GenBank MN128538; Identities = 569/615 (86.75 %), 10 gaps (1 %)), *Favolaschia calocera* (voucher: Dia20086, GenBank MZ661792; Identities = 569/615 (86.36 %), 10 gaps (1 %)). Further, the closest hit using the **LSU** sequence of KFRIMH1503 had highest similarity to *Favolaschia manipularis* (Sqe2, GenBank MZ914395; Identities = 934/1025 (91 %), 31 gaps (3 %)), *Poromycena* sp. (RV.PR114, GenBank AF261421; Identities = 902/980 (92 %), 24 gaps (2 %)), *Mycenoporella griseipora* (strain JM95/156, GenBank AF261428; Identities = 872/938 (93 %), 18 gaps (1 %)), *Filoboletus gracilis* (strain JEJ.PR.253, GenBank AF261422; Identities = 901/980 (92 %), 24 gaps (2 %)) and *Filoboletus manipularis* (isolate PL110619, GenBank MZ827877; Identities = 868/937 (93 %), 17 gaps (1 %)).

Filoboletus keralensis has an overall morphological similarity to *F. manipularis*, except for its smaller basidia as well as basidiospores. In addition, *F. keralensis* has distinct gill-like structures underneath the pileus, while it is not so distinct in *F. manipularis.* Phylogenetic analysis revealed that the *F. keralensis* is closely related to *F. pallescens* (voucher BAP 654) and distinct from *F. manipularis*.

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Geastrum albofibrosum

Fungal Planet 1513 – 29 June 2023

Geastrum albofibrosum R.L. Oliveira, Dourado-Barbosa, R. Cruz, M.P. Martín & Baseia, *sp. nov.*

Etymology. In reference to the white colouration of the fibrous layer.

Classification — *Geastraceae*, *Geastrales*, *Agaricomycetes*.

Unexpanded *basidiomata* absent. Expanded basidiomata, 4.9–5.2 mm high (including peristome) × 8.2–8.4 mm wide. *Rhizomorphs* absent. *Exoperidium* splitting into 7–8 triangular rays, involute, non-hygroscopic, arched. *Mycelial layer* cotonous, heavily encrusted, white (1A1 Kornerup & Wanscher 1978). *Fibrous layer* coriaceous to tomentose, persistent, white to yellowish white (4A1, 4A2). Pseudoparenchymatous no-persistent, slightly rimose, detaching irregularly from the basidiomata at maturation, collar absent, olive brown (4E5). *Endoperidial body* globose, 2.9–3.1 mm high (including peristome) × 3.2–3.4 mm wide, surface glabra, light brown (5D4). *Apophysis* absent. *Stalk* 0.4–0.6 mm high × 0.2–0.3 mm wide, concolourous with endoperidium. *Peristome*, slightly mamiform, non-delimited, 0.3–0.4 mm high. *Gleba* pulverulent, brown (5F4). *Mycelial layer* composed of hyphae, 1.2–3.4 µm, thick-walled (0.4–0.8 µm), slightly encrusted, sinuous, non-branched, low evident lumen, hyaline. *Fibrous layer* composed of hyphae, 1.9–4.5 µm, thick-walled (0.6–1.2 µm), slightly encrusted, non-branched, lumen evident, hyaline. *Pseudoparenchymatous layers* composed of subglobose cells, 8.1–33.2 × 5.8–27.9, thin-walled (0.3–1.5 µm), hyaline. *Eucapillitium* 2.1–5.0 µm, thick walls (0.5–1.7 µm) not-encrusted, low evident lumen, not branched, light brown. *Basidiospores* subglobose, 3.9–5.0 × 3.4–4.8 µm (x = 4.4 ± 0.2 × 4.1 ± 0.3, Q_m = 1.06, n = 30), ornamentation conspicuous under light microscope and verrucose under scanning electron microscope (SEM); warts columnar (0.5–0.9 µm high), with some confluent tips; apiculous conspicuous, yellowish to brownish.

Habit & Habitat — Basidiomata gregarious, growing in moist soil, along with leaf litter.

Typus. Brazil, Paraíba, Cuité, Serra de Cuité, in moist soil along with leaf litter, 11 Apr. 2018, *R.L. Oliveira* (holotype UFRN-Fungos 3064; ITS and LSU sequences GenBank OP856849 and OP856848; MycoBank MB 846451).

Additional material examined. Brazil, Paraíba, Cuité, Serra de Cuité, 11 Apr. 2018, *R.L. Oliveira* (UFRN-Fungos 3638).

Notes — *Geastrum albofibrosum* belongs to Section *Geastrum* subsect. *Quadrifida* (Horner et al. 1995, Zamora et al. 2015). This species is characterised by a pseudoparenchymatous layer that falls almost completely at maturity, extremely small basidiomata and a discreet pedicel almost imperceptible to the naked eye. *Geastrum albofibrosum* resembles *G. austrominimum, G. calcium*, *G. granulosum*, *G. kuharii*, *G. quadrifidum* and *G. marginatum* by presenting verrucous ornamentation (Zamora et al. 2015, Finy et al. 2021). *Geastrum albofibrosum* has an arched and non-fornicated basidiome, similar to *G. quadrifidum*, however *G. albofibrosum* has a delicate pedicel, discrepant from the most evident pedicel of *G. quadrifidum* (Persoon 1794, Sunhede 1989). *Geastrum kuharii* and *G. albofibrosum* are similar in having non-hygroscopic rays, however, *G. albofibrosum* has small basidiomes with 7–8 involute triangular rays on the exoperidium, and is easily differentiated from the former by the much more robust basidiomes and commonly having 8–11 rays in the exoperidium (Kuhar 2013). *Geastrum albofibrosum* and *G. marginatum* are similar in their fibrillar peristome; however, in *G. albofibrosum* is undelimited, and in *G. marginatum* is distinctly delimited (Vittadini 1842). Two other species morphologically similar to *G. albofibrosum* are *G. calceum* and *G. austrominimum*; however, *G. calceum* differs by not presenting the pedicel with the same colour that the endoperidium, and by presenting a well-developed apophysis when present, and *G. austrominimum* differs by presenting a light brown to greyish brown pedicel (Lloyd 1907, Zamora et al. 2015). *Geastrum granulosum* is also closely related to *G. albofibrosum*, as both species have aqueous rays. However, *G. albofibrosum* is a dry and hot climate species, while *G. granulosum* is typically from holarctic regions (Fuckel 1860). A similar species to *G. albofibrosum* is *G. dolomiticum*, but the fibrous layer of *G. albofibrosum* varies from leathery to tomentose, whereas *G. dolomiticum* shows the papyraceous type; in addition, *G. albofibrosum* has a much smaller endoperidium than the *G. dolomiticum*, which can reach up to 9 mm diam in *G. dolomiticum* (Finy et al. 2021).

Colour illustrations. Brazil, Paraíba, Cuité, Serra de Cuité, where the specimens were collected. From top to bottom: basidiospores under SEM; capillitium under SEM; close up of mature basidioma *in situ*; mature basidiomata *in situ*. Scale bars = 2 µm and 5 µm (SEM photos), 5 mm (basidioma), 10 mm (basidiomata).

Supplementary material

FP1513 Phylogenetic tree.

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Halocryptovalsa endophytica

Fungal Planet 1514 – 29 June 2023

Halocryptovalsa endophytica G. Delgado, T. Nau & Maciá-Vicente, *sp. nov.*

Etymology. Named after the root endophytic lifestyle of the fungus.

Classification — *Diatrypaceae*, *Xylariales*, *Sordariomycetes*.

Root endophyte isolated on culture media from surface-sterilised roots of living plants. *Mycelium* composed of branched, septate, smooth, hyaline, thin-walled *hyphae*, 1.5–4 µm wide. *Chlamydospores* present, terminal or intercalary, solitary or catenate and in short chains of up to 6, cylindrical, subcylindrical or elongated, sometimes constricted at the centre, pale brown to brown or dark brown, thick-walled, smooth, aseptate, 7–17(–21) × 3–5 µm.

Culture characteristics — Colonies on malt extract agar (MEA) moderately fast growing, reaching 27–37 mm diam after 2 wk at 23–24 °C, cream, flat, slightly raised and producing chlamydospores around the centre, sometimes with a reduced amount of aerial mycelium, margin diffuse, reverse yellowish cream. On potato dextrose agar (PDA) reaching 29–35 mm diam, off-white, flat, sparsely cottony, cream-colour and slightly raised at the centre with a concentric ring of aerial mycelium, margin diffuse, reverse creamy white to dull white. Cultures sterile.

Habitat & Distribution — Root endophyte. Known so far from southeast Spain and possibly Iran.

Typus. Spain, Alicante, Santa Pola, N38°11'50.5" W0°34'42.4", 0 m a.s.l., isolated from surface-sterilised, asymptomatic roots of a wild plant of *Salicornia patula* (*Amaranthaceae*), 15 June 2013, coll. *J.G. Maciá-Vicente*, isol. *T. Nau*, P1589 (holotype permanently preserved in a metabolically inactive state CBS 149761; culture ex-type CBS 149761; ITS, LSU, SSU and *tef1* sequences GenBank KU933993, OQ592846, OQ588704 and OQ595099; MycoBank MB 847915).

Additional material examined. Spain, Alicante, Santa Pola, N38°11'50.5" W0°34'42.4", 0 m a.s.l., isolated from surface-sterilised, asymptomatic roots of a wild plant of *S. patula*, 15 June 2013, coll. *J.G. Maciá-Vicente*, isol. *T. Nau*, P2003, ITS sequence GenBank OQ587950.

Notes — Several genera of diatrypaceous fungi have been found associated with halophytic plants or those well adapted to conditions of high salinity in marine environments (Klaysuban et al. 2014, Dayarathne et al. 2016, 2020, Abdel-Wahab et al. 2017). One of them is *Halocryptovalsa*, which was introduced to accommodate two saprobic diatrypaceous marine taxa (Dayarathne et al. 2020). The type species, *H. avicenniae*, was originally described from intertidal decayed wood of the mangrove *Avicennia marina* in Saudi Arabia, whereas *H. salicorniae* was collected on decaying stem of the salt marsh plant *Salicornia* sp. in Thailand. They are distinct from other diatrypaceous genera in having poorly developed stromata with perithecia that lack horizontal or vertical furrows within the relatively long, wide ascomatal necks lacking a white powdery entostroma, and are deeply immersed in the wood of the host forming small papillae that protrude above the substrate. The third species introduced here, *H. endophytica*, was isolated during a sampling for root endophytic fungi associated with amaranthaceous halophytes in southeast Spain (Maciá-Vicente et al. 2016). Both strains were obtained from roots of *Salicornia patula*, a common halophyte in saline ecosystems of the Mediterranean region (Sánchez-Gavilán et al. 2021). Phylogenetically, they clustered together with a third isolate identified as '*Libertella* sp. F6' in a strongly supported monophyletic clade (95 BS/0.99 BPP). However, despite the identical geographical origin of the strains of *H. endophytica*, pairwise comparisons show some variation in their ITS sequences which can be attributed to intra-genomic variability between ITS copies. Curiously, the *Libertella* sp. F6 isolate, represented in GenBank by an unpublished ITS sequence, was obtained from *Juncus acutus* in Iran according to the available annotations. Unfortunately, it was not possible to infer which part of the host plant it was obtained from or its lifestyle and ecology, but *J. acutus* is a known halotolerant species with a wide ecological range which is frequent on dunes in zones of estuaries and tolerates well soils with high levels of sulphates and chlorides (Boscaiu et al. 2011). Furthermore, its ITS sequence is highly similar to that of CBS 149761, the ex-type culture of *H. endophytica*, and therefore this isolate could be considered conspecific with our fungus based on molecular and ecological evidence. Similarly, Macia-Vicente et al. (2008) previously reported a root endophyte identified as *Libertella* sp. based on morphological features, and isolated from the halophyte *Frankenia corymbosa* in a coastal salt marsh of Alicante, Spain, 20 km north from the location where strains of *H. endophytica* were obtained. Lack of molecular data precludes comparison with *H. endophytica*, but this finding suggests that libertella-like fungi are widespread among different members of this ecological group of plants. Abdel-Wahab et al. (2017), on the other hand, reported a libertella-like asexual morph for *H. avicenniae* forming globose to subglobose, ostiolate pycnidia deeply immersed in the stromata of the sexual morph and having aseptate, filiform, straight, curved or hook-like, hyaline conidia. *Libertella* species have been previously regarded as the conidial morphs of diatrypaceous fungi (Sutton 1980, Adamčíková et al. 2011) but rarely mentioned in association with halophytic hosts (Rashmi et al. 2019). Our strains remained sterile in all the media used and a morphological comparison with previously described species of *Halocryptovalsa* or *Libertella* was not possible. They grouped sister to both known species of *Halocryptovalsa* with strong support (99 BS/1 BPP). A third strain of *H. avicenniae*, NFCCI-4389, isolated from *A. marina* in India, grouped distant from this clade but within the well-supported lineage (96 BS/1 BPP) representing the genus *Halocryptovalsa*.

(Notes continued on Supplementary page)

Colour illustrations. Salt marsh with *Salicornia patula* plants near Santa Pola, Alicante, Spain, where the species was isolated. Colonies on MEA and PDA surface view; mycelium with hyphae; chlamydospores. Scale bars = 10 µm (hyphae), 5 µm (chlamydospores).

Supplementary material

FP1514-1 Phylogenetic tree.

FP1514-2 Table. List of strains included in this study and their GenBank accession numbers.

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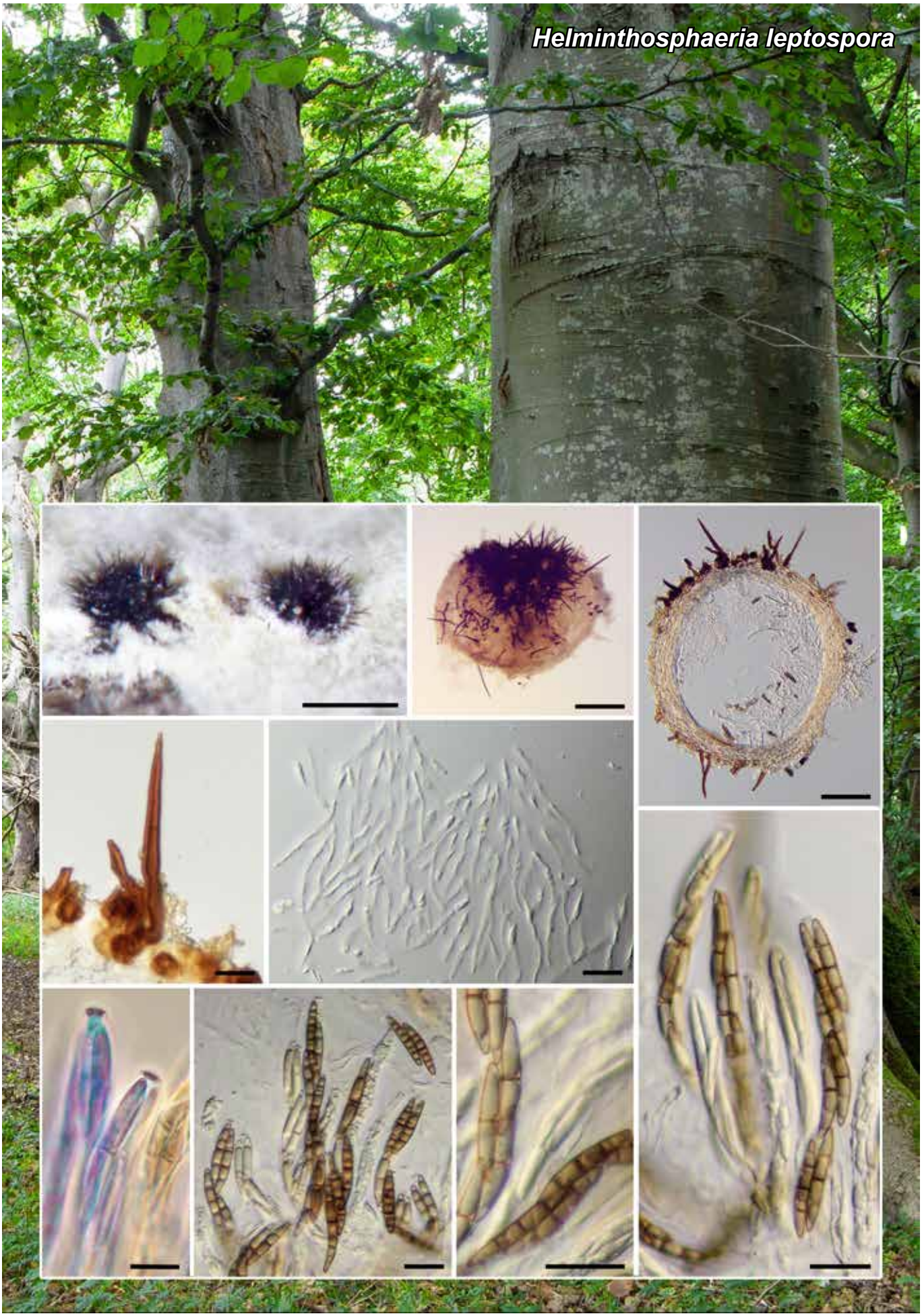

Helminthosphaeria leptospora

Fungal Planet 1515 – 29 June 2023

Helminthosphaeria leptospora A.N. Mill. & Læssøe, *sp. nov.*

Etymology. Name refers to the long, slender ascospores.

Classification — *Helminthosphaeriaceae*, *Sordariales, Sordariomycetidae*, *Sordariomycetes*.

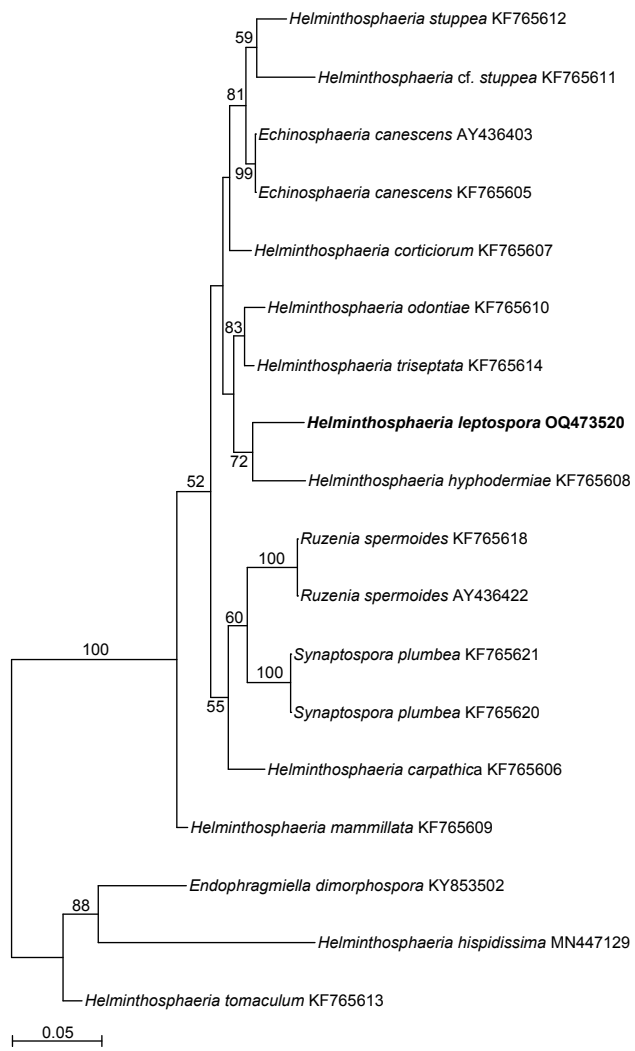
Ascomata globose to subglobose, slightly papillate, neck indistinct, 300–500 µm diam, numerous, scattered, brown when dry, pale yellowish in water, sparsely setose in lower two-thirds, densely setose and black in upper third above mycelial mat, setae brown, 40–170 × 6–12 µm, walls 1.5–3 µm wide, ends acute; ascomata emerging from a basidioma of *Neohypochnicium cremicolor* on hardwood, probably *Fagus sylvatica*. *Ascomatal wall* of *textura angularis* in surface view, in longitudinal section 2-layered, 40–60 µm thick, inner layer *textura prismatica*, 10–20 µm thick, composed of 2–5 layers of elongate, flattened, thin-walled, hyaline to pale brown cells; outer layer *textura angularis*, 30–40 µm thick, composed of several layers of thick-walled, pale brown cells, walls 1.5–2 µm thick; setae projecting from outer wall cells. *Ascomatal apex* black, densely setose, indistinct. *Paraphyses* filiform, 1.5–5 µm wide, hyaline, abundant, septate, unbranched, persistent. *Asci* broadly clavate, 100–130 × 8.5–11 µm, stipitate, unitunicate, thin-walled, apex truncate; ring narrow, 1.5 µm wide, shallow, wedge-like, refractive, I-, not stained by blue and blue-black inks; with eight bi- to triseriate ascospores. *Ascospores* fusiform, with subacute ends, 29.5–45(–49.5) × 4–6.5 µm (av. 34.5 × 5; n = 32), hyaline and aseptate in the ascus before maturity, eventually brown and 1–3-septate, first-formed septum median, not constricted; with large guttules in all cells, smooth-walled, without sheath or appendages.

Habitat & Distribution — Deciduous, *Fagus*-dominated forest; fungicolous on *Neohypochnicium cremicolor*. Known only from Denmark.

Typus. Denmark, Lolland, Favrsted Skov, 54.7256N 11.5465E, deciduous forest, on the corticioid *Neohypochnicium cremicolor,* 14 Oct. 2020, *M.S. Christiansen & T. Læssøe*, DMS-10149277 (holotype ILLS00121778 (ILLS); LSU sequence GenBank OQ473520; MycoBank MB 847668).

Colour illustrations. Background photo of a deciduous forest near the type locality, Denmark (photo credit Jens H. Petersen). Ascomata; ascoma; longitudinal section through ascoma; setae; paraphyses; asci; ascal apices; ascospores. Scale bars = 500 µm (ascomata), 100 µm (ascoma, section), 20 µm (setae, paraphyses, asci, ascospores), 10 µm (ascal apices) (photos A. Miller). More images at: https://svampe.databasen.org/observations/10149277.

Notes — *Helminthosphaeria leptospora* is distinguished by its growth on a resupinate basidiomycete, ascomata with a densely setose apex, and long, eventually 3-septate, fusiform ascospores. Three other species in the genus occur on resupinate basidiomycetes: *H. corticiorum*, *H. hyphodermiae*, and *H. odontiae* (Samuels et al. 1997, Miller et al. 2014). Although *H. leptospora* is closely related to *H. hyphodermiae*, the other two species are more distantly related suggesting that this host ecology arose multiple times. The ascospores in *H. hyphodermiae* are ellipsoidal, aseptate and 7.2–16 µm long, whereas the ascospores in *H. leptospora* are long fusiform, up to 3-septate, and 29.5–49.5 µm long. A dematiaceous hyphomycete is also present in the type material but would appear not to be connected with the *Helminthosphaeria* (M. Reblova in litt.).



Maximum Likelihood tree generated using PhyML in SeaView v. 5.0.4 (Gouy et al. 2010). *Helminthosphaeria leptospora* is in **bold**. Numbers above or below branches refer to bootstrap support values from 1 000 bootstrap replicates. GenBank accession numbers for the LSU region are given after taxon names. The alignment and trees are publicly available in TreeBase (TB2:S30194).

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Inocybe amygdaliolens

Fungal Planet 1516 – 29 June 2023

Inocybe amygdaliolens Esteve-Rav., Pancorbo & Dovana, *sp. nov.*

Etymology. The name derives from the Latin 'amygdalus', which refers to the almond tree, and 'olens', the present active participle of 'oleo', which means smell. It refers to the characteristic bitter almond smell of the species.

Classification — *Inocybaceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata agaricoid and stipitate. *Pileus* 20–40(–50) mm, at first campanulate-convex, soon convex to plano-convex, broadly umbonate to subumbonate; margin straight to decurved, regular to sometimes wavy with age, fissurate at times; colour yellow ochraceous to yellowish brown or buff brown (Mu 2.5Y 7/6-8; 10Y/R 7/6-8, 6/6-8), uniform but in some cases slightly paler in the centre by the presence of an ephemeral whitish velipellis; surface initially smooth, delicately tomentose to fibrillose, often broken into appressed small squamulae towards the margin, dry, not or hardly hygrophanous, radially fibrous at the margin, not rimose. *Velipellis* generally absent or very ephemeral, when present as a white arachnoid patch or sparse remains, especially in young basidiomata. *Lamellae* crowded (L = 45–50(–60); l = (0–)1(–2), free to narrowly adnate, hardly to slightly ventricose, initially whitish, becoming pale grey to beige, often showing a rosaceous reflection, then pale brown ochraceous to yellowish brown, edge white, entire to finely crenulate. *Stipe* 20–50(–80) × 4–8(–10) mm, straight or often curved towards the base, cylindrical, tapering towards the apex, often claviform to rarely subbulbous; colour initially white, soon dirty white to beige, in some collections taking on a pink to flesh-coloured tinge at the upper end (Mu 5YR 7/4-6); surface densely pruinose along the entire surface without veil remains. *Cortina* absent. *Context* fibrous, whitish, with a similar colour to the stipe surface, exceptionally pinkish at the upper part of the stipe. *Smell* initially subspermatic herbaceous when cut, in aged basidiomata developing a typical smell of bitter almonds, especially remarkable when kept in a closed box, *taste* non-particular. *Spores* (7.6–)8.1–*9.1*–10.7(–12.4) × (4.9–)5.1–*5.7*–6.3(–6.9) µm (n = 317 / N = 4); Q: (1.34–)1.40–*1.50*–1.99(–2.36), smooth, ovoid in frontal view, amygdaloid in profile, with a rather faint suprahilar depression, apex mostly rounded, sometimes subacute. *Basidia* (20.9–)22.1–*26.8*–31.5(–32.8) × (6.9–)7.3–*8.8*–10.7(–11.3) µm; Q: (2.08–)2.51–*3.00*–3.47(–3.88), 4-spored, rarely 2-spored, clavate, sterigmata 3.5–5 µm long. *Lamella edge* practically sterile, composed of numerous protruding hyaline cheilocystidia mixed with abundant mostly hyaline clavate paracystidia. *Cheilocystidia* (29.6–)31.2–*37.8*–48.3(–53.9) × (9.6–)10.5–*13.4*–16.3(–18.3) µm; Q: (2.06–)2.35–*2.90*–3.51(–4.16), similar in size and shape to pleurocystidia. *Pleurocystidia* (31.2–)33.5–*41.1*–48.4(–58.3) × (8.2–)10.0–*12.4*–14.7(–15.7) µm; (2.18–)2.54–*3.30*–4.15(–5.24), (n = 152 / N = 4), broadly fusiform to subfusiform, hyaline, base often attenuate, sometimes pedicellate, mainly crystalliferous at the apex, walls (1.08–)1.26–*1.80*–2.59(–3.05) µm thick, reaching –3.5 µm at the apex, yellowish in 10 % NH_4OH. *Stipitipellis* a cutis of parallel hyphae (2.8–)3.7–5.0–6.7(–6.8) µm, bearing caulocystidia mainly in the upper part of the stipe, scarce in the lower part, (38.2–)38.3–*45.9*–58.3(–62.0) × (10.8–)10.9–*13.0*–16.5(–17.2) µm; Q: (2.75–)2.95–*3.50*–4.20(–4.50) (n = 57 / N = 3), similar in shape to hymenial cystidia, mixed with clavate to subcylindrical hyaline paracystidia. *Pileipellis* a cutis formed by parallel cylindrical cells, 6–11 µm wide, somewhat constricted at septa, showing an encrusting and diffusely intracellular yellowish ochraceous pigmentation. *Hymenophoral trama* of parallel hyphae, 3–7 µm broad, hyaline. *Subhymenium* pseudoparenchymatic in appearance, with subglobose to polygonal cells 7.5 × 6.4 µm in average. *Clamp connections* abundant.

Habitat & Distribution — See Supplementary page.

Typus. Spain, Madrid, Rozas de Puerto Real, El Tejar, N40°16'06" W4°32'42", 675 m a.s.l., in mixed *Quercus suber*, *Q. ilex*, *Pinus pinaster* and *P. pinea* forest, in acidic, sandy soil, 16 Nov. 2018, *J.C. Campos & M. Hinojosa* (holotype AH 50978, isotype FP18111603; ITS and LSU sequences GenBank OQ379324 and OQ379363; MycoBank MB 846991).

Additional materials examined. See Supplementary page.

Notes — Colour codes are taken from Munsell (1994), and terminology follows Vellinga (1988) and Kuyper (1986). The macro and micro-morphological characters, and especially the typical bitter almond smell, place *I. amygdaliolens* in the *Inocybe hirtella* group (Bandini et al. 2022a). Apart from a different ITS/LSU sequence, two characteristics seem to be especially diagnostic in *I. amygdaliolens*: 1) its Mediterranean distribution, with a marked preference for acid and sandy soils; and 2) its small hymenial cystidia, with a clear claviform to fusiform tendency. This type of cystidia would place it in proximity to *I. brevicystis*, *I. mycenoides* and *I. somae*, which we have already discussed when dealing with the Mediterranean *I. pityusarum*. This last species inhabits limestone soils and exhibits wider spores and slightly larger cystidia. On the other hand, *Inocybe brevicystis* is a taxon of a doubtful interpretation, originally described by Métrod (1956) from humid continental forests of central Europe, with a scaly cap in the centre and no indication of the smell was made. The differences with respect to *I. mycenoides* and *I. somae* are discussed in the observations of *I. pityusarum*. The GenBank sequence KY349119 (as *I.* cf. *brevicystis*) corresponds to *I. amygdaliolens*. In our ITS/LSU phylogenetic analysis, *I. amygdaliolens* grouped in a well-supported clade (ML-BS 98 %, BPP 1) with *I. mycenoides*, *I. pityusarum* and *I. somae*. Comparison of ITS sequences showed that the *I. amygdaliolens* sequence (GenBank OQ379324) has 567/576 (98 %) identity and seven gaps with the *I. pityusarum* holotype sequence (GenBank OQ379324), 623/641(97 %) identity and 10 gaps with *I. mycenoides* (GenBank OK057156) and 623/639 (97 %) identity and eight gaps with *I. somae* (GenBank OK057148).

Colour illustrations. *Inocybe amygdaliolens* habitat from the type locality in Rozas de Puerto Real, Spain. *Quercus suber*, *Q. ilex*, *Pinus pinaster* and *P. pinea* forest, in acidic, sandy soil. In situ basidiomata of the holotype (AH 50978); photos of basidiospores; pleurocystidia; cheilocystidia; caulocystidia in the upper third of the stipe. Scale bars = 10 mm (basidiomata), 50 µm (cystidia), 10 µm (spores).

Supplementary material

FP1516 Phylogenetic tree.

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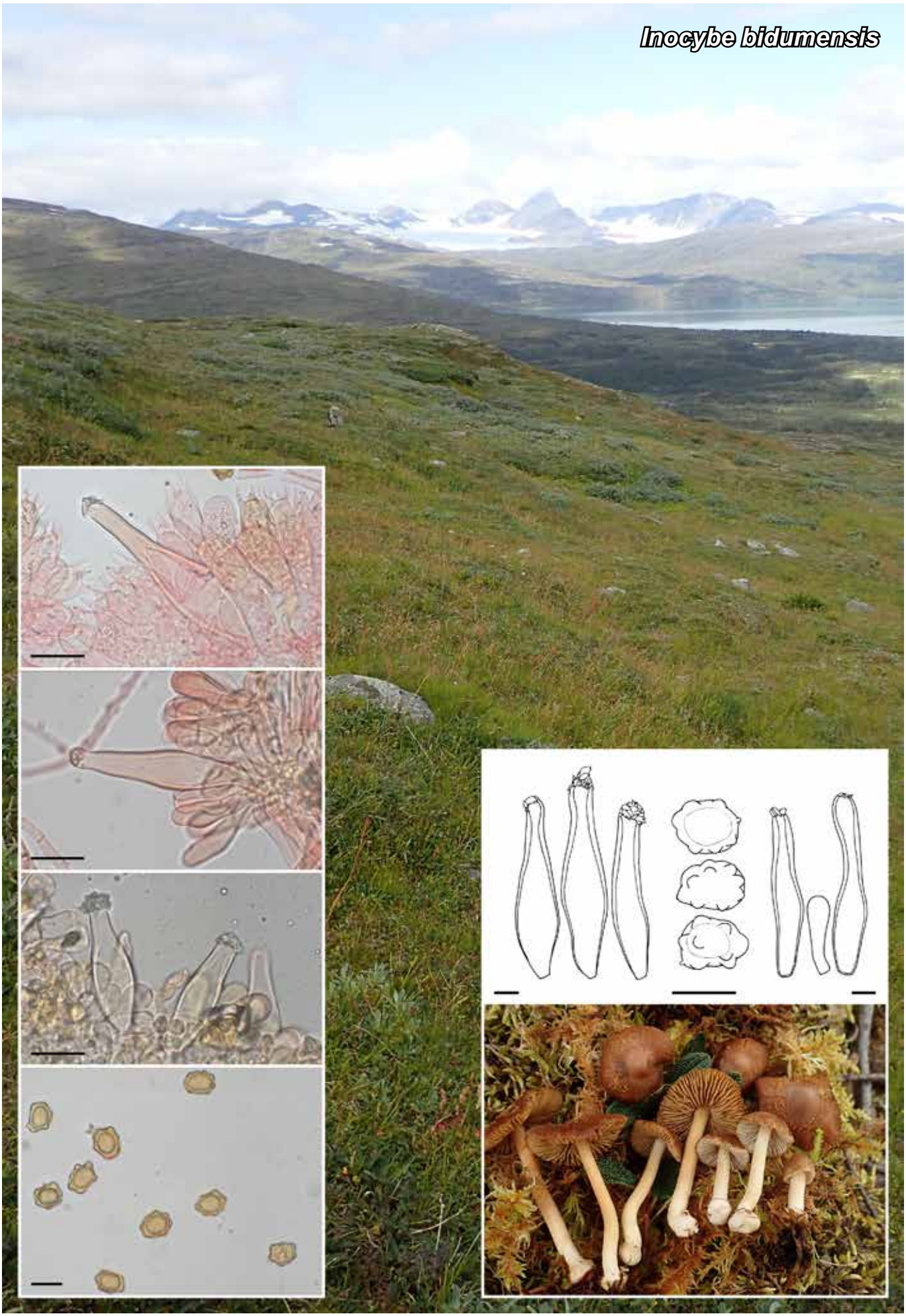
Inocybe bidumensis

Fungal Planet 1517 – 29 June 2023

Inocybe bidumensis E. Larss. & Vauras, *sp. nov.*

Etymology. Refers to the Sami name for the region of the type locality, Pite lappmark.

Classification — *Inocybaceae*, *Agaricales*, *Agaricomycetes*.

Pileus 8–30 mm diam, conical to convex, umbonate or with an obtuse to broad umbo, later plano-convex to plane with broad umbo, as young with slightly incurved margin later plane to decurved, often with undulate margin, dry, rather uniformly coloured yellowish brown to ochraceous brown, at centre smooth to matted fibrillose, radially fibrillose to weakly rimose towards the margin, with age coarsely fibrillose, adpressed scaly to scaly towards the margin, cortina absent, velipellis thin, fugacious, white, visible in young basidiomata, soon disappearing. *Lamellae* moderately crowded, interspersed with lamellulae, L = 30–50, adnexed to almost free, first white with a greyish tone, later pale ochraceous brown, edge pale to concolorous. *Stipe* 15–45 × 3–5 mm, cylindrical with a distinct rounded prominent white basal bulb, with age often a bit curved, pruinose for the entire length, as young whitish to pale straw, later with a yellowish-brown tone, longitudinally striate pruinose, solid, darkening upon drying. *Context* in pileus pale ochraceous brown, in stipe pale ochraceous brown, base white. *Smell* and taste indistinct. *Basidiospores* (9.5–)10.4–*10.9*–11.4(–12.6) × (6.3–)7.6–*7.9*–8.2(–8.8) µm, n = 120, Q = 1.20–*1.37*–1.45, variable, angular-nodulose, prominent rounded obtuse nodules and a small apiculus, pale ochraceous brown. *Basidia* 30–*36*–43 × 11–*13*–15 µm, n = 26, clavate, 4-spored, hyaline, sterigmata 6–7.5 µm. *Pleurocystidia* 58–*77*–95 × 14–*17*–24 µm, n = 50, lageniform to utriform to fusiform, with short pedicel, thick-walled (2–)2.5–3.5(–4) µm, thicker towards the apex, with abundant crystals, hyaline to slightly yellow in KOH solution. *Cheilocystidia* similar to pleurocystidia but shorter, 45–*53*–71 × 12–*16*–23 µm, n = 35, pedicellate to truncate-variable or with rounded base, thick-walled, paracystidia rather abundant. *Caulocystidia* over the entire length, less dense in the lower part, similar to pleurocystidia but narrower and longer at stipe apex, abundant with crystals, less so in the lower part, 40–*60*–90 × 11–*12*–18 µm, n = 57, fusiform to more cylindrical, hyaline to slightly yellow in KOH solution. *Cauloparacystidia* 20–30 × 8–12 µm, n = 30, clavate to pyriform, abundant. *Pileipellis* a cutis of cylindrical to inflated hyphae with 7–16 µm wide, encrusted, yellowish-brown pigmented. *Clamp connections* present.

Ecology & Distribution — Occurs in the arctic and alpine zone growing in moist areas in mosses associated with *Salix reticulata*, *S. polaris*, *S. herbacea* and *Bistorta vivipara*, and seems to be favored by calcareous ground. Known from Sweden, Norway and Svalbard. Blast search of NCBIs GenBank nucleotide database and the UNITE database recovered no additional data.

Typus. Sweden, Pite lappmark, Arjeplog, North-east side of mount Áhkáris. Fen on slope in the alpine zone on calcareous ground, associated with *Salix herbacea*, *S. reticulata*, *Betula nana* and *Bistorta vivipara*, 14 Aug. 2018, *J. Vauras & E. Larsson*, EL168-18 (holotype GB-0207649, isotype TUR-A 208248; ITS-LSU sequence GenBank OQ572784; MycoBank MB 847905).

Additional materials examined. Norway, Hordaland, Ulvik, Finse, Kongsnuten, Blåisen, in moist place with *Salix herbacea*, 11 Aug. 2005, *E. Larsson*, EL35-05, GB-0207652 (ITS sequence GenBank AM882989); Oppland, Dovre, Grimsdalen, Verkensetra, in moist area with *Salix reticulata*, *Bistorta vivipara* and *Betula nana*, 13 Aug. 2021, *E. Larsson*, EL44-21, GB-0207654 (ITS sequence GenBank OQ572787). – Svalbard and Jan Mayen, Svalbard, Nordenskiöld Land, Bolterdalen, with *Salix polaris* and *Bistorta vivipara*, 13 Aug. 2015, *E. Larsson*, EL89-15, GB-0207650 (ITS-LSU sequence GenBank OQ572786). – Sweden, Lule lappmark, Jokkmokk, Padjelanta, Unna Duvgge, in alpine zone, moist area with *Salix herbacea* and *Bistorta vivipara*, 15 Aug. 2016, *E. Larsson*, EL177-16, GB-0207653 (ITS-LSU sequence GenBank OQ572785); Lule lappmark, Jokkmokk, Padjelanta, Sårjåsjaure, in alpine zone, moist area with *Salix reticulata, S. herbacea* and *Bistorta vivipara*, 17 Aug. 2016, *E. Larsson*, EL203-16, GB-0207651 (ITS-LSU sequence GenBank OQ572788).

Notes — *Inocybe bidumensis* is characterised by the uniformly coloured ochraceous brown radially fibrose to scaly pileus with obtuse to broad umbo, pale to yellowish brown often curved stipe with a prominent white basal bulb, long thick-walled pleuro- and caulocystidia, and angular-nodulose spores with rounded obtuse nodules. Like *I. subrimosa*, a rather common species in parks and grazed forest meadows in the Nordic countries, *I. bidumensis* develops darkening of the stipe upon drying (Esteve-Raventós et al. 2022). In alpine habitats there are several similar species that can cause confusion; *I. hirculus* differs by having somewhat slender basidiomata and a less distinct bulbous stipe base; *I. alpinomarginata* shares with *I. bidumensis* the greyish tone in young lamellae and uniformly coloured ochraceous brown radially fibrose to scaly pileus, but has a less coloured stipe and less bulbous stipe base (Cripps et al. 2020). Other nodulose-spored species in the alpine zone include *I. substellata*, that differs by having a greyish yellow-brown colour of the pileus, often with abundant white velipellis; *I. obtusiuscula* that differs by the acute umbonate pileus, slender basidiomata and less distinct bulbous stipe base, and *I. caprimulgi* that has a more strongly rimose pileus, a marginate bulbous stipe base and different ecology (Kühner 1988, Vauras & Larsson 2016). *Inocybe oreina* has on average larger spores and a distinct marginate basal bulb (Favre 1955). The sequence difference in the ITS region between *I. bidumensis* and its sister species *I. subrimosa* are 11 substitutions, two 5 bp, one 2 bp and 5 single bp insertion/deletion events.

Colour illustrations. *Inocybe bidumensis* habitat in the alpine zone, Pite lappmark, Arjeplog, Áhkáris. Basidiomata of the holotype (GB-0207649); photos of pleuro-, caulo-, cheilocystidia and basidiospores; drawing of pleurocystidia (left), basidiospores, caulocystidia (right). Scale bars = 10 µm (spores and drawing), 20 µm (pleuro, caulo- and cheilocystidia).

Supplementary material

FP1517 Phylogenetic tree.

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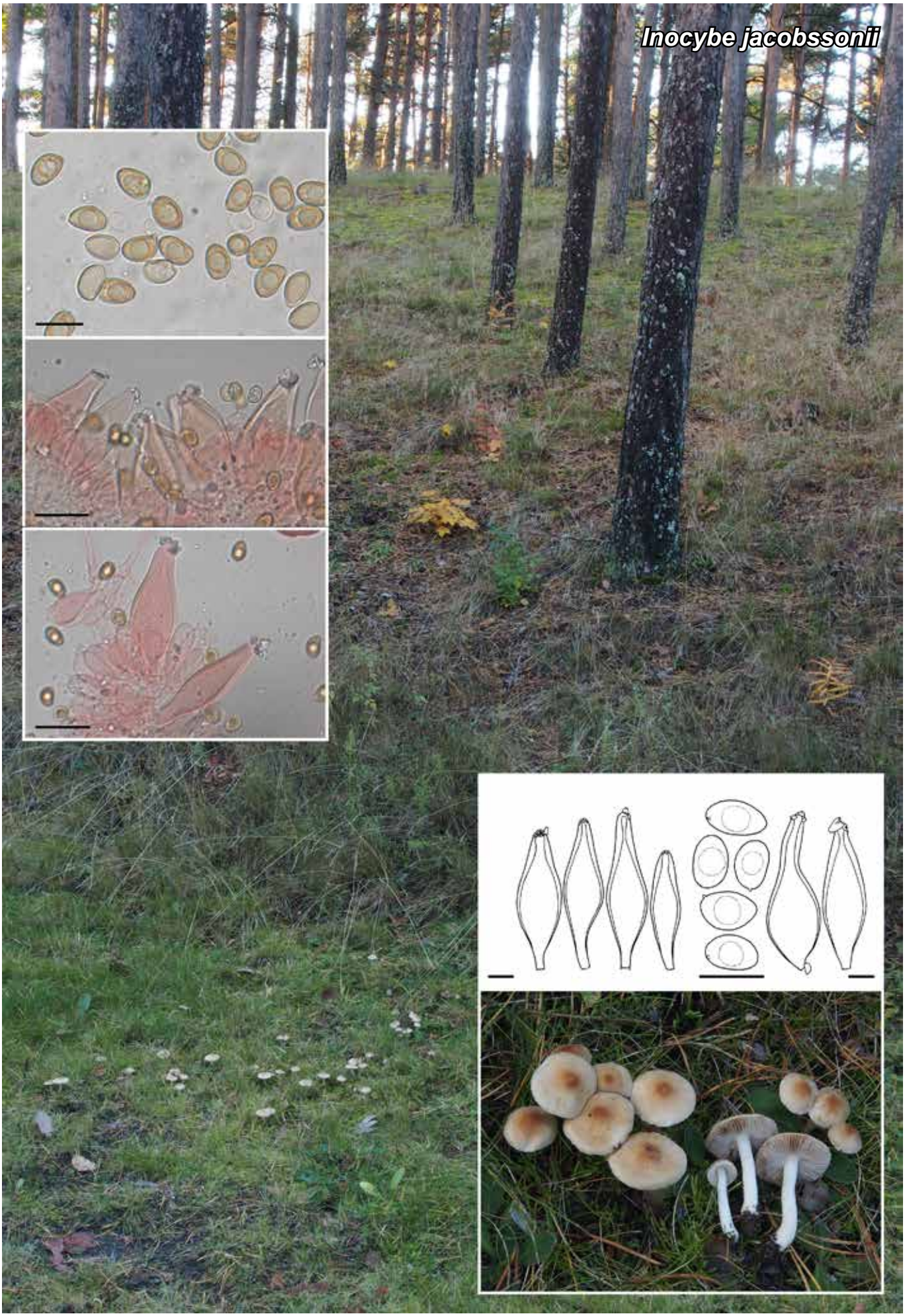
Inocybe jacobssonii

Fungal Planet 1518 – 29 June 2023

Inocybe jacobssonii Vauras & E. Larss., *sp. nov.*

Etymology. In honour of Stig Jacobsson for his contributions to the knowledge of *Inocybaceae* in Fennoscandia.

Classification — *Inocybaceae*, *Agaricales*, *Agaricomycetes*.

Pileus 15–45 mm diam, as young hemisphaerical to campanulate, later becoming convex to expanded, at first without, later with more or less pronounced umbo, margin at first inflexed, later deflexed to reflexed, colour ochraceous to brown around centre, outwards gradually paler, at margin creme to whitish, surface at first sericeous-smooth, later towards the margin sericeous-fibrillose, subviscid when moist. *Cortina* whitish in young basidiomata, rather abundant, but soon disappearing. *Lamellae* moderately crowded, interspersed with lamellulae, to 7 mm broad, ventricose, mainly narrowly adnate, first whitish to pale greyish, then grey, brown-grey, later grey-brown, edge fimbriate, pale. *Stipe* 25–60 × 3–8 mm, equal, slightly clavate to subbulbous, solid, rather fragile, white, later also ocher tinged, at apex white pruinose, downwards smooth to slightly fibrillose. *Context* whitish, pale greyish, pale yellowish to pale brownish. *Smell* spermatic. *Basidiospores* (7.4–)7.7–*8.4*–9.2(–9.9) × (4.6–)4.8–*5.4*–5.9(–6.4) µm, n = 140, Q = (1.3–)1.4–1.75(–1.85), Q mean = 1.57, smooth, ellipsoid to subamygdaliform, with obtuse apex and small apiculus, rather pale yellowish brown. *Basidia* (23–)24–30(–31) × 8–10(–11) µm, n = 40, subclavate to clavate, 4-spored, hyaline. *Pleurocystidia* (46–)49–*57*–66(–72) × (10–)14–*17*–20(–25) µm, Q mean = 3.4, n = 140, mainly fusiform, often with a pedicel, crystalliferous at apex, thick-walled, wall to 3 µm thick, yellowish. *Cheilocystidia* (35–)38–*49*–59(–62) × (12–)13–*16*–20 µm, n = 40, similar to pleurocystidia, mainly fusiform but more variable and on average shorter. *Paracystidia* 15–26 × 8–12 µm, n = 40, oval, pyriform to clavate, hyaline. *Caulocystidia* at apex similar to pleurocystidia but on average longer, abundant, with crystals, (42–)48–*61*–85(–92) × (12–)13–*17*–23(–28) µm, n = 70, less so further down, fusiform to more cylindrical, *cauloparacystidia* (16–)20–34(–36) × 8–14(–18) µm, n = 40, mainly clavate. *Clamp connections* frequent.

Ecology & Distribution — Has preference for dry forests and park habitats on calcareous soils, where it often occurs in larger groups. It is found mainly with *Pinus sylvestris,* but also in deciduous forests with *Tilia cordata*, *Quercus robur* and *Corylus avellana*. It is known from the hemiboreal and nemoral zones in Europe. Blast search of NCBIs GenBank nucleotide database and the UNITE database gave matches of ITS data of from *Epipogon* root community studies in Italy suggesting the species to have broad host preferences.

Typus. Finland, Regio aboënsis, Turku, the cemetery Turun hautausmaa, on lawn at margin of park forest with *Pinus sylvestris,* 35 m a.s.l., 1 Oct. 2022, *J. Vauras*, 33634F (holotype TUR-A 215830, isotype GB-0207655; ITS-LSU sequence GenBank OQ520012; MycoBank MB 847861).

Additional materials examined. Estonia, Läänemaa, Taebla, Palivere, forest with *Picea abies, Pinus sylvestris*, *Corylus avellana* and *Salix caprea*, 27 Sept. 2008, *J. Vauras*, 26717 (TUR-A 182548, GB). – Finland, Regio aboënsis, Halikko, Märynummi, margin of lawn, near *Pinus sylvestris,* 22 Sept. 2017, *J. Vauras*, 32379 (TUR-A 204942, GB, ITS-LSU sequence GenBank OQ520016); Regio aboënsis, Parainen, Ersby, margin of an old abandoned limestone quarry in forest with *Pinus sylvestris, Picea abies* and *Salix*, 24 Sept. 1986, *J. Vauras*, 2527 (TUR-A 147834, WTU, ITS and LSU sequences GenBank KY990556 and KY990512); ibid., forest with *Pinus sylvestris,* 6 Oct. 2022, *J. Vauras*, 33657 (TUR-A 215831, GB, ITS-LSU sequence GenBank OQ520015); Parainen, Tennby, mixed forest with *Betula pendula*, *Corylus avellana*, *Pinus sylvestris* and *Picea abies*, 28 Sept. 2021, *J. Vauras*, 33226 (TUR-A 209514, GB); Nylandia, Hanko, Tvärminne, at the old brick plant, under *Pinus sylvestris*, 11 Oct. 2011, *J. Vauras*, 28850 (TUR-A 190868, GB, ITS-LSU sequence GenBank OQ520014). – Slovakia, Banskobystricky Kraj, Muránska Planina National Park, Murán, Velka Lúka, in mixed coniferous forest, 10 Oct. 2008, *E. Larsson*, EL260-08, GB-0207656 (ITS-LSU GenBank OQ520022). – Sweden, Bohuslän, Håby, Lammö, in deciduous forest under *Quercus*, *Corylus* and *Tilia*, 29 Sept. 2014, *E. Larsson*, EL200-14, GB-0207658 (ITS-LSU GenBank OQ520018). Gotland, Ardre, Mullvalds strandskog, under *Pinus sylvestris* on sandy soil, 18 Oct. 2021, *E. Larsson*, EL190-21, GB-0207657 (ITS-LSU GenBank OQ520020).

Notes — *Inocybe jacobssonii* belongs in the *I. geophylla* group, that is identified to host a high phylogenetic diversity (Ryberg et al. 2008). Several new species have recently been described within the group (Matheny & Swenie 2018, Crous et al. 2020a, Bandini et al. 2021, 2022b, Kaygusuz et al. 2022, Tan et al. 2022). *Inocybe jacobssonii* is a medium-sized species, characterised by a pileus that has a distinct ochre to darker brown disc and is outwards remarkably pale when older. Both in morphology and molecular data it is close to *I. udicola*, but differs by having slightly smaller spores and average Q value, on average larger pleurocystidia and different ecology (Tan et al. 2022). A similar species in the hemiboreal zone is *I. bellidiana* that has a paler pileus and spores with bulgy dorsal sides and grows in parks mainly with *Quercus robur*. Also, *I. orionis* associated with *Fagus sylvatica, Carpinus betulus* and *Quercus robur* has rather similar colours as *I. jacobssonii,* but has narrower spores and a larger Q value and smaller pleurocystidia (Bandini et al. 2021). In the Nordic countries *I. jacobssonii* has earlier been identified as *I. posterula* (Jacobsson & Larsson 2012, Ludwig 2017) and *I. xanthodisca* (Kytövuori et al. 2005). The sequence difference in the ITS region between *I. jacobssonii* and its sister species *I. udicola* are 13 substitutions, two 3 bp, one 2 bp and 7 single bp insertion/deletion events.

Colour illustrations. Inocybe jacobssonii habitat from the type locality in Turun hautausmaa, Finland: lawn at a cemetery park forest in the hemiboreal zone, growing associated with *Pinus sylvestris. In situ* basidiomata of the holotype (TUR-A 215830); photos of cheilocystidia and basidiospores; drawing of pleurocystidia (left), basidiospores, caulocystidia (right). Scale bars = 20 µm (cheilocystidia ans pleurocystidia), 10 µm (spores and drawing).

Supplementary material

FP1518 Phylogenetic tree.

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Inocybe pityusarum

Fungal Planet 1519 – 29 June 2023

Inocybe pityusarum Esteve-Rav., Pancorbo, Siquier & Dovana, *sp. nov.*

Etymology. The name is derived from the Greek 'Pityoessai', which means abundant in pines. In fact, the smaller islands of the Balearic Islands are Ibiza and Formentera, which are called the Pitiusas Islands.

Classification — *Inocybaceae*, *Agaricales*, *Agaricomycetes.*

Basidiomata agaricoid and stipitate. *Pileus* 15–25 mm, at first campanulate-convex, soon convex to plano-convex, broadly umbonate to subumbonate; margin straight, regular to sometimes wavy with age, fissurate at times, often covered with appendiculate traces of the velipellis; colour tawny brownish to orange ochraceous (Mu 7.5YR 6/4-6; 5/8) or yellow brown (Mu 10YR 5/6-8), sometimes slightly paler in the centre due to the whitish velipellis; surface delicately tomentose to fibrillose, often lacerated into appressed small squamulae (in one collection of old basidiomata, AH 40235, the surface can be covered with erect recurved scales), dry, not hygrophanous, radially fibrous at the margin. Velipellis present, generally rather persistent as white arachnoid remains. *Lamellae* moderately crowded to subdistant (L = 35–45; l = (0–)1–2(–3), free to narrowly adnate, rather ventricose, initially whitish, becoming pale grey to beige, then pale brown ochraceous, edge white, entire to finely crenulate. *Stipe* 20–30(–50) × 3–5 mm, straight to curved towards the base, cylindrical, tapering towards the apex, sometimes claviform to subbulbous; colour initially white, soon dirty white to beige, in some collections (AH 50987, AH 51001) taking on a slight orange to fulvous ochraceous tinge (not reddish nor pinkish) at the upper part (Mu 10YR 6/6, 7/6); surface densely pruinose along the entire surface. *Cortina* absent. *Context* fibrous, whitish, with a similar colour to the stipe surface. *Smell* subspermatic herbaceous when cut in young basidiomata, also typically of bitter almonds in more aged specimens, clearly cyanic when kept in a closed box for 24 h, *taste* not recorded. *Spores* (8.7–)9.1–*9.8*–11.0(–11.6) × (5.3–)5.8–*6.5*–7.2(–7.8) µm, Q: (1.2–)1.4–*1.5*–1.6(–1.8) (n = 397 / N = 4), smooth, ovoid in frontal view, amygdaloid in profile, with a rather faint suprahilar depression, apex mostly rounded, sometimes subacute. *Basidia* (21.9–)25.9–*29.5*–33.1(–34.9) × (7.6–)7.9–*9.5*–10.6(–11.3) µm; Q: (2.5–)2.6–*3.1*–3.5(–4.2), 4-spored, rarely 2-spored, clavate, sterigmata 3–7 µm long. *Lamella edge* practically sterile, composed of numerous protruding hyaline cheilocystidia mixed with abundant mostly hyaline clavate paracystidia. *Pleurocystidia* abundant, (33.7–)38.7–*45.9*–54.2(–56.4) × (10.9–)12.1–*14.9*–18.3(–19.5) µm, Q: (2.3–)2.4–*3.1*–4.0(–4.7), (n = 168 / N = 4), fusiform to subcylindrical, hyaline, base often attenuate, sometimes pedicellate, rather crystalliferous at the apex (in some collections provided with microcrystals), walls (1.5–)1.8–*2.4*–3.0(–3.5) µm thick, reaching –4 µm at the apex, hyaline to hardly yellowish in 10 % NH_4OH. *Cheilocystidia* (31.5–)34.1–*42.4*–51.7(–59.3) × (12.1–)13.0–*15.4*–17.9(–19.2) µm, Q: (2.2–)2.3–*2.8*–3.6(–3.9), similar in size and shape to pleurocystidia. *Stipitipellis* a cutis of parallel hyphae (3.1–)3.5–*5.6*–7.8(–8.2) µm, bearing caulocystidia along the entire length of the stipe, (33.9–)40.7–*47.3*–55.4(–56.6) × (9.9–)10.5–*13.0*–16.9(–17.2) µm, Q: (2.7–)2.8–*3.7*–4.6(–4.8) (n = 22 / N = 2), similar in shape to hymenial cystidia, mixed with numerous clavate to subcylindrical hyaline paracystidia. *Pileipellis* a cutis formed by parallel cylindrical cells, 4.5–9.5 µm wide, somewhat constricted at septa, showing minute pale yellow ochraceous pigment, minutely encrusting and also diffuse intracellular. *Lamellar trama* of parallel hyphae, 3–6.5 µm broad, hyaline. *Clamp connections* abundant.

Habitat & Distribution — Gregarious in calcareous soil, usually in mossy and humid places; all collections have been found in Ibiza and Formentera (Balearic Islands), in Mediterranean Aleppo pine (*Pinus halepensis*) forests, with abundant macchia with the presence of *Cistus albidus*, *Juniperus oxycedrus, J. phoenicea*, *Arbutus unedo* and *Pistacia lentiscus*, sometimes also mixed with holm oaks (*Quercus coccifera*). A matching sequence deposited in GenBank (accession HQ204678) by Richard and co-workers in 2011, from ectomycorrhizae in *Quercus ilex*-dominated forests, confirms that the species is also present in southern France.

Typus. Spain, Illes Balears, Ibiza, Sant Antoni de Portmany, ses Planes d'en Frencolí, N39°01'25" E01°21'46", 156 m a.s.l., under *Pinus halepensis*, *Cistus albidus*, *Quercus coccifera* and *Pistacia lentiscus* in calcareous soil, 5 Dec. 2018, *F. Pancorbo*, *A. Altés*, *J.L. Siquier, J.C. Salom, J. Llistosella* & *F. Esteve-Raventós* (holotype AH 51001; ITS and LSU sequences GenBank OQ379317 and OQ379320; MycoBank MB 846408).

Additional materials examined. See Supplementary page.

Notes — Colour codes are taken from Munsell (1994), and terminology follows Vellinga (1988) and Kuyper (1986). Due to its characteristic bitter almond smell and macro- and microscopic characters, *I. pityusarum* is included in the 'hirtella' complex. According to the study by Bandini et al. (2022a) of this group, it would fit phylogenetically into a clade paraphyletic to the type (*I. hirtella*), which includes those species with cystidia of small size, not exceeding 50 µm in length on average. This clade hosts *I. somae*, *I. mycenoides* and most probably *I. brevicystis*. All these species grow in Europe in temperate humid forests of continental type, especially deciduous, but also under conifers. *Inocybe somae*, so far only known from Germany, shows a pale and smooth straw-yellow pileus and narrow spores (Q = 1.7–2.1) and grows in humid *Salicaceae* forests (*Populus*, *Salix*). *Inocybe mycenoides* (= *I. hirtellarum s*. Bandini et al. 2022a) has very narrow and small cystidia (9–13 µm wide), and originally yellow lamellae (Kuyper 1986, L!).

(Notes continued on Supplementary page)

Colour illustrations. Spain, Illes Balears, Ibiza, Sant Antoni de Portmany, Planes den Frencolí, *Pinus halepensis*, *Cistus albidus*, *Quercus coccifera* in mossy soil, locality where the holotype was collected. Basidiomata; spores; pleurocystidia; cheilocystidia; caulocystidia at stipe base. Scale bars = 10 mm (basidiomata), 50 µm (cystidia), 10 µm (spores).

Supplementary material

FP1516 Phylogenetic tree with *Inocybe amygdaliolens*.

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Inocybe roseobulbipes

Fungal Planet 1520 – 29 June 2023

Inocybe roseobulbipes Esteve-Rav., Pancorbo & E. Larss., *sp. nov.*

Etymology. The name derives from Latin 'roseus', which means pink or pinkish, 'bulbus', which means bulb and 'pes', which refers to the stipe. In reference to the bulbous pink stipe.

Classification — *Inocybaceae*, *Agaricales*, *Agaricomycetes.*

Basidiomata agaricoid and stipitate. *Pileus* 15–40 mm, initially campanulate-convex, soon convex to plano-convex, broadly umbonate to subumbonate; margin straight, regular to sometimes wavy with age, sometimes fissured, occasionally with sparse and ephemeral traces of velipellis; colour uniform or slightly darker on the umbo or central area, from cinnamon to fulvous (Mu 7.5YR 6/4-6; 5/3-4) to brown or chestnut brown (7.5YR 4/4-6; 5YR 4/4), sometimes mimicked by the development of the velipellis; surface uniformly fibrillose and smooth, very rarely broken into small irregular and appressed flakes (due to the development of velipellis) or lacerated radially (as in AH 56204), the umbo remaining smooth and mostly covered by the persistent velipellis, dry, not hygrophanous, radially fibrous to subrimose at the margin, especially with age. *Velipellis* rather persistent as a white arachnoid patch (it can almost disappear in rainy weather). *Lamellae* moderately crowded to subdistant (L = 38–45; l = 1(–2), free to narrowly adnate, ventricose, 5–7 mm broad, initially whitish, becoming pale grey to beige, then pale brown ochraceous to yellow ochraceous, edge white or paler, entire to finely crenulate. *Stipe* 20–50(–60) × 5–8(–9) mm, straight, sometimes curved towards the base, cylindrical, or rarely tapering towards the apex, the base always clearly bulbous, sometimes abruptly bulbous, not marginate (–12 mm), exceptionally subbulbous in some specimens (AH 46979); surface pale pinkish cream or salmon when young, deep pink to less often pink ochraceous when mature (Mu 5YR 7/6; 6/3-6), paling towards the base, which is whitish in the bulb; surface densely pruinose throughout, sometimes scattered pruinose fibrillose in the lower 1/3. *Cortina* absent. *Context* fibrous, whitish in the pileus and stipe, pinkish to rosy in the cortical part of the stipe. *Smell* subspermatic when cut in young basidiomata, *taste* not recorded. *Basidiospores* (6.5–)7.5–*8.6*–9.9(–10.7) × (4.5–)5.0–*5.5*–6.1(–6.6) µm, Q = (1.3–)1.4–*1.5*–1.8(–2.1) (n = 390 / N = 3), smooth, elliptic to ovoid in frontal view, amygdaloid in profile, with a rather faint suprahilar depression, apex usually acute, sometimes subacute to rounded, often with a 'pseudocallus'. *Basidia* (23.1–)25.2–*28.9*–33.2(–33.6) × (6.2–)7.0–*8.5*–10.1(–11.1) µm, 4-spored, rarely 2-spored, clavate, sterigmata 3–8.5 µm long. *Lamella edge* sterile, consisting of numerous protruding cheilocystidia mixed with abundant hyaline clavate paracystidia. *Pleurocystidia* abundant, (40.6–)44.5–*54.9*–65.6(–81.3) × (10.2–)11.9–*14.9*–18.8(–22.7) µm, (n = 195 / N = 3), lageniform to sublageniform to subfusiform, the apex often tapering and acute, crystalliferous, mostly provided with microcrystals, hyaline, the base sometimes attenuated into a short pedicel, walls (1.4–)1.8–*2.6*–3.7(–4.2) µm thick, often coalescent at the apex, yellowish in 10 % NH_4OH. *Cheilocystidia* (37.0–)42.5–*52.4*–62.8(–71.6) × (11.2–)12.0–*14.8*–18.2(–20) µm, similar in size and shape to pleurocystidia, some of them with a greyish ochre intracellular content. *Stipitipellis* a cutis of parallel hyphae (1.9–)2.0–*4.1*–5.5(–6.4) µm, bearing caulocystidia along the entire length of the stipe, (40.4–)49.6–*65.6*–81.0(–90.9) × (9.2–)12.7–*16.2*–21.0(–26.7) µm, (n = 119 / N = 3), similar in shape to hymenial cystidia, mixed with numerous clavate to subcylindrical hyaline paracystidia. *Pileipellis* a cutis formed by parallel cylindrical cells, 21.8–51.7 × 5.9–14.0 µm, constricted at the septa, with ochraceous brown pigment, minutely encrusted and diffuse intracellular. *Lamellar trama* of parallel hyphae, 3.4–7.3 µm wide, hyaline. *Clamp connections* abundant.

Ecology & Distribution — Currently known from the Iberian Peninsula (Spain and Portugal). Found on acidic soils with a sandy texture of the fanglomerates or 'rañas' type. Growing in reforested 'maritime pine' forests (*Pinus pinaster*) in a *Quercus ilex/Q.pyrenaica* potential vegetation on a meso-mediterranean level; the undergrowth usually formed by *Cistus ladanifer* or *C. laurifolius* shrubs, accompanied by *Juniperus phoenicea*. Blast searches of NCBIs GenBank nucleotide database and the UNITE database recovered three sequences from ectomycorrhizae studies, accessions FJ013061, JQ975964 and FJ897195, and confirm the presence in central Spain and in northeastern Portugal, in previously burned *Pinus pinaster* forests (Rincón et al. 2014) and from holm oak forests on acidic serpentine soils (Branco & Ree 2010).

Typus. Spain, Castilla-La Mancha, Guadalajara, Tamajón, road to El Vado reservoir, barranco La Jara, N41°01'30.85" W3°16'37.28", 1035 m a.s.l., in a reforested forest of *Pinus pinaster* with scattered thickets of *Cistus ladanifer* and *Juniperus phoenicea*, on acidic soils consisting of fanglomerates or glacis with stones ('rañas'), with a sandy texture, 5 Nov. 2021, *A. Altés*, *Y. Turégano* & *F. Esteve-Raventós* (holotype AH 56204, isotype GB; ITS-LSU sequence GenBank OQ300086; MycoBank MB 847335).

Additional material examined. Spain, Castilla-La Mancha, Guadalajara, Tamajón, Holgada Honda, N40°56'40.41" W3°15'50.32", 1040 m a.s.l., in *Pinus pinaster* reforested forest with *Cistus ladanifer* and *Juniperus phoenicea*, in acid soils ('rañas') with sandy texture, 19 Nov. 2008, *A. Altés & F. Esteve-Raventós* (AH 36409, ITS-LSU sequence GenBank OQ300078); same locality and habitat as the holotype, 12 Nov. 2018, *A. Altés & F. Esteve-Raventós* (AH 46831, ITS-LSU sequence GenBank OQ300079); ibid., 15 Nov. 2019, *A. Altés* (AH 46979).

Notes — Colour codes are taken from Munsell (1994), and terminology follows Vellinga (1988) and Kuyper (1986). *Inocybe roseobulbipes* can be separated from *I. subbrunnea* (Kühner 1955, G!) based on morphological, ecological and molecular characters.

(Notes continued on Supplementary page)

Colour illustrations. *Inocybe roseobulbipes* habitat from the type locality in Tamajón, Spain. *Pinus pinaster* reforested forest and *Cistus ladanifer* shrubs in acidic soil. *In situ* basidiomata of the holotype (AH 56204); photos of basidiospores; pleurocystidia; cheilocystidia; caulocystidia at stipe base. Scale bars = 50 µm (cystidia), 10 µm (spores).

Supplementary material

FP1520 Phylogenetic tree.

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Laetiporus pratigiensis
20 µm
1
20 µm
4
50 µm
2
3

Fungal Planet 1521 – 29 June 2023

Laetiporus pratigiensis C.D. Santos, J.L. Bezerra, J.P.A.F. Oliveira, P.A.S. Marbach & G. Marques, *sp. nov.*

Etymology. The name refers to the locality of the type specimens (Pratigi Environmental Protection Area, Montane Tropical Atlantic Rainforest).

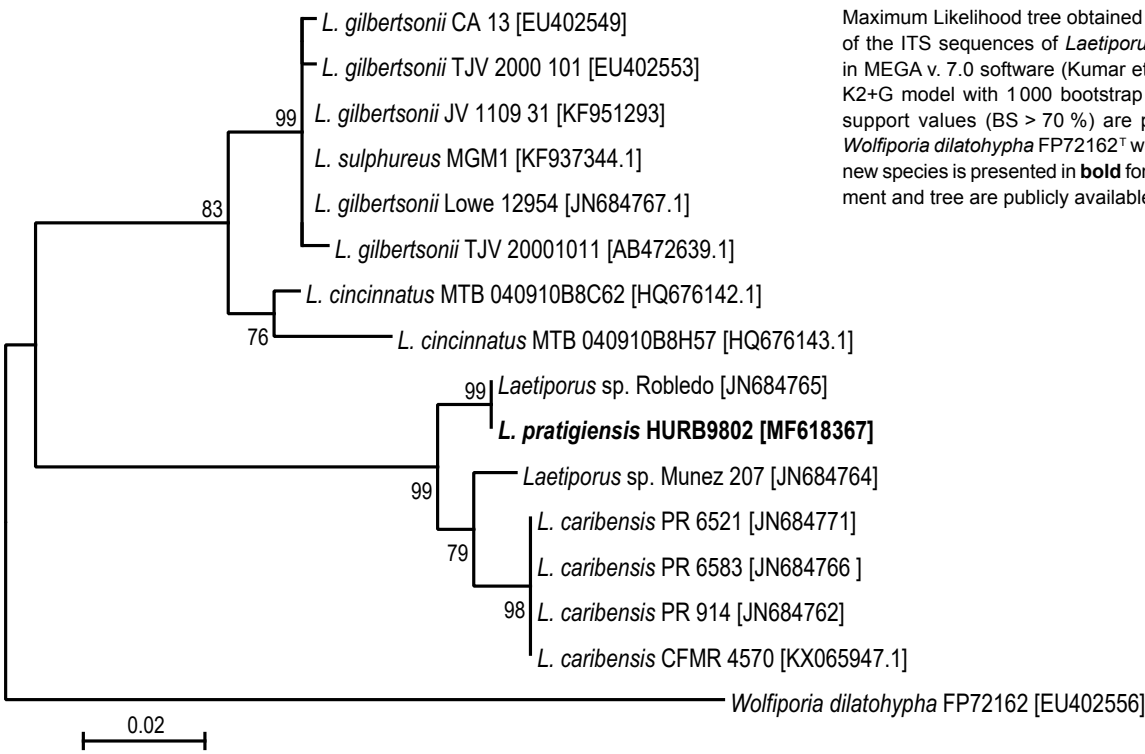
Classification — *Laetiporaceae*, *Polyporales*, *Agaricomycetes.*

Basidiocarps annual, sessile, dimidiate, imbricate clusters, 30 × 18 cm broad, fleshy when fresh and crumbly when dry. Pileal surface tomentose, zonate, intense orange, fading to cream when dry. Context soft, friable, yellowish, darker near attachment to the substrate, showing no reaction to KOH; yellow to yellow orange pore surface, becoming cream to pale yellow when dry; pores rounded to angular, 5–7 per mm; dissepiments entire and thick. *Odour* and *taste* pleasant. *Hyphal structure* hyphal system dimitic, inamyloid; generative hyphae parallel, septate, hyaline, lacking clamp connections; skeletal hyphae subparallel, occasionally septate, branching at right angles, lacking clamp connections. *Basidia* clavate, hyaline, thin-walled, bearing two sterigmata. *Basidiospores* abundant, ovoid to ellipsoid, hyaline, smooth, usually with a central oil drop, inamyloid, undextrinoid, 2–4 × 2–3 µm, Xm = 2.45–3.1; Q = 0.8–2.0; Qm = 1.32 (n = 30/1).

Ecology & Distribution — Growing on a living hardwood tree. Presently known exclusively from the Brazilian Atlantic Rainforest, Pratigi Environmental Protection Area, Bahia State. However, phylogenetic analysis suggest that it could occur in other regions of South America.

Typus. Brazil, Bahia, Pratigi environmental protection area, Montane Tropical Atlantic Rainforest, S13°54' W39°27', growing in a trunk of a living unknown hardwood tree species, 14 Apr. 2014, *C.D. Santos* (holotype HURB 9802 (dried culture); culture ex-type CCMB715 = CDS–2017a; ITS sequence GenBank MF618367; MycoBank MB 847914).

Notes — A phylogenetic analysis was performed to assess the relative position of the new taxon within the *Laetiporus sulphureus* species complex. Results showed the new species forming a well-supported lineage (99 % ML) with an undescribed *Laetiporus* sp. (Robledo strain 1122 from Argentina), belonging to clade M of Banik et al. (2012). Morphologically *L. pratigiensis* is very similar to species in the *L. sulphureus* complex, sharing the shape and colour of the basidioma, but differing by the bright orange pileal surface, yellow orange pore surface, smaller basidiospores (2–4 × 2–3 µm) and smaller pores (5–7 per mm) than other species of the genus.



Maximum Likelihood tree obtained by phylogenetic analysis of the ITS sequences of *Laetiporus pratigiensis* performed in MEGA v. 7.0 software (Kumar et al. 2016) employing the K2+G model with 1 000 bootstrap re-samplings. Bootstrap support values (BS > 70 %) are presented at the nodes. *Wolfiporia dilatohypha* FP72162^{T} was used as outgroup. The new species is presented in **bold** font (^{T} = ex-type). The alignment and tree are publicly available in TreeBASE ID 30214.

Colour illustrations. Basidiocarp of *L. pratigiensis* on a trunk of a living hardwood tree species in the Montane Tropical Atlantic Rainforest of Pratigi environmental protection area, located in Bahia, Brazil. Basidiocarp; hyphal structure; basidia; basidiospores. Scale bars = 20 µm, except hyphal structure = 50 µm.

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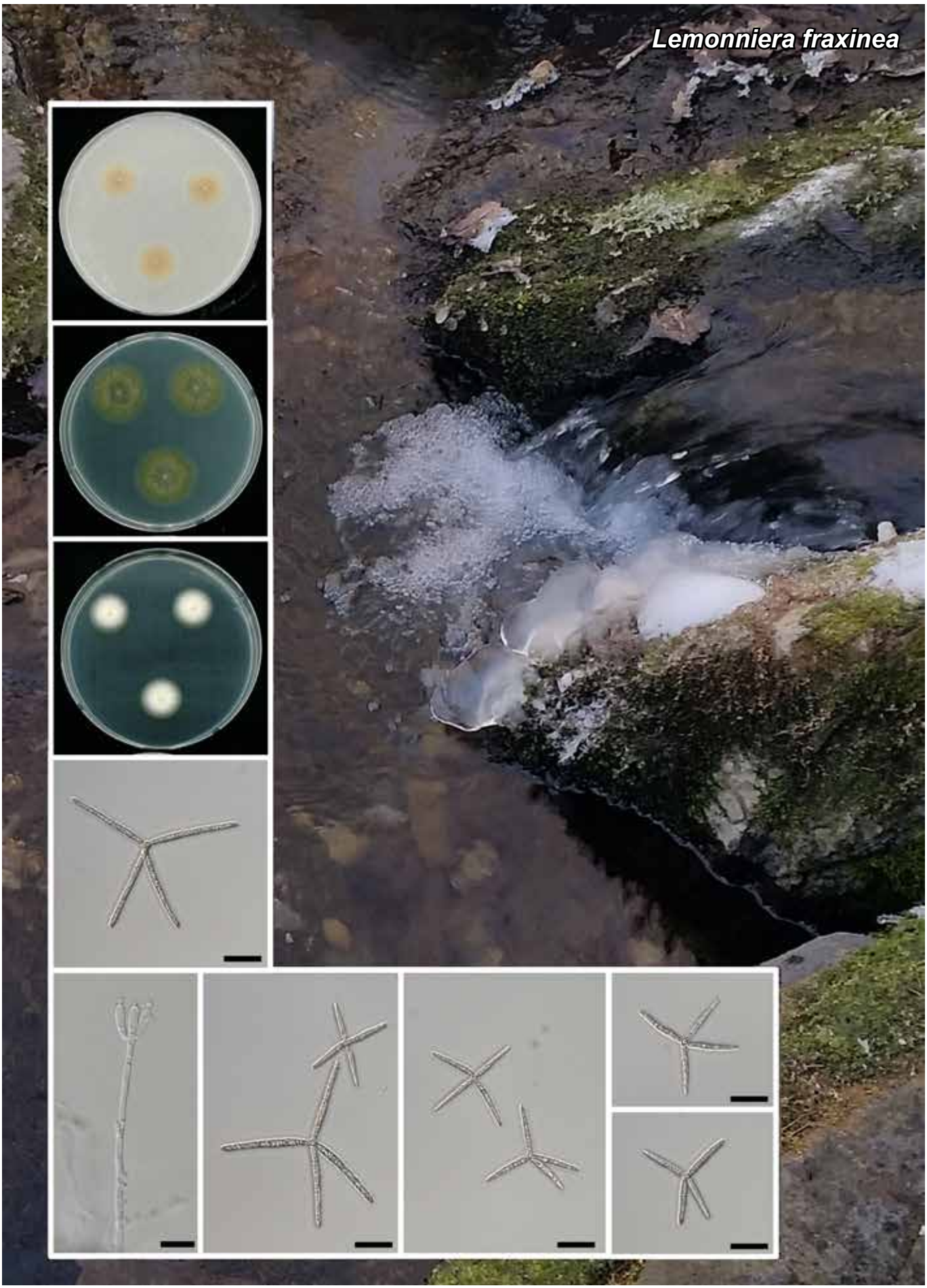

Lemonniera fraxinea

Fungal Planet 1522 – 29 June 2023

Lemonniera fraxinea Mun & J. Goh, *sp. nov.*

Etymology. In reference to the host genus *Fraxinus*.

Classification — *Discinellaceae*, *Helotiales*, *Leotiomycetes*.

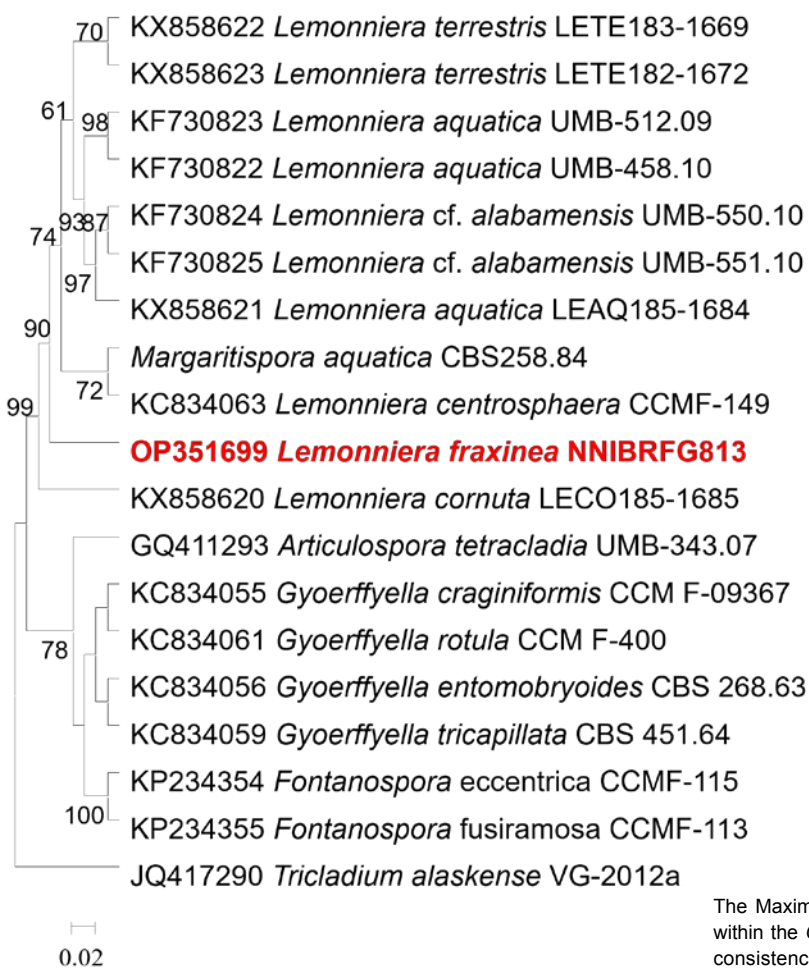
Conidiophores and conidia formed under submerged conditions. *Conidiophores* unbranched straight, branched near free end to two to eight phialides. *Conidia* with four long divergent arms, septate, hyaline, 23–49 × 3–5 µm. Conidial branches almost equal in length, and arms attached via a narrow isthmus to central cell.

Culture characteristics — Colonies with moderate aerial mycelium, very slow growth, 3 mm/d diam at 15 °C. *Lemonniera fraxinea* grew best at 15 °C on malt extract agar (MEA). On oatmeal agar (OA) surface and reverse pale pink. On MEA surface and reverse olive green. On potato dextrose agar (PDA) surface white, reverse yellow.

Typus. South Korea, Gyeongsangbuk-do, Sangju-si, on decaying leaves of *Fraxinus* sp. from pond, 3 Feb. 2016, *H.Y. Mun* (holotype preserved as metabolically inactive culture NNIBRFG813; culture ex-type NNIBRFG813; ITS sequence GenBank OP351699; MycoBank MB 845500).

Notes — Since *Lemonniera* was established by De Wildeman (1894) from submerged decaying leaves of alder and willow, nine species have to date been described in *Lemonniera*. *Lemonniera* forms conidia and conidiophores below the water surface. Conidia consist of four long divergent arms (Ingold 1942). Conidia of *L. fraxinea* are shorter and thicker than in *L. aquarica*. Although a central cell is present in conidia of *L. centrosphaera*, *L. cornuta* and *L. terrestris*, the arms are not as narrow, and the central cell is ellipsoidal or globose.

Based on a blast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Lemonniera terrestris* (strain 183-1669; GenBank KU519116.1; Identities 501/508 (98.62 %), one gap), *Margaritispora aquatica* (strain DSM 105081; GenBank MK353139.1; Identities 501/508 (98.62 %), one gap), *L. centrosphaera* (strain CCM F-149; GenBank NR_155313.1; Identities 501/508 (98.62 %), one gap), *L. pseudofloscula* (strain VG30-2; Genbank OM907742.1; Identities 499/506 (98.62 %), no gaps). *Lemonniera* and *Margaritispora* are phylogenetically closely related, but differ morphologically with regard to their conidia.



The Maximum Parsimony (MP) tree inferred from the ITS region of taxa within the *Gyoreffyella* clade using MEGA v. 11 (Tamura et al. 2021). The consistency index is 0.832258 (0.682927), retention index is 0.868687 (0.868687), and the composite index is 0.722972 (0.593250) for all sites and parsimony-informative sites, respectively. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1 000 replicates) is shown next to the branches. The MP tree was obtained using the Tree-Bisection-Regrafting (TBR) algorithm. This analysis involved 19 nucleotide sequences and a total of 472 positions in the final dataset.

Colour illustrations. Geomryongso-pond with plant litter in Taebaek-si, South Korea. Colonies: OA, MEA, PDA; conidiophores; conidia. Scale bars = 20 µm.

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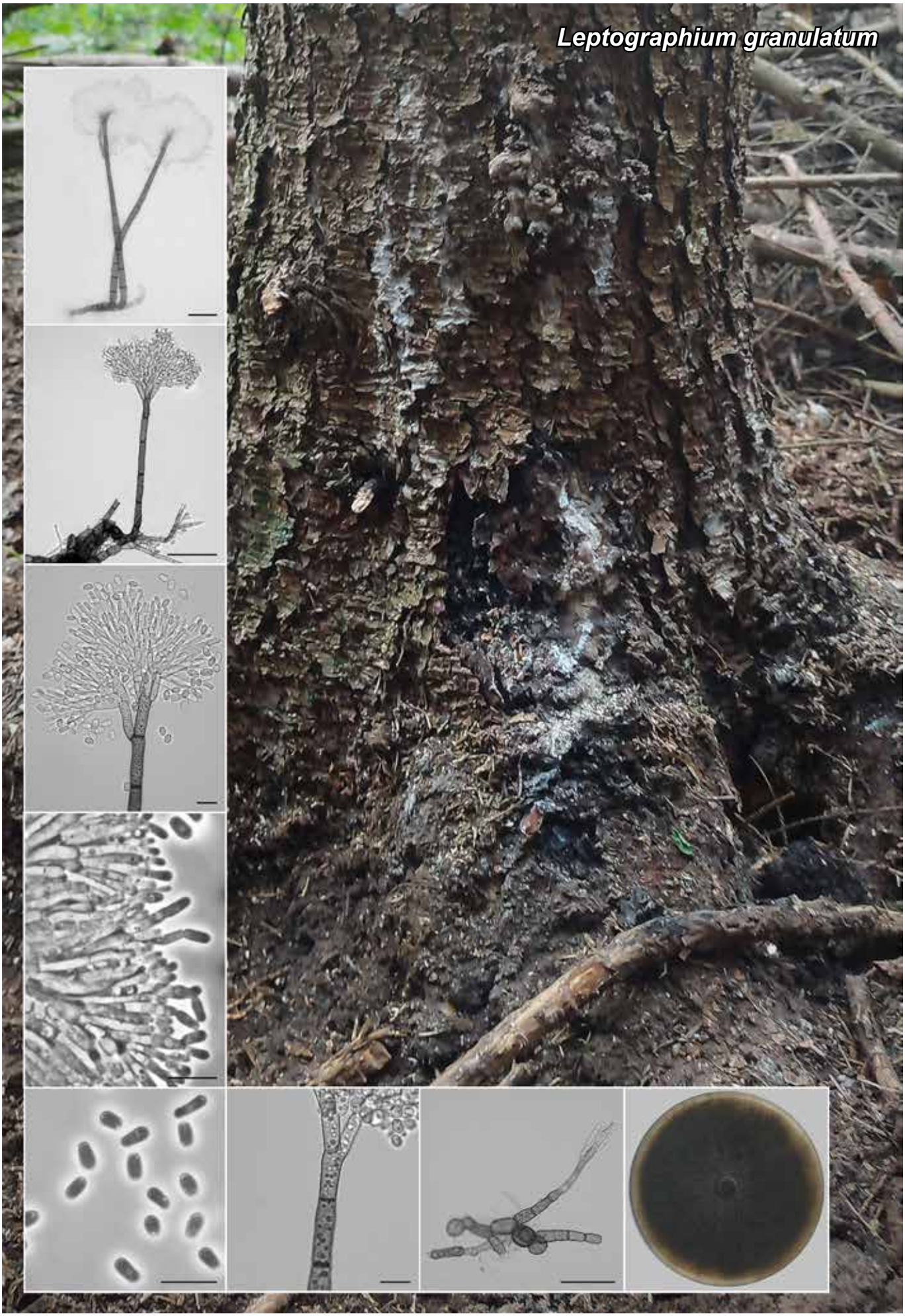
Leptographium granulatum

Fungal Planet 1523 – 29 June 2023

Leptographium granulatum R. Jankowiak & P. Bilański, *sp. nov.*

Etymology. The epithet *granulatum* (Latin) refers to the conidiophores containing granules inside their cells.

Classification — *Ophiostomataceae*, *Ophiostomatales*, *Sordariomycetes*.

Sexual morph not observed. *Conidiophores* macronematous, mononematous, arising from mycelium, often developing from swollen hyphal cells, erect, solitary or in small, loose groups, with granular cytoplasm, without rhizoidal hyphae at the bases, (76–)201–367(–463) µm long including the conidiogenous apparatus. *Stipes* olive (1E5; Kornerup & Wanscher 1978), 6–11-septate, (49.5–)132.5–278(–382) µm long (from first basal septum to below primary branches), (3.5–)5–8.5(–10.5) µm wide at base, basal cell often swollen. *Conidiogenous apparatus* (45–)53.5–105(–144) µm long (excluding conidial mass), consisting of 3–4 series (occasionally 5) of cylindrical branches. Primary branches 2–3 (occasionally 4), arrangement of primary branches-type B (more than two branches), greyish yellow (1B5), with granular cytoplasm, swollen, smooth, (11–)26.5–59(–140.5) × (3.5–)4.5–7(–8.5) µm. *Conidiogenous cells* 2–3 per branch, hyaline, cylindrical, tapering from base to apex, (7–)10.5–14(–17) × (1.5–)2–2.5(–3) µm. *Conidia* hyaline, obovoid to broadly ellipsoidal, occasionally oblong, (3.5–)4.5–5.5(–6.5) × 2–3 µm, accumulating around the conidiogenous apparatus as a creamy mucilaginous mass.

Cultural characteristics — Colonies with optimal growth at 20 °C on 2 % MEA, reaching 74 mm (± 3.05 mm) diam in 7 d, with a radial growth rate of 5.29 (± 0.22) mm/d. Colonies dark brown (6F8), margin smooth. Hyphae submerged in agar with very little aerial mycelium, olive yellow (2D7), smooth or occasionally roughened, often with granular material and swollen cells, occasionally constricted at the septa, (0.9–)2.3–5.9(–9.9) µm wide.

Cardinal temperature for growth — Minimum 10 °C, optimum 20 °C, maximum 25 °C.

Typus. Poland, south-western Poland, Ołdrzychowice Kłodzkie, isolated from a gallery of *Dendroctonus micans* on *Picea abies*, Oct. 2021, *R. Jankowiak* (holotype O-F- 259634; culture ex-type CBS 149325 = KFL436H; ITS, LSU, *ACT*, βT, *CAL* and *TEF1-α* sequences GenBank OP872581, OP872581, OP870051, OP870075, OP870059 and OP870067; MycoBank MB 847451).

Additional materials examined. Poland, south-western Poland, Ołdrzychowice Kłodzkie, isolated from a gallery of *Dendroctonus micans* on *Picea abies*, Oct. 2021, *R. Jankowiak*, culture CBS 149326 = KFL434H, ITS, LSU, *ACT*, βT, *CAL* and *TEF1-α* sequences GenBank OP872579, OP872579, OP870049, OP870073, OP870057 and OP870065, culture CBS 149327 = KFL433H, ITS, LSU, *ACT*, βT, *CAL* and *TEF1-α* sequences GenBank OP872578, OP872578, OP870048, OP870072, OP870056 and OP870064.

Notes — Phylogenetically, *L. granulatum* resides in a strongly supported clade and shares a common ancestor with *L. albopini*. Together with *Grosmannia huntii*, these species form the *Leptographium incertae sedis* group, which are adjacent to species from the *L. lundbergii* and *L. clavigerum* species complexes (De Beer et al. 2022). In a multigene phylogeny of the ITS, LSU, βT, and *TEF1-α* gene regions, *L. granulatum* differs from *L. albopini* (CBS 170.93, based only on **ITS** and **LSU** sequences) by 0.84 %, *L. pinicola* (CMW 2398) by 5.40 %, *Grosmannia huntii* (CBS 274.65) by 5.46 %, *L. truncatum* (CBS 929.85) by 5.68 %, and *L. koreanum* (CMW 14199) by 5.71 %. *Leptographium granulatum* is similar to *L. albopini* in the conidial dimension but differs in having obovoid conidia rather than oblong. The conidiophores, stipes and the conidiogenous apparatus of *L. granulatum* are shorter, and the primary branches are longer as those of *L. albopini* (Wingfield et al. 1994). *Leptographium granulatum* also can be distinguished by conidiophores developing often from swollen hyphal cells and cells containing abundant granules. In addition, cultures of *L. granulatum* have optimum growth at 20 °C followed by 15 °C, while in *L. albopini* the growth rate at 20 °C is almost the same as its optimal growth recorded at 25 °C (Wingfield et al. 1994). *Leptographium granulatum* is associated with *Dendroctonus micans* on *Picea abies* in Poland.

Colour illustrations. *Picea abies* infested by *Dendroctonus micans*, Ołdrzychowice Kłodzkie, Poland. Typical conidiophores; conidiogenous apparatus; conidiogenous cells; conidia; part of the conidiophore containing granules inside cells; the conidiophore develops from swollen hyphal cells; colony on MEA. Scale bar = 50 µm (conidiophores at the very top and swollen hyphal cells), 10 µm (all others).

Supplementary material

FP1523-1 Phylogenetic tree.

FP1523-2 Table. GenBank accession numbers for reference sequences used in the phylogenetic tree.

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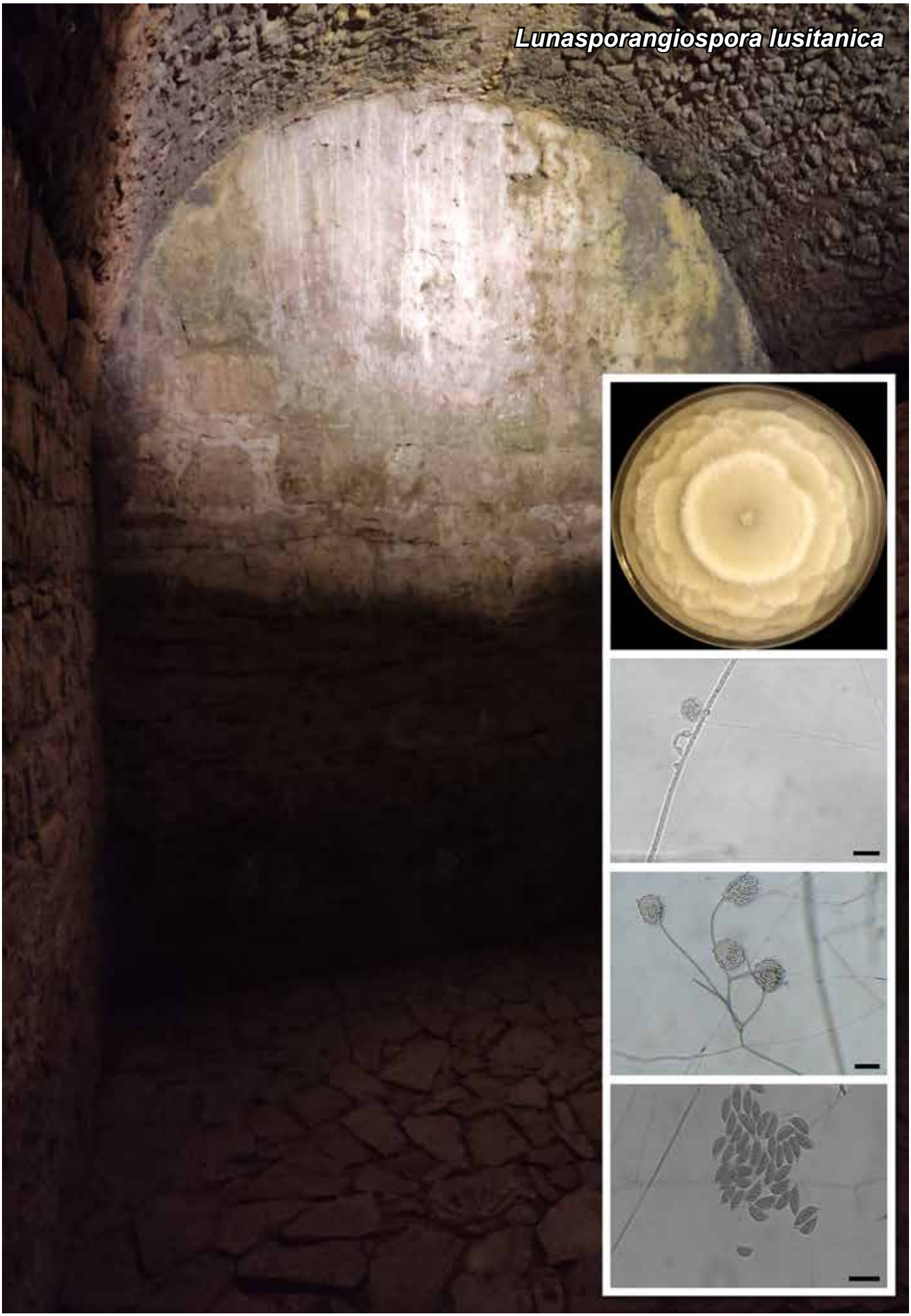

Lunasporangiospora lusitanica

Fungal Planet 1524 – 29 June 2023

Lunasporangiospora lusitanica J. Trovão, J. Pawłowska & A. Portugal, *sp. nov.*

Etymology. From the Latin *Lusitania* (the name of the Roman province in the Iberian Peninsula which today encompasses most of Portugal) denoting where the isolates were collected.

Classification — *Mortierellaceae*, *Mortierellales*, *Mortierellomycetes*.

Hyphae hyaline, 3.5–6.5 µm wide, forming solitary gemmae. *Gemmae* hyaline, intercalary and terminal, often formed in reduced lateral stalks 4–5 µm wide, without anastomosis, globose, 9.5–23.5 (av. = 16.9; SD = 4.5) µm diam, with smooth cell wall, 0.75–1.45 (mean = 0.96; SD = 0.18) µm thick. *Sporangiophores* hyaline, fragile, arising from substratum hyphae, slightly immersed into the agar, with 1–4 basal sympodial ramifications, 100–700 µm long. *Sporangia* subglobose, columella strongly reduced, 40–130 (av. = 69.8; SD = 26.52) × 30–118 (av. = 61.5; SD = 23.09) µm. *Sporangiospores* lunate, smooth-walled, 13.5–19 (av. = 15.9; SD = 1.53) × 6–9.5 (av. = 7.9; SD = 0.82) µm.

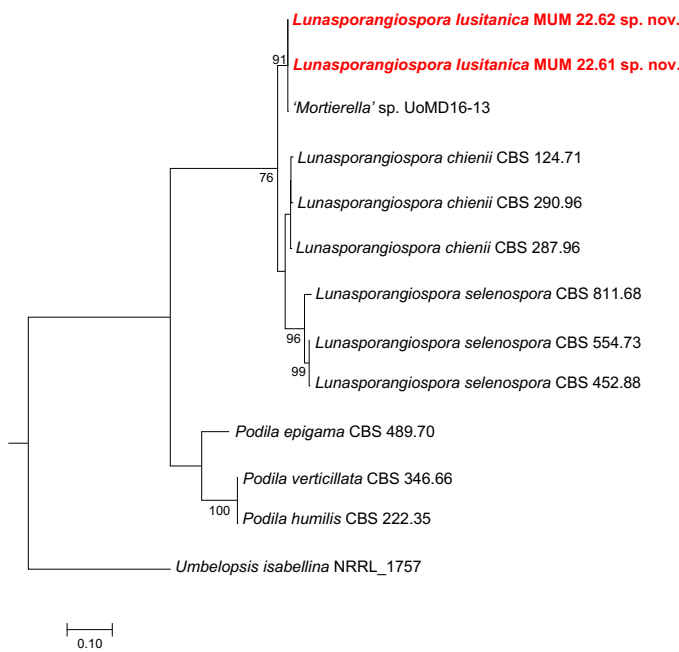
Culture characteristics — On 2 % Potato dextrose agar (PDA), after 7 d at 25 °C in the dark, fast-growing colonies, radiate, with zonate growth, forming a lobate pattern on the edge and daily growth of 2–5 mm. Colonies white on top and yellowish in reverse. No garlic odour detected. Reproductive structures detected on 2 % water agar (WA), Czapek dox agar (CZA) and malt extract agar (MEA) supplemented with 5 % $CaCO_3$, mainly after 60 d. However, the characteristic colony shape does not develop in these media. No chlamydospores or zygospores detected.

Typus. Portugal, Coimbra, isolated from a biofilm covering a biodeteriorated limestone wall in the Machado de Castro National Museum Cryptoporticus, 4 Apr. 2019, *J. Trovão* (holotype MUM-H 22.61; culture ex-type MUM 22.61; ITS and LSU sequences GenBank OP686543 and OP686519; MycoBank MB 846444).

Additional material examined. Portugal, Coimbra, isolated from a biofilm covering a biodeteriorated limestone wall in the Machado de Castro National Museum Cryptoporticus, 4 Apr. 2019, *J. Trovão,* MUM 22.62, ITS and LSU sequences GenBank OP686544 and OP686520.

Notes — Molecular analysis shows that these isolates belong to the genus *Lunasporangiospora* (Vandepol et al. 2020), with 98 % LSU sequence similarity to *Lunasporangiospora chienii* (CBS 290.96) and 88 % ITS sequence similarity to *Lunasporangiospora chienii* (CBS 124.71). The genus currently encompasses two species (*L. chienii* and *L. selenospora*) exhibiting distinctive lunate sporangiospores and being typically found in mushroom compost and forest soils (Vandepol et al. 2020). Ecologically, this species is distinctive, since it was isolated from a biofilm colonising a hypogean limestone monument. Moreover, a redundant GenBank sequence labelled as '*Mortierella* sp.' (GenBank MF967427) isolated from Australian spiders (Gibbons et al. 2019), also clusters with the sequences obtained in this study. This is in accordance with the previously raised hypothesis that arthropod-vectored fungal dispersion plays an important ecological role at the Machado de Castro National Museum Cryptoporticus (Soares et al. 2022). In addition, at 1.5 % threshold, our clade represents SH1274621.09FU known from eDNA analysis in UNITE (https://unite.ut.ee/) which is known also from Cuba and Puerto Rico.

Morphologically, the new species forms smooth sporangiospores with a lunate shape, typical for the genus. It can be distinguished from both *L. chienii* and *L. selenospora* by the presence of gemmae; from *L. chienii* by sporangiospore size (7–10 × 3–4 µm); and additionally, from *L. selenospora* by the absence of rare terminal chlamydospores (Chien 1972, Gams 1977, Vandepol et al. 2020). Considering the morphological differences, the sequence similarity values, and the phylogenetic placement, we propose to delineate these isolates as a distinct species.



Phylogenetic tree obtained from the concatenated ClustalX (Larkin et al. 2007) ITS (671 nucleotides including gaps) and LSU (991 nucleotides including gaps) alignments using the HKY+I for ITS and TrN+G4 for LSU substitution models, as implemented in raxml (Kozlov et al. 2019). The new species is indicated in red and in bold. The scale bar indicates the expected number of substitutions per site and the bootstrap support values (>75 %) are also shown. The alignment and tree were deposited in figshare (10.6084/m9.figshare.21429420).

Colour illustrations. The sampled biofilm in the Machado de Castro National Museum Cryptoporticus, Portugal (photo credit J. Trovão). Seven-day-old colony on PDA; gemmae; sporangiophores and sporangia; sporangiospores. Scale bars = 20 µm (gemmae; sporangiospores), 100 µm (sporangiophores and sporangia).

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Lyophyllum obscurum

Fungal Planet 1525 – 29 June 2023

Lyophyllum obscurum F. Mondello, Loizides, N. Privitera, G. Vasquez, Faulwetter & Bellanger, *sp. nov*.

Etymology. Refers to the rapid darkening of basidiomata upon bruising or ageing.

Classification — *Lyophyllaceae*, *Agaricales*, *Agaricomycetes*.

Pileus 2–5 cm, initially convex to subcampanulate, then convex to applanate but maintaining a broad, flattened, or at times centrally depressed umbo, with an involute, rarely undulated margin; cuticle dry, somewhat pruinose in dry conditions, glabrous and viscid in moist conditions, radially fibrillose and often concentrically guttulate, grey-brown to brown, usually darker blackish grey at the umbo; blackening when bruised or when aged. *Lamellae* adnexed to emarginate, intercepted by lamellulae of variable lengths, not very thick, straw-coloured to pale grey, becoming charcoal grey or blackish brown in old age or upon drying; edges entire, concolourous. *Stipe* 3 – 6 × 0.4–1 cm, cylindrical, sometimes bent, longitudinally striate-fibrillose, dull argillaceous grey to dirty grey, blackening when handled; base densely covered with a bristly white mycelial felt. *Context* thick, pale grey, blackening slowly when cut, with a weak, somewhat farinaceous *odour* and an unpleasant *taste*. *Spore deposit* pure white. *Basidiospores* (5.8–)6.4–7.4(–7.7) × (3.2–)3.6–4.2(–4.4) µm, Qm = 1.8, ellipsoid, hyaline, depressed near the apiculum, with one or more guttules, smooth. *Basidia* 23–33 × 5–8 µm, clavate, tetrasporic, carminophilic with diffuse granulations; sterigmata 1–2 µm. *Marginal cells* 18–30 × 6–7.5 µm, clavate to subcapitate, rarely cylindrical-flexuous, thick walled (< 1 µm). *Hymenophoral trama* composed of tightly packed, ± parallel, thick-walled and sparsely septate hyphae < 8 µm wide. *Pileipellis* a cutis, composed of parallel, inflated and thick-walled hyphae 7–19 µm wide. *Clamp connections* present.

Habit, Habitat & Distribution — Solitary to gregarious or rarely sub-fasciculate, growing in thermophilous *Pinus* or *Pinus*/*Quercus* woodlands on calcareous, basic or volcanic soils from November to January. So far known from Cyprus, Greece and Italy (Sicily), but probably widespread in *Pinus*-dominated woodlands of the Mediterranean.

Typus. Italy, Sicily, Messina, Ucria, under *Pinus pinea* and *Quercus ilex*, on acidic soil, c. 700 m a.s.l., 4 Nov. 2021, *F. Mondello* (holotype in Herbarium of C.d.C.M. Messina, No. 1263; isotype in herb. pers. F. Mondello No. 1263; ITS and LSU sequences GenBank OP626152 and OP626154; MycoBank MB 847866).

Additional materials examined. Cyprus, Platania, under *Pinus brutia* and *Quercus alnifolia* on basic soil, 7 Jan. 2016, *M. Loizides*, ML6117LA (ITS sequence GenBank OP626150). – Greece, Peloponnese, Strofylia National Park, coastal pine forest, under *P. nigra* with occasional *Q. coccifera* and *Myrtus communis*, on a sandy soil, 14 Jan. 2018, *S. Faulwetter*, FR2017560 (ITS sequence GenBank OP626151). – Italy, Sicily, Catania, Nicolosi, Mt.i.Rossi, 921 m a.s.l., under *P. halepensis* & *Q. ilex*, on a deep sandy-lavic soil with lapilli and volcanic scoriae, 21 Nov. 2018, *N. Privitera*, NP20181121; ibid., 930 m a.s.l., under *P. halepensis* & *P. nigra* subsp. *calabrica*, 18 Nov. 2019, *N. Privitera*, NP20191118; ibid., 925 m a.s.l., under *P. halepensis* & *Q. ilex*, 7 Dec. 2020, *N. Privitera*, NP20201207; ibid., 940 m a.s.l., under *P. halepensis, P. pinea* & *Q.* spp., 12 Dec. 2020, *N. Privitera*, NP20201212; ibid., 937 m a.s.l., under *P. halepensis* & *P. pinea* & *Q.* spp., 1 Jan. 2021, *N. Privitera*, NP20210101 (ITS sequence GenBank OP626153); Messina, Ucria, under *Pinus pinea* and *Quercus ilex*, on acidic soil, c. 690 m a.s.l., 4 Nov. 2021, *F. Mondello*, Mondello1264.

Notes — *Lyophyllum obscurum* represents a well-delimited lineage within Clade Va sensu Bellanger et al. (2015), displaying three polymorphic sites and distant from the closest species by 11 substitutions + two indels (2 % of sequence divergence) at the ITS locus. The lack of reference sequences for most classical and recently described species prevents from formally naming the phylospecies (see supplementary material), that are for this reason labelled as '*Lyophyllum* sp. Va-1–Va-15', according to Bellanger et al. (2015). Only sp. Va-9 can now be nomenclaturally linked to *L. semitale* var. *intermedium*, after we could successfully sequence the holotype of this old taxon from Romagnesi (1987). For the same reason, *L. obscurum* may have been collected repeatedly under Mediterranean *Pinus* spp. but misidentified as other blackening *Lyophyllum* species, particularly in the Canary Islands (Dähncke et al. 2009). Other blackening *Lyophyllum* taxa with similar habit and ellipsoid spores have been described in Europe but none displays the combination of macro-morphological and ecological features of *L. obscurum*. The widespread *L. semitale*, quite polymorphic, can produce similar basidiomata but lamellae are usually not so dark, blackening is usually slower, while spores and basidia are larger (Vesterholt & Ludwig 2012). *Lyophyllum ignobile* (Clémençon 1982) and *L. pulvis-horrei* (Ludwig 2001), share many macro- and microscopic features with *L. obscurum*, but these species are described from Fennoscandia and Germany, respectively, and are unlikely to be present in thermophilous *Pinus* woodlands of the Mediterranean. The cespitose and blackening *L. fuscobrunneum* (Contu & Vizzini 2011), described from the same biome as the present species, produces stouter basidiomata with cream lamellae when young and longer basidia. *Lyophyllum aemiliae* (Consiglio 1998), *L. maleolens* (Melis & Contu 2000) and *L. semitale* var. *intermedium* (Romagnesi 1987), have lamellae staining tawny-rusty or yellow before blackening, in addition to other micro-anatomical differences.

Colour illustrations. Holotype collection area at Ucria (ME), Italy (Sicily). Basidiomata *in situ*, holotype collection (top left); coll. Mondello1264 (middle left); siderophilic basidia in acetate carmine (bottom left, holotype collection); basidiospores in Cotton Blue (bottom right, holotype collection). Scale bars = 1 cm (basidiomata), 5 µm (micromorphology).

Supplementary material

FP1525 Phylogenetic tree.

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Mallocybe ahmadii

Fungal Planet 1526 – 29 June 2023

Mallocybe ahmadii I. Rauf & Saba, *sp. nov.*

Etymology. The species epithet '*ahmadii*' refers to the Sultan Ahmad, a pioneering Pakistani mycologist.

Classification — *Inocybaceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata stipitate, small-sized, in clusters. *Pileus* 2.4–4.5 cm, convex when young, become broadly convex to plano-convex at maturity, without umbo, slightly depressed at the centre, margin initially straight, then deflexed with age, undulating, not rimose, fibrillose-tomentose to woolly tomentose with scurfy appressed squamules, moderate orange yellow (10YRf 7/8) to deep yellowish brown (10YR 3/6) and becoming darker in colour with age. *Lamellae* crowded, 2–4 mm, narrow, adnate, regular, free, crisped, margin wavy, moderate orange yellow (10YR 7/8) and becoming deep yellowish brown (10YR 3/6) with age, concolourous. *Stipe* 2.4–5 × 0.4–1 cm, cylindrical, hollow to fistulose, equal, somewhat subbulbous at base, pale yellow to deep yellowish brown in aged basidiomata, moderate orange yellow (10YR 7/8) to deep yellow brown (10YR 3/6), white cortina present in young basidiomata. *Context* brownish in pileus, somewhat ochraceous brown in stipe. *Taste* indistinct. *Annulus* absent. *Basidiospores* (9.3–)10.4–12.9(–14.6) × (5.2–)6.0–7.3(–7.7) µm, Q = (1.4–)1.5–2.0(–2.2), thin-walled, smooth, yellowish in 5 % KOH, ellipsoid to ovoid, amygdaliform in side view, ellipsoid in frontal view. *Basidia* 26–37 × 10–13 µm, clavate to cylindrical, narrowly clavate, 4-spored, sometimes 2-spored, with inner olivaceous guttulae and brown necropigment, sterigmata up to 3 µm long. *Pleurocystidia* absent. *Cheilocystidia* numerous, 39–65 × 8–14 µm, hyaline, thin-walled, variable in shape, cylindrical to clavate, less often broadly clavate or ventricose, occasionally utriform, pyriform, rounded at apex. *Caulocystidia* absent. *Hymenophoral trama* 13–22 µm regular to subregular, hyaline to yellowish, cylindrical, thin-walled. *Stiptipellis* a cutis, often with long extended hyphae, cylindrical, yellowish when aggregated, 4–10 µm wide, encrusted. *Pileipellis* a cutis, with bundles of hyphae, cylindrical to inflated, yellowish brown when aggregated, 8–23 µm wide, thickened. *Clamp connections* present in all tissues.

Habit, Habitat & Distribution — Solitary to gregarious, on soil under pine trees (*Pinus roxburghii*) at QAU Botanical garden.

Typus. Pakistan, Islamabad, QAU Botanical Garden, N30°26'30" E69°21'35", 507 m a.s.l., under *Pinus roxburghii* (*Pinaceae*), 5 Aug. 2021, *I. Rauf & M. Saba*, MIR2 (holotype LAH37801 ITS and LSU sequences GenBank OP997541 and OP997544; MycoBank MB 848105).

Additional materials examined. Pakistan, Islamabad, QAU Botanical Garden, N30°26'30" E69°21'35", 507 m a.s.l., under *P. roxburghii*, 8 Sept. 2022, *I. Rauf & M. Saba*, MIR2 (paratype LAH37802, ITS and LSU sequences GenBank OP997542 and OP997545).

Notes — Terminology for descriptive terms follows Kuyper (1986) and Vellinga (1988) and colour codes are taken from Munsell (1994). In our phylogeny, *Mallocybe ahmadii* belongs to a well-supported clade (bootstrap support value = 100 %) together with *M. aurantiodisca*, *M. longicystis*, *M. unicolor*, and *M. multispora* (GenBank OM179935, OM179927, MN178524, MN178509, respectively). *Mallocybe ahmadii* is described here from Pakistan, growing on soil under *Pinus roxburghii*. Characteristic morphological features include rather fleshy, predominately deep yellowish brown basidioma, a fibrillose-tomentose to woolly tomentose pileus with scurfy appressed squamules, ellipsoid to ovoid, amygdaliform and comparatively large basidiospores. In addition, cheilocystidia are cylindrical to clavate, less often broadly clavate or ventricose, occasionally utriform, pyriform and rounded at the apex. *Mallocybe aurantiodisca* is morphologically quite close to *M. ahmadii* and occurs in subtropical evergreen broad-leaved forests dominated by *Castanopsis* (China), but distinguished by its orange to reddish brown, becoming pale yellow brown with orange tinged pileus with tomentose squamules and somewhat smaller basidiospores, (7.9–)8.1–9.1–10.2(–11.8) × (4.1–)4.2–5.0–5.4(–6.2) µm (Hu et al. 2023). Other morphologically closely related taxa that cluster in the same clade are *M. longicystis* (originally described from China) and *M. unicolor* (originally described from New York). The former can be differentiated by its umber coloured pileus with erect squamules and smaller basidiospores (8.8–10.2 × 4.3–5.6 µm). Furthermore, the latter can be distinguished by the fibrillose-fleshy context of its stipe, and smaller basidiospores (8–11.5 × 4–6 µm) (Kuo 2017).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Mallocybe aurantiodisca* (GenBank OM179937, OM179935; Identities = 95.43 %). Closest hits using the **LSU** sequence are also *Mallocybe aurantiodisca* (GenBank OM138835, OM138834; Identities = 98.76 %).

Colour illustrations. *Pinus roxburghii* trees in the QAU Botanical Garden in Islamabad, Pakistan (photo credit I. Rauf). *Mallocybe ahmadii* basidiomata in habitat; basidiospores; basidia and cheilocystidia. Scale bars = 10 µm.

Supplementary material

FP1526 Phylogenetic tree.

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Melanogaster anatolicus

Fungal Planet 1527 – 29 June 2023

Melanogaster anatolicus Kaygusuz, G. Moreno & Türkekul, *sp. nov.*

Etymology. From 'griego Ανατολή Anatolḗ', which is presently known as Anatolia, the Turkish Peninsula where this species was collected.

Classification — *Paxillaceae*, *Boletales*, *Agaricomycetes*.

Basidiomata 35–100 mm wide, hypogeous or semi-hypogeous, subglobose or irregularly tuberous, wrinkled exteriorly, showing mostly an irregular shape, slightly lobed, frequently with an irregular apical depression, occasionally folded inside. *Surface* smooth, slightly velvety, frequently cracked, at first light ginger yellow to light yellowish brown, then cream yellow to matt or dull yellowish brown to ochre yellow brown, darkening in areas exposed to air; dark brown or dark rhizomorphs arranged laterally, simple or aggregated. *Gleba* shiny gelatinous, overall black at maturity, with cells delimited by irregular distinct whitish veins on the walls of the glebal chambers, which are angular to subglobose, usually exuding a bright dark black liquid, which spot an ink-blot appearance when cut. The *smell* is slightly acidic for mature specimens. *Peridium* 150–360 µm thick, consisting of two types of elements: *Peridiopellis* 27.5–75(–90) × 4.5–13.5 µm, composed of interwoven to parallel hyphae with conspicuous erect hyphae, very variable in shape: from tortuous-cylindrical, elongate cylindrical, cylindro-clavate to subfusiform, lageniform, often irregularly shaped, smooth, thin- to slightly thick-walled, sometimes with evenly dissolved pale yellowish brown intracellular pigment. *Dermatocystidium* 40–110(–135) × 6–30(–48) µm, various in shape, fusiform to ventricose-fusiform, with obtuse to acute apex, sometimes with a hypha-like base; broadly utriform to narrowly lageniform to broadly lageniform, short- to long necked or with a broad apex, thick-walled, with evenly dissolved pale brown intracellular pigment. *Gleba* 150–850 µm thick, composed of layers of subglobose to globose to irregularly ellipsoid cells, separated by veins consisting of gelatinised, slightly thick-walled. *Basidiospores* (6.3–)6.7–11.5(–12.0) × (4.1–)4.4–6.0(–6.4) µm, $L^m \times W^m$ = 8.9 × 5.0 µm, Q = (1.4–)1.5–2.1(–2.3), Q^m = 1.8, mostly oblong to broadly fusiform, sometimes ellipsoid or subcylindrical, smooth, thick-walled, yellowish brown to brown to dark brown in 3 % KOH. *Basidia* 25.0–35.0(–40.0) × 5.9–8.0 µm, narrowly clavate to clavate, with a long and sinuous stipe, mostly 4-spored, sometimes 2-spored, with short cylindrical sterigmata, thin-walled, hyaline. *Basidioles* numerous, 15.0–35.0(–40.5) × 4.5–8.5 µm, clavate to subclavate or flexuose, with sometimes mucronate to distinct subcapitate apex, thin-walled. *Clamp connections* present in all parts examined.

Habitat & Distribution — Gregarious or sometimes in small groups, hypogeous or semi hypogeous, between early June and late August, mostly present at elev. 1 000–1 700 m, always under *Cedrus libani*, which grows on clay loamy soils, which are rich in calcium.

Colour illustrations. Cedrus libani Forest at the Kızıldağ National Park, located in the Isparta Province, Türkiye. Ascomata; peridium and gleba; detail of the outermost layer of the peridium with prosenchymatic structure; prosenchymatic gleba, basidia and basidiospores; basidiospores (holotype OKA-TR142441). Scale bars = 10 mm (basidiomata), 100 µm (cortex; (peridiopellis), 10 µm (basidia and spores).

Typus. Türkiye, Isparta Province, Şarkikaraağaç District, around Kızıldağ National Park, *Cedrus libani* forest, 1 700 m a.s.l., 3 June 2018, *O. Kaygusuz* (holotype OKA-TR142441, isotype in AH 51471; ITS and LSU sequences GenBank OP548645 and OP548640; MycoBank MB 845757).

Additional materials examined. *Melanogaster anatolicus*: Türkiye, Isparta Province, Şarkikaraağaç District, around Kızıldağ National Park, under *Cedrus libani,* 1 690 m a.s.l., 5 July 2020, *O. Kaygusuz* (OKA-TR142442, ITS and LSU sequences GenBank OP548646 and OP548641); ibid., 25 June 2021, *O. Kaygusuz* (OKA-TR142443, ITS and LSU sequences GenBank OP548647 and OP548642); ibid., Süleyman Demirel University West Campus, under *C. libani,* 1 000 m a.s.l., 28 Aug. 2022, *O. Kaygusuz* (OKA-TR142444, ITS and LSU sequences GenBank OP548648 and OP548643).

Notes — *Melanogaster anatolicus* is morphologically characterised by its large and broad basidiospores (Q^m = 1.8) with an obtuse apex, differently shaped and sized peridiopellis and dermatocystidium, and growing under *Cedrus libani*. Based on the ITS and LSU sequences, the new species is genetically quite different from the other known species of *Melanogaster*. *Melanogaster anatolicus* is phylogenetically and morphologically related to *M. broomeanus* and *M. variegatus*. However, *Melanogaster broomeanus* and *M. variegatus* differ from *M. anatolicus* by forming slightly smaller basidiospores (6.0–8.4 × 3.5–4.0 µm and 7.5–10.3 × 5.0–7.5 µm, respectively) (Zeller & Dodge 1937). Other European species similar to *M. anatolicus* are *M. luteus* and *M. rivularis*. The smaller size of the basidiomata and basidiospores and different growing habitats of *M. luteus* and *M. rivularis* clearly distinguish them from *M. anatolicus* (Zeller 1939, Moreau et al. 2011). Microscopically, the basidiospore sizes of *M. anatolicus* are clearly smaller than those of *Melanogaster* species such as *M. ambiguous* (8–17 × 5.5–8.5 µm), *M. intermedius* (11–13 × 7.4–8 µm), and *M. eurysperm* (12–15 × 8–11 µm) (Zeller & Dodge 1937, Zeller 1939).

The genus *Melanogaster* was recently divided into four genera: *Alpova*, *Melanogaster*, *Neoalpova*, and *Paralpova*, according to their peridium being entirely prosenchymatic or the peridium entirely (or at least the subpellis) pseudoparenchymatic, and the colour of the glebal sterile tissue (Alvarado et al. 2021). As a result of the study carried out to resolve the phylogenetic relationships between these genera, *Alpova* was found to be strictly associated with *Alnus* (Alvarado et al. 2021).

Supplementary material

FP1527 Phylogenetic tree.

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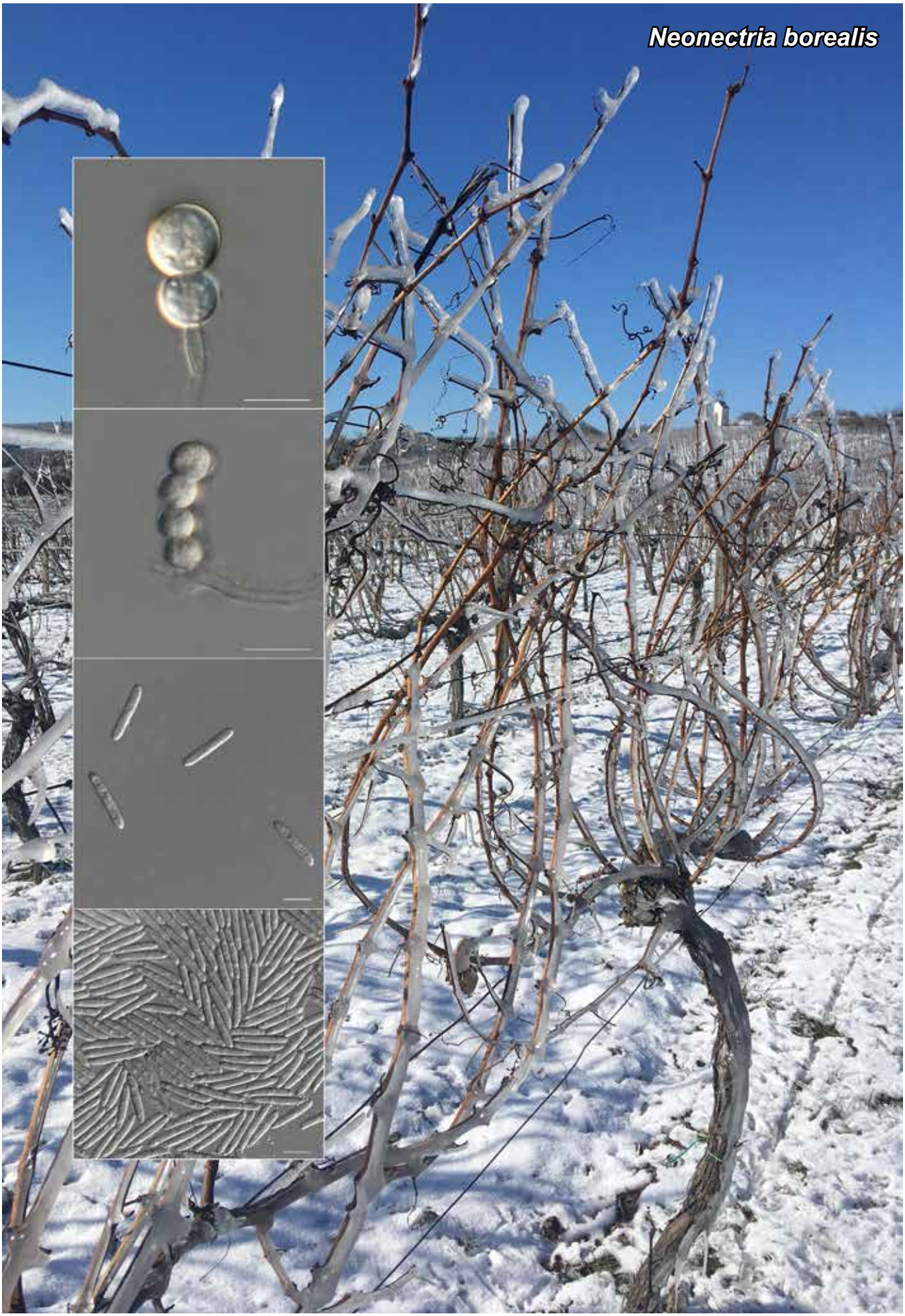

Neonectria borealis

Fungal Planet 1528 – 29 June 2023

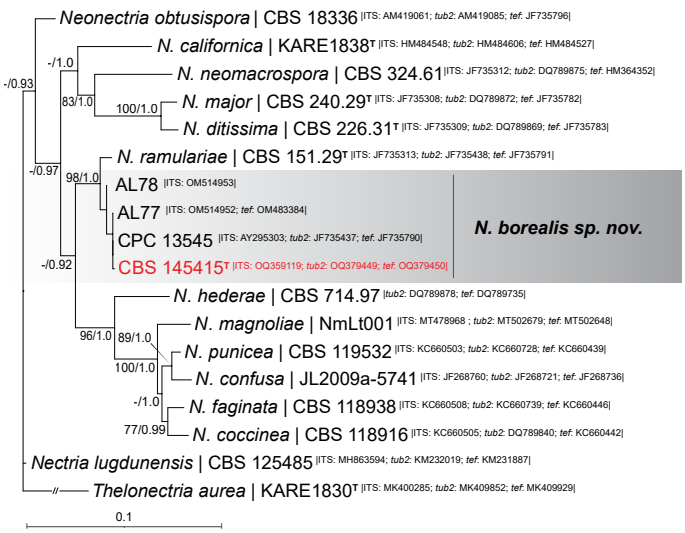
Neonectria borealis Spetik, Eichmeier & Gramaje, *sp. nov*.

Etymology. Name refers to Northern Spain, where the fungus was isolated.

Classification — *Nectriaceae*, *Hypocreales*, *Sordariomycetes*.

Conidiophores simple or complex. Simple conidiophores unbranched or some branched, 1–2-septate, 25–53 µm long. *Phialides* monophialidic, more or less cylindrical, tapering slightly towards the apex, 16–27 µm long, 1.5–3 µm wide at the base, 2–3.5 µm at the widest point, 1.5–2.5 µm near the aperture. Sporodochial conidiophores irregularly branched. *Macroconidia* (1–)2-septate, straight, cylindrical, with both ends more or less broadly rounded, mostly with a visible centrally located hilum; 1-septate (19.5–)22.5–24(–31) × (4–)5–5.5 (–6.5) µm (av. 23 × 5 µm), L/W ratio (3–)3.5–4.5(–5.5) (av. 4), 2-septate (28–)32.5–40.1(–45) × (5.5–)7.0–8.5(–9) µm (av. 35.5 × 8 µm), L/W ratio (2.5–)4–5.5(–7) (av. 4.2). *Microconidia* rarely formed, 0–1-septate, aseptate microconidia mostly ellipsoidal, (7.5–)9–11.5(–9.5) × (4.5–)5.5–6(–7) (av. 11 × 6 µm), L/W ratio (1.3–)1.5–1.8(–2.1) (av. 1.7); 1-septate, ellipsoidal to oblong, (10.5–)16–23.5(–25) × (6.5–)7–8.5(–9) (av. 21.5 × 7.5 µm), L/W ratio (2–)2.5–3(–3.3) (av. 2.8). *Chlamydospores* observed on SNA, globose to subglobose, 6–10 × 7–11 µm diam, smooth but often appearing rough due to deposits, thick-walled, mainly in chains, hyaline, becoming medium brown.

Culture characteristics — Mycelium felty with average density in both oatmeal agar (OA) and potato dextrose agar (PDA). Surface on OA straw to buff towards the edge; margin buff. Surface on PDA straw to buff towards the centre; margin straw. Zonation present in both PDA and OA, transparency homogenous and margin even in both OA and PDA. Reverse similar to surface, except in colour, chestnut on OA and chestnut to sienna on PDA. Colonies reaching a radius of 24.5 mm after 7 d at 25 ºC. Minimum temperature for growth 5 ºC, optimum 18.8 ºC, maximum 30 ºC.



A phylogram showing relationships in *Neonectria* based on combined ITS, *tef* and *tub2* sequences. The dataset contained sequences of 18 strains including two outgroup taxa (*Nectria lugdunensis* CBS 125485^{T} and *Thelonectria aurea* KARE1830^{T}) and a total of 1465 characters of which 418 were variable and 177 parsimony-informative. The maximum likelihood (ML) tree was constructed using IQ-TREE v. 2 (Minh et al. 2020). The best models for the ML analyses were selected based on the Akaike Information Criterion (AIC). The most suitable substitution model for Bayesian analyses (BI) was determined separately for each loci using jModelTest v. 2.1.7 (Ronquist & Huelsenbeck 2003): HKY+G (ITS, *tef*) and GTR+G (*tub2*). The BI analysis employed MrBayes v. 3.2.7 (Ronquist et al. 2012) and included four parallel runs of 50 M generation starting from a random tree topology; every 1000 generations were sampled and the first 25 % of the trees were discarded as the 'burn-in'. The ML bootstrap support values (BS) above 75 % obtained from 1000 bootstrap replicates and posterior probabilities (PP) above 0.95 are shown at the nodes (BS/PP). The novel species is highlighted in **bold** in a grey block and the strain isolated in this study in red. The alignment, trees and barcodes used for phylogenetic analyses are available in figshare (10.6084/m9.figshare.21997043).

Colour illustrations. *Vitis vinifera* in winter. Chlamydospores; conidia. Scale bars = 10 µm.

Typus. Spain, Navarra, Larraga, on roots of 110 Richter grapevine rootstock (*Vitis berlandieri* × *Vitis rupestris*), 2018, *C. Berlanas* (holotype CBS H-23885; culture ex-type CBS 145415 = BV-1396; ITS, *tub2*, *tef*, *rpb2* and *his3* sequences GenBank OQ359119, OQ379449, OQ379450, OQ379451 and OQ379452; MycoBank MB 847494).

Notes — *Neonectria borealis* (CBS 145415) is > 99.7 % identical (3 nt differences in the combined *tub2*, *tef* and *his3* dataset) to isolate CPC 13545 which was deposited in GenBank as *Cylindrocarpon* sp. in the study of Cabral et al. (2012); a similar scenario was observed comparing ex-type strain of *N. borealis* with isolates AL77 (3 nt differences in the combined ITS, *tef* and *his3* dataset) and AL78 (3 nts in the combined ITS and *his3* dataset) which were deposited in GenBank as *Neonectria* sp. 1 in the study of Capote et al. (2022). Thus, we decided to group the isolates described above with our newly obtained isolate (CBS 145415) as a taxonomic novelty *N. borealis*. *Neonectria borealis* is located in a well-supported (98/1.0) clade together with ex-type strain of *N. ramulariae* (CBS 151.29). Both species can be distinguish based on size of conidia; *N. borealis* has wider conidia, av. 23 × 5 µm vs 16.0–29.2 × 1.3–2.9 µm in *N. ramularia* (Hirooka et al. 2012). Comparing ex-type strain of both species there are 12 pairwise nucleotide differences in *tef*, 12 nts in *tub2* and 25 nts in *his3*.

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Neophaeosphaeria livistonae

Fungal Planet 1529 – 29 June 2023

Neophaeosphaeria livistonae Tennakoon & C.H. Kuo, *sp. nov*.

Etymology. Named after the host genus from which it was collected, *Livistona*.

Classification — *Neophaeosphaeriaceae*, *Pleosporales*, *Dothideomycetes*.

Ascomata separate, immersed to semi-immersed, partly erumpent, solitary or scattered, globose, unilocular, brown, 80 µm diam, with central papillate ostiole; wall of 2–3 layers of brown *textura angularis*. *Pseudoparaphyse*s cellular, hyaline, smooth, branched, septate, anastomosing, 1.5–2 µm diam. *Asci* bitunicate, 8-spored, cylindrical-clavate, fissitunicate, slightly curved, rounded apex, with low ocular chamber, 5 µm diam, 1–2 µm high (visible only in young asci), with a short pedicel, 55–65 × 16–25 µm. *Ascospores* bi- to tri-seriate, ellipsoidal to obovoid, with rounded ends, widest in middle of second cell from apex, developing a central septum and then becoming muriformly septate, slightly constricted at the septa, hyaline when immature and golden brown at maturity, guttulate, 16–18 × 6–8 µm.

Culture characteristics — Colonies reaching 20 mm diam after 2 wk at 25 °C. On MEA colonies folded, with sparse aerial mycelium and smooth, even margin; surface pale olivaceous grey, reverse olivaceous grey. On PDA surface pale olivaceous-grey, with patches of olivaceous-grey, reverse olivaceous grey.

Typus. China, Taiwan region, Miaoli city, Huoyan Mountain, on dead leaf of *Livistona rotundifolia* (*Arecaceae*), 14 Sept. 2018, *D.S. Tennakoon*, DST33 (holotype NCYU 19-0403; cultures ex-type NCYUCC 19-0393–19-0395; ITS, LSU, SSU and *tef1* sequences GenBank OQ437390–OQ437392, OQ437387–OQ437389, OQ437393–OQ437395 and OQ436029–OQ436031; MycoBank MB 847563).

Notes — *Neophaeosphaeria* was introduced by Câmara et al. (2003) to accommodate four species, namely *N. filamentosa*, *N. barrii*, *N. conglomerata* and *N. quadriseptata*. Subsequently, *N. agaves* and *N. phragmiticola* were added by Crous et al. (2013) and Hyde et al. (2018), respectively. The phylogeny inferred from the ITS, LSU, SSU and *tef1* sequences demonstrated that the new species *N. livistonae* nested in the *Neophaeosphaeria* clade and forms an independent lineage sister to *N. phragmiticola* (KUMCC 16-0216) with full statistical support (100 %). Interestingly, both *N. livistonae* and *N. phragmiticola* have muriform spores, but in different morphs (sexual and asexual). Therefore, we compared the *tef1* and LSU base pair differences between our collection and *N. phragmiticola*. There are 28 base pair differences (3 %) across 926 nucleotides across the *tef1* gene region and three base pair differences across the LSU gene region. *Neophaeosphaeria livistonae* differs from the sexual morph of other *Neophaeosphaeria* species in having muriform ascospores (Ellis & Everhart 1888, Barr 1992, Câmara et al. 2003). In addition, *N. livistonae* can be distinguished from *N. filamentosa* in distinct size differences of asci (55–65 × 16–25 vs 75–80 × 7–8 µm) and ascospores (16–18 × 6–8 vs 12–15 × 4–5 µm) (Ellis & Everhart 1888). *Neophaeosphaeria quadriseptata* also differs from *N. livistonae* in their asci dimensions (76–110 × 11–14 vs 55–65 × 16–25 µm) (Barr 1992). Thus, we introduce our collection as a new species from *Livistona rotundifolia*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to an uncultured fungus (strain G2_BG11, GenBank JX043146; Identities = 541/566 (96 %), five gaps (0.8 %)), uncultured fungus (strain G2_CC1, GenBank JX043148; Identities = 541/566 (96 %), five gaps (0.8 %)) and uncultured fungus (strain G2_DG5, GenBank JX043147; Identities = 530/566 (93 %), 18 gaps (3 %)). Closest hits using the **LSU** sequence are *Leptosphaerulina nitida* (strain CBS 450.84, GenBank MH873454; Identities = 867/877 (99 %), two gaps (0.3 %)), *Pleosporineae* sp. (strain 18BPLE022, GenBank MT646040; Identities = 861/877 (98 %), two gaps (0.2 %)) and *N. agaves* (strain CPC 21264, GenBank NG_058045; Identities = 862/877 (98 %), two gaps (0.2 %)).

Colour illustrations. Holotype collection area in the Miaoli city, Huoyan Mountain, Taiwan region, China (photo credit Yi Jyun Chen). Appearance of ascomata on dead leaf of *Livistona rotundifolia*; vertical section of ascoma; asci; ascospores. Scale bars = 50 µm (section), 30 µm (asci), 10 µm (ascospores).

Supplementary material

FP1529-1 Phylogenetic tree.

FP1529-2 Table. Cultural collection and GenBank accession numbers of isolates included in phylogenetic analyses.

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Neosetophoma fici

Fungal Planet 1530 – 29 June 2023

Neosetophoma fici A. Ahmadpour, Z. Heidarian, F. Alavi, Z. Alavi & Y. Ghosta, *sp. nov.*

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

Classification — *Phaeosphaeriaceae*, *Pleosporales*, *Dothideomycetes*.

Conidiomata pycnidial, (semi-)immersed in the agar or produced on the agar surface, mostly solitary, scattered, papillate, sometimes the confluent pycnidia merge with age, brown, erumpent, globose, (100–)120–180(–200) × (100–)120–200(–220) µm diam with 1(–2) ostioles; *conidiomatal wall* of 3–4 layers of brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining inner cavity. *Conidiogenous cells* single, phialidic, unbranched, aseptate, hyaline, smooth-walled, doliiform to ampulliform, 4–8 × 4–6 µm. *Conidia* solitary, aseptate, hyaline, smooth-walled, subcylindrical to ellipsoid, straight to slightly curved, apex round to obtuse, attenuate or truncate at the base, yellowish-brown at maturity as a mass, 3–4 × 1(–1.5) µm, with one polar guttule. *Sexual morph* unknown.

Culture characteristics — Colony on oatmeal agar (OA) reaching 25 mm diam after 7 d, margin regular, floccose, aerial mycelium sparse, floccose, white to greenish olivaceous; reverse white to pale brown, olivaceous near the centre. On potato dextrose agar (PDA) reaching 28 mm diam at 25 °C after 7 d, margin regular, aerial mycelium sparse, floccose, white in outer ring grey olivaceous towards to the centre; reverse with pale olivaceous near the centre. On malt extract agar (MEA) reaching 23 mm diam after 7 d, margin regular, aerial mycelium sparse, floccose, white in outer ring grey olivaceous towards to the centre; reverse pale brown near the center.

Typus. Iran, West Azarbaijan Province, Miyandoab city, on infected leaves of *Ficus elastica* (*Moraceae*), 20 Sept. 2021, *A. Ahmadpour* (holotype IRAN 18106F; ex-type living culture IRAN 4234C; ITS, LSU, *RPB2* and *TUB2* sequences GenBank OP806395, OP805934, OP838919 and OP838921; MycoBank MB 846431).

Additional materials examined. Iran, West Azarbaijan province, Miyandoab city, on infected leaves of *F. elastica*, 30 Sept. 2021, *A. Ahmadpour*, FCCUU 1902, ITS, LSU, *RPB2* and *TUB2* sequences GenBank OP806396, OP805935, OP838920 and OP838922.

Notes — The two isolates studied of *N. fici* form a fully-supported clade distinct from known *Neosetophoma* species. *Neosetophoma fici* is phylogenetically closely related to *N. ulmi* (nom. inval., Art. 40.8; Shenzhen) (strain CCTUE1042) with a fully-supported node encompassing both species. *Neosetophoma fici* can be easily distinguished from *N. ulmi* by the size of its conidia (3–4 × 1(–1.5) µm in *N. fici* vs 4–7.3 × 1.3–2 µm in *N. ulmi*). Moreover, *N. fici* produces larger conidiomata (120–200 µm diam vs 69–146 µm diam in *N. ulmi*) (Ahmadi et al. 2021). If the two species are however later shown to be synonymous, the name *N. fici* would have preference, as *N. ulmi* was invalidly described.

Based on a megablast search of NCBI nucleotide database, the closest hits using the **ITS** sequence had the highest similarity to *Neosetophoma samarorum* (strain 88SA1, GenBank KY950236.1; Identities = 491/494 (99 %), with one gap (0 %)), *Neosetophoma samarorum* (strain AW1325, GenBank MK049885.1; Identities = 488/494 (99 %), with one gap (0 %)) and *Neosetophoma* sp. (= *N. ulmi*) (strain C12-A2, GenBank MW432173.1; Identities = 488/494 (99 %), three gaps (0 %)). The closest hits using the **LSU** sequence had the highest similarity to *Neosetophoma* sp. (= *N. ulmi*) (strain C12-A2 GenBank MW432172.1; Identities = 808/813 (99 %), four gaps (0 %)), *Ascochyta eriobotryae* (strain CBS 448.73, GenBank MH878377.1; Identities = 808/813 (99 %), five gaps (0 %)) and *Neosetophoma rosarum* (strain MFLU 17-0308, GenBank MG829036.1; Identities = 808/813 (99 %), with five gaps (0 %)). Closest hits using the ***RPB2*** sequence are *Neosetophoma cerealis* (strain CBS 518.74, GenBank MT223692.1; Identities = 708/782 (91 %), no gaps), *Neosetophoma buxi* (strain CBS 146845/MEND-F-0059, GenBank MW628872.1; Identities = 706/782 (90 %), no gaps) and *Brunneomurispora lonicerae* (strain KUMCC 18-0157, GenBank MK359079.1; Identities = 702/783 (90 %), no gaps). The closest hits using the ***TUB2*** sequence had the highest similarity to *Phaeosphaeria* (strain IG115, GenBank MH001471.1; Identities = 251/271 (93 %), four gaps (1 %)), *Neosetophoma cerealis* (strain CBS 443.82, GenBank MT223739.1; Identities = 246/271 (91 %), three gaps (1 %)) and *Neosetophoma* sp. (= *N. ulmi*) (strain C12-A2, GenBank MW442587.1; Identities = 182/183 (99 %), no gaps).

Colour illustrations. *Ficus elastica* growing in Iran. Symptom on leaves with pycnidia; colony on OA, PDA and MEA after 7 d (front and reverse); pycnidia produced on OA, PDA and MEA; pycnidium; conidiogenous cells and conidia. Scale bars = 50 µm (pycnidium) and 10 µm (conidiogenous cells and conidia).

Supplementary material

FP1530 Phylogenetic tree.

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Niesslia parviseta

Fungal Planet 1531 – 29 June 2023

Niesslia parviseta Darmostuk, Etayo & Flakus, *sp. nov.*

Etymology. Named after the small hairs on the perithecia.

Classification — *Niessliaceae*, *Hypocreales*, *Sordariomycetes*.

Ascomata situated on the apothecial disk and on the lower and upper surface of the host thallus, usually aggregated, black, subglobose, sessile, collapsing cup-like when dry, with a central ostiole, setose, (85–)90–130(–170) µm diam (n = 25). *Setae* numerous, simple, dark brown, 12–23 µm long, tapering from 3–5 µm at the base towards pointed apex; intermixed with hyaline, capitate, thick-walled, monocilium-like conidiophores, 22–25 × 2–2.5 µm. *Exciple* dark orange brown, homogeneously pigmented (only the inner portion paler to hyaline), 10–20 µm wide, KOH+ greenish brown, composed of several rows of thick-walled angular cells, 2–7 × 1–4 µm in transversal section. *Periphyses* formed around the ostiole, hyaline, 1-septate, 10–12 × 1–2 µm, thin-walled. *Paraphyses* not observed. *Asci* sub-cylindrical, with a short foot at the base and a truncate apex, unitunicate, 8-spored, I–, K/I–, 35–38 × 4–6 µm. *Ascospores* uniseriate, ellipsoid, smooth, without perispore, with round ends, hyaline, rather thick-walls, medianly 1-septate, (5.0–)5.5–6.8(–7) × (2.0–)2.9–3.3(–3.5) µm (n = 35).

Habit, Habitat & Distribution — *Niesslia parviseta* is known from a single specimen in an open area with shrubs at the upper limit of Yungas cloud forest, where it grew on the thallus and apothecial discs of *Erioderma barbellatum* on twigs.

Typus. Bolivia, Department Cochabamba, Tiraque Province, Parque Nacional Carrasco, close to Antenas Sillar-Cotany Alto road, S17°14'22" W65°43'07", 3870 m a.s.l., open area with shrubs, on the lower part and apothecial disc of *Erioderma barbellatum* (*Pannariaceae*) on twig, 30 Nov. 2014, *J. Etayo*, 34214 (holotype KRAM L-73346, isotypes LPB, herb. Etayo; ITS, LSU, *tef1* sequences GenBank OQ600193, OQ600191 and OQ606818; MycoBank MB 847848).

Notes — The genus *Niesslia* is characterised by small, setose perithecia that collapse into cup-like shapes when dry and monocillium-like asexual morphs (Gams et al. 2019). Mostly, *Niesslia* species inhabit decaying plant substrates, but some are also lichenicolous, fungicolous or parasites of nematodes. The newly described *Niesslia parviseta* is characterised by black, subglobose, perithecioid ascomata, (85–)90–130(–170) µm diam, covered by short setae, 12–23 µm long, excipulum evidently reacting KOH+ greenish brown, 8-spored asci and 1-septate, small ascospores, (5–)5.5–6.8(–7) × (2–)2.9–3.3(–3.5) µm. However, there are two *Niesslia* species previously described from *Erioderma* hosts. The first one is *Niesslia echinoides* growing on *Erioderma barbellatum* from Bolivia which differs from the new species by having the ascomata wall with two different layers, longer asci, 47–57 µm, and longer ascospores, 13–15 µm, which break in half within the asci (Etayo et al. 2013). The other species, *Niesslia evae* is known from Ecuador, where it is growing on *Erioderma* spp., and can be distinguished by larger, obpyriform, grey brown, ascomata, 150–200 µm wide, a thicker and complex ascomatal wall, 35–40 µm thick and multi-spored asci with 22–32 globose spore fragments (Etayo 2017). The newly generated sequence of *N. parviseta* forms a well-supported clade together with *Niesslia cladoniicola*. The latter species was described from *Cladonia rangiformis* in Great Britain and later reported from numerous localities mainly across the Holarctic region (Hawksworth 1975, Brackel 2014, Zhurbenko & Pino-Bodas 2017). Both species are morphologically similar and have the same KOH+ reaction of excipulum, but *Niesslia cladoniicola* can be distinguished by having longer setae, 20–30 µm, longer and narrower ascospores, (6.5–)8.3–10.3(–13.1) × (1.6–)2.2–2.6(–3.0) µm, and different host selection.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had the highest similarity to *Niesslia cladoniicola* (strain CBS 960.73, GenBank MG827042; Identities = 96 %, eight gaps (1 %)). The closest hits using the **LSU** sequence are *Niesslia cladoniicola* (strain CBS 960.73, GenBank MG826850; Identities = 99.88 %, no gaps), *Niesslia ilicifolia* (strain CBS 459.74, GenBank MG826798; Identities = 99.27 %, no gaps) and *Niesslia exilis* (strain CBS 357.70, GenBank AY489718; Identities = 99.15 %, no gaps). The closest hits using the ***tef1*** sequence are *Tolypocladium reniformisporum* (strain YFCC 1805002, GenBank MK984570; Identities = 91.67 %, six gaps (0 %)) and *Tolypocladium ophioglossoides* (strain NBRC 8992, GenBank AB968601; Identities = 91.46 %, six gaps (0 %)).

Colour illustrations. Open vegetation at the upper limit of Yungas cloud forest, next to the roadside in Parque Nacional Carrasco, Bolivia (photo credit A. Flakus). A habit of the ascomata on the host thallus; cross-section of the ascomata (right mounted in water, left in KOH); squash of the ascomata (right mounted in water, left in KOH); ascospores (mounted in water). Scale bars = 250 µm (habit), 25 µm (section and squash preparation), 5 µm (ascospores).

Supplementary material

FP1531-1 Phylogenetic tree.

FP1531-2 Table.GenBank and voucher accession numbers of sequences included in the phylogenetic analyses.

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Penicillium acericola

Fungal Planet 1532 – 29 June 2023

Penicillium acericola Mack & Overy, *sp. nov.*

Etymology. Name referring to the host plant (*Acer saccharum*) from which this fungus was first isolated.

Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetes*.

Conidiophores biverticilliate, smooth, 100–500 × 3–3.5 µm, bearing 3–5 metulae, 7.5–12 × 3.5–4.5 µm. *Conidiogenous cells* phialides, ampulliform, occurring 4–8 per metulae, 6–9 × 2.5–3 µm. *Conidia* occurring in chains, rough walled, ellipsoid to slightly obclavate, 3–4 × 2–3 µm.

Culture characteristics — (25 °C, 7 d): On Czapek yeast autolysate agar (CYA): colonies 18–22 mm (15 °C: 3–6 mm; 20 °C: 16–18 mm; 30 °C: 4–6 mm) moderately elevated, radially sulcate, slightly crateriform; margin entire, low and thin; mycelia white to pale yellow (3A3; Kornerup & Wanscher 1978); texture velvety; sporulation abundant, conidia *en masse* dark green (25F3); Soluble pigments inconspicuous yellowish; reverse snuff (5F7). On Malt extract agar (MEA): colonies 21–23 mm flat; margin entire, flat, wide; mycelia yellow (3C3); texture cottony; sporulation abundant, conidia *en masse* dark green (26F3); soluble pigments absent; reverse clay (5D5). On yeast extract sucrose agar (YES): colonies 14–20 mm moderately raised, radially and concentrically sulcate; margin entire, wide, immersed; mycelia white to light yellow (3A5) and light orange (5A4); texture velvety; sporulation poor, conidia *en masse* white to greyish blue (23C5); soluble pigments absent; reverse light brown (5D6). On dichloran 18 % glycerol agar (DG18): colonies 23–27 mm faintly radially sulcate, flat; margin entire, flat, wide; mycelia white to orange (5B8); texture velvety; sporulation abundant, conidia *en masse* dull green (25E3); soluble pigments inconspicuous, pale yellow (3A3); reverse pale yellow to brownish orange (7C7). On Oatmeal agar (OA): colonies 18–24 mm flat, low; margin entire, thin, flat; mycelia immersed pale to yellow or green; texture flocculose or cottony; sporulation abundant, conidia *en masse* dark green (28F5); soluble pigments absent; reverse greyish green (29D4). On creatine sucrose agar (CREA): growth weak, acid production weak.

Habit, Habitat & Distribution — Isolated from bark of *Acer saccharum*, currently only known from Canada.

Typus. Canada, Ottawa, Ontario, N45°26' W75°39', isolated using particle filtration/dilution culturing from dead bark of *Acer saccharum* (*Sapindaceae*), Apr. 2021, *J. Mack* (holotype: DAOM 985060 (dried specimen in metabolically inactive state); culture ex-type CHEM 2781 = DAOMC 252603; ITS, *BenA*, *CaM*, and *RPB2* sequences: GenBank OQ299442, OQ290898, OQ290901 and OQ290904; MycoBank MB 847213).

Notes — *Penicillium acericola* is similar to species of section *Sclerotiorum* series *Herqueorum* by producing yellow to orange hyphae and symmetrically biverticilliate conidiophores (Visagie & Yilmaz 2022). *Penicillium acericola* is phylogenetically most closely related to *P. umkhoba*, *P. verrucisporum*, *P. herquei* and *P. malachitum*. *Penicillium acericola* grow slower than *P. umkhoba* on CYA (18–22 vs 28–31 mm) and MEA (21–24 vs 28–32 mm) (Visagie & Yilmaz 2022) while *P. verrucisporum* grow faster on YES (43–44 vs 14–20 mm) and MEA (36–37 vs 21–24 mm) (Wang et al. 2017) and *P. herquei* grow faster than *P. acericola* on YES (30–40 vs 14–20 mm) (Visagie & Yilmaz 2022). *Penicillium malachiteum* produce cleistothecia in culture (Houbraken & Samson 2011) which are absent in *P. acericola*.

Colour illustrations. Living *Acer saccharum* growing in Ontario, Canada. Conidiophore morphology on CYA; conidia; colonies at 7 d of *Penicillium acericola* DAOMC 252603 (top row from left to right CYA, MEA, YES, OA, bottom row from left to right CYA reverse, MEA reverse, DG18, CREA). Scale bars = 10 µm (conidiophores), 5 µm (conidia).

Supplementary material

FP1532-1 – FP1532-4 Phylogenetic trees.

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Penicillium corticola

Fungal Planet 1533 – 29 June 2023

Penicillium corticola Mack & Overy, *sp. nov.*

Etymology. Named for inhabiting bark, the substrate from which this fungus was first isolated.

Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetes*.

Conidiophores monoverticillate, finely roughened, 100–200 (–300) × 2.5–3.5 µm, terminating in smooth vesicles, 5–7 µm. *Conidiogenous cells* phialides, ampulliform, 10–13 per vesicle, (7–)8–10(–11) × (2–)2.5–3.5(–4) µm. *Conidia* occurring in chains, smooth, ellipsoid, 2.5–3.5 × 1.5–2.5(–3) µm. *Sclerotia* produced on CYA, MEA and OA, white when young, turning orange with age, of thick-walled polygonal cells, globose, 300–500 µm.

Culture characteristics — (25 °C, 7 d): On Czapek yeast autolysate agar (CYA): Colonies 35–38 mm (15 °C: 11–13 mm; 20 °C: 21–26 mm; 30 °C: 34–37 mm), raised in the center, slightly sulcate; margins entire, wide; mycelia white; texture floccose; sporulation sparse to moderate, conidia *en masse* dull green (25E4; Kornerup & Wanscher 1978); soluble pigments absent; exudates clear; reverse cream (4A3); sclerotia abundant, greyish orange (5B6). On malt extract agar (MEA): Colonies 26–28 mm, flat, loosely funiculose; margin poorly differentiated; mycelia, loosely funiculose, white; texture floccose; sporulation moderate, conidia *en masse* grayish green (25C4); soluble pigments greenish white (30A2); exudates absent; reverse pale green; sclerotia moderately produced, white. On yeast extract sucrose agar (YES): Colonies 18–21 mm, raised in the centre, sulcate; margins entire; mycelia compact, white; texture velvety; sporulation sparse, conidia *en masse* greenish grey (25B2); soluble pigments inconspicuous, cream (4A3); exudates absent; reverse yellow (4B4); sclerotia absent. On dichloran 18 % glycerol agar (DG18): Colonies 30–33 mm, flat; margin narrow, entire; mycelia white; texture velvety, sporulation dense, conidia *en masse* greyish turquoise (24E3); soluble pigments inconspicuous pale yellow (2A3); reverse greyish green (30B4); sclerotia absent. On oatmeal agar (OA): Colonies 35–39 mm, flat; margin entire, narrow; mycelia loosely funiculose; sporulation moderate, conidia *en masse* greyish turquoise (24E4); soluble pigments pale green (30A3); exudates clear; sclerotia orange white (4A2). On creatine sucrose agar (CREA): growth weak, acid production very weak.

Habit, Habitat & Distribution — Isolated from bark of dead *Acer saccharum*, currently only known from Canada.

Typus. Canada, Ontario, Ottawa, N45°26' W75°39', isolated using particle filtration/dilution culturing from dead bark of *Acer saccharum* (*Sapindaceae*), Nov 2019, *J. Mack* (holotype: DAOM 985059 (dried specimen in metabolically inactive state); culture ex-type CHEM 2207 = DAOMC 252605; ITS, *BenA*, *CaM* and *RPB2* sequences: GenBank OQ299440, OQ290896, OQ290899 and OQ290902; MycoBank MB 847212).

Notes — *Penicillium corticola* is similar to other species classified in section *Aspergilloides* series *Thomii* by producing hard orange sclerotia on CYA and OA, and monoverticilliate conidiophores, with finely roughened stipes and ellipsoidal conidia (Houbraken et al. 2014). *Penicillium corticola* is phylogenetically most closely related to *P. aurantioviolaceum*, *P. cartierense, P. fusisporum*, *P. roseoviride* and *P. valentinum*. Morphologically, *P. cartierense* differs from *P. corticola* by producing sclerotia that do not turn orange in less than a week, wider conidia and by growing faster on CYA, MEA and YES (Houbraken et al. 2014). *Penicillium aurantioviolaceum* differ by its lack of sclerotia, longer conidiophore up to 400 µm and profuse sporulation on CYA (Raper & Thom 1949). *Penicillium fusisporum* produce cinnamon coloured sclerotia and longer fusiform conidia (Wang et al. 2014). *Penicillium roseoviride* differ by the absence of sclerotia (Pitt 1980) and *P. valentinum* differ by the production of amber pigments on MEA and absence of sclerotia on CYA (Ramirez & Martinez 1980).

Colour illustrations. Detail of the bark of a living *Acer saccharum* growing in Canada. Sclerotia on CYA; conidiophores; conidia; colonies at 7 d of *Penicillium corticola* DAOMC 252605 (top row from left to right CYA, MEA, YEA, OA, bottom row from left to right CYA reverse, MEA reverse, DG18, CREA). Scale bars = 10 µm (conidiophore), 5 µm (conidia).

Supplementary material

FP1533-1 – FP1533-4 Phylogenetic trees.

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Penicillium nudgee

Fungal Planet 1534 – 29 June 2023

Penicillium nudgee Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

Etymology. Named after Nudgee, a residential suburb of the city of Brisbane thought to be derived from an Aboriginal word meaning a wild or black duck. The suburb includes St Joseph's Nudgee College, an educational institution with extensive school grounds that include diverse native bushland. St Joseph's Nudgee College acknowledges the Turrbal people, traditional custodians of the lands and waterways known as Nudgee. This fungus was isolated from soil under a *Melaleuca quinquenervia* tree. The soil was collected by Year 8 students at St Joseph's Nudgee College as part of a mycology project organised by their science teacher Belinda Drury. The students were Nick Cheney, Jordan Cordingley, Finn Curran, Jackson Dalton, Henry Dennis, Oliver Douyere, Joshua Eckersall, Xander Eyles, Eric Fitzgerald, Toby Gall, William Gibson, Angus Glyde, Hayden Hamilton, Toby Harvey, Mark Hili, Samuel Howard, Lucas Jebreen, Dean Keys, Lachlan Mills, Paddy Williams, Lincoln Wright, and Nicholas Zeitoun.

Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetes*.

Conidiophores mono- and biverticillate, mostly unbranched. *Stipes* smooth, 50–200 × 2–3.5 µm. *Metulae* typically 3, cylindrical, 13–25 × 2–3 µm, vesicle 3–4 µm. *Phialides* ampulliform, in verticils of 3–9 per metula, 5–9 × 2–3 µm. *Conidia* globose to subglobose, 2–3 µm, smooth, catenulate. *Ascomata* or *sclerotia* not observed.

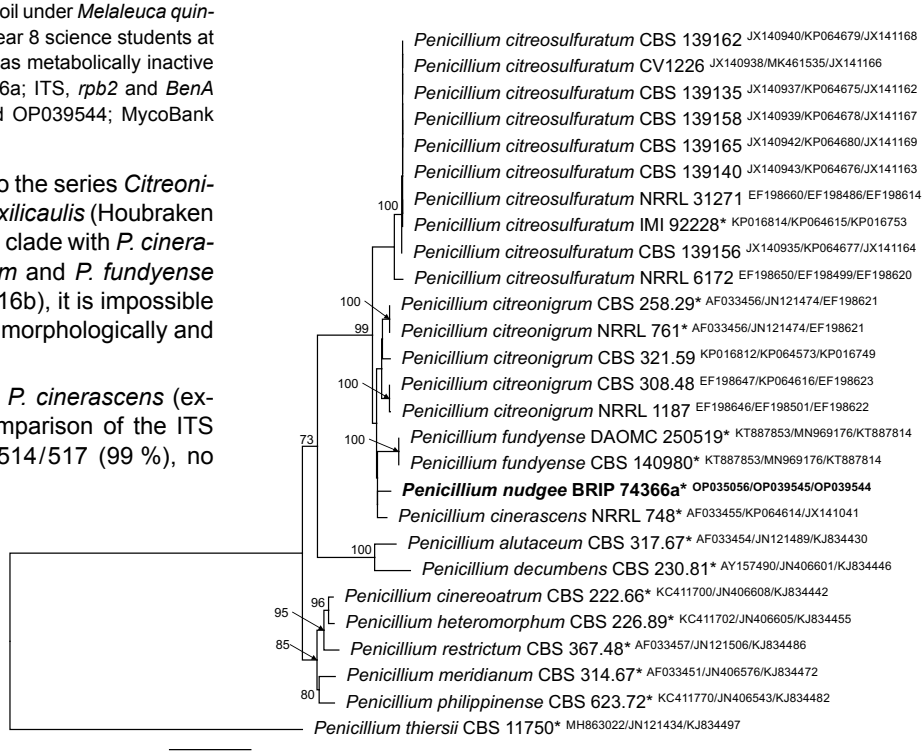
Culture characteristics (25 °C, 10 d, in darkness) — Colonies on potato dextrose agar (PDA) 4–4.5 cm diam, margin regular, yellow green, white at margins; reverse sulphur yellow.

Typus. Australia, Queensland, Brisbane, from soil under *Melaleuca quinquenervia* (*Myrtaceae*), 2 Nov. 2021, *B. Drury* & Year 8 science students at St Joseph's Nudgee College (holotype preserved as metabolically inactive culture BRIP 74366a; culture ex-type BRIP 74366a; ITS, *rpb2* and *BenA* sequences GenBank OP035056, OP039545 and OP039544; MycoBank MB 845975).

Notes — *Penicillium nudgee* belongs to the series *Citreonigra* sensu Visagie (2016a) in the section *Exilicaulis* (Houbraken et al. 2020). *Penicillium nudgee* sits in this clade with *P. cinerascens, P. citreonigrum*, *P. citreosulfuratum* and *P. fundyense* (Visagie 2016b). As noted by Visagie (2016b), it is impossible to distinguish the species of this complex morphologically and DNA barcode sequences are required.

Penicillium nudgee is distinguished from *P. cinerascens* (ex-type strain NRRL 748) by sequence comparison of the ITS region (GenBank AF033455; Identities 514/517 (99 %), no gaps; unique nucleotide at positions 389(G), 465(C), 500(C)), *rpb2* (GenBank KP064614; Identities 563/571 (99 %), no gaps; unique nucleotide at positions 79(T), 163(A), 244(C), 295(C), 307(A), 325(C), 355(T), 508(T)) and *tub2* (GenBank JX141041; Identities 437/446 (98 %), two gaps; unique nucleotide at positions 18(C), 21(C), 48(C), 76(T), 77(G), 268(T), 271(G)).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence are *P. citreonigrum* (strain NRRL 761, GenBank NR_138264, Identities 517/517 (100 %)), *P.* cf. *restrictum* (strain IHEM 28039, GenBank OU989466, Identities 517/517 (100 %)) and *P. fundyense* (strain DAOMC 250519, GenBank NR_171586, Identities 516/517 (99 %)). The closest hits using the ***rpb2*** sequence are *P. cinerascens* (strain NRRL 748, GenBank KP064614, Identities 563/571 (99 %)), *P. fundyense* (strain CBS 140980, GenBank MN969176, Identities 806/826 (98 %)) and *P. citreonigrum* (strain NRRL 761, GenBank EF198500, Identities 838/859 (98 %)). The closest hits using the ***tub2*** sequence are *P. citreonigrum* (strain NRRL 35629, GenBank EF198553, Identities 426/431 (99 %)), *P. aeneum* (strain CBS 321.59, GenBank KP016749, Identities 434/441 (98 %)) and *P. cinerascens* (strain IMI 092234, GenBank JX141041, Identities 437/446 (98 %), two gaps).



Phylogenetic tree of selected *Penicillium* species in section *Exilicaulis* based on a maximum likelihood analysis of the ITS, *rpb2* and *BenA* gene regions. The ML analysis was done on the IQ-TREE web server (Trifinopoulos et al. 2016) based on the GTR substitution model with gamma-distribution rate variation. GenBank accession numbers are indicated (superscript ITS/*rpb2*/*BenA*). *Penicillium thiersii* ex-type strain CBS 117503 was used as outgroup. Novel taxon is indicated in **bold**. Ex-type strains indicated with an asterisk (*). The alignment and trees are publicly available in 10.5281/zenodo.7726428.

Colour illustrations. Grove of *Melaleuca quinquenervia*, St Joseph's Nudgee College, Brisbane, Queensland, Australia (photo credit Belinda Drury). Colony sporulating on PDA (top and reverse); conidiophores; conidia. Scale bars = 1 cm (colony), 10 µm (all others).

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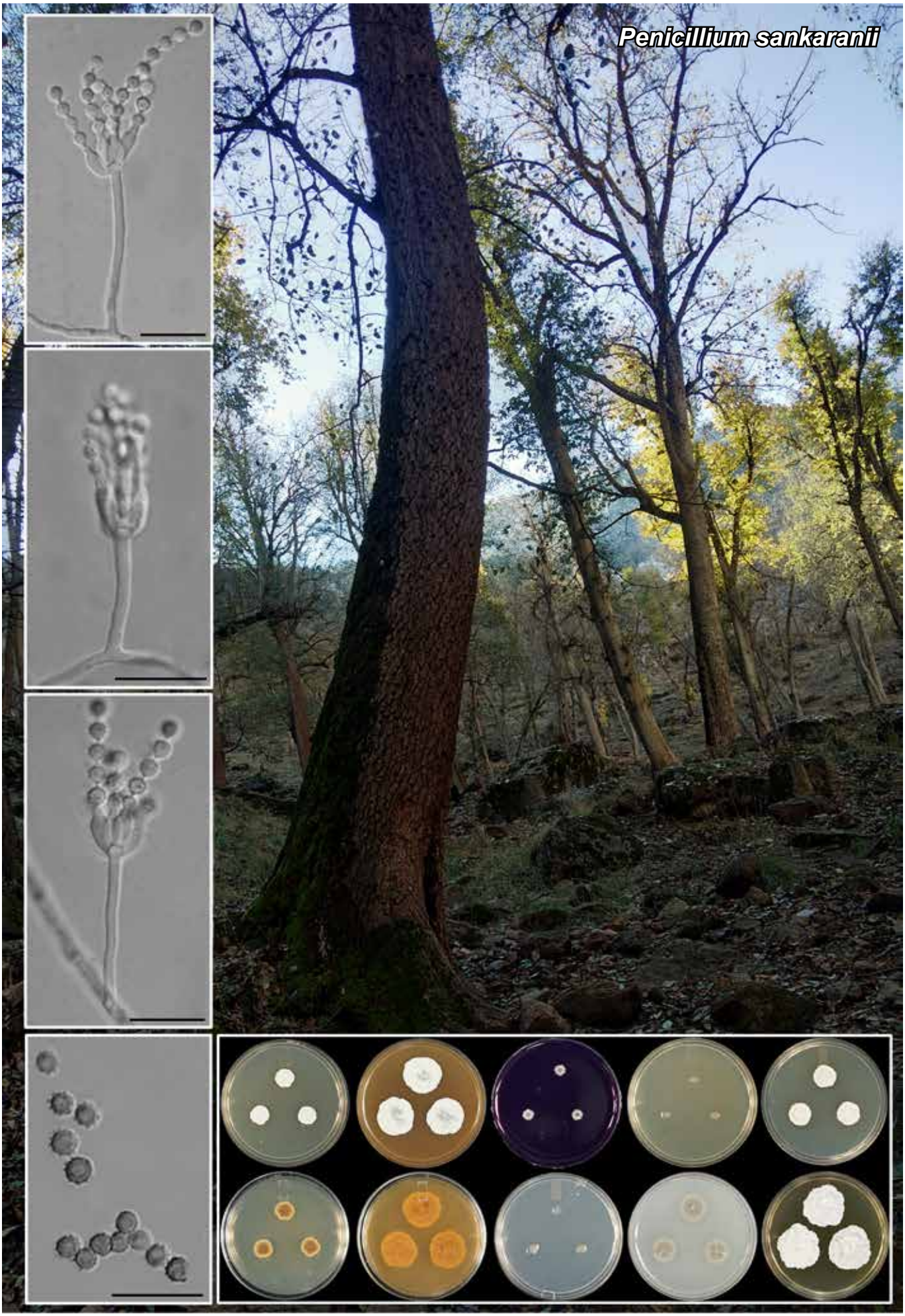
Penicillium sankaranii

Fungal Planet 1535 – 29 June 2023

Penicillium sankaranii Rajeshk., N. Ashtekar, G. Anand, Yilmaz & Visagie, *sp. nov.*

Etymology. Named after Dr K.V. Sankaran, former Director of the Kerala Forest Research Institute (KFRI) in Peechi, India, for his contributions to Indian Mycology.

Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetes*.

Conidiophores monoverticillate, rarely biverticillate. *Stipes* smooth to finely roughened, 12–51(–107) × 1.5–3 µm. *Metulae* in verticils of two of unequal lengths, 9–35 × 2–2.5 µm. *Phialides* ampulliform, in verticils of 4–8 per stipe/metula, 6–9.5 × 2–3 µm. *Conidia* globose, spinulose, 2–3 × 2–3 µm, borne in well-defined columns, distinct connectors visible.

Culture characteristics (25 °C, 7 d, in darkness) — Colonies on Czapek yeast autolysate agar (CYA) 16–17 mm diam, deep, radially sulcate, centrally convolute; margins irregular, deep; mycelia white; texture floccose; sporulation sparse, greenish white (25D2; Kornerup & Wanscher 1978) centrally, white (1A1) towards periphery; exudates absent; soluble pigments absent; reverse brown (5E5) centrally, greyish yellow (4B4) towards periphery, yellowish white (2A2) at margin. Colonies on malt extract agar (MEA) 24–26 mm diam, deep, slight radial sulcations, centrally convolute; margin irregular, deep; mycelia pale yellow (2A3) to white (1A1); texture velutinous; sporulation sparse, greenish grey (25D2); exudates clear, dispersed all over the colony; soluble pigments absent; reverse golden blonde (5C4) centrally, yellowish white (4A2) at margin. Colonies on CYA with 5 % NaCl (CYAS) 5–6 mm diam; margin irregular, deep; texture butyrous; sporulation absent, yellowish white (4A2) margin; exudates absent; soluble pigments absent; reverse champagne (4B4) centrally, pale yellow (4A3) at margin. Colonies on oatmeal agar (OA) 14–17 mm diam, superficial, slightly convolute; margin regular, superficial; mycelia greenish grey (26C2); texture floccose; sporulation dense, greyish brown (5D3); exudates absent; soluble pigments absent; reverse hair brown (5E4) centrally, white (1A1) at margin. Colonies on Czapek's agar (CZ) 19–20 mm diam, superficial, radially sulcate, centrally convolute; margins irregular, deep; mycelia white (1A1); texture velutinous; sporulation sparse, greenish white (27A2); exudates clear, dispersed all over the colony; soluble pigments absent; reverse raw amber (5F8) to coffee (5F7) centrally, towards periphery amber yellow (4B6), white (1A1) at margin. Colonies on dichloran 18 % glycerol agar (DG18) 6 mm diam, deep; margin irregular, deep; mycelia white (1A1); texture butyrous; sporulation absent; exudates absent; soluble pigments absent, reverse white (1A1) entire. Colonies on yeast extract sucrose agar (YES) 26–28 mm diam, deep; highly sulcate, slightly convolute; margins irregular, deep; mycelia pale yellow (4A3); texture velutinous; sporulation sparse, greyish green (26C3) centrally, golden blonde (5C4) towards periphery; exudates absent; soluble pigments absent; reverse coffee (5F7) centrally, towards periphery greyish orange (5B4), yellowish white (2A2) at margin. Colonies on Creatine Sucrose agar (CREA) 8–9 mm diam, acid production absent.

Typus. India, Uttarakhand, Dehradun, N30°34'38" E77°99'96", 700 m a.s.l., from soil, 23 Mar. 2019, *G. Anand, K.C. Rajeshkumar & N. Ashtekar* (holotype preserved in metabolically inactive state AMH 10481; culture ex-type NFCCI 5424; ITS, LSU, *BenA*, *CaM* and *RPB2* sequences GenBank OQ355036, OQ449451, OQ362166, OQ361667, OQ361668; MycoBank MB 847860).

Notes — A megablast search of the *BenA* sequence of NFCCI 5424 against the NCBI GenBank nucleotide database revealed it belonged to *Penicillium* sect. *Exilicaulis* ser. *Restricta*, with *Penicillium arabicum* (GenBank KP016750; Identities = 391/397 (98 %), one gap (0 %)), *Penicillium kurssanovii* (GenBank KP016758; Identities = 387/397 (97 %), one gap (0 %)) and *Penicillium chalabudae* (GenBank KP016748; Identities = 387/397 (97 %), one gap (0 %)) as the closest hits. Phylogenetic analyses of series *Restricta* (see Suppl. material) resolved NFCCI 5424 as a new species, closely related to *P. cinereoatrum* and *P. heteromorphum*. Morphological comparisons between*, P. heteromorphum, P. sankaranii,* and *P. cinereoatrum* revealed that the novel species have intermediate stipes (from 6 µm vs 12 µm vs 60 µm) and has globose conidia with prominent spinulose ornamentation, compared to the spheroidal to subspheroidal conidia with smooth to finely roughened ornamentation of *P. cinereoatrum* (Chalabuda 1950) and globose to subglobose conidia with roughened ornamentation of *P. heteromorphum* (Kong & Qi 1988). *Penicillium* ser. *Restricta* now contains 14 accepted species (Houbraken et al. 2020), but is in need of a taxonomic revision as noted previously (Visagie et al. 2016a).

Colour illustrations. Collection site Dehradun, Uttarakhand, India. Monoverticillate conidiophores; conidia; colonies after 7 d at 25 ± 2 °C (CYA and MEA obverse and reverse, CREA obverse, CYAS obverse, CZA obverse, DG18 obverse). Scale bars =10 µm.

Supplementary material

FP1535-1 Combined phylogenetic tree.
FP1535-2 Single gene phylogenies.

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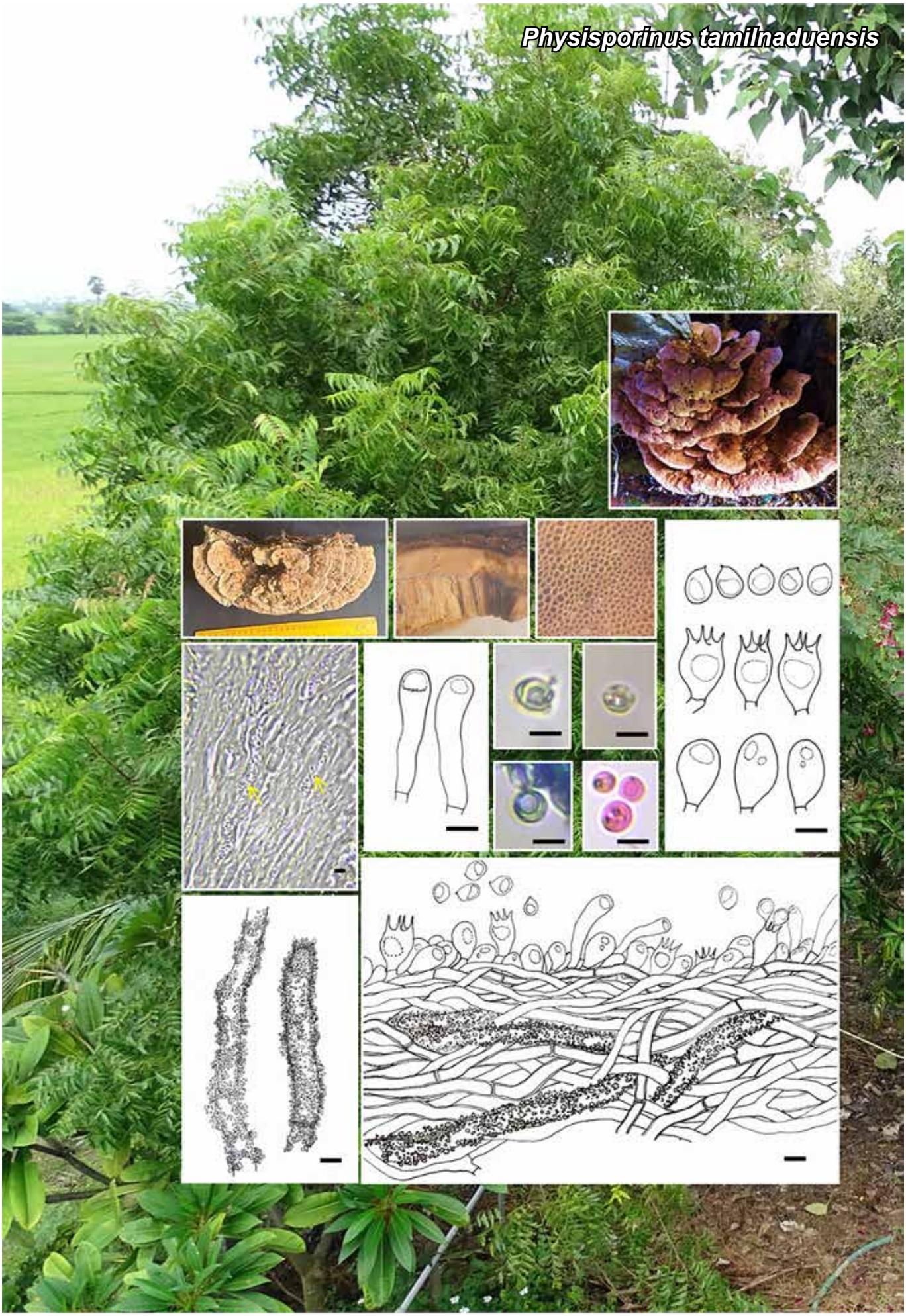
Physisporinus tamilnaduensis

Fungal Planet 1536 – 29 June 2023

Physisporinus tamilnaduensis Kaliyaperumal, Kezo & Bhat, *sp. nov.*

Etymology. The species epithet *tamilnaduensis* refers to the collection locality.

Classification — *Meripilaceae*, *Polyporales*, *Agaricomycetes*.

Basidiomata annual, clustered to imbricate, pileate, leathery when fresh, becoming hard and light when dry. *Pilei* dimidiate to elongated, projecting up to 13 cm long, 30 cm wide, and 1 cm thick at the base. Pileal surface glabrous, warted, weakly zonate, brownish orange (6C4; Kornerup & Wanscher 1981) towards the margin and light brown (6D5) towards attachment when fresh, becoming brownish orange (5C5) towards margin and brown (6E5) at the attachment when dry. *Margin* obtuse and white (6A1) when fresh, becoming yellowish white (4A2), sharp and incurved when dry. *Hymenial surface* light brown (6D5) when fresh, brown (6E5) when dry; pores round to angular, 6–8 per mm. *Context* duplex, upper context brown (6E5), lower context brownish orange (5C5) up to 4 mm thick. Tubes concolourous with the pore surface, up to 5 mm long. *Hyphal system* monomitic; hyphae simple septate, IKI-, moderately CB+, unchanged in KOH. *Context* hyphae hyaline, fairly thick-walled with a large lumen, rarely branched and frequently septate, slightly straight to flexuous, more or less interwoven, 2.5–5 µm diam. *Tramal* hyphae hyaline, thin- to slightly thick-walled with a wide lumen, occasionally branched, frequently simple septate, more or less straight, loosely interwoven, 2–3.3 µm diam. *Cystidia* present, embedded along the trama, coarsely encrusted, 40–100 µm and 4–7 µm wide; Cystidioles present project out from the trama, bearing a guttule at the apex, 28–35.5 × 4.5–7.25 µm. *Basidia* broadly clavate, bearing a large guttule, four sterigmata and a simple basal septum, 12.5–17.5 × 5–7.25 µm. *Basidioles* broadly clavate, 10–16.5 × 4.25–7.25 µm. *Basidiospores* broadly ellipsoid to subglobose, hyaline, thin-walled, smooth, bearing a large guttule, (4.3–)4.5–5.8(–6.0) × (3.8–)4.0–5.0(–5.5) µm (n = 30/2), IKI-, CB-, Q = 1.1 (Q range 1.1–1.23).

Habit & Distribution — On the trunk of *Azadirachta indica*, the collection site is located in Southern India.

Typus. India, Tamil Nadu, Chidambaram district, Chokkankollai, N11°30'02.1" E79°38'52.3", on the trunk of *Azadirachta indica* (*Meliaceae*), 31 Dec. 2022, *M. Kaliyaperumal* (holotype MUBL1045; ITS and LSU sequences GenBank OQ553779 and OQ553783; MycoBank MB 847833).

Additional materials examined. India, Tamil Nadu, Chidambaram district, Chokkankollai, N11°29'54.7" E79°38'47.3", on the trunk of *A. indica*, 31 Dec. 2022, *M. Kaliyaperumal* (isotype KDM01a, ITS and LSU sequence GenBank OQ553780 and OQ553784).

Notes — *Physisporinus tamilnaduensis* is characterised by its imbricate basidiomata, presence of encrusted cystidia, and subglobose to broadly ellipsoid basidiospores. Our new species, *P. tamilnaduensis,* shares similar characters with *P. crataegi* by having an incurved margin and pore size (6–8 per mm), monomitic hyphal system and broadly ellipsoid to subglobose basidiospores. However, the latter differs in having effused-reflexed basidiomata, absence of cystidia and smaller basidiospores ((4.0–)4.2–5.0(–5.2) × (3.0–)3.2–4.2 µm; Wu et al. 2017). *Physisporinus tamilnaduensis* shares similar characters with *P. lineatus*; similar pore size (6–9 per mm), monomitic hyphal system presence of encrusted cystidia but the latter differs in having effused-reflexed basidiomata, thin-walled, larger globose basidiospores (5–6 × 4–5 µm; Núñez & Ryvarden 2001). *Physisporinus cinereus* differs from our species by having an effused reflexed basidiocarp, bigger pores (5–6/mm) and globose basidiospores (5–4.2 µm diam; Núñez & Ryvarden 2001). Our observations on morpho-microscopic illustrations are consistent with the phylogenetic analyses. Both maximum likelihood (ML) and Bayesian inference (BI) analyses inferred from the combined dataset of ITS and nLSU of *Physisporinus* spp. revealed that *P. tamilnaduensis* formed a new lineage sister to *P. cinereus* and *P. crataegi* (0.98 BIPP / 83 % MLBS) with *P.* lineatus as nearest basal sister lineage (1 BIPP / 95 % MLBS) clade.

Physisporinus tamilnaduensis shares similar characters with *P. lavendulus* by having pileate basidiomata, incurved margin on drying, monomitic hyphae and presence of cystidia. However, the latter differs by having a smaller basidiocarp (projecting up to 2 cm tall, 5 cm wide and 5 mm thick), smaller pore size (9–10/mm), apically encrusted cystidia and smaller globose basidiospores ((4.1–)4.2–5.0(–5.1) × 4.0–5.0 µm; Wu et al. 2017). *Physisporinus sulphureus* differs from *P. tamilnaduensis* by having resupinate basidiomata and smaller thin-walled subglobose spores (4.0–5.0(–5.1) × (3.0–)3.5–4.0 µm; Dai & Dai 2018). *Physisporinus castanopsidis, P. rivulosu, P. roseus, P. subcrocatus* and *P. tibeticus* share a resupinate basidiocarp while *P. tamilnaduensis* differs by having imbricate pilei and larger basidiospores (Wu et al. 2017).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to Rigidoporus sp. (strain PY1757, GenBank MK659920; Identities = 566/568 (99 %), two gaps (0 %)), *Meripilus giganteus* (isolate 17, GenBank KU366500; Identities = 565/568 (99 %), two gaps (0 %)) and *Meripilus giganteus* (culture CBS 116.142, GenBank GQ355959; Identities = 565/568 (99 %), two gaps (0 %)). Closest hit using **LSU** sequence had highest similarity to *Physisporinus* sp. 4 (strain Cui 16903, GenBank MT309489; Identities = 973/1012 (96 %), four gaps (0 %)), *Physisporinus* sp. 4 (voucher Cui 16856, GenBank MT309488; Identities = 973/1012 (96 %), four gaps (0 %)) and *Physisporinus* sp. (voucher JV_0509_47, GenBank OM669988; Identities = 974/1013 (96 %), five gaps (0 %)).

Colour illustrations. Holotype collection site, India. Habitat; pilear surface; transvers section; pore surface; basidiospores in water, Melzer's, cotton blue and phloxine; camera lucida illustration; basidiospore, basidia, basidioles, cystidia, cystidioles and transvers section of tube. Scale bars = 5 µm.

Supplementary material

FP1536-1 Phylogenetic tree.

FP1536-2 Table. Species, strains and accession numbers of the specimens used in phylogenetic tree.

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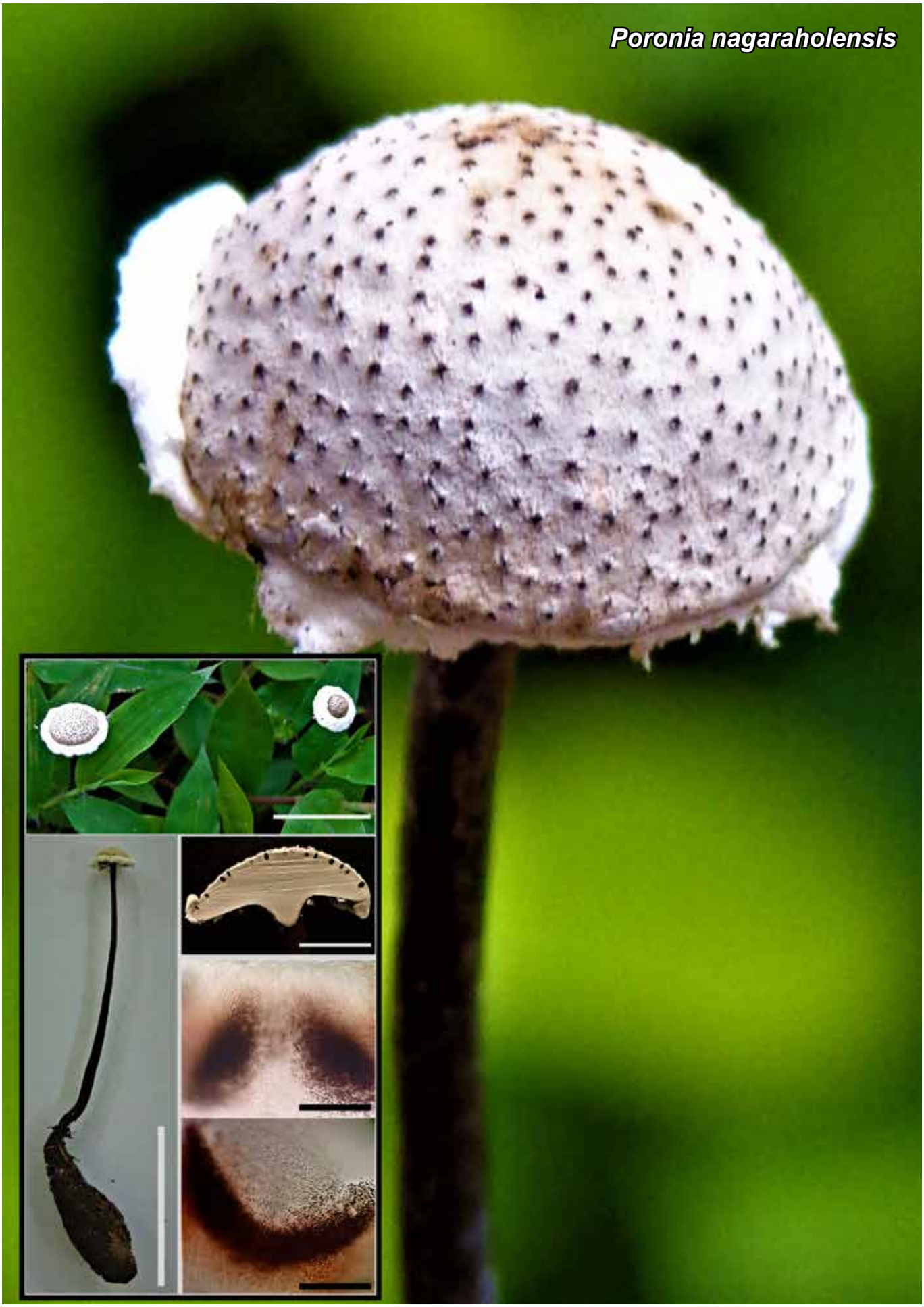

Poronia nagaraholensis

Fungal Planet 1537 – 29 June 2023

Poronia nagaraholensis Mahadevak., Sarma, D. Chalasani, A.R. Podile & Chandran., *sp.nov.*

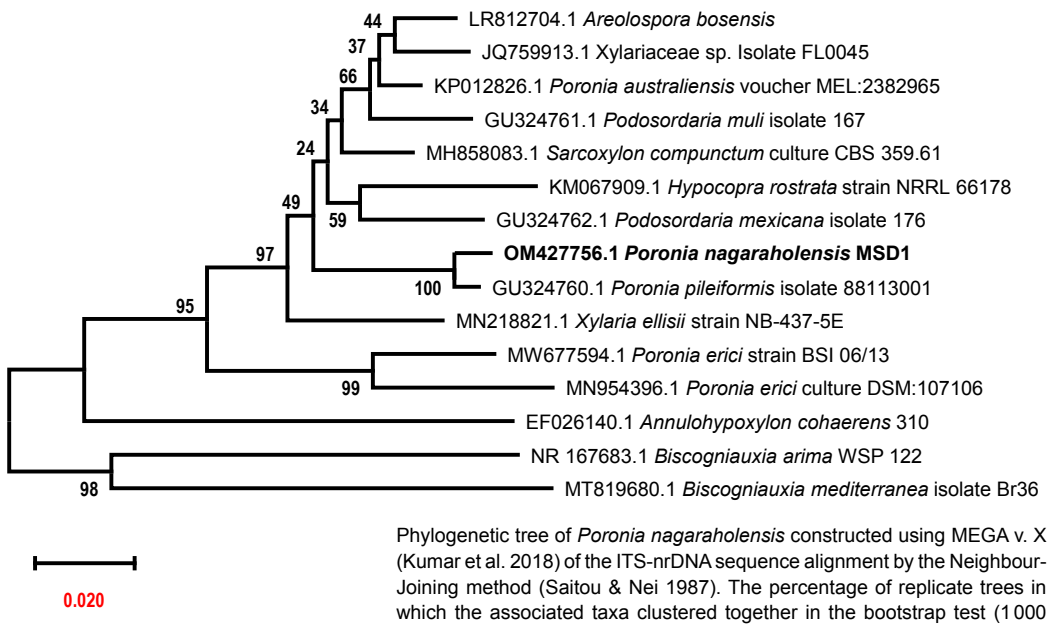
Etymology. Name refers to the place, Nagarahole, Madikeri, Karnataka, India, where this specimen was collected.

Classification — *Xylariaceae*, *Xylariales*, *Xylariomycetidae, Sordariomycetes.*

Stromata long, solitary, unbranched, (6.8–)10.2–22.46 (–24.8) cm × (1.4–)2.0–6.8(–9.2) mm; stromata attached to a rhizomorph, rhizomorph, (3.0–)4.2–12.2(–14.6) × (1.1–) 2.0–2.4(–3.2) cm; fertile part consisting of 0.8–1.3 cm broad head on the top of the stalk; dark brown at the base and whitish at the top with black papillate ostioles, stroma smooth, becomes hard on maturity. *Stroma* solid, filled with cream coloured matrix. *Perithecia* (450.0–)522.8–614.3(–708.0) × (395.0–)460.1–524.4(–586.0) µm, ovate with a tiny neck. *Asci* and *ascospores* not observed.

Typus. India, Karnataka, Madikeri, Nagarahole Wild Life Sanctuary, on elephant dung, 17 Sept. 2017, *S. Mahadevakumar, P.V.S.R.N. Sarma* & *C. Danteswari*, MSD1 (holotype AMH-10454; ITS and LSU sequences GenBank OM427756 and OP442524; MycoBank MB 844003).

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closesthits using the **ITS** sequence of MSD1 had highest similarity to *Poronia pileiformis* (WSP 88113001, GenBank GU324760; Identities = 468/497 (94 %), 18 gaps (3 %)), *Areolospora bosensis* (culture FMR 17563, GenBank LR812704; Identities = 421/450 (94 %), nine gaps (3 %)) and *Areolospora bosensis* (culture CBS 572.63, GenBank MH858360; Identities = 420/450 (93 %), 10 gaps (2 %)). Similarly, the closest hit using **LSU** region sequence of MSD1 had highest similarity to *Xylaria badia* (strain P5256, GenBank JQ862643, Identities = 1 211/1 234 (98.14 %), eight gaps (0 %)), *Hypocopra rostrata* (isolate NRRL 66178, GenBank KM067909, Identities = 1 206/1 231 (97.97 %), five gaps (0 %)), *Poronia punctata* (culture CBS 656.78, GenBank KY610496, Identities = 1 181/1 200 (98.42 %), four gaps (0 %)) and *Poronia erici* (isolate DSM 107106, GenBank MN954397, Identities = 1 173/1 191 (98.49 %), four gaps (0 %)). Morphologically, *P. nagaraholensis* has similar characters to *P. pileiformis* on the substrate it is associated with, and stipe and stromata. However, *P. nagaraholensis* is morphologically distinct from other known *Poronia* species (*P. punctata* and *P. pileiformis*) with respect to stromata and perithecia. *Poronia punctata* has a very short stalk and expanded fertile head, and quite larger than *P. nagaraholensis*. Similarly, *P. pileiformis* is has a smaller fertile head (4–6 mm diam) than *P. nagaraholensis* (8–13 mm diam). Due to lack of mature spore details for *P. nagaraholensis* and *P. punctata*, a comparative account on spore morphology was not possible, but the two species are phylogenetically distinct.



Phylogenetic tree of *Poronia nagaraholensis* constructed using MEGA v. X (Kumar et al. 2018) of the ITS-nrDNA sequence alignment by the Neighbour-Joining method (Saitou & Nei 1987). The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1 000 replicates) are shown next to the branches (Felsenstein 1985). The evolutionary distances were computed using the Kimura 2-parameter method (Kimura 1980) and are in the units of the number of base substitutions per site. This analysis involved 16 nucleotide sequences and a total of 2 124 positions in the final dataset. All ambiguous positions were removed for each sequence pair (pairwise deletion option). The phylogenetic position of *P. nagaraholensis* is indicated in **bold**. The alignment and trees are publicly available in 10.6084/m9.figshare.22255426.

Colour illustrations. Poronia nagaraholensis (holotype specimen AMH10454) growing on elephant dung in India. *Poronia nagaraholensis* samples appearance in top view; close-up view of sporocarp with attached rhizomorph; cross section of stromata showing perithecia; microscopic views of perithecia showing hypha and no spores were observed. Scale bars = 3 cm (top and left panel), 5 mm (free hand section of fertile cap), 100 µm (microscopic views).

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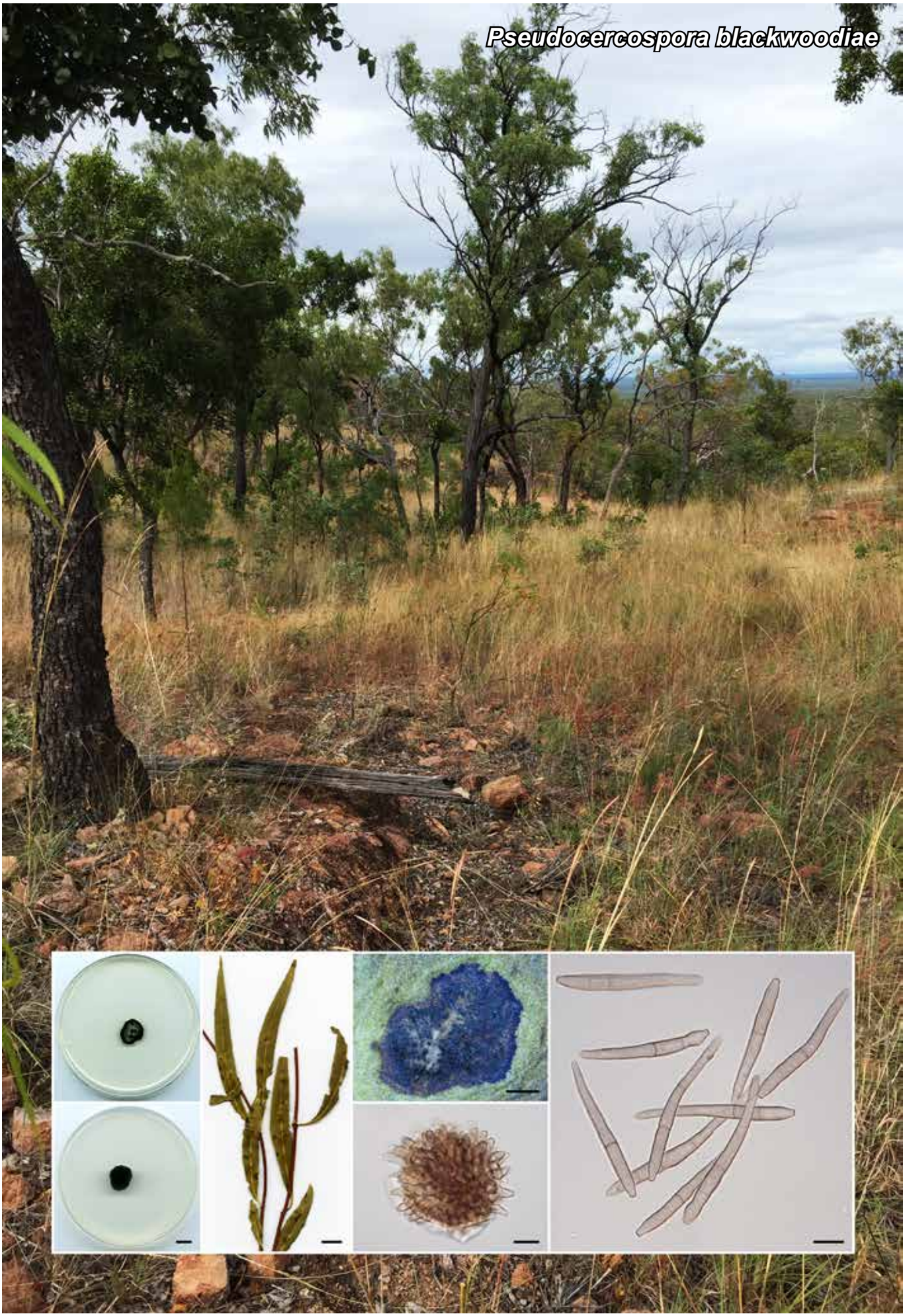
Pseudocercospora blackwoodiae

Fungal Planet 1538 – 29 June 2023

Pseudocercospora blackwoodiae Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

Etymology. Named after Dame Margaret Blackwood (1909–1986), a distinguished Australian botanist and plant geneticist. Margaret Blackwood lectured at the University of Melbourne for most of her career, becoming its first female deputy chancellor in 1980. In 1989, Margaret Blackwood was commemorated by *Phyllosticta blackwoodiae*, an Australian leaf-inhabiting fungus found on *Tristania grandis* in Western Australia.

Classification — *Mycosphaerellaceae*, *Mycosphaerellales*, *Dothideomycetes*.

Leaf spots on *Persoonia falcata*, amphigenous, irregular with rounded edges, blackish brown to dark brown, 2–7 mm diam. *Mycelium* internal. *Caespituli* amphigenous, punctiform, dense, dark grey to black, with masses of conidia. *Stromata* epidermal, erumpent, 40–60 µm diam, brown. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* densely situated on the upper part of stromata, straight, subcylindrical to obpyriform, unbranched, 8–13 × 4–6 µm, subhyaline to pale brown, smooth, rounded at the apex, with unthickened loci. *Conidia* solitary, obclavate, straight or curved, 35–75 × 4–5 µm, (2–)3–4(–5)-septate, pale brown, smooth to finely roughened, rounded at the apex, obconically truncate at base; hila unthickened, neither darkened nor refractive, 2 µm diam.

Culture characteristics (25 °C, 7 d, in darkness) — Colonies on potato dextrose agar (PDA) after 4 wk 15–18 mm diam, compact with sparse aerial mycelium, smooth lobate margins, olivaceous black with patches of scant glaucous grey mycelium; reverse olivaceous black.

Typus. Australia, Queensland, Mount Surprise, from leaf spot of *Persoonia falcata* (*Proteaceae*), 21 Apr. 2021, *K.L. Bransgrove, M.D.E. Shivas & R.G. Shivas* (BRIP 72387b preserved as metabolically inactive culture, ITS, *actA* and *tef1α* sequences GenBank OP584786, OP559500 and OP559501, MycoBank MB 845794).

Colour illustrations. Woodland in northern Queensland. Colony surfaces (upper and reverse) on PDA; leaf spots on *Persoonia falcata*; leaf spot with caespituli; stroma with conidiogenous cells; conidia. Scale bars = 1 cm; 1 cm; 1 mm, 10 µm; 10 µm.

Notes — *Pseudocercospora blackwoodiae* is distinguished from *P. longispora* (ex-type strain CBS 122470) by sequence comparison of the ITS region (GenBank GU269734; Identities 479/500 (96 %), five gaps (1 %); unique nucleotide at positions 185(T), 216(A), 219(T), 245(A), 249(G), 305(T), 493(G), 509(T), 516(T), 537(T), 548(T), 558(T), 596(A), 597(T), 598(A), 618(T)), *actA* (GenBank GU320436; Identities 191/209 (91 %), two gaps; unique nucleotide at positions 49(T), 53(T), 67(G), 69(G), 70(C), 76(G), 85(T), 136(G), 141(T), 158(C), 160(G), 170(G), 176(G), 177(C), 198(C)) and *tef1α* (GenBank GU384447; Identities 262/322 (81 %), 16 gaps (4 %); unique nucleotide at positions 13(T), 15(C), 17(A), 20(A), 22(T), 23(A), 28(C), 32(T), 40(G), 48(G), 56(G), 62(C), 66(C), 72(C), 89(A), 129(G), 151(T), 152(C), 154(C), 171(C), 191(T), 194(T), 198(T), 202(T), 207(A), 215(C), 217(C), 219(T), 223(T), 235(T), 236(A), 242(C), 244(T), 245(T), 247(C), 248(G), 251(C), 253(A), 254(G), 256(G), 258(A), 264(G), 267(T), 300(T)). *Pseudocercospora blackwoodiae* is distinguished from *P. musae* (strain CBS 116634) by sequence comparison of the ITS region (GenBank EU514265; Identities 482/509 (95 %), five gaps; unique nucleotide at positions 189(G), 216(A), 219(T), 236(A), 245(A), 249(G), 280(A), 293(T), 295(G), 317(A), 493(G), 509(T), 516(T), 517(T), 528(T), 529(T), 537(T),548(T), 578(A), 585(T), 596(A), 598(A)), *actA* (GenBank GU320449; Identities 193/212 (91 %), two gaps; unique nucleotide at positions 49(T), 53(T), 66(C), 67(G), 69(G), 70(C), 76(G), 84(A), 85(T), 136(G), 140(A), 141(T), 158(C), 160(G), 170(G), 176(G), 177(C)), and *tef1α* (GenBank GU384459; Identities 263/324 (81 %), 20 gaps (6 %); unique nucleotide at positions 13(T), 15(C), 17(A), 20(A), 22(T), 28(C),32(T), 40(G), 44(G), 48(G), 56(G), 62(C), 66(C), 88(A), 129(G), 151(T), 152(C), 154(C), 171(C), 191(T), 194(T), 195(G), 197(C), 202(T), 207(A), 215(C), 217(C), 219(T), 223(T), 235(T), 240(G), 245(T), 246(T), 248(G), 250(A), 252(C), 256(G), 258(A), 264(G), 267(T), 300(T)). Morphologically, *P. blackwoodiae* shares some morphological characters with *P. musae*; and has shorter conidia than *P. longispora* (cf. 82–120 µm) (Arzanlou et al. 2008).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using ***actA*** sequence are *P. subtorulosa* (strain CBS 117230, GenBank GU320518, Identities 202/212 (95 %), one gap), *P. acericola* (strain CBS 122279, GenBank GU320358, Identities 200/212 (94 %), one gap) and *P. nandinae* (strain MAFF 237633, GenBank KX462568, Identities 199/212 (94 %), no gap). The closest hits using the ***tef1α*** sequence are *P. jahnii* (strain CPC 24235, GenBank KM393284, Identities 431/516 (84 %), 23 gaps (4 %)), *P. parapseudarthriae* (strain CBS 137996, GenBank KJ869238, Identities 431/517 (83 %), 21 gaps (4 %)) and *P. xanthocercidis* (strain CBS 131593, GenBank JQ325005, Identities 428/516 (83 %), 18 gaps (3 %)).

Supplementary material

FP1538 & FP1539 Phylogenetic tree.

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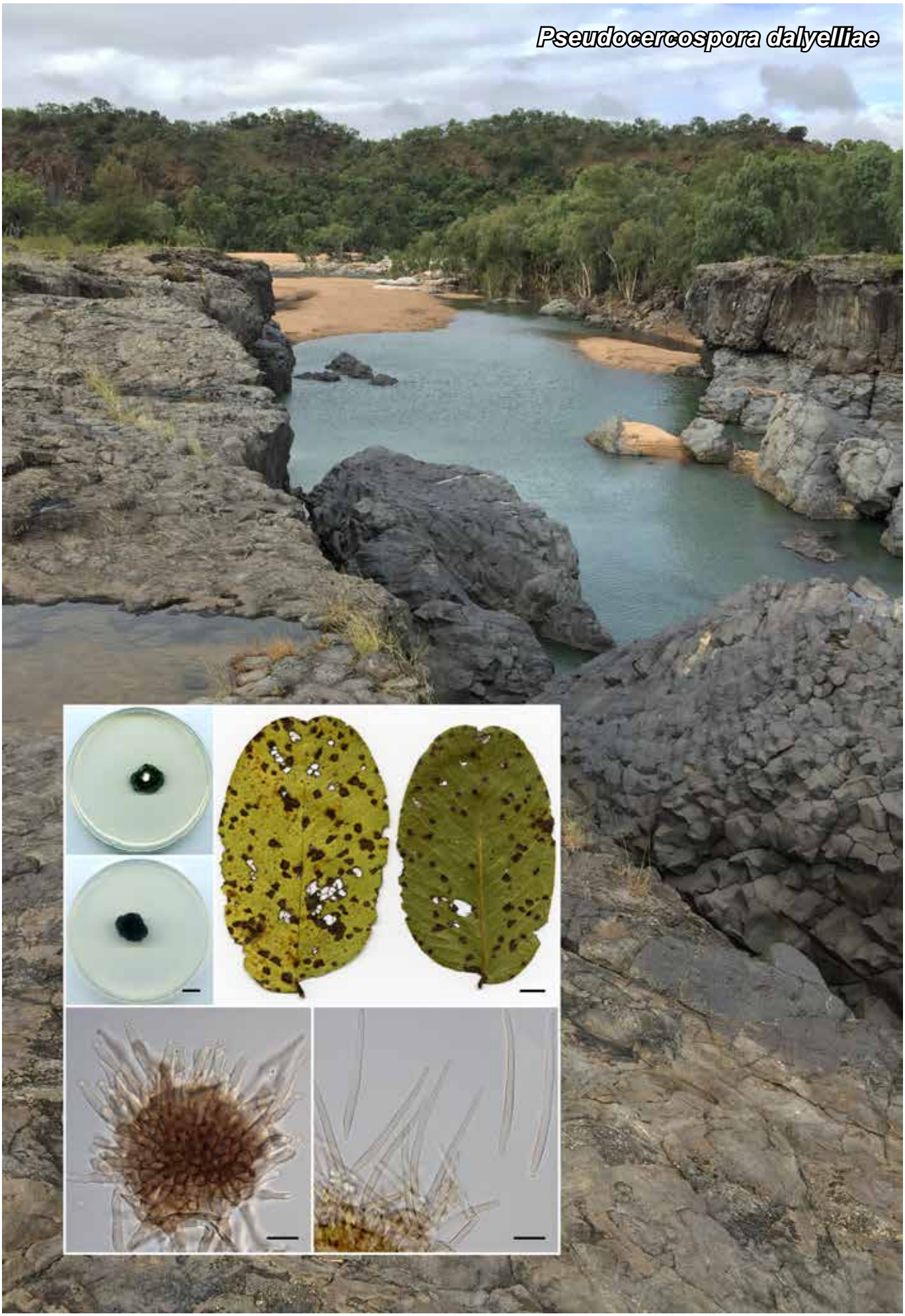
Pseudocercospora dalyelliae

Fungal Planet 1539 – 29 June 2023

Pseudocercospora dalyelliae Y.P. Tan, Bishop-Hurley & R.G. Shivas, *sp. nov.*

Etymology. Named after Elsie Jean Dalyell (1881–1948), a pioneering Australian medical doctor. In 1912, Elsie Dalyell became the first Australian woman to receive the Beit Memorial Fellowship for Medical Research, which took her to the Lister Institute of Preventative Medicine in London, where she studied gastroenterology in children. She left the institute when World War I broke out in 1914 and applied for service with the Royal Army Medical Corps but was rejected on the grounds that she was a woman. She then volunteered with the Serbian Relief Fund during the typhus epidemic in Macedonia. Subsequently, she served on the Western Front in an all-female medical unit of the Scottish Women's Hospital. In 1916, Elsie Dalyell joined the Royal Army Medical Corps when army policy changed. In 1923, she returned to Australia as an internationally renowned pathologist.

Classification — *Mycosphaerellaceae*, *Mycosphaerellales*, *Dothideomycetes*.

Leaf spots on *Senna alata*, amphigenous, irregular, often bordered by veins, dark brown, 3–5 mm. *Mycelium* internal. *Caespituli* amphigenous, punctiform, dense, dark grey to black, with masses of conidia. *Stromata* epidermal, erumpent, 30–80 µm diam, brown. *Conidiophores* in loose fascicles, subcylindrical, swollen at base, unbranched, straight to sinuous, subcylindrical, 25–50 × 3–4 µm, subhyaline to pale brown, 0–3-septate, smooth. *Conidiogenous cells* terminal, unbranched, subcylindrical and sometimes geniculate near the apex, 10–20 × 2.5–4 µm, rounded to truncate at apex, smooth. *Conidia* solitary, subcylindrical to narrowly obclavate, straight or curved, 30–80 × 3.5–4.5 µm, 3–4-septate, pale brown, smooth, rounded at the apex, gradually tapered towards the truncate base; hila unthickened, neither darkened nor refractive, 1.5 µm diam.

Culture characteristics (25 °C, 7 d, in darkness) — Colonies on potato dextrose agar (PDA) after 4 wk, 15–25 mm diam, compact with sparse aerial mycelium, smooth lobate margins, olivaceous black with patches of grey aerial mycelium; reverse olivaceous black.

Typus. Australia, Queensland, Georgetown, leaf spot of *Senna alata* (*Fabaceae*), 22 Apr. 2021, *K.L. Bransgrove, T.S. Marney, M.J. Ryley, S.M. Thompson, M.D.E. Shivas & R.G. Shivas* (holotype preserved as metabolically inactive culture BRIP 72389f; culture ex-type BRIP 72389f; ITS, *actA* and *tef1α* sequences GenBank OP584787, OP559502 and OP559503; MycoBank MB 745795).

Notes — *Pseudocercospora dalyelliae* is distinguished from *P. zanthoxyli* (strain CPC 10065 as *P. xanthoxyli*) by sequence comparison of the ITS region (GenBank GU269832; Identities 493/501 (98 %), one gap; unique nucleotide at positions 254(A), 255(C), 281(T), 282(T), 522(G), 523(T), 626(A)), *actA* (GenBank GU320536; Identities 184/202 (91 %), four gaps (1 %); unique nucleotide at positions 16(C), 49(C), 51(G), 53(T), 60(T), 61(T), 88(A), 93(T), 139(G), 144(A), 153(C), 154(T), 159(A), 191(T)) and *tef1α* (GenBank GU384544; Identities 270/306 (88 %), nine gaps (2 %); unique nucleotide at positions 10(A), 20(A), 33(T), 42(A), 55(T), 116(G), 164(C), 165(T), 175(A), 187(G), 190(A), 203(C), 227(T), 230(A), 235(C), 246(C), 248(G), 250(C), 251(A), 254(A), 257(G), 260(A), 263(T), 268(T), 279(T), 285(T), 294(C)).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest relevant hits using the **ITS** region are *P. fuligena* (strain CPC 12296, GenBank GU214675, Identities 678/680 (99 %), two gaps), *P. chengtuensis* (strain CPC 10785, GenBank GU214672, Identities 678/680 (99 %), two gaps) and *P. atromarginalis* (strain CPC 11372, GenBank GU214671, Identities 677/680 (99 %), two gaps). The closest relevant hits using the ***actA*** sequence are *P. amelanchieris* (strain MAFF 237782, GenBank KX462550, Identities 189/199 (95 %), two gaps (1 %)), *P. atromarginalis* (strain CCTU 1052, GenBank KM452827, Identities 188/198 (95 %), no gap) and *P. puderi* (strain MUCC 906, GenBank GU320467, Identities 189/199 (95 %), two gaps (1 %)). The closest hits using the ***tef1α*** sequence are *P. jagerae* (strain BRIP 58549, GenBank KM055438, Identities 441/501 (88 %), 12 gaps (2 %)), *P. diplusodonis* (strain CPC 25179, GenBank KT290189, Identities 441/505 (87 %), 14 gaps (2 %)) and *P. perae* (strain CPC 25171, GenBank KT290186, Identities 440/505 (87 %), 15 gaps (2 %)).

Colour illustrations. Copperfield Gorge, northern Queensland, Australia. Colony surfaces (upper and reverse) on PDA; leaf spots on lower surface (left) and upper surface (right) of *Senna alata*, stroma with conidiogenous cells; conidia. Scale bars = 1 cm (colonies and leaves), 10 µm (micromorphology).

Supplementary material

FP1538 & FP1539 Phylogenetic tree.

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Scytalidium synnematicum

Fungal Planet 1540 – 29 June 2023

Scytalidium synnematicum G.G. Barreto & Gusmão, *sp. nov.*

Etymology. Name refers to the formation of synnemata.

Classification — *Helotiaceae*, *Helotiales*, *Leotiomycetes*.

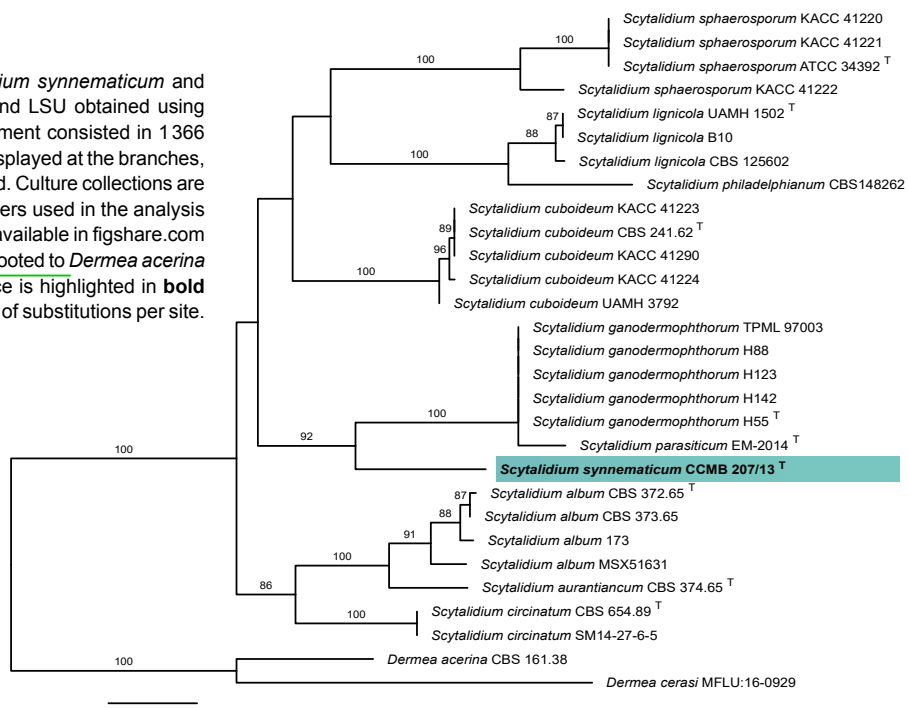
Conidiomata determinate, synnemata; mycelium mostly immersed. *Synnemata* solitary, somewhat cylindric, straight, base formed by inconspicuous stroma-like structures composed by pale brown rounded cells that give rise to a fertile hypha, 340–500 × 35–70 µm. *Fertile hyphae* simple, straight or flexuous, smooth, cylindrical, unbranched, initially pigmented, developing in parallel synnemata, producing a terminal dry mass of hyaline arthroconidia. *Conidia* thallic-arthric, schizogenous, cylindrical, smooth, aseptate, dry, guttulate, hyaline, 6.2–7.5 × 2.5–3.5 µm.

Culture characteristics — Colonies on cornmeal carrot agar (CMCA; 30 g of cornmeal, 30 g of carrot, 13 g of agar for 1 L of distilled water) flat, with an entire edge, spreading and lacking aerial mycelium, reaching 50 mm diam after 2 wk at 25 °C. The surface and reverse of CMCA pale brown. Sporulation abundant once synnemata produced. Synnemata on water agar initially hyaline, then becoming light purple, and when mature, turning pale brown.

Typus. Brazil, Manaus, Amazonas, Reserva Florestal Adolpho Ducke, on dead twigs of unidentified plant, 3 Mar. 2013, *B.M.P. Ottoni* (holotype HUEFS 252282; culture ex-type CCMB 207/13; ITS and LSU sequences GenBank OQ430525 and OQ430526; MycoBank MB 847900).

Notes — *Scytalidium synnematicum* is closely related to *S. ganodermophtorum* and *S. parasiticum*, which are both parasites of *Ganoderma* spp. The former was first described occurring on *G. lucidum* in South Korea and has hyaline to yellow, rectangular to cylindrical arthroconidia, 1.5–4 × 1.5–3 µm (Kang et al. 2010). The latter was found parasitising *G. boninense* in Malaysia and has hyaline to pale yellow, smooth, cuboidal to oblong or cylindrical arthroconidia, 1.7–6.6 × 1.3–2.7 µm (Goh et al. 2015). *Scytalidium synnematicum* can be distinguished from both species based on its saprobic habitat, production of synnemata, and the dimensions of its hyaline arthroconidia. Moreover, phylogenetic data confirms that *S. synnematicum* is a distinct species. The type species, *Scytalidium lignicola*, is morphologically similar in terms of arthroconidial dimensions (5–8 × 2 µm) but has 0–1-septate arthroconidia and produces chlamydospores (Ellis 1971). Additionally, DNA data places *S. lignicola* in a separate clade.

Based on a megablast search of NCBIs GenBank nucleotide database, the **ITS** sequence had the highest similarity to *S. ganodermatophtorum* (strain UAMH 10320, GenBank NR_137727.1; Identities = 471/520 (91 %), 16 gaps (3 %)), *Scytalidium circinatum* (strain CBS 654.89, GenBank NR_160180.1; Identities = 471/523 (90 %), 18 gaps (3 %)) and *S. lignicola* (strain UAMH 1502, GenBank NR_121314.1; Identities = 478/538 (89 %), 18 gaps (3 %)). The closest hits using the **LSU** sequence were *S. lignicola* (strain DSM 105466, GenBank MG815782.1; Identities = 794/813 (98 %), no gaps), *Scytalidium candidum* (strain 3C, GenBank MG018250.1; Identities = 787/813 (97 %), no gaps) and *S. ganodermatophtorum* (strain CBS 187.69, GenBank MG018251.1; Identities = 782/813 (96 %), no gaps).



Maximum Likelihood phylogenetic tree of *Scytalidium synnematicum* and closely related species based on combined ITS and LSU obtained using IQ-TREE v. 1.6.12 (Nguyen et al. 2015). The alignment consisted in 1366 nucleotides. Bootstrap support values > 70 % are displayed at the branches, and values > 95 % are considered strongly supported. Culture collections are indicated for all species, GenBank accession numbers used in the analysis are in the supplementary table and the alignment is available in figshare.com (doi: 10.6084/m9.figshare.22094654). The tree was rooted to *Dermea acerina* and *Dermea cerasi*. The newly generated sequence is highlighted in **bold** font. The scale bar represents the expected number of substitutions per site.

Colour illustrations. *Scytalidium synnematicum* growing inside a soft twig at Reserva Florestal Adolpho Ducke, Brazil (photo credit J.D.P. Bezerra). Conidiomata growing on natural substrate, with conidiophores disarticulating to form arthroconidia. Scale bars = 100 µm (synnema), 20 µm (all others).

Supplementary material

FP1540 Table. Species, strains and accession numbers of the specimens used in phylogenetic tree.

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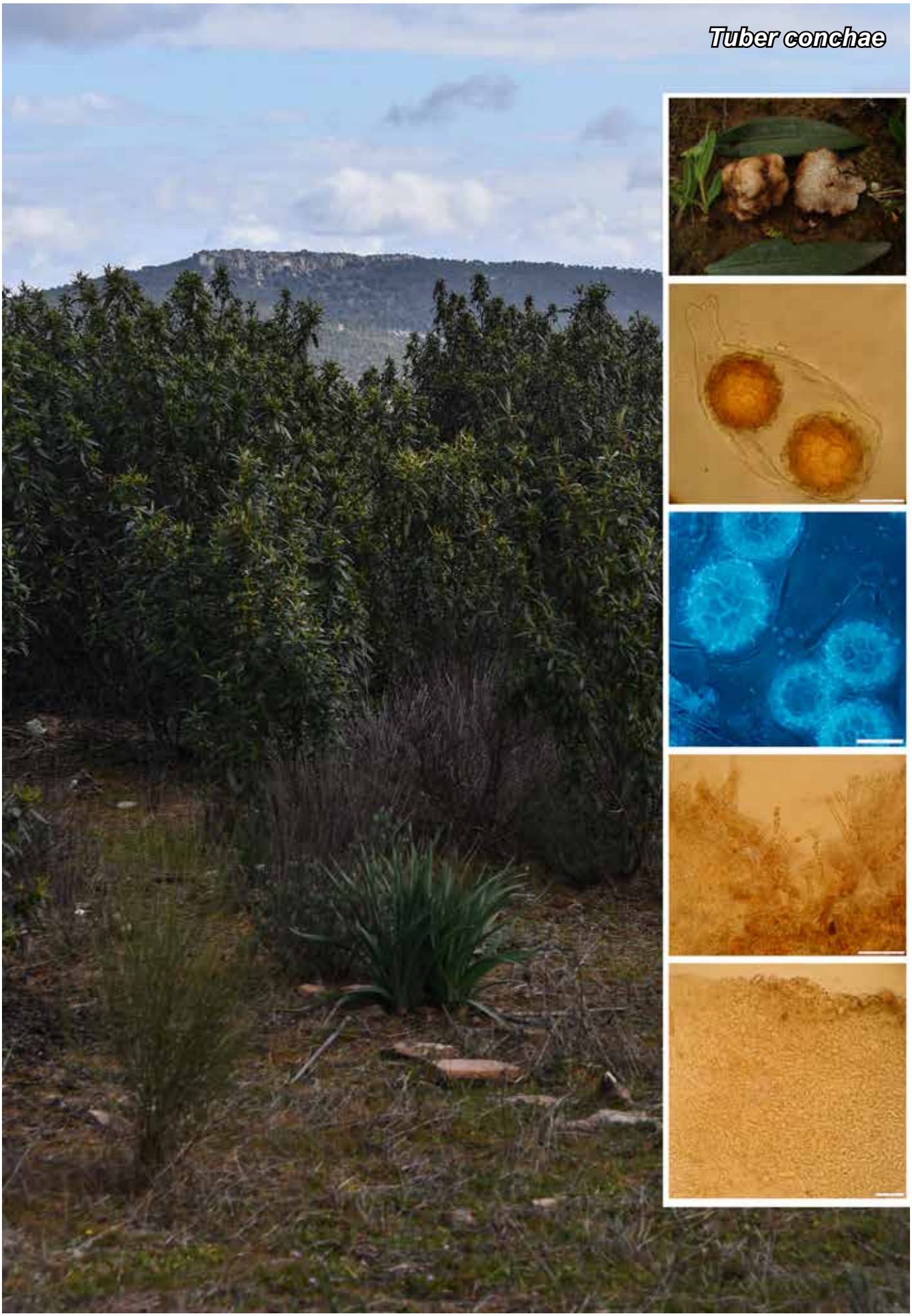
Tuber conchae

Fungal Planet 1541 – 29 June 2023

Tuber conchae M. Romero & P. Alvarado, *sp. nov*.

Etymology. The epithet refers to Ms. Concha Martín, wife of the first author, one of the collectors of the holotype.

Classification — *Tuberaceae*, *Pezizales*, *Pezizomycetes*.

Ascomata hypogeous, 1–4 cm diam, subglobose to irregularly lobulate or tuberculiform, tough, surface slightly pubescent, beige to light brown in colour with whitish areas, turning to dark brown in age. *Gleba* marbled, with elongated greyish white fertile areas that turn pale to dark brown with age, separated by short and thick white sterile veins. *Odour* weak in young specimens, strongly unpleasant (goat-like) in mature samples. *Peridium* thin, similar in colour to the surface, 200–300 µm thick, composed of: 1) external suprapellis with hyphal tips and some cystidia, 12–30 × 1.5–2 µm, straight, septate, inflated at septa, some of them with acute tips, sometimes forming a palisade, others crushed by plates of dark brown pigment; and 2) an underlying pellis arranged as a prosenchyma, composed of interwoven short hyphal elements, 2–4 µm diam, parallel to the surface, septate. *Asci* strongly dextrinoid (young ones), mostly pyriform with a long stalk (100–130 × 42–45 µm, including stalk), or else ovoid to subglobose (80–90 × 75–83 µm, including stalk), containing (1–)2–3(–4) ascospores. *Ascospores* golden yellow to pale brown in water, dextrinoid (immature ones), subglobose to broadly ellipsoid, some oculiform in immature asci, (27.5–)30.9–40.2(–45.9) × (23.4–)25.4–37.2(–41.5) µm, Q = 1–1.3(–1.4), M_e = 35.5 × 31.6 µm, Q_e = 1.1 (n = 25, measurements including spore ornaments), ornamented with 3–5 µm high spines forming a polygonal reticulum, often with 6–8 µm hexagonal alveoli, 3–5 in number across the spore diameter.

Distribution — Currently known only from acidic soils of central-western Spain, sporulating isolated or in small groups underground, between February and May, in clear areas near *Cistus ladanifer* plants.

Typus. Spain, Extremadura, Badajoz, Quintana de la Serena, Sierra de los Vuelos, soil near *Cistus ladanifer* (*Cistaceae*), 22 Apr. 2018, *M. Romero & C. Martín*, MRG486 (holotype AH49384; ITS and LSU sequences GenBank OQ565276 and OQ565275; MycoBank MB 847835).

Additional materials examined. ***Tuber conchae***. Spain, Extremadura, Badajoz, Quintana de la Serena, Fuente Quemada, near *Cistus ladanifer* and *Genista scorpius*, 10 May 2018, *M. Romero*, MRG505 (ITS sequence GenBank OQ565277). ***Tuber lacunosum.*** Spain, Extremadura, Badajoz, Quintana de la Serena, soil under *Tuberaria gutatta* and *Retama sphaerocarpa*, 19 Apr. 2015, *M. Romero*, MRG358 (ITS sequence GenBank OQ565279); ibid., 12 Apr. 2021, *M. Romero*, MRG692 (ITS sequence GenBank OQ565280); ibid., soil under *Tuberaria gutatta*, *Quercus ilex* and *Retama sphaerocarpa*, 21 Apr. 2022, *M. Romero*, MRG762 (ITS sequence GenBank OQ565281); ibid., *Tuberaria gutatta*, *Quercus ilex* and *Cistus ladanifer*, 12 May 2018, *M. Romero*, MRG498 (ITS sequence GenBank OQ565282). ***Tuber gennadii***. Spain, Extremadura, Badajoz, Quintana de la Serena, soil under *Tuberaria gutatta*, *Quercus ilex* and *Retama sphaerocarpa*, 7 May 2018, *M. Romero*, MRG496 (ITS sequence GenBank OQ565278).

Notes — *Tuber conchae* is a whitish truffle of the /gennadii clade, characterised by its subglobose to irregularly lobulate or tuberculiform ascomata, 1–4 cm diam, where the marbled gleba does not crack with age. It has a prosenchymatic pellis, globose or broadly ellipsoid ascospores, a strong unpleasant goat-like odour, and it seems to sporulate near *Cistus ladanifer* in acidic soils. According to BLAST results, ITS rDNA sequences of *T. conchae* are 84–92 % similar to those of *T. gennadii*, *T. lacunosum* and *T. lucentum*. Morphologically, *T. conchae* differs from *T. gennadii* (Chatin 1896, Montecchi & Sarasini 2000, Alvarado et al. 2012), because the latter has smaller (0.5–2 cm diam) and globose or subglobose ascomata (rarely wrinkled or lobulated), develops long cracks or locules in the gleba with age, and is probably associated to a different host plant (*Tuberaria guttata*). *Tuber lacunosum* (Mattirolo 1900) is also associated to *Tuberaria guttata*, has minute isolated locules in the gleba, and a pseudoparenchymatic pellis. *Tuber lucentum* (Crous et al. 2019b) produces minute globose ascomata, and grows in basic soils associated with *Helianthemum violaceum*, *H. syriacum* and *Fumana thymifolia*. Other whitish *Tuber* species resembling *T. conchae* can be found in Extremadura, but not in the same habitat (*Cistus ladanifer*). *Tuber davidlopezii* (Crous et al. 2022), which belongs to the /maculatum clade, has smaller ascomata with a two-layered peridium (the most external one pseudoparenchymatic), smaller globose to subglobose ascospores, and grows in dehesas, probably associated to *Quercus ilex* subsp. *ballota*. Finally, *T. lusitanicum* (Crous et al. 2020a), another member of the /maculatum clade, has also a two-layered peridium, including a pseudoparenchymatic external layer formed by globose to subangular thick-walled elements giving rise to external hairs. It is also associated with *Quercus* spp. in dehesa formations.

Colour illustrations. Spain, Extremadura, Badajoz, Quintana de la Serena, Mediterranean maquis with *Cistus ladanifer* and *Retama sphaerocarpa* where the holotype of *Tuber conchae* was found. Ascoma of the holotype; ascus in water; ascospores in KOH; suprapellis in water; pellis in water. Scale bars = 20 µm.

Supplementary material

FP1541 Phylogenetic tree.

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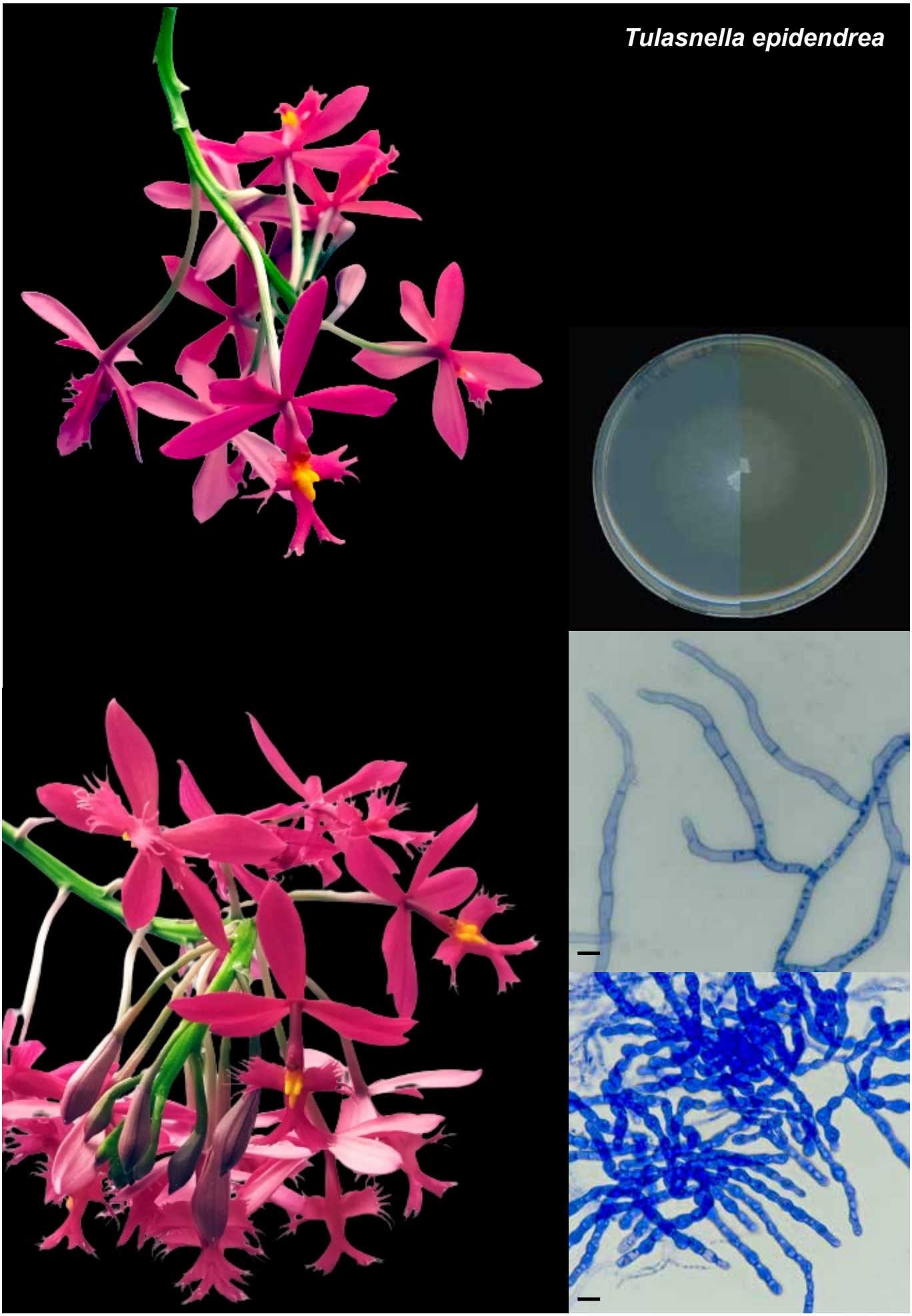

Tulasnella epidendrea

Fungal Planet 1542 – 29 June 2023

Tulasnella epidendrea Nkomo, Hammerb., B.D. Wingf. & T. Bose, *sp. nov.*

Etymology. Name refers to the orchid genus *Epidendrum*, the roots of *Epidendrum* × *obrienianum* yielded both isolates.

Classification — *Tulasnellaceae*, *Cantharellales*, *Agaricomycetes*.

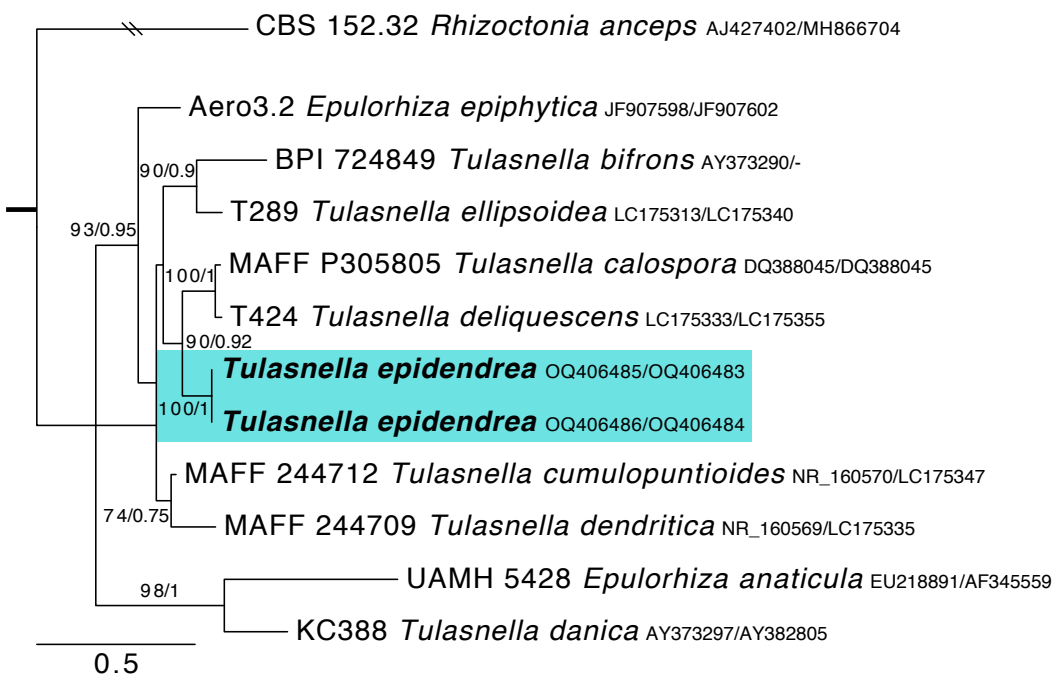
Hyphae smooth, septate, compartments measuring 25–50(–75) × 5–7.5(–9.3) µm, cylindrical, thin-walled, hyphal anastomosis rare; septa often slightly constricted, hyphae branched; branches mostly at right angles, arising below the septa or from the middle of the compartment, base of branch minutely constricted; hyphae lacking clamp connections; terminal cells of hyphae short, often bulbous above the septa, measuring 20–27.5 (–32.5) × 6.25–12.5 µm, numerous dark stain storage bodies in the older hyphae; monilioid cells, catenulate, caespitose; each cell doliiform in shape, walls slightly thicker than hyphae, with one large (often 2–3) guttules, measuring 12.5–20.3(–27.5) × 10–14.5(–16.2) µm. *Sexual morph* not observed.

Culture characteristics — On half strength potato dextrose agar (PDA), colony off white in colour (top and reverse; Rayner 1970), compact, flat, radiating, margin filamentous, mycelia mostly submerged, with mycelial knots on older cultures (21 d or older), growth rate 5.8 ± 0.2 mm/d at 25 °C. On malt extract agar (MEA), similar to 1/2 PDA except the fungus forms concentric growth rings, growth rate 4.6 ± 0.1 mm/d at 25 °C.

Typus. South Africa, Gauteng Province, Pretoria, isolated from the roots of *Epidendrum* × *obrienianum* (*Orchidaceae*), 2022, *T. Nkomo* (holotype PREM 63347; culture ex-type CMW 60269 = CMW-IA 1199; ITS and LSU sequences GenBank OQ406485 and OQ406483; MycoBank MB 847501).

Additional materials examined. South Africa, Gauteng Province, Pretoria, isolated from the roots of *Epidendrum* × *obrienianum*, 2022, *T. Nkomo*, culture CMW 60270 = CMW-IA 1200, ITS and LSU sequences GenBank OQ406486 and OQ406484.

Notes — *Tulasnella epidendrea* emerged as the sister clade to *T. calospora* and *T. deliquescens* in the ITS, LSU and concatenated phylogenetic trees. There is currently a taxonomic disagreement between these two species. *Tulasnella calospora* and *T. deliquescens* are likely synonymous (Roberts 1999, Suárez et al. 2006, Linde et al. 2017). We aligned many ITS and LSU sequences from both species. There were a few single-base-pair polymorphisms between the isolates of either species, but they were inconsistent. *Tulasnella epidendrea*, however, differs significantly from *T. calospora* and *T. deliquescens* in the ITS and LSU gene regions, as well as in morphology. For example, we found no sexual reproductive structures in *T. epidendrea*, and the shape of monilioid cells differs significantly across these fungi. Regardless, all of these species have been recognised as orchid symbionts.



The maximum likelihood (ML) tree of selected fungal species from *Tulasnellaceae* was constructed using IQ-TREE v. 1.6.12 (Minh et al. 2020) using the concatenated dataset, ITS and LSU with 500 bootstrap replicates. Bayesian analysis of the dataset was done using MrBayes v. 3.2.7a (Huelsenbeck & Ronquist 2001). *Rhizoctonia anceps* served as the outgroup. Branch labels indicate ML bootstrap support values / Bayesian posterior probabilities. Only bootstrap support values ≥ 70 % and posterior probability above ≥ 0.80 are shown. Isolates recovered in this study are in boldface and highlighted in blue. GenBank accession numbers are listed as suffixes after each taxon (ITS/LSU).

Colour illustrations. Inflorescences of *Epidendrum* × *obrienianum*. Colony morphology of *Tulasnella epidendrea* on 1/2 PDA (left) and 2 % MEA (right); mycelia; monilioid cells. Scale bars = 10 µm.

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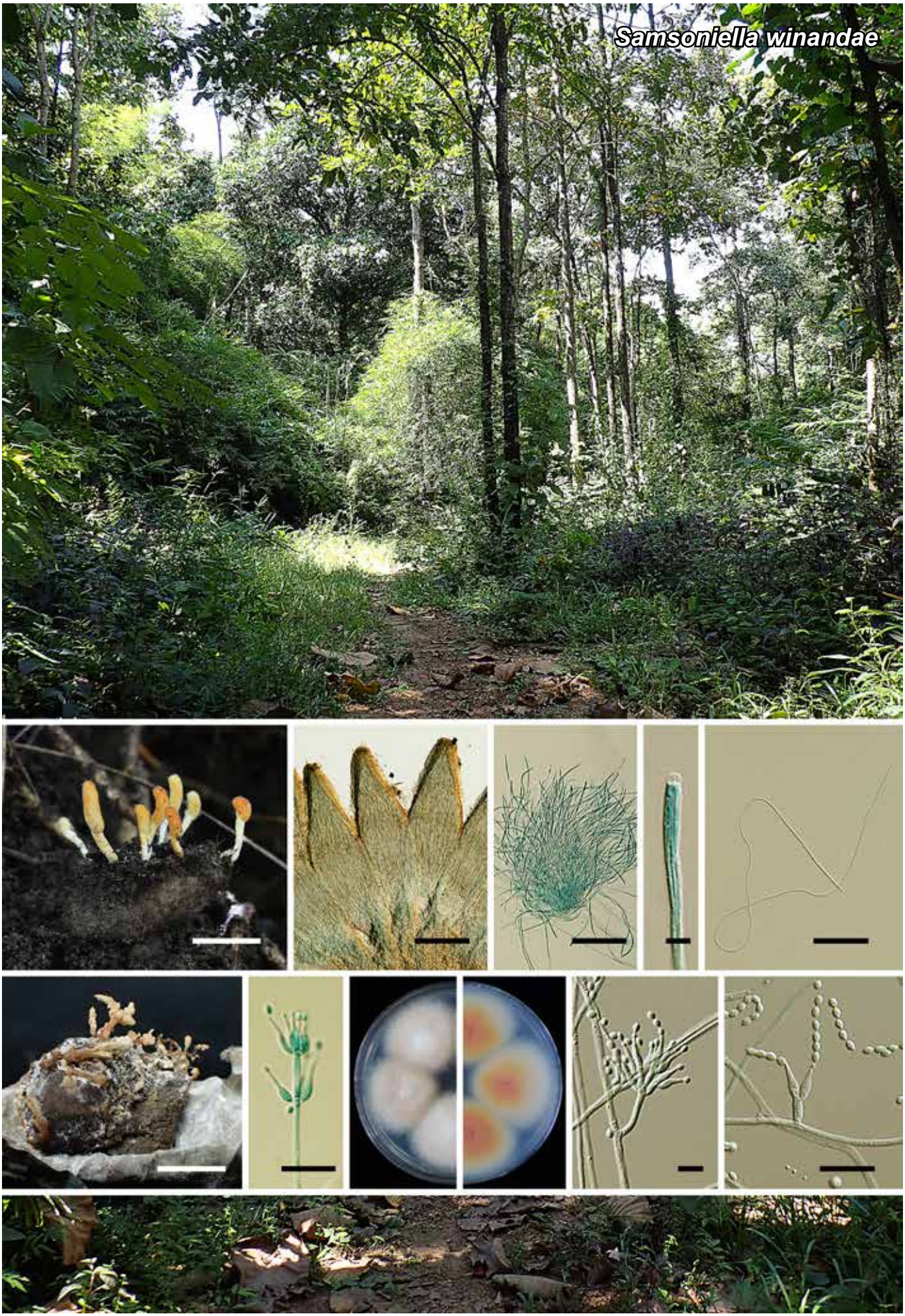
Samsoniella winandae

Fungal Planet 1543 – 29 June 2023

Samsoniella winandae Mongkols., Noisrip. & Luangsa-ard, *sp. nov.*

Etymology. Named after Dr. Winanda Himaman, colleague and researcher from the Department of National Parks, Wildlife and Plant Conservation.

Classification — *Cordycipitaceae*, *Hypocreales*, *Sordariomycetes*.

Stromata multiple, unbranched, 8–20 mm long and 0.5–2 mm broad, cream, cylindrical to enlarging apically, arising from the pupa in a cocoon (*Lepidoptera*). *Fertile part* orange yellow (23C; Royal Horticultural Society 2015), 2–8 mm long, 2–3 mm broad. *Perithecia* superficial, narrowly ovoid, 500–570(–580) × (120–)135–180 µm. *Asci* cylindrical, 8-spored, up to 300 × 4–5 µm, with caps 2–3 µm thick. *Ascospores* hyaline, whole, bola-shaped, 3- or 5-septate, (180–)200–265(–300) × 0.5–1 µm, central part filiform, terminal part very narrowly fusiform, (20–)25–45(–50) × 1–1.5 µm. *Asexual morph* isaria-like. *Synnemata* multiple, unbranched, up to 12 mm long, 2 mm broad, moderate orange (170C), cylindrical to clavate, arising from the pupa of *Limacodidae* (*Lepidoptera*) in a cocoon, white mass of conidia produced towards the apex of synnemata. *Phialides* verticillate, in whorls of 2–5, 5–12 × 2–3 µm, with basal portion swollen to ellipsoidal, tapering into a distinct neck, 4–6 × 1 µm. *Conidia* in chains, ellipsoidal, aseptate, white, 1.5–3 × 1–2 µm.

Culture characteristics — Colonies on potato dextrose agar (PDA) moderately fast-growing, c. 3 cm diam in 14 d at 25 °C, pale yellow pink (29C–D), consisting of a basal felt and cottony, floccose overgrowth, reverse strong orange (25A–B). Prostrate hyphae smooth, septate, hyaline, 2–3 µm diam. *Conidial* structures consisting of erect conidiophores usually arising from the aerial hyphae, verticillate with phialides in whorls of 2–5. *Phialides* (5–)5.5–10.5(–12) × 1–2(–3) µm, flask-shaped, tapering into long necks. *Conidia* in chains, oval with a pointed end, aseptate, white, 1.5–3 × 2–2.5(–3) µm.

Typus. Thailand, Chiang Mai Province, Ban Chan Upriver Forest, N18°58'42.62" E98°17'13.01", on *Lepidoptera* pupa, buried in soil, 11 Nov. 2020, *J.J. Luangsa-ard*, *K. Tasanathai*, *A. Khonsanit*, *S. Mongkolsamrit*, *W. Noisripoom*, *S. Sommai & P. Khamsuntorn* (holotype BBH 49043; culture ex-type MY 12469.01 = TBRC 17511; ITS, LSU, *tef1, rpb1* and *rpb2* sequences GenBank OM491228, OM491231, OM687896, OM687901 and OM687899; MycoBank MB 847002).

Additional materials examined. Thailand, Chiang Mai Province, Ban Chan Upriver Forest, N18°58'42.62" E98°17'13.01", on pupa of *Limacodidae* (*Lepidoptera*) in a cocoon, buried in soil, 11 Nov. 2020, *J.J. Luangsa-ard*, *K. Tasanathai*, *A. Khonsanit*, *S. Mongkolsamrit*, *W. Noisripoom*, *S. Sommai & P. Khamsuntorn*, BBH 49043, culture MY 12469.02 = TBRC 17512, ITS, LSU, *tef1, rpb1* and *rpb2* sequences GenBank OM491229, OM491232, OM687897, OM687902 and OM687900; ibid., BBH 48948, culture MY 12500 = TBRC 17510, ITS, LSU, *tef1* and *rpb1* sequences GenBank OM491230, OM491233, OM687898 and OM687903.

Notes — Species in *Samsoniella* have been reported occurring on various substrates and hosts, such as soil, fungi, and insects, e.g., *Coleoptera*, *Lepidoptera*, *Hymenoptera* (Samson 1974, Mongkolsamrit et al. 2018, Chen et al. 2020, Wang et al. 2020, 2022). Amongst the insect hosts of *Samsoniella* species, *Lepidoptera* is the major order. According to our phylogenetic analyses, *S. winandae* is closely related to *S. pseudotortricidae* (Wang et al. 2022). Based on the sexual morph, both species are parasitic on *Lepidoptera* pupae that can be found buried in soil. The macromorphologies of the natural samples of *S. winandae* resemble *S. pseudotortricidae* by producing several unbranched stromata with orange ascomata. The perithecia in these two species are superficial and narrowly ovoid. *Samsoniella winandae* is distinctly different from *S. pseudotortricidae* due to its larger perithecia (500–580 × 120–180 µm; 285.7–313.2 × 149.2–154.9 µm). The asexual morph of *S. winandae* in nature closely resembles *S. ramosa* by occurring on the pupae of *Limacodidae* in a cocoon and producing a white mass of conidia toward the apex of stipes. However, the colour of colonies on PDA in *S. winandae* differs significantly from *S. pseudotortricidae* and *S. ramosa*. In *S. winandae*, colonies are pale yellow pink in colour, whereas *S. pseudotortricidae* and *S. ramosa* have white colonies (Wang et al. 2020, 2022).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of TBRC 17511 had highest similarity to *Isaria farinosa* (strain GZU4718, GenBank KJ522469; Identities = 476/476 (100 %), no gaps), *Samsoniella* sp. (strain A19501, GenBank MT626376; Identities = 476/476 (100 %), no gaps), and *Cordyceps farinosa* (strain HLS, GenBank MK976001; Identities = 475/476 (99 %), no gaps). Closest hits using the **LSU** sequence are *Cordyceps farinosa* (culture CBS 156.65, GenBank MH870163; Identities = 811/811 (100 %), no gaps), *Akanthomyces waltergamsii* (strain TBRC 7251, GenBank MF140713; Identities = 811/811 (100 %), no gaps) and *Samsoniella* sp. (strain KY11321, GenBank ON502839; Identities = 811/811 (100 %), no gaps). Closest hits using the ***tef1*** sequence are *Cordyceps farinosa* (strain BUC418, GenBank MH879661; Identities = 929/934 (99 %), no gaps), *Samsoniella* sp. (strain XY4, GenBank ON804527; Identities = 926/934 (99 %), no gaps) and *Samsoniella cristata* (strain YFCC 7004, GenBank MN576963; Identities = 926/934 (99 %), no gaps). Closest hits using the ***rpb1*** sequence are *Isaria* sp. (strain TNS 16333, GenBank MF416662; Identities = 708/717 (99 %), no gaps), *Samsoniella farinospora* (strain YFCC 8774, GenBank ON676504; Identities = 708/717 (99 %), no gaps) and *Samsoniella* sp. (strain RCEF5406, GenBank OM751890; Identities = 707/716 (99 %), no gaps). Closest hits using the ***rpb2*** sequence are *Samsoniella sinensis* (strain YFCC 8766, GenBank ON568694; Identities = 964/968 (99 %), no gaps), *Samsoniella* sp. (strain RCEF2831, GenBank OM802500; Identities = 964/968 (99 %), no gaps) and *Samsoniella tortricidae* (strain YFCC 6142, GenBank MN576922; Identities = 964/968 (99 %), no gaps).

Colour illustrations. Background photo of forest in Thailand. Fungi on hosts; perithecia; asci ascus tip and bola-ascospore; fungi on hosts; asexual morph (isaria-like); culture on PDA (obverse and reverse); phialides with conidia on PDA. Scale bars = 10 mm (fungi on insect host), 150 µm (perithecia), 100 µm (asci), 20 µm (ascospores), 10 µm (phialides), 5 µm (ascus tip).

Supplementary material

FP1543-1 Phylogenetic tree.
FP1543-2 Table: List of species and GenBank accession numbers of sequences used in this study.

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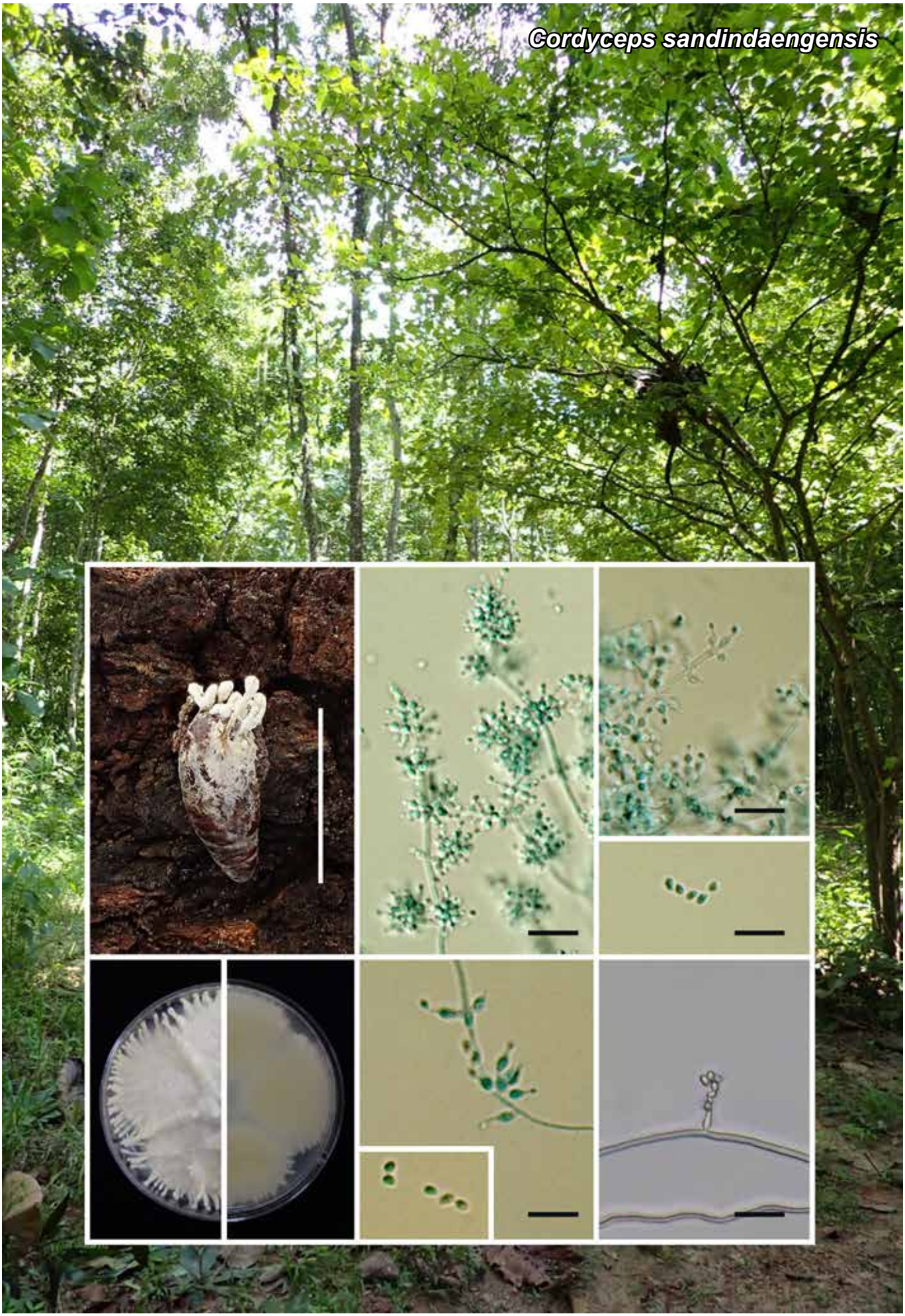
Cordyceps sandindaengensis

Fungal Planet 1544 – 29 June 2023

Cordyceps sandindaengensis Mongkols., Noisrip. & Luangsa-ard, *sp. nov.*

Etymology. Named after Ban San Din Daeng in Chiang Mai Province, the location where the specimen was found.

Classification — *Cordycipitaceae*, *Hypocreales*, *Sordariomycetes*.

Synnemata multiple, unbranched, up to 2–8 mm long and 1–2 mm broad, cream, cylindrical to clavate, arising from the upper part of a *Lepidoptera* pupa. *Fertile part* white, 3–5 mm long, white, conidia mass produced near the apex of synnemata. *Conidiogenous cells* isaria-like. *Phialides* verticillate, in whorls of 2–5, 5–6(–7) × 2–2.5 µm, with globose to flask-shaped basal portion, distinct neck, 1–2 × 0.5 µm. *Conidia* in dry chains, white, ovoid to obovoid, aseptate, 1.5–3 × 1–2 µm. *Sexual morph* unknown.

Culture characteristics — Colonies on potato dextrose agar (PDA) moderately fast-growing, c 3.5 cm diam in 14 d at 25 °C, white, consisting of a basal felt and cottony white with high mycelium density, reverse white. *Phialides* arising from prostrate hyphae, solitary, or in whorls of two to five on each branch, (3–)4.5–8.5(–12) × 2–3 µm, with a globose to slightly flask-shaped basal portion, distinct neck, 1–2 × 0.5 µm. *Conidia* ovoid to obovoid, aseptate, 1.5–2.5(–3) × 1.5–2 µm. *Conidial* arrangement evlachovaea-like. *Synnemata* observed after 20 d, white.

Typus. Thailand, Chiang Mai Province, Ban San Din Daeng, N18°58'42.62" E98°17'13.01", on *Lepidoptera* pupa, buried in soil, 24 Aug. 2022, *J.J. Luangsa-ard*, *S. Mongkolsamrit*, *W. Noisripoom*, *U. Pinruan, S. Sommai* & *P. Khamsuntorn* (holotype BBH 49633; culture ex-type MY 12914 = BCC 95817; ITS, LSU, *tef1* and *rpb2* sequences GenBank OQ540839, OQ540838, OQ473659 and OQ473660; MycoBank MB 847880).

Notes — Available sequences of four strains of *C. cateniannulata* (ARSEF 6240, ARSEF 6242, IYL-01 and IYYC-01) were retrieved from the GenBank nucleotide database and used in this study. Our phylogenetic tree clearly showed that the four strains formed a lineage with *C. sandindaengensis* (BCC 95817) with full support (MLB = 100 % / BPP = 1.00), which is an independent lineage separate from the ex-type of *C. cateniannulata* (CBS 152.83). They are thus proposed here as a new species and named *C. sandindaengensis*. According to the ARSEF dataset (2023) and this study, *C. sandindaengensis* occurs on *Lepidoptera* pupae and *Lymantria dissolute* (*Lymantriinae*), while *C. cateniannulata* is found on *Coleoptera* and a spider (TBRC 7258). The macromorphology of *C. sandindaengensis* collected in Thailand resembles the asexual morph of *C. cicadae* by producing a white powdery conidial mass near the apex of synnemata but differs significantly in the host (Luangsa-ard et al. 2007). Based on culture characteristics, *C. sandindaengensis* more closely resembles *C. blackwelliae* in the colour of colonies, producing synnemata when older, and the shape of phialides. The colour of colonies in both species is white with a conidial mass, their phialides are globose to flask-shaped with distinct necks (Mongkolsamrit et al. 2018). However, *C. sandindaengensis* differs significantly from *C. blackwelliae* in the shape and size of the conidia which are ovoid to obovoid in *C. sandindaengensis*. Meanwhile, the conidia in *C. blackwelliae* are cylindrical to ellipsoidal or reniform. The size of conidia in *C. sandindaengensis* is smaller than reported in *C. blackwelliae* (1.5–3 × 1.5–2 µm; 3–8 × 2–3.5 µm). Moreover, the arrangement of conidia on PDA, in *C. sandindaengensis* was evlachovaea-like, while isaria-like was observed in *C. blackwelliae*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of BCC 95817 had highest similarity to *Cordyceps cateniannulata* (strain IYL-01, GenBank MG345097; Identities = 511/511 (100 %), no gaps), *C. cateniannulata* (strain IYYC-01, GenBank MG345096; Identities = 511/511 (100 %), no gaps) and *C. cateniannulata* (strain ILT-01, GenBank MG345091; Identities = 511/511 (100 %), no gaps). Closest hits using the **LSU** sequence are *Cordyceps farinosa* (culture CBS 142.24, GenBank MH877764; Identities = 812/812 (100 %), no gaps), *Cordyceps sphingum* (culture CBS 114.22, GenBank MH866223; Identities = 812/812 (100 %), no gaps) and *Cordyceps* sp. (strain NTUCC 18-147, GenBank MT974263; Identities = 812/812 (100 %), no gaps). Closest hits using the ***tef1*** sequence are *Cordyceps cateniannulata* (strain RCEF3440, GenBank MW723086; Identities = 866/866 (100 %), no gaps), *Isaria cateniannulata* (strain ARSEF 6240, GenBank GU734758; Identities = 856/858 (99 %), no gaps) and *Cordyceps cateniannulata* (strain RCEF3340, GenBank OM482379; Identities = 840/840 (100 %), no gaps). Closest hits using the ***rpb2*** sequence are *Cordyceps cateniannulata* (strain BUC207, GenBank MH879631; Identities = 820/840 (98 %), no gaps), *Cordyceps cateniannulata* (strain BUC207, GenBank MH879612; Identities = 820/840 (98 %), no gaps) and *Cordyceps cateniannulata* (strain RCEF5406, GenBank MW426476; Identities = 820/840 (98 %), no gaps).

Colour illustrations. Background photo of a forest in Thailand. Fungus on insect host; phialides with conidia from the specimen; culture on PDA (obverse and reverse); phialides with conidia on PDA. Scale bars = 10 mm (fungi on insect host), 10 µm (phialides and conidia).

Supplementary material

FP1544-1 Phylogenetic tree.

FP1544-2 Table: List of species and GenBank accession numbers of sequences used in this study.

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Ophiocordyceps kuchinaraiensis

Fungal Planet 1545 – 29 June 2023

Ophiocordyceps kuchinaraiensis Khons., Thanakitp. & Luangsa-ard, *sp. nov.*

Etymology. Refers to the place where the type specimen was found, Khok Pa Si community forest, Kuchinarai District, Kalasin Province, Thailand.

Classification — *Ophiocordycipitaceae*, *Hypocreales*, *Sordariomycetes*.

Stromata single or double on *Coleoptera* larvae, brown, dark brown to black, cylindrical, slightly curved to curved, emerging from the fallen off feet pairs of the larva, 5.5–10 cm long and 2–3 mm broad, enlarging abruptly at the fertile head. *Fertile head* terminal, brown to dark brown, ovoid, limoniform, with ostioles slightly protruding on the surface of the fertile stroma, 5–7 mm long and 3–4 mm broad. *Perithecia* semi-immersed, obclavate, (630–)669–790(–820) × (210–)222–282(–300) µm. *Asci* cylindrical, (305–)364–485(–525) × (4.5–)5(–5.5) µm. *Asci-caps* convex, 3–4 × 5–5.5 µm. *Ascospores* filiform, multiseptate and breaking into 64 part-spores, (430–)480–569(–615) × 1–2 µm. *Part-spores* cylindrical with truncated apices, (5–)5.5–11(–20) × 1–2 µm.

Culture characteristics — Colony on potato dextrose agar (PDA) grew slowly, attaining 2.7–3 mm diam in white light/dark cycles for 4 wk at 25 °C, brown in the middle and white at the margins, colony reverse dark brown in the middle and brown at the margins. *Conidial* structures consisting of erect conidiophores arising from the aerial hyphae. *Phialides* solitary, smooth-walled, elongate-ampulliform and truncated at the base (7.0–)10.6–24.1(–38.0) × (2.0–)2.4–3.6(–4.0) µm. *Conidia* cylindrical with rounded ends, ellipsoid, fusoid and ovoid, white to cream, (3.0–)4.5–8.8(–12.0) × (2.0–)2.2–3.3(–4.0) µm.

Typus. Thailand, Kalasin Province, Kuchinarai District, Khok Pa Si Community Forest, on *Coleoptera* larva, buried in soil, 8 June 2021, *A. Khonsanit*, *D.Thanakitpipattana* & *K. Tasanathai* (holotype MY12719; culture ex-type = BCC 95830; ITS, LSU, *tef1,* and *rpb2* sequences GenBank OQ627396, OQ627397, OQ625474, and OQ625475; MycoBank MB 847858).

Additional material examined. THAILAND, Kalasin Province, Kuchinarai District, Khok Pa Si Community Forest, on *Coleoptera* larva, buried in soil, 8 June 2021, *A. Khonsanit*, *D.Thanakitpipattana* & *K. Tasanathai* (MY12720).

Notes — The gross morphological characters in *O. kuchinaraiensis* and *O. barnesii* (Thwaites) are very similar by occurring on *Coleoptera* larva and producing brown to dark brown stromata. However, *O. kuchinaraiensis* differs from *O. barnesii* by producing a shorter fertile head, longer perithecia, asci and ascospores. Moreover, *O. kuchinaraiensis* has multi-septate ascospores and breaks into 64 part-spores, while in *O. barnesii* the ascospores only have three septa and break into four part-spores (Luangsa-ard et al. 2010). Phylogenetically, *O. kuchinaraiensis* is closely related to *O. krachonicola* (Thanakitpipattana et al. 2020). Both species produce brown to dark brown stromata, as well as synglioclad ium-like asexual morph on culture media and are found buried in the soil. However, they can be distinguished from each other by host; *O. kuchinaraiensis* is found on *Coleoptera* larvae, while *O. krachonicola* is found on mole crickets. Additionally, *O. kuchinaraiensis* differs from *O. krachonicola* in having smaller stromata, shorter fertile head, longer perithecia, asci, ascospores and part-spores.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of BCC 95830 had highest similarity to *Tolypocladium* sp. (strain iNAT:16829892, GenBank ON243900; Identities = 491/594 (83 %), 42 gaps (7 %)), *Tolypocladium bacillisporum* (strain C53, GenBank LC684523; Identities = 490/594 (82 %), 45 gaps (7 %)) and *Ophiocordyceps* sp. (strain NHJ01339, GenBank JN942623; Identities = 430/508 (85 %), 40 gaps (7 %)). Closest hits using the **LSU** sequence are *Ophiocordyceps krachonicola* (strain BCC79667, GenBank MK632081; Identities = 783/809 (97 %), seven gaps (0 %)), *Ophiocordyceps sobolifera* (strain JCS-3, GenBank OM780146; Identities = 764/812 (94 %), 11 gaps (1 %)) and *Ophiocordyceps kniphofioides* var. *monacidis* (strain MF74, GenBank KX713605; Identities = 757/806 (94 %), eight gaps (0 %)). Closest hits using the ***tef1*** sequence are *Ophiocordyceps houaynhangensis* (strain MY10729, GenBank MH092896; Identities = 901/945 (95 %), no gaps), *Ophiocordyceps krachonicola* (strain BCC79666, GenBank MK632054; Identities = 856/894 (96 %), no gaps) and *Ophiocordyceps myrmicarum* (strain CG1357, GenBank MG922554; Identities = 872/945 (92 %), no gaps). Closest hits using the ***rpb2*** sequence are *Ophiocordyceps krachonicola* (strain BCC79666, GenBank MK632132; Identities = 732/792 (92 %), no gaps), *Tolypocladium* sp. (strain NBRC 106958, GenBank OP223137; Identities = 787/880 (89 %), two gaps (0 %)) and *Tolypocladium paradoxum* (strain NBRC 106958, GenBank AB968561; Identities = 787/880 (89 %), two gaps (0 %)).

Colour illustrations. Background photo of Khok Pa Si Community Forest, Kuchinarai District, Kalasin Province, Thailand. Stroma on *Coleoptera* larva; fertile head; perithecia; asci; asci-caps; filiform ascospores; part-spores; colony obverse and reverse on PDA; phialides with conidia on PDA. Scale bars = 10 mm (stroma on *Coleoptera* larva), 5 mm (fertile head, colony obverse and reverse on PDA), 500 µm (perithecia), 100 µm (asci, filiform ascospores), 10 µm (asci-caps, part-spores, phialides with conidia on PDA).

Supplementary material

FP1545-1 Phylogenetic tree.

FP1545-2 Table: List of species and GenBank accession numbers of sequences used in this study.

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Lapidomyces epipinicola

Fungal Planet 1546 – 29 June 2023

Lapidomyces epipinicola Piątek, Czachura & Stryjak-Bogacka, *sp. nov.*

Etymology. Name refers to the occurrence on the surface of *Pinus nigra* needles.

Classification — *Teratosphaeriaceae*, *Mycosphaerellales*, *Dothideomycetes*.

Mycelium composed of branched, septate, pale brown to olive brown, smooth or verruculose, thick-walled hyphae, 2.5–6 µm wide, consisting of elongated cells, sometimes constricted at septa; hyphae develop into arthroconidia or aggregate into a dense, dark brown sporodochial stroma, with conidiophores developed on the external layer. *Arthroconidia* ellipsoid, broadly ellipsoidal or elongated, pale brown to brown, smooth to finely verruculose, 1(–3)-septate, 8.5–30 × 4.5–8.5 µm, produced terminally or rarely intercalary, in simple or branched chains. *Conidiophores* reduced to doliiform or subcylindrical, hyaline, phialidic conidiogenous cells, 4–9 × 1.5–4 µm. *Conidia* produced singly, ellipsoid to subcylindrical, often with obtuse ends and narrowed at the centre, hyaline, smooth to finely verruculose, aseptate or rarely with one indistinct septum, 5.5–14 × 4–7.5 µm.

Culture characteristics — Colony on malt extract agar (MEA), oatmeal agar (OA) and potato dextrose agar (PDA) erumpent, spreading, compact and greenish olivaceous, surface cerebriform at the centre and zonate at the margin, with even and lobate margin, reaching 5 mm diam after 2 wk growth at 25 °C, and 9 mm diam after 1 mo growth at 25 °C. Reverse black.

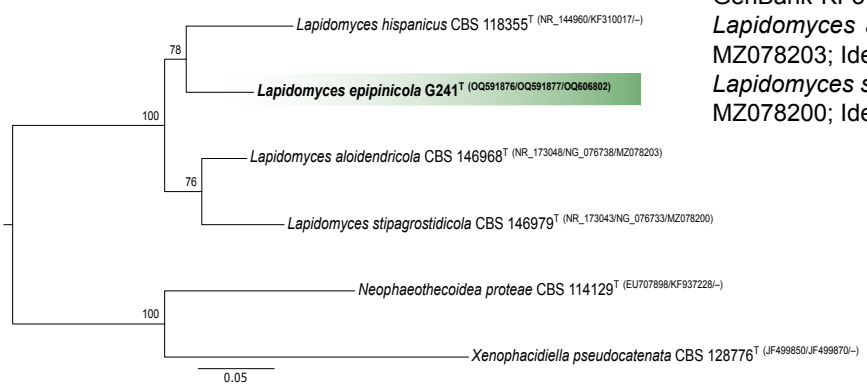
Typus. Poland, Podkarpackie Province, Rzeszów County, Rzeszów-Kmity, municipal greenery, isolated from sooty mould community on *Pinus nigra* (*Pinaceae*) needles, 17 Sept. 2018, *M. Piątek, W. Bartoszek & P. Czachura* (holotype KRAM F-59827; culture ex-type G241 = CBS 149898; ITS, LSU, and *rpb2* sequences GenBank OQ591876, OQ591877 and OQ606802; MycoBank MB 848116).

Notes — The genus *Lapidomyces* was described for the sterile rock-inhabiting fungus *Lapidomyces hispanicus* producing hyaline to pale brown, thick-walled, branched hyphae (Egidi et al. 2014, Crous et al. 2019a). Two other species, *Lapidomyces aloidendricola* and *Lapidomyces stipagrostidicola*, have been described for fungi isolated from plants, *Aloidendron dichotomum* (*Asphodelaceae*) and *Stipagrostis* cf. *ciliata* (*Poaceae*) in South Africa and Namibia, respectively (Crous et al. 2021a). Both of them produced asexual morphs in culture with conidiophores and conidia developed on sporodochial stroma and in pycnidial conidiomata, respectively.

Cultures of *L. epipinicola* proved to be fertile like those of *L. aloidendricola* and *L. stipagrostidicola*. Morphologically it is similar to *L. aloidendricola* in developing a sporodochial stroma, but it differs in having hyaline, ellipsoid to subcylindrical, larger conidia and abundant arthroconidia (conidia are brown, ellipsoid to ovoid, (7–)8–10(–12) × 6(–7) µm and arthroconidia are absent in *L. aloidendricola*). Phylogenetically, *Lapidomyces epipinicola* is most closely related to *L. hispanicus*.

All described *Lapidomyces* species have been isolated from extremophilic habitats – rocks in Spain, brown stems of *Aloidendron dichotomum* in South Africa, leaves of *Stipagrostis* cf. *ciliata* in Namibia, and a sooty mould community on *Pinus nigra* needles in Poland. It is also noteworthy that *L. hispanicus* cannot grow at 25 °C in culture, suggesting it prefers colder environments, despite the fact that it was isolated from mountains in the Mediterranean (Egidi et al. 2014). However, the other species do grow readily at this temperature (Crous et al. 2021a, this study).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence are *Lapidomyces aloidendricola* (culture CBS 146968, GenBank NR_173048; Identities = 514/528 (97 %), three gaps (0 %)), *Lapidomyces hispanicus* (culture CBS 118355, GenBank NR_144960; Identities = 453/468 (97 %), three gaps (0 %)) and *Lapidomyces stipagrostidicola* (culture CBS 146979, GenBank NR_173043; Identities = 509/531 (96 %), six gaps (1 %)). The closest hits using the **LSU** sequence are *Lapidomyces aloidendricola* (culture CBS 146968, GenBank NG_076738; Identities = 838/841 (99 %), no gaps), *Lapidomyces stipagrostidicola* (culture CBS 146979, GenBank NG_076733; Identities = 833/841 (99 %), no gaps) and *Phaeothecoidea melaleuca* (culture CPC 17223, GenBank HQ599595; Identities = 828/842 (98 %), four gaps (0 %)). The closest hits using the ***rpb2*** sequence are *Lapidomyces hispanicus* (culture CBS 118764, GenBank KF310076; Identities = 203/225 (90 %), no gaps), *Lapidomyces aloidendricola* (culture CPC 38703, GenBank MZ078203; Identities = 694/842 (82 %), four gaps (0 %)) and *Lapidomyces stipagrostidicola* (culture CPC 38938, GenBank MZ078200; Identities = 591/724 (82 %), 10 gaps (1 %)).



Phylogenetic tree of *Lapidomyces* species obtained from a maximum likelihood analysis of the combined multi-locus alignment (2 157 nucleotides: ITS, LSU, *rpb2*). The maximum likelihood analysis was performed using RAxML-NG v. 1.1.0 (Kozlov et al. 2019). The position of *Lapidomyces epipinicola* is indicated in **bold**. Ex-type cultures are indicated with superscript T. Numbers above branches indicate maximum likelihood bootstrap support values > 70 %. *Neophaeothecoidea proteae* and *Xenophacidiella pseudocatenata* were used as an outgroup. The scale bar represents the expected number of changes per site. The alignment was deposited at figshare.com (10.6084/m9.figshare.22303279).

Colour illustrations. Needles of *Pinus nigra* with sooty mould communities, Poland. Colony on MEA; hyphae and arthroconidia; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

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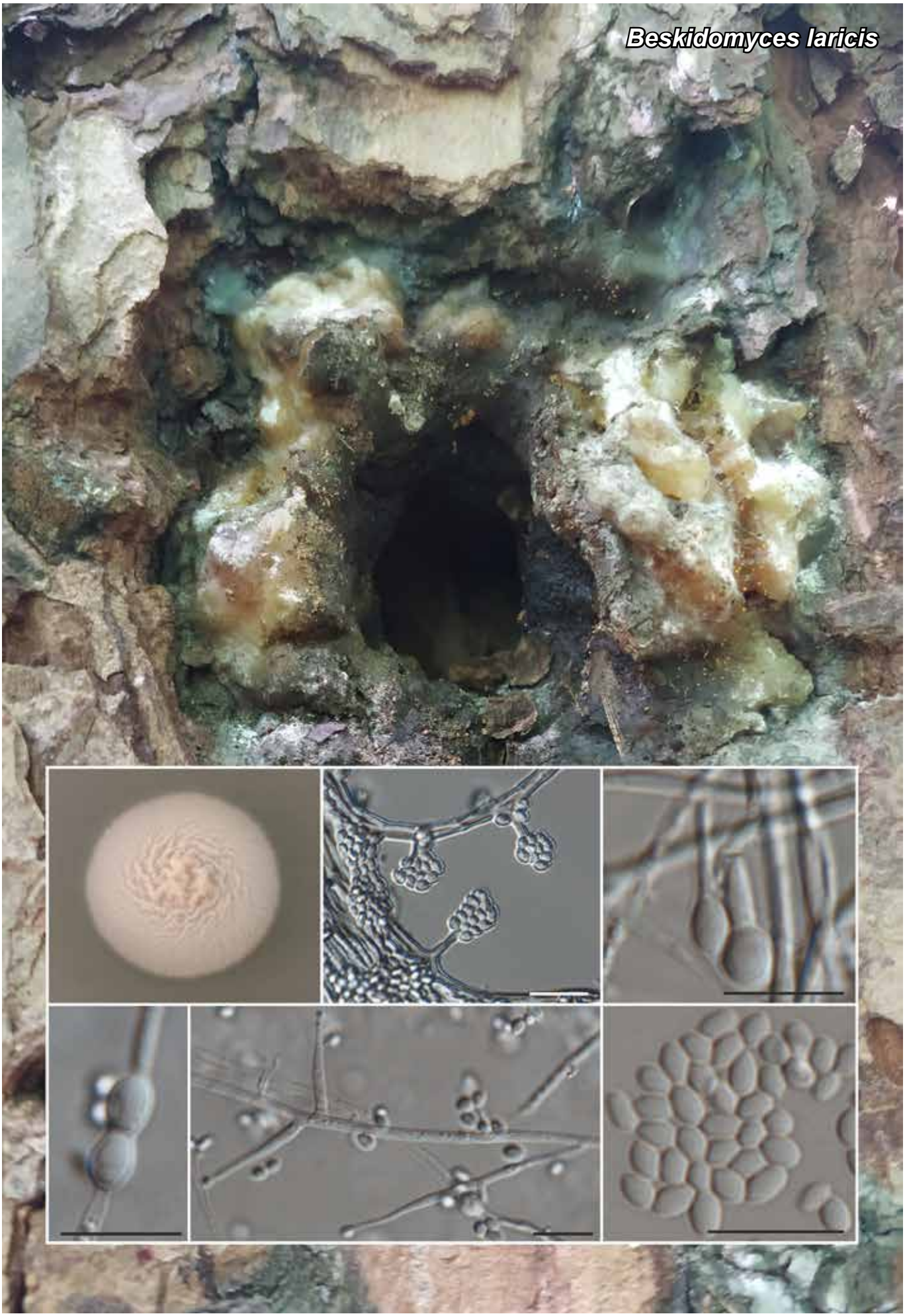
Beskidomyces laricis

Fungal Planet 1547 – 29 June 2023

Beskidomyces Czachura & Piątek, *gen. nov*.

Etymology. Named after Beskidy Mts, the mountains within the Carpathians, where the new fungus was discovered.

Classification — *Pseudeurotiaceae*, *Thelebolales*, *Leotiomycetes*.

Mycelium composed of branched, septate, hyaline, smooth hyphae, sometimes in fascicles; hyphae develop into macroconidia and phialides with microconidia. *Macroconidia* intercalary or terminal on hyphae or side branches, solitary or rarely in short chains, globose, subglobose or broadly ellipsoid, hyaline, smooth. *Conidiophores* reduced to phialides, cylindrical or elongated, hyaline, smooth, with indistinct collarettes. *Microconidia* ellipsoidal, hyaline, smooth, at first accumulating at the apices of the phialides, but later readily disintegrating.

Type species. *Beskidomyces laricis* Czachura & Piątek MycoBank MB 848108.

Beskidomyces laricis Czachura & Piątek, *sp. nov.*

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

Mycelium composed of sparsely branched, sparsely septate, hyaline, smooth hyphae, 1.5–2 µm wide, sometimes in fascicles up to 40 µm wide (especially at the aerial mycelium in slide cultures); hyphae develop into intercalary or terminal macroconidia and phialides with microconidia. *Macroconidia* intercalary or terminal on hyphae or side branches, solitary or rarely 2–3 in chains, globose, subglobose or broadly ellipsoid, hyaline, smooth, (3.5–)4.5–5.5 × 3–4.5 µm, wall c. 0.5 µm thick. *Conidiophores* reduced to phialides, cylindrical or elongated, hyaline, smooth, with indistinct collarettes, 2.5–14 × 1.5–2.5 µm (or up to 35 × 2 µm in slide cultures). *Microconidia* ellipsoidal, hyaline, smooth, 2.5–4 × 1.5–2.5 µm, at first accumulating at the apices of the phialides, but later readily disintegrating.

Culture characteristics — Colonies globose, umbonate or low convex on MEA and PDA, respectively, flat on OA, with fimbriate margin, whitish to pale cream, reaching 14 mm diam after 2 wk at 15 °C and 22 mm diam after 2 wk at 25 °C. Reverse whitish to pale cream on malt extract agar (MEA), potato dextrose agar (PDA) and oatmeal agar (OA).

Typus. Poland, Podkarpackie Province, Krosno County, Modrzyna Reserve, c. 13 km south of Dukla city, isolated from resin of *Larix decidua* ssp. *polonica* (*Pinaceae*), 22 Oct. 2020, *P. Czachura* (holotype KRAM F-59828; culture ex-type PLM19; ITS, LSU, *rpb2*, and *tef1* (second part) sequences GenBank OQ600167, OQ600166, OQ606813 and OQ606812; MycoBank MB 848110).

Gymnostellatospora Ugadawa et al., Mycotaxon 48: 158. 1993

Gymnostellatospora bhattii (Samson) Piątek & Czachura, *comb. nov*. MycoBank MB 848111

Basionym. *Pseudogymnoascus bhattii* Samson, Acta Bot. Neerl. 21: 519. 1972.

Synonym. *Gymnostellatospora bhattii* (Samson) Zhi.Y. Zhang et al., Frontiers in Microbiology 11: 5. 2020, nom. inval., Art. F.5.1 (Shenzhen).

Notes — *Beskidomyces* is a new genus in the family *Pseudeurotiaceae* of the order *Thelebolales* characterised by production of two types of conidia: macroconidia formed intercalary or terminally on hyphae or side branches (with appearance and equivalent to typical conidia known in other genera of the *Pseudeurotiaceae*; they are named here as macroconidia to distinguish them from microconidia) and microconidia produced on phialides with indistinct collarettes. Phylogenetic analyses placed *Beskidomyces laricis* in an isolated position within *Pseudeurotiaceae*, sister to a lineage formed by representatives of predominantly soil-inhabiting genera *Solomyces*, *Geomyces*, *Gymnostellatospora*, *Pseudogeomyces*, *Ovadendron* and *Pseudogymnoascus*. The next closely related genus is *Leuconeurospora*. Phylogenetic placement of *Ovadendron* (Sigler & Carmichael 1976) within *Thelebolales* is revealed here for the first time. Morphologically, the production of two types of conidia distinguishes *Beskidomyces* from most other related genera in the *Pseudeurotiaceae* (e.g., Sigler & Carmichael 1976, Sigler et al. 2000, Sogonov et al. 2005, Zhang et al. 2020, 2021, 2023; though *Leuconeurospora* sometimes may produce both conidia and arthroconidia, Malloch et al. 2016). The type species, *Beskidomyces laricis*, was isolated only once from the resin of *Larix decidua* ssp. *polonica* growing in an old mixed forest in the Polish Carpathians (specifically, in the Beskid Niski Mts, which is part of the Beskidy Mts). Megablast searches in GenBank did not reveal any sequence that could belong to this species. The resinous habitat occupied by *Beskidomyces laricis* is a new ecological niche for *Thelebolales*.

Sequences from the ex-type culture of *Pseudogymnoascus bhattii* (CBS 760.71) cluster with sequences of *Gymnostellatospora* species, similar as in the study of Zhang et al. (2020). Thus, this species belongs to *Gymnostellatospora* and is the oldest described species in this genus. *Pseudogymnoascus bhattii* is reallocated here to *Gymnostellatospora* since the previous combination in this genus was invalid (Zhang et al. 2020).

(Notes continued on Supplementary page)

Colour illustrations. Resin on the bark of *Larix decidua* ssp. *polonica*, Poland. Colony on MEA; hyphae and phialides with microconidia observed in slide cultures; terminal and intercalary macroconidia; phialides and microconidia; microconidia. Scale bars = 10 µm.

Supplementary material

FP1547 Phylogenetic tree.

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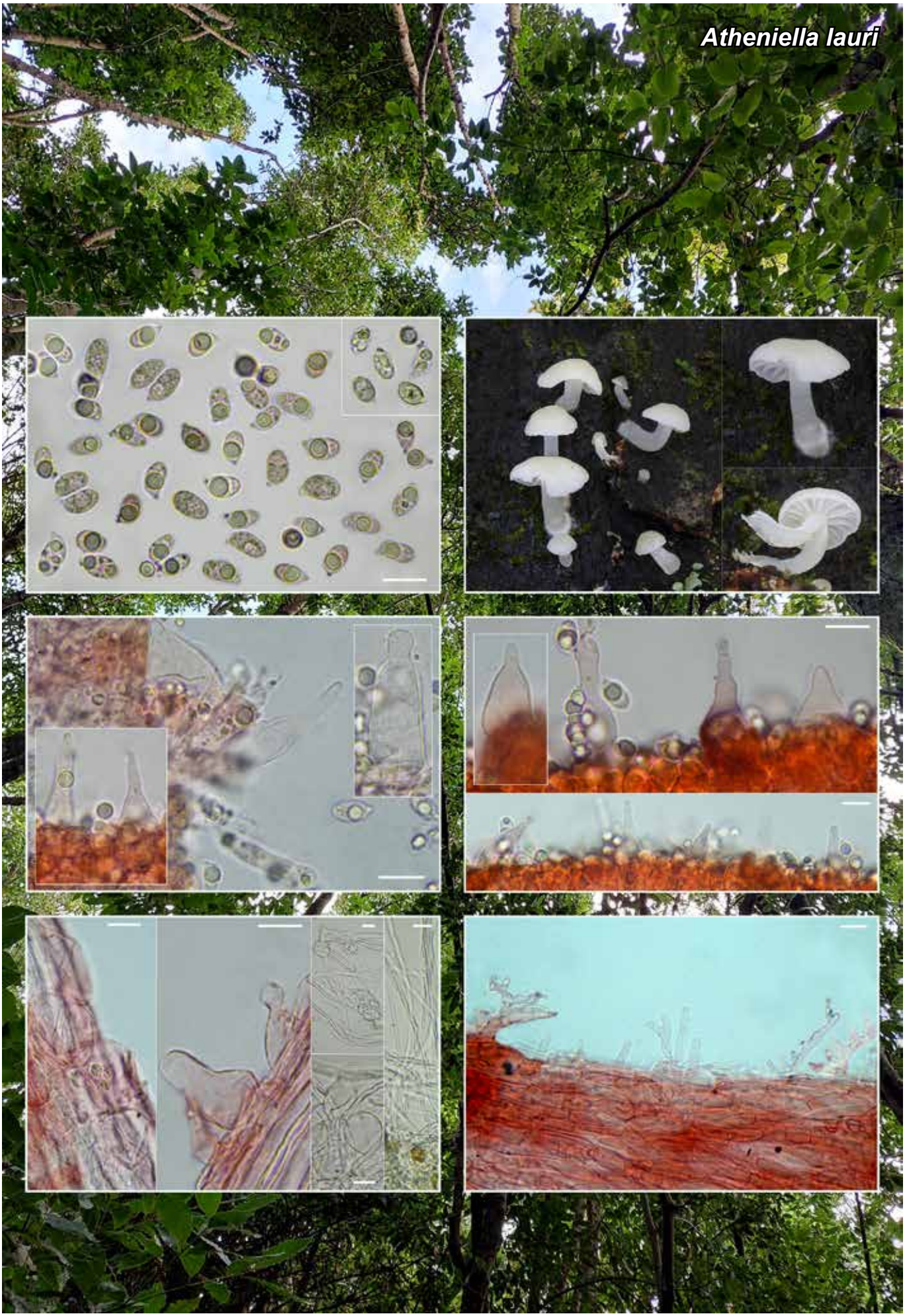
Atheniella lauri

Fungal Planet 1548 – 29 June 2023

Atheniella lauri De la Peña-Lastra, A. Mateos, Pérez-de-Greg. & Plaza, *sp. nov*.

Etymology. The specific epithet refers to the host on which it grows, *Laurus nobilis*.

Classification — *Mycenaceae*, *Agaricales*, *Agaricomycetes*.

Pileus 1.5–7.5 mm diam, hemispherical, conical to campanulate, sometimes with a small mamelon when young, then obtuse-flattened in centre, margin involute at first, hygrophanous, somewhat striated by transparency, whitish-translucent or greyish, whitish yellowish (Ség. 270; Séguy 1936) especially in centre, yellowing more distinctly on drying or ageing, pale or white at margin. *Lamellae* separate, L = 8–12, with abundant lamellulae (1 L = 1–3 lam), thick, adnate, arcuate-decurrent, well developed, some somewhat ventricose, white, with the edge concolourous and somewhat pubescent. *Stipe* up to 4–8 × 0.6–1.0 mm, cylindrical, claviform, with very broadened base (up to 2 mm), straight or curved, translucent white, hyaline, entirely pruinose, insititious and sometimes with white basal hairs or rhizoids. *Context* exiguous, whitish, no discernible *odour*, taste *indistinct*. *Basidiospores* (6.0–)7.0–*8.2*–9.2(–10.7) × (3.8–)4.3–*4.8*–5.3(–6.0) µm, Q = (1.4–)1.5–*1.7*–1.9(–2.1); n = 50; Ve = 99 µm^3, ellipsoidal, broadly ellipsoidal, subcylindrical, smooth, hyaline, non-amyloid, with one large guttule, sometimes with two more and opaque contents. *Basidia* (21.3–)25.9–*30.1*–36.5 × (4.8–)5.7–*6.4*–6.9(–7.2) µm, bisporic and some monosporic, claviform, with sterigmata 3.1–6.0 µm high. *Cheilocystidia* 33–50 × 9–15 µm, thin-walled, fusiform, lageniform, lanceolate, many with elongate upper end, apex rounded and sometimes mucronate. *Pleurocystidia* 37–58 × 7–19 µm, thin-walled to somewhat thick-walled, fusoid, lageniform, tapering into a short to long subcylindrical neck, apex rounded or mucronate. *Pileipellis* in cutis consisting of radially arranged, diverticulate, thin-walled hyphae, 2–6 µm wide; diverticula up to 40 × 4 µm, flexuous, smooth and obtuse or digitate and branched up to 20 × 2 µm; *subpileipellis* consisting of very broad (up to 13 µm) hyphae with ellipsoid to broadly fusoid elements. *Stipitipellis* with a cutis of parallel, cylindrical, slightly thick-walled, smooth, outer hyphae 2–5 µm and inner hyphae 5–9 µm wide. *Caulocystidia* 15–26 × 3.5–14 µm, irregular, fusoid, lageniform, sometimes capitate, globose or subglobose, thin-walled or somewhat thick-walled, hyaline. *Basal hairs* cylindrical, 3 µm wide on average and 5–7 µm wide at base, thick-walled (1 µm), lower part with widened hyphae (physaloids) up to 14 µm wide and with subglobose cells up to 17 µm wide. *Clamp connections* present on hyphae of epicutis and caulocutis.

Distribution — Currently known only from the type location in north-western Spain.

Typus. Spain, Galicia, Pontevedra, Parque Nacional de las Islas Atlánticas de Galicia, Illa de Cortegada, N42°37'10.29" W8°47'16.85", 17 m a.s.l., scattered to gregarious on the bark of fallen trees of *Laurus nobilis*, 27 Nov. 2020, *S. De la Peña-Lastra* (holotype AMI-SPL538; ITS and LSU sequences GenBank OQ539683 and OQ539684; MycoBank MB 847761).

Notes — The genus *Atheniella* is characterised macroscopically by its mycenoid appearance, small basidiomata, white lamellae, and white, yellow, orange, pink or red coloured pileus and stipes. The 12 species described worldwide are saprophytes, growing directly on wood or various plant debris. Their main chemical characteristic is the absence of amyloid reaction in contact with iodine reagents, which largely distinguishes them from the genus *Mycena* (Redhead et al. 2012). *Atheniella lauri* is characterised by its small size, white, greyish white or slightly yellowish colouration, arcuate-decurrent lamellae and two types of caulocystidia (type fusoid/lageniform and globose), and its growth on mossy bark of *Laurus nobilis*. Macroscopically, the most similar species would be *Hemimycena delectabilis* var. *bispora*; however, it is larger, up to 16 mm diam, has more decurrent lamellae, nitrous odour, and grows on plant debris and conifer roots, with a northern and central European distribution (Antonín & Noordeloos 2004); from a molecular point of view, it is also distant from our species. The closest species phylogenetically would be *A. amabilissima*; this taxon, of American distribution, has received different interpretations, both Maas Gesteranus (1992: 432) and Robich (2003: 27), have considered it a synonym of *Mycena adonis*, now *Atheniella adonis*. According to the description of Smith (1947: 180), or the more recent description by Landry & Labbé (2023), it is a species associated with conifers, with tetrasporic basidia, narrower spores (3–4 µm), and pinkish shades, without yellowish tones. *Atheniella flavoalba*, a cosmopolitan and very common species, with a much larger size (up to 16 mm diam), light yellowish shades, ascending and adnate lamellae, tetrasporic and sometimes bisporic, and grows among mosses, leaf litter or conifer needles (ITS 94.5 % match). *Atheniella rutila* with deep salmon to bright red pileus, without caulocystidia, growing on dead wood (ITS 93.8 % match). *Atheniella taoyao* a light pink-salmon pileus and decurrent lamellae is microscopically similar to *A. lauri,* except the pileipellis has numerous short excrescences, growing on living *Cephalotaxus* or *Cunninghamia* trees (Ge et al. 2021) (ITS 94.1 % match). On the other hand, none of these species mentioned growth in association with *Laurus nobilis*.

Colour illustrations. Spain, Pontevedra, P. Nacional Illas Atlánticas de Galicia, Illa de Cortegada, forest of *Laurus nobilis*, where the holotype of *Atheniella lauri* was collected. Right column: basidiomata in upper photo correspond with the holotype; middle photo corresponds with cheilocystidia (RC); and the bottom photo is pileipellis (RC). Left column: in upper photo correspond basidiospores (H_2O, MLZ in upper detail); middle photo corresponds with pleurocystidia, and the bottom photo is caulocystidia and stipitipellis (two pictures on the left, RC) and physaloids cells, subglobose cells and basal hairs (three pictures on the right, H_2O). Scale bars = 10 µm.

Supplementary material

FP1548-1 Phylogenetic tree.

FP1548-2 Table: List of species and GenBank accession numbers of sequences used in this study.

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Geoglossum azoricum

Fungal Planet 1549 – 29 June 2023

Geoglossum azoricum A. Mateos, De la Peña-Lastra & Plaza, *sp. nov.*

Etymology. The epithet refers to the place where it was found (Azores archipelago, Portugal).

Classification — *Geoglossaceae*, *Geoglossales*, *Geoglossomycetes*.

Apothecia gracile *44–70 mm high, dry, shiny when wet, furrowed, blackish, velvety. *Ascogenous portion* *19–20 × 4.2–4.8 mm, cylindrical, clavate to lanceolate, subcylindrical to spatulate in cross section, compressed, 1.7–2.2 mm thick, with one or more longitudinal furrows, 1/4 or 1/2 of the total length ascocarp, felted, smooth or somewhat wrinkled, blackish, brownish in the area near the stipe; sometimes the ascogenous portion and the sterile portion are not clearly distinguishable, junction between the two fairly regular. *Sterile portion* *24–50 × 1.0–1.8 mm, terete, usually recurved; scaly; greyish blackish or brownish, paler brownish at apex. *Flesh* greyish. *Asci* *180–220(–250) × 15–19(–25) µm; unitunicate, consistently 8-spored, clavate, fusiform, with rounded apex, narrowed below, with pleurorhynchous base provided with croziers, apical pore hemiamyloid (RR) in IKI 2 solution (potassium iodide 6 g; resublimated iodine 2 g; distilled water, up to 100 mL). *Paraphyses* protruding above asci, fragile, filiform and hyaline towards the base, 5–6.5 µm wide, constricted at septa, frequently or moderately septate, with greenish-greyish or brownish-full parietal and encrusting pigment, last elements capitate, pyriform, obovoid, claviform, straight, flexuous or curved and less frequently hooked, usually 90°, sometimes proliferate, *15–30 × 5–11(–17) µm. *Pseudoparaphyses* rare, moniliform, with ovoid elements, 9–22 × 4–10 µm, with more conspicuous, dark greenish encrusting pigment. *Ascospores* *(65.0–)72.7–*84.1*–93.7(–99.4) × (4.7–)5.0–*5.4*–6.1(–6.3) µm; Q = (13.1–)13.7–*15.5*–17.5(–18.6); n = 30; cylindrical-clavate, sub-fusiform, somewhat curved, basal end more acute; initially hyaline and aseptate, finally dark brown and 7-septate, rarely 3- or 6-septate; *pluriguttulate (LBs). *Subhymenial trama* with intricate texture. *Medullary excipulum* banal, composed of compact porrecta-prismatic texture, elements *(17.1–)27.8–*34.3*–45.7(–50.3) × (6.5–)6.9–*8.5*–11.3(–11.5) µm. *Ectal excipulum* consisting of chains of 3–6 elements, *58–127 µm long, moniliform, with greenish brown or greyish parietal pigment, apical elements ovoid, ellipsoid or setiform, *15–30 × 5.5–10 µm, remaining elements subcylindrical or claviform.

Habitat & Distribution — Gregarious, in more or less numerous groups in laurel forest areas, growing on *Sphagnum* spp. Known from one island (Terceira, Azores, Portugal).

Typus. Portugal, Azores, Terceira, Angra do Heroísmo, pr. Algar do Carvão, Terra Brava, N38°44'09" W27°12'0.4", 670 m a.s.l., gregarious growing on mossy areas of laurel forest areas planted with *Cryptomeria japonica*, 14 Jan. 2022, *A. Mateos* & *S. De la Peña* (holotype AMI-SPL1247; ITS and LSU sequences GenBank OQ618223 and OQ618224; MycoBank MB 847843).

Additional material examined. Portugal, Azores, Terceira, Angra do Heroísmo, pr. Algar do Carvão, Terra Brava, N38°44'09" W27°12'0.4", 670 m a.s.l., gregarious growing on mossy areas of laurel forest areas planted with *C. japonica*, 14 Jan. 2022, *A. Mateos* & *S. De la Peña* (AMI-SPL1264; ITS sequence GenBank OQ617305).

Notes — *Geoglossum azoricum* is characterised by its gracile and very slender apothecia, partially brownish clavula near the foot and brown in the upper third of the foot and with scaly decoration, pigmented ascospores, with seven septa and plurigutulate, with hemiamyloid apical pore asci, and with paraphyses of polymorphous terminal elements, it grows on *Sphagnum*. Morphologically similar is *G. scabripes* (Arauzo & Iglesias 2014), but it has many dissimilarities: smaller size, different clavula, shorter asci, (146.0–)155.3–190.4(–205.0) µm, different paraphyses and pseudoparaphyses, smaller ascospores, (55.5–)62.8–73.7(–79.1) × (4.6–)5.3–5.7(–6.5) µm) and different habitat to *G. azoricum*; it is phylogenetically close (ITS 96.67 % match). Also similar is *G. brunneipes* (Arauzo & Iglesias 2014), smooth-footed, with smaller asci (164–190 × 17.2–21.8 µm), distinct paraphyses and no pseudoparaphyses, smaller ascospores ((60.2–)66.6–68.7(–75.1) × (4.5–)5.3–5.6(–6.5) µm) and different habitat; (ITS 95.18 % match). *Geoglossum azoricum* is phylogenetically more closely related to *G. subbarlae* nom. prov. sp. 'ERRO 2012121800' (Arauzo & Iglesias 2014) (ITS 97.7 % match, differs by 8 nucleotides and 3 indels), with smaller and less slender, black ascomata, with smaller asci ((169.0–)176.3–186.7(–195.0) × 20.1–22.7 µm), somewhat different paraphyses, smaller ascospores ((62.3–)75.7–80.5(–90.3) × (4.9–)5.5–5.8(–6.8) µm), ectal excipulum and different habitat. *Geoglossum barlae* 'voucher ILLS:61034' (Hustad 2015) (ITS 97.23 % match, differs in 15 nucleotides and 6 indels), smaller and darker, glabrous foot, somewhat smaller asci (150–190 × 16–19 µm), euamyloid reaction, smaller ascospores (66–73 × 5–6 µm), different paraphyses, no pseudoparaphyses and different habitat. *Geoglossum laurisilvae* (Crous et al. 2022b) (ITS 95 % match, differs in 19 nucleotides and 5 indels), darker coloured, shorter asci (160.0–)175.5–*182.7*–190.0(–205.0) µm and with euamyloid apical pore, without pseudoparaphyses and with somewhat smaller spores, (65.0–)71.6–*79.3*–86.0(–90.0) × (4.8–)5.0–*5.8*–6.47(–6.5) µm.

Colour illustrations. Portugal, Azores, Terceira, Algar do Carvão, laurel forests planted with *Cryptomeria japonica*, place where the holotype of *Geoglossum azoricum* was collected. Right column: apothecia in upper photo correspond with the holotype; middle photo corresponds with: detail of *ascus apex, detail base ascus with crozier (one pictures, H_2O) and mature asci (two pictures) in *IKI 2; the bottom photo is *pseudoparaphyses (left) *ectal excipulum (middle) and *medullary excipulum (right) in H_2O. Left column: middle photo ascospores (right *RC, left *H_2O); the bottom photo is paraphyses (*H_2O). * = living. Scale bars = 25 µm (ascospores), 10 µm (all others).

Supplementary material

FP1549-1 Phylogenetic tree.

FP1549-2 Table: List of species and GenBank accession numbers of sequences used in this study.

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