Persoonia 48, 2022: 261–371
www.ingentaconnect.com/content/nhn/pimj

RESEARCH ARTICLE

ISSN (Online) 1878-9080
https://doi.org/10.3767/persoonia.2022.48.08

Fungal Planet description sheets: 1383–1435

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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**, *Agaricus albofoetidus*, *Agaricus aureoelephanti* and *Agaricus parviumbrus* on soil, *Fusarium ramsdenii* from stem cankers of *Araucaria cunninghamii*, *Keissleriella sporoboli* from stem of *Sporobolus natalensis*, *Leptosphaerulina queenslandica* and *Pestalotiopsis chiaroscuro* from leaves of *Sporobolus natalensis*, *Serendipita petricolae* as endophyte from roots of *Eriochilus petricola*, *Stagonospora tauntonensis* from stem of *Sporobolus natalensis*, *Teratosphaeria carnegiei* from leaves of *Eucalyptus grandis* × *E. camaldulensis* and *Wongia ficherai* from roots of *Eragrostis curvula.* **Canada**, *Lulworthia fundyensis* from intertidal wood and *Newbrunswickomyces abietophilus* (incl. *Newbrunswickomyces* gen. nov.) on buds of *Abies balsamea.* **Czech Republic**, *Geosmithia funiculosa* from a bark beetle gallery on *Ulmus minor* and *Neoherpotrichiella juglandicola* (incl. *Neoherpotrichiella* gen. nov.) from wood of *Juglans regia.* **France**, *Aspergillus rouenensis* and *Neoacrodontium gallica* (incl. *Neoacrodontium* gen. nov.) from bore dust of *Xestobium rufovillosum* feeding on *Quercus* wood, *Endoradiciella communis* (incl. *Endoradiciella* gen. nov.) endophytic in roots of *Microthlaspi perfoliatum* and *Entoloma simulans* on soil. **India**, *Amanita konajensis* on soil and *Keithomyces indicus* from soil. **Israel**, *Microascus rothbergiorum* from *Stylophora pistillata.* **Italy**, *Calonarius ligusticus* on soil. **Netherlands**, *Appendopyricularia juncicola* (incl. *Appendopyricularia* gen. nov.), *Eriospora juncicola* and *Tetraploa juncicola* on dead culms of *Juncus effusus*, *Gonatophragmium physciae* on *Physcia caesia* and *Paracosmospora physciae* (incl. *Paracosmospora* gen. nov.) on *Physcia tenella*, *Myrmecridium phragmitigenum* on dead culm of *Phragmites australis*, *Neochalara lolae* on stems of *Pteridium aquilinum*, *Niesslia nieuwwulvenica* on dead culm of undetermined *Poaceae*, *Nothodevriesia narthecii* (incl. *Nothodevriesia* gen. nov.) on dead leaves of *Narthecium ossifragum* and *Parastenospora pini* (incl. *Parastenospora* gen. nov.) on dead twigs of *Pinus sylvestris.* **Norway**, *Verticillium bjoernoeyanum* from sand grains attached to a piece of driftwood on a sandy beach. **Portugal**, *Collybiopsis cimrmanii* on the base of living *Quercus ilex* and amongst dead leaves of *Laurus* and herbs. **South Africa**, *Paraproliferophorum hyphaenes* (incl. *Paraproliferophorum* gen. nov.) on living leaves of *Hyphaene* sp. and *Saccothecium widdringtoniae* on twigs of *Widdringtonia wallichii.* **Spain**, *Cortinarius dryosalor* on soil, *Cyphellophora endoradicis* endophytic in roots of *Microthlaspi perfoliatum*, *Geoglossum laurisilvae* on soil, *Leptographium gemmatum* from fluvial sediments, *Physalacria auricularioides* from a dead twig of *Castanea sativa*, *Terfezia bertae* and *Tuber davidlopezii* in soil. **Sweden**, *Alpova larskersii*, *Inocybe alpestris* and *Inocybe boreogodeyi* on soil. **Thailand**, *Russula banwatchanensis*, *Russula purpureoviridis* and *Russula lilacina* on soil. **Ukraine**, *Nectriella adonidis* on overwintered stems of *Adonis vernalis.* **USA**, *Microcyclus jacquiniae* from living leaves of *Jacquinia keyensis* and *Penicillium neoherquei* from a minute mushroom sporocarp. Morphological and culture characteristics are supported by DNA barcodes.

Citation: Crous PW, Boers J, Holdom D, et al. 2022. Fungal Planet description sheets: 1383–1435. Persoonia 48: 261–371. https://doi.org/10.3767/persoonia.2022.48.08.
Effectively published online: 12 July 2022 [Received: 10 April 2022; Accepted: 20 May 2022].

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Acknowledgements Teresa Lebel and colleagues acknowledge the Royal Botanic Gardens Victoria and the Friends of the Royal Botanic Gardens Victoria for funding and support for Northern Territory field and laboratory work; Northern Territory Herbarium staff for space and laboratory access and help with collection curation; State Herbarium of South Australia for support of the undergraduate intern J. Broadbridge. This research was also supported through funding from Australian Biological Resources Study grant (4-EHOJ161) to the State Herbarium of South Australia. Ellen Larsson acknowledges the Swedish Taxonomy Initiative, SLU, Artdatabanken, Uppsala (dha.2019.4.3-13) and the curators of herbaria O, S, UME and UPS. Fernando Esteve-Raventós acknowledges the FEDER/Ministerio de Ciencia, Innovación y Universidades – Agencia Estatal de Investigación, Spain (Project CGL2017-86540-P). Jordi Vila (Institut d'Estudis Catalans) is thanked for sending us material and a photograph of *Inocybe alpestris*. The studies of Hana Ševčíková and Vladimír Antonín was facilitated via institutional support of the long-term conceptual development of research institutions for the Moravian Museum provided by the Czech Ministry of Culture (ref. MK000094862). François Armada and colleagues acknowledge Clotilde & Didier Borgarino and Patrice Tanchaud for collections, and Francisco Donaire (JA-CUSSTA), as fungarium curator. Gregorio Delgado is grateful to William Colbert and Kamash Pillai (Eurofins EMLab P&K) for provision of laboratory facilities. Jose G. Maciá-Vicente acknowledges support from the German Research Foundation under grant MA7171/1-1, and 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). Kandikere R. Sridhar and colleagues are thankful to Prof. Sajeewa S.N. Maharachchikumbura, University of Electronic Science and Technology of China, P.R. China for facilitating phylogenetic tree construction and interpretation. Kai Reschke and colleagues thank Machiel E. Noordeloos for extensive support with their *Entoloma* research. The work of Bálint Dima was supported by the ELTE Thematic Excellence Programme 2020 (TKP2020-IKA-05), financed by the National Research, Development and Innovation Office of Hungary. Antonio Mateos and colleagues thank Amalio Gutiérrez for his collaboration and cooperation in the field collections in Extremadura. Ajay C. Lagashetti and colleagues thank the Director, MACS-Agharkar Research Institute, Pune, for providing necessary facilities, the CSIR, New Delhi for a Senior Research Fellowship (SRF) and S.P. Pune University for granting permission to register for a PhD degree. The study of Daniel Torres-Garcia and colleagues was partially supported by the Spanish Ministerio de Economía, Industria y Competitividad (grant CGL2017-88094-P). Lukasz Istel and co-authors thank Jan Dijksterhuis for the examination of *Microascus rothbergiorum* using Scanning Electron Microscopy. Oded Yarden and Nofar Lifshitz were funded by the Israel Science Foundation. The research of Milan Spetik and co-authors was supported by project No. IGA-ZF/2021-ST2003. Saúl De la Peña-Lastra and colleagues thank the Atlantic Islands National Maritime-Terrestrial Park authorities and guards, especially Víctor Rivas Iglesias, and also Cristóbal Burgos Morillo for his generous help in processing the images. Tracey Steinrucken and colleagues were supported by AgriFutures Australia (Rural Industries Research and Development Corporation), through funding from the Australian Government Department of Agriculture, Water and the Environment, as part of its Rural Research and Development for Profit program (PRJ-010527). Janneke Aylward and colleagues are grateful for funding received from the Department of Science and Innovation (DSI)-National Research Foundation (NRF) Centre of Excellence in Plant Health Biotechnology (CPHB), South Africa and the DST-NRF SARChI chair in Fungal Genomics. Julio Cabero acknowledges Berta Martín from the regional administration of Zamora (Spain) for supporting this work, as well as Hipólito Hernandez, environmental agent in the area of Sanabria, for sharing his knowledge about local flora and ecology. Asunción Morte is grateful to Fundación Séneca- Agencia de Ciencia y Tecnología de la Región de Murcia (20866/PI/18) for financial support. Umpawa Pinruan and colleagues were financially supported by the Platform Technology Management Section, National Center for Genetic Engineering and Biotechnology (BIOTEC), Project Grant No. P19-50231. Konstanze Bensch (Westerdijk Fungal Biodiversity Institute, Utrecht) is thanked for correcting the spelling of various Latin epithets.


Appendopyricularia juncicola

Fungal Planet 1383 – 12 July 2022

Appendopyricularia Crous & Osieck, *gen. nov.*

Etymology. Name refers to a morphological similarity to *Pyricularia*, but with apical conidial appendices.

Classification — *Barbatosphaeriaceae*, *Sordariomycetes incertae sedis*, *Sordariomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate hyphae. *Conidiophores* dimorphic, solitary or in fascicles of 2–3. *Microconidiophores* subcylindrical, hyaline, smooth, geniculate-sinuous. *Macroconidiophores* subcylindrical, straight to curved to geniculate-sinuous, brown, thick-walled, smooth, base swollen or not so, 1–2-septate. *Conidiogenous cells* integrated, terminal, subcylindrical, at times slightly clavate; subdenticulate, denticles cylindrical, with one to several per conidiogenous cell. *Conidia* solitary, hyaline, smooth, guttulate, fusoid to fusoid-ellipsoid, 0–2-septate, hilum truncate, with flexuous central apical appendage.

Type species. *Appendopyricularia juncicola* Crous & Osieck MycoBank MB 844242.

Appendopyricularia juncicola Crous & Osieck, *sp. nov.*

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

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* dimorphic, solitary or in fascicles of 2–3. *Microconidiophores* subcylindrical, hyaline, smooth, geniculate-sinuous, 7–30 × 3–4 µm. *Macroconidiophores* subcylindrical, straight to curved to geniculate-sinuous, brown, thick-walled, smooth, base swollen or not so, 4–7 µm diam, 1–2-septate, 40–80 × 4–5 µm. *Conidiogenous cells* integrated, terminal, subcylindrical, at times slightly clavate, (7–)25–40 × 3–5 µm; subdenticulate, denticles cylindrical, 1–2 × 1 µm, with one to several per conidiogenous cell. *Conidia* (13–)15–20(–22) × 3(–4) µm, solitary, hyaline, smooth, guttulate, fusoid to fusoid-ellipsoid, 0–2-septate, hilum truncate, 1–1.5 µm diam with flexuous central apical appendage, 4–15 µm long.

Culture characteristics — Colonies erumpent, spreading, with sparse to moderate aerial mycelium and feathery margins, reaching 6 mm diam in 2 wk. On MEA surface smoke grey, reverse honey; on PDA surface smoke grey, reverse pale mouse grey; on OA surface pale mouse grey.

Typus. Netherlands, Utrecht Province, Nieuw Wulven, near Houten, 1.5 m a.s.l., N52°02'41" E05°09'49", on dead culm of *Juncus effusus* (*Juncaceae*), 25 Feb. 2021, *E.R. Osieck*, HPC 3600 = WI-26/#4224 (holotype CBS H-24981, cultures ex-type CPC 41278 = CBS 149232, CPC 41279, ITS, LSU, *actA* and *tef1* (first part) sequences GenBank ON603767.1, ON603787.1, ON605619.1, ON605627.1 and ON605635.1, MycoBank MB 844243).

Additional material examined. Netherlands, Utrecht Province, Nieuw Wulven, near Houten, 1.5 m a.s.l., N52°02'45" E05°10'34", on dead culm of *J. effusus*, 24 June 2021, *E.R. Osieck*, HPC 3659 = WI-41/#4274, culture CPC 42171 = CBS 149233, ITS, LSU and *tef1* (first part) sequences GenBank ON603768.1, ON603788.1, ON605628.1 and ON605636.1.

Colour illustrations. *Juncus effusus* growing at Nieuw Wulven, near Houten in Utrecht. Conidiophores giving rise to conidia on SNA; conidiogenous cell with conidia; conidia with apical appendage. Scale bars = 10 µm.

Notes — *Appendopyricularia* resembles genera in the *Pyricularia* complex (Klaubauf et al. 2014), in that it has solitary, pigmented conidiophores that terminate in denticulate conidiogenous cells. It is distinct in that the conidia are hyaline, fusoid to fusoid-ellipsoid, and have a characteristic flexuous central apical appendage, with conidia arranged in an apical circle, curved upwards, bowl-like, when viewed under a dissecting microscope.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 41278 had highest similarity to *Phialemoniopsis curvata* (strain EXF-8700, GenBank KP035004.1; Identities = 389/462 (84 %), 29 gaps (6 %)), *Phialemoniopsis limonesiae* (strain CBS 146752, GenBank NR_172355.1; Identities = 388/461 (84 %), 27 gaps (5 %)) and *Thyridium curvatum* (strain UTHSC R-3448, GenBank HE599292.1; Identities = 387/462 (84 %), 29 gaps (6 %)). The ITS sequences of CPC 41278 and 42171 differ by one substitution and two gaps caused by two separate single nucleotide repeat strings (484/487 nt (99 %), including two gaps). Closest hits using the **LSU** sequence of CPC 41278 are *Barbatosphaeria varioseptata* (strain CBS 137797, GenBank NG_058674.1; Identities = 776/816 (95 %), five gaps (0 %)), *Paradiplococcium singulare* (strain CBS 126091, GenBank NG_066271.1; Identities = 775/815 (95 %), three gaps (0 %)) and *Fluminicola striata* (strain MFLUCC 18-0990, GenBank MW287770.1; Identities = 767/808 (95 %), five gaps (0 %)). The LSU sequences of CPC 41278 and 42171 differ by one gap caused by an extra C in a single nucleotide repeat string (659/660 nt (99 %), including one gap). Closest hits using the ***actA*** sequence of CPC 41278 did not reveal any significant hits, only a very distant association with *Xylariales*. Closest hits using the ***tef1*** (first part) sequence of CPC 41278 did not reveal any significant hits, only a very distant association with *Sordariales* and *Hypocreales*. The *tef1* sequences of CPC 41278 and 42171 differ by one gap caused by an extra C in a single nucleotide repeat string (447/448 nt (99 %), including one gap). Closest hits using the ***tub2*** sequence of CPC 41278 did not reveal any significant hits, only a very distant association with *Glomerellales* and *Xylariales*. The *tub2* sequences of CPC 41278 and 42171 are identical (678/678 nt).

Supplementary material

FP1383-1 Phylogenetic ITS tree.

FP1383-2 Phylogenetic LSU tree.

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Myrmecridium phragmitigenum

Fungal Planet 1384 – 12 July 2022

Myrmecridium phragmitigenum Crous & Osieck, *sp. nov.*

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

Classification — *Myrmecridiaceae*, *Myrmecridiales*, *Sordariomycetidae*, *Sordariomycetes*.

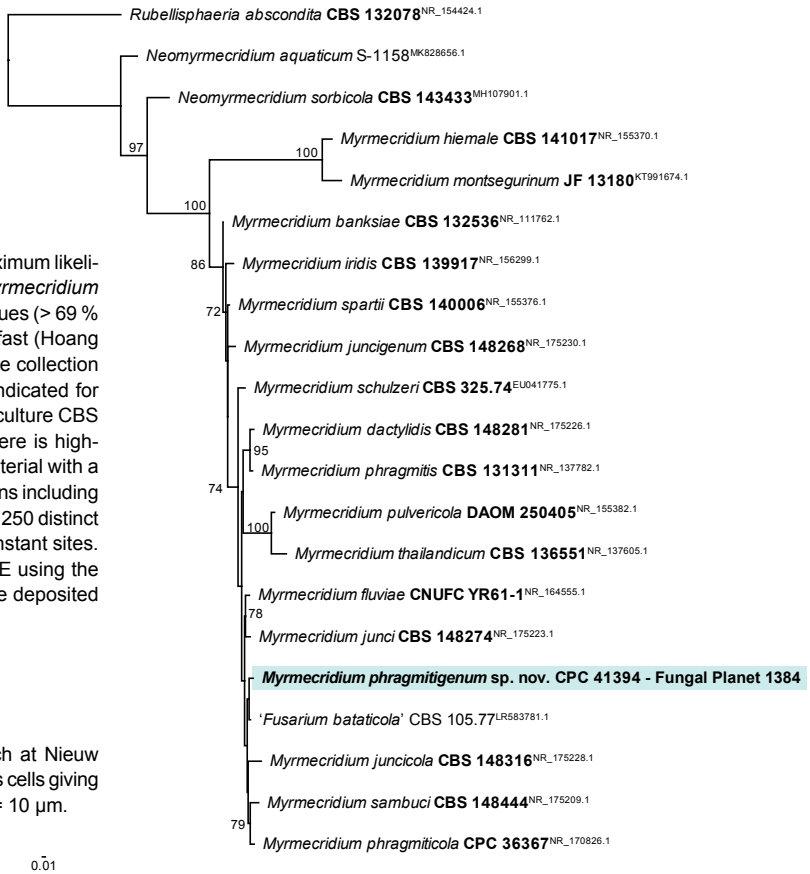
On SNA. *Mycelium* consisting of hyaline, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* unbranched, erect, straight, flexuous, medium brown, at times with nodulose swellings, thick-walled, 3–8-septate, up to 140 µm tall, 3–4 µm diam, with T-shaped basal cell, lacking rhizoids. *Conidiogenous cells* terminal, integrated, subcylindrical, 20–45 µm long, pale brown, forming a rachis with pimple-shaped denticles less than 1 µm long, 0.5 µm diam, slightly thickened. *Conidia* solitary, aseptate, pale brown, thin- and smooth-walled, guttulate with wing-like gelatinous sheath in middle, fusoid, (6–)7–8(–10) × 2.5(–3) µm; hilum unthickened but slightly darkened, 0.5 µm diam.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, even margin, reaching 45 mm diam after 2 wk at 25 °C. On MEA surface hazel, reverse hazel to isabelline; on PDA surface and reverse buff; on OA surface hazel.

Typus. Netherlands, Utrecht Province, Nieuw Wulven, near Houten, 1.5 m a.s.l., N52°03'03" E05°09'46", on dead culm of *Phragmites australis* (*Poaceae*), 25 Feb. 2021, *E.R. Osieck*, HPC 3613 = WI-32/#4221 (holotype CBS H-24955, cultures ex-type CPC 41394 = CBS 148945, ITS and LSU sequences GenBank ON603769.1 and ON603789.1, MycoBank MB 844244).

Notes — *Myrmecridium phragmitigenum* is closely related to *M. phragmiticola* known from *Phragmites australis* in Ukraine (conidia ellipsoid to fusoid, (7–)8–9 × (2.5–)3 µm, conidiophores 2–4-septate, up to 70 µm tall, 3–3.5 µm diam; basal cell 4–6 µm diam; Crous et al. 2020b) and *M. sambuci*, known from *Sambucus nigra* in the Netherlands (conidia ellipsoid to fusoid, (7–)8–9(–10) × (2.5–)3(–3.5) µm, conidiophores (1–)3–7-septate, up to 170 µm tall, 2.5–3 µm diam; Crous et al. 2021c). It can be distinguished from *M. phragmiticola* by its longer, multiseptate conidiophores, but is best distinguished from *M. sambuci* based on DNA data, as the two species are morphologically similar, but phylogenetically distinct. A further species occurring on *Phragmites*, *M. phragmites* has similar ellipsoid to obovoid or fusoid conidia, (6.5–)7–8(–9) × (2.5–)3(–3.5) µm, but shorter conidiophores, 1–4-septate, up to 100 µm tall (Crous et al. 2011).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to '*Neocosmospora striata* / *Fusarium bataticola*' (strain CBS 105.77, GenBank LR583781.1; Identities = 528/535 (99 %), one gap (0 %)), *Myrmecridium schulzeri* (strain CBS 188.96, GenBank EU041772.1; Identities = 508/518 (98 %), three gaps (0 %)) and *Myrmecridium sambuci* (strain CBS 148444, GenBank NR_175209.1; Identities = 523/534 (98 %), two gaps (0 %)). Closest hits using the **LSU** sequence are *Myrmecridium phragmiticola* (strain CPC 36367, GenBank NG_074444.1; Identities = 776/779 (99 %), no gaps), *Myrmecridium schulzeri* (strain CBS 188.96, GenBank EU041829.1; Identities = 775/779 (99 %), no gaps) and *Myrmecridium spartii* (strain CPC 24953, GenBank KR611902.1; Identities = 773/779 (99 %), no gaps).



Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Myrmecridium phragmitigenum* ITS nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast (Hoang et al. 2018) 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 *Rubellisphaeria abscondita* (culture CBS 132078; GenBank NR_154424.1) 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: 21 strains including the outgroup; 565 characters including alignment gaps analysed: 250 distinct patterns, 135 parsimony-informative, 70 singleton sites, 360 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was TIM2e+R2. The alignment and tree were deposited at figshare.com (10.6084/m9.figshare.19745380).

Colour illustrations. Phragmites australis growing along ditch at Nieuw Wulven, near Houten in Utrecht. Conidiophores and conidiogenous cells giving rise to conidia on SNA; conidia with mucoid sheath. Scale bars = 10 µm.

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Paraproliferophorum hyphaenes

Fungal Planet 1385 – 12 July 2022

Paraproliferophorum Crous, *gen. nov.*

Etymology. Name refers to the fact that it is related to the genus *Proliferophorum*.

Classification — *Diaporthomycetidae incertae sedis*, *Diaporthomycetidae*, *Sordariomycetes*.

Mycelium consisting of pale brown, smooth, branched, septate hyphae. *Conidiophores* solitary, erect, subcylindrical, olivaceous brown to medium brown, unbranched or branched above, finely verruculose, 1–2-septate. *Conidiogenous cells* terminal and intercalary, olivaceous brown, smooth to finely verruculose, subcylindrical with slight apical taper, with aggregated cluster of apical denticles, loci slightly darkened. *Conidia* olivaceous brown, smooth, guttulate, fusoid, 0(–1)-septate, tapering to truncate ends, darkened, thickened; with age apical locus elongating sympodially to become ramoconidia, giving rise to 1–2 secondary conidia, fusoid, apex subobtuse, base truncate, hilum darkened, thickened, pale brown, guttulate, smooth.

Type species. *Paraproliferophorum hyphaenes* Crous
MycoBank MB 844245.

Paraproliferophorum hyphaenes Crous, *sp. nov.*

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

Mycelium consisting of pale brown, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* solitary, erect, subcylindrical, olivaceous brown to medium brown, unbranched or branched above, finely verruculose, 1–2-septate, 20–60 × 3–4 µm. *Conidiogenous cells* terminal and intercalary, olivaceous brown, smooth to finely verruculose, subcylindrical with slight apical taper, 15–45 × 2.5–3 µm, with aggregated cluster of apical denticles, 0.5 × 0.5–1 µm, slightly darkened. *Conidia* olivaceous brown, smooth, guttulate, fusoid, 0(–1)-septate, tapering to truncate ends, darkened, thickened, 0.5–1 µm diam, (8–)10–12(–15) × (2.5–)3(–4) µm; with age apical locus elongating sympodially to become ramoconidia, giving rise to 1–2 secondary conidia, fusoid, apex subobtuse, base truncate, hilum darkened, thickened, 0.5 µm diam, pale brown, guttulate, smooth, 4–6 × 2–2.5 µm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with sparse aerial mycelium and smooth, even margin, reaching 8 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse isabelline.

Typus. South Africa, near Mozambique, on living leaves of *Hyphaene* sp. (*Arecaceae*), 19 Oct. 2017, *M.J. Wingfield & J. Roux*, HPC 3501 (holotype CBS H-24949, culture ex-type CPC 40103 = CBS 148939, ITS, LSU, *rpb1* and *tef1* (second part) sequences GenBank ON603770.1, ON603790.1, ON605643.1 and ON605632.1, MycoBank MB 844246).

Colour illustrations. *Hyphaene* sp. in South Africa near Mozambique. Conidiophores and conidiogenous cells giving rise to conidia on SNA; conidia. Scale bars = 10 µm.

Notes — *Paraproliferophorum* is phylogenetically related to *Proliferophorum* (Phookamsak et al. 2019), but distinct from the latter genus in that the conidiophores do not proliferate percurrently, have terminal and intercalary clusters of subdenticulate conidiogenous loci, and form ramoconidia that give rise to secondary conidia with slightly thickened hila. Morphologically *Paraproliferophorum* resembles *Semipseudocercospora* and *Veronaeopsis*, although the former genus has longer, more flexuous conidiophores with terminal conidiogenous cells, and *Veronaeopsis* tends to form a rachis of conidiogenous loci (Arzanlou et al. 2007, Braun et al. 2015).

Based on a blastn search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Proliferophorum thailandicum* (strain MFLUCC 17-0293, GenBank MK028344.1; Identities = 352/422 (83 %), 18 gaps (4 %)), *Plagiosphaera immersa* (strain D270, GenBank MN727889.1; Identities = 178/209 (85 %), two gaps (0 %)) and *Pseudopyricularia higginsii* (strain 09/2007/1470, GenBank KM484875.1; Identities = 183/216 (85 %), eight gaps (3 %)). Closest hits using the **LSU** sequence are *Proliferophorum thailandicum* (strain MFLUCC 17-0293, GenBank MK028343.1; Identities = 802/848 (95 %), ten gaps (1 %)), *Ophiostoma saponiodorum* (strain CBS 128125, GenBank MH877992.1; Identities = 741/845 (88 %), 19 gaps (2 %)) and *Ophiostoma pallidulum* (strain VPRI 43846, GenBank MW046139.1; Identities = 741/845 (88 %), 19 gaps (2 %)). No significant hits were obtained when the ***rpb1*** sequence was used in blastn and megablast searches. Closest hits using the ***tef1*** (second part) sequence had distant similarity to *Phaeoacremonium sphinctrophorum* (strain MFLUCC 11-0629, GenBank KU940202.1; Identities = 481/514 (94 %), no gaps), *Phaeoacremonium minimum* (strain AFTOL-ID 924, GenBank DQ471083.2; Identities = 476/514 (93 %), no gaps) and *Codinaea amazonensis* (strain MUCL 41171, GenBank OL653996.1; Identities = 472/512 (92 %), no gaps).

Supplementary material

FP1385 Phylogenetic tree.

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Niesslia nieuwwulvenica

Fungal Planet 1386 – 12 July 2022

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

Etymology. Name refers to Nieuw Wulven where it was collected.

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

Mycelium consisting of smooth, septate, hyaline, branched, 1.5–2 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells, erect, flexuous, solitary or aggregated, subcylindrical, hyaline, smooth, thick-walled, 65–100 × 2–2.5 µm, swollen in middle part with wavy apical region, terminating in a phialidic apex with non-flared collarette up to 1 µm long, 1.5–2 µm diam. *Stipes* intermingled among conidiophores, straight to flexuous, shorter than conidiophores, 20–40 µm long, thick-walled, terminating in sphaeropedunculate vesicle, 5–6 µm diam. *Conidia* solitary, aseptate, hyaline, smooth, subcylindrical, straight, apex subobtuse, base truncate, (8–)10–12(–13) × 2.5(–3) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, even margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse luteous; on PDA surface and reverse dirty white; on OA surface pale luteous.

Typus. Netherlands, Utrecht Province, Nieuw Wulven, near Houten, 1.5 m a.s.l., N52°02'48" E05°10'33", on dead culm of undetermined *Poaceae*, 19 Mar. 2021, *E.R. Osieck*, HPC 3623 = WI-38/#4238 (holotype CBS H-24953, cultures ex-type CPC 41374 = CBS 148943, ITS, LSU, *actA*, *tef1* (first part) and *tub2* sequences GenBank ON603771.1, ON603791.1, ON605620.1, ON605629.1 and ON605637.1, MycoBank MB 844247).

Notes — Using the key of Gams et al. (2019), *N. nieuwwulvenica* is identified as *N. curvisetosa*, which has much smaller dimorphic conidia, with globose conidia (3.5–)4.0–4.5 µm diam and ellipsoid conidia 3.5–6 × 1.5–2.0 µm. Phylogenetically, *N. nieuwwulvenica* is related to *N. aemula* (conidia cylindrical, 4.5–6.5 × 1.2–2.0 µm) and *N. indica* (conidia guttiliform to clavate, 3-5–4.7 × 1.8–2.2(–3) µm and *N. neoexosporioides* (conidia subcylindrical, (7–)8–10(–14) × 2(–2.5) µm (Gams et al. 2019, Crous et al. 2021b), which differ based on their conidial dimensions.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Niesslia aemula* (strain CBS 556.75, GenBank MG827004.1; Identities = 535/564 (95 %), 15 gaps (2 %)), *Niesslia indica* (strain CBS 313.61, GenBank MH858063.1; Identities = 516/545 (95 %), 17 gaps (3 %)) and *Niesslia neoexosporioides* (strain CBS 146810, GenBank NR_173014.1; Identities = 533/563 (95 %), 14 gaps (2 %)). Closest hits using the **LSU** sequence are *Niesslia exosporioides* (strain CBS 515.72 I, GenBank MH872254.1; Identities = 788/798 (99 %), no gaps), *Niesslia neoexosporioides* (strain CBS 146810, GenBank NG_076714.1; Identities = 791/802 (99 %), one gap (0 %)) and *Niesslia aemula* (strain CBS 556.75, GenBank MG826805.1; Identities = 791/804 (98 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Niesslia neoexosporioides* (strain CPC 38177, GenBank MW890027.1; Identities = 519/574 (90 %), 14 gaps (2 %)) and the protein-coding part of the sequences of *Coccinonectria pachysandricola* (strain CBS 501.63, GenBank KM231167.1; Identities = 398/418 (95 %), no gaps) and *Gliocephalotrichum bulbilium* (strain CBS 242.62, GenBank KM231118.1; Identities = 398/419 (95 %), no gaps). Closest hits using the ***tef1*** (first part) sequence had highest similarity to *Niesslia neoexosporioides* (strain CPC 38177, GenBank MW890097.1; Identities = 284/348 (82 %), 27 gaps (7 %)) and the protein-coding part of the sequences of *Alfaria ossiformis* (strain CBS 324.54, GenBank KU846009.1; Identities = 202/234 (86 %), 9 gaps (3 %)) and *Trichoderma applanatum* (strain 7781, GenBank KJ634757.1; Identities = 144/150 (96 %), no gaps). No significant hits were obtained when the ***tub2*** sequence was used in blastn and megablast searches. However, a blast2 comparison against *Niesslia* beta-tubulin sequences in GenBank revealed highest similarity to *Niesslia ilicifolia* (strain CBS 459.74, GenBank MG896293.1 (unverified sequence); Identities = 244/296 (82 %), 12 gaps (4 %)), *Niesslia exilis* (strain CBS 389.70A, GenBank MG896278.1 (unverified sequence); Identities = 235/293 (80 %), eight gaps (2 %)) and *Monocillium constrictum* (strain CBS 407.70A, GenBank MG896289.1 (unverified sequence); Identities = 239/304 (79 %), 15 gaps (4 %)).

Colour illustrations. *Poaceae* with *Juncus effusus* clumps along ditches in open woodland, in Nieuw Wulven, near Houten in Utrecht. Conidiophores with conidia on SNA; sphaeropedunculate vesicles; conidia. Scale bars = 10 µm.

Supplementary material

FP1386 Phylogenetic tree.

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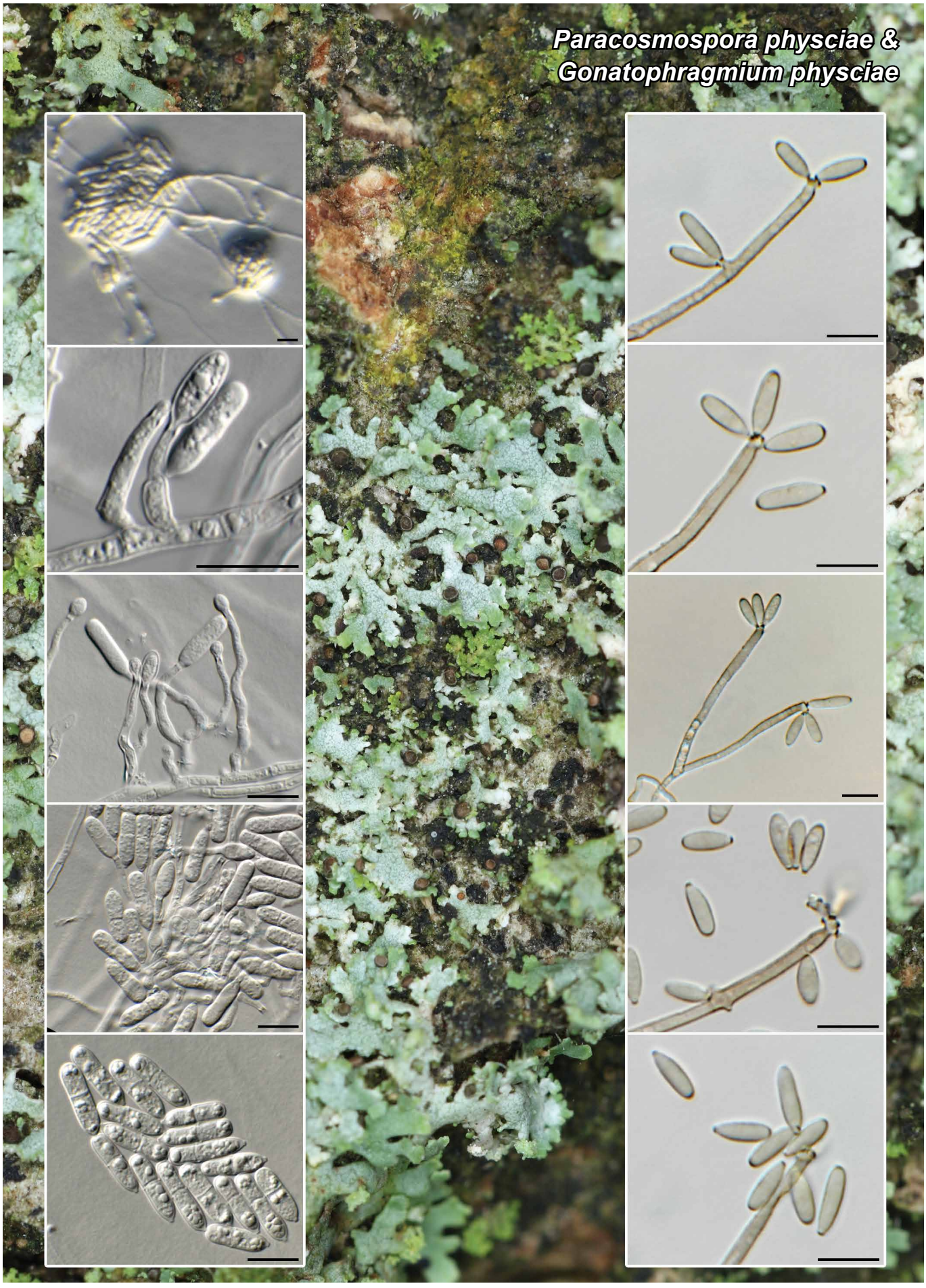
Paracosmospora physciae &
Gonatophragmium physciae

Fungal Planet 1387 & 1388 – 12 July 2022

Paracosmospora Crous & Boers, *gen. nov.*

Etymology. Name refers to its phylogenetic relationship with the genus *Cosmospora*.

Classification — *Hypocreales incertae sedis*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*.

Mycelium consisting of hyaline, smooth, septate, branched hyphae. *Conidiophores* solitary, but mostly aggregated in clusters, forming sporodochia, subcylindrical, smooth, hyaline, erect to wavy, branched or not, 1–2-septate. *Conidiogenous cells* terminal or intercalary, subcylindrical, hyaline, smooth, apex phialidic, with periclinal thickening. *Conidia* solitary, hyaline, smooth, guttulate, subcylindrical, medianly 1-septate, straight, apex obtuse to somewhat flattened, base tapering to truncate scar.

Type species. *Paracosmospora physciae* Crous & Boers MycoBank MB 844248.

Paracosmospora physciae Crous & Boers, *sp. nov.*

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

Mycelium consisting of hyaline, smooth, septate, branched, 2.5–3 µm diam hyphae. *Conidiophores* solitary, but mostly aggregated in clusters, forming sporodochia, subcylindrical, smooth, hyaline, erect to wavy, branched or not, 1–2-septate, 20–50 × 2.5–3 µm. *Conidiogenous cells* terminal or intercalary, subcylindrical, hyaline, smooth, 15–25 µm long, apex phialidic, with periclinal thickening. *Conidia* solitary, hyaline, smooth, guttulate, subcylindrical, medianly 1-septate, straight, apex obtuse to somewhat flattened, base tapering to truncate scar, 1–1.5 µm diam, (11–)13–15(–18) × 4(–4.5) µm.

Culture characteristics — Colonies flat, spreading, with folded surface and moderate aerial mycelium with smooth, lobate margin, reaching 25 mm diam after 2 wk at 25 °C. On MEA surface saffron, reverse sienna; on PDA surface saffron, reverse orange; on OA surface saffron.

Typus. Netherlands, Drenthe Province, Dwingeloo, 52.8358892, 6.3644129, on *Physcia tenella* (*Physciaceae)*, 10 Mar. 2021, *J. Boers*, HPC 3602 (holotype CBS H-24952 culture ex-type CPC 41288 = CBS 148942, ITS, LSU and *tef1* (first part) sequences GenBank ON603772.1, ON603792.1 and ON605630.1, MycoBank MB 844249).

Notes — *Paracosmospora* resembles genera in the *Cosmospora* complex and is allied to *Pseudocosmospora*. It is morphologically distinct, however, in that *Pseudocosmospora* has acremonium-like to verticillium-like asexual morphs with aseptate, ellipsoidal, ovoid, or reniform conidia (Herrera et al. 2013).

(Notes continues on Supplementary material page FP1387 & 1388)

Gonatophragmium physciae Crous & Boers, *sp. nov.*

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

Classification — *Acrospermaceae*, *Acrospermales*, *Dothideomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* solitary, erect, unbranched, subcylindrical, pale brown, smooth, 1–3-septate, 30–60 × 2.5–3 µm. *Conidiogenous cells* terminal, subcylindrical, smooth, pale brown, 10–30 × 2–2.5 µm, with terminal and intercalary loci, consisting of swollen areas with denticulate loci, 0.5–1 µm, darkened, not thickened. *Conidia* pale brown, smooth, (7–)8–9(–10) × (2.5–)3 µm, solitary, subcylindrical to narrowly ellipsoid, aseptate, apex obtuse, base obconically truncate, darkened, 0.5–1 µm diam.

Culture characteristics — Colonies erumpent, spreading, with folded surface and moderate aerial mycelium and smooth, even margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface sienna to isabelline and diffuse scarlet pigment, reverse bay; on PDA surface fulvous, reverse sienna; on OA surface umber.

Typus. Netherlands, Drenthe Province, Dwingeloo graveyard, 52.831376, 6.365404, on *Physcia caesia* (*Physciaceae)*, 28 Mar. 2021, *J. Boers*, HPC 3614 (holotype CBS H-24967, culture ex-type CPC 41464 = CBS 149048, ITS and LSU sequences GenBank ON603773.1 and ON603793.1, MycoBank MB 844250).

Additional material examined. Netherlands, Drenthe Province, Dwingeloo graveyard, 52.831376, 6.365404, on *Physcia tenella* (*Physciaceae)*, 28 Mar. 2021, *J. Boers*, HPC 3614, CPC 41466, 41467, ITS and LSU sequences of CPC 41466 GenBank ON603774.1 and ON603794.1.

Notes — Hudson et al. (2019) suggested that although the asexual morph of *Acrospermum* is not known, close relatives include *Gonatophragmium*, *Pseudovirgaria* and *Radulidium*. Furthermore, Crous et al. (2021b) also added *Pseudoacrospermum* to the complex. If these taxa are congeneric, then the older name *Acrospermum* (1790) would have precedence. However, the type species, *A. compressum* (on dry stems of *Heracleum sphondylium*, Germany), is not yet known from culture or DNA. It thus remains to be determined whether *Acrospermum* is monophyletic. Based on its morphology, we have tentatively described the present taxon in *Gonatophragmium. Gonatophragmium physciae* should also be compared to *G. lichenophilum* (on *Xanthoria parietina* in Austria), although the latter has longer, septate conidia ((7–)9–15(–17) × (2.5–)3–4(–4.5) µm, (0–)1(–2)-septate) (see key in Berger et al. 2015).

(Notes continues on Supplementary material page FP1387 & 1388)

Colour illustrations. *Physcia tenella* at Dwingeloo graveyard. *Paracosmospora physciae* (left column). Sporodochia on SNA; conidiophores and conidiogenous cells giving rise to conidia; conidia. *Gonatophragmium physciae* (right column). Conidiophores and conidiogenous cells giving rise to conidia. Scale bars = 10 µm.

Supplementary material

FP1387-1 *Paracosmospora physciae* phylogenetic ITS tree.

FP1387-2 *Paracosmospora physciae* phylogenetic LSU tree.

FP1388 *Gonatophragmium physciae* phylogenetic ITS tree.

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Neoacrodontium gallicum

Fungal Planet 1389 – 12 July 2022

Neoacrodontium Crous & Decock, *gen. nov.*

Etymology. Name refers to the morphologically similar genus *Acrodontium*.

Classification — *Amplistromataceae*, *Amplistromatales*, *Sordariomycetidae*, *Sordariomycetes*.

Mycelium consisting of subhyaline to pale olivaceous, smooth, thin-walled, septate, branched, hyphae. *Conidiophores* erect, arising from hyphae, brown at base, becoming subhyaline toward apex, branched subverticillately, septate. *Conidiogenous cells* integrated, terminal and intercalary, basal part flask-shaped, with long flexuous, elongated neck, proliferating sympodially to form a long rachis; denticles pimple-like or elongated. *Conidia* solitary, subhyaline, subglobose, base with unthickened truncate scar.

Type species. Neoacrodontium gallicum Crous & Decock MycoBank MB 844251.

Neoacrodontium gallicum Crous & Decock, *sp. nov.*

Etymology. Name refers to France where it was collected.

Mycelium consisting of subhyaline to pale olivaceous, smooth, thin-walled, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* erect, arising from hyphae, brown at base, becoming subhyaline toward apex, branched subverticillately, 1–3-septate. *Conidiogenous cells* integrated, terminal and intercalary, basal part flask-shaped, with long flexuous, elongated neck, proliferating sympodially to form a long rachis, 20–60 × 2–3 µm; denticles pimple-like, 0.5 µm diam, or elongated, up to 2 µm long, 0.5 µm diam. *Conidia* 2–3 µm diam, solitary, subhyaline, subglobose, base with truncate scar, 0.5 µm diam.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, even margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA surface and reverse ochreous; on PDA surface and reverse saffron; on OA surface ochreous.

Typus. France, Ile de France, Paris, 7ième arrondissement, in house, from bore dust of *Xestobium rufovillosum* feeding on *Quercus* wood (death-watch beetle), Sept. 2020, *C. Decock* (holotype CBS H-24951 culture ex-type CPC 41118 = CBS 148941 = MUCL 58099, ITS and LSU sequences GenBank ON603775.1 and ON603795.1, MycoBank MB 844252).

Notes — *Neoacrodontium* (*Amplistromataceae*) is phylogenetically distinct from morphologically similar genera such as *Acrodontium* (*Teratosphaeriaceae*; Videira et al. 2016) and *Xenoacrodontium* (*Xenoacrodontiaceae*; Crous et al. 2021c). *Neoacrodontium gallicum* clusters with CBS 349.55 (unknown country, keratinous substrate, F. Blank, 3 Jan. 1955), which was identified as *Acrodontium hydnicola* (De Hoog 1972), and belongs to the same genus.

Neoacrodontium hydnicola (Peck) Crous & Decock, *comb. nov.* — MycoBank MB 844253

Basionym. *Virgaria hydnicola* Peck, Ann. Rep. N.Y. State Mus. 42: 128. 1889.
Synonyms. *Tritirachium hydnicola* (Peck) Hughes, Canad. J. Bot. 31: 604. 1953.
Acrodontium hydnicola (Peck) de Hoog, Stud. Mycol. 1: 31. 1972.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to '*Acrodontium*' *hydnicola* (strain CBS 349.55, GenBank MH857507.1; Identities = 515/602 (86 %), 44 gaps (7 %)), '*Acrodontium*' *simplex* (strain CBS 127.53, GenBank MH857128.1; Identities = 378/462 (82 %), 41 gaps (8 %)) and *Acidothrix acidophila* (strain MH566, GenBank FJ430780.3; Identities = 341/420 (81 %), 28 gaps (6 %)). Closest hits using the **LSU** sequence are '*Acrodontium*' *hydnicola* (strain CBS 349.55, GenBank MH869047.1; Identities = 806/833 (97 %), two gaps (0 %)), *Wallrothiella congregata* (strain SMH1760, GenBank FJ532375.1; Identities = 753/839 (90 %), 16 gaps (1 %)) and *Amplistroma erinaceum* (strain CBS 134881, GenBank MH877572.1; Identities = 655/733 (89 %), 17 gaps (2 %)).

Colour illustrations. *Quercus* wood with beetle damage. Insect galleries in wood; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Supplementary material

FP1389-1 Phylogenetic ITS tree.

FP1389-2 Phylogenetic LSU tree.

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Parastenospora pini

Fungal Planet 1390 – 12 July 2022

Parastenospora Crous, *gen. nov.*

Etymology. Name refers to *Stenospora*, which is morphologically similar to this genus.

Classification — *Incertae sedis*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes.*

Mycelium consisting of hyaline, smooth, branched, septate hyphae. *Conidiophores* terminal on hyphae, or intercalary, erect, solitary, subcylindrical, straight to flexuous, hyaline, smooth, septate, branched below or unbranched. *Conidiogenous cells* subcylindrical, hyaline, smooth, terminal or intercalary, holoblastic with one to several denticulate loci, unthickened, not darkened, frequently with rosette of denticulate loci. *Conidia* solitary, hyaline, smooth, guttulate, obclavate, apex subobtuse, base obconically truncate, straight to curved, septate; hilum unthickened, not darkened.

Type species. *Parastenospora pini* Crous
MycoBank MB 844254.

Parastenospora pini Crous, *sp. nov.*

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

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* terminal on hyphae, or intercalary, erect, solitary, subcylindrical, straight to flexuous, hyaline, smooth, 0–3-septate, branched below or unbranched, 10–30 × 2.5–3 µm. *Conidiogenous cells* 3–10 × 2–5 µm, subcylindrical, hyaline, smooth, terminal or intercalary, holoblastic with one to several denticulate loci, 1–3 × 1.5–2 µm, unthickened, not darkened, frequently with rosette of denticulate loci. *Conidia* solitary, hyaline, smooth, guttulate, obclavate, apex subobtuse, base obconically truncate, straight to curved, (1–)3(–6)-septate, (25–)45–70(–85) × (3–)4(–5) µm; hilum unthickened, not darkened, 1.5–2 µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, even margin, reaching 5 mm diam after 2 wk at 25 °C. On MEA surface and reverse ochreous; on PDA surface and reverse dirty white; on OA surface dirty white.

Typus. Netherlands, Utrecht Province, Soest, De Zoom, on dead twigs of *Pinus sylvestris* (*Pinaceae*), 1 Nov. 2020, *A.L. van Iperen*, HPC 3492 (holotype CBS H-24950, culture ex-type CPC 40385 = CBS 148940, ITS, LSU, *rpb2* and *tub2* sequences GenBank ON603776.1, ON603796.1, ON605622.1 and ON605638.1, MycoBank MB 844255).

Notes — *Parastenospora* is reminiscent of *Condylospora* and *Stenospora*. However, *Stenospora* is mycoparasitic, and has slightly thickened scars and hila (Braun et al. 2013), while *Condylospora* is aquatic, having unique L- or N-shaped conidia (Yen et al. 2012). The latter genera are thus morphologically and phylogenetically distinct from *Parastenospora*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had distant similarity over mainly the 5.8S nrRNA gene to *Neocamarosporium solicola* (strain IBRC M 30257, GenBank KX817217.1; Identities = 347/393 (88 %), ten gaps (2 %)), *Didymocyrtis cladoniicola* (strain 19E070, GenBank MZ206178.1; Identities = 373/431 (87 %), 11 gaps (2 %)),and *Ascochyta manawaorae* (strain 1213, GenBank MZ400577.1; Identities = 373/432 (86 %), 11 gaps (2 %)). Closest hits using the **LSU** sequence are *Pseudopyrenochaeta lycopersici* (strain CBS 306.65, GenBank NG_057799.1; Identities = 847/860 (98 %), no gaps), *Subplenodomus galicola* (voucher MFLU 15-1368, GenBank NG_070410.1; Identities = 843/863 (98 %), no gaps) and *Subplenodomus urticae* (voucher MFLU 17-1694, GenBank NG_073768.1; Identities = 843/863 (98 %), no gaps). Distant hits were obtained using the ***rpb2*** sequence, with highest similarity to *Podonectria kuwanaspis* (strain SICAUCC 21-0007, GenBank MW462123.1; Identities = 617/735 (84 %), no gaps), *Neocucurbitaria aetnensis* (strain C261, GenBank MF795811.1; Identities = 609/736 (83 %), no gaps) and *Neocucurbitaria cinereae* (strain KU9, GenBank MF795813.1; Identities = 607/736 (82 %), no gaps). Distant hits were obtained using the ***tub2*** sequence, with highest similarity to *Parafenestella pseudosalicis* (strain C301, GenBank MK357620.1; Identities = 253/291 (87 %), one gap (0 %)), *Parafenestella vindobonensis* (strain C302, GenBank MK357632.1; Identities = 258/300 (86 %), 11 gaps (3 %)) and *Neocucurbitaria keratinophila* (strain CNM-CM 6401, GenBank LT992261.1; Identities = 255/295 (86 %), one gap (0 %)).

Colour illustrations. Pinus sylvestris in De Zoom, Soest. Conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Supplementary material

FP1390 Phylogenetic tree.

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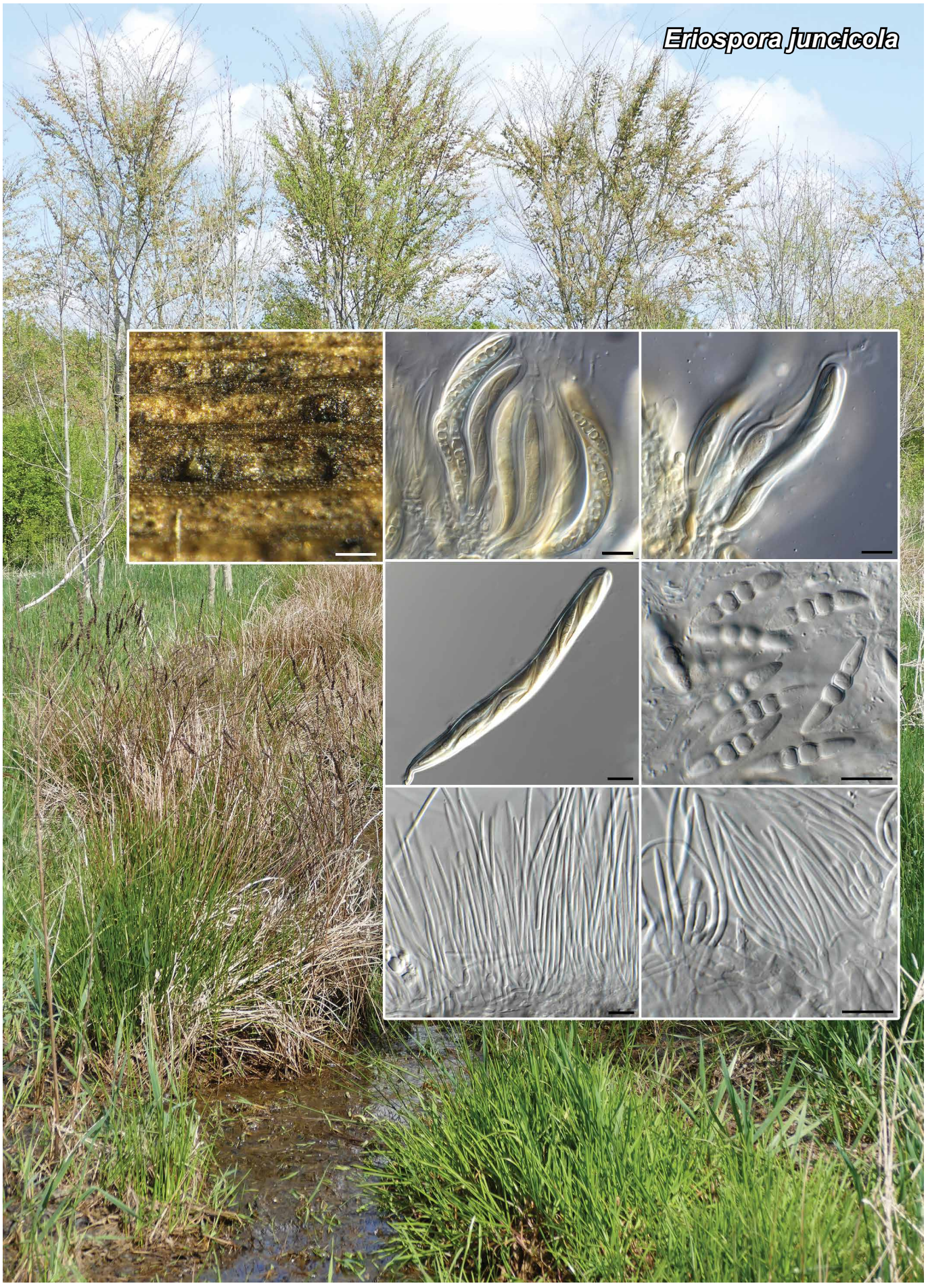
Eriospora juncicola

Fungal Planet 1391 – 12 July 2022

Eriospora juncicola Crous & Osieck, *sp. nov.*

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

Classification — *Stictidaceae*, *Ostropales*, *Ostropomycetidae*, OSLEUM clade, *Lecanoromycetes*.

Ascomata pseudothecial, immersed in host tissue, globose, 250–300 µm diam, with central ostiole; wall of 2–3 layers of brown *textura angularis*. *Pseudoparaphyses* trabeculae-like, hyaline, smooth, branched, septate, anastomosing, 1.5–2 µm diam. *Asci* hyaline, smooth, fusoid-ellipsoid, apex obtuse with stipitate base, ocular chamber well defined, bitunicate with 2–3 seriate ascospores, 100–130 × 15–17 µm. *Ascospores* hyaline, smooth, guttulate, fusoid ellipsoid, initially medianly septate, becoming 3-septate, constricted at septa, prominently swollen in cell above median septum, encased in 5–7 µm diam thick mucoid sheath, (22–)24–26(–30) × 5(–6) µm (in Melzer). *Conidiomata* pycnidial, immersed in agar, separate, globose, unilocular with thick wall and central ostiole. *Conidiophores* reduced to conidiogenous cells that proliferate sympodially at apex, subcylindrical, hyaline, smooth, 5–10 × 1.5–2 µm. *Conidia* frequently remaining attached to conidiogenous cells, hyaline, smooth, curved, multi-septate, cylindrical with obtuse ends, 30–100 × 1.5–2 µm.

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

Typus. Netherlands, Utrecht Province, Nieuw Wulven, near Houten, N52°02'48" E05°10'33", on dead culm of *Juncus effusus* (*Juncaceae*), 19 Mar. 2021, *E.R. Osieck*, HPC 3620 = WI-35/#4233 (holotype CBS H-24958, culture ex-type CPC 41498 = CBS 148948, ITS and LSU sequences GenBank ON603777.1 and ON603797.1, MycoBank MB 844256).

Notes — *Eriospora* is a genus of saprobic coelomycetes for which there was no known sexual morph (Sutton 1980). The type species, *E. leucostoma*, was treated by Crous et al. (2020c), with cultures from *Typha* sp. (the type host genus), and *Juncus effusus*. *Eriospora juncicola* has a sexual morph, which distinguishes it from the asexual *E. leucostoma.* The two species have morphologically similar asexual morphs, but are phylogenetically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Eriospora leucostoma* (strain CPC 35594, GenBank MT223795.1; Identities = 589/651 (90 %), 15 gaps (2 %)), *Neofitzroyomyces nerii* (strain CBS 145088, GenBank NR_161144.1; Identities = 580/656 (88 %), 38 gaps (5 %)) and *Fitzroyomyces cyperacearum* (strain MFLU 19-2725, GenBank MW293953.1; Identities = 391/441 (89 %), 14 gaps (3 %)). Closest hits using the **LSU** sequence are *Eriospora leucostoma* (strain CPC 35594, GenBank MT223890.1; Identities = 778/780 (99 %), no gaps), *Neofitzroyomyces nerii* (strain CBS 145088, GenBank NG_068278.1; Identities = 778/786 (99 %), no gaps) and *Phacidiella alsophilae* (strain CPC 37041, GenBank MT373344.1; Identities = 728/769 (95 %), five gaps (0 %)).

Colour illustrations. *Juncus effusus* in Nieuw Wulven, near Houten, Utrecht. Ascomata immersed in host tissue; asci and pseudoparaphyses; ascus; ascospores; conidiogenous cells giving rise to branched conidia. Scale bars: ascomata = 300 µm, all others = 10 µm.

Supplementary material

FP1391 Phylogenetic tree.

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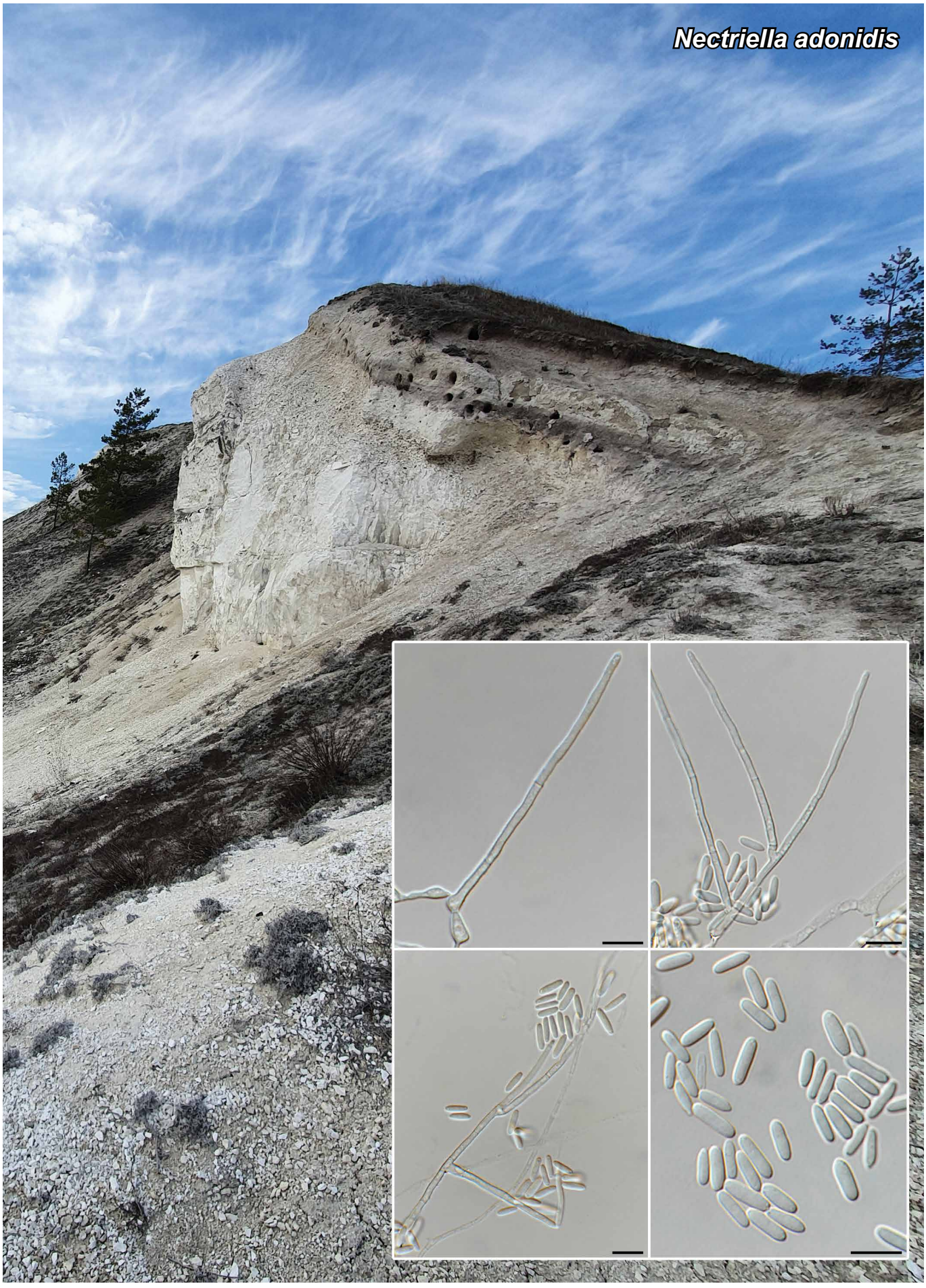

Nectriella adonidis

Fungal Planet 1392 – 12 July 2022

Nectriella adonidis Crous & Akulov, *sp. nov.*

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

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

Mycelium consisting of hyaline, septate, smooth, branched, 1.5–2 µm diam hyphae. *Conidiophores* erect, solitary, unbranched or subverticillately branched with terminal and intercalary conidiogenous cells. *Conidiogenous cells* acremonium-like, monophialidic, somewhat thick-walled, cylindrical, flexuous, with slight apical taper, 35–80 × 2.5–3 µm. *Conidia* hyaline, smooth, aseptate, thin-walled, guttulate, fusoid-ellipsoid, ends obtuse, straight, hilum bluntly rounded to truncate, 1.5 µm diam, (7–)8–10(–11) × (2–)2.5(–3) µm. *Sexual morph* unknown.

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

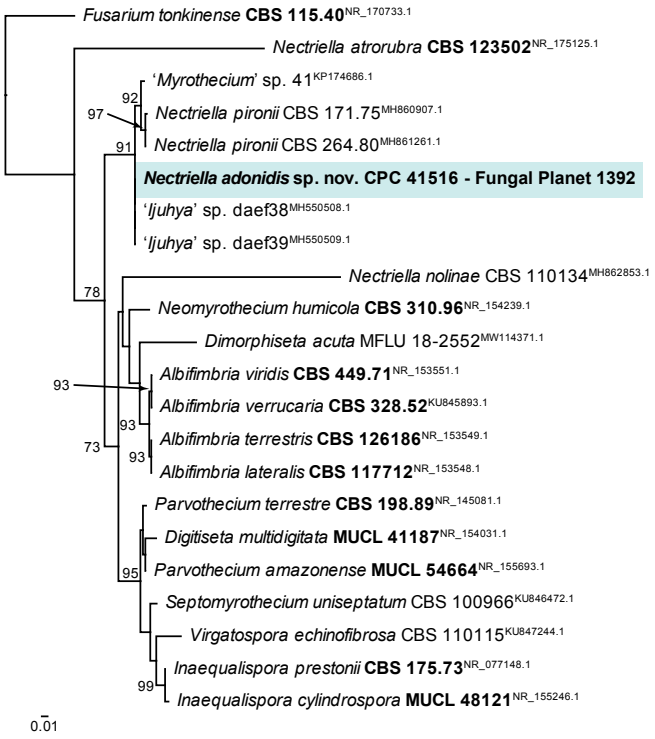
Typus. Ukraine, Kharkiv region, Dvorichna district, Krasne Pershe village, National Park Dvorichanskyi, on overwintered stems of *Adonis vernalis* (*Ranunculaceae*), 11 Apr. 2021, *A. Akulov*, ex CWU (MYC) AS 8121, HPC 3630 (holotype CBS H-24960, culture ex-type CPC 41516 = CBS 148950, ITS and LSU sequences GenBank ON603778.1 and ON603798.1, MycoBank MB 844257).

Notes — *Nectriella* (based on *N. fuckellii*) is characterised by white to pale yellow or pale brown ascomatal perithecia (frequently immersed) and ellipsoid to fusoid, 1-septate, hyaline, smooth to faintly spinulose to striate ascospores. Where known from culture, species produce kutilakesa-like sporodochia, and acremonium-like asexual morphs (Alfieri & Samuels 1979, Rossman et al. 1999). However, most *Nectriella* spp. occur on dead wood and herbaceous substrates, and are not considered plant pathogenic (Rossman et al. 1999). Based on the few cultures that are available, *Nectriella* is paraphyletic, and the only plant pathogen, *N. pironii*, together with *N. adonidis* probably represents a distinct genus.

Nectriella adonidis is closely related to *N. pironii*, which produces kutilakesa-like sporodochia on PDA, and an acremonium-like asexual morph on corn meal agar. *Nectriella adonidis* was isolated from orange sporodochia, but sporulated only on SNA, producing an acremonium-like morph, and no sporodochia, making it difficult to compare to other known species. This is the first *Nectriella* species described from *Adonis vernalis*, which occurs in the dry meadows and steppes of Eurasia.

Colour illustrations. National Park Dvorichanskyi, Krasne Pershe village, Kharkiv region, Ukraine. Conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to '*Ijuhya* sp.' (strain daef39, GenBank MH550509.1; Identities = 555/555 (100 %), no gaps), *Nectriella pironii* (strain CBS 264.80, GenBank MH861261.1; Identities = 548/555 (99 %), no gaps) and *Parvothecium terrestre* (strain CBS 198.89, GenBank NR_145081.1; Identities = 516/557 (93 %), 12 gaps (2 %)). Closest hits using the **LSU** sequence are '*Sarcopodium circinatum*' (strain CBS 376.81, GenBank HQ232167.1; Identities = 788/788 (100 %), no gaps), *Nectriella pironii* (strain CBS 264.80, GenBank MH873030.1; Identities = 780/788 (99 %), one gap (0 %)) and *Pseudoachroiostachys krabiense* (strain MFLUCC 16-0325, GenBank NG_068839.1; Identities = 774/788 (98 %), three gaps (0 %)).



Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Nectriella adonidis* ITS nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5000 ultrafast (Hoang et al. 2018) 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 *Fusarium tonkinense* (culture CBS 115.40; GenBank NR_170733.1) 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: 22 strains including the outgroup; 644 characters including alignment gaps analysed: 228 distinct patterns, 88 parsimony-informative, 113 singleton sites, 443 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was TNe+R2. The alignment and tree were deposited at figshare.com (10.6084/m9.figshare.19745380).

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Nothodevriesia narthecii

Fungal Planet 1393 – 12 July 2022

Nothodevriesia Crous & Boers, *gen. nov.*

Etymology. Phylogenetically related but distinct from *Devriesia*.

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

Saprobic on leaf litter. *Ascomata* pseudothecial, amphigenous, immersed to erumpent, superficial, globose, ostiole inconspicuous; ascomata linked by immersed brown hyphal network; hyphae medium brown, smooth, constricted at septa; ascomatal wall consisting of 2–3 layers of medium brown *textura angularis*. *Asci* aparaphysate, bitunicate, subsessile, obovoid to broadly ellipsoid, 8-spored. *Ascospores* multiseriate, overlapping, hyaline to pale brown (verruculose upon discharge), guttulate, thin-walled, straight, obovoid, ends obtuse, widest in middle of apical cell, medianly 1-septate, constricted at septum, tapering towards both ends, but more prominently towards lower end.

Type species. *Nothodevriesia narthecii* Crous & Boers MycoBank MB 844258.

Nothodevriesia narthecii Crous & Boers, *sp. nov.*

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

Leaf spots absent, associated with leaf litter. *Ascomata* pseudothecial, amphigenous, immersed to erumpent, superficial, globose, 30–45 µm diam, ostiole inconspicuous; ascomata linked by immersed brown hyphal network; hyphae medium brown, smooth, 4–5 µm diam, constricted at septa; ascomatal wall consisting of 2–3 layers of medium brown *textura angularis*. *Asci* aparaphysate, bitunicate, subsessile, obovoid to broadly ellipsoid, 8-spored, 15–20 × 9–10 µm. *Ascospores* multiseriate, overlapping, hyaline to pale brown (verruculose upon discharge), guttulate, thin-walled, straight, obovoid, ends obtuse, widest in middle of apical cell, medianly 1-septate, constricted at septum, tapering towards both ends, but more prominently towards lower end, (7–)8–9(–10) × (2.5–)3 µm. Germinating from one end, with germ tube at angle to the long axis.

Culture characteristics — Colonies erumpent, spreading, surface folded with moderate aerial mycelium and lobate, even margin, reaching 4 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse iron-grey.

Typus. Netherlands, Drenthe Province, Dwingelderveld National Park, 52.829188, 6.432495, on dead leaves of *Narthecium ossifragum* (*Nartheciaceae*), 13 July 2021, *J. Boers*, HPC 3655 (holotype CBS H-24985, cultures ex-type CPC 42166 = CBS 149066, ITS, LSU, *actA*, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank ON603779.1, ON603799.1, ON605621.1, ON605623.1, ON605631.1 and ON605639.1, MycoBank MB 844259).

Notes — *Nothodevriesia narthecii* represents a sexual morph in the *Teratosphaeriaceae* occurring on dead leaves of *Narthecium ossifragum*. Although related, it is morphologically and phylogenetically distinct from *Devriesia*, which includes hyphomycetous species that are soil-borne, as well as saprobic taxa found in dead plant material (Seifert et al. 2004, Crous & Groenewald 2011, Chang et al. 2022).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phaeothecoidea melaleuca* (strain CPC 17223, GenBank HQ599594.1; Identities = 444/501 (89 %), 11 gaps (2 %)), *Teratosphaeria jonkershoekensis* (strain CBS 122897, GenBank EU707864.1; Identities = 443/503 (88 %), 14 gaps (2 %)) and *Neocatenulostroma microsporum* (strain HFJN1, GenBank MH349092.1; Identities = 433/485 (89 %), 13 gaps (2 %)). Closest hits using the **LSU** sequence are *Devriesia thermodurans* (strain CBS 115878, GenBank NG_059078.1; Identities = 802/833 (96 %), no gaps), *Teratosphaeria hortaea* (strain CBS 124156, GenBank MH874881.1; Identities = 798/834 (96 %), five gaps (0 %)) and *Readeriella considenianae* (strain CMW37676, GenBank JQ732948.1; Identities = 798/834 (96 %), five gaps (0 %)). Closest hits using the ***actA*** sequence had highest similarity to *Neocatenulostroma germanicum* (strain CAT104, GenBank KU612288.1; Identities = 444/508 (87 %), 12 gaps (2 %)), *Teratosphaeria dunnii* (strain CBS 145548, GenBank MK876463.1; Identities = 372/404 (92 %), no gaps) and *Teratosphaeria gracilis* (strain CBS 145090, GenBank MK047523.1; Identities = 442/507 (87 %), nine gaps (1 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Teratosphaeria corymbiicola* (strain CBS 146047, GenBank MN556802.1; Identities = 472/623 (76 %), ten gaps (1 %)), *Teratosphaeria eucalypti* (strain CPC 12552, GenBank KX348102.1; Identities = 509/685 (74 %), 10 gaps (1 %)) and *Teratosphaeria biformis* (strain CBS 124578, GenBank KX348100.1; Identities = 471/624 (75 %), 12 gaps (1 %)). No significant hits were obtained when the ***tef1*** (first part) and ***tub2*** sequences were used in blastn and megablast searches.

Colour illustrations. *Narthecium ossifragum* in Dwingelderveld National Park. Ascomata in host tissue; broken ascoma with asci; brown ascospores on host tissue; germinating ascospores on MEA. Scale bars: intact ascomata = 30 and 45 µm, respectively, all others = 10 µm.

Supplementary material

FP1393-1 *Nothodevriesia narthecii* phylogenetic ITS tree.

FP1393-2 *Nothodevriesia narthecii* phylogenetic LSU tree.

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Tetraploa juncicola

Fungal Planet 1394 – 12 July 2022

Tetraploa juncicola Crous & Osieck, *sp. nov.*

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

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

Mycelium consisting of medium brown, verruculose, septate, branched, 2–3 µm diam hyphae. *Conidiogenous cells* monoblastic, intercalary on hyphae, doliiform to ellipsoid, 3–6 × 3–5 µm. *Conidia* solitary, dry, composed on basal conidial body and 1–4 brown, septate apical appendages; conidia body (17–)20–30(–35) × (15–)18–20(–23) µm, medium brown, guttulate, verruculose, narrowly ellipsoid to subcylindrical, composed of brown, verruculose, four vertical columns of cells, 3–5 distoseptate. *Appendages* 30–100 µm long, medium brown, 3–8-septate, thick-walled, guttulate, smooth-walled.

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

Typus. Netherlands, Flevoland Province, Horsterwold, N52°18'52" E05°28'10", on dead culm of *Juncus inflexus* (*Juncaceae*), 31 Mar. 2021, *E.R. Osieck*, HPC 3631 = WI-39/#4240 (holotype CBS H-24965, culture ex-type CPC 41580 = CBS 149046, ITS, LSU and *rpb2* sequences GenBank ON603780.1, ON603800.1 and ON605624.1, MycoBank MB 844260).

Notes — *Tetraploa* (= *Tetraplosphaeria*), based on *T. aristata*, is characterised by micronematous conidiophores, monoblastic conidiogenous cells and tetraploate conidia (4-euseptate, short-cylindrical, brown, vertical columns that are verrucose at the base, with 4-setose, divergent, short or long septate appendages at the apex; Tanaka et al. 2009). *Tetraploa aristata*, long believed to be a single species with high ecological variation, is considered by Tanaka (loc. cit.) as species complex. Approximately 20 species are known (Bao et al. 2021), of which some have been linked to a massarina-like sexual morph (Crous et al. 2021a). *Tetraploa juncicola* is similar to *T. aquatica* and *T. thailandica*, having monoblastic conidiogenous cells and four vertical columns, with up to four apical appendages. It is distinct in that vertical columns of *T. aquatica* are 2–3-septate, while conidia of *T. juncicola* and *T. thailandica* are 3–5-septate, but *T. thailandica* has longer appendages, being 73–136 µm long, 5–10-distoseptate (Bao et al. 2021). It is also rather similar to *T. aristata* which has a slightly larger conidial body with 3–6 columns and somewhat shorter appendages (Ellis 1949). *Tetraploa* species are saprobic mostly on monocotyledons (more than half of the species) and/or in freshwater habitats. *Tetraploa juncicola* is the 3rd *Tetraploa* species recorded from Europe.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Tetraploa yunnanensis* (strain MFLUCC 19-0319, GenBank NR_171886.1; Identities = 522/544 (96 %), six gaps (1 %)), *Tetraploa sasicola* (strain 5-1, GenBank KX440178.1; Identities = 513/535 (96 %), four gaps (0 %)) and *Tetraploa endophytica* (strain P6086, GenBank KT270279.1; Identities = 489/515 (95 %), nine gaps (1 %)). Closest hits using the **LSU** sequence are *Tetraploa endophytica* (strain CBS 147114, GenBank MW659165.1; Identities = 678/683 (99 %), one gap (0 %)), *Tetraploa sasicola* (voucher HHUF 27566, GenBank NG_042329.1; Identities = 758/766 (99 %), no gaps) and *Tetraploa yunnanensis* (strain MFLUCC 18-0652, GenBank MN913697.1; Identities = 767/776 (99 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Tetraploa yunnanensis* (strain MFLUCC 19-0319, GenBank MT878451.1; Identities = 677/737 (92 %), no gaps), *Melanomma pulvis-pyrius* (strain KH 77, GenBank LC203400.1; Identities = 542/740 (73 %), 12 gaps (1 %)) and *Ernakulamia krabiensis* (strain MFLUCC 18-0237, GenBank MK434872.1; Identities = 535/734 (73 %), seven gaps (0 %)).

Colour illustrations. *Juncus inflexus* in woodland border, Horsterwold, Flevoland Province. Conidiogenous cells giving rise to conidia; conidia with apical appendages. Scale bars = 10 µm.

Supplementary material

FP1394 Phylogenetic tree.

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Neochalara lolae

Fungal Planet 1395 – 12 July 2022

Neochalara lolae Crous, *sp. nov.*

Etymology. Named after Lola, a Labradoodle member of the Crous family, who indicated where to collect this specimen in her favourite forest.

Classification — *Pezizellaceae*, *Rhytismatales*, *Leotiomycetes.*

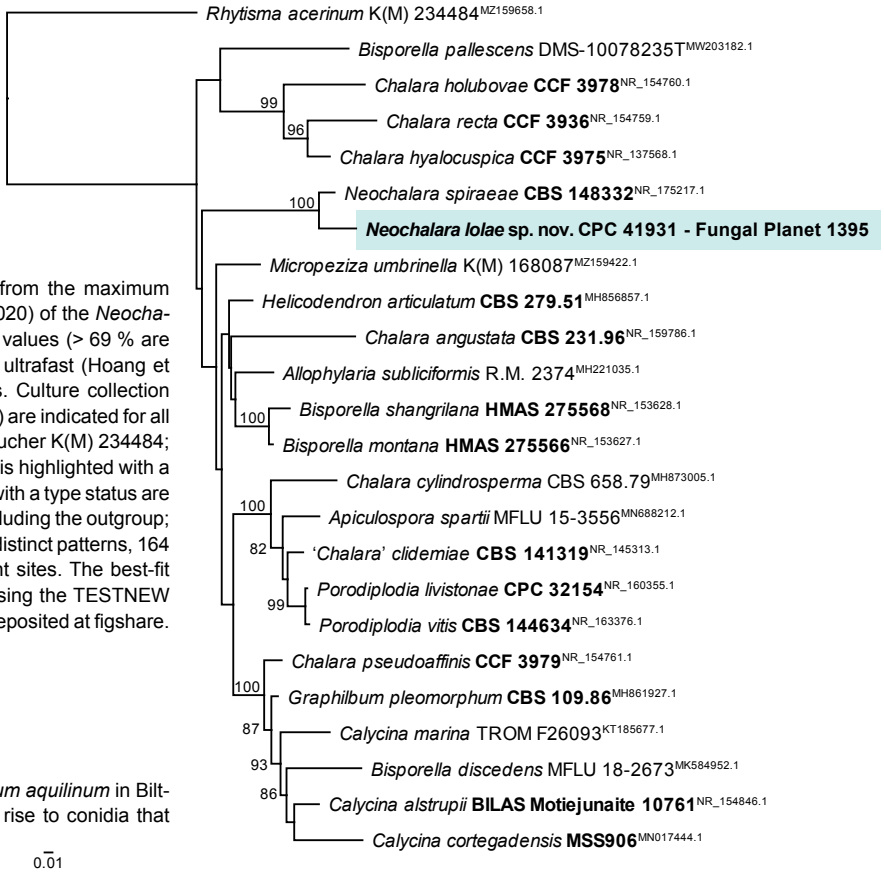
Mycelium consisting of hyaline, smooth, branched, 2–2.5 µm diam hyphae. *Conidiophores* solitary, erect, medium brown, smooth, 1–2-septate, with gradual transition between venter and neck; conidiophores 50–70 µm tall; venter 20–30 × 4–6 µm, without any sign of percurrent rejuvenation; neck cylindrical, 10–25 × 3–4 µm. *Conidia* occurring in long flexuous, unbranched chains, hyaline, smooth, thin-walled, guttulate, ends bluntly rounded, (9–)12–16(–28) × (2.5–)3 µm, 1–3(–4)-septate.

Culture characteristics — Colonies erumpent, with sparse aerial mycelium and lobate, even margin, reaching 6 mm diam after 2 wk at 25 °C. On MEA surface and reverse ochreous; on PDA surface dirty white, reverse ochreous; on OA surface ochreous.

Typus. Netherlands, Utrecht Province, Bilthoven, on stems of *Pteridium aquilinum* (*Dennstaedtiaceae)*, 24 May 2021, *P.W. Crous*, *K.L. Crous & L. Crous*, HPC 3644 (holotype CBS H-24986, culture ex-type CPC 41931 = CBS 149065, ITS, LSU, *rpb1* and *tub2* sequences GenBank ON603781.1, ON603801.1, ON605644.1 and ON605640.1, MycoBank MB 844261).

Notes — *Neochalara lolae* is common on the fronds of *Pteridium aquilinum* in the Netherlands, and forms extremely long conidial chains. It must be compared with *C. pteridina*, that occurs on this host in Europe. It differs from the latter that has single or short conidial chains, conidiophores with percurrent rejuvenation, a wider venter (5–9.2 µm), longer collarettes (12–44(–50) × 3–4.5 µm), and mostly 3-septate conidia, (8–)12(–18) × (2–)2.5(–3) µm (Nag Raj & Kendrick 1975). *Neochalara lolae* is similar to *N. spiraeae*, which also has septate conidia with truncate ends (on *Spiraea japonica*, Netherlands), but is distinct in that the latter species has smaller, 1-septate conidia ((11–)12–14(–16) × (3–)4(–4.5) µm, av. 13 × 4 µm; Crous et al. 2021c).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neochalara spiraeae* (strain CBS 148332, GenBank NR_175217.1; Identities = 457/489 (93 %), 16 gaps (3 %)), *Lambertella advenula* (strain FC-1007, GenBank AB705236.1; Identities = 336/380 (88 %), 25 gaps (6 %)) and *Orbiliopsis callistea* (voucher PDD 97932, GenBank HQ533049.1; Identities = 403/461 (87 %), nine gaps (1 %)). Closest hits using the **LSU** sequence are *Neochalara spiraeae* (strain CPC 39565, GenBank OK663754.1; Identities = 806/817 (99 %), no gaps), *Calycina citrina* (voucher G.M. 2014-12-14-4, GenBank KY462815.1; Identities = 785/817 (96 %), no gaps) and *Bisporella citrina* (strain M253, GenBank EU940087.1; Identities = 785/817 (96 %), no gaps). No significant hits were obtained when the ***rpb1*** and ***tub2*** sequences were used in blastn and megablast searches.



Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Neochalara lolae* ITS nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5000 ultrafast (Hoang et al. 2018) 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 *Rhytisma acerinum* (voucher K(M) 234484; GenBank MZ159658.1) 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: 24 strains including the outgroup; 579 characters including alignment gaps analysed: 299 distinct patterns, 164 parsimony-informative, 83 singleton sites, 332 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was TIM2e+I+G4. The alignment and tree were deposited at figshare.com (10.6084/m9.figshare.19745380).

Colour illustrations. Lola inspecting stems of *Pteridium aquilinum* in Bilthoven. Conidiophores with conidiogenous cells giving rise to conidia that form in chains; conidia. Scale bars = 10 µm.

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Aspergillus rouenensis

Fungal Planet 1396 – 12 July 2022

Aspergillus rouenensis Crous & Decock, *sp. nov.*

Etymology. Name refers to Rouen, capital of the northern French region of Normandy, where this species was collected.

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

Mycelium consisting of hyaline, smooth, branched, septate, 2–2.5 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells arising laterally from hyphae, erect, hyaline, smooth, subcylindrical to narrowly ampulliform, phialidic, at times with inconspicuous percurrent proliferation, 4–20 × 2.5–3 µm. *Conidia* occurring in short chains (–15), ovoid to ellipsoid to ovoid, apex obtuse, base truncate, thick-walled, aseptate, guttulate, hyaline, smooth, becoming somewhat verruculose and on MEA greenish (hyaline on SNA), (3.5–)4–5 × (3.5–)4–5 µm.

Culture characteristics — Colonies erumpent, spreading, surface folded with moderate aerial mycelium and smooth, lobate margin, reaching 6 mm diam after 2 wk at 25 °C. On MEA surface olivaceous buff, reverse olivaceous; on PDA surface and reverse olivaceous buff; on OA surface olivaceous buff.

Typus. France, Normandy, Rouen, in house, bore dust of *Xestobium rufovillosum* feeding on *Quercus* wood (death-watch beetle), Feb. 2021, *C. Decock* 376a (holotype CBS H-24987, culture ex-type CPC 41585 = CBS 149067 = MUCL 58110, ITS, LSU, *BenA* , *CaM* and *rpb2* sequences GenBank ON603782.1, ON603802.1, ON605641.1, ON653193.1 and ON653194.1, MycoBank MB 844262).

Additional material examined. France, Normandie, Rouen, in house, bore dust of *Xestobium rufovillosum* feeding on *Quercus* wood (death-watch beetle), Feb. 2021, *C. Decock* 376a, culture CBS 149068 = CPC 41586 = MUCL 58109, ITS, LSU and *tub2* sequences GenBank ON603783.1, ON603803.1 and ON605642.1.

Notes — *Aspergillus* is subdivided in six subgenera with 27 sections (Houbraken et al. 2020, Visagie et al. 2021). *Aspergillus rouenensis* is phylogenetically distinct and is sister to a clade containing *A. baarnensis*, *A. loretoensis*, *A. salinarum* and *A. salisburgensis*. Houbraken et al. (2020) accepted 17 species in *Aspergillus* subgenus *Polypaecilum* (currently 20 species are accepted), and introduced six series in the subgenus: *Canini*, *Kalimarum*, *Noonimiarum*, *Polypaecilum*, *Salinarum* and *Whitfieldiorum*. *Aspergillus rouenensis* belongs to series *Salinarum* and shares the production of simple, solitary, monophialidic conidiogenous cells borne laterally or terminally on hyphae. No chlamydospores were observed in *A. rouenensis*, while these structures were observed in *A. salinarum* and *A. salisburgensis* cultures. *Aspergillus baarnensis*, *A. loretensis* and *A. salinarum* are strict halophiles (unable to grow in medium without NaCl) in contrast to *A. rouenensis* that is able to grow on media without NaCl. *Aspergillus loretensis* also differs by production of smaller conidia (2.5–4 µm vs (3.5–)4–5 µm).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 41585 had highest similarity to *Aspergillus baarnensis* (strain CBS 348.68, GenBank MH859155.1; Identities = 551/598 (92 %), nine gaps (1 %)), *Aspergillus salinarum* (strain CBS 138583, GenBank NR_157473.1; Identities = 548/596 (92 %), nine gaps (1 %)) and *Aspergillus kalimae* (strain CBS 143506, GenBank NR_156332.1; Identities = 546/594 (92 %), 16 gaps (2 %)). The ITS sequences of CPC 41585 and 41586 are identical (575/575 nt). Closest hits using the **LSU** sequence of CPC 41585 are *Aspergillus caninus* (strain CBS 128032, GenBank NG_064243.1; Identities = 815/831 (98 %), no gaps), *Aspergillus limoniformis* (strain FZ4148-2, GenBank MK328972.1; Identities = 813/829 (98 %), one gap (0 %)) and *Aspergillus baarnensis* (strain CBS 129.65, GenBank MH870150.1; Identities = 816/836 (98 %), five gaps (0 %)). The LSU sequences of CPC 41585 and 41586 are identical (831/831 nt). Closest hits using the ***BenA*** sequence of CPC 41585 had highest similarity to *Aspergillus salisburgensis* (strain CBS 142047, GenBank MN969414.1; Identities = 238/271 (88 %), no gaps), *Aspergillus baarnensis* (strain DAOMC 251735, GenBank KY980551.1; Identities = 236/271 (87 %), six gaps (2 %)) and *Aspergillus phialosimplex* (strain LC12658, GenBank MK336099.1; Identities = 218/256 (85 %), two gaps (0 %)). The *tub2* sequences of CPC 41585 and 41586 are identical (381/381 nt). Closest hits using the ***CaM*** sequence had highest similarity to *Aspergillus salinarum* (strain CBS 138583, GenBank KY980583.1; Identities = 433/508 (85 %), 15 gaps (2 %)), *Aspergillus baarnensis* (strain CBS 380.74, GenBank KY980585.1; Identities = 432/513 (84 %), 21 gaps (4 %)) and *Aspergillus telluris* (as *Aspergillus* sp.; strain CGMCC3.19701, GenBank MN635264.1; Identities = 432/514 (84 %), 24 gaps (4 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Aspergillus salisburgensis* (strain CBS 142047, GenBank MN969191.1; Identities = 589/632 (93 %), no gaps), *Aspergillus baarnensis* (strain CBS 380.74, GenBank JN121509.1; Identities = 597/643 (93 %), no gaps) and *Aspergillus loretoensis* (strain CM-CNRG 624, GenBank MK312162.1; Identities = 657/710 (93 %), no gaps).

Colour illustrations. Roof of house with beetle damage in Rouen, Normandy. Conidiogenous cells on SNA giving rise to conidia; conidial chains. Scale bars = 10 µm.

Supplementary material

FP1396-1 Phylogenetic *BenA* tree.

FP1396-2 Phylogenetic *rpb2* tree.

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Newbrunswickomyces abietophilus

Fungal Planet 1397 – 12 July 2022

Newbrunswickomyces Crous & Malloch, *gen. nov.*

Etymology. Name refers to New Brunswick, Canada, where this species was collected.

Classification — *Pezizales incertae sedis*, *Pezizales*, *Pezizomycetes*.

Mycelium consisting of hyaline to brown, smooth to verruculose, branched, septate hyphae. *Sporodochia* developing on agar surface with mucoid conidial mass. *Conidiophores* aggregated in sporodochia, erect, branched, septate. *Conidiogenous cells* terminal and intercalary, subcylindrical, hyaline, smooth, phialidic with inconspicuous percurrent proliferation at apex. *Conidia* solitary, hyaline, subcylindrical to narrowly ellipsoid, apex obtuse, tapering to truncate hilum, septate.

Type species. Newbrunswickomyces abietophilus Crous & Malloch MycoBank MB 844263.

Newbrunswickomyces abietophilus Crous & Malloch, *sp. nov.*

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

Mycelium consisting of hyaline to brown, smooth to verruculose, branched, septate, 2–3 µm diam hyphae. *Sporodochia* developing on agar surface with mucoid conidial mass. *Conidiophores* aggregated in sporodochia, erect, branched, 1–5-septate, up to 80 µm tall. *Conidiogenous cells* terminal and intercalary, subcylindrical, hyaline, smooth, phialidic with inconspicuous percurrent proliferation at apex, 5–15 × 3–4 µm. *Conidia* solitary, hyaline, subcylindrical to narrowly ellipsoid, apex obtuse, tapering to truncate hilum, 2.5–3 µm diam, 3-septate, (14–)16–18(–21) × (4–)5 µm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and lobate, even margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse greenish black.

Typus. Canada, New Brunswick, Charlotte Co., 1.5 km SW of Little Lepreau, 45.135614° -66.492269°, on buds of *Abies balsamea* (*Pinaceae*), 4 May 2021, *D.W. Malloch*, HPC 3633 (holotype CBS H-24961, culture ex-type CPC 41918 = CBS 149042, ITS, LSU, *rpb1* and SSU sequences GenBank ON603784.1, ON603804.1, ON605645.1 and ON603974.1, MycoBank MB 844264).

Notes — *Newbrunswickomyces abietophilus* is phylogenetically closely related to *Phialea strobilina* (CBS 643.85), which has *Chalara strobilina* as asexual morph (Gams & Philippi 1992), and is thus morphologically quite distinct. Although future research might resolve *Newbrunswickomyces* as asexual morph for one of the known sexual genera in *Pezizales*, we have been unable to resolve this question and have therefore chosen to name it in a new genus.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phialea strobilina* (strain CBS 643.85, GenBank EF596821.1; Identities = 513/551 (93 %), nine gaps (1 %)), *Scleropezicula alnicola* (strain CBS 200.46, GenBank AF141168.1; Identities = 512/551 (93 %), 10 gaps (1 %)) and *Mollisina uncinata* (voucher KUS-F52307, GenBank JN033404.1; Identities = 481/518 (93 %), 11 gaps (2 %)). Closest hits using the **LSU** sequence are *Phialea strobilina* (strain CBS 643.85, GenBank EF596821.1; Identities = 799/810 (99 %), no gaps), *Rhytisma acerinum* (voucher J. Platt (DUKE), GenBank AF356696.1; Identities = 775/787 (98 %), two gaps (0 %)) and *Calycellina fagina* (voucher SBRH925, GenBank OM218631.1; Identities = 795/810 (98 %), no gaps). No significant hits were obtained when the ***rpb1*** sequence was used in blastn and megablast searches. Closest hits using the **SSU** sequence are *Rhytisma acerinum* (voucher J. Platt (DUKE), GenBank AF356695.1; Identities = 865/878 (99 %), no gaps), *Dicephalospora huangshanica* (voucher MFLU 18-1828, GenBank MK585051.1; Identities = 864/878 (98 %), no gaps) and *Dicephalospora rufocornea* (voucher MFLU 18-1827, GenBank MK585050.1; Identities = 863/878 (98 %), no gaps).

Colour illustrations. Abies balsamea in Charlotte Co., New Brunswick. Conidiophores and conidiogenous cells on SNA giving rise to septate conidia. Scale bars = 10 µm.

Supplementary material

FP1397 Phylogenetic tree.

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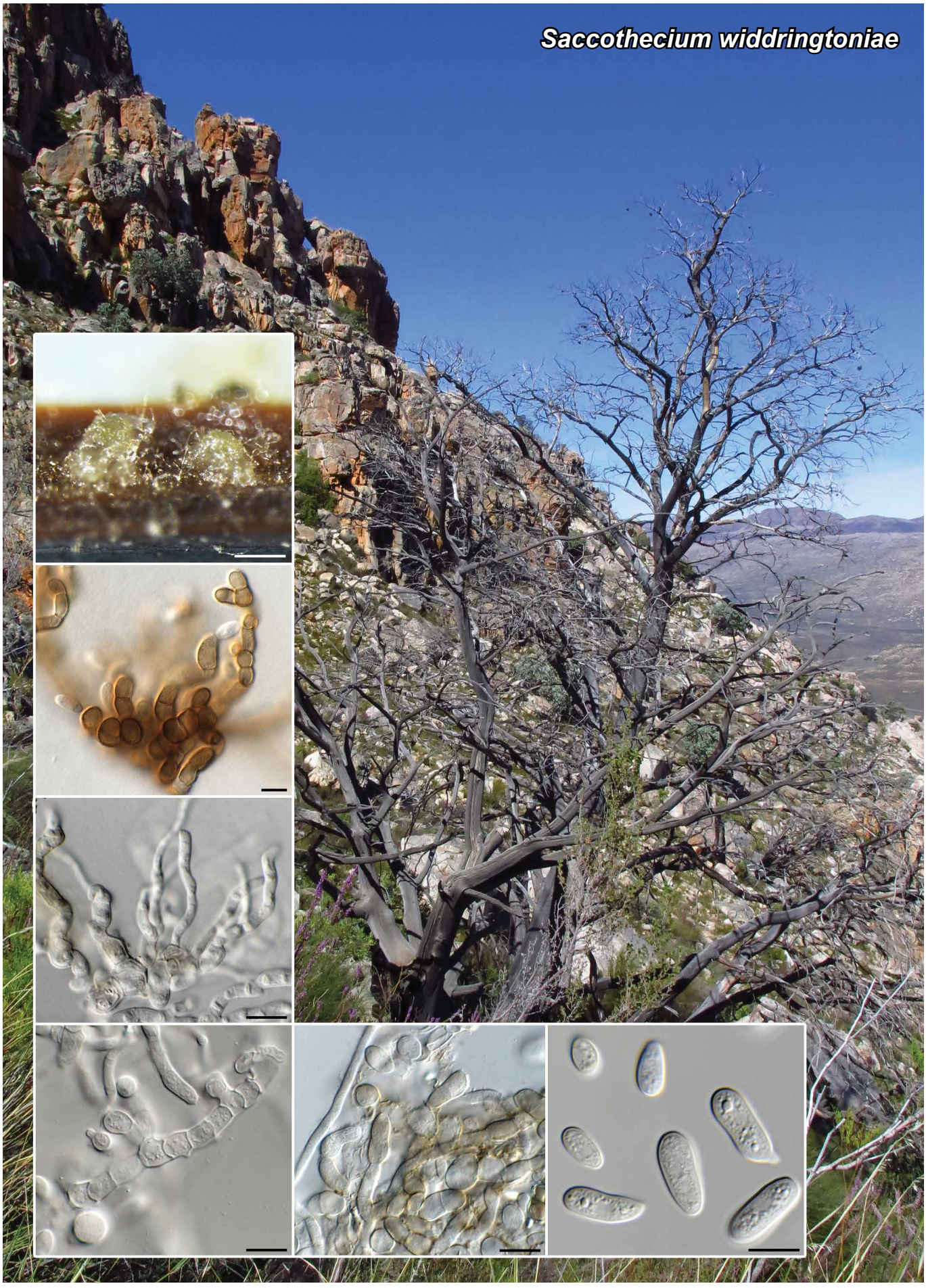

Saccothecium widdringtoniae

Fungal Planet 1398 – 12 July 2022

Saccothecium widdringtoniae Crous, *sp. nov.*

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

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

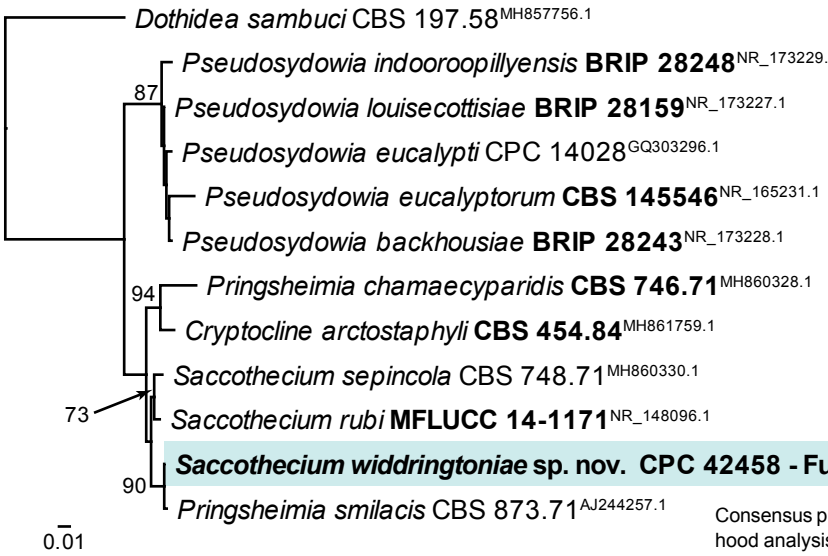
Sporodochia solitary, superficial, hyaline, becoming pale brown, up to 250 µm diam, giving rise to mucoid conidial mass. *Conidiophores* reduced to conidiogenous cells which are solitary loci on hyphae forming sporodochia, intercalary, subdenticulate, pale brown, smooth. *Conidia* solitary, 0–1-septate, hyaline to brown, smooth, fusoid-ellipsoid, straight to slightly curved, (10–)12–14(–18) × (5–)6–7(–8) µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and lobate, smooth margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface brown vinaceous, reverse grey olivaceous.

Typus. South Africa, Northern Cape Province, Cederberg, on twigs of *Widdringtonia wallichii* (*Cupressaceae*), 3 Sept. 2018, *F. Roets & M.J. Wingfield*, HPC 3770 (holotype CBS H-24973, culture ex-type CPC 42458 = CBS 149071, ITS, LSU, *rpb2* and *tef1* (second part) sequences GenBank ON603785.1, ON603805.1, ON605625.1 and ON605633.1, MycoBank MB 844265).

Notes — *Saccothecium widdringtoniae* was isolated from sporodochia occurring on twigs of *Widdringtonia wallichii* in the Cederberg, South Africa. Only the aureobasidium-like morph (Barr 1972) of *Saccothecium* was found, complicating its generic placement. However, given its phylogenetic similarity to other taxa in the genus, *Saccothecium* is appropriate.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pringsheimia smilacis* (strain CBS 873.71, GenBank AJ244257.1; Identities = 520/525 (99 %), four gaps (0 %; all due to variability in number of nucleotide repeats)), *Saccothecium rubi* (strain MFLUCC 14-1171, GenBank NR_148096.1; Identities = 519/531 (98 %), five gaps (0 %)) and *Saccothecium sepincola* (strain CBS 748.71, GenBank MH860330.1; Identities = 512/527 (97 %), six gaps (1 %)). Closest hits using the **LSU** sequence are *Saccothecium rubi* (strain MFLUCC 14-1171, GenBank NG_059644.1; Identities = 756/765 (99 %), no gaps), *Cryptocline arctostaphyli* (strain 19GCAS004, GenBank MW077311.1; Identities = 755/765 (99 %), no gaps) and *Pseudosydowia indooroopillyensis* (strain BRIP 28248, GenBank MW443081.1; Identities = 753/765 (98 %), two gaps (0 %)). The LSU sequence of *Pringsheimia smilacis* (strain CBS 873.71, GenBank FJ150970.1) is only 94 % similar (Identities = 521/557 (94 %), four gaps (0 %)). No significant hits were obtained when the ***rpb2*** and ***tef1*** (second part) sequences were used in blastn and megablast searches.



Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Saccothecium widdringtoniae* ITS nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5000 ultrafast (Hoang et al. 2018) 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 *Dothidea sambuci* (culture CBS 197.58; GenBank MH857756.1) 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: 12 strains including the outgroup; 615 characters including alignment gaps analysed: 117 distinct patterns, 40 parsimony-informative, 57 singleton sites, 518 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was TIM2e+G4. The alignment and tree were deposited at figshare.com (10.6084/m9.figshare.19745380).

Colour illustrations. *Widdringtonia wallichii* in Cederberg, Northern Cape Province. Sporodochia on pine needle agar; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars: sporodochia = 250 µm, all others = 10 µm.

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Verticillium bjoernoeyanum

Fungal Planet 1399 – 12 July 2022

Verticillium bjoernoeyanum Crous & Rämä, *sp. nov.*

Etymology. Name refers to Bear Island (Bjørnøya in Norwegian), an island in the Barents Sea where the fungus was collected.

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

Mycelium consisting of hyaline, smooth, branched, septate, 2–3 µm diam hyphae. *Microsclerotia* not seen. *Conidiophores* erect, subcylindrical, branched or not, hyaline, smooth, arising from superficial hyphae, 1–2-septate. *Conidiogenous cells* phialidic, solitary, or verticillate to subverticillate on hyphae, subulate, with slight apical taper, (8–)20–30(–40) × 2.5–3.5 µm, apex 1.5 µm diam, with non-flared collarette, 0.5–1.5 µm long. *Conidia* hyaline, smooth, 0–2-septate, subcylindrical with obtuse ends, dimorphic, smaller 0–1-septate conidia (7–)10–15(–17) × 2–3 µm, whereas longer conidia 1–2-septate, 18–25(–32) × 3 µm; conidia accumulating in crystalline mucoid mass, with both conidial types developing on the same phialide. On SNA developing chains or small clusters of chlamydospores, hyaline, smooth, ellipsoid, 5–11 µm diam.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and smooth, even margin, reaching 5 mm diam after 2 wk at 25 °C MEA and PDA, 35 mm diam on OA. On MEA surface and reverse ochreous; on PDA and OA surface and reverse dirty white.

Typus. Norway, Svalbard, Bjørnøya, Kvalrossfjæra, isolated from sand grains attached to a piece of driftwood that was found on a sandy beach, N74°30'10" E18°58'11", 21 Aug. 2020, *T. Rämä*, TRä3203I, (Governor of Svalbard´s collection permission RiS-ID 11551) (holotype CBS H-25000, culture ex-type 149167 = CPC 43267, ITS, LSU, *rpb1*, *rpb2*, SSU and *tef1* (second part) sequences GenBank ON603786.1, ON603806.1, ON605646.1, ON605626.1, ON603975.1 and ON605634.1, MycoBank MB 844266).

Notes — There are currently three *Verticillium* species that are considered as marine fungi. These include *V. dahliae*, *V. cellulosae* and *V. terrestre*, according to the marinefungi.org website (Jones et al. 2019). These species are encountered both in the terrestrial and the marine environments, whereas *V. bjoernoeyanum* described in this study has thus far only been found in the marine environment. *Verticillium bjoernoeyanum* was isolated on an autoclaved agar medium consisting of freeze-dried diatom (*Porosira glacialis*) pellets (2 g/L), and Sigma Sea salts (40 g/L). The isolation was done by streaking sand grains attached to a piece of driftwood (2 cm diam, 17 cm long) over the agar surface. The fungus was subcultured on corn meal agar and malt extract agar supplemented with Sigma Sea salts. The isolation site was a sandy beach of Kvalrossfjæra that is located on the Northern shore of Bear Island, alongside the weather station. The ITS sequence and sequences from three protein-coding genes showed that *V. bjoernoeyanum* falls in the genus but is phylogenetically distinct from other marine and terrestrial species of *Verticillium*. The morphological observations and culture characteristics provided by Inderbitzin et al. (2011) support this conclusion.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Verticillium tricorpus* (strain CBS 237.75, GenBank MH860910.1; Identities = 523/543 (96 %), eight gaps (1 %)), *V. albo-atrum* (strain CBS 127169, GenBank MH864456.1; Identities = 521/546 (95 %), nine gaps (1 %)) and *V. longisporum* (strain CBS 128316, GenBank MH864843.1; Identities = 520/546 (95 %), nine gaps (1 %)). Closest hits using the **LSU** sequence are *Verticillium zaregamsianum* (strain CBS 130342, GenBank NG_069489.1; Identities = 812/818 (99 %), two gaps (0 %)), *V. klebahnii* (strain CBS 130344, GenBank NG_069486.1; Identities = 812/818 (99 %), two gaps (0 %)) and *V. isaacii* (strain CBS 130343, GenBank NG_069485.1; Identities = 812/818 (99 %), two gaps (0 %)). Closest hits using the ***rpb1*** sequence had highest similarity to *Verticillium isaacii* (strain NO-1, GenBank AB548758.1; Identities = 525/591 (89 %), three gaps (0 %)), *V. tricorpus* (strain CE98Vt1, GenBank AB545917.1; Identities = 523/591 (88 %), three gaps (0 %)) and *V. zaregamsianum* (strain Shichi6, GenBank AB545914.1; Identities = 522/591 (88 %), three gaps (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Verticillium albo-atrum* (strain CBS 130340, GenBank LR026233.1; Identities = 385/440 (88 %), no gaps), *V. zaregamsianum* (strain V204, GenBank KJ443183.1; Identities = 385/441 (87 %), two gaps (0 %)) and *V. tricorpus* (strain CBS 803.97, GenBank LR026285.1; Identities = 378/437 (86 %), no gaps). Closest hits using the **SSU** sequence are *Verticillium zaregamsianum* (strain V202, GenBank KJ443093.1; Identities = 1020/1021 (99 %), no gaps), *V. nonalfalfae* (strain CBS 382.66, GenBank CP069146.1; Identities = 1018/1021 (99 %), no gaps) and *V. dahliae* (strain ATCC 16535, GenBank AY489705.1; Identities = 1018/1021 (99 %), no gaps). Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Verticillium nonalfalfae* (strain CBS 321.91, GenBank LR026579.1; Identities = 356/374 (95 %), no gaps), *V. alfalfae* (strain CBS 127169, GenBank LR026546.1; Identities = 356/374 (95 %), no gaps) and *V. albo-atrum* (strain CBS 102464, GenBank LR026541.1; Identities = 355/375 (95 %), two gaps (0 %)).

Colour illustrations. Kvalrossfjæra on the northern shore of Bear Island, the type location of *V. bjoernoeyanum*. Sporulating colony on SNA; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Supplementary material

FP1399 Phylogenetic tree.

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Agaricus albofoetidus

Fungal Planet 1400 – 12 July 2022

Agaricus albofoetidus Boxshall, Broadbridge & T. Lebel, *sp. nov.*

Etymology. Named for the large white basidiomata with strong persistent phenol odour.

Classification — *Agaricaceae*, *Agaricales*, *Agaricomycetes.*

Pileus 25–65(–75) mm diam, apex and general shape square when young, becoming hemispherical with flattened apex (square) with age; appearing shiny and smooth with very fine fibrils and scales scattered over surface, white or barely tinged cream-coloured, margin of pileus can appear slightly roughened with veil remnants; context staining bright yellow immediately. *Lamellae* free, crowded, thin, pale pink becoming dull brown; lamellulae in four series. *Stipe* (25–)38–70(–90) × 5–13 mm, central, cylindrical, tapering slightly to apex, with a very slightly bulbous base, surface silky, appearing smooth above and below the annulus, white handling slightly reddish brown; context staining bright yellow immediately. *Annulus* sub-apical to supra-median, very broad, becoming pendent with maturity, comprising universal and partial veils as a 'double annulus'; universal veil thick, pale to light brown, friable ridge breaking into large fragments; partial veil thin and elastic, lower surface floccose, white becoming beige-light brown towards margins with age, sometimes producing pale yellowish brown droplets at margins, connected to stipe by robust, arachnoid fibres that may break upon drying causing annulus to become moveable. *Odour* strong, persistently of phenol when fresh and dried. *Basidiospores* 5–6.5 × (2.8–)3–3.5(–4.0) µm, (5.53 ± 0.34 × 3.35 ± 0.28, Q = 1.37–2.01, n = 36), ellipsoid to elongate ellipsoid, smooth, brown when mature, hyaline when immature, thick-walled 0.5–0.8 µm, germ pore absent; 2-spored 6.4–7 × (3.6–)4–4.9(–5.1) µm, (6.64 ± 0.2 × 4.39 ± 0.48, Q = 1.28–1.77, n = 8), thick-walled. *Basidia* 15–20 × (4.5–)5–8 µm, clavate, hyaline, mostly 4-spored, some 2-spored; sterigmata inconspicuous. *Cheilocystidia* absent. *Pleurocystidia* absent. *Hymenophoral trama* composed of interwoven, septate, hyaline hyphae, 3–4 µm wide; *subhymenium* 17–20 µm wide, composed of 3–4 parenchymatous cells, 6.4–8 × 4.5–7.0 µm. *Pileipellis* a cutis composed of hyaline, smooth, unpigmented, septate hyphae, 3–5 µm wide, cylindrical, smooth, sometimes constricted at the septa; terminal elements cylindrical and apex obtuse. *Pileus context* of interwoven hyphae, slightly inflated, 6–8 µm wide. *Clamp connections* not observed.

Habit, Habitat & Distribution — Sporulating singly or in groups, sometimes caespitose at base. Sporulating in deep leaf litter along roadside embankments in open *Eucalyptus* and *Acacia* woodland. Known from two locations in the Northern Territory and in south-eastern Queensland.

Typus. Australia, Northern Territory, Fogg Dam, 1st parking bay, 24 Jan. 2014, *G.M. Bonito*, *M.D. Barrett*, *T. Lebel* & *C.N. Barrett*, GB538 (holotype MEL2382883, ITS-LSU sequence GenBank KP012754, MycoBank MB 843302).

Colour illustrations. Subtropical rainforest, Fogg Dam, Northern Territory, Australia, holotype site. Basidiomata showing pale pileus with some scattered fibrils; double annulus, with partial veil still attached; (inset) showing two sizes of basidiospores; basidiomes showing pale pileus and immature lamellae; closeup of double annulus, composed of universal and partial veils. Scale bar = 10 µm. (Photo credit C.N. Barrett, M. Barrett & J. Broadbridge (spores)).

Additional material examined. Australia, Northern Territory, Fogg Dam site2, parking area at end of dam, 24 Jan. 2014, *G.M. Bonito*, *M.D. Barrett*, *T. Lebel* & *C.N. Barrett*, GB545, MEL2382890 (ITS-LSU sequence GenBank KP012761); Litchfield National Park, site 3 on roadside, 25 Jan. 2014, *G.M. Bonito*, *M.D. Barrett*, *T. Lebel* & *C.N. Barrett*, GB561, MEL2382906 (ITS-LSU sequence GenBank KP012775); Queensland, Lamington National Park, Caves track, Binna Burra, 1 Mar. 2003, *N.A. Fechner & A.M. Young*, LNP893, BRI-AQ794575 (ITS and LSU sequences GenBank OM955546 and OM955549); Queensland, 12 Mar. 2016, *P. Leonard*, 1120316, BRI-AQ (ITS and LSU sequences GenBank OM955545 and OM955548).

Notes — According to phylogenetic analyses, *A. albofoetidus* and *A. atrodiscus* appear as an unbranched, strongly supported lineage arising near the common ancestor of the clade named Xan III by Thongklang et al. (2014), which is one of the three major clades constituting the section *Xanthodermatei*. Many of the species in this broader clade, *A. atrodiscus*, *A. daliensis*, *A. endoxanthus*, *A. rotalis*, *A. punjabensi*s and *A. xanthosarcus*, have dark pigmented pilei, a strong chemical odour and robust veils (Thongklang et al. 2014, Liu et al. 2015, Chen et al. 2016, Zhou et al. 2016, Bashir et al. 2021). *Agaricus albofoetidus* is unique in this clade in having a white pileus and lacking any darkly pigmented fibrils. Morphologically, *A. albofoetidus* and *A. atrodiscus* are easily distinguished. In *A. albofoetidus* the context stains bright yellow immediately (no staining observed in *A. atrodiscus*), the sporocarps are smaller (cap up to 75 mm diam vs 90–130 mm), cheilocystidia are absent, and the spores are longer (*A. atrodiscus* 4.7–5.9 × 3–3.6 µm). *Agaricus atrodiscus* is currently found amongst bamboo in subtropical vegetation while *A. albofoetidus* is found in subtropical open eucalypt and *Acacia* woodland. Differences in the ITS gene region are small (less than 5 bp) between Australian collections from Queensland and the Northern Territory, and *A. albofoetidus* and *A. atrodiscus* from Thailand. Further sampling from both northern Australia and Thailand, and analysing other genes such as *tef1-α* or *rpb2* (which have been found useful in distinguishing other closely related pairs of *Agaricus*), will potentially aid in further discriminating *A. albofoetidus* and *A. atrodiscus*.

Another species in the same lineage, *Agaricus daliensis* from China, varies in the degree of dark fibrils on the pileus from dots with dark apical disc to almost completely covered in dark scales, the stipe surface changing to reddish brown when touched, and spores 4.3–5.1 × 2.7–3.2 µm (Zhou et al. 2016).

Supplementary material

FP1400 Phylogenetic tree.

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Agaricus aureoelephanti

Fungal Planet 1401 – 12 July 2022

Agaricus aureoelephanti Broadbridge, Boxshall & T. Lebel, *sp. nov.*

Etymology. In reference to the overall colour and texture of the sporocarps. *L* = golden (*aureo*) elephant (*elephanti*).

Classification — *Agaricaceae*, *Agaricales*, *Agaricomycetes.*

Pileus 18–48 mm diam, convex, pale cream to tawny white, ageing to brownish orange cream or sometimes very pale brown in centre, smooth, dry, fibrils forming indistinct, broad, flat scales 2–4 mm across, that show as a tessellated pattern on drying (pellis becoming slightly leathery and shiny on drying); context staining slowly but distinctly yellowish/brownish. *Lamellae* dull, pale pink, becoming dark chocolate brown when mature, densely crowded, 2–3 series of short lamellulae; margins appearing slightly eroded. *Stipe* 30–65 mm long × 4.5–8.5 mm diam, 4 mm diam at apex widening to 8–13 mm in clavate to elongate-bulbous base, central, cylindrical, smooth, white to pale cream, but bruising yellowish orange upon handling; outer parts of solid context flesh and lower 3/4 of stipe staining slowly but distinctly yellowish brown. *Annulus* comprising partial veil, fragile and easily lost or malformed, milky white to buff at margin, matte, margin uneven, becoming thin towards stipe attachment. *Odour* unpleasant, very strong mushroom to 'hot-asphalt' scent or of almonds (MEL2382663). *Basidiospores* 6.20–7.40 × 4.50–5.30 µm, (6.86 ± 0.36 × 4.80 ± 0.25, Q = 1.31–1.61, n = 15), broadly ellipsoid, smooth, brown when mature, hyaline when immature, thick-walled ± 0.5 µm, germ pore absent. *Basidia* 22–27 × 8–9.5 µm, clavate, hyaline, 4-spored; sterigmata inconspicuous. *Cheilocystidia* absent. *Pleurocystidia* absent. *Hymenophoral trama* composed of interwoven, septate hyaline hyphae 4–11 µm wide; *subhymenium* 17–20 µm wide, composed of 2–4 parenchymatous cells 4–8 × 4–7 µm. *Pileipellis* a narrow cutis, 30–40 µm wide, composed of hyaline, smooth, unpigmented, septate hyphae, 4–6 µm wide, cylindrical, smooth, terminal elements cylindrical with an obtuse apex, repent to upright. *Pileus context* a broad layer 200–400 µm wide, of interwoven hyaline hyphae 3–5 µm wide. *Clamp connections* not observed.

Habit, Habitat & Distribution — On soil in fairly dense *Eucalyptus miniata* woodland with understory shrub layer of *Erythrophleum chlorostachys* and other shrubs, with deep litter layer; long unburnt or subtropical mixed forest of *Eucalyptus*, *Acacia*, *Callitris* with open understory of herbs and grasses.

Typus. Australia, Northern Territory, Palmerston, Howard Springs Reserve, Site 1 approximately 500 m from entrance, 23 Jan. 2014, *G.M. Bonito*, *M.D. Barrett*, *T. Lebel* & *C.N. Barrett*, GB513 (holotype MEL2382860, ITS-LSU sequence GenBank KP012734, MycoBank MB 843303).

Additional material examined. Australia, Northern Territory, Darwin, Palmerston, NE corner of Buscall Terrace and Chung-wa Terrace, *M.D. Barrett*, *G.M. Bonito*, *T. Lebel* & *C.N. Barrett*, MD F71/14, MEL2382663 (ITS-LSU sequence GenBank KP013026).

Colour illustrations. *Eucalyptus* woodland, Palmerston, Northern Territory, Australia. Basidiomata of *Agaricus aureoelephanti*; lamellae and (inset) closeup of serrated lamellae margins; showing stipe context with some yellow-orange staining in cross section; golden-scaled pileus, more densely pigmented at centre. (Photo credit C.N. Barrett & M. Barrett).

Notes — *Agaricus aureoelephanti* is the first recorded member of subgenus *Spissicaules* section *Rarolentes* in Australasia. Kerrigan (2016) and Santana-Ortiz et al. (2021) state that members of subgenus *Spissicaules* section *Rarolentes* occur in tropical to subtropical habitats, have pilei that are pale toned and convex with fibrils ranging from cream to brown, pink-toned gills that darken to chocolate brown with maturity, an unchanging or locally sordid stipe context, an odour of solvent, rubber or sometimes almonds or anise.

Phylogenetically it is placed in a poorly supported clade with an unnamed species from Queensland (tle2660), *A. brunneodiscus* (India), *A. leucolepidotus* (Thailand), *A. albosquamosus* (Thailand) and more distantly *A. butyreburneus* (USA) and *A. furfuripes* (Martinique). *Agaricus aureoelephanti* resembles *A. leucolepidotus* and *A. albosquamosus*, but has a smaller pileus and sordid brown staining reaction which is lacking in Thai material. The spore size is more similar to *A. leucolepidotus* than *A. albosquamosus*. *Agaricus brunneodiscus* from India has much larger basidiomata, an anise odour, narrower basidiospores, and abundant cheilocystidia (Arya et al. 2022).

Supplementary material

FP1401 Phylogenetic tree.

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Agaricus parviumbrus

Fungal Planet 1402 – 12 July 2022

Agaricus parviumbrus Broadbridge, Boxshall & T. Lebel, *sp. nov.*

Etymology. In reference to the overall shape of the pileus, darkening with maturity, and the small shadow cast by this species; *L. parvi* (small), *umbra* (a little shadow).

Classification — *Agaricaceae*, *Agaricales*, *Agaricomycetes.*

Pileus 12–35 mm diam, convex becoming planoconvex and slightly umbonate, dry, minutely fibrillose, with purple to brownish fibrils scattered over pileus surface, becoming dark dull brown overall, margin faintly striate when young; no context staining. *Lamellae* free, crowded, lamellulae present in series of > 3, pale pinkish brown, becoming pinkish brown to dark brown. *Stipe* 3–6 mm wide × 16–65 mm long, central, cylindrical, tapering slightly at apex and slightly bulbous at base, white, finely fibrillose, silky, bruising orange with handling; context immediately stains yellow to orange-brown, becoming brown. *Universal veil* cortina-like, forming a thick web enclosing the entire pileus, creamy to golden, bruising strong orange upon handling, remnants of universal veil present on base to lower third of stipe as broken strands resembling roughly broken tufts of fibrils, remnants may also be visible on pileus margin or lower partial veil surface in young specimens. *Partial veil* initially erect becoming pendent, white, fragile, upper surface finely striate, lower surface finely floccose, attached to upper third of stipe with white, arachnoid fibres. *Odour* almond-scented. *Basidiospores* 5.4–6.3(–6.7) × 3.5–4.7 µm (5.96 ± 0.35 × 3.93 ± 0.33 µm, Q= 1.19–1.81, n = 23) ellipsoid, thick walled, 0.2–0.5 µm, brown, smooth, germ pore absent. *Basidia* 15–22(–26.5) × 6.5–8(–9.0) µm, mostly 4-spored, clavate, hyaline to broadly clavate; sterigmata conspicuous. *Cheilocystidia* absent. *Pleurocystidia* absent. *Hymenophoral trama* composed of irregularly inflated interwoven hyphae, 5–12.5 µm wide, septate and indented around septa; *subhymenium* 14–20 µm wide, composed of 3–5 parenchymatous cells, 4–10.5 × 4–10.5 µm, with scattered much larger cells, 12–20 × 10–17 µm. *Pileipellis* a cutis 30–60 µm wide, composed of hyaline and golden brown (KOH) to brown (water) pigmented septate hyphae, 4–8 µm diam, terminal elements cylindrical with an obtuse apex, repent to upright. *Pileus context* 200–400 µm wide, composed of interwoven hyaline hyphae 4–7 µm diam and inflated elements 10–18 µm diam more common towards the cutis, with hyphae 4–8 µm diam becoming more consistent and interwoven towards the hymenophoral trama. *Clamp connections* not observed.

Habit, Habitat & Distribution — Solitary or in small groups, in scattered leaf litter and bare soil in open eucalypt woodland and subtropical mixed forest of *Acacia*, *Callitris* and *Eucalyptus* with open understory of herbs and grasses.

Typus. Australia, Northern Territory, Howard Springs Reserve Site 1 approximately 500 m from entrance, 23 Jan. 2014, *G.M. Bonito*, *M.D. Barrett*, *T. Lebel* & *C.N. Barrett*, GB511 (holotype MEL2382858, ITS-LSU sequence GenBank KP012732, MycoBank MB 843301).

Additional material examined: Australia, Northern Territory, Palmerston, Territory Wildlife Park, walking track to Goose Lagoon, 21 Jan. 2014, *G.M. Bonito*, *M.D. Barrett*, *T. Lebel* & *C.N. Barrett*, GB487, MEL2382834 (ITS-LSU sequence GenBank KP012709).

Notes — *Agaricus parviumbrus* is in section *Minores* but placement is currently unresolved, with poor branch support in deeper nodes, utilising only the nuclear ITS gene region. While the smallish basidiome size and almond smell are also typical of the closely related sects. *Minoriopsis* and *Kerrigania*, our analyses support placement in the very diverse sect. *Minores* (Gui et al. 2015, Chen et al. 2017). The lack of yellow staining and orange bruising are uncommon characters of species in this section (Kerrigan 2016).

Colour illustrations. Eucalypt and subtropical mixed woodland with open understory of herbs and grasses, Territory Wildlife Park, Palmerston, Northern Territory, Australia, paratype site. Basidiomes of *Agaricus parviumbrus*, showing colour and texture of pileus, including faintly striate margin in younger specimens; basidiomes of *A. parviumbrus* in deep leaf litter; lamellae and partial veil; (inset) orange bruising of button, and partial and universal veils visible; pileus texture; and yellow to orange-brown bruising of stipe context in older specimen. (Photo credit C.N. Barrett & M. Barrett).

Supplementary material

FP1402 Phylogenetic tree.

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Alpova larskersii

Fungal Planet 1403 – 12 July 2022

Alpova larskersii Jeppson & E. Larss., *sp. nov.*

Etymology. The name refers to the Swedish botanist Lars Erik Kers (1931–2017) who made important contributions to the knowledge of hypogeous fungi in Sweden.

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

Basidiomata hypogeous to emergent, subglobose, irregularly lobed, 10–25 mm diam. *Peridial* surface smooth to finely felted, when young whitish ochraceous, with age yellow brown to reddish brown, when dry dark brown to almost black. Fresh peridium turning reddish brown on handling. No rhizomorphs covering the peridial surface although inconspicuous rhizomorphs may sometimes be present in the basal area. *Peridium* yellowish brown in section 0.4–1.0 mm thick fresh, dry 0.2–0.3 mm, turning slightly reddish brown on exposure. *Gleba* composed of gelatinised, olivaceous brown to blackish brown chambers divided by distinct narrow, whitish to yellowish brown walls. *Peridium* with an exterior peridiopellis 20–50 µm thick, of brownish to yellowish, smooth to slightly encrusted hyphae, 2–8 µm diam with slightly thickened walls and occasional clamps. Interior part of peridium (subpellis) 180–300 µm thick, composed of more or less hyaline, cylindrical to isodiametric cells forming a pseudoparenchymatic structure with occasional larger follicle-like features and bundles of compacted hyphae. *Clamps* present but difficult to discern. Walls of the glebal chambers composed of compacted hyaline to yellowish hyphae and pseudoparenchymatic cells. *Basidia* club-shaped, 8–12 × 4–5 µm, with a short tapering, elongate base, in mature specimens largely collapsed, with up to eight basidiospores developing on thin and short sterigmata. *Basidiospores* narrowly ellipsoid to cylindrical or allantoid, in KOH hyaline-pale yellowish grey, smooth, 5.0–5.3–6.5 × 2.0–2.5–3.0 µm, Q = 2.1– 2.5, sometimes biguttulate.

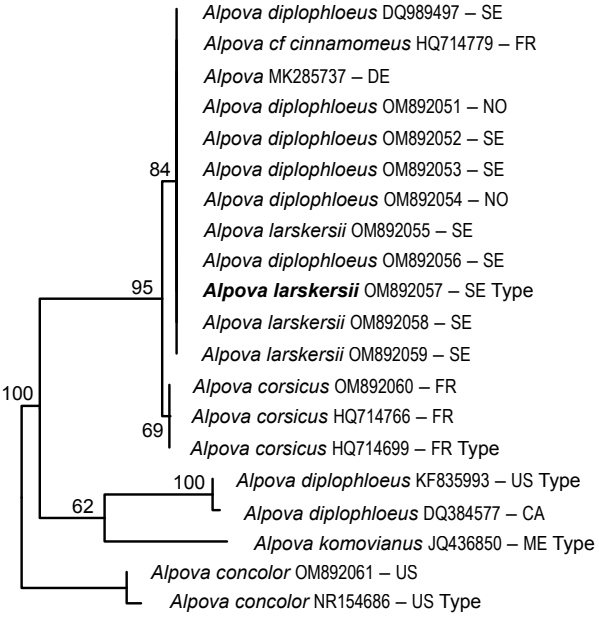
Ecology & Distribution — Associated with *Alnus alnobetula*, *A. glutinosa* and *A. incana* in alder fens and along lake shores and streams lined with alders. In Northern Europe with *A. glutinosa* and *A. incana* in hemiboreal and boreal areas of Norway and Sweden. It is also recorded under *A. alnobetula* in the French Alps (Moreau et al. 2011; HQ714779) and ITS sequence data from environmental samples from Germany (Schwarzwald; GenBank MK285737) and Slovenia (UNITE UDB009830), suggest a wider distribution also comprising montane habitats in Central Europe.

Typus. Sweden, Västergötland, Amnehärad s:n, Kvarntorpet, c. 9.6 km SSW of Amnehärad church, c. 4 km S of Otterbäcken, c. 600 m NNO of Kvarntorpet, on the south bank of the rivulet Kvarntorpsbäcken, under *Alnus glutinosa*, *Corylus avellana*, *Picea abies* and *Populus tremula*, N58.910305° E14.021087°, 24 July 2009, *R. Carlsson*, 2009-07-24:3 (holotype S-F413318, ITS-LSU sequence GenBank OM892057, MycoBank MB 843356).

Additional materials examined. ***Alpova corsicus***: France, Corsica, Moltifao, Campo Longo, Valdo, under *Alnus glutinosa* along stream, 7 Nov. 2019, *M. Jeppson*, *E. Larsson*, *P.A. Moreau* et al., MJ10823 (GB-0207628). ***Alpova larskersii***: Norway, Møre og Romsdal, Nesset, Eikesdalen, along path at Vike, under *Alnus incana*, *Corylus* and *Betula*, 16 Sept. 2011, *J.-O. Aarnes* (O-21018); Oppland, Lunner, S. Oppdalen, mold-rich soil, roadside verge, 28 July 1979, *T.E. Brandrud 52-79* (O-F151994); Oslo, SW Sognsvann, along stream with old *Picea* and scattered *Alnus* and *Betula*, 17 Sept. 1985, *J. Nitare* & *M. Jeppson* (O-F88449); Viken, Larvik, at Gjønnesvannet, south of Kvelde, 2018, *J.T. Jensen* (GB-0207627). – Sweden, Ångermanland, Nordingrå, 1 km N Röksta, slope towards Ullåkersfjärden, under *Alnus incana* and *Picea abies*, 21 July 1989, *R. Carlsson*, 447 (S-F410823); Dalarna, Leksand, Åsledens fäbod, Åsledsberget, under *Alnus incana*, 21 Sept. 1987, *L.E. Kers*, 6681 (S-F410837); Jämtland, Ragunda, below Vättaberget, near Skaltjärn, under *Alnus incana*, 6 Aug. 1986. *L.E. Kers* & *R. Carlsson* (S-F410832); Småland, Hörreda, Kulla, N57.616439° E14.843744°, under *Alnus glutinosa*, *L.E. Kers* & *R. Carlsson* (S-F413316); Värmland, Nordmark, 1 km N of Motjärnshyttan, under *Alnus incana*, 14 Sept. 1988, *L.E. Kers* & *R. Carlsson*, 8812 (S-F410846); Västergötland, Amnehärad, 4.3 km SSV of Otterbäcken, just S of Kvarntorpsbäcken, 16 Aug. 1980, *J. Nitare* (UPS-F153582); ibid., UME33851; Hova, 1.5 km N of Mälltorp, 27 June 1981, *C. Eriksson* (UPS-F153581).

Colour illustrations. *Alpova larskersii* habitat from the type locality in Västergötland, Sweden. Basidiomata (fresh); basidiospores (holotype). Scale bars = 10 mm (basidiomata), 10 µm (basidiospores).

Notes — *Alpova larskersii* is closely related to *A. corsicus*, a species that appears to be endemic to Corsica (France) (Moreau et al. 2011). In contrast to *A. corsicus*, *A. larskersii* has a wide European distribution particularly in montane and boreal regions. In morphology it differs from *A. corsicus* by slightly larger spores. Based on molecular data it differs by a single insertion/deletion event in ITS1 and three substitutions in ITS2. *Alpova larskersii* was first reported and illustrated with line drawings from Scandinavia by Kers (1981, 1983, 1986) under the name *A. diplophloeus*. Hayward et al. (2014) provided an extensive description of a Swedish sample (as *Alpova* sp.) collected by L.E. Kers and also provided ITS data. They further concluded that a previously published French record (as *A*. cf. *cinnamomeus*; Moreau et al. 2011) was conspecific. In macromorphology *A. larskersii* is reminiscent of *Melanogaster luteus* with which it shares its habitat under *Alnus* spp. The latter can be readily recognised under the microscope by its yellowish brown, thick-walled, wider spores with a truncate base and a conspicuous sterigmal remnant.



Phylogram obtained using PAUP v. 4.0a (Swofford 2003) based on ITS data showing the position of *A. larskersii* as a sister species to *A. corsicus*. Heuristic searches with 1 000 random-addition sequence replicates and tree bisection-reconnection (TBR) branch swapping were performed. Relative robustness of clades was assessed by the bootstrap method using 1 000 heuristic search replicates with 100 random taxon addition sequence replicates and TBR branch swapping. Bootstrap support values are indicated on branches, the holotype of *A. larskersii* is indicated and marked in **bold**.

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Amanita konajensis

Fungal Planet 1404 – 12 July 2022

Amanita konajensis K.R. Sridhar, Mahadevak., B.R. Nuthan & N.C. Karun, *sp. nov.*

Etymology. Name refers to the place / region, Konaje, Mangalore, Karnataka, India where this species was collected.

Classification — *Amanitaceae*, *Agaricales*, *Agaricomycetidae*, *Agaricomycetes*.

The immature *sporocarp* is oval to dumbbell-shaped, (0.5–)0.6–1.9(–2.1) × (0.4–)1.2–1.6(–2.0) cm (n = 11); mature sporocarp (5.4–)5.5–10.6(–11.3) cm (n = 28); *pileus* pale grey to greyish brown, hemispherical to convex at maturity, smooth, viscid, non-striated, (1.2–)1.5–6.1(–6.3) cm; lamellae white, free, narrow to inflated, crowded, regular, short gills of 3–4 lengths. Stipes white to smokey white with age, fibrillose, cylindrical stuffed, equal or slightly tapering towards the apex, (3.5–)3.7–8.0(–8.4) × (0.4–)0.5–1.2(–1.4) cm (n = 28); *Annulus* white, membranous, superior, skirt-like, flaring, persistent, striate on the upper surface, smooth to the silky inner surface, emerging out from the apex region, (0.6–)0.7–1.8(–1.9) cm (n = 28); *volva* white, saccate, membranous, lobed, smooth, spongy to puffy, (1.4–)1.6–2.9(–3.3) × (1.3–)1.4–2.4(–2.6) cm (n = 28); *basidia* hyaline, long, cylindrical, thin-walled, club-shaped with 4 sterigmata with each basidiospore, (15.6–)18.2–28.6(–31.2) × (5.2–)7.8–11.7(–13) µm (n = 25); *basidiospores* hyaline, smooth, thin-walled sub-spherical to broadly ellipsoidal, (7.8–)9.1–11.7(–13) × (5.2–)6.5–9.1(–10.4) µm (n = 50); *cheilocystidia* are hyaline, short broadly clavate. *Taste* edible in immature stage and not edible in mature state.

Habit & Habitat — Ectomycorrhizal on hosts *Acacia auriculiformis*, *Acacia mangium* and *Anacardium occidentale*. Basidiomata growing solitary on moist soil near the forest of Konaje.

Typus. India, Karnataka, Mangalore on scrub jungles of Konaje on the basins of *Acacia auriculiformis*, *Acacia mangium* and *Anacardium occidentale* 15 June 2013, *K.R. Sridhar* (holotype UOM2021-10; ITS sequence GenBank MW354955, MycoBank MB 840212).

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence of UOM2021-10 had highest similarity to *Amanita marmorata* (voucher RET 685-9, GenBank MG252696; Identities = 587/611 (96 %), six gaps (0 %)), *Amanita eucalypti* (voucher PERTH 8809828, GenBank KU057396; Identities = 579/610 (95 %), five gaps (0 %)) and the type of *Amanita gardneri* (voucher PERTH 08776121, GenBank NR_169902; Identities = 569/615 (93 %), ten gaps (1 %)). Morphologically, *A. konajensis* has similar characters to *A. marmorata* except for the pileus, stipe, and annulus characteristics. The pileus in *A. marmorata* is pale grey to dried dull brown, broadly convex, with no signs of a universal veil. However, in *A. konajensis* it is pale grey to greyish brown, hemi-spherical to convex at maturity, smooth, viscid and non-striate. The stipe in *A. marmorata* is white, equal or enlarging to form a clavate base, slightly raised with loose fibrils, and in *A. konajensis*, it is white to smoky white, with age fibrillose, cylindrical, stuffed, and equal or slightly tapering towards the apex. The annulus in *A. marmorata* is white, skirt-like, superior, and often almost at the lamellae. In contrast, in *A. konajensis* it is white, membranous, superior, skirt-like, flaring, persistent, striating on the upper surface, smooth to the silky inner surface, and emerging from the apex region.

Colour illustrations. *Amanita konajensis* (holotype specimen, Collection UOM2021-10) on soil in Konaje, Karnataka, India. Immature basidioma; mature basidioma with pileus; basidium with sterigmata with immature basidiospores. Scale bars: 20 mm – specimen *in situ* (left panel); 20 µm – basidium and basidiospores (right panel).

Supplementary material

FP1404 Phylogenetic tree.

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Calonarius ligusticus

Fungal Planet 1405 – 12 July 2022

Calonarius ligusticus Calledda, Boccardo & Dovana, *sp. nov.*

Etymology. The epithet '*ligusticus*' reflects the name Liguria, a region in Italy where the holotype was collected.

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

Basidiomata small-sized, phlegmacioid. *Pileus* 25–45 mm diam, hemispherical, then convex to plano-convex, when old depressed, slightly viscid to dry, radially fibrillose, centre with a few whitish to pale brown veil remnants, margin involute for a long time then inflexed; cream, ochraceous to ochraceous brown with some faint brown hues and with pinkish to violaceous tinges. *Lamellae* moderately distant, emarginate to adnate with decurrent tooth, edge even to slightly crenulated, violet at the beginning, darkening to rusty brown with age. *Stipe* 20–40 × 6–12 mm, cylindrical, with a relatively broad marginate bulb up to 20 mm diam long, violet, later becoming brownish, solid, covered with fibrils of the partial veil; bulbipellis whitish with a lilac tinge, that becomes brownish when old; whitish to lilac universal veil on the bulb margin; mycelial strands white. *Cortina* fairly sparse, whitish, with age heavily covered with rust-brown spore powder. *Context* whitish to ochraceous in the pileus, with blue tinge in the stipe, brown in the bulb of older specimens. *Odour* and *taste* not distinctive. Macrochemical reaction 30 % KOH on pileus orange-brown, in context pale orange-brown, brown on bulb edge surface. *Basidiospores* (10.5–)10.7–*11.7*–12.6(–14.5) × (5.0–)5.9–*6.4*–6.9(–7.5) µm Q = (1.49–)1.61–*1.83*–2.05(–2.36) citriform, amygdaliform to subamygdaliform, strongly and coarsely, net-like verrucose, suprahilar plage indistinct, apiculus smooth. *Basidia* 27–32 × 8–10 µm, clavate, four-spored, thin-walled and hyaline in KOH, sterigmata up to 3.5 µm long. *Lamella edge* fertile, presence of cystidioid cylindrical elements. *Cheilocystidia* and *pleurocystidia* not observed. *Pileipellis* as an ixocutis, hyphae hyaline, yellow to brown, cylindrical to slightly moniliform with subcapitate terminal elements 4–6 µm wide. *Pigments* cytoplasmic and parietal. *Clamp connections* frequent at all septa.

Habitat & Distribution — In deciduous forest with *Quercus ilex* on calcareous soil. Found, so far as we know, only in North Italy in Liguria Region.

Typus. Italy, Zoagli, Località Le Grazie, in a dense forest of *Quercus ilex*, near the path, on calcareous soil, 30 Nov. 2019, *F. Calledda*, *M. Carbone* & *E. Pini* (holotype GDOR5237, ITS and LSU sequences GenBank OM980183 and OM980184, MycoBank MB 843353).

Notes — Spore dimensions are expressed as (a)b–*c*–d(e), where (a) = minimum value, b = (average – standard deviation), *c* = average, d = (average + standard deviation) and (e) = maximum value. *Calonarius ligusticus* is characterised by a small basidioma, cream to ochraceous brown fibrillose pileus with pinkish to light violaceous tinges and with some brown hues, lamellae moderately distant and distinctly violaceous, violaceous stipe with broad marginate bulb covered by whitish to lilac universal veil, mycelial strands white and orange alkaline reaction on the pileus surface and in the context. Microscopically, *Calonarius ligusticus* shows high variability in spore shape (citriform, amygdaliform to subamygdaliform, Q = 1.49–2.36) and size (10.5–14.5 × 5.0–7.5 µm) and a pileipellis as an ixocutis, with brown subcapitate terminal elements. In the nrITS phylogenetic analysis, *Calonarius ligusticus* is in a well-supported /Calochroi clade (maximim-likelihood bootstrap, MLB = 98 %), and it is a sister species of *Calonarius laberiae* (MLB = 100 %), with which it shares 97 % bp. Based on a megablast search of NCBIs GenBank nucleotide database, the best hit using the LSU sequence is *Calonarius sodagnitus* (voucher AFTOL-ID 811, GenBank; Identities = 909/915 (99 %), no gaps). Morphologically, *C. laberiae* differs mainly from *C. ligusticus* by yellow to yellow-ochraceous pileus, greyish white lamellae, white to ochraceous stipe, smaller basidiospores (9.3–12.2 × 5.9–7.3 µm) and different habitat under *Abies* and *Picea* (Münzmay et al. 2009). *Calonarius sodagnitus* is easily distinguished from *C. ligusticus* by its violaceous pileus with dark spots, intense alkaline reactions on bulbipellis and pileus and smaller basidiospores (8.5–10 × 5–6 um) (Brandrud et al. 1992).

Colour illustrations. Zoagli, Italy, *Quercus ilex* forest. *Calonarius ligusticus* basidiomata in habitat; basidiospores and pileipellis. Scale bars = 10 µm.

Supplementary material

FP1405 Phylogenetic tree.

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Collybiopsis cimrmanii

Fungal Planet 1406 – 12 July 2022

Collybiopsis cimrmanii Ševčíková & P.-A. Moreau, *sp. nov.*

Etymology. *cimrmanii* in honour of 'The greatest Czech Jára Cimrman', a great playwright, poet, musician, teacher, traveller, philosopher, inventor, scientist, criminologist and athlete.

Classification — *Omphalotaceae*, *Agaricales*, *Agaricomycetes.*

Pileus 7–12 mm broad, hemispherical to convex, then applanate, obtuse or with or without small umbo at centre, slightly involute then straight at margin, sulcate or non-striate, indistinctly undulate or crenulate at the margin, very finely tomentose, whitish, with very pale ochre to brownish tinge at the centre, not striate, not hygrophanous. *Lamellae* moderately close, L = c. 20, l = 3–4, ± emarginated and broadly adnate, anastomosed when old, white, with concolourous edge. *Stipe* 10–25 × 0.5–1.5 mm, cylindrical or slightly attenuated towards base, minutely pubescent, even finely floccose when young, white at apex, pale ochre then pale brown at lower half, chestnut brown at the base. *Smell* none. *Basidiospores* 7.0–9.0 × (2.25–)2.5–3.0(–3.5) µm, av. 7.8 × 2.7 µm, E = 2.3–3.2, Q = 2.9, narrowly fusoid, almost lacrimoid, cylindrical-ellipsoid, thin-walled, separate, rarely in tetrads in preparations. *Basidia* 15.5–20 × 5.5–6.0 µm, 4-spored, clavate or subfusoid. *Cheilocystidia* 25–60(–75) × 16–30 µm, in the form of broom cells of both the Siccus- and Rotalis-type, broadly clavate to vesiculose or (sub)fusoid, rarely clavate, thin-walled, mostly diverticulate, rarely smooth or rostrate, hyaline, colourless. *Pleurocystidia* absent. *Pileipellis* a cutis of diverticulate, 3.0–10 µm wide hyphae and solitary broom cells of the Rotalis-type. *Stipitipellis* hyphae 3.0–9.5 µm broad, cylindrical. *Caulocystidia* 30–60 × 5.0–22 µm, variable in shape, clavate, subulate, (sub)cylindrical, submoniliform, irregular, smooth or diverticulate, thin-walled. *Clamp connections* present.

Habit, Habitat & Distribution — In groups on the base of living *Quercus ilex* and amongst dead leaves *Laurus* and herbs. So far known only from Madeira, Portugal.

Typus. Portugal, Madeira, a way from Ribeiro Frio to Portela, Levada do Furado, on the base of living *Quercus ilex* (*Fagaceae*), 520–870 m a.s.l., 23 Sept. 2015, leg. *H. Ševčíková*, (holotype BRNM 828679; GenBank sequences ITS, LSU and *EF1-a* MW924062, OM333232 and OM675755, MycoBank MB 839325).

Additional material examined. Portugal, Ribeiro Frio, trail PR11, Vereda dos Balcoes, amongst the dead leaves *Laurus novocanariensis* and herbs along the trail, 21 July 2019, leg. *P.-A. Moreau*, BRNM 828680, GenBank sequences ITS, LSU and *EF1-a* MW924061, OM333231 and OM675754.

Notes — The morphologically similar species *C. ramealis* has larger spores on average, 7.5–11(–12.5) × 2.5–4.5(–5.5) µm; yellow upper parts of cheilocystidia in KOH; shorter stipe, often a darker stipe base and a pileus (Antonín & Noordeloos 2010). Our unpublished results show a wider variability in *C. ramealis*, with some basidiomata being paler, and their stipes may be longer than the 20 mm mentioned by Antonín & Noordeloos (2010). *Collybiopsis ramealis* may grow on rotting leaves or decomposed plants. *Marasmiellus subramealis* differs by its narrowly adnexed to subfree lamellae, wider spores, cheilocystidia only up to 55 × 21 µm, slightly thicker hyphae of upper stipe portion and longer caulocystidia (Singer & Digilio 1951, Singer 1973). African *Gymnopus ugandensis* (= *Marasmiellus ugandensis*) differs by having a brown stipe, shorter basidiospores, 5–7.5 × 2.5–3.5 µm, narrower cheilocystidia and different caulocystidia (Pegler 1977, Desjardin & Perry 2017). *Marasmiellus antarcticus* differs by its glabrous pileus, smaller cheilocystidia; and caulocystidia of different size and shape (Singer 1969). *Marasmiellus atrostipitatus* differs by a radially sulcate-striate pileus, broader spores, 7–9 × 3.5–4.5 µm, mostly clavate cheilocystidia; and clavate to subcylindrical, smooth or with a few irregular, knob-like diverticula (Takahashi 2000). Old basidiomata smell alliaceous. A phylogenetically closely related species, *C. foliiphila*, differs by a thinner stipe (< 1 mm), greyish yellow to buff-brown at the base; smaller cheilocystidia up to 31(–37) × 12(–18) µm and the absence of the pileipellis broom cells; it grows on leaves of dicotyledonous plants in India (Dutta et al. 2015); *C. filamentipes* has a pinkish buff coloured pileus, more distant lamellae (L = 12–13), adnexed to subdecurrent, lamellar edge with diverticulate hyphae and narrower cheilocystidia with long projections, presence of pleurocystidia, different caulocystidia, and grows apparently associated with *Poaceae* (Petersen & Hughes 2021); *C. furtiva* differs by a darker pileus, lamellae adnexed to decurrent by tooth and sometimes almost pale olive buff or buff when fresh, a shorter (4–11 × 0.3–1.2 mm) stipe sometimes abruptly pinched at base, different cheilocystidia and well-developed pleurocystidia (Petersen & Hughes 2021); *C. californica* has a pinkish buff to cinnamon pileus, buff coloured lamellae, slightly narrower, thick-walled cheilocystidia which are sometimes pale yellow and smaller, never diverticulate caulocystidia, 18–30 × 3.6–9 µm (Desjardin 1987).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to Uncultured *Gymnopus* (FONf09, GenBank HM488468, Identities = 528/545 (97 %), seven gaps (1 %)) and *Collybiopsis filamentipes* type (TENN F-065861, GenBank NR_174048; Identities = 619/644 (96 %), 12 gaps (1 %)). Closest hits using the *EF1-a* sequence are *Chaetocalathus* cf. *columellifer* (MCA2538, GenBank AY916688, Identities = 350/394 (89 %), 13 gaps (3 %)) and *Marasmius* sp. (MCA1708, GenBank AY916722, Identities = 341/385 (89 %), seven gaps (1 %)). Closest hits using the LSU sequence are Uncultured soil fungus (NCD_LSU_otu2179, GenBank KF567149, Identities = 611/619 (99 %), no gaps) and *Collybiopsis filamentipes* (TFB13962, GenBank MN897832, Identities = 609/619 (98 %), no gaps).

Colour illustrations. Type locality, Madeira island, Levada do Furado, laurisilva. Drawings: *Collybiopsis cimrmanii* holotype BRNM 828679 from top to bottom: cheilocystidia, basidiospores, basidia, pileipellis elements, caulocystidia. Photo: *Collybiopsis cimrmanii* basidiomata BRNM 828680. Scale bars = 10 µm (micro characters).

Supplementary material

FP1406 Phylogenetic tree.

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Cortinarius dryosalor

Fungal Planet 1407 – 12 July 2022

Cortinarius dryosalor Armada, Bidaud, Bellanger & Loizides, *sp. nov*.

Synonym. *Cortinarius largodelibutus* var. *caducifolius* Bidaud, Journal des J.E.C. 13: 5. 2011.

Etymology. From the Greek word *δρῦς* (= oak) and *salor*, referring to the species' putative association with oaks and close resemblance to *C. salor*.

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

Pileus 20–105 mm diam, subglobose at first, then campanulate to convex or plano-convex, broadly umbonate, with an inrolled, sometimes dented or contracted margin; coating viscous, smooth or finely felted-fibrillated under the magnifying glass, dull to bright sky-blue, lilac, lavender or mauve when fresh, paler ochre-yellow, livid ivory to ochraceous in the centre, not reacting to 5 % KOH but strongly gold yellow with TI_4. *Lamellae* up to 9 mm wide, fairly thick, adnate to emarginate, grey-blue to mauve when immature, becoming rusty brown to grey brown at full maturity; edges paler, smooth to crenate. *Stipe* 33–110(–220) × 6–25(–31) mm, cylindrical to clavate, often enlarged towards the base and then attenuated to rooting, sometimes bent or somewhat twisted, surface smooth to fibrillose or somewhat speckled and bluish lilac at the apex, pure white with occasional faint bluish hues elsewhere, often staining ochre-brown, with a fleeting cortina forming a fibrillose orange-rust annular zone at the apex. *Context* thick and firm in young basidiomata, whitish with bluish tinges in the upper stipe, yellowish at the stipe base, odour weak but complex, fruity, herbaceous, honey-like or raddish-like; *taste* mild; reacting to TI_4 (yellow), null or grey yellowish in 5 % KOH, null or grey-blue in $AgNO_3$, null or golden yellow in phenolaniline, null in gaïacol, formol, FMP and $FeSO_4$. *Basidiospores* 7–9.5(–11) × 6–7.5(–8.5) µm, Me = 9 × 7.1 µm; Q = 1.13–1.42; Qm = 1.26, ovoid to subglobose, thick-walled, fairly densely ornamented by unconnected spiny warts, tapering to an obligue hilar appendage. *Lamellar edge* fertile. *Basidia* 30–52 × 8–12 µm, tetrasporic, cylindro-clavate, thick-walled, with a basal clamp. *Hymenophoral trama* composed of tightly packed, septate, 2–12 µm wide hyphae. *Marginal cells* abundant, 3–13 µm wide, thick-walled, cylindro-clavate or ± cylindrical, frequently bifurcate, with a basal clamp. *Pileipellis* a cutis, composed of a thick layer of long (2.5–)3–6 µm wide hyphae overlying an undifferentiated or weakly differentiated layer of slightly wider parallel hyphae < 15(–19) µm with yellowish parietal pigmentation, encrusted or finely zebra-like in Congo red, appearing more subtly encrusted in KOH, rarely smooth. *Clamp connections* abundant throughout.

Habit, Habitat & Distribution — In small groups near *Quercus*, on calcareous or basic soil. So far known from southern Spain, Cyprus and Mediterranean or relatively thermophilous localities in France.

Typus. Spain, Granada, Huétor de Santillán, Arroyo Palacios, under *Quercus ilex*, *Q. faginea*, and scattered *Pinus halepensis* and *P. pinaster* on calcareous soil, 1300 m a.s.l., 24 Nov. 2018, *F. Armada* & *M.-J. Díaz de Haro* (holotype in Herbarium of Granada: JA-CUSSTA 9619; isotype in herb. pers. *F. Armada*: FA 4700, ITS and LSU sequences GenBank OM964838 and ON032996, MycoBank MB 844316).

Additional material examined. See Supplementary material page.

Notes — Two clades are currently candidates for the widely applied binomial *Cortinarius salor*, referred to as '*C. salor*' and '*C. salor* II' in the reference phylogeny by Garnica et al. (2016). The species described here constitutes a third well-supported lineage distinct from both these clades (Supplementary material), distant from them by 9 SNPs + 3 indels, and 4 SNPs + 5 indels, respectively (data not shown). *Cortinarius dryosalor* has been previously described at an infraspecific rank as *C. largodelibutus* var. *caducifolius* by Bidaud (2011). We refrain from recombining this variety at species level because the epithet is unfortunately grammatically incorrect and would literally translate as '*Cortinarius* with deciduous leaves' also not accurately describing the ecology of this species which is frequently found with evergreen oaks. Therefore the new name *C. dryosalor* is proposed for this lineage.

Morphologically, these three species are all very similar, but *C. dryosalor* usually displays somewhat paler sky-blue to grey-blue tinges on the pileus whereas '*C. salor*' and '*C. salor* II' display generally more vibrant violet colours. The new species can additionally be distinguished by its ecology and biogeography. Available data so far indicate that *C. dryosalor* is present in the distribution area of *Q. ilex*, *Q. calliprinos* s.lat. and *Q. alnifolia* in southern Europe, but also in thermophilous woodlands populated by *Q. pubescens* or *Q. cerris* in more continental localities. Conversely, sequenced collections of '*C. salor*' and '*C. salor* II' originate from colder/moister localities dominated by conifers and *Fagus sylvatica* in lower latitudes or, e.g., *Tilia cordata* in northern European ecoregions. It is thus unlikely that *C. dryosalor* co-occurs with either of the two *C. salor* candidates and reports of *C. salor* from the Mediterranean or the Atlantic coast (e.g., https://www.mycocharentes.fr/pdf1/1104.pdf), most likely correspond to the new species described here. A collection from Cyprus (ML902151CS) previously reported as '*C. salor*' in Loizides et al. (2011) also represents *C. dryosalor*, as probably do Mediterranean collections identified as *C. largodelibutus*.

Colour illustrations. Holotype collection area at Huétor de Santillán, Spain; basidiomata *in situ*, holotype coll. JA-CUSSTA 9619 (top left, scale bar = 10 cm); coll. DB041143 (top right, scale bar = 5 cm); marginal cells in congo red (bottom left, coll. JA-CUSSTA 9619, scale bar = 20 µm); basidiospores in congo red (bottom right, coll. DB041143, scale bar = 10 µm).

Supplementary material

FP1407 Phylogeny of *Cortinarius* sect. *Delibuti*.

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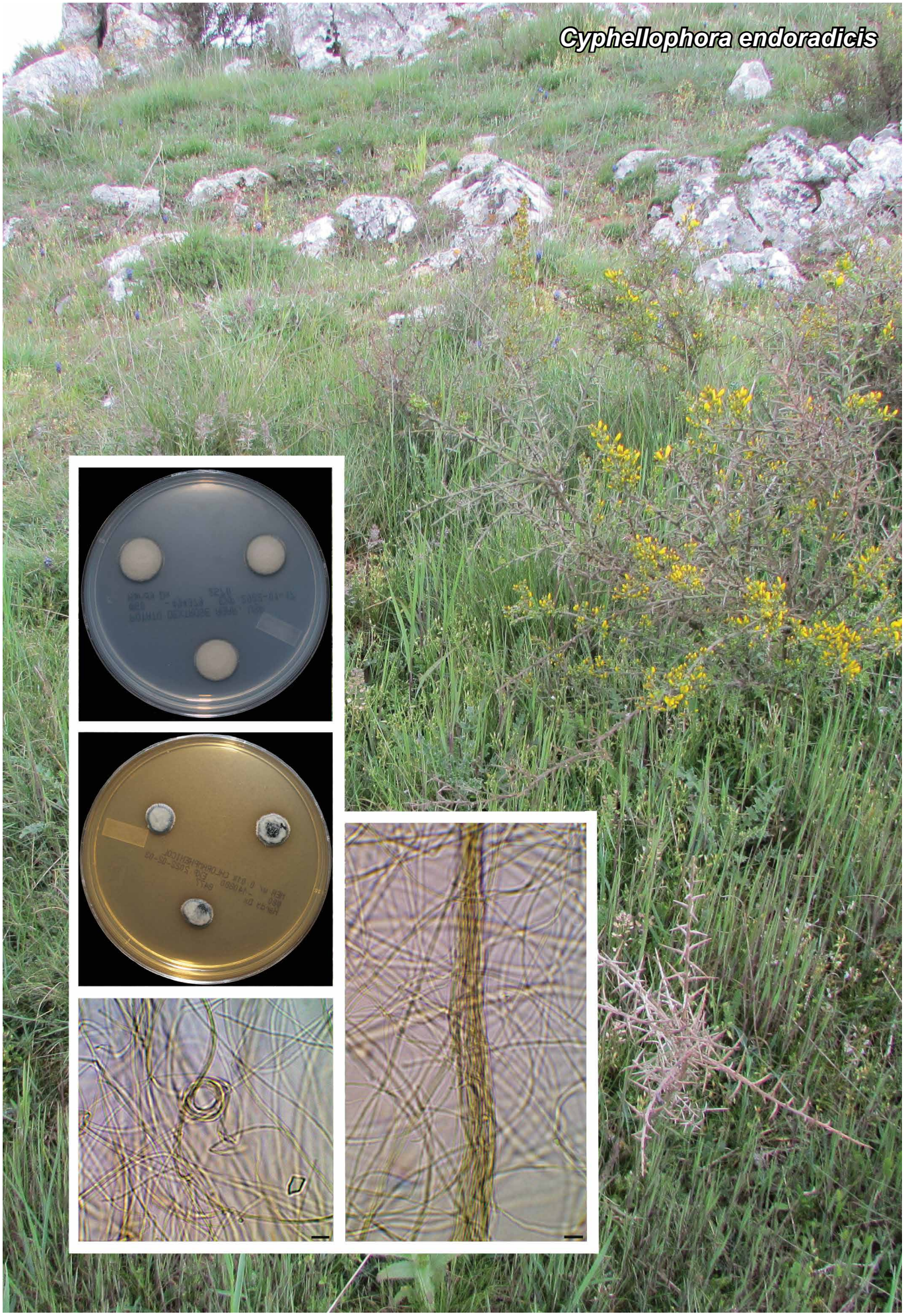
Cyphellophora endoradicis

Fungal Planet 1408 – 12 July 2022

Cyphellophora endoradicis G. Delgado & Maciá-Vicente, *sp. nov.*

Etymology. Epithet refers to the isolation source, inside the root tissues of the host plant.

Classification — *Cyphellophoraceae*, *Chaetothyriales*, *Eurotiomycetes*.

Root endophyte isolated on culture media from surface-sterilised roots of living plants. *Mycelium* composed of hyaline, subhyaline to pale brown or pale olivaceous, branched, septate, smooth, thin-walled *hyphae*, 1–2(–3) µm wide, at first pale olivaceous brown in mass turning brown to dark brown with age, single or often aggregated in tightly packed, brown hyphal cords up to 56 µm wide, rarely forming hyphal coils.

Culture characteristics — Colonies on potato dextrose agar (PDA) moderately slow growing, reaching 10–15 mm diam after 2 wk at 25 °C, velvety, pale grey to grey, circular, convex and slightly raised up to 2 mm, margin entire, reverse blackish grey; culture P1380 smaller, 10–11 mm diam, umbonate, with darker grey centre often developing a concentric ring. On malt extract agar (MEA) reaching 10–14 mm diam, grey, circular, pulvinate and raised up to 5 mm, margin entire or slightly undulose, dark grey to black, reverse black. Cultures sterile.

Typus. Spain, Palencia, Grijera, endophytic in roots of *Microthlaspi perfoliatum* (*Brassicaceae*), N42°48'36.0" W4°15'00.0", 1055 m a.s.l., isolated from surface-sterilised, asymptomatic roots of a wild plant, 16 May 2013, coll. *K. Glynou* & *J.G. Maciá-Vicente*, isol. *K. Glynou*, culture P1577 (holotype and culture ex-type permanently preserved in a metabolically inactive state CBS 148862, ITS, LSU, *tub2* and *tef1* sequences GenBank KT268871, OM527235, OM574614 and OM574612, MycoBank MB 843143) (= culture DSM 111321).

Additional materials examined. France, Auvergne-Rhône-Alpes, Drôme, near Ruisseau d'Establet, endophytic in roots of *M. perfoliatum*, N44°29'31.7" E5°26'35.7", 742 m a.s.l., isolated from surface-sterilised, asymptomatic roots of a wild plant, 8 May 2013, coll. *A.-K. Buch* & *X. Xia*, isol. *K. Glynou*, culture P2009 = CBS 146853, ITS, LSU, *tub2* and *tef1* sequences GenBank KT269272, OM527236, OM574615 and OM574613; Nouvelle-Aquitaine, Vienne, Celle-Lévescault, ibid., N46°24'29.9" E0°12'54.5", 115 m a.s.l., ibid., 5 May 2013, coll. & isol. *K. Glynou* & *J.G. Maciá-Vicente*, culture P2429, ITS sequence GenBank KT269660. – Germany, Baden-Württemberg, Bad Mergentheim, endophytic in roots of *Microthlaspi erraticum* (*Brassicaceae*), N49°27'09.7" E9°49'09.6", 273 m a.s.l., ibid., coll. & isol. *K. Glynou* & *J.G. Maciá-Vicente*, 6 June 2013, culture P2927, ITS sequence GenBank KT270124. – Spain, Granada, Puebla de Don Fadrique, Puerto del Pinar, ibid., N38°02'40.9" W2°28'54.8", 1636 m a.s.l., ibid., 2 May 2013, coll. & isol. *J.G. Maciá-Vicente*, culture P1380 = CBS 148861, ITS, LSU and *tef1* sequences GenBank KT268675, OM527234, and OM574611.

Notes — Among the 35 described species of *Cyphellophora* (http://www. indexfungorum.org; search date 01.31.2022), only *C. guyanensis*, *C. indica* and *C. vermispora* have been isolated as plant endophytes (Walz & De Hoog 1987, Jacob & Bhat 2000, Azuddin et al. 2021). However, there are several reports of *Cyphellophora* taxa determined only to genus level that occur as endophytes in different plant hosts (Liu et al. 2017, Li et al. 2018, Abdelrazek et al. 2020), suggesting that the endophytic lifestyle is probably widespread among its members and further novelties still await formal description. *Cyphellophora endoradicis* was isolated during an extensive sampling for root endophytic fungi across Europe (Glynou et al. 2016). It was recovered as a sterile endophyte and none of the five isolates studied sporulated in any of the culture media used, even after an extended incubation period of over 3 mo. Phylogenetically, they clustered in a fully supported monophyletic group (100 % BS, 1 BPP) with several other root endophytic *Cyphellophora* strains, represented in GenBank mainly by their ITS sequences. They are *Cyphellophora* sp. Cyph2 (GenBank MN450628), isolated from roots of *Cephalanthera rubra* (*Orchidaceae*) in France (Bell et al. 2020), and *Cyphellophora* sp. TU18 (GenBank MN537681) and MD68 (GenBank MN537651), both root endophyte isolates obtained from the grass *Stipa krylovii* (*Poaceae*) in Mongolia (Knapp et al. 2019). Phylogenetic analyses suggest that they may be conspecific with *C. endoradicis* and the latter two isolates expand its distribution from Europe to north-central Asia. Moreover, strains of *C. endoradicis* were phylogenetically close but distinct from *C. chlamydospora*, another sterile species isolated from soil in Spain and characterised by the production of abundant chlamydospores in culture (Madrid et al. 2016).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of *Cyphellophora endoradicis* (CBS 148862) are *Cyphellophora* sp. (isolate Cyph2, GenBank MN450628.1; Identities = 577/580 (99 %), no gaps), *Cyphellophora* sp. (isolate TU18, GenBank MN537681.1; Identities = 479/483 (99 %), no gaps) and *Cyphellophora* sp. (isolate MD68, GenBank MN537651.1; Identities = 474/484 (98 %), three gaps (0 %)). Closest hits using the **LSU** sequence are *Cyphellophora europaea* (strain CBS 101466, GenBank KC455259.1; Identities = 913/920 (99 %), no gaps), *Cyphellophora europaea* (strain CBS 129.96, GenBank NG_067264.1; Identities = 975/983 (99 %), no gaps) and *Cyphellophora olivacea* (strain CBS 123.74, GenBank NG_067280.1; Identities = 970/983 (99 %), no gaps). The closest hits using the ***tub2*** sequence are *Cyphellophora phyllostachydis* (strain HLHNZWYZZ08, GenBank KP122929.1; Identities = 321/369 (87 %), three gaps (0 %)), *Cyphellophora europaea* (strain CBS 129.96, GenBank JQ766364.1; Identities = 312/364 (86 %), three gaps (0 %)) and *Cyphellophora europaea* (strain CBS 656.82, GenBank JQ766367.1; Identities = 311/364 (85 %), three gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Cyphellophora europaea* (strain CBS 101466, GenBank XM_008714006.1; Identities = 758/812 (93 %), four gaps (0 %)), *Phialophora attae* (strain CBS 131958, GenBank XM_018148973.1; Identities = 730/798 (91 %), no gaps) and *Cladophialophora immunda* (strain CBS 83496, GenBank XM_016388514.1; Identities = 705/792 (89 %), two gaps (0 %)).

Colour illustrations. Grassland near Grijera (Palencia, Spain), with the stand of *Microthlaspi perfoliatum* from where the type specimen was isolated. Colonies on PDA and MEA (after 2 wk at 25 °C) on surface view; mycelium with hyphae forming hyphal coil and cord. Scale bars = 10 µm.

Supplementary material

FP1408 Phylogenetic tree.

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Endoradiciella communis

Fungal Planet 1409 – 12 July 2022

Endoradiciella G. Delgado & Maciá-Vicente, *gen. nov*.

Etymology. Name refers to the fungus lifestyle as a root endophyte.

Classification — *Porodiplodiaceae*, *Helotiales*, *Leotiomycetes*.

Root-colonising endophyte living on a variety of plant species. Mycelium sterile and isolated on culture media from surface-sterilised roots of plant hosts. Hyphae often aggregated in tightly packed hyphal cords, with intercalary or terminal, thin-walled chlamydospore-like cells and formation of crystal bundles in large and complex structures. The genus differs from its closest phylogenetic relative, *Chalara clidemiae* (CBS 141319, ex-type culture), by unique fixed alleles in the ITS and LSU loci based on alignments of each separate locus deposited in figshare (10.6084/m9.figshare.19310963). ITS positions: 13 (G), 60 (C), 72 (T), 82 (T), 84 (G), 87 (A), 94 (A), 114 (T), 117 (T), 128 (G), 151 (deletion), 152 (A), 155 (C), 399 (G), 405 (C), 467 (C), 475 (T), 486 (G), 503 (C), 504 (T); LSU positions: 36 (A), 37 (G), 38 (C), 114 (C), 115-116 (T), 119 (insertion), 329 (T), 384 (C), 395 (C), 413 (T), 433 (T), 434 (C), 435 (G), 445 (G).

Type species. *Endoradiciella communis* G. Delgado & Maciá-Vicente MycoBank MB 843305.

Endoradiciella communis G. Delgado & Maciá-Vicente, *sp. nov.*

Etymology. Epithet refers to the apparent widespread distribution of the fungus.

Mycelium composed of branched, septate, smooth, hyaline or subhyaline 1–2 µm wide hyphae, single or often aggregated in tightly packed hyphal cords, hyaline when young, reddish brown to blackish brown with age, up to 75 µm wide, rarely forming hyphal coils and often with swollen, intercalary or terminal, thin-walled, uni- or bicellular chlamydospore-like cells, 4–7 µm wide.

Culture characteristics — Colonies on potato dextrose agar (PDA) moderately fast growing, reaching 27–30 mm diam after 2 wk at 25 °C, velvety, whitish to pale cream, circular, flat, sometimes slightly raised in the centre and whitish cream or pale orange to orange, margin diffuse, reverse whitish cream. On malt extract agar (MEA) reaching 18–22 mm diam, whitish cream, floccose and funiculose in the centre, with hyphal cords visible under the dissecting microscope and brown in colour, velvety and flattening toward the edge, margin diffuse, reverse whitish yellow, brown in the centre; formation of greenish yellow bundles of needle-shaped or thin rectangular-bladed crystals, often in large and complex structures, was observed after 2 mo of incubation. Cultures sterile.

Typus. France, Côte-d'Or, Auxonne, endophytic in roots of *Microthlaspi perfoliatum* (*Brassicaceae*), N47°10'43.1" E5°27'21.0", 211 m a.s.l., isolated from surface-sterilised, asymptomatic roots of a wild plant, 4 May 2013, coll. *A.-K. Buch* & *X. Xia*, isol. *K. Glynou*, culture P2333 (holotype and culture ex-type permanently preserved in a metabolically inactive state CBS 148863, ITS and LSU sequences GenBank KT269568 and OM527237, MycoBank MB 843306).

Additional material examined. France, Vienne, Celle-Lévescault, endophytic in roots of *M. perfoliatum*, N46°24'29.9" E0°12'54.5", 115 m a.s.l., isolated from surface-sterilised, asymptomatic roots of a wild plant, 5 May 2013, coll. *K. Glynou* & *J.G. Maciá-Vicente*, isol. *K. Glynou*, culture P2433, ITS GenBank KT269664. – Germany, Baden-Württemberg, Bad Mergentheim, endophytic in roots of *Microthlaspi erraticum* (*Brassicaceae*), N49°27'09.7" E9°49'09.6", 273 m a.s.l., isolated from surface-sterilised, asymptomatic roots of a wild plant, 6 June 2013, coll. *K. Glynou* & *J.G. Maciá-Vicente*, isol. *K. Glynou*, culture P2928, ITS sequence GenBank KT270125.

Notes — The recently introduced helotialean family *Porodiplodiaceae* currently includes coelomycetous and chalara-like asexual morphs inhabiting living leaves or saprobic on dead plant material belonging to different hosts (Crous et al. 2016, 2018, 2019, Wijayawardene et al. 2016, 2021). However, none of its members has been reported so far as a plant endophyte. The novel genus *Endoradiciella* is introduced to accommodate a sterile root endophyte which strains did not sporulate in any culture medium used even after an extended incubation period of over 2 mo. Similar to previously described taxa (Crous et al. 2021a), *Endoradiciella communis* was isolated during an extensive sampling for root endophytic fungi across Europe (Glynou et al. 2016). Blast searches of the fungus ITS sequences reveal a considerable number of isolates available in GenBank annotated as *Helotiaceae* sp. or *Helotiales* sp. that are identical or almost identical to *Endoradiciella.* They share a similar root endophytic lifestyle whereas phylogenetic analyses suggest they might be conspecific with *E. communis.* Most of them have been isolated from several locations all over Europe, including roots of *Vitis vinifera* subsp. *sylvestris* (*Vitaceae*) in Bosnia and Herzegovina and Croatia (Radic et al. 2021), *Cephalanthera rubra* (*Orchidaceae*) in France (Bell et al. 2020) and *Fragaria vesca* (*Rosaceae*) in the UK (Yokoya et al. 2017). Moreover, the distribution of *Endoradiciella* is apparently not limited to Europe but also includes western North America and China. Available ITS sequences also suggest several conspecific isolates recovered from roots of *Pinus flexilis* (*Pinaceae*) seedlings in the US state of California (Shemesh et al. 2020) and *Populus* spp. (*Salicaceae*) in Oregon, Washington, and the Canadian province of British Columbia (Bonito et al. 2016). A further isolate named *Helotiales* sp. FT2G58 (GenBank KT291427.1) was obtained as an endophyte of *Dysphania ambrosioides* (*Amaranthaceae*), a hyperaccumulator of heavy metals in contaminated soils of China (Li et al. 2016). Phylogenetically, these isolates of disparate geographical origins clustered with our strains in a strongly supported monophyletic group (100 % BS but lacking significant BPP) and they all formed a well-distinct lineage within the family *Porodiplodiaceae*. The presence of needle-shaped crystals in bundles on the hyphae of *E. communis* could be tentatively attributed to calcium oxalate but their true nature remains pending of future chemical analysis.

(Notes continued on Supplementary page)

Colour illustrations. Plants of *Microthlaspi erraticum* near Bad Mergentheim, Germany. Colonies on PDA and MEA (after 2 wk at 25 °C) on surface view; hyphal cords, hyphae with swollen chlamydospore-like cells, bundles of needle-shaped crystals. Scale bars (from left to right) = 10 µm, 5 µm, 10 µm.

Supplementary material

FP1409 Phylogenetic tree.

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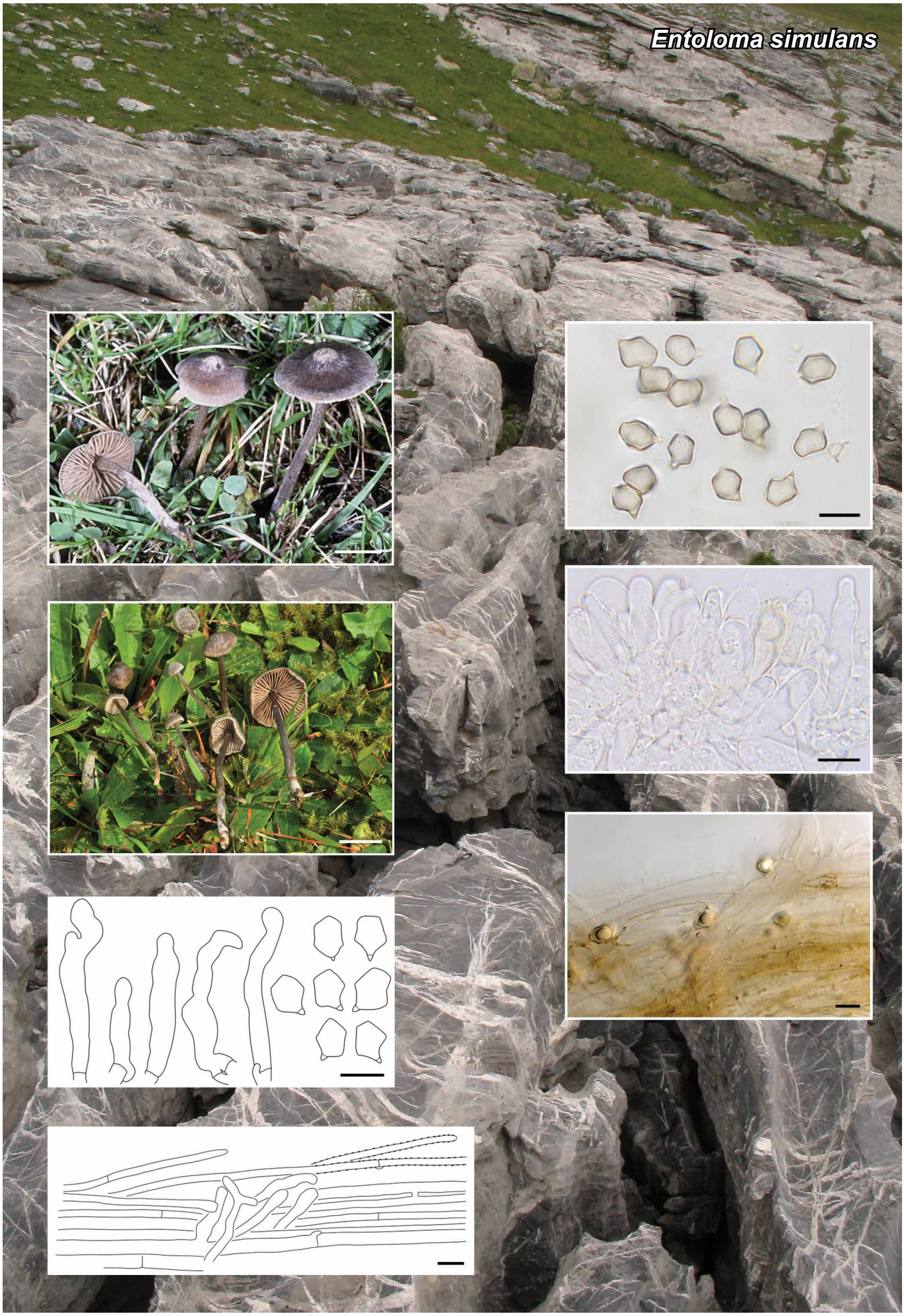
Entoloma simulans

Fungal Planet 1410 – 12 July 2022

Entoloma simulans Reschke, Karich, Corriol, G.M. Jansen & Dima, *sp. nov.*

Etymology. *simulans* (L.) = pretending, i.e., referring to the fact that this species pretends to belong to subgenus *Nolanea*.

Classification — *Entolomataceae*, *Agaricales*, *Agaricomycetes*.

Basidiocarps nolaneoid (mycenoid). Pileus 3–22 mm, conico-convex to convex, finally flattened, with or without small papilla, sordid yellow-brown to grey-brown, mostly not or only slightly translucently striate at the margin, predominantly with somewhat fibrillose, silvery-greyish pruina, especially in the centre, sometimes smooth, finely felted, particularly at centre, becoming more distinctly translucently striate up to centre in fragile or soaked specimens, thin-fleshed. *Lamellae* L = 20–30, l = 1–3(–5), moderately distant, narrowly adnate, sometimes with small, decurrent tooth, ventricose, brownish pink to dark greyish with concolourous edge. *Stipe* 15–70 × 0.8–2 mm, filiform to cylindrical, sometimes almost polished, but often whitish fibrillose, concolorous with pileus, sometimes darker towards base. Basal mycelium white, somewhat cottony, without conspicuous rhizomorphs. *Odour* and *taste* predominantly weak, sometimes farinaceous. *Basidiospores* 8.0–11.0 × 6.0–8.5 µm, av. 9.0–9.6 × 6.6–7.1 µm, Q = 1.15–1.60, Qav 1.3–1.4, heterodiametrical, 5–6-angled with pronounced and sharp angles. *Basidia* 25–45 × 9–13 µm, clavate, mainly 4-spored, few 2-spored, clamped. Lamella edge heterogenous, with scattered cheilocystidia slightly exceeding the hymenium. *Cheilocystidia* 20–50 × 3.5–9.0 µm, subcylindrical, somewhat moniliform to subclavate, often subcapitate, clamped. *Hymenophoral trama* regular, made up of slightly inflated hyphae, 4.5–20 µm wide, with pale brown, incrusting pigment. *Pileipellis* a cutis of cylindrical hyphae, 4–12 µm wide, with transitions to a loose trichoderm, particularly at centre, with rather frequent, variable terminal cells often emerging from below the suprapellis. Pigment incrusting and faintly intracellular. *Stipitipellis* a cutis with somewhat loose suprapellis of often relatively wide hyphae, 4.5–12 µm, and a dense subcutis of narrow hyphae, 2–4 µm wide, with pale brown, minutely incrusting pigment; scattered terminal cells of the suprapellis cylindric-clavate to irregular, often (sub-)capitate, or rather moniliform. *Clamp connections* abundant in all parts.

Habitat & Distribution — In poorly managed, nutrient-poor grasslands and parks, and in heath-like vegetations on poor soil. Known from Estonia, France, Denmark, Germany, Latvia, Norway, and The Netherlands.

Colour illustrations. Subalpine site with grassland patches near Garvarnie ski station, holotype location. Basidiocarps of GC03091006, holotype, and IHI-20Ent06; drawings (from holotype) of cheilocystidia and basidiospores; drawing (from holotype) of the pileipellis with incrusting pigment indicated on hyphae at the right; microscopical pictures of basidiospores (from holotype), hymenium with cheilocystidia among immature basidia (from holotype), and pileipellis (from L-0607897). Scale bars = 10 mm (basidiocarps), 20 µm (drawing of pileipellis with incrusting pigment), 10 µm (all others).

Typus. France, Hautes-Pyrénées, Gavarnie ski station, 1850 m a.s.l., in a grazed subalpine nutrient poor basophilous grassland with other *Entoloma* species, 10 Sept. 2003, *G. Corriol*, GC03091006 (holotype in BBF; ITS-LSU sequence GenBank ON006551, MycoBank MB 843348).

Additional materials examined. Denmark, Biowide 089 Eskebjerg Vesterlyng, 23 Sept. 2015, *T. Læssøe*, DMS-718511, ITS sequence GenBank ON006557; Biowide 079 Melby Hede, 18 Sept. 2020, *T. Læssøe*, DMS-716711, ITS sequence GenBank ON006556. – Germany, Lückendorf, Parkwiese, 19 Sept. 2019, *A. Karich*, IHI-19Ent01, ITS sequence GenBank ON006552; 2 Sept. 2021, *A. Karich*, IHI-20Ent06, ITS sequence GenBank ON006554; Herrnhut, Gottesacker, 23 Sept. 2020, *A. Karich*, IHI-20Ent05, ITS sequence GenBank ON006553. – Netherlands, Utrecht Province, Soesterberg, former military airport, 30 Sept. 2019, *M.E. Noordeloos*, *J. van Dongen & JP. Keizer*, L-0607879, ITS sequence GenBank ON006558. – Norway, Telemark, Porsgrunn, Heistad, Lundebukta, 11 Oct. 2013, *A. Molia & T. Læssøe*, O-F-21950, ITS sequence GenBank ON006555.

Notes — This study is part of a large-scale molecular phylogenetic and morphological revision of the genus *Entoloma* in Europe (Noordeloos et al. 2022). *Entoloma simulans* belongs to the subgenus *Leptonia*, where it occupies an isolated position. It is distinctive by its rather small basidiocarps with mycenoid habit and fibrillose-pruinose pileus surface, a heterogenous lamella edge with scattered, rather undifferentiated cheilocystidia, rather simple, heterodiametrical spores with sharp angles, and abundant clamp connections. It has some affinity to *E. sanvitalense*, which has, however, a translucently striate pileus about halfway to the centre, a blackish stipe, and a fertile lamella edge (Noordeloos & Hausknecht 1998, Vila et al. 2013). Specimens of *E. simulans* with rather smooth pileus and stipe may resemble *E. clandestinum*. This species has, however, differently shaped spores with 6–8, relatively blunt angles, a fertile lamella edge, and a regular cutis without conspicuous trichodermal parts (Noordeloos 1980). Molecularly it is quite distant, belonging to another subgenus (*Nolanea*).

Supplementary material

FP1410 Phylogenetic tree.

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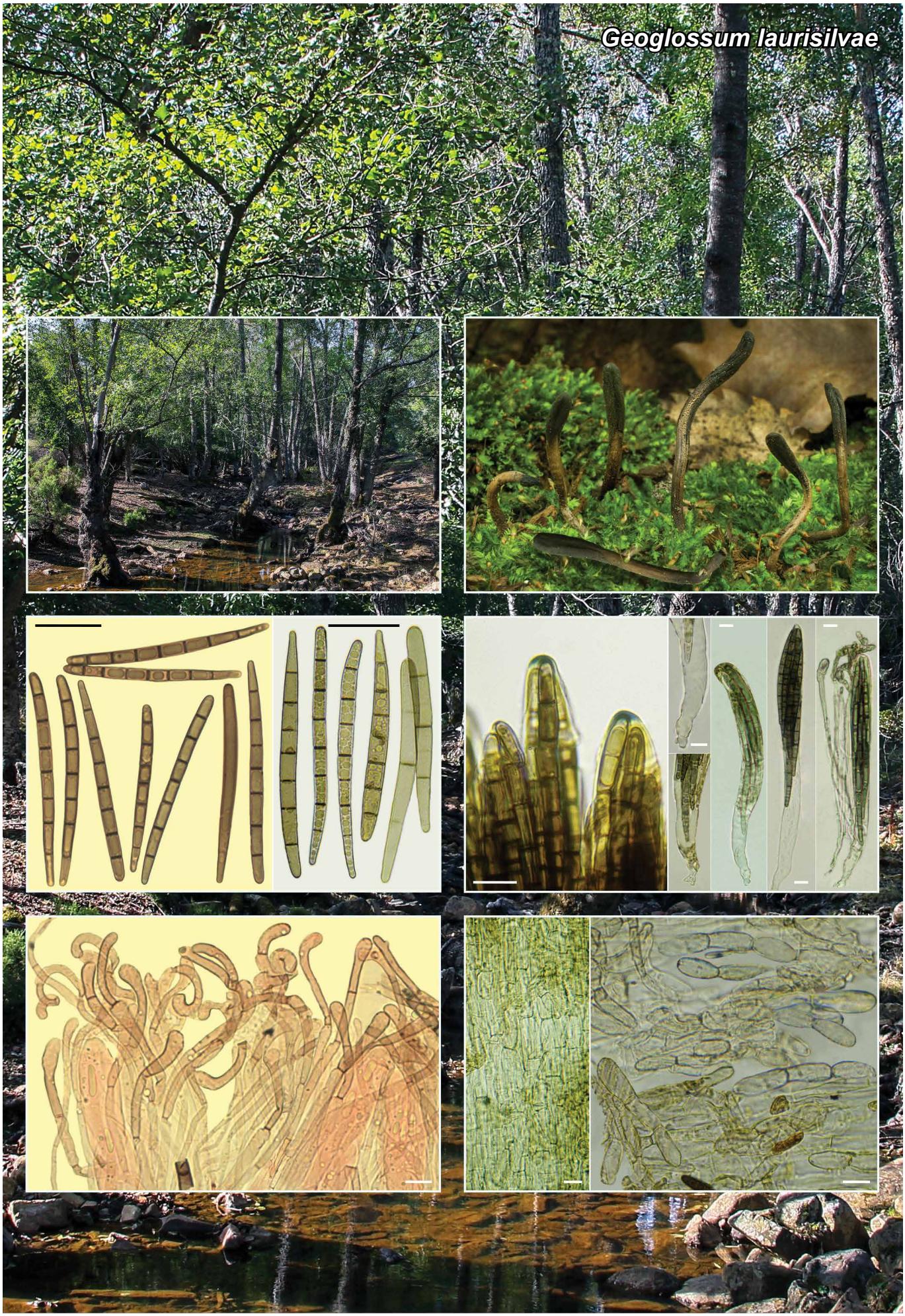
Geoglossum laurisilvae

Fungal Planet 1411 – 12 July 2022

Geoglossum laurisilvae A. Mateos, S. De la Peña-Lastra, Arauzo & P. Iglesias, *sp. nov.*

Etymology. The specific epithet refers to the ecosystem where it was found, evergreen laurel forest, commonly called 'laurisilva'.

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

Apothecia gracile *14–48 mm high, dry, cylindrical or subcapitate but usually clavate, dull grey blackish, dark brown or blackish. *Ascogenous portion* *5–17 × 1.5–4 mm, cylindrical to clavate, frequently flattened (spatulate), sometimes longitudinally furrowed, (1/4) 1/3 or 40 % of the total apothecium, felted in appearance and with grey-blackish colour in general; ascogenous portion and sterile portion they are not clearly distinguishable, at times lower on one side or the other, smoothly shaped. *Sterile portion* *9–37 × 1.1–2.2 mm, terete, sometimes compressed lobed with longitudinal furrow, generally recurved, occasionally serpentiform, narrowed towards the base, which ends somewhat widened; upper part finely fibrillose and with small scales, more abundant near fertile part; lower part more cylindrical, with surface more uniform and smooth, sometimes granulate; colour is greyish brown especially in dry weather and blackish towards the base, darker in wet weather, the hairs shorter and finer than fertile part along the whole length. *Flesh* somewhat fistulous at ascogenous portion, with a slight pleasant odour, whitish when cut, but soon turning greyish and brownish on the underside of the stipe, blackish at the apex of fertile part. *Asci* *(160–)175.5–*182.7*–190(–205) × (14.4–)14.7–*15.6*–16(–19) µm; Q = (10–)10.8–*11.8*–12.67(–12.7), unitunicate, consistently 8-spored, clavate, cylindrical or fusiform, with rounded apex, narrowed below, pore I^+ euamylloid, with pretreatment in KOH and later in Lugol's solution (IKI 2), apical ring strongly amyloid (bb) deep blue-greenish, with pleurorhynchous base provided with croziers. *Paraphyses* slightly protruding above the asci, fragile, filiform and hyaline towards the base, 2.5–3.5 mm wide, constricted at the septa, last elements with parietal or encrusting grey-fuliginous pigment, distinctly and variously enlarged, broadly clavate, capitate, pyriform or obovoid, sometimes with appendage or somewhat curved or flexuous, hook-like or circinate, usually 180–270(–360) degrees, *(14–)17–37 × (5–)5.5–8(–11) µm. *Ascospores* *(65–)71.6–*79.3*–86(–90) × (4.8–)5–*5.8*–6.47(–6.5) µm; Q = (10.8–)11.2–*13.8*–17(–17.4); N = 20; Vm = 1416 µm^3; cylindrical-clavate, sub-fusiform, somewhat curved, acute basal end; initially hyaline and aseptate, finally dark brownish full-brown and with well-marked 7-septate, rarely with 1- or 3-septate; ˙pluriguttulate (LBs) and sometimes with larger guttules forming a more or less complete row. *Medullary excipulum* banal composed of rather compact *textura porrecta-prismatica*, elements *(20–)22.2–*29.1*–36.1(–50) × (8.2–)8.4–*11.7*–14.3(–15) µm, shallower hyphae with abundant encrusting pigment. *Subhymenial trama* with globose elements up to 15 × 10 µm. *Ectal excipulum* composed of cauline hairs *(35–)50–65(–90) µm long, consisting of chains of 3–5 elements, moniliform, light brown parietal pigment. Basal element clavate, all other elements are elliptic, ovoid or subglobose *(10–)13–18(–20) × 6–9 µm.

Habitat & Distribution — Gregarious, in more or less numerous groups in laurel forest areas, among the leaf litter of *Prunus lusitanica* subsp*. lusitanica*. Known from two different and distant laurel forest locations, one continental (Cáceres, Spain) and one island (Madeira, Portugal).

Typus. Spain, Cáceres, Alía, Lorera de la Trucha, N39°32'50.57" W5°14'55.08", 640 m a.s.l., gregarious growth on a slope near a watercourse, under *Prunus lusitanica* subsp. *lusitanica* (*Rosaceae*) in acidic soils, 20 Feb. 2021, *A. Mateos*, *S. De la Peña* & *A. Gutiérrez* (holotype AMI-SPL642, ITS and LSU sequences GenBank OM691497 and OM691457, MycoBank MB 843160).

Additional materials examined. Portugal, Madeira, Ribeiro Frío, N32°44'08.0" W16°53'11.0", 888 m a.s.l., in wet area under laurel forest (*Laurus novocanariensis*), 23 Nov. 2018, *P. Iglesias*, *J. Fernández*, *R. Ibarretxe* & *R. Martínez* (ERRO2018112301, ITS sequence GenBank OM691496). – Spain, Cáceres, Alía, Lorera de la Trucha, N39°32'50.57" W5°14'55.08", 640 m a.s.l., gregarious growth on a slope near a watercourse, under *Prunus lusitanica* subsp. *lusitanica* in acidic soils, 20 Feb. 2021, *A. Mateos*, *S. De la Peña* & *A. Gutiérrez* (AMI-SPL641).

Notes — *Geoglossum laurisilvae* is morphologically characterised by gracile and slender apothecia, brown stipe with scaly decoration, paraphyses with variously shaped terminal elements and ascospores with seven pluriguttulate septa. Closely related species are: *G. subumbratile* nom. prov. 'sp. SA-2015c' (Arauzo & Iglesias 2014) with more robust and black hymenium and stipe, partially similar but less claviform and more curved paraphyses, the ectal excipulum has generally claviform cells; *G. pseudoumbratile* nom. prov. 'sp. SA-2015a' (Arauzo & Iglesias 2014), has much larger apothecia, with wider and blacker clavula and stipe, the paraphyses without hooks and larger spores; *G. umbratile* with larger ascomata, no scaly stipe, with monotonous, only slightly claviform paraphyses and somewhat larger spores; although *G. gesteranii* is also close, it differs mainly by the paraphyses with very thickened and curved apex, and the spores with non-acute base and much smaller spores. *Geoglossum brunneipes* and *G. scabripes*, despite their morphological and phylogenetic affinity, differ well in having the pore of the asci hemiamyloid, paraphyses never circinate and smaller spores. The most closely phylogenetically related species appearing in the same clade in our analyses are *G. subbarlae* nom. prov. 'sp. SA-2015b' (ITS 95.2 % match), *G. scabripes* (ITS 94.1 % match) and *G. brunneipes* (ITS 91.4 % match). *Geoglossum scabripes* and *G. subbarlae* differ in having a more strongly ornamented stipe, hemiamyloid ascal pore and frequent pseudoparaphyses; *G. brunneipes* differs in having a smooth stipe, hemiamyloid ascal pore and shorter ascospores (Arauzo & Iglesias 2014).

Colour illustrations. Spain, Alía, Lorera de la Trucha, laurissilva of *Prunus lusitanica* subsp. *lusitanica*, where the holotype of *Geoglossum laurisilvae* was collected. Right column: apothecia in upper photo correspond with the holotype; middle photo corresponds with: detail of *ascus apex (IKI 2), detail base ascus with crozier (two pictures) and mature asci (three pictures) in *H_2O; the bottom photo is *medullary excipulum (left) and *ectal excipulum (right) (H_2O). Left column: middle photo ascospores (left †RC, right *H_2O); the bottom photo is paraphyses (†RC). † = dead, * = living. Scale bars = 25 µm (ascospores), 10 µm (all others).

Supplementary material

FP1411 Phylogenetic tree.

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Geosmithia funiculosa

Fungal Planet 1412 – 12 July 2022

Geosmithia funiculosa Pepori, M. Kolařík, Nigrone & Santini, *sp. nov*.

Etymology. Named after the funiculose mycelium.

Classification — *Bionectriaceae*, *Hypocreales*, *Sordariomycetes.*

On MEA, 25 °C, 7 d: *Conidiophores* penicillium-like, arising from surface or aerial mycelium, verrucose, septate; base with our without a peg foot; *stipe* erect (20–)39–93(–162) × (1.1–)2.2–3.7(–5.0) µm; *penicillus* symmetrical, often with short branch appressed to each other, 1–5 × branched, (17–)23–40(–120) × (14–)19–37(–80) µm, primary branches (5–)6.5–11.5(–20) × 2.1–3.0 µm, 2–4 per cluster; secondary branches (5–)6.5–9.3(–17) × 1.7–2.6 µm, 2–3 per cluster, *metulae* 3–12 × (2–)2.5–3.7 µm, 2–3(–4) per cluster; *phialides* cylindrical without distinct neck, 5–7(–10) × 1.5–2.1 µm, 2–3 per cluster. *Conidial* chains not persistent, not forming crust. *Conidia* cylindrical, (1.6–)3.1–4.2(–5) × (0.9–)1.4–2.1(–2.5) µm. *Substrate conidia* absent. *Sexual morph* unknown.

Culture characteristics — On malt extract agar (MEA), margin narrow, entire, substrate mycelium hyaline; aerial mycelium hyaline; surface and texture plane, with velutinose, floccose and funicolose (typically in the centre) areas; sporulation weak to moderate, yellowish brown (5E 8–5, 5D 6–5), light brown (6D 8–5); reverse dull yellow (3B3); soluble pigment absent. On Czapek Yeast Autolysate Agar (CYA), similar to MEA, but sometimes radially furrowed, zonate, aerial mycelium more evolved, sporulation weak, reverse browning in the inner part (old part of mycelium). On Czapek Dox Agar (CZD), similar to MEA, substrate mycelium less shiny, sporulation weak, reverse pale grey. Yeast-like colonies absent. Colony diam, 14 d (mm): MEA at 25 °C: 39–48; CYA at 25 °C: 45–62; CZD at 25 °C: 40–74; MEA at 37 °C: no growth. Colour codes based on Kornerup & Wanscher (1981).

Distribution & Habitat — Italy, Czech Republic (Pepori et al. 2015, this study), Bulgaria, Hungary, Poland (Kolařík & Jankowiak 2013, Strzałka et al. 2021). Seems to be absent in other regions, such as Mediterranean basin (Kolařík et al. 2007), China (Zhang et al. 2022) and the USA (Kolařík et al. 2017) where *Geosmithia* was studied. Associated with broad spectrum of bark beetle species feeding on host plants from families *Fagaceae*, *Oleaceae*, *Pinaceae*, *Rosaceae*, *Tiliaceae* and *Ulmaceae*. See the distribution and host list of *Geosmithia* sp. 5 in Kolařík & Jankowiak (2013), Pepori et al. (2015) and Strzałka et al. (2021).

Typus. Czech Republic, Velký Osek, Libický Luh, from a bark beetle gallery on *Ulmus minor* (*Ulmaceae*), 11 Oct. 2009, *A. Pepori & M. Kolařík* (holotype CNR48, dried culture on MEA, Fungal Collection Institute for Sustainable Plant Protection (CNR), Florence, Italy; ITS, *tub2*, *tef1* sequences GenBank KR229897, KP990579, KR135506, ex-type culture CBS 149063, MycoBank MB 843066). *Geosmithia* sp. 5 in Pepori et al. (2015).

Additional materials examined. Bulgaria, Rodopy Mts, Bačkovo, from *Ernoporus tiliae* on *Tilia* sp., 16 Sept. 2005, *M. Kolařík*, *tub2*, *rpb2*, *tef1* sequences GenBank HG799812, HG799903, HG799849. – Czech Republic, Libický Luh, Velký Osek, from a bark beetle gallery on *Ulmus minor*, 11 Oct. 2009, *A.L. Pepori & M. Kolařík*, CNR31, CNR 33, ITS, *tub2*, *tef1* sequences GenBank for CNR31: KR229887, KP990567, KF484889, for CNR33: KR229889, KP990569, KR135495; from a bark beetle gallery on *U. laevis*, 11 Oct. 2009, *A.L. Pepori & M. Kolařík*, CNR 30, ITS, *tub2*, *tef1* sequences GenBank KR229886, KP990566, KR135493; *Scolytus intricatus* on *Quercus petraea*, 1998, *A. Kubátová*, CCF3341 (= AK 108/97) ITS, *tub2*, *rpb2*, *tef1* sequences GenBank AJ578487, HG799801, HG799891, HG799837; Sušice, Maršovice, from a bark beetle gallery on *U. glabra*, 17 Oct. 2009, *A.L. Pepori & M. Kolařík*, CNR49, *tef1* sequences GenBank KR135507; Libochovice, Hoštěnice, from a bark beetle gallery on *U. glabra*, 17 Oct. 2009, *A.L. Pepori & M. Kolařík*, CNR63, ITS, *tub2*, *tef1* sequences GenBank KR229906, KP990588, KR135517. – Italy, Florence, from a bark beetle gallery on *U. minor*, 3 Nov. 2010, *A.L. Pepori*, CNR142.

Notes — *Geosmithia funiculosa* was previously classified as a broad species *G. pallida*, where it was distinguished as an own group *G. pallida* RAPD-type V 'funiculosa' by RAPD fingerprinting (Kolařík et al. 2004). Later, based on DNA sequence data, the group was treated as *Geosmithia* sp. 5, without a formal description (Kolařík & Jankowiak 2013, Pepori et al. 2015, Strzałka et al. 2021). Diagnostic features of *G. funiculosa* include beige shades of sporulation and funiculose texture of colonies, short conidiophore stipes and branches, and small cylindrical conidia. *Geosmithia funiculosa* grows faster on CZD than on the other substrates and does not grow at 37 °C. It is morphologically similar to other species from the *G. pallida* species complex, namely *G. pumila* and *G. pulverea* (Zhang et al. 2022). Some slight phenotypic differences are observed: *G. pumila* has a surface texture mostly velutinous and reverse less pigmented than *G. funiculosa*, especially on CZD. *Geosmithia pulverea* differs by its strictly velutinous colonies on MEA and smaller conidia. All *G. funiculosa* strains exhibited almost identical morphology, differing in colony growth rate only.

Colour illustrations. *Ulmus minor* plain forest. *Geosmithia funiculosa* colonies on (top to bottom) CYA, CZD, MEA; conidiophores and small cylindrical conidia. Scale bars = 10 µm.

Supplementary materials

FP1412-1 Maximum likelihood tree.

FP1412-2 One of the three equally most parsimonious trees.

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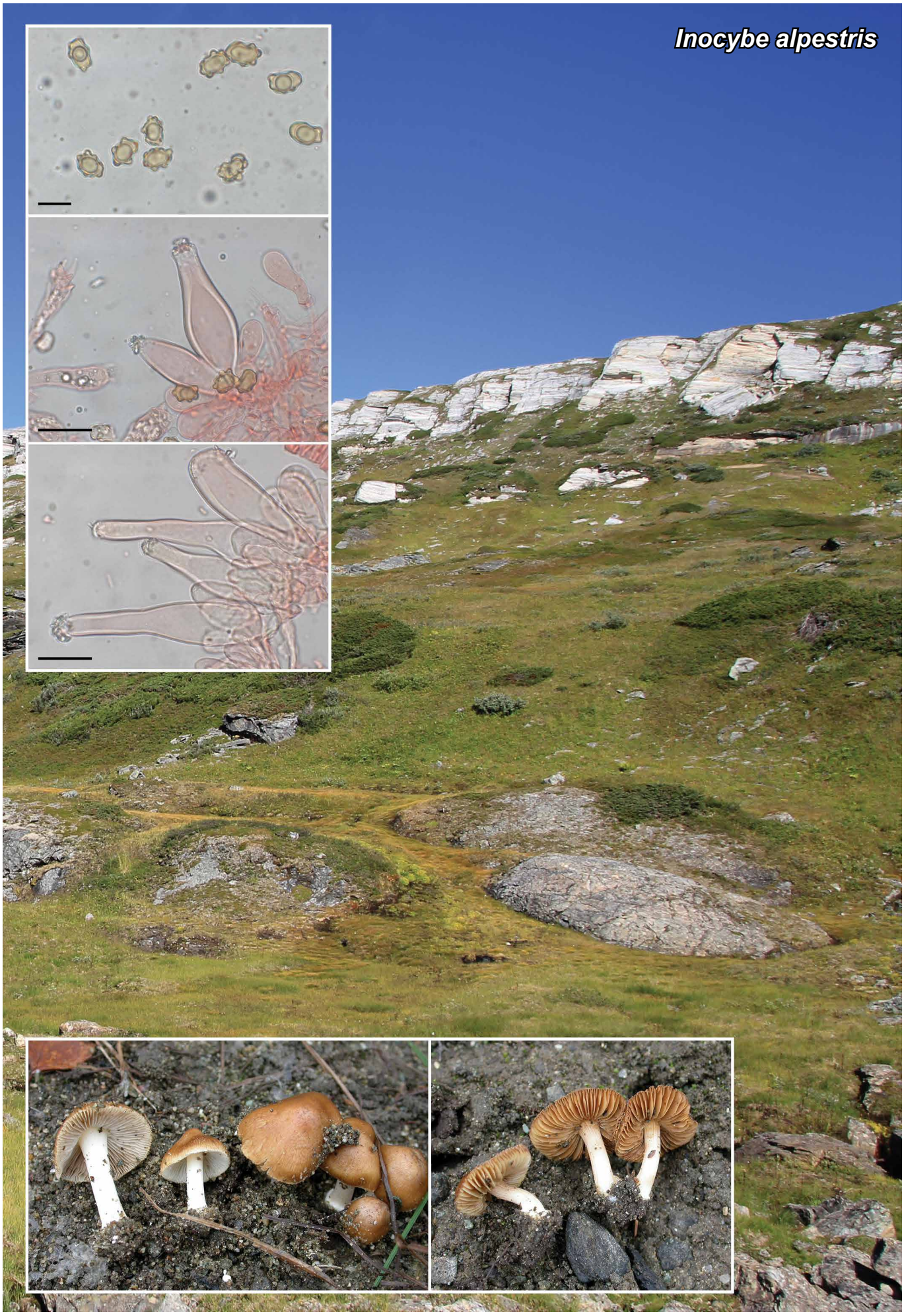
Inocybe alpestris

Fungal Planet 1413 – 12 July 2022

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

Etymology. Refers to the ecology, growing in the alpine zone.

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

Pileus 10–35 mm diam, as young campanulate, conical to convex, umbonate or with an obtuse to broad umbo, later planoconvex to plane with or without broad umbo, as young with slightly incurved margin later plane to decurved, sometimes with undulate margin, dry, rather uniformly coloured yellowish brown to ochraceous brown, at centre smooth to matted fibrillose, radially fibrillose with depressed scale and rimose towards the margin, cortina absent, velipellis thin fugacious white visible in young basidiomata, soon disappearing. *Lamellae* moderately crowded L 46–60, interspersed with lamellulae, adnexed to almost free, first white with a greyish tone, later pale ochraceous brown, edge concolourous to pale. *Stipe* 15–45 × 3–8 mm, more or less equal with a distinctly marginate basal bulb, sometimes with a fibrillose false volva as a result of the remains of the velipellis, with age often a bit curved at the base, pruinose for the entire length, as young white and later with pale straw to a yellowish brown tone, longitudinally striate, solid. *Context* in pileus pale yellowish brown, in stipe whitish to pale buff, base white. *Smell* weakly spermatic to indistinct, *taste* indistinct. *Basidiospores* (9.2–)10.2–*10.5*–11.1(–12.7) × (5.5–)6.5–*6.9*–7.1(–8.5) µm, n = 95, Q = 1.34–*1.51*–1.80, variable, angular-nodulose, with about 7–10 prominent rounded obtuse nodules and a small apiculus, pale ochraceous brown. *Basidia* 30–*34*–40 × 10–*11*–13 µm, n = 25, clavate, 4-spored, hyaline, sterigmata 6.0–7.5 µm. *Pleurocystidia* 60–90 × 16–26 µm, n = 35, lageniform to utriform to fusiform, with short pedicel, pedicellate to truncate-variable or with rounded base, thick-walled (1.5–)2–4(–5) µm, thicker towards the apex, with abundant crystals, hyaline to slightly yellow in ammonia solution. *Cheilocystidia* similar to pleurocystidia but shorter, 45–75 × 12–24 µm, n = 30, thick-walled, mixed with clavate paracystidia (1.5–)2–4(–5) µm, hyaline. *Caulocystidia* numerous over the entire length, similar to pleurocystidia, longer at stipe apex, abundant, with crystals, less so further down 50–100 × 10–20 µm, n = 30, fusiform to more cylindrical, with abundant crystals, cauloparacystidia clavate to pyriform abundant. *Pileipellis* a cutis of cylindrical to inflated thin-walled, 7–15 µm wide hyphae. *Clamp connections* present.

Ecology & Distribution — Occurs in the alpine zone growing associated with *Dryas octopetala*, *Salix reticulata* and *S. retusa*, also in the subalpine zone associated with *S. lapponum*. Based on the three studied collections it seems to be favoured by more nutrient rich soils and neutral to calcareous ground. It is known from Sweden and Spain, and from an ITS sequence generated from a soil sample in China originating from a northern temperate forest. The Chinese ITS sequence differs in a few base pairs from the ITS of the European collections.

Typus. Sweden, Härjedalen, Tännäs, Andersborgsvägen, subalpine area on sandy soil, associated with *Salix lapponum* (*Salicaceae*), 15 Aug. 2006, *E. Larsson*, EL85-06 (holotype GB-0207621, isotype AH, ITS-LSU sequence GenBank FN550892, MycoBank MB 843360).

Additional materials examined. Spain, Catalonia, Girona, Vall de Núria, Ras de l´Ortigar, 2250 m a.s.l., alpine meadows with *Dryas octopetala* and *Salix retusa* on calcareous soil, 23 July 1999, *J. Vila* 990723-8, AH26730 (ITS sequence GenBank OM891092). – Sweden, Lule lappmark, Jokkmokk, Padjelanta, Oarjep Slampet-Jåhkkå, in mosaic rich alpine vegetation on calcareous ground associated with *Salix reticulata* and *Dryas octopetala*, 18 Aug. 2016, *E. Larsson*, EL244A-16, GB-0207622 (ITS-LSU sequence GenBank OM891091).

Notes — *Inocybe alpestris* is characterised by the uniformly coloured, warm brown, smooth, radially fibrose pileus, entire white pruinose stipe with a distinct to volvate marginate bulb, hardly darkening context and prominent cystidia. In alpine habitats there are similar species that can cause confusion (Cripps et al. 2020); *I. phaeocystidiosa* (*I. salicis-herbaceae*) differs by having somewhat more robust basidiomata, yellowish brown appressed scaly to rimose pileus, stipe and context that becomes brownish, less distinct bulbous stipe base and broader spores. *Inocybe occulta* and *I. alpinomarginata* share with *I. alpestris* the greyish tone in young lamellae and not so darkening context; *I. occulta* belongs to the *I. mixtilis* group (Esteve-Raventós et al. 2018) characterised by more yellowish brown radially fibrose pileus, rounded stipe base and different shorter cystidia; otherwise *I. alpinomarginata* is similar to *I. phaeocystidiosa* but clearly differs by the less marginate stipe base, hardly darkening flesh and in ITS sequence data. In micro-morphology they all have distinct nodulose spores but the average number of prominent nodules vary, in *I. phaeocystidiosa* (10–14), *I. occulta* (8–13), *I. alpestris* (7–10) and in *I. alpinomarginata* (6–8). The pleurocystidia of *I. phaeocystidiosa* are distinctly yellow-brown in NH_4OH, while they are pale to only pale yellowish in *I. occulta*, *I. alpinomarginata* and *I. alpetris*. Another nodulose species in the alpine zone is *I. substellata*, that differs by having a grey-brown colour of the pileus, often abundant white velipellis and larger spores (Vauras & Larsson 2016).

Colour illustrations. Inocybe alpestris habitat in the alpine zone, Padjelanta, Oarjep Slampet-Jåhkkå. *In situ* basidiomata of the holotype (GB-0207621); photos of basidiospores, cheilo- and caulocystidia. Scale bars = 20 µm (cheilo- and caulocystidia), 10 µm (spores).

Supplementary material

FP1413 Phylogenetic tree.

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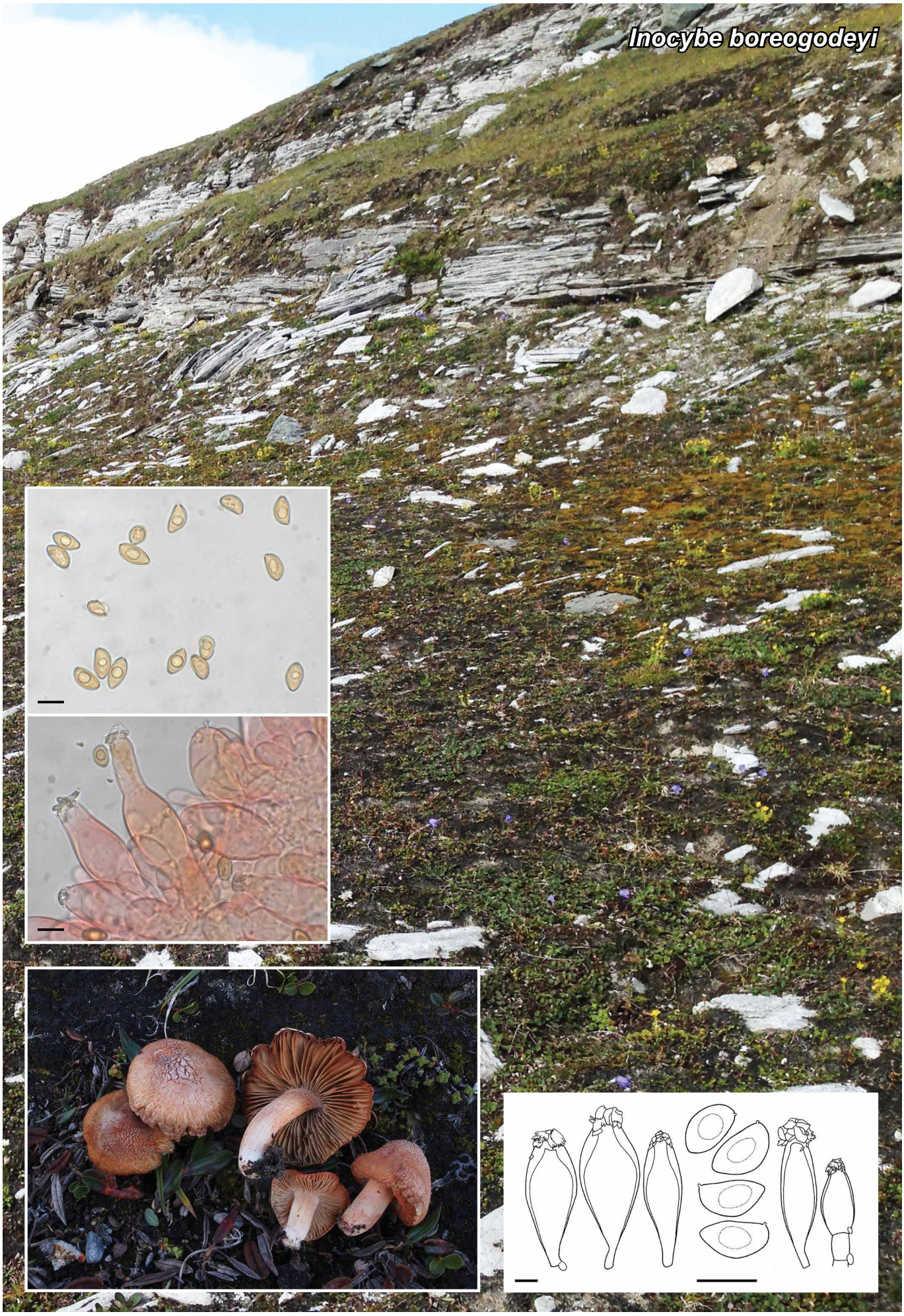
Inocybe boreogodeyi

Fungal Planet 1414 – 12 July 2022

Inocybe boreogodeyi Vauras, Kokkonen & E. Larss., *sp. nov.*

Etymology. Refers to the boreal distribution, and being closely related to *Inocybe godeyi*.

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

Pileus 10–33 mm diam, when young hemispherical or obtusely conical, later convex to plano-convex, sometimes with broad umbo, margin at first inflexed to deflexed, later often reflexed; surface smooth, slightly viscid to dry, innately fibrillose, sometimes cracking into small squares, centre at times with whitish velipellis, often abundantly in high altitudes; colour at first pale yellow-orange, reddish cream, brownish yellow to yellow-brown, later darkening and soon reddening to brownish red to red-brown, umbo often paler, yellowish or greyish; no cortina observed. *Lamellae* moderately crowded, up to 8 mm broad, narrowly adnate to emarginate, at first pale grey, then grey, later pale brown or grey-brown, reddening first at edges or as few red spots, later sometimes totally red; edge fimbriate, pale, concolourous, or red. *Stipe* 15–42 × 2.5–7 (bulb –8) mm, equal, often bulbous but not marginately so; when young white, soon partly pale yellow-brown, red-brown, brownish red to red, rarely turning red when touched or damaged; white-pruinose all over or visibly pruinose on the upper part, longitudinally striate. *Context* in pileus pale grey, brownish to watery pale red, in stipe whitish, pale red, or brownish. *Smell* slightly spermatic when cut. *Basidiospores* (8.9–)9.4–*10.4*–11.3(–11.7) × (5.4–)5.7–*6.2*–6.6(–6.8) µm, Q = (1.4–)1.5–*1.67*–1.9(–2.0) (n = 105/6), smooth, subamygdaloid, some with bulgy dorsal side, without or with suprahilar depression, apex obtuse, subacute to subpapillate, yellow-brown with reddish tinge. *Basidia* (24–)26–*33*–40(–44) × 9–*11*–13 µm (n = 40/3), subclavate to clavate, mainly 4-spored. *Pleurocystidia* (42–)50–*60*–74(–84) × (15–)16–*21*–26(–28) µm (n = 130/5), Qaw = 2.9, mainly subfusiform, broadly subfusiform to subclavate, with or without pedicel, walls up to 2 µm, yellowish in 10 % NH_4OH, apex crystalliferous. *Cheilocystidia* similar to pleurocystidia, or shorter and broadly clavate, rarely yellow-brown inside, intermixed with abundant subclavate to pyriform thin-walled paracystidia. *Caulocystidia* present down to the base, similar to cheilocystidia but in general shorter, abundant, (25–)32–*46*–62(–64) × 11–*16*–20(–22) µm (n = 40/1), apex mostly crystalliferous. *Clamps* abundant.

Ecology & Distribution — The species is found both in the alpine zone and in boreal lowlands, likely associated with *Salix* spp. on calcareous soils. In the Scandinavian Mountains found growing with dwarf *Salix* and *Bistorta viviparia*, and in Finland on a boreal lake shore close to mixed forest as well as from a margin of fen. Additional ITS data from soil and environmental samples suggest a broader distribution and host preferences with occurrences in a wooded meadow in Estonia and associated with *Dryas integrifolia* in Alaska, Fairbanks.

Typus. Sweden, Lule lappmark, Jokkmokk, Padjelanta NP, Vielggisbákte, alpine fjeld area, S slope, under limestone cliff with *Salix herbacea*, *S. reticulata* (*Salicaceae*) and *Bistorta vivipara* (*Polygonaceae*), 760 m a.s.l., 12 Aug. 2016, *J. Vauras*, 31472F (holotype TUR-A 204256, isotype GB-0207623; ITS-LSU sequence GenBank OM859009, MycoBank MB 843268).

Additional materials examined. Finland, Pohjois-Savo, Kuopio, Säyneinen, Huosiaisniemi Nature Reserve, lake shore, near *Salix myrsinifolia*, *Alnus incana*, *Betula*, *Picea abies* and *Populus tremula*, 96 m a.s.l., 20 Sept. 2013, *K. Kokkonen*, 463/13, TUR-A 209628 (ITS sequence GenBank OM859015); ibid., 16 Sept. 2014, *K. Kokkonen*, 129/14, TUR-A 209629; ibid., 2. Sept. 2021, *J. Vauras*, 33447, TUR-A 209525 (ITS sequence GenBank OM859016); Oulun Pohjanmaa, Oulu, Kiiminki, Keskikylä, Vehmaansuo, margin of fen, 45 m a.s.l., 24 Aug. 1969, *M. Ohenoja*, OULU. – Sweden, Lule lappmark, Jokkmokk, Padjelanta NP, Vielggisbákte, alpine fjeld area, S slope, under limestone cliff with *Salix herbacea*, *S. reticulata* and *Bistorta vivipara*, 760 m a.s.l., 12 Aug. 2016, *J. Vauras*, 31473, TUR-A 204298, GB-0207626 (ITS-LSU sequence GenBank OM859010); ibid., *J. Vauras*, 31485F, TUR-A 204321, GB-0207624; Padjelanta NP, N side of Slahpejávrre, S slope, on sandy, calcareous soil with *Salix herbacea* and *Bistorta vivipara*, 790 m a.s.l., 14 Aug. 2016, *J. Vauras*, 31528, TUR-A 204263, GB-0207625 (ITS-LSU sequence GenBank OM859011).

Notes — *Inocybe boreogodeyi* is characterised by the reddening basidiomata, entirely pruinose stipe, smooth and rather dark variable spores. It is a medium-sized species with a northern alpine and boreal distribution, and is clearly rare. In the phylogeny it comes out as a sister species to *I. godeyi*, that also must be regarded as rare but has a wide distribution in temperate and Mediterranean Europe in deciduous woods and parks associated with *Fagus*, *Tilia*, *Corylus* and *Quercus* on calcareous soils (Kuyper 1986, Jacobsson & Larsson 2018). The species are morphologically very similar but *I. boreogodeyi* has on average slightly longer spores and pleurocystidia. The average size of spores of *I. godeyi* in our measurements was 10.1 × 6.2 µm (n = 100/5) and of pleurocystidia 55 × 20 µm (n = 64/5). Further, the spores of *I. boreogodeyi* are darker in 10 % NH_4OH. Both species have rather variable spores, as depicted by Stangl (1989) of *I. godeyi*. *Inocybe roseifolia* described from Florida, USA, is a species that belongs to the same species group but does not seem to occur in Europe. Also *I. amelandica*, described from dunes of the Netherlands is genetically closely related but does not have reddening basidiomata (Bandini et al. 2020).

Colour illustrations. *Inocybe boreogodeyi* habitat in the alpine zone with *Salix herbacea*, *S. reticulata* and *Bistorta vivipara*, Padjelanta NP, Lule lappmark, Sweden. *In situ* basidiomata of the holotype (TUR-A 204256); hymenial cheilocystidia; basidiospores. Drawing of pleurocystidia (left); basidiospores; caulocystidia (right). Scale bars = 10 µm.

Supplementary material

FP1414-1 Phylogenetic tree.

FP1414-2 Photo of *Inocybe boreogodeyi* from the southern boreal zone (Kokkonen 129/14).

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Keithomyces indicus
ॐ नमः शिवाय॥

Fungal Planet 1415 – 12 July 2022

Keithomyces indicus Lagashetti, S.K. Singh & P.N. Singh, *sp. nov.*

Etymology. Name refers to India, the country from where this fungus was isolated.

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

Mycelium in simple or in parallel hyphal bundles, branched, septate, pigmented, hyaline, thin- and smooth-walled, 0.7–4.9 µm wide. *Conidiophores* mononematous unbranched arising laterally from superficial hyphae, smooth-walled, hyaline, simple to verticillate, 11.25–112.5 × 0.85–3.15 µm. *Phialides* solitary, sometimes produced directly from superficial hyphae or in groups of 2–5, produced terminally from conidiophores, acerose with elongated neck, straight to slightly tapered towards neck, base narrow, smooth-walled, hyaline, 7–85.5 × 1.3–3.5 µm. *Conidia* globose to subglobose to rarely fusoid, catenate, echinulate, hyaline, 1.7–3.9 × 1.6–3.2 µm. *Stroma* and *chlamydospores* absent.

Culture characteristics — Colonies on potato dextrose agar (PDA) 16–18 mm diam after 7 d at 25 °C, circular, floccose, umbonate, colony from below white (1A1; Methuen handbook of colour) to pinkish white (9A2), reverse orange yellow (4B8) to pastel yellow (3A4), exudate lacking, margin regular, entire, smooth producing soluble yellow pigment diffused in media.

Typus. India, Maharashtra, Pune, Bhamburda, Vetal Hill, saprophyte from soil, 1 Oct. 2020, *A.C. Lagashetti* & *S.K. Singh* (holotype NFCCI 5106, preserved as metabolically inactive culture, culture ex-type SF-8; ITS, LSU, SSU, *tef1* and *rpb2* sequences GenBank OL584171, OL584177, OL584174, OM032806 and OM032809, MycoBank MB 842441).

Notes — Initially, members of the genus *Keithomyces* were placed in the genus *Metarrhizium* due to morphological similarity. A recent study on *Clavicipitaceae* especially *Metarhizium* using six genomic loci (ITS, SSU, LSU, *tef*, *rpb1*, *rpb2*), showed that the genus *Keithomyces* presently comprises of three species which includes *K. aciculare*, *K. carneus* and *K. neogunnii* (Mongkolsamrit et al. 2020). Among them, *K. aciculare* and *K. carneus* were isolated from soil in temperate regions, whereas *K. neogunnii* was isolated from *Lepidoptera* larvae. Morphologically, *K. indicus* is distinct from other species of *Keithomyces*. Conidiophores of *K. indicus* are significantly longer as compared to conidiophores in *K. aciculare* and *K. neogunnii*, while it is shorter in *K. carneus.* Similarly, the phialides of *K. indicus* are longer as compared to all other species of *Keithomyces*. The conidia are echinulate or spinulose in *K. indicus*, similar to those in *K. carneus*, *K. neogunnii* and *K. aciculare.*

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Keithomyces carneus* (strain WCPX-FS04, GenBank KR296911.1; Identities = 521/521 (100 %), no gaps), *Keithomyces carneus* (strain GZDXIFR-XJ73-2, GenBank DQ836183.1; Identities = 521/525 (99 %), three gaps (0 %)) and *Metarhizium flavoviride* (strain SC01B03, GenBank MW113262.1; Identities = 523/524 (99 %), one gap (0 %)). Closest hits using the **LSU** sequence are *Keithomyces carneus* (strain CBS 126563, GenBank MT078856.1; Identities = 889/916 (97 %), no gaps), *Metarhizium viride* (strain VS10220, GenBank MH014982.1; Identities = 888/916 (97 %), two gaps (0 %)), *Metarhizium granulomatis* (culture collection MUT:5385, GenBank KU314964.1; Identities = 877/902 (97 %), one gap (0 %)), and *Drechmeria gunnii* (GenBank HM119590.1; Identities = 889/916 (97 %), no gaps). Closest hits using the **SSU** sequence are *Metarhizium aciculare* (strain JCM 33284, GenBank NG_067656.1; Identities = 1059/1064 (99 %), no gaps), *Metarhizium granulomatis* (strain UAMH 11028, GenBank NG_064956.1; Identities = 1059/1064 (99 %), no gaps), *Keithomyces carneus* (strain JCM 6870, GenBank AB103379.1; Identities = 1059/1064 (99 %), no gaps) and *Metarhizium viride* (strain CBS 348.65, GenBank NG_062608.1; Identities = 1059/1064 (99 %), no gaps). Closest hits using the ***tef*** sequence are *Metarhizium robertsii* (strain TMGJ01, GenBank LT220799.1; Identities = 922/959 (96 %), no gaps), *Metarhizium guizhouense* (culture-collection CBS 258.90, GenBank EU248862.1; Identities = 922/959 (96 %), no gaps), *Metarhizium novozealandicum* (voucher ARSEF 4661, GenBank KJ398811.1; Identities = 921/959 (96 %), no gaps) and *Metacordyceps taii* (strain YHMG0928, GenBank KC244318.1; Identities = 919/956 (96 %), no gaps). Closest hits using the ***rpb2*** sequence are *Cordyceps gunnii* (strain HMIGD 20873, GenBank EF495088.1; Identities = 917/1028 (89 %), no gaps), *Rotiferophthora angustispora* (strain RCEF4111, GenBank KP324768.1; Identities = 883/1004 (88 %), no gaps), and *Metarhizium viride* (voucher ARSEF 2456, GenBank KJ398717.1; Identities = 885/1025 (86 %), no gaps).

Colour illustrations. Vetal Hill, Bhamburda, Pune, Maharashtra, India. Conidiophore bearing conidia; phialide directly emerging from superficial hyphae bearing conidium; rough-walled, globose to subglobose, echinulate conidia; conidia at higher magnification. Scale bars = 2 µm.

Supplementary material

FP1415-1 Phylogenetic tree.

FP1415-2 Table showing taxa used for phylogenetic analysis and their corresponding GenBank accession numbers.

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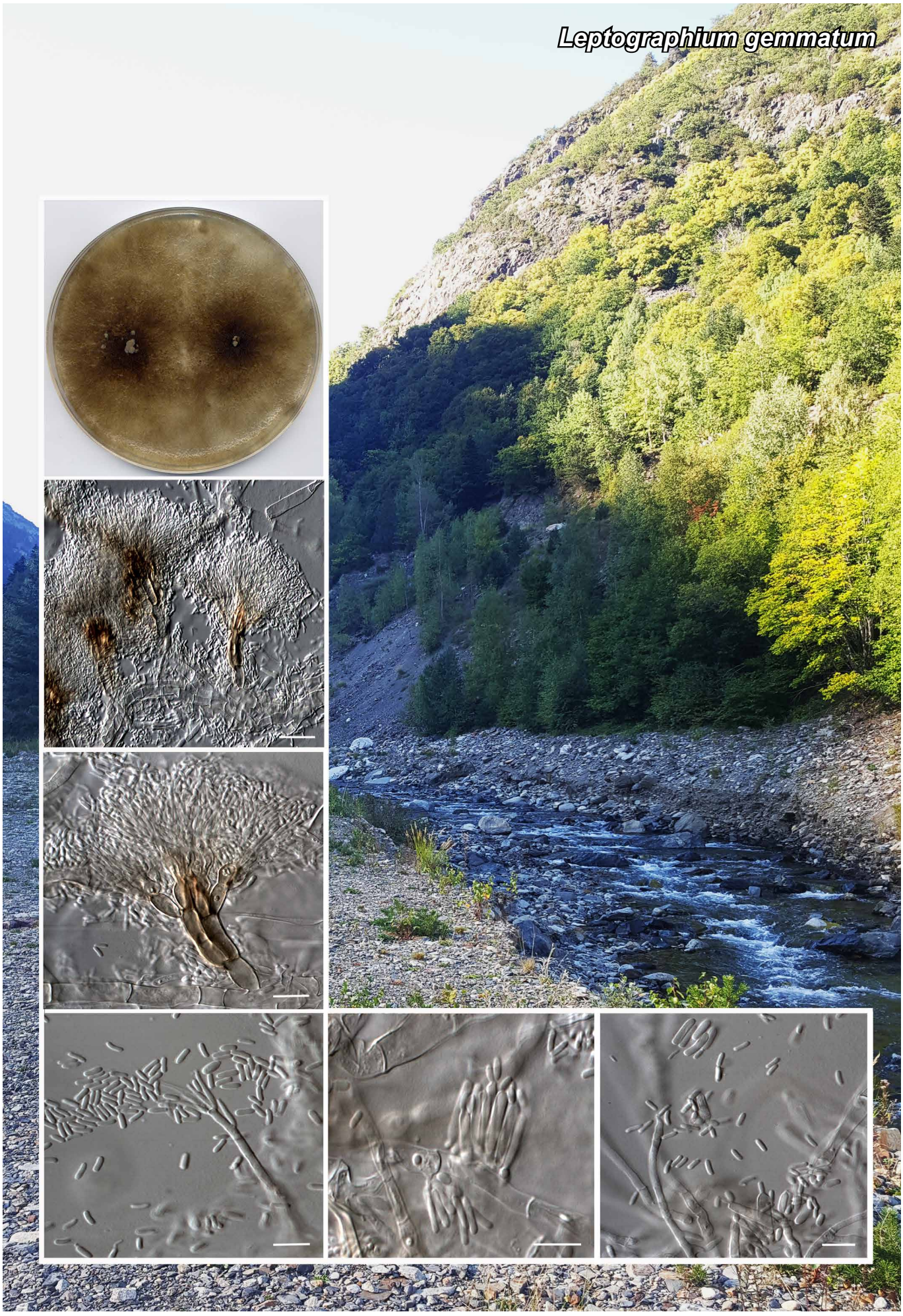
Leptographium gemmatum

Fungal Planet 1416 – 12 July 2022

Leptographium gemmatum Torres-Garcia, Dania García & Gené, *sp. nov.*

Etymology. Name refers to the ability to produce yeast-like cells in culture.

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

On malt extract agar (MEA) at 25 °C. *Mycelium* mostly immersed, composed of branched, septate, septa often irregularly distributed along hyaline, subhyaline to brown, smooth, thin- to thick-walled hyphae, 9–11.5 µm wide. *Conidiophores* micronematous, semi-macronematous or macronematous occurring simultaneously on vegetative hyphae; micronemateous conidiophores consisting in intercalary conidiogenous cells with a lateral peg, up to 4 × 2 µm, arising directly from vegetative hyphae; semi-macronematous unbranched to slightly branched, with hyaline, smooth and cylindrical stipes, bearing terminal or lateral conidiogenous cells, up to 50 × 2–3 µm; macronematous conidiophores branched, with stipes short, brown, smooth, cylindrical to slightly swollen, 0–1-septate, 10–25 × 4.5–7 µm, 1–4 stages of branching, each branch bearing terminally a group of 3–6 appressed conidiogenous cells, 40–110 µm long. *Conidiogenous cells* annellidic, hyaline, smooth, cylindrical, tapering at the apex, 10–20.5 × 0.5–1.5 µm. *Conidia* slimy, aseptate, hyaline, smooth- and thin-walled, narrowly oblong, some slightly curved; conidia from micronematous conidiophores 15–22 × 1.5–3 µm; conidia from semi- to macronematous conidiophores 3–8.5(–13) × 0.5–1.5(–2) µm. Pear-shaped cells not observed. Yeast-like cells present on MEA and potato dextrose agar (PDA) after 1 wk, 0(–1)-septate, hyaline, smooth- and thick-walled, cylindrical, somewhat curved, 13–15.5 × 2.5–3 µm, with terminal or subterminal conidiogenous loci. *Sexual morph* not observed.

Culture characteristics at 25 °C in 1 wk — Colonies on PDA reaching 82–85 mm diam, with granular surface and irregular cottony masses at the centre, olive brown (4E5) (Kornerup & Wanscher 1978), margin diffuse; reverse colourless to olive brown (4E5); abundant sporulation. On MEA it showed the same growth rate as on PDA, but colonies were flat, with superficial mycelium radially distributed, cream coloured (4A2) at centre, brown (5E5) towards periphery, margin fimbriate; reverse colourless to brown (5E5); sporulation moderate.

Cardinal temperature for growth — Minimum 5 °C, optimum 25 °C, maximum 30 °C.

Typus. Spain, Aragón, Huesca, Remáscaro stream, fluvial sediments, Sept. 2018, *D. Torres-Garcia* (holotype CBS H-24942, culture ex-type CBS 149024 = FMR 17558; ITS, LSU and *tub*2 sequences GenBank LR989050, LR990372 and LR989052, MycoBank MB 842301).

Notes — Based on a megablast search of NCBIs GenBank database, the **LSU** sequence of *L. gemmatum* showed a similarity of 98 % (532/542) with sequences of *L. piriforme* (CMW 52066, GenBank MH74031; KFL10618DA, GenBank MN901002), 97.45 % (529/542) with *L. crassivaginatum* (CMW 134, GenBank MN901003) and 97 % (528/542) with those of *L. alni* (CBS 144901-T, GenBank MN900997; CBS 144902, GenBank MN900994; CBS 144900, GenBank MN901000); the similarity with **ITS** sequences ranged from 94.4 % (559/587–590/625) with *L. piriforme* (UAMH 10680-T, GenBank DQ885241, KFL10618DA, GenBank MN901002; CMW 52066, GenBank MN901001) to 91 % (465/511) with those of *L. alni* (CBS 144901-T, GenBank MN900997; CBS 144902, GenBank MN900994; CBS 144900, GenBank MN9010009) and *L. crassivaginatum* (CMW 134, GenBank MN901003). Whereas the similarity using ***tub*2** sequences was 99 % (374/375) with *L. piriforme* (CMW 52066, GenBank MH740984; KFL10618DA, GenBank MN901011) and 83 % or lower regarding sequences of the other *Leptographium* species mentioned above. Our phylogenetic reconstruction with the three gene markers places *L. gemmatum*, together with *L. alni*, *L. crassivaginatum* and *L. piriforme*, in a fully-supported clade distant from other *Leptographium* clades representing different species complexes described in the genus (De Beer & Wingfield 2013, Yin et al. 2019, Strzałka et al. 2020), with *L. piriforme* as its closest relative.

Relevant morphological features that distinguish *L. gemmatum* from the other species in the clade are the production of large yeast-like cells and the lack of pear-shaped cells. In addition, *L. gemmatum* differs from *L. alni* and *L. crassivaginata* (Greif et al. 2006, Strzałka et al. 2020) by the absence of a sexual morph and the presence of a micronematous conidial morph, and from *L. piriforme* (Greif et al. 2006) by showing macronematous conidiophores with shorter stipes (up to 25 µm vs up to 45.6 µm), longer conidiogenous cells (up to 20.5 µm vs up to 15.4 µm) and usually straight and longer conidia (3–13 µm vs curved and 2.4–4.6 µm long). In addition, *L. gemmatum* has an optimal temperature for growth at 25 °C, while *L. piriforme* grows optimally at 30–35 °C (Greif et al. 2006, Jankowiak & Kolařík 2010).

Colour illustrations. Cerler, Aragón, Spain. Colony on PDA after 1 wk at 25 °C; conidiophores and conidia after 7 d at 25 °C. Scale bars = 25 µm (habitat on MEA), 10 µm (microscopic structures on MEA).

Supplementary material

FP1416 Phylogenetic tree.

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Lulworthia fundyensis

Fungal Planet 1417 – 12 July 2022

Lulworthia fundyensis V.A. Taylor, S.J. Adams, B.M. Robicheau & A.K. Walker, *sp. nov.*

Etymology. Named after the region where it was collected, the Bay of Fundy, Nova Scotia, Canada.

Classification — *Lulworthiaceae*, *Lulworthiales*, *Sordariomycetes*.

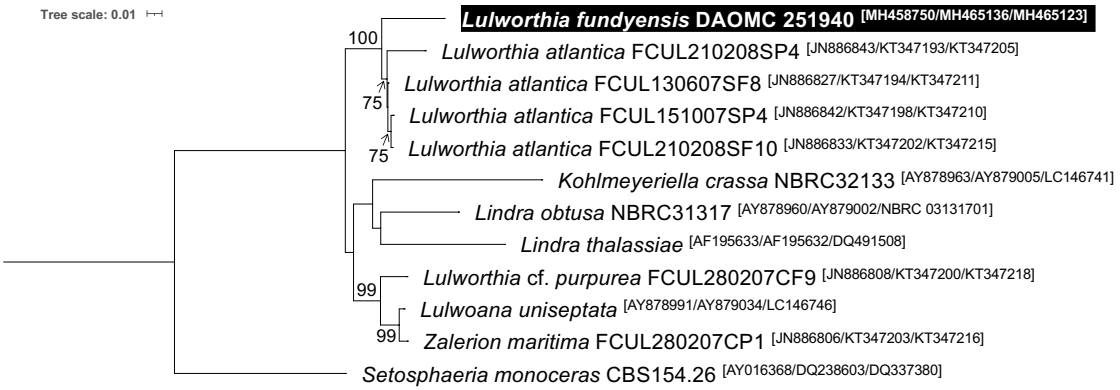
Ascomata perithecial, known only from culture. Immature perithecia were observed after 2 mo on 50 % seawater malt extract agar (MEA) plates at 4 °C and were dark brown to grey and globose, 39–41 mm in width (based on small sample size, n = 6). *Asci* and *ascospores* were not observed after 3 yr incubation at several temperatures and on several media types. After 10 mo, no *perithecia* were observed on wood block inoculations. *Chlamydospores* were observed after 3 mo on 50 % seawater cornmeal agar (CMA) at 21 °C; cultures grown at 4 °C either lacked or had few chlamydospores. *Chlamydospores* formed chains and were hyaline and globose to subglobose with thick walls, measuring (7.18–)9.09–14.30(–18.55) µm in length and (6.61–)8.01–12.42(–15.18) µm in width (av. = 11.23 × 10.27 µm, S.D. 1.98, 1.71, n1 = 100, n2 = 100).

Culture characteristics — Colonies reaching 25 mm diam after 2 wk on 50 % seawater corn meal agar (CMA; Sigma) at 21 °C. Cultures were dark to pale brown/grey, velvety, appressed, with low dense white aerial mycelium. Diffusion of a dark brown pigment was observed in the media.

Typus. Canada, Nova Scotia, Cumberland County, Edgett's Beach, N45°27'23.7" W64°51'10.7", dried perithecia from culture obtained from direct plating of recently exposed buried intertidal wood onto 50 % seawater CMA, 19 June 2017, *S.J. Adams*, *E. Adams* & *S. Winters* (holotype DAOMC 251940, ex-type culture ACAD21000F; ITS, LSU and SSU nrDNA sequences GenBank MH465123, MH458750 and MH465136, MycoBank MB 836622).

Notes — Wood samples were collected from Edgett's Beach Sandbar, Nova Scotia, Canada after a spring storm. The storm redirected a tidal stream, exposing fragments of buried marine wood which had been buried in beach sediment for over 100 years.

Lulworthia presently includes approximately 13 species of obligate marine fungi (Jones et al. 2015, Azevedo et al. 2017) occurring on marine substrates such as submerged wood. A three-gene phylogeny (LSU, SSU, ITS rDNA concatenated gene ML tree) shows support for *Lulworthia fundyensis* as a sister species to *Lulworthia atlantica*. *Lulworthia fundyensis* reached 25 mm diam on 50 % seawater CMA after 14 d; *L. atlantica* reached 50 mm diam on 50 % seawater CMA after 15 d (Azevedo et al. 2017). *Lulworthia fundyensis* was pale brown to grey, with low dense white aerial mycelium and a dark brown pigment diffused in the medium. In contrast, under the same culture conditions, *L. atlantica* was green to pale brown, producing sparse aerial mycelia and no diffused pigments (Azevedo et al. 2017). Chlamydospores of *L. fundyensis* were almost twice as large as those reported for *L. atlantica* (Azevedo et al. 2017). For a key to other lignicolous species of *Lulworthia*, see Azevedo et al. (2017).



Maximum likelihood tree built from concatenated 28S/18S/ITS sequences. Bootstrap support values > 70 % (from 1000 replicates) are shown midbranch. Tree was built in MEGA v. 7 (Kumar et al. 2016) using a TrN+G model; nucleotide sites with missing data/gaps were excluded from the analysis. Alignment was trimmed to start and end positions without a gap. Tree was visualised in iTOL v. 5.6.2 (Letunic & Bork 2019). TreeBASE Study Accession URL: http://purl.org/phylo/treebase/phylows/study/TB2:S29426.

Colour illustrations. Intertidal wood at Bay of Fundy, Nova Scotia, Canada. Clockwise from top left: immature ascomata (MEA at 10 °C), scale bar = 100 µm; chlamydospores forming chains (after 3 mo on CMA at 21 °C), scale bar = 50 µm; culture macromorphology (after 4 mo on CMA at 21 °C). All plates contained 50 % artificial seawater.

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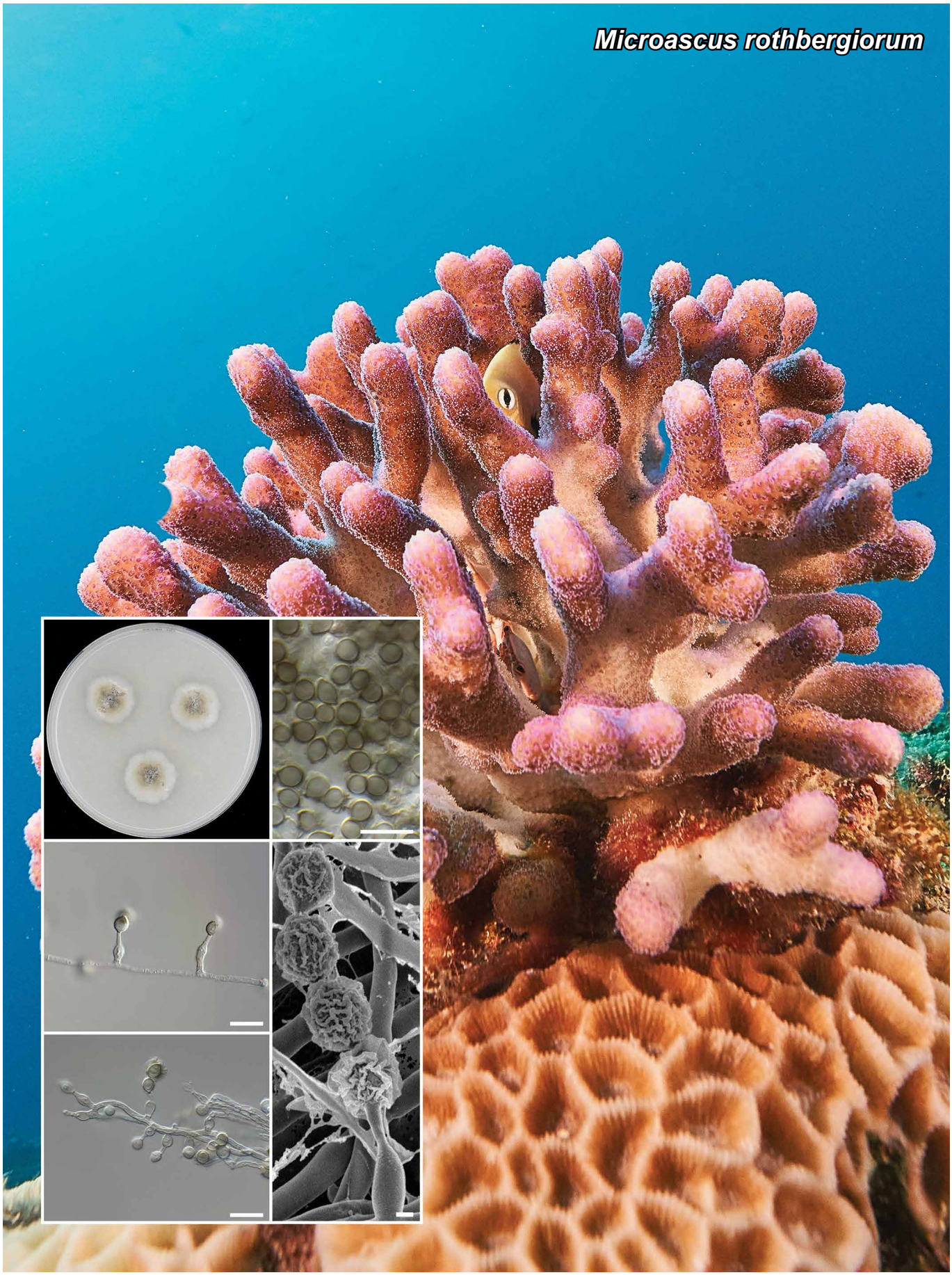

Microascus rothbergiorum

Fungal Planet 1418 – 12 July 2022

Microascus rothbergiorum Houbraken, Istel & Yarden, *sp. nov*.

Etymology. Name refers to the Rothberg family, in recognition of continuous support of studies on marine environments.

Classification — *Microascaceae*, *Microascales*, *Sordariomycetes*.

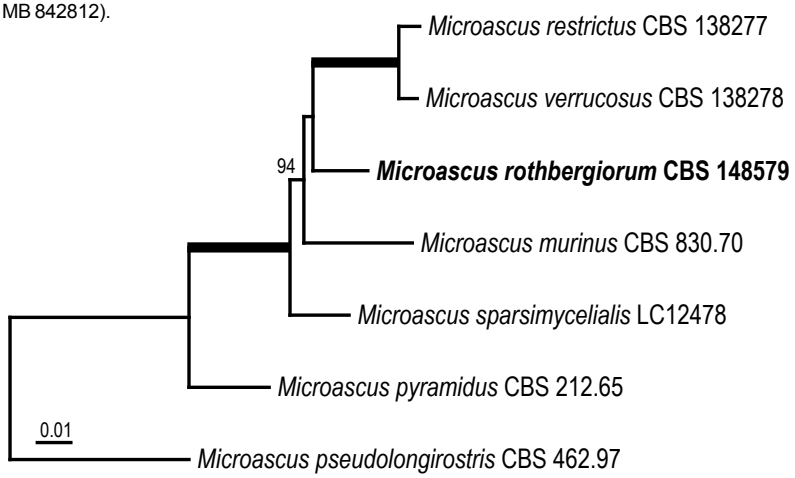
Vegetative hyphae septate, subhyaline, smooth- and thin-walled. *Conidiogenous cells* annellidic, solitary, somewhat lageniform, (6–)7.5–11.5(–13.5) µm long, 2.5–4.5(–6) µm broad at the widest part, tapering to a distinct neck, 1–2.5 µm wide. *Conidia* subglobose to broadly ellipsoidal, with a small, distinct apical base, highly reticulate, 4–5.5 × (3–)3.5–4.5 µm, dull green to greenish grey en masse, arranged in short chains. *Sexual morph* not observed.

Culture characteristics (14 d) — Malt extract agar (MEA), 15 °C: Colonies 4 mm diam, elevated in centre, flat at the margins; mycelium white; sporulation absent; reverse pastel yellow. MEA, 25 °C: Colonies 21–24 mm diam, slightly elevated; margin irregular; texture velvety to lanose; mycelium white; sporulation sparse, present in darker spots of the colony, under aerial hyphae; reverse pale yellow to yellowish white, with greenish grey spots. MEA, 37 °C: no growth. Dichloran 18 % Glycerol agar (DG18), 25 °C: Colonies 22–28 mm, umbonate; margin regular, immersed; mycelium white to greyish; sporulation absent; reverse yellowish grey to greenish grey. Oatmeal agar (OA), 25 °C: Colonies 23–25 mm, flat, dull yellow to pale yellow with floccose spots in olive; texture velvety, floccose in centre; margins white, slightly irregular; sporulation sparse to moderate; mycelium white; reverse greenish white.

Typus. Israel, Eilat, N29.5° E34.9°, from *Stylophora pistillata* (*Pocilloporidae*), Jan. 2019, *N. Lifshitz* (holotype CBS H-24913, culture ex-type CBS 148579 = DTO 454-F5; ITS, LSU, *tub2* and *tef* sequences GenBank OM509733, OM509736, OM470474 and OM470475, MycoBank MB 842812).

Notes — *Microascus rothbergiorum* is phylogenetically distinct and related to *M. murinus*, *M. restrictus*, *M. sparsimycelialis* and *M. verrucosus*. This species can be easily distinguished from those species by its conidial ornamentation, as it is the only species that produces reticulate conidia. In contrast, the conidia of *M. verrucosus* are distinctively rough and *M. murinus*, *M. restrictus* and *M. sparsimycelialis* produce smooth to finely ornamented conidia (Sandoval-Denis et al. 2016, Woudenberg et al. 2017, Zhang et al. 2021).

A megablast search of the NCBIs nucleotide database using the ITS sequence revealed similarity with *M. restrictus* (GenBank KX923928; Identities = 444/459 (97 %), 3 gaps), *M. verrucosus* (GenBank KX923950; Identities = 450/470 (96 %), 5 gaps) and *M. murinus* (GenBank KX923908; Identities 411/431 (95 %), 7 gaps).



Maximum likelihood tree of *M. rothbergiorum* and phylogenetically closely related species based on 2264 aligned nucleotides (combined ITS, LSU, *tef* and *tub2* sequences). GenBank accession numbers used in the analysis can be found in Woudenberg et al. (2017) and Zhang et al. (2021). Analysis performed using RAxML v. 8.2.12 (Stamatakis 2014). Bootstrap support from 1000 re-samplings; only bootstrap support values above 70 % are presented at the nodes and branches of > 95 % are thickened. *Microascus pseudolongirostris* was used as outgroup. The scale bar indicates the expected number of substitutions per site.

Colour illustrations. *Stylophora pistllata* (photo credit Guilhem Banc-Prandi). Colonies on OA (14 d, 25 °C); conidia; annellides with conidia. Scale bars = 10 µm (light microscopical pictures), 1 µm (SEM picture).

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Microcyclus jacquiniae

Fungal Planet 1419 – 12 July 2022

Microcyclus jacquiniae Raja & J.L. Crane, *sp. nov.*

Etymology. Named after the host plant, *Jacquinia keyensis* from which the fungus is described.

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

Ascostromata 320–480 µm wide, pulvinate, irregularly shaped, developing from the adaxial surface of the leaf by lifting the upper epidermis, superficial, multilocular, composed of pseudoparenchymatous cells; *textura angularis* to *textura prismatica*, 10–20 µm wide, thick-walled, reddish brown, ostiole papillate, 28–30 µm wide, with periphyses. *Asci* 82–124 × 8–12 µm (av. = 96 × 10 µm), 8-spored, thick-walled, bitunicate, fissitunicate, cylindrical to clavate, with a pedicel, 10–17 µm long, with bulbous base. *Ascospores* 17–20 × 2–4 µm (av. = 18 × 3 µm), biseriate partially overlapping, 1-septate, fusiform, upper cell wider than lower cell, slightly constricted at the septum, smooth-walled granular, hyaline, with two bipolar pad-like appendages apparent only in fresh material in water, staining in aqueous nigrosin. *Asexual morph* not present.

Habitat & Distribution — Biotrophic on leaves, known only from Florida.

Typus. USA, Florida, Monroe County, Long Key State Recreation Area, East of Layton, Salt Pan Area, on living leaves of *Jacquinia keyensis* (*Primulaceae*), N24.8145, W80.8196, 2 Jan. 1988, *J.L. Crane* & *J.D. Schoknecht*, F263 (holotype ILLS00151164, isotypes BPI, NY; ITS-LSU sequence GenBank ON006513, MycoBank MB 843362).

Additional materials examined. USA, Florida, Monroe County, Long Key State Recreation Area, East of Layton, Salt Pan Area, on living leaves of *Jacquinia keyensis*, N24.8145, W80.8196, 1 Jan. 1989, *J.L. Crane* & *J.D. Schoknecht*, 89-482, ILLS00151165; ibid., 30 Dec. 1991, *J.L. Crane* & *J.D. Schoknecht*, F265. ILLS00151166; ibid., 2 Jan. 1992, *J.L. Crane* & *J.D. Schoknecht*, 92-567, ILLS00151167; ibid., 1 Jan. 1995, *J.L. Crane* & *J.D. Schoknecht*, 95-875, ILLS00151168; ibid., 26 Jan. 1996, *J.L. Crane* & *J.D. Schoknecht*, 96-29a, ILLS00151169; ibid., 18 May 1998, *J.L. Crane* & *Payam M. Fallah*, 98-249, ILLS00151170; ibid., 28 Dec. 2001, *J.L. Crane*, 01-393, ILLS00151171; ibid., 15 Mar. 2012, ILLS00151172; ibid., 10 Feb. 2015, *J.L. Crane* & *J.D. Schoknecht*, F267, ILLS00151173.

Notes — The new species from Florida, *M. jacquiniae*, agrees with the generic circumscription of *Microcyclus*, which is characterised as biotrophic and necrotrophic on leaves and stems of tropical and subtropical plants with irregularly-shaped multilocular ascostromata, composed of thick-walled, *textura angularis* cells, 8-spored, thick-walled, bitunicate, cylindrical to clavate asci, with an ocular chamber, periphysate ostiole, and 1-septate ascospores (Cannon et al. 1995, Monkai et al. 2013).

The Florida material agrees in all respects with the protologue of *M. angolensis*, the type species of the genus, but differs in being an epiphyllous biotrophic parasite on living leaves of *Jacquinia keyensis*, whereas *M. angolensis* was described from living leaves of *Millettiae thonningii*. The ascospores of *M. jacquiniae* show bipolar pad-like appendages, apparent only in fresh material in water stained with nigrosin. In contrast, the pad-like appendages are absent in the ascospores of *M. angolensis.* The genus appears to be polyphyletic and this is substantiated by the numerous asexual morphs associated with *Microcyclus* (Cannon et al. 1995, Da Hora Júnior et al. 2014). However, no asexual morph was found associated with *M. jacquiniae*. The host plant, *J. keyensis*, is native to Florida and the Greater Antilles and is found on the Keys and the coastal Everglades from areas subjected to extremes of salt spray, periods of saltwater inundation (Salt Pan Areas) and dryness.

Based on Maximum likelihood analysis using partial LSU, *M. jacquiniae* shows phylogenetic affinities to the *Mycosphaerellaceae*, *Mycosphaerellales* (Monkai et al. 2013, Videira et al. 2017). We believe this study is the second report of molecular data from *Microcyclus* and might help shed light on the phylogenetic relationships of this poorly studied genus, which includes 36 species (Index Fungorum; Monkai et al. 2013). Recently, Da Hora Júnior et al. (2014) transferred the pleomorphic rubber pathogen, *Microcylus ulei*, to *Pseudocercospora ulei* based on a multi-gene phylogeny as it clustered with the *Pseudocercospora* s.str. clade within the *Mycosphaerellaceae*.

Colour illustrations. Background photo of *Jacquinia keyensis* (picture credit R.A. Hattaway). *Microcyclus jacquiniae* on living leaves of *Jacquinia keyensis* (picture credit J. Karakehian); ascomata on host; longitudinal section through ascomal wall; asci; ascospores. Scale bars = 50 µm and 200 µm (ascomata), 20 µm (all others).

Supplementary material

FP1419 Phylogenetic tree.

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Neoherpotrichiella juglandicola

Fungal Planet 1420 – 12 July 2022

Neoherpotrichiella Spetik, Eichmeier, Mahamedi & Berraf-Tebbal, *gen. nov*.

Etymology. Refers to the *Herpotrichiellaceae*, where the genus is accommodated.

Classification — *Herpotrichiellaceae*, *Chaetothyriales*, *Chaetothyriomycetes.*

Mycelium consisting of hyaline, septate hyphae. *Conidiophores* smooth, septate, arising from vegetative hyphae, bearing intercalary and/or terminal phialides. *Conidiogenous cells* solitary or in clusters of 2–3, phialidic, ampulliform to broadly ellipsoid, intercalary and/or terminal on conidiophores or reduced to subcylindrical conidiogenous loci on vegetative hyphae, producing conidia in slimy masses. *Conidia* dimorphic, hyaline, unicellular, aseptate, ellipsoid and subcylindrical.

Type genus. *Neoherpotrichiella juglandicola* Spetik, Eichmeier, Mahamedi & Berraf-Tebbal
MycoBank MB 843906.

Neoherpotrichiella juglandicola Spetik, Eichmeier, Mahamedi & Berraf-Tebbal, *sp*. *nov*.

Etymology. Name refers to the host genus, *Juglans*.

Sexual morph: not observed. Asexual morph: *Mycelium* consisting of hyaline, septate, 1.9–2.2 µm diam hyphae. *Conidiophores* 17–36 µm long, brown, smooth, 1–4-septate, arising from vegetative hyphae, bearing intercalary and/or terminal phialides. *Conidiogenous cells* 2.7–7.5 × 1.9–2.7 µm, solitary or in clusters of 2–3, brown, smooth, phialidic, ampulliform to broadly ellipsoid, intercalary and terminal on conidiophores or intercalary as subcylindrical loci on vegetative hyphae, producing conidia in slimy masses. *Chlamydospores* forming in culture after 4 wk, intercalary or terminal, smooth, brown, thick-walled. *Conidia* hyaline, smooth, aseptate, dimorphic: ellipsoidal conidia (1.9–)2.5–2.8(–3.4) × (1.7–)2.1–2.3(–2.9) µm, (av. ± S.D. 2.7 ± 0.4 × 2.2 ± 0.3 µm, L/W ration = 1.2); subcylindrical conidia (3.5–)4.4–5(–6.2) × (1.5–)1.8–2(–3.3) µm (av. ± S.D. 4.7 ± 0.8 × 1.9 ± 0.3 µm, L/W ration = 5.6).

Culture characteristics — Colonies on potato dextrose agar (PDA) circular, raised, entire margin, velvety with grey aerial mycelium, reverse greyish black, slow growing, 9.3 mm diam after 2 wk at 25 °C. On malt extract agar (MEA) circular, umbonate, entire margin, velvety with grey aerial mycelium, reverse greyish black, slow growing, 9 mm diam after 2 wk at 25 °C. Colonies on oatmeal agar (OA) circular, raised, entire margin, velvety, olivaceous grey with grey aerial mycelium, slimy in the centre, reverse greyish black, slow growing, 8.7 mm diam after 2 wk at 25 °C. On corn meal agar (centre) circular, raised, entire margin, velvety with grey aerial mycelium, reverse greyish black, slow growing, 8.3 mm diam after 2 wk at 25 °C. On yeast mannitol agar (YMA) circular, raised with entire margin, velvety, olivaceous grey in centre, grey in outer ring, reverse greyish black, slow growing, 10 mm diam after 2 wk at 25 °C.

Typus. Czech Republic, Boleradice, isolated from wood of *Juglans regia* (*Juglandaceae*), 2018, *M. Spetik* (holotype CBS H-24969, ex-type culture CBS 147585 = MEND-F-0548, ITS, LSU, *tub2* and *tef1-α* sequences GenBank ON110815, ON111439, ON181438 and ON314831, MycoBank MB 843907).

Notes — *Neoherpotrichiella* represents a new genus accommodated in the *Herpotrichiellaceae*, being morphologically similar to *Exophiala* and the synasexual morph of *Thysanorea* (Hernández-Restrepo et al. 2020). However, it is phylogenetically distinct from both genera.

Based on a megablast search of NCBIs nucleotide database, the closest hits using the **ITS** sequence had the highest similarity to *Veronaea japonica* (strain D28, GenBank KX302057; Identities = 535/579 (93 %), 19/579 gaps (3 %)), *Exophiala brunnea* (CBS 587.66, GenBank MH858890; Identities = 530/577 (92 %), 17/577 gaps (2 %)) *Veronaea aquatica* (strain JAUCC2549, GenBank MW046892; Identities = 531/580 (92 %), 20/580 gaps (3 %)); the closest hits using the **LSU** sequence had the highest similarity to *Annellophorella ellisii* (strain CBS 738.70, GenBank MH871721; Identities = 817/833 (98 %), 2/833 gaps (0.2 %)), *Exophiala* sp. (strain LY-2021a, GenBank MZ779229; Identities = 817/833 (98 %), 2/833 gaps (0.2 %)) and *Rhinocladiella coryli* (strain CPC 26654, GenBank NG_059697; Identities = 815/831 (98 %), 4/831 gaps (0.5 %)); the closest hits using the ***tub2*** sequence had the highest similarity to *Veronaea botryose* (strain DI15-135, GenBank MN477327; Identities = 343/430 (80 %), 23/430 gaps (5 %)); *Exophiala cancerae* (strain CBS 117491, GenBank JN112446; Identities = 269/332 (81 %), 11/332 gaps (3 %)) and *Exophiala psychrophila* (strain CBS 191.87, GenBank JN112497; Identities = 272/334 (81 %), 13/334 gaps (3 %)); the closest hits using the ***tef1-α*** sequence had the highest similarity to *Exophiala embothrii* (strain CBS 146558, GenBank MW055980; Identities = 101/124 (81 %), 10/124 gaps (8 %)), *Exophiala* sp. (strain CBS 122268, GenBank JN128794; Identities = 101/124 (81 %), 10/124 gaps (8 %)), *Exophiala salmonis* (strain CBS 120274, GenBank JN128802; Identities = 99/122 (81 %), 8/122 gaps (6 %)).

Colour illustrations. Walnut tree in Lednice, Czech Republic. Mycelium with conidial masses; conidiogenous cells; conidiophores bearing conidiogenous cells; conidia. Scale bars = 10 µm.

Supplementary material

FP1420 Phylogenetic tree.

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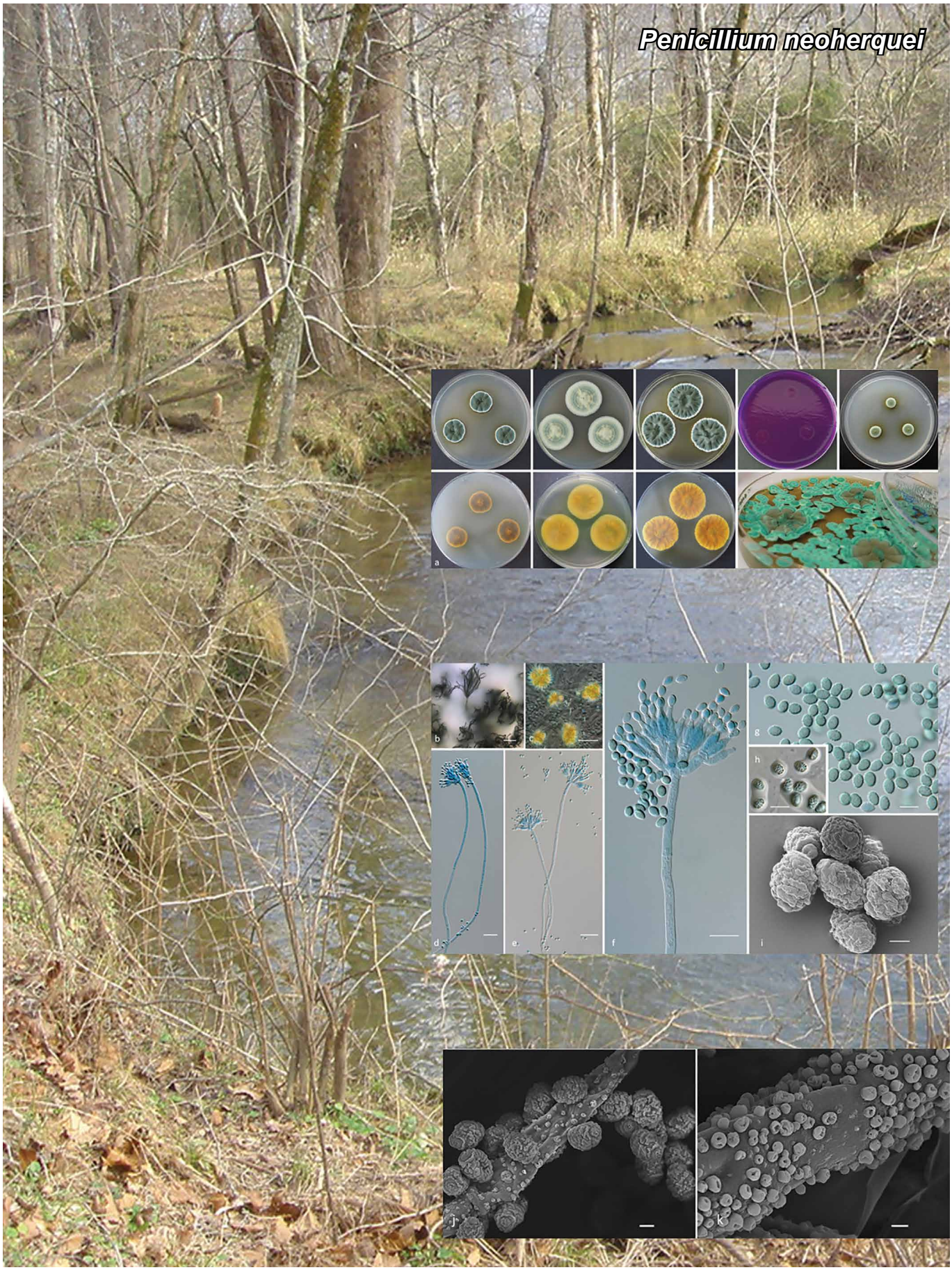
Penicillium neoherquei
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Fungal Planet 1421 – 12 July 2022

Penicillium neoherquei Labuda, Kubátová, J. Nebesářová, Oberlies & Raja, *sp. nov.*

Etymology. Latin, *neoherquei* refers to its resemblance with *P. herquei*.

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

Conidiophores strictly biverticillate, born from surface or aerial hyphae; *stipes* (180–)250–480(–520) × (2–)3–3.5(–4) µm, hyaline, smooth-walled when young, coarsely rough to tuberculate (visible in water mounts) in older parts, non-vesicular to slightly swollen tip; *metulae* appressed, 5–6(–7) per stipe, (7–)8–12(–15) × (3–)3.5–4(–4.5) µm, terminally slightly swollen; *phialides* flask-shaped (ampulliform), in verticils of 5–7, (6.5–)8–10(–10.5) × (2.5–)3–3.5(–4) µm, with short necks; *conidia* ellipsoidal to slightly apiculate, (3–)3.5–4(–4.5) × 2.2–2.5(–3) µm (av. = 3.7 ± 0.3 × 2.5 ± 0.2 µm, n = 50), coarsely roughened and often striate (micro-tuberculate to lobate-reticulate under Scanning Electron Microscope; SEM), produced in short to long, tangled chains. *Sclerotia* not observed.

Culture characteristics — (in darkness, 25 °C, 7 d): Colonies on Czapek agar (CZ) slow growing, 10–12 mm diam, plane, centrally slightly umbonate, texture velutinous to granulose, margins narrow; aerial mycelium inconspicuous, white at the margins, yellowish at the centre; sporulation good, dark dull green; exudate absent; soluble pigment produced, amber yellow; reverse orange to dark yellow brown. Colonies on Czapek yeast extract agar (CYA) slow growing, 18–22 mm diam, centrally slightly umbonate to crateriform, radially and slightly concentrically wrinkled, texture velutinous to floccose centrally, margins narrow and slightly lobate; aerial mycelium white to yellowish; sporulation strong, dark dull green; exudate absent or as very minute yellowish droplets; soluble pigment produced, amber yellow becoming green after prolonged incubation (after 12 d); reverse ochre to dark olive green with vivid orange areas especially at the centres and at the margins turning dark green after 14 d. Colonies on malt extract agar (MEA) moderately growing, 25–30 mm diam, plane, texture velutinous to slightly floccose centrally, margins filiform to fimbriate; aerial mycelium usually inconspicuous centrally and at the margins (sometimes also abundant yellow mycelium giving colonies a yellow character), white to yellowish; sporulation poor to good, dull dark green to glaucous blue green; exudate absent to very minute yellowish droplets; soluble pigment produced, amber yellow becoming green after prolonged incubation (after 9 d); reverse in orange yellow colours with green areas at subcentral and central parts. Colonies on yeast extract agar (YES) moderately growing, 27–30 mm diam, centrally strongly umbonate and crateriform, radially and concentrically deep furcate, margins narrow and slightly lobate, texture velutinous to deeply floccose; aerial mycelium white to yellowish; sporulation good, dark green to glaucous blue green; exudate absent; soluble pigment produced, amber yellow; reverse yellow brown with olive green at the centres. Colonies on creatine sucrose agar (CREA), poor and profusely growing, 8–10 mm diam, no acid production. Aerial mycelium of the colonies on CYA during the storage in fridge (7–10 °C) turned its colour to vivid malachite green. Growth (in mm, after 7 d) at 32 °C (CYA, MEA = 0, no spore germination), 31 °C (CYA = 5–8, MEA = 3–8), 30 °C (CYA = 8–11, MEA = 13–15), 20 °C (CYA = 11–14, MEA = 19–21), 15 °C (CYA = 7–8, MEA = 11–12), 12 °C (CYA = 5–7, MEA = 10–11), 10 °C (CYA = 3–4, MEA = 4–7), 8 °C (CYA = 0, MEA = 1–2), 5 °C (CYA = 0, no spore germination, MEA = 0, spore germination). Spectrum of the extrolites was recently published (Al Subeh et al. 2021).

Typus. USA, Connecticut, Hebron, N41°41.26776 W72°26.52564, from a minute mushroom sporocarp, which was growing out of submerged wood collected in Jan. 2019 from a freshwater stream, isol. *H. Raja* (holotype PRM 956035 (dried culture), culture ex-type G1071 = CCF 6604 = CBS 148692; ITS, *BenA*, *CaM* and *RPB2* sequences GenBank MW341222, OL840853 & OL840854, OL840855 & OL840856 and MW349119 & MW349120, MycoBank MB 842267).

Notes — See Supplementary material page.

Colour illustrations. A stream in the USA, Dec. 2021. *Penicillium neoherquei* G1071. Colonies on CYA, MEA, YES, CREA and CZ, rows, from top to bottom: obverses after 7 d, and reverse after 7 d at 25 °C; right bottom: unusually coloured colonies (malachite green) on CYA following 25 °C incubation and after storage in a fridge for 3 wk; conidiophores with conidia in long chains (*in situ*, on MEA, after 7 d); crystals formed on MEA; conidiophores with conidia (MEA, after 7 d); conidia (on MEA, after 7 d); conidia in air bubbles (on MEA, after 7 d); scanning electron microscopy of conidia (on MEA, after 7 d). Scale bars = 50 µm (b), 20 µm (c–e), 10 µm (f), 5 µm (g–h), 1 µm (i–j), 0.5 µm (k).

Supplementary material

FP1421-1 Table - Sequence identities and DNA gap frequencies among *Penicillium neoherquei* sp. nov. and close related species in series *Herqueorum* (section *Sclerotiorum*) *.

FP1421-2 Table - Comparison of the key phenotypic characteristics of *Penicillium* species (series *Herqueorum*, section *Sclerotiorum*).

FP1421-3 SEM of conidia of ex-type culture of *P. herquei* CCF 2769 (= MUCL 29213) (on MEA, after 7 d). Scale bar = 1 µm.

FP1421-4 Phylogenetic tree.

FP1421-5 Cartoon version of phylogeny.

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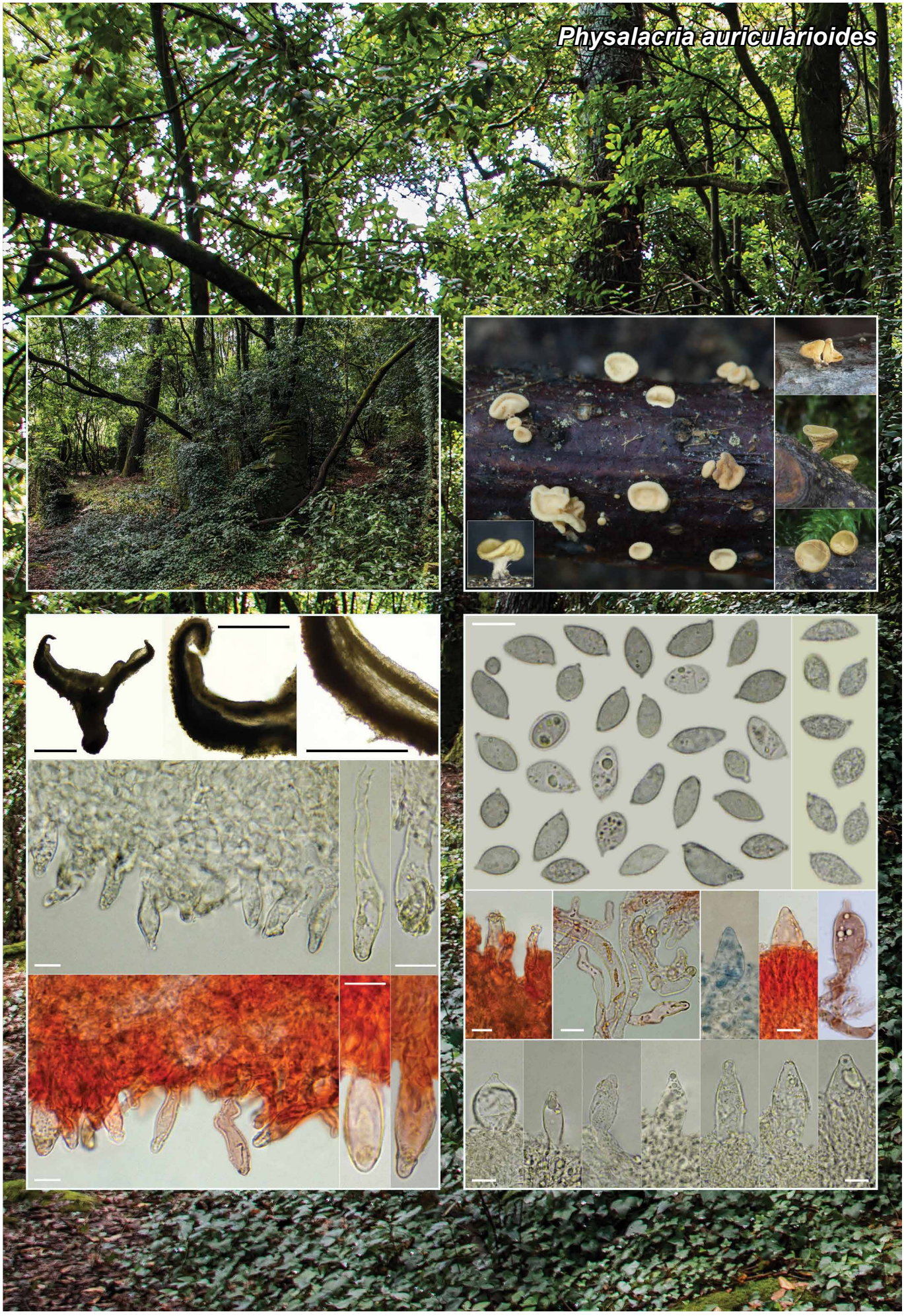
Physalacria auricularioides

Fungal Planet 1422 – 12 July 2022

Physalacria auricularioides S. De la Peña-Lastra, A. Mateos, M. Saavedra & P. Alvarado, *sp. nov*.

Etymology. The epithet refers to the shape of the apothecium, similar to that of *Auricularia* spp.

Classification — *Physalacriaceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata gregarious, isolated or in groups of 3–5 specimens, (1–)2.4–3.0 × 2.4–2.7(–3) mm, discoid-peltate, cupulate, lenticular when at the primordial state, usually regular in shape, but often laterally compressed or lobed; interior of the *hymenial receptacle* auriculiform, veined, concave, but sometimes flat-convex or with raised, wavy centre; hymenium surface smooth, gelatinous, pale beige, brownish orange or yellowish when mature or after drying; margin thick, rounded, 0.3 mm wide; outer surface irregular, covered with a fine pruina and transparent granules up to the edge. With a *stipe* or rudimentary *pseudo-stipe* 0.6 × 0.4 mm, somewhat broadened at the top and base (0.6 mm), tomentose, pale or concolourous with the outer surface, blackening at the base, sometimes sessile. *Flesh* hard and leathery. *Basidia* cylindrical or slightly clavate, fusiform when immature and fusoid when young (like basidioles), with two or four sterigmata up to 5 µm long, 26.6–*35.2*–42.0 × 6.7–*9.2*–12.5 µm. *Basidiospores* hyaline, smooth, thin-walled and inamyloid, ellipsoid to broadly ellipsoid or nearly subglobose, subovoid, subcitriform, lacrymoid, elongated pip-shaped or broadly navicular, (7–)8.4–*10.6*–12.5(–14) × (4.2–)5.1–*5.9*–6.8(–7.3) µm; Q = (1.3–)1.4–*1.8*–2.1(–2.6); N = 95; Ve = 199 µm^3, generally with medium or small oily droplets. *Gloeocystidia hymenial* protruded, fusiform to fusiform-acuminate or sometimes subglobose, with apical resinous droplets, (25.2–)31.2–*38.7*–49.0(–55.5) × (5.7–)7.1–*10.5*–14.5(–17.6) µm, with rounded capitate or uncapitate apices. *Subhymenial hyphae* 2.3–4.5 µm diam, sparsely interwoven, cylindrical, hyaline, thin-walled. *Outer surface* of the dome (sub-hymenium) sterile, with abundant cystidia, claviform, fusiform or capitate with rounded apex, thick-walled, with encrusting pigment, cyanophilic, covered with resinaceous exudates at the apex, and with yellowish pigment, (26.6–)31.2–*36.1*–42.9(–44) × (6.8–)7.0–*8.2*–9.8(–10.1) µm. *Cortical hyphae* 3–7 µm diam, cylindrical, protruding, smooth, hyaline, thick-walled. *Stipe* with subfusiform or subcylindrical thick-walled caulocystidia, 22.8–42.6 × 4.6–9.5 µm, with resinaceous exudates attached at apex. *Clamp connections* present in all tissues.

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

Colour illustrations. Spain, Pontevedra, Parque Nacional de las Islas Atlánticas de Galicia, Illa de Cortegada, laurel forest with specimens of *Castanea sativa*, place where the holotype of *Physalacria auricularioides* was collected. Right column: basidiomata in upper photo correspond with the holotype AMI-SPL688 (left) and MSS937 (right); the bottom photo corresponds with: in upper basidiospores (H_2O, MLZ); in middle, caulocystidia (left) (RC), cortical hyphae (centre) (RC), hymenial gloecystidia (right and the bottom) (BL70, RC, H_2O). Left column: basidiomata section in upper photo, middle and the bottom photo are outer cystidia (H_2O, RC). Scale bar = 1 mm (section), 10 µm (all others). RC = Congo Red, MLZ= Melzer, BL70 = Blue Lactofenol heated to 70 °C.

Phylogeny — The analysis of 28S rDNA suggests that the specimens analysed belong to the genus *Physalacria* (FP1422 Suppl. Mat.). The ITS and 28S rDNA sequences produced do not match any other in public nucleotide databases. The ITS rDNA is only 91 % similar to multiple sequences of *Cylindrobasidium* and a few *Physalacria*, but with a very low coverage (< 45 %); LSU is 97.26 % close to *Ph. corticola* (GenBank DQ284913) and other species of *Physalacria*; finally, LSU is 99.13 % similar to *Cylindrobasidium laeve* (GenBank AF518576), and only 98.79 % close to some other sequences of *Physalacria* and *Mycotribulus*. A low coverage (< 40 %) can be seen also when the ITS rDNA sequences of *P. lacrymispora* (GenBank NR_154322, KT201648) are BLASTed. Both clades are by now interpreted as deviant lineages of genus *Physalacria*.

Typus. Spain, Galicia, Pontevedra, Parque Nacional de las Islas Atlánticas de Galicia, Illa de Cortegada, N42°36'56.27" W8°47'6.30", 20 m a.s.l., several apothecia found together on a dead twig of *Castanea sativa* (*Fagaceae*), 28 July 2021, *S. De la Peña-Lastra* (holotype AMI-SPL676, ITS and LSU sequences GenBank OM964475 and OM964480, MycoBank MB 843221).

Additional materials examined. See Supplementary material page.

Notes — *Physalacria auricularioides* is characterised by its discoid-peltate and cupulate basidiomata with an auriculiform hymenium surface and negative geotropism. Only *Ph. subpeltata* resembles it in some way, but it is not cupulate (only discoid to lenticular), its stipe is slenderer (up to 1 mm long × 0.125 mm wide), has smaller spores (10–12.5 × 4.5–5 µm), lacks hymenial cystidia, and the cystidia of the sterile tissues are somewhat different (Redhead 1979, Berthier 1985). These features led to this species being classified in section *Pileolina* by Singer (1976: 31), but he later (Singer 1986) transferred this section to genus *Deigloria*, which has sessile-cupulate basidiomata (Agerer 1980). Finally, Horak & Desjardín (1994) accommodated it in the new genus *Anastrophella*. This is not the case of *Ph. auricularioides*, which can have a rudimentary stipe or be almost sessile, presents fusiform or claviform, capitate or not capitate, hymenial and subhymenial oleocystidia (Corner 1950, cystidia with resinous droplets sensu Berthier 1985) with cyanophilic walls, and inamyloid spores, which are typical characters of the genus *Physalacria* (1882). *Physalacria* currently includes more than 40 known species (Quin & Yang 2016), almost all of which are saprophytic and have been found in the Southern Hemisphere and the tropics. The species found in the Northern Hemisphere are thought to have been introduced there together with their host plants (Cochard & Réaudin 2019). Furthermore, *Ph. stilboidea* (host species *Griselinia littoralis*) and *Ph. cryptomeriae* (host species *Cryptomeria japonica*; Laessøe & Spooner 1993), are the only species of *Physalacria* known to occur in Europe. Therefore, *Ph. auricularioides* is the first species to be described in Europe.

Supplementary material

FP1422 Phylogenetic tree.

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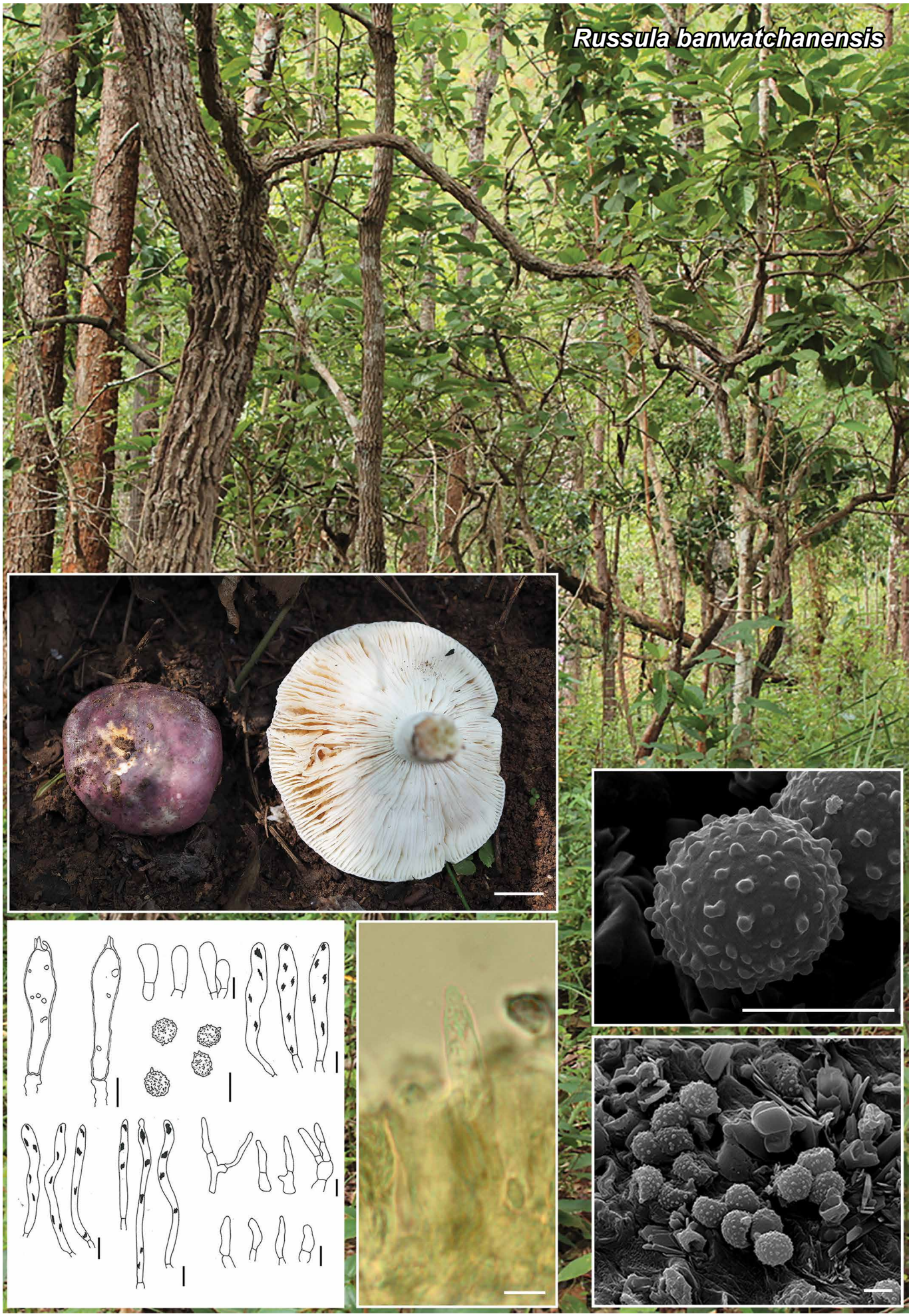
Russula banwatchanensis

Fungal Planet 1423 – 12 July 2022

Russula banwatchanensis Sommai, Pinruan, Somrith. & Luangsa-ard, *sp. nov.*

Etymology. Refers to the location where the fungus was collected, Banwatchan watershed forest, Kanlayaniwattana district, Chiang Mai province, Thailand.

Classification — *Russulaceae*, *Russulales*, *Agaricomycetes.*

Pileus medium-sized, 3.2–5.5 cm diam, pulvinate when young, plano-convex when mature, centre depressed with age; margin even, sometimes cracking; surface smooth, viscid when moist, greyish reddish purple (N77C, colour chart of RHS 2015) when young, greyish purplish red (N77D) when mature, unchanging when bruised. *Lamellae* free close, narrow, average, crowded, often forking, with scattered lamellulae, equal, white (N155D). *Stipe* 1.0–1.2 × 2.5–3.0 cm, central, equal sometimes tapering, longitudinally, smooth, dry, striate, solid, rigid, chalky, white (N155D), unchanging when bruised. *Context* 1.0–3.0 mm thick, firm, white (NN155D), unchanging when cut or bruised. *Odour* indistinct. *Taste* unrecorded. *Spore print* not obtained. *Basidiospores* (30/3/1) 5.7–7.5(–8.5) × 4.2–6.9 µm (Q = 0.83–1.61, Qm = 1.30 ± 0.19), globose to subglobose; ornamentation amyloid; minute warts, not exceeding 1.0–2.0 µm in height; suprahilar plage indistinct; hilar appendix distinct, not amyloid; hyaline in 10 % KOH. *Basidia* (20.4–)21.7–35.3 × 4.0–8.2(–8.8) µm, 4-spored with some 2-spored basidia present but rarely, clavate; sterigmata 4.0–6.0 µm in length, thick-walled. *Lamellar trama* mainly composed of hyphae, 5.0–6.0 µm width, without sphaerocysts. *Hymenial cystidia* numerous, c. 2133/mm^2, 24.0–43.0(–65.0) × 2.5–8.0 µm abundant, clavate to subfusiform, thin-walled, apex round and some mucronate; contents completely heteromorphous (granular or crystalline), reacting weakly greyish in sulfovanillin; abundant near the lamellae edges, 47.5–65.0 × 7.5–8.8 µm, similar to those on the sides. Lamellae edges fertile; *marginal cells* 12.5–23.8 × 3.8–7.5 µm, usually broadly clavate and shorter than basidia. *Pileipellis* metachromatic in Cresyl Blue, not sharply delimited from underlying context, 100–120 µm, deep, not gelatinised, a trichodermium, composed of hyphae 2.0–6.0 µm wide, thin-walled, septate. *Acid-resistant incrustations* absent. Hyphal terminations near the pileus margin occasionally branched, flexuous, thin-walled, septate, terminal cells 12.5–27.5 × 2.5–5.0 µm, conical, subulate, lageniform or cylindrical, thin-walled, branched. Terminal cells of hyphae near the pileus centre cylindrical, 12.5–20.0 × 2.5–5.0 µm. *Pileus trama* interwoven with sphaerocysts. *Pileocystidia* near the pileus margin very abundant, always 1-celled, cylindrical, often very long and originating in the context, 42.5–127.5 × 2.5–5.0 µm, thin-walled, with dispersed granulations or locally heteromorphous-banded, non-reaction in sulfovanillin. *Pileocystidia* near the pileus centre similar. *Stipitipellis* a cutis, composed of hyphae 2.0–5.0 µm wide, thin-walled, septate. *Caulocystidia* and *clamp connection*s absent.

Habitat & Distribution — Currently known only from the type locality, in association with *Dipterocarpus* spp. (*Dipterocarpaceae*).

Typus. Thailand, Chiang Mai, Kanlayaniwattana district, on soil under *Dipterocarpus* (*Dipterocarpaceae*) trees, 6 Nov. 2019, *S. Sommai* (holotype BBH 49228; ITS, LSU and *rpb2* sequences GenBank MT940813, MT940823 and MT965687, MycoBank MB 841176).

Additional material examined. Thailand, Chiang Mai, Kanlayaniwattana district, on soil under *Dipterocarpus* trees, 6 Nov. 2019, *S. Khamsuntorn*, BBH 49230; ITS, LSU and *rpb2* sequences GenBank MT940814, MT940824 and MT965688.

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the ITS sequence of the type collection has the closest GenBank BLAST match (99.5 %) with a sequence identified as unidentified *Russula* from Laos (GenBank MT252583) and similar sequences identified as *R. variata* (97.8 %). The nrLSU sequence of the type collection has the closest GenBank BLAST match (98.2 %) with a sequence identified as *Russula lotus* from China (GenBank MG214695).

The phylogenetic analyses showed *R. banwatchanensis* formed a highly supported sister group to the other species of subg. *Heterophyllidia* subsection *Cyanoxanthinae*. *Russula banwatchanensis* morphologically resembles other species in *Cyanoxanthinae* in the size of its pileus, colour of lamellae, the shape and size of basidia and basidiospores. Macromorphologically, apart from the difference in cap colour, the lamellae of *R. banwatchanensis* often fork from the centre of pileus to the margin as seen in *R. lotus*, *R. phloginea* and *R. subpallidirosea*, but forked lamellae are rare in *R. dinghuensis* and are absent in *R. lilacina* and *R. purpureoviridis*. Micromorphologically, the warts of basidiospores of *R. banwatchanensis* are similar to other species in *Cyanoxanthinae*. As for the structure of pleurocystidia, those of *R. banwatchanensis* are abundant and the same size as those of *R. lilacina* and *R. purpureoviridis*, while those of *R. dinghuensis* and *R. subpallidirosea* are abundant but larger in size, and those of *R. lotus* and *R. phloginea* are larger in size and not abundant. The cheilocystidia of *R. banwatchanensis* are similar to but smaller than those of *R. dinghuensis*, *R. lotus*, *R. phloginea* and *R. subpallidirosea*. Pileocystidia of *R. banwatchanensis* are absent, like *R. lotus*, *R. lilacina* and *R. purpureoviridis* while they are present in *R. dinghuensis*, *R. phloginea* and *R. subpallidirosea*. The caulocystidia of *R. banwatchanensis* are absent, similar to *R. lotus* while it is present in other species in *Cyanoxanthinae*.

Colour illustrations. The dipterocarp forest in Banwatchan watershed, Kanlayaniwattana district, Chiang Mai province, where the holotype was collected. Left top: Basidiomata growing on the soil BBH 49228. Right top and bottom: Scanning electron photograph of spores from BBH 49228. Left bottom: Line drawings all from holotype BBH 49228; basidia (left top), marginal cells and basidiospores (centre), hymenial cystidia near the lamellae edges (right top), pileocystidia near the pileus centre (left bottom), pileocystidia near the pileus margin (centre), hypha terminations near the pileus centre (right centre) and hypha terminations near the pileus margin (right bottom). Centre: hymenial cystidia near the lamellae sides. Scale bars = 10 mm (basidiomata), 10 µm (all other microscopic structures), 5 µm (spores).

Supplementary material

FP1423–1425-1 Table. Sequence data of *Russula* spp. used in this study.

FP1423–1425-2 Phylogenetic ITS tree.

FP1423–1425-3 Phylogenetic LSU tree.

FP1423–1425-4 Phylogenetic 3-gene tree.

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Russula purpureoviridis

Fungal Planet 1424 – 12 July 2022

Russula purpureoviridis Khamsuntorn, Lueangjaroenkit, Sommai & Pinruan, *sp. nov.*

Etymology. Refers to the purplish green colour of pileus.

Classification — *Russulaceae*, *Russulales*, *Agaricomycetes.*

Pileus medium to large-sized, 1.8–7.0 cm diam, convex, expanding to applanate when mature, centre infundibuliform with age; margin even, arched when old, sometime cracking, surface smooth, viscid when moist, greyish purple (N187B, colour chart of RHS 2015) when young, purplish green when mature, unchanging when bruised. *Lamellae* decurrent, narrow, crowded, equal, average, white (NN155C–D), unchanging when bruised. *Stipe* 1.0–1.8 × 2.0–5.5 cm, central, tapering, longitudinally, smooth, dry, striate, firm, solid, white (NN155D), unchanging when bruised. *Context* 1.0–3.0 mm thick, white (NN155C–D), without colour changing when bruised. *Odour* indistinct. *Taste* unrecorded. *Spore print* not obtained. *Basidiospores* (31/2/1) 6.1–9.3 × 6–8 µm (Q = 0.89–1.59, Qm = 1.20 ± 0.17), globose to subglobose or broadly ellipsoid; ornamentation amyloid; minute warts to bluntly conical to subcylindrical, not exceeding 1.0–2.0 µm in height; suprahilar plage indistinct; hilar appendix distinct, 1.0–1.5 µm in height, not amyloid; hyaline in 10 % KOH. *Basidia* 30.9–43.8(–47.6) × 5.0–9.0 µm, 4-spored with some 2-spored basidia present, narrowly clavate to clavate; sterigmata 3.0–6.0 µm in length. *Lamellar trama* mainly composed of nested sphaerocysts, 15.0–25.0 µm diam, and filamentous hyphae 3.0–6.5 µm thick, hyaline. *Hymenial cystidia* dispersed to moderately numerous, c. 800/mm², (34.0–)36.3–49.7 × 4.3–7.0(–8.2) µm abundant, clavate to subfusiform, with oil-content, thin-walled, round or mucronate apex, non-reaction in sulfovanillin; abundant near the lamellae edges, 45.0–77.5 × 7.5–10.0 µm, similar to those on the sides. Lamellae edges fertile; *marginal cells* 10.0–32.5 × 7.5–12.5 µm, mainly clavate and shorter than basidia. *Pileipellis* metachromatic in Cresyl Blue, not sharply delimited from underlying context, 25.0–62.5 µm, deep, not gelatinised, a trichodermium, composed of hyphae 2.0–5.0 µm wide, thin-walled, septate. *Acid-resistant incrustations* absent. Hyphal terminations near the pileus margin scarcely branched, occasionally flexuous, thin-walled, septate, terminal cells 12.5–20.0 × 3.8–5.0 µm, occasionally cylindrical, rarely clavate, fusiform, some irregularly inflated near the base. Terminal cells of hyphae near the pileus centre, often clavate and longer 22.5–32.5 × 3.8–7.0 µm. *Pileus trama* interwoven with sphaerocysts. *Pileocystidia* near the pileus margin mainly 1-celled, clavate-pedicelate, often with strongly constricted and attenuated basal part, thin-walled, 52.5–87.5 × 5.0–8.3 µm, non-reaction in sulfovanillin. *Pileocystidia* near the pileus centre similar. *Stipitipellis* a cutis, composed of hyphae 2–4.5 µm in width, thin-walled, septate. *Caulocystidia* 38.5–42.5 × 5–6.5 (–7.2) µm, cylindrical, not abundant. *Clamp connections* absent.

Habitat & Distribution — Currently known only from the type locality, in association with *Pinus merkusii* (*Pinaceae*).

Typus. Thailand, Chiang Mai, Kanlayaniwattana district, on soil under *Pinus merkusii* trees (*Pinaceae*), 7 Nov. 2019, *S. Khamsuntorn* (holotype BBH 49226; ITS, LSU and *rpb2* sequences GenBank MT940807, MT940817 and MT965684, MycoBank MB 841177).

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the ITS sequence of the type collection has the closest GenBank BLAST match (94.5 %) with a sequence identified as unidentified *Russula* from Malaysia (GenBank GQ268649) and similar sequences identified as *R. cyanoxantha* (93.7 %) and *R. variata* (93.5 %).

The nrLSU sequence of the type collection has the closest GenBank BLAST match (97 %) with a sequence identified as *Russula lotus* from China (GenBank MG214695).

Russula purpureoviridis is proposed here as new to science based on morphological features and the phylogenetic analyses of DNA sequence data of ITS and LSU rDNA, and *RPB2* gene, that consistently confirm that these two new taxa are placed into *Russula* subg. *Heterophyllidia* subsection *Cyanoxanthinae.* The phylogenetic analyses showed *R. purpureoviridis* and *R. lilacina* formed a highly supported sister group to the other species in subsection *Cyanoxanthinae*. The morphology of *R. purpureoviridis* is similar to *R. lilacina* in the size of basidiospores and the absence of cheilocystidia, pileocystidia and clamp connections. However, the morphological differences between the two species are obvious. The pileus colour of *R. purpureoviridis* is purplish green and unchanged with 3 % KOH while those of *R. lilacina* is lilac/purple and turn to pale yellow with 3 % KOH. Lamellae of *R. purpureoviridis* unchanged when bruised while they turn to pale purplish pink when bruised in *R. lilacina*. Moreover, *R. purpureoviridis* has larger basidia and smaller lamellar trama than those of *R. lilacina.* The pleurocystidia are abundant in *R. purpureoviridis* but rarely found in *R. lilacina.* The caulocystidia are slightly larger and abundant in *R. lilacina* but smaller and not abundant in *R. purpureoviridis.*

Colour illustrations. The dipterocarp forest in Banwatchan watershed, Kanlayaniwattana district, Chiang Mai province, where the holotype was collected. Left: basidiomata growing on the soil BBH 49226. Centre top; scanning electron photograph of spores from BBH 49226. Centre bottom; hymenial cystidia near the lamellae sides. Line drawings all from holotype BBH 49226. Left: basidia (left top), marginal cells and basidiospores (centre), hymenial cystidia near the lamellae edges (right top), pileocystidia near the pileus centre (left bottom), pileocystidia near the pileus margin (centre), hypha terminations near the pileus centre (right centre), and hypha terminations near the pileus margin (right bottom). Scale bars = 10 mm (basidiomata), 10 µm (all other microscopic structures), 5 µm (spores).

Supplementary material

FP1423–1425-1 Table. Sequence data of *Russula* spp. used in this study.

FP1423–1425-2 Phylogenetic ITS tree.

FP1423–1425-3 Phylogenetic LSU tree.

FP1423–1425-4 Phylogenetic 3-gene tree.

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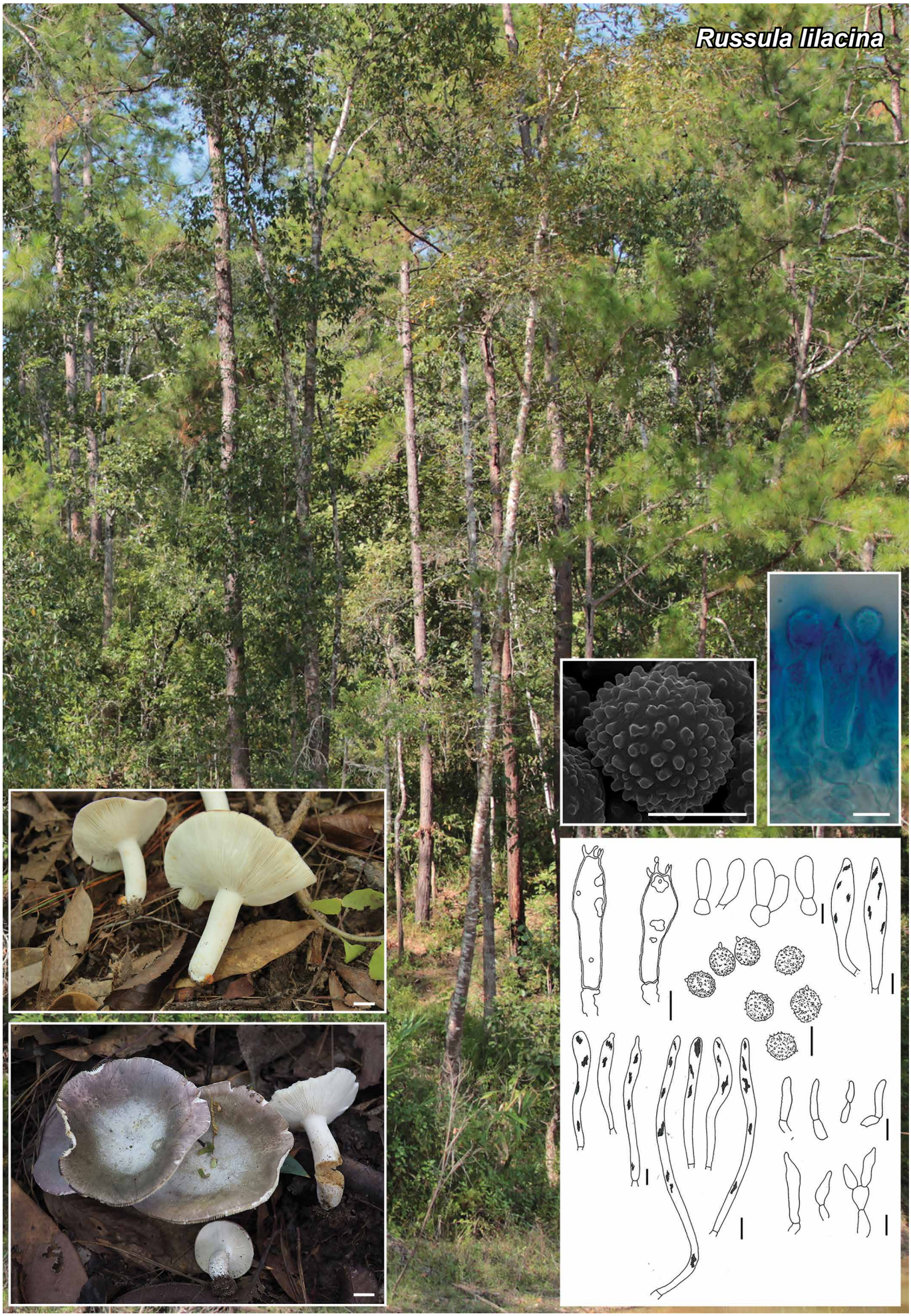
Russula lilacina

Fungal Planet 1425 – 12 July 2022

Russula lilacina Sakolrak, Jangsantear, Sommai & Pinruan, *sp. nov.*

Etymology. Refers to the lilac colour of the pileus.

Classification — *Russulaceae*, *Russulales*, *Agaricomycetes*.

Pileus medium to large-sized, 0.4–8.0 cm diam, hemispheric when young, becoming plano-convex to applanate when mature, often slightly depressed at centre or to funnel-shaped (infundibuliform), surface smooth, viscid when moist, light brownish grey (201A, colour chart of RHS 2015) when young, greyish lilac (N77C) when mature with yellowish white (155D) at the centre of pileus, unchanging when bruised, turning light yellow with 3 % KOH. *Lamellae* decurrent, narrow, crowded, even, equal, pale purplish pink (62D) when bruised. *Stipe* 0.7–1.3 × 2.0–4.8 cm, central, equal, longitudinally, smooth, dry, striate, firm, solid, unchanging when bruised, turning light yellow to yellow with 3 % KOH, white (NN155D). *Context* 1–4 mm, thick, white (NN155D), spongy to firm changing when cut pale purplish pink (62D). *Odour* indistinct. *Taste* unrecorded. *Spore print* not obtained. *Basidiospores* (30/3/1) 6.2–9.7 × 5.8–8.8 µm (Q = 0.9–1.61, Qm = 1.15 ± 0.26), globose to subglobose or broadly ellipsoid; ornamentation amyloid; minute warts, not exceeding 1.0–2.0 µm in height; suprahilar plage indistinct; hilar appendix distinct, 1–1.5 µm in height, not amyloid; hyaline in 10 % KOH. *Basidia* (20.4–)22.0–35.3(–39.5) × 5.6–9.4(–10.6) µm, 4-spored with some 2-spored basidia present, narrowly clavate to clavate; sterigmata 4.0–6.0 µm in length. *Lamellar trama* mainly composed of nested sphaerocysts, 8.0–35.0 µm diam, and filamentous hyphae 3.0–5.0 µm thick, hyaline. *Hymenial cystidia* numerous, c. 1600/mm^2, 32.2–46.9 × 4.1–9(–10) µm, rarely, clavate to subfusiform, with oil-content, thin-walled, round apex, weakly greyish in sulfovanillin; abundant near the lamellae edges, 35.0–57.5 × 10.0–10.5 µm, similar to those on the sides. Lamellae edges fertile; *marginal cells* 17.5–22.5 × 5.0–10.0 µm, mainly clavate and shorter than basidia. *Pileipellis* metachromatic in Cresyl Blue, not sharply delimited from underlying context, 30.0–40.0 µm, deep, not gelatinised, a trichodermium, composed of hyphae 2.0–7.0 µm wide, thin-walled, septate. *Acid-resistant incrustations* absent. Hyphal terminations near the pileus margin occasionally branched, flexuous, thin-walled, septate, terminal cells 17.5–35.0 × 3.8–5.0 µm, mainly lageniform, pyriform or clavate, apical obtuse and often with glutinous coating not colouring in any reagent. Terminal cells of hyphae near the pileus centre, often cylindrical and smaller, 10.0–17.5 × 2.5–4.5 µm. *Pileus trama* interwoven with sphaerocysts. *Pileocystidia* near the pileus margin relatively numerous, 1-celled, cylindrical, rarely lanceolate, often very long and originating in the context, thin-walled, 62.5–137.5 × 3.8–7.5 µm, with dispersed granulations or locally heteromorphous-banded, weakly greyish in sulfovanillin. *Pileocystidia* near the pileus centre similar and shorter. *Stipitipellis* a cutis, composed of hyphae 2.0–5.0 µm wide, thin-walled, septate. *Caulocystidia* 35.5–45.8 × 8.5–10.3(–12.5) µm, cylindrical to digitate, abundant. *Clamp connections* absent.

Habitat & Distribution — Currently known only from the type locality, in association with *Pinus merkusii* (*Pinaceae*).

Typus. Thailand, Chiang Mai, Kanlayaniwattana district, on soil under *Pinus merkusii* trees (*Pinaceae*), 7 Nov. 2019, *S. Sommai* (holotype BBH 49227; ITS, LSU and *rpb2* sequences GenBank, MT940809, MT940819 and MT965685, MycoBank MB 841178).

Additional material examined. Thailand, Chiang Mai, Kanlayaniwattana district, on soil under *P. merkusii* trees, 7 Nov. 2019, *S. Sommai*, BBH 49229; ITS, LSU and *rpb2* sequences GenBank MT940810, MT940820 and MT965686.

Notes — See notes under *Russula purpureoviridis* (FP1424).

Colour illustrations. The pine forest, Kanlayaniwattana district, Chiang Mai province, where the holotype was collected. Left top and bottom: basidiomata growing on the soil BBH 49227. Right top: scanning electron photograph of spores from BBH 49227 and hymenial cystidia near the lamellae sides. Right bottom; line drawings all from holotype BBH 49227; basidia (left top), marginal cells and basidiospores (centre), hymenial cystidia near the lamellae edges (right top), pileocystidia near the pileus centre (left bottom), pileocystidia near the pileus margin (centre), hypha terminations near the pileus centre (right centre) and hypha terminations near the pileus margin (right bottom). Scale bars = 10 mm (basidiomata), 10 µm (all other microscopic structures), 5 µm (spores).

Supplementary material

FP1423–1425-1 Table. Sequence data of *Russula* spp. used in this study.

FP1423–1425-2 Phylogenetic ITS tree.

FP1423–1425-3 Phylogenetic LSU tree.

FP1423–1425-4 Phylogenetic 3-gene tree.

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Serendipita petricolae

Fungal Planet 1426 – 12 July 2022

Serendipita petricolae Dearnaley, Hidmi & C.C. Linde, *sp. nov.*

Etymology. Name refers to the rocky location from where it was collected.

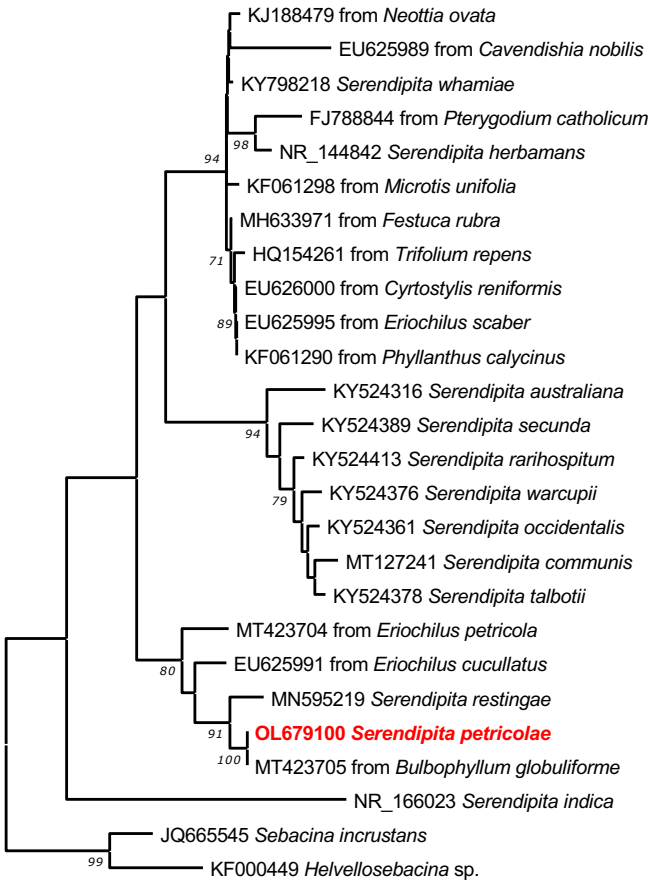
Classification — *Serendipitaceae*, *Sebacinales*, *Agaricomycetes*.

Sporophore produced by the soil on agar method (Warcup & Talbot 1967), cream-coloured, resupinate hyphae growing on the surface of soil clods. *Probasidia* ovate 8–10 × 6–7 µm diam, without sub-basidial cells. *Metabasidia*, *basidia*, *sterigmata* and *basidiospores* not seen.

Culture characteristics — Colonies on potato dextrose agar (PDA) up to 6 cm diam after 3 wk growth at 22 °C, cream, appressed, without aerial mycelium, margins irregular and translucent, surface wrinkled in the central part, reverse cream. *Hyphae* hyaline, thin-walled, lacking clamps, 1–3 µm in width. *Monilioid cells* globose, 4–7 µm diam, in short chains of 3–4 cells.

Typus. Australia, Queensland, Mt Mee, D'Aguilar National Park, open *Eucalyptus* woodland, S27°06'29" E151°42'21", 527 m a.s.l., isolated as an endophyte from roots of *Eriochilus petricola* (*Orchidaceae*), 3 Apr. 2018, *J.D.W. Dearnaley*, JDEADA2.4 (holotype BRIP 71159, preserved as metabolically inactive culture, culture ex-type BRIP 71159; ITS and LSU sequences GenBank OL679100 and OM327581, MycoBank MB 842605).

Notes — *Serendipita* spp. are cultivable agaricomycetous fungi found as mycobionts in a variety of plant hosts worldwide including grasses, ericoids, liverworts and orchids (Weiss et al. 2016). Recent descriptions include *S. australiana*, *S. communis*, *S. occidentalis*, *S. rarihospitum*, *S. restingae*, *S. secunda*, *S. talbotii*, *S. warcupii* and *S. whamiae* (Fritsche et al. 2021, Crous et al. 2020a, Oktalira et al. 2021). *Serendipita petricolae* is a new species of *Serendipitaceae* with some similarities to the recently described *S. whamiae* from the Australian terrestrial orchid *Eriochilus cucullatus*, including globose monilioid cells in chains and a growth rate on PDA of 3 mm/d. It differs from *S. whamiae* in that it has ovate probasidia without sub-basidial cells. Compared to other sequenced *Serendipita* taxa, *S. petricolae* is identical to the mycobiont isolated from the epiphytic Australian orchid, *Bulbophyllum globuliforme* (GenBank MT423705). It is distinct on BLAST matches from another *Serendipita* isolate (JDEADA2.1) from *Eriochilus petricola* (ITS; 82 % identity over 649 bp; GenBank MT423704) and *S. restingae* (ITS; 89 % identity over 640 bp; GenBank MN595219; Fritsche et al. 2021).



Maximum Likelihood tree obtained by analysis of ITS DNA from *S. petricolae* (red, bold) and related *Sebacinales* species in GenBank. Phylogenetic analysis was conducted in MEGA v. 11 (Tamura et al. 2021) using ClustalW for alignment (422 bp in the final dataset) and Tamura-Nei parameters, Gamma distribution and 1 000 bootstrap re-samplings to build the tree. *Helvellosebacina* sp. (KF000449) and *Sebacina incrustans* (JQ665545) were used as outgroups. Scale bar = 0.10.

Colour illustrations. *Eriochilus petricola* in *Eucalyptus* woodland at D'Aguilar National Park. *Serendipita petricolae* (descending order) colony on PDA; monilioid cells; probasidia. Scale bars = 1 cm (host plant and colony), 10 µm (monilioid cells and probasidia).

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Keissleriella sporoboli

Fungal Planet 1427 – 12 July 2022

Keissleriella sporoboli Steinrucken, Vitelli, Holdom, Y.P. Tan & R.G. Shivas, *sp. nov.*

Etymology. Named after *Sporobolus*, the grass on which the fungus was found.

Classification — *Lentitheciaceae*, *Pleosporales*, *Dothideomycetes*.

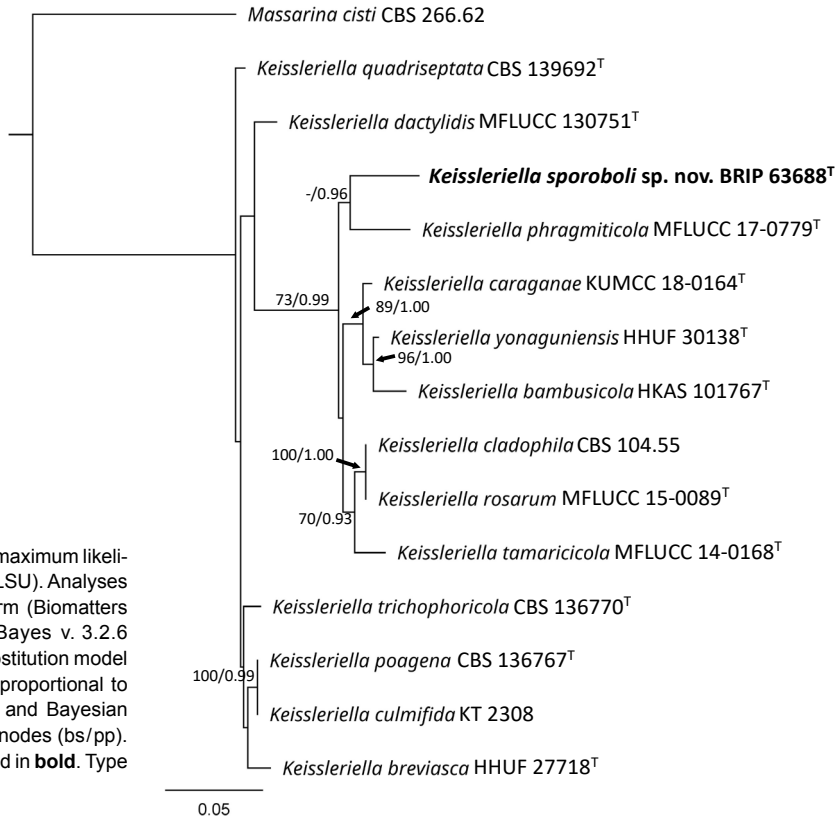
Conidia cylindrical, (19–)23–26(–28) × (5.5–)6–7(–7.5) µm, hyaline to subhyaline, rounded at apex, slightly truncate at base, 3-septate, straight, slightly constricted at septa, smooth-walled, cells with conspicuous guttules. *Conidiomata*, *conidiophores*, *conidiogenous cells* and *sexual morph* not seen.

Culture characteristics — Colonies on 1/2 potato dextrose agar (PDA) after 10 d in the dark at 23 °C reaching 22 mm diam, circular, olivaceous grey with a narrow pale grey margin, adpressed with scant aerial mycelium; reverse cream to pale yellow, with conidiomata apparent as small dark patches.

Typus. Australia, Queensland, Taunton, Williams Way, S24°26'48.04" E151°47'41.10", from stem of *Sporobolus natalensis* (*Poaceae*), 13 Nov. 2015, *J.S. Vitelli* (holotype BRIP 63688, preserved as metabolically inactive culture, culture ex-type BRIP 63688; ITS and LSU sequences GenBank MW682816 and MW682815, MycoBank MB 842477).

Notes — Phylogenetic analysis of the ITS region placed *K. sporoboli* in a well-supported monophyletic clade with sister *K. phragmiticola*, a saprobe of *Phragmites* sp. (*Poaceae*), first described from Dorset, UK (Wanasinghe et al. 2018). The asexual morph was described from isolates of woody *P. communis* in Cardiff Bay, Wales (Devadatha et al. 2020).

A BLASTn search of NCBIs GenBank shows that the closest hits using the **ITS** sequence were *K. yonaguniensis* (GenBank NR_155212; identities 477/527 (91 %); 11 gaps (2 %)), *K. caraganae* (GenBank NR_164447; identities 475/525 (90 %); 11 gaps (2 %)) and *K. bambusicola* (GenBank NR_165917; identities 474/530 (89 %); 15 gaps (2 %)). A BLASTn search of NCBIs GenBank shows that the closest hits using the **LSU** sequence were *K. yonaguniensis* (GenBank NG_059402; identities 823/828 (99 %); no gaps), *K. caraganae* (GenBank MK359439; identities 821/828 (99 %); no gaps) and *Murilentithecium rosae* (GenBank MG829030; identities 821/828 (99 %); no gaps).



Phylogenetic tree of selected *Keissleriella* species based on maximum likelihood analysis of a combined multilocus alignment (ITS and LSU). Analyses were performed on the Geneious Prime ® 2021.0.3 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. Branch lengths are proportional to distance. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). *Massarina cisti* was used as outgroup. Novel taxon is indicated in **bold**. Type specimens indicated with T.

Colour illustrations. Invasive *Sporobolus* spp. infestation of a paddock in Taunton, Queensland. Colony on 1/2 PDA at 1 wk; conidia. Scale bars = 1 cm (colony), 10 µm (conidia).

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Leptosphaerulina queenslandica

Fungal Planet 1428 – 12 July 2022

Leptosphaerulina queenslandica Steinrucken, Vitelli, Holdom, Y.P. Tan & R.G. Shivas, *sp. nov.*

Etymology. Named after Queensland, where this fungus was collected.

Classification — *Didymellaceae*, *Pleosporales*, *Dothideomycetes*.

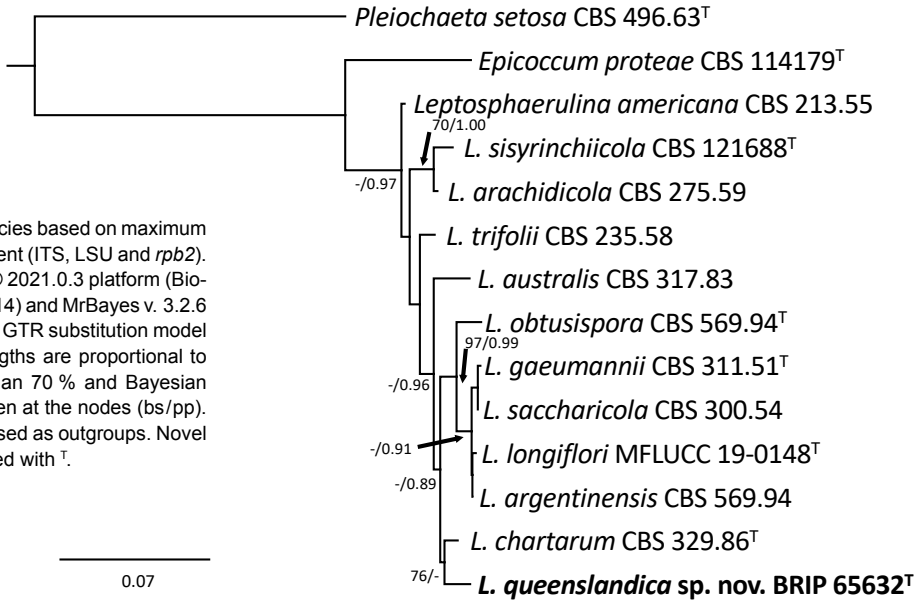
Ascomata 75–200 µm diam, pseudothecial, abundant and clustered on potato dextrose agar (PDA), solitary and scattered on straw pieces on Sach's agar, immersed to erumpent, uniloculate, brown to dark brown, subglobose to cylindrical, pseudoparenchymatous, ostiolate; peridium composed of several layers of brown to dark cells of *textura angularis*. *Asci* 80–100 × 55–75 µm, 8-spored, bitunicate, broadly obovoid, short pedicellate, apically rounded. *Ascospores* 29–34 × 10–14 µm, ellipsoid to obovoid, hyaline, muriform, with 5 transverse septa, and 1–2 longitudinal septa, smooth-walled, surrounded by a mucilaginous sheath.

Culture characteristics — Colonies on PDA reaching 60 mm diam after 10 d at 24 °C, velvety, cream to grey, with irregular dark scattered patches, darker at the centre; reverse dark brown to black, margin pale grey.

Typus. Australia, Queensland, Taunton, Tablelands Road, S24°27'0.47" E151°48'2.80", from leaves of *Sporobolus natalensis* (*Poaceae*), 8 Feb. 2017, *J.S. Vitelli* (holotype BRIP 65632, preserved as metabolically inactive culture, culture ex-type BRIP 65632; ITS, LSU and *rpb2* sequences GenBank MW481667, MW481664 and MW626889, MycoBank MB 842478).

Notes — *Leptosphaerulina queenslandica* is morphologically similar to other species of *Leptosphaerulina* in having 8-spored, bitunicate asci and hyaline, muriform ascospores (Tennakoon et al. 2019). The size of the ascospores of *L. queenslandica* overlaps with several species, including the type of the genus, *L. australis* (McAlpine 1902), which was isolated from leaves of *Prunus armeniaca* in Queensland. There are 63 *Leptosphaerulina* epithets in MycoBank, but only16 have molecular data in GenBank (October 2020). Species of *Leptosphaerulina* include plant pathogens (e.g., *L. australis*; Mitkowski & Browning 2004) and saprobes (e.g., *L. chartarum*; Roux 1986). Multilocus (ITS, LSU and *rpb2*) phylogenetic analysis placed *L. queenslandica* in a monophyletic clade with *L. australis* (the generic type). *Leptosphaerulina queenslandica* is sister to *L. chartarum*, which was isolated from *Galenia* sp. (*Aizoaceae*) (Hou et al. 2020).

A BLASTn search of NCBIs GenBank shows that the closest hits using the **ITS** sequence were *L. argentinensis* (GenBank MH862490^{T}), *L. australis* (GenBank MH857766^{T}) and *L. trifolii* (GenBank MH857454^{T}), all 100 % identical (522/522 nucleotides, no gaps). A BLASTn search of NCBIs GenBank shows that the closest hits using the **LSU** sequence were *L. longiflori* (GenBank NG_070082^{T}), *Epicoccum pruni* (GenBank NG_069437^{T}) and *Nothophoma anigozanthi* (GenBank NG_069045^{T}) all 99 % identical (998/1 008 nucleotides, two gaps (0 %)). A BLASTn search of NCBIs GenBank shows that the closest hits using the ***rpb2*** sequence were *L. saccharicola* (GenBank KF670714^{T}; Identities 815/885 (92 %), no gaps), *Saccothecium sepincola* (GenBank GU371745^{T}; Identities 815/885 (92 %), no gaps) and *L. americana* (GenBank MT649487; Identities 808/885 (91 %), no gaps).



Phylogenetic tree of selected *Leptosphaerulina* species based on maximum likelihood analysis of a combined multilocus alignment (ITS, LSU and *rpb2*). Analyses were performed on the Geneious Prime ® 2021.0.3 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. Branch lengths are proportional to distance. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). *Pleiochaeta setosa* and *Epicoccum proteae* were used as outgroups. Novel taxon is indicated in **bold**. Type specimens indicated with ^{T}.

Colour illustrations. *Sporobolus natalensis* infestation in Taunton, Queensland, *Leptosphaerulina queenslandica*. Colony on PDA at 10 d (upper and reverse); pseudothecia forming on Sabourad's dextrose agar; pseudothecium; ascus and ascospores. Scale bars = 1 cm (colony), 100 µm (pseudothecia on agar), 10 µm (pseudothecium, ascus and ascospores).

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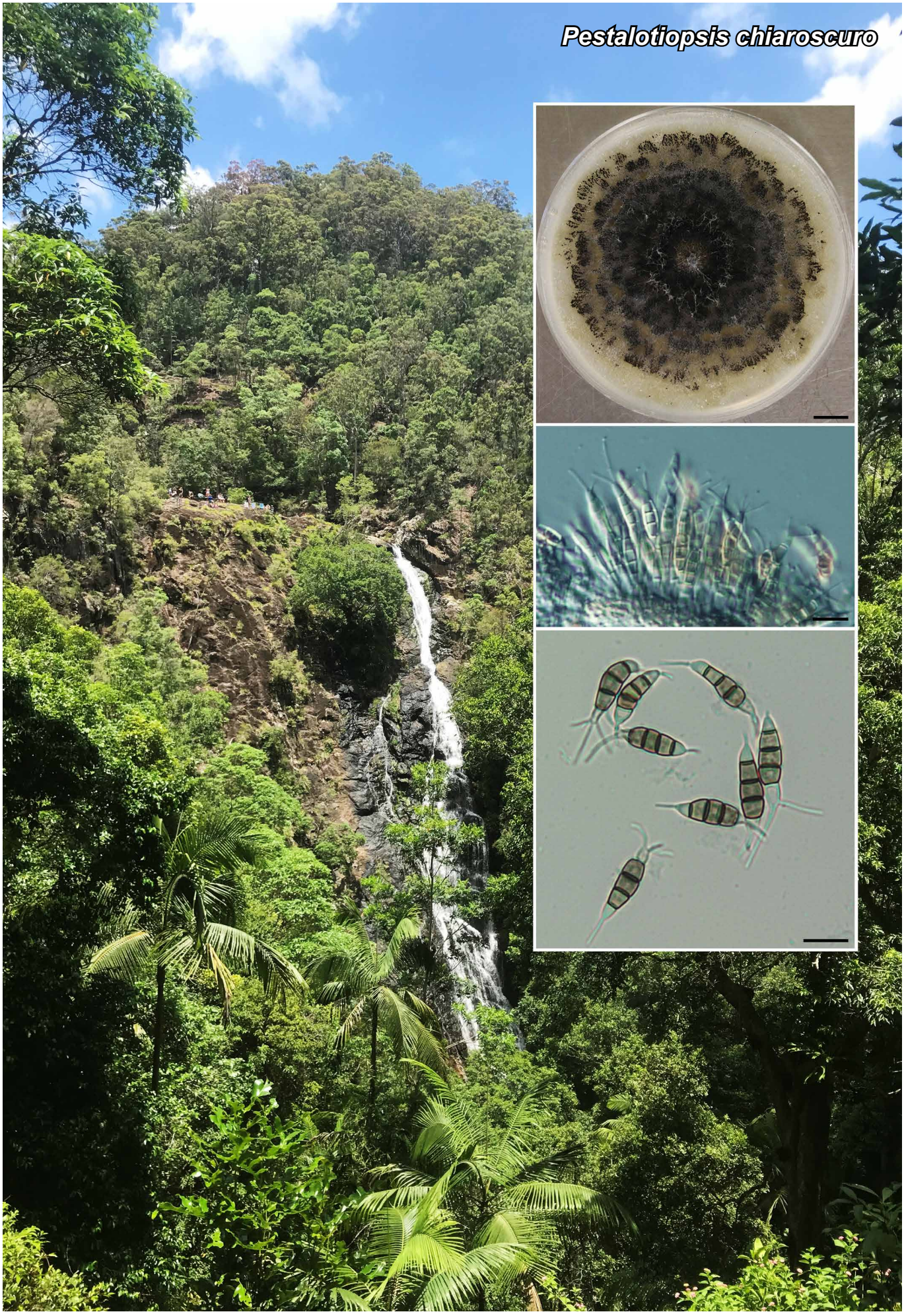

Pestalotiopsis chiaroscuro

Fungal Planet 1429 – 12 July 2022

Pestalotiopsis chiaroscuro Rapley, Steinrucken, Vitelli, Holdom & Y.P. Tan, *sp. nov.*

Etymology. From *chiaroscuro*, which refers to the effect of contrasted light and dark. This is a reference to different colonies of the fungus that varied in colour from white to dark grey when grown on culture plates.

Classification — *Pestalotiopsidaceae*, *Xylariales*, *Sordariomycetes*.

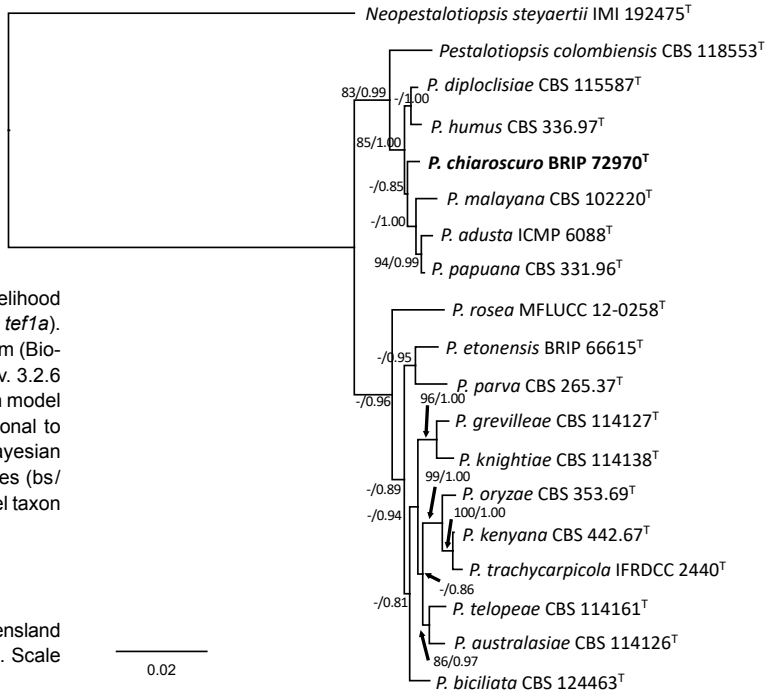
Conidiomata acervular on 1/2 PDA, globose or clavate, scattered or aggregated, immersed or semi-immersed, dark brown to black, up to 500 µm diam; exuding dark brown to black conidial masses. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* discrete, cylindrical, hyaline, smooth, 5–10 × 1–2 µm. *Conidia* fusoid, cylindrical, straight to slightly curved, 4-septate, 16–20 × 4–7 µm, basal cell conic, hyaline, smooth and thin-walled, 2–5 µm long; three median cells doliiform, 12–18 µm long, smooth, concolorous, septa darker than the rest of the cell; apical cell 2–4.5 µm long, hyaline, conic, thin-walled, smooth; with three tubular apical appendages, unbranched, filiform, 10–18 µm; basal appendage tubular, centric, 2–8 µm long. *Sexual morph* not seen.

Culture characteristics — Colonies on potato dextrose agar (PDA) after 7 d reach 8 cm diam, adpressed with scant aerial mycelium, margin entire, with radiating patches of dark brown to black acervuli in the centre becoming lighter towards the margin.

Typus. Australia, Queensland, Murgon, S26°08'38.5" E151°49'58.7", on leaf of *Sporobolus natalensis* (*Poaceae*), 31 May 2021, *J. Mitchell* (holotype BRIP 72970a, preserved as metabolically inactive culture, culture ex-type BRIP 72970a; ITS, LSU, *tub2* and *tef1a* sequences GenBank OK422510, OK422511, OK423752 and OK423753, MycoBank MB 842479).

Notes — *Pestalotiopsis chiaroscuro* was isolated from leaves and stems of giant rat's tail grass (*Sporobolus natalensis*), an introduced weedy pasture species in Australia. *Pestalotiopsis chiaroscuro* is a plant pathogen under investigation by Biosecurity Queensland for use as a potential biological control agent for this exotic grass in Queensland. *Pestalotiopsis* is a large genus of endophytes, saprobes or pathogens across diverse hosts and environments (Maharachchikumbura et al. 2011, 2014).

A multilocus phylogenetic analysis of the ITS, LSU, *tub2* and *tef1a* loci placed *P. chiaroscuro* in a well-supported clade with *P. malayana*, *P. adusta*, *P. papuana*, *P. humus*, *P. diploclisiae* and *P. colombiensis*. A blastn search of NCBIs GenBank nucleotide database found the closest hits of **ITS** sequence were *P. papuana* (GenBank KU715152; Identities 539/539 (100 %), no gaps) and *P. microspora* (GenBank MT597837; identities 537/539 (99 %), no gaps). A BLASTn search of NCBIs GenBank nucleotide database found the closest hits of **LSU** sequence were *P. thailandica* (GenBank NG_070088; Identities 846/846 (100 %), no gaps), *P. rhizophorae* (GenBank NG_070087; Identities 846/846 (100 %), no gaps) and *P. papuana* (GenBank NG_069219; Identities 846/846 (100 %), no gaps). A BLASTn search of NCBIs GenBank nucleotide database found the closest hits of ***tub2*** sequence were *P. diploclisia* (GenBank KM199417; Identities 771/777 (99 %), no gaps), *P. humus* (GenBank KM199418; Identities 766/772 (99 %), no gaps) and *P. malayana* (GenBank KM199411; Identities 767/774 (99 %), no gaps). A BLASTn search of NCBIs GenBank nucleotide database found the closest hits of ***tef1a*** sequence were *P. humicola* (GenBank MH554563; Identities 465/469 (99 %), no gaps), *P. aggestorum* (GenBank KY464151; Identities 465/469 (99 %), no gaps) and *P. humus* (GenBank KM199484; Identities 465/469 (99 %), no gaps).



Phylogenetic tree of *Pestalotiopsis* species based on maximum likelihood analysis of a combined multilocus alignment (ITS, LSU, *tub2* and *tef1a*). Analyses were completed on the Geneious Prime ® 2022.0.1 platform (Biomatters Ltd.) using RAxML v. 8.2. (Stamatakis 2014) and MrBayes v. 3.2.6 (Huelsenbeck & Ronquist 2001), both based on the GTR substitution model with gamma-distribution rate variation. Branch lengths are proportional to distance. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the branches (bs/pp). *Neopestalotiopsis steyaertii* was used as the outgroup. The novel taxon is indicated in **bold**. Ex-type strains are marked with T.

Colour illustrations. Kondalilla Falls, Kondalilla National Park, Queensland (photo credit T..V. Steinrucken). Colony on PDA; acervulus; conidia. Scale bars = 1 cm (colony) and 10 µm (acervulus and conidia).

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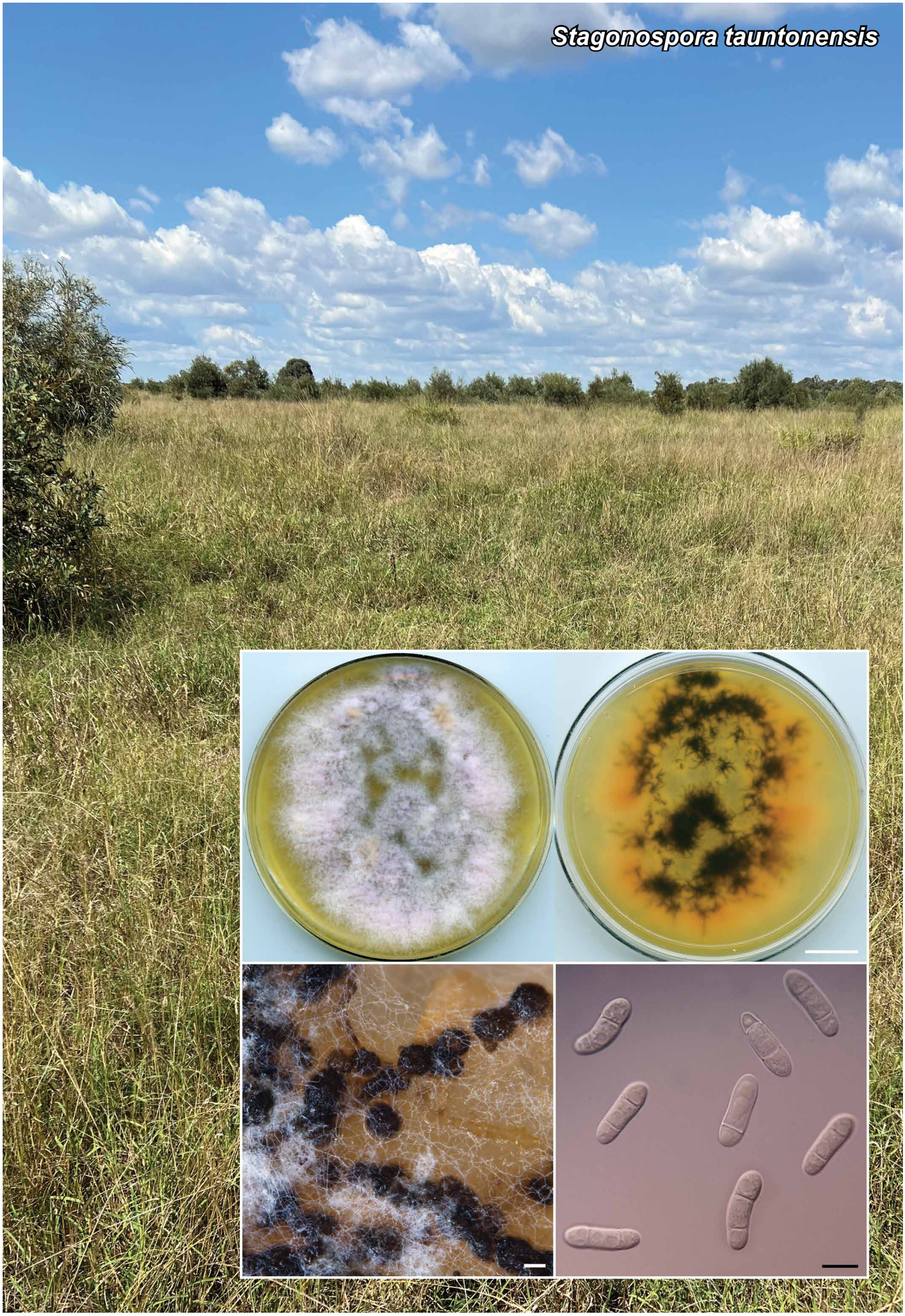

Stagonospora tauntonensis

Fungal Planet 1430 – 12 July 2022

Stagonospora tauntonensis Steinrucken, Vitelli, Holdom, Y.P. Tan & R.G. Shivas, *sp. nov.*

Etymology. Named after Taunton, the rural locality where the fungus was collected.

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

Conidiomata abundant on potato carrot agar (PCA) after 3 wk at 25 °C, superficial and immersed, aggregated and often in irregular lines radiating from clusters, globose, 150–280 µm diam, dark brown, glabrous, with central ostiole. *Conidiophores* reduced to conidiogenous cells, hyaline, smooth, ampulliform. *Conidia* hyaline, smooth, guttulate, cylindrical to obclavate with rounded ends, (1–)2(–3)-septate, straight or curved, slightly constricted at septa, 20–25 × 5–7 µm.

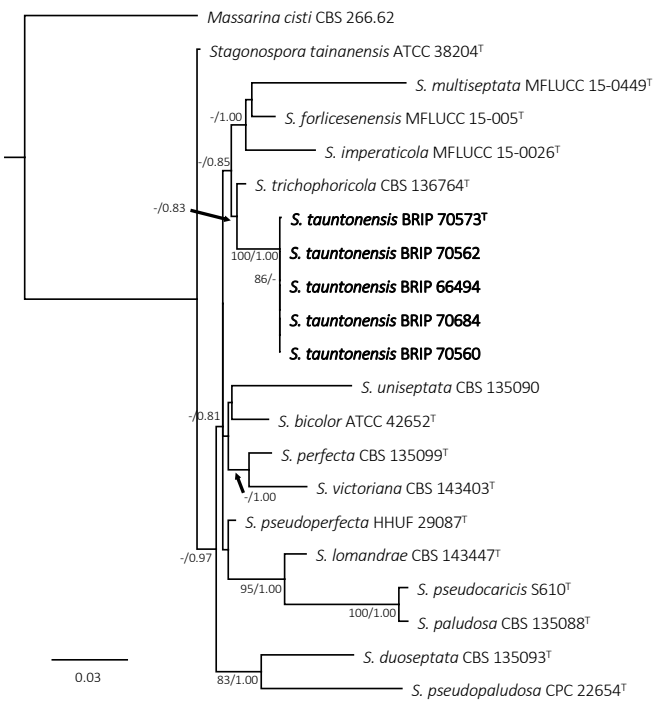
Culture characteristics — Colonies on PCA after 2 wk at 25 °C cover the surface of 5.5 cm diam plates, aerial mycelium sparse, rosy vinaceous, with darker patches corresponding to aggregations of conidiomata; reverse pale peach with aggregations of conidiomata visible as dark patches.

Typus. Australia, Queensland, Taunton, Williams Way, S24°26'58.0" E151°47'05.6", on stem of *Sporobolus natalensis* (*Poaceae*), 30 Nov. 2017, *J.S. Vitelli* (holotype BRIP 70573, preserved as a metabolically inactive culture, culture ex-type BRIP 70573; ITS, LSU and *tef1a* sequences GenBank MW481668, MW481662 and OM219059, MycoBank MB 842475).

Additional materials examined. Australia, Queensland, Gladstone Region, on leaf of *Sporobolus natalensis*, 25 July 2017, *J.S. Vitelli*, BRIP 70684a (ITS, LSU and *tef1a* sequences GenBank OM220030, OM220036 and OM219058); Mareeba, Mareeba Dimbulah Road, on leaf of *Sporobolus natalensis*, 1 Nov. 2017, *J.S. Vitelli*, BRIP 70562 (ITS, LSU and *tef1a* sequences GenBank OM220029, OM220035 and OM219057); Mutchilba, Mareeba Dimbulah Road, on roots of *Sporobolus natalensis*, 30 Nov. 2017, *J.S. Vitelli*, BRIP 70560 (ITS, LSU and *tef1a* sequences GenBank OM220028, OM220034 and OM219056); Delaney's Creek, Newman Road, on leaf of *Sporobolus natalensis*, Nov. 2017, *D.G. Holdom*, BRIP 66494 (ITS, LSU and *tef1a* sequences GenBank OM220027, OM220033 and OM219055).

Notes — *Stagonospora tauntonensis* is only known from *Sporobolus natalensis* and has been collected from multiple locations in eastern Queensland as part of a survey of the invasive rat's tail grasses (*S. natalensis* and *S. pyramidalis*). It is currently under assessment as a potential biological control agent for these agricultural weeds.

Phylogenetic analysis of the ITS gene placed *S. tauntonensis* in a monophyletic clade with sister *S. trichophoricola* from *Trichophorum cespitosum* in the Netherlands (Crous et al. 2014) and closest relatives *S. forlicesenensis* from *Phragmites australis* in Italy (Hyde et al. 2016) and *S. multiseptata* (Thambugala et al. 2017) and *S. imperaticola* from grasses. A BLASTn search of NCBIs GenBank shows that the closest hits using the **ITS** sequence were *S. trichophoricola* (GenBank MT228943; Identities 517/527 (98 %), two gaps (0 %)), *S. bicolor* (GenBank MT446144; Identities 516/527 (98 %), one gap (0 %)) and *S. pseudoperfecta* (GenBank MK442625; Identities 513/523 (98 %), two gaps (0 %)). A BLASTn search of NCBIs GenBank shows that the closest hits using the **LSU** sequence were *S. tainanensis* (GenBank AB807580; Identities 1000/1008 (99 %), two gaps (0 %)), *S. paspali* (GenBank EU754172; Identities 999/1008 (99 %), two gaps (0 %)) and *S. pseudoperfecta* (GenBank NG_059399; Identities 998/1008 (99 %), two gaps (0 %)). A BLASTn search of NCBIs GenBank shows that the closest hits using the ***tef1a*** sequence were *S. tainanensis* (GenBank AB808556; Identities 537/551 (97 %), no gaps), *S. pseudoperfecta* (GenBank AB808553; Identities 536/551 (97 %), no gaps) and *S. perfecta* (GenBank AB808555l; Identities 529/551 (96 %), no gaps).



Phylogenetic tree of selected *Stagonospora* species based on maximum likelihood analysis of the ITS, LSU and *tef1a* gene. Analyses were performed on the Geneious Prime ® 2021.0.3 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. Branch lengths are proportional to distance. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). *Massarina cisti* was used as outgroup. Novel taxon is indicated in **bold**. Ex-type strains indicated with T.

Colour illustrations. Pasture in central Queensland. *Stagonospora tauntonensis* (BRIP 70562) on PDA after 3 wk at 25 °C. Colony upper surface (left) and lower surface (right); conidiomata; conidia. Scale bars = 1 cm (colony), 100 µm (conidiomata), 10 µm (conidia).

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Wongia ficherai

Fungal Planet 1431 – 12 July 2022

Wongia ficherai Steinrucken, Vitelli, Holdom, Y.P. Tan & R.G. Shivas, *sp. nov.*

Etymology. In honour of Giovanni (Gio) Fichera, our friend and colleague, in the year of his retirement after three and a half decades of providing research and technical support, and friendship to the Tropical Weed Biological Control teams at the Commonwealth Scientific and Industrial Research Organisation, Brisbane.

Classification — *Papulosaceae*, *Xenospadicoidales*, *Sordariomycetes*.

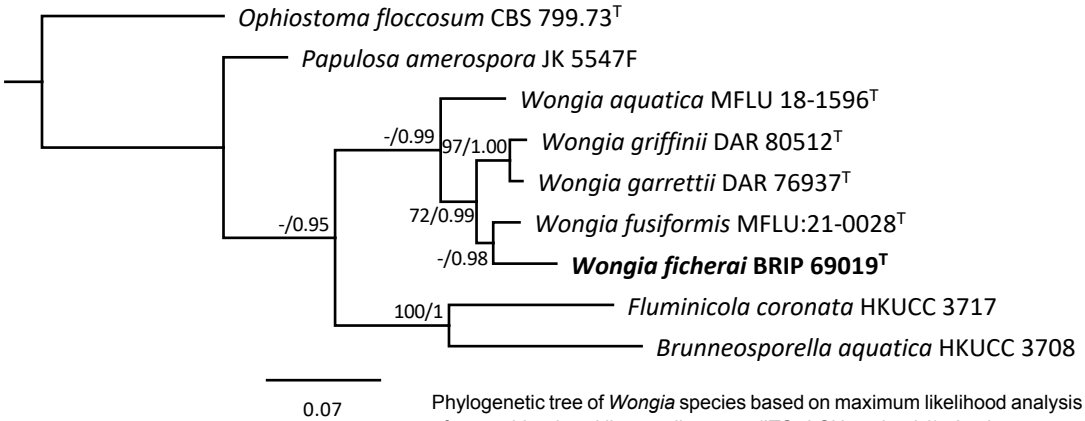
Conidiophores subcylindrical, 70–120 × 3–5 µm, unbranched, solitary, septate, erect, straight or slightly flexuous, pale brown, smooth-walled. *Conidiogenous cells* subcylindrical, 18–30 × 2–4 µm, narrowed towards the apex, polyblastic, conspicuously denticulate, terminal, subhyaline to pale brown. *Conidia* 8–16 × 3–4 µm, solitary cylindrical to fusiform, rounded at the ends, 1–2-septate, pale brown, slightly constricted at the septa, smooth-walled.

Culture characteristics — Colonies on potato dextrose agar (PDA) reaching 60 mm diam after 10 d at 24 °C, velvety, umber, reverse fuscous black.

Typus. Australia, Queensland, Taunton, Williams Way, S24°26'58.0" E151°47'05.6", from roots of *Eragrostis curvula* (*Poaceae*), 18 May 2018, *J.S. Vitelli* (holotype BRIP 69019, preserved as metabolically inactive culture, culture ex-type BRIP 69019; ITS, LSU and *rpb2* sequences GenBank OM230139, OM230140 and OM162025, MycoBank MB842476).

Notes — *Wongia ficherai* was discovered during a survey in Australia for pathogenic fungi on leaves and stems of the introduced grasses, *Sporobolus natalensis*, *S. pyramidalis* and *Eragrostis curvula*, which have become weedy in pastures. *Wongia ficherai* is currently under investigation as a potential biological control agent for these exotic grasses in Queensland. *Wongia* contains four other species, two (*W. garrettii* and *W. griffinii*) that are associated with disease symptoms in some grasses (Wong et al. 2012, Khemmuk et al. 2016), and two (*W. aquatica* and *W. fusiformis*) that have been isolated as saprobes on decayed wood in freshwater habitats (Bao et al. 2021).

A multilocus phylogenetic analysis of the ITS, LSU and *rpb2* loci placed *W. ficherai* in a well-supported monophyletic clade with ex-types sequences of the four known species of *Wongia* (including the generic type *W. garrettii*). A blastn search of NCBIs GenBank nucleotide database shows that the closest hits using the **ITS** sequence were *W. fusiformis* MFLU 21-0029 (GenBank MZ412515; Identities 476/525 (91 %), 20 gaps (3 %)), *W. fusiformis* MFLU 21-0028^{T} (GenBank MZ412517; Identities 450/495 (91 %), 18 gaps (3 %)) and *W. garrettii* DAR 79637 ^{T} (GenBank KU850474; Identities 446/493 (90 %), 16 gaps (3 %)). A blastn search of NCBIs GenBank nucleotide database shows that the closest hits using the **LSU** sequence were *Wongia fusiformis* DLUCC 1767 (GenBank MZ420761; Identities 982/994 (99 %), two gaps (0 %)), *W. fusiformis* MFLU 21-0029 (GenBank MZ412527; Identities 710/719 (99 %), no gaps) and W. *fusiformis* MFLU 21-0028^{T} (GenBank MZ412529; Identities 698/707 (99 %), no gaps). A blastn search of NCBIs GenBank nucleotide database shows that the closest hits using the ***rpb2*** sequence were *W. aquatica* MFLU 18-1596^{T} (GenBank MN124536; Identities 677/752 (90 %), no gaps), *Ceratosphaeria abietis* CBS 125235^{T} (GenBank JX066698; Identities 569/715 (80 %), 14 gaps (1 %)) and *Ceratostomella cuspidata* ICMP 17629 (GenBank KT991651; Identities 541/693 (78 %), 18 gaps (2 %)).



Phylogenetic tree of *Wongia* species based on maximum likelihood analysis of a combined multilocus alignment (ITS, LSU and *rpb2*). Analyses were performed on the Geneious Prime ® 2021.0.3 platform (Biomatters Ltd.) using RAxML v. 8.2. (Stamatakis 2014) and MrBayes v. 3.2.6 (Huelsenbeck & Ronquist 2001), both based on the GTR substitution model with gamma-distribution rate variation. Branch lengths are proportional to distance. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the branches (bs/pp). *Ophiostoma floccosum* CBS 799.73 was used as the outgroup. The novel taxon is indicated in **bold**. Ex-type strains are marked with ^{T}.

Colour illustrations. Queensland Hinterland. Colony on PDA after 4 wk; conidiophore and conidia. Scale bars = 1 cm (colony), 10 µm (all others).

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Teratosphaeria carnegiei

Fungal Planet 1432 – 12 July 2022

Teratosphaeria carnegiei Aylward, Marinc. & M.J. Wingf., *sp. nov.*

Etymology. Named for Dr Angus J. Carnegie who collected a population of *Teratosphaeria* isolates amongst which this species was found, and in recognition of his outstanding contributions to the study of *Eucalyptus* diseases.

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

Conidiomata on oatmeal agar (OA), stromatic, pycnidioid, superficial, embedded in white fluffy mycelia, exudating conidial mass at apex. *Conidiophores* borne along hymenial layer, often reduced to conidiogenous cells, mostly simple, rarely branched. *Conidiogenous cells* enteroblastic, discrete, hyaline to subhyaline, smooth to verruculous, ampulliform to sub-cylindrical, 3.5–12 × 2–5 µm. *Conidia* hyaline when young, becoming sub-hyaline when mature, greenish brown in mass, cylindrical to filiform, tapering toward apex, with blunt base, sometimes with marginal frills, curved in various ways, smooth, becoming verruculose when old, 0–1-septate, septation inconspicuous, mostly sub-median, (30–)36.5–44.5(–49) × (2–)3(–3.5) µm.

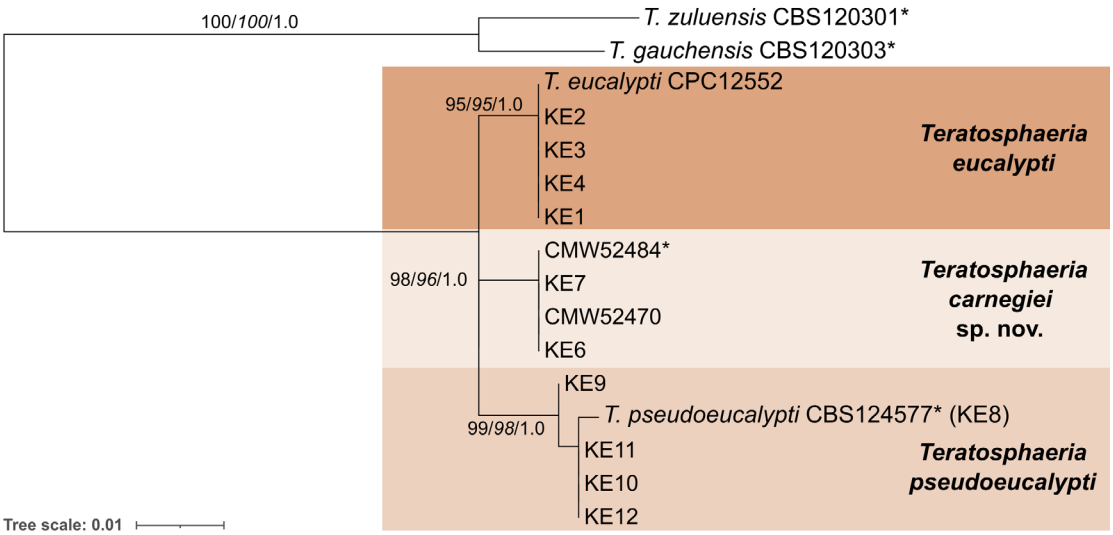
Culture characteristics — Colonies on 2 % malt extract agar (MEA) after 48 d in the dark at 25 °C producing slimy brown conidial mass, growing circular with lobate edges, raised, densely compact causing cracks on media, covered with short aerial hyphae, olivaceous grey with sporadic and intermixed patches of iron-grey and rosy buff on the surface and greenish black on reverse. Optimum growth temperature at 25 °C reaching 17.6 mm diam in 48 d, followed by at 20 °C (13.1 mm), 15 °C (9.5 mm), 10 °C (6.2 mm), 30 °C (5.7 mm) and no growth at 5 °C and 35 °C.

Typus. Australia, New South Wales, Mallanganee, Sandilands plantation, on leaf of *Eucalyptus grandis* × *E. camaldulensis* (*Myrtaceae*), 18 Apr. 2018, *A.J. Carnegie* (holotype PREM 63266, culture ex-type culture CMW 52484 = PPRI 29907; ITS, *EF1-α* and *Btub* sequences GenBank MZ285070, MZ318165 and MZ318163, MycoBank MB 841347).

Additional material examined. Australia, New South Wales, Mallanganee, on leaf of *Eucalyptus grandis* × *E. camaldulensis*, 2018, *A.J. Carnegie*, PREM 63267, culture CMW 52470 = PPRI 29908; ITS, *EF1-α* and *Btub* sequences GenBank MZ285069, MZ318164 and MZ318162.

Notes — *Teratosphaeria* species are primarily leaf-infecting fungi, many of which are also important pathogens of *Eucalyptus* (Quaedvlieg et al. 2014, Burgess & Wingfield 2017). *Teratosphaeria carnegiei* is closely related to the aggressive *Eucalyptus* pathogens *T. eucalypti* and *T. pseudoeucalypti*. It was first detected as a variant of *T. eucalypti* in New South Wales (NSW) that comprised distinct 'KE' haplotypes (Andjic et al. 2010) and was later isolated as part of a *T. pseudoeucalypti* population genetics study (Aylward et al. 2021), also in NSW. Molecular phylogenies and microsatellite genotypes (based on Havenga et al. 2020) clearly distinguish the NSW variants as a distinct and cryptic species.

Three *Teratosphaeria* species are morphologically similar with only small differences in conidial dimensions and the number of septa (Cooke 1889, Walker et al. 1992, Andjic et al. 2010). Conidial dimensions for the three species have been reported as follows: *T. eucalypti* 25–48 × 2–3 µm with 0–2 septa (Walker et al. 1992), *T. pseudoeucalypti* 26–58 × 2–3.5 (av. 35 × 2.2) µm *in vivo*, 27–43 × 1.5–3 (av. 35 × 2.5) µm in vitro with 0–3 septa (Andjic et al. 2010) and *T. carnegiei* 30–49 × 2–3.5 (av. 40 × 3) µm with 0–1 septa in vitro (this study).



Maximum likelihood phylogeny constructed from the combined *Btub* and ITS sequences of *Teratosphaeria eucalypti* and *T. pseudoeucalypti* 'KE' haplotypes (Andjic et al. 2010) and ex-type (*) isolates. Support values for the three species clades represent bootstrap support for the maximum likelihood analysis in RAxML-NG v. 1.0.2 (Kozlov et al. 2019) and parsimony analysis in PAUP v. 4.0a (Swofford 2003) and the Bayesian posterior probabilities determined with MrBayes v. 3.2.7a (Ronquist et al. 2012), respectively.

Colour illustrations. *Eucalyptus* tree in the native range. Colony on oatmeal agar showing conidial mass exudated from conidiomata; conidiogenous cells (arrows); conidia (×400); conidia (×1000). Scale bars = 1 mm (colony), 50 µm (conidia ×400), 10 µm (all others).

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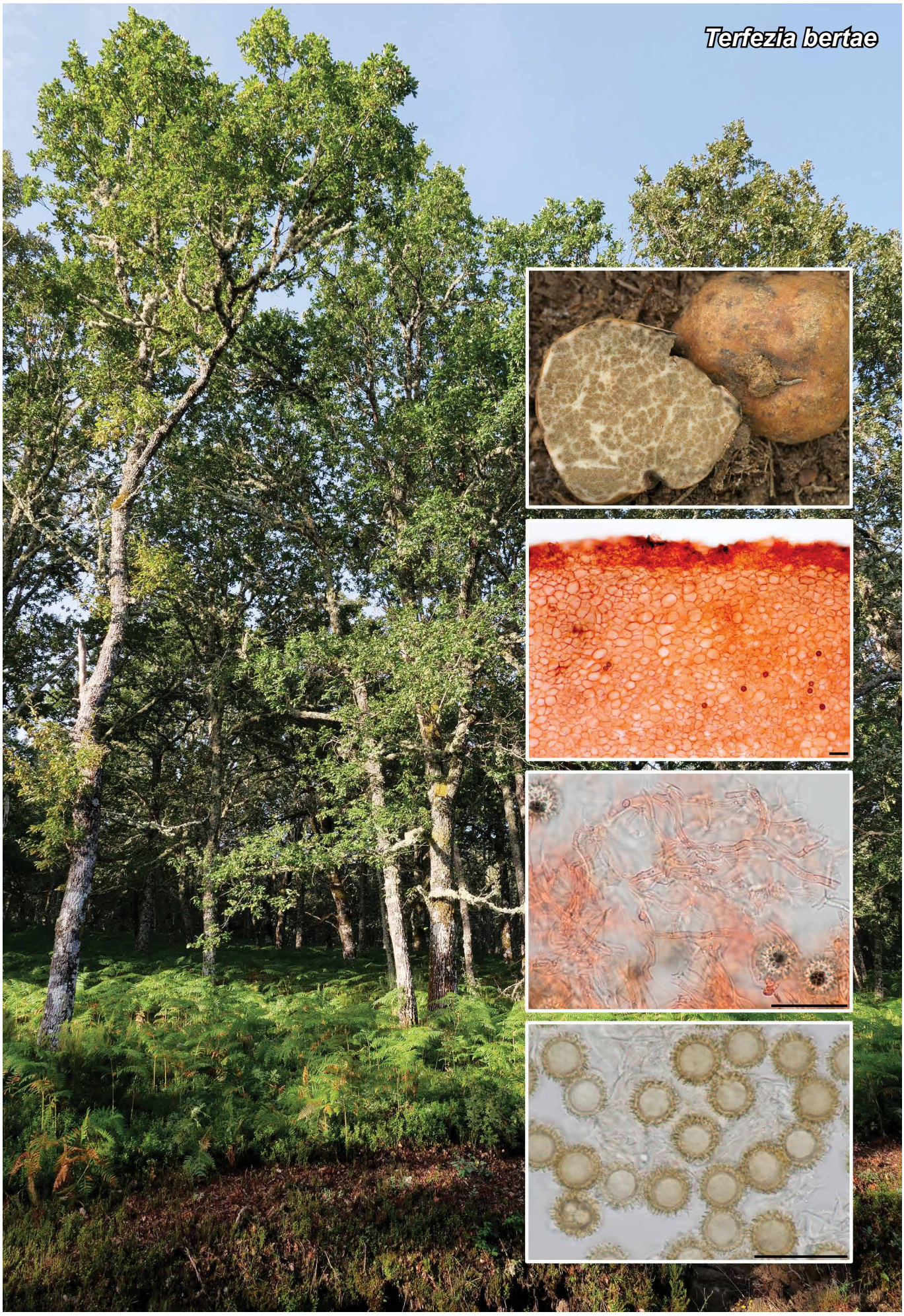

Terfezia bertae

Fungal Planet 1433 – 12 July 2022

Terfezia bertae Cabero, P. Alvarado & Ant. Rodr., *sp. nov*.

Etymology. Named in honour of Berta Martín, a technician of the regional administration of Zamora (Spain), and supporter of the study of hypogeous fungi in this region.

Classification — *Terfeziaceae*, *Pezizales*, *Ascomycota*.

Ascomata globose, smooth, with small or subtle depressions, ocherish cream in colour when young, then reddish brown with darker areas, blackening when mature; 2–3 cm diam, showing a small tuft of mycelium in the base; odour slightly acidic. *Gleba* stuffed, whitish, with small dark cream irregular pockets containing fertile tissue. *Trama* formed by densely packed sterile irregular hyphae, septate, bifurcate, (1.23–)1.31–2.13(–2.36) µm diam. *Peridium* 300–400 µm thick, completely pseudoparenchymatic, formed by slightly angular cells measuring 45–60 µm, yellowish to reddish cells near the surface, which become globose and smaller, about 20–35 µm, in the inner layers. *Asci* subglobose to ovoid, 65–82 × 50–55 µm, sessile, inamyloid and indehiscent, developing 7–8 ascospores. *Ascospores* spherical, (13.92–)13.93–14.57–15.19(–15.20) µm, ornamented with conical spikes, 2.26–2.48 µm high.

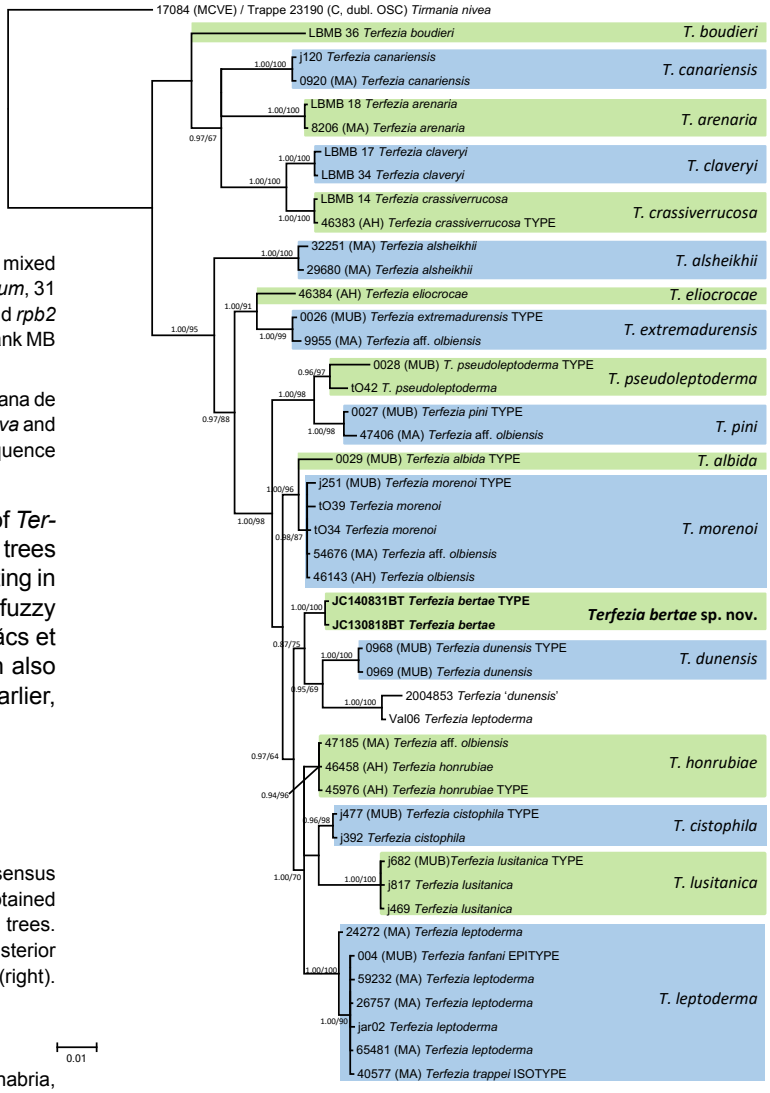
Distribution — Currently known only from the type locality in Zamora (central Spain). Occurring in mixed forests with *Quercus pyrenaica* and *Castanea sativa*, apparently without *Cistaceae* plants. Sporocarps found 2–3 cm deep in acidic soils (pH 5.5 approx.). In summer (July–Aug.).

Phylogeny — *Terfezia bertae* is probably closely related to *T. dunensis*, and also to *T. honrubiae*, *T. cistophila*, *T. lusitanica* and *T. leptoderma*. The two samples analysed form a significantly monophyletic clade (PP 1.00, BP 100) without any genetic difference between them. The ITS rDNA sequences of *T. bertae* are only 95–96 % similar to the closest species of *Terfezia*; 28S rDNA is < 99 % similar to homologous sequences of *T. morenoi*, *T. honrubiae* and *T. leptoderma*.

Typus. Spain, Castilla y León, Zamora, Ilanes de Sanabria, soil of a mixed forest with *Quercus pyrenaica*, *Castanea sativa* and *Pteridium aquilinum*, 31 Aug. 2014, *J. Cabero*, JC140831BT (holotype AH:51463; ITS, LSU and *rpb2* sequences GenBank ON009054, ON009056 and ON012516, MycoBank MB 843364).

Additional material examined. Spain, Castilla y León, Zamora, Quintana de Sanabria, soil of a mixed forest with *Quercus pyrenaica*, *Castanea sativa* and *Pteridium aquilinum*, 13 Aug. 2018, *J. Cabero* (JC130818BT, ITS sequence GenBank ON009055).

Notes — *Terfezia bertae* differs from all other species of *Terfezia* because of its ecology, being linked with broadleaved trees (instead of *Cistaceae* or *Pinaceae*) in acidic soils, sporulating in summer (instead of spring), and the presence of irregular fuzzy dark fertile pockets in the gleba. *Terfezia alsheikhii* (Kovăcs et al. 2011) and *T. olbiensis* (Tulasne & Tulasne 1851) can also occur in broadleaved forests, but they sporulate much earlier, in winter or spring, and the former has reticulate spores.



Phylogenetic tree. A 50 % majority rule ITS rDNA-28S rDNA consensus phylogram of the genus *Terfezia* (with *Tirmania nivea* as outgroup) obtained using MrBayes v. 3.2.6 (Ronquist et al. 2012) from 1275 sampled trees. Nodes were annotated if they were supported by ≥ 0.95 Bayesian posterior probability (left) or ≥ 70 % maximum likelihood bootstrap proportions (right). Sequences newly generated in this study are in **bold**.

Colour illustrations. Spain, Castilla y León, Zamora, Ilanes de Sanabria, mixed forest with *Quercus pyrenaica* and *Castanea sativa* where the holotype was found. Ascoma; peridium; tramal hyphae; ascospores. Scale bars = 40 µm (micro plates).

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Tuber davidlopezii

Fungal Planet 1434 – 12 July 2022

Tuber davidlopezii Ant. Rodr., Morte & Muñ.-Moh., *sp. nov.*

Etymology. Named after David López Carreño, a prestigious Spanish mycological chef, for his valuable contribution to the dissemination of truffles in gastronomy.

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

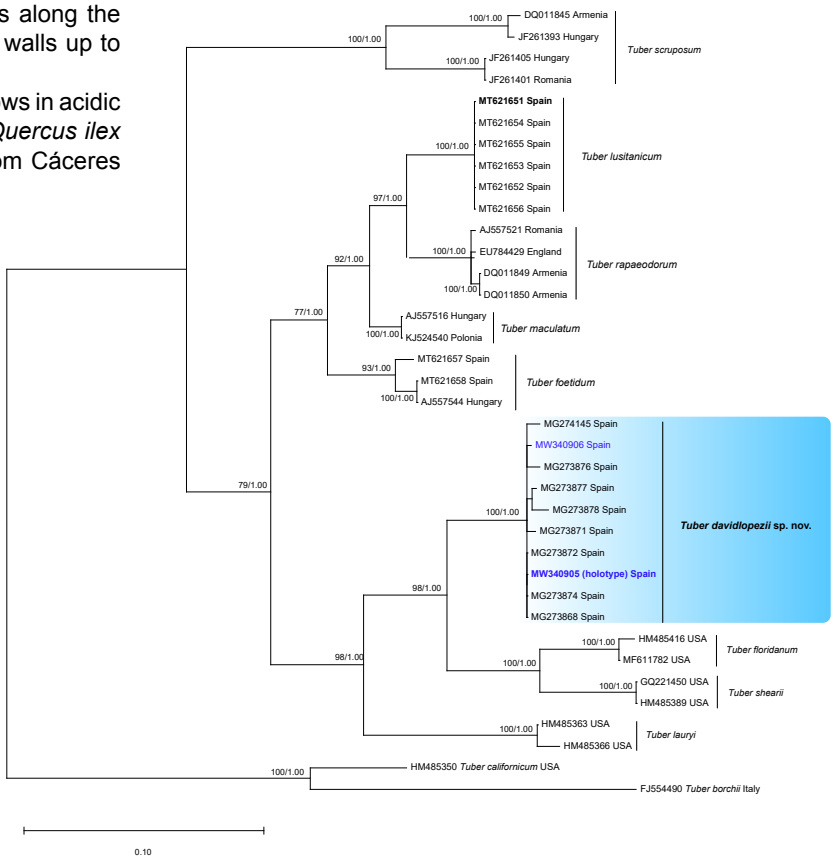
Ascomata hypogeous, 0.5–1 cm in size, subglobose or irregular in form and gibbous, solid, firm, whitish at first, pale brown at maturity, smooth. *Peridium* 200–300 µm thick, two-layered: the outermost pseudoparenchymatous, 50–100 µm thick, composed of subglobose or subangular cells, 5–25 µm diam, hyaline to yellowish, thick-walled; the inner layer 100–200 µm thick, composed of hyaline, thin-walled, interwoven hyphae up to 8 µm broad at the septum, gradually intermixing into gleba. *Gleba* whitish when immature, becoming dark brown at maturity, marbled with thin, white veins. *Odour* slight and not distinctive. *Asci* inamyloid, 70–100 × 50–80 µm, the walls up to 2.5 µm thick, ellipsoid to subglobose, sessile or short-stalked, 1–4(–5)-spored. *Ascospores* globose to subglobose, 24–42 × 23–40 µm (av. Q = 1.02), excluding ornamentation, the walls 2–4 µm thick, at first hyaline, becoming yellowish brown at maturity; reticulum with 4–6(–8) alveolar meshes along the spore length, polygonal (5–6 sides), the alveolar walls up to 6 µm high.

Ecology & Distribution — *Tuber davidlopezii* grows in acidic soils of Spain dehesas forming mycorrhiza with *Quercus ilex* subsp. *ballota* in spring. Currently known only from Cáceres and Sevilla, Spain.

Typus. Spain, Cáceres, Talayuela, in acidic soil, under *Quercus ilex* subsp. *ballota* (*Fagaceae*), 13 Apr. 2006, *A. Rodriguez* (holotype MUB Fung-1001; ITS and LSU sequences GenBank MW340905 and MW547121, MycoBank MB 838176).

Additional material examined. Spain, Cáceres, Talayuela, in acidic soil, under *Quercus ilex* subsp. *ballota*, 5 May 2006, *A. Rodriguez*, MUB Fung-1002, ITS sequence GenBank MW340906.

Notes — Recently published DNA phylogenetic studies on *Tuber* have shown that the genus is more diverse than previously suspected (Eberhart et al. 2020), containing many still undescribed taxa. Among these, *T. davidlopezii* is a whitish truffle that clusters in the maculatum clade, and is characterised by its white-cream smooth peridium, brown gleba marbled with thin, white veins and globose, reticulate-alveolate spores. *Tuber davidlopezii* differs from all other species of the maculatum clade by its globose spores and unique DNA sequence data. *Tuber rapaedorum* has larger, ellipsoid spores (Ceruti et al. 2003). *Tuber maculatum* has a prosenchymatous peridium and ellipsoid spores (Mello et al. 2000).



Phylogenetic tree. Maximum likelihood phylogeny based on the ITS nuclear rDNA sequences showing placement of *Tuber davidlopezii* among other taxa in the maculatum clade. Type specimens are indicated in **bold**. Newly generated sequences are in blue. The new species is marked in blue square. Support values on branches indicate Maximum likelihood (ML) bootstrap values (BS) ≥ 70 % and Bayesian posterior probability values (PP) > 95 % (BS/PP). *Tuber californicum* and *T. borchii* were used as the outgroup. The scale bar indicates the expected number of changes per site. The ML analysis was done in IQ-TREE v. 1.6.12 (Nguyen et al. 2015) using the non-parametric bootstrap (1 000 replicates) and the best-fit model (TN+F+G4), according to BIC, determined with ModelFinder (Kalyaanamoorthy et al. 2017). Bayesian (PP) inference was done in MrBayes v. 3.2.6 (1 million generations), allowing the software to estimate the evolutionary model (Ronquist et al. 2012). All other settings were left as default. Both ML and Bayesian analysis resulted in identical overall topology and therefore only the ML tree is shown.

Colour illustrations. Spain, Cáceres, Talayuela dehesa where the holotype specimen was collected. Ascocarps; mature ascospores. Scale bar = 20 µm.

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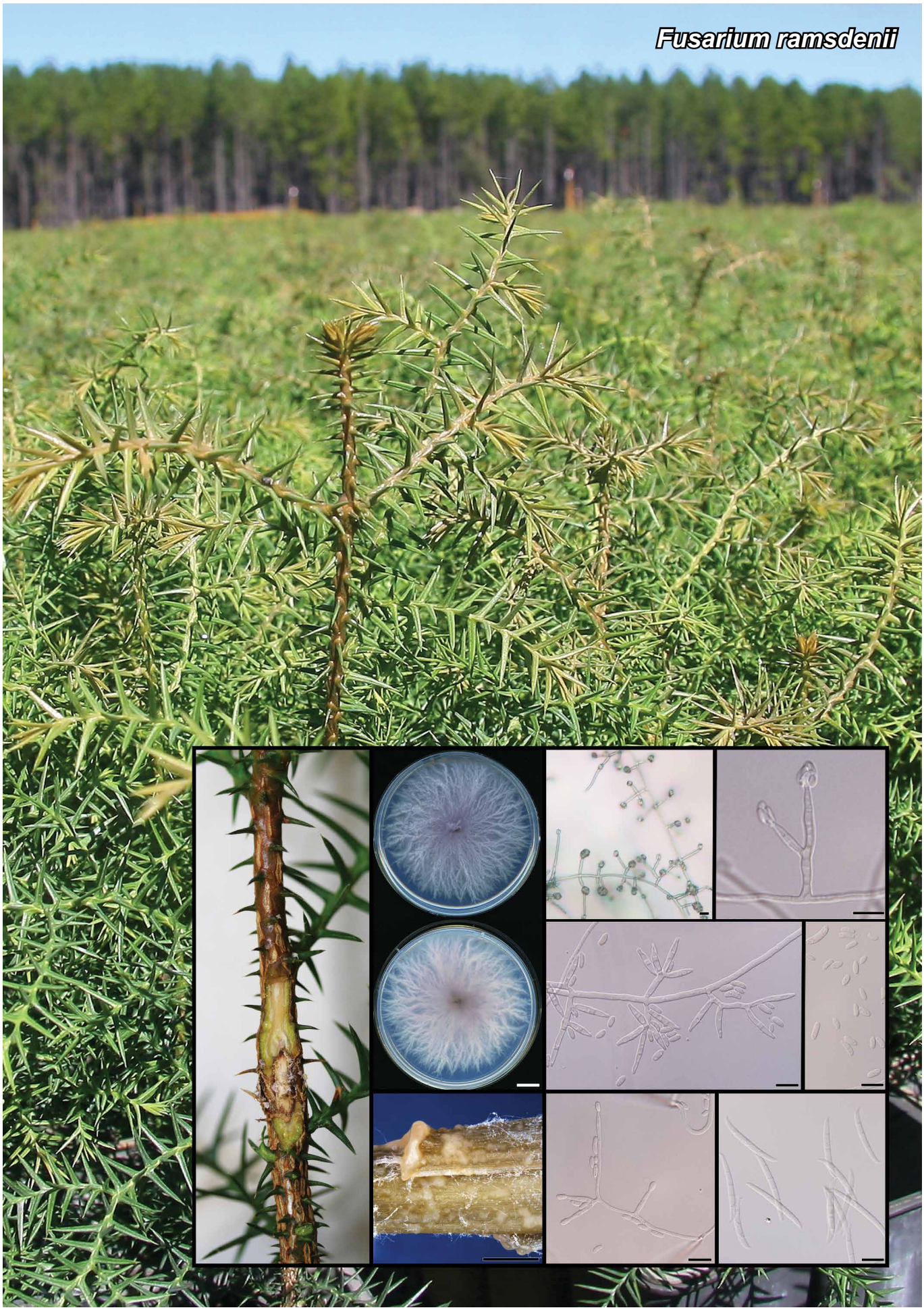

Fusarium ramsdenii

Fungal Planet 1435 – 12 July 2022

Fusarium ramsdenii Y.P. Tan, Pegg, A.G. Manners, A.W. Cooke & R.G. Shivas, *sp. nov.*

Etymology. Named after Michael Ramsden, an Australian forest health specialist, who has decades of experience protecting forest plantations in Queensland from major insect pests and fungal pathogens.

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

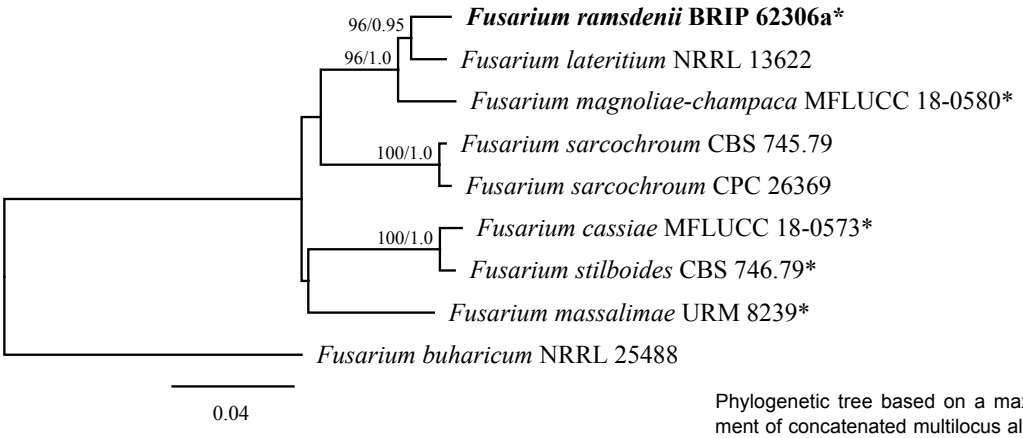
Characters on CLA. Aerial mycelium absent or sparsely developed. *Sporodochia* formed on carnation leaf pieces. *Conidiophores* formed laterally on hyphae or terminal, simple or branched. *Conidiogenous cell*s monophialides and rarely polyphialides, abundant on sporodochia and mycelium on agar, cylindrical to lageniform, 7–70 × 2–3 um, sometimes in terminal whorls. *Microconidia* produced on agar and carnation leaf pieces, formed singly or in false heads, 0–1-septate, elliptical to oval or cylindrical, straight or slightly curved, 4.5–16 × 2–4 um, hyaline. *Macroconidia* produced in the sporodochia apparent as cream-coloured slimy patches, fusiform, straight to slightly curved, 32–42 × 3–4 um, tapered towards the ends, apical cell papillate, basal cell notched, 3–4-septate, hyaline. *Chlamydospores* absent.

Culture characteristics — Colonies on (PDA) growing under 12 h ultraviolet light / 12 h dark cycle reach 6 cm diam after 4 wk at 23 °C, with sparse aerial mycelium. Colony pale violet becoming paler towards the irregularly filamentous margin, surface of colony with irregularly branched radial strands, reverse similar to the upper surface.

Typus. Australia, Queensland, Toolara, from stem canker of *Araucaria cunninghamii* (*Auracariaceae*), 19 Mar. 2015, *M. Ramsden* (holotype BRIP 62306a, preserved in a metabolically inactive state; culture ex-type BRIP 62306a; LSU, ITS, *rpb2*, *tef1* and *tub2* sequences GenBank OL330777, OL330776, OL332733, OL332732 and OL332734; MycoBank MB 843258).

Notes — *Fusarium ramsdenii* is phylogenetically related to members of the *Fusarium lateritium* species complex. *Fusarium ramsdenii* differs from *F. lateritium* sensu Geiser et al. (2005) by sequence comparison of *rpb2* (GenBank JX171571.1; Identities 842/859 (98 %)) and *tef1* (GenBank AY707173.1; Identities 613/632 (97 %)). Several species, *F. oxysporum*, *F. robustum* and *F. solani* (= *Neocosmospora solani*), have been isolated from *Araucaria* spp. in Argentina (Gerlach 1977) and Australia (Kamara et al. 1981). The identity of these isolates was not determined by molecular methods. Colonies of *F. ramsdenii* produced microconidia and a violet pigment, which differed from *F. lateritium* as described by Gerlach & Nirenberg (1982).

Araucaria cunninghamii seedlings with sunken stem cankers girdling the main stem about 3 cm above the soil line were found in about 1 % of plants in a production nursery in 2014. Samples were submitted for diagnostic testing to Grow Help Australia in 2015. Isolates of *Fusarium* from the discoloured vascular tissue were consistently obtained on PDA amended with streptomycin (SPDA). A single conidial culture of isolate BRIP 62306 was used in pathogenicity studies on stems with and without wounds made by a sterile scalpel. Stems were inoculated by placing a disc of either colonised or sterile SPDA on the wound, which were then wrapped in Parafilm. Five replicates were completed for each treatment. Plants were kept under high humidity for 1 wk (enclosed in plastic bags) and then grown without plastic bags in glasshouses. All plants were assessed 4 wk after inoculation. Cankers exuding resin were found only in seedlings that had been both wounded and inoculated. These symptomatic plants also had discoloured purplish vascular tissue below the cankers. All other treatments were asymptomatic. *Fusarium ramsdenii* was only reisolated from the cankers on inoculated and wounded seedlings, fulfilling Koch's postulates.



Phylogenetic tree based on a maximum likelihood analysis of an alignment of concatenated multilocus alignment (*rpb2* and *tef1*) from *Fusarium lateritium* species complex. Analysis was performed on the Geneious Prime 2022 platform using RAxML v. 8.2.11, based on the GTR substitution model with gamma-distribution rate variation. Bayesian posterior probabilities (pp) and RAxML bootstrap values (bs) are given at the nodes (bs/pp). *Fusarium buharicum* strain NRRL 25488 was used as the outgroup. Branch lengths are proportional to substitutions per site. Novel taxon is indicated in **bold**. Ex-type strains are marked with an asterisk (*).

Colour illustrations. Araucaria cunninghamii seedlings in a nursery in south-east Queensland (image by Michael Ramsden); seedling stem canker symptoms (left); upper and reverse surfaces of colonies on half-strength PDA (top and middle rows); microconidia in false heads (top row); phialides in whorls (middle row); microconidia (middle row); sporodochia on carnation leaf pieces (bottom row); conidiophores and microconidia; monophialides (bottom row); macroconidia (bottom row). Scale bars = 1 cm (plates), 1 mm (sporodochia), 10 µm (others).

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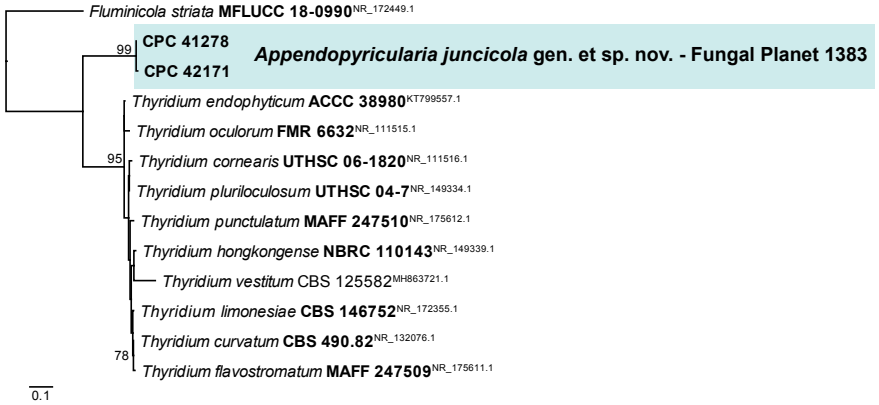
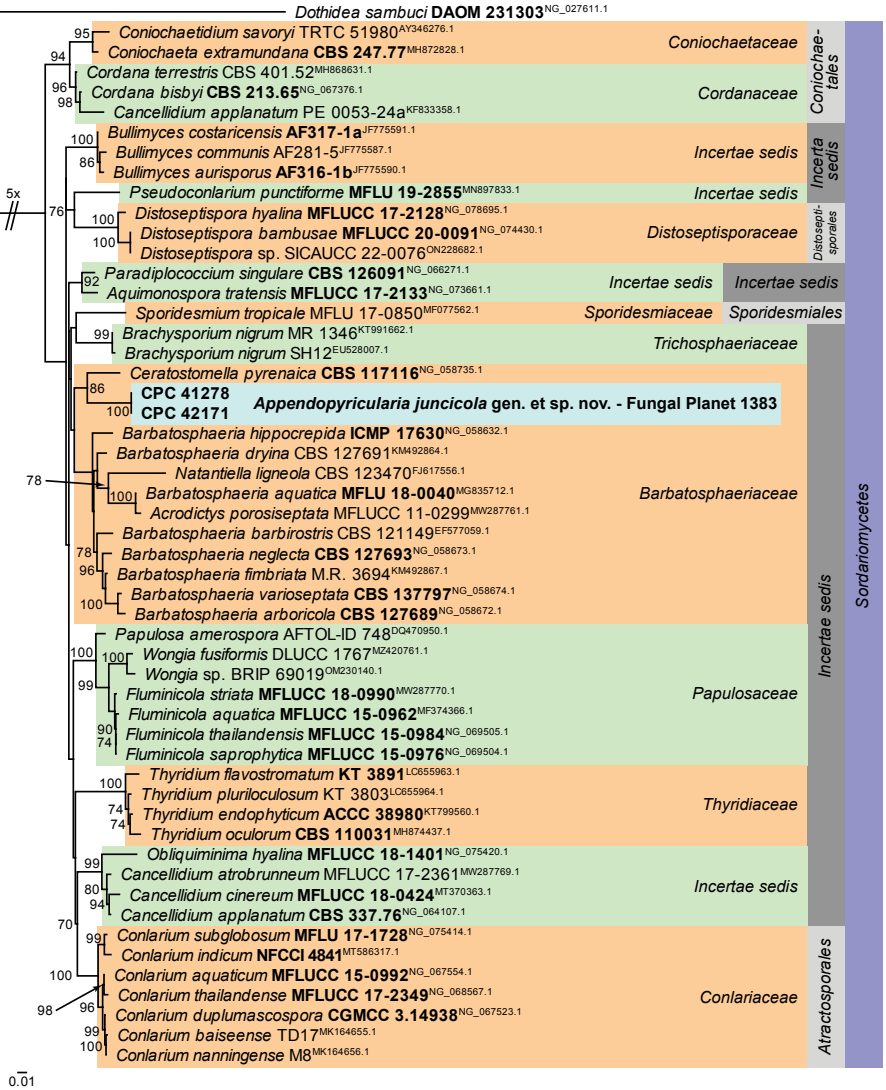
Fungal Planet 1383 – *Appendopyricularia juncicola*

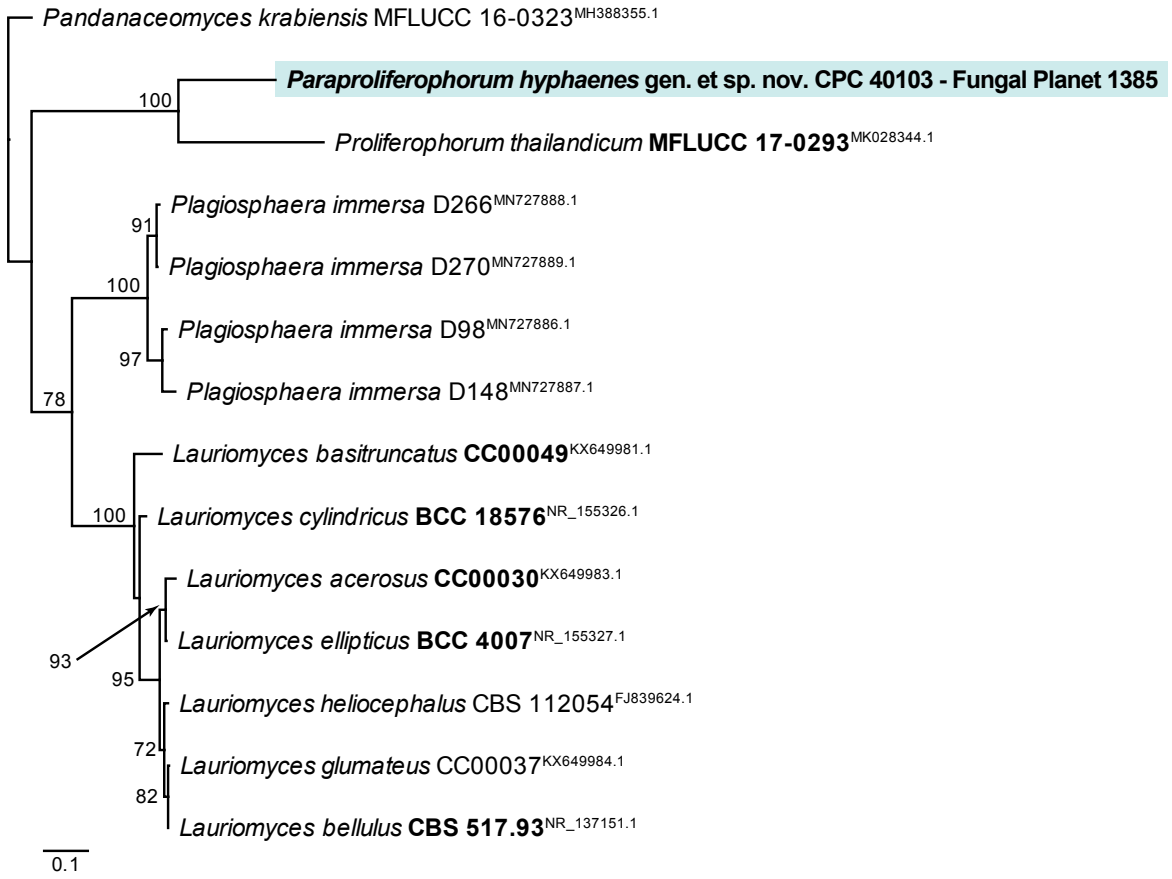


FP1383-1 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Appendopyricularia juncicola* ITS nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast (Hoang et al. 2018) 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 *Fluminicola striata* (culture MFLUCC 18-0990; GenBank NR_172449.1) 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: 13 strains including the outgroup; 545 characters including alignment gaps analysed: 159 distinct patterns, 94 parsimony-informative, 76 singleton sites, 375 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was TIM2e+R2. The alignment and tree were deposited at figshare.com (10.6084/m9.figshare.19745380).



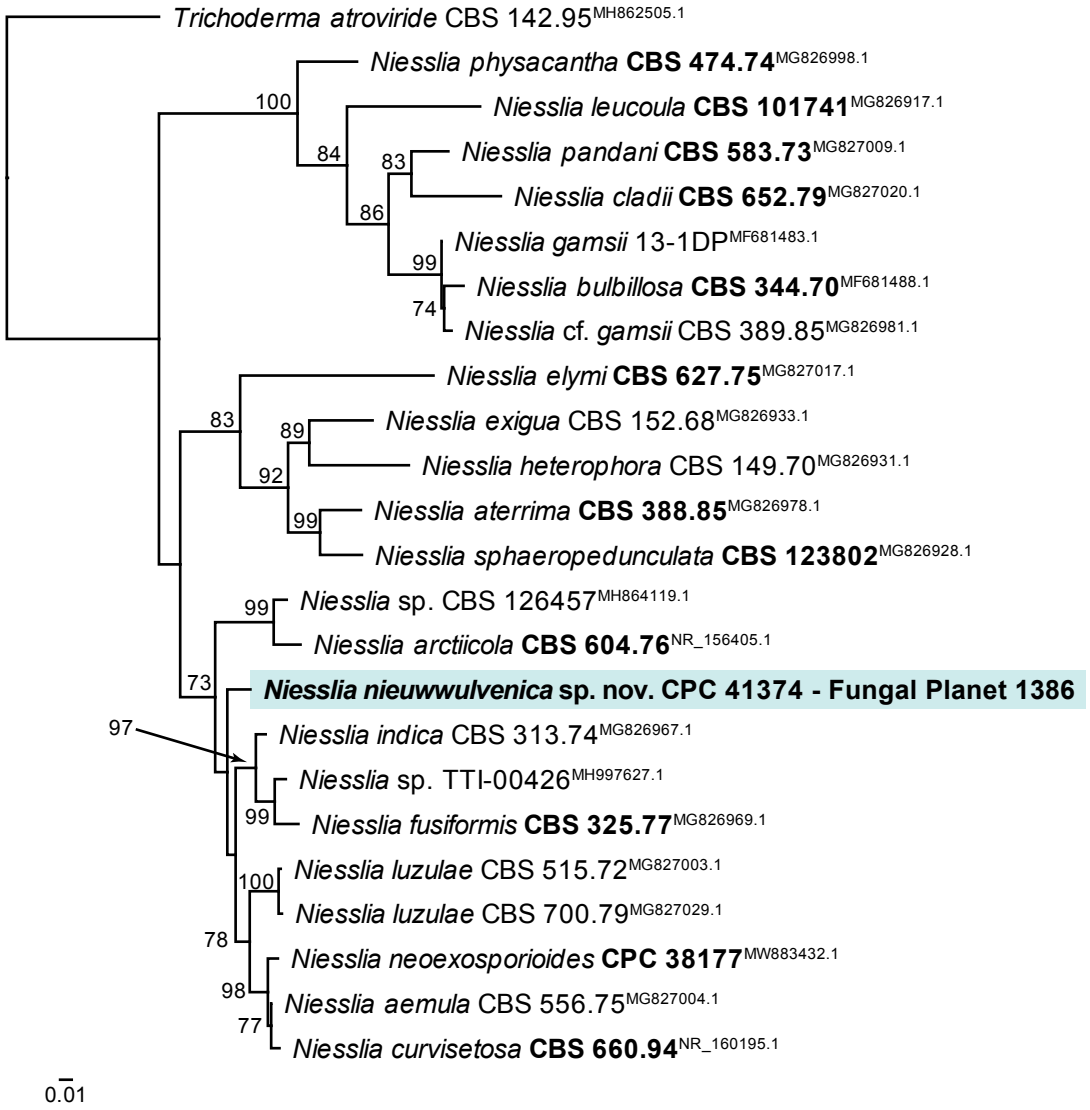
FP1383-2 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Appendopyricularia juncicola* LSU nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast (Hoang et al. 2018) 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 *Dothidea sambuci* (culture DAOM 231303; GenBank NG_027611.1) 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: 53 strains including the outgroup; 857 characters including alignment gaps analysed: 245 distinct patterns, 152 parsimony-informative, 82 singleton sites, 623 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was TIM3e+R4. The alignment and tree were deposited at figshare.com (10.6084/m9.figshare.19745380).

Fungal Planet 1385 – *Paraproliferophorum hyphaenes*



FP1385 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Paraproliferophorum hyphaenes* ITS nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5000 ultrafast (Hoang et al. 2018) 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 *Pandanaceomyces krabiensis* (culture MFLUCC 16-0323; GenBank MH388355.1) 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: 14 strains including the outgroup; 677 characters including alignment gaps analysed: 330 distinct patterns, 180 parsimony-informative, 139 singleton sites, 358 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was TNe+R2. The alignment and tree were deposited at figshare.com (10.6084/m9.figshare.19745380).

Fungal Planet 1386 – *Niesslia nieuwwulvenica*



FP1386 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Niesslia nieuwwulvenica* ITS nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast (Hoang et al. 2018) 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 *Trichoderma atroviride* (culture CBS 142.95; GenBank MH862505.1) 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: 24 strains including the outgroup; 698 characters including alignment gaps analysed: 321 distinct patterns, 164 parsimony-informative, 94 singleton sites, 440 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was TIM2+F+G4. The alignment and tree were deposited at figshare.com (10.6084/m9.figshare.19745380).

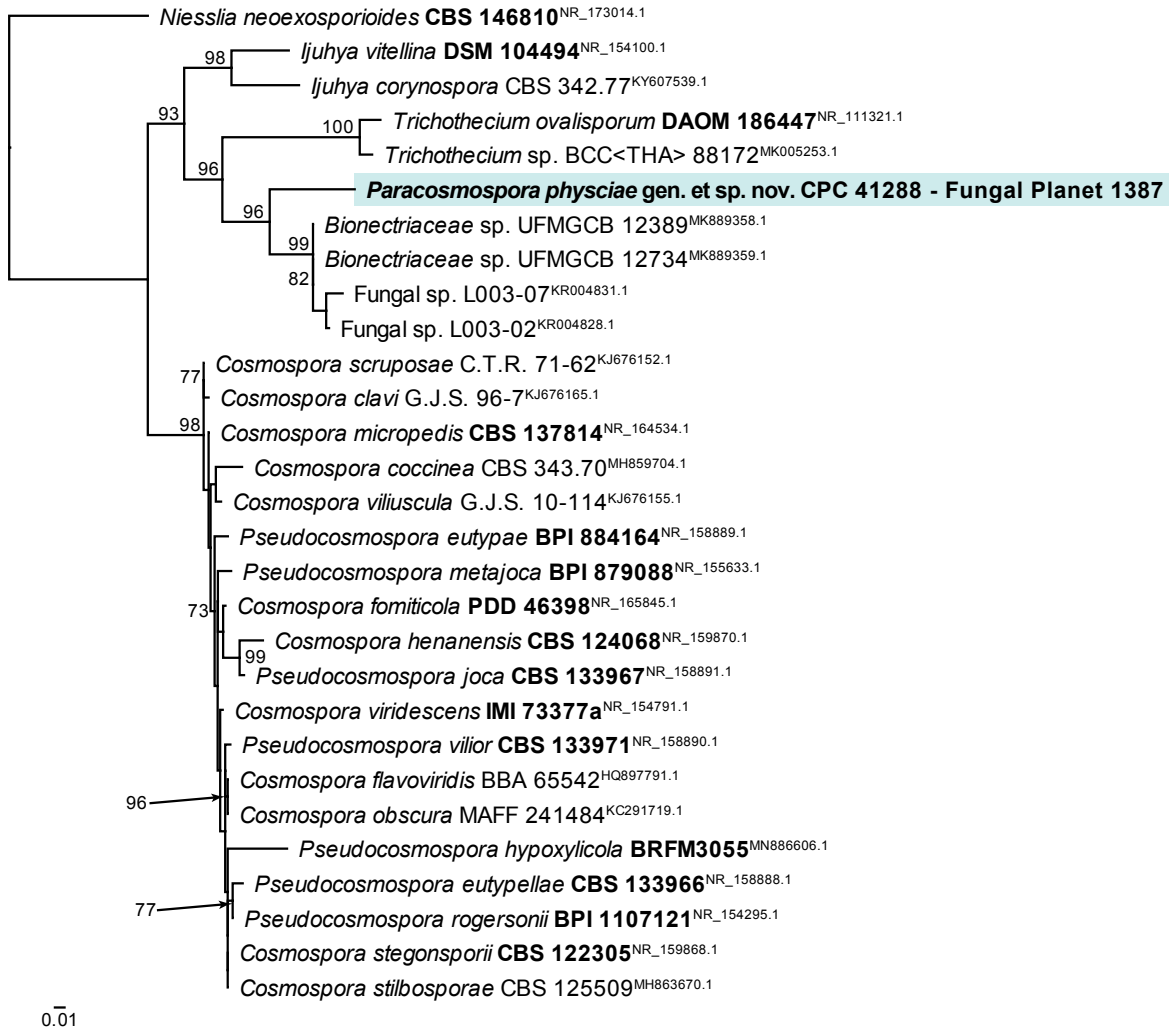
Fungal Planet 1387 & 1388 – *Paracosmospora physciae & Gonatophragmium physciae*

(Notes *Paracosmospora physciae* continued)

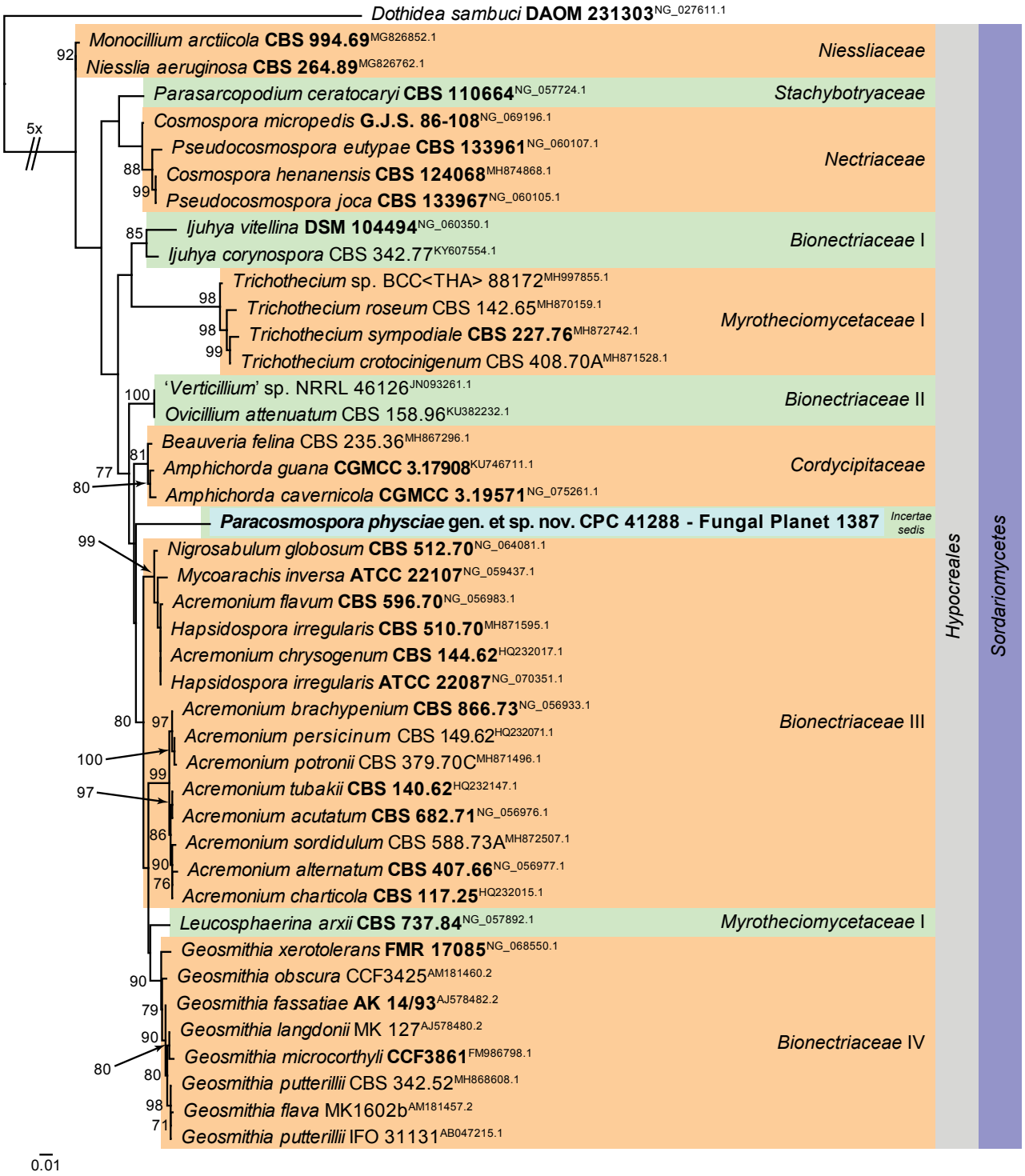
Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pseudocosmospora vilior* (strain P.C. 1246, GenBank KC291738.1; Identities = 506/571 (89 %), 34 gaps (5 %)), *Pseudocosmospora eutypellae* (strain CBS 133966, GenBank NR_158888.1; Identities = 504/572 (88 %), 36 gaps (6 %)) and *Acremonium domschii* (strain CBS 385.70B, GenBank MH859747.1; Identities = 500/569 (88 %), 35 gaps (6 %)). Closest hits using the **LSU** sequence are *Acremonium acutatum* (strain CBS 682.71, GenBank MH872055.1; Identities = 802/844 (95 %), six gaps (0 %)), *Amphichorda guana* (strain LC5815, GenBank KU746711.1; Identities = 801/843 (95 %), six gaps (1 %)) and *Acremonium flavum* (strain CBS 596.70, GenBank MH871649.1; Identities = 801/844 (95 %), six gaps (0 %)). No significant hits were obtained when the ***tef1*** (first part) sequence was used in blastn and megablast searches.

(Notes *Gonatophragmium physciae* continued)

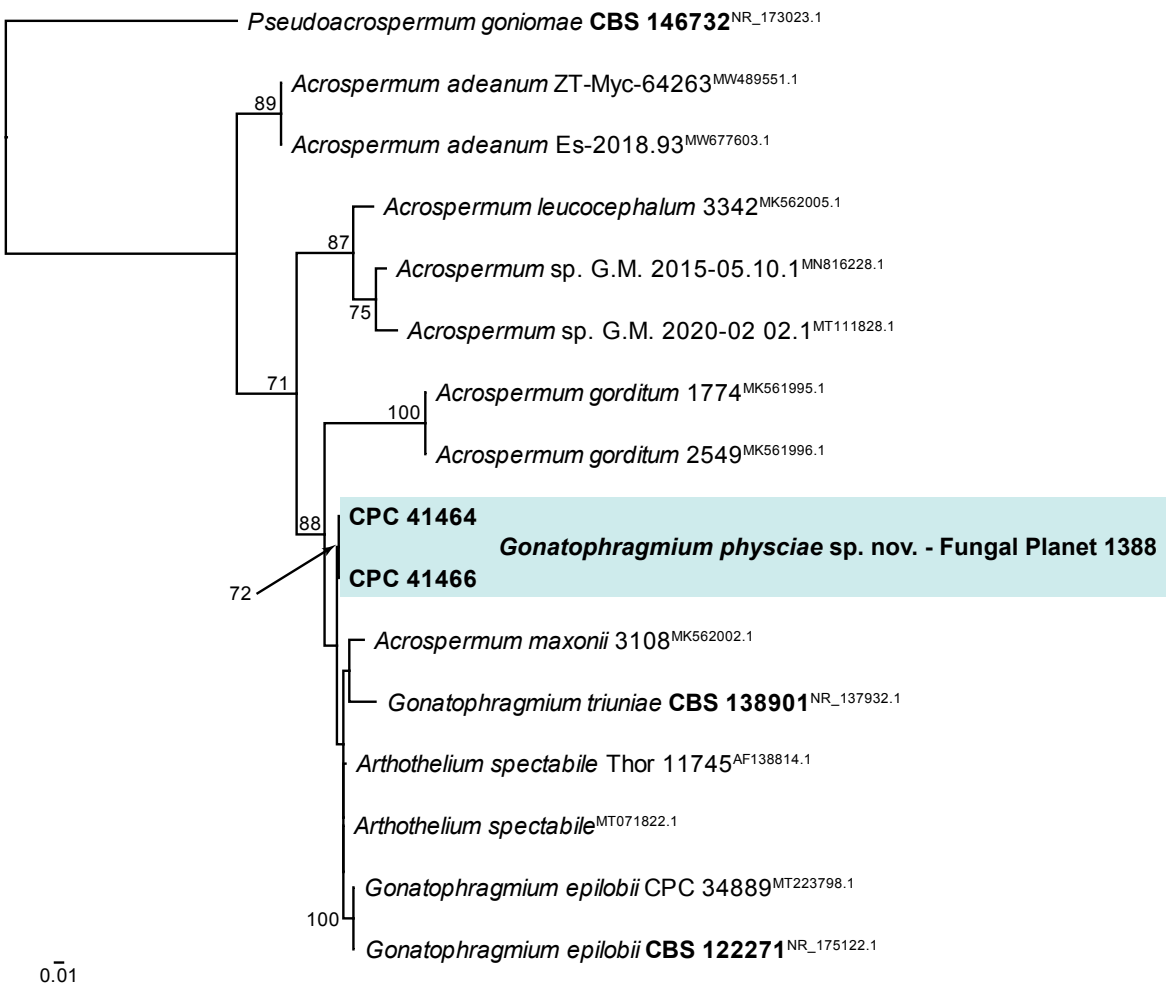
Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 41464 had highest similarity to *Arthothelium spectabile* (strain 190821-029, GenBank MT071823.1; Identities = 485/490 (99 %), one gap (0 %)), *Gonatophragmium epilobii* (strain CBS 122271, GenBank NR_175122.1; Identities = 479/489 (98 %), one gap (0 %)) and *Acrospermum maxonii* (voucher 3381, GenBank MK562006.1; Identities = 507/519 (98 %), one gap (0 %)). The ITS sequences of CPC 41464 and 41466 are identical (518/518 nt). Closest hits using the **LSU** sequence of CPC 41464 are *Acrospermum maxonii* (voucher 3381, GenBank MK561989.1; Identities = 775/776 (99 %), no gaps), *Gonatophragmium epilobii* (strain CPC 34889, GenBank MT223893.1; Identities = 808/811 (99 %), no gaps) and *Gonatophragmium triuniae* (strain CBS 138901, GenBank NG_058117.1; Identities = 808/812 (99 %), no gaps). The LSU sequences of CPC 41464 and 41466 are identical (822/822 nt).



FP1387-1 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Paracosmospora physciae* ITS nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast (Hoang et al. 2018) 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 *Niesslia neoexosporioides* (culture CBS 146810; GenBank NR_173014.1) 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: 29 strains including the outgroup; 629 characters including alignment gaps analysed: 226 distinct patterns, 107 parsimony-informative, 71 singleton sites, 451 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was TIM2+F+I+G4. The alignment and tree were deposited at figshare.com (10.6084/m9.figshare.19745380).

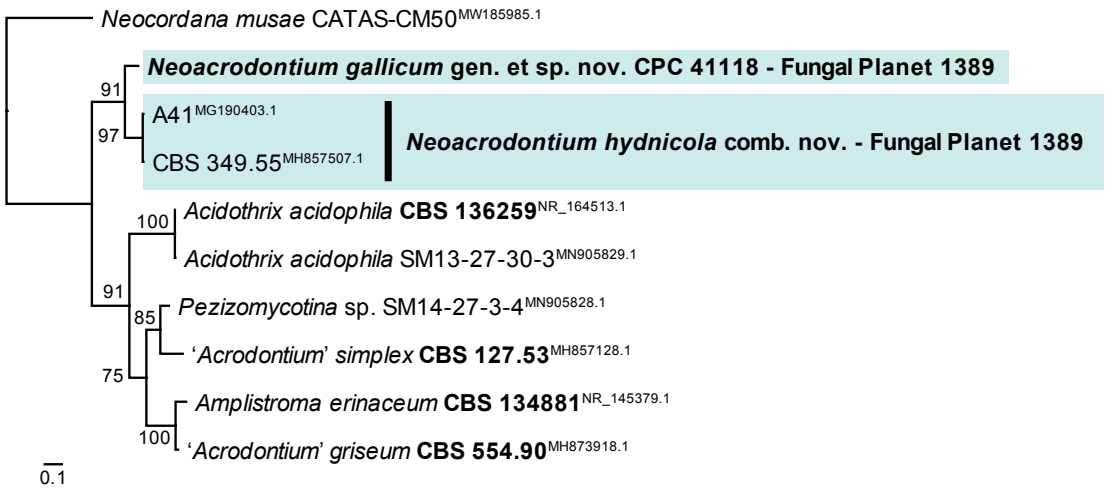


FP1387-2 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Paracosmospora physciae* LSU nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast (Hoang et al. 2018) 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 *Dothidea sambuci* (culture DAOM 231303; GenBank NG_027611.1) 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: 43 strains including the outgroup; 904 characters including alignment gaps analysed: 285 distinct patterns, 113 parsimony-informative, 94 singleton sites, 697 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was TNe+I+G4. The alignment and tree were deposited at figshare.com (10.6084/m9.figshare.19745380).

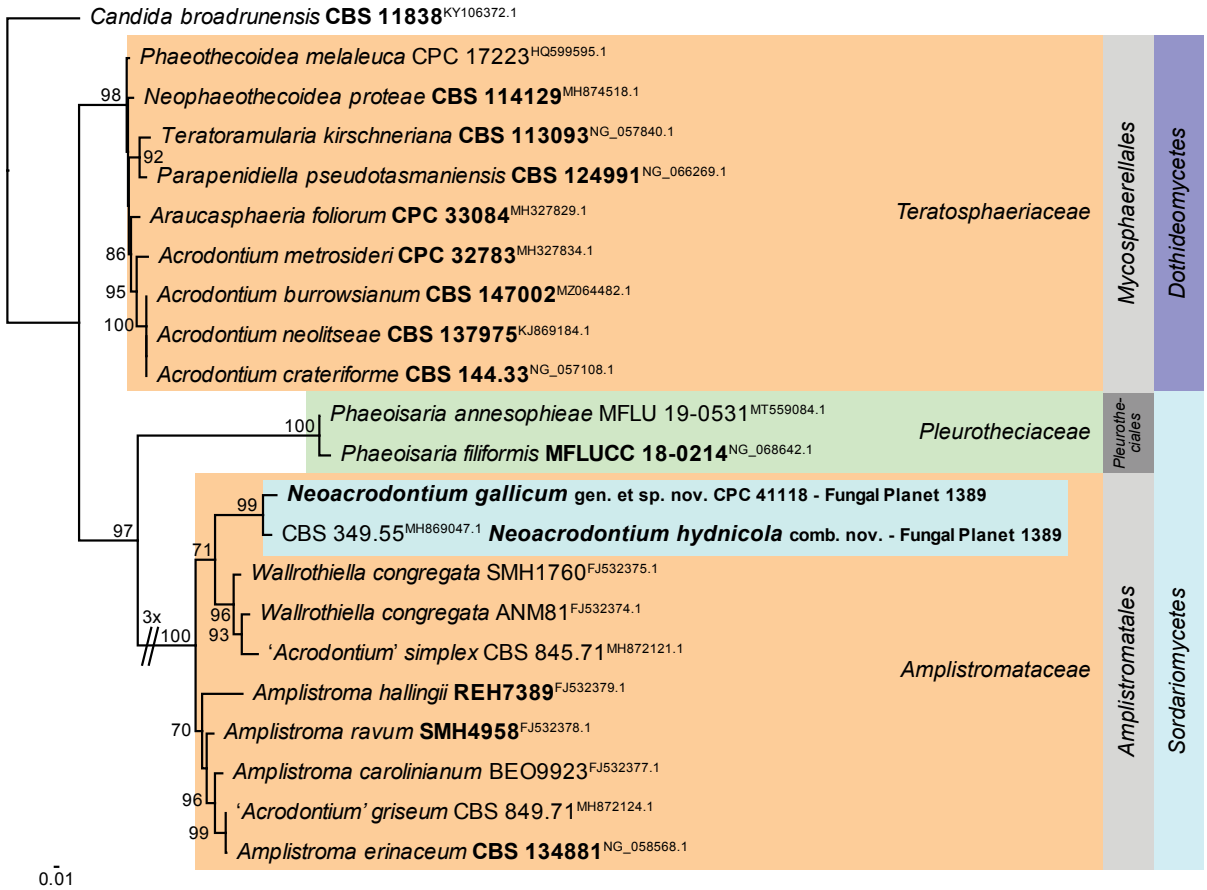


FP1388 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Gonatophragmium physciae* ITS nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast (Hoang et al. 2018) 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 *Pseudoacrospermum goniomae* (culture CBS 146732; GenBank NR_173023.1) 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: 16 strains including the outgroup; 554 characters including alignment gaps analysed: 165 distinct patterns, 105 parsimony-informative, 50 singleton sites, 399 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was TNe+G4. The alignment and tree were deposited at figshare.com (10.6084/m9.figshare.19745380).

Fungal Planet 1389 – *Neoacrodontium gallicum*

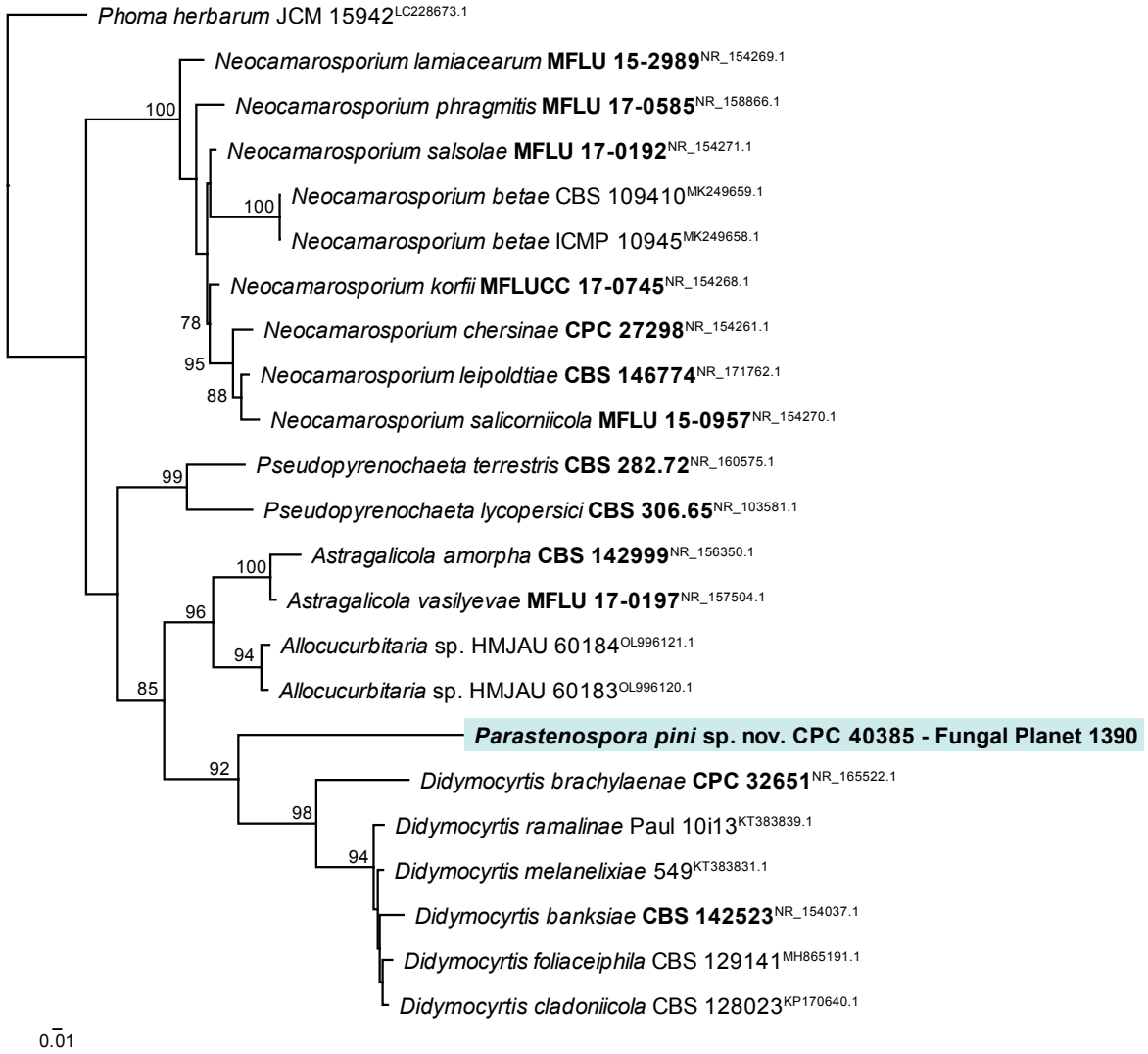


FP1389-1 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Neoacrodontium gallicum* and *Neoacrodontium hydnicola* ITS nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5000 ultrafast (Hoang et al. 2018) 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 *Neocordana musae* (culture CATAS-CM50; GenBank MW185985.1) and the novelties described here are highlighted with coloured blocks and **bold** font. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: ten strains including the outgroup; 751 characters including alignment gaps analysed: 357 distinct patterns, 226 parsimony-informative, 107 singleton sites, 418 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was TIM2+F+G4. The alignment and tree were deposited at figshare.com (10.6084/m9.figshare.19745380).



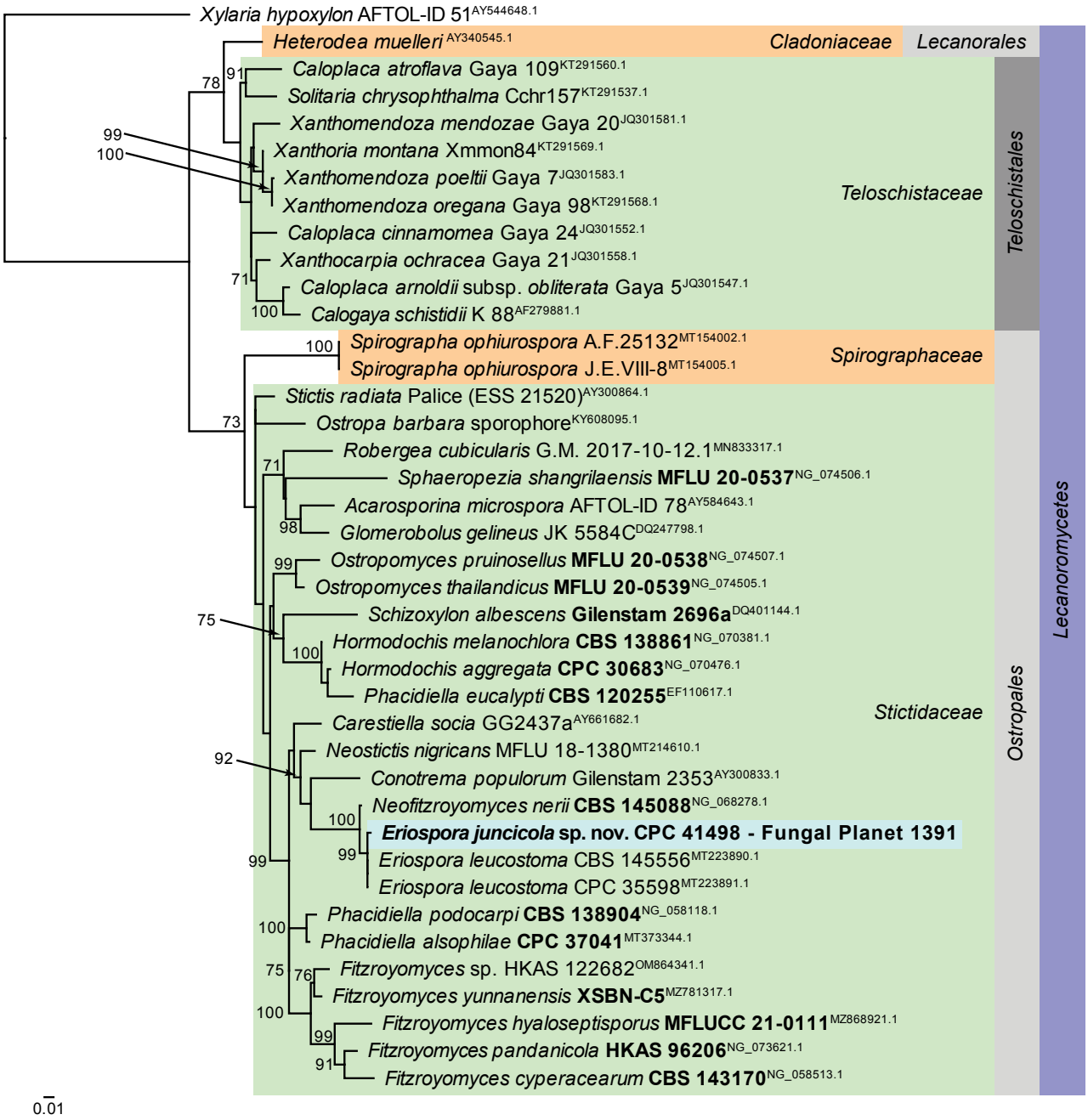
FP1389-2 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Neoacrodontium gallicum* and *Neoacrodontium hydnicola* LSU nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5000 ultrafast (Hoang et al. 2018) 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 *Candida broadrunensis* (culture CBS 11838; GenBank KY106372.1) and the novelties described here are highlighted with coloured blocks and **bold** font. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 22 strains including the outgroup; 976 characters including alignment gaps analysed: 389 distinct patterns, 316 parsimony-informative, 63 singleton sites, 597 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was TN+F+I+G4. The alignment and tree were deposited at figshare.com (10.6084/m9.figshare.19745380).

Fungal Planet 1390 – *Parastenospora pini*



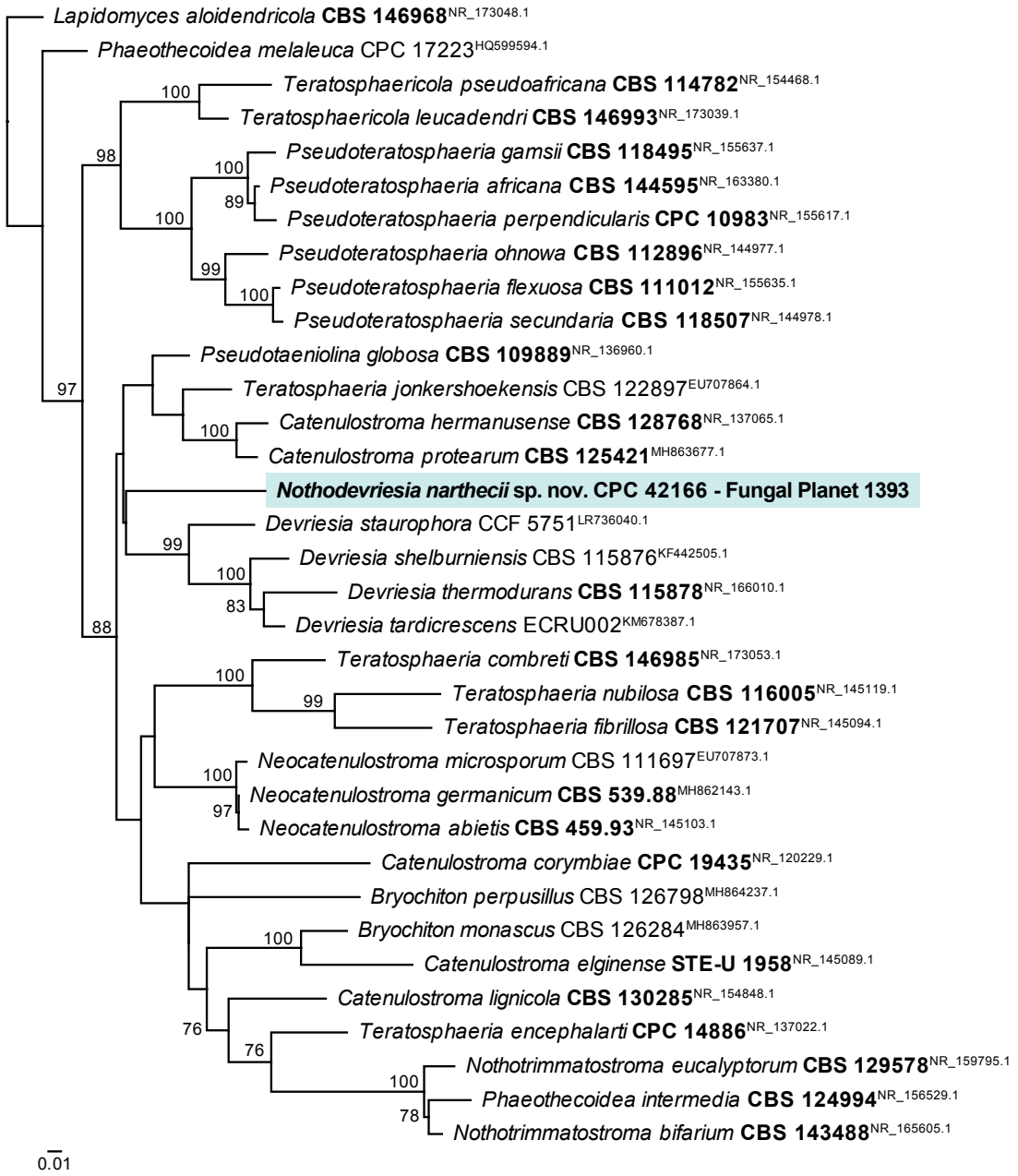
FP1390 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Hyphomycete genus* CPC 40385 ITS nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast (Hoang et al. 2018) 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 *Phoma herbarum* (culture JCM 15942; GenBank LC228673.1) 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: 23 strains including the outgroup; 586 characters including alignment gaps analysed: 268 distinct patterns, 189 parsimony-informative, 34 singleton sites, 363 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was SYM+G4. The alignment and tree were deposited at figshare.com (10.6084/m9.figshare.19745380).

Fungal Planet 1391 – *Eriospora juncicola*

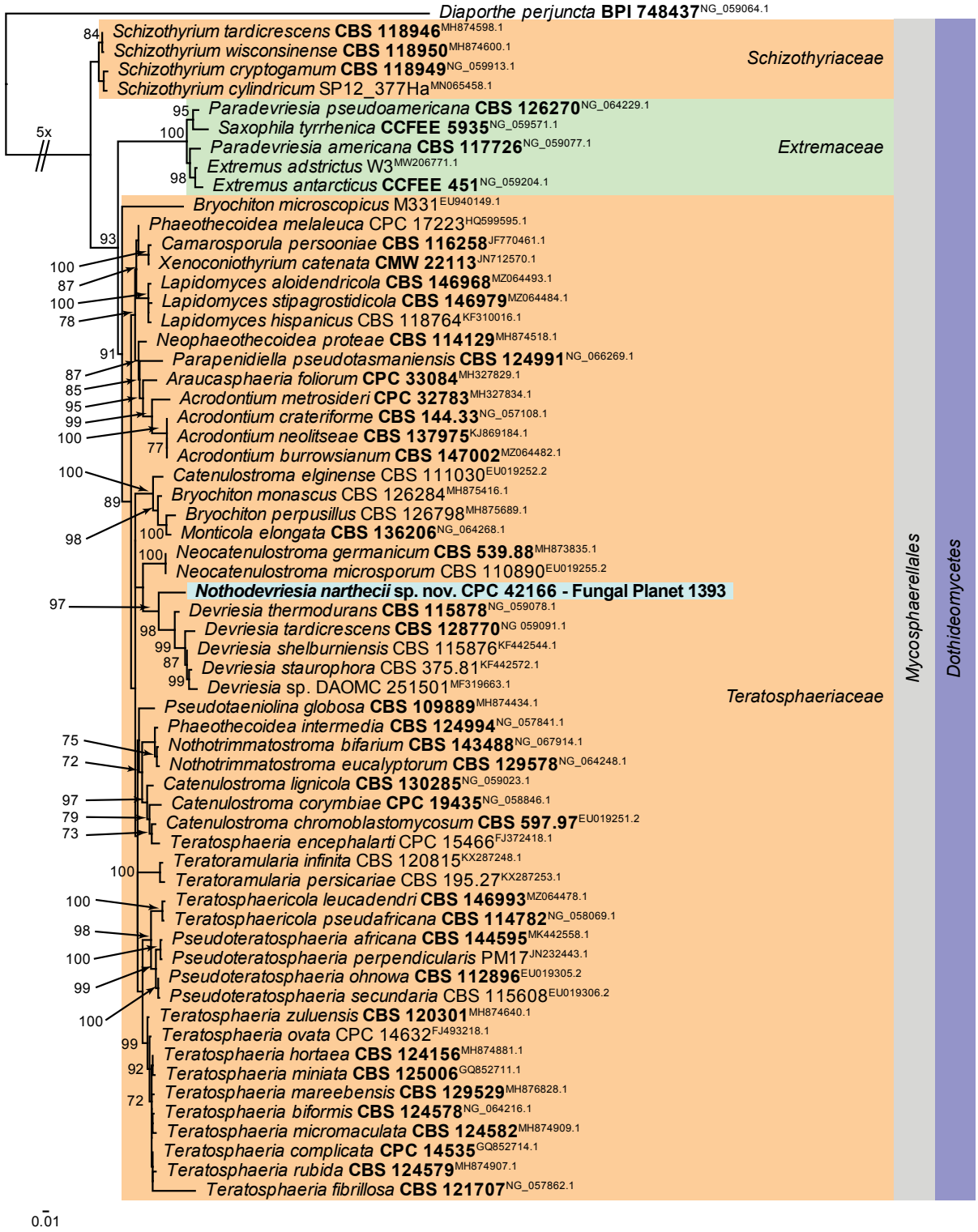


FP1391 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Eriospora juncicola* LSU nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast (Hoang et al. 2018) 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 *Xylaria hypoxylon* (voucher OSC 100004; GenBank AY544648.1) 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: 40 strains including the outgroup; 936 characters including alignment gaps analysed: 351 distinct patterns, 205 parsimony-informative, 112 singleton sites, 619 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was TNe+I+G4. The alignment and tree were deposited at figshare.com (10.6084/m9.figshare.19745380).

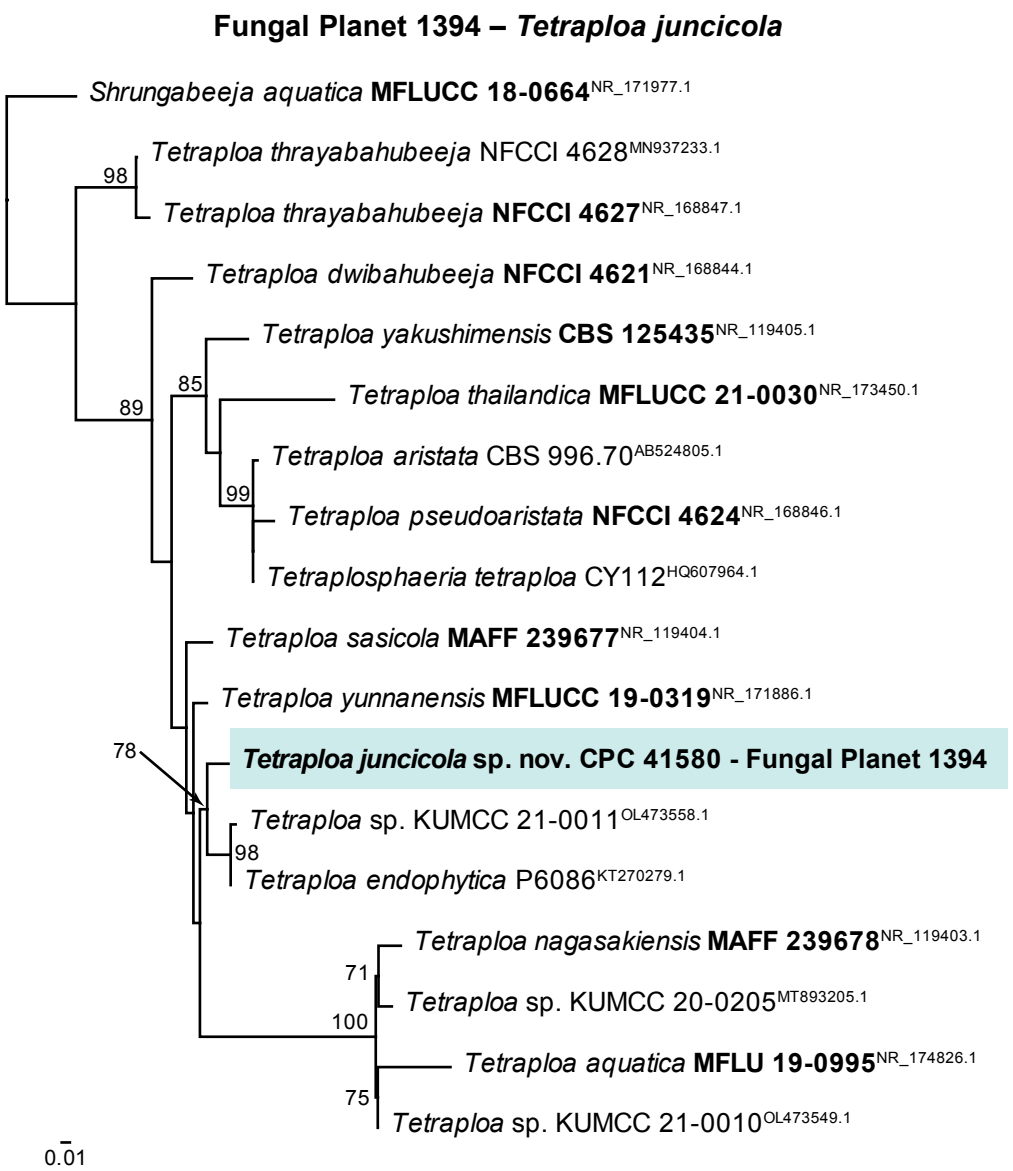
Fungal Planet 1393 – *Nothodevriesia narthecii*



FP1393-1 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Nothodevriesia narthecii* ITS nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast (Hoang et al. 2018) 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 *Lapidomyces aloidendricola* (culture CBS 146968; GenBank NR_173048.1) 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: 34 strains including the outgroup; 560 characters including alignment gaps analysed: 283 distinct patterns, 170 parsimony-informative, 62 singleton sites, 328 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was TIM2e+G4. The alignment and tree were deposited at figshare.com (10.6084/m9.figshare.19745380).

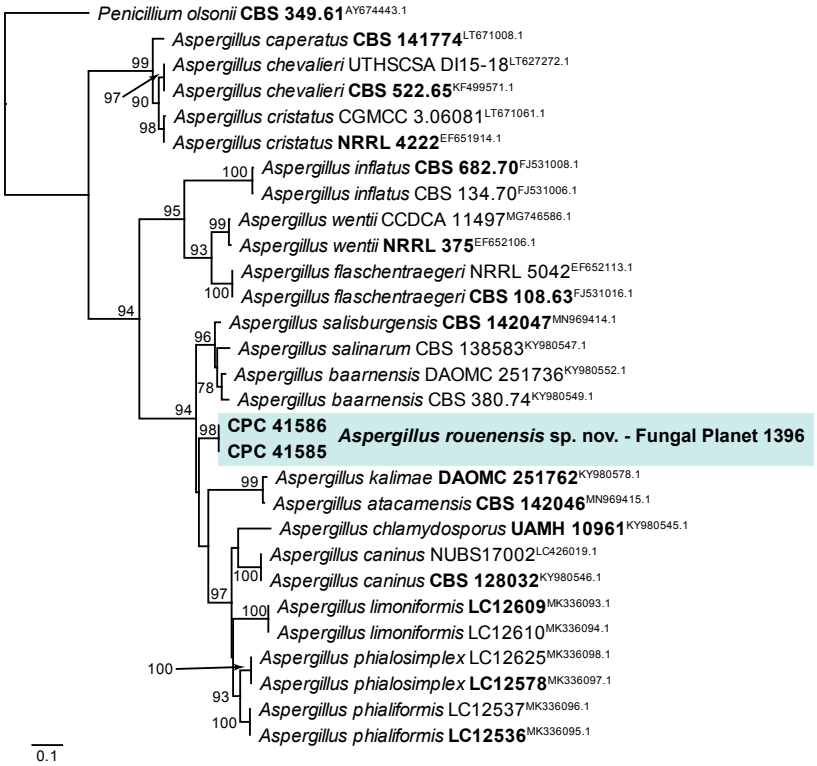


FP1393-2 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Nothodevriesia narthecii* ITS nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast (Hoang et al. 2018) 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 *Diaporthe perjuncta* (voucher BPI_748437; GenBank NG_059064.1) 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: 62 strains including the outgroup; 874 characters including alignment gaps analysed: 279 distinct patterns, 153 parsimony-informative, 102 singleton sites, 619 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was TN+F+I+G4. The alignment and tree were deposited at figshare.com (10.6084/m9.figshare.19745380).

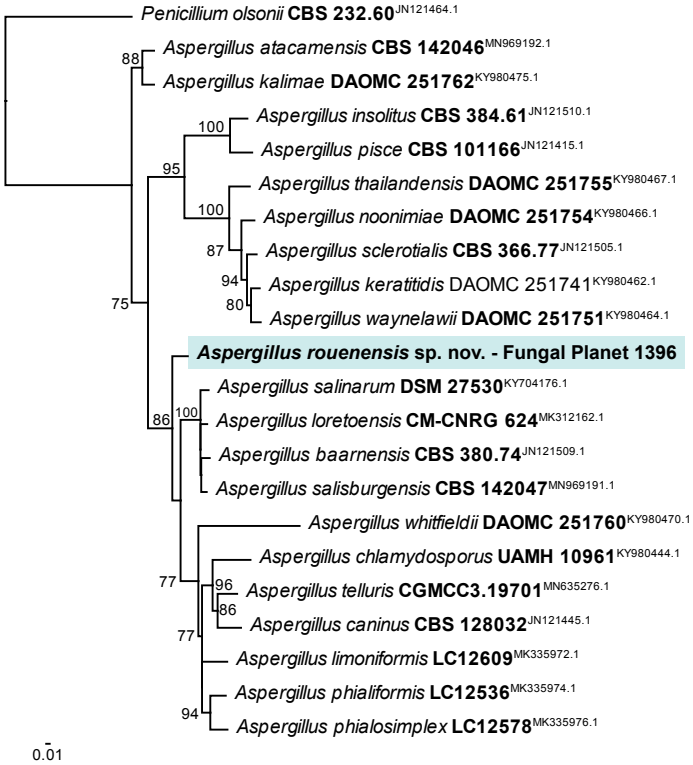


FP1394 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Tetraploa juncicola* ITS nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5000 ultrafast (Hoang et al. 2018) 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 *Shrungabeeja aquatica* (culture MFLUCC 18-0664; GenBank NR_171977.1) 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: 18 strains including the outgroup; 590 characters including alignment gaps analysed: 212 distinct patterns, 127 parsimony-informative, 52 singleton sites, 411 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was TPM2+F+G4. The alignment and tree were deposited at figshare.com (10.6084/m9.figshare.19745380).

Fungal Planet 1396 – *Aspergillus rouenensis*

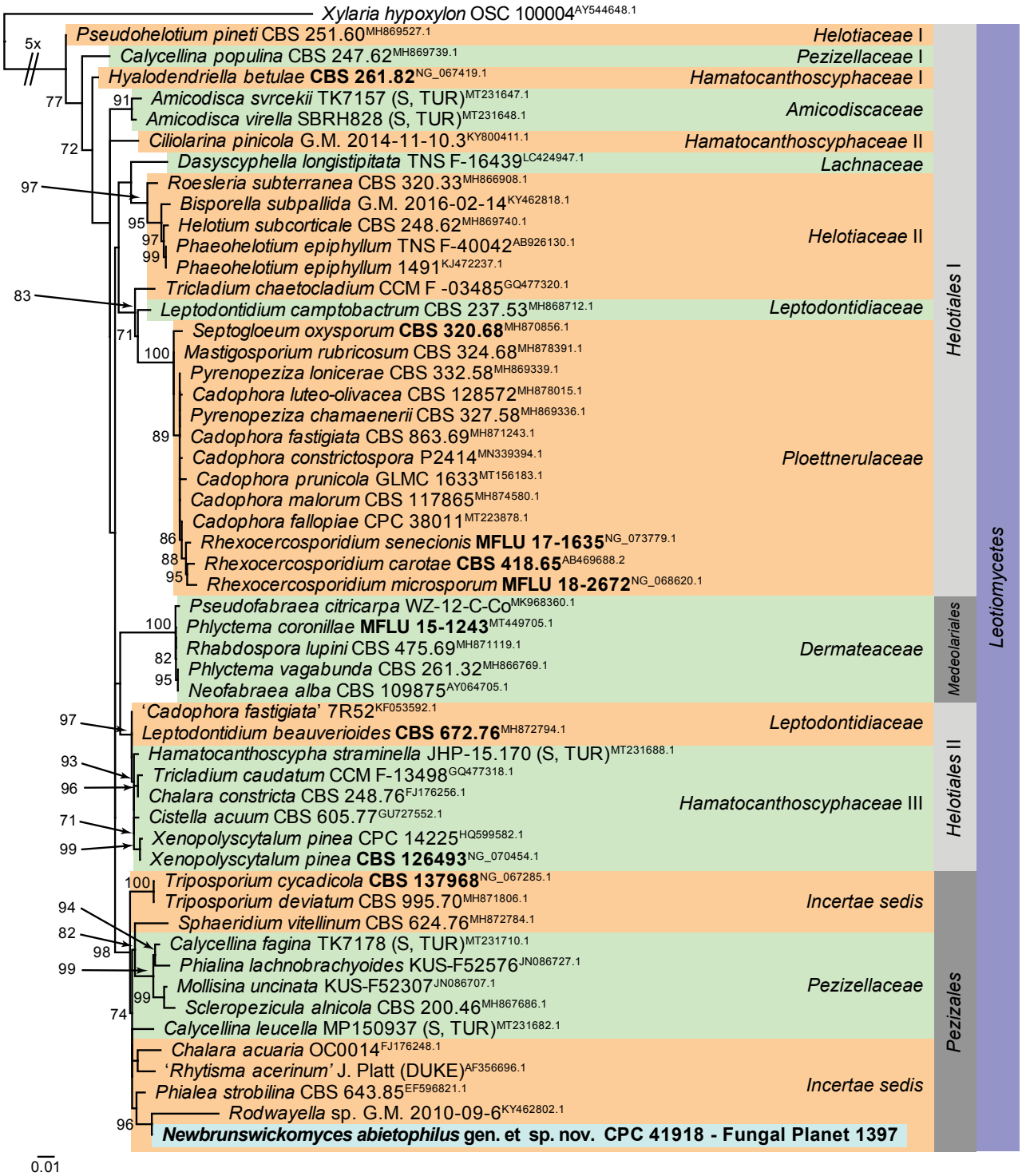


FP1396-1 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Aspergillus rouenensis BenA* nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast (Hoang et al. 2018) 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 *Penicillium olsonii* (culture CBS 349.61; GenBank AY674443.1) 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: 29 strains including the outgroup; 521 characters including alignment gaps analysed: 327 distinct patterns, 242 parsimony-informative, 34 singleton sites, 245 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was TNe+G4. The alignment and tree were deposited at figshare.com (10.6084/m9.figshare.19745380).



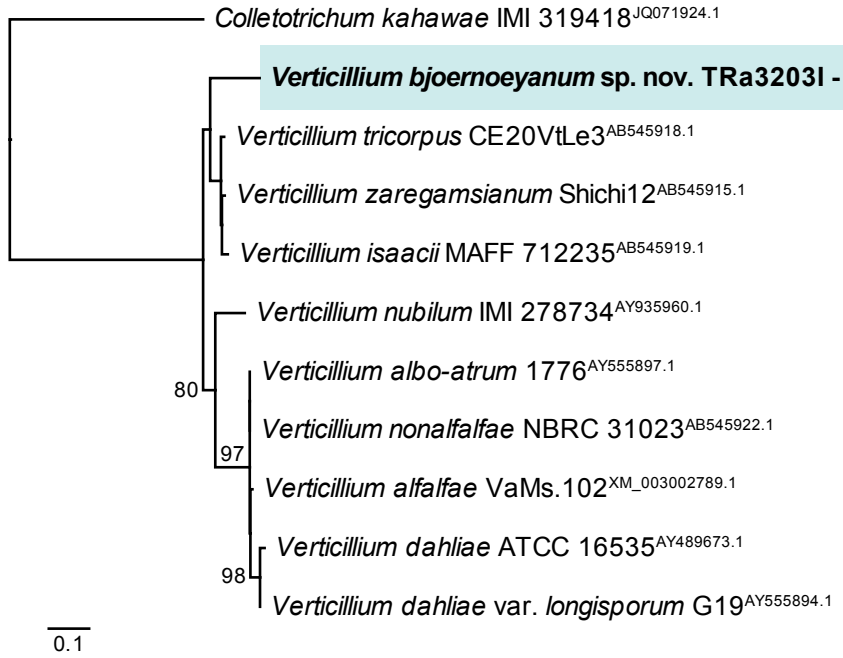
FP1396-2 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Aspergillus rouenensis rpb2* nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast (Hoang et al. 2018) 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 *Penicillium olsonii* (culture CBS 349.61; GenBank JN121464.1) 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: 22 strains including the outgroup; 957 characters including alignment gaps analysed: 413 distinct patterns, 302 parsimony-informative, 80 singleton sites, 575 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was TN+F+G4. The alignment and tree were deposited at figshare.com (10.6084/m9.figshare.19745380).

Fungal Planet 1397 – *Newbrunswickomyces abietophilus*



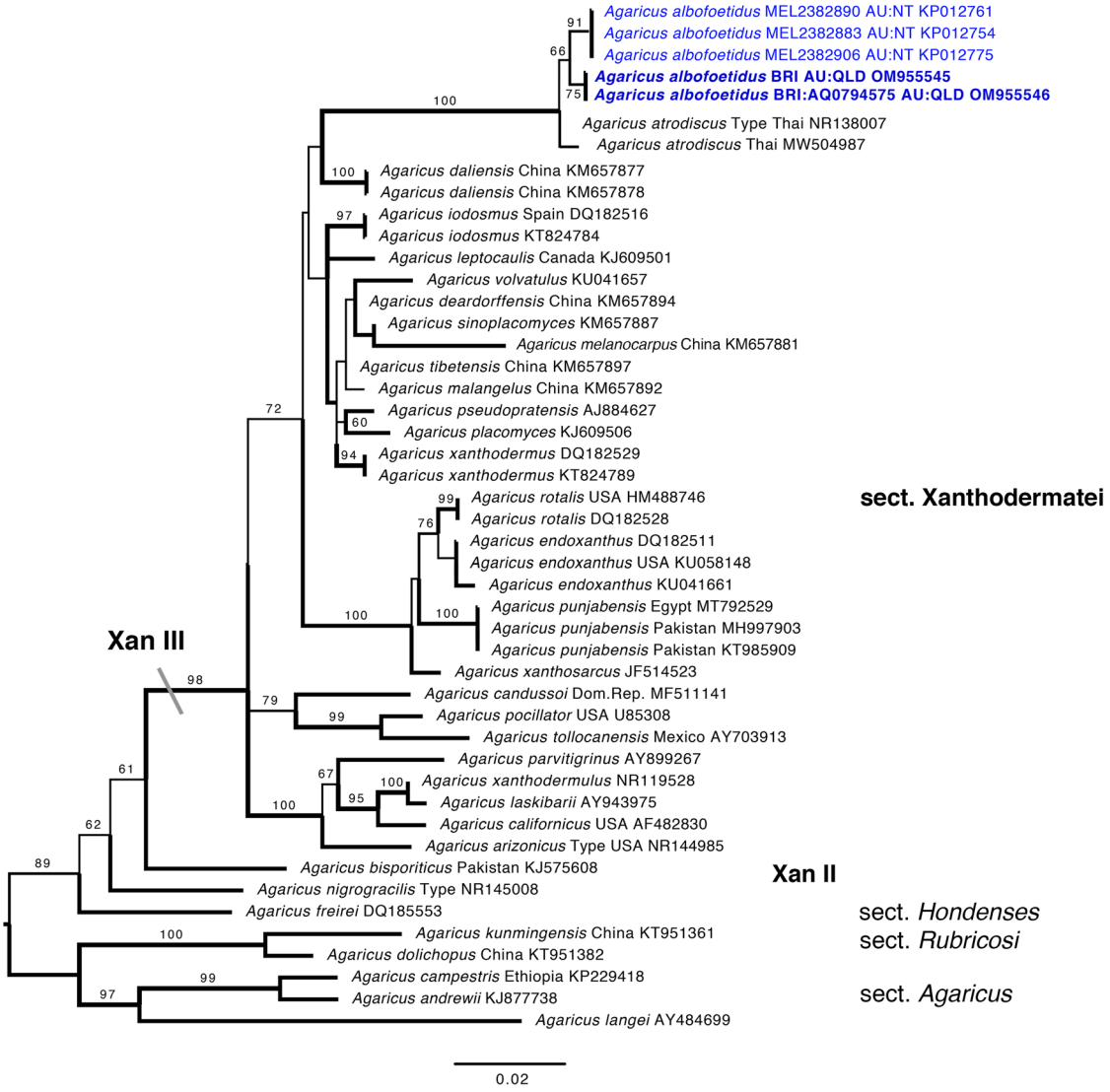
FP1397 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Newbrunswickomyces abietophilus* LSU nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5000 ultrafast (Hoang et al. 2018) 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 *Xylaria hypoxylon* (voucher OSC 100004; GenBank AY544648.1) 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: 54 strains including the outgroup; 881 characters including alignment gaps analysed: 212 distinct patterns, 100 parsimony-informative, 90 singleton sites, 691 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was TN+F+R3. The alignment and tree were deposited at figshare.com (10.6084/m9.figshare.19745380).

Fungal Planet 1399 – *Verticillium bjoernoeyanu*



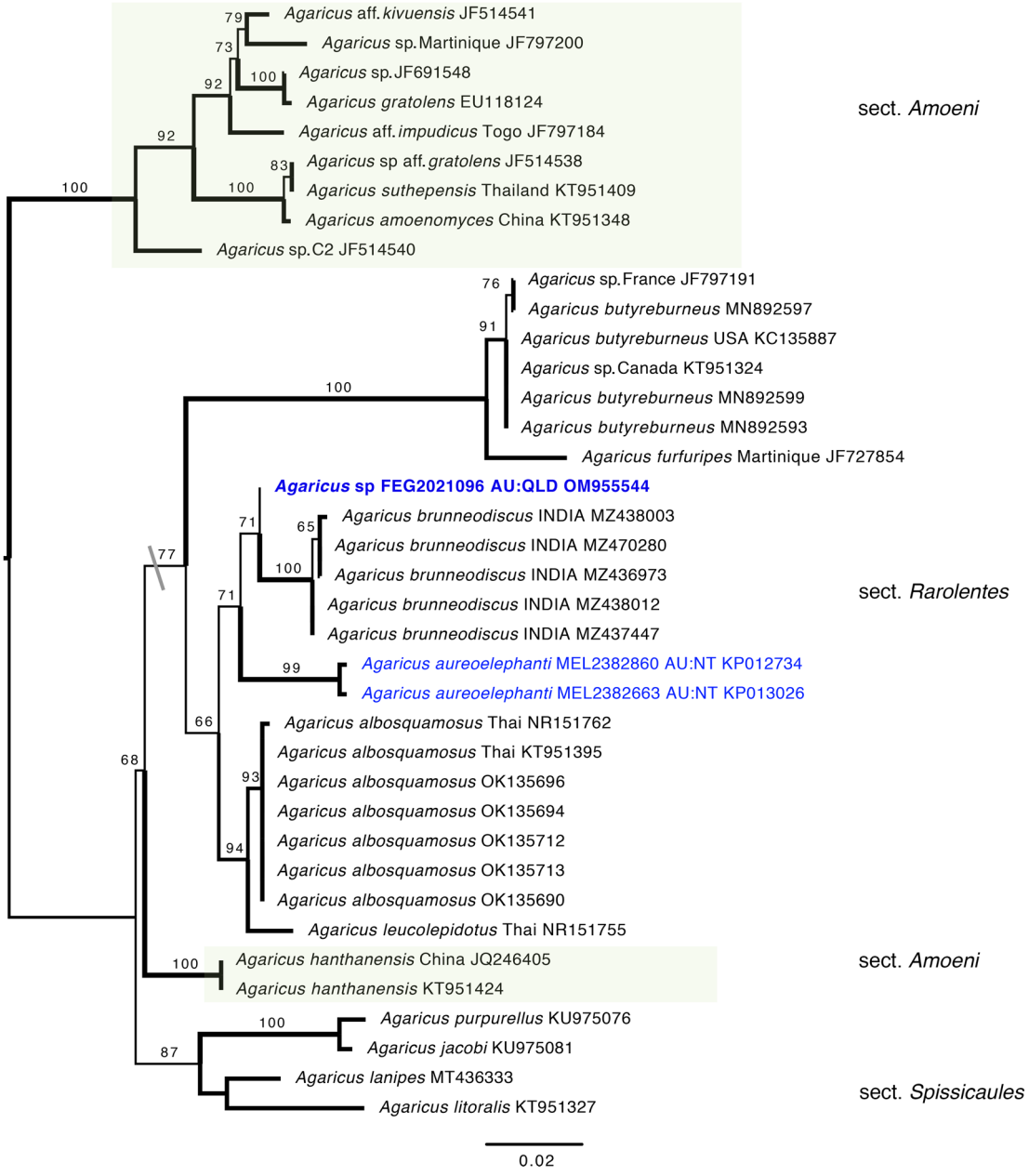
FP1399 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Minh et al. 2020) of the *Verticillium bjoernoeyanum rpb1* nucleotide alignment. Bootstrap support values (> 69 % are shown; only values > 94 % are significant) from 5 000 ultrafast (Hoang et al. 2018) 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 *Colletotrichum kahawae* (culture IMI 319418; GenBank JQ071924.1) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 11 strains including the outgroup; 692 characters including alignment gaps analysed: 175 distinct patterns, 111 parsimony-informative, 153 singleton sites, 428 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was TIM3e+G4. The alignment and tree were deposited at figshare.com (10.6084/m9.figshare.19745380).

Fungal Planet 1400 – *Agaricus albofoetidus*



FP1400 Maximum likelihood phylogenetic tree of a selection of taxa in *Agaricus* section *Xanthodermatei*; analyses performed using RAxML v. 8.2.12 (Stamatakis 2014) using the rapid bootstrapping and search algorithm, with GTR+GAMMA nucleotide substitution model, and 100 bootstrap replicates, as implemented in Geneious Prime v. 2021.2.2 (http://www.geneious.com; Kearse et al. 2012). ML bootstrap values indicated when > 50 %. Thickened lines indicate PP support ≥ 0.95. Yellow box indicates members of clade XanII in section *Xanthodermatei*. **Bold** sequences are new.

Fungal Planet 1401 – *Agaricus aureoelephanti*

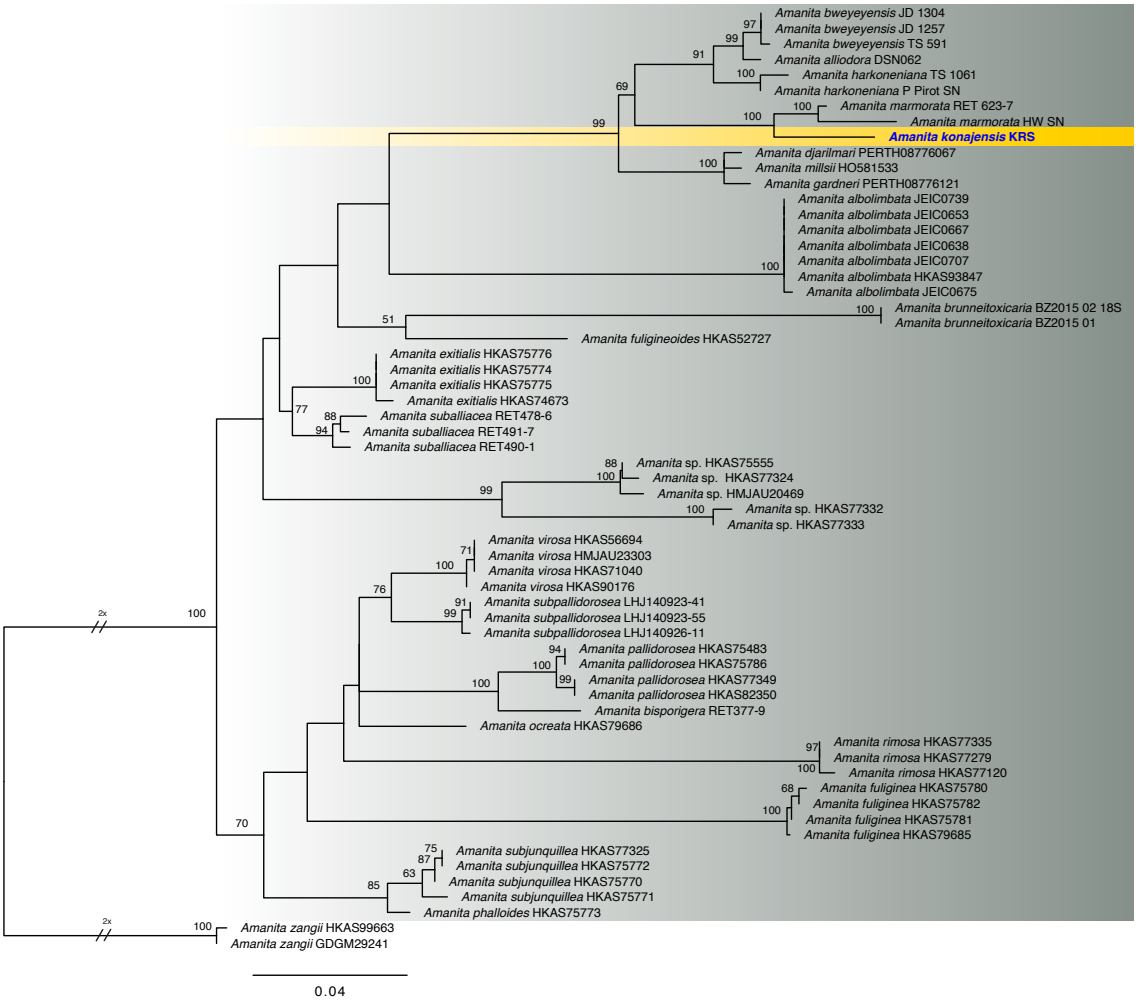


FP1401 Maximum likelihood phylogenetic tree of a selection of taxa in *Agaricus* section *Spissicaules*, analyses performed using RAxML v. 8.2.12 (Stamatakis 2014) using the rapid bootstrapping and search algorithm, with GTR+GAMMA nucleotide substitution model, and 100 bootstrap replicates, as implemented in Geneious Prime v. 2021.2.2 (http://www.geneious.com; Kearse et al. 2012). ML bootstrap values indicated when > 50 %. Thickened lines indicate PP support ≥ 0.90. **Bold** sequences are new.

Fungal Planet 1402 – *Agaricus parviumbrus*

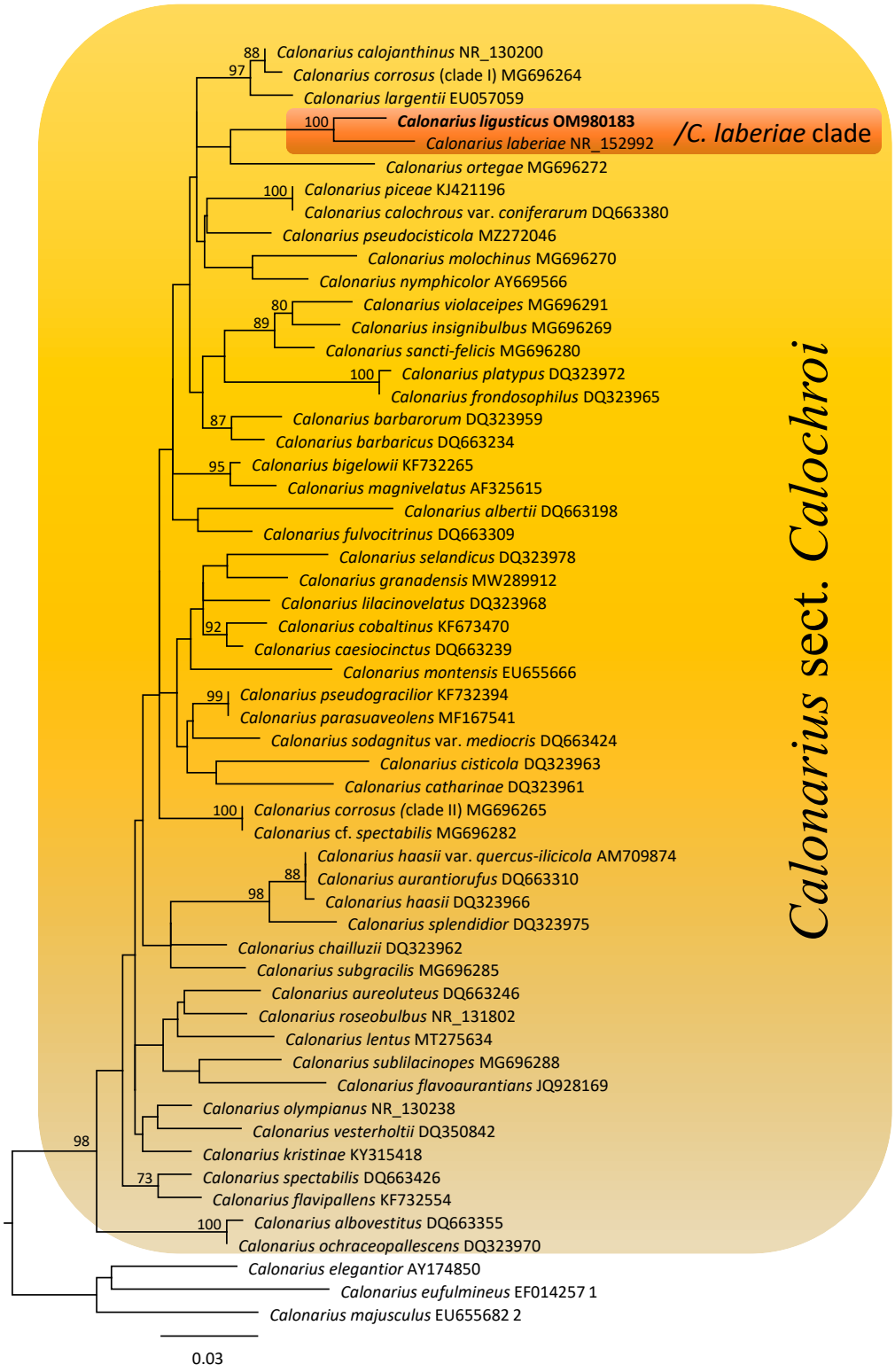
FP1402 Maximum likelihood phylogenetic tree of a selection of taxa in *Agaricus* section *Minores*; analyses performed using RAxML v. 8.2.12 (Stamatakis 2014) using the rapid bootstrapping and search algorithm, with GTR+GAMMA nucleotide substitution model, and 100 bootstrap replicates, as implemented in Geneious Prime v. 2021.2.2 (http://www.geneious.com; Kearse et al. 2012). ML bootstrap values indicated when > 50 %. Thickened lines indicate PP support ≥ 0.95.

Fungal Planet 1404 – *Amanita konajensis*



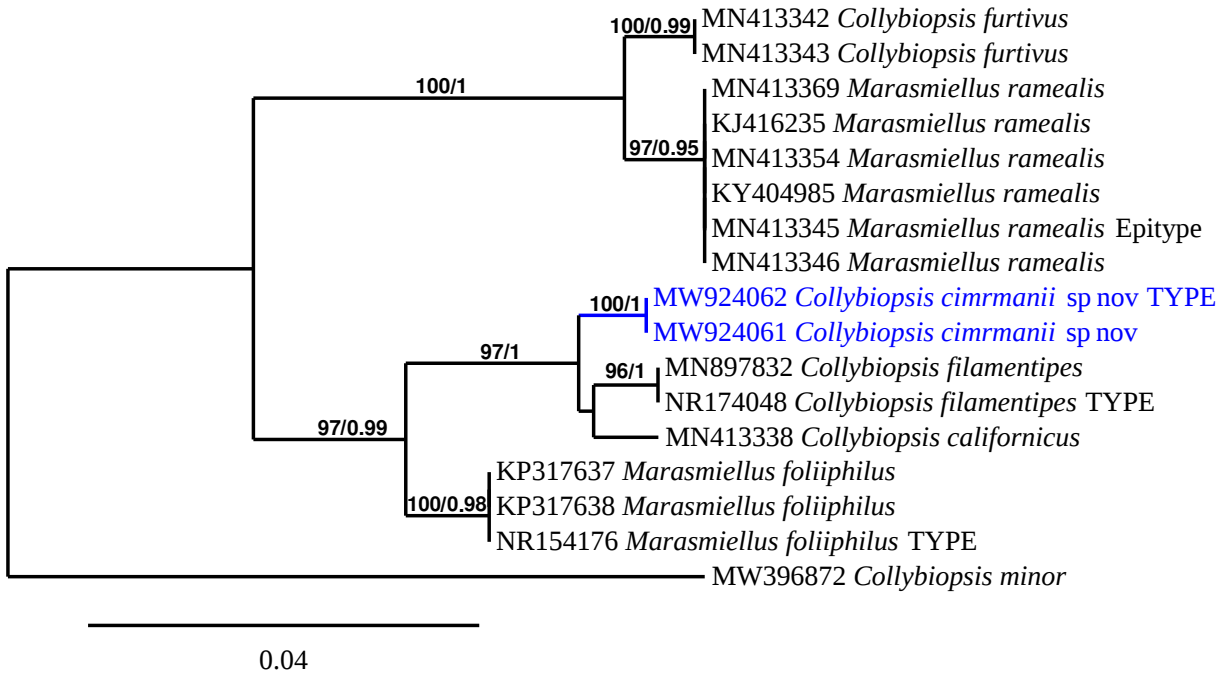
FP1404 Phylogenetic tree of *Amanita* species constructed using RAxML-HPC2 on XSEDE v. 8.2.8 (Stamatakis et al. 2008, Stamatakis 2014) on the CIPRES science gateway platform (http://www.phylo.org) (Miller et al. 2010) of the ITS region alignment. Bootstrap support values ≥ 50 % are given at the nodes. The phylogenetic position of *Amanita konajensis* is indicated in yellow. The alignment is available in figshare.com (10.6084/m9.figshare.20231331).

Fungal Planet 1405 – *Calonarius ligusticus*



FP1405 Maximum-likelihood analysis of the nrITS region of *Calonarius* was performed with RAxML v. 8 (Stamatakis 2014) using the GTR+G model (1 000 bootstrap replicates, bootstrap support values ≥ 70 % are shown) as implemented in Geneious v. 11.1.5 (Kearse et al. 2012). The scale bar represents the expected number of nucleotide changes per site.

Fungal Planet 1406 – *Collybiopsis cimrmanii*

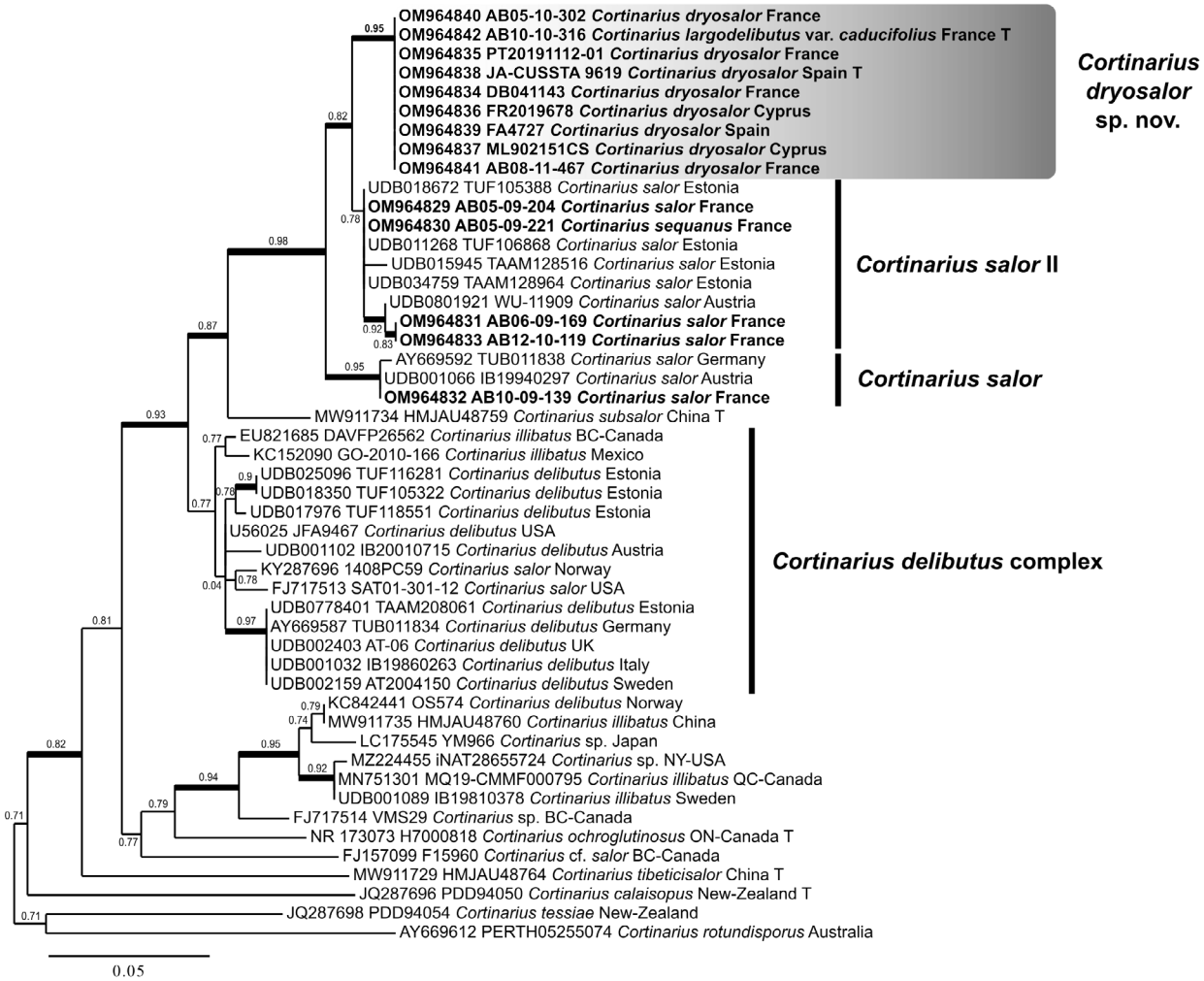


FP1406 Phylogenetic tree based on ITS sequence data for *Collybiopsis cimrmanii* was generated using Maximum likelihood analysis with PhyML v. 3.0 (Guindon et al. 2010); and using Bayesian Inference (MrBayes v. 3.2.7a; Ronquist et al. 2012). Bootstrap support values for ML greater than 80 % and Bayesian Inference posterior probabilities ≥ 0.95 are given above branches. The newly generated nucleotide sequences (indicated in blue) were compared against the GenBank nucleotide database (http://www.ncbi.nlm. nih.gov/). *Collybiopsis minor* MW396872 was used as outgroup.

Fungal Planet 1407 – *Cortinarius dryosalor*

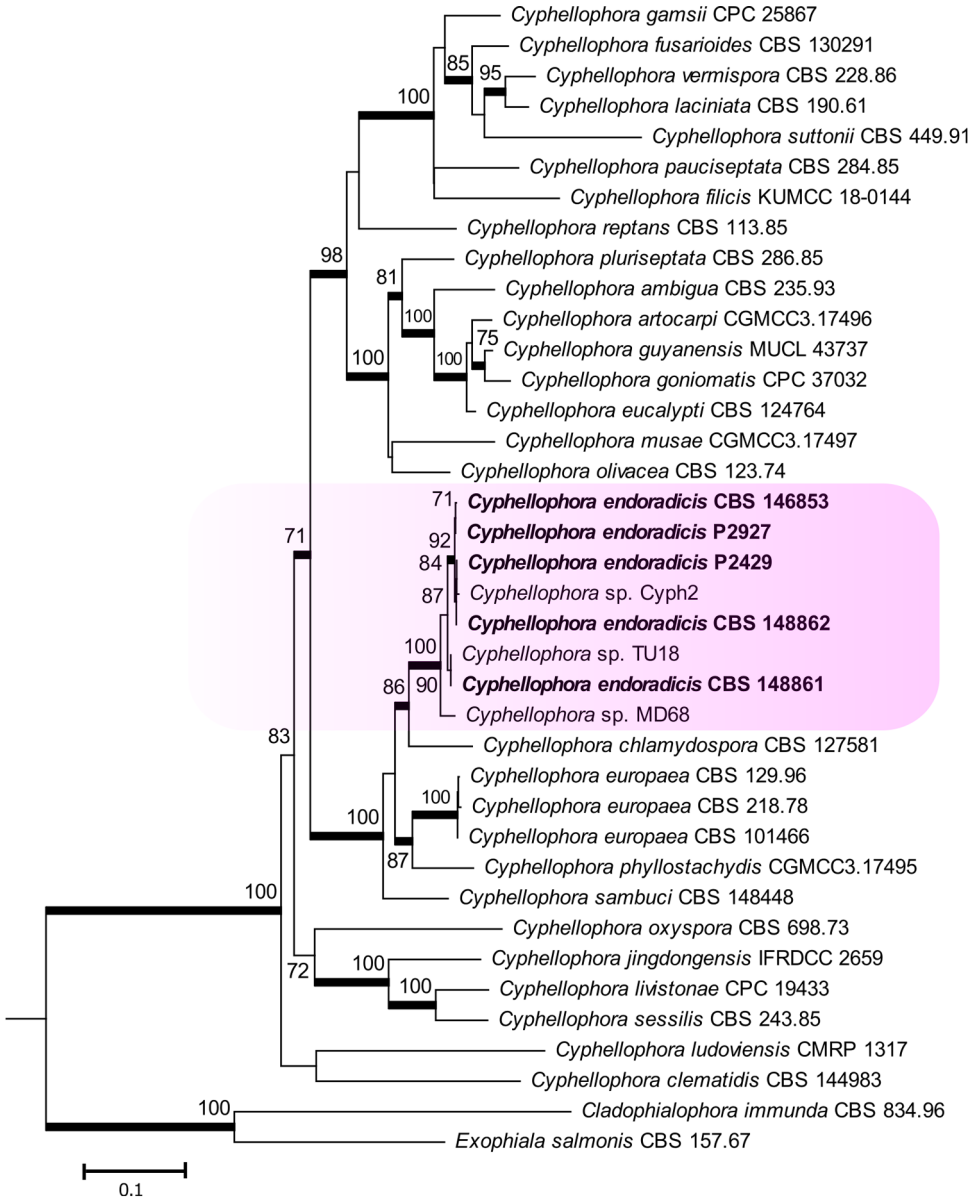
(Additional material examined)

Additional material examined. Cyprus, Mesa Potamos, along path in mixed forest on basic soil, c. 750 m a.s.l., 1 Dec. 2019, *J.-M. Bellanger* & *M. Loizides*, FR2019678 (ITS sequence GenBank OM964836); Kannaviou, under *Pinus brutia*, *Quercus alnifolia* and *Acer obtusifolium* on basic soil, c. 800 m a.s.l., 15 Dec. 2009, *M. Loizides*, ML902151CS (ITS sequence GenBank OM964837). – France, Vaucluse, Cadenet, la Royère, under *Q. pubescens*, *Q. ilex* and *P. halepensis* on calcareous soil, 7 Dec. 2004, *C.* & *D. Borgarino*, DB041143 (ITS sequence GenBank OM964834); Côte-d'Or, Vernot, bois de Nonceuil, under deciduous trees (*Quercus* spp., *Carpinus betulus*) on calcareous soil, 400 m a.s.l., 14 Oct. 2005, *J. Gane*, AB 05-10-302 (ITS sequence GenBank OM964840); Ardèche, Saint-Remèze, la Barthe, under *Q. ilex* on calcareous soil, 330 m a.s.l., 10 Nov. 2008, *A. Bidaud*, AB 08-11-467 (ITS sequence GenBank OM964841); Ain, Cerin, le Réservoir, under *Q. pubescens*, *C. betulus* & *Fagus sylvatica* on calcareous soil, 650 m a.sl., 21 Oct. 2010, *A. Bidaud*, AB 10-10-316 (holotype of *C. largodelibutus* var. *caducifolius*, ITS sequence GenBank OM964842); Charentes-maritimes, Douhet, under *Q. ilex* and other *Quercus* spp. on calcareous soil, 50 m a.s.l., 12 Nov. 2019, *P. Tanchaud*, PT20191112-01 (ITS sequence GenBank OM964835). – Spain, Granada, Huétor de Santillán, Arroyo Palacios, under *Q. ilex*, *Q. faginea*, and scattered *P. halepensis* and *P. pinaster* on calcareous soil, 1300 m a.s.l., 28 Nov. 2018, *F. Armada*, FA 4727 (ITS sequence GenBank OM964839). ***Cortinarius salor***: France, Ain, Champdor-Corcelles, Longeagne, under *Picea abies* on calcareous soil, 900 m a.s.l., 10 Sept. 2010, *A. Bidaud*, AB 10-09-139 (ITS sequence GenBank OM964832). ***Cortinarius salor* II**: France, Isère, Corrençon-en-Vercors, Clot de la Balme, under *Abies alba* and *F. sylvatica* on calcareous soil, 1250 m a.s.l., 21 Sept. 2005, *A. Bidaud*, AB 05-09-204 (ITS sequence GenBank OM964829); Haute-Savoie, Bernex, Crêt Thollon, under *P. abies* on calcareous soil, 950 m a.s.l., 27 Sept. 2005, *A. Bidaud*, AB 05-09-221 (ITS sequence GenBank OM964830); Ain, Thézillieu, Lacha, under *A. alba* and *F. sylvatica* on calcareous soil, 880 m a.s.l., 26 Sept. 2006, *A. Bidaud*, AB 06-09-169 (ITS sequence GenBank OM964831); ibid., 6 Oct. 2012, *A. Bidaud*, AB 12-10-119 (ITS sequence GenBank OM964833).



FP1407 Phylogeny of *Cortinarius* sect. *Delibuti*. Maximum Likelihood phylogenetic analysis of 49 ITS sequences belonging in sect. *Delibuti*, as defined by, e.g., Soop et al. (2019), performed online at http//phylogeny.lirmm.fr (Dereeper et al. 2008). Numbers on branches indicate SH-aLRT support values, significant when > 0.81 (Bellanger et al. 2015, thick branches). Sequences from type material are ended by a T suffix, those generated for the present study are highlighted in **bold**.

Fungal Planet 1408 – *Cyphellophora endoradicis*

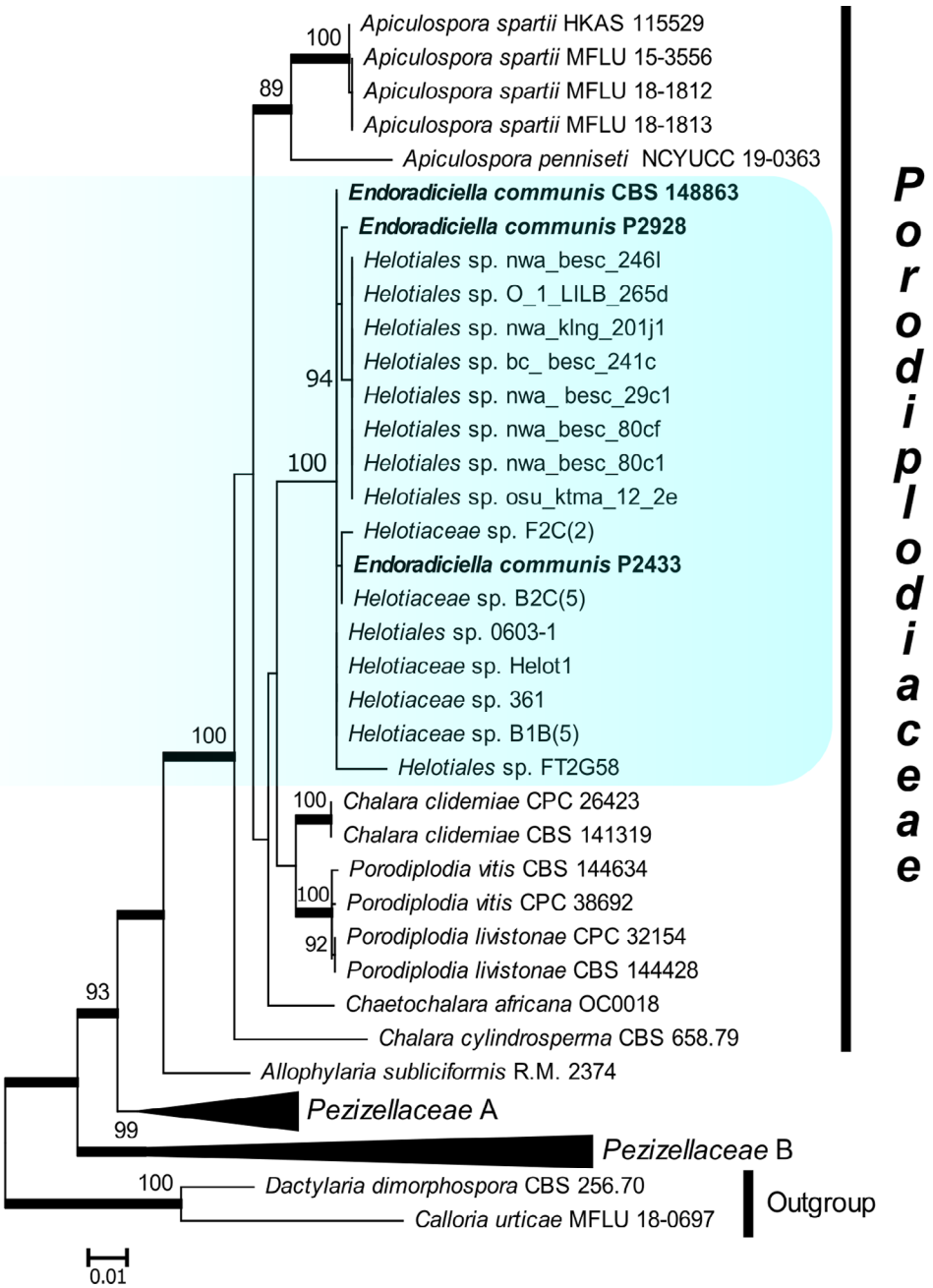


FP1408 Phylogenetic tree obtained from Maximum likelihood (ML) and Bayesian inference (BI) analyses of concatenated ITS, LSU and *tub2* sequences of *Cyphellophora* species, showing the placement of *C. endoradicis* within the genus. Alignment was based on the dataset of Jayawardena et al. (2019) and Crous et al. (2021c). Sequences were aligned with MAFFT v. 7.475 (Katoh & Standley 2013) on the online server and the final dataset consisted of 38 sequences and 1 843 positions including the outgroups. The ML analysis was conducted on the CIPRES Science Gateway server (Miller et al. 2010) using RAxML v. 8.2.12 (Stamatakis 2014) and employed the rapid bootstrapping algorithm under the GTRCAT model with 1 000 bootstrap iterations. The best substitution model as determined in MEGA v. 6.06 (Tamura et al. 2013) was the GTR + G + I. The BI analysis was performed with MrBayes v. 3.2.7a (Ronquist & Huelsenbeck 2003) and consisted of two independent runs of 10 M generations sampled every 100th generation and the first 25 % of trees was discarded as burn-in. Bootstrap support values ≥ 70 % are indicated by numbers close to nodes and Bayesian posterior probabilities ≥ 0.95 by thickened branches. The *C. endoradicis* clade is highlighted in a purple-coloured box and strains obtained during this work are in **bold**. The tree is rooted with *C. immunda* (CBS 834.96) and *Exophiala salmonis* CBS (157.67). Alignments and trees were deposited in figshare (10.6084/m9.figshare.19213929).

Fungal Planet 1409 – *Endoradiciella communis*

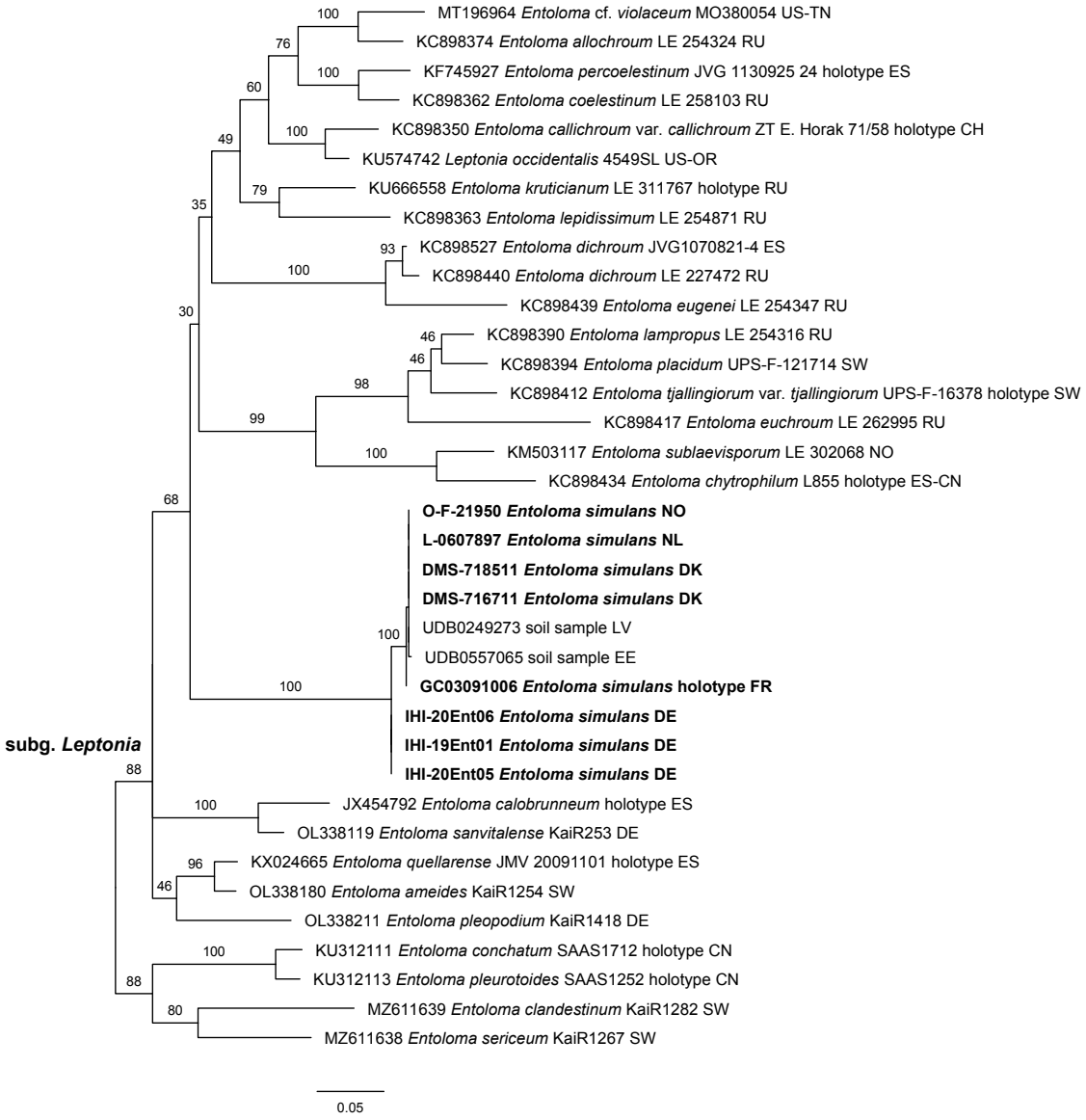
Notes (cont.)

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of *Endoradiciella communis* (CBS 148863) include 15 sequences identified as *Helotiaceae* sp. or *Helotiales* sp. (Identities = 99–100 %, no gaps); the next closest hits at the species level are '*Chalara*' *clidemiae* (strain CBS 141319^{T}, GenBank NR_145313.1; Identities = 492/512 (96 %), one gap (0 %)), *Porodiplodia vitis* (strain CBS 144634^{T}, GenBank NR_163376.1; Identities = 487/512 (95 %), two gaps (0 %)) and *Porodiplodia vitis* (strain CPC 38692, GenBank MW883445.1; Identities = 487/512 (95 %), two gaps (0 %)). Closest hits using the **LSU** sequence are *Bisporella citrina* (isolate AFTOL-ID 1301, GenBank FJ176871.1; Identities = 1273/1325 (96 %), two gaps (0 %)), *Bisporella citrina* (isolate M253, GenBank EU940087.1; Identities = 1275/1329 (96 %), two gaps (0 %)) and *Calycina alstrupii* (isolate Pz167, GenBank KY305098.1; Identities = 1248/1303 (96 %), four gaps (0 %)).



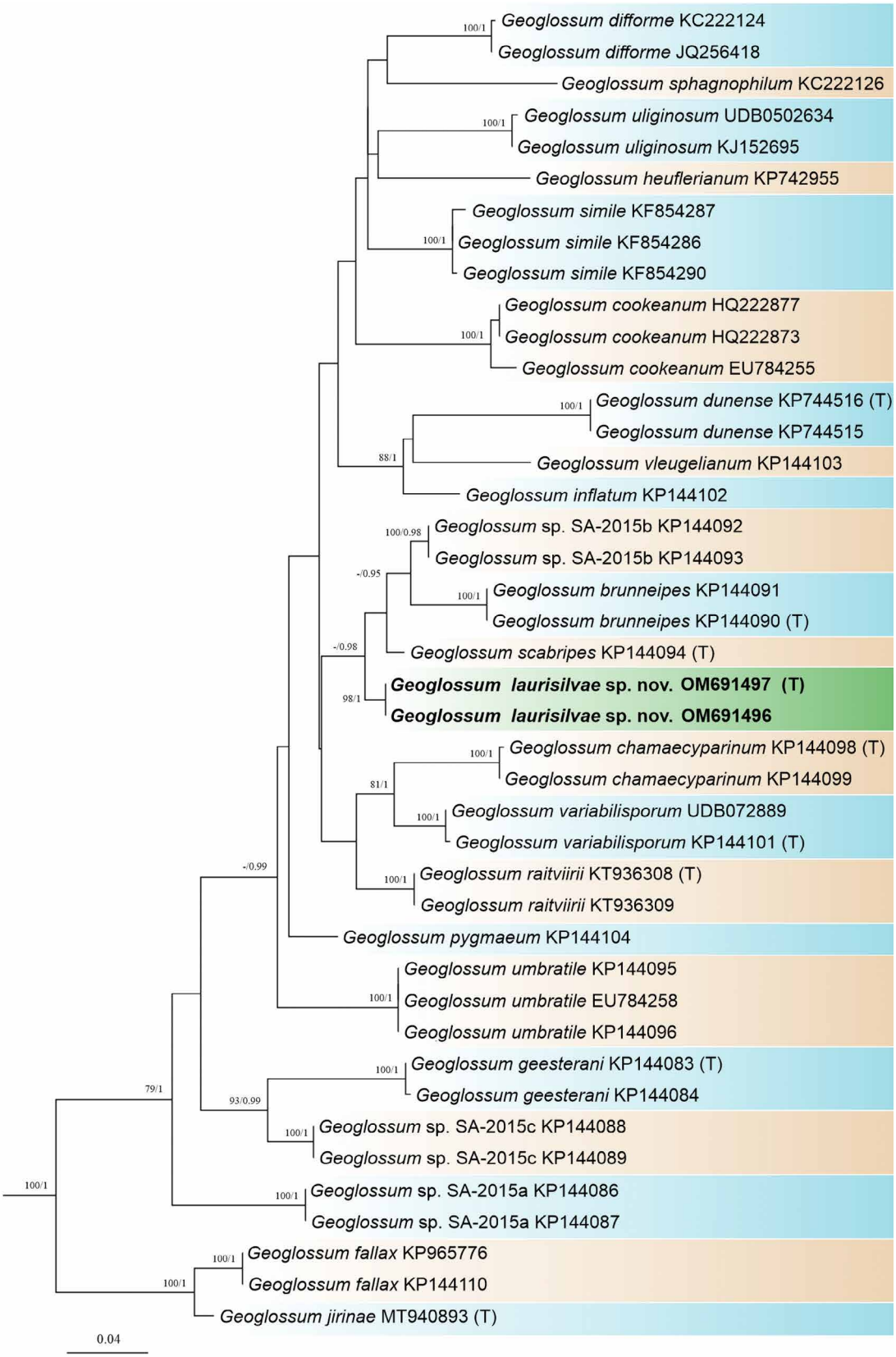
FP1409 A best scoring maximum likelihood (ML) phylogenetic tree inferred from concatenated ITS and LSU sequences of *Endoradiciella communis* strains and others retrieved from GenBank, showing the species placement within the family *Porodiplodiaceae* (*Helotiales, Leotiomycetes*). Taxon sampling followed Karunarathna et al. (2021) and Wijayawardene et al. (2021). Sequences were aligned with MAFFT v. 7.475 (Katoh & Standley 2013) on the online server and the final dataset included 53 sequences and 1343 positions including the outgroups. The ML and Bayesian Inference approaches were run using RAxML v. 8.2.12 (Stamatakis 2014) on the CIPRES Science Gateway server (Miller et al. 2010) and MrBayes v. .3.2.7a (Ronquist & Huelsenbeck 2003), respectively. Settings for both analyses followed Crous et al. (2021a). Bootstrap support values ≥ 70 % are indicated by numbers close to nodes and Bayesian posterior probabilities ≥ 0.95 by thickened branches. The *E. communis* clade is highlighted with an aqua-coloured box and strains studied in this work are marked in **bold**. The tree is rooted with *Dactylaria dimorphospora* (CBS 256.70) and *Calloria urticae* (MFLU 18-0697). Alignments and trees were deposited in figshare (10.6084/m9.figshare.19310963).

Fungal Planet 1410 – *Entoloma simulans*



FP1410 Phylogenetic tree derived from Maximum Likelihood (ML) analysis based on nrITS1-5.8S-ITS2 sequence data. Analysis was performed in RAxML v. 8.2.11 (Stamatakis 2014) using the GTRGAMMA model with 45 per site rate categories, and 500 rapid bootstrap replications. The ML bootstrap support values are shown at the branches. Scale bar = expected changes / nucleotide. Novel sequences are indicated in **bold** and country code abbreviations follow ISO 3166.

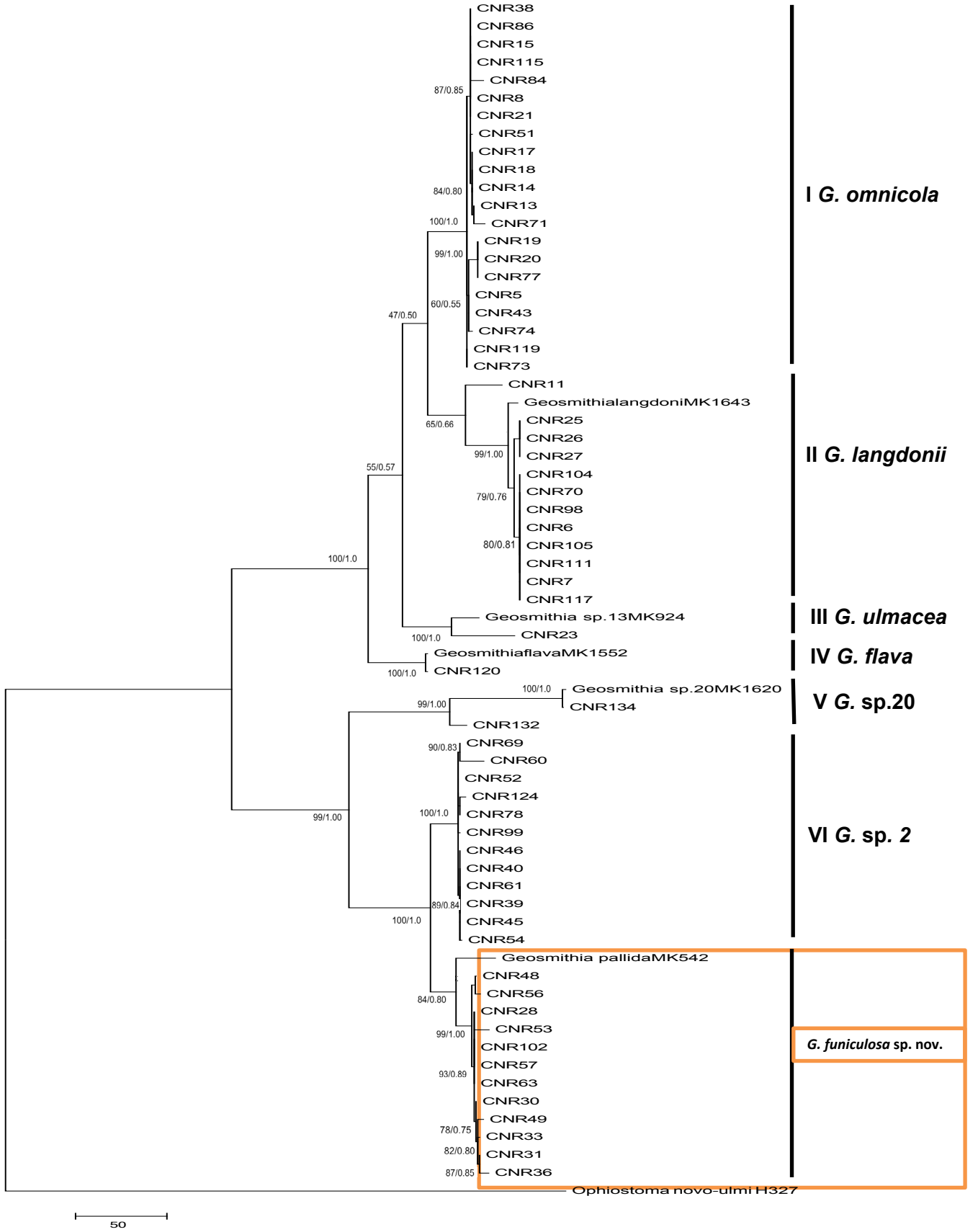
Fungal Planet 1411 – *Geoglossum laurisilvae*



FP1411 Best phylogenetic tree obtained from the maximum likelihood analysis with RAxML v. 8.2.12 (Stamatakis 2014) of the *Geoglossum* ITS nucleotide alignment. Maximum likelihood bootstrap support values from 1 000 replicates and ≥ 75 % are shown at the nodes. Bayesian Inference obtained with MrBayes v. 3.2.7a (Ronquist et al. 2012), the posterior probabilities support values from 2 M generations and ≥ 0.95 are shown. The sequence *Sabuloglossum arenarium* GenBank JQ256426 was used as outgroup (not shown in the tree). New sequences generated in this study are indicated in **bold** text and species types are indicated with (T). The scale bar represents the expected number of nucleotide changes per site.

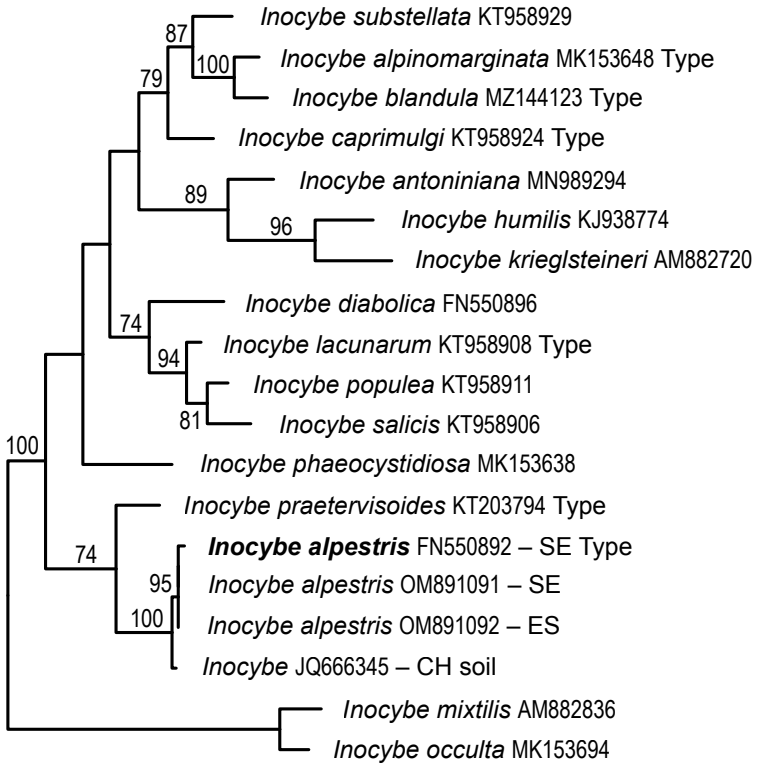
Fungal Planet 1412 – *Geosmithia funiculosa*

FP1412-1 Maximum likelihood tree illustrating relationships in terms of distance, derived from partial sequences of the ITS regions. The tree was built by using PhyML v. 3.1 in Geneious Prime version 2022.1 (Biomatters Ltd., Auckland, New Zealand). Numbers alongside branches represent the percentage of congruent clusters in 1 000 bootstrap replicates when the values were greater than 50 %. Scale bar = 0.05. Strains from Pepori et al. (2015) and Zhang et al. (2022) were included in the phylogenetic tree.



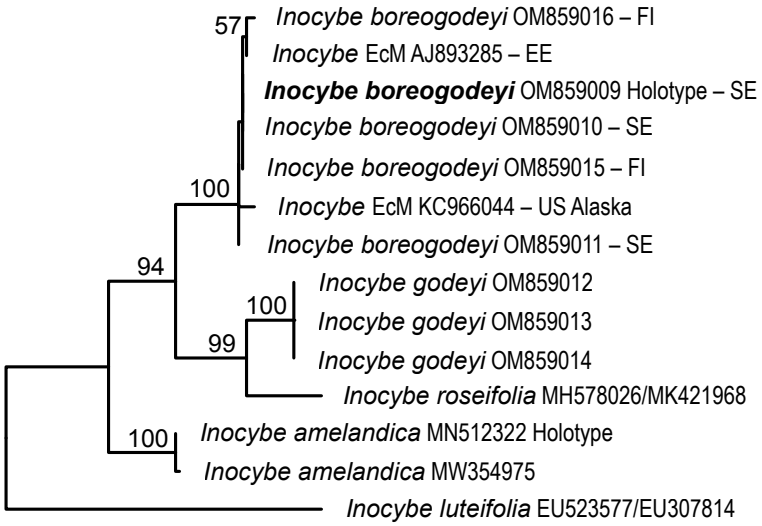
FP1412-2 One of the three equally most parsimonious trees (length = 788) from the combined sequence datasets of the ITS rDNA, *tub2*, *tef1* loci is shown (CI = 0.687, RI = 0.928, RC = 0.788, HI = 0.723). The aligned datasets were analysed with PAUP (Phylogenetic Analyses Using Parsimony) v. 4.0b10, using a heuristic search option with 1000 random sequence additions. The alignment and tree were uploaded to TreeBASE. In addition, datasets were analysed using Bayesian inference (BI) with MrBayes v. 3.1.2. The MP and Bayesian posterior probability are indicated next to the branches. *Ophiostoma novo-ulmi* sequences are used as outgroup (Pepori et al. 2015).

Fungal Planet 1413 – *Inocybe alpestris*



FP1413 Phylogram obtained from a parsimony analysis using PAUP v. 4.0a (Swofford 2003) based on ITS and LSU data showing the position of *I. alpestris* among its closest relatives in section *Marginatae*. Heuristic searches with 1 000 random-addition sequence replicates and tree bisection-reconnection (TBR) branch swapping were performed. Relative robustness of clades was assessed by the bootstrap method using 1 000 heuristic search replicates with 100 random taxon addition sequence replicates and TBR branch swapping. Bootstrap support values are indicated on branches. The holotype of *I. alpestris* is indicated and marked in **bold**.

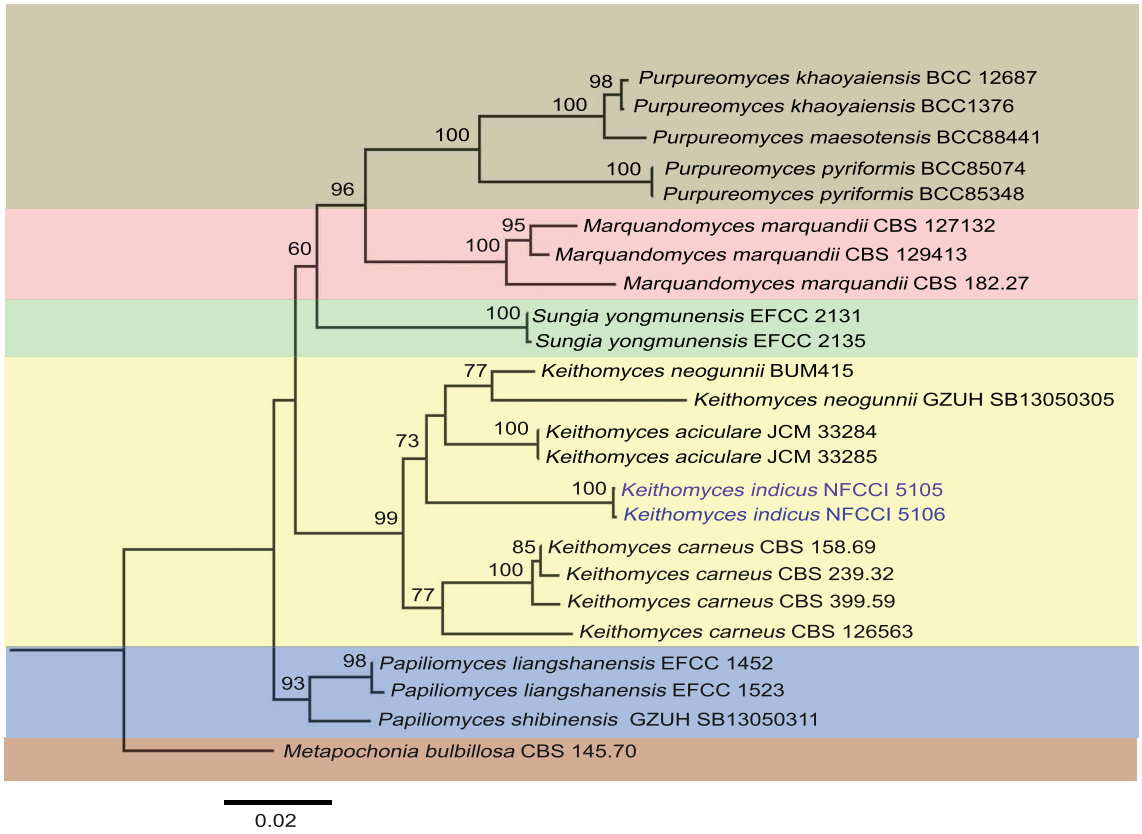
Fungal Planet 1414 – *Inocybe boreogodeyi*



FP1414-1 Phylogram obtained using a parsimony analysis in PAUP v. 4.0a (Swofford 2003) based on ITS and LSU data showing the position of *I. boreogodeyi* as a sister species to *I. godeyi*. Heuristic searches with 1 000 random-addition sequence replicates and tree bisection-reconnection (TBR) branch swapping were performed. Relative robustness of clades was assessed by the bootstrap method using 1 000 heuristic search replicates with 100 random taxon addition sequence replicates and TBR branch swapping. Bootstrap support values are indicated on branches. The holotype of *I. boreogodeyi* is indicated and marked in **bold**.

FP1414-2 Photo of *Inocybe boreogodeyi* from the southern boreal zone (Kokkonen 129/14).

Fungal Planet 1415 – *Keithomyces indicus*

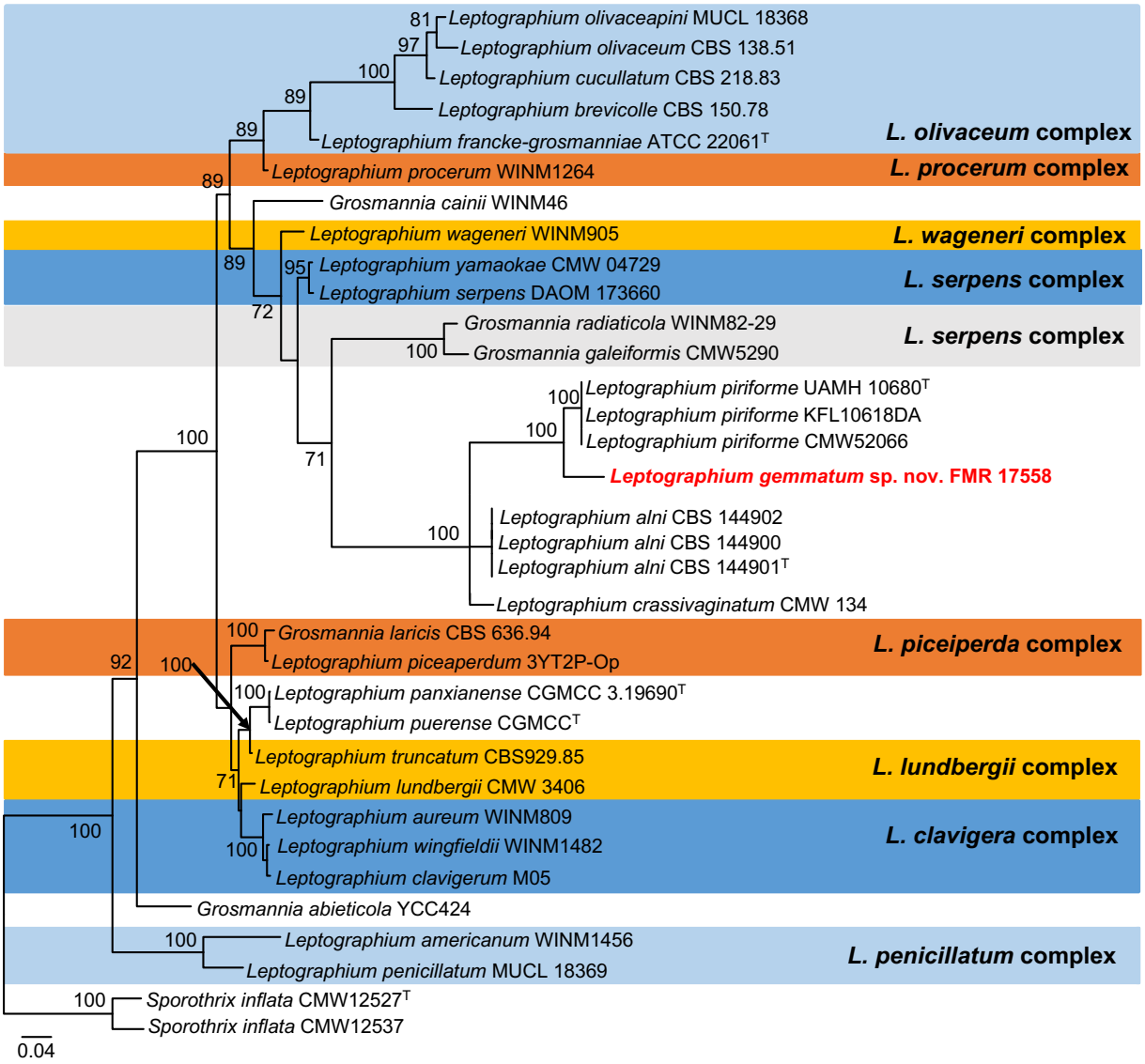


FP1415-1 Phylogenetic tree of *Keithomyces indicus* based on combined ITS, LSU, SSU, *tef1* and *rpb2* sequence data. IQ-TREE multicore v. 1.6.11 (Nguyen et al. 2015) was used for construction of the phylogenetic tree by Maximum Likelihood (ML) method. Bootstrap support values > 50 % are shown at the nodes. The novel species is indicated with coloured text. TreeBASE submission ID: 29152.

FP1415-2 Taxa used for phylogenetic analysis and their corresponding GenBank accession numbers.

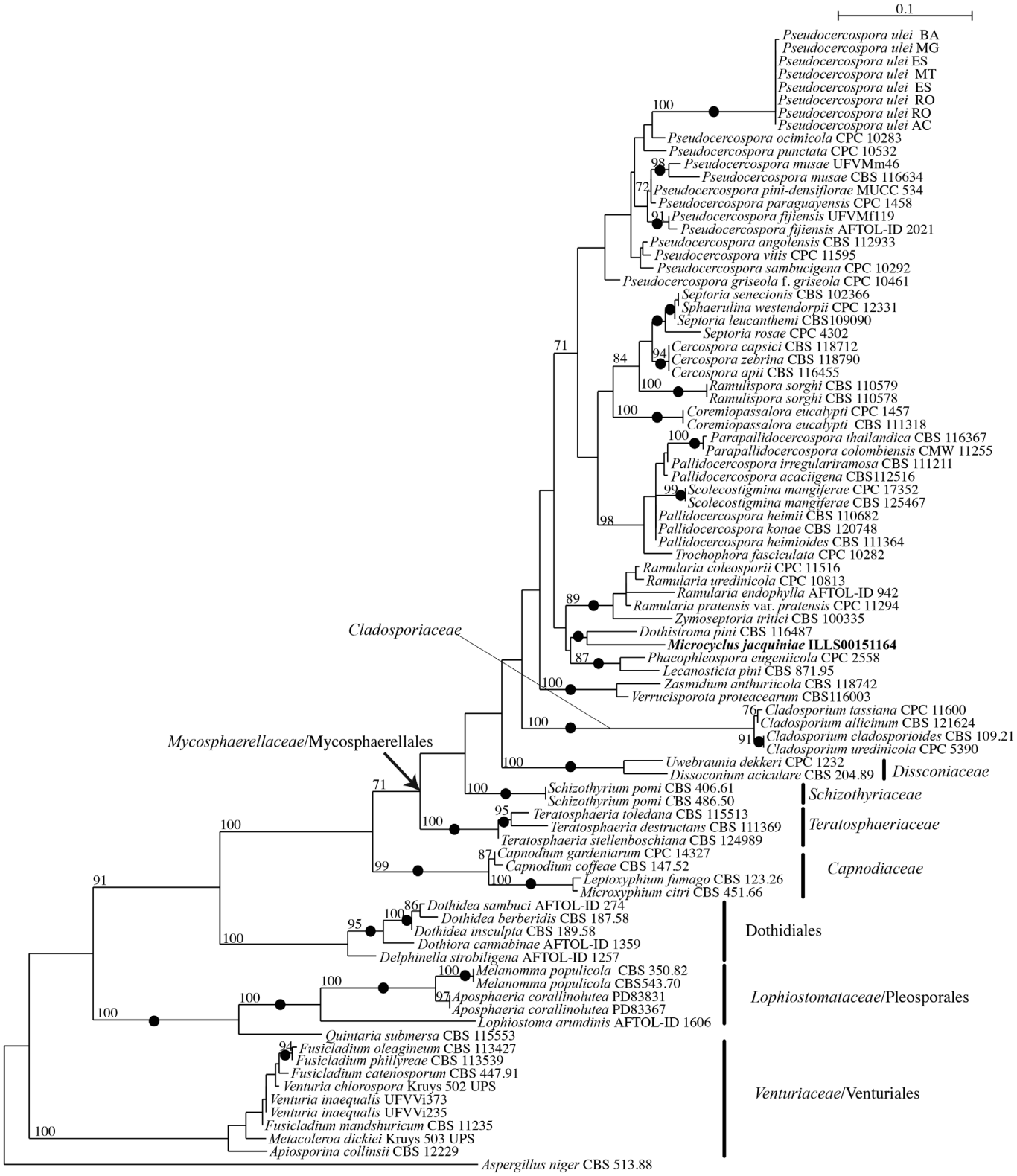
Taxa	Strain	Country	Substrate	GenBank accession numbers				
				ITS	LSU	SSU	*tef1*	*rpb2*
Keithomyces indica	NFCCI 5105	India	Plant detritus	OL584170	OL584176	OL584173	OM032805	OM032808
Keithomyces indica	**NFCCI 5106**	**India**	**Soil**	**OL584171**	**OL584177**	**OL584174**	**OM032806**	**OM032809**
Keithomyces aciculare	JCM 33284	Japan	Soil	NR_164567	LC435741	LC435738	LC462188	–
Keithomyces aciculare	JCM 33285	Japan	Soil	LC463198	LC435742	LC435739	LC462189	–
Keithomyces carneus	CBS 158.69	USA	Soil	MT078886	–	–	–	–
Keithomyces carneus	CBS 399.59	USA	Soil	MT078887	EF468842	EF468989	EF468788	EF468939
Keithomyces carneus	CBS 239.32	France	Sand dune	AY624171	EF468843	EF468988	EF468789	EF468938
Keithomyces carneus	CBS 126563	Tanzania	Soil	MT078883	MT078856	MT078871	MT078848	MT078921
Keithomyces neogunnii	BUM415	China	*Lepidoptera* larva	MH143811	MH143828	MH143845	MH143861	MH143891
Keithomyces neogunnii	GZUH SB13050305	China	*Lepidoptera* larva	KY423507	–	KU729724	KU729729	–
Marquandomyces marquandii	CBS 127132	USA	Soil	MT078882	MT078857	MT078872	MT078849	MT078922
Marquandomyces marquandii	CBS 129413	USA	Soil	MT561567	MT078859	MT078874	MT078851	–
Marquandomyces marquandii	CBS 182.27	USA	Soil	AY624193	EF468845	EF468990	EF468793	EF468942
Metapochonia bulbillosa	CBS 145.70	Denmark	*Picea abies*	AJ292410	AF339542	AF339591	EF468796	EF468943
Papiliomyces liangshanensis	EFCC 1452	Korea	*Lepidoptera*	–	EF468815	EF468962	EF468756	–
Papiliomyces liangshanensis	EFCC 1523	Korea	*Lepidoptera*	–	EF468814	EF468961	EF468755	EF468918
Papiliomyces shibinensis	GZUH SB13050311	China	*Lepidoptera*	NR_154178	–	KR153588	KR153589	–
Purpureomyces khaoyaiensis	BCC1376	Thailand	*Lepidoptera* larva	KX983460	KX983462	KX983468	KX983457	KX983465
Purpureomyces khaoyaiensis	BCC 12687	Thailand	*Lepidoptera* larva	JN049868	JF415971	–	KJ398796	KJ398703
Purpureomyces maesotensis	BCC88441	Thailand	*Lepidoptera* larva	MN781916	MN781877	–	MN781734	MN781824
Purpureomyces pyriformis	BCC85074	Thailand	*Lepidoptera* larva	MN781929	MN781873	–	MN781730	MN781821
Purpureomyces pyriformis	BCC85348	Thailand	*Lepidoptera* larva	MN781927	MN781871	–	MN781728	MN781820
Sungia yongmunensis	EFCC 2131	Korea	*Lepidoptera*	JN049856	EF468833	EF468977	EF468770	KJ398690
Sungia yongmunensis	EFCC 2135	Korea	*Lepidoptera*	–	EF468834	EF468979	EF468769	–

Fungal Planet 1416 – *Leptographium gemmatum*



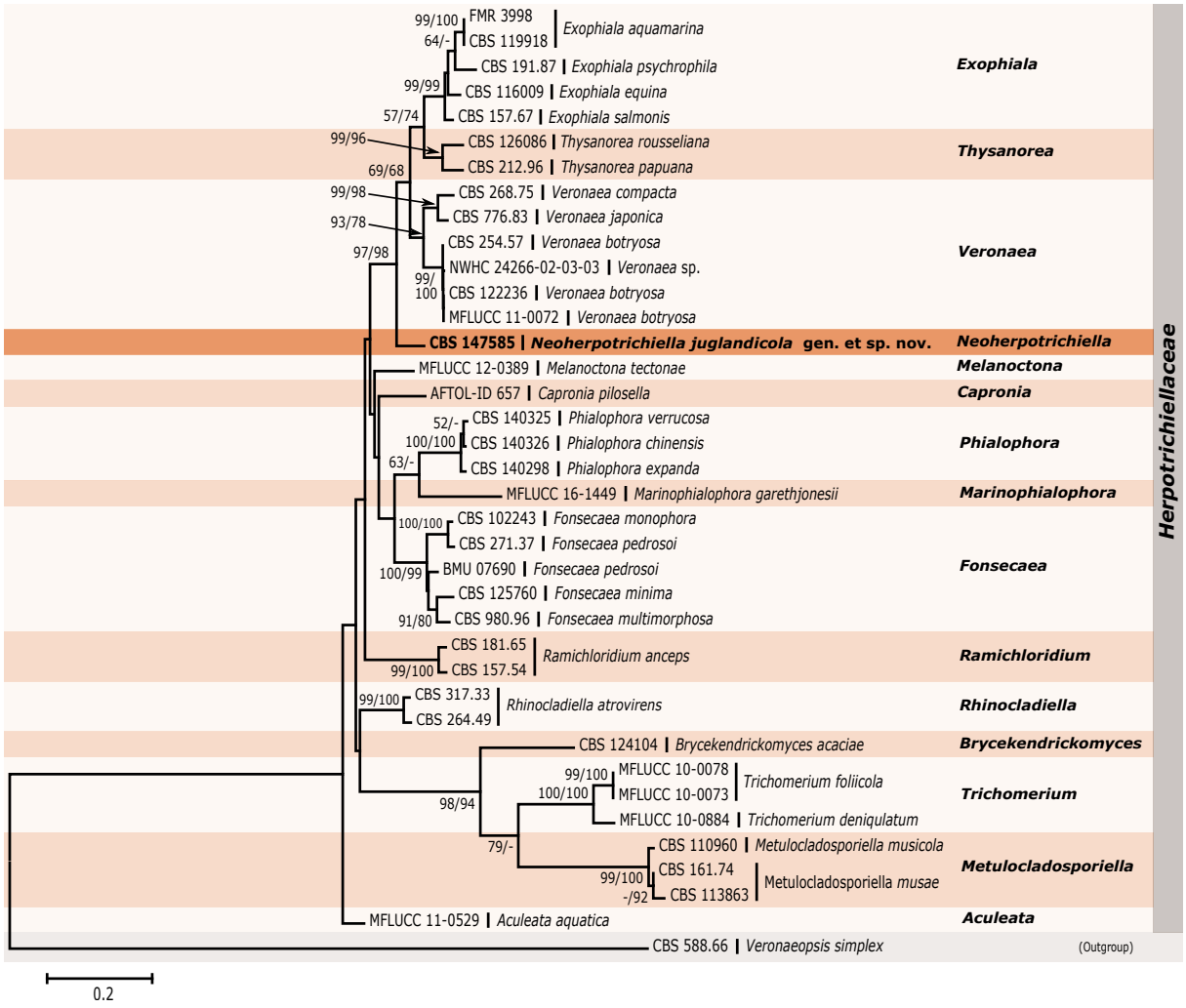
FP1416 Phylogenetic tree based on Maximum likelihood analysis obtained by RAxML v. 8.2.12 (Stamatakis et al. 2014) using the combined LSU, ITS, and *tub2* sequences of *Leptographium* species representing some of the species complex currently recognised in *Leptographium* s.lat. (Yin et al. 2019, Strzałka et al. 2020). Bootstrap support values above 70 % are indicated on the nodes. The alignment included 1771 bp and was performed using Tamura 3-parameter with Gamma distribution (T93+G) as the best nucleotide substitution model. The tree was rooted with two strains of *Sporothrix inflata*: CMW 12527 and CMW 12537. The alignment was performed with MEGA v. 6 software (Tamura et al. 2013). The new species proposed in this study is indicated in red and **bold** face. A superscript T denotes ex-type cultures.

Fungal Planet 1419 – *Microcyclus jacquiniae*



FP1419 Maximum likelihood tree (−lnL = 5681.45) generated from a PhyML v. 3.0. (Guindon et al. 2010) analysis of a partial LSU alignment (793 bp) of 82 sequences of various *Dothideomycetes* lineages. *Microcyclus jacquiniae* is shown in **bold**. Bootstrap branch support values ≥ 75 % are shown above or below nodes. The bold circles indicate significant Bayesian posterior probabilities ≥ 0.95 implemented using MrBayes v. 3.2. (Ronquist & Huelsenbeck 2003). Taxon sampling from Da Hora Júnior et al. (2014). *Aspergillus niger* CBS 513.88 was used as an outgroup.

Fungal Planet 1420 – *Neoherpotrichiella juglandicola*



FP1420 Maximum likelihood tree obtained from the ITS, LSU and *tub2* gene sequences of our isolates and sequences of *Herpotrichiellaceae* species retrieved from GenBank. The tree was built using the Maximum likelihood (ML) and maximum parsimony (MP) methods, under MEGA-X v. 10.2.6 (Kumar et al. 2018). The combined ITS, LSU and *tub2* sequence data set consisted of 37 *Herpotrichiellaceae* taxa with *Veronaeopsis simplex* (CBS 588.66) as outgroup and consisted of 1915 characters. Of these 1066 were constant, 79 were excluded, 230 were variable and parsimony-uninformative and 540 were parsimony-informative. A heuristic search of these 540 parsimony-informative characters resulted in 1000 equally parsimonious trees of 2169 steps with CI = 0.55, RI = 0.68 and HI = 0.45. The ML analysis yielded a best scoring tree with the final ML optimization likelihood value of –12163.29 (ln) and a gamma distribution shape parameter value of 0.3425. All individual trees obtained from single gene datasets were essentially similar in topology and not substantially different from the tree generated from the concatenated dataset. One of the two ML trees obtained is presented with ML/MP bootstrap support values at the nodes. The alignment and tree are available at figshare.com (10.6084/m9.figshare.19904407).

Fungal Planet 1421 – *Penicillium neoherquei*

Notes — Based on a search of NCBIs GenBank nucleotide database, the closest hit for *P. neoherquei* using the **ITS** sequence is *P. herquei* CBS 336.48 (NR_103659.1; identity 532/544 (98 %) and two gaps (0 %)) and *P. malachiteum* CBS 647.95 (NR_120271.1; identity 543/555 (98 %) and three gaps (0 %)). FP1421-1 summarises the sequence identities and DNA gap frequencies among *P. neoherquei* sp. nov. and the closest related species within series *Herqueorum*. According to Raper & Thom (1949) and Ramirez (1982), conidia of *P. herquei* are somewhat smooth, while in *P. neoherquei* they are conspicuously roughened to striate. Under SEM, there is some similarity in topology of ornamentation in both species. Conidiophores of *P. herquei* can reach up to 1 000 µm, while in *P. neoherquei* up to c. 500 µm (Raper & Thom 1949). An ex-type culture of *P. herquei* CCF 2769 (= MUCL 29213) exhibited faster growth on all media tested (i.e., 25–45 % growth rate difference between *P. herquei* and *P. neoherquei*), brighter colours (yellow-orange) of mycelium and reverses especially on MEA (bright orange) and YES (reddish orange) at 25 °C. The main distinguishing phenotypic characteristics of the new species compared with the other taxa within series *Herqueorum* are listed in the Supplementary data. A molecular phylogenetic analysis of a 4-gene dataset (*BenA, CaM*, ITS, *RPB2*) sequences also clearly separates *P. neoherquei* from all species within series *Herqueorum* in the section *Sclerotiorum*. Molecular phylogenetic analysis of four genes (*BenA, CaM*, ITS, *RPB2*) of *Penicillium* section *Sclerotiora* sequences reveal strain G1071 occurs on an isolated clade and is described herein as a new species of *Penicillium*.

FP1421-1 Sequence identities and DNA gap frequencies among *Penicillium neoherquei* sp. nov. and close related species in series *Herqueorum* (section *Sclerotiorum*) *.

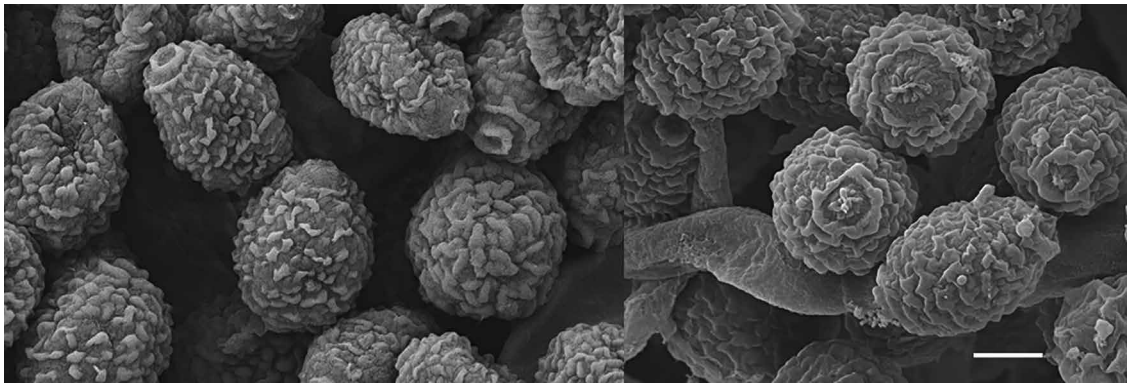
	P. choerospondiatis HMAS 248813	*P. herquei* CBS 336.48	*P. sanshaense* HMAS 248820	*P. malachiteum* CBS 647.95	*P. verrucisporum* HMAS 248819
			Identities (%) / gaps (%)		
ITS	489 / 506 (97 %) 6 / 506 (1 %)	532 / 544 (98 %) 2 / 544 (0 %)	492 / 504 (98 %) 3 / 504 (0 %)	533 / 544 (98 %) 4 / 544(0 %)	490 / 504 (97 %) 5 / 504 (0 %)
Ben	401 / 449 (89 %) 4 / 449 (0 %)	419 / 471 (89 %) 5 / 471 (1 %)	408 / 449 (91 %) 3 / 449 (0 %)	368 / 410 (90 %) 4 / 410 (0 %)	400 / 448 (89 %) 2 / 448 (0 %)
CaM	384 / 452 (85 %) 24 / 452 (5 %)	400 / 461 (87 %) 24 / 461 (5 %)	388 / 458 (85 %) 23 / 458 (5 %)	320 / 377 (85 %) 24 / 377 (6 %)	400 / 459 (87 %) 23 / 459 (5 %)
RPB2	791 / 854 (93 %) 0 / 854 (0 %)	784 / 854 (92 %) 0 / 854 (0 %)	–	793 / 863 (92 %) 0 / 853 (0 %)	783 / 854 (92 %) 0 / 854 (0 %)

* Ex-type cultures.

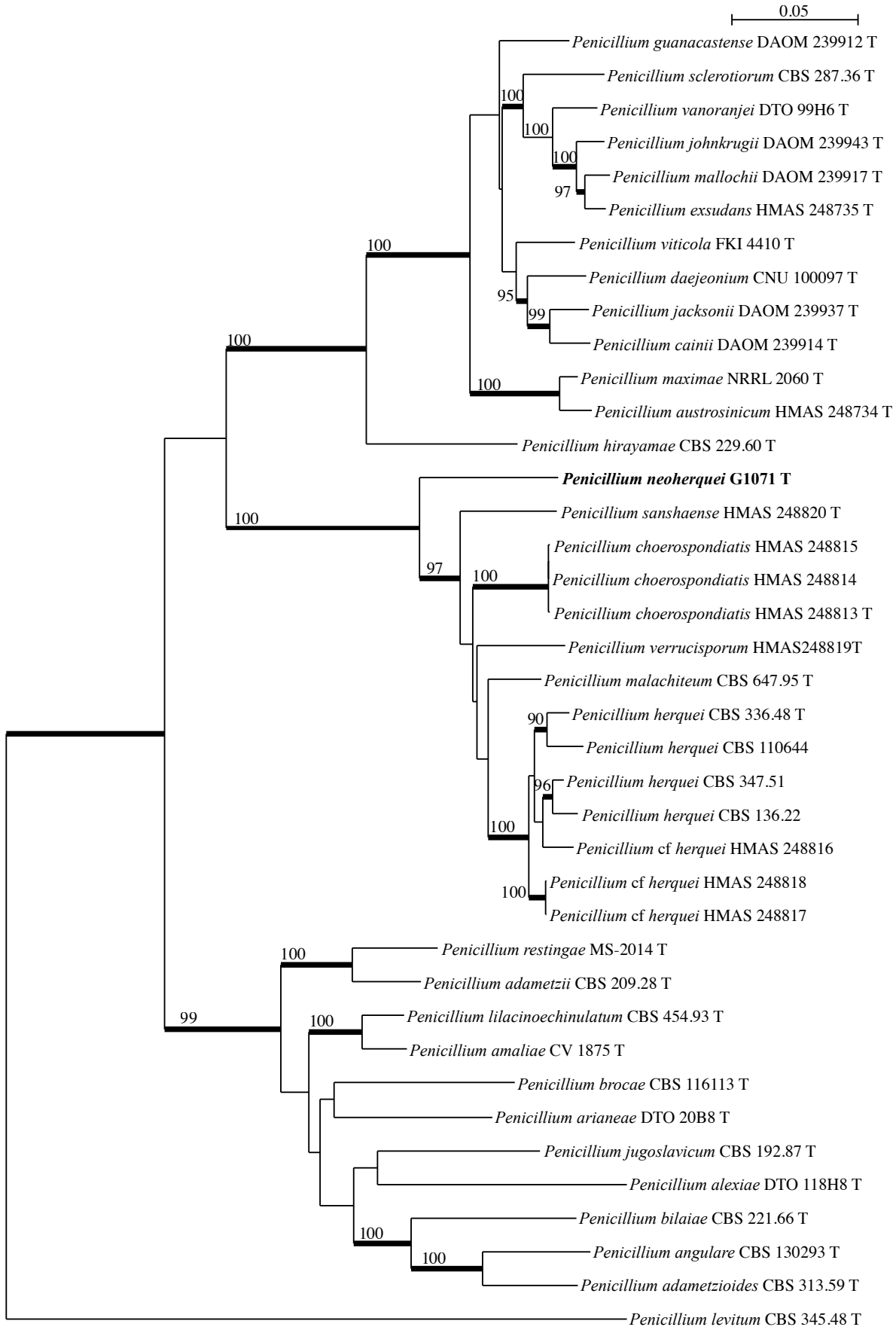
FP1421-2 Comparison of the key phenotypic characteristics of *Penicillium* species (series *Herqueorum*, section *Sclerotiorum*).

Species	Conidiophores (stipes)		Metulae		Conidia	
	length (µm)	wall	number	size (µm)	wall	size (µm)
P. neoherquei sp. nov.	180–520	rough*	5–7	7–15 × 3–4.5	rough	3–4.5 × 2.2–3
P. choerospondiatis[1]	100–135	smooth	3–5	10.5–15 × 3.5–4.5	rough	4.5–6.5 × 3.3–4.5
P. herquei[2,3,5]	200–1000	rough	4–10	10–15 × 4.0–5.5	smooth to rough**	3.5–4.5 × 2.2–3
P. sanshaense[1]	200–500	smooth to rough	6–8	9–12 × 4–6.5	smooth	3–3.5 × 2–2.5
P. malachiteum[4]	200–320	rough	4–8	8–14 × 2.5–5	smooth	3–5 × 1.5–3.5
P. verrucisporum[1]	125–200	rough	5–8	9–10.5 × 3.5–5.5	rough	3–3.5 × 2.5–3

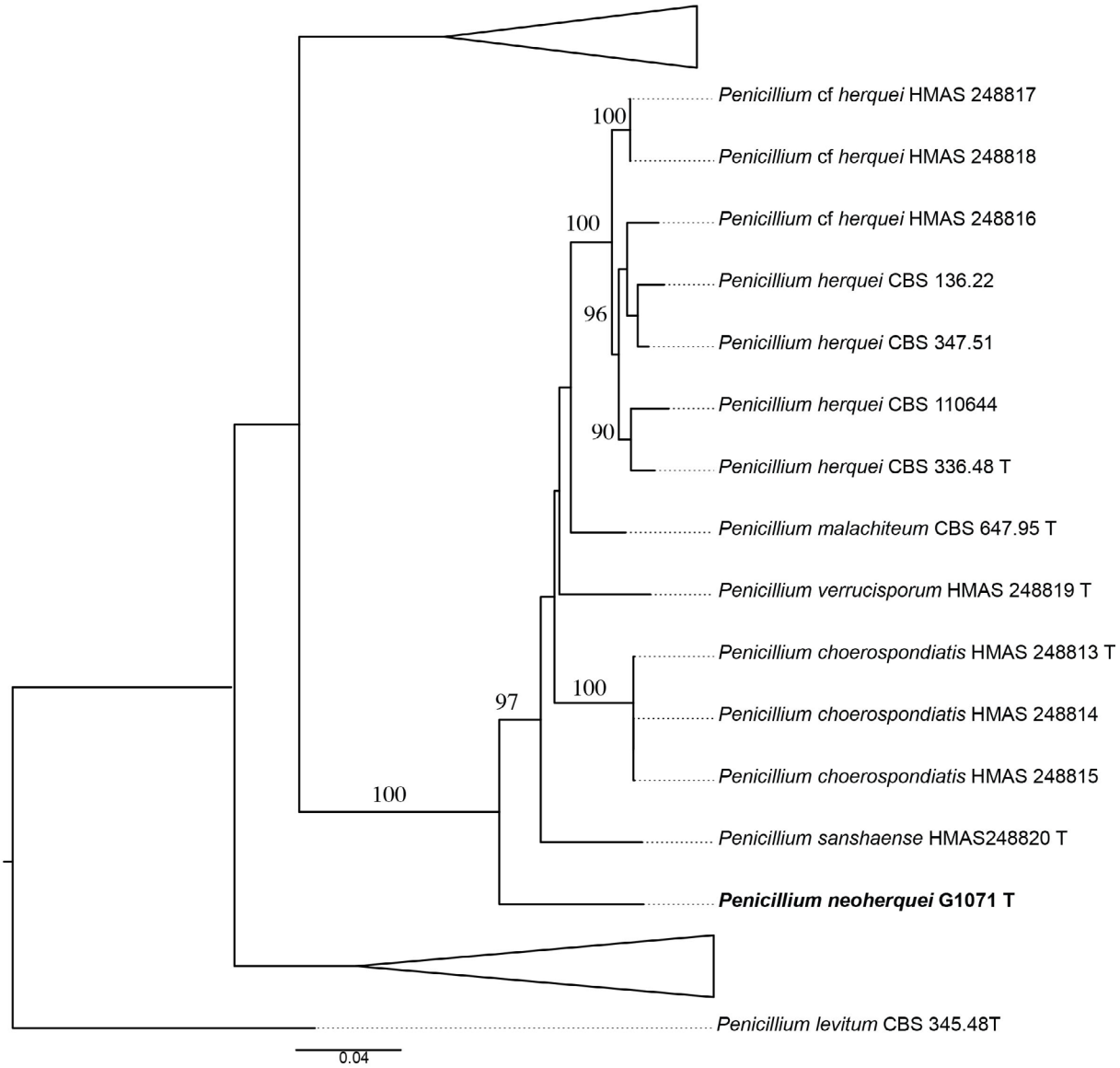
[1]Wang et al. (2017), [2]Raper & Thom (1949), [3]Ramirez (1982), [4]Yaguchi (1993), [5]Pitt (1980).
* Observed in water mounts.
** Smooth to nearly so ([2,3]) smooth to conspicuously roughened ([5]).



FP1421-3 Scanning electron microscopy (SEM) of conidia of ex-type culture of *P. herquei* CCF 2769 (= MUCL 29213) (on MEA, after 7 d). Scale bar = 1 µm.



FP1421-4 Molecular phylogenetic analysis of a 4-gene alignment (*BenA, CaM*, ITS, *RPB2*) of *Penicillium* section *Sclerotiora* sequences reveal strain G1071 occurs on an isolated lineage and is described herein as a new species of *Penicillium*. Phylogram of the most likely tree (−lnL = 15119.34) from a Maximum Likelihood analysis of 39 sequences based on 4-gene concatenated dataset (2 186 bp) using IQ-TREE (Nguyen et al. 2015) in PhyloSuite v. 1.2.1. (Zhang et al. 2020). Numbers refer to UFBoot support values ≥ 90 % based on 5 000 replicates. Bayesian analysis was implemented using MrBayes v. 3.2. (Ronquist & Huelsenbeck 2003). The thickened branches indicate significant Bayesian posterior probabilities ≥ 95 %. Nodes ≥ 95 are considered strongly supported. *Penicillium levitum,* strain CBS 345.48 T was used as outgroup. Bar indicates nucleotide substitutions per site. T, ex-type culture.

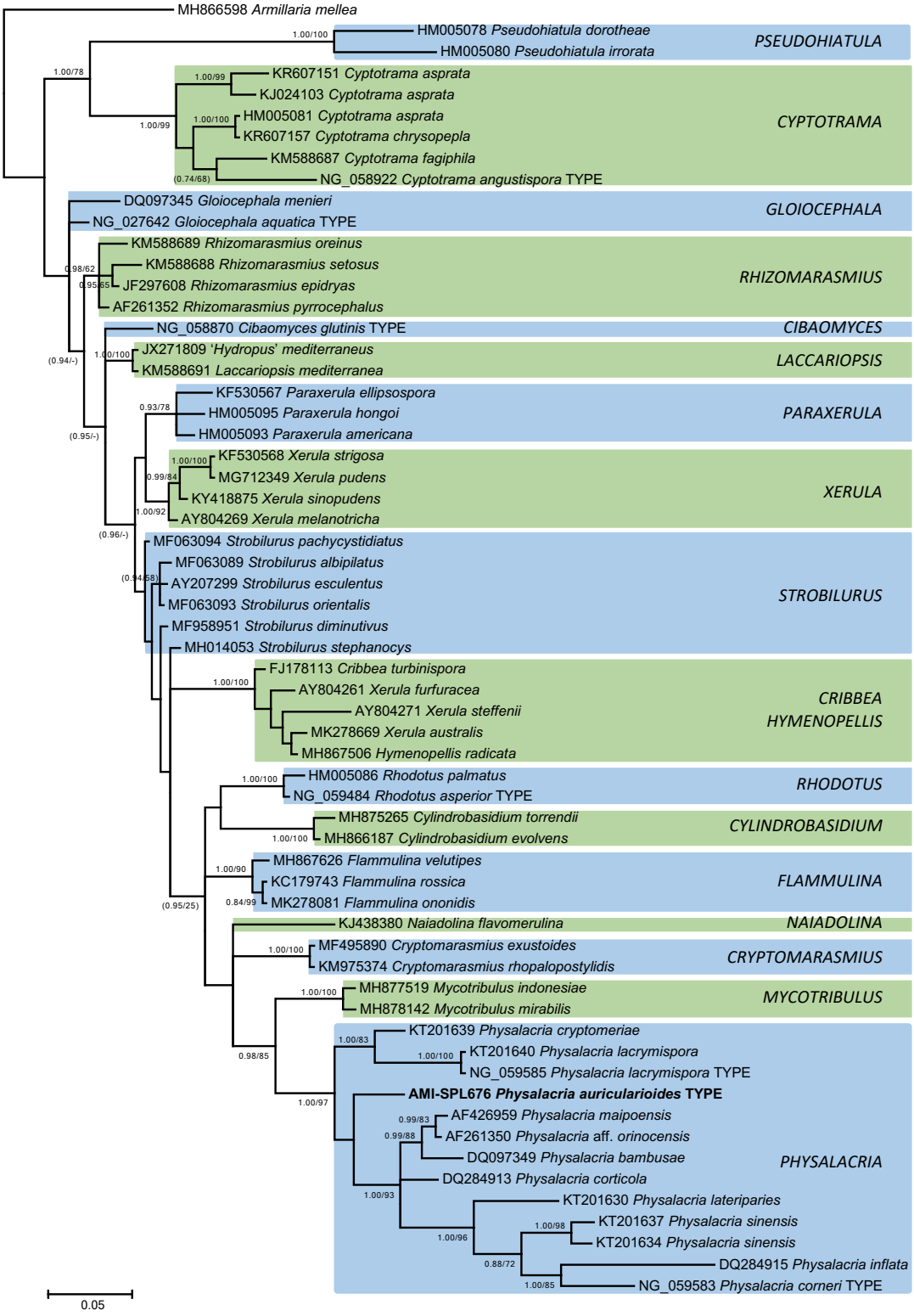


FP1421-5 Cartoon version of phylogeny, highlighting the new species in **bold** within the series *Herqueorum.*

Fungal Planet 1422 – *Physalacria auricularioides*

(Additional materials examined)

Additional materials examined. Spain, Galicia, Pontevedra, Parque Nacional de las Islas Atlánticas de Galicia, Illa de Cortegada, N42°36'56.27" W8°47'6.30", 20 m a.s.l., several apothecia found together on a dead twig of *Castanea sativa*, 18 Aug. 2021, *S. De la Peña-Lastra, A. Mateos* & *A. Rego*, AMI-SPL688; ibid., N42°37'9.19" W8°47'1.70", 18 m a.s.l., several apothecia found together on a dead twig of *Castanea sativa*, 17 Jan. 2018, *S. De la Peña-Lastra,* MSS937 (ITS, LSU and SSU sequences GenBank OM964476, OM964481 and OM964477); ibid., 17 Nov. 2018, *S. De la Peña-Lastra* & *M. Saavedra*, MSS1018 (ITS and LSU sequences GenBank OM964474 and OM964479).



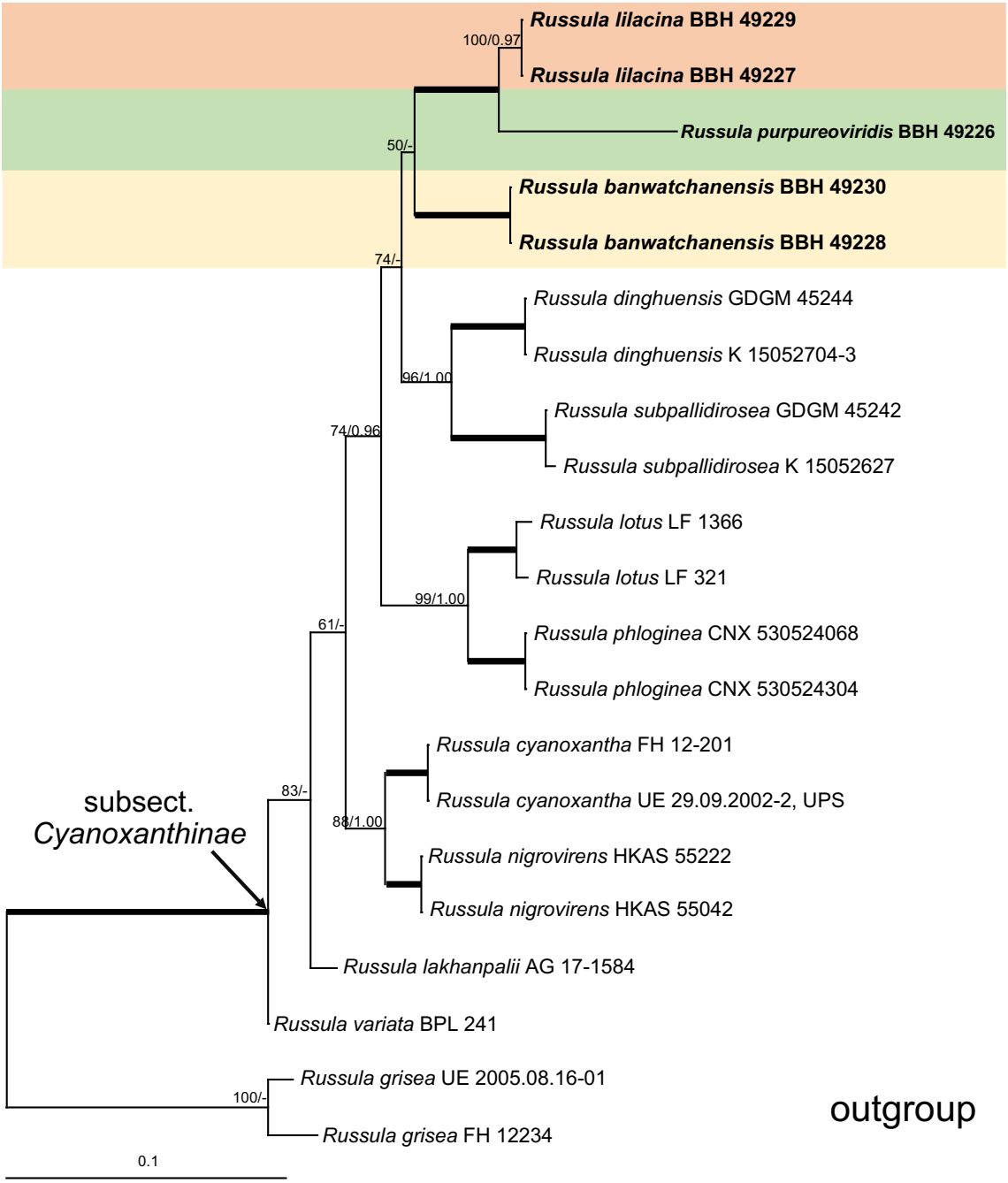
FP1422 A 50 % majority rule 28S rDNA consensus phylogram of the family *Physalacriaceae* (suborder *Marasmiineae*, order *Agaricales*) (with *Armillaria mellea* as outgroup) obtained using MrBayes from 109 275 sampled trees. Nodes were annotated if they were supported by ≥ 0.95 Bayesian posterior probability (left) or ≥ 70 % maximum likelihood bootstrap proportions (right). Non-significant support values are exceptionally represented inside parentheses. Sequences newly generated in this study are in **bold**.

Fungal Planet 1423–1425 –

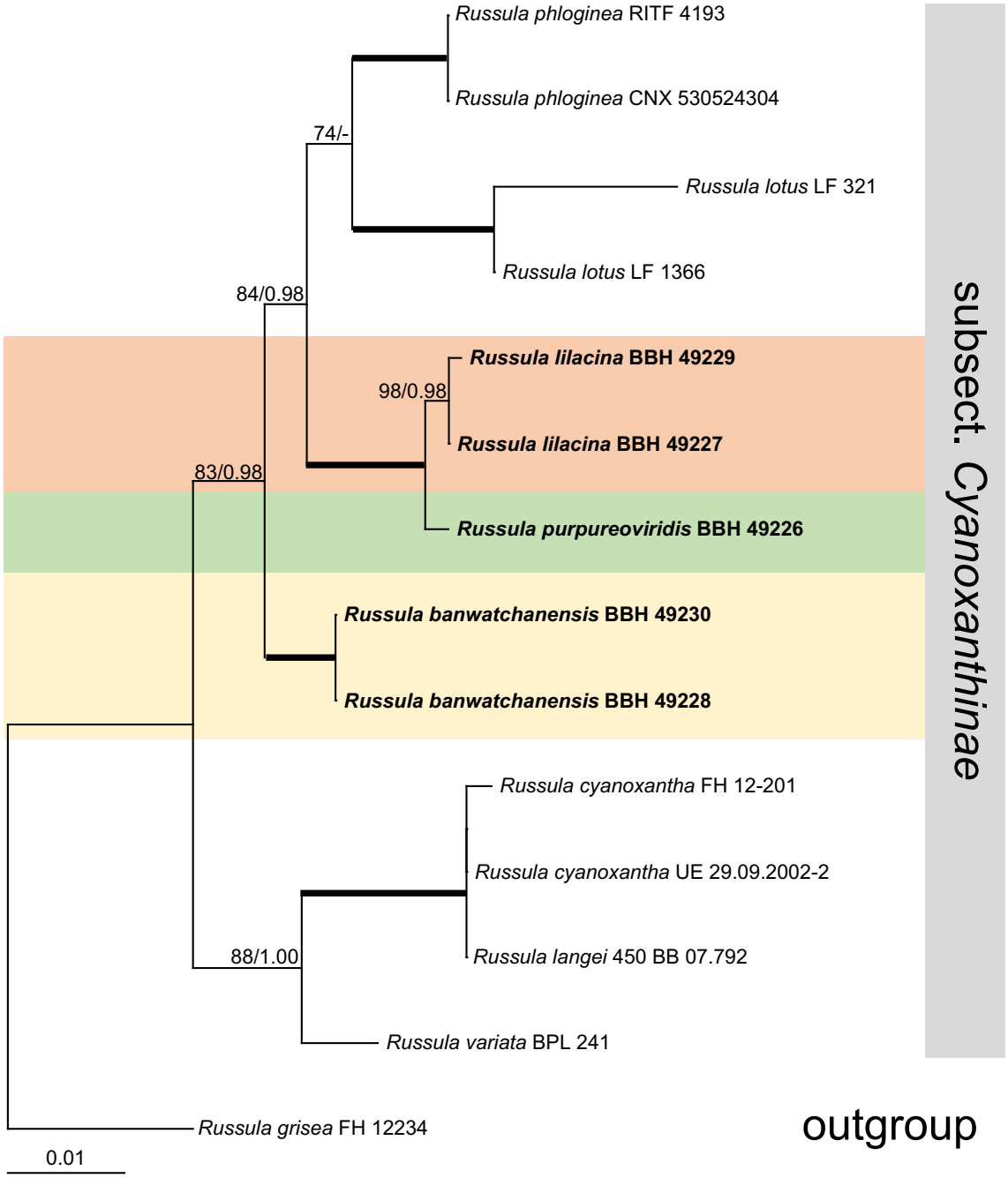
Russula banwatchanensis, Russula purpureoviridis & Russula lilacina

FP1423–1425-1 Sequence data of *Russula* spp. used in this study.

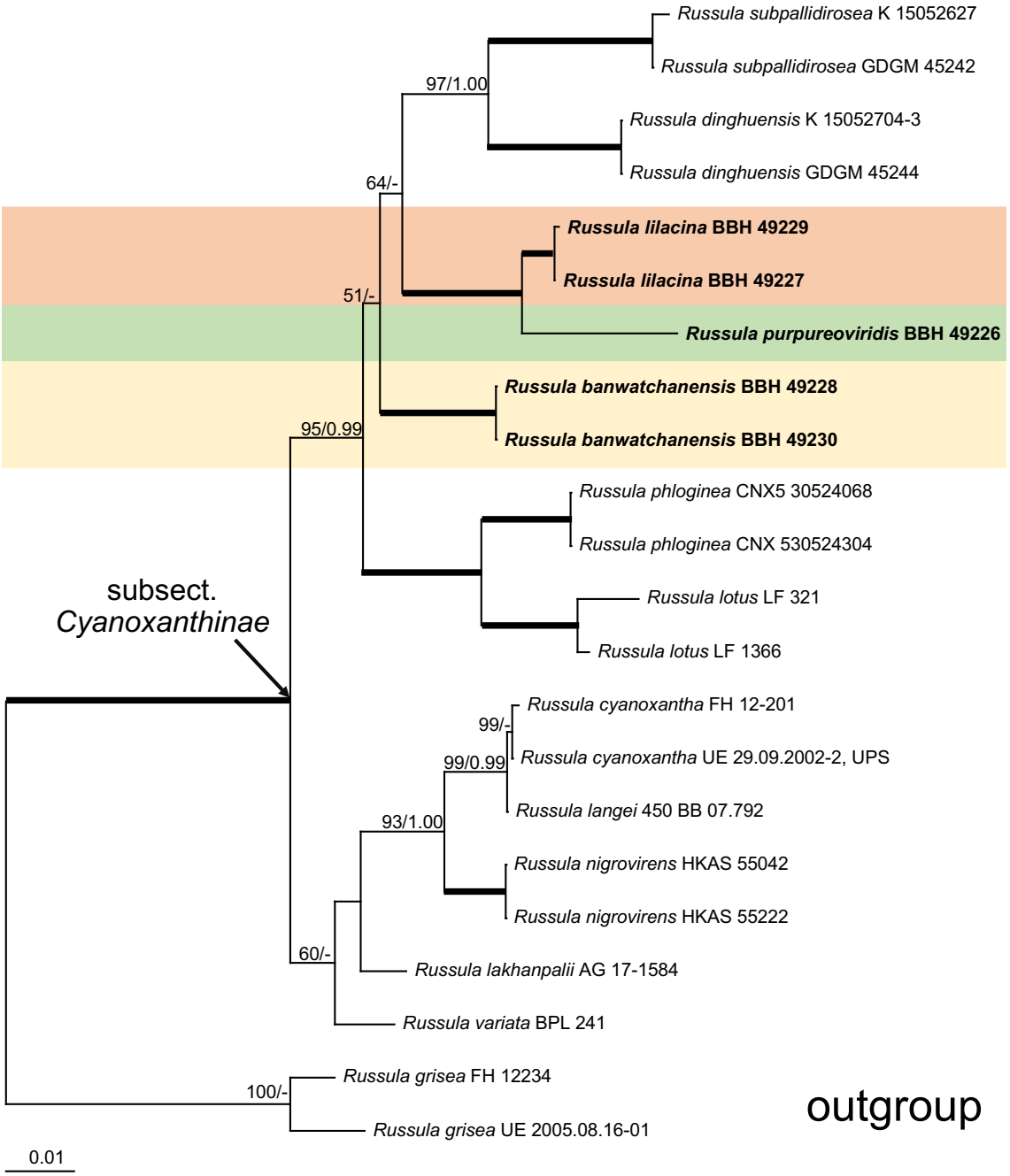
Taxa	Voucher	ITS	LSU	*rpb2*
Russula banwatchanensis	**BBH 49228**	**MT940813**	**MT940823**	**MT965687**
Russula banwatchanensis	**BBH 49230**	**MT940814**	**MT940824**	**MT965688**
Russula bubalina	K15052614	MG018742	–	–
Russula castanopsidis	KUN-HKAS 96547	–	MN134541	MN134541
Russula castanopsidis	KUN-HKAS 104880	–	MN134540	MN134540
Russula cheelii	JET1002	JX266623	JX266623	–
Russula cyanoxantha	FH 12-201	KR364093	KR364093	–
Russula cyanoxantha	UE29.09.2002-2	DQ422033	DQ422033	DQ421970
Russula delica	FH 12-272	–	KR364224	–
Russula dinghuensis	GDGM45244	KU863579	–	–
Russula dinghuensis	K15052704-3	KU863581	–	–
Russula emetica	OSAMY-7802	LC192780	–	–
Russula emetica	DG18	JQ888196	–	–
Russula grisea	UE2005.08.16-01	DQ422030	–	DQ422030
Russula heterophylla	UE20.08.2004-2	DQ422006	–	DQ422006
Russula ilicis	563IC52	AY061682	–	–
Russula intervenosa	CAL-1272	–	KU928135	–
Russula lakhanpalii	AG 17-1584	MN262088	–	–
Russula langei	450 BB 07.792	–	KU237510	KU237510
Russula lilacina	**BBH 49227**	**MT940809**	**MT940819**	**MT965685**
Russula lilacina	**BBH 49229**	**MT940810**	**MT940820**	**MT965686**
Russula lotus	LF321	MG214687	MG214687	–
Russula lotus	LF1366	MG214688	MG214688	–
Russula maguanensis	KUN-HKAS 102277	MH724918	MH724918	MH724918
Russula nigrovirens	HKAS 55042	KP171174	–	–
Russula nigrovirens	HKAS 55222	KP171173	–	–
Russula nauseosa	FH12173	–	KT933846	–
Russula orientipurpurea	SFC20170725-37	MT017548	–	–
Russula pauriensis	CAL1395	MF535185	–	–
Russula phloginea	CNX530524068	MK860701	MK860704	–
Russula phloginea	CNX530524304	MK860700	MK860703	–
Russula purpureogracilis	FH-12-055	MN130099	–	MN130099
Russula purpureoviridis	**BBH 49226**	**MT940807**	**MT940817**	**MT965684**
Russula rostraticystidia	H6165	EU019938	–	–
Russula shingbaensis	KD11-094 (BSHC)	KM386692	–	–
Russula subpallidirosea	K15052627	KU863578	–	–
Russula subpallidirosea	GDGM45242	KU863582	–	–
Russula subpallidirosea	RITF 4083	–	MK860702	–
Russula substriata	KUN-HKAS 102278	MH724921	MH724921	MH724921
Russula variata	BPL241	KT933959	KT933959	KT933959
Russula variispora	H5855	EU019934	–	–
Russula verrucospora	K16091205	MG786053	–	–
Russula vesca	AT2002091	DQ422018	–	DQ422018
Russula vinosa	UPSF124791	–	KX812900	–
Russula violeipes	SFC20121010-06	KF361808	KF361808	KF361808
Russula viridicinnamomea	K15091418	MK049972	–	–
Russula werneri	IB1997 0786	DQ422021	–	–



FP1423–1425-2 Phylogenetic relationships of *Russula* subsect. *Cyanoxanthinae* inferred from ITS sequences. The maximum likelihood analysis was performed on the CIPRES supercomputer using the program RAxML-HPC2 v. 8.2.12 on XSEDE (Miller et al. 2010). The Bayesian analysis was performed using MrBayes v. 3.0b4 (Huelsenbeck & Ronquist 2001). Numbers at the significant nodes represent ML bootstrap support values (BSML) /Bayesian posterior probabilities (BPP). Bold lines in the tree represent BSML = 100 % and BPP = 1.00.



FP1423–1425-3 Phylogenetic relationships of *Russula* subsect. *Cyanoxanthinae* inferred from LSU sequences. The maximum likelihood analysis was performed on the CIPRES supercomputer using the program RAxML-HPC2 v. 8.2.12 on XSEDE (Miller et al. 2010). The Bayesian analysis was performed using MrBayes v. 3.0b4 (Huelsenbeck & Ronquist 2001). Numbers at the significant nodes represent ML bootstrap support values (BSML) /Bayesian posterior probabilities (BPP). Bold lines in the tree represent BSML = 100 % and BPP = 1.00.



FP1423–1425-4 Phylogenetic relationships of *Russula* subsect. *Cyanoxanthinae* from a combined ITS, LSU and *rpb2* analyses. The maximum likelihood analysis was performed on the CIPRES supercomputer using the program RAxML-HPC2 v. 8.2.12 on XSEDE (Miller et al. 2010). The Bayesian analysis was performed using MrBayes v. 3.0b4 (Huelsenbeck & Ronquist 2001). Numbers at the significant nodes represent ML bootstrap support values (BSML) /Bayesian posterior probabilities (BPP). Bold lines in the tree represent BSML = 100 % and BPP = 1.00.