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Abstract: Novel species of fungi described in this study include those from various countries as follows: **Antarctica**, *Leuconeurospora bharatiensis* from accumulated snow sediment sample. **Argentina**, *Pseudocercospora quetri* on leaf spots of *Luma apiculata*. **Australia**, *Polychaetomyces verrucosus* on submerged decaying wood in sea water, *Ustilaginoidea cookiorum* on *Scleria levis*, *Xylaria guardiae* as endophyte from healthy leaves of *Macaranga tanarius*. **Belgium**, *Iodophanus taxi* on leaf of *Taxus baccata*. **Belize**, *Hygrocybe mirabilis* on soil. **Brazil**, *Gongronella irregularis* from soil, *Linodochium splendidum* on decaying sheath of *Euterpe oleracea*, *Nothophysalospora agapanthi* (incl. *Nothophysalospora gen. nov.*) on flower stalks of *Agapanthus praecox*, *Phaeosphaeria tabebuiae* on leaf of *Tabebuia* sp., *Verrucohypha endophytica* (incl. *Verrucohypha gen. nov.*) from healthy roots of *Acrocomia aculeata*. **Estonia**, *Inosperma apricum* on soil under *Quercus robur*. **Greece**, *Monosporascus solitarius* isolated from surface-sterilised, asymptomatic roots of *Microthlaspi perfoliatum*. **India**, *Diaporthe neocapsici* on young seedling stems of *Capsicum annuum*, *Fuscoporia naditirana* on dead wood, *Sebacina spongicarpa* on soil, *Torula kanvae* from the gut of a *Copris signatus* beetle. **Iran**, *Sarcinomyces pruni* from twig and petiole tissues of *Prunus persica* and *Prunus armeniaca*, *Xenodidymella quercicola* from leaf spots of *Quercus brantii*. **Italy**, *Agaricus aereiceps* on grass, *Agaricus bellui* in meadows, *Agaricus fabrianensis* in urban grasslands, *Beaucarneamyces muscorum* on moss growing in forest, *Xenoanthostomella quercus* on leaf litter of *Quercus ilex*. **Netherlands**, *Alfaria neerlandica* on stem lesions of *Cortaderia selloana*, *Neodictyosporium juncicola* on culms of *Juncus maritimus*, *Penicillium geertdesnooi* from soil under *Papaver rhoeas*, *Russula abscondita* on rich calcareous soil with *Quercus*, *Russula multiseptata* on rich clay soil with *Quercus*, *Russula purpureopallescens* on soil with *Populus*, *Sarocladium caricicola* on leaves of *Carex riparia*. **Pakistan**, *Circinaria shimlaensis* on limestone rocks. **Panama**, *Acrocalymma philodendri* on leaf spots of *Philodendron* sp., *Caligospora panamaensis* on leaf litter, *Chlamydocillium simulans* associated with a *Xylaria* sp., *Corynesporina panamaensis* on leaf litter, *Cylindromonium panamaense* on twig litter of angiosperm, *Cyphellophora panamaensis* on twig litter of angiosperm, *Microcera panamensis* on leaf litter of fern, *Pseudotricholoma pusillum* in tropical montane forest dominated by *Quercus* spp., *Striaticonidium panamaense* on leaf litter, *Yunnanomyces panamaensis* on leaf litter. **Poland**, *Albocremella abscondita* (incl. *Albocremella gen. nov.*) from rhizoids of liverwort *Conocephalum salebrosum*. **Portugal**, *Agaricus occidualis* in meadows. **South Africa**, *Alternaria elsarustiae* on culms of unidentified *Poaceae*, *Capronia capensis* on dead twig of unidentified angiosperm, *Codinaeella bulbinicola* on dead leaves of *Bulbine frutescens*, *Cytospora carpobroticola* on leaf of *Carpobrotus quadrifidus*, *Neophaeomoniella watsoniae* on leaf of *Watsonia* sp., *Neoplatysporoides aloigena* on leaf of *Aloe khamiesensis*, *Nothodactylaria comitabilis* on living leaf of *Itea rhamnoides*, *Nothopenidiella beaucarneae* (incl. *Nothopenidiella gen. nov*.) on dead leaves of *Beaucarnea stricta*, *Orbilia kirstenboschensis* on dead flower stalks of *Agapanthus praecox*, *Phragmocephala agapanthi* on dead flower stalks of *Agapanthus praecox*, *Podocarpigena hagahagaensis* (incl. *Podocarpigena gen. nov.*) on leaf spots of

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Abstract: *Podocarpus falcatus*, *Sporisorium enterogonipteri* from the gut of *Gonipterus* sp., *Synnemapestaloides searsiae* on leaf of *Searsia populifolia*, *Xenophragmocapnias diospyri* (incl. *Xenophragmocapnias gen. nov.*) on leaf spots of *Diospyros* sp., *Yunnanomyces hagahagaensis* on leaf spots of *Sideroxylon inerme*. **Spain**, *Agaricus basicinctus* in meadows, *Agaricus quercetorum* among leaf litter in oak forests, *Coprinopsis palaciosii* on degraded woody debris, *Inocybe complutensis* in calcareous loamy soil, *Inocybe tanitiae* in calcareous sandy soil, *Mycena subfragosa* on dead leaves of *Salix atrocinerea*, *Pseudobaeospora cortegadensis* in laurel forests, *Trichoderma sedimenticola* from fluvial sediments. **Sweden**, *Inocybe badjelanndana* on calcareous soil. **Ukraine**, *Beaucarneamyces lupini* on overwintered stems of *Lupinus polyphyllus*, *Protocreopsis globulosa* on thallus and apothecia of *Lecania cyrtella* on bark of *Populus* sp., *Thyridium tiliae* on dead twigs of *Tilia* sp. **USA**, *Cladosporium louisianense*, *Cyphellophora americana* from a bedroom vent, *Extremus massachusettsianus* from lyse buffer, *Myxotrichum tapetae* on carpet in basement, *Neospissiomyces floridanus* (incl. *Neospissiomyces gen. nov.*) on swab from hospital, *Polychaetomyces marinus* (incl. *Polychaetomyces gen. nov.*) on submerged driftwood in sea water, *Steccherinum fragrans* on hardwood fallen on the beach, *Steinbeckomyces carnegieae* (incl. *Steinbeckomyces gen. nov.*) on *Carnegiea gigantea*, *Tolypocladium pennsylvanicum* from air sampled in basement. **Vietnam**, *Acidomyces ducanhii* from *Aglaia* flowers, *Acidomyces paludis* from dead bark of *Acacia* sp., *Phakopsora sageretiae* on *Sageretia theezans*, *Puccinia stixis* on *Stixis scandens*. Morphological and culture characteristics are supported by DNA barcodes.

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Hubka acknowledges support from Talking microbes - understanding microbial interactions within One Health framework (CZ.02.01.01/00/22_008/0004597) and Czech Academy of Sciences Long-term Research Development Project (RVO: 61388971). The study of P. Eisvand and M. Mehrabi-Koushki was financially supported by grant (SCU. AP1403.294) from the Research Council of Shahid Chamran University of Ahvaz. The study of M. Piątek and M. Stryjak-Bogacka was supported by the statutory funds of the W. Szafer Institute of Botany, Polish Academy of Sciences, Kraków. Institutional support for the institutes of the Czech Academy of Sciences (J. Borovička) was provided by the Long-term Development Projects RVO67985831 and RVO61389005.


Nothodactylaria comitabilis

Fungal Planet 1697

MycoBank MB 856066

Nothodactylaria comitabilis Crous, ***sp. nov.***

Etymology: Name refers to an association with a *Meliola* sp.

Classification: *Nothodactylariaceae*, *Xylariales*, *Xylariomycetidae*, *Sordariomycetes*.

Mycelium consisting of 1.5–2 μm diam hyphae, smooth, initially hyaline, but becoming pigmented closer to conidiophores. *Conidiophores* reduced to conidiogenous cells, solitary, erect, subcylindrical, brown, smooth, geniculate-sinuous, 5–20 × 3–4 μm; apical region with several polyblastic sympodial denticles, 1–2 × 1 μm, not thickened, nor darkened. *Conidia* solitary, hyaline, smooth, guttulate, 1-septate in upper third of conidium, wedge-shaped, apex truncate, tapering to 1 μm diam truncate hilum, (20–)22–23(–25) × (2.5–)3 μm.

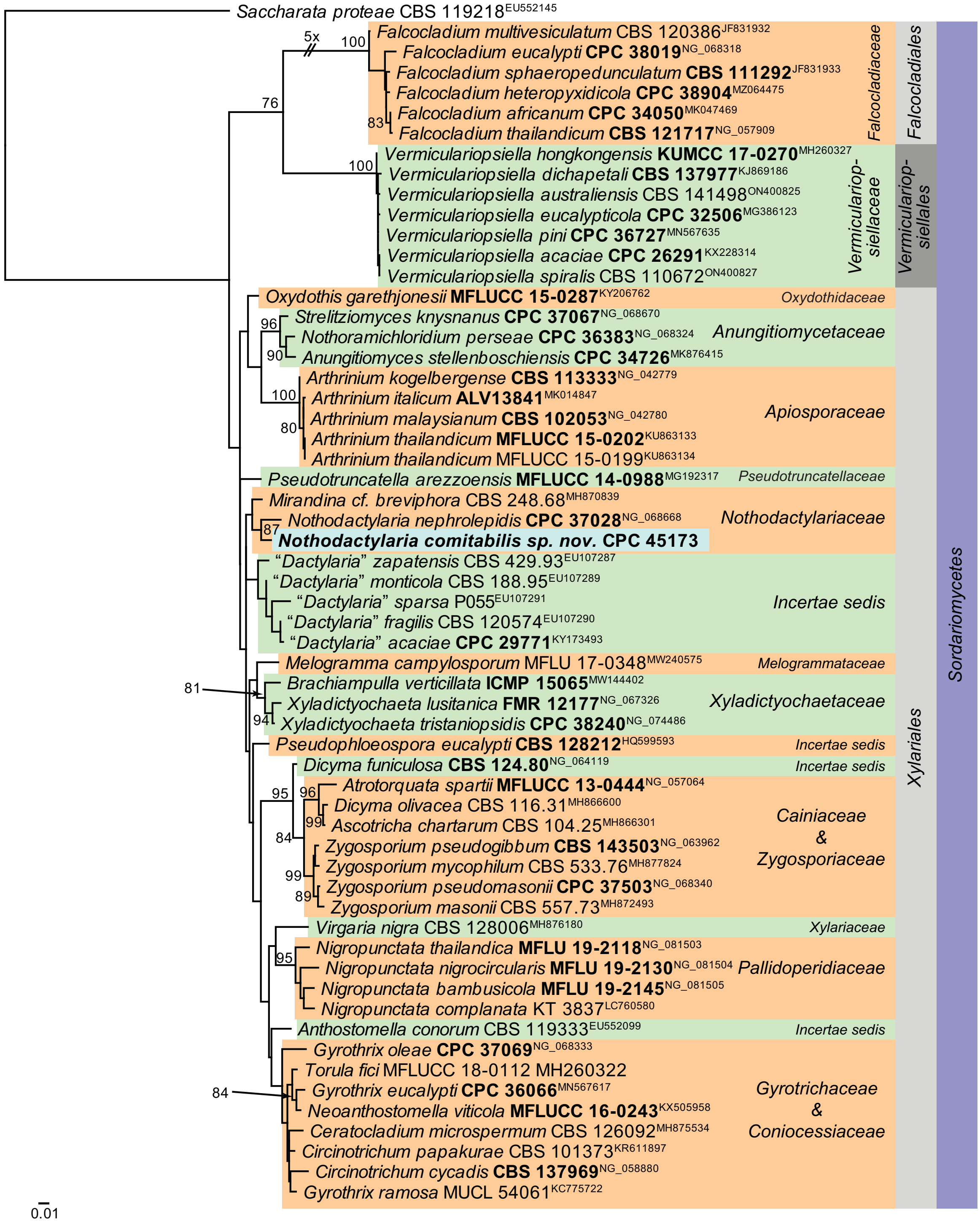
Culture characteristics: Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, lobate margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA surface ochreous, reverse sienna; on PDA and OA surface and reverse isabelline.

Typus: **South Africa**, Mpumalanga Province, Buffelskloof Nature Reserve, on living leaf of *Itea rhamnoides* (*Escalloniaceae*) with *Meliola* sp., 5 Aug. 2022, *P.W. Crous*, HPC 3977 (**holotype** CBS H-25281; culture ex-type CPC 45173 = CBS 150068; ITS and LSU sequences GenBank PQ498925 and PQ498974).

Colour illustrations: Leaves of *Itea rhamnoides* at Buffelskloof Nature Reserve, South Africa. Conidiophores and conidiogenous cells giving rise to conidia on SNA; conidia. Scale bars = 10 μm.

Notes: *Nothodactylaria comitabilis* is the second species described in the genus but is morphologically quite distinct from *N. nephrolepidis* (on leaves of *Nephrolepis exaltata*, Knysna, South Africa) having 1(–3)-septate, hyaline, subcylindrical to fusoid-ellipsoid conidia. Both species share hyaline to pale brown conidiogenous cells, with polyblastic sympodial denticles, and hyaline conidia (Crous *et al.* 2019).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Dactylaria* sp. TKPB-2017 [strain FeF108a, GenBank MZ493066.1; Identities = 513/567 (90 %), 19 gaps (3 %)], *Mirandina breviphora* (*nom. inval.*) [strain CBS 248.68, GenBank MH859127.1; Identities = 511/572 (89 %), 18 gaps (3 %)], and *Dactylaria acerosa* [strain ICMP 13178, GenBank OR543730.1; Identities = 511/575 (89 %), 30 gaps (5 %)]. Closest hits using the **LSU** sequence are *Nothodactylaria nephrolepidis* [strain CPC 37028, GenBank NG_068668.1; Identities = 824/843 (98 %), two gaps (0 %)], *Mirandina breviphora* (*nom. inval.*) [strain CBS 248.68, GenBank MH870839.1; Identities = 851/875 (97 %), two gaps (0 %)], and *Dactylella microaquatica* [strain CBS 216.59, GenBank MH869383.1; Identities = 815/842 (97 %), two gaps (0 %)].



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Nothodactylaria* LSU nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Saccharata proteae* (CBS 119218; GenBank EU552145) and the novelty described here is highlighted with a coloured block and **bold** font. Families, orders and the class are shown to the right of the tree in coloured blocks. The branch of *Falcocladiaceae* was shortened to facilitate layout. Alignment statistics: 59 strains including the outgroup; 826 characters including alignment gaps analysed: 277distinct patterns, 228 parsimony-informative, 50 singleton sites, 548 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: SYM+R3. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Neodictyosporium juncicola

Fungal Planet 1698 MycoBank MB 856067

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

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

Classification: *Incertae sedis*, *incertae sedis*, *Sordariomycetidae*, *Sordariomycetes*.

Conidiomata pycnidial, brown, superficial to immersed in agar, up to 300 µm diam, opening via irregular rupture; wall of 15–20 µm diam, consisting of several layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells or 1–3-septate, subcylindrical, pale brown, lining the basal cavity. *Conidiogenous cells* subcylindrical to doliiform, subhyaline to pale brown, smooth, holoblastic, 4–6 × 3–4 µm. *Conidia* 17–30(–40) µm tall, (12–)15–17(–22) µm diam, medium brown, becoming pale brown towards apex, complanate, dictyospores, with 5–12 rows of cells, each row with 3–7 cells, 3–4 µm diam, narrowing towards apex; basal cell medium brown with truncate hilum.

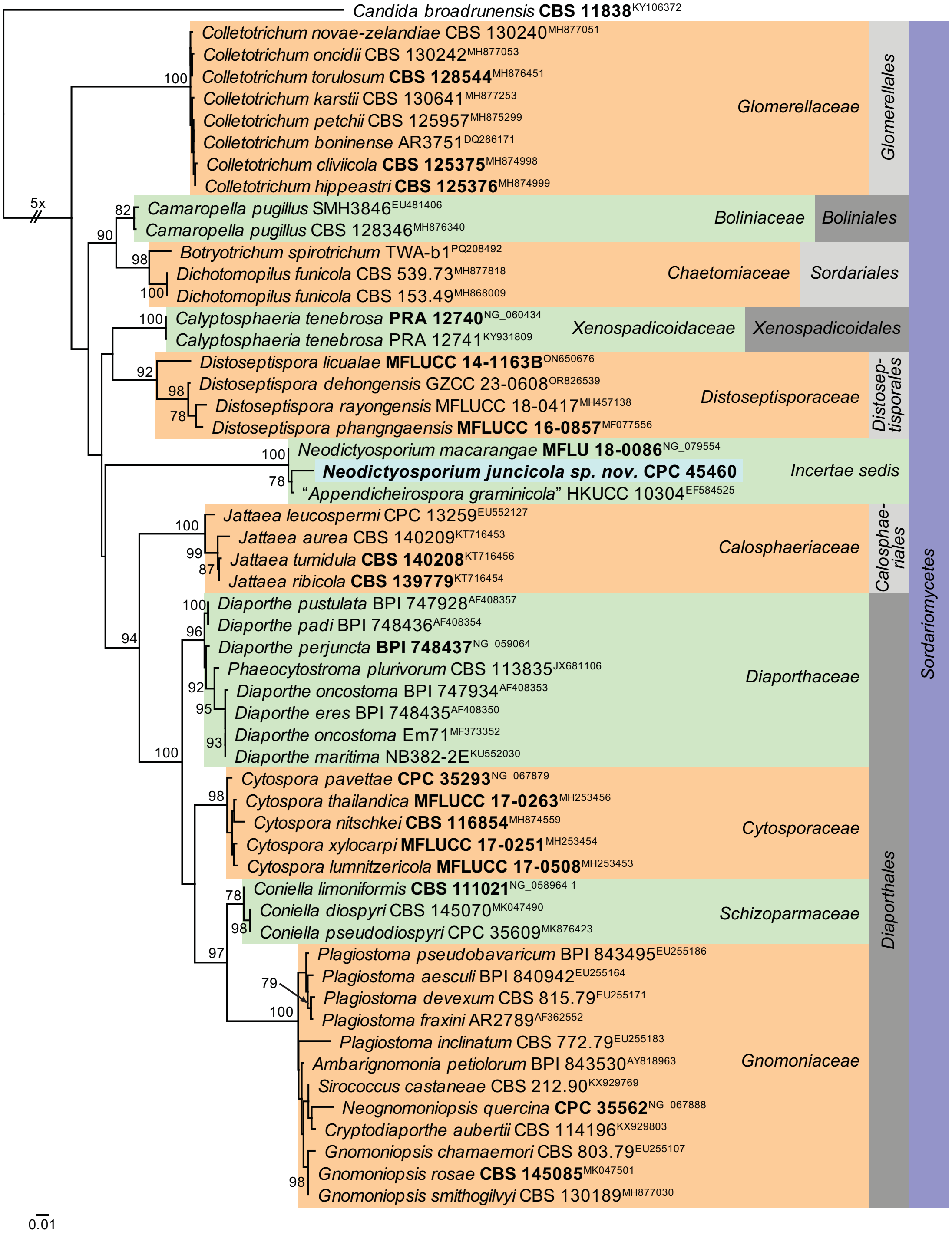
Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth, even margin, reaching 25 mm diam after 2 wk at 25 °C. On MEA surface and reverse umber; on PDA surface and reverse olivaceous grey.

Typus: **Netherlands**, North Holland Province, Texel, Den Hoorn, Mokbaai, N53°00’41’’, E04°44’38’’, on culms of *Juncus maritimus* (*Juncaceae*), 9 Dec. 2022, *E.R. Osieck*, HPC 4097 = WI-70/#4601 (**holotype** CBS H-25291; culture ex-type CPC 45460 = CBS 150187; ITS, LSU, *rpb2* and *tub2* sequences GenBank PQ498926, PQ498975, PQ497718 and PQ497771).

Colour illustrations: Mokbaai, Texel, the Netherlands. Conidiomata on oatmeal agar; conidiophores and conidiogenous cells giving rise to conidia; conidium. Scale bars = 10 µm.

Notes: *Neodictyosporium juncicola* is the second species of *Neodictyosporium* described to date. It differs morphologically from *N. macarangae* (leaf petioles of *Macaranga tanarius*, Taiwan) in that the latter is dimorphic, having smaller, pigmented, dictyosporous conidia, 22–26(–32) × (11–)13–17 µm, with 5–6 rows of cells, and clavate to obovoid, 3-septate conidia (Tennakoon *et al.* 2021). The conidia of *N. juncicola* are reminiscent of those of the (unrelated) *Coelodictyosporium* (*Lophiostoma*) *pseudodictyosporium* but its conidia are somewhat wider and “regularly consisting of 6–8 rows of cells” (Liu *et al.* 2015). Wijayawardene (2016) noted also resemblance of conidia of *Psammina* with the latter species but *P. bommerae* has many more radiating arms (Sutton 1980). Species belonging to *Dictyosporium* (also with cheiroid conidia) are sporodochial.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Dictyosporium* sp. [strain KT 2028, GenBank MZ363675.1; Identities = 419/467 (90 %), 13 gaps (2 %)], and very distant hits to *Tubakia dryina* [strain CBS 114920, GenBank MG591856.1; Identities = 323/377 (86 %), 19 gaps (5 %)], and *Tubakia melnikiana* [strain CPC 32249, GenBank MG591889.1; Identities = 320/374 (86 %), 18 gaps (4 %)]. Closest hits using the ***rpb2*** (first part) sequence had distant similarity to “*Appendicheirospora graminicola*” [strain HKUCC 10304, GenBank EF584526.1; Identities = 557/650 (86 %), one gap (0 %)], *Platytrachelon abietis* [strain CBS 125235, GenBank JX066698.1; Identities = 624/771 (81 %), no gaps], and *Aquimonospora tratensis* [strain MFLUCC 17-2133, GenBank MK344654.1; Identities = 613/767 (80 %), no gaps]. Closest hits using the **LSU** sequence are “*Appendicheirospora graminicola*” [strain HKUCC 10304, GenBank EF584525.1; Identities = 843/857 (98 %), no gaps], *Neodictyosporium macarangae* [voucher MFLU 18-0086, GenBank NG_079554.1; Identities = 845/863 (98 %), two gaps (0 %)], and *Fluminicola aquatica* [strain MFLUCC 15-0962, GenBank MF374366.1; Identities = 792/875 (91 %), nine gaps (1 %)]. No significant hits were obtained when the ***tub2*** sequence was used in blastn and megablast searches.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Neodictyosporium* LSU nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Candida broadrunensis* (CBS 11838; GenBank KY106372) and the novelty described here is highlighted with a coloured block and **bold** font. Families, orders and the class are shown to the right of the tree in coloured blocks. The root branch was shortened to facilitate layout. Alignment statistics: 55 strains including the outgroup; 869 characters including alignment gaps analysed: 308 distinct patterns, 241 parsimony-informative, 67 singleton sites, 561 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIMe+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Sarocladium caricicola

Fungal Planet 1699 MycoBank MB 856068

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

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

Classification: *Sarocladiaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* solitary, erect, subcylindrical, hyaline, smooth, 1–2-septate, 20–50 × 2–2.5 µm. *Conidiogenous cells* integrated, phialidic, hyaline, smooth, subcylindrical with apical taper, 15–40 × 2–2.5 µm; collarette inconspicuous, not flared. *Conidia* solitary, subcylindrical with obtuse ends, aggregating in mucoid mass, aseptate, hyaline, smooth, guttulate, (4–)5–7 × (1.5–)2 µm.

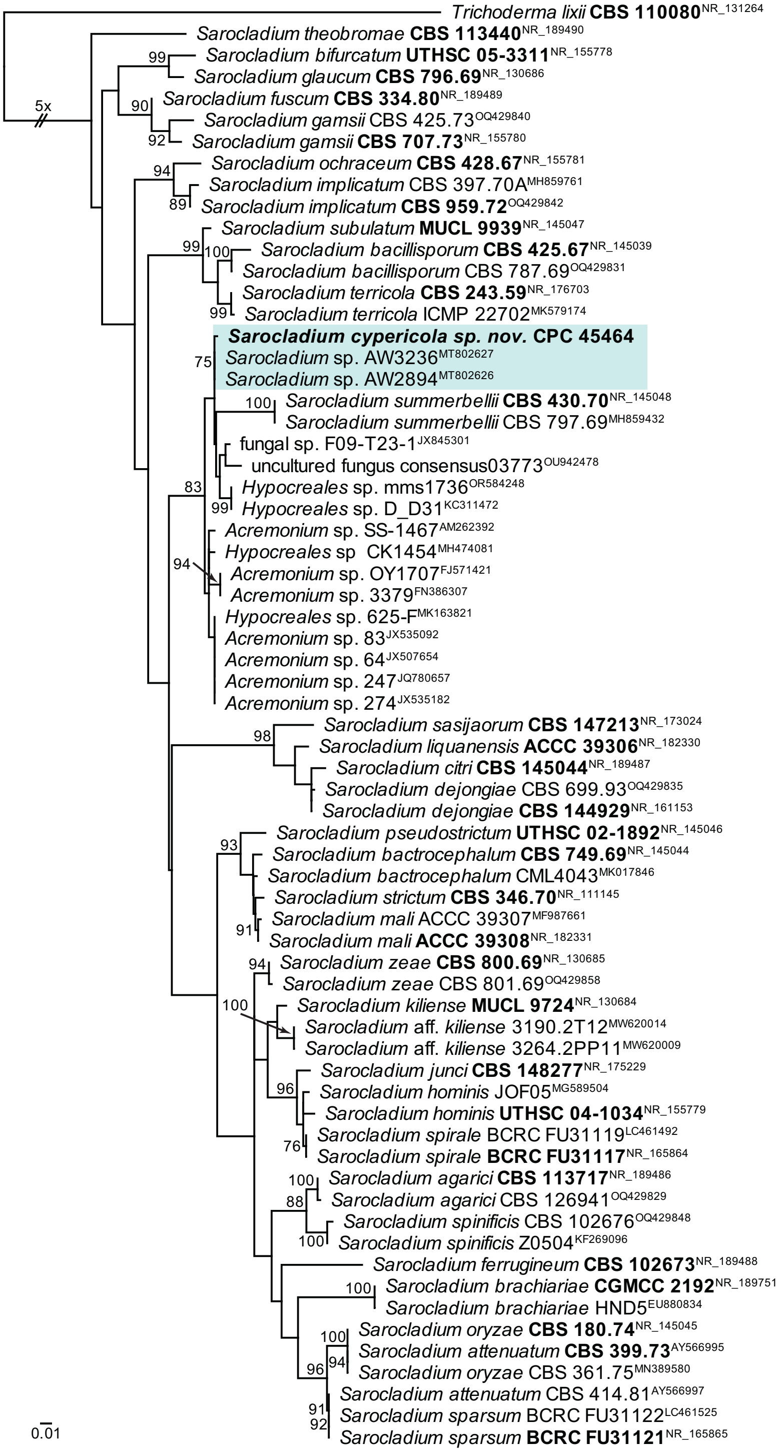
Culture characteristics: Colonies flat, spreading, surface folded, with sparse aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface saffron, reverse saffron to peach.

Typus: **Netherlands**, Utrecht Province, Langbroek, Leeuwenburgh, N52°01’24’’, E05°18’24’’, on leaves of *Carex riparia* (*Cyperaceae*), 25 Jan. 2023, *E.R. Osieck*, HPC 4106 = WI-73 / #4613 (**holotype** CBS H-25309; culture ex-type CPC 45464 = CBS 150792; ITS and LSU sequences GenBank PQ498927 and PQ498976).

Notes: *Sarocladium caricicola* resides in a clade with several isolates identified as *Acremonium* sp., or *Sarocladium* sp. *Sarocladium* was recently treated by Hou *et al.* (2023). *Sarocladium caricicola* is closely related to *S. summerbellii*, which has conidia of similar dimensions, but they tend to be fusoid, with pointed ends (Giraldo *et al.* 2015).

Based on a megablast search tof NCBI’s GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Sarocladium* sp. [voucher AW3236, GenBank MT802627.1; Identities = 502/503 (99 %), no gaps], *Sarocladium summerbellii* [voucher MEL 7371, GenBank OP437860.1; Identities = 494/516 (96 %), four gaps (0 %)], and *Sarocladium ochraceum* [strain IHEM 10207, GenBank OW984568.1; Identities = 519/544 (95 %), four gaps (0 %)]. Closest hits using the **LSU** sequence are *Acremonium* sp. 83 OA-2013 [strain 83, GenBank JX535093.1; Identities = 842/842 (100 %), no gaps], *Sarocladium implicatum* [strain CBS 125892, GenBank MH875549.1; Identities = 841/842 (99 %), no gaps], and *Sarocladium kiliense* [strain CBS 400.52, GenBank KM231729.1; Identities = 818/831 (98 %), one gap (0 %)].

Colour illustrations: Leeuwenburgh, Langbroek, the Netherlands. Conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Sarocladium* ITS nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Trichoderma lixii* (CBS 110080; GenBank NR_131264) and the novelty described here is highlighted with a coloured block and **bold** font. The root branch was shortened to facilitate layout. Alignment statistics: 67 strains including the outgroup; 597 characters including alignment gaps analysed: 271 distinct patterns, 144 parsimony-informative, 69 singleton sites, 384 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2+F+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Penicillium geertdesnooi

Fungal Planet 1700

MycoBank MB 855809

Penicillium geertdesnooi Crous, Sandoval-Denis & Hern.-Restr., ***sp. nov.***

Etymology: Named for Prof. dr Geert de Snoo, who was Director of the Netherlands Institute of Ecology (NIOO-KNAW) of the Royal Dutch Academy of Arts and Sciences (2019–2024). During his term as Director, he actively stimulated biodiversity research collaboration between the NIOO-KNAW, and the Westerdijk Fungal Biodiversity Institute (WI-KNAW), who in turn have the genus *Penicillium* as the logo of their institute. *Penicillium geertdesnooi* is described as a novel species to reflect this new research collaboration. The fungus was isolated from soil under *Papaver rhoeas* (Geert's favourite flower), in Zeist, the town in the Netherlands where he was born, as part of a Citizen Science project with Dutch school children known as "Fungi for the Future".

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

Sclerotia absent. *Conidiophores* monoverticillate, simple, erect, straight to flexuous, 43–121 µm long, 2–4 µm wide, smooth- and thick-walled, widening progressively towards the apex, ending in a slightly vesiculate upper region, 3.5–6 µm wide, bearing multiple conidiogenous cells; rarely non-vesiculate, with a single terminal conidiogenous cell. *Conidiogenous cells* phialidic, (1–)3–8 per stipe, ampulliform, (7.5–)9–10.5(–13) × (2–)2.5–3.5(–4) µm, smooth- and thin-walled. *Conidia* globose, subglobose to obovate, (2.5–)3.5–4 × (2–)2.5–3.5(–4) µm, smooth- and thick-walled, dark green to dull green in mass.

Culture characteristics: Colonies on CYA and MEA reaching 14–19 mm diam after 7d, erumpent and radially folded, velvety, cottony to floccose, leek green to greyish green (Rayner 1970), radial straw to primrose patches and pale sulphur yellow, scarlet to red excretions may be present, aerial mycelium abundant in irregular clusters, margin undulate to filiform. Reverse pale luteous, dark vinaceous red at centre, with pale herbage green to yellow green diffusible pigment.

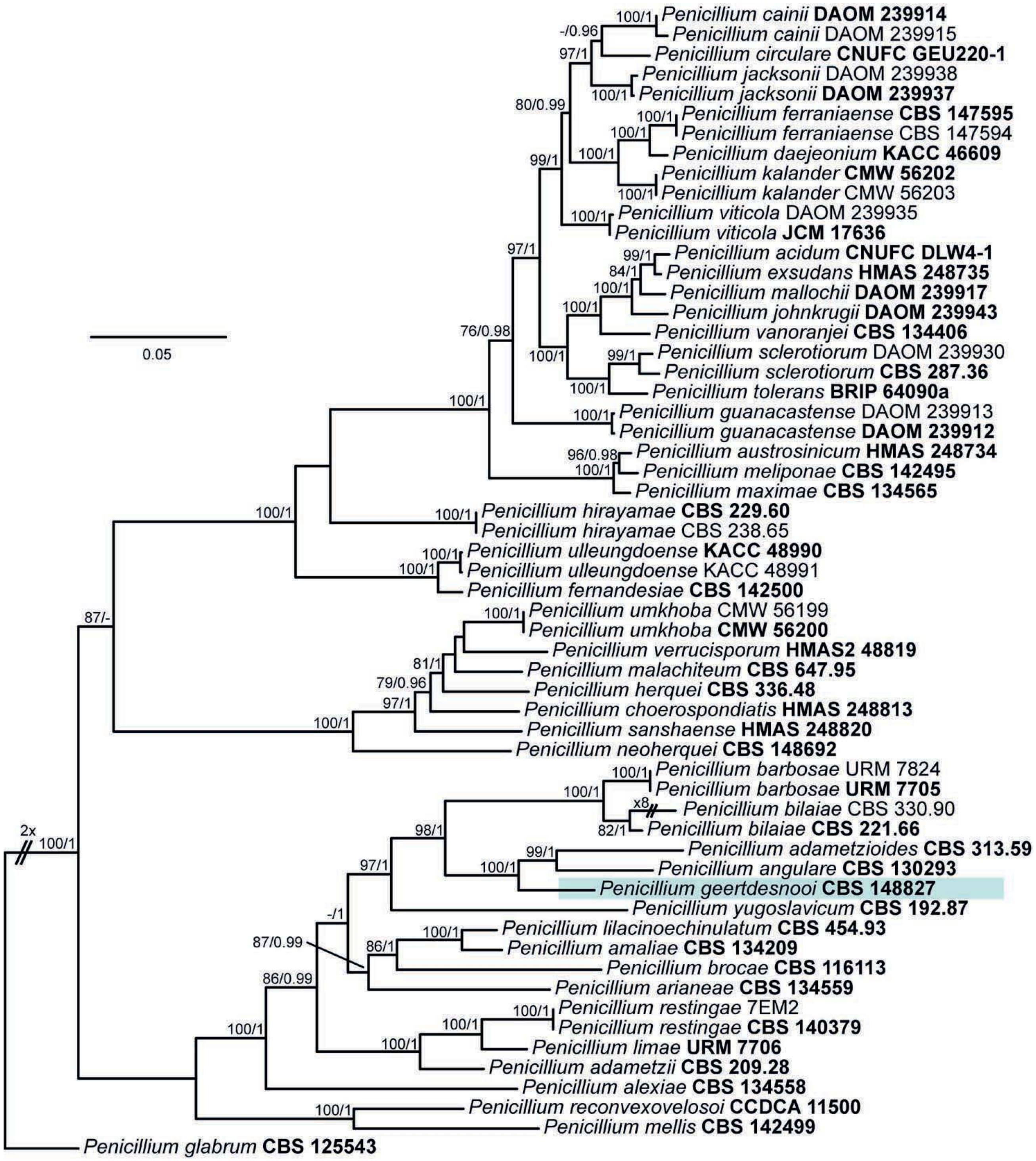
Typus: **Netherlands**, Utrecht Province, Zeist, from soil under *Papaver rhoeas* (*Papaveraceae*), 13 May 2021, *M. & V. van Rooijen & M. Hernandez-Restrepo* [**holotype** CBS 148827, preserved in a metabolically inactive state, culture ex-type CBS 148827 = SPC 81.14; ITS, LSU, *BenA*, *CaM*, *rpb2* and *tef1* (second part) sequences GenBank PQ498928, PQ498977, PQ497772, PQ497711, PQ497719 and PQ497756].

Colour illustrations: *Papaver rhoeas*, Zeist, the Netherlands (photo by J.Z. Groenewald). Colony on CYA, conidia and conidiophores. Scale bars = 10 µm.

Notes: *Penicillium geertdesnooi* groups within series *Adametziorum*, section *Sclerotiorum*, subgenus *Aspergilloides* of *Penicillium*, being closely related to *Penicillium adatmetzioides* and *P. angulare*. The three species clustered in a strongly supported branch in all single-gene and multilocus phylogenetic analyses (supplementary files); the three taxa, however, are clearly differentiated phylogenetically by all the standard phylogenetic markers used for *Penicillium*, including ITS. Morphologically, *P. geertdesnooi* differs from its closest siblings by its green colonies producing pale green soluble pigments and yellow to red exudates (*vs* greyish colonies in *P. adametzioides* and *P. angulare*, with yellow to pale brown pigment in *P. adametzioides* and absence of diffusible pigments, but producing clear exudates in *P. angulare*). Additionally, *P. geertdesnooi* has a restricted growth rate, wider phialides and larger conidia which distinguishes it from *P. adametizioides*; while the presence of noticeable conidiophore vesicles differentiates the novel species from *P. angulare*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Penicillium* sp. [strain NWHC 44736-21-02-02, GenBank KX148633.1; Identities = 476/478 (99 %), 2 gaps (0 %)], and *Penicillium angulare* [strain DTO190B8, GenBank KC773829.1; Identities = 470/485 (97 %), 5 gaps (1 %)]. Closest hits using the ***BenA*** sequence are *Penicillium angulare* [strain P448, GenBank MZ078822.1; Identities = 411/443 (93 %), 6 gaps (1 %)], and *Penicillium adametzioides* [strain YT-QM2, GenBank MG696875.1; Identities = 417/460 (91 %), 9 gaps (1 %)]. Closest hits using the ***CaM*** sequence had highest similarity to *Penicillium* sp. [strain SZMC 27950, GenBank OP765561.1; Identities = 465/487 (95 %), 5 gaps (1 %)], *Penicillium glabrum* [strain NRRL 35626, GenBank EF198580.1; Identities = 481/514 (94 %), 7 gaps (1 %)], and *Penicillium adametzioides* [strain CBS 313.59, GenBank JN686387.1; Identities = 475/511 (93 %), 4 gaps (0 %)]. Closest hits using the ***rpb2*** sequence had highest similarity to *Penicillium angulare* [strain DTO 3A6, GenBank JN406554.1; Identities = 365/395 (92 %), no gaps], *Penicillium adametzioides* [strain CBS 313.59, GenBank JN406578.1; Identities = 357/389 (92 %), no gaps], and *Penicillium yugoslavicum* [as *P. jugoslavicum*, strain CBS 192.87, GenBank JN406618.1; Identities = 360/395 (91 %), no gaps].

Supplementary material: doi: 10.6084/m9.figshare.27275988 (alignment with individual gene trees).



Most likely phylogram obtained from the maximum likelihood analysis with raxmlGUI v. 2.0 (Edler *et al.* 2020) of the combined *BenA*, *CaM*, ITS and *rpb2* nucleotide alignment. Numbers at the nodes are bootstrap support values from 1 000 non-parametric bootstrap replicates (> 70 % are shown), followed by posterior probability values from a Bayesian analysis with MrBayes v. 3.2.7 (Ronquist *et al*. 2012). Culture collection numbers are indicated for all strains. Sequences from material with a type status are indicated in bold font. The tree was rooted to *Penicillium glabrum* CBS 125543 and the novelty described here is highlighted with a coloured block. The root and a terminal branch were shortened to facilitate layout. Alignment statistics: 58 strains including the outgroup; 2 524 characters including alignment gaps analysed: 1 056 distinct patterns, 855 parsimony-informative, 196 singleton sites, 1 410 constant sites. The best-fit model identified for all gene-partitions in ML and BI using MrModeltest2 (Nylander 2004) was: GTR+I+G. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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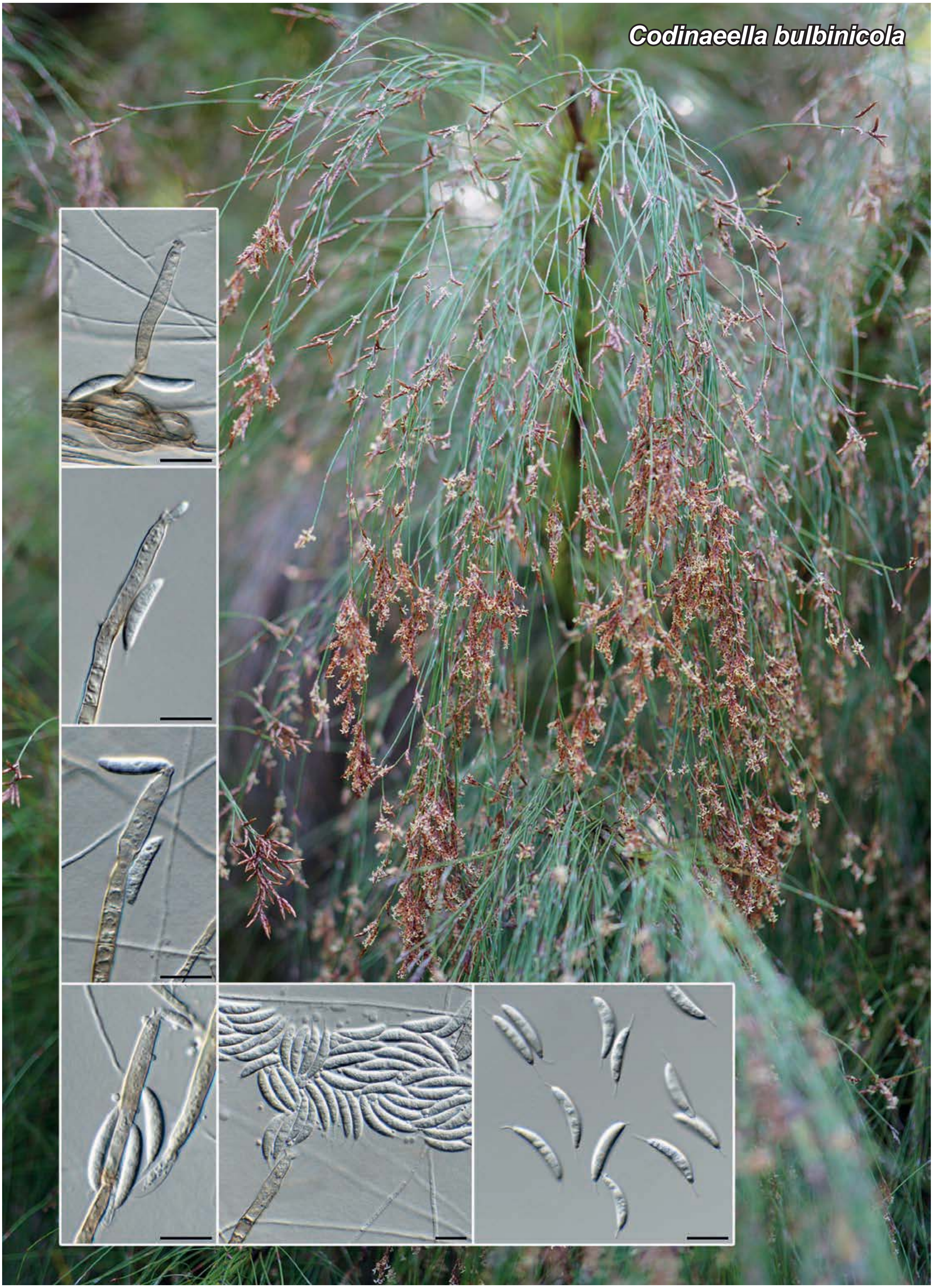

Codinaeella bulbinicola

Fungal Planet 1701 MycoBank MB 856070

Codinaeella bulbinicola Crous, *sp. nov.*

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

Classification: *Chaetosphaeriaceae*, *Chaetosphaeriales*, *Sordariomycetidae*, *Sordariomycetes*.

Mycelium consisting of smooth, pale brown, branched, septate, 1.5–2 μm diam hyphae, forming hyphal coils, typically giving rise to several conidiophores. *Setae* medium brown, erect, multiseptate, terminal on hyphae, up to 150 μm tall, 3–4 μm wide in swollen apical region; apex subobtuse, pale brown than stipe. *Conidiophores* solitary, subcylindrical, straight to flexuous, multiseptate, 30–50 × 3–4 μm. *Conidiogenous cells* integrated, terminal, subcylindrical, 30–40 × 3–5 μm, with terminal funnel-shaped collarette, 3–4 μm diam. *Conidia* solitary, aggregating in mucoid mass, hyaline, smooth, granular, aseptate, curved, fusoid-ellipsoid, more prominently curved on dorsal side, setulate, setae 3–5 μm long, apical seta central, basal seta attached on inner plane, apex subobtuse, hilum truncate, conidia (12–)14–16(–17) × (3–)4 μm.

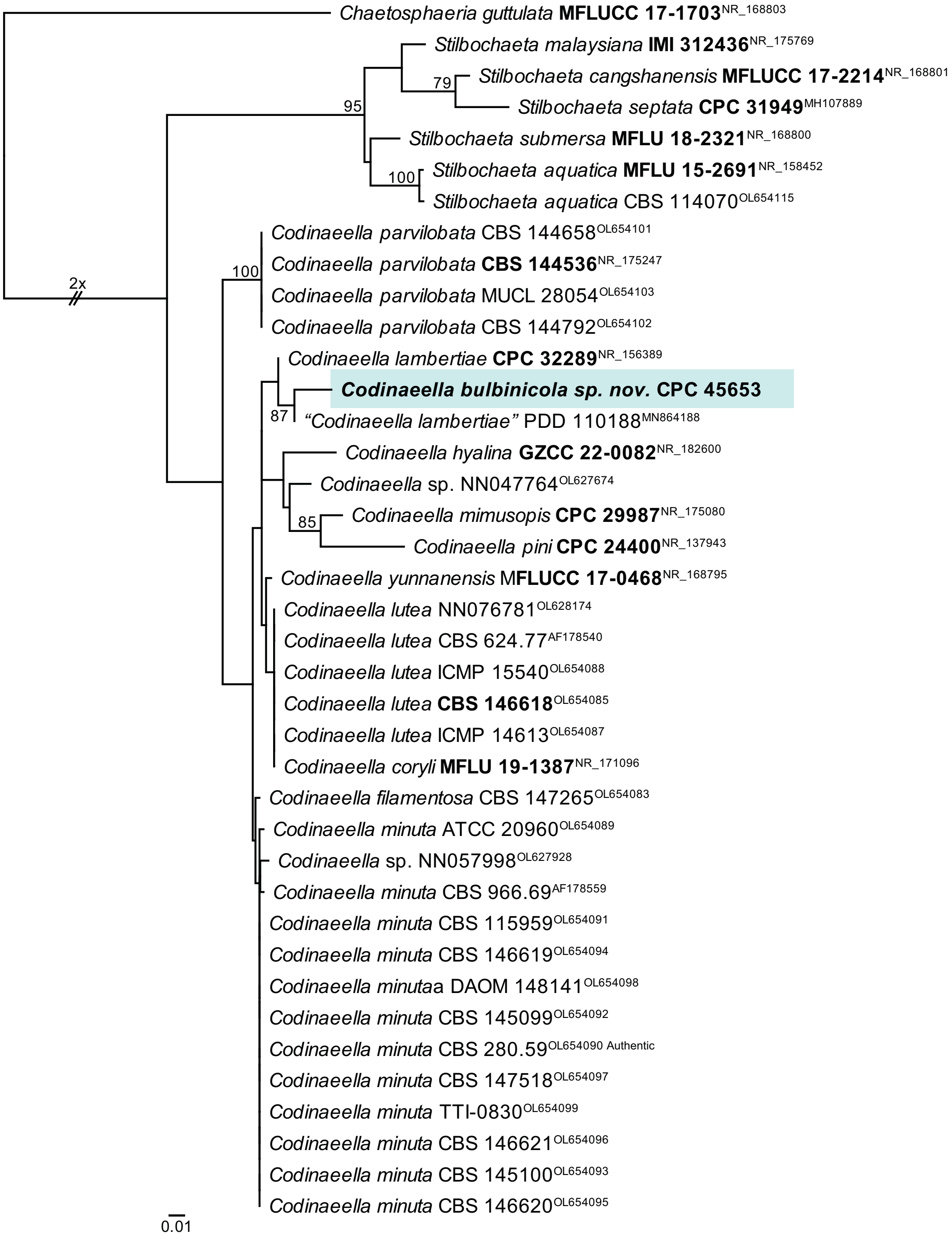
Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface pale olivaceous grey and reverse luteous; on PDA surface and reverse pale olivaceous grey; on OA surface ochreous with patches of cream.

Typus: **South Africa**, Western Cape Province, Stellenbosch Botanical Garden, on dead leaves of *Bulbine frutescens* (*Asphodelaceae*), 4 Mar. 2023, *P.W. Crous*, HPC 4119 [**holotype** CBS H-25318; culture ex-type CPC 45653 = CBS 150801; ITS, LSU, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank PQ498929, PQ498978, PQ497720, PQ497764 and PQ497773].

Colour illustrations: *Bulbine frutescens* in Stellenbosch Botanical Garden, South Africa. Conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 μm.

Notes: Species of *Codinaeella* are usually found as saprobes on dead leaves, bark, and fruits. *Codinaeella* **bulbinicola** is closely related to *C. lambertiae*, but can be distingsuished as the latter has smaller conidia, 11.5–14.5 × 2.5–3 μm, longer conidiophores, 128–362 μm long, and lacks setae (Réblová *et al.* 2021).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Codinaeella lambertiae* [strain CBS 143419, GenBank NR_156389.1; Identities = 511/524 (98 %), one gap (0 %)], *Dictyochaeta simplex* [strain 417E, GenBank MZ078594.1; Identities = 542/560 (97 %), one gap (0 %)], and *Codinaeella minuta* [strain ATCC 20960, GenBank OL654089.1; Identities = 452/468 (97 %), one gap (0 %)]. Closest hits using the **LSU** sequence are *Codinaeella filamentosa* [strain CBS 147265, GenBank OL654140.1; Identities = 857/864 (99 %), no gaps], *Codinaeella lutea* [strain CBS 624.77, GenBank OL654143.1; Identities = 855/864 (99 %), no gaps], and *Codinaeella yunnanensis* [strain MFLUCC 17-0468, GenBank NG_068630.1; Identities = 834/843 (99 %), no gaps]. Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Codinaeella yunnanensis* [voucher MFLU 18-1611, GenBank MN156517.1; Identities = 541/583 (93 %), no gaps], *Zignoella ovoidea* [strain SMH2605, GenBank AY780173.1; Identities = 720/831 (87 %), two gaps (0 %)], and *Menispora tortuosa* [strain AFTOL-ID 278, GenBank DQ836884.1; Identities = 718/831 (86 %), two gaps (0 %)]. Distant hits were obtained using the ***tef1*** (first part) sequence in a blastn search and had highest similarity to *Scolecofusarium ciliatum* [strain 295Jb14, GenBank KU516644.1; Identities = 420/505 (83 %), 27 gaps (5 %)], and *Stilbochaeta septata* [strain CBS 143386, GenBank MH108015.1; Identities = 211/238 (89 %), 6 gaps (2 %)]. Distant hits were obtained using the ***tub2*** sequence and had highest similarity to *Chloridium moratum* [strain FMR 11343, GenBank OP465102.1; Identities = 450/578 (78 %), 43 gaps (7 %)], *Chloridium caudigerum* [strain FMR 11338, GenBank OP465061.1; Identities = 444/579 (77 %), 43 gaps (7 %)], and *Chloridium volubile* [strain CBS 144661, GenBank OP465123.1; Identities = 440/566 (78 %), 42 gaps (7 %)].



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Codinaeella* ITS nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Chaetosphaeria guttulata* (MFLUCC 17-1703; GenBank NR_168803) and the novelty described here is highlighted with a coloured block and **bold** font. The root branch was shortened to facilitate layout. Alignment statistics: 39 strains including the outgroup; 481 characters including alignment gaps analysed: 154 distinct patterns, 76 parsimony-informative, 58 singleton sites, 347 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988)

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Nothopenidiella beaucarneae

Fungal Planet 1702

MycoBank MB 856071

Nothopenidiella **Crous, *gen. nov.***

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

Classification: *Microthyriaceae*, *Microthyriales*, *incertae sedis*, *Dothideomycetes*.

Mycelium consisting of hyaline to pale brown, smooth, branched, septate hyphae. *Conidiophores* arising from superficial hyphae, erect, solitary, subcylindrical, mostly unbranched, pale brown, smooth, septate. *Conidiogenous cells* integrated, terminal, polyblastic; scars truncate, not darkened nor thickened. *Conidia* mostly in unbranched chains, fusoid-ellipsoid, hyaline, smooth, guttulate, septate; hila unthickened, not darkened.

Type species: *Nothopenidiella beaucarneae* Crous

MycoBank MB 856072

Nothopenidiella beaucarneae **Crous, *sp. nov.***

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

Mycelium consisting of hyaline to pale brown, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* arising from superficial hyphae, erect, solitary, subcylindrical, mostly unbranched, pale brown, smooth, 1–4-septate, 15–40 × 2.5–3 µm. *Conidiogenous cells* integrated, terminal, polyblastic, 7–15 × 2.5–3 µm; scars truncate, not darkened nor thickened, 1–1.5 µm diam. *Conidia* mostly in unbranched chains (–15), fusoid-ellipsoid, hyaline, smooth, guttulate, 0–2-septate, (16–)18–20 × 3(–3.5) µm; hila unthickened, not darkened, 1–1.5 µm diam.

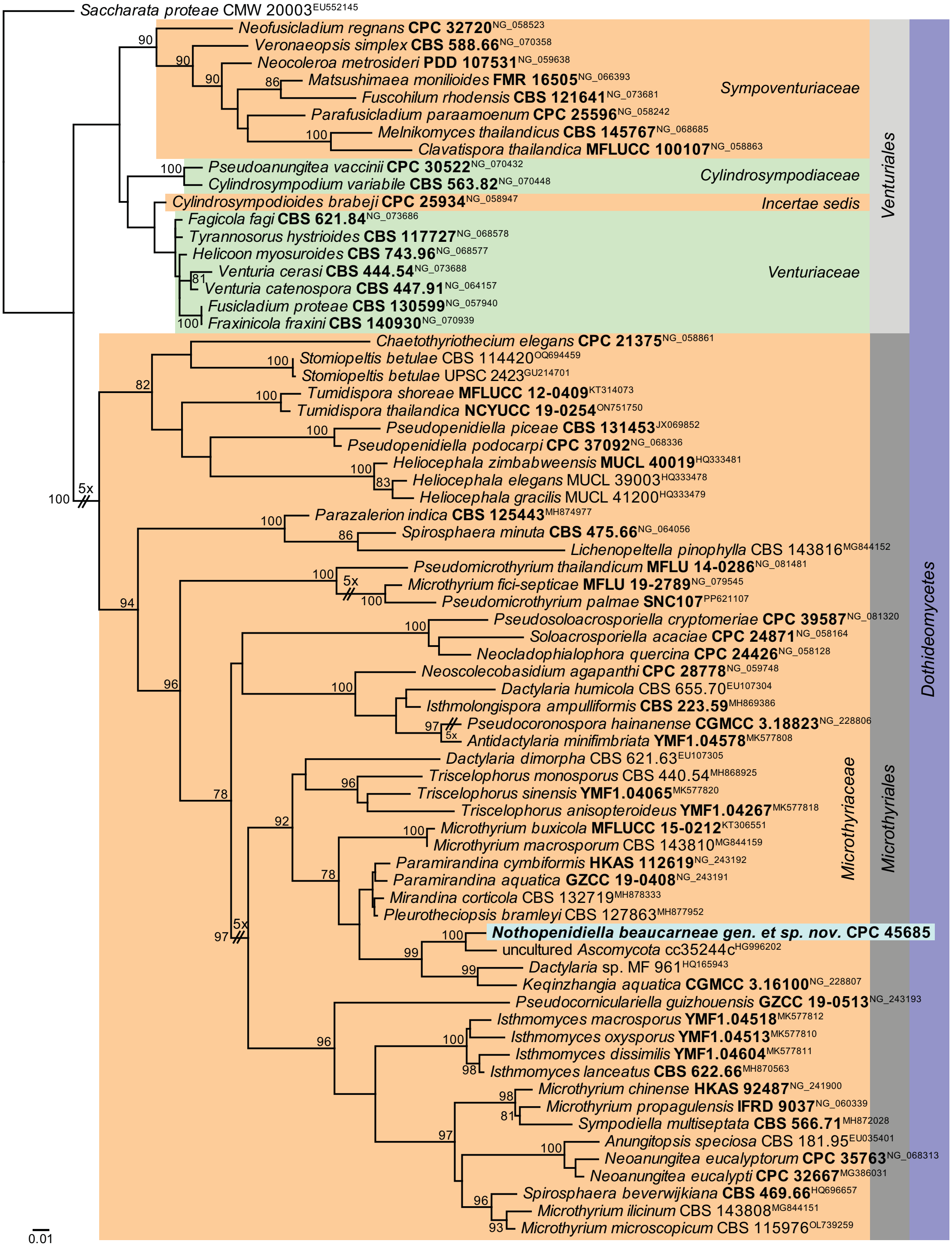
Culture characteristics: Colonies erumpent, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 7 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus: **South Africa**, Western Cape Province, Stellenbosch Botanical Garden, on dead leaves of *Beaucarnea stricta* (*Asparagaceae*), 4 Mar. 2023, *P.W. Crous*, HPC 4112 (**holotype** CBS H-25323; culture ex-type CPC 45685 = CBS 150807; ITS and LSU sequences GenBank PQ498930 and PQ498979).

Colour illustrations: *Beaucarnea stricta* in Stellenbosch Botanical Garden, South Africa. Conidiophores and conidiogenous cells giving rise to conidial chains. Scale bars = 10 µm.

Notes: *Nothopenidiella* is reminiscent of *Penidiella* (Crous *et al*. 2007), except that it has mostly unbranched conidial chains, and hyaline conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the distant hits using the **ITS** sequence had highest similarity to *Nothomicrothyrium beaucarneae* [strain CBS 150084, GenBank OR680761.1; Identities = 376/448 (84 %), 17 gaps (3 %)], *Hemibeltrania mitrata* [strain ICMP 15465, GenBank EF029228.1; Identities = 321/371 (87 %), nine gaps (2 %)], and *Pseudosoloacrosporiella cryptomeriae* [strain CBS 148441, GenBank NR_175206.1; Identities = 181/191 (95 %), one gap (0 %)]. Closest hits using the **LSU** sequence are *Mirandina corticola* [strain CBS 132719, GenBank MH878333.1; Identities = 805/849 (95 %), no gaps], *Pleurotheciopsis bramleyi* [strain CBS 127863, GenBank MH877952.1; Identities = 805/850 (95 %), two gaps (0 %)], and *Paramirandina aquatica* [strain GZCC 19-0408, GenBank NG_243191.1; Identities = 789/836 (94 %), four gaps (0 %)]. Of these three species, an ITS sequence is only available for *Paramirandina aquatica*; that ITS sequence has only partial similarity over the 5.8S nrDNA [192/197 (97 %), including two gaps] to the ITS sequence of CPC 45685.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Microthyriaceae* LSU nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Saccharata proteae* (CMW 20003; GenBank EU552145) and the novelty described here is highlighted with a coloured block and **bold** font. Families, orders and the class are shown to the right of the tree in coloured blocks. The branch of *Microthyriaceae* was shortened to facilitate layout. Alignment statistics: 71 strains including the outgroup; 831 characters including alignment gaps analysed: 445 distinct patterns, 339 parsimony-informative, 56 singleton sites, 436 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM3e+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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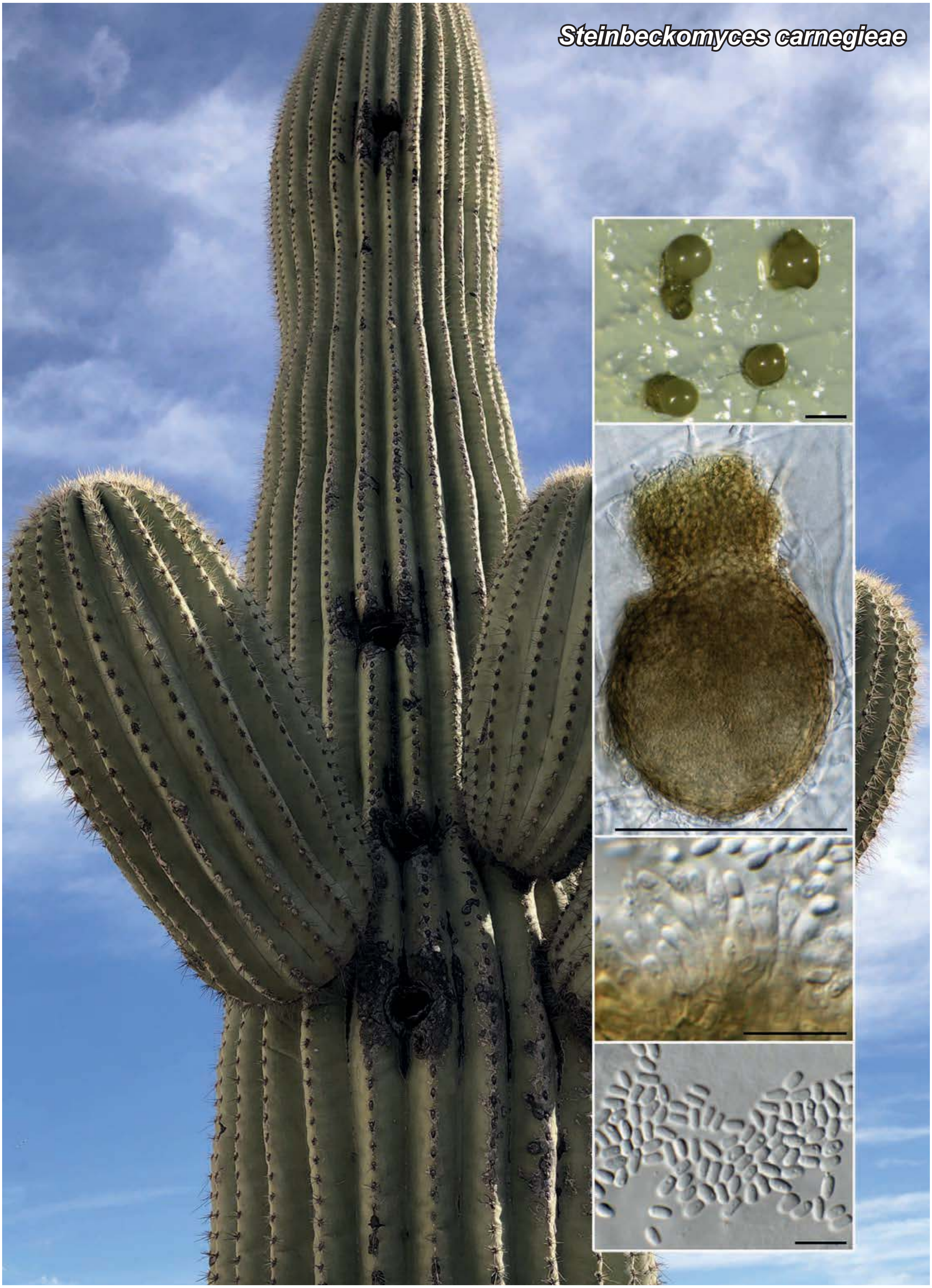

Steinbeckomyces carnegieae

Fungal Planet 1703

MycoBank MB 856073

Steinbeckomyces Crous & Jurjević, ***gen. nov.***

Etymology: Named for John Ernst Steinbeck, an American author, who won the 1962 Nobel Prize in Literature, and who wrote a novel titled *Tortilla Flat* (1935), the location where this fungus was collected.

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

Conidiomata pycnidial, subglobose, brown, with long neck, straight to curved, and apical ostiole. *Conidiophores* reduced to conidiogenous cells lining inner cavity, hyaline, smooth, ampulliform, phialidic. *Conidia* solitary, hyaline, smooth, aseptate, subcylindrical with obtuse ends.

Type species: *Steinbeckomyces carnegieae* Crous & Jurjević

MycoBank MB 856074

Steinbeckomyces carnegieae Crous & Jurjević, ***sp. nov.***

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

Conidiomata pycnidial, subglobose, brown, 140–270 × 90–140 μm (incl. neck), with long neck, straight to curved, up to 150 μm long, apical ostiole up to 50 μm diam. *Conidiophores* reduced to conidiogenous cells lining inner cavity, hyaline, smooth, ampulliform, phialidic, 5–7 × 2.5–3 μm. *Conidia* solitary, hyaline, smooth, aseptate, subcylindrical with obtuse ends, 3–4 × 2–2.5 μm.

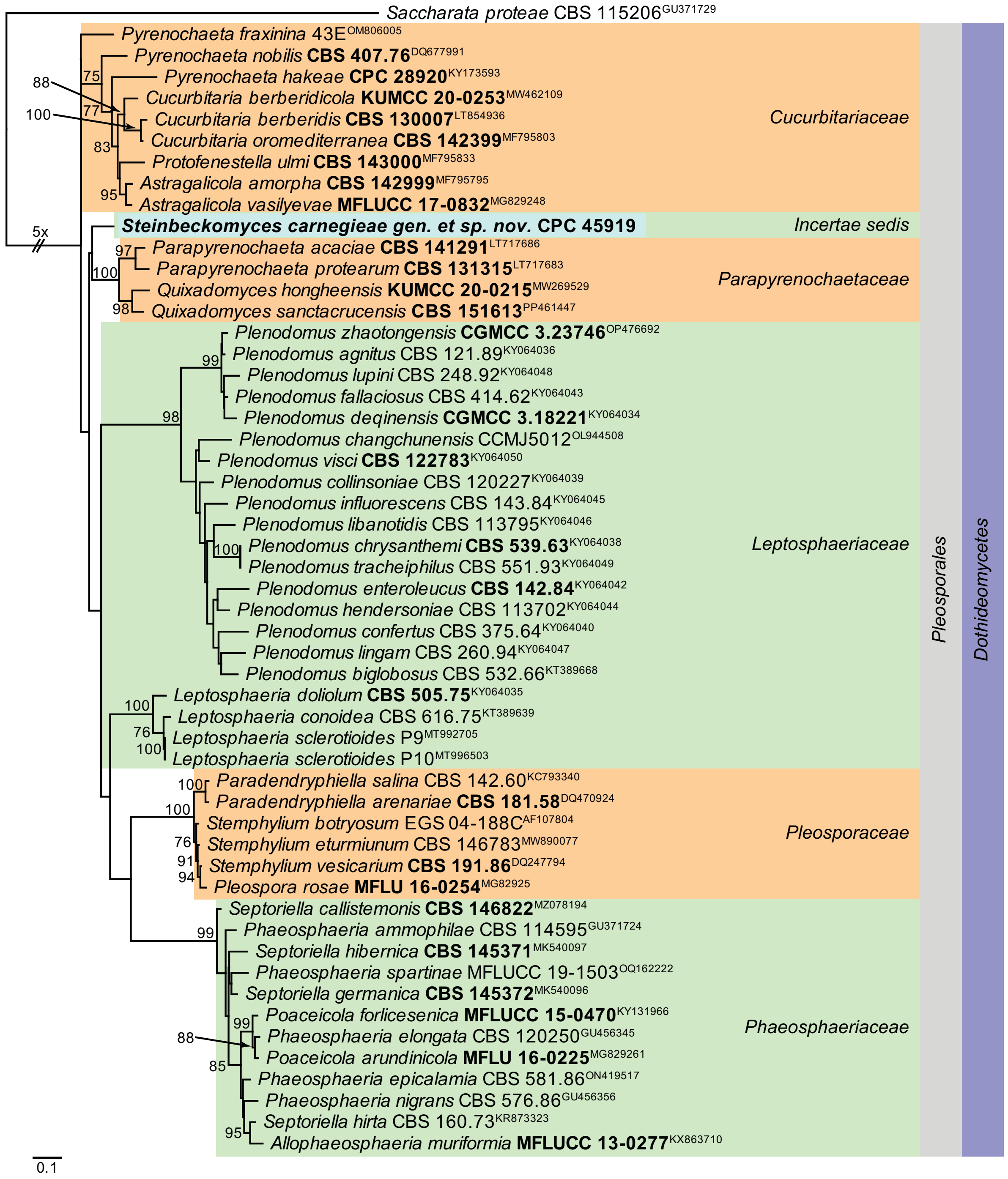
Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth, even margin, covering dish after 2 wk at 25 °C. On MEA surface and reverse olivaceous grey; on PDA and OA surface and reverse fuscous black.

Typus: **USA**, Arizona, Tortilla Flat (Apache trail), on *Carnegiea gigantea* (*Cactaceae*), Mar. 2023, *Z. Jurjević*, 5818 (**holotype** CBS H-25333; culture ex-type CPC 45919 = CBS 150815; ITS, LSU, *actA*, *rpb2* and *tub2* sequences GenBank PQ498931, PQ498980, PQ497707, PQ497721 and PQ497774).

Notes: *Steinbeckomyces* adds another new phoma-like genus to the *Pleosporales* (Hou *et al.* 2023), being characterised by subglobose pycnidial conidiomata with papillate necks, phialidic conidiogenous cells, and hyaline, aseptate conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pyrenochaeta gentianicola* [voucher UNASAM-FUN-0107, GenBank MK216330.1; Identities = 438/458 (96 %), four gaps (0 %)], *Subplenodomus drobnjacensis* [strain PRG11-03, GenBank AB819762.1; Identities = 433/453 (96 %), four gaps (0 %)], and *Paraleptosphaeria padi* [voucher MFLU 15-2756, GenBank NR_189797.1; Identities = 436/459 (95 %), five gaps (1 %)]. Closest hits using the **LSU** sequence are *Plenodomus hendersoniae* [strain LTO, GenBank MF795790.1; Identities = 865/870 (99 %), no gaps], *Plenodomus enteroleucus* [strain CBS 142.84, GenBank NG_067270.1; Identities = 862/867 (99 %), no gaps], and *Plenodomus confertus* [strain CBS 375.64, GenBank JF740277.1; Identities = 862/867 (99 %), no gaps]. Closest hits using the ***actA*** sequence had highest similarity to *Cnidariophoma eilatica* [strain CPC 44117, GenBank OQ627931.1; Identities = 546/617 (88 %), 18 gaps (2 %)], *Setosphaeria holmii* [strain CBS 128053, GenBank LT837663.1; Identities = 466/515 (90 %), three gaps (0 %)], and *Setosphaeria rostrata* [strain BRIP 11426, GenBank LT837589.1; Identities = 466/515 (90 %), three gaps (0 %)]. Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Pyrenochaeta fraxinina* [strain 43E, GenBank OM806005.1; Identities = 726/846 (86 %), no gaps], *Parapyrenochaeta acaciae* [strain CBS 141291, GenBank LT717686.1; Identities = 682/801 (85 %), no gaps], and *Astragalicola vasilyevae* [strain MFLUCC 17-0832, GenBank MG829248.1; Identities = 681/804 (85 %), two gaps (0 %)]. Closest hits using the ***tub2*** sequence had highest similarity to *Cucitella opali* [strain FV, GenBank MF795884.1; Identities = 386/454 (85 %), 15 gaps (3 %)], *Paracucurbitaria corni* [strain 10F, GenBank MT547860.1; Identities = 382/453 (84 %), 13 gaps (2 %)], and *Parafenestella pseudosalicis* [strain C301, GenBank MK357620.1; Identities = 388/462 (84 %), 15 gaps (3 %)].

Colour illustrations: *Carnegiea gigantea* in Arizona, USA. Conidioma on synthetic nutrient-poor agar; conidioma; conidiogenous cells giving rise to conidia; conidia. Scale bars: conidiomata = 200 μm, all others = 10 μm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Pleosporales rpb2* nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Saccharata proteae* (CBS 115206; GenBank GU371729) and the novelty described here is highlighted with a coloured block and **bold** font. Families, the order and the class are shown to the right of the tree in coloured blocks. The root branch was shortened to facilitate layout. Alignment statistics: 54 strains including the outgroup; 810 characters including alignment gaps analysed: 410 distinct patterns, 356 parsimony-informative, 75 singleton sites, 379 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2+F+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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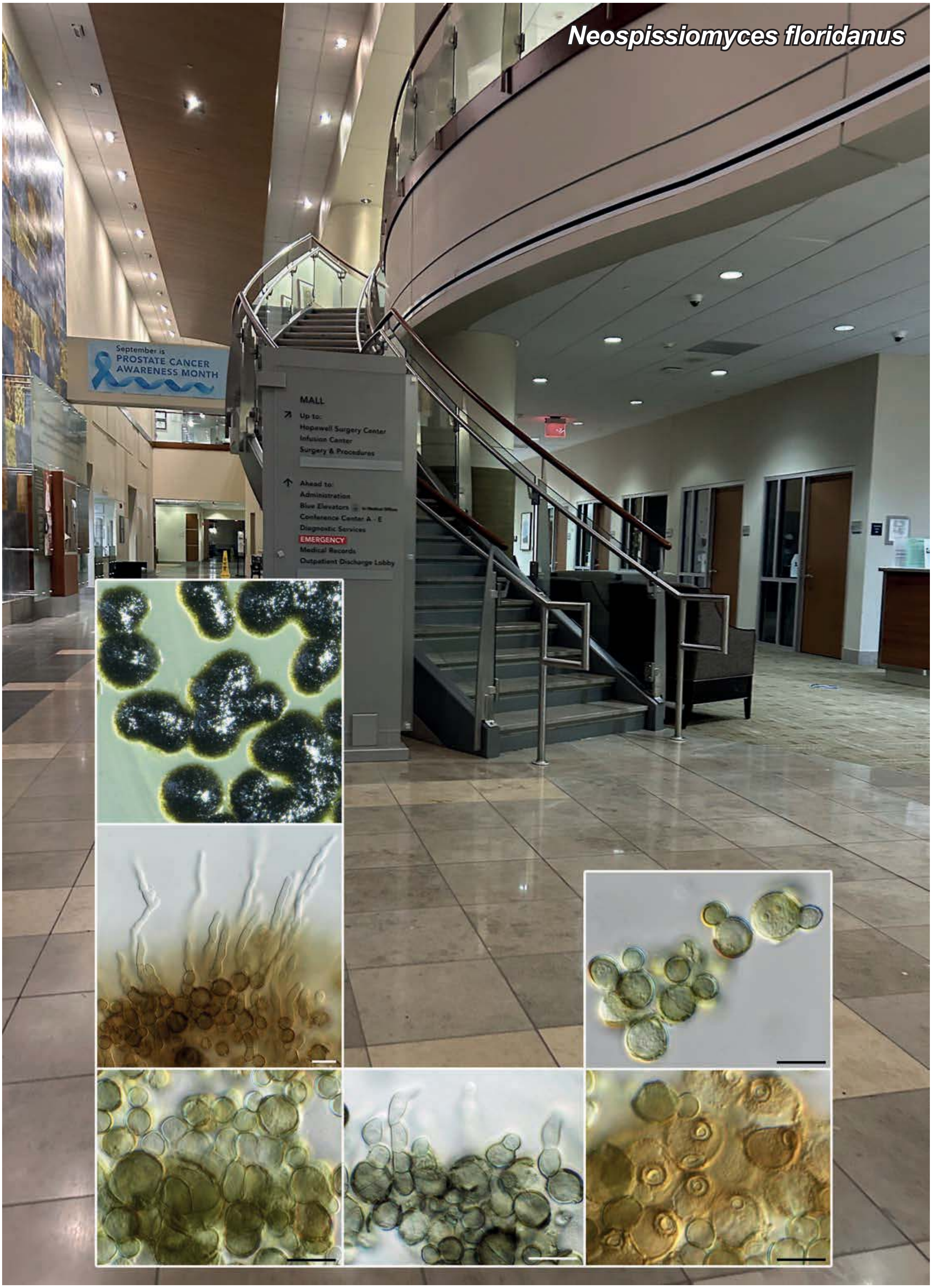

Neospissiomyces floridanus
September is
PROSTATE CANCER
AWARENESS MONTH
MALL
Up to:
Hopewell Surgery Center
Infusion Center
Surgery & Procedures
Ahead to:
Administration
Blue Elevators
Conference Center A - E
Diagnostic Services
EMERGENCY
Medical Records
Outpatient Discharge Lobby

Fungal Planet 1704 MycoBank MB 856075

Neospissiomyces Crous & Jurjević, *gen. nov.*

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

Classification: *Incertae sedis*, *incertae sedis*, *incertae sedis*, *Dothideomycetes*.

Sporodochia superficial, brown, round, with basal stroma that gives rise to upper layer of *conidiogenous cells*, globose, brown, verruculose, with single apical ostiole, proliferating percurrently, giving rise to solitary *conidia*, globose to ovoid, brown to dark brown, aseptate, verruculose to warty, thick-walled, becoming transversely or obliquely septate, dividing into endoconidia, or forming a conidiogenous cell, giving rise to secondary conidia via microcyclic conidiation.

Type species: *Neospissiomyces floridanus* Crous & Jurjević

MycoBank MB 856076

Neospissiomyces floridanus Crous & Jurjević, *sp. nov.*

Etymology: Name refers to the American state of Florida from where it was collected.

Sporodochia superficial, brown, round, with basal stroma that gives rise to upper layer of *conidiogenous cells*, globose, brown, verruculose, 8–12 × 8–10 µm, with single apical ostiole, 3–4 µm diam, proliferating percurrently, giving rise to solitary *conidia*, globose to ovoid, brown to dark brown, aseptate, verruculose to warty, 5–10 µm diam, thick-walled, becoming transversely or obliquely septate, dividing into endoconidia, or forming a conidiogenous cell, giving rise to secondary conidia via microcyclic conidiation.

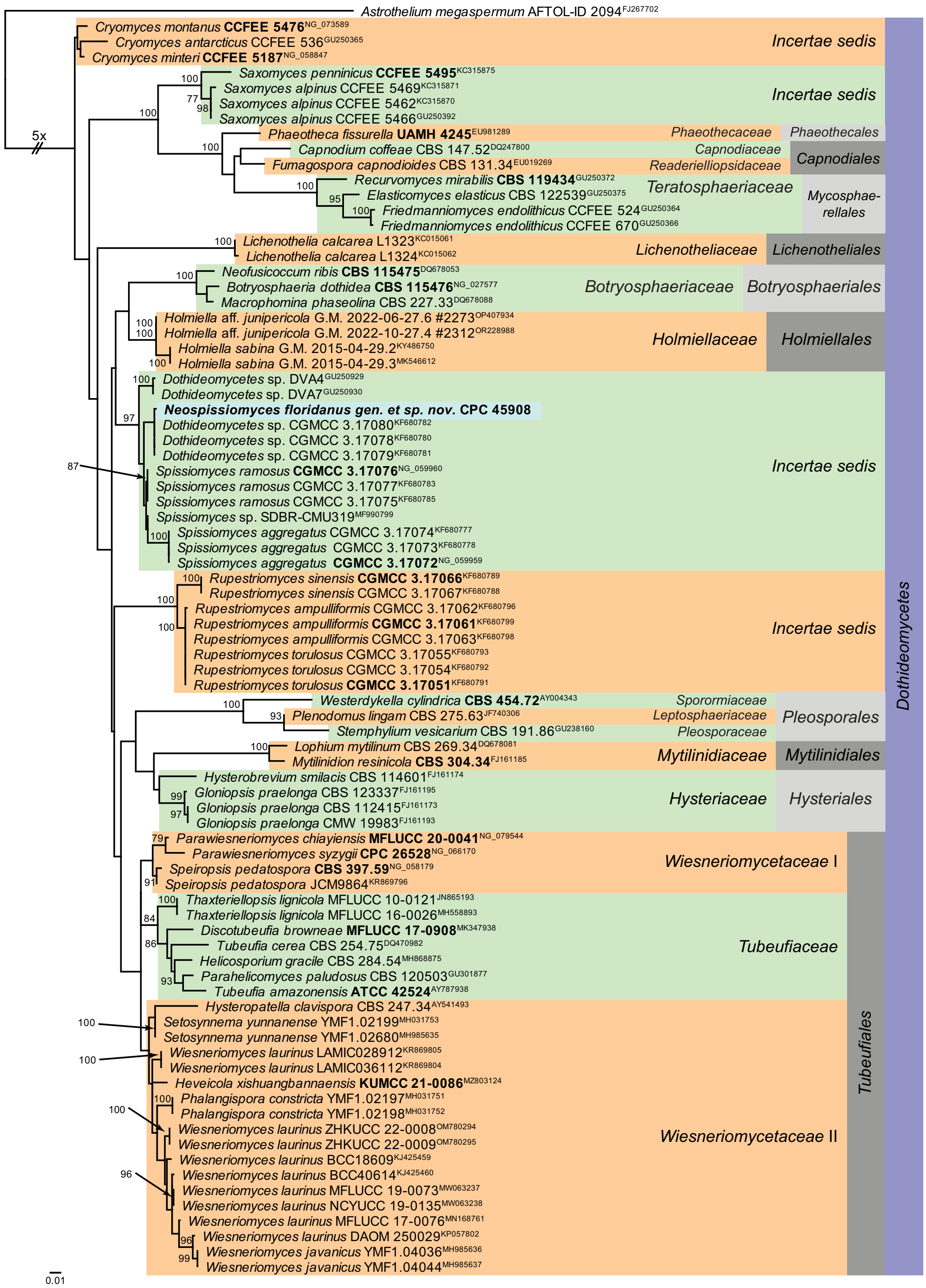
Culture characteristics: Colonies erumpent, slow growing, without aerial mycelium, margins smooth, even, 5–7 mm diam after 2 wk at 25 °C. On MEA, PDA, OA and modified cellulose agar surface and reverse fuscous black.

Typus: **USA**, Florida, Fort Lauderdale, hospital, swab, 2023, *Z. Jurjević*, 5804 (**holotype** CBS H-25457; culture ex-type CPC 45908 = CBS 152209; ITS, LSU, *rpb1* and *rpb2* sequences GenBank PQ498932, PQ498981, PQ497757 and PQ497722).

Notes: *Neospissiomyces* is related to *Spissiomyces*, a rock-inhabiting fungus described from China, characterised by pigmented, thick-walled hyphae and swollen cells (Su *et al*. 2015). *Neospissiomyces* was isolated from a hospital swab, and its ecological niche remains unknown. However, it is distinguished from *Spissiomyces* by forming sporodochia with conidiogenous cells in culture that give rise to solitary conidia, that can again form endoconidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to Fungal sp. [strain TRN170, GenBank AY843070.1; Identities = 509/511 (99 %), no gaps], *Dothideomycetes* sp. [strain FJII_L1_SW_P2, GenBank MT704879.1; Identities = 553/558 (99 %), no gaps], and *Spissiomyces ramosus* [as *Dothideomycetes* sp. LS-2013h; strain CGMMCC 3.17077, GenBank KF513515.1; Identities = 516/569 (91 %), 12 gaps (2 %)], and distant hits with *Sarea difformis* [strain JMEKa, GenBank MT809271.1; Identities = 478/571 (84 %), 28 gaps (4 %)], and *Hormococcus conorum* [strain RS3-S2-12, GenBank MN547392.1; Identities = 476/570 (84 %), 24 gaps (4 %)]. Closest hits using the **LSU** sequence are *Dothideomycetes* sp. LS-2013g [strain CGMCC 3.17080, GenBank KF680782.1; Identities = 813/815 (99 %), one gap (0 %)], *Spissiomyces ramosus* [strain CGMCC 3.17076, GenBank NG_059960.1; Identities = 805/815 (99 %), no gaps], and *Spissiomyces aggregatus* [strain CGMCC 3.17072, GenBank NG_059959.1; Identities = 793/817 (97 %), one gap (0 %)]. Distant hits were obtained using the ***rpb1*** sequence in a blastn search and had highest similarity to *Dothideomycetes* sp. [strain AN13, GenBank GU250945.1; Identities = 503/655 (77 %), two gaps (0 %)], *Superstratomyces flavomucosus* [strain DTO 305-C3, GenBank KX950493.1; Identities = 476/659 (72 %), 20 gaps (3 %)], and *Superstratomyces albomucosus* [strain DTO 277-D2, GenBank KX950494.1; Identities = 474/658 (72 %), 18 gaps (2 %)]. There are currently no *rpb1* sequences available for *Spissiomyces* on GenBank. Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Dothideomycetes* sp. LS-2013g [strain CGMCC 3.17078, GenBank KJ733735.1; Identities = 728/734 (99 %), no gaps], *Spissiomyces aggregatus* [strain CGMCC 3.17072, GenBank KJ733736.1; Identities = 659/731 (90 %), no gaps], and *Spissiomyces ramosus* [strain CGMCC 3.17077, GenBank KJ733734.1; Identities = 641/731 (88 %), no gaps].

Colour illustrations: Fort Lauderdale hospital, Florida, USA. Sporodochia on PDA; hyphae and conidiogenous cells; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Neospissiomyces* LSU nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Astrothelium megaspermum* (AFTOL-ID 2094; GenBank FJ267702) and the novelty described here is highlighted with a coloured block and **bold** font. Families, orders and the class are shown to the right of the tree in coloured blocks. The root branch was shortened to facilitate layout. Alignment statistics: 83 strains including the outgroup; 818 characters including alignment gaps analysed: 323 distinct patterns, 248 parsimony-informative, 93 singleton sites, 477 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TNe+R3. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Cylindromonium panamaense

Fungal Planet 1705

MycoBank MB 856077

Cylindromonium panamaense Crous, *sp. nov.*

Etymology: Name refers to Panama, the country where it was collected.

Classification: *Nectriaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*.

Conidiophores arising from superficial mycelium, solitary, flexuous, subcylindrical, unbranched or branched at base, 120–180 × 2.5–3 µm, multiseptate, tapering to truncate monophialidic apex with flared collarette. *Conidiogenous cells* integrated, terminal subcylindrical, hyaline, smooth, 40–60 × 1–1.5 µm. *Conidia* solitary, fusoid, straight to curved, hyaline, smooth, 4–6-septate, tapering to subobtuse apex, base tapering to truncate hilum, 0.5–1 µm diam, 38–43 × 3.5 µm; conidia remain at apex of conidiophore and form a mucoid cluster that eventually anastomoses via the basal conidial cells, forming a cheiroid conidial propagule.

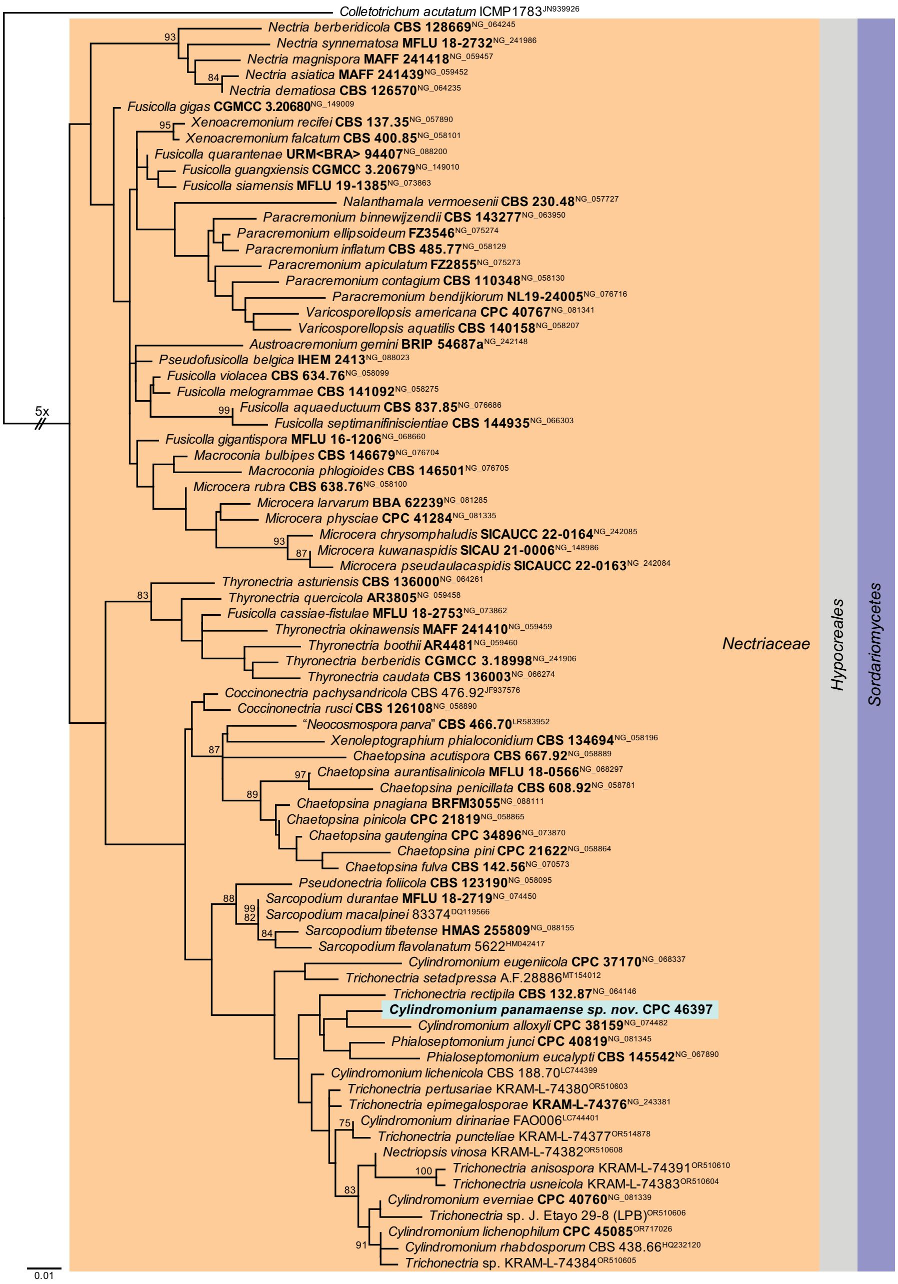
Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium, and smooth, lobate margin, 10 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse salmon.

Typus: **Panama**, Colon Province, Soberania National Park, Pipeline Road, close to Gamboa, on twig litter of angiosperm, 6 Aug. 2023, *P.W. Crous*, HPC 4219 [**holotype** CBS H-25461; culture ex-type CPC 46397 = CBS 152311; ITS, LSU, *actA*, *his3*, *tef1* (first part) and *tub2* sequences GenBank PQ498933, PQ498982, PQ497708, PQ497717, PQ497765 and PQ497775].

Notes: *Cylindromonium* includes acremonium-like taxa with unbranched, hyaline, phialidic conidiophores, and cylindrical, 1-septate conidia (Crous *et al*. 2019). *Cylindromonium panamaense* is unique in the genus as it has multi-septate conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cylindromonium alloxyli* [strain CBS 146806, GenBank NR_171760.1; Identities = 528/549 (96 %), four gaps (0 %)], *Cylindromonium lichenicola* [strain CBS 188.70, GenBank MH859549.1; Identities = 516/564 (91 %), 20 gaps (3 %)], and *Phialoseptomonium eucalypti* [strain CBS 145542, GenBank NR_165572.1; Identities = 512/560 (91 %), 14 gaps (2 %)]. Closest hits using the **LSU** sequence are *Cylindromonium lichenicola* [strain CBS 303.70, GenBank OQ055452.1; Identities = 765/778 (98 %), two gaps (0 %)], *Trichonectria pertusariae* [voucher KRAM-L-74380, GenBank OR510603.1; Identities = 800/816 (98 %), no gaps], and *Phialoseptomonium junci* [strain CBS 148307, GenBank NG_081345.1; Identities = 792/809 (98 %), no gaps]. No significant hits were obtained when the ***actA*** sequence was used in blastn and megablast searches. Closest hits using the ***his3*** sequence had highest similarity to *Cylindromonium alloxyli* [strain CPC 38159, GenBank MW173108.1; Identities = 307/352 (87 %), nine gaps (2 %)], *Volutella rosea* [strain CBS 128258, GenBank KM231492.1; Identities = 285/330 (86 %), 14 gaps (4 %)], and *Volutella ciliata* [strain CBS 100447, GenBank MH936793.1; Identities = 280/326 (86 %), nine gaps (2 %)]. Closest hits using the ***tef1*** (first part) sequence had had distant similarity over the exon to *Trichoderma pseudolacteum* [strain TUFC 61505, GenBank JX238496.1; Identities = 206/239 (86 %), nine gaps (3 %)], *Semifissispora natalis* [strain CPC 25383, GenBank KT950878.1; Identities = 203/236 (86 %), seven gaps (2 %)], and *Cucurbitaria berberidis* [strain C39, GenBank MF795844.1; Identities = 206/240 (86 %), five gaps (2 %)]. A blast2 search with the blastn algorithm against the available *Cylindromonium tef1* sequences in GenBank revealed low similarity to *Cylindromonium alloxyli* [strain CPC 38159, GenBank MW173120.1; Identities = 189/232 (81 %), 15 gaps (6 %)], *Cylindromonium rhabdosporum* [strain CBS 438.66, GenBank OR683713.1; Identities = 134/151 (89 %), no gaps], and *Cylindromonium lichenophilum* [strain CPC 45085, GenBank OR683711.1; Identities = 128/145 (88 %), no gaps]. No significant hits were obtained when the ***tub2*** sequence was used in blastn and megablast searches.

Colour illustrations: Soberania National Park, Panama. Conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Nectriaceae* LSU nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Colletotrichum acutatum* (ICMP1783; GenBank JN939926) and the novelty described here is highlighted with a coloured block and **bold** font. The family, order and class are shown to the right of the tree in coloured blocks. The root branch was shortened to facilitate layout. Alignment statistics: 80 strains including the outgroup; 789 characters including alignment gaps analysed: 219 distinct patterns, 119 parsimony-informative, 69 singleton sites, 601 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM3e+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Striaticonidium panamaense

Fungal Planet 1706 MycoBank MB 856078

Striaticonidium panamaense Crous, ***sp. nov.***

Etymology: Name refers to Panama, the country where it was collected.

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

Conidiomata synnemata, solitary, erect, straight to somewhat flexuous, arising from a hyaline stroma, consisting of tightly aggregated bundles of conidiophores, subcylindrical, olivaceous green, verruculose, multiseptate, 400–600 × 60–80 µm, giving rise to a globose head of mucoid conidia. *Terminal cells* giving rise to 1–4 conidiogenous cells, becoming smooth and hyaline towards apex, subcylindrical, 20–40 × 2–3 µm; phialidic, with minute apex and collarette. *Conidia* solitary, aseptate, longitudinally striate, fusoid, green olivaceous, finely guttulate, apex subacute, base truncate, 1 µm diam, (13–)14(–15) × 4(–4.5) µm.

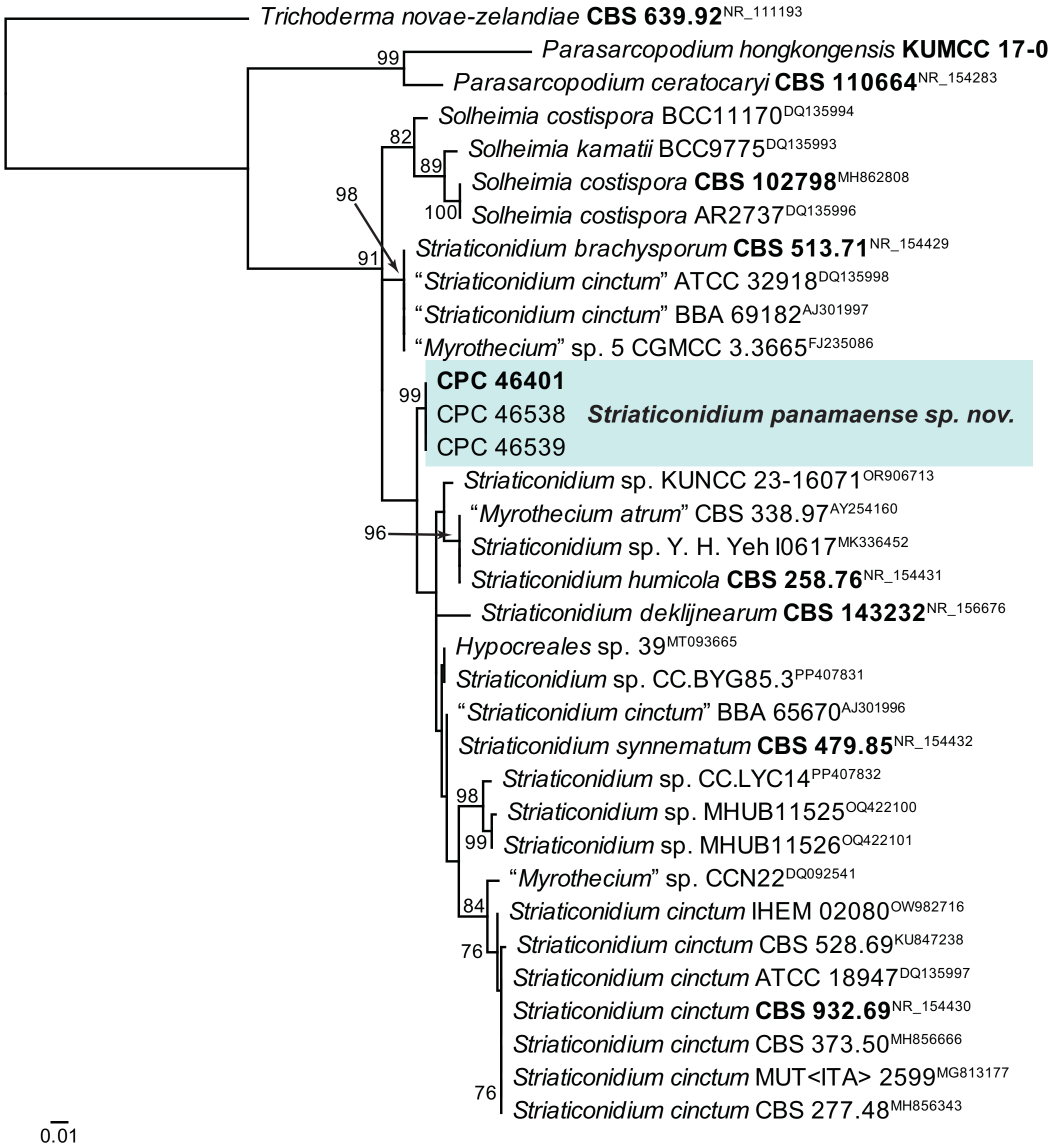
Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium, surface folded, and smooth, lobate margin, reaching up to 35 mm diam after 2 wk at 25 °C. On MEA, PDA surface and OA surface dirty white, reverse luteous.

Typus: **Panama**, Colon Province, Soberania National Park, Pipeline Road, close to Gamboa, on leaf litter, 6 Aug. 2023, *P.W. Crous*, HPC 4224 (**holotype** CBS H-25462; culture ex-type CPC 46401 = CBS 152312; ITS, LSU, *rpb2* and *tub2* sequences GenBank PQ498934, PQ498983, PQ497723 and PQ497776); *idem.*, cultures CPC 46538 = CBS 152316 (ITS, LSU, *CaM*, *rpb2* and *tub2* sequences GenBank PQ498935, PQ498984, PQ497712, PQ497724 and PQ497777), CPC 46539 = CBS 152317 (ITS, LSU, *CaM*, *rpb2* and *tub2* sequences GenBank PQ498936, PQ498985, PQ497713, PQ497725 and PQ504942).

Notes: *Striaticonidium* was introduced by Lombard *et al*. (2016) for myrothecium-like fungi characterised by striate conidia and synnematous or sporodochial conidiomata. *Striaticonidium panamaense* is related to *S. deklijnearum*, but distinct in that the latter has sporodochia, and smaller conidia, (5–)6–8(–9) × 2–3 µm (Crous *et al.* 2017).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 46401 had highest similarity to *Striaticonidium synnematum* [strain CBS 479.85, GenBank NR_154432.1; Identities = 528/548 (96 %), 14 gaps (2 %)], *Striaticonidium cinctum* [strain 80388, GenBank OR761593.1; Identities = 512/532 (96 %), 14 gaps (2 %)], and *Striaticonidium humicola* [strain CBS 258.76, GenBank NR_154431.1; Identities = 528/549 (96 %), 13 gaps (2 %)]. The ITS sequence of CPC 46401 is identical to those of CPC 46538 and 46539 (542/542 and 544/544 nt, respectively). Closest hits using the **LSU** sequence of CPC 46401 are *Striaticonidium synnematum* [strain IGu24, GenBank ON986784.1; Identities = 795/797 (99 %), no gaps], *Striaticonidium humicola* [strain CBS 258.76, GenBank NG_058228.1; Identities = 789/797 (99 %), two gaps (0 %)], and *Striaticonidium cinctum* [strain CBS 528.69, GenBank MH871132.1; Identities = 788/797 (99 %), no gaps]. The LSU sequence of CPC 46401 is identical to those of CPC 46538 and 46539 (783/783 and 794/794 nt, respectively). Closest hits using the ***cmdA*** sequence of CPC 46538 had highest similarity to *Striaticonidium brachysporum* [strain CBS 513.71, GenBank KU847209.1; Identities = 541/632 (86 %), 15 gaps (2 %)], *Striaticonidium synnematum* [strain CBS 479.85, GenBank KU847218.1; Identities = 529/636 (83 %), 18 gaps (2 %)], and *Striaticonidium cinctum* [strain CBS 528.69, GenBank KU847215.1; Identities = 526/634 (83 %), 14 gaps (2 %)]. The *cmdA* sequences of CPC 46538 and 46539 are identical (709/709 nt). Closest hits using the ***rpb2*** (first part) sequence of CPC 46538 had highest similarity to *Striaticonidium cinctum* [strain CBS 277.48, GenBank KU847288.1; Identities = 639/721 (89 %), no gaps], *Striaticonidium brachysporum* [strain CBS 126552, GenBank KU847285.1; Identities = 635/721 (88 %), no gaps], and *Striaticonidium synnematum* [strain CBS 479.85, GenBank KU847292.1; Identities = 631/721 (88 %), no gaps]. The *rpb2* sequence of CPC 46401 is identical to those of CPC 46538 and 46539 (778/778 and 742/742 nt, respectively). Closest hits using the ***tub2*** sequence of CPC 46538 had highest similarity to *Striaticonidium deklijnearum* [strain CBS 143232, GenBank MG386171.1; Identities = 570/664 (86 %), 35 gaps (5 %)], *Striaticonidium brachysporum* [strain CBS 126552, GenBank KU847323.1; Identities = 315/347 (91 %), four gaps (1 %)], and *Coccinonectria pachysandricola* [strain JAC 18-79, GenBank MT341239.1; Identities = 305/351 (87 %), 11 gaps (3 %)]. The *tub2* sequence of CPC 46401 is identical to those of CPC 46538 and 46539 (343/343 and 343/343 nt, respectively).

Colour illustrations: Soberania National Park, Panama. Synnemata on pine needle agar; synnemata and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Striaticonidium* ITS nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Trichoderma novae-zelandiae* (CBS 639.92; GenBank NR_111193) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 34 strains including the outgroup; 612 characters including alignment gaps analysed: 172 distinct patterns, 75 parsimony-informative, 72 singleton sites, 465 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+R2. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Chlamydocillium simulans

Fungal Planet 1707

MycoBank MB 856079

Chlamydocillium simulans Crous, ***sp. nov.***

Etymology: *Simul* = Latin, occurring together.

Classification: *Sarocladiaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate, 1–1.5 µm diam hyphae, forming hyphal coils. *Conidiophores* solitary, erect, subcylindrical, flexuous, unbranched or branched below, hyaline, smooth, somewhat thick-walled at base, 1–3-septate, 50–80 × 2–2.5 µm. *Conidiogenous cells* integrated, terminal, monophialidic, 47–70 × 2 µm; apical collarette minute, not flared. *Conidia* aggregating in mucoid mass, hyaline, smooth, reniform, aseptate, ends subobtuse, 5–6(–10) × 2 µm. *Chlamydospores* not seen.

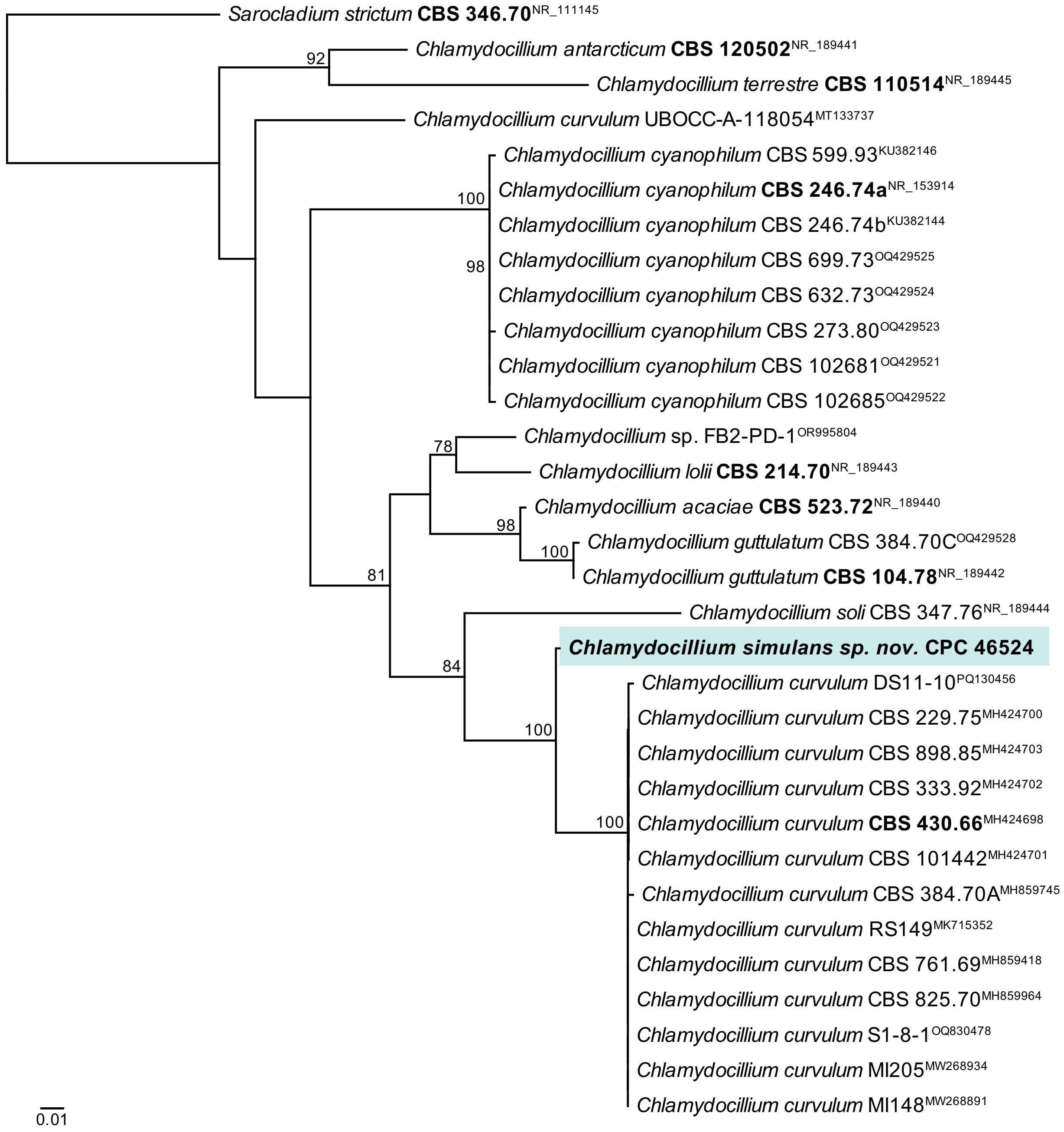
Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium, surface folded, and smooth, lobate margin, reaching 30mm diam after 2 wk at 25 °C. On MEA surface peach, reverse ochreous; on PDA surface and reverse dirty white; on OA surface dirty white.

Typus: **Panama**, Colon Province, Soberania National Park, Pipeline Road, close to Gamboa, on leaf litter, associated with *Xylaria* sp., 6 Aug. 2023, *P.W. Crous*, HPC 4217 [**holotype** CBS H-25463; culture ex-type CPC 46524 = CBS 152313; ITS, LSU, *rpb1*, *rpb2* and *tef1* (second part) sequences GenBank PQ498937, PQ498986, PQ497758, PQ497726 and PQ497741].

Notes: *Chlamydocillium* was established for verticillium-like asexual morphs with abundant intercalary chlamydospores (Zare & Gams 2016). *Chlamydocillium simulans* is related to *C. curvulum* (conidia cylindrical, ellipsoid, or short reniform, 3.2–8.2 × 2–2.6 µm; Hou *et al.* 2023), and *C. soli* (conidia cylindrical, allantoid, oblong, 4–7.8(–10.3) × 1.6–2.4 µm; Hou *et al.* 2023), but is phylogenetically and morphologically distinct.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Chlamydocillium curvulum* [as *Kiflimonium curvulum*; strain MUT<ITA> 6656, GenBank OP161512.1; Identities = 410/422 (97 %), one gap (0 %)], *Kiflimonium junci* [strain CBS 148279, GenBank NR_175233.1; Identities = 478/534 (90 %), 22 gaps (4 %)], and *Chlamydocillium lolii* [strain CBS 214.70, GenBank NR_189443.1; Identities = 433/484 (89 %), 17 gaps (3 %)]. Closest hits using the **LSU** sequence are *Chlamydocillium curvulum* [strain CBS 229.75, GenBank HQ232021.1; Identities = 789/802 (98 %), two gaps (0 %)], *Chlamydocillium guttulatum* [strain CBS 104.78, GenBank NG_242044.1; Identities = 767/782 (98 %), two gaps (0 %)], and *Chlamydocillium soli* [strain CBS 347.76, GenBank NG_242046.1; Identities = 765/780 (98 %), two gaps (0 %)]. Distant hits obtained using the ***rpb1*** sequence had highest similarity to *Trichoderma leucopus* [voucher spat 06-234, GenBank MF416650.1; Identities = 565/705 (80 %), 11 gaps (1 %)], *Trichoderma deliquescens* [as *Hypocrea lutea*; strain ATCC 208838, GenBank AY489662.1; Identities = 531/664 (80 %), ten gaps (1 %)], and *Trichoderma americanum* [as *Hypocrea americana*; strain AFTOL-ID 52, GenBank DQ522853.1; Identities = 564/706 (80 %), 13 gaps (1 %)]. Distant hits obtained using the ***rpb2*** (first part) sequence had highest similarity to *Thyronectria sinopica* [strain CBS 127386, GenBank HM534890.1; Identities = 664/882 (75 %), 26 gaps (2 %)], *Fusarium albidum* [strain BBA 67603, GenBank HQ897738.1; Identities = 673/891 (76 %), 44 gaps (4 %)], and *Thyronectria quercicola* [strain CBS 128976, GenBank KM232411.1; Identities = 654/869 (75 %), 16 gaps (1 %)]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Chlamydocillium curvulum* [strain CBS 229.75, GenBank OQ470810.1; Identities = 746/772 (97 %), two gaps (0 %)], *Sarocladium theobromae* [strain CBS 113440, GenBank OQ471188.1; Identities = 739/770 (96 %), no gaps], and *Sarocladium pseudostrictum* [strain CBS 137660, GenBank OQ471178.1; Identities = 734/772 (95 %), two gaps (0 %)].

Colour illustrations: Soberania National Park, Panama. Conidiophores on SNA; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Chlamydocillium* ITS nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Sarocladium strictum* (CBS 346.70; GenBank NR_111145) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 32 strains including the outgroup; 536 characters including alignment gaps analysed: 218 distinct patterns, 113 parsimony-informative, 64 singleton sites, 359 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Corynesporina panamaensis & Yunnanomyces panamaensis

Fungal Planet 1708 and 1709 MycoBank MB 856080

Corynesporina panamaensis Crous, *sp. nov.*

Etymology: Name refers to Panama, the country where it was collected.

Classification: *Incertae sedis*, *incertae sedis*, *Sordariomycetidae*, *Sordariomycetes*.

Mycelium consisting of pale brown, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* solitary, erect, subcylindrical, brown, smooth, 30–70 × 3–4 µm, 1–2-septate, unbranched. *Conidiogenous cells* integrated, terminal, medium brown, smooth, subcylindrical, 15–40 × 3–4 µm, with solitary tretic apical locus. *Conidia* obovoid, brown, smooth, 1–3-distoseptate (wall 1.5–2 µm thick), straight to slightly curved, occurring in short chains, apex and hilum darkened, thickened, 2–3 µm diam, (55–)60–65(–70) × 6–7 µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium, surface folded, and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA and PDA surface and reverse olivaceous grey; on OA surface olivaceous grey in centre, cream in outer region.

Typus: **Panama**, Colon Province, Soberania National Park, Pipeline Road, close to Gamboa, on leaf litter, 6 Aug. 2023, *P.W. Crous*, HPC 4222 [**holotype** CBS H-25465; culture ex-type CPC 46532 = CBS 152315; ITS, LSU and *tef1* (second part) sequences GenBank PQ498938, PQ498987 and PQ497742].

Notes: *Corynesporina* is based on *C. elegans* (on litter of *Smilax calophylla*, Singapore; conidia 2–3-distoseptate, 24–42 × 4–8 µm; Subramanian 1994), a genus validated by Gams *et al*. (2009). The genus has remained monotypic, and its phylogeny is unresolved, due to the absence of culture or DNA data. The present collection fits the genus in having distoseptate, tretic conidia formed in short chains, but represents a new species with slightly longer conidia. *Corynesporina panamaensis* clusters close to *Sporidesmium tropicale*, but the latter is not congeneric with the genus *Sporidesmium*, and needs to be allocated elsewhere.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pseudoproboscispora caudae-suis* [strain A336-2d, GenBank KU975068.1; Identities = 346/413 (84 %), 25 gaps (6 %)], *Neoeriomycopsis wadeae* [strain BRIP 71660a, GenBank NR_191350.1; Identities = 338/412 (82 %), 21 gaps (5 %)], and *Sydowiella stellatifolii* [strain CBS:119342, GenBank NR_132825.1; Identities = 343/418 (82 %), 28 gaps (6 %)]. Closest hits using the **LSU** sequence are *Sporidesmium tropicale* [strain MFLUCC 17-0344, GenBank OL782088.1; Identities = 748/806 (93 %), three gaps (0 %)], *Heinzbutinia microspora* [as *Ophiostoma microsporum*; strain CMW 17152, GenBank OM514758.1; Identities = 737/798 (92 %), five gaps (0 %)], and *Pararamichloridium livistonae* [strain CBS 143166, GenBank NG_058504.1; Identities = 746/809 (92 %), eight gaps (0 %)]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Stilbochaeta ramulosetula* [strain IMI 313452, GenBank OL654062.1; Identities = 822/879 (94 %), no gaps], *Stilbochaeta malaysiana* [strain IMI 312436, GenBank OL654059.1; Identities = 830/892 (93 %), no gaps], and *Thozetella effusa* [strain CBS 115044, GenBank OL654066.1; Identities = 842/905 (93 %), no gaps].

MycoBank MB 856083

Yunnanomyces panamaensis Crous, *sp. nov.*

Etymology: Name refers to Panama, the country where it was collected.

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

Mycelium consisting of hyaline, smooth, septate, branched, 1.5–2 µm diam hyphae that give rise to conidiophores. *Conidiophores* solitary, erect, unbranched, subcylindrical, straight to slightly flexuous, medium brown, smooth- and thick-walled, base lacking rhizoids, 2–4-septate, 25–60 × 2.5–3 µm. *Conidiogenous cells* integrated, terminal, darker brown than conidiophore, slightly roughened, with numerous minute denticle-like loci covering the conidiogenous cell, 22–30 × 3 µm (slightly wider than basal part of conidiophore). *Conidia* solitary, dry, medianly 1-septate, straight, medium brown, finely roughened, ellipsoid, but widest at obtuse base, tapering towards subobtuse apex, 5–6(–7) × 2–2.5 µm.

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

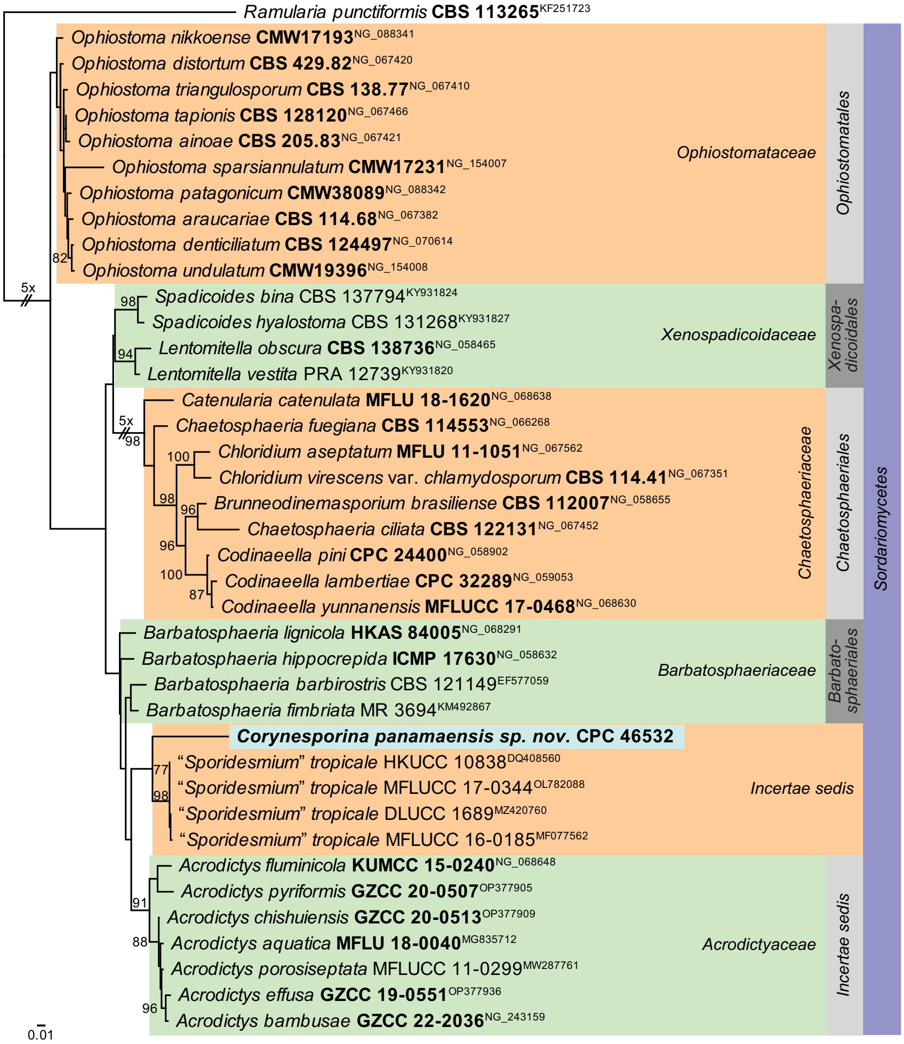
Typus: **Panama**, Colon Province, Soberania National Park, Pipeline Road, close to Gamboa, on leaf litter, 6 Aug. 2023, *P.W. Crous*, HPC 4218 [**holotype** CBS H-25469; culture ex-type CPC 46559 = CBS 152319; ITS, LSU, *rpb2* and *tef1* (first part) sequences GenBank PQ498939, PQ498988, PQ497727 and PQ497766].

Notes: *Yunnanomyces* is a genus of *Sympoventuriaceae*, which was revised by Wei *et al.* (2022). The genus is characterised by its globose to broadly oval, yellow to brown, muriformly septate conidia (Tibpromma *et al*. 2018). *Yunnanomyces panamaensis* is a morphologically distinct species, having brown, ellipsoid, medianly 1-septate conidia.

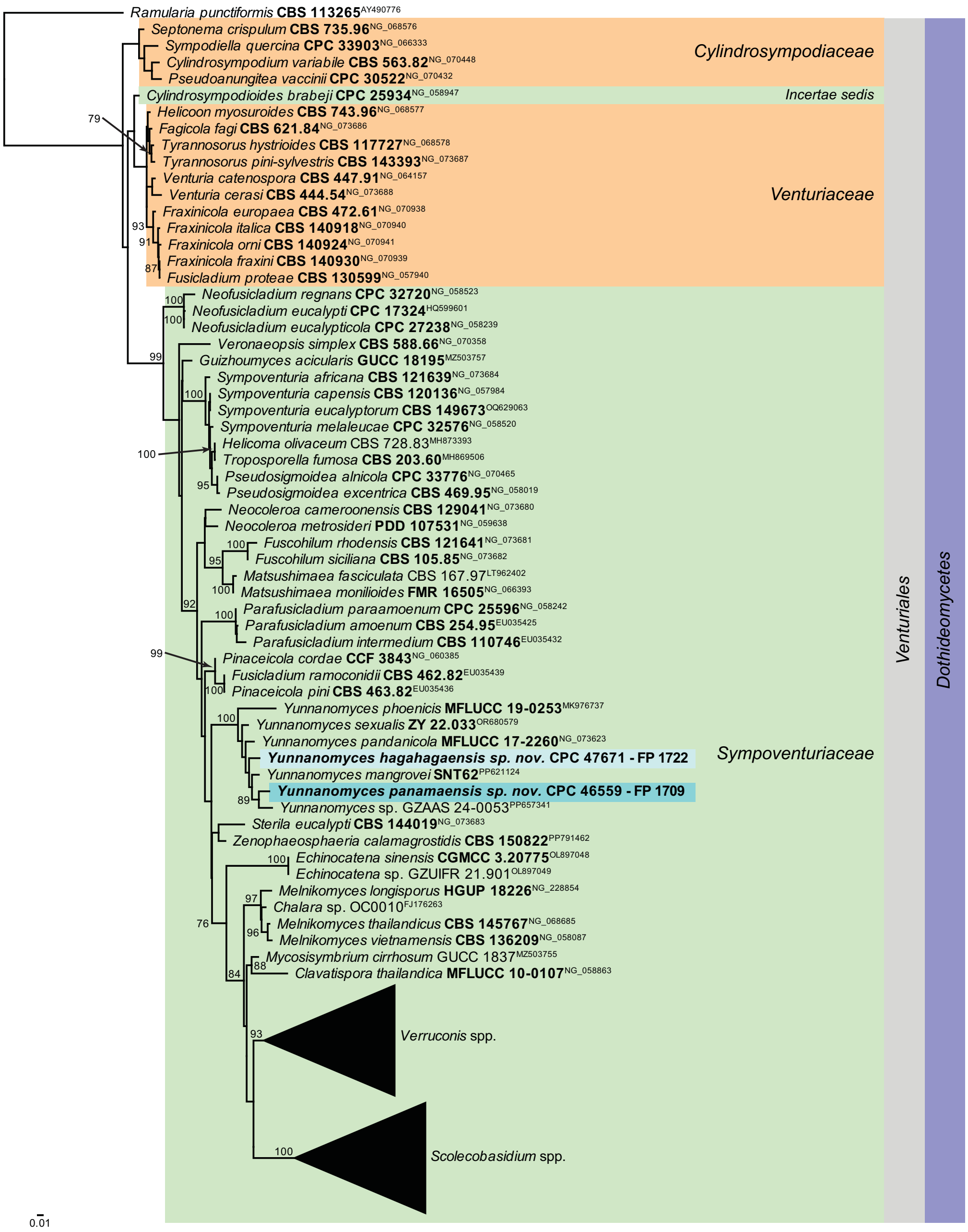
Colour illustrations: Soberania National Park, Panama. Left column (CPC 46532): Conidiophores and conidiogenous cells giving rise to conidia; conidia. Right column (CPC 46559): Conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had distant similarity to *Yunnanomyces* sp. NGL-2024a [voucher GZAAS 24-0053, GenBank PP657299.1; Identities = 316/372 (85 %), 25 gaps (6 %)], *Pinaceicola cordae* [strain CBS 126959, GenBank NR_166037.1; Identities = 351/434 (81 %), 43 gaps (9 %)], *Matsushimaea monilioides* [strain FMR 16505, GenBank NR_160581.1; Identities = 297/361 (82 %), 19 gaps (5 %)], and *Fuscohilum siciliana* [strain CBS 105.85, GenBank NR_168753.1; Identities = 290/348 (83 %), 13 gaps (3 %)]. Closest hits using the **LSU** sequence are *Yunnanomyces* sp. NGL-2024a [voucher GZAAS 24-0053, GenBank PP657341.1; Identities = 771/793 (97 %), one gap (0 %)], *Yunnanomyces pandanicola* [strain MFLUCC 17-2260, GenBank NG_073623.1; Identities = 765/793 (96 %), one gap (0 %)], *Zenophaeosphaeria calamagrostidis* [strain CPC 46090, GenBank PP791462.1; Identities = 752/797 (94 %), five gaps (0 %)], and *Pinaceicola pini* [strain CBS 463.82, GenBank MH873264.1; Identities = 748/795 (94 %), three gaps (0 %)]. Closest hits using the ***rpb2*** (first part) sequence had distant similarity to *Ochroconis anomala* [strain Lx CH40, GenBank HE575205.1; Identities = 653/835 (78 %), 16 gaps (1 %)], *Yunnanomyces phoenicis* [strain MFLUCC 19-0254, GenBank MK986484.1; Identities = 646/835 (77 %), 16 gaps (1 %)], and *Scolecobasidium longiphorum* [strain ZY 22.032, GenBank OR842928.1; Identities = 650/837 (78 %), 20 gaps (2 %)]. No significant hits were obtained when the ***tef1*** (first part) sequence was used in blastn and megablast searches.

Culture CPC 46559 is distantly related to CPC 47671 described elsewhere in this document (ITS: 234/257 nt incl. eight gaps; LSU: 765/793 nt incl. one gap) as *Yunnanomyces hagahagaensis* (FP 1722). For a species level phylogeny, see the ITS phylogeny provided under that species.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Corynesporina* LSU nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Ramularia punctiformis* (CBS 113265; GenBank KF251723) and the novelty described here is highlighted with a coloured block and **bold** font. Families, orders and the class are shown to the right of the tree in coloured blocks. Some branches were shortened to facilitate layout. Alignment statistics: 40 strains including the outgroup; 822 characters including alignment gaps analysed: 254 distinct patterns, 182 parsimony-informative, 70 singleton sites, 570 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM3+F+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Venturiales* LSU nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Ramularia punctiformis* (CBS 113265; GenBank AY490776) and the novelties described here are highlighted with coloured blocks and **bold** font. Families, the order and the class are shown to the right of the tree in coloured blocks. Two of the clades were collapsed to facilitate layout; the uncollapsed tree is deposited at figshare.com. Alignment statistics: 93 strains including the outgroup; 790 characters including alignment gaps analysed: 311 distinct patterns, 250 parsimony-informative, 50 singleton sites, 490 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TN+F+R5. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Beaucarneamyces lupini

Fungal Planet 1710 MycoBank MB 856084

Beaucarneamyces lupini Crous & Akulov, ***sp. nov.***

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

Classification: *Neodactylariaceae*, *Neodactylariales*, *Pleosporomycetidae*, *Dothideomycetes*.

Mycelium consisting of pale brown, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* arising from superficial hyphae, erect, medium brown, smooth, subcylindrical, 1–2-septate, unbranched, straight to once geniculate, 10–30 × 3–4 µm, or reduced to conidiogenous cells. *Conidiogenous cells* integrated, terminal, 10–20 × 3–4 µm, medium brown, smooth, with several flat-tipped denticle-like sympodial loci, 1–2 × 1 µm. *Conidia* solitary, dry, hyaline, smooth, narrowly obclavate to subcylindrical, straight to slightly flexuous, apex subobtuse, base obconically truncate, 1–1.5 µm diam, not thickened nor darkened, 1–13-septate, guttulate, (10–)50–60(–70) × 2.5–3 µm.

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

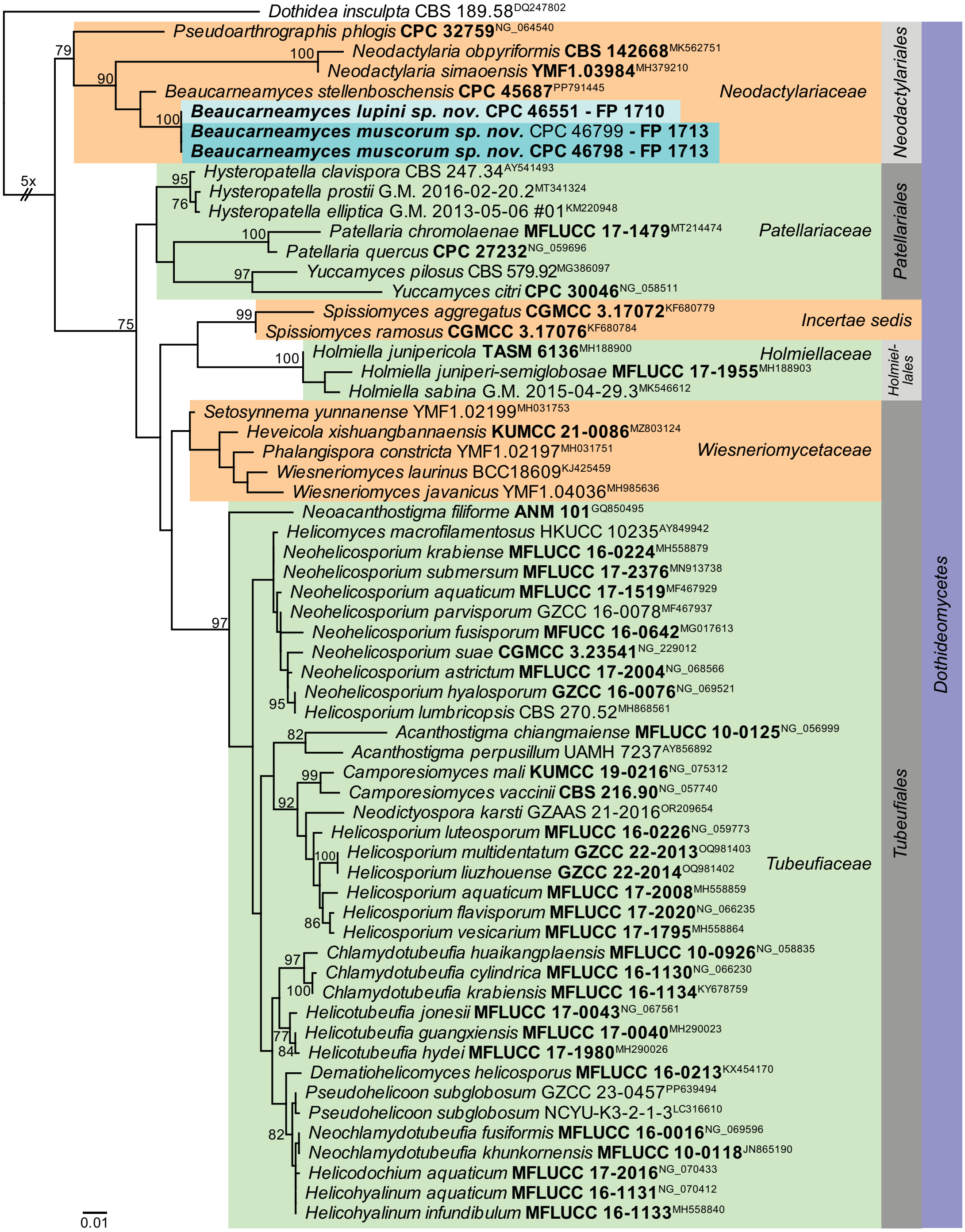
Typus: **Ukraine**, Kharkiv region, Zolochiv district, cottage village Alpha near Chepeline village, on overwintered stems of *Lupinus polyphyllus* (*Fabaceae*), 10 Jun. 2023, *A. Akulov*, HPC 4243, CWU (Myc) AS 8604 (**holotype** CBS H-25468; culture ex-type CPC 46551 = CBS 152213; ITS and LSU sequences GenBank PQ498940 and PQ498989).

Notes: *Beaucarneamyces* was introduced for *B. stellenboschensis* (on dead leaves of *Beaucarnea stricta*, South Africa), characterised by conidiophores reduced to conidiogenous cells on hyphae, with polyblastic, aggregated truncate apical denticles, and solitary, fusoid-ellipsoid, septate conidia, with the two central cells being pale brown (Crous *et al.* 2024). *Beaucarneamyces lupini* has medium brown conidiogenous cells, and flexuous, multiseptate, hyaline conidia, thus broadening the concept of *Beaucarneamyces.*

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to "*Pseudoarthrographis phlogis*" [strain SGSF544, GenBank MT947191.1; Identities = 468/469 (99 %), no gaps], *Beaucarneamyces stellenboschensis* [strain CPC 45687, GenBank PP791416.1; Identities = 526/567 (93 %), ten gaps (1 %)], *Pseudoarthrographis phlogis* [strain CPC 32759, GenBank NR_160349.1; Identities = 477/570 (84 %), 28 gaps (4 %)], *Neodactylaria simaoensis* [strain YMF1.03984, GenBank MH379209.1; Identities = 474/578 (82 %), 37 gaps (6 %)], and *Neodactylaria obpyriformis* [strain FMR 14604, GenBank NR_154267.1; Identities = 471/576 (82 %), 37 gaps (6 %)]. Closest hits using the **LSU** sequence are *Beaucarneamyces stellenboschensis* [strain CPC 45687, GenBank PP791445.1; Identities = 811/826 (98 %), no gaps], *Pseudoarthrographis phlogis* [strain CPC 32759, GenBank NG_064540.1; Identities = 785/826 (95 %), no gaps], and *Helicohyalinum aquaticum* [as *Tubeufiaceae* sp. YZL-2018e; strain MFLUCC 16-0014, GenBank MH558839.1; Identities = 784/829 (95 %), six gaps (0 %)].

The culture CPC 46551 is closely related to CPC 46798 and 46799 (ITS: 538/543 nt incl. one gap and 470/474 nt; LSU: both 826/826 nt) described elsewhere in this document as *Beaucarneamyces muscorum* (FP 1713). For a species level phylogeny, see the ITS phylogeny provided under that species.

Colour illustrations: Zolochiv district, Ukraine. Conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Neodactylariaceae* LSU nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Dothidea insculpta* (CBS 189.58; GenBank DQ247802) and the novelties described here are highlighted with coloured blocks and **bold** font. Families, orders and the class are shown to the right of the tree in coloured blocks. The root branch was shortened to facilitate layout. Alignment statistics: 61 strains including the outgroup; 822 characters including alignment gaps analysed: 236 distinct patterns, 146 parsimony-informative, 64 singleton sites, 612 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM3e+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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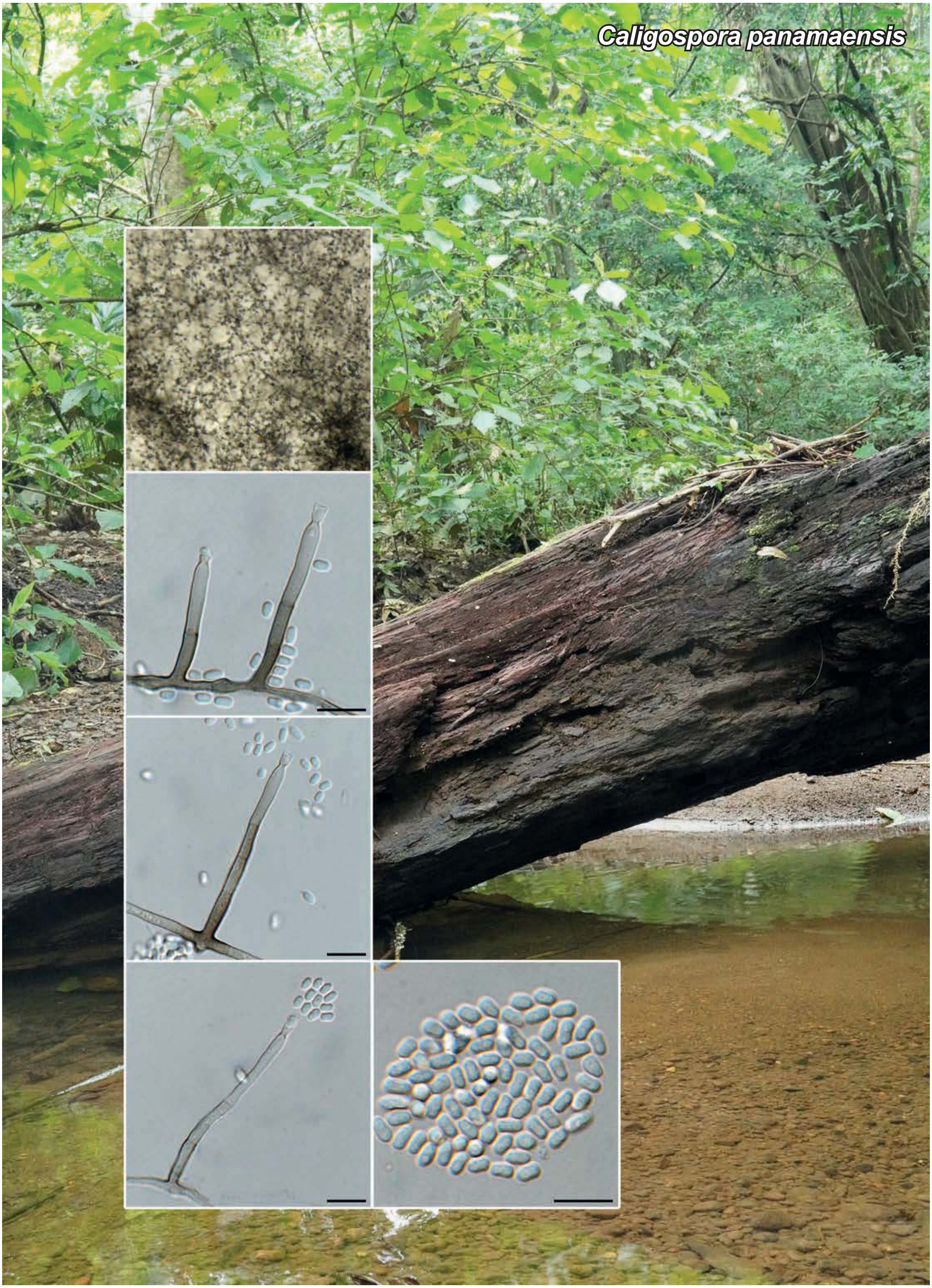

Caligospora panamaensis

Fungal Planet 1711

MycoBank MB 856085

Caligospora panamaensis Crous, *sp. nov.*

Etymology: Name refers to Panama, the country where it was collected.

Classification: *Chaetosphaeriaceae*, *Chaetosphaeriales*, *Sordariomycetidae*, *Sordariomycetes*.

Mycelium consisting of pale brown, smooth to finely roughened, branched, septate, 1.5–2 µm diam hyphae. *Setae* intermingled among conidiophores, erect, unbranched, subcylindrical with clavate apex, brown, smooth, becoming pale brown at clavate apex, thicker walled at basal region, 1–4-septate, 40–70 × 4–5 µm. *Conidiophores* solitary, unbranched, subcylindrical, erect, straight to slightly flexuous, brown, smooth, 3–5-septate, 40–70 × 3–3.5 µm. *Conidiogenous cells* 25–35 µm long, integrated, terminal, brown, paler towards apex, smooth, with cylindrical collarette, slightly flared, constricted at base, 3–5 × 3.5–4 µm. *Conidia* aggregating in mucoid mass, hyaline, smooth, thin-walled, ellipsoid to subcylindrical, apex obtuse, base truncate, (3–)4–5(–7.5) × 2.5–3 µm.

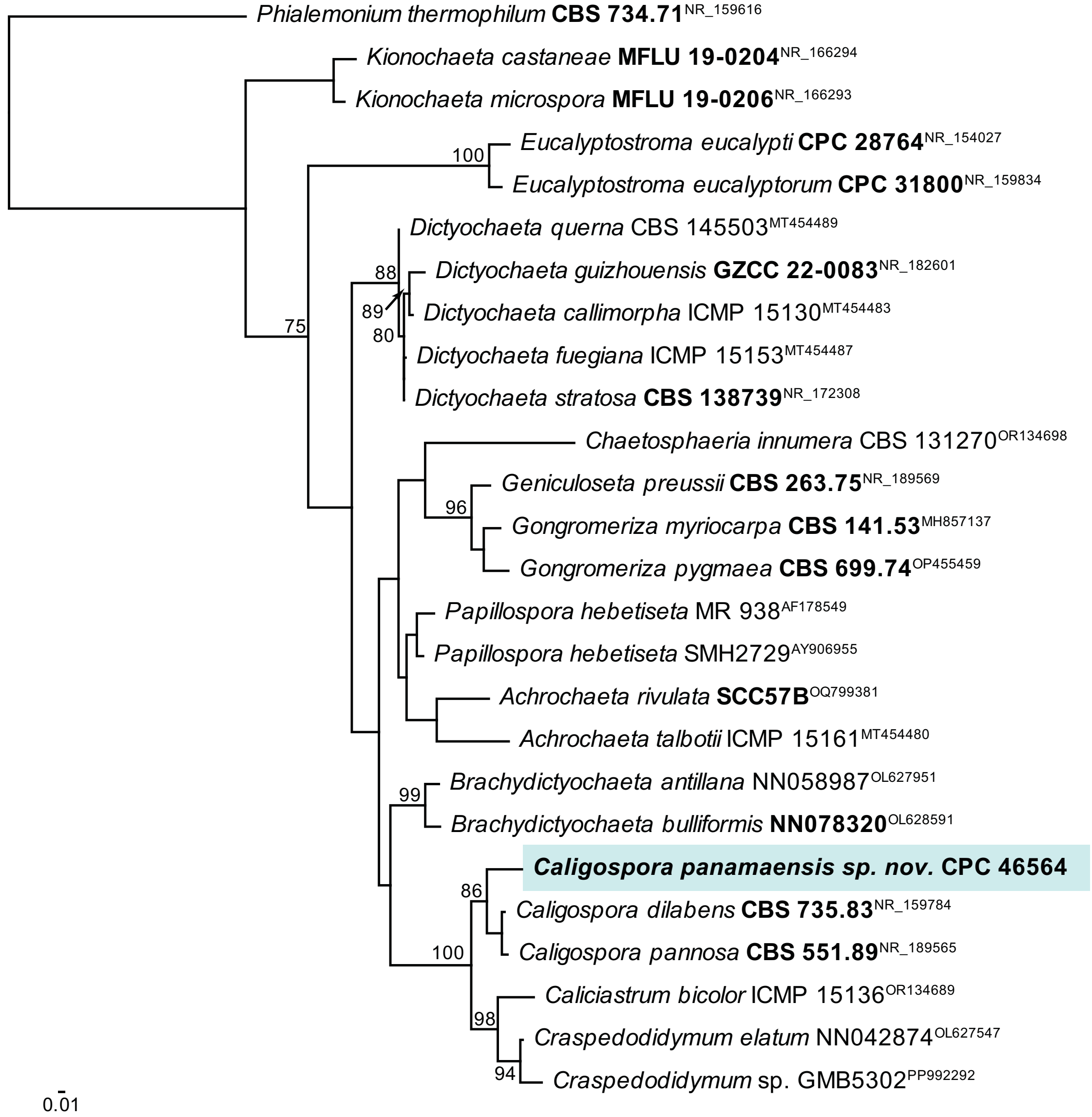
Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium, surface folded, and smooth, lobate margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse fuscous black.

Typus: **Panama**, Colon Province, Soberania National Park, Pipeline Road, close to Gamboa, on leaf litter, 6 Aug. 2023, *P.W. Crous*, HPC 4214 [**holotype** CBS H-25470; culture ex-type CPC 46564 = CBS 152320; ITS, LSU and *tef1* (second part) sequences GenBank PQ498941, PQ498990 and PQ497743].

Notes: *Caligospora panamaensis* clusters with species of *Caligospora* (Réblová & Nekvindová 2023) but is distinct in that the latter presently contains species with strongly pigmented conidia, suggesting that it might even represent yet another genus in *Chaetosphaeriaceae*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Chaetosphaeria* sp. DMH-2018a [clone N1_5, GenBank OR079896.1; Identities = 502/506 (99 %), two gaps (0 %)], *Caligospora pannosa* [strain CBS 551.89, GenBank NR_189565.1; Identities = 464/494 (94 %), seven gaps (1 %)], *Caligospora dilabens* [strain CBS 735.83, GenBank NR_159784.1; Identities = 445/472 (94 %), seven gaps (1 %)], and *Caliciastrum bicolor* [strain ICMP 15136, GenBank OR134689.1; Identities = 442/491 (90 %), four gaps (0 %)]. Closest hits using the **LSU** sequence are *Caligospora pannosa* [strain CBS 551.89, GenBank OR134637.1; Identities = 807/812 (99 %), no gaps], *Chaetosphaeria* sp. DMH-2018a [clone N1_5, GenBank OR079903.1; Identities = 811/817 (99 %), five gaps (0 %)], and *Caligospora dilabens* [strain CBS 734.83, GenBank OR134636.1; Identities = 806/812 (99 %), no gaps]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Caligospora pannosa* [strain CBS 551.89, GenBank OR130772.1; Identities = 845/895 (94 %), no gaps], *Cryptophiale udagawae* [strain MFLUCC 18-0428, GenBank OP473067.1; Identities = 840/892 (94 %), no gaps], and *Caligospora dilabens* [strain CBS 734.83, GenBank OR130771.1; Identities = 839/892 (94 %), no gaps].

Colour illustrations: Soberania National Park, Panama. Conidiophores on SNA; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Caligospora* ITS nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Phialemonium thermophilum* (CBS 734.71; GenBank NR_159616) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 26 strains including the outgroup; 599 characters including alignment gaps analysed: 273 distinct patterns, 160 parsimony-informative, 72 singleton sites, 367 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2+F+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Alfaria neerlandica

Fungal Planet 1712 MycoBank MB 856086

Alfaria neerlandica Crous, *sp. nov.*

Etymology: Name refers to the Netherlands, where it was collected.

Classification: *Stachybotriaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*.

Conidiomata sporodochial, 250–400 µm diam, with black mucoid conidial mass. *Setae* intermingled throughout sporodochium, olivaceous green, thick-walled, flexuous, septate, finely roughened, tapering to subobtuse apex, 120–220 × 6–7 µm. *Conidiophores* in tightly aggregated mass, arising from basal stroma, hyaline, smooth, branched, septate, 20–30 × 2.5–3 µm. *Conidiogenous cells* phialidic, cylindrical, hyaline, smooth, 7–10 × 2.5–3 µm, with inconspicuous collarettes. *Conidia* aseptate, smooth, subcylindrical, straight, apex subobtuse, base truncate, 8–9(–10) × 2 µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium, surface folded, and smooth, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white, reverse luteous.

Typus: **Netherlands**, Utrecht Province, Bilthoven, on stem lesions of *Cortaderia selloana* (*Poaceae*), 10 Sep. 2023, *P.W. Crous*, HPC 4258 [**holotype** CBS H-25471; culture ex-type CPC 46776 = CBS 152214; ITS, LSU, *gapdh*, SSU, *tef1* (first part) and *tef1* (second part) sequences GenBank PQ498942, PQ498991, PQ497715, PQ498970, PQ497767 and PQ497744].

Notes: *Alfaria terrestris* (from soil, Turkey, CBS 477.91) was introduced by Lombard *et al.* (2016), and at the time it included considerable intraspecific phylogenetic variation. *Alfaria neerlandica* is distinct from *A. terrestris*, as the latter lacks setae, and has smaller, ellipsoidal to limoniform conidia, (4–)5–7× 2–3 µm (av. 6 × 2 µm).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Alfaria* sp. [strain ICMP 1074, GenBank OR514933.1; Identities = 548/548 (100 %), no gaps], *Myrothecium gramineum* [strain ZLW0801-19, GenBank JX077058.1; Identities = 425/431 (99 %), one gap (0 %)], *Xepicula leucotricha* [strain F26-03, GenBank KX664359.1; Identities = 547/555 (99 %), two gaps (0 %)], and *Alfaria terrestris* [strain CBS 477.91, GenBank NR_145069.1; Identities = 552/561 (98 %), two gaps (0 %)]. Closest hits using the **LSU** sequence are *Alfaria terrestris* [strain CBS 168.97, GenBank KU845996.1; Identities = 811/811 (100 %), no gaps], *Amerosporium platense* [strain CBS 658.73, GenBank MH872519.1; Identities = 810/811 (99 %), no gaps], *Amerosporium atrum* [strain CBS 151.69, GenBank MH877704.1; Identities = 810/811 (99 %), no gaps], and *Alfaria dandenongensis* [strain CBS 143399, GenBank NG_069537.1; Identities = 810/811 (99 %), no gaps]. The closest hit using the ***gapdh*** sequence had highest similarity to *Myrothecium gramineum* [strain MUCL 39210, GenBank EF486690.1; Identities = 288/319 (90 %), no gaps]. Closest hits using the **SSU** sequence are *Xepicula leucotricha* [as *Myrothecium leucotrichum*; strain BBA 65577, GenBank AJ301992.1; Identities = 983/987 (99 %), one gap (0 %)], *Stachybotrys bisbyi* [strain UAMH 1526, GenBank DQ680057.1; Identities = 978/987 (99 %), one gap (0 %)], and *Koorchaloma bambusae* [voucher MFLU 19-2899, GenBank MT214958.1; Identities = 977/988 (99 %), four gaps (0 %)]. Closest hits using the ***tef1*** (first part) sequence had highest similarity to *Alfaria terrestris* [strain CBS 127305, GenBank KU846012.1; Identities = 370/400 (93 %), one gap (0 %)], *Albifimbria viridis* [strain CBS 127346, GenBank KU845956.1; Identities = 210/232 (91 %), eight gaps (3 %)], and *Myxospora crassiseta* [strain CBS 121141, GenBank KU846521.1; Identities = 206/230 (90 %), three gaps (1 %)]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Alfaria cyperi-esculenti* [voucher MFLU 18-0908, GenBank OL606737.1; Identities = 842/874 (96 %), no gaps], *Alfaria avenellae* [strain MFLUCC 15-0828, GenBank MG264368.1; Identities = 829/874 (95 %), no gaps], and *Koorchaloma bambusae* [voucher MFLU 19-2899, GenBank MT454027.1; Identities = 825/872 (95 %), no gaps].

Colour illustrations: Stem lesions of *Cortaderia selloana*, Bilthoven, Netherlands. Conidiomata on SNA; setae, conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Alfaria* ITS nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Neocosmospora falciformis* (CBS 475.67; GenBank NR_164424) and the novelty described here is highlighted with a coloured block and **bold** font. Families, orders and the class are shown to the right of the tree in coloured blocks. The root branch was shortened to facilitate layout. Alignment statistics: 39 strains including the outgroup; 540 characters including alignment gaps analysed: 132 distinct patterns, 47 parsimony-informative, 71 singleton sites, 422 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2+F+R2. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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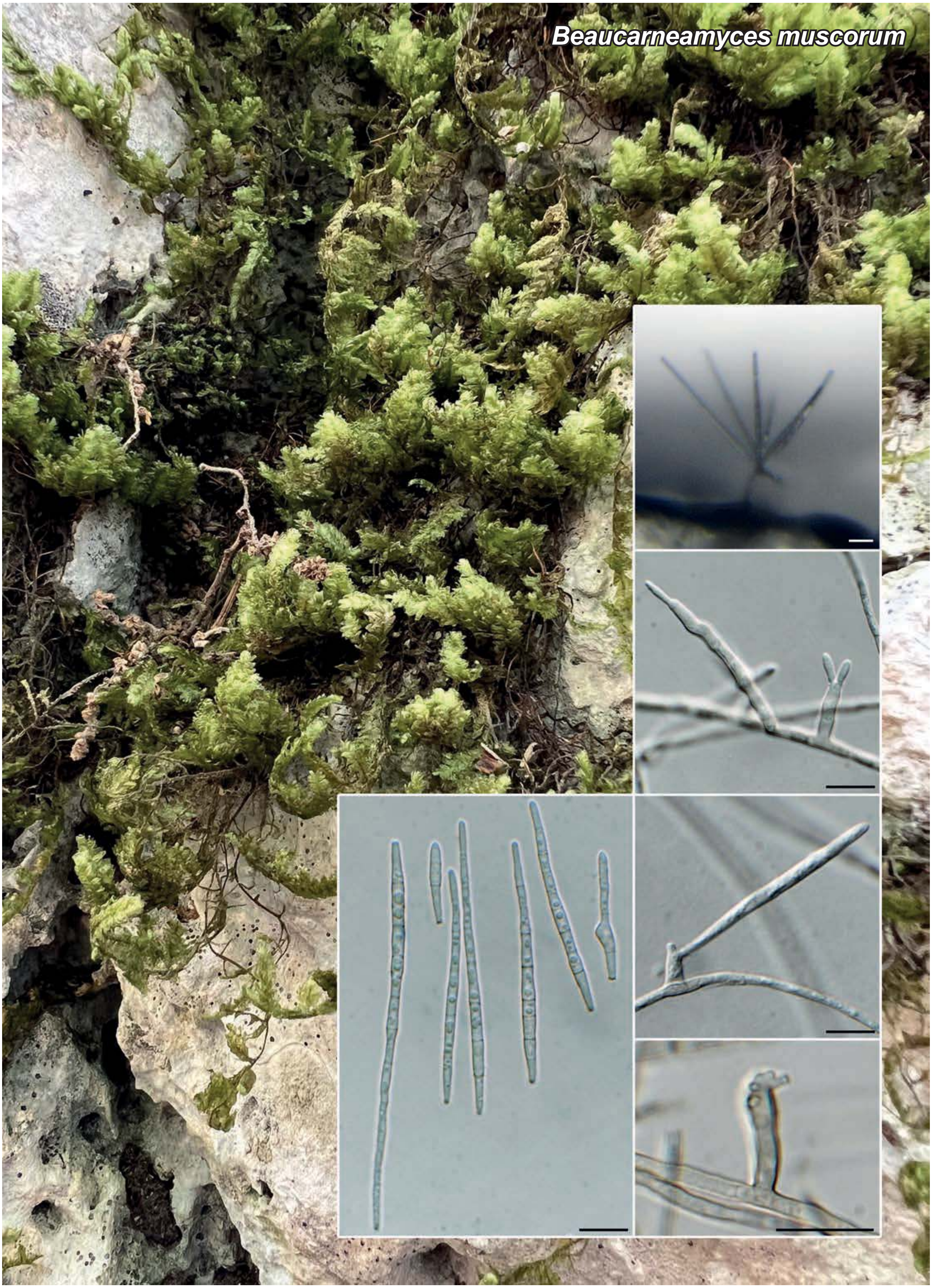

Beaucarneamyces muscorum

Fungal Planet 1713 MycoBank MB 856087

Beaucarneamyces muscorum Crous, *sp. nov.*

Etymology: *Muscus* = Latin for moss.

Classification: *Neodactylariaceae*, *Neodactylariales*, *Pleosporomycetidae*, *Dothideomycetes*.

Mycelium consisting of hyaline to pale brown, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* solitary, erect, straight to geniculate-sinuous, subcylindrical, pale brown, smooth, 1–3-septate, 6–30 × 2.5–4 µm. *Conidiogenous cells* integrated, terminal, subcylindrical, pale brown, smooth, 6–20 × 2.5–3 µm, terminating with several sympodial denticles, 1–3 × 1.5–2 µm, not thickened nor darkened. *Conidia* solitary, dry, hyaline, smooth, granular, subcylindrical to narrowly obclavate, apex obtuse, base long obconically truncate, 1–15-septate, 25–100 × 2.5–3 µm; conidia undergoing microcyclic conidiation in culture.

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

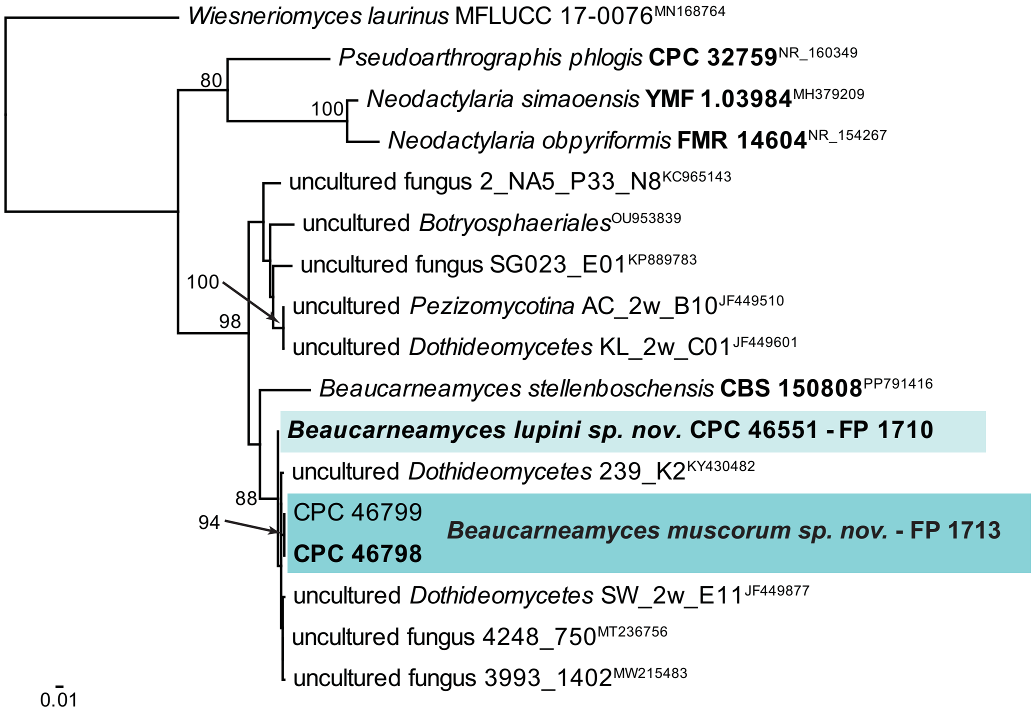
Typus: **Italy**, Spoleto, on moss growing in forest, 6 Sep. 2023, *P.W. Crous*, HPC 4263 (**holotype** CBS H-25472; culture ex-type CPC 46798 = CBS 152215; ITS and LSU sequences GenBank PQ498943 and PQ498992); *idem.*, culture CPC 46799 (ITS and LSU sequences GenBank PQ498944 and PQ498993).

Notes: *Beaucarneamyces muscorum* is phylogenetically closely related to *B. lupini* [on overwintered stems of *Lupinus polyphyllus*, Ukraine; conidia (10–)50–60(–70) × 2.5–3 µm], but is morphologically distinct in that it has longer conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to "*Pseudoarthrographis phlogis*" [strain SGSF544, GenBank MT947191.1; Identities = 465/469 (99 %), one gap (0 %)], *Beaucarneamyces stellenboschensis* [strain CPC 45687, GenBank PP791416.1; Identities = 509/551 (92 %), 13 gaps (2 %)], *Pseudoarthrographis phlogis* [strain CPC 32759, GenBank NR_160349.1; Identities = 459/553 (83 %), 29 gaps (5 %)], and *Neodactylaria obpyriformis* [strain FMR 14604, GenBank NR_154267.1; Identities = 399/479 (83 %), 22 gaps (4 %)]. The ITS sequences of CPC 46798 and 46799 are identical (905/905 nt). Closest hits using the **LSU** sequence are *Beaucarneamyces stellenboschensis* [strain CPC 45687, GenBank PP791445.1; Identities = 812/827 (98 %), no gaps], *Pseudoarthrographis phlogis* [strain CPC 32759, GenBank NG_064540.1; Identities = 786/827 (95 %), no gaps], *Helicohyalinum aquaticum* [as *Tubeufiaceae* sp. YZL-2018e; strain MFLUCC 16-0014, GenBank MH558839.1; Identities = 785/830 (95 %), six gaps (0 %)], and *Pseudohelicoon subglobosum* [strain GZCC 23-0457, GenBank PP639494.1; Identities = 785/830 (95 %), six gaps (0 %)]. The LSU sequences of CPC 46798 and 46799 are identical (827/827 nt).

The cultures CPC 46798 and 46799 are closely related to *Beaucarneamyces lupini* (CPC 46551) (ITS: 538/543 nt incl. one gap and 470/474 nt; LSU: both 826/826 nt) described elsewhere in this document (FP 1710). For a higher order phylogeny, see the LSU phylogeny provided under that species.

Colour illustrations: Moss growing on rocks in Spoleto, Italy. Conidiophores on SNA; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Beaucarneamyces* ITS nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Wiesneriomyces laurinus* (MFLUCC 17-0076; GenBank MN168764) and the novelties described here are highlighted with coloured blocks and **bold** font. Alignment statistics: 17 strains including the outgroup; 567 characters including alignment gaps analysed: 218 distinct patterns, 122 parsimony-informative, 94 singleton sites, 351 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TN+F+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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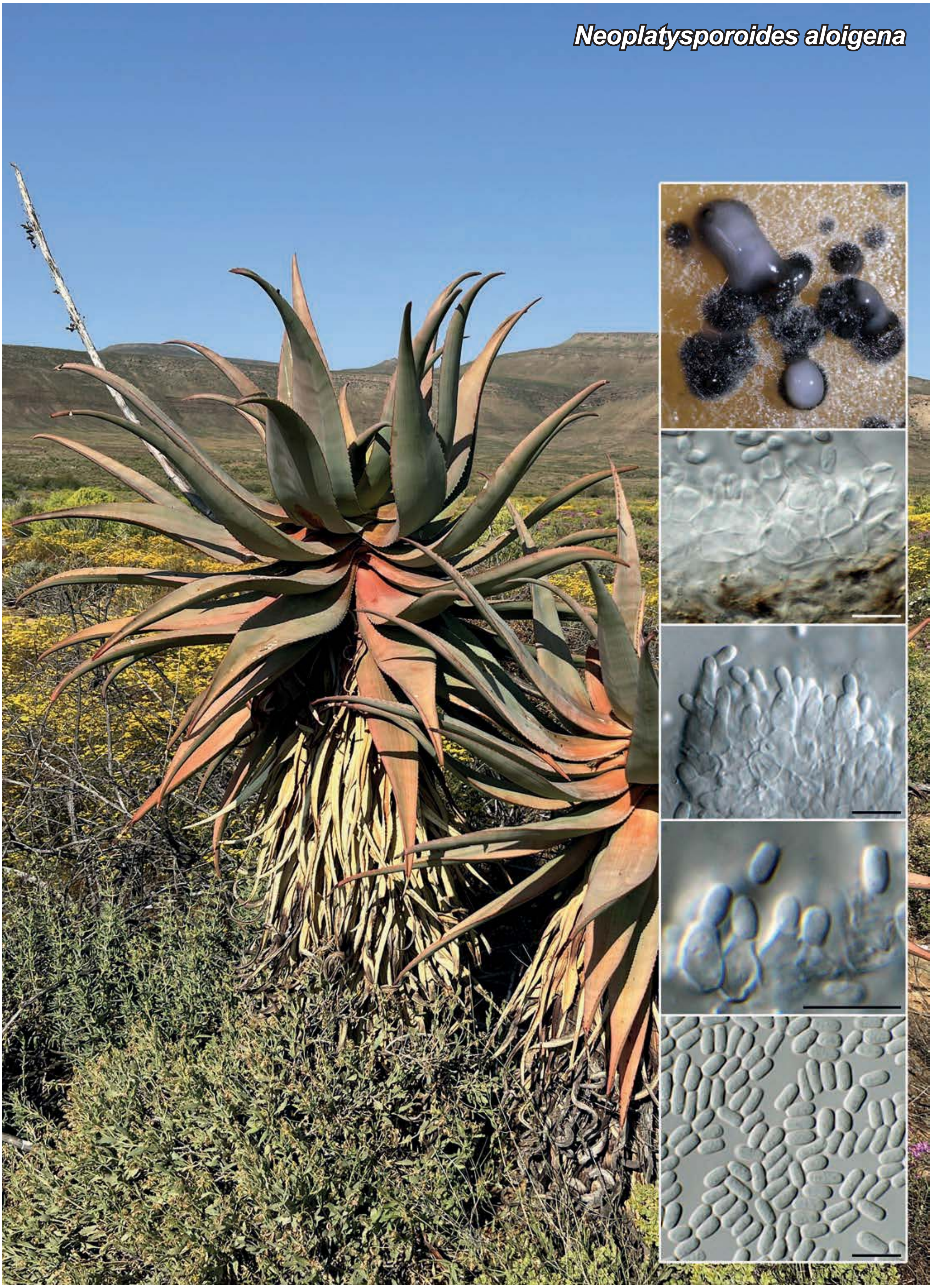

Neoplatysporoides aloigena

Fungal Planet 1714

MycoBank MB 856088

Neoplatysporoides aloigena Crous, *sp. nov.*

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

Classification: *Libertasomycetaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*.

Conidiomata pycnidial, aggregated in clusters, each pycnidium with clearly developed central ostiole; pycnidia brown, globose, 300–350 µm diam, outer layer covered in brown hyphae; wall of 3–6 layers of brown *textura angularis. Conidiophores* tightly aggregated, hyaline, smooth, subcylindrical to doliiform, reduced to conidiogenous cells or elongated, septate, developing conidiogenous cells terminally and intercalary. *Conidiogenous cells* subcylindrical to doliiform, hyaline, smooth, proliferating percurrently, 3–10 × 3–5 µm. *Conidia* solitary, exuding in creamy to pinkish mucoid mass, hyaline, smooth, aseptate, guttulate, subcylindrical, apex obtuse, base truncate, 4–5 × 2.5–3 µm.

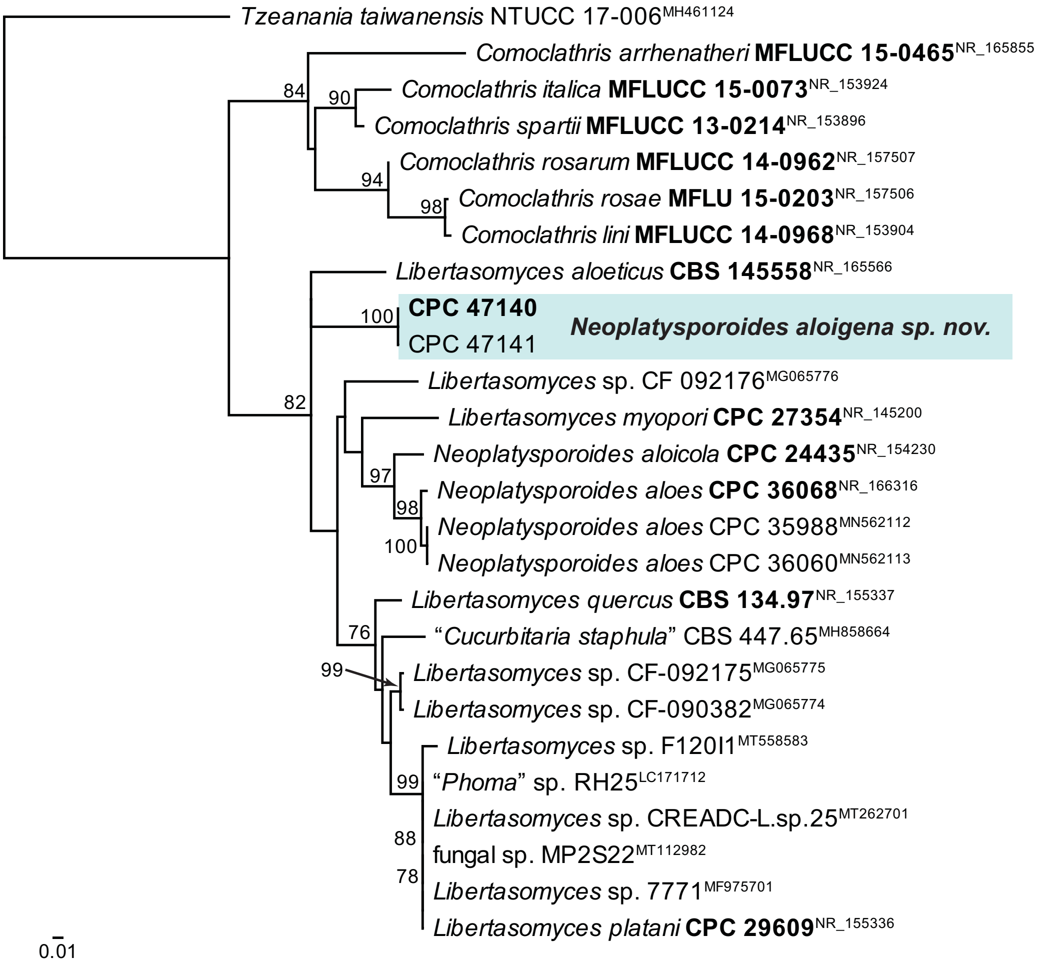
Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium, surface folded, and smooth, lobate margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA surface olivaceous grey in centre, luteous in outer region, reverse luteous with patches of umber; on PDA surface and reverse ochreous; on OA surface pale luteous.

Typus: **South Africa**, Western Cape Province, Cederberg, Botterkloof Pass, on leaf of *Aloe khamiesensis* (*Asphodelaceae*), Sep. 2023, *M.J. Wingfield*, HPC 4283 (**holotype** CBS H-25477; culture ex-type CPC 47140 = CBS 152218; ITS and LSU sequences GenBank PQ498945 and PQ498994); *idem.*, culture CPC 47141 = CBS 152219 (ITS and LSU sequences GenBank PQ498946 and PQ498995).

Colour illustrations: *Aloe khamiesensis* in Cederberg, South Africa. Conidiomata on oatmeal agar; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Notes: *Neoplatysporoides aloigena* needs to be compared with *N. aloes* [conidia brown, 0–1-septate, (7–)8–9(–10) × (4–)4.5(–5) µm; Crous *et al.* 2019] and *N. aloicola* (conidia golden brown, 0–1-septate, (8–)9–10(–12) × (4–)5(–6) µm; Crous *et al.* 2015b), which both have pigmented, and larger conidia than in *N. aloigena.* Phylogenetically, it appears to cluster more basal to *Neoplatysporoides* and *Libertasomyces*, and might even represent a third genus in this complex.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 47140 had highest similarity to *Libertasomyces aloeticus* [strain CBS 145558, GenBank NR_165566.1; Identities = 502/554 (91 %), 11 gaps (1 %)], *Neoplatysporoides aloicola* [strain CBS 139901, GenBank NR_154230.1; Identities = 500/552 (91 %), 12 gaps (2 %)], and *Neoplatysporoides aloes* [strain CPC 36068, GenBank NR_166316.1; Identities = 499/551 (91 %), 12 gaps (2 %)]. The ITS sequences of CPC 47140 and 47141 are identical (541/541 nt). Closest hits using the **LSU** sequence of CPC 47140 are *Neoplatysporoides aloes* [strain CPC 35988, GenBank MN567620.1; Identities = 810/815 (99 %), one gap (0 %)], *Neoplatysporoides aloicola* [strain CBS 139901, GenBank NG_058160.1; Identities = 806/814 (99 %), one gap (0 %)], and *Neocamarosporium betae* [strain CBS 109410, GenBank EU754178.1; Identities = 805/816 (99 %), three gaps (0 %)]. The LSU sequences of CPC 47140 and 47141 are identical (814/814 nt).



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Neoplatysporoides* ITS nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Tzeanania taiwanensis* (NTUCC 17-006; GenBank MH461124) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 26 strains including the outgroup; 542 characters including alignment gaps analysed: 218 distinct patterns, 133 parsimony-informative, 50 singleton sites, 359 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Synnemapestaloides searsiae

Fungal Planet 1715 MycoBank MB 856090

Synnemapestaloides searsiae Crous, ***sp. nov.***

Etymology: Name refers to *Searsia*, the host it was isolated from.

Classification: *Sporocadaceae*, *Xylariales*, *Xylariomycetidae*, *Sordariomycetes*.

Ascomata perithecial, brown, solitary to aggregated, globose, 250–350 µm diam, with punctiform apex and central ostiole; wall of 3–6 layers of brown *textura angularis. Paraphyses* intermingled among asci, hyaline, smooth, septate, hyphae-like, 5–7 µm diam. *Asci* sessile, ellipsoid, unitunicate, apical mechanism not straining in Melzer, 70–80 × 20-24 µm; 8-spored, with tri- to multiseriate ascospores. *Ascospores* hyaline, smooth, guttulate, ellipsoid with central septum, not constricted at septum, becoming 3-septate, enclosed in mucoid sheath, widest above apical septum, (21–)23–25(–27) × (7–)8–9 µm.

Culture characteristics: Colonies flat, spreading, with sparse to moderate aerial mycelium, and smooth, lobate margin, reaching 17 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse umber.

Typus: **South Africa**, Western Cape Province, Cederberg, Cederberg City Hall, on leaf of *Searsia populifolia* (*Anacardiaceae*), Sep. 2023, *M.J. Wingfield*, HPC 4292 [**holotype** CBS H-25480; culture ex-type CPC 47153 = CBS 152220; ITS, LSU, *rpb2*, SSU, *tef1* (first part) and *tef1* (second part) sequences GenBank PQ498947, PQ498996, PQ497728, PQ498971, PQ504941 and PQ497745].

Notes: Handa *et al*. (2004) introduced *Synnemapestaloides* (based on *S. rhododendri*) for a synnematous hyphomycete. Liu *et al*. (2019) emended the description to also include taxa with sporodochia, and having conidia that lacked appendages. *Synnemapestaloides searsiae* represents a sexual genus that clusters among species described in *Synnemapestaloides*, but as no asexual morph developed in culture, a morphological comparison was not possible.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Sarcostroma bisetulatum* [strain CBS 122695, GenBank EU552155.1; Identities = 496/522 (95 %), eight gaps (1 %)], *Sarcostroma restionis* [strain CPC 29466, GenBank MH823021.1; Identities = 496/522 (95 %), eight gaps (1 %)], and *Seimatosporium hakeae* [strain NBRC 32678, GenBank AB594804.1; Identities = 480/506 (95 %), eight gaps (1 %)]. Closest hits using the **LSU** sequence are *Discosia ravennica* [voucher MFLU 18-0131, GenBank NG_075366.1; Identities = 812/817 (99 %), no gaps], *Discosia fraxinea* [strain NTIT469, GenBank KF827439.1; Identities = 810/817 (99 %), no gaps], *Synnemapestaloides shangrilaensis* [strain SHLA-14, GenBank MZ387994.1; Identities = 809/817 (99 %), no gaps], and *Sarcostroma australiense* [strain CBS 144160, GenBank MH554340.1; Identities = 809/817 (99 %), no gaps]. Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Synnemapestaloides shangrilaensis* [voucher HKAS 113188, GenBank MZ389340.1; Identities = 659/735 (90 %), no gaps], *Synnemapestaloides juniperi* [strain CBS 477.77, GenBank MH554966.1; Identities = 643/737 (87 %), four gaps (0 %)], and *Discosia fraxinea* [strain NTIT469, GenBank KF827476.1; Identities = 634/735 (86 %), no gaps]. Closest hits using the **SSU** sequence are *Immersidiscosia eucalypti* [strain KT2115, GenBank AB593701.1; Identities = 994/994 (100 %), no gaps], *Discosia fraxinea* [strain NTIT469, GenBank KF827443.1; Identities = 994/994 (100 %), no gaps], and *Discosia brasiliensis* [strain NTCL094-2, GenBank KF827440.1; Identities = 993/994 (99 %), no gaps]. Closest hits using the ***tef1*** (first part) sequence had distant similarity to *Sporocadus brevis* [strain ROC 095, GenBank OL814541.2; Identities = 300/373 (80 %), 34 gaps (9 %)], *Allelochaeta neocylindrospora* [strain CBS 144176, GenBank MH823133.1; Identities = 217/241 (90 %), nine gaps (3 %)], and *Allelochaeta parafalcata* [strain CBS 144185, GenBank MH823139.1; Identities = 214/239 (90 %), nine gaps (3 %)]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Sporocadus rosigena* [strain MV-B1, GenBank OQ434078.1; Identities = 761/794 (96 %), no gaps], *Neopestalotiopsis sichuanensis* [strain CC.HK12, GenBank PP496595.1; Identities = 809/857 (94 %), no gaps], *Pestalotiopsis microspora* [GenBank PQ114718.1; Identities = 814/863 (94 %), no gaps] , and *Sarcostroma restionis* [strain RBG7301, GenBank OP066942.1; Identities = 380/396 (96 %), no gaps].

Colour illustrations: *Searsia populifolia* in Cederberg, South Africa. Ascomata on SNA; asci; ascospores (stained in Melzer); asci; ascospores with sheath. Scale bars = 10 µm.

Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Synnemapestaloides* ITS nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Xylaria necrophora* (CBS 146542; GenBank NR_182818) and the novelty described here is highlighted with a coloured block and **bold** font. The root branch was shortened to facilitate layout. Alignment statistics: 75 strains including the outgroup; 550 characters including alignment gaps analysed: 226 distinct patterns, 135 parsimony-informative, 59 singleton sites, 356 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TPM3+F+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Iodophanus taxi

Fungal Planet 1716

MycoBank MB 856091

Iodophanus taxi Crous & Declercq, ***sp. nov.***

Etymology: Name refers to *Taxus*, the host it was isolated from.

Classification: *Ascobolaceae*, *Pezizales*, *Pezizomycetes*.

Mycelium consisting of hyaline, smooth, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* solitary, subcylindrical, erect, flexuous, hyaline, smooth, 10–15-septate, 200–450 µm tall. *Conidiogenous cells* integrated, terminal, globose to sphaeropedunculate, 25–30 µm diam, covered in numerous denticles, 1–2 × 1 µm. *Conidia* solitary, aseptate, fusoid-ellipsoid, hyaline, smooth, apex subobtuse, base truncate, 1 µm diam, with marginal frill, (20–)25–27(–30) × 9–10(–11) µm.

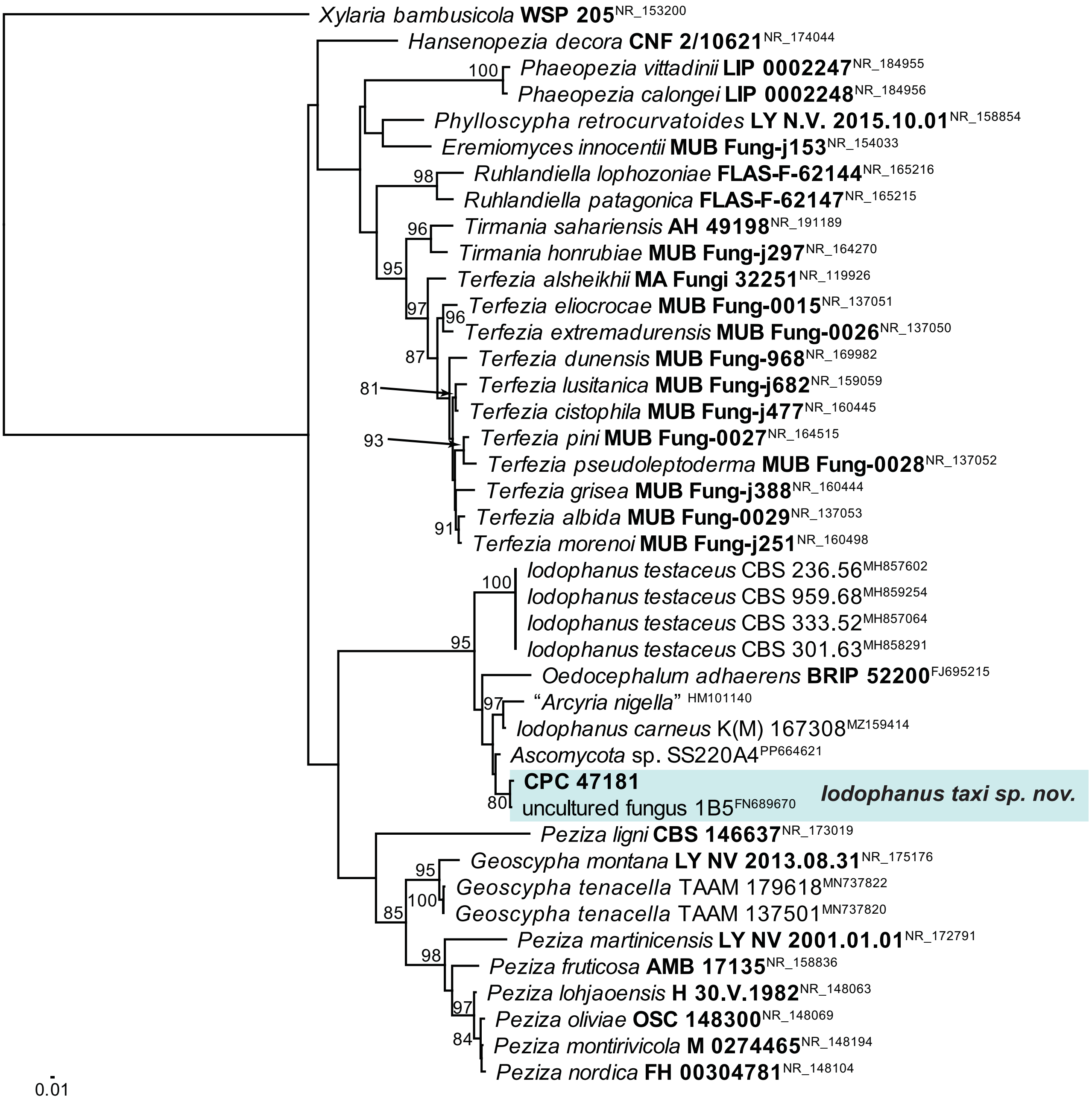
Culture characteristics: Colonies flat, spreading, lacking aerial mycelium, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse pale luteous.

Typus: **Belgium**, Sint-Niklaas, heikapel, on leaf of *Taxus baccata* (*Taxaceae*), 6 Dec. 2022, *B. Declercq*, HPC 4270, BD 22/037 (**holotype** CBS H-25481; culture ex-type CPC 47181 = CBS 152221; ITS and LSU sequences GenBank PQ498948 and PQ498997).

Colour illustrations: *Taxus baccata*, Sint-Niklaas, Belgium. Conidiophores on SNA; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars: Conidiophores = 20 µm, all others = 10 µm.

Notes: *Oedocephalum* asexual morphs have been linked to genera such as *Peziza* and *Iodophanus* (Clinto *et al*. 2007). Phylogenetically *I. taxi* appears to represent a novel species of *Iodophanus*. Because it is known only from its asexual morph, morphological comparisons are impossible.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Iodophanus carneus* [voucher K(M):167308, GenBank MZ159414.1; Identities = 566/617 (92 %), 32 gaps (5 %)], *Oedocephalum adhaerens* [strain BRIP 52200, GenBank FJ695215.1; Identities = 553/627 (88 %), 50 gaps (7 %)], and *Arcyria nigella* [GenBank HM101140.1; Identities = 533/604 (88 %), 39 gaps (6 %)]. Closest hits using the **LSU** sequence are *Iodophanus carneus* [voucher JHP 00.027 (C), GenBank AY500534.1; Identities = 877/882 (99 %), no gaps], *Iodophanus testaceus* [strain CBS 236.56, GenBank MH869150.1; Identities = 874/882 (99 %), no gaps], and *Oedocephalum adhaerens* [strain CBS 125450, GenBank NG_064222.1; Identities = 863/882 (98 %), no gaps].



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Iodophanus* ITS nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Xylaria bambusicola* (WSP 205; GenBank NR_153200) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 41 strains including the outgroup; 675 characters including alignment gaps analysed: 464 distinct patterns, 337 parsimony-informative, 90 singleton sites, 248 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: GTR+F+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Cyphellophora panamaensis

Fungal Planet 1717 MycoBank MB 856092

Cyphellophora panamaensis Crous, ***sp. nov.***

Etymology: Name refers to Panama, where it was collected.

Classification: *Cyphellophoraceae*, *Chaetothyriales*, *Chaetothyriomycetidae*, *Eurotiomycetes*.

Mycelium consisting of pale brown, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* solitary, erect, brown, smooth, subcylindrical, unbranched, 1–3-septate, 3–40 × 2–2.5 µm. *Conidiogenous cells* integrated, terminal, subcylindrical, pale brown, smooth, 3–25 × 1.5–2 µm, terminating in a rachis of a few sympodially arranged slightly darkened loci, 0.5 µm diam. *Conidia* solitary, narrowly fusoid, widest in middle, tapering toward both ends, (1–)3-septate, pale brown, smooth, guttulate, hilum slightly darkened, 0.5 µm diam, (6–)11–17(–27) × 2 µm.

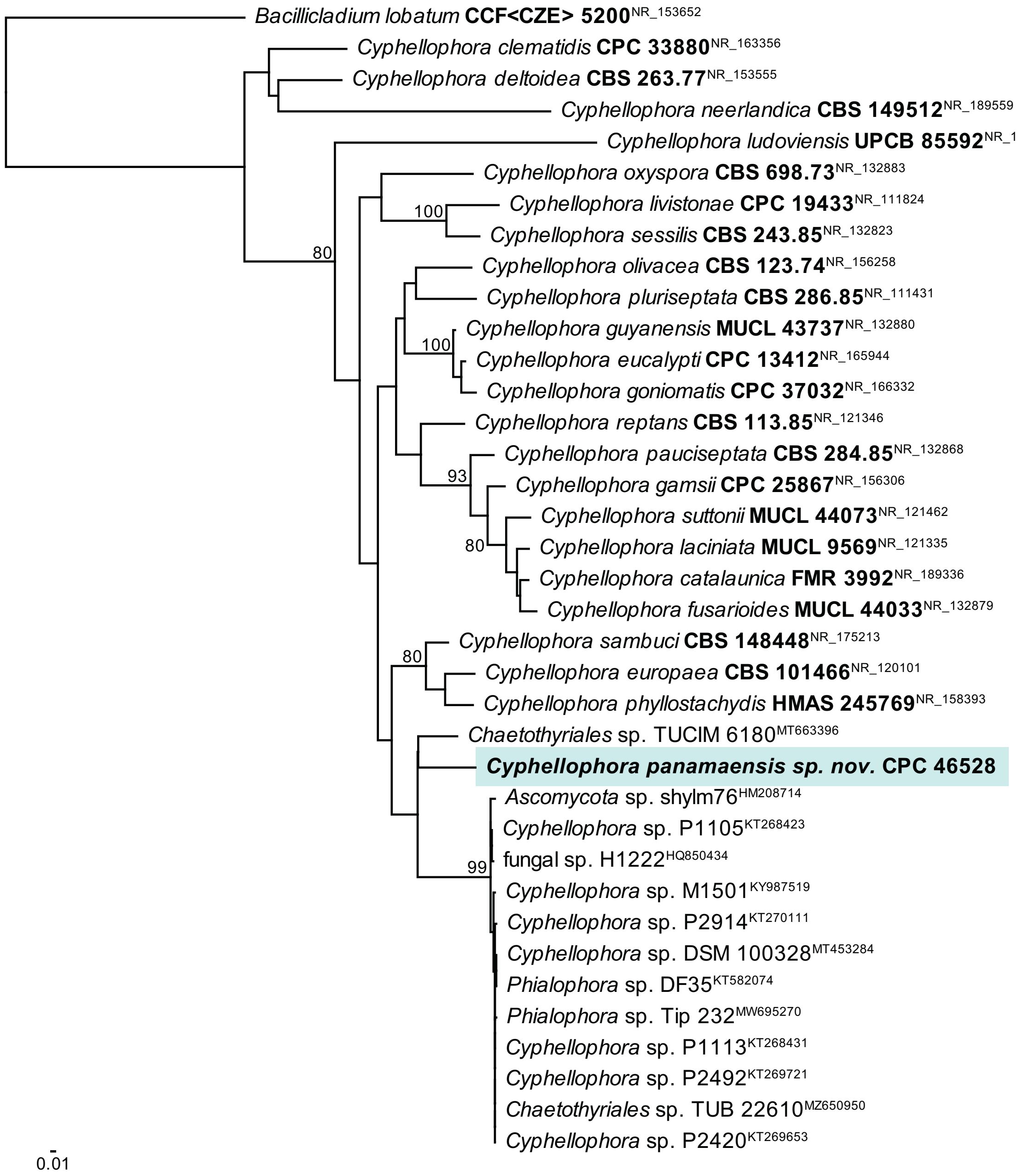
Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium, surface folded, and smooth, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus: **Panama**, Colon Province, Soberania National Park, Pipeline Road, close to Gamboa, on twig litter of angiosperm, 6 Aug. 2023, *P.W. Crous*, HPC 4219 (**holotype** CBS H-25464; culture ex-type CPC 46528 = CBS 152314; ITS, LSU and *tub2* sequences GenBank PQ498949, PQ498998 and PQ497778).

Notes: *Cyphellophora*, based on *C. laciniata*, was emended by Réblová *et al*. (2013) to also include taxa with aseptate conidia, and flask-shaped phialidic collarettes. *Cyphellophora panamaensis* adds an unusual species to the genus, as it lacks visible phialidic conidiogenous cells, but rather has sympodially arranged slightly darkened loci (at least when viewed under a compound microscope), which morphologically, suggests this to not be a true *Cyphellophora*. For the present however, it is best accommodated in *Cyphellophora*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cyphellophora reptans* [strain CCFEE 6373, GenBank MZ573432.1; Identities = 472/521 (91 %), 15 gaps (2 %)], *Cyphellophora europaea* [strain A457_7, GenBank MH063219.1; Identities = 472/523 (90 %), 12 gaps (2 %)], and *Cyphellophora sambuci* [strain CBS 148448, GenBank NR_175213.1; Identities = 523/584 (90 %), 18 gaps (3 %)]. Closest hits using the **LSU** sequence are *Cyphellophora musae* [strain HMAS 245771, GenBank NG_068524.1; Identities = 809/819 (99 %), two gaps (0 %)], *Cyphellophora olivacea* [strain CBS 123.74, GenBank NG_067280.1; Identities = 806/818 (99 %), two gaps (0 %)], and *Cyphellophora sambuci* [strain CBS 148448, GenBank NG_081322.1; Identities = 791/803 (99 %), one gap (0 %)]. Closest hits using the ***tub2*** sequence in a blastn search had highest similarity to *Cyphellophora sambuci* [strain CPC 39957, GenBank OK651206.1; Identities = 403/532 (76 %), 38 gaps (7 %)], *Cyphellophora aestiva* [strain CBS 497.80, GenBank MW297547.1; Identities = 328/420 (78 %), 14 gaps (3 %)], and *Cyphellophora olivacea* [strain CBS 123.74, GenBank KC455231.1; Identities = 325/415 (78 %), 14 gaps (3 %)].

Colour illustrations: Soberania National Park, Panama. Conidiophores on SNA; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Cyphellophora* ITS nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Bacillicladium lobatum* (CCF<CZE> 5200; GenBank NR_153652) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 37 strains including the outgroup; 624 characters including alignment gaps analysed: 302 distinct patterns, 192 parsimony-informative, 84 singleton sites, 348 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: GTR+F+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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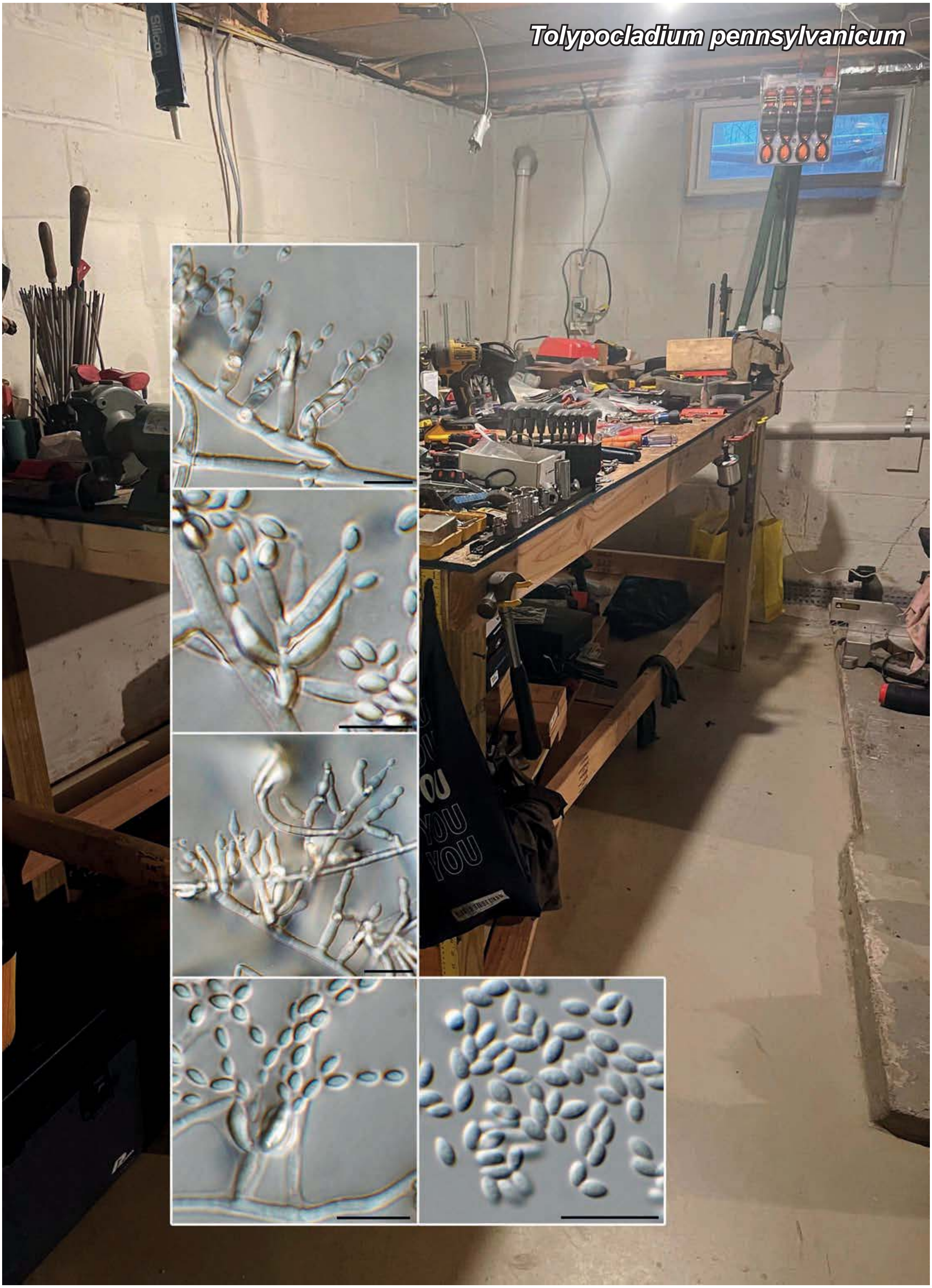

Tolypocladium pennsylvanicum

Fungal Planet 1718 MycoBank MB 856093

Tolypocladium pennsylvanicum Crous & Jurjević, ***sp. nov.***

Etymology: Name refers to the American state of Pennsylvania where it was collected.

Classification: *Ophiocordycipitaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2.5 µm diam hyphae. *Conidiophores* erect, arising from superficial hyphae, solitary or in clusters, subcylindrical, hyaline, smooth, 1–4-septate, 20–35 × 2.5–3 µm, with primary branches terminal and intercalary, 4–8 × 2–2.5 µm, giving rise to conidiogenous cells, solitary or in clusters of up to four. *Conidiogenous cells* hyaline, smooth, ampulliform to ellipsoid, straight to curved, phialidic, 3–8 × 2–2.5 µm. *Conidia* in dry, unbranched chains, hyaline, smooth, guttulate, ellipsoid, aseptate, 3–4 × (1.5–)2 µm.

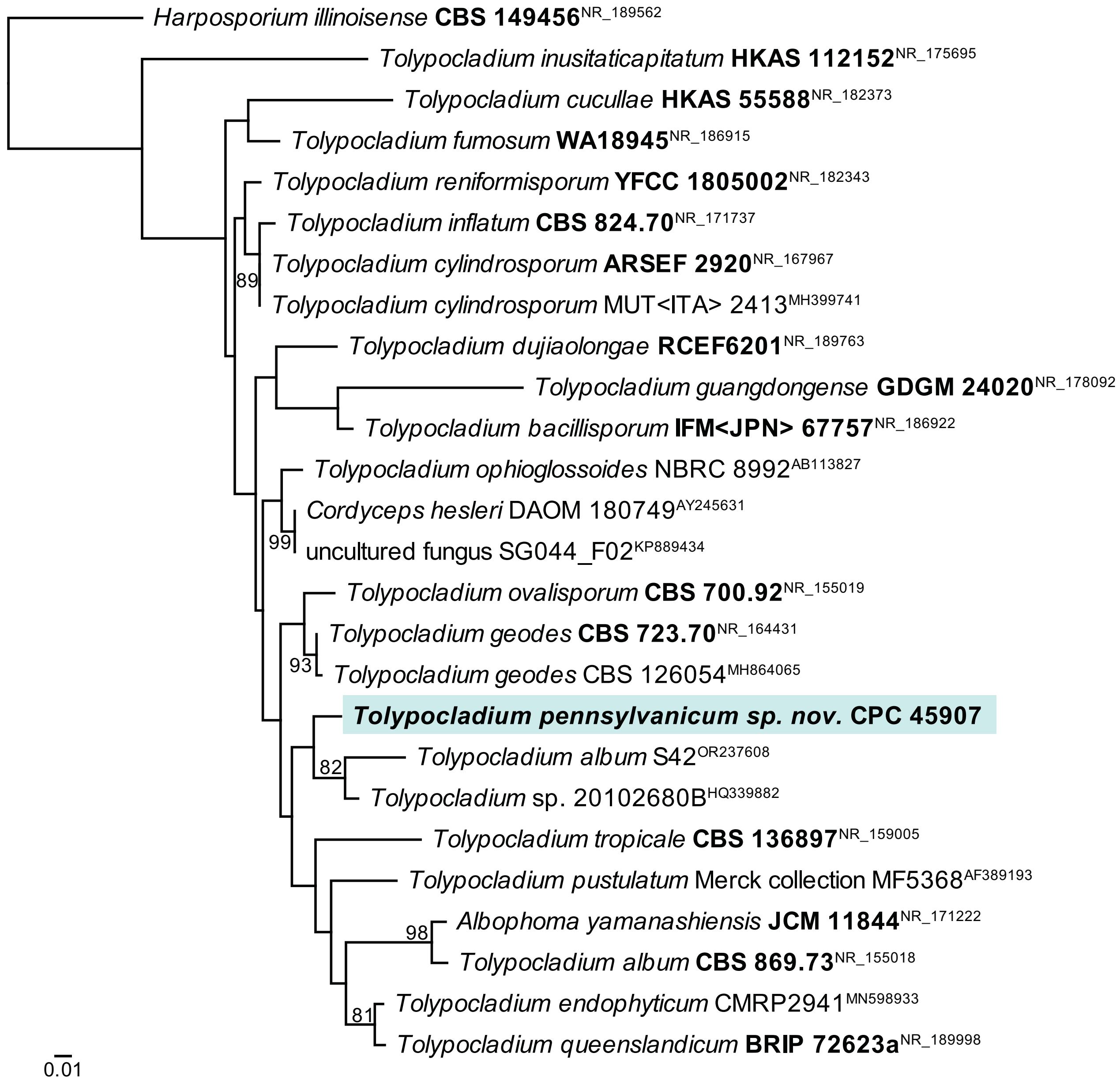
Culture characteristics: Colonies erumpent, spreading, with abundant aerial mycelium, surface folded, and smooth, lobate margin, on CYA radially moderate deep sulcate, covering dish after 2 wk at 25 °C. On CYA, MEA, PDA and OA surface white, and reverse white to pale luteous.

Typus: **USA**, Pennsylvania, Bath, basement air, Jan. 2023, *Z. Jurjević*, 5800 [**holotype** CBS H-25456; culture ex-type CPC 45907 = CBS 152275; ITS, LSU, *rpb1*, *tef1* (second part) and *tub2* sequences GenBank PQ498950, PQ498999, PQ497759, PQ497746 and PQ497779].

Notes: *Tolypocladium pennsylvanicum* was sampled from air in a basement in Pennsylvania. Phylogenetically, it is distinct from presently accepted taxa (Quandt *et al.* 2014, Soares *et al.* 2023), and is thus introduced as a novel species.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Tolypocladium endophyticum* [strain CMRP2941, GenBank MN598933.1; Identities = 525/550 (95 %), 12 gaps (2 %)], *Tolypocladium cylindrosporum* [strain CBS 280.80B, GenBank MH861264.1; Identities = 530/558 (95 %), 21 gaps (3 %)], and *Tolypocladium inflatum* [strain CANU E1032, GenBank FJ411408.1; Identities = 523/551 (95 %), 21 gaps (3 %)]. Closest hits using the **LSU** sequence are *Tolypocladium amazonense* [strain MS533, GenBank KF747142.1; Identities = 800/805 (99 %), no gaps], *Tolypocladium ophioglossoides* [strain DM1086, GenBank MT644894.1; Identities = 816/822 (99 %), no gaps], and *Tolypocladium endophyticum* [strain MX65, GenBank KF747156.1; Identities = 799/805 (99 %), no gaps]. Closest hits using the ***rpb1*** sequence had highest similarity to *Ophiocordyceps sinensis* [strain J82, GenBank KC242735.1; Identities = 621/668 (93 %), three gaps (0 %)], *Cordyceps inegoensis* [voucher SU-15, GenBank DQ127243.1; Identities = 660/711 (93 %), one gap (0 %)], *Elaphocordyceps subsessilis* [strain OSC 71235, GenBank EF469090.1; Identities = 608/655 (93 %), three gaps (0 %)], and *Tolypocladium tropicale* [strain IQ45, GenBank KF747207.1; Identities = 612/662 (92 %), four gaps (0 %)]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Tolypocladium* sp. [strain KNUF-22-014, GenBank LC802124.1; Identities = 741/778 (95 %), no gaps], *Tolypocladium cylindrosporum* [strain ARSEF 2920, GenBank MG228390.1; Identities = 739/778 (95 %), no gaps], and *Tolypocladium paradoxum* [strain NBRC 100945, GenBank AB968599.1; Identities = 738/778 (95 %), no gaps]. Closest hits using the ***tub2*** sequence had distant similarity to *Tolypocladium cylindrosporum* [strain Tc_RK, GenBank MT944105.1; Identities = 224/252 (89 %), four gaps (1 %)], *Emericellopsis synnematicola* [strain CBS 176.60, GenBank AY632681.1; Identities = 249/289 (86 %), eight gaps (2 %)], and *Striatibotrys atypica* [strain CPC 18423, GenBank KU847187.1; Identities = 252/293 (86 %), eight gaps (2 %)].

Colour illustrations: Basement in Bath, Pennsylvania, USA. Conidiophores on SNA; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Tolypocladium* ITS nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Harposporium illinoisense* (CBS 149456; GenBank NR_189562) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 26 strains including the outgroup; 583 characters including alignment gaps analysed: 191 distinct patterns, 92 parsimony-informative, 70 singleton sites, 421 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TPM3+F+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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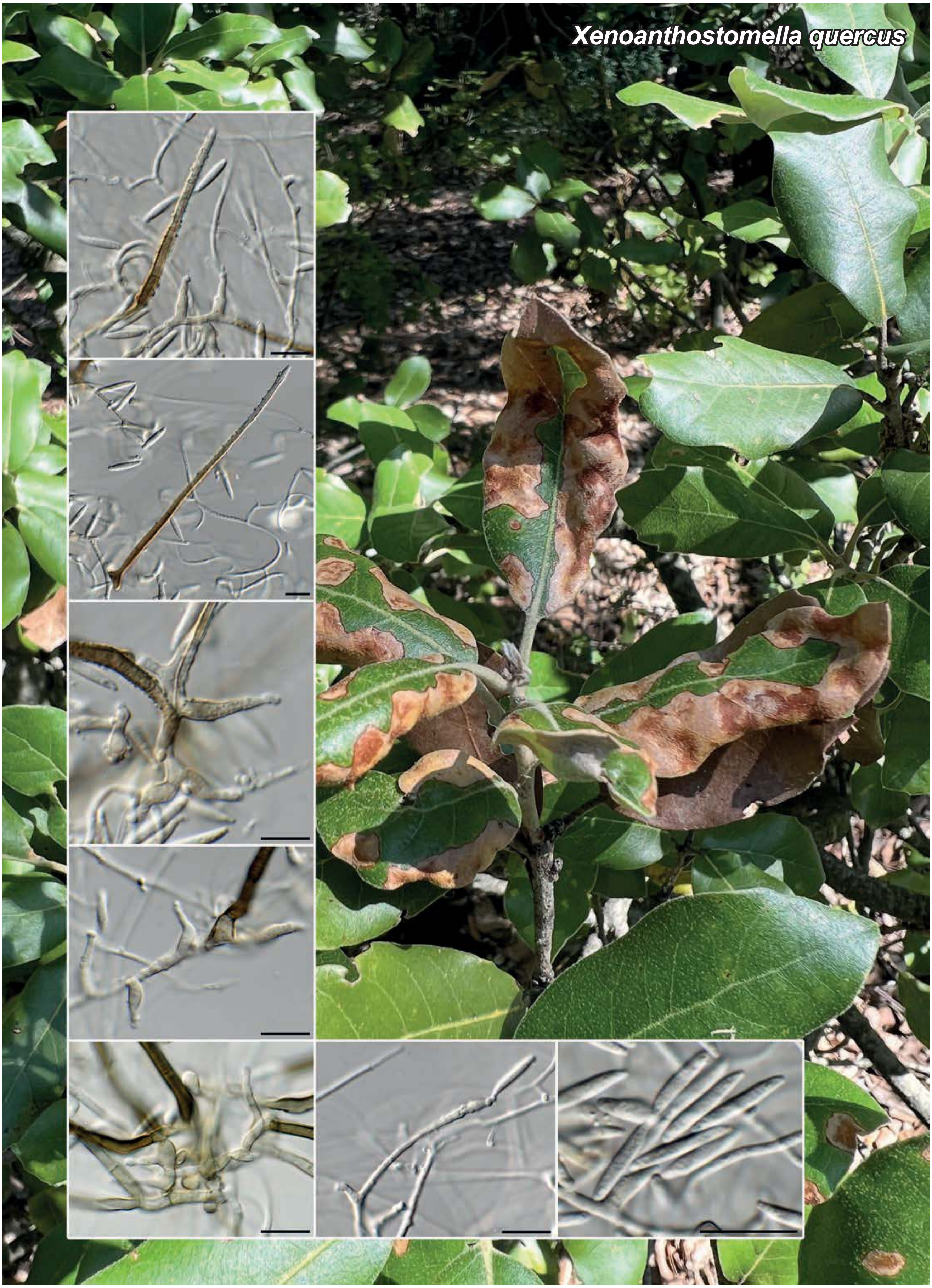

Xenoanthostomella quercus

Fungal Planet 1719 MycoBank MB 856094

Xenoanthostomella quercus Crous, ***sp. nov.***

Etymology: Name refers to *Quercus*, the tree genus from which it was isolated.

Classification: *Gyrotrichaceae*, *Xylariales*, *Xylariomycetidae*, *Sordariomycetes*.

Mycelium consisting of hyaline to pale brown, smooth, branched, septate, 1.5–2 µm diam hyphae. *Setae* erect, solitary, unbranched, dark brown, thick-walled, verruculose and warty, base lacking rhizoids, apex curved, 60–130 × 3–4 µm, 3–6-septate. *Conidiophores* reduced to clusters of *conidiogenous cells* around the base of setae, medium brown, smooth to warty, subcylindrical to ampulliform to doliiform, proliferating sympodially, polyblastic, with visible truncate apical scars to subdenticulate, 0.5 µm diam, 10–20 × 3.5–5 µm. *Conidia* solitary, hyaline, smooth, aseptate, guttulate, subcylindrical, straight, base truncate, inner plane straight, outer plane curved, tapering to subobtuse apex, (8–)11–13(–14) × (2–)2.5(–3) µm.

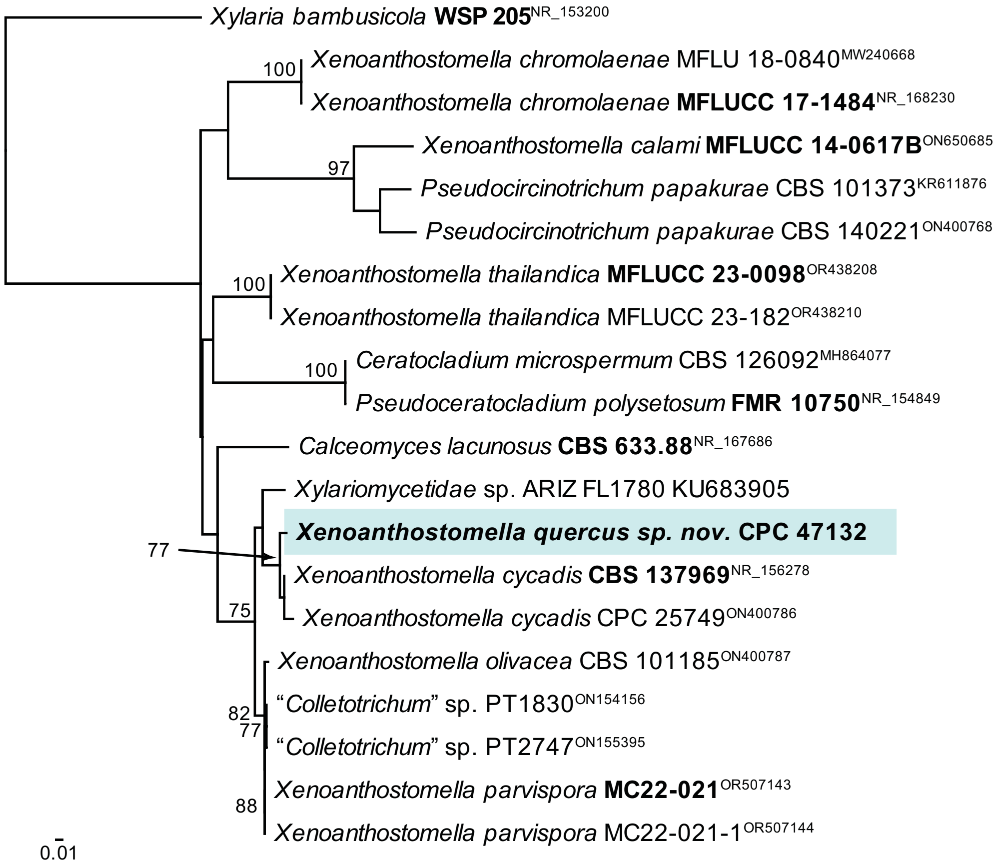
Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium, surface folded, and smooth, lobate margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA surface pale olivaceous grey, reverse luteous; on PDA surface and reverse pale olivaceous grey; on OA surface pale olivaceous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

Typus: **Italy**, Spoleto, on leaf litter of *Quercus ilex* (*Fagaceae*), 6 Sep. 2023, *P.W. Crous*, HPC 4262 (**holotype** CBS H-25476; culture ex-type CPC 47132 = CBS 152278; ITS, LSU and *rpb2* sequences GenBank PQ498951, PQ499000 and PQ497729).

Notes: *Xenoanthostomella quercus* has simple, curled setae, similar to those of *X. cycadis*, to which it is phylogenetically related. It is morphologically distinct, however, in having wider setae than those of *X. cycadis* [setae 2–3 µm diam, conidia (8–)9–11(–13) × 2(–2.5) µm] and slightly larger conidia (Crous *et al.* 2014, Hernández-Restrepo *et al.* 2022).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Xenoanthostomella cycadis* [strain CBS 137969, GenBank NR_156278.1; Identities = 542/550 (99 %), five gaps (0 %)], *Xenoanthostomella olivacea* [strain CBS 101185, GenBank ON400787.1; Identities = 530/548 (97 %), five gaps (0 %)], and *Calceomyces lacunosus* [strain CBS 633.88, GenBank NR_167686.1; Identities = 507/562 (90 %), 24 gaps (4 %)]. Closest hits using the **LSU** sequence are *Xenoanthostomella cycadis* [strain CBS 137969, GenBank NG_058880.1; Identities = 808/818 (99 %), two gaps (0 %)], *Xenoanthostomella calami* [strain MFLUCC 14-0617A, GenBank NG_228977.1; Identities = 805/816 (99 %), no gaps], and *Xenoanthostomella chromolaenae* [strain MFLUCC 17-1484, GenBank NG_068915.1; Identities = 803/816 (98 %), no gaps]. Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Xenoanthostomella cycadis* [strain CBS 137969, GenBank ON399350.1; Identities = 667/720 (93 %), no gaps], *Xenoanthostomella olivacea* [strain CBS 101185, GenBank ON399351.1; Identities = 596/647 (92 %), no gaps], and *Calceomyces lacunosus* [strain CBS 633.88, GenBank KY624293.1; Identities = 700/812 (86 %), six gaps (0 %)].

Colour illustrations: *Quercus ilex* in Spoleto, Italy. Conidiogenous cells on SNA; setae, and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Xenoanthostomella* ITS nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Xylaria bambusicola* (WSP 205; GenBank NR_153200) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 20 strains including the outgroup; 575 characters including alignment gaps analysed: 250 distinct patterns, 161 parsimony-informative, 60 singleton sites, 354 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIMe+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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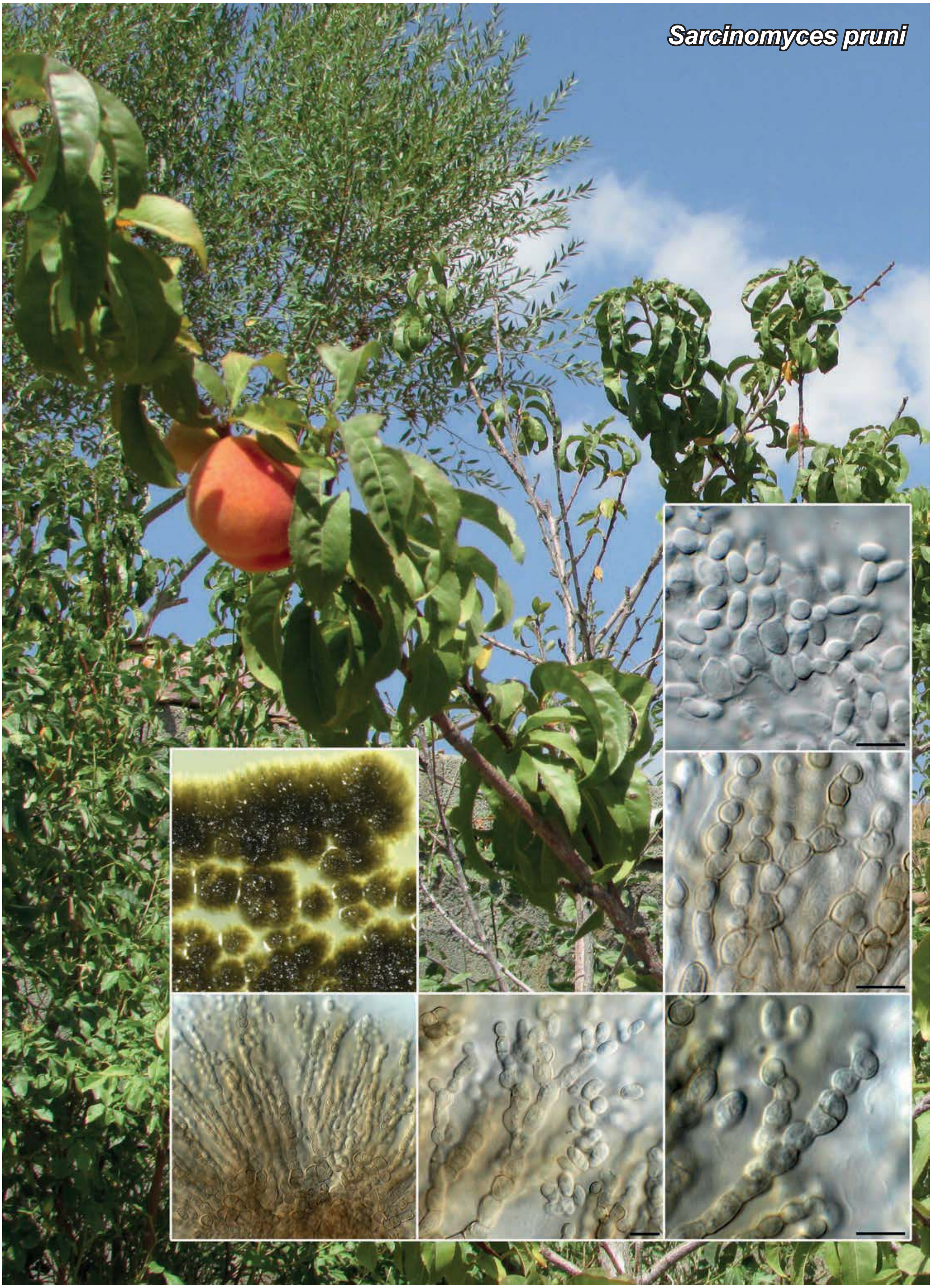

Sarcinomyces pruni

Fungal Planet 1720 MycoBank MB 856095

Sarcinomyces pruni Ketabchi, Thines, Zafari, Crous & Atashi Khalilabad, ***sp. nov.***

Etymology: Name refers to *Prunus*, the tree genus from which it was isolated.

Classification: *Incertae sedis*, *Dothideales*, *Dothideomycetidae*, *Dothideomycetes*.

Colonies forming a central brown stroma of pseudoparenchymatal cells, 7–15 µm diam, becoming muriformly septate, and on SNA forming radiating hyphal strands with cells 4–10 × 4–7 µm, becoming fertile, giving rise to hyaline conidia; loci circular, phialidic, 1.5–2 µm diam. *Conidia* hyaline, smooth, thin-walled, ellipsoid, 0–1-septate, 5–10 × 3–4 µm; undergoing microcyclic conidiation.

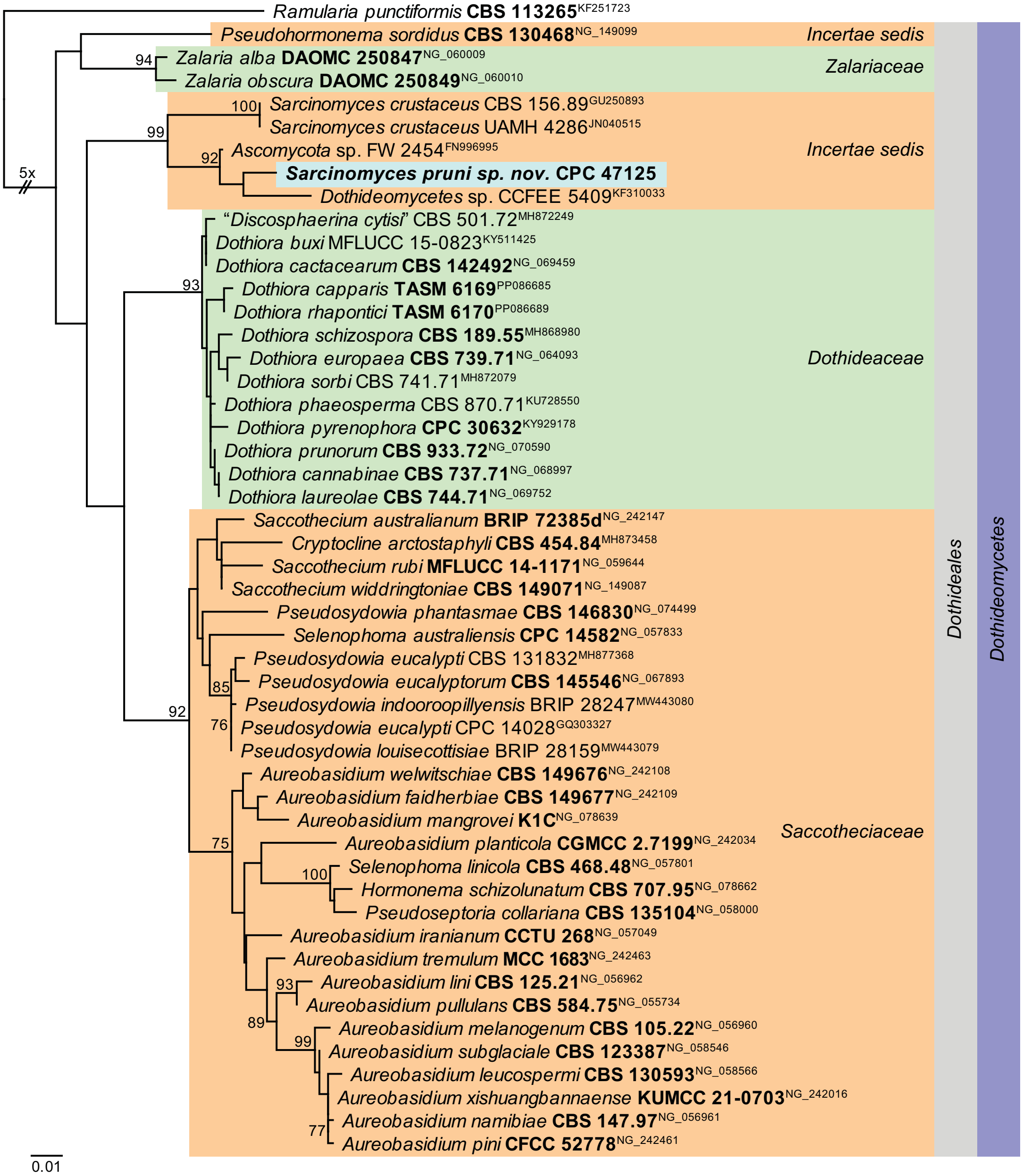
Culture characteristics: Colonies erumpent, spreading, aerial mycelium absent, and smooth, lobate margin, reaching 4 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse leaden black.

Typus: **Iran**, Hamedan Province, Nashar, 34°40’38’’N 48°52’0’’E, from twig and petiole tissues of *Prunus persica* and *Prunus armeniaca*, 8 Sep. 2021, *M. Ketabchi* (**holotype** IRAN Fungarium IRAN18264F; **isotype** CBS H-25475; culture ex-type IRAN Collection IRAN4846C = CBS 152277 = CPC 47125; ITS, LSU and SSU sequences GenBank OR944892, OR944893 and PQ498972).

Colour illustrations: Peach and apricot orchard in Hamedan Province, Iran. Colonies on SNA; hyphae and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Notes: *Sarcinomyces,* based on *S. crustaceus* is a melanised genus of yeasts commonly isolated from diverse substrates, including wood and stone. *Sarcinomyces pruni* is introduced as a new species from Iran, where it was associated with twig and petiol tissues of *Prunus* spp. Phylogenetically it is distinct from species presently known from culture.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Ascomycota* sp. [strain Bc6, GenBank KX611080.1; Identities = 597/613 (97 %), seven gaps (1 %)], *Phaeosclera dematioides* [strain CBS 157.81, GenBank MH861313.1; Identities = 512/619 (83 %), 46 gaps (7 %)], and *Sarcinomyces crustaceus* [strain UAMH 4286, GenBank NR_121503.1; Identities = 521/642 (81 %), 54 gaps (8 %)]. Closest hits using the **LSU** sequence are *Sarcinomyces crustaceus* [strain UAMH 4286, GenBank JN040515.1; Identities = 801/844 (95 %), 13 gaps (1 %)], *Dothiora ceratoniae* [strain CBS 290.72, GenBank KU728539.1; Identities = 788/844 (93 %), eight gaps (0 %)], and *Neodothiora populina* [strain CPC 39399, GenBank MW175405.1; Identities = 786/844 (93 %), seven gaps (0 %)]. Closest hits using the **SSU** sequence are *Phaeosclera dematioides* [strain CBS 157.81, GenBank GU296184.1; Identities = 998/1 003 (99 %), no gaps], *Aureobasidium pullulans* [strain 19LSOL004, GenBank MW131849.1; Identities = 1 004/1 014 (99 %), no gaps], and *Coniozyma leucospermi* [as *Coniothyrium leucospermi*; strain CBS 114035, GenBank AY720711.1; Identities = 1 004/1 015 (99 %), one gap (0 %)].



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Dothideales* LSU nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Ramularia punctiformis* (CBS 113265; GenBank KF251723) and the novelty described here is highlighted with a coloured block and **bold** font. Families, orders and the class are shown to the right of the tree in coloured blocks. The root branch was shortened to facilitate layout. Alignment statistics: 50 strains including the outgroup; 777 characters including alignment gaps analysed: 197 distinct patterns, 114 parsimony-informative, 64 singleton sites, 599 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TNe+R2. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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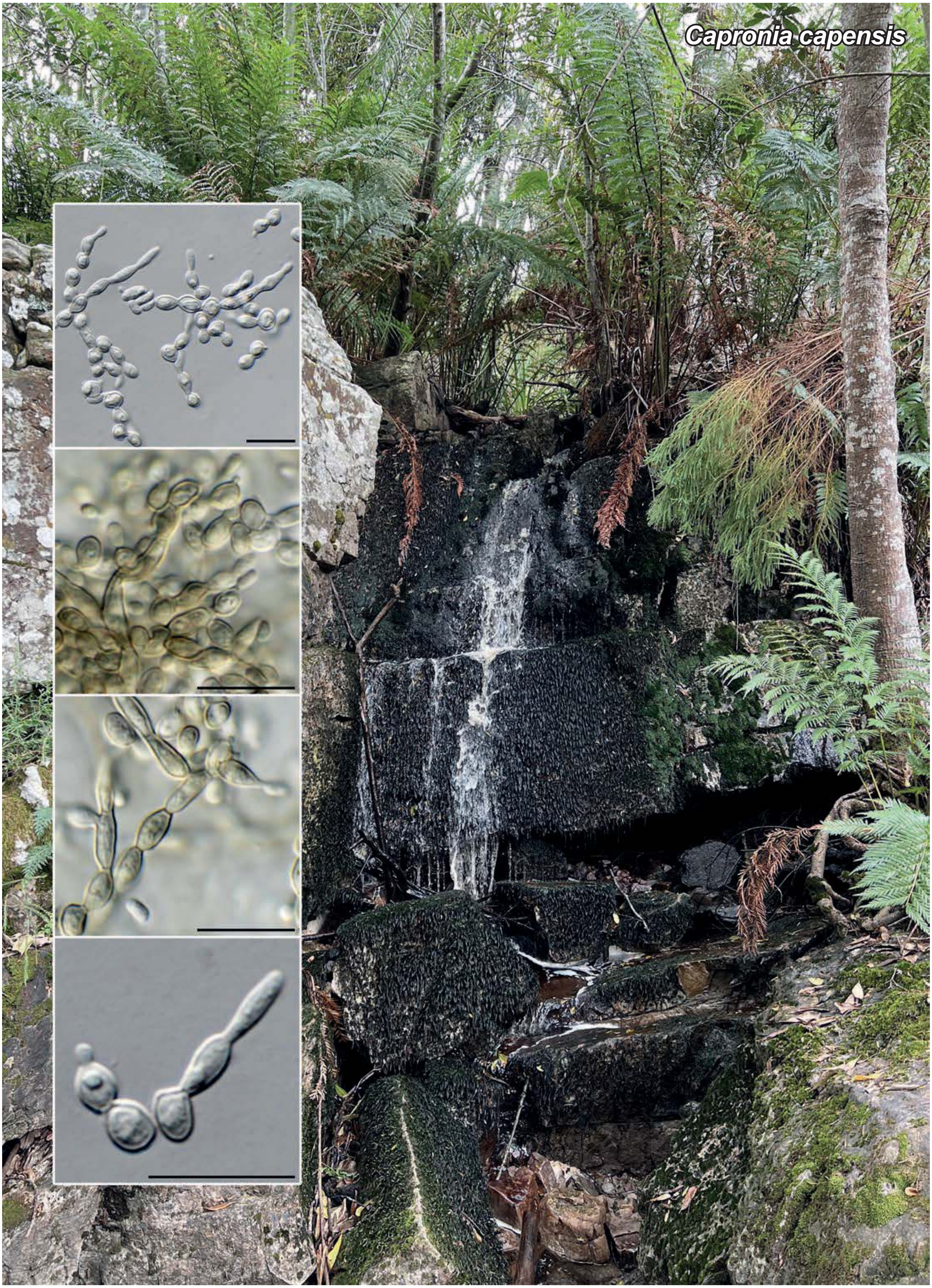
Capronia capensis

Fungal Planet 1721

MycoBank MB 856096

Capronia capensis Crous, ***sp. nov.***

Etymology: Name refers to the Western Cape Province of South Africa, where it was collected.

Classification: *Herpotrichiellaceae*, *Chaetothyriales*, *Chaetothyriomycetidae*, *Eurotiomycetes*.

Stroma black, of pseudoparenchymatal cells, occurring on dead wood, containing empty pseudothecia of a *Capronia* sp. Cultures were derived via cultivation from asexual morph that developed during moist chamber incubation. *Mycelium* consisting of pale brown, smooth, guttulate hyphae, 2–3 µm diam, forming chains of toruloid hyphae that radiate outwards, cells ellipsoid, 3–4 µm diam, becoming fertile, phialidic, loci 0.5 µm diam, giving rise to ellipsoid *conidia*, 3–5 × 2–3 µm, becoming brown with age, undergoing microcyclic conidiation.

Culture characteristics: Colonies erumpent, spreading, lacking aerial mycelium, and smooth, lobate margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse fuscous black.

Typus: **South Africa**, Western Cape Province, Silvermine, on dead twig of unidentified angiosperm, 1 Dec. 2023, *P.W. Crous*, HPC 4345 [**holotype** CBS H-25491; culture ex-type CPC 47666 = CBS 152290; ITS, LSU, *rpb1* and *tef1* (second part) sequences GenBank PQ498952, PQ499001, PQ497760 and PQ497747].

Notes: *Capronia capensis* was cultured from empty pseudothecia occurring on dead twigs of an unidentified woody host, and is only known from its asexual morph, making a morphological comparison difficult. Phylogenetically it is related but distinct from *Capronia pilosella*, a taxon which also commonly occurs on rotten woody substrates.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Capronia pilosella* [strain DAOM 208453, GenBank AF050255.1; Identities = 560/574 (98 %), four gaps (0 %)], *Capronia lijiangensis* [strain CGMCC 3.20501, GenBank NR_176765.1; Identities = 535/554 (97 %), seven gaps (1 %)], and *Capronia pulcherrima* [strain DAOM 216384, GenBank AF050256.1; Identities = 552/575 (96 %), five gaps (0 %)]. Closest hits using the **LSU** sequence are *Capronia pulcherrima* [strain DAOM 216384, GenBank AF050256.1; Identities = 771/773 (99 %), one gap (0 %)], *Capronia lijiangensis* [strain CGMCC 3.20501, GenBank NG_081534.1; Identities = 771/774 (99 %), one gap (0 %)], and *Capronia pilosella* [strain AFTOL-ID 657, GenBank DQ823099.1; Identities = 768/773 (99 %), no gaps]. Closest hits using the ***rpb1*** sequence had highest similarity to *Capronia pilosella* [strain DAOM 208453, GenBank JN989447.1; Identities = 570/609 (94 %), no gaps], *Fonsecaea multimorphosa* [strain CBS 102226, GenBank XM_016781560.1; Identities = 350/428 (82 %), no gaps], and *Rhinocladiella mackenziei* [strain CBS 650.93, GenBank XM_013419726.1; Identities = 354/435 (81 %), no gaps]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Exophiala xenobiotic* [strain NCPF 2375, GenBank LT594743.1; Identities = 793/861 (92 %), no gaps], *Fonsecaea pedrosoi* [strain CBS 271.37, GenBank XM_013426453.1; Identities = 838/912 (92 %), no gaps], and *Capronia coronata* [strain CBS 617.96, GenBank XM_007726769.1; Identities = 838/912 (92 %), no gaps].

Colour illustrations: Silvermine, Western Cape Province, South Africa. Hyphae and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Capronia* ITS nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Penicillium saturniforme* (CBS 122276; GenBank NR_190913) and the novelty described here is highlighted with a coloured block and **bold** font. statistics: 29 strains including the outgroup; 612 characters including alignment gaps analysed: 302 distinct patterns, 184 parsimony-informative, 112 singleton sites, 316 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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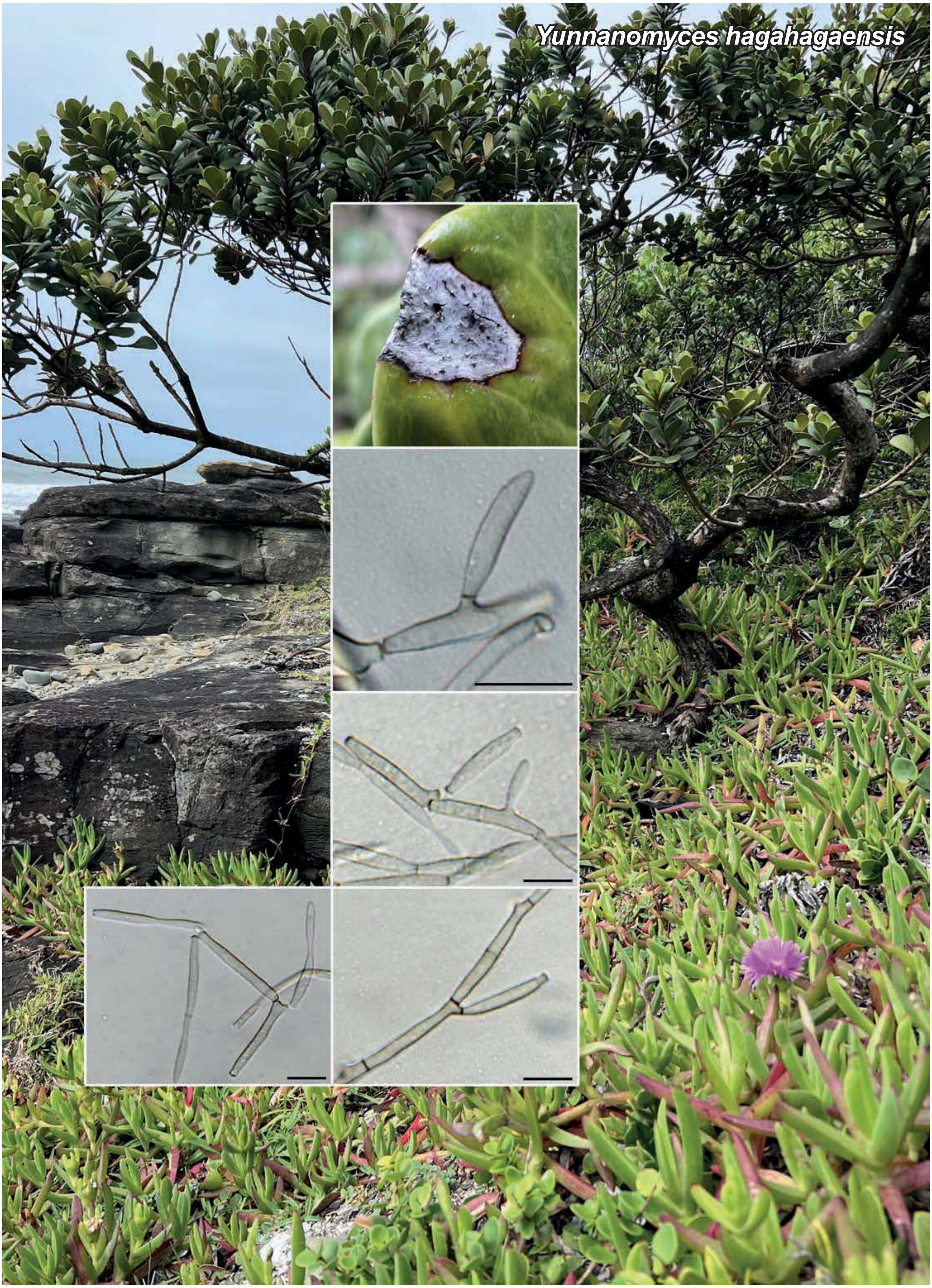

Yunnanomyces hagahagaensis

Fungal Planet 1722 MycoBank MB 856097

Yunnanomyces hagahagaensis Crous, ***sp. nov.***

Etymology: Name refers to Haga Haga in the Eastern Cape of South Africa, where it was collected.

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

Mycelium consisting of pale brown, smooth, septate, branched, 2.5–3 µm diam hyphae. *Conidiophores* 0–1-septate, subcylindrical, pale brown, smooth, erect, arising from superficial hyphae, 3–40 × 1.5–3 µm. *Conidiogenous cells* integrated, terminal, subcylindrical, pale brown, smooth, 3–25 × 1.5–2.5 µm, proliferating sympodially at apex. *Conidia* in branched chains, subcylindrical with truncate ends, 2–3 µm diam, 0–1-septate, pale brown, smooth, guttulate, (17–)20–27(–40) × 2.5–3 µm.

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

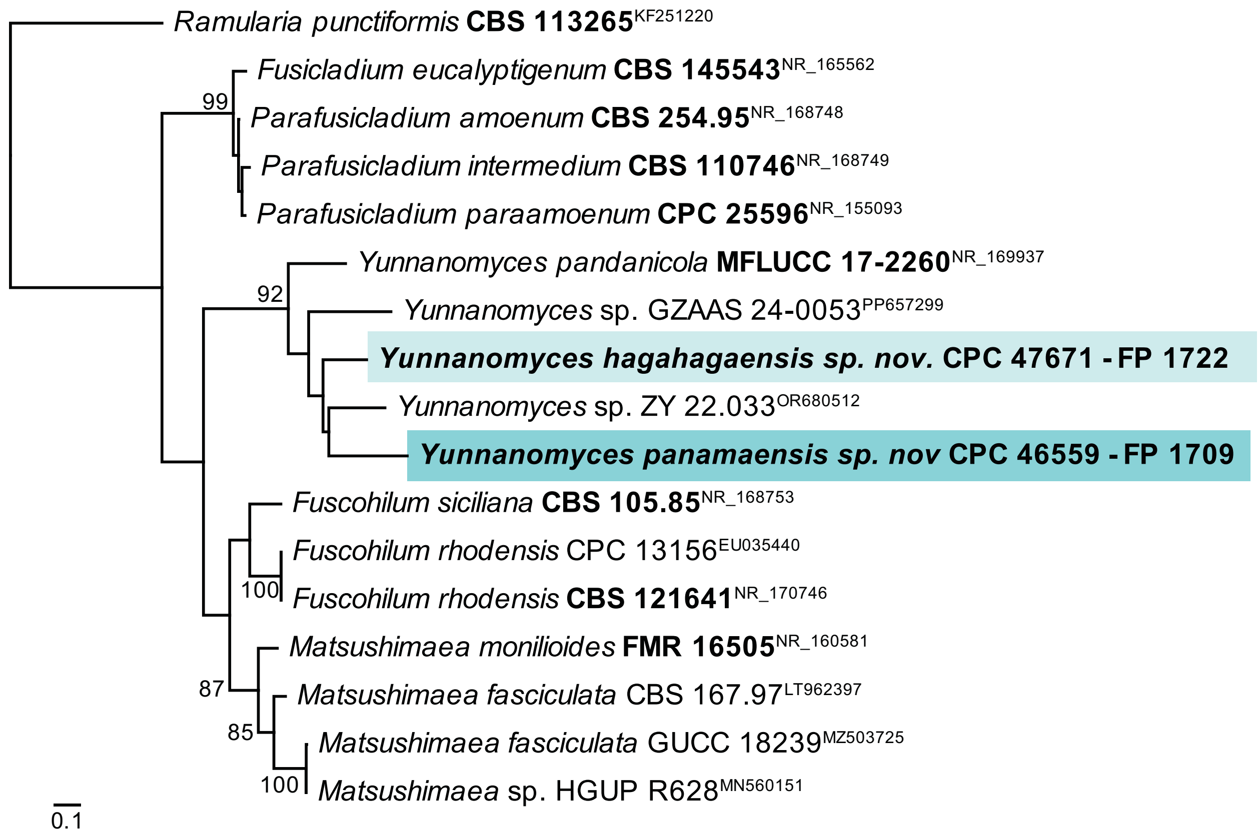
Typus: **South Africa**, Eastern Cape Province, Haga Haga, Amathole, on leaf spots of *Sideroxylon inerme* (*Sapotaceae*), 1 Dec. 2022, *M.J. Wingfield*, HPC 4353 [**holotype** CBS H-25492; culture ex-type CPC 47671 = CBS 152291; ITS, LSU, *rpb2* and *tef1* (second part) sequences GenBank PQ498953, PQ499002, PQ497730 and PQ497748].

Notes: *Yunnanomyces* is characterised by having globose to broadly oval, yellow to brown, muriformly septate conidia (Tibpromma *et al*. 2018), which is morphologically different from the morphology of *Y. hagahagaensis*, suggesting that this could be a generic complex requiring further study.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Yunnanomyces pandanicola* [strain MFLUCC 17-2260, GenBank NR_169937.1; Identities = 364/438 (83 %), 28 gaps (6 %)], *Fuscohilum rhodensis* [strain CBS 121641, GenBank NR_170746.1; Identities = 253/286 (88 %), eight gaps (2 %)], *Matsushimaea monilioides* [strain FMR 16505, GenBank NR_160581.1; Identities = 234/259 (90 %), six gaps (2 %)], and *Fuscohilum siciliana* [strain CBS 105.85, GenBank NR_168753.1; Identities = 302/362 (83 %), ten gaps (2 %)]. Closest hits using the **LSU** sequence are *Yunnanomyces* sp. SZ-2024a [strain SNT62, GenBank PP621124.1; Identities = 781/802 (97 %), two gaps (0 %)], *Yunnanomyces pandanicola* [strain MFLUCC 17-2260, GenBank NG_073623.1; Identities = 780/801 (97 %), no gaps], and *Pinaceicola cordae* [strain CBS 675.82, GenBank MH873281.1; Identities = 759/803 (95 %), two gaps (0 %)]. Closest hits using the ***rpb2*** (first part) sequence in a blastn search had highest similarity to *Scolecobasidium musicola* [strain CIRADCMR 2064, GenBank MW070921.1; Identities = 667/847 (79 %), eight gaps (0 %)], *Ochroconis musicola* [strain CPC 32927, GenBank MH327876.1; Identities = 660/845 (78 %), six gaps (0 %)], *Mycosisymbrium cirrhosum* [strain GUFCC 18012, GenBank KR349124.1; Identities = 651/844 (77 %), two gaps (0 %)], and *Yunnanomyces phoenicis* [strain MFLUCC 19-0253, GenBank MK986483.1; Identities = 642/834 (77 %), eight gaps (0 %)]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Yunnanomyces* sp. NGL-2024a [voucher GZAAS 24-0053, GenBank PP869701.1; Identities = 842/894 (94 %), no gaps], *Pseudohelminthosporium clematidis* [strain MFLUCC 17-2086, GenBank MT394627.1; Identities = 809/868 (93 %), no gaps], and *Acrocalymma medicaginis* [strain MFLUCC 17-1423, GenBank MT235797.1; Identities = 846/908 (93 %), two gaps (0 %)].

Culture CPC 47671 is distantly related to CPC 46559 described elsewhere in this document (ITS: 234/257 nt incl. eight gaps; LSU: 765/793 nt incl. one gap) as *Yunnanomyces panamaensis* (FP 1709). For a higher order phylogeny, see the LSU phylogeny provided under that species.

Colour illustrations: Haga Haga, Eastern Cape Province, South Africa. Leaf spot on *Sideroxylon inerme*; hyphae, conidiophores and conidiogenous cells giving rise to conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Yunnanomyces* ITS nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Ramularia punctiformis* (CBS 113265; GenBank KF251220) and the novelties described here are highlighted with coloured blocks and **bold** font. Alignment statistics: 17 strains including the outgroup; 637 characters including alignment gaps analysed: 380 distinct patterns, 258 parsimony-informative, 99 singleton sites, 280 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TNe+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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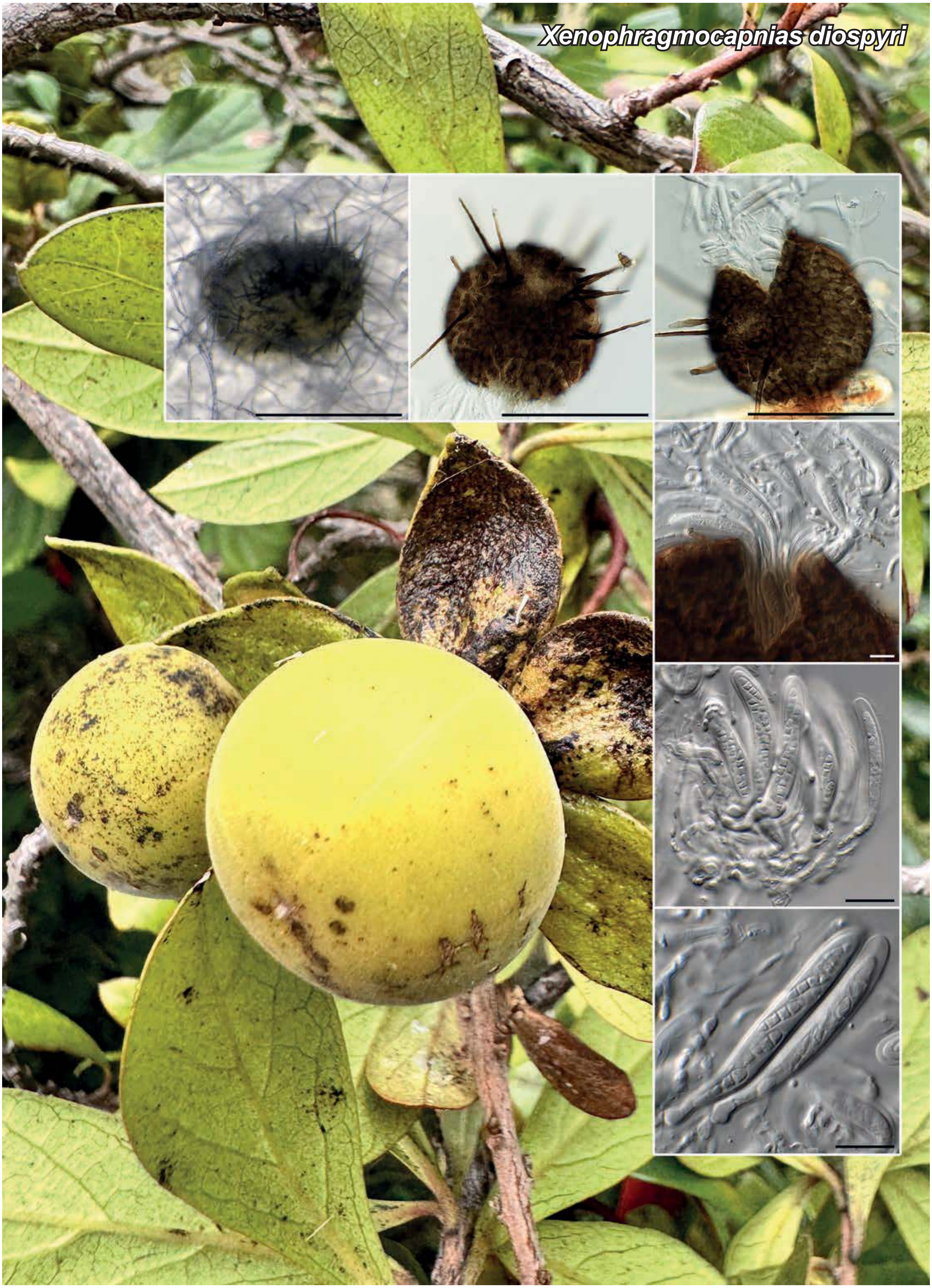

Xenophragmocapnias diospyri

Fungal Planet 1723 MycoBank MB 856098

Xenophragmocapnias Crous, ***gen. nov.***

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

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

Ascomata pseudothecial, occurring on the underside of leaves, superficial, adhering to leaf surface or leaf trichomes, solitary, globose, brown, surface appearing “flaky” due to overlapping brown cells of *textura prismatica*, ostiole central, periphysate. *Setae* on ascomatal surface erect, unbranched, brown, straight, thick-walled, ends obtuse, aseptate. *Pseudoparaphyses* intermingled among asci, hyaline, smooth, septate, hyphae-like. *Asci* fusoid-ellipsoid, straight to incurved, apex obtuse, stipitate, with apical ocular chamber, bitunicate, 8-spored. *Ascospores* multiseriate, hyaline, smooth, guttulate, septate, widest at upper septum, fusoid-ellipsoid, apex obtuse, tapering towards subobtuse base. *Conidiomata* developing in culture, globose, brown, immersed to erumpent; wall of 6–10 layers of brown pseudoparenchymatal cells with central ostiole; outer surface covered in brown setae, unbranched, aseptate, thick-walled. *Conidiophores* lining the inner cavity, subcylindrical, hyaline, smooth, branched at base, septate. *Conidiogenous cells* subcylindrical, hyaline, smooth, terminal and intercalary, 8phialidic with flared collarette. *Conidia* solitary, hyaline, smooth, guttulate, ellipsoid to subcylindrical, aseptate, ends obtuse.

Type species: *Xenophragmocapnias diospyri* Crous

MycoBank MB 856099

Xenophragmocapnias diospyri Crous, ***sp. nov.***

Etymology: Name refers to *Diospyros*, the tree genus from which it was isolated.

Ascomata pseudothecial, occurring on the underside of leaves, superficial, adhering to leaf surface or leaf trichomes, solitary, globose, brown, 90–150 µm diam, surface appearing “flaky” due to overlapping brown cells of *textura prismatica*, ostiole central, 20–25 µm diam, periphysate. *Setae* on ascomatal surface erect, unbranched, brown, straight, thick-walled, ends obtuse, 40–100 × 3–6 µm, aseptate. *Pseudoparaphyses* intermingled among asci, hyaline, smooth, septate, hyphae-like, 1.5–2.5 µm. *Asci* fusoid-ellipsoid, straight to incurved, apex obtuse, stipitate, with apical ocular chamber, 1–1.5 µm diam, bitunicate, 8-spored, 43–50 × 6–7 µm. *Ascospores* multiseriate, hyaline, smooth, guttulate, 3-septate, widest at upper septum, fusoid-ellipsoid, apex obtuse, tapering towards subobtuse base, 8–12 × 2.5–3 µm. *Conidiomata* developing in culture, globose, brown, immersed to erumpent, 100–150 µm diam; wall of 6–10 layers of brown pseudoparenchymatal cells with central ostiole; outer surface covered in brown setae, unbranched, aseptate, thick-walled, 40–70 × 3–5 µm. *Conidiophores* lining the inner cavity, subcylindrical, hyaline, smooth, branched at base, 1–2-septate, 15–25 × 2.5–3 µm. *Conidiogenous cells* subcylindrical, hyaline, smooth, terminal and intercalary, 8–15 × 2–2.5 µm, phialidic with flared collarette, 1–2.5 µm long. *Conidia* solitary, hyaline, smooth, guttulate, ellipsoid to subcylindrical, aseptate, ends obtuse, 3–7 × 2–3 µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium, surface folded, and smooth, lobate margin, reaching 12 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface ochreous and reverse ochreous to umber; on PDA and OA with diffuse umber pigment.

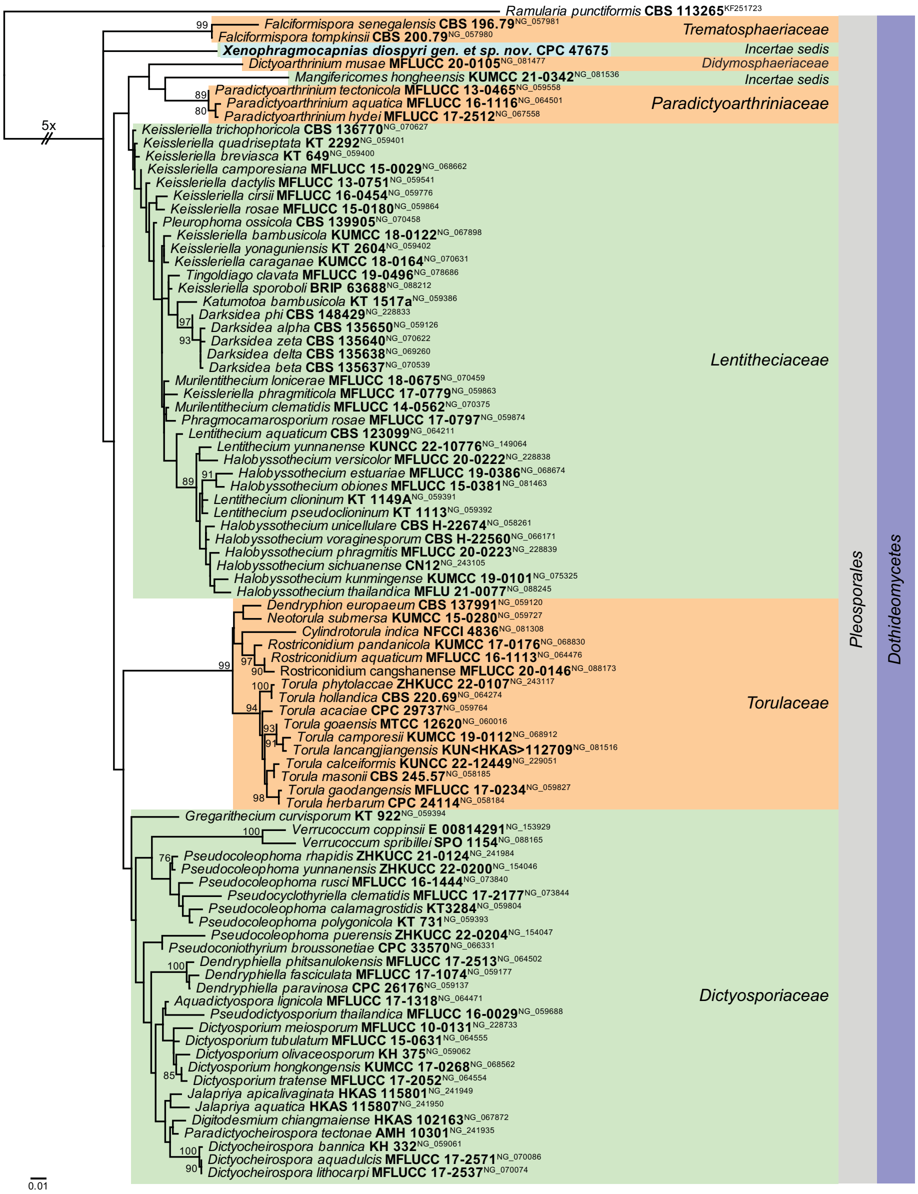
Colour illustrations: *Diospyros* sp., Haga Haga, Eastern Cape, South Africa. Conidioma on SNA; ascomata *in vivo*, exuding asci; asci and ascospores. Scale bars: Conidioma and ascomata = 150 µm, all others = 10 µm.

Typus: **South Africa**, Eastern Cape Province, Haga Haga, Amathole, on leaf spots of *Diospyros* sp. (*Ebenaceae*), Dec. 2023, *M.J. Wingfield*, HPC 4354 [**holotype** CBS H-25493; culture ex-type CPC 47675 = CBS 152292; ITS, LSU, *rpb2*, SSU and *tef1* (second part) sequences GenBank PQ498954, PQ499003, PQ497731, PQ498973 and PQ497749].

Notes: The monotypic genus *Xenophragmocapnias* is based on *X. diospyri*, but is phylogenetically distinct in *Pleosporales*. Morphologically it is reminiscent of the sooty mould *Phragmocapnias*, but is phylogenetically unrelated to that genus. It is characterised by having superficial ascomata covered in setae, occurring among the leaf hairs of a *Diospyros* sp., and producing an asexual morph in culture with brown pycnidial conidiomata also covered in setae.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the **ITS** sequence had distant similarity to *Herpotrichia juniperi* [strain agrFF1619, GenBank HE584897.1; Identities = 353/412 (86 %), 14 gaps (3 %)], *Fusiconidium indicum* [strain NFCCI 4039, GenBank NR_154045.1; Identities = 258/297 (87 %), 13 gaps (4 %)], and *Corylicola italica* [strain HKAS122732, GenBank OQ158920.1; Identities = 410/521 (79 %), 31 gaps (5 %)]. Closest hits using the **LSU** sequence are *Fuscostagonospora sasae* [strain HHUF 29106, GenBank NG_059395.1; Identities = 733/776 (94 %), six gaps (0 %)], *Medicopsis chiangmaiensis* [strain MFLUCC 17-2457, GenBank MG873481.1; Identities = 731/775 (94 %), six gaps (0 %)], and *Fuscostagonospora camporesii* [voucher MFLU 16-1362, GenBank MN750590.1; Identities = 731/777 (94 %), eight gaps (1 %)]. Closest hits using the ***rpb2*** (first part) sequence in a blastn search had highest similarity to *Bambusicola massarinia* [strain MFLUCC 11-0135, GenBank KU940169.1; Identities = 527/662 (80 %), four gaps (0 %)], *Bambusicola sichuanensis* [voucher SICAU 16-0004, GenBank MK262830.1; Identities = 523/662 (79 %), no gaps], and *Bambusicola massarinia* [voucher MFLU 11-0389, GenBank KP761716.1; Identities = 526/662 (79 %), four gaps (0 %)]. Closest hits using the **SSU** sequence are *Keissleriella cladophila* [strain CBS 104.55, GenBank GU296155.1; Identities = 973/997 (98 %), two gaps

(0 %)], *Keissleriella rosarum* [strain MFLUCC 15-0089, GenBank NG_063685.1; Identities = 982/1007 (98 %), three gaps (0 %)], and *Pleurophoma pleurospora* [strain TASM 6115, GenBank MG829159.1; Identities = 982/1 007 (98 %), three gaps (0 %)]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Cucurbitaria berberidis* [strain CBS 394.84, GenBank XM_040935051.1; Identities = 826/916 (90 %), four gaps (0 %)], *Parafenestella ulmicola* [voucher HMJAU 60181, GenBank OL944599.1; Identities = 798/891 (90 %), two gaps (0 %)], and *Parafenestella ulmi* [voucher HMJAU 60178, GenBank OL944596.1; Identities = 797/891 (89 %), two gaps (0 %)].



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Pleosporales* LSU nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Ramularia punctiformis* (CBS 113265; GenBank KF251723) and the novelty described here is highlighted with a coloured block and **bold** font. Families, the order and the class are shown to the right of the tree in coloured blocks. The root branch was shortened to facilitate layout. Alignment statistics: 89 strains including the outgroup; 798 characters including alignment gaps analysed: 261 distinct patterns, 156 parsimony-informative, 93 singleton sites, 549 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TNe+R3. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Microcera panamensis

Fungal Planet 1724

MycoBank MB 856100

Microcera panamensis Crous, ***sp. nov.***

Etymology: Name refers to Panama, where it was collected.

Classification: *Nectriaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*.

Sporodochia orange, up to 500 µm diam, exuding mucoid conidial mass; basal stroma giving rise to *conidiophores*, subcylindrical, hyaline, smooth, branched below, 1–3-septate, 15–50 × 3–3.5 µm. *Conidiogenous cells* hyaline, smooth, integrated, terminal and intercalary, subcylindrical, monophialidic, 20–35 × 2.5–3 µm. *Conidia* hyaline, smooth, guttulate, slender, curved with parallel walls, apex curved, basal cell also curved without foot-cell, but both ends with mucoid cap, but not persistent, 3(–4)-septate, (60–)65–70(–80) × (3.5–)4 µm.

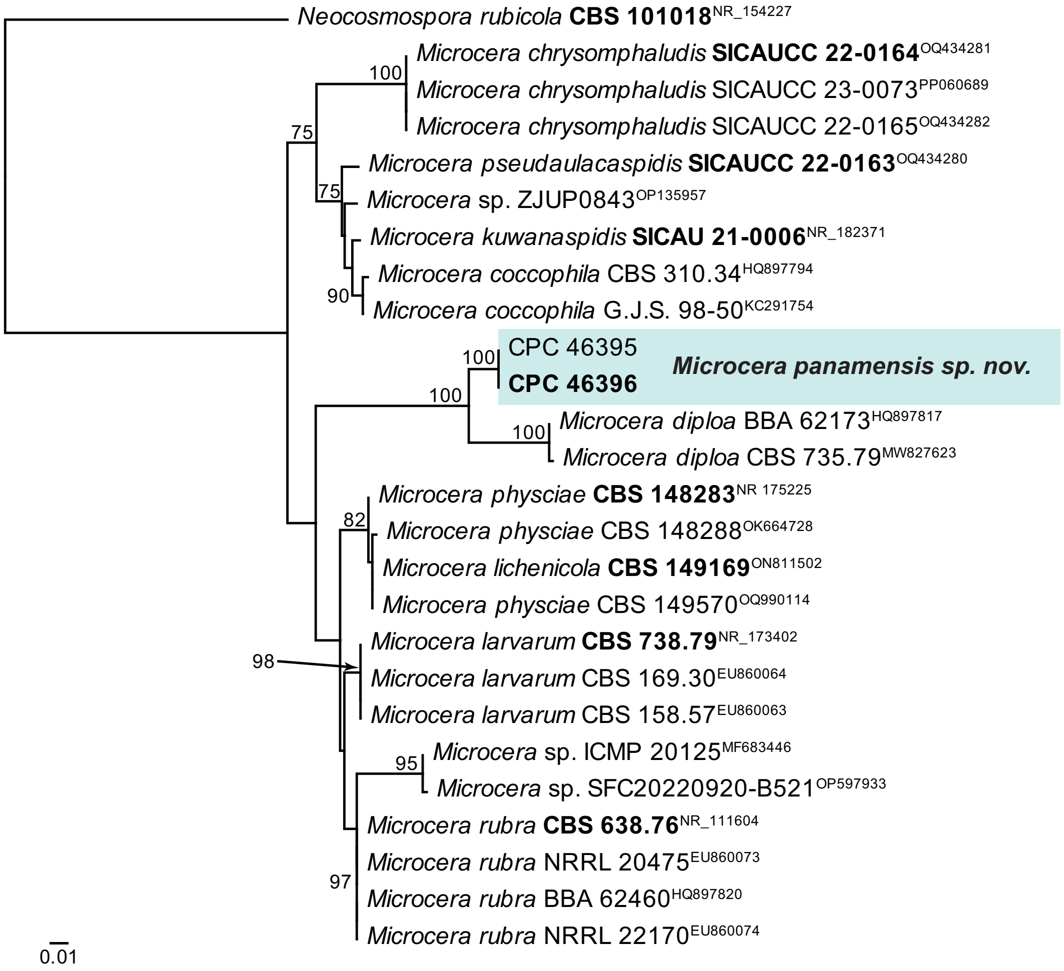
Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium, and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface and reverse orange; on PDA surface and reverse saffron; on OA surface pale luteous.

Typus: **Panama**, Colon Province, Soberania National Park, Pipeline Road, close to Gamboa, on leaf litter of fern, 6 Aug. 2023, *P.W. Crous*, HPC 4216 (**holotype** CBS H-25460; cultures ex-type CPC 46396 = CBS 152310; ITS, LSU and *rpb1* sequences GenBank PQ498955, PQ499004 and PQ497761); *idem*., culture CPC 46395 = CBS 152309 (ITS, LSU and *rpb1* sequences GenBank PQ498956, PQ499005 and PQ497762).

Notes: Species of *Microcera* are commonly associated with scale insects, soil, lichens, and litter (Crous *et al.* 2021b). *Microcera panamensis* is phylogenetically related to *M. diploa*, an entomogenous species reported from many tropical and subtropical regions. It is morphologically distinct, however, as *M. diploa* has longer macroconidia, 3–5-septate, 40–120 × 3–5 µm long (Gerlach & Nirenberg 1982, Gräfenhan *et al.* 2011).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 46395 had highest similarity to *Microcera diploa* [strain BBA 62173, GenBank HQ897817.1; Identities = 530/572 (93 %), 20 gaps (3 %)], *Microcera cf. rubra* [strain KoLRI_053251, GenBank MZ855423.1; Identities = 504/558 (90 %), 30 gaps (5 %)], and *Microcera lichenicola* [strain CBS 149169, GenBank ON811502.1; Identities = 501/557 (90 %), 30 gaps (5 %)]. The ITS sequences of CPC 46395 and 46396 are identical (552/552 nt). Closest hits using the **LSU** sequence of CPC 46395 are *Microcera chrysomphaludis* [strain SICAUCC 22-0164, GenBank NG_242085.1; Identities = 805/823 (98 %), one gap (0 %)], *Microcera coccophila* [strain CBS 793.70, GenBank MH871747.1; Identities = 784/802 (98 %), two gaps (0 %)], and *Corallomycetella repens* [strain CBS 313.72, GenBank MH872202.1; Identities = 800/824 (97 %), three gaps (0 %)]. The LSU sequences of CPC 46395 and 46396 are identical (813/813 nt). Closest hits using the ***rpb1*** sequence of CPC 46395 had highest similarity to *Microcera chrysomphaludis* [strain SICAUCC 22-0164, GenBank OQ569747.1; Identities = 461/513 (90 %), no gaps], *Microcera kuwanaspidis* [strain SICAUCC 21-0009, GenBank MZ044041.1; Identities = 463/519 (89 %), no gaps], and *Microcera coccophila* [strain G.J.S. 98-50, GenBank KC291897.1; Identities = 463/520 (89 %), no gaps]. The *rpb1* sequences of CPC 46395 and 46396 are identical (523/523 nt).

Colour illustrations: Soberania National Park, Panama. Sporodochium on oatmeal agar; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Microcera* ITS nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Neocosmospora rubicola* (CBS 101018; GenBank NR_154227) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 26 strains including the outgroup; 552 characters including alignment gaps analysed: 160 distinct patterns, 96 parsimony-informative, 43 singleton sites, 413 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TNe+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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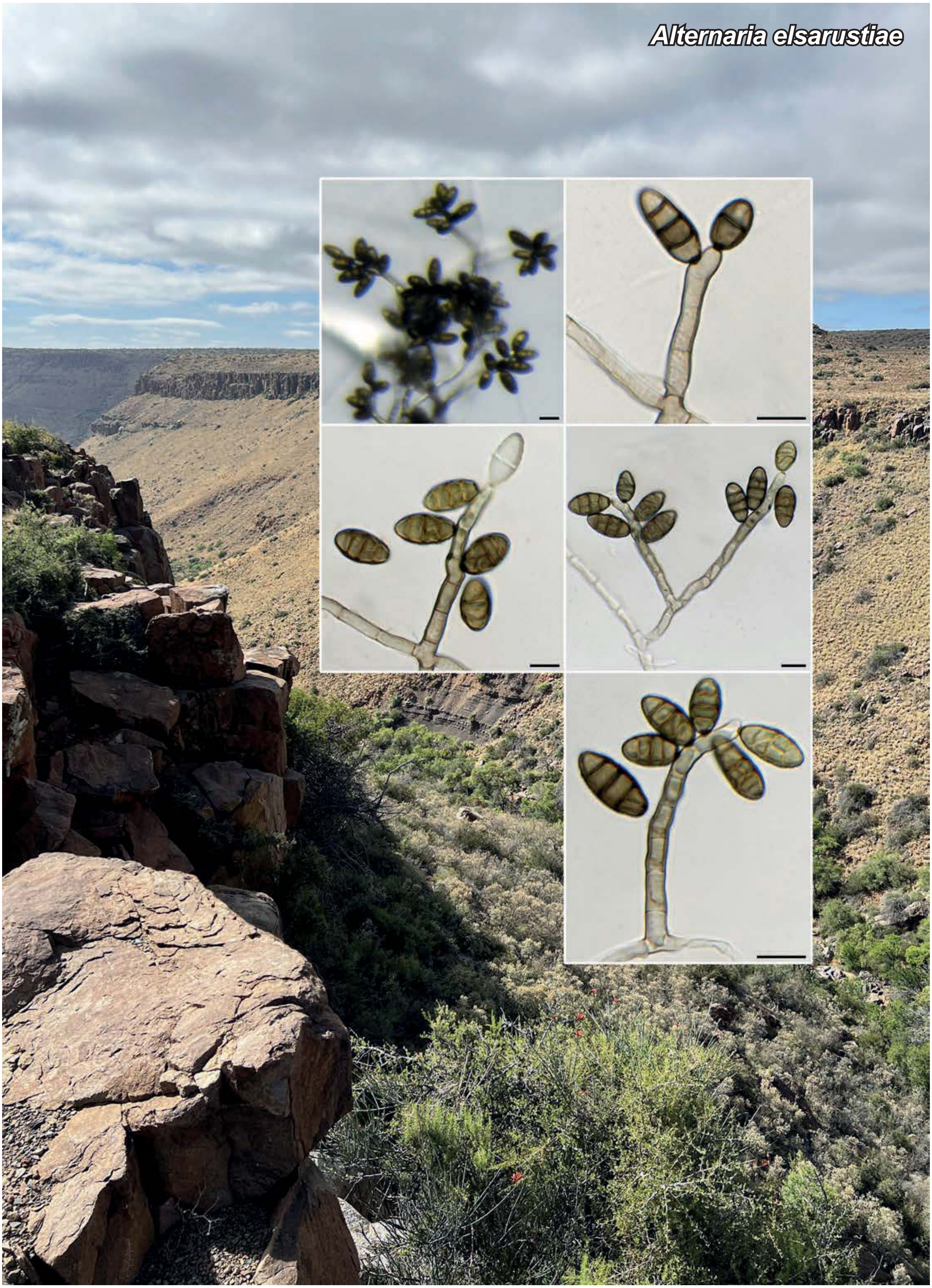

Alternaria elsarustiae

Fungal Planet 1725 MycoBank MB 856101

Alternaria elsarustiae Crous, ***sp. nov.***

Etymology: In loving memory of my mother, Elsa Carolina Rust (Asmus), born in the Karoo, a semi-desert natural region of South Africa, where she also now rests (9 Aug. 1938 – 7 Apr. 2023).

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

Mycelium consisting of pale brown, smooth, septate, branched, 4–5 µm diam hyphae. *Conidiophores* erect, solitary, subcylindrical, pale brown, smooth, unbranched, 3–12-septate, 35–80 × 4–5 µm. *Conidiogenous cells* integrated, terminal and intercalary, subcylindrical, pale brown, smooth, 7–15 × 4–5 µm; tretic, scars round, thickened, darkened, 2–2.5 µm diam. *Conidia* solitary, ovoid, brown, verruculose, guttulate, apex obtuse, base rounded, hilum thickened, darkened, 2.5–3 µm diam, muriformly septate, horizontally 3-septate, with 1–2 oblique to vertical septa, thick-walled, (13–)17–20(–23) × (7–)8(–9) µm.

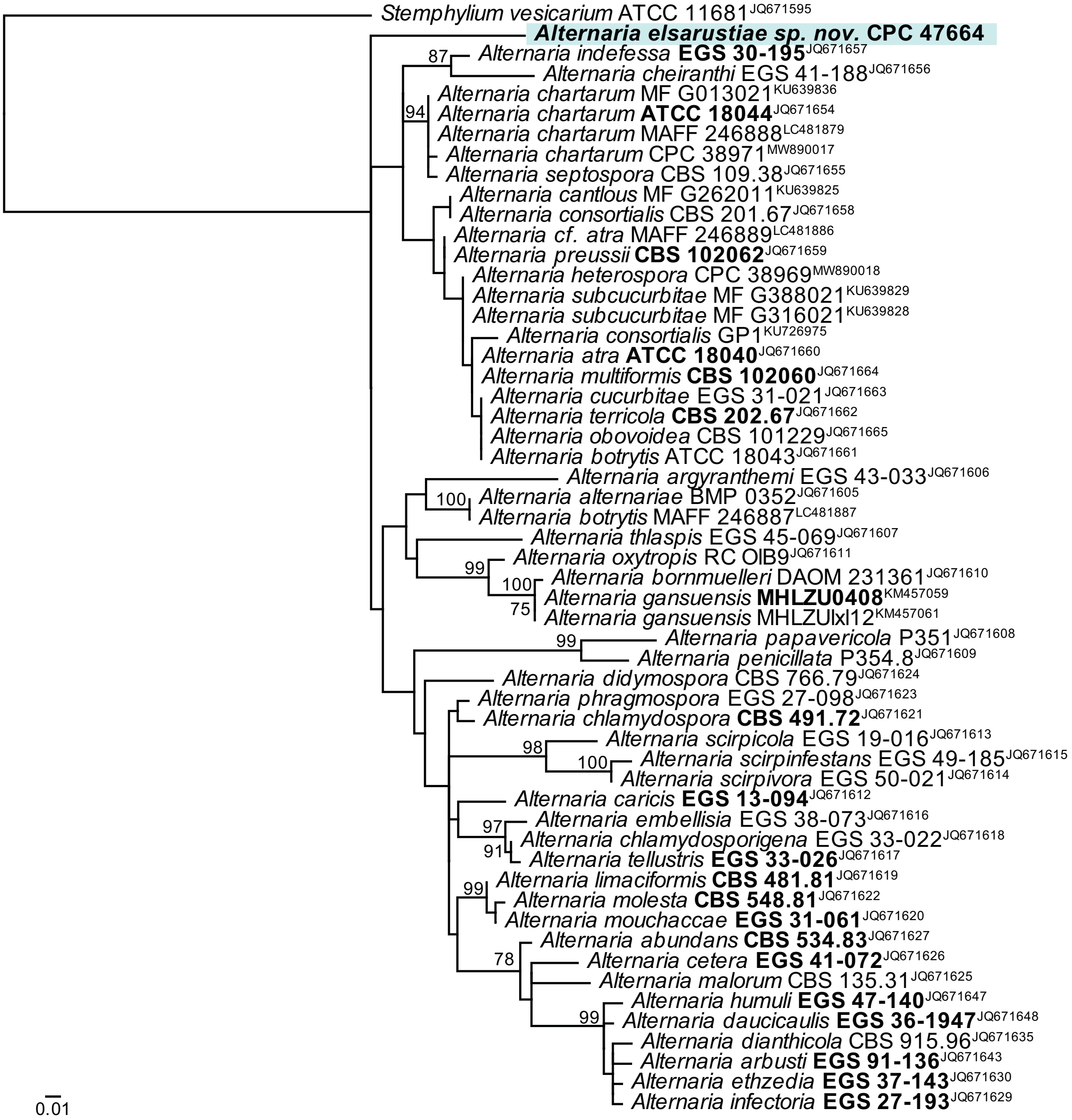
Culture characteristics: Colonies erumpent, spreading, with moderate to abundant aerial mycelium, and smooth, lobate margin, reaching 60 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus: **South Africa**, Northern Cape Province, Karoo, Beaufort West, on culms of unidentified *Poaceae*, 4 Dec. 2023, *P.W. Crous*, HPC 4338 [**holotype** CBS H-25490; culture ex-type CPC 47664 = CBS 152289; ITS, LSU, *actA*, *chs-1*, *gapdh*, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank PQ498957, PQ499006, PQ497709, PQ497714, PQ497716, PQ497732, PQ497768 and PQ504943].

Notes: *Alternaria elsarustiae* is a phylogenetically distinct species of *Alternaria.* Based on ITS sequence data, the closest species is *A. penicillata* [conidia 17–30(–35) × (4–)5–7(–8) µm, with 3–4(–6) transverse septa; Inderbitzin *et al*. 2006], from which it is morphologically distinct.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Dendryphiella triticicola* [strain RR 248, GenBank AJ876894.1; Identities = 559/571 (98 %), two gaps (0 %)], *Alternaria penicillata* [strain CBS 208.50, GenBank MH856590.1; Identities = 559/571 (98 %), two gaps (0 %)], and *Crivellia papaveracea* [strain A1-s_HU, GenBank GQ995476.1; Identities = 558/571 (98 %), two gaps (0 %)]. Closest hits using the **LSU** sequence are *Alternaria penicillata* [strain CBS 117147, GenBank LT963459.1; Identities = 807/807 (100 %), no gaps], *Alternaria papavericola* [strain CBS 116606, GenBank MH874555.1; Identities = 807/807 (100 %), no gaps], and *Septonema secedens* [strain CBS 469.48, GenBank MH867983.1; Identities = 807/809 (99 %), two gaps (0 %)]. Closest hits using the ***actA*** sequence had highest similarity to *Alternaria thlaspis* [strain EGS 45-069, GenBank JQ671607.1; Identities = 504/515 (98 %), two gaps (0 %)], *Alternaria indefessa* [strain EGS 30-195, GenBank JQ671657.1; Identities = 503/514 (98 %), one gap (0 %)], and *Alternaria cheiranthi* [strain EGS 41-188, GenBank JQ671656.1; Identities = 503/514 (98 %), one gap (0 %)]. Closest hits using the ***chs-1*** sequence had highest similarity to *Alternaria novae-zelandiae* [strain BMP 2774, GenBank XM_049401464.1; Identities = 248/259 (96 %), no gaps], *Alternaria ethzedia* [strain BMP 0044, GenBank XM_049373339.1; Identities = 247/259 (95 %), no gaps], and *Alternaria conjuncta* [strain BMP 0040, GenBank XM_051470870.1; Identities = 247/259 (95 %), no gaps]. Closest hits using the ***gapdh*** sequence had highest similarity to *Alternaria botrytis* [strain KBP F-146, GenBank OR777273.1; Identities = 487/527 (92 %), two gaps (0 %)], *Ulocladium alternariae* [strain BMP 3141005, GenBank AY278815.1; Identities = 518/566 (92 %), four gaps (0 %)], and *Ulocladium obovoideum* [strain HSAUP_XF031144, GenBank AY762952.1; Identities = 518/566 (92 %), four gaps (0 %)]. Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Alternaria alternariae* [strain CBS 126989, GenBank KC584470.1; Identities = 780/828 (94 %), no gaps], *Alternaria capsici-annui* [strain CBS 504.74, GenBank KC584385.1; Identities = 779/828 (94 %), no gaps], and *Alternaria indefessa* [strain CBS 536.83, GenBank KC584458.1; Identities = 775/828 (94 %), no gaps]. Closest hits using the ***tef1*** (first part) sequence had highest similarity to *Alternaria chartarum* [strain CPC 38971, GenBank MW890080.1; Identities = 412/458 (90 %), 11 gaps (2 %)], *Alternaria cucurbitae* [strain ICMP 1424, GenBank OM522547.1; Identities = 410/456 (90 %), nine gaps (1 %)], and *Alternaria argyranthemi* [strain ICMP 13570, GenBank OM522530.1; Identities = 407/455 (89 %), eight gaps (1 %)]. Closest hits using the ***tub2*** sequence had highest similarity to *Alternaria heterospora* [strain CPC 38969, GenBank MW890119.1; Identities = 410/455 (90 %), 12 gaps (2 %)], *Alternaria chartarum* [strain CPC 38971, GenBank MW890118.1; Identities = 408/454 (90 %), nine gaps (1 %)], and *Embellisia astragali* [strain MHLZU0408, GenBank KM457077.1; Identities = 425/484 (88 %), 11 gaps (2 %)].

Colour illustrations: Beaufort West, Northern Cape Province, South Africa. Conidiophores on SNA; conidiophores and conidiogenous cells giving rise to conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Alternaria actA* nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Stemphylium vesicarium* (ATCC 11681; GenBank JQ671595) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 55 strains including the outgroup; 232 characters including alignment gaps analysed: 143 distinct patterns, 84 parsimony-informative, 39 singleton sites, 109 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: HKY+F+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Phragmocephala agapanthi

Fungal Planet 1726 MycoBank MB 856102

Phragmocephala agapanthi Crous, *sp. nov.*

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

Classification: *Melanommataceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*.

Mycelium consisting of pale brown, smooth, septate, branched, 3–4 µm diam hyphae. *Conidiophores* fasciculate, unbranched, straight, arising from a brown basal stroma, subcylindrical, 3–6-septate, 40–80 × 6–8 µm. *Conidiogenous cells* monoblastic, pale brown, terminal, integrated, 15–35 × 6–8 µm. *Conidia* (25–)26–28(–30) × (15–)17–18 µm, (3–)4–5-septate, dark brown, paler at both ends, with middle cells dark brown, apex obtuse, base truncate, ellipsoid to subglobose; after release, tubular part of conidiogenous cell remains attached to conidium.

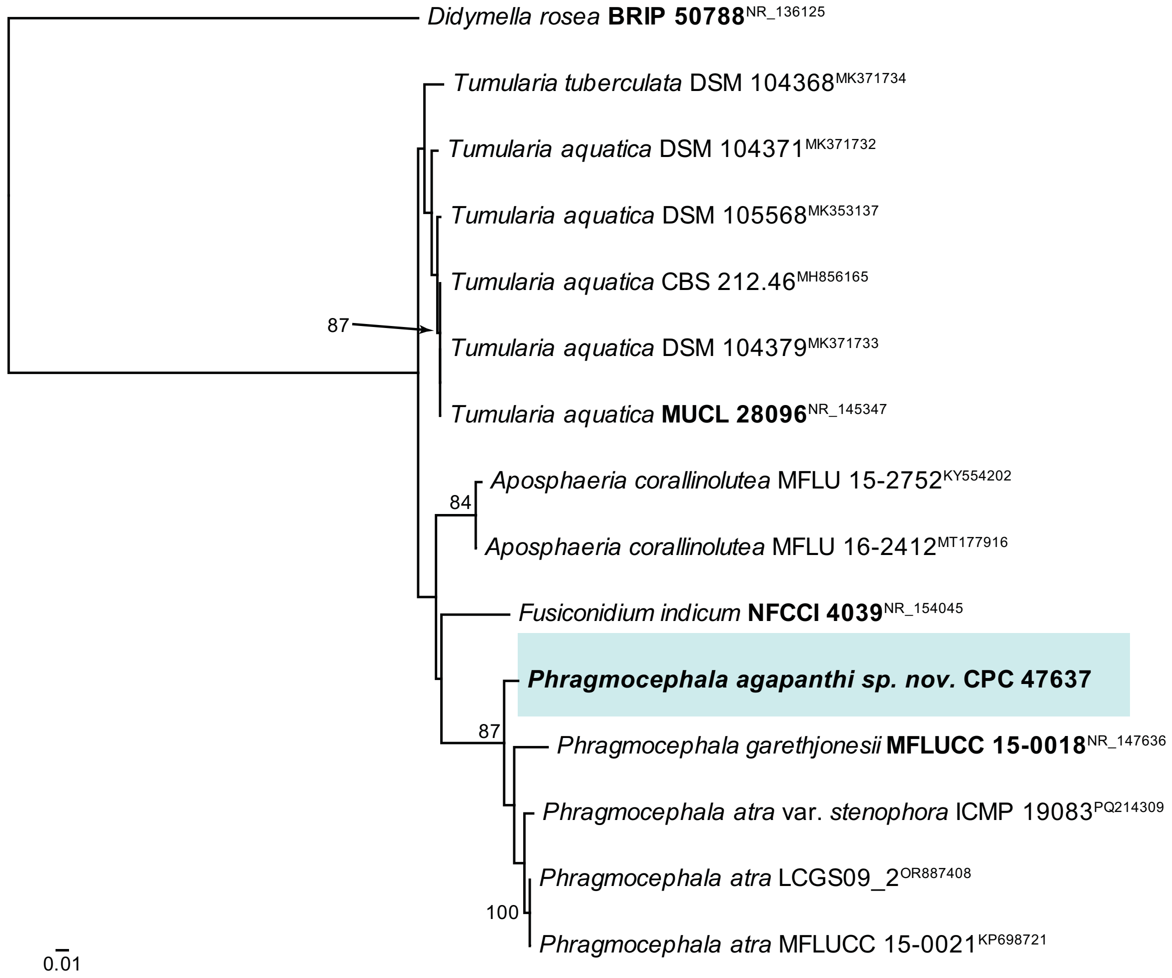
Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium, surface folded, and smooth, lobate margin, reaching 25 mm diam after 2 wk at 25 °C. On MEA surface orange to sienna, reverse sienna; on PDA surface orange to sienna, reverse orange; on OA surface sienna.

Typus: **South Africa**, Western Cape Province, Cape Town, Kirstenbosch, on dead flower stalks of *Agapanthus praecox* (*Amaryllidaceae*), Nov. 2023, *P.W. Crous*, HPC 4318 [**holotype** CBS H-25488; culture ex-type CPC 47637 = CBS 152287; ITS, LSU, *rpb2* and *tef1* (second part) sequences GenBank PQ498958, PQ499007, PQ497733 and PQ497750].

Notes: *Phragmocephala agapanthi* is related to *P. atra* (conidia 30–35 × 15–18 µm), and *P. garethjonesii* (conidia 28–35 × 16.5–20.5 µm), but is distinct based on its conidial dimensions. Furthermore, its two conidial end cells are also pale brown as in *P. garethjonesii*, but the latter has 5–6-septate conidia (Su *et al*. 2015).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phragmocephala atra* [strain LCGS09_2, GenBank OR887408.1; Identities = 492/507 (97 %), two gaps (0 %)], *Phragmocephala garethjonesii* [strain MFLUCC 15-0018, GenBank NR_147636.1; Identities = 491/508 (97 %), four gaps (0 %)], and *Camposporium cambrense* [strain CBS 132486, GenBank MH866029.1; Identities = 480/509 (94 %), five gaps (0 %)]. Closest hits using the **LSU** sequence are *Phragmocephala atra* [strain MFLUCC 15-0021, GenBank KP698725.1; Identities = 816/819 (99 %), no gaps], *Phragmocephala garethjonesii* [strain MFLUCC 15-0018, GenBank NG_059548.1; Identities = 815/819 (99 %), no gaps], and *Camposporium pellucidum* [strain CBS 135.53, GenBank MH868668.1; Identities = 812/820 (99 %), one gap (0 %)]. Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Phragmocephala garethjonesii* [strain KUMCC 20-0166, GenBank MZ394068.1; Identities = 772/801 (96 %), no gaps], *Bertiella ellipsoidea* [strain MFLUCC 17-2015, GenBank MG547224.1; Identities = 668/807 (83 %), nine gaps (1 %)], and *Flammeascoma lignicola* [strain MFLUCC 10-0128c, GenBank KT324586.1; Identities = 605/814 (74 %), 26 gaps (3 %)]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Phragmocephala garethjonesii* [strain KUMCC 20-0166, GenBank MZ394067.1; Identities = 771/799 (96 %), no gaps], *Melanomma pulvis-pyrius* [strain CBS 124080, GenBank GU456265.1; Identities = 721/770 (94 %), no gaps], and *Uzbekistanica yakutkhanika* [strain MFLUCC 17-0842, GenBank MG829245.1; Identities = 748/799 (94 %), no gaps].

Colour illustrations: *Agapanthus praecox* in Kirstenbosch, South Africa. Conidiophores on SNA; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Phragmocephala* ITS nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Didymella rosea* (BRIP 50788; GenBank NR_136125) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 15 strains including the outgroup; 497 characters including alignment gaps analysed: 104 distinct patterns, 48 parsimony-informative, 84 singleton sites, 365 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+R2. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Neophaeomoniella watsoniae

Fungal Planet 1727 MycoBank MB 856103

Neophaeomoniella watsoniae Crous, ***sp. nov.***

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

Classification: *Phaeomoniellaceae*, *Phaeomoniellales*, *Chaetothyriomycetidae*, *Eurotiomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate, 2.5–4 µm diam hyphae, prominently constricted at septa. *Conidiophores* reduced to conidiogenous cells, intercalary on hyphae, phialidic loci inconspicuous, 0.5 µm diam, giving rise to conidia that aggregate in mucoid mass. *Conidia* subcylindrical, hyaline, smooth, aseptate, guttulate, ends obtuse, mostly straight, 3–4(–5) × 1.5(–2) µm, becoming swollen with age, 5–7 × 2–3 µm. On host tissue isolates were obtained from immersed conidiomata, globose, 80–120 µm diam, with central ostiole.

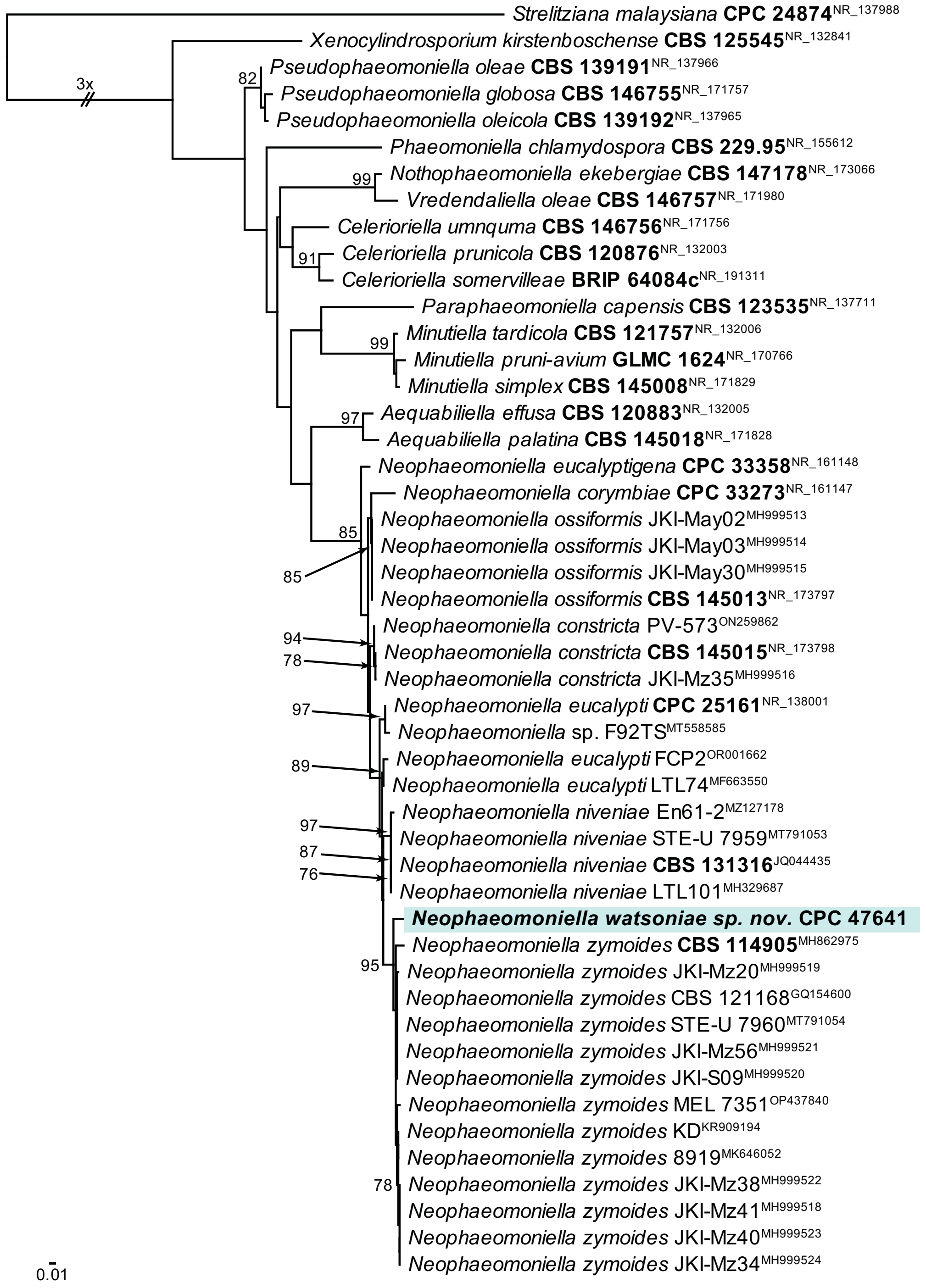
Culture characteristics: Colonies erumpent, spreading, lacking aerial mycelium, surface folded, and smooth, lobate margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse pale luteous.

Typus: **South Africa**, Western Cape Province, Knysna, on leaf of *Watsonia* sp. (*Iridaceae*), 6 Dec. 2023, *P.W. Crous*, HPC 4332 [**holotype** CBS H-25489; culture ex-type CPC 47641 = CBS 152288; ITS, LSU and *tef1* (first part) sequences GenBank PQ498959, PQ499008 and PQ497769].

Notes: *Neophaeomoniella* is related to *Phaeomoniella*, but lacks the characteristic hyphomycetous morph of the latter (Crous *et al.* 2015b). *Neophaeomoniella watsoniae* resembles *N. zymoides* (conidia unicellular, narrowly ellipsoid, (2.6–)3.5–6(–7) × 0.8–1.9 µm; Lee *et al*. 2006), but has shorter conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neophaeomoniella zymoides* [strain JKI-S09, GenBank MH999520.1; Identities = 578/590 (98 %), two gaps (0 %)], *Neophaeomoniella niveniae* [strain En61-2, GenBank MZ127178.1; Identities = 573/591 (97 %), three gaps (0 %)], and *Neophaeomoniella eucalypti* [strain LTL74, GenBank MF663550.1; Identities = 568/592 (96 %), nine gaps (1 %)]. Closest hits using the **LSU** sequence are *Neophaeomoniella zymoides* [strain CBS 114905, GenBank MH874535.1; Identities = 826/827 (99 %), no gaps], *Neophaeomoniella niveniae* [strain En61-2, GenBank OK380948.1; Identities = 823/830 (99 %), three gaps (0 %)], and *Neophaeomoniella eucalypti* [strain CBS 139919, GenBank NG_058174.1; Identities = 805/813 (99 %), four gaps (0 %)]. Closest hits using the ***tef1*** (first part) sequence used in a blastn search had highest similarity to *Neophaeomoniella eucalyptigena* [strain CBS 145093, GenBank MK047569.1; Identities = 301/353 (85 %), 15 gaps (4 %)], *Neophaeomoniella niveniae* [strain En61-2, GenBank OQ384107.1; Identities = 184/209 (88 %), five gaps (2 %)], and *Phaeomoniella chlamydospora* [strain IBVD01, GenBank KP213113.1; Identities = 247/305 (81 %), 18 gaps (5 %)].

Colour illustrations: *Watsonia* sp. in Knysna, South Africa. Colony on SNA; hyphae and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Neophaeomoniella* ITS nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Strelitziana malaysiana* (CPC 24874; GenBank NR_137988) and the novelty described here is highlighted with a coloured block and **bold** font. The root branch was shortened to facilitate layout. Alignment statistics: 48 strains including the outgroup; 597 characters including alignment gaps analysed: 286 distinct patterns, 177 parsimony-informative, 100 singleton sites, 320 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Orbilia kirstenboschensis

Fungal Planet 1728

MycoBank MB 856104

Orbilia kirstenboschensis Crous, ***sp. nov.***

Etymology: Name refers to Kirstenbosch in the Western Cape of South Africa where it was collected.

Classification: *Orbiliaceae*, *Orbiliales*, *Orbiliomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate, 2–3 µm diam hyphae, forming hyphal coils. *Conidiophores* solitary, flexuous, subcylindrical, hyaline, smooth, 2–3-septate, 45–80 × 3–4 µm. *Conidiogenous cells* hyaline, smooth, subcylindrical, monoblastic, 25–50 × 2–3 µm. *Conidia* solitary, hyaline, smooth, guttulate, straight, rarely slightly curved, fusoid, widest in apical third, apex subobtuse, tapering to long narrowed base, hilum truncate, 2–2.5 µm diam, (4–)7–8(–11)-septate, (48–)50–60(–70) × (6–)7–8 µm.

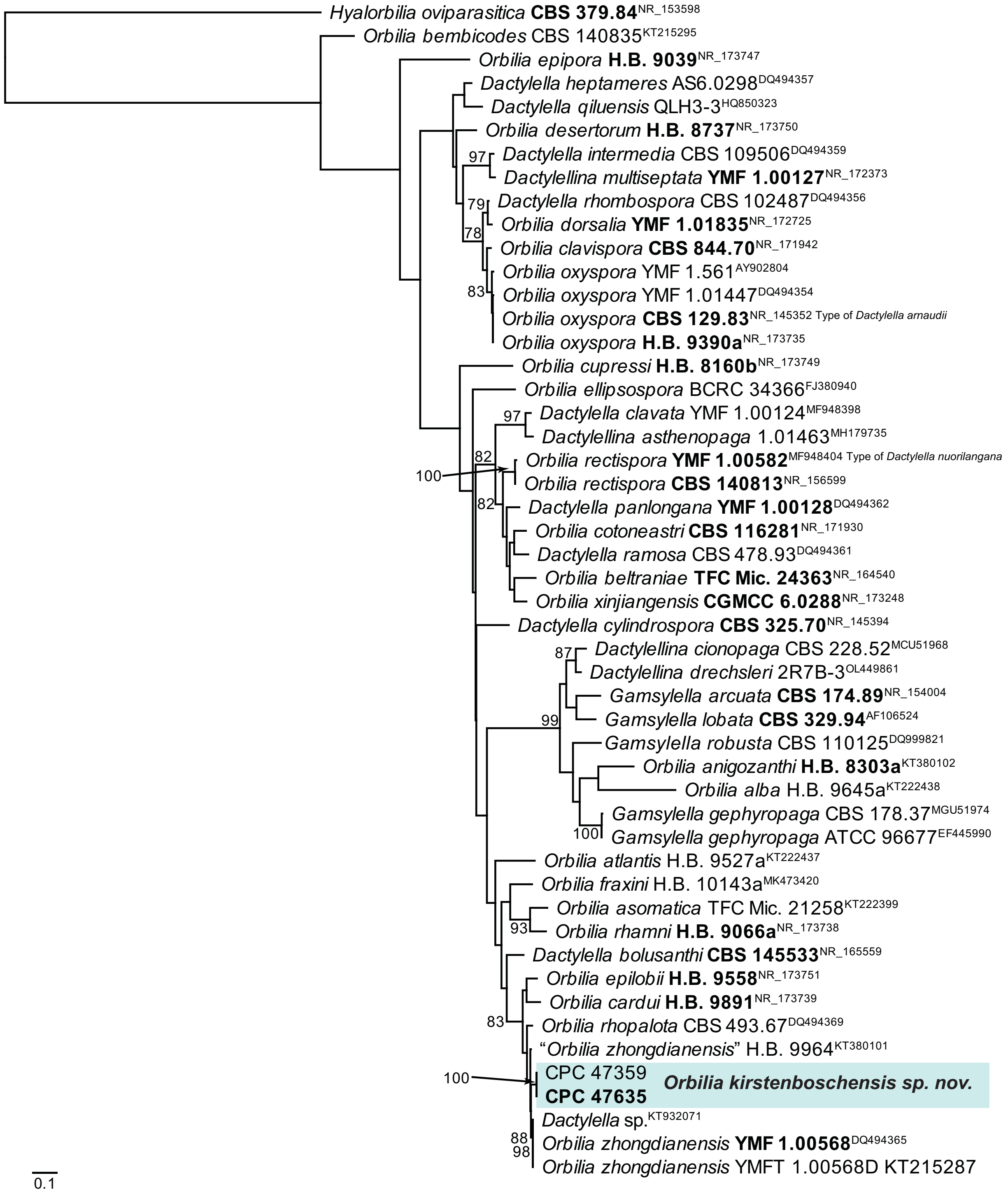
Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium, and feathery, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse saffron.

Typus: **South Africa**, Western Cape Province, Cape Town, Kirstenbosch, on dead flower stalks of *Agapanthus praecox* (*Amaryllidaceae*), Nov. 2023, *P.W. Crous*, HPC 4318 (**holotype** CBS H-25487; culture ex-type CPC 47635 = CBS 152286; ITS and LSU sequences GenBank PQ498960 and PQ499009), *idem.*, culture CPC 47359 = CBS 152283 (ITS and LSU sequences GenBank PQ498961 and PQ499010).

Notes: *Orbilia kirstenboschensis* is related to *O. zhongdianensis* [conidia (17.5–)22–34(–37.5) × (5–)5.7–7(–8) µm, (2–)3–4(–6)-septate; Baral *et al.* 2020], but is morphologically distinct in having larger conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Orbilia zhongdianensis* [as *Dactylella zhongdianensis*; voucher H.B. 9964, GenBank KT380101.1; Identities = 905/942 (96 %), 13 gaps (1 %)], *Orbilia epilobii* [voucher B.C. 080615, GenBank KY419180.1; Identities = 847/952 (89 %), 27 gaps (2 %)], and *Arthrobotrys cylindrospora* [strain CBS 325.70, GenBank U51953.1; Identities = 801/997 (80 %), 90 gaps (9 %)]. The ITS sequences of CPC 47635 and 47359 are identical (920/920 nt). Closest hits using the **LSU** sequence are *Orbilia zhongdianensis* [as *Dactylella zhongdianensis*; voucher H.B. 9964, GenBank KT380101.1; Identities = 708/710 (99 %), no gaps], *Orbilia epilobii* [voucher B.C. 080615, GenBank KY419180.1; Identities = 701/710 (99 %), no gaps], and *Orbilia rhopalota* [strain CBS 493.67, GenBank AY261177.1; Identities = 700/710 (99 %), no gaps]. The LSU sequences of CPC 47635 and 47359 are identical (710/710 nt).

Colour illustrations: *Agapanthus praecox* in Kirstenbosch, South Africa. Conidiophores on pine needle agar; hyphal coils and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Orbilia* ITS nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Hyalorbilia oviparasitica* (CBS 379.84; GenBank NR_153598) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 50 strains including the outgroup; 734 characters including alignment gaps analysed: 461 distinct patterns, 283 parsimony-informative, 132 singleton sites, 319 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Extremus massachusettsianus
Promega
Maxwell RSC48

Fungal Planet 1729 MycoBank MB 856105

Extremus massachusettsianus Crous & Jurjević, ***sp. nov.***

Etymology: Name refers to the American state of Massachusetts ,where it was collected.

Classification: *Extremaceae*, *Mycosphaerellales*, *Dothideomycetidae*, *Dothideomycetes*.

Mycelium consisting of pale brown, smooth, branched, septate, 2–2.5 µm diam hyphae. *Conidiophores* solitary, aggregating into clusters to form sporodochia, pale brown, smooth, subcylindrical, branched extensively at apex, giving rise to clusters of conidiogenous cells, up to 50 µm tall, 2–3 µm wide. *Conidiogenous cells* integrated, terminal and intercalary, reduced to conidiogenous loci, or ellipsoid, 3–5 × 2–2.5 µm, phialidic with flared collarette. *Conidia* solitary, ellipsoid, apex subobtuse, base truncate, aseptate, brown, smooth, (3–)4(–5) × 2(–2.5) µm.

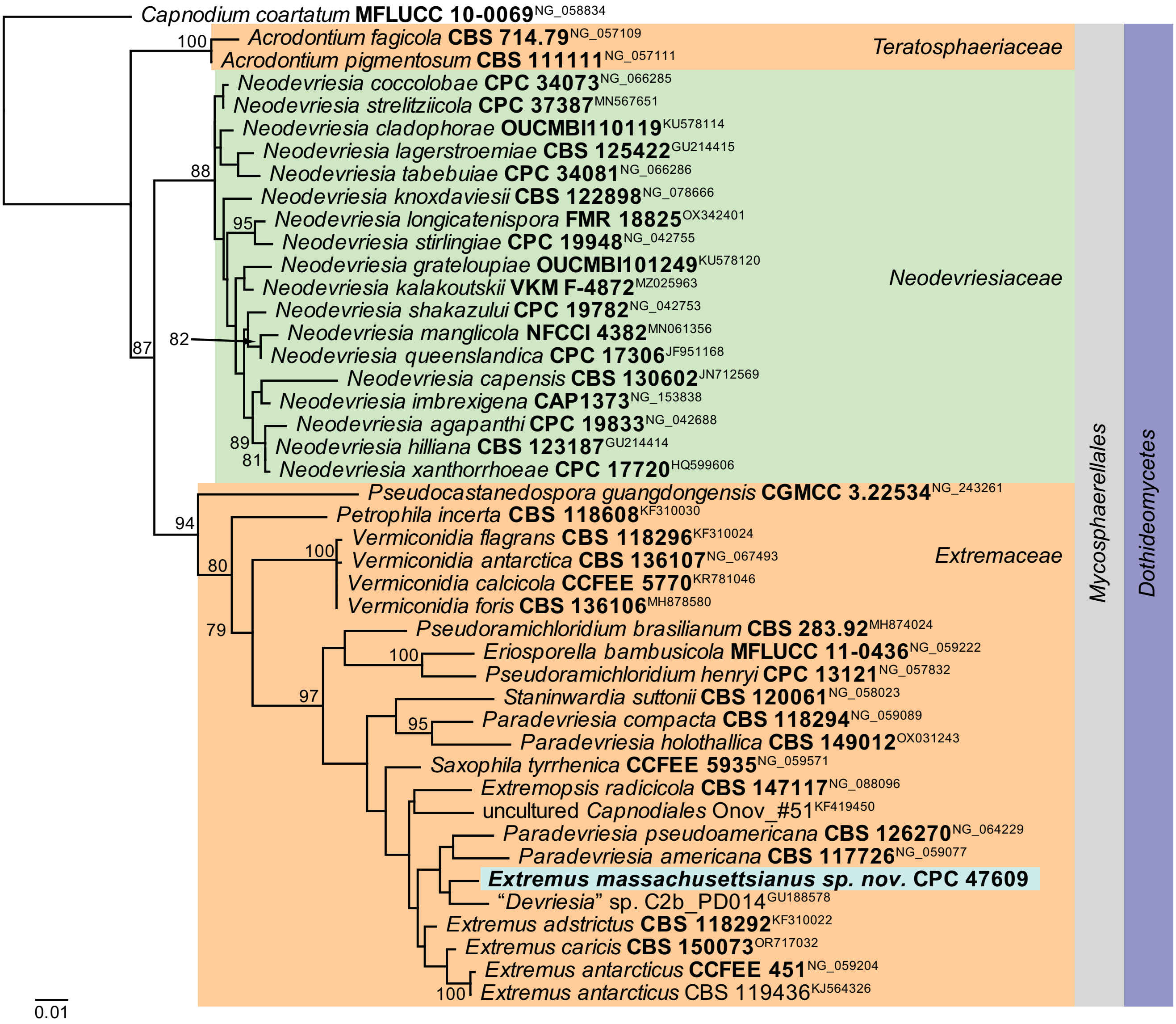
Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium, surface folded, and irregular, lobate margin, reaching 5 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus: **USA**, Massachusetts, Charlestown, from lyse buffer, Aug. 2023, *Z. Jurjević*, 5869 (**holotype** CBS H-25485; culture ex-type CPC 47609 = CBS 152285; ITS, LSU and *rpb2* sequences GenBank PQ498962, PQ499011 and PQ497734).

Notes: Species of *Extremus* are commonly associated with a rock-inhabiting habitat (Egidi *et al*. 2014), being characterised by pigmented, usually sterile or poorly sporulating colonies. *Extremus massachusettsianus* represents a novel lineage in the genus, distinct from all presently described species.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Paradevriesia pseudoamericana* [strain CBS 126270, GenBank NR_171743.1; Identities = 475/511 (93 %), ten gaps (1 %)], *Extremus caricis* [strain CBS 150073, GenBank OR680778.1; Identities = 484/523 (93 %), 16 gaps (3 %)], and *Incertomyces vagans* [strain CCFEE 5393, GenBank NR_154064.1; Identities = 433/470 (92 %), ten gaps (2 %)]. Closest hits using the **LSU** sequence are *Extremus caricis* [strain CPC 45099, GenBank OR717032.1; Identities = 759/775 (98 %), two gaps (0 %)], *Extremus adstrictus* [strain TRN96, GenBank KF310022.1; Identities = 710/725 (98 %), two gaps (0 %)], and *Saxophila tyrrhenica* [strain CCFEE 5935, GenBank NG_059571.1; Identities = 787/806 (98 %), no gaps]. Closest hits using the ***rpb2*** (first part) sequence had distant similarity to *Saxophila tyrrhenica* [strain CCFEE 5935, GenBank XM_064801695.1; Identities = 441/565 (78 %), no gaps], *Extremus caricis* [strain CPC 45099, GenBank OR683731.1; Identities = 420/568 (74 %), three gaps (0 %)], and *Fusoidiella anethi* [strain CBS 117584, GenBank MF951500.1; Identities = 379/567 (67 %), 20 gaps (3 %)].

Colour illustrations: Laboratory in Charlestown, USA. Sporodochia with conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Extremus* LSU nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Capnodium coartatum* (MFLUCC 10-0069; GenBank NG_058834) and the novelty described here is highlighted with a coloured block and **bold** font. Families, the order and the class are shown to the right of the tree in coloured blocks. Alignment statistics: 44 strains including the outgroup; 822 characters including alignment gaps analysed: 218 distinct patterns, 126 parsimony-informative, 52 singleton sites, 644 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TNe+R3. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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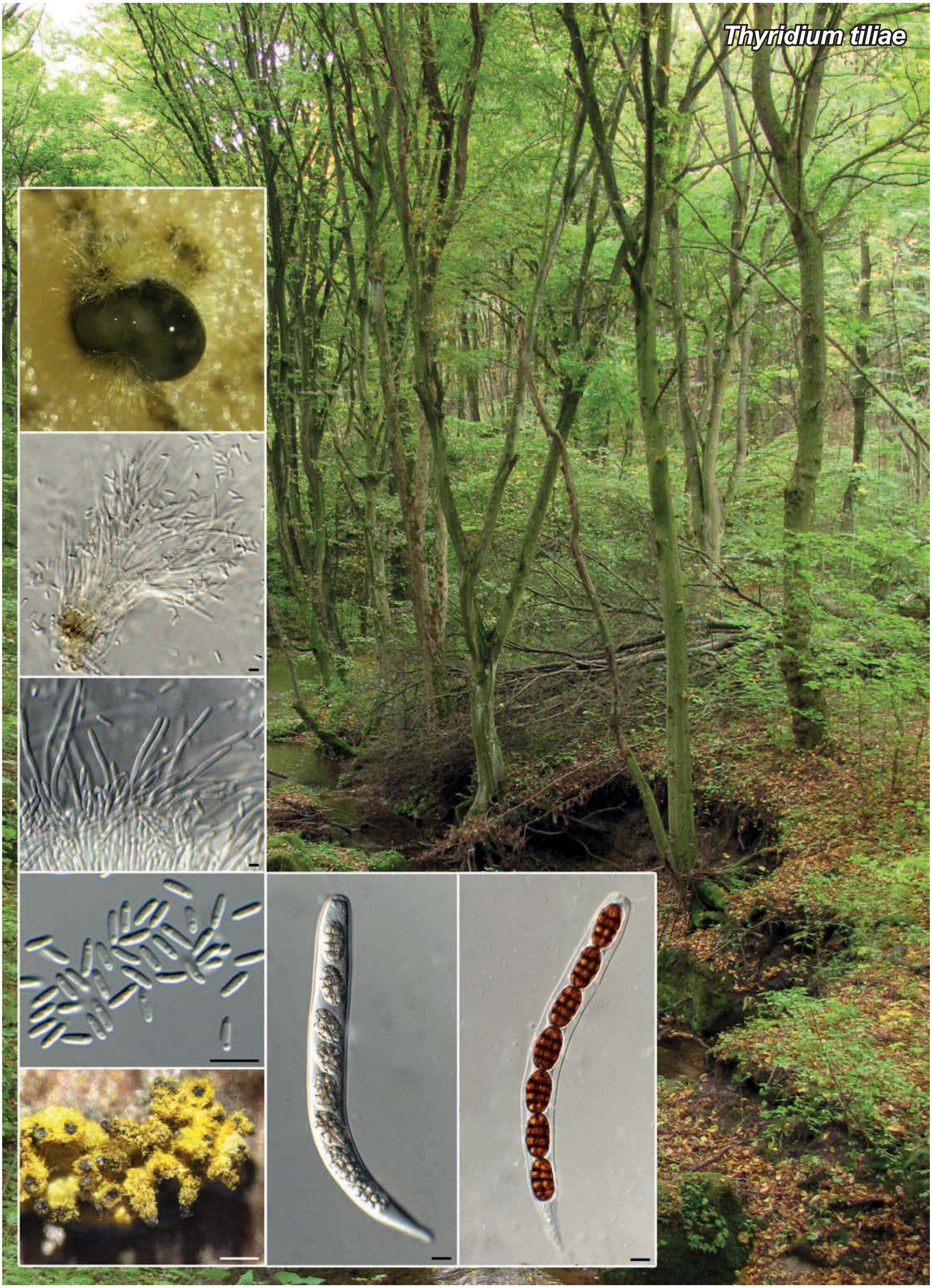

Thyridium tiliae

Fungal Planet 1730

MycoBank MB 856106

Thyridium tiliae Crous & Akulov, ***sp. nov.***

Etymology: Name refers to *Tillia*, the tree genus from which it was isolated.

Classification: *Thyridiaceae*, *Thyridiales*, *Sordariomycetidae*, *Sordariomycetes*.

Stromata scattered, pulvinate, circular in outline, submerged, becoming erumpent through bark, dark brown, 1(–2) mm diam. *Ascomata* perithecial, subglobose, up to 350 µm diam, immersed in stromata; wall of 6–10 layers of dark brown cells with long cylindrical necks, up to 600 µm tall, 120–180 µm wide, periphysate, with yellow outer mycelium developing when incubated in moist chambers. *Paraphyses* septate, unbranched, cylindrical, up to 120 µm tall, 4–6 µm wide. *Asci* unitunicate, cylindrical, 150–200 × 13–15 µm, broadly rounded at apex, non-amyloid annulus, pedicellate, (6–)8-spored. *Ascospores* fusoid-ellipsoid, brown, smooth, with 3 transverse and 3–4 oblique or vertical septa, (18–)20–22(–26) × 11–12(–14) µm. *Conidiomata* pycnidial to acervular, brown, globose, solitary to aggregated, 250–300 µm diam. *Conidiophores* hyaline, smooth, up to 100 µm tall, smooth, extensively branched, cylindrical with terminal and intercalary phialides. *Conidiogenous cells* phialidic, subcylindrical, hyaline, smooth, 12–30 × 1.5–2 µm. *Conidia* hyaline, smooth, guttulate, aseptate, subcylindrical, straight to curved, ends subobtuse, (4–)5–6 × 1.5(–2) µm.

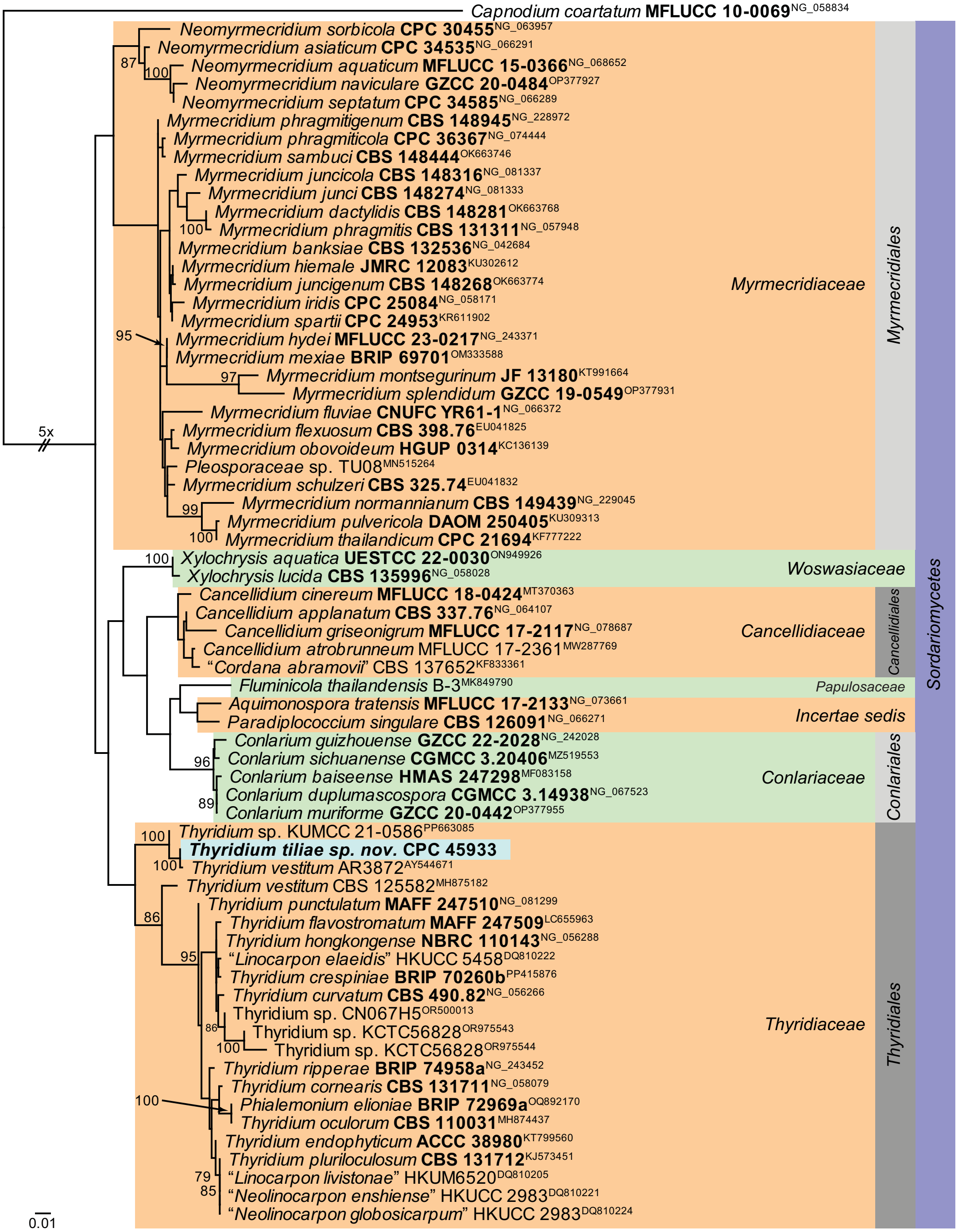
Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium, and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA surface and reverse luteous; on PDA surface and reverse ochreous; on OA surface pale luteous.

Typus: **Ukraine**, Ternopil region, Chortkiv district, Krutyliv village, on dead twigs of *Tilia* sp. (*Tiliaceae*), 4 Nov. 2022, *A. Akulov*, HPC 4171, CWU (Myc) AS 8483 [**holotype** CBS H-25496; culture ex-type CPC 45933 = CBS 152297; ITS, LSU, *rpb2* and *tef1* (second part) sequences GenBank PQ498963, PQ499012, PQ497735 and PQ497751].

Colour illustrations: Krutyliv village, Ukraine. Conidioma on oatmeal agar; conidiophores and conidiogenous cells giving rise to conidia; conidia; ascomata *in vivo*; asci with ascospores. Scale bars: conidiophores = 20 µm, ascomata = 350 µm, all others = 10 µm.

Notes: *Thyridium* includes approx. 33 species, occurring on various plants as saprobic or hemibiotrophic fungi (Sugita & Tanaka 2022). *Thyridium tiliae* is related but distinct from various isolates identified as *T. vestitum* (ascospores 3–5(–8) transverse septa), although the latter requires typification to settle the application of the name.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Thyridium* sp. [strain KUMCC21-0586, GenBank PP663078.1; Identities = 541/546 (99 %), no gaps], *Thyridium vestitum* [strain NWFVA6251, GenBank ON710904.1; Identities = 511/549 (93 %), 11 gaps (2 %)], and *Thyridium pluriloculosum* [strain CBS 131712, GenBank MH865904.1; Identities = 498/548 (91 %), 16 gaps (2 %)]. Closest hits using the **LSU** sequence are *Thyridium vestitum* [strain AFTOL-ID 172 = CBS 113027, GenBank AY544671.1; Identities = 810/812 (99 %), one gap (0 %)], *Thyridium vestitums* [strain CBS 125582, GenBank MH875182.1; Identities = 778/812 (96 %), three gaps (0 %)], *Xylochrysis aquatica* [as *Xylochrysis* sp. XY-2022a; strain UESTCC 22.0030, GenBank ON949926.1; Identities = 771/811 (95 %), four gaps (0 %)], and *Cancellidium applanatum* [strain CBS 337.76, GenBank NG_064107.1; Identities = 772/813 (95 %), five gaps (0 %)]. Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Thyridium vestitum* [strain AFTOL-ID 172 = CBS 113027, GenBank DQ470890.1; Identities = 706/717 (98 %), five gaps (0 %)], *Thyridium* sp. [strain BRIP 70260b, GenBank PP438398.1; Identities = 654/807 (81 %), six gaps (0 %)], and *Apiorhynchostoma curreyi* [strain UAMH 11088, GenBank KY931926.1; Identities = 302/376 (80 %), no gaps]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Thyridium vestitum* [strain AFTOL-ID 172 = CBS 113027, GenBank DQ471058.1; Identities = 919/919 (100 %), no gaps], *Thyridium pluriloculosum* [strain KT 3803, GenBank LC655972.1; Identities = 810/897 (90 %), four gaps (0 %)], and *Phialemonium obovatum* [strain CBS 279.76, GenBank LT634003.1; Identities = 827/920 (90 %), six gaps (0 %)].



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Thyridiaceae* LSU nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Capnodium coartatum* (MFLUCC 10-0069; GenBank NG_058834) and the novelty described here is highlighted with a coloured block and **bold** font. Families, orders and the class are shown to the right of the tree in coloured blocks. The root branch was shortened to facilitate layout. Alignment statistics: 67 strains including the outgroup; 800 characters including alignment gaps analysed: 235 distinct patterns, 145 parsimony-informative, 87 singleton sites, 568 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM3e+R3. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Myxotrichum tapetae

Fungal Planet 1731 MycoBank MB 856107

Myxotrichum tapetae Crous & Jurjević, ***sp. nov.***

Etymology: Name refers to the fact that it was isolated from a floor carpet.

Classification: *Myxotrichaceae*, *incertae sedis*, *Leotiomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. Fertile branches lateral, frequently opposite each other on hyphae, forming clusters, erect, sinuous, 2.5–3 µm diam, forming terminal and intercalary arthroconidia. *Conidia* enteroarthric, hyaline, smooth, thick-walled, separated by evanescent connective cells, subcylindrical upon release, becoming globose, 2.5–3 µm diam, aseptate, rounded at both ends, with minute marginal frill due to rhexolytic secession. *Chlamydospores* not observed.

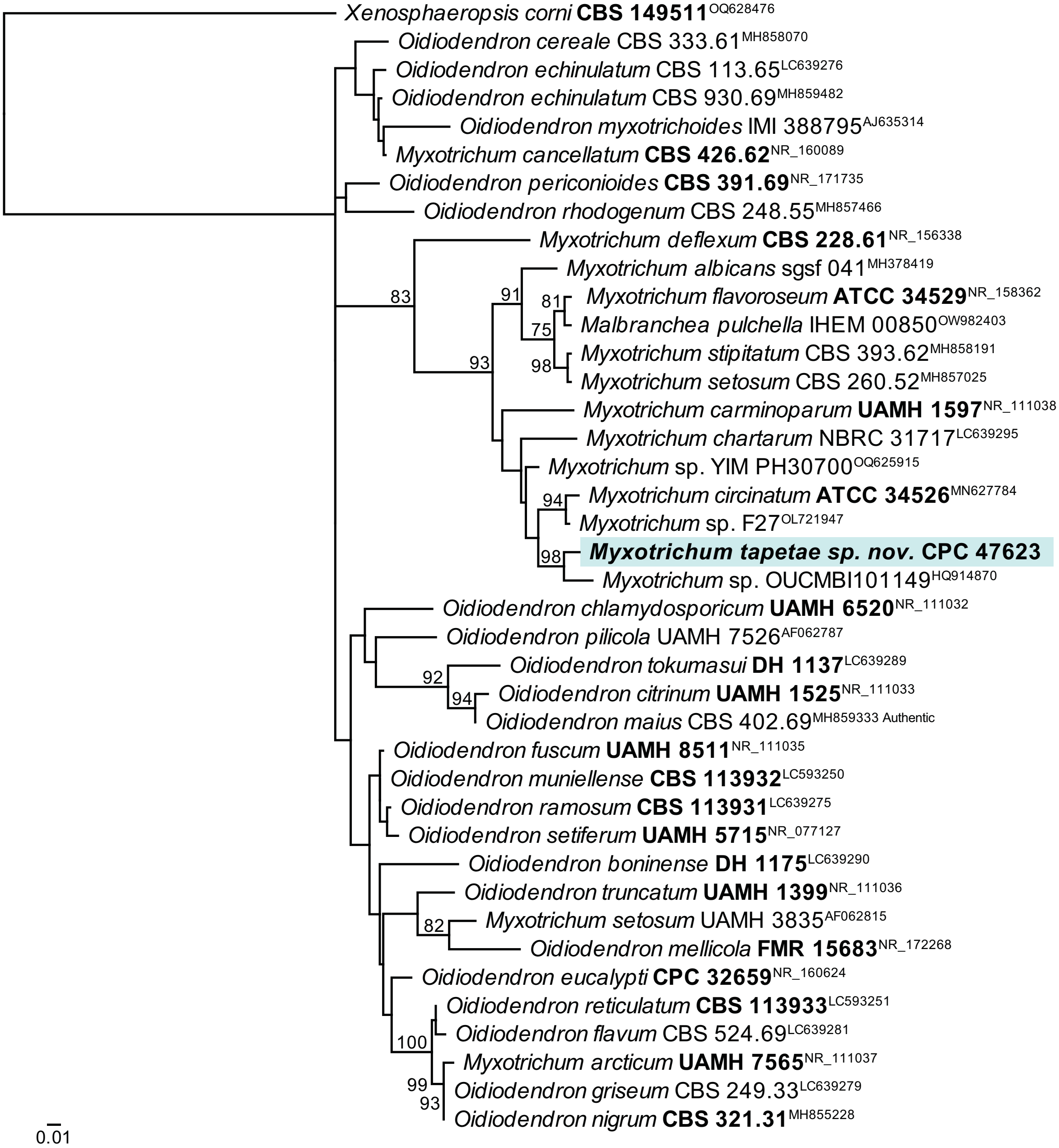
Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium, and smooth, lobate margin, reaching 25 mm diam after 2 wk at 25 °C. On MEA surface pale luteous, occasionally clear abundant exudate, large droplets after 7 d, reverse sienna; on PDA surface and reverse dirty white; on OA surface dirty white.

Typus: **USA**, Pennsylvania, Feasterville, on carpet in basement, Nov. 2023, *Z. Jurjević*, 5889 (**holotype** CBS H-25499; culture ex-type CPC 47623 = CBS 152303; ITS, LSU and *rpb1* sequences GenBank PQ498964, PQ499013 and PQ497763).

Notes: The *Malbrachea* complex was recently revised by Rodríguez-Andrade *et al.* (2021), who excluded *Malbranchea circinata* and *M. flavorosea* from the genus. In a subsequent study, Mehrabi *et al*. (2024), placed these two species in *Myxotrichum. Myxotrichum tapetae* is closely related to *M. circinata*, but is phylogenetically and morphologically distinct in lacking gymnothecia and “antler-like” appendages (Sigler & Carmichael 1976).

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Myxotrichum chartarum* [strain NBRC 31717, GenBank LC639295.1; Identities = 492/524 (94 %), six gaps (1 %)], *Malbranchea circinata* [strain IFM 41295, GenBank LC639294.1; Identities = 496/518 (96 %), five gaps (0 %)], and *Malbranchea flavorosea* [strain ATCC 34529, GenBank NR_158362.1; Identities = 485/518 (94 %), five gaps (0 %)]. Closest hits using the **LSU** sequence are *Myxotrichum stipitatum* [strain CBS 393.62, GenBank MH869789.1; Identities = 786/803 (98 %), one gap (0 %)], *Myxotrichum setosum* [strain CBS 260.52, GenBank MH868555.1; Identities = 785/802 (98 %), no gaps], and *Myxotrichum albicans* [strain SGSF041, GenBank MH971222.1; Identities = 790/809 (98 %), no gaps]. Closest hits using the ***rpb1*** sequence had highest similarity to *Myxotrichum chartarum* [strain NBRC 31717, GenBank LC639271.1; Identities = 522/572 (91 %), no gaps], *Myxotrichum stipitatum* [strain NBRC 31721, GenBank LC639272.1; Identities = 535/632 (85 %), four gaps (0 %)], and *Malbranchea flavorosea* [strain IFM 41293, GenBank LC639269.1; Identities = 534/631 (85 %), two gaps (0 %)].

Colour illustrations: Carpet in basement, Feasterville, Pennsylvania, USA. Hyphae disarticulating into conidia; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Myxotrichum* ITS nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Xenosphaeropsis corni* (CBS 149511; GenBank OQ628476) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 40 strains including the outgroup; 525 characters including alignment gaps analysed: 216 distinct patterns, 120 parsimony-informative, 60 singleton sites, 345 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TNe+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Cytospora carpobroticola

Fungal Planet 1732

MycoBank MB 856108

Cytospora carpobroticola Crous, *sp. nov.*

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

Classification: *Valsaceae*, *Diaporthales*, *Sordariomycetidae*, *Sordariomycetes*.

Conidiomata stromatic, unilocular, cytosporoid, greenish grey, ovoid, up to 350 µm diam, with central papillate neck and periphysate ostiole. *Conidiophores* hyaline, branched, tightly aggregated, septate, giving rise to 1–4 conidiogenous cells, up to 30 µm tall, 2.5–3 µm wide. *Conidiogenous cells* phialidic, subcylindrical with apical taper and minute collarettes, 6–12 × 2–3 µm. Conidia hyaline, smooth, eguttulate, aseptate, allantoid, (4–)5–6 × (1–)1.5 µm.

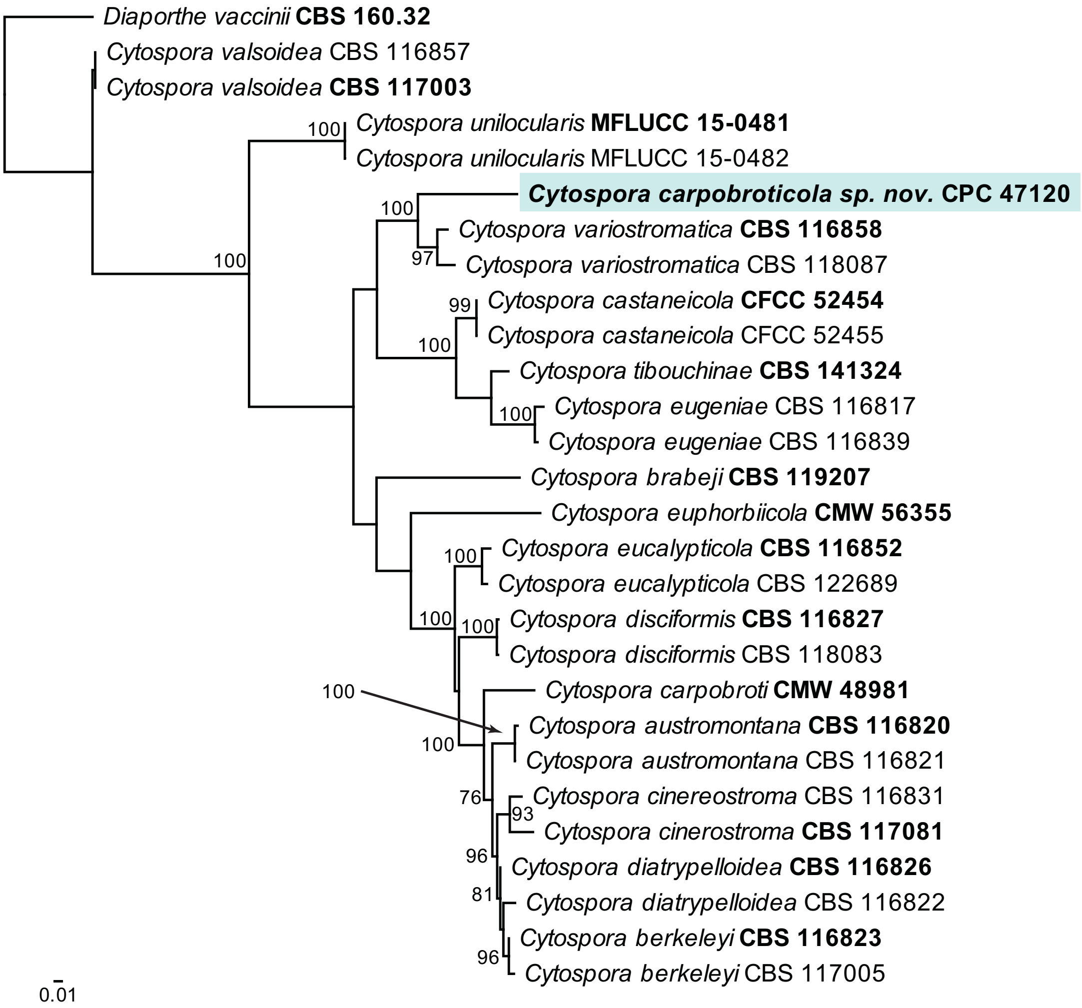
Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus: **South Africa**, Western Cape Province, Cederberg, Clanwilliam, on leaf of *Carpobrotus quadrifidus* (*Aizoaceae*), Sep. 2023, *M.J. Wingfield*, HPC 4291 [**holotype** CBS H-25500; culture ex-type CPC 47120 = CBS 152300; ITS, LSU, *actA*, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank PQ498965, PQ499014, PQ497710, PQ497736, PQ497770 and PQ497780].

Notes: Occurring on *Carpobrotus*, *C. carpobroticola* needs to be compared specifically to *C. carpobroti* (Jami *et al.* 2018), as well as to other species in the genus (Lin *et al.* 2024), all from which it is phylogenetically distinct. *Cytospora carpobroti* has conidiomata that develop up to five elongated necks, and shorter conidiophores, 8.5–11 × 2.5–3.5 µm (Jami *et al.* 2018), thus is also morphologically distinct.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cytospora variostromatica* [strain JSP 01-11 A 1.1, GenBank KR093848.1; Identities = 561/581 (97 %), 12 gaps (2 %)], *Waydora typica* [voucher PDD 103894, GenBank KF727412.1; Identities = 561/581 (97 %), 12 gaps (2 %)], and *Cytospora valsoidea* [strain CBS 117003, GenBank MH863010.1; Identities = 536/566 (95 %), 19 gaps (3 %)]. Closest hits using the **LSU** sequence are *Waydora typica* [voucher PDD 103894, GenBank KF727413.1; Identities = 803/811 (99 %), no gaps], *Cytospora fraxiicola* [voucher MFLU 17-2392, GenBank MN764356.1; Identities = 801/811 (99 %), no gaps], and *Cytospora carbonacea* [strain CBS 219.54, GenBank MH868831.1; Identities = 800/811 (99 %), no gaps]. The closest hit using the ***actA*** sequence had highest similarity to *Cytospora pavettae* [strain CBS 145562, GenBank MK876457.1; Identities = 591/641 (92 %), 12 gaps (1 %)]. Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Cytospora eucalypticola* [strain RBG7257, GenBank OP066958.1; Identities = 719/785 (92 %), no gaps], *Cytospora pistaciae* [strain CPC 34211, GenBank MN078082.1; Identities = 694/758 (92 %), no gaps], and *Cytospora salicacearum* [strain shd162, GenBank MW824357.1; Identities = 707/786 (90 %), no gaps]. Closest hits using the ***tef1*** (first part) sequence had highest similarity to *Cytospora granati* [strain 6F-45, GenBank MG971514.1; Identities = 470/575 (82 %), 32 gaps (5 %)], *Cytospora pistaciae* [strain KARE441, GenBank MG971515.1; Identities = 463/572 (81 %), 31 gaps (5 %)], and *Cytospora parapistaciae* [strain KARE270, GenBank MG971519.1; Identities = 461/572 (81 %), 31 gaps (5 %)]. Closest hits using the ***tub2*** sequence had highest similarity to *Cytospora cincta* [strain CFCC 89956, GenBank KR045665.1; Identities = 517/661 (78 %), 45 gaps (6 %)], *Cytospora chrysosperma* [voucher BJFC-S978, GenBank KP321973.1; Identities = 533/693 (77 %), 66 gaps (9 %)], and *Cytospora platycladi* [strain CFCC 50504, GenBank MH933581.1; Identities = 516/670 (77 %), 39 gaps (5 %)].

Colour illustrations: *Carpobrotus quadrifidus* in Cederberg, South Africa. Conidioma on pine needle agar; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Cytospora* ITS-*actA*-*rpb2*-*tef1*-*tub2* nucleotide alignment (1–580; 581–890; 891–1 541; 1 542–2 309; 2 310–2 859, respectively). Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers are indicated for all species. GenBank accession numbers can be found in Lin *et al.* (2024), from which this alignment represents a subset. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Diaporthe vaccinii* (CBS 160.32) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 28 strains including the outgroup; 2 859 characters including alignment gaps analysed: 1 183 distinct patterns, 689 parsimony-informative, 350 singleton sites, 1 820 constant sites. The best-fit models identified for the individual loci in IQ-TREE using the TESTNEW option were: TNe+G4; K2P+G4; TIM2e+G4; TPM2+F+I+G4; HKY+F+G4, respectively. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Podocarpigena hagahagaensis

Fungal Planet 1733

MycoBank MB 856109

Podocarpigena Crous, ***gen. nov.***

Etymology: Name refers to *Podocarpus*, the tree genus from which it was isolated.

Classification: *Asterosporiaceae*, *Diaporthales*, *Sordariomycetidae*, *Sordariomycetes*.

Conidiomata solitary, pycnidial to acervular; wall of 3–8 layers of brown *textura epidermoidea. Conidiophores* hyaline, smooth, subcylindrical, branched, with terminal and intercalary conidiogenous cells. *Conidiogenous cells* hyaline, smooth, subcylindrical, proliferating percurrently at apex. *Conidia* solitary, hyaline, smooth, guttulate, fusoid-ellipsoid to clavate, widest in upper third, straight to irregularly curved, apex subobtuse, tapering to truncate base, with marginal frill; a few conidia were observed to develop up to 3 transverse septa, and 1–2 vertical/oblique septa with age.

Type species: *Podocarpigena hagahagaensis* Crous

MycoBank MB 85611

Podocarpigena hagahagaensis Crous, ***sp. nov.***

Etymology: Name refers to the village of Haga Haga in the Eastern Cape Province, South Africa where it was collected.

Conidiomata solitary, pycnidial to acervular, up to 350 µm diam; wall of 3–8 layers of brown *textura epidermoidea. Conidiophores* hyaline, smooth, subcylindrical, branched, up to 100 µm tall, with terminal and intercalary conidiogenous cells. *Conidiogenous cells* hyaline, smooth, subcylindrical, 7–30 × 3–3.5 µm, proliferating percurrently at apex. *Conidia* solitary, hyaline, smooth, guttulate, fusoid-ellipsoid to clavate, widest in upper third, straight to irregularly curved, apex subobtuse, tapering to truncate base, 2–3 µm diam, with marginal frill, (16–)20–25(–35) × (6–)7(–7.5) µm; a few conidia were observed to develop up to 3 transverse septa, and 1–2 vertical/oblique septa with age.

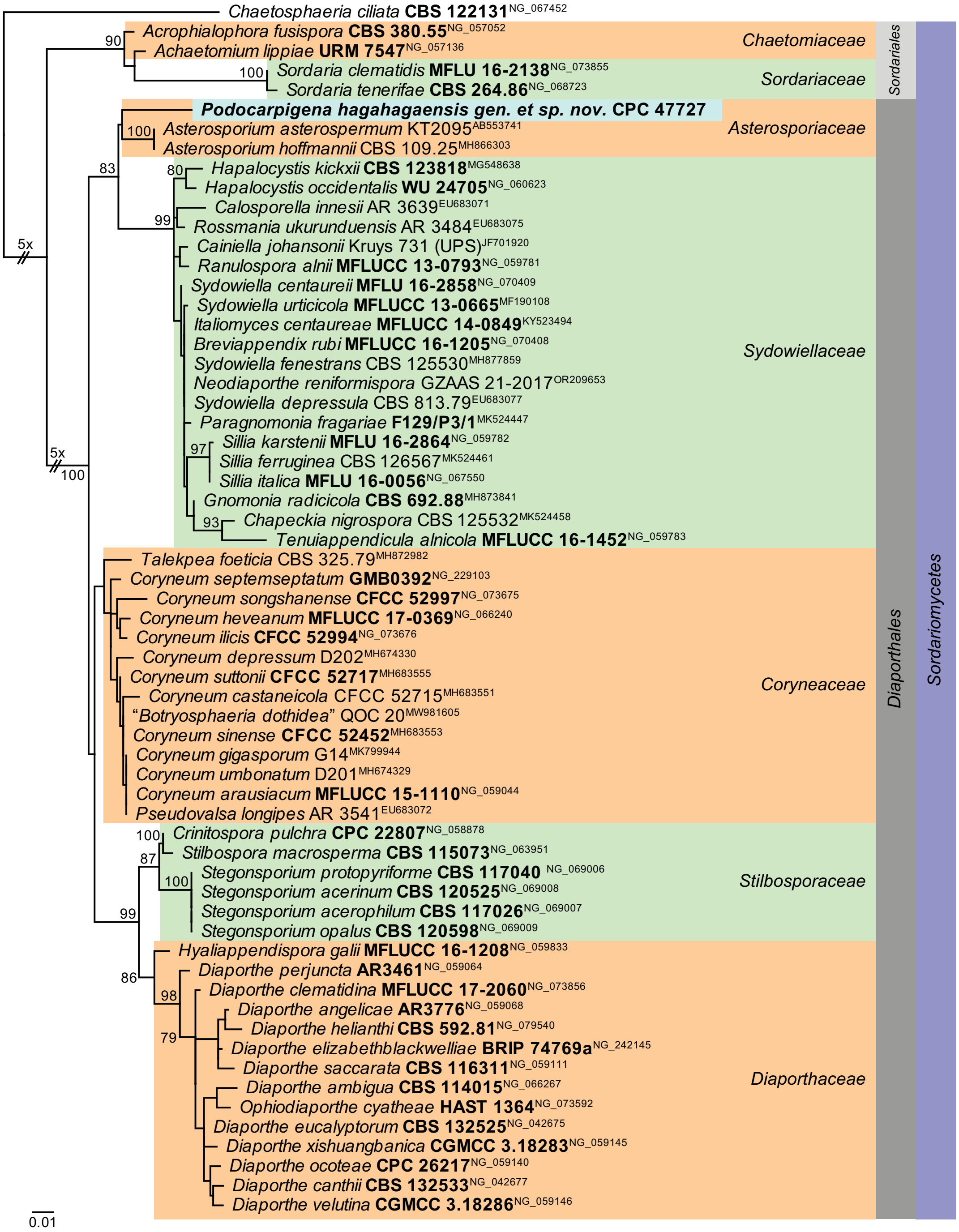
Culture characteristics: Colonies erumpent, slow-growing, with sparse aerial mycelium, and smooth, lobate margin, reaching 2–5 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus: **South Africa**, Eastern Cape Province, Haga Haga, Amathole, on leaf spots of *Podocarpus falcatus* (*Podocarpaceae*), 1 Dec. 2022, *M.J. Wingfield*, HPC 4352 [**holotype** CBS H-25501 culture ex-type CPC 47727 = CBS 152308; ITS, LSU, *rpb2*, *tef1* (second part) and *tub2* sequences GenBank PQ498966, PQ499015, PQ497737, PQ497752 and PQ497781].

Notes: *Podocarpigena* represents a novel genus in the *Diaporthales* (Senanayake *et al.* 2017), tentatively placed in the *Asterosporiaceae.* This monotypic genus is based on *P. hagahagaensis*, which was associated with leaf spots of *Podocarpus falcatus*, suggesting that it might have a role as pathogen, although this must be confirmed in pathogenicity tests. *Podocarpigena* is characterised by pycnidial conidiomata, long, flexuous conidiophores, terminating in conidiogenous cells with percurrent proliferation, and hyaline, fusoid-ellipsoid to clavate conidia that are mostly aseptate, but become muriformly septate with age.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Lamproconium desmazieri* [strain MFLUCC 17-1401, GenBank MW159906.1; Identities = 356/423 (84 %), 33 gaps (7 %)], *Pseudoplagiostoma* sp. [strain SAUCC WZ0152, GenBank OP810626.1; Identities = 365/447 (82 %), 33 gaps (7 %)], and *Hyaloterminalis alishanensis* [voucher MFLU 20-0428, GenBank NR_172183.1; Identities = 329/398 (83 %), 27 gaps (6 %)]. Closest hits using the **LSU** sequence are *Asterosporium hoffmannii* [strain CBS 109.25, GenBank MH866303.1; Identities = 766/790 (97 %), one gap (0 %)], *Asterosporium asterospermum* [strain KT2095, GenBank AB553741.1; Identities = 761/785 (97 %), one gap (0 %)], and *Hapalocystis occidentalis* [strain WU 24705, GenBank NG_060623.1; Identities = 759/791 (96 %), three gaps (0 %)]. Closest hits using the ***rpb2*** (first part) sequence had distant similarity to *Stegonsporium galeatum* [strain D70, GenBank KF570176.1; Identities = 647/822 (79 %), three gaps (0 %)], *Caudospora iranica* [strain D189, GenBank MG495988.1; Identities = 650/828 (79 %), nine gaps (1 %)], and *Stilbospora longicornuta* [strain D33, GenBank KF570192.1; Identities = 644/824 (78 %), three gaps (0 %)]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Cytospora punicae* [GenBank KX983930.1; Identities = 751/819 (92 %), no gaps], *Diaporthe pseudomangiferae* [strain SICAUCC 22-0131, GenBank OQ281369.1; Identities = 747/819 (91 %), no gaps], and *Diaporthe amygdali* [strain CAA958, GenBank XM_053136773.1; Identities = 746/819 (91 %), no gaps]. Closest hits using the ***tub2*** sequence had highest similarity to *Caudospora taleola* [strain D186, GenBank MG496006.1; Identities = 550/723 (76 %), 56 gaps (7 %)], and *Caudospora iranica* [strain D189, GenBank MG496004.1; Identities = 548/723 (76 %), 60 gaps (8 %)].

Colour illustrations: Haga Haga, Eastern Cape Province, South Africa. Conidiomata on SNA; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars: Conidiomata = 350 µm, all others = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Diaporthales* LSU nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Chaetosphaeria ciliata* (CBS 122131; GenBank NG_067452) and the novelty described here is highlighted with a coloured block and **bold** font. Families, orders and the class are shown to the right of the tree in coloured blocks. Some branches were shortened to facilitate layout. Alignment statistics: 62 strains including the outgroup; 809 characters including alignment gaps analysed: 183 distinct patterns, 144 parsimony-informative, 47 singleton sites, 618 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TNe+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Nothophysalospora agapanthi

Fungal Planet 1734 MycoBank MB 856111

Nothophysalospora Crous & R.W. Barreto, *gen. nov.*

Etymology: Name refers to its similarity to *Physalospora*, from which it is distinct.

Classification: *Incertae sedis*, *incertae sedis*, *Sordariomycetidae*, *Sordariomycetes*.

Leaf spots brown, amphigenous, with darker brown margin. *Ascomata* erumpent, perithecial, separate, globose, black on host, brown in culture, 100–300 µm diam, with central periphysate ostiole; wall of 3–4 layers of *brown textura angularis. Paraphyses* intermingled among asci, hyaline, smooth, constricted at septa, 3–4 µm diam, hyphae-like. *Asci* unitunicate, hyaline, smooth, subcylindrical, straight to slightly curved, apex obtuse to bluntly rounded, stipitate; apical mechanism not straining in Melzer's reagent. *Ascospores* uniseriate, fusoid-ellipsoid, aseptate, hyaline, smooth, guttulate, widest in middle, ends subobtuse, surrounded by a non-persistent mucoid sheath.

Type species: *Nothophysalospora agapanthi* Crous & R.W. Barreto

MycoBank MB 856112

Nothophysalospora agapanthi Crous & R.W. Barreto, *sp. nov.*

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

Leaf spots brown, amphigenous, up to 15 mm diam, with darker brown margin. Description based on CPC 47788 in culture. *Ascomata* erumpent, perithecial, separate, globose, black on host, brown in culture, immersed, 100–300 µm diam, with central periphysate ostiole; wall of 3–4 layers of *brown textura angularis. Paraphyses* intermingled among asci, hyaline, smooth, constricted at septa, 3–4 µm diam, hyphae-like. *Asci* unitunicate, hyaline, smooth, subcylindrical, straight to slightly curved, apex obtuse to bluntly rounded, stipitate, 75–90 × 9–15 µm; apical mechanism not straining in Melzer's reagent. *Ascospores* uniseriate, fusoid-ellipsoid, aseptate, hyaline, smooth, guttulate, widest in middle, ends subobtuse, surrounded by a non-persistent mucoid sheath, (13–)15–17(–19) × (7–)8 µm.

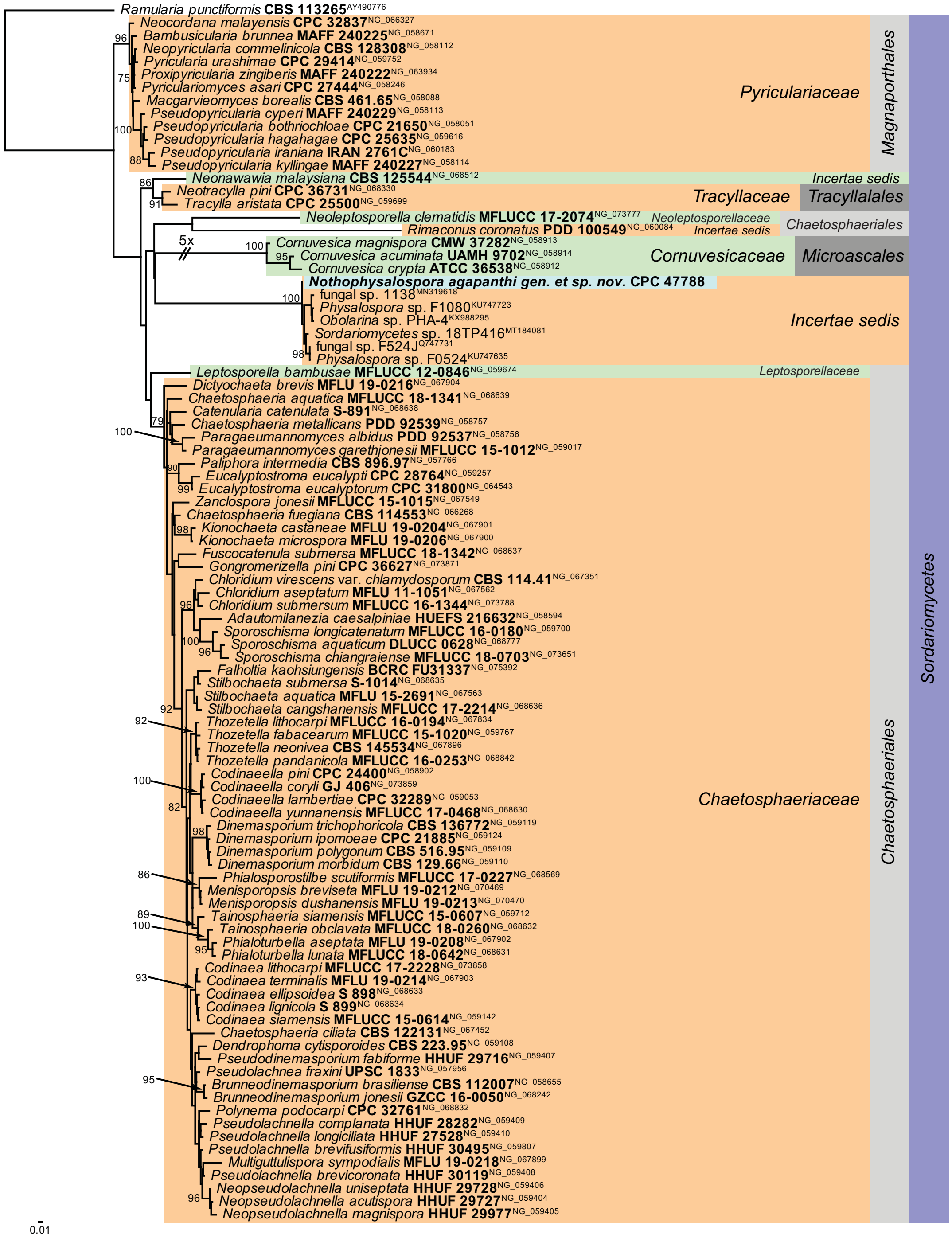
Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium, and smooth, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse ochreous.

Typus: **Brazil**, Minas Gerais, Viçosa campus, on flower stalks of *Agapanthus praecox* (*Amaryllidaceae*), 2024, *P.W. Crous & R. Barreto*, HPC 4391 [**holotype** CBS H-25503; culture ex-type CPC 47788 = CBS 152325; ITS, LSU, *rpb2*, *tef1* (second part) and *tub2* sequences GenBank PQ498967, PQ499016, PQ497738, PQ497753 and PQ497782].

Notes: *Physalospora*, based on *P. alpestris*, is a genus in *Hyphonectriaceae* (on leaves of *Carex*, Europe). The genus is characterised by being saprobic, and having immersed, brown ascomata, fusoid-ellipsoid asci intermingled among thread-like paraphyses, and 2–3-seriate, hyaline, fusoid ascospores (Arx & Müller 1954). As far as we could establish, there is no authentic material of *Physalospora*, and the type species will have to be recollected. *Nothophysalospora* is distinct from *Physalospora* as it is associated with leaf spots, has cylindrical asci, unitunicate ascospores, and paraphyses that are prominently constricted at their septa.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Coniochaeta navarrae* [strain CBS 141016, GenBank NR_154808.1; Identities = 343/407 (84 %), 21 gaps (5 %)], *Coniochaeta ellipsoidea* [strain CBS 138.68, GenBank MH859092.1; Identities = 341/407 (84 %), 22 gaps (5 %)], and *Coniochaeta taeniospora* [strain LTA1, GenBank KU762325.1; Identities = 341/407 (84 %), 22 gaps (5 %)]. Closest hits using the **LSU** sequence are *Lasiosphaeria ovina* [strain SMH4605, GenBank AY436413.1; Identities = 725/837 (87 %), 17 gaps (2 %)], *Lasiosphaeria sorbina* [strain GJS L555, GenBank AY436415.1; Identities = 724/837 (86 %), 17 gaps (2 %)], and *Lasiosphaeria similisorbina* [voucher ILLS:81088, GenBank MF806375.1; Identities = 725/839 (86 %), 19 gaps (2 %)]. Closest hits using the ***rpb2*** (first part) sequence had distant similarity to *Camarops tubulina* [strain SMH4614, GenBank AY780157.1; Identities = 641/828 (77 %), 12 gaps (1 %)], *Camarops amorpha* [strain SMH1450, GenBank AY780156.1; Identities = 639/825 (77 %), six gaps (0 %)], and *Camarops ustulinoides* [strain AFTOL-ID 72, GenBank DQ470882.1; Identities = 630/828 (76 %), 12 gaps (1 %)]. Closest hits using the ***tef1*** (second part) sequence had distant similarity to *Phaeoacremonium sphinctrophorum* [strain MFLUCC 11-0629, GenBank KU940202.1; Identities = 795/861 (92 %), no gaps], *Thozetella effusa* [strain CBS 115044, GenBank OL654066.1; Identities = 792/861 (92 %), no gaps], and *Colletotrichum siamense* [strain Cg363, GenBank XM_036644039.1; Identities = 789/859 (92 %), two gaps (0 %)]. No significant hits were obtained using the ***tub2*** sequence in megablast and blastn searches.

Colour illustrations: *Agapanthus praecox*, Viçosa University campus, Brazil. Asci with ascospores. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Sordariomycetes* LSU nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Ramularia punctiformis* (CBS 113265; GenBank AY490776) and the novelty described here is highlighted with a coloured block and **bold** font. Families, orders and the class are shown to the right of the tree in coloured blocks. The branch of *Cornuvesicaceae* was shortened to facilitate layout. Alignment statistics: 94 strains including the outgroup; 892 characters including alignment gaps analysed: 506 distinct patterns, 352 parsimony-informative, 95 singleton sites, 445 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TN+F+R4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Phaeosphaeria tabebuiae

Fungal Planet 1735 MycoBank MB 856113

Phaeosphaeria tabebuiae Crous, Alfenas & R.F. Alfenas, ***sp. nov.***

Etymology: Name refers to *Tabebuia*, the tree genus from which it was isolated.

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

Ascomata solitary or aggregated in clusters, globose, brown, 200–250 µm diam, central ostiole up to 60 µm diam; wall of 3–6 layers of brown *textura angularis*. *Pseudoparaphyses* intermingled among asci, hyaline, smooth, septate, 3–4 µm diam, hyphae-like. *Asci* bitunicate, subcylindrical, stipitate, 8-spored, apiculus 1 µm diam, 55–80 × 8–11 µm. *Ascospores* bi- to triseriate, fusoid-ellipsoid, ends subobtuse, golden brown, verruculose, 3-septate, widest in second cell from apex, (19–)20–22(–25) × 4(–5) µm. Cultures also forming brown, globose, pycnidial conidiomata, 150–200 µm diam, giving rise to scolecosporous, subcylindrical, flexuous, brown, smooth *conidia*, apex subobtuse, base truncate, 3(–4)-septate, 25–35 × 2.5–3 µm.

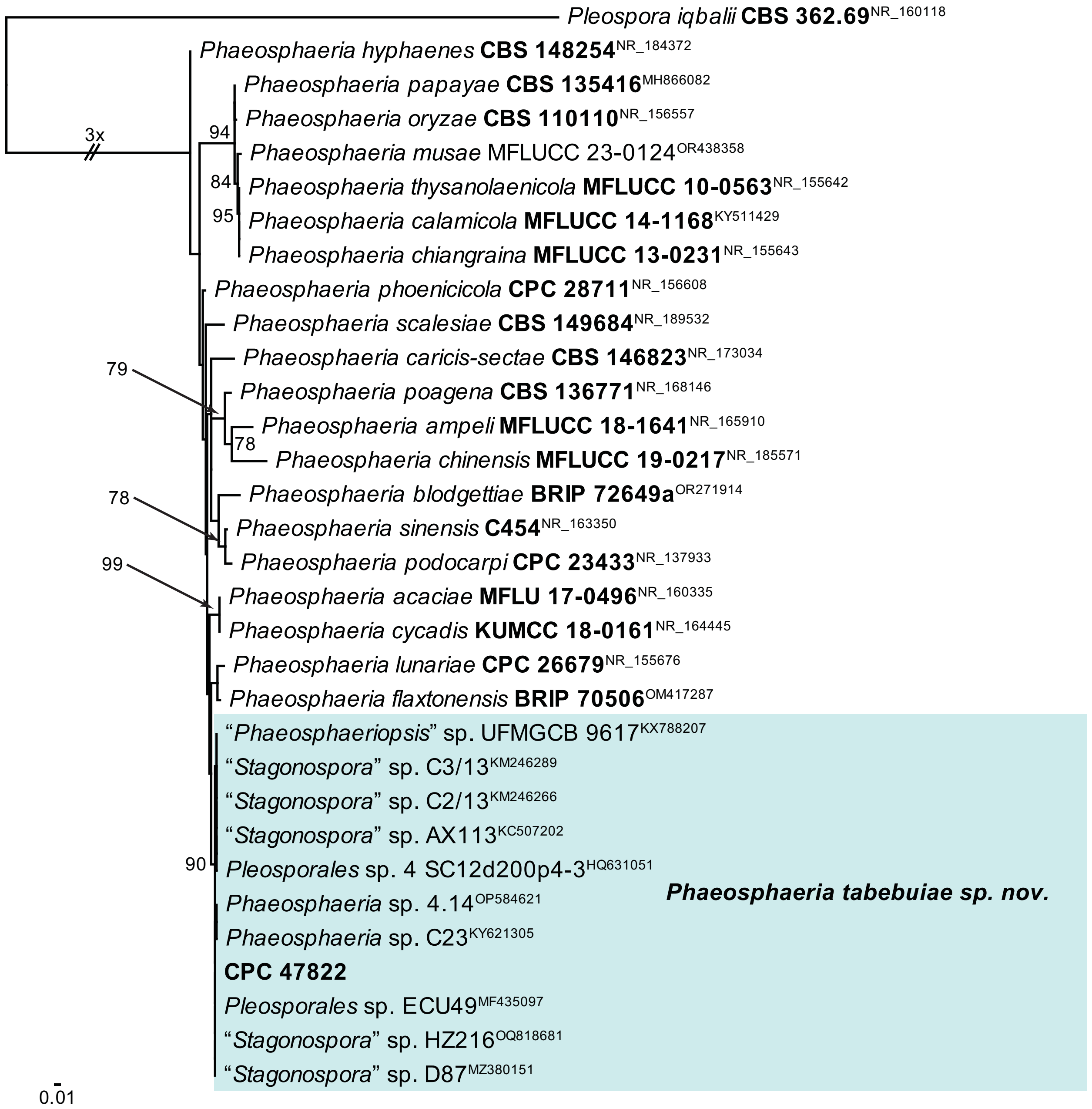
Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus: **Brazil**, Minas Gerais, Brumadinho, Inhotim Gardens, on leaf of *Tabebuia* sp. (*Bignoniaceae*), 21 Feb. 2024, *P.W. Crous*, HPC 4414 [**holotype** CBS H-25505; culture ex-type CPC 47822 = CBS 152330; ITS, LSU, *rpb2* and *tef1* (second part) sequences GenBank PQ498968, PQ499017, PQ497739 and PQ497754].

Colour illustrations: Inhotim Gardens, Brazil. Asci with ascospores; conidia. Scale bars = 10 µm.

Notes: *Phaeosphaeria tabebuiae* was isolated from leaves of *Tabebuia* sp. in Brazil. Phylogenetically it showed similarities with *P. lunariae* [conidia 1(–3)-septate, (9–)12–13(–15) × (2–)2.5–3(–3.5) µm; Hernández-Restrepo *et al*. 2016], *P. acaciae* [conidia 1(–3)-septate, (9–)12–13(–15) × (2–)2.5–3(–3.5) µm; Hyde *et al.* 2017], and *P. phoenicicola* [conidia 1–3-septate, (8–)12–14(–16) × (2–)2.5(–3) *µ*m; Crous *et al.* 2016a], from which it is morpophologically distinct.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phaeosphaeria* sp. [strain 4.14, GenBank OP584621.1; Identities = 510/511 (99 %), no gaps], *Phaeosphaeria lunariae* [strain Ct-LC17, GenBank MK619277.1; Identities = 452/460 (98 %), one gap (0 %)], *Phaeosphaeria acaciae* [strain KUMCC 20-0214, GenBank MW078431.1; Identities = 503/512 (98 %), one gap (0 %)], and *Phaeosphaeria phoenicicola* [strain CPC 28711, GenBank NR_156608.1; Identities = 502/512 (98 %), one gap (0 %)]. Closest hits using the **LSU** sequence are *Phaeosphaeria lunariae* [strain CPC 26679, GenBank KX306791.1; Identities = 800/800 (100 %), no gaps], *Phaeosphaeria acaciae* [voucher MFLU 17-0496, GenBank NG_069453.1; Identities = X800/800 (100 %), no gaps], and *Phaeosphaeria cycadis* [strain KUMCC 18-0161, GenBank NG_070078.1; Identities = 800/800 (100 %), no gaps]. Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Phaeosphaeria acaciae* [strain KUMCC 20-0214, GenBank MW192765.1; Identities = 834/867 (96 %), no gaps], *Phaeosphaeria caricis-sectae* [strain CPC 38771, GenBank MZ078195.1; Identities = 798/867 (92 %), no gaps], and *Phaeosphaeria oryzae* [strain CBS 110110, GenBank ON419520.1; Identities = 796/867 (92 %), no gaps]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Phaeosphaeria cycadis* [strain KUMCC 18-0161, GenBank MK359069.1; Identities = 845/858 (98 %), no gaps], *Phaeosphaeria musae* [strain MFLUCC 11-0133, GenBank KM434296.1; Identities = 840/858 (98 %), no gaps], and *Phaeosphaeria chinensis* [strain MFLUCC 18-1552, GenBank MK360072.1; Identities = 840/858 (98 %), no gaps].



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Phaeosphaeria* ITS nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Pleospora iqbalii* (CBS 362.69; GenBank NR_160118) and the novelty described here is highlighted with a coloured block and **bold** font. The root branch was shortened to facilitate layout. Alignment statistics: 32 strains including the outgroup; 501 characters including alignment gaps analysed: 167 distinct patterns, 58 parsimony-informative, 95 singleton sites, 348 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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Acrocalymma philodendri

Fungal Planet 1736 MycoBank MB 856114

Acrocalymma philodendri Crous, *sp. nov.*

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

Classification: *Acrocalymmaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*.

Conidiomata pycnidial, brown, globose, solitary, 200–250 µm diam, with central ostiole; wall of 3–6 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining inner cavity, hyaline, smooth, ampulliform to subcylindrical, 5–7 × 3–4 µm, proliferating percurrently at apex. *Conidia* solitary, hyaline, smooth, guttulate, aseptate, subcylindrical, apex subobtuse, base tapered, truncate hilum, apex with mucoid cap, 2 µm tall, 2–3 µm wide, (10–)11–12(–13) × 3(–3.5) µm.

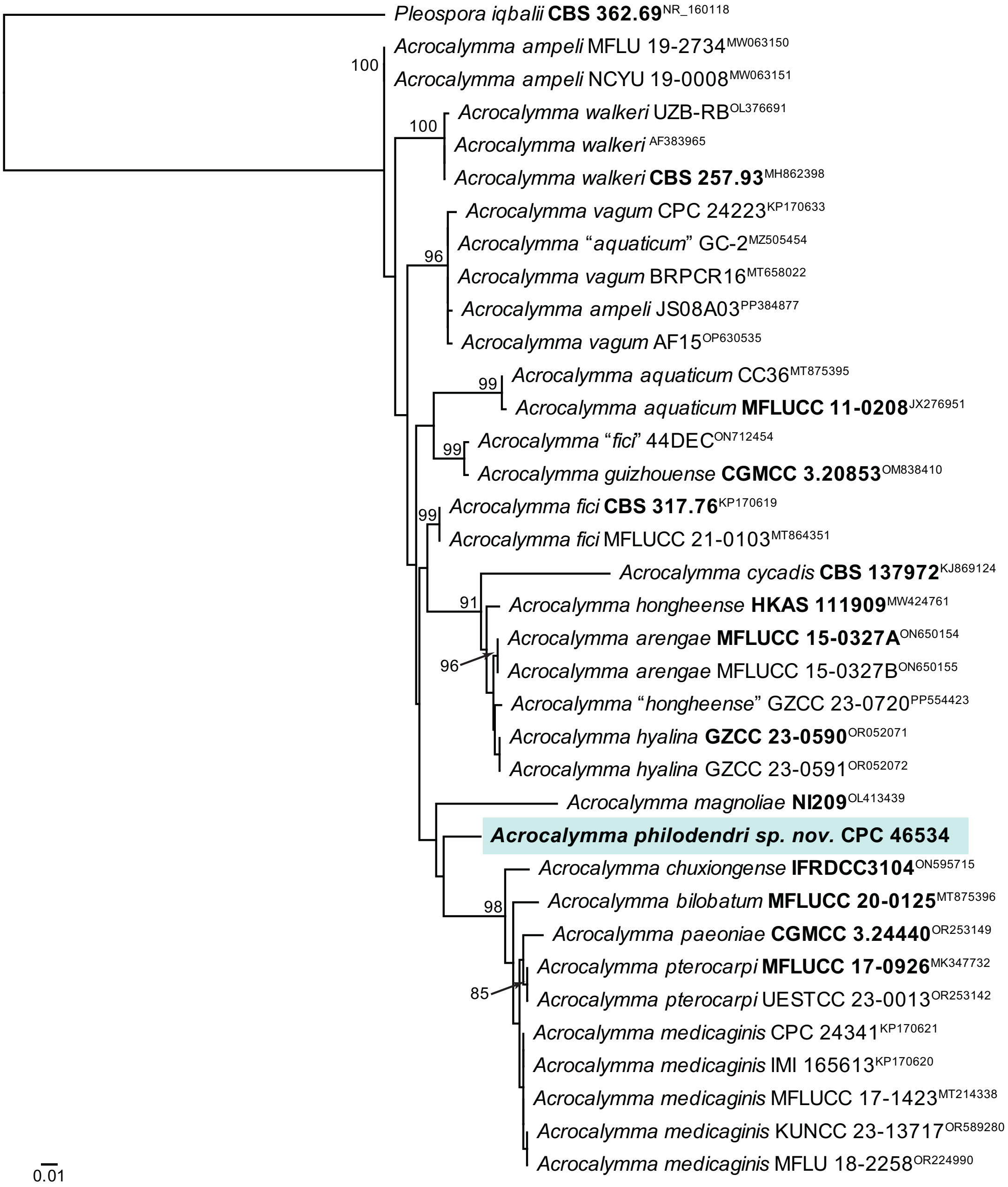
Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus: **Panama**, Colon Province, Soberania National Park, Pipeline Road, close to Gamboa, on leaf spots of *Philodendron* sp. (*Araceae*), 6 Aug. 2023, *P.W. Crous*, HPC 4223 [**holotype** CBS H-25506; culture ex-type CPC 46534 = CBS 152331; ITS, LSU, *rpb2* and *tef1* (second part) sequences GenBank PQ498969, PQ499018, PQ497740 and PQ497755].

Notes: *Acrocalymma* and similar coelomycetous genera with hyaline conidia and mucoid caps were treated by Trakunyingcharoen *et al.* (2014), and *Acrocalymma* shown to represent a new family, *Acrocalymmaceae*. Of all the species presently known in the genus, *A. philodendri* is phylogenetically distinct, being closely related to *A. magnoliae* (conidia 22–30 × 5–7 µm, 2–3-septate; de Silva *et al*. 2022].

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Rhizopycnis vagum* [strain agrFF1761, GenBank HE585021.1; Identities = 816/846 (96 %), 12 gaps (1 %)], *Acrocalymma arengae* [as *Acrocalymma* sp. SK-2022a; strain MFLUCC 15-0327B, GenBank ON650155.1; Identities = 828/891 (93 %), 16 gaps (1 %)], and *Acrocalymma hongheense* [strain GZCC 23-0720, GenBank PP554423.1; Identities = 797/864 (92 %), 15 gaps (1 %)]. Closest hits using the **LSU** sequence are *Acrocalymma medicaginis* [strain CPC 24342, GenBank KP170715.1; Identities = 796/800 (99 %), no gaps], *Acrocalymma walkeri* [strain NI214, GenBank OK655821.1; Identities = 795/800 (99 %), no gaps], and *Acrocalymma paeoniae* [strain CGMCC 3.24440, GenBank OR253308.1; Identities = 795/800 (99 %), no gaps]. Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Acrocalymma arengae* [strain MFLUCC 15-0327B, GenBank ON734015.1; Identities = 740/852 (87 %), four gaps (0 %)], *Acrocalymma walkeri* [strain UTHSC DI16-195, GenBank LT796992.1; Identities = 728/850 (86 %), no gaps], and *Neodidymelliopsis negundinis* [strain JZB380020, GenBank MH628157.1; Identities = 674/859 (78 %), 17 gaps (1 %)]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Acrocalymma medicaginis* [strain MFLUCC 17-1423, GenBank MT235797.1; Identities = 896/913 (98 %), no gaps], *Acrocalymma chuxiongense* [strain IFRDCC 3104, GenBank ON604684.1; Identities = 913/943 (97 %), no gaps], and *Acrocalymma pterocarpi* [strain KUMCC 21-0675, GenBank OR613417.1; Identities = 906/933 (97 %), no gaps].

Colour illustrations: Soberania National Park, Panama. Conidioma on pine needle agar; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Acrocalymma* ITS nucleotide alignment. Bootstrap support values from 1 000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Pleospora iqbalii* (CBS 362.69; GenBank NR_160118) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 36 strains including the outgroup; 503 characters including alignment gaps analysed: 189 distinct patterns, 76 parsimony-informative, 79 singleton sites, 348 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27275988).

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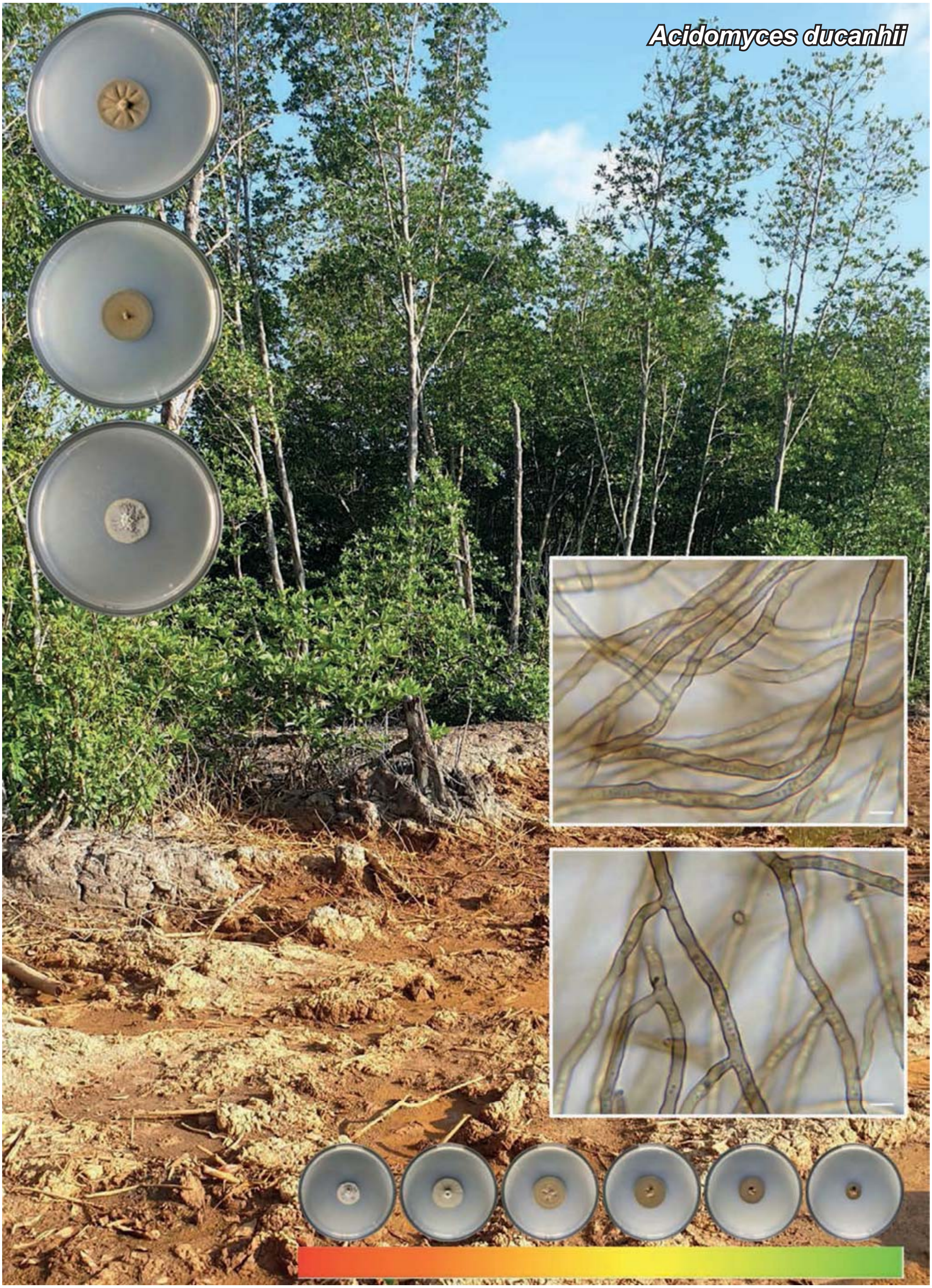

Acidomyces ducanhii

Fungal Planet 1737 MycoBank MB 855291

Acidomyces ducanhii V.N. Thanh, N.T. Thuy, L.T.M. Hanh, J. Larsbrink & L. Olsson, ***sp. nov.***

Etymology: Name given in memory of our colleague, Dr Nguyen Duc Anh.

Classification: *Teratosphaeriaceae*, *Mycosphaerellales*, *Dothideomycetes*.

Sexual structures not observed. *Hyphae* pale to dark brown, smooth, with regular constriction, 1.7–3.5 µm diam, branched, septate; *aerial mycelia* often forming clusters.

Culture characteristics: Growth restricted, slow, optimal at pH 2.0–3.0. On PDA, colonies raised, rugose, entire, velvet, chestnut brown, reverse black, reaching 20–24 mm diam after 3 wk at 29 °C. On MEA colonies flat, velvet, entire, chestnut brown, 19–25 mm diam. On MEA containing 1 % sulfuric acid, colonies greenish grey to dark grey, with moderate aerial mycelium, diam 17–21 mm.

Habit, habitat and distribution: *Acidomyces ducanhii* is an acidophilic fungus, obtained by cultivation of living and dead plant materials collected from acidic environments using a selective medium containing 1 % sulfuric acid.

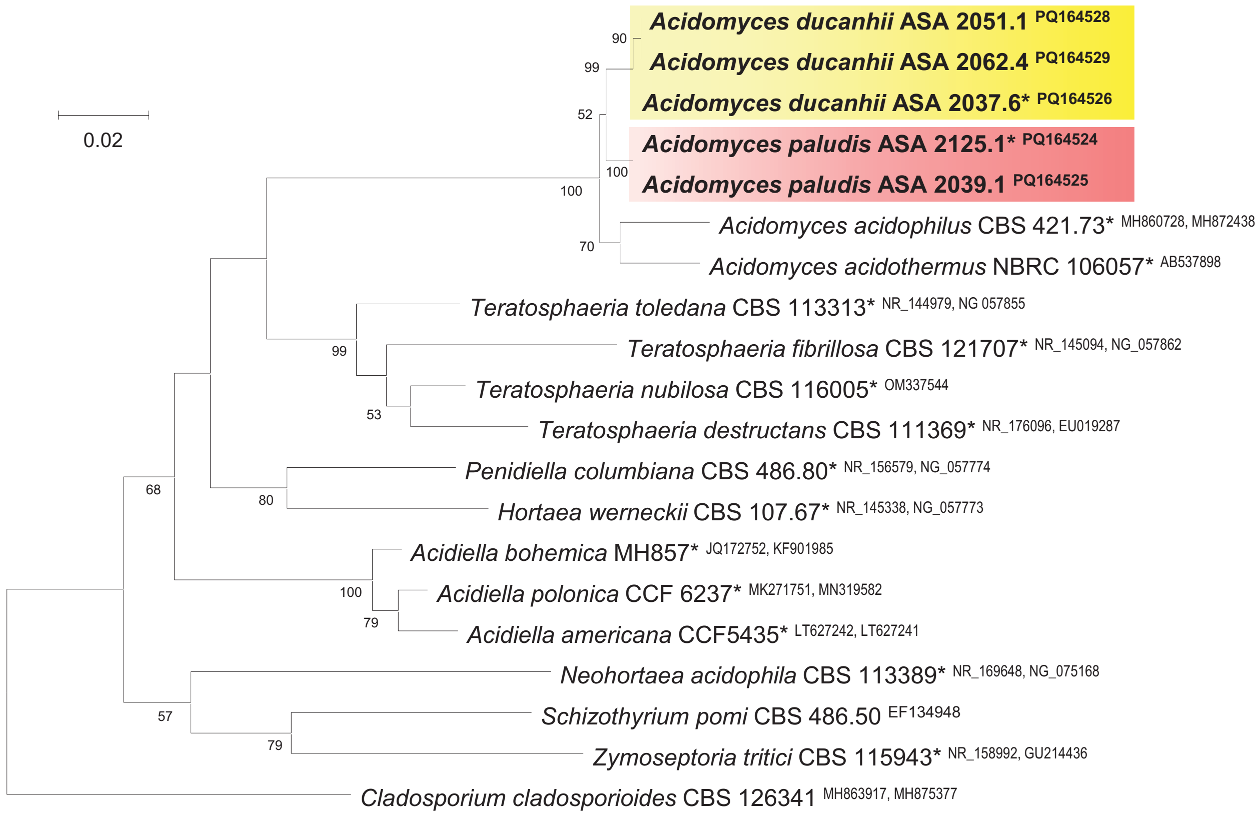
Typus: **Vietnam**, Dong Nai, 10°38’N 106°58’E, 1 m a.s.l., flowers of *Aglaia* collected near a disrupted mangrove (*Rhizophora*) forest by selective isolation on MEA containing 1 % sulfuric acid, Jan. 2024, *V.N. Thanh* (**holotype** and culture ex-type permanently preserved in a metabolically inactive state ASA 2037.6; ITS-LSU, *tef1*, *rpb2*, *tub2*, and *cmdA* sequences GenBank PQ164526, PQ186862, PQ186866, PQ186869, and PQ186873).

Additional material examined: **Vietnam**, Dong Nai, 10°38’N 106°58’E, 1 m a.s.l., decaying fruit of *Rhizophora* at a disrupted mangrove forest by selective isolation on MEA containing 1 % sulfuric acid from, Jan. 2024, *V.N. Thanh*, lyophilised culture ASA 2062.4; ITS and LSU, *tef1*, *rpb2*, *tub2*, and *cmdA* sequences GenBank PQ164529, PQ186864, PQ186868, PQ186872, and PQ186874.

Colour illustrations: Vietnam, Dong Nai, part of the *Rhizophora* mangrove forest affected by road construction activities causing ground acidification (photo credit V.N. Thanh). Larger plates, from top: colony on PDA, MEA, and MEA containing 1 % sulfuric acid after 21 d at 29 °C; Bottom plates, from left: colonies on MEA in buffered media with pH 1, 2, 3, 4, 5, 6 after 21 d; Colour bar illustrates pH gradient from 1 to 6. All plates = 90 mm diam, scale bar = 5 µm.

Notes: In a study on the diversity of acidotolerant and acidophilic fungi in Vietnam, from plant residues and tissues, 38 strains of *Acidomyces* were obtained using selective isolation on MEA containing 1 % sulfuric acid. Identification by ITS sequencing indicated that 23 strains belong to *A. acidothermus* and five strains to *A. acidophilus*. Two novel *Acidomyces* species were found and assigned as *A. paludis* (two strains; described elsewhere in this study) and *A. ducanhii* (eight strains). *Acidomyces ducanhii* differs from *A. paludis* by 12/513 (2 %) positions in ITS, 4/1 322 (0 %) in LSU, 39/980 (4 %) in *tef1*, and 54/1 062 (5 %) in *rpb2*. Both species are acidophilic but differ from each other in the level of acid tolerance, micromorphology, and culture morphology. *Acidomyces ducanhii* has the slowest growth rate and least level of acid tolerance among *Acidomyces* spp.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Acidomyces acidophilus* [strain CBS 125382, GenBank MH863600.1; Identities = 482/509 (95 %), three gaps (0 %)], and *Teratosphaeria acidotherma* (= *Acidomyces acidothermus*) [strain NBRC 106057T, GenBank AB537898.1; Identities = 483/511 (95 %), six gaps (1 %)]. Closest hits using the LSU sequence are *Teratosphaeria nubilosa* [strain CBS 116005, GenBank NG_057854.1; Identities = 1 276/1 330 (96 %) four gaps (0 %)], *Teratosphaeria stellenboschiana* [strain CPC 10886, GenBank EU019295.2; Identities = 1 275/1 330 (96 %), four gaps (0 %)]. The closest hit using the *tef1* sequence is *Baudoinia panamericana* [strain UAMH 10762, GenBank XM_007673622.1; Identities = 861/978 (88 %), two gaps (0 %)]. The closest hit using the *rpb2* sequence is *Schizothyrium pomi* [strain CBS 486.50, GenBank MF951735.1; Identities = 327/418 (78 %), two gaps (0 %)]. The closest hit using the *tub2* sequence is a distant match with a *Neofusicoccum* sp. [strain JFRL 03-778, GenBank OQ207635.1; Identities = 229/276 (83 %), 12 gaps (4 %)]. Closest hit using the *cmdA* sequence is *Queenslandipenidiella californica* [strain CPC 45493, GenBank PP780602.1; Identities = 277/297 (93 %), no gaps].



Phylogenetic tree based on a maximum likelihood analysis of a concatenated alignment (ITS and LSU) of *Acidomyces* spp. and related species of *Teratosphaeriaceae*. The maximum likelihood analysis was performed using Tamura-Nei model (Tamura & Nei 1993) in MEGA v. 11 (Tamura *et al*. 2021). Bootstrap support values greater than 50 % are given at the nodes. GenBank accession numbers are indicated (superscript ITS, LSU). Novel taxa are indicated in **bold**, with this species highlighted in yellow and *Acidomyces paludis* (FP 1738, described elsewhere in this publication) highlighted in red. Ex-type strains indicated with asterisks (*). The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27210066).

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Acidomyces paludis

Fungal Planet 1738

MycoBank MB 855257

Acidomyces paludis V.N. Thanh, N.T. Thuy, L.T.M. Hanh, J. Larsbrink & L. Olsson, ***sp. nov.***

Etymology: Name refers to the habitat where the fungus was found (disrupted wetlands, mangrove forest).

Classification: *Teratosphaeriaceae*, *Mycosphaerellales*, *Dothideomycetes*.

Sexual structures not observed. *Hyphae* pale brown to chestnut brown, varying in size, 1.7–4.5 µm diam, branched, septate with slight constrictions; *aerial mycelia* may be interconnected by slender tendril-like mycelia, often forming clusters or ring-like structures; *substrate mycelia* actively branch in agar containing 1 % sulfuric acid. *Arthroconidia* present but rare. *Chlamydospores* terminal, intercalary or sessile in old cultures, 5.5–9.2 × 5.8–12.5 µm.

Culture characteristics: Growth restricted, slow, optimal at pH below 2.5. On potato dextrose agar (PDA), colonies raised, rugose, velvet, chestnut brown, reverse black, reaching 26–33 mm diam after 3 wk at 29 °C. On malt extract agar (MEA) colonies flat, entire, grey, chestnut brown, 28–34 mm diam. On MEA containing 1 % sulfuric acid, colonies lighter in colour, with moderate aerial mycelium, grow faster, 41–43 mm diam.

Habit, habitat and distribution: *Acidomyces paludis* is an extreme acidophilic fungus, obtained by cultivation of plant residues collected from acidic environments using a selective medium containing 1 % sulfuric acid.

Typus: **Vietnam**, Hau Giang, 9°44’N 105°41’E, 2 m a.s.l., dead bark of *Acacia* on dried mud by selective isolation on MEA containing 1 % sulfuric acid, Jan. 2024, *V.N. Thanh* (**holotype** and culture ex-type permanently preserved in a metabolically inactive state ASA 2125.1; ITS-LSU, *tef1*, and *rpb2* sequences GenBank PQ164524, PQ186860, and PQ186865).

Colour illustrations: Vietnam, Dong Nai, *Rhizophora* in the mangrove forest next to a road construction (photo credit V.N. Thanh). Larger plates, from top: colony on PDA, MEA, and MEA containing 1 % sulfuric acid after 21 d at 29 °C; Bottom plates, from left: colonies on MEA in buffered media with pH 1, 2, 3, 4, 5, 6 after 21 d; Colour bar illustrates pH gradient from 1 to 6. All plates = 90 mm diam, scale bar = 5 µm.

Additional material examined: **Vietnam**, Dong Nai, 10°38’N 106°58’E, 1 m a.s.l., insect frass on *Rhizophora* at a disrupted mangrove forest by selective isolation on MEA containing 1 % sulfuric acid, Jan. 2024, *V.N. Thanh*, lyophilised culture ASA 2039.1; ITS-LSU, and *tef1* sequences GenBank PQ164525 and PQ186861.

Notes: Using MEA containing 1 % sulfuric acid as a selective medium, isolations from plant residues collected in Vietnam resulted in 38 strains of *Acidomyces* being obtained. The ITS sequences indicated that 23 strains belong to *A. acidothermus,* and five strains to *A. acidophilus*. The remaining ten strains represent two novel species and are assigned as *A. paludis* (two strains) and *A. ducanhii* (eight strains; described elsewhere in this study). The two species differ from each other by 12/513 (2 %) positions in ITS, 4/1 322 (0 %) in LSU, 39/980 (4 %) in *tef1*, and 54/1 062 (5 %) in *rpb2*. Both are acidophilic but vary in the level of acid tolerance, micromorphology, and culture morphology. *Acidomyces ducanhii* has the slowest growth rate and least level of acid tolerance among *Acidomyces* spp.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Teratosphaeria acidotherma* (=*Acidomyces acidothermus*) [strain NBRC 106057^{T}, GenBank AB537898.1; Identities = 484/510 (95 %), four gaps (0 %)], *Acidomyces acidophilus* [strain CBS 272.74, GenBank MH860851.1; Identities = 488/515 (95 %), three gaps (0 %)]. Closest hits using the LSU sequence are *Catenulostroma chromoblastomycosum* [strain CBS 597.97, GenBank EU019251.2; Identities = 1 289/1 343 (96 %), two gaps (0 %)], *Teratosphaeria nubilosa* [strain CBS 116005^{T}, GenBank NG_057854.1; Identities = 1 290/1 345 (96 %), four gaps (0 %)]. The closest hit using the *tef1* sequence is *Neohortaea acidophila* [strain CBS 113389^{T}, GenBank XM_033732699.1; Identities = 862/978 (88 %), five gaps (0 %)]. The closest hit using the *rpb2* sequence is *Fusoidiella anethi* [strain CBS 117584, GenBank MF951500.1; Identities = 507/673 (75 %), 16 gaps (2 %)].

For phylogenetic tree, see *Acidomyces ducanhii* (FP 1737).

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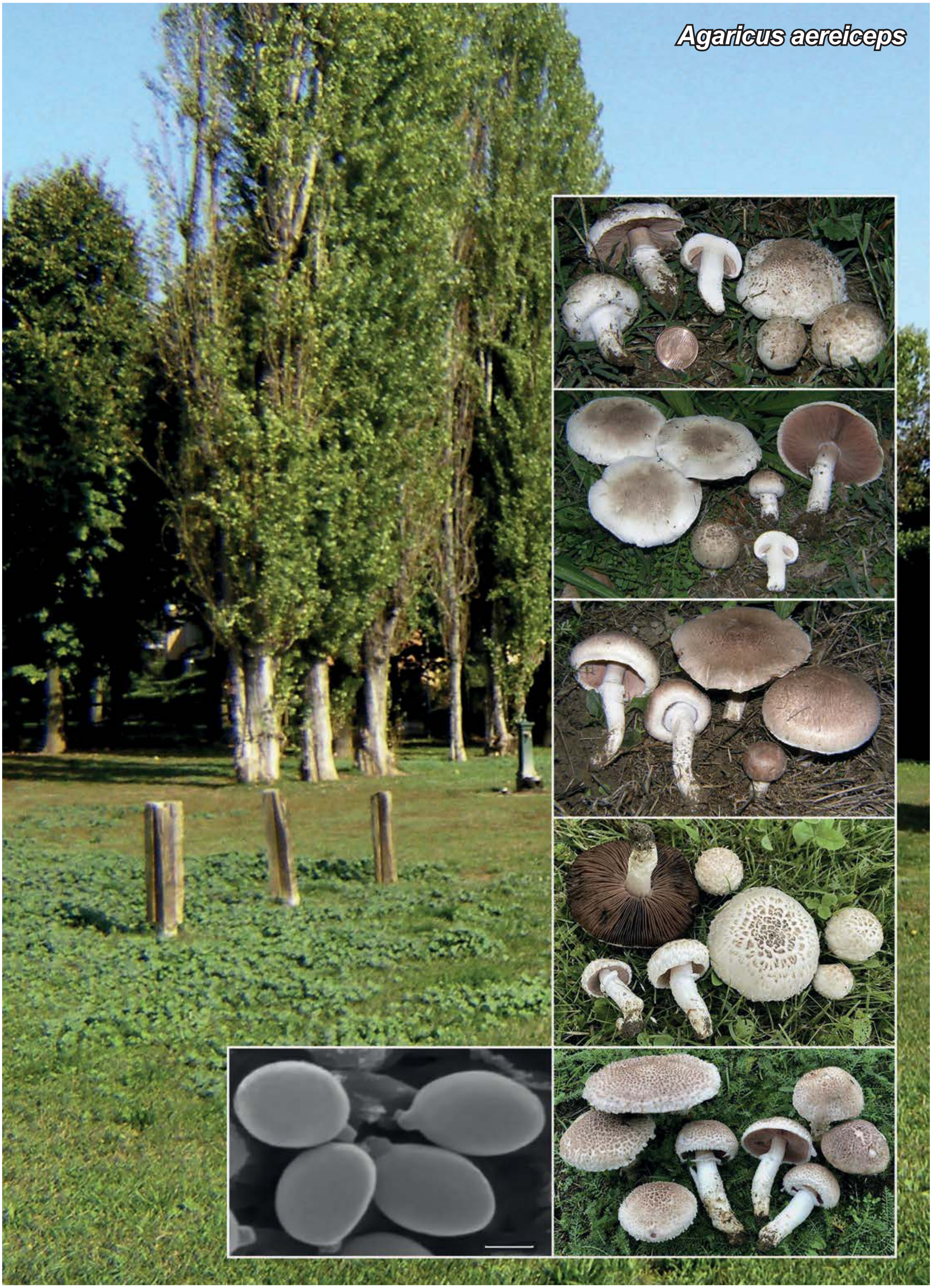

Agaricus aereiceps

Fungal Planet 1739

MycoBank MB 856128

Agaricus aereiceps Cappelli, L.A. Parra, Lucchini & Linda J. Chen, ***sp. nov.***

Etymology: Named for the bronze colour of the surface of the pileus. (Latin) *aereum* bronze colour and *ceps* head, pileus.

Classification: *Agaricaceae*, *Agaricales*, *Agaricomycetes*.

Pileus 25–85 mm diam, at first globose, then hemispherical to rarely truncate-conical, finally planoconvex. Surface completely radially silky fibrillose of a bronze colour, or covered with bronze minute punctate to triangular, sometimes upturned, concentrically arranged scales on a white or cream-white background, but also frequently with a more or less broad white margin. Margin thin, exceeding the lamellae up to 2 mm, fibrillose, finely denticulate or with small irregular appendiculate remnants of the annulus. *Lamellae* free, up to 8 mm broad, crowded, with intercalated lamellulae, first pinkish, then bright pink, later reddish brown and finally dark brown almost black, with a concolourous edge. *Stipe* 35–75 × 7–14 mm, central, cylindrical or, more often fusiform, solid, with an annulus generally in its upper half, above the annulus pale pink, smooth or slightly fibrillose, below the annulus white, fibrillose to slightly scaly, sometimes with some transverse linear bronze-coloured bands near the base. *Annulus* superous, up to 5 mm wide, white, simple, thin, narrow, fragile, with fimbriated margin. Context white on cutting, remaining unchanged with time. *Odour* indistinct, weak or fungoid. *Basidiospores* (5.7–)6.1–7.8 × 4.3–5.4 µm; 6.8 × 4.9 µm av., Q = (1.21–)1.28–1.50(–1.56); 1.38 av., ellipsoid, brown, thick-walled, some with a rudimentary apical pore. *Basidia* 21–29(–36) × 6–9 µm, mostly 4-spored, clavate or slightly truncate at the apex, with sterigmata up to 3 µm long. *Cheilocystidia* absent. *Pleurocystidia* absent. *Annulus lower surface* composed of cylindrical, hyaline, smooth, unpigmented, septate hyphae, 4–23(–30) µm wide, the broader the more constricted at septa. *Pileipellis* a cutis composed of cylindrical hyaline, smooth, unpigmented or with reddish brown granular pigment, septate hyphae, 4–28 µm wide, the broader the more constricted at septa, with terminal elements with progressively attenuated rounded apex up to 11 µm wide. *Clamp connections* absent.

Macrochemical reactions: Schäffer’s and KOH (30 %) reactions negative on pileus surface.

Habit, habitat and distribution: Solitary or in groups, usually up to 10 basidiomata, in grassy places of parks, gardens, forest clearings and roadsides. Currently know from Italy in the Lombard plain north of Milan, and Switzerland in the Lepontine Alps.

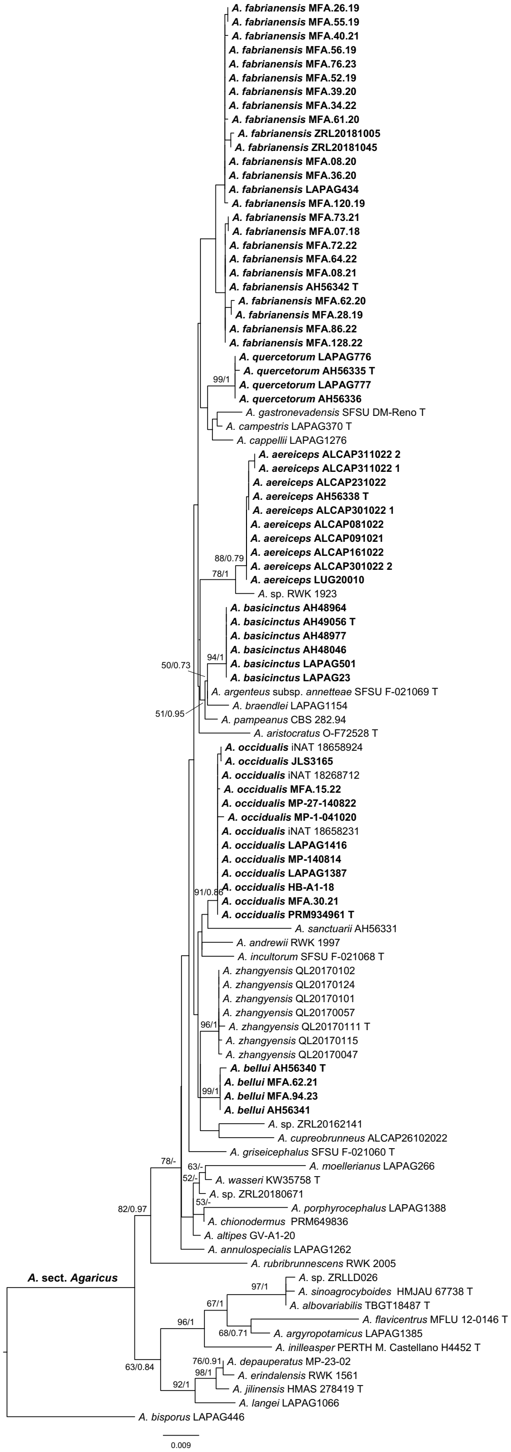
Colour illustrations: Dog park in Via Buraschi, Saronno, Varese, Italy, holotype site. From top to bottom: Holotype, ALCAP161022, ALCAP301022-2, LUG20010 and ALCAP231022; scanning electron micrograph of the spores from the holotype. Scale bar = 2 µm [Photo credit A. Cappelli, G. Lucchini, M. Cartabia & G. Moreno (spores)].

Typus: **Italy**, Varese, Saronno, dog park in via Buraschi, N45°38’08.07’’ W9°03’04.25’’, 220 m a.s.l., 19 Oct. 2022, *A. Cappelli* (**holotype** AH56338, ITS, LSU and *TEF* sequences GenBank PP776067, PP809863 and PP789271; **isotypes** ALCAP191022 in A. Cappelli private fungarium, ALCAP, and LAPAG1405 in L.A. Parra private fungarium, LAPAG).

Additional materials examined: **Italy**, Monza e della Brianza (MB), Seveso, Villa Dho park, N45°38’31.05’’ W9°07’59.58’’, 230 m a.s.l., 30 Oct. 2022, *A. Cappelli*, ALCAP 301022-1 (ITS sequence GenBank PP776069); Villa Dho park, N45°38’29.27’’ W9°08’00.57’’, 228 m a.s.l., 30 Oct. 2022, *A. Cappelli*, ALCAP301022-2 (ITS sequence GenBank PP776070); Varese (VA), Bolladello di Cairate, Via Montello, N45°41’29.82’’ W8°50’40.95’’, 283 m a.s.l., 23 Oct. 2022, *M. Cartabia* & *N. Gambirasio*, ALCAP231022 (ITS, LSU and *TEF* sequences GenBank PP776071, PP809864 and PP789272); Varese (VA), Saronno, Via Radice, N45°38’25.87’’ W9°02’59.42’’, 224 m a.s.l., 9 Oct. 2021, *A. Cappelli* ALCAP 091021(ITS sequence GenBank PP776063); Via Don Mazzolari, N45°37’55.56’’ W9°02’53.36’’, 218 m a.s.l., 8 Oct. 2022, *A. Cappelli*, ALCAP 081022 (ITS, LSU and *TEF* sequences GenBank PP776064, PP809862 and PP789273); Via Radice, N45°38’26.40’’ W9°02’56.47’’, 224 m a.s.l., 16 Oct. 2022, *A. Cappelli*, AH56339 (duplicate in ALCAP 161022) (ITS sequence GenBank PP776068); Parco del Lura, N45°38’25.14’’ W9°02’27.64’’, 218 m a.s.l., 31 Oct. 2022, *A. Cappelli*, ALCAP 311022-1 (ITS sequence GenBank PP776065); Parco del Lura, N45°38’25.17’’ W9°02’28.02’’, 218 m a.s.l., 31 Oct. 2022, *A. Cappelli*, ALCAP 311022-2 (ITS sequence GenBank PP776066). All with duplicates in L.A. Parra private fungarium (LAPAG). **Switzerland**, Canton Ticino, Lepontine Alps, Val Leventina, Faido, Via Balcengo, N46°28’44.49’’ W8°48’05.59’’, 720 m a.s.l., 27 Jun. 2022, *G. Lucchini*, LUG20010 (duplicate in LAPAG1407) (ITS sequence GenBank PP776072).

Notes: *Agaricus aereiceps* belongs to *Agaricus* sect. *Agaricus*. According to our phylogenetic analyses, *A. aereiceps* forms a strongly supported and well-defined clade. The ITS region of *Agaricus aereiceps* does not possess any species-specific markers in *Agaricus* sect. *Agaricus*. However, it shares an exclusive single nucleotide accct[C]tcgaa at position 245 in the alignment with one undescribed species RWK1923 (GenBank OP749431) from the USA. Morphologically, *A. aereiceps* can be distinguished from the remaining taxa in *Agaricus* sect. *Agaricus* in having a campestroid habit, a bronze colour of the pileus, an unchanging context and small spores. *Agaricus braendlei*, *A. cupreobrunneus*, *A. erindalensis* and *A. incultorum*, with campestroid habit, have or may have similar colours on the pileus, but all of these species have much larger spores (8.6 × 6.2 µm, 7.9 × 5.4 µm, 7.9 × 5.2 µm and 8.1 × 5.8 µm on average, respectively). In addition, *A. erindalensis* becomes reddish when bruised.

Supplementary material: doi: https://doi.org/10.6084/m9.figshare.26372614 (Two alignments, two tables and two trees).



Maximum likelihood (ML) tree of *Agaricus* sect. *Agaricus* based on ITS, LSU and *tef1-α* sequence data with *A. bisporus* (LAPAG446) used as outgroup. The maximum likelihood (ML) analysis was performed in RAxMLHPC2 v. 8.2.12 (Stamatakis 2014) as implemented on the Cipres portal (Miller *et al*. 2010), under a GTRGAMMA model with 1 000 rapid bootstrap (BS) replicates. Bayesian inference (BI) analysis was performed in MrBayes v. 3.1.2 (Ronquist & Huelsenbeck 2003). The bootstrap support values > 50 % and Bayesian posterior probabilities > 0.7 are indicated. New species are in **bold**. T = Type specimens. The alignment and trees are publicly available in figshare.com: (doi: org/10.6084/m9.figshare.26372614).

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Agaricus basicinctus
1 cm

Fungal Planet 1740 MycoBank MB 856129

Agaricus basicinctus L.A. Parra, G. Moreno & Linda J. Chen, ***sp. nov.***

Etymology: *basicinctus* (Latin) from *basis* (base) and *cinctus* (encircled, girdled) by the stem usually ornamented by a reddish brown girdle near the base.

Classification: *Agaricaceae*, *Agaricales*, *Agaricomycetes*.

Pileus 40–80 mm diam, at first globose, then hemispherical, finally plano-convex with a flat or sometimes shallowly depressed centre. Surface smooth, radially fibrillose or turning into more or less large, triangular, appressed, concentrically-arranged, scales, first white then becoming increasingly ochraceous, later increasingly darkening to red or brown with age, sometimes vinaceous brown from the beginning, on a whitish background. Margin thin, exceeding the lamellae up to 2 mm and often appendiculate by abundant denticulate annulus remnants. *Lamellae* free, up to 7 mm broad, crowded, with intercalated lamellulae, first pale pink, then bright pink, later progressively reddish brown, finally dark brown almost black with a concolourous edge in mature basidiomata. *Stipe* 2.5–4.5(–6.5) × 8–20 mm, central, solid, cylindrical almost always tapering downwards, with an annulus in its upper half, above the annulus white, smooth or sometimes slightly squamulose, below white, fibrillose, usually with a single vinaceous brown linear girdle towards the base. *Annulus* superous or intermediate, simple, thin and narrow, fragile, fibrillose to membranous, sometimes with a double margin, white, up to 4 mm broad. *Context* firm and solid, white when cut, unchanging. *Odour* usually absent or fungoid. *Basidiospores* (7.1–)7.7–10.8(–11.3) × (4.7–)5.7–7.2(–7.7) µm; 9.2 × 6.4 µm av., Q = 1.25–1.80(–1.83); 1.48 av., broadly ellipsoidal to elongate, brown, thick-walled, often with a rudimentary apical pore. *Basidia* 20–35 × 8–12 µm, mostly 4-spored, clavate or slightly truncate at the apex, with sterigmata up to 5 µm long. In LAPAG 23, cystidiform hyaline basidia 25–32 × 16–18 µm are also observed. *Cheilocystidia* absent. *Pleurocystidia* absent. *Annulus lower surface* composed of hyaline, smooth, unpigmented, septate hyphae, 4–17 µm wide, the broader the more constricted at septa, in the specimens, and terminal elements with tapering rounded apex up to 8 µm wide. *Pileipellis* a cutis composed of cylindrical, hyaline, smooth, unpigmented, septate hyphae, 4–13 µm wide, the broader the more constricted at septa, with abundant terminal elements with tapering rounded apex up to 9 µm wide. *Clamp connections* absent.

Colour illustrations: Basic meadow in Alcalá de Henares, University Campus, near the hangars, holotype site. Basidiomata in the collecting spot, from top to bottom: holotype, AH48964, LAPAG23, LAPAG150; scanning electron micrograph of the spores from the holotype. Scale bar = 5 µm [Photo credit G. Moreno & L.A. Parra & G. Moreno (spores)].

Macrochemical reactions: Schäffer's and KOH (30 %) reactions negative on pileus surface in dried specimens.

Habit, habitat and distribution: Gregarious in small groups or in fairy rings, in meadows, pastures and among leaf litter under *Pinus halepensis*. Known only from central Spain.

Typus: **Spain**, Madrid, Alcalá de Henares, University Campus, near the hangars, N40°30'25.6" W3°20'25.6", 600 m a.s.l., 18 Apr. 2018, *J.R. Carlavilla, J.A. Picado & G. Moreno* (**holotype** AH 49056, ITS, LSU and *TEF* sequences GenBank PP776085, PP809868 and PP779513; **isotype** LAPAG1412 in L.A. Parra private fungarium, LAPAG).

Additional materials examined: **Spain**, Madrid, Moncloa-Aravaca, Finca Bartolo, N40°28'28.5" W3°45'07.8" 600 m a.s.l., 15 Nov. 1994, *L.A. Parra*, LAPAG 23 (ITS sequence GenBank PP776086); Moncloa-Aravaca, Finca Bartolo, N40°28'28.5" W3°45'07.8" 600 m a.s.l., 6 Nov. 2005, *L.A. Parra*, LAPAG 501 (ITS and *TEF* sequences GenBank PP776087 and PP779516); Alcalá de Henares, University Campus, Biology building parking, N40°30'16.0" W3°20'13.8", 600 m a.s.l., 19 Apr. 2016, *G. Moreno*, AH 48046 (ITS, LSU and *TEF* sequences GenBank PP776082, PP809865 and PP779514); Alcalá de Henares, University Campus, between Science Faculty and RENFE station, N 40°30'18.8"; W3°20'11.8", 600 m a.s.l., 15 Mar. 2018, *J.A. Picado, J.R. Carlavilla, G. Moreno & Á. López-Villalba*, AH 48977 (ITS, LSU and *TEF* sequences GenBank PP776084, PP809867 and PP779512); Alcalá de Henares, University Campus, between the Science Faculty and the hangars, N 40°30'23.07"; W3°20'26.97", 600 m a.s.l., 17 Apr. 2018, *J.A. Picado*, AH 48964 (ITS, LSU and *TEF* sequences GenBank PP776083, PP809866 and PP779515). All with duplicates in L.A. Parra private fungarium (LAPAG).

Notes: *Agaricus basicinctus* belongs to *Agaricus* sect. *Agaricus*. According to our phylogenetic analyses, *A. basicinctus* forms a strongly supported and well-defined clade. The ITS region of *Agaricus basicinctus* possesses one species-specific nucleotide acact[A]gcga- at position 605 in the alignment in *Agaricus* sect. *Agaricus*. Morphologically, specimens of *A. basicinctus* can be distinguished from the remaining taxa in *Agaricus* sect. *Agaricus* in having usually a single vinaceous brown linear girdle towards the base, unchanging context and stipe surface and spores 9.2 × 6.4 µm on average, and Q coefficient 1.40 on average. Other species of *Agaricus* sect. *Agaricus* which can have dark coloured girdles at the stipe base are *A. braendlei*, *A. cupreobrunneus*, *Agaricus erindalensis* and *A. fabrianensis*. In fact, LAPAG 23 was previously published as *A. cupreobrunneus* in Parra (2008). They differ in having smaller spores (8.6 × 6.2 µm, 7.9 × 5.4 µm, 7.9 × 5.2 µm and 7.1 × 5.1 µm on average, respectively). In addition, *A. fabrianensis* possesses a reddish discolouration on the surface, and a yellow discolouration in the context, at the stipe base, and *Agaricus erindalensis* discolours red when bruised. *Agaricus braendlei* is morphologically (macro- and microscopically) very similar and very difficult to distinguish unequivocally from *A. basicinctus*. Molecularly, it is also very similar to *A. braendlei*, differing only in four positions in the ITS sequence (acttt**A**ttg/rtg, acact**A**gcgag, and gctct**- -** gtgtt, instead G, G and CT respectively in *A. braendlei*). However, both species are easily distinguished by ten differences in their *TEF1-α* sequences (gccga**T**tgtgc, ccaat**T**a(t/w)aat, ttcat**T**aagaa, agtcc**G**ccaag, aagta**G**gtgtt, tccca**C**agaca, ccaat**T**taag(g/r), aag(g/r)t**T**ctcaa, tgtcg**C**taagg, gctat**C**g(a/m)cgc, instead C, C, C, A, A, G, C, C, T and T respectively in *A. braendlei*).

For phylogenetic tree, see *Agaricus aereiceps* (FP 1739).

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Agaricus bellui

Fungal Planet 1741 MycoBank MB 856130

Agaricus bellui Faraoni, L.A. Parra & Linda J. Chen, ***sp. nov.***

Etymology: The specific Latin epithet *bellui* honours our good friend, and excellent Italian mycologist, Francesco Bellù, who passed away in 2022.

Classification: *Agaricaceae*, *Agaricales*, *Agaricomycetes*.

Pileus 47–114 mm diam, at first subglobose, then from convex to truncated-conical, finally plano-convex with slightly applanate centre. Surface fibrillose-squamulose with small appressed, or coarser and sparser, sometimes upturned scales, initially whitish discolouring yellowish to dark ochraceous when bruised or with age. Margin thick, exceeding the lamellae up to 2 mm, fibrillose irregularly appendiculate by annulus remnants. *Lamellae* free, up to 9 mm broad, crowded, with intercalated lamellulae, first bright pink, then dark brown almost black. *Stipe* 45–80 × 17–30 mm, central, cylindrical or tapering downwards, solid and firm, with an annulus in its upper half, above the annulus whitish, smooth, below white, slightly yellowish ochraceous at the base when handled, smooth, sometimes near the lower surface of the annulus with a fragile and thin woolly whitish-ochraceous bracelet. *Annulus* superous or intermediate, up to 10 mm wide but usually thick and narrow, membranous, double with a lacerated denticulated margin, upper side smooth and white, underside fibrillose or fibrillose-squamose and white. *Context* white when cut, soon discolouring yellow in the lower part of the stipe, later ochraceous. *Odour* absent to slightly anise-like at the stipe base context. *Basidiospores* (6.6–)7.4–10.1(–10.8) × (4.7–)5.2–6.8(–7.8) µm; 8.1 × 5.7 µm av., Q = 1.20–1.74; 1.45 av., broadly ellipsoidal to elongate, brown, thick-walled, without a rudimentary apical pore. In MFA.94.23, some large-sized rare spores of large dimensions, *e.g.* up to 14.5 × 7.8 µm, can be observed. *Basidia* 11–36(–39) × 5–13(–18) µm, mostly 4-spored, clavate or slightly truncated at the apex, with sterigmata up to 5.5 µm long. *Cheilocystidia* absent. *Pleurocystidia* absent. *Annulus lower surface* composed of hyaline, smooth, unpigmented, septate hyphae, 3–38 µm wide, the broader the more constricted at septa. *Pileipellis* a cutis composed of cylindrical, hyaline, smooth, unpigmented, septate hyphae, 3–24 µm wide the broader the more constricted at septa, with terminal elements with rounded apex up to 12 µm wide. *Clamp connections* absent.

Colour illustrations: Rocky sloping grasslands of Cupi, Visso, Monti Sibillini National Park, Italy, holotype site. Basidiomata in the collecting spot; close-up of the cog-wheel on the lower margin of the annulus; close-up of the stipe, the annulus and the solid context of the stipe; yellow discolouration at the stipe base; scanning electron micrograph of the spores. All from the holotype. Scale bar = 5 µm [Photo credit M. Faraoni & G. Moreno (spores)].

Macrochemical reactions: Schäffer's and KOH (30 %) reactions negative on pileus surface.

Habit, habitat and distribution: Gregarious in small groups or in fairy rings in meadows and pastures, including rocky and sloping grasslands. Known only from central Italy.

Typus: **Italy**, Marche, Macerata, Monti Sibillini National Park, Visso, Cupi, N42°59'55.9" E13°07'46.5", 1 337 m a.s.l., 6 Oct. 2020, *M. Faraoni* (**holotype** AH56340, ITS and *TEF* sequences GenBank PP776100 and PP779519; **isotypes** MFA.42.20 in Mauro Faraoni private fungarium MFA and LAPAG1408 in L.A. Parra private fungarium, LAPAG).

Additional materials examined: **Italy**, Marche, Macerata, Sefro, Monte Vermenone N43°08'48.7" E12°55'11.3", 1 320 m a.s.l., 17 Oct. 2020, *M. Faraoni, S. Morettini* & *G. Spinaci*, AH56341 (duplicate in MFA.66.20) (ITS, LSU and *TEF* sequences GenBank PP776098, PP809869 and PP779517); Macerata, Fiuminata, Monte Vermenone, N43°08'50.6" E12°55'12.0" 1 330 m a.s.l., 18 Nov. 2023, *G. Spinaci*, MFA.94.23 (ITS, LSU and *TEF* sequences GenBank PP776101, PP809870 and PP779520); Umbria, Perugia Nocera Umbra, Cellerano, Pian di Faeto, N43°11'49.0" E12°49'40.0", 1 192 m a.s.l., 19 Oct. 2021, *P. Carnevali*, MFA.62.21 (ITS and *TEF* sequences GenBank PP776099 and PP779518). All with duplicates in L.A. Parra private fungarium (LAPAG).

Notes: *Agaricus bellui* belongs to *Agaricus* sect. *Agaricus*. According to our phylogenetic analyses, *A. bellui* forms a strongly supported and well-defined clade. The ITS region of *Agaricus bellui* possesses one species specific nucleotide tgggc[A]tttcat at position 276 in the alignment in *Agaricus* sect. *Agaricus*. Morphologically, *A. bellui* can be distinguished from the remaining taxa in *Agaricus* sect. *Agaricus* in having a campestroid habit, a squamose pileus, a membranous thick annulus dissociated into a cog-wheel in the lower margin, a context discolouring yellow at the stipe base and spores 8.1 × 5.7 µm and Q coefficient 1.45 on average. *Agaricus cappellii* can be macroscopically very similar but microscopically differs in having larger spores (8.7 × 6.4 µm on average) and lower Q coeficient (1.36 on average).

For phylogenetic tree, see *Agaricus aereiceps* (FP 1739).

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Agaricus fabrianensis
1 cm
ZRL20181045

Fungal Planet 1742 MycoBank MB 856131

Agaricus fabrianensis Faraoni, L.A. Parra, R.L. Zhao & Linda J. Chen, ***sp. nov.***

Etymology: *fabrianensis* (Latin) meaning from Fabriano, the city where the first collection of this taxon was identified as a new species.

Classification: *Agaricaceae*, *Agaricales*, *Agaricomycetes.*

Pileus 40–100 mm diam, at first globose, then hemispherical to convex-campanulate, finally plano-convex to obtusely umbonate, with a flat or sometimes shallowly depressed centre. Surface radially fibrillose-silky, or turning into more or less large, triangular, appressed, concentrically-arranged, scales, first white then becoming increasingly ochraceous, then increasingly darkening with age, sometimes vinaceous-brownish purple from the beginning, on a whitish background, ochraceous, pink or light vinaceous when rubbed then darker. Margin thin, exceeding the lamellae up to 3 mm and often appendiculate by abundant annulus remnants. *Lamellae* free, up to 8 mm broad, crowded, with intercalated lamellulae, first pale pink, then bright pink, later progressively reddish-brown, finally dark brown almost black. *Stipe* 40–70 × 8–20 mm, central, solid, cylindrical almost always tapering downwards, with an annulus in its upper half, above the annulus white to pale pink, smooth or sometimes slightly squamulose, below white, cottony scaly specially near the annulus, usually with one or more brown to purple vinaceous linear girdles towards the base which discolours ochraceous to pale red under manipulation or even spontaneously. *Annulus* superous or intermediate, simple, rarely double, thin and narrow, fragile, up to 4–5 mm broad, upper side and underside white and fibrillose, with fimbriate margin. *Context* firm and solid, white when cut, reddening in the pileus near the lamellae and often discolouring pale yellow at the base. *Odour* usually absent or fungoid, sometimes anise-like or of bitter almonds at the stipe base, more evident after rubbing. *Basidiospores* 6.2–8.5(–10.1) × 4.6–5.9(–6.3) µm; 7.1 × 5.1 µm av., Q = (1.13–)1.17–1.61; 1.40 av., broadly ellipsoidal to ellipsoidal, brown, thick-walled, some with a rudimentary apical pore. *Basidia* 14–36 × 6–11 µm, mostly 4-spored, clavate or slightly truncated at the apex, with sterigmata up to 4.5 µm long. *Cheilocystidia* absent. *Pleurocystidia* absent. *Annulus lower surface* composed of hyaline, smooth, unpigmented, septate hyphae, 3–17(–25) µm wide, the broader the more constricted at septa, in the specimens MFA.63.22 and MFA.64.22 easily disarticulated into isolate elements with round ends. *Pileipellis* a cutis composed of cylindrical, hyaline, smooth, unpigmented, septate hyphae, 3–17 µm wide, the broader the more constricted at septa, with terminal elements with rounded apex up to 10 µm wide. *Clamp connections* absent.

Macrochemical reactions: Schäffer's and KOH (30 %) reactions negative on pileus surface in dried specimens.

Colour illustrations: Pasture with limestone rock outcrops in Passo Godi, Scanno, Abruzzo, Lazio and Molise National Park, holotype site. Basidiomata in the collecting spot and yellow discolouration at the stipe base, from top to bottom: holotype, MFA.56.19, MFA.120.19, MFA.08.21, holotype, ZRL20181045; scanning electron micrograph of the spores: MFA.64.22. Scale bar = 2 µm [Photo credit M. Faraoni, R.-L. Zhao & G. Moreno (spores)].

Habit, habitat and distribution: Solitary or gregarious in small groups or in fairy rings, in urban grasslands, meadows, and pastures with lush grass or gravel with limestone rock outcrops. Known only from China, Italy and Spain.

Typus: **Italy**, Abruzzo, L'Aquila, Parco Nazionale d'Abruzzo, Lazio e Molise, Scanno, Passo Godi, N41°49'54.1" E13°55'51.2", 1 550 m a.s.l., 8 Oct. 2022, *M. Faraoni* (**holotype** AH56342, ITS and *TEF* sequences GenBank PP776106 and PP779525; **isotypes** MFA.63.22 in Mauro Faraoni private fungarium MFA and LAPAG1410 in L.A. Parra private fungarium, LAPAG).

Additional materials examined: **China**, Gansu Province, Wuwei City, Hualong Conservation Station of Qilian Mountain Nature Reserve, N36°54'36.6" E102°38'8.03", 3 395 m a.s.l., 20 Aug. 2018, *R.-L. Zhao, B. Cao, J.-X. Li*, ZRL20181005 (*TEF* sequence GenBank PQ049123); Gansu Province, Wuwei City, Hualong Conservation Station of Qilian Mountain Nature Reserve, N36°54'36.6" E102°38'8.03", 3 395 m a.s.l., 20 Aug. 2018, *R.-L. Zhao, B. Cao, J.-X. Li*, ZRL20181045 (*TEF* sequence GenBank PQ049124). **Italy**, Marche, Ancona, Parco Naturale Gola della Rossa e Frasassi, Fabriano, Monte Valmontagnana, N43°23'26.1" E12°57'40.9", 879 m a.s.l., 10 Oct. 2019, *M. Faraoni*, MFA.52.19 (ITS and *TEF* sequences GenBank PQ039707 and PQ049115); Marche, Ancona, Parco Naturale Gola della Rossa e Frasassi, Fabriano, Monte Valmontagnana, N43°23'17.3" E12°57'36.8", 874 m a.s.l., 10 Oct. 2019, *M. Faraoni*, MFA.55.19 (ITS and *TEF* sequences GenBank PQ039708 and PQ049116); Marche, Ancona, Parco Naturale Gola della Rossa e Frasassi, Fabriano, Monte Valmontagnana, N43°23'16.4" E12°57'36.5", 868 m a.s.l., 10 Oct. 2019, *M. Faraoni*, AH56343 (duplicate in MFA.56.19) (ITS and *TEF* sequences GenBank PP776105 and PP779524); Marche, Ancona, Parco Naturale Gola della Rossa e Frasassi, Fabriano, Monte Valmontagnana, N43°23'30.7" E12°57'29.4", 823 m a.s.l., 16 Sep. 2021, *M. Faraoni*, MFA.08.21(ITS and *TEF* sequences GenBank PP776102 and PP779521); Marche, Macerata, Matelica, Vocabolo Giardino, 357 m a.s.l., N43°14'56.5" E13°00'45.8'', 28 Nov. 2019, *C. Chirielli* & *M. Faraoni*, MFA.120.19 (ITS and *TEF* sequences GenBank PP776104 and PP779523); Marche**,** Macerata, Pioraco, unnamed peaks between Monte Tre Pizzi and Monte Castel Santa Maria, N43°12'11.7" E12°58'01.4", 1 170 m a.s.l., 25 Oct. 2021, *M. Faraoni*, MFA.73.21(ITS and *TEF* sequences GenBank PQ039701 and PQ049109); Marche, Ancona, Fabriano, Monte Pizzinetto di Mutola, N43°13'55.3" E12°53'47.6", 1 086 m a.s.l., 1 Oct. 2022, *M. Faraoni* & *G. Spinaci*, MFA.34.22 (ITS and *TEF* sequences GenBank PQ039698 and PQ049106); Marche, Macerata, Parco Nazionale dei Monti Sibillini, Visso, Cupi, N42°59'26.0" E13°08'05.1", 1 389 m a.s.l., 17 Jun. 2020, *M. Faraoni, S. Morettini* & *G. Spinaci*, MFA.08.20 (ITS and *TEF* sequences GenBank PQ039709 and PQ049117); Marche, Macerata, Parco Nazionale dei Monti Sibillini, Visso, Cupi, N42°59'26.1" E13°08'08.9", 1 403 m a.s.l., 6 Oct. 2020, *M. Faraoni*, MFA.36.20 (ITS and *TEF* sequences GenBank PQ039710 and

PQ049118); Marche, Macerata, Parco Nazionale dei Monti Sibillini, Visso, Cupi, N42°59’25.9” E13°08’01.0”, 1 367 m a.s.l, 6 Oct. 2020, *M. Faraoni*, MFA.39.20 (ITS and *TEF* sequences GenBank PQ039700 and PQ049108); Marche, Macerata, Parco Nazionale dei Monti Sibillini, Visso, Cupi, N42°59’24.5” E13°08’14.1”, 1 422 m a.s.l., 13 Oct. 2020, *M. Faraoni*, MFA.61.20 (ITS and *TEF* sequences GenBank PQ039711 and PQ049119); Marche, Macerata, Parco Nazionale dei Monti Sibillini, Visso, Cupi, N42°59’23.8” E13°08’17.8”, 1 441 m a.s.l., 13 Oct. 2020, *M. Faraoni*, MFA.62.20 (ITS and *TEF* sequences GenBank PQ039712 and PQ049120); Marche, Macerata, Parco Nazionale dei Monti Sibillini, Visso, Cupi, N42°59’35.5” E13°08’01.8”, 1 349 m a.s.l., 19 Oct. 2022, *M. Faraoni*, MFA.72.22 (ITS and *TEF* sequences GenBank PQ039699 and PQ049107); Marche, Macerata, Parco Nazionale dei Monti Sibillini, Visso, Cupi, N42°59’25.9” E13°08’01.1”, 1 365 m a.s.l., 19 Oct. 2022, *M. Faraoni*, MFA.86.22 (ITS and *TEF* sequences GenBank PQ039703 and PQ049111); Marche, Macerata, Parco Nazionale dei Monti Sibillini, Visso, Cupi, N42°59’22.2” E13°08’13.8”, 1 399 m a.s.l., 30 Oct. 2023, *C. Chirielli* & *M. Faraoni*, MFA.76.23 (ITS and *TEF* sequences GenBank PQ039714 and PQ049122); Marche, Macerata, Parco Nazionale dei Monti Sibillini, Ussita, Monte Croce di Monte Rotondo, N42°58’07.0” E13°09’57.9”, 1 710 m a.s.l., 8 Sep. 2018, *M. Faraoni*, MFA.07.18 (ITS and *TEF* sequences GenBank PQ039704 and PQ049112); Marche, Ancona, Sassoferrato, Casalvento, Monte Miesola, N43°23’07.9” E12°48’00.9”, 770 m a.s.l., 30 Sept. 2019, *M. Faraoni*, MFA.26.19 (ITS and *TEF* sequences GenBank PQ039705 and PQ049113); Marche, Ancona, Sassoferrato, Casalvento, Monte Miesola, N43°23’16.1” E12°47’53.4”, 685 m a.s.l., 30 Sep. 2019, *M. Faraoni*, MFA.28.19 (ITS and *TEF* sequences GenBank PQ039706 and PQ049114); Abruzzo, L’Aquila, Parco Nazionale d’Abruzzo, Lazio e Molise, Scanno, Passo Godi, 1 542 m a.s.l., N41°50’05.8” E13°55’52.7”, 8 Oct. 2022, *M. Faraoni*, MFA.64.22 (ITS, LSU and *TEF* sequences GenBank PP776103, PP809871 and PP779522). Umbria, Perugia, Nocera Umbra, Cellerano**,** N43°11’34.6” E12°50’26.0”, 950 m a.s.l., 12 Oct. 2021, *M. Faraoni*, MFA.40.21 (ITS and *TEF* sequences GenBank PQ039713 and PQ049121); Umbria, Perugia, Passignano sul Trasimeno, San Vito, N43°10’36.2” E12°11’10.0”, 268 m a.s.l., 26 Dec. 2022*, M. Faraoni* & *P. Poeta*, MFA.128.22 (ITS and *TEF* sequences GenBank PQ039702 and PQ049110); All with duplicates in L.A. Parra private herbarium (LAPAG). **Spain**, Burgos, Caleruega, Fuente del Rey, N41°52’08.3” W3°27’14.1”, 1 022 m a.s.l., 5 Oct. 2006, *L.A. Parra*, LAPAG434 (ITS and *TEF* sequences GenBank PP776107 and GenBank PP779526).

Notes: *Agaricus fabrianensis* belongs to *Agaricus* sect. *Agaricus*. According to our phylogenetic analysis, samples of *A. fabrianensis* formed a well-defined clade but without significant support. This is due to the high number of polymorphic positions revealed in the ITS sequences of *A. fabrianensis*. In addition to 13 polymorphic positions listed in the second supplementary table, 20 more polymorphic positions that was found only in a single sequence are not shown. Such a level of intra-specific variation is not frequently observed in the genus. Further, the ITS region of *Agaricus fabrianensis* lacks any species-specific nucleotides in *Agaricus* sect. *Agaricus*. Morphologically, specimens with the campestroid habit of *A. fabrianensis* can be distinguished from the remaining taxa in *Agaricus* sect. *Agaricus* in having one or more brown to purple vinaceous linear bracelets towards the stipe base, which discolours ochraceous to pale red under manipulation or even spontaneously on the surface and yellow in the context, and spores 7.1 × 5.1 µm on average with a Q coefficient 1.40 on average. Other species of *Agaricus* sect. *Agaricus* which can have dark coloured bracelets at the stipe base are *A. basicinctus*, *A. braendlei* and *A. cupreobrunneus*, but all of these have much larger spores (9.2 × 6.4 µm, 8.6 × 6.2 µm and 7.9 × 5.4 µm on average, respectively), stipe not reddening at the base and context without yellow discolouration when cut. *Agaricus erindalensis* discolours red when bruised but it differs in having a context not discolouring yellow at the stipe base and larger spores (7.9 × 5.2 µm on average). When *A. fabrianensis* has a slender habit and almost white surfaces, as in the specimen MFA.08.21, it is, morphologically, very similar to several species of *Agaricus* sect. *Agaricus* with this habit and colour surfaces and molecular characters are crucial for an unequivocal identification.

For phylogenetic tree and supplementary tables, see *Agaricus aereiceps* (FP 1739).

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Agaricus occidualis

Fungal Planet 1743 MycoBank MB 856132

Agaricus occidualis L.A. Parra, Callac†, Faraoni, Weholt, Borovička, Siquier, B.A. Roy & Linda J. Chen, *sp. nov.*

Etymology: Named for its distribution in Western Europe and Western USA. (Latin) *occidualis* meaning “western”, but in this case it is also a pun taking into account that *dualis* in Latin means “containing two”, and this species has a Western area of distribution in two continents.

Classification: *Agaricaceae*, *Agaricales*, *Agaricomycetes*.

Pileus 35–50 mm diam, at first globose, then hemispherical, finally plano-convex or shallowly depressed in the centre. Surface completely radially silky fibrillose with sometimes smooth centre, or covered with appressed, concentrically arranged triangular scales denser and darker at the centre. Fibrils and scales rarely white, usually pale creamy, ochraceous yellow, orangish, or ochraceous brown, on a white background. Margin thin, exceeding the lamellae up to 3 mm, fibrillose or squamose, sometimes appendiculate by annulus remnants. *Lamellae* free, up to 8 mm broad, crowded, with intercalated lamellulae, first pale pink, then bright pink, later reddish-brown and finally dark brown almost black with a concolourous, or very slightly paler, edge. *Stipe* 17–65 × 7–20 mm, central, claviform, cylindrical or cylindrical tapering downwards, at first stuffed, later narrowly fistulous, with an annulus in the middle or in its upper half, above the annulus white, fibrillose, below white, fibrillose to slightly squamose, sometimes slightly pale ochre at the extreme base with time or manipulation. *Annulus* superous or intermediate, up to 5 mm wide, white, simple, thin, very narrow, fragile, fibrillose with fimbriate margin. *Context* white on cutting, reddening only in the upper cortex of the stipe and in the pileus near the lamellae. *Odour* indistinct, weak or fungoid. *Basidiospores* 6.1–10.3 × 3.9–6.3(–6.9) µm; 8.1 × 5.2 µm av., Q = 1.25–1.80; 1.55 av., broadly ellipsoid to ellipsoid, or elongate, brown, thick-walled, usually with a rudimentary apical pore. In all collections some isolated large-sized spores. For example, in MFA.30.21 and PRM AH56335 spores measuring 11.5 × 7.5 µm and 11.4 × 6.2 µm, respectively, can be observed. *Basidia* 13–33 × 6–12 µm, mostly 4-spored, but in MFA.30.21 and LAPAG1416 bisporic are also abundant and in LAPAG1416 monosporic are also observed, clavate or slightly truncate at the apex, hyaline or in HBA1-18 with internal diffuse dark brown pigment, with sterigmata up to 4 µm long. *Cheilocystidia* absent. *Annulus lower surface* composed of cylindrical, hyaline, smooth, unpigmented, septate hyphae, 4–11 µm wide, the broader the more constricted at septa. *Pileipellis* a cutis composed of cylindrical, hyaline, smooth, unpigmented, septate hyphae, 2–17(–22) µm wide, the broader the more constricted at septa, with terminal elements with rounded apex up to 11 µm wide. *Clamp connections* absent.

Colour illustrations: Grassy place at Pico de Areiro, near the top, holotype site. Basidiomata in the collecting spot, from top to bottom: holotype, JLS3165, MP-1-140814, MFA.30.21, OSC 171755, LAPAG138; on the right LAPAG1416; scanning electron micrograph of the spores: JLS3165. Scale bar = 2 µm [Photo credit J. Borovička, J.L. Siquier, M. Pettersen, M. Faraoni, M. Hicks, L.A. Parra, P. Callac & G. Moreno (spores)].

Macrochemical reactions: Schäffer’s reaction negative or weakly positive on dried specimens, and KOH (30 %) negative on pileus surface on fresh and dried specimens.

Habit, habitat and distribution: Solitary or gregarious in small groups, in meadows, prairies, pastures, lawns and grassy clearings, sometimes near deciduous (*Alnus, Betula, Populus, Quercus, Salix, Tilia*), or coniferous (*Picea, Pinus*) trees. The North American collections grew in native wetland prairies dominated by *Deschampsia cespitosa* (tufted hairgrass, *Poaceae*) within 30 m of *Quercus garryana*, and OSC 171755 and OSC 171837 in areas burned about five weeks prior to collection.

Typus: **Portugal**, Madeira, Santana, Pico de Areiro, N32°44’07.2’’ W16°55’43.8’’24, 1 800 m a.s.l., 23 Sep. 2015, *J. Borovička* (**holotype** PRM934961, ITS, LSU and *TEF* sequences GenBank PP776090, PP809872 and PP779527; **isotype** LAPAG1081 in L.A. Parra private fungarium).

Additional material examined: **Italy**, Marche, Ancona, Fabriano, Pizzinetto di Mutola, N43°13’53.5” E12°53’52.6”, 1 100 m a.s.l., 9 Oct. 2021, *M. Faraoni* & *G. Spinaci*, MFA.30.21 (ITS, LSU and *TEF* sequences GenBank PP776096, PP809874 and PP779528); Marche, Macerata, Pioraco, unnamed mountain between mount Tre Pizzi and mount Castel Santa Maria, N43°12’10.4” E12°58’03.1”, 1 168 m a.s.l., 21 Sep. 2022, *M. Faraoni*, MFA.15.22 (ITS, LSU and *TEF* sequences GenBank PP776097, PP809875 and PP779529). **Norway**, Østfold, Sarpsborg, Hafslundparken, N59°16’23’’ E11°08’17’’, 53 m a.s.l., 14 Aug. 2014, *M. Pettersen*, MP-140814 (ITS sequence GenBank PP776092; duplicate LAPAG1105); Akershus, Ås, Dogga, N59°45’04.0’’ E10°48’38.8’’, 77 m a.s.l., 26 Aug. 2018, *H. Bøås*, HBA1-18 (ITS sequence GenBank PP776093); Østfold, Fredrikstad, Borge chapel, N59°13’26’’ E11°02’09’’, 39 m a.s.l., 4 Oct. 2020, *M. Pettersen*, MP-1-041020 (ITS sequence GenBank PP776094); Østfold, Sarpsborg, Hafslundparken, N59°16’23’’ E11°08’17’’, 53 m a.s.l., 14 Aug. 2022, *M. Pettersen*, MP-27-140822 (ITS sequence GenBank PP776095). All with duplicates in LAPAG except for MP-27-140822. **Portugal**, Algarve, Lagos, Atalaia, 24 Nov. 2005, *P. Callac*, LAPAG1416 (ITS sequence GenBank PP776089); Azores islands, São Miguel, Ponta Delgada, Parque Século XXI, N37°45’03.5’’ W25°39’13.2’’24, 96 m a.s.l., 11 Oct. 2023, *L.A. Parra*, LAPAG1387 (ITS sequence GenBank PP776088). **Spain**, Burgos, Vizcaínos, Pedroso river bank, N42°05’48.60” W3°15’49.20”E, 1 050 m a.s.l., 11 Nov. 2010, *J.L. Siquier*, JLS 3165 in J.L. Siquier private fungarium (ITS and LSU sequences GenBank PP776091 and PP809873; duplicate LAPAG729). **USA**, Oregon, Lane, Eugene, Fisher Butte Fern Ridge Wetlands Wildlife Area, N44°03’13.2” W123°15’18.2”, 114 m a.s.l., 9 Nov. 2014, *M. Hicks* & *K. Alexander*, WEW007 = iNat18268712, OSC 171755 (with duplicate in LAPAM200) (ITS sequence GenBank OM203495); Oregon, Lane, Malabon, Fern Ridge Reservoir Dike2, N44°06’09.1’’ W123°15’30.2’’, 115 m. a.s.l., 7 Nov. 2015, *A. Nelson*, WEW048 = iNat18658231, OSC171806 (ITS sequence GenBank OM203496); Oregon, Lane, Eugene, Fisher Butte Fern Ridge Wetlands Wildlife Area, N44°03’33.6” W123°15’34.4”, 114 m a.s.l., 15 Nov. 2015, *S. Holmes* & *B. Roy*, WEW061 = iNat18658924, OSC 171837 (ITS sequence GenBank OM203497).

Notes: *Agaricus occidualis* belongs to *Agaricus* sect. *Agaricus*. According to our phylogenetic analyses, *A. occidualis* forms a well-supported and well-defined clade. The ITS region of *Agaricus occidualis* possesses two species specific nucleotides tcagc[T]tatca at position 131, and tatag[A]agggc at position 492 in the alignment in *Agaricus* sect. *Agaricus*. *Agaricus occidualis* can be distinguished from other species of *Agaricus* sect. *Agaricus* with a squat habit in having a pileus without dark fibrils or scales, rarely white, a stipe surface and context white, unchanging when fresh, without dark coloured girdles near the base, spores with a patent rudimentary apical pore measuring 8.1 × 5.2 µm on average and habitat in grassy places. *Agaricus bellui*, *A. cupreobruneus*, *A. incultorum* and *fabrianensis* have similar spore size and habit. *Agaricus bellui* and *A. fabrianensis* differ in having a context with yellow discolouration at the stipe base and the latter has usually dark coloured girdles at the stipe base. *Agaricus cupreobrunneus* and *A. incultorum* have a coppery brown pileus when young with concolourous girdles at the stipe base. When *A. occidualis* has a white pileus, it is morphologically, very similar to several species of *Agaricus* sect. *Agaricus* as for example some collections of *A. andrewii*, *A. fabrianensis*, *A. braendlei* or *A. campestris*, or when the pileus is unusually dark coloured resembling *A. cupreobrunneus* or *A. incultorum*, molecular characters are crucial for an unequivocal identification.

For phylogenetic tree, see *Agaricus aereiceps* (FP 1739).

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Agaricus quercetorum

Fungal Planet 1744 MycoBank MB 856133

Agaricus quercetorum L.A. Parra, A. Caballero† & Linda J. Chen, ***sp. nov.***

Etymology: Named for its habitat in *Quercus ilex* forests. From Latin *quercetorum* genitive plural of *quercetum* meaning “from the *Quercus* forests”.

Classification: *Agaricaceae*, *Agaricales*, *Agaricomycetes*.

Pileus 46–70 mm diam, at first globose, then hemispherical to truncate-conical, finally plano-convex or shallowly depressed in the centre. Surface completely radially silky fibrillose to woolly fibrillose, with sometimes smooth centre, completely white, ochraceous, dark greyish brown or with a coloured centre and white margin. Margin thin, exceeding the lamellae up to 2 mm, fibrillose, sometimes appendiculate by annulus remnants. *Lamellae* free, up to 8 mm broad, crowded, with intercalated lamellulae, first pinkish, then bright pink, later reddish brown and finally dark brown almost black with a concolourous edge. *Stipe* 35–70 × 10–20 mm, central, claviform, cylindrical or cylindrical with attenuated base, at first stuffed, later narrowly fistulous, provided with an annulus generally in its upper half, above the annulus white, smooth or fibrillose, below white or slightly ochraceous at the base, fibrillose to slightly squamose. *Annulus* superous, up to 5 mm wide, white, simple, thin, very narrow, fragile, fibrillose with fimbriate to membranous margin. *Context* white on cutting, reddening only in the pileus near the lamellae. *Odour* indistinct, weak or fungoid. *Basidiospores* 7.3–10.3 × 5.1–6.3 µm; 8.8 × 5.5 µm av., Q = 1.34–1.76(–1.84); 1.59 av., ellipsoid, brown, thick-walled, some with a rudimentary apical pore. In AH56335 and LAPAG776 some isolated large-sized spores, *e.g*. up to 10.3 × 6.3 µm and 15 × 6 µm, respectively, can be observed. *Basidia* 24–34 × (7–)10–15 µm, mostly 4-spored, clavate or slightly truncate at the apex, with sterigmata up to 5 µm long. *Cheilocystidia* isolated or absent. In AH56335 rare, hyaline, globose, ovoid or clavate, generally simple measuring 24–42 × 14–31 µm, absent in the remaining specimens. *Pleurocystidia* very rare in AH56335 similar to the cheilocystidia, *e.g*. 36 × 16 µm or 52 × 19 µm, absent in the remaining specimens. *Annulus lower surface* composed of cylindrical, hyaline, smooth, unpigmented, septate hyphae, 6–24 µm wide, the broader the more constricted at septa. *Pileipellis* a cutis composed of cylindrical, hyaline, smooth, unpigmented, septate hyphae, 5–22 µm wide, the broader the more constricted at septa, with terminal elements with rounded apex up to 10 µm wide. *Clamp connections* absent.

Colour illustrations: Holm oak forest of Villalba de Duero, Burgos, Spain, holotype site. Basidiomata at the collecting spots; scanning electron micrograph of the spores. The two upper images and the spores are from the holotype, the two remaining images are from AH56336. Scale bar = 2 µm [Photo credit L.A. Parra & G. Moreno (spores)].

Macrochemical reactions: Schäffer’s and KOH (30 %) reactions negative on pileus surface.

Habit, habitat and distribution: Solitary or in small groups, in holm oak forests (*Quercus ilex* subsp. *ballota*) in areas with abundant leaf litter without grass. Known only from Spain.

Typus: **Spain**, Burgos, Villalba de Duero, near the smallest lagoon, N41°40’25.2’’ W3°45’32.7’’, 785 m a.s.l., 6 Dec. 2021, *M.L. Vázquez* (**holotype** AH56335; ITS, LSU and *TEF* sequences GenBank PP776078, PP809876 and PP779510; **isotype** LAPAG1355 in L.A. Parra private fungarium).

Additional materials examined: **Spain**, La Rioja, Villarroya, 800 m a.s.l., 22 Nov. 1997, *A. Caballero*, LAPAG776 in L.A. Parra private fungarium (ITS sequence GenBank PP776080; duplicate AC2148 in A. Caballero private fungarium); La Rioja, Villarroya, 800 m a.s.l., 2 Oct. 1994, *A. Caballero*, LAPAG777 in L.A. Parra private fungarium (ITS sequence GenBank PP776081; duplicate AC1868 in A. Caballero private fungarium); Málaga, Parauta, Sierra de las Nieves Natural Park, near the Cortijo Las Navas de los Pinsapos, N36°39’48.6’’ W5°03’27.9’’, 1 130 m a.s.l., 23 Nov. 2021, *J.F. Ramírez*, AH56336 (ITS, LSU and *TEF* sequences GenBank PP776079, PP809877 and PP779511; duplicate LAPAG 1354 in L.A. Parra private fungarium).

Notes: *Agaricus quercetorum* belongs to *Agaricus* sect. *Agaricus*. According to our phylogenetic analyses, *A. quercetorum* forms a strongly supported and well-defined clade. The ITS region of *A. quercetorum* possesses two species specific nucleotides acttg[A] tt--g at position 527, and t---g[G]gacaa at position 660 in the alignment in *Agaricus* sect. *Agaricus*. *Agaricus quercetorum* can be distinguished from other species of *Agaricus* sect. *Agaricus* with a squat habit in having a silvicolous habitat. Other species of this section with squat habit are found in grasslands or among grass under trees or in clearings but never in forests under trees in a dense grassless leaf litter as it occurs in *A. quercetorum*. The holotype specimen (AH56335) possesses isolated macrocystidia which are absent in the remaining specimens of this species and very rare in other taxa of *A.* sect. *Agaricus*.

For phylogenetic tree, see *Agaricus aereiceps* (FP 1739).

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Albocremella abscondita

Fungal Planet 1745

MycoBank MB 856142

Albocremella Piątek & Stryjak-Bogacka, ***gen. nov.***

Etymology: Name refers to the white and pale cream colour of the fungal colonies.

Classification: *Vandijckellaceae*, *Helotiales*, *Leotiomycetes*.

Colonies erumpent, spreading, umbonate or flat, white to pale cream, surface radially folded or not, with sparse aerial mycelium, margin finely crenate or entire. *Mycelium* composed of sparsely branched, septate, hyaline, straight, smooth hyphae, sometimes with swellings; hyphae develop into arthroconidia. *Arthroconidia* subcylindrical, hyaline, smooth, aseptate or with one indistinct septum, usually narrowed at the centre, produced intercalary or terminally, in chains.

Type species: *Albocremella abscondita* Piątek & Stryjak-Bogacka

MycoBank MB 856143

Albocremella abscondita Piątek & Stryjak-Bogacka, ***sp. nov.***

Etymology: Name derived from Latin *absconditus* – hidden, in reference to the hidden nature of this fungus.

Mycelium composed of sparsely branched, septate, hyaline, straight, smooth, 1.5–3.5 µm wide hyphae, sometimes with swellings; hyphae develop into arthroconidia. *Arthroconidia* subcylindrical, hyaline, smooth, aseptate or with one indistinct septum, 12–21 × 2.5–4.5 µm, usually narrowed at the centre, produced intercalary or terminally, in chains [description based on malt extract agar (MEA)].

Culture characteristics: Colonies on MEA erumpent, spreading, umbonate, white to pale cream, reaching 16 mm diam after 2 wk growth at 15 °C and 9 mm diam after 2 wk growth at 25 °C, surface radially folded, with weak aerial mycelium at the centre, margin finely crenate. Reverse cream-coloured. Colonies on potato dextrose agar (PDA) erumpent, spreading, umbonate, white to pale cream, reaching 16 mm diam after 2 wk growth at 15 °C and 9 mm diam after 2 wk growth at 25 °C, surface radially folded, with sparse aerial mycelium, margin entire. Reverse cream-coloured. Colonies on oatmeal agar (OA) spreading, flat, white to pale cream, reaching 18 mm diam after 2 wk growth at 15 °C and 7 mm diam after 2 wk growth at 25 °C, surface with sparse aerial mycelium at the centre, margin entire. Reverse cream-coloured.

Typus: **Poland**, Małopolska Province, Tarnów County: slopes of Wąwóz Wodospad (Waterfall Ravine), *ca*. 1 km S of Ciężkowice, 367 m a.s.l., isolated from rhizoids of liverwort *Conocephalum salebrosum*, 30 Jun. 2018, *B. Cykowska-Marzencka* (**holotype** KRAM F-60033; culture ex-type P02; ITS, LSU, SSU, and *rpb2* sequences GenBank PQ321308, PQ321307, PQ321309, PQ335014).

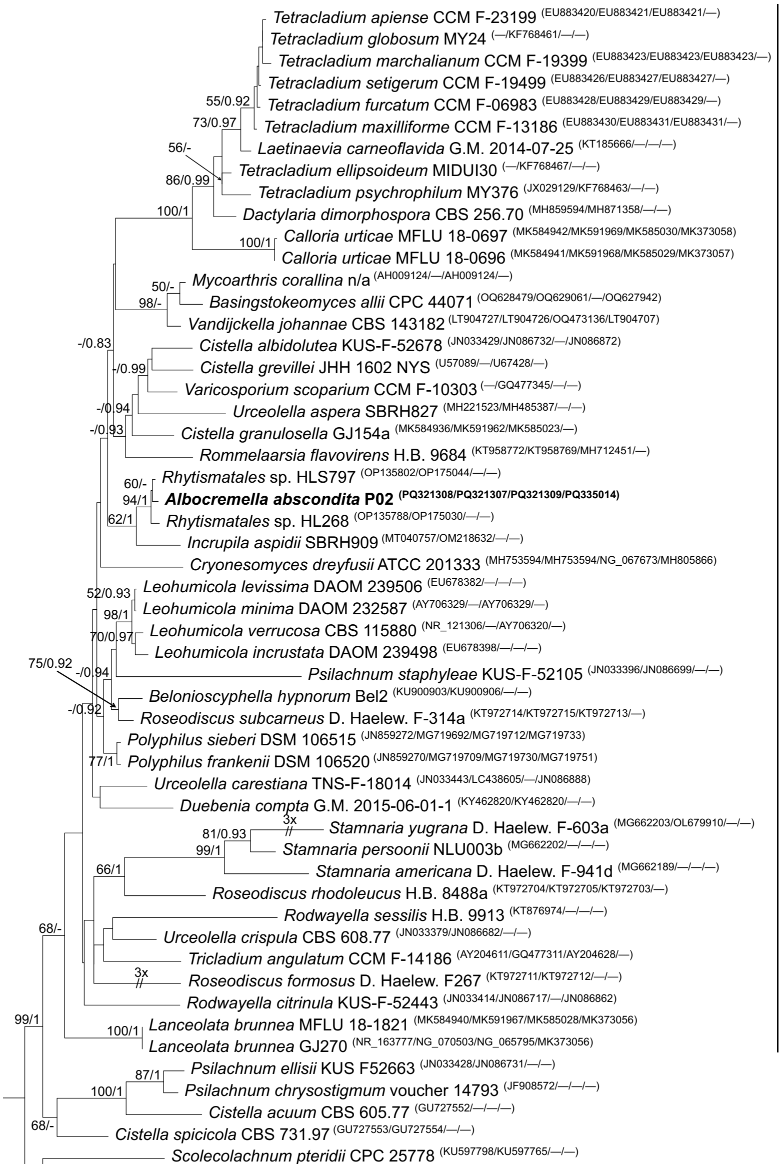
Notes: The family *Vandijckellaceae* (Crous *et al*. 2017, Ashrafi *et al.* 2018, Johnston *et al*. 2019, Untereiner *et al.* 2019) has been described for a *Hyaloscyphaceae sensu lato* Clade 9 recognised by Han *et al*. (2014). The family *Callorinaceae* (Baral & Marson 2019, Ekanayaka *et al.* 2019) was described later and applied to the same lineage, and may be synonymous with *Vandijckellaceae*. The number of the genera included in this family is insufficiently known but the family includes endophytes, saprotrophs as well as soil-borne, water and nematophagous fungi, and some of them are associated with bryophytes (*Belonioscyphella hypnorum*, *Cryonesomyces dreyfussii*, *Roseodiscus formosus*, *R. subcarneus*).

Albocremella is a new genus that resides in the family *Vandijckellaceae*. It is closely related to the genus *Incrupila*, typified by *I. aspidii* (Raitviir 1970). In culture *A. abscondita* produces only hyphae with rare, subcylindrical, aseptate or indistinctly 1-septate arthroconidia. It is however phylogenetically distinct from *I. aspidii*, which is a discomycete with septate, thick-walled, incrusted hairs and cylindrical paraphyses (Raitviir 1970). *Albocremella abscondita* has been isolated from the surface-sterilised (using 75 % ethanol for 1 min, then 2 % sodium hypochlorite for 3 min, and finally 75 % ethanol for 0.5 min) rhizoids of the liverwort *Conocephalum salebrosum*. This suggests its endophytic lifestyle in the rhizoids of this liverwort. The megablast search of NCBIs GenBank nucleotide database resulted with numerous sequences not assigned to species (many marked as belonging to “uncultured” fungus/ectomycorrhiza/*Helotiales* or to “*Rhytismatales* sp.”) with about 98–99 % threshold similarity with the ITS sequence of *A. abscondita*. They were mainly obtained from soil, roots of vascular plants or as plant endophytes. These sequences may belong either to *A. abscondita* or to closely related undescribed species.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits of the named species using the **ITS** sequence are “*Polyphilus sieberi*” [strain SGSF543, GenBank MT947190; Identities = 482/488 (99 %), two gaps (0 %)], *Incrupila aspidii* [voucher SBRH909, GenBank MT040757; Identities = 461/485 (95 %), one gap (0 %)] and “*Polyphilus sieberi*” [strain ES59, GenBank MN218785; Identities = 500/528 (95 %), three gaps (0 %)]. The closest hits using the **LSU** sequence are *Vandijckella johannae* [strain CBS 143182, GenBank NG_075222; Identities = 747/758 (99 %), no gaps], *Pseudoanguillospora stricta* [strain DSM 104335, GenBank OR243773; Identities = 746/758 (98 %), no gaps] and *Basingstokeomyces allii* [strain CBS

Colour illustrations: Wąwóz Wodospad (Waterfall Ravine), Poland. Colony on MEA; hyphae; arthroconidia. Scale bars = 10 µm.

149671, GenBank NG_242104; Identities = 745/758 (98 %), no gaps]. The closest hits using the **SSU** sequence are *Microscypha cajaniensis* [isolate M147, GenBank EU940037; Identities = 993/999 (99 %), no gaps], *Hyphodiscus hyaloscyphoides* [strain NBRC 104869, GenBank NG_067655; Identities = 993/999 (99 %), no gaps] and *Polyphilus sieberi* [strain REF057, GenBank MG719716; Identities = 991/999 (99 %), no gaps]. The closest hits using the ***rpb2*** sequence are *Polyphilus sieberi* [strain REF059, GenBank MG719739; Identities = 630/759 (83 %), four gaps (0 %)], *Polyphilus frankenii* [strain REF050, GenBank MG719751; Identities = 630/760 (83 %), four gaps (0 %)] and *Cistella blauvikensis* [strain CPC 45252, GenBank OR683722; Identities = 632/785 (81 %), 12 gaps (1 %)].



Phylogenetic tree of representatives of the family *Vandijckellaceae* obtained from a maximum likelihood analysis of the combined multi-locus alignment (3 181 nucleotides: ITS, LSU, SSU, *rpb2*). The maximum likelihood analysis was performed using RAxML-NG v. 1.1.0 (Kozlov *et al*. 2019) and the Bayesian inference was performed using MrBayes v. 3.2.6 (Ronquist *et al*. 2012). The position of *Albocremella abscondita* is indicated in **bold** and marked by coloured block. Numbers above branches indicate maximum likelihood bootstrap (MLB) support values > 50 % and Bayesian posterior probabilities (BPP) > 0.9, respectively (MLB/BPP). *Hyphodiscus hymeniophilus* and *Scolecolachnum pteridii* were used as an outgroup. The scale bar represents the expected number of changes per site. The alignment was deposited at figshare.com (doi: 10.6084/m9.figshare.27014554.v1).

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Circinaria shimlaensis

Fungal Planet 1746 MycoBank MB 852876

Circinaria shimlaensis A. Noor, Saba & W. Akram, *sp. nov.*

Etymology: The epithet "*shimlaensis*" refers to the locality Shimla Hills, KPK province of Pakistan, from where the type specimen was collected.

Classification: *Megasporaceae*, *Pertusariales*, *Lecanoromycetes.*

Thallus crustose, areolate, 5–7 cm broad, rounded to angular, flat to concave areolate, areoles 0.5–1.2 mm diam, non-contiguous. *Prothallus* absent. *Surface* greyish white to pale grey when dry, no change when wet, slightly pruinose, shiny. *Prothallus* absent. *Upper cortex* 25–40 µm thick, hyaline, with a thick, dark brown epinecral layer, 30–32µm thick; medulla hyaline. *Photobiont* green thick continuous layer, 60–70 µm thick, chlorococoid cells, 9–20 µm diam. *Apothecia* immersed, rounded, 1 per areole, 0.2–0.8 mm diam; thalline margin whitish grey, distinct, with radially compact greyish pruinose thalline areole; disc flat, circular to slightly concave, black, densely greyish white pruinose; proper margin, distinct; hymenium hyaline, 210–250 µm high, I+ blue; paraphyses thin, septate and anastomosing 3–5 µm wide and 70–90 µm in length, slightly swollen at tips; submoniliform (2–3 globose apical cells), epithecium, 26 µm high, light brown; hypothecium hyaline, 30–40 µm high, I+ blue. *Asci* cylindrical to clavate, 20–25 × 110–120 µm, *Ascospores Aspicilia*-type, 4–6 per ascus, hyaline, ellipsoid to subglobose 12–20 × 25–28 µm diam (n = 15). *Pycnidia* rarely present, rounded, black *ca*. 180 µm diam. *Conidia* filiform, straight, 1–3 × 5–7 µm (n = 30). *Odour* not recorded.

Chemistry: Spot tests: cortex K–, C–, P–, medulla K–, C–, P–. No lichen substance detected by TLC.

Habitat: Coniferous forest is dominated by species of *Cedrus deodara*, *Pinus roxburghii* and *Quercus* species. Moderate rainfall with varying moderate temperature from 20–30 °C during the summer to average 4 °C during the winter.

Typus: **Pakistan**, KPK province, Shimla Hill in the northwest Himalaya range on limestone rocks: 31°61'81''N, 77°10'73''E, alt. 2 206 m a.s.l., 17 Sep. 2023, *A. Noor*, *LT17* (**holotype** ISBAN03; ITS sequence GenBank PQ324268).

Additional material examined: **Pakistan**, KPK province, Shimla Hill in the northwest Himalaya range on limestone rocks: 31°61'81''N, 77°10'73''E, alt. 2 206 m a.s.l., 12 Aug. 2023, *A. Noor*, *LT16* (ISBAN04; ITS sequence GenBank PQ324269).

Notes: The taxon is characterised by a greyish white to pale grey pruinose thallus, whitish grey epruinose black apothecia with distinct white margins, flat to slightly concave areoles, a hymenium of 180 µm in height, ascospores 12–20 × 25–28 µm, and the presence of pycnidia.

Approximately 59 species of the genus *Circinaria* have been described globally to date (Index Fungorum, accessed on 13 Mar. 2024) but out of these taxa, only five species have been reported from Pakistan (Aptroot & Iqbal 2010, Iqbal 2023 & Rizwana *et al*. 2023). *Circinaria shimlaensis* is a new addition to science and lichen biota of Pakistan. This species closely resembles *C. pakistanica* both morphologically and phylogenetically.

Circinaria pakistanica is known by its whitish grey coloured thallus, greyish white epruinose apothecia, epihymenium, olive brown, hymenium 110–200 µm in height, larger ascospores, 22–38 × 18–32 µm, and absence of pycnidia (Iqbal *et al*. 2023). *Circinaria shimlaensis* can be distinguished mainly from the other species of this genus by a thicker squamulose-areolate thallus of greyish white or rusty white cracked areoles, black apothecia with distinct white margin, presence of pycnidia and smaller ascospores, 12–20 × 25–28 µm. The type specimen can also be compared with *C. hoffmanniana*, having a non-continuous areolate thallus as the latter is distinct in having a continuous thallus structure brownish grey in colour. Another similar calcareous lichen is *C. contorta*, which can also be distinguished from *C. shimlaensis* in having flat to convex areoles and larger ascospores (Fletcher *et al.* 2009, Nimis 2016).

In the phylogenetic analysis based on ITS sequences, *Circinaria shimlaensis*, is found to be a close relative of *C. pakistanica* (PP431557) reported from Pakistan (Iqbal *et al.* 2023), *C. contorta* (KX550106) with strong bootstrap value (99 %). Apart from ITS sequence, *C. pakistanica* is phylogenetically close to the *C. shimlaensis* and can be distinguished due to a combination of morpho-anatomical characteristics such whitish grey to blackish grey, non-contiguous with flat to slightly concave areoles and flat to slightly convex, (epruinose *vs* immersed in *C. shimlaensis*), Ascospores globose to subglobose. and Pycnidia (Absent *vs* present in *C. shimlaensis*). (Iqbal *et al.* 2023).

Circinaria contorta differs from *C. shimlaensis* by its rounded areolate, chalk white to pale grey thallus color, concave to flat, pruinose apothecia, areolate (flat to convex *vs* flat to concave in *C. shimlaensis*), Ascospores (clavate *vs* aspicilia type in shimlaensis). (Fletcher *et al.* 2009).

Based on a BLAST search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence shows 93 % similarity with *Circinaria* sp. (voucher CBM FL-41412**,** GenBank LC547496), 92.5 % similarity with *Circinaria pakistanica* (voucher LAH36028**,** GenBank OP584496), and 93 % similarity *Circinaria contorta* submitted from Turkey (voucher MGH 0.139**,** GenBank KX550106).

Supplementary material: doi: 10.6084/m9.figshare. 27013477. v1 (Table).

Colour illustrations: Pakistan, Punjab, Khyber Pakhtunkhwa, District Abbottabad, Shimla Hills rocks dominated by *Cedrus deodara, Pinus roxburgii* and *Taxus baccata* (photo credit A. Noor). Thallus of *Circinaria shimlaensis* in natural habitat; dissecting microscope picture of areolate thallus; microscopic cross section of apothecia; anatomy of ascus, ascospores, algal cells. Scale bars: thallus = 1 cm; micromorphology = 5 µm.

Molecular phylogenetic tree inferred from the nrITS sequence alignment. The evolutionary analysis was conducted in MEGA v. X, using Maximum Likelihood (ML) (Kumar *et al.* 2018). Branches are labelled with ML bootstrap support values from 1000 resamplings. The tree was rooted with *Lobothallia radiosa* (MN989285). The new species is shown in **bold**. The alignment and tree are available in TreeBASE (ID: S31697).

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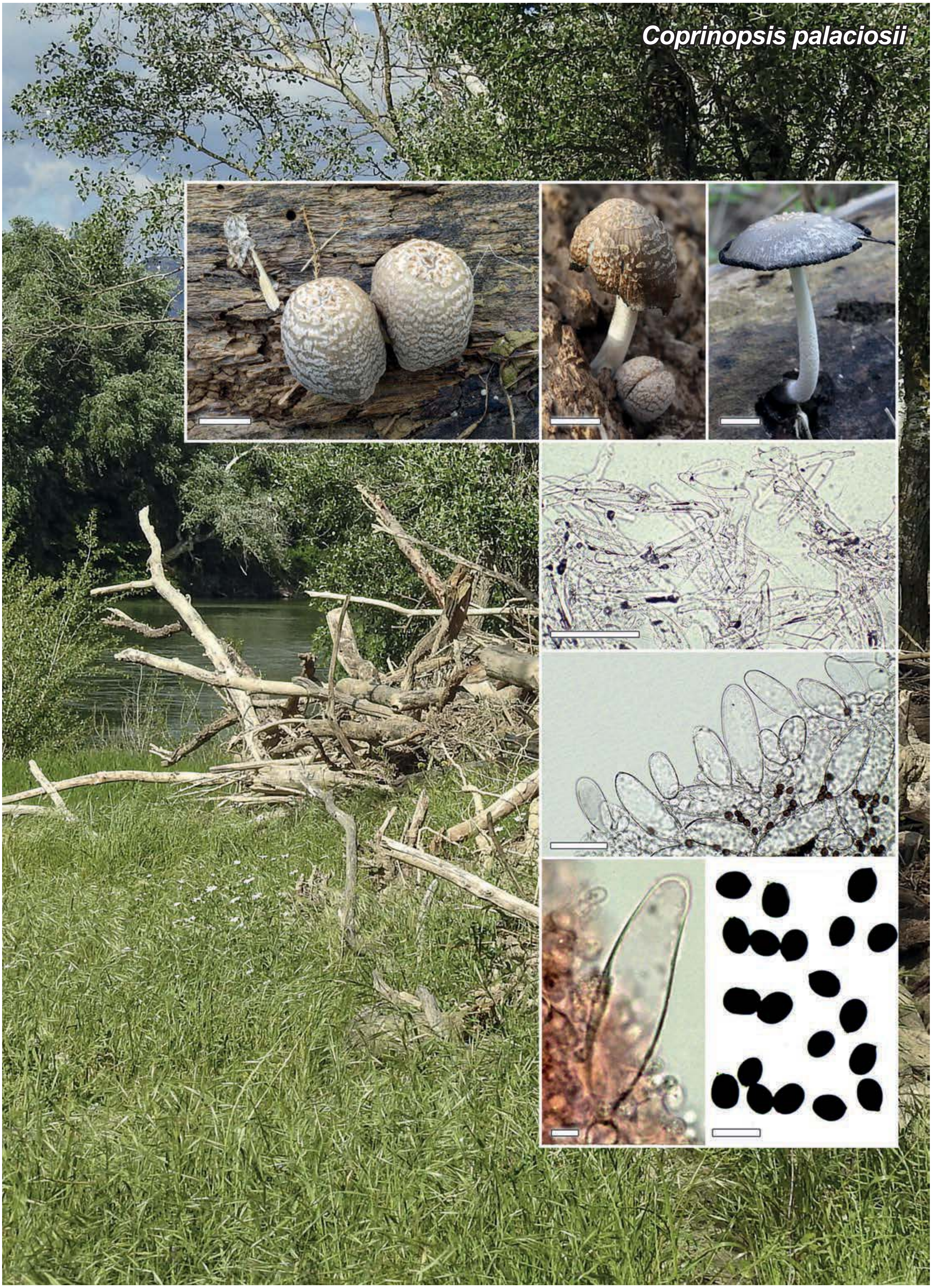

Coprinopsis palaciosii

Fungal Planet 1747

MycoBank MB 854363

Coprinopsis palaciosii A. Ruiz, G. Moreno & P. Alvarado, ***sp. nov.***

Etymology: Named in honour of the Basque mycologist Daniel Palacios.

Classification: *Psathyrellaceae*, *Agaricales*, *Agaricomycetes*.

Cap 1–2 cm diam, ovoid to campanulate, finally expanding to almost flat, but not becoming concave; when fully expanded it can measure up to 4 cm diam, with a fissured and slightly revolute margin. *Universal veil* white in colour, with brown or greyish brown scales, progressively fissuring into plaques with the development of the basidiome, revealing the underlying pileus surface, which is white to off-white or greyish brown. *Hymenophore* composed of deliquescent, lanceolate, somewhat ventricose, very dense, free lamellae; white at first, later becoming brownish, and finally black due to spore maturation. *Stem* cylindrical, up to 60 mm in length and 7 mm diam, robust, white, occasionally with an annular zone at the base resulting from the rupture of the whitish and pruinose universal veil, sometimes stained black by spore deposition. *Flesh* very scarce, without any remarkable *odour* and *taste*. *Basidia* 6.4–6.9 × 4.9–5.4 µm, clavate, tetrasporic. *Spores* 7.2–8.1 × 5.5–6.4 µm, Me = 7.65 × 5.95 µm, Qe = 1.2, broadly ellipsoidal, smooth, blackish with reddish tones under the microscope, with a central germ pore and marked hilar appendix. *Cheilocystidia* 47.6–89.3 × 18.6–25.9 µm, abundant, variable in shape, either cylindrical to fusiform or lageniform. *Pleurocystidia* 99.1–114.7 × 19.3–28.7 µm, mostly fusiform or sometimes cylindrical. *Pileipellis* arranged as a cutis, formed by elongated cells. *Vellipellis* formed by intermingled cells 5.2–8.5 µm in diameter, concatenated, cylindrical and diverticulate, thin-walled, generally hyaline, but some areas with yellowish-brown intracellular pigmentation. *Stipitipellis* similar to pileipellis, with remnants of structures from the universal veil. *Clamp connections* present.

Habitat and distribution: On degraded wood of riparian trees, in woody deposits caused by the floods of the Ebro river.

Typus: **Spain**, Navarra, Ribaforada, La Barca, on degraded woody debris, 31 Oct. 2023, *A. Ruiz* (**holotype** AH 49301; ITS, LSU and *TEF1* sequences GenBank PP907120, PP907118 and PP974473).

Additional specimens examined: **Spain**, Navarra, Ribaforada, La Barca, on degraded woody debris, 28 Oct. 2023, *A. Ruiz* (**paratype** AH 49300; ITS, LSU and *TEF1* sequences GenBank PP907119, PP907117, and PP910696); Ribaforada, El Vado, on fallen trunk of *Populus* sp., 3 Nov. 2023, *A. Ruiz* (ARMCO435); *idem.*, on woody debris, 18 Nov. 2023 (ARMCO436); Ribaforada, El Vado, on fallen trunk of *Populus* sp., 21 May 2024 (ARMCO439); Fustiñana, Sotos del Ebro, on degraded woody debris, 3 Nov. 2023 (ARMCO437).

Colour illustrations: Spain, Navarra, Ribaforada, La Barca, on degraded woody remains. Basidiomata (holotype and paratype); velipellis, cheilocystidia, pleurocystidium and spores (holotype). Scale bars: basidiomata = 0.5 cm; velipellis and cheilocystida = 50 µm, cheilocystidium and spores = 10 µm.

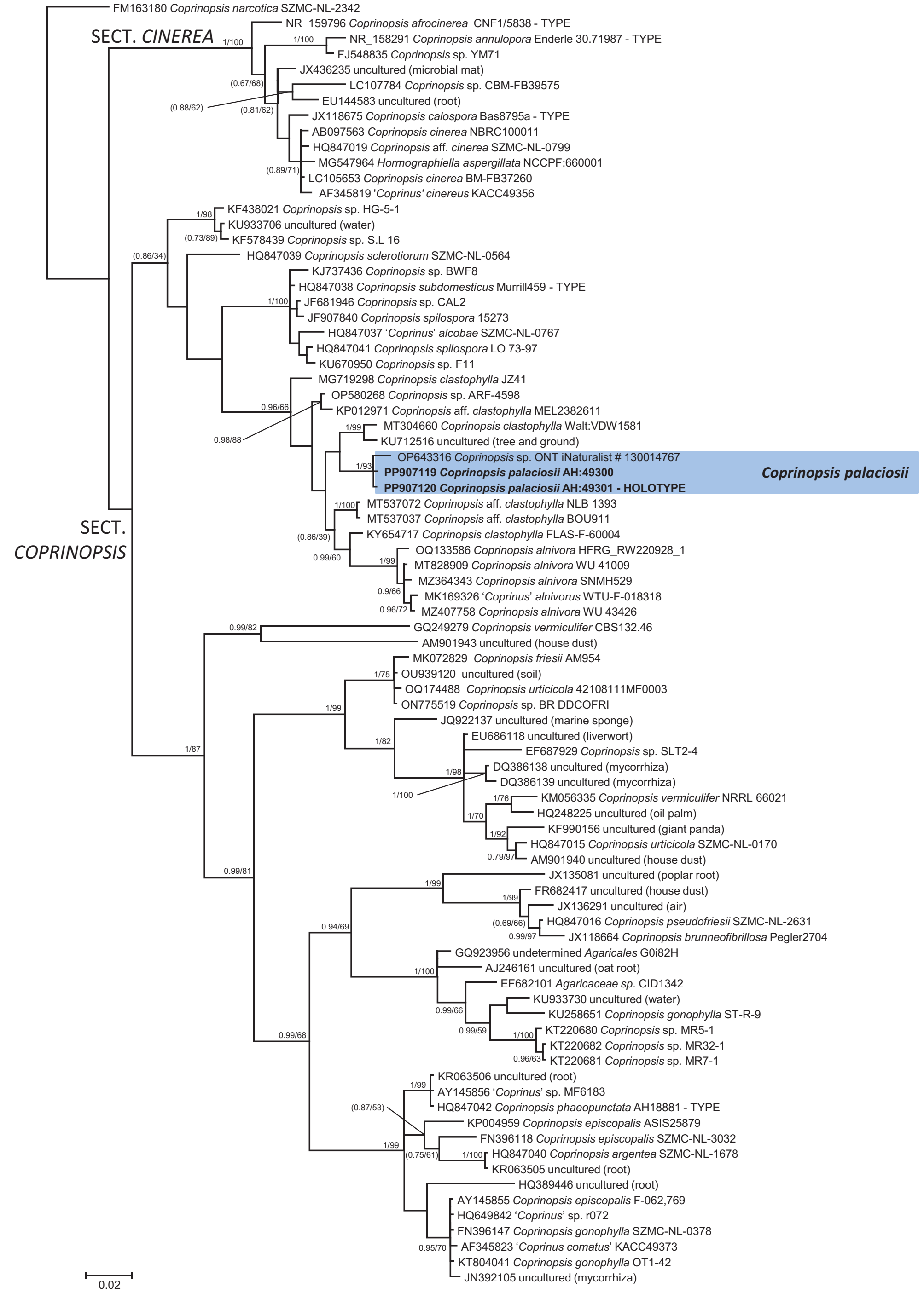
Notes: *Coprinopsis palaciosii* is characterized by its lignicolus habitat, growing solitary or in small groups on decaying wood of riparian trees, and the presence of persistent scales of the universal veil on the pileus. It belongs to section *Coprinopsis*, which includes small lignicolous or graminicolous species showing a universal veil formed by concatenated diverticulate hyphae. Molecularly, the ITS sequences produced are almost identical to GenBank OP643316, obtained from the undetermined sample iNaturalist #130014767 (Indiana, USA). They are also closely related (98.2 %) to sequences obtained from samples identified as *C. clastophylla* (*i.e.* KP012971, MT304660), but very different from the sequence (NR_154756) obtained from the type collection of this species (CBS 473.70). The LSU sequence is also close (99.57 %) to homologous sequences from *C.* aff. *clastophylla* (*i.e.* MT537072), and finally, *TEF1* is only 85 % close to the few homologous sequences of *Coprinopsis* available in databases.

Coprinopsis palaciosii seems to be closely related to several samples identified as *C. clastophylla* (considered a synonym of *C. lilacina*) and *C. alnivora*, two extra-European taxa with a similar lignicolous habitat, universal veil formed by thin-walled hyphae, cylindrical cystidia, and broadly ellipsoidal spores. The sexual morph of *C. lilacina*, was first described as *C. clastophylla* (Maniotis 1964), whose sporocarps were obtained *in vitro* from asexual material of *Rhacophyllus lilacinus* collected on wood remnants of *Quercus virginiana* in Texas (USA). It differs from *C. palaciosii* by having smaller basidiomata and slightly larger spores. *Coprinopsis alnivora* was first found in Washington (USA), growing on wood of *Alnus* sp. (Bogart 1976). It differs from *C. palaciosii* by its considerably larger spores and the presence of a ring on the stipe. The exact identity of these species needs to be fixed by sequencing type material (selecting epitypes if necessary), as there are probably multiple taxa identified with these names in databases.

Other genetically related, but more distant species include *C. spilospora*, with spores having a very conspicuous suprahilar plage (Romagnesi 1951), and *C. alcobae* with a non-lignicolous habitat (Ortega & Esteve-Raventós 2003). Other closely related lignicolous taxa with diverticulated, thin-walled veil hyphae include *C. urticicola* var. *salicicola*, which is much smaller in size and has partially diverticulated cystidia (Uljé & Noordeloos 1997); *C. gelatinosa*, an African species with larger spores and initially gelatinised veil (Reid & Eicker 1990); and *C. paleotropica*, another African taxon similar to *C. gelatinosa* (Redhead & Traquair 1981).

The remaining lignicolous species in the section *Coprinopsis* (Wächter & Melzer 2020) differ in various characteristics but mainly by their coralloid universal veil. Although belonging to another section, perhaps the species most likely to be confused with *C. palaciosii* is *C. mitrispora* (sect. *Mitraesporae*). The macroscopic resemblance is astonishing, and it occurs also in small groups on dead wood of riparian trees. However, unlike *C. palaciosii*, its universal veil is not formed by diverticulated elements (Bohus 1970). *Coprinopsis mexicana* has some similar microscopic features, but its basidiomata have very evident orange colours and, genetically, it belongs to a different section (Angelini et al. 2023)

Supplementary material: doi: 10.6084/m9.figshare.27169044.



A 50 % majority rule ITS consensus phylogram of selected species of genus *Coprinopsis* sections *Coprinopsis* and *Cinerea* (*Psathyrellaceae*, *Agaricales*) (with *C. narcotica* of section *Narcoticae* as outgroup) obtained using MrBayes v. 3.2.6 (Ronquist *et al.* 2012) from 12 000 sampled trees. Nodes were annotated if they were supported by ≥ 0.95 Bayesian posterior probability (left) or ≥ 70 % maximum likelihood bootstrap proportions (right) obtained in RAxML v. 8.2.12 (Stamatakis 2014). Non-significant support values are exceptionally represented inside parentheses. Sequences newly generated in this study are in **bold**. The alignment, Table and tree were deposited in Figshare.com (doi: 10.6084/m9.figshare.27169044).

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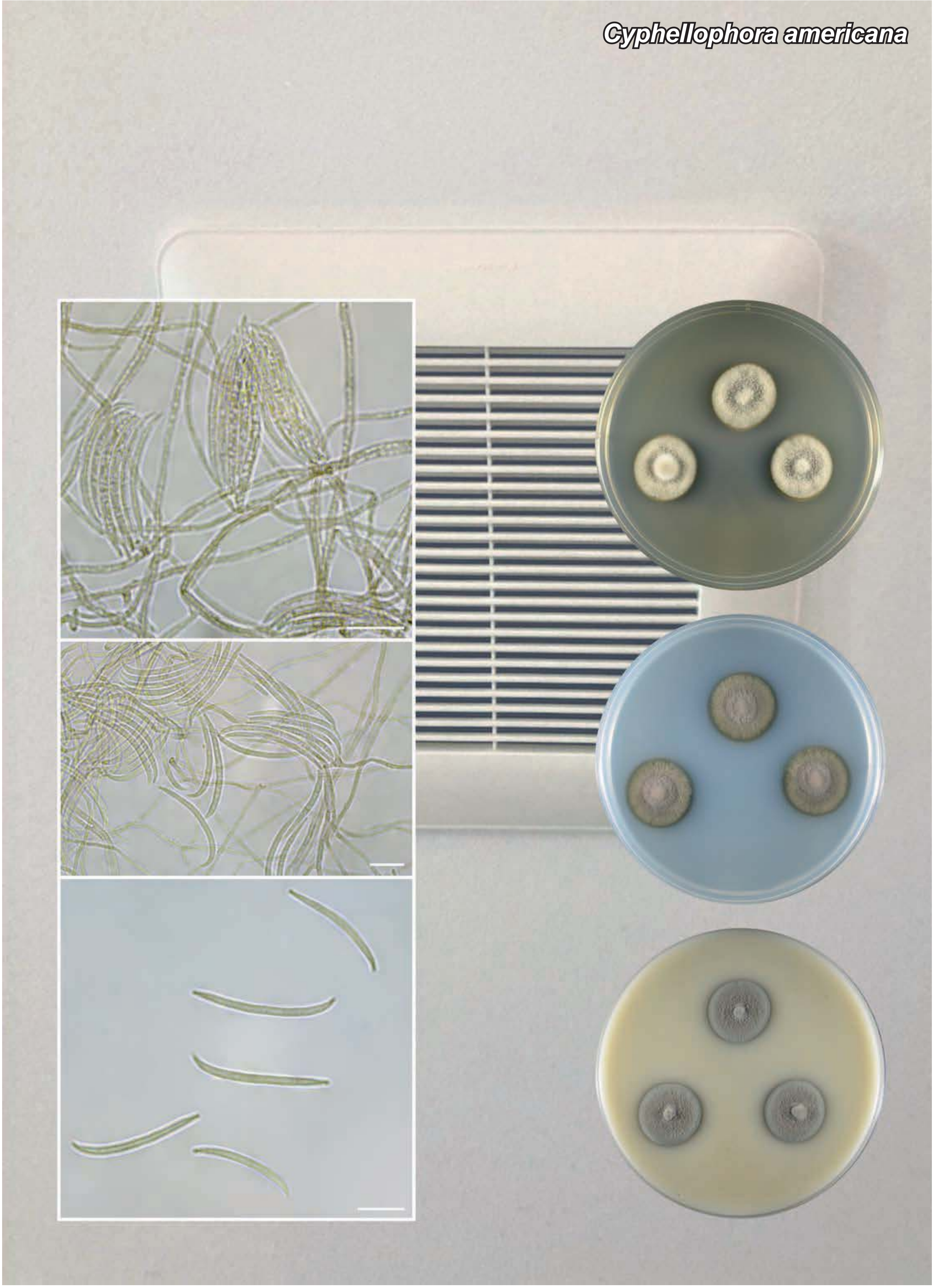

Cyphellophora americana

Fungal Planet 1748 MycoBank MB 843714

Cyphellophora americana Jurjević & Hubka, ***sp. nov.***

Etymology: Name refers to the country where it was collected, USA.

Classification: *Cyphellophoraceae*, *Chaetothyriales*, *Eurotiomycetes.*

Micromorphology (on malt extract agar; MEA): *Hyphae* pale greyish to pale brown, septate, smooth, thin-walled, 1.5–2.5 µm diam, rope-like structures present. *Conidiophores* reduced to conidiogenous cells on hyphae, pale grey brown, smooth, commonly cylindrical, 2–6 × 2–3.5 µm diam, apex with flared collarette, 1–1.5 µm long. *Conidia* subhyaline to pale brown, smooth, thin-walled, lunate to straight, 0–3-septate, (17–)22–32(–38) × 2–3 µm diam, commonly in small bundles. *Chlamydospores* and *sclerotia* absent. *Sexual morph* not observed.

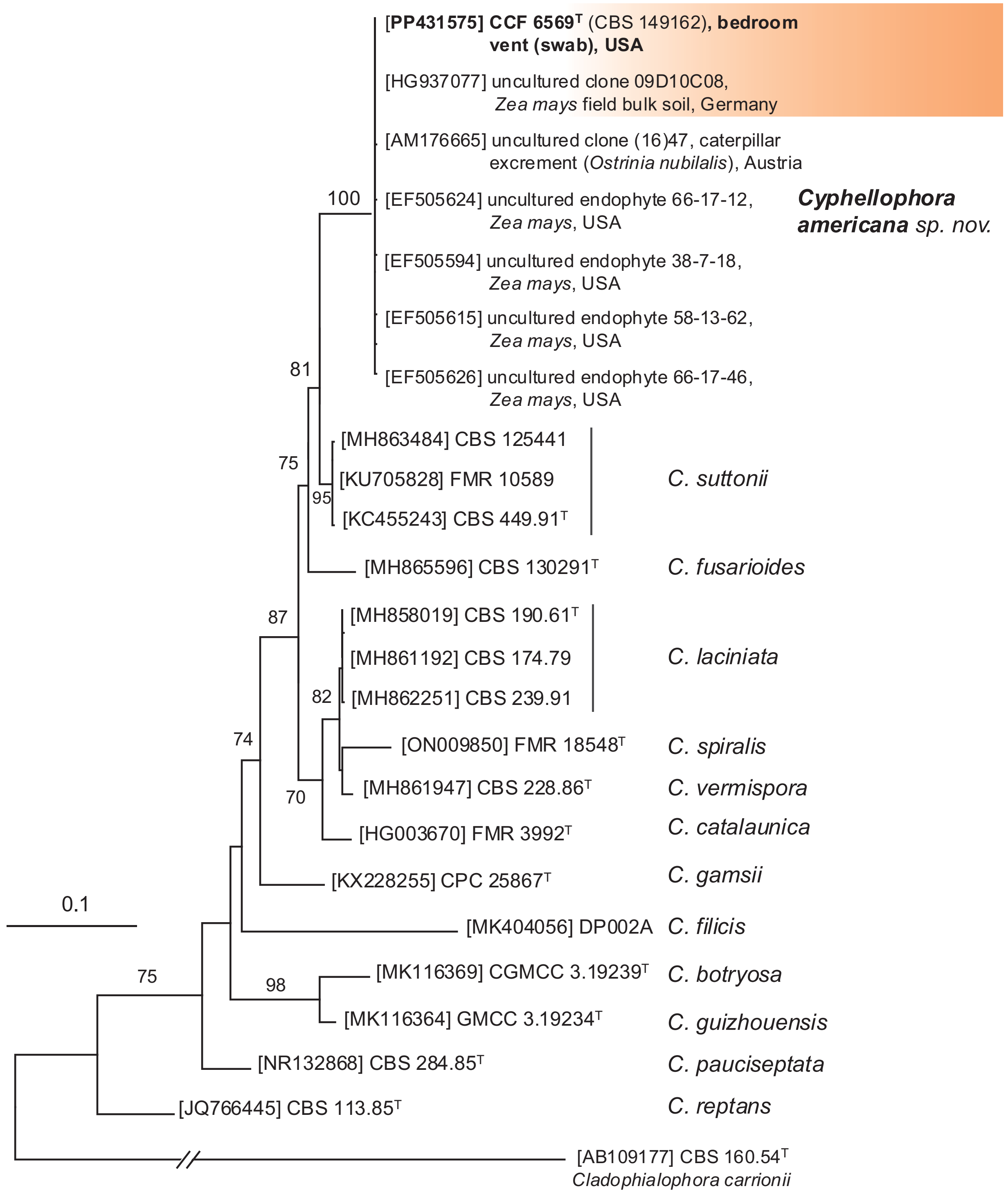
Culture characteristics: (in darkness, 25 °C after 14 d): Colonies on MEA 20–23 mm diam, floccose to lightly funiculose, mycelium peal smoke grey to smoke grey [R46; Ridgway (1912)], umbonate, sporulation very good, exudate absent, soluble pigments absent, reverse deep greyish olive to olivaceous black (R46). Colonies on Czapek yeast autolysate agar (CYA) 22–13 mm diam, floccose to lightly funiculose, moderate deep radially sulcate, mycelium light greyish olive to dark greyish olive (R46), sporulation very poor, exudate absent, soluble pigments absent, reverse deep greyish olive to dark greyish olive (R46). Colonies on potato dextrose agar (PDA) 24–25 mm diam, floccose to lightly funiculose, mycelium pale smoke grey to greyish olive (R46), umbonate, sporulation very poor, exudate absent, soluble pigments absent, reverse olivaceous black to greyish olive at margins (R46). Colonies on oatmeal agar (OA) 22–24 mm diam, floccose to lightly funiculose, mycelium light mineral grey to mineral grey (R46), sporulation poor to good, exudate absent, soluble pigments absent. Colony diam (in mm after 14 d) at 20 °C/30 °C; MEA 17–18/19–20; CYA 17–18/19–20; OA --/19–21. No growth on MEA, CYA, PDA and OA at 35 °C or 37 °C.

Typus: **USA**, Illinois, Lake Zurich, bedroom vent (swab), 29 Sep. 2016, *Ž. Jurjević* (**holotype** CBS H-25005, culture ex-type CBS 149162 = CCF 6569 = EMSL 3646; ITS, LSU and SSU sequences GenBank PP431575, PP431637 and PP431974).

Notes: BLAST analyses with the ITS, LSU and SSU sequences of *C. americana* showed greatest similarity with *C. suttonii* CBS 449.91^T (95.9 %, KC455243; 99.5 %, KC455256; and 99.9 %, KC455300, respectively), *C. catalaunica* FMR 3992^T (95.6 %, HG003670; 97.9 %, HG003673; and absent in GenBank, respectively) and *C. fusarioides* CBS 130291^T (94.1 %, MH865596; 99.1 %, MH877022; and absent in GenBank, respectively).

The strain from which the new species is described originates from an indoor environment in the USA. However, based on data available in GenBank (see isolates with identical ITS sequences in the phylogenetic tree), it appears to be associated with maize. Identical ITS sequences were found in maize field bulk soil in Germany (Moll *et al.* 2016; GenBank HG937077), in the excrement of the caterpillar of the maize pest *Ostrinia nubilalis* in Austria (Molnár *et al.* 2008; GenBank AM176665), and it was also recorded as an endophyte of maize (Pan *et al*. 2008; GenBank EF505624, EF505594, EF505615 and EF505626). *Cyphellophora americana* can be distinguished from its close relatives *C. suttonii* and *C. fusarioides* by conidia septation and size: *Cyphellophora americana* 0–3-septate, (17–)22–32(–38) × 2–3 µm diam, while *C. suttonii* 3–6-septate, 18–30 × 1–1.2 µm diam (Réblová *et al*. 2013), and *C. fusarioides* 1(–2)-septate, 11–20 × 2–2.5 µm (Réblová *et al*. 2013). Somewhat less, but still related species: *C. laciniata* 1–3-septate, 11–25 × 2–5 µm diam (Réblová *et al.* 2013); *C. vermispora* 4–8-septate, 30–55 × 1.2–1.5 µm diam (Réblová *et al*. 2013); *C. spiralis* 0–2(–3)-septate, 9–18 × 1–2 µm diam (Torres-Garcia *et al*. 2023); *C. catalaunica* 0–3-septate, (11–)15.5–26(–28) × 1.5–2 µm diam (Crous *et al.* 2013); *C. gamsii* (0–)3-septate, (22–)30–40(–50) × 1.5(–2) µm diam (Crous *et al*. 2016b).

Colour illustrations: Bedroom in Lake Zurich, Illinois, USA. 14-d-old cultures of *Cyphellophora americana* at 25 °C, (top to bottom MEA, PDA, OA); conidia and conidiophores on MEA. Scale bars = 10 µm.



A maximum likelihood (ML) tree based on the ITS regions shows the relationships of *Cyphellophora americana* and its close relatives. The alignment was performed using the FFT-NS-i option implemented in the MAFFT online interface (Katoh *et al.* 2019) and included 24 taxa and a total of 612 characters of which 203 were variable. The ML tree was constructed in IQ-TREE v. 2.2.2.6 (Minh *et al.* 2020) with nodal support determined by ultrafast bootstrapping (BS) with 100 000 replicates. The TIM2e+G4 model was selected as the best substitution model for ITS1 region, K2P+I+G4 for the 5.8S region and TNe+G4 for the ITS2 region. Only support values ≥ 70 % are shown; ex-type strains are indicated by a superscript T; novel species is indicated in bold font. The tree was rooted with *Cladophialophora carrionii*. The alignment and tree were deposited in TreeBASE/figshare/Zenodo/etc.

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Diaporthe neocapsici

Fungal Planet 1749 MycoBank MB 855675

Diaporthe neocapsici Ajithk., Savitha, Keerthana, Renuka & Mahadevak., ***sp. nov.***

Etymology: Named after the host genus, *Capsicum*, with the prefix "neo" to distinguish it from earlier reported species, *Diaporthe capsici*.

Classification: *Diaporthaceae*, *Diaporthales*, *Soradariomycetes*.

Phytopathogenic, associated with seedling blight of chilli. *Conidiomata* not observed on infected tissues. *Sexual morph*: not found. *Asexual morph* (on culture media): *Conidiomata* pycnidial, solitary, rarely aggregated, subglobose, dark brown to black, embedded in tissues, 187–324 µm diam, covered with hyphal out growths, superficial, ostiole absent, exuding a creamy mucoid conidial mass; pseudoparenchymatous, dark brown, outer layer thick walled and inner layer thin walled. *Conidiophores* formed in fascicles, macronematous, reduced to conidiogenous cells, cylindrical, smooth, hyaline to olivaceous. *Conidiogenous cells* (9.4–)12.1–16.3(–19.8) × (1.2–)1.6–2.3 (–2.8) µm, mostly phialidic, terminal, often intermingled with paraphyses. *Alpha conidia* ellipsoidal, hyaline, smooth, thin-walled, aseptate, bi-guttulate, straight to slightly curved, (4.9–)6.2–7.9(–9.4) × (1.2–)1.4–1.7(–1.9) µm. *Beta conidia* abundant, hyaline, filiform, hamate, eguttulate, aseptate, (24.9–)29.2–33.7(–37.6) × (1.1–)1.4–1.8(–2.1) µm.

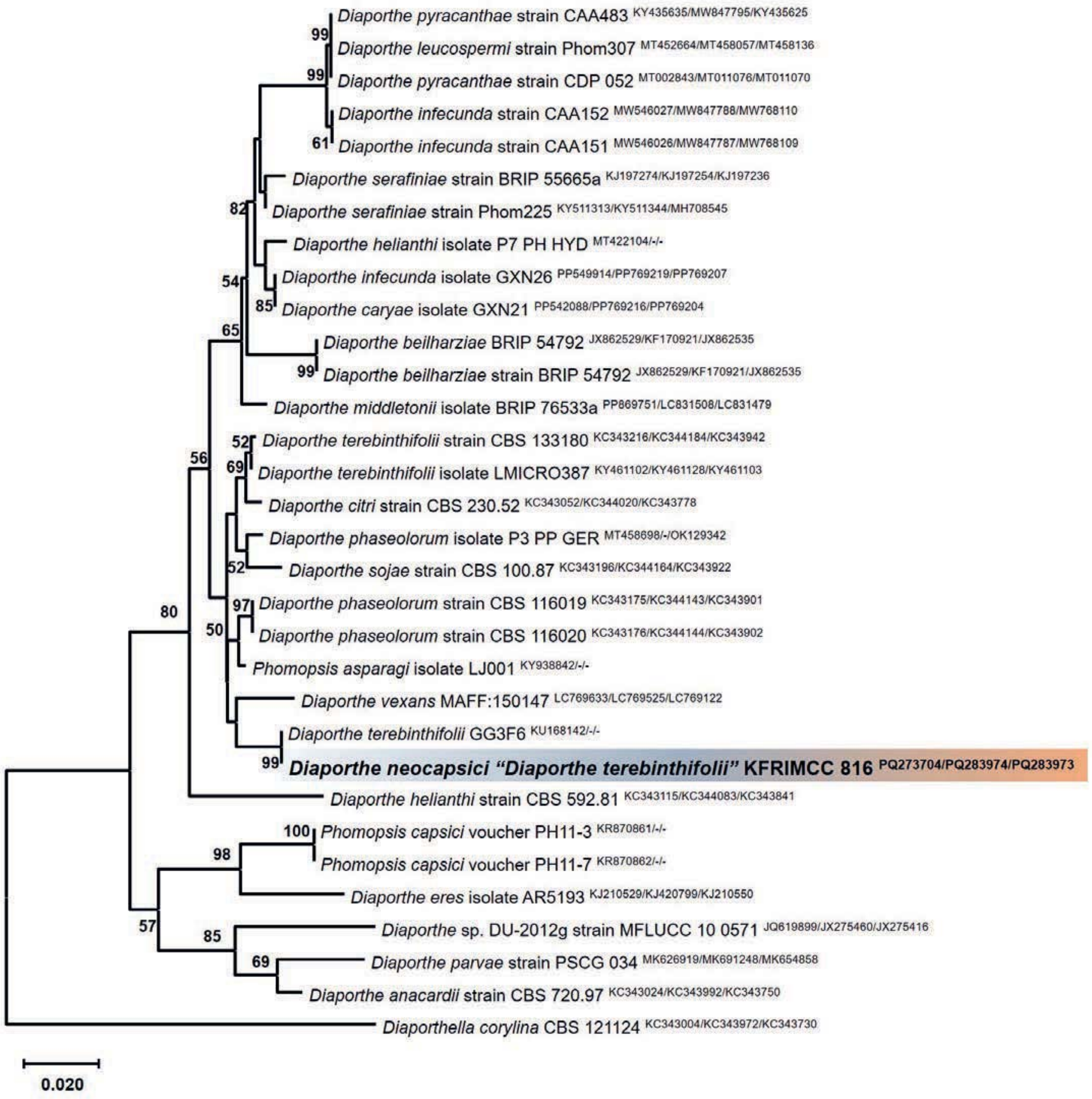
Culture characteristics: Colonies on potato dextrose agar (PDA) reaching 40 mm diam after 7 d at 28 °C. Surface flat, velvety, with uniform margin, whitish to pale. Reverse pale yellowish and become buff towards the centre. Conidiomata pycnidial, solitary or aggregated, half-immersed, pale brown to dark brown or black.

Typus: **India**, Karnataka, Raichur, University of Agricultural Sciences, Experimental Plot of Department of Plant Pathology, on young seedlings (stem portion) of *Capsicum annuum* (*Solanaceae*), 28 Aug. 2022, *A.S. Savitha, K. Ajithkumar & K.S. Keerthana* (**holotype** specimen KFRI-MH 816; living culture ex-type KFRIMCC 816; ITS, *tub2*, and *tef-1α* sequences GenBank PQ273704, PQ283974, and PQ283973).

Notes: Culturally and morphologically *D. neocapsici* is closely related to *D. vexans* but morphologically they differ with respect to the shape of their beta conidia and length of their conidiogenous cells. Furthermore, ITS nrDNA, *tef-1α* and *tub2* gene sequence data did not share any similarity with *D. vexans*. However, the concatenated sequence alignment of ITS-*tub2*-*tef-1α* shared a common clade with *D. terbinthifolii* (GenBank KU168142) an endophytic isolate obtained from *Glycyrrhiza glabra* which was identified based on ITS sequence data alone. However, ex-type strains/isolates of *D. terbinthifolii* (CBS 133180 & LMICRO387) are distantly placed in the phylogram, thus confirming that the *Diaporthe* species from the present investigation is not *D. terbinthifolii*. Based on the multi-locus phylogenetic analysis, the *Diaporthe* species isolated from chilli tissues is herewith introduced as a new species.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of *D. neocapsici* had highest similarity to *Phomopsis asparagi* [isolate LJ001, GenBank KY938892; Identities = 630/666 (94.59 %), 12 gaps (1 %)], *D. phaseolorum* [isolate P12_PP_GER, GenBank MT458702; Identities = 593/621 (95.49 %), ten gaps (1 %)), *D. phaseolorum* (isolate P3_PP_GER, GenBank MT458698; Identities = 589/620 (95 %), nine gaps (1 %)], *D. terbinthifolii* [isolate GG3F6, GenBank KU168142; Identities = 506/508 (99.61 %), one gap (0 %)] and *D. helianthi* [isolate P7_PH_HYD, GenBank MT422104; Identities 546/570 (95.79 %) two gaps (0 %)]. The ***tub2*** gene sequence shared highest similarity to *D. leucospermi* [strain CAA152, GenBank MW847788; Identities = 385/460 (83.70 %) eight gaps (1%))], *D. leucospermi* [strain CAA 151, GenBank MW847787; Identities = 385/460 (83.70 %) eight gaps (1 %)], *D. pyracanthe* [strain CDP 052, GenBank MT01107; Identities = 384/459 (83.66 %) two gaps (1 %)], *D. pyracanthe* [strain CAA483, GenBank KY435666; Identities = 308/347 (88.76 %) two gaps (0 %)], *D. beilharziae* [strain BRIP 54792, GenBank KF170921; Identities = 308/347 (88.76 %) two gaps (0 %)] and *D. serafiniae* [strain BRIP 55665b, GenBank KJ197254; Identities = 307/347 (88.47 %) two gaps (0 %)]. Further, the closest hits using the ***tef-1α*** gene sequence had highest similarity to *D. middletonii* [strain BRIP 76533a, GenBank LC831479; Identities = 309/373 (82.84 %), nine gaps (2 %)], *D. infecunda* [isolate GXN26, GenBank PP769207; Identities = 311/376 (82.71 %), 11 gaps (2 %)], *D. leucospermi* [strain Phom307, GenBank MT458136; Identities = 309/374 (82.62 %), 12 gaps (3 %)], *D. caryae* [isolate GXN21, GenBank PP769204; Identities = 306/370 (82.70 %), 11 gaps (2 %)], *D. beilharziae* [strain BRIP 54792, GenBank JX862535; Identities = 299/361 (82.83 %), 11 gaps (3 %)], *D. pyracanthe* [strain CDP 052, GenBank MT011070; Identities = 309/376 (82.18 %), 12 gaps (3 %)] and *D. serafiniae* [isolate Phom225, GenBank MH708545; Identities = 298/361 (82.55 %), 12 gaps (3 %)].

Colour illustrations: Seedlings of *Capsicum annuum* found infected with a seedling blight disease in an experimental plot of the University of Agricultural Science, Raichur; Karnataka. Left panel from top: Seedlings affected with *Diaporthe neocapsici*, active culture of *D. neocapsici* top and reverse view of PDA plate, conidiomatal structures developed from the culture; right panel from top to bottom: conidiogenous cells, alpha conidia and beta conidia of *D. neocapsici*. Scale bars = 10 µm.



Phylogenetic tree of *Diaporthe neocapsici* constructed using MEGA v. X (Kumar *et al.* 2018) of the ITS-*tub*2-*tef*-1α concatenated sequence alignment by Maximum-Likelihood Method (Saitou & Nei 1987). The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1 000 replicates) are shown next to the branches (Felsenstein 1985). The evolutionary distances were computed using the Kimura 2-parameter method (Kimura 1980) and are in the units of the number of base substitutions per site. This analysis involved 32 nucleotide sequences, including the outgroup. All positions containing gaps and missing data were eliminated (complete deletion option). There were a total of 372 positions in the final dataset. The phylogenetic position of *D. neocapsici* is indicated in **bold**. The alignment and tree were deposited in figshare.com (doi: 10.6084/m9.figshare.27172776).

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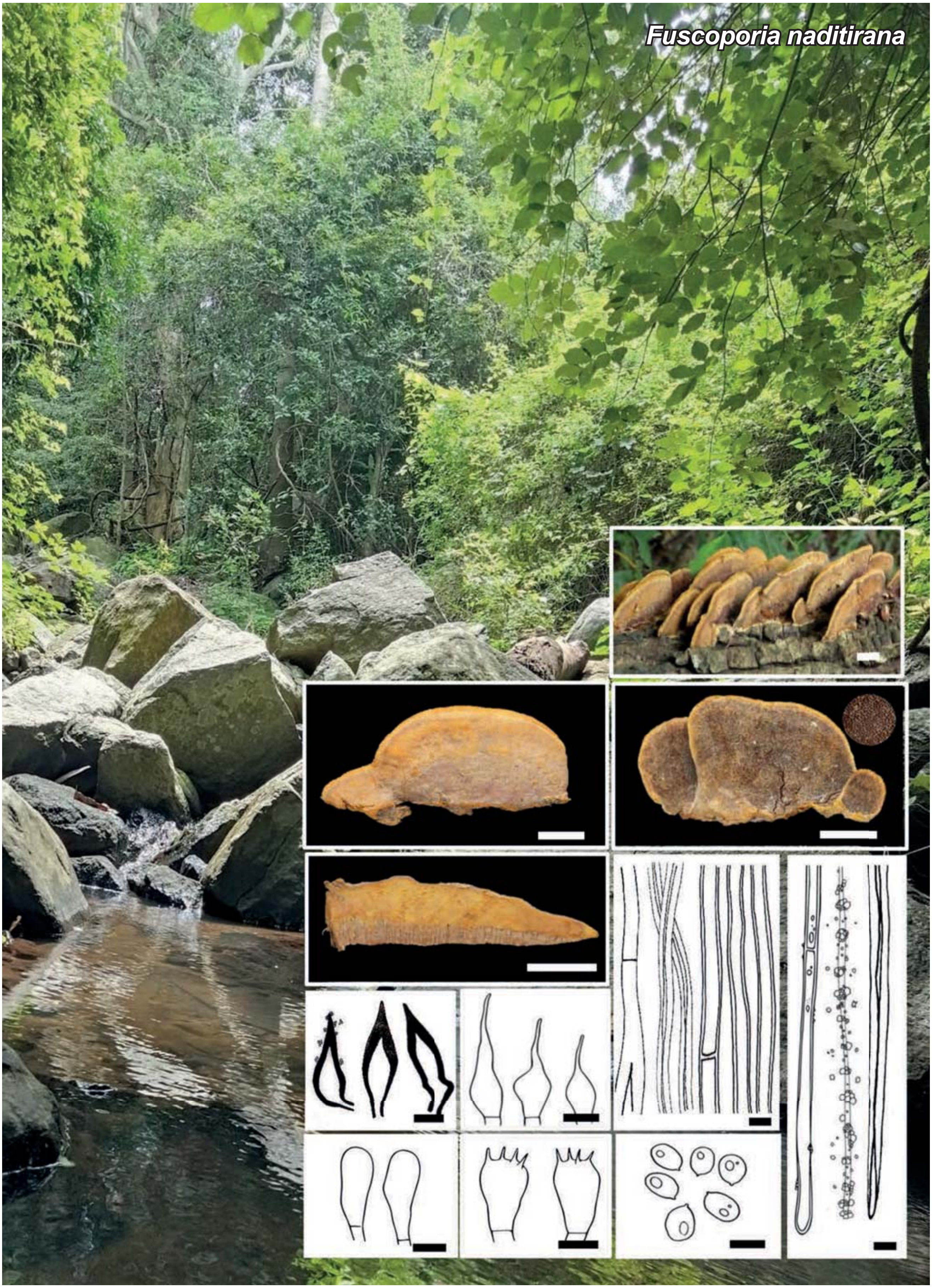

Fuscoporia naditirana

Fungal Planet 1750

MycoBank MB 855669

Fuscoporia naditirana S. Gunaseelan, E. Arumugam & M. Kaliyaperumal, ***sp. nov.***

Etymology: The species epithet "*naditirana*" is a Sanskrit word, referring to the bank of a stream where the specimen was collected.

Classification: *Hymenochaetaceae*, *Hymenochaetales*, *Agaricomycetes*.

Basidiomes annual to biennial, applanate, pileate, appears to be imbricate, soft to light corky when dry. *Pilei* dimidiate, broadly attached, convex, projecting up to 4.2 cm long, 5.7 cm broad, and 1.5 cm thick at the base. *Pileal surface* smooth, glabrous, brown (7E6; Kornerup & Wanscher 1978) to brownish yellow (5C8) near the attachment, yellowish brown (5D8) towards margin, smooth, indistinctly zonate. *Margin* distinct, yellowish brown (5D8), acute, 1 mm thick. *Pore surface* pale brown (5F8) to dark brown (6F8), glancing. *Pores* round to angular, 9–12 / mm. *Context* brownish yellow (5C8), homogenous, up to 3.2 mm thick. *Tube layer* yellowish brown (5D6), hard corky, tubes stratified up to 2 mm thick. *Hyphal system* dimitic; generative hyphae simple, septate; tissue darkening but otherwise unchanged in KOH. *Context* generative hyphae hyaline, thin- to slightly thick-walled, branched, thin-walled hyphae frequently encrusted, simple septate, 2.1–3.4 µm wide; skeletal hyphae dominant, rust-brown, thick walled with a medium to wide lumen, branched, occasionally septate, straight, more or less straight and regularly arranged, 2.4–3.4 µm wide. *Trama* generative hyphae dominant at dissepiment edges, thin-walled, encrusted, frequently branched and simple septate, hyaline, 2.1–3.2 µm wide; skeletal hyphae dominant, thick-walled with a medium to wide lumen, infrequently septate, more or less straight, subparallel along the tubes, yellow to golden yellow, 2.4–3.2 µm diam. *Hymenial setae* subulate to ventricose, acute to acuminate at the apex, infrequently apically encrusted, occasionally bi-radicated, originating from tramal hyphae, dark brown, thick walled, 12–35 × 6–9 µm; *Cystidioles* hyaline to pale yellow in water, changing to yellow in KOH, fusoid to subulate, rare, tapering at the end, 6–32 × 2.5–6.7 µm. *Basidioles* broadly clavate, 8–16 × 4.5–6.3 µm size. *Basidia* broadly clavate, yellow, four sterigmata, 9–17 × 2.5–6.7 µm. *Basidiospores* hyaline, thin-walled, smooth, ellipsoid, CB$^-$, IKI$^-$, (3.0–)3.2–3.8(–4.2) × (2.0–)2.2–2.5µm, Q = 1.5, Q = 1.3–1.6, (n = 30/2).

Typus: **India**, Tamil Nadu, Kallakurichi, 11°96'N, 78°77'E, on dead wood, 18 Mar. 2019, *M. Kaliyaperumal* (**holotype** MUBL1105; ITS, LSU, *rpb2* and *tef1-α* sequences GenBank PQ098039, PP390499, PQ346367 and PQ346369).

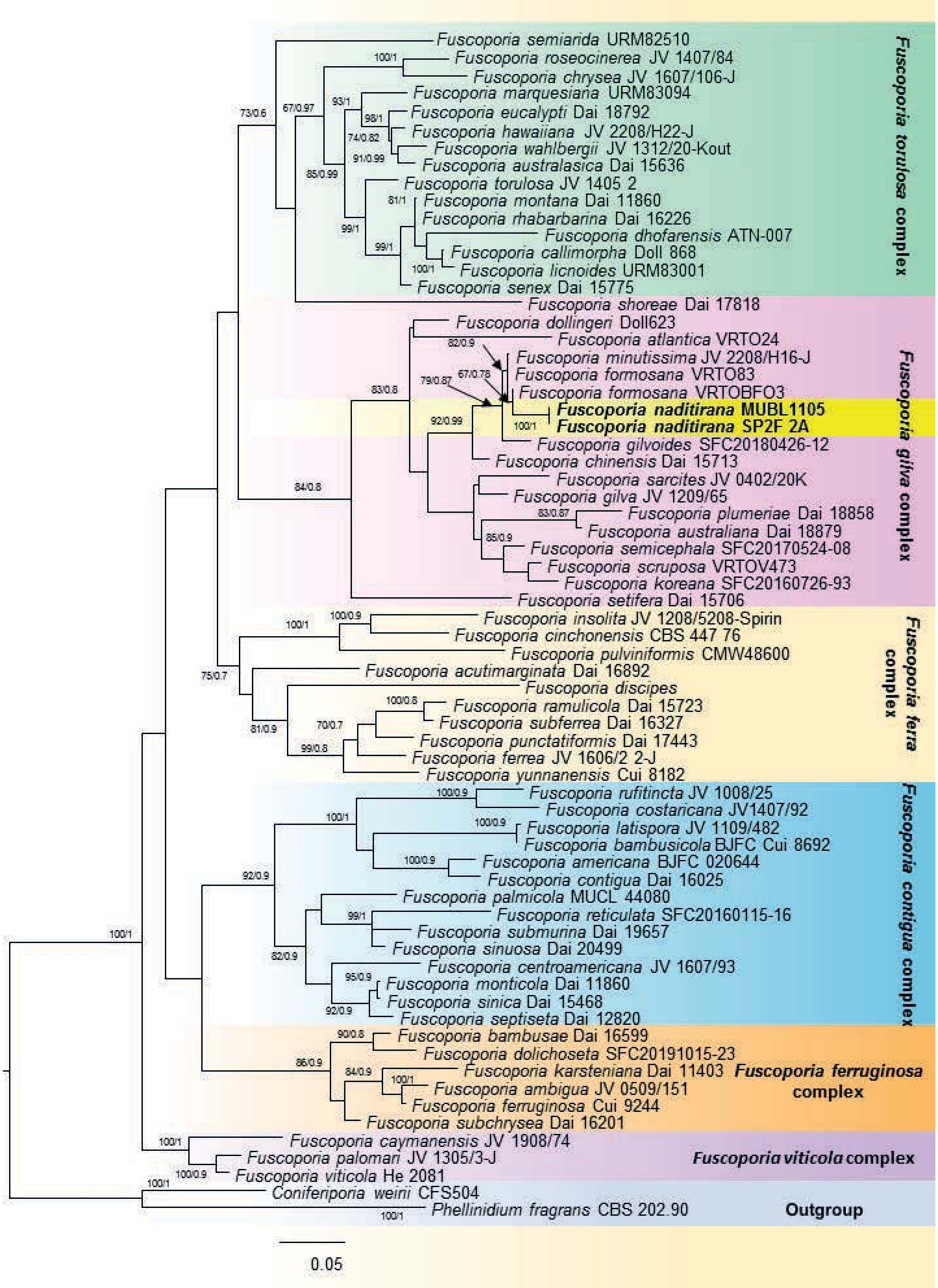
Additional material examined: **India**, Tamil Nadu, Kallakurichi, 11°96'N, 78°77'E, on dead wood, 18 Mar. 2019, *M. Kaliyaperumal* (**paratype** SP2FA; ITS, LSU, *rpb2* and *tef1-α* sequences GenBank PQ098040, PQ113748, PQ346368 and PQ346370).

Colour illustrations: *Fuscoporia naditirana* growing next to the stream in Serapattu, Kalvarayan Hills, India. Habitat; pilear surface; pore surface; transverse section of basidiomata; *camera lucida* drawing of holotype: contextual hyphae, tramal hyphae; seate; cystidioles; basidioles; basidia; basidiospores. Scale bars: basidiocarps = 1 cm; all other structures = 5 µm.

Notes: Multigene phylogenetic analyses inferred from ITS, LSU, *rpb2* and *tef1-α* revealed that *F. naditirana* formed a distinct lineage (100 % ML, 1.0 BI) in the *F. gilva* clade (Cho *et al*. 2023) with other related *Fuscoporia* spp. (*viz*. *F. formosana*, *F. minutissima*, *F. gilvoides* and *F. chinensis*). *Fuscoporia naditirana* differs from *F. formosana* in having smooth, indistinctly zonate basidiomes with smaller pores (9–12 / mm), a dimitic hyphal system, and cystidioles, whereas *F. formosana* has coarsely tomentose to hispid, narrowly zonate basidiomes, a strictly monomitic hyphal system, no cystidioles and larger pores (3–5 / mm) (Wu *et al*. 2022). *Fuscoporia naditirana*, *F. minutissima* and *F. gilvoides* resemble *F. naditirana* in having dimitic hyphae and cystidioles. However, the former differs by having annual to biennial weakly zonate, glabrous, smooth basidiomes and smaller basidiospores, whereas *F. minutissima* and *F. gilvoides* are perennial, concentrically sulcate, zonate basidiomes with larger basidiospores (Chen *et al*. 2023, Cho *et al*. 2023). *Fuscoporia naditirana* differs from *F. chinensis* by having applanate, glabrous basidiomes, an acute margin and smaller pores, whereas the latter has an effused reflex, pileal surface and radially rugose, obtuse margin with larger pores (7–8 / mm) (Wu *et al.* 2022).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Fuscoporia gilva* [strain JP107, GenBank OR827617; Identities = 556/600 (93 %), 17 gaps (2 %)], *Fuscoporia minutissima* [strain JV 2208/H12-J, GenBank OQ817711; Identities = 556/600 (93 %), 17 gaps (2 %)], and *Fuscoporia gilva* [strain UOC KAUNP MK 42, GenBank KT037022; Identities = 556/600 (93 %), 17 gaps (2 %)]. Closest hits using the **LSU** sequence are *Fuscoporia minutissima* [strain JV 2208/H12-J, GenBank OQ817857; Identities = 1 283/1 287 (99 %), two gaps (0 %)], *Fuscoporia minutissima* [strain JV 2208/H16-J, GenBank OQ817858; Identities = 1 282/1 287 (99 %), two gaps (0 %)], and *Fuscoporia plumeriae* [strain Dai 18858, GenBank MN810010; Identities = 1 279/1 287 (99 %), 2 gaps (0 %)]. Closest hits using the ***rpb2*** sequence are *Fuscoporia gilvoides* [voucher MUGBt, GenBank ON479791; Identities = 589/609 (97 %), no gaps (0 %)], *Fuscoporia chinensis* [voucher Dai 17282, GenBank MN848772; Identities = 591/612 (97 %), no gaps (0 %)] and *Fuscoporia gilva* [isolate Dai 15681, GenBank MN159389; Identities = 590/611 (97 %), no gaps (0 %)]. Closest hits using the ***tef1-α*** sequence are *Fuscoporia plumeriae* [voucher Dai 17814, GenBank MN848845; Identities = 493/499 (99 %), no gaps (0 %)], *Fuscoporia plumeriae* [voucher Dai 18858, GenBank MN848843; Identities = 492/499 (99 %), no gaps (0 %)] and *Fuscoporia gilvoides* [voucher SFC20150701-23, GenBank ON479815; Identities = 478/499 (96 %), no gaps (0 %)]

Supplementary material: doi: 10.6084/m9.figshare.27190245 (Table and Alignment).



Multigene phylogenetic analyses from ITS, LSU, *rpb2* and *tef1-α* sequences of *Fuscoporia naditirana* (MUBL1105, holotype and SP2F 2A) and related species rooted with *Coniferiporia weirii* (CFS504) and *Phellinidium fragrans* (CBS 202.90). The maximum likelihood (ML) analysis was performed using MEGA v. X (Kumar *et al*. 2018) and the same data were used for a Bayesian analysis using MrBayes v. 3.2.7 (Ronquist *et al*. 2012). Branches are labelled with ML bootstrap support and Bayesian posterior probabilities values (BPP). Novel species is in **bold**. The tree is available from TreeBASE (study ID: S31691).

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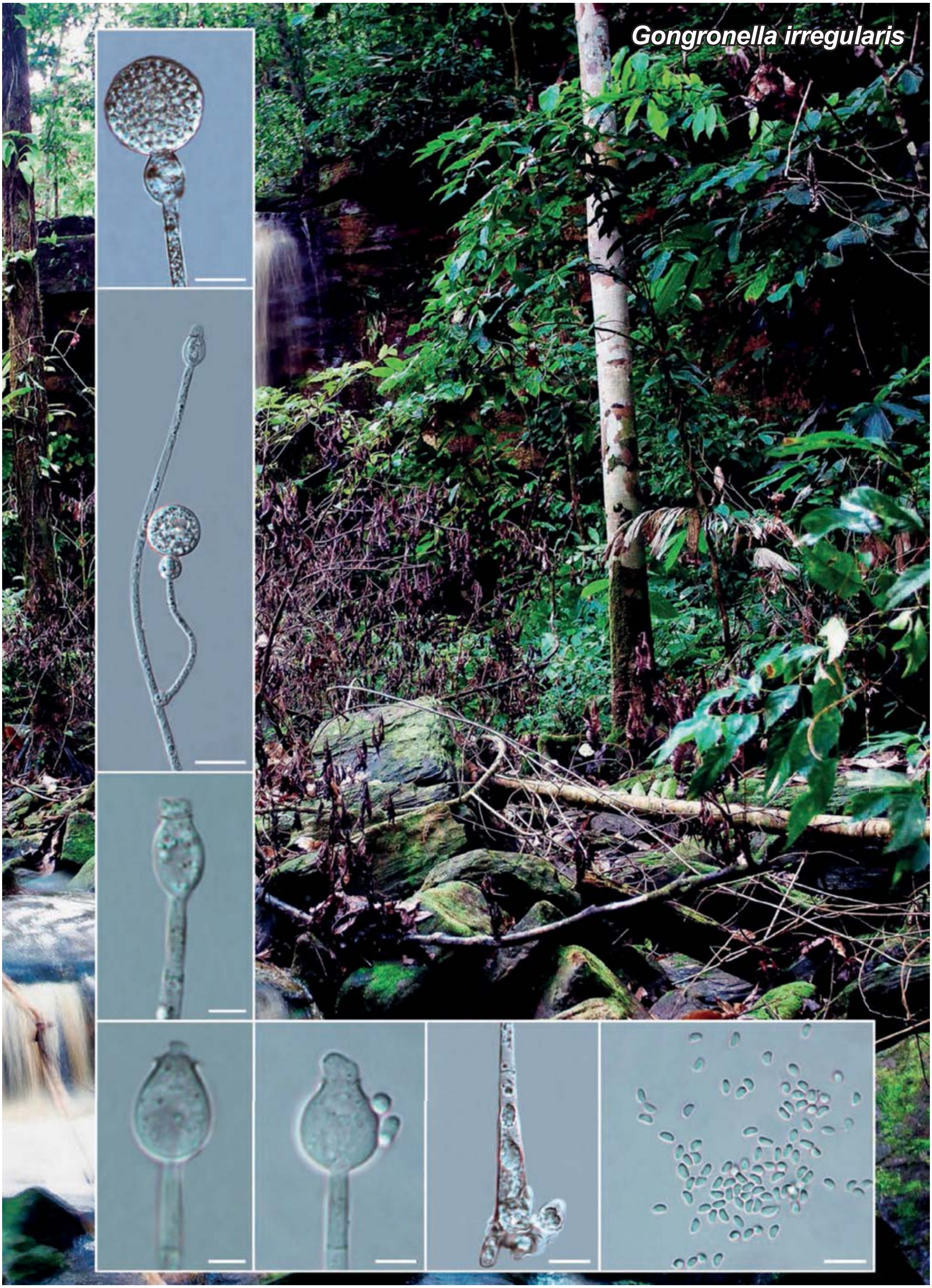

Gongronella irregularis

Fungal Planet 1751

MycoBank MB 855455

Gongronella irregularis L.S.W Freitas, S.B.G da Silva & A.L. Santiago, ***sp. nov.***

Etymology: Referring to the irregularly-shaped columellae.

Classification: *Cunninghamellaceae*, *Mucorales*, *Mucoromycota*, *Mucoromycetes*.

Mycelium hyaline with oil contents. *Colony* with cottony aspect, white; reverse cream with regular margin. *Rhizoids* hyaline, with branches arising from the same point, septate or not at the base, commonly bulbous, some irregularly-shaped, 12–120 × 7–12 µm. *Stolons* hyaline, coenocytic. *Sporangiophores* hyaline with a septum below the apophysis, rarely with two septa, simple or sympodially branched up to four times, rarely forming monopodial branches, (70–)240–540(–720) × 2.5–4.5 µm, with swelling at the base, 4.5–7 µm in width. Short branches 24–55 × 2–6 µm and long branches 40–90 × 2–4 µm. *Sporangia* yellow, globose, 7–20 µm diam, wall deliquescent, leaving a collar. *Sterile sporangia* frequent, hyaline, globose or subglobose, located at the apex of the main sporophore or on its lateral branches, 5–15 µm diam. *Columellae* hyaline, nipple-shaped, hemispherical, subglobose, angular, irregularly-shaped, and some inconspicuous, 2–5.5 × 3–6.5 µm. *Apophyses* vasiform, some elongated, elliptical, 5–20 × 3–9.5 µm. *Sporangiospores* hyaline, reniform, 2.5–6 × 2–5 µm. *Chlamydospores* abundant, hyaline, globose, 2.5–9 µm diam. *Zygosporangia* absent.

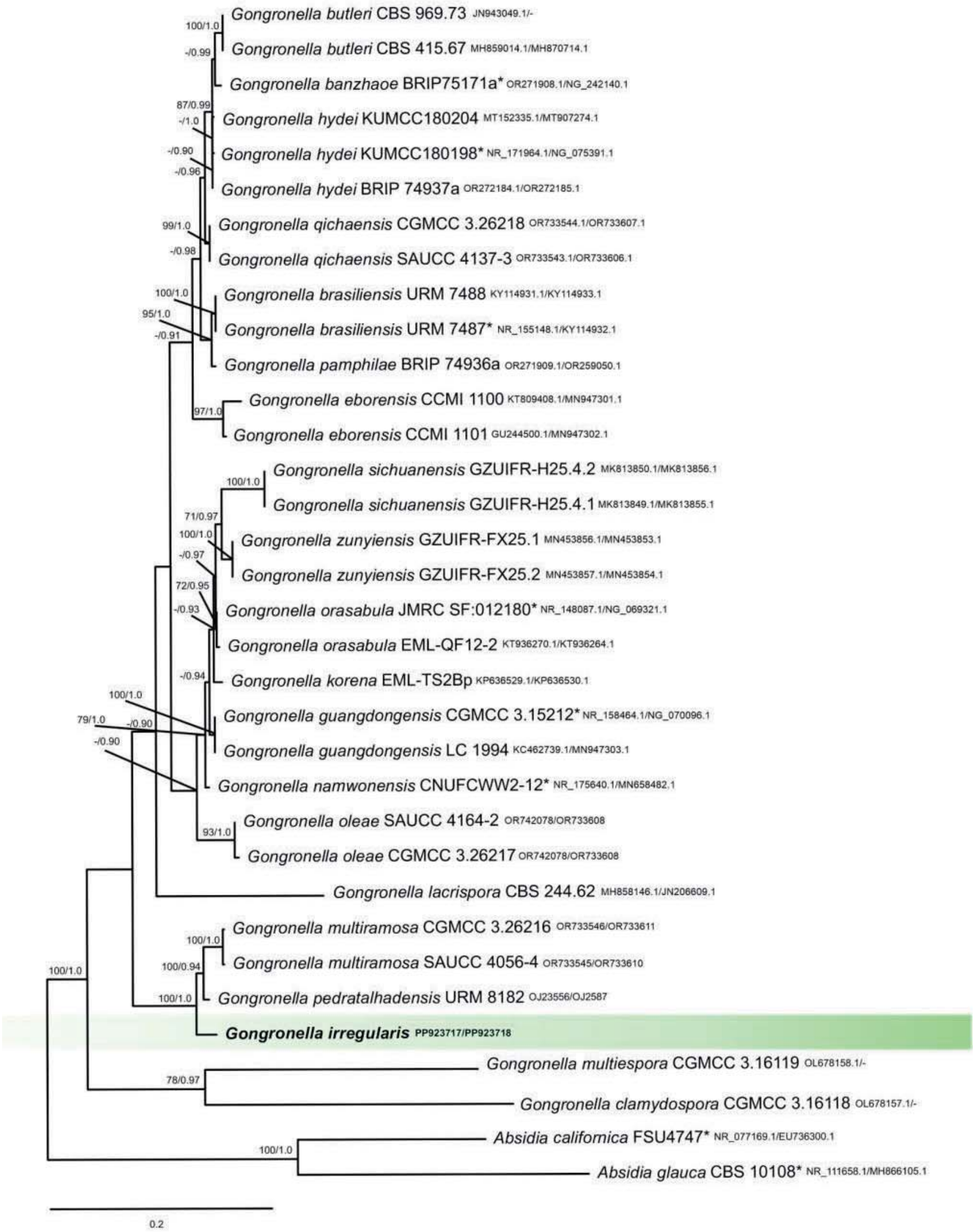
Culture characteristics: Colonies with cottony aspect, white; reverse with regular margin, light honey, growing 8.5 cm diam after 8 d on PDA at 25 °C. On PDA: at 10 °C – lack of growth; 15 °C – slow growth (3.1 cm diam after 5 d) with poor sporulation; at 20 °C – slow growth (2.5 cm diam after 5 d), and good sporulation; at 25 °C – better growth (5.3 cm diam after 5 d) with excellent sporulation; at 30 °C – slow growth (3.4 cm diam after 5 d) good sporulation; at 35 °C – lack of growth. Sterile sporangia are more common at temperatures of 25 and 30 °C. On MEA: at 10 °C – lack of growth; 15 °C – slow growth (1.1 cm diam after 5 d) and poor sporulation; at 20 °C – slow growth (2.5 cm diam after 5 d), and good sporulation; at 25 °C –better growth (9 cm diam after 5 d) with excellent sporulation; at 30 °C – slow growth (3.1 cm diam after 5 d) good sporulation; at 35 °C – lack of growth.

Colour illustrations: Brazil, Mato Grosso, Cristalino State Park (type locality). Sporangiophore with apophysate sporangium; branched sporangiophore with terminal columella and lateral sporangium; sporangiophore with irregular columella, sporangiophore with nipple-shaped columella, sporangiophore with irregular columella, sporangiophore with rhizoid, sporangiospores. Scale bars: other microscopic structures = 10 µm; columellae = 5 µm.

Typus: **Brazil**, Mato Grosso State, Novo Mundo, Parque Estadual do Cristalino, S09°37’59” W55°29’22”, isolated from soil samples, coll. 9 Dec. 2022, *B.T. Goto*, isol. 5 Mar. 2023, *L.W.S. de Freitas* (**holotype** URMB 95619, culture ex-type URM 9013; ITS and LSU sequences GenBank PP923717 and PP923718).

Notes: During a survey on the diversity of *Mucoromycota* from the Amazon Rainforest in the Mato Grosso state of Brazil, one strain belonging to *Gongronella* that is morphologically and genetically [internal transcribed spacer (ITS) and large subunit (LSU) rDNA] distinct from other species, was isolated. In the phylogenetic tree, the strain clustered in a fully supported clade, closer to *G. pedratalhadensis,* but also close to *G. multiramosa*. *Gongronella irregularis* differs morphologically from *G*. *pedratalhadensis* as the latter forms rhizoids with globules but not with nodular basal structures as is observed in *G. irregularis.* Sporangiophores of *G. pedratalhadensis* are simple and weakly sympodially branched (up to 2 times), and columellae are commonly hemispheric, with some subglobose, and short hemispheric (de Freitas *et al*. 2021), whereas the new species forms sporangiophores simple and sympodially branched up to four times, and columellae varied-shaped, many angular and irregular, some inconspicuous. *Gongronella multiramosa* differs from *G. irregularis* by not forming stolons and by forming giant cells, while the new species forms stolons but not giant cells. Yet, *G. multiramosa* forms sporangiophores strongly sympodially branched (up to seven times) with columellae mostly hemispherical, sometimes sub-hemispherical (Wang *et al.* 2023), thus differing from the ones of *G*. *irregularis*.

Based on a megablast search of NCBIs GenBank nucleotide database, *G*. *pedratalhadensis* is also the closest relevant hit using ITS [strain URM 8182, GenBank MN912511; Identities = 611/639 (96 %), nine gaps (1 %)] and LSU [strain URM 8182, GenBank MN912508; Identities = 626/639 (98 %), no gaps].



Phylogenetic tree derived from a Maximum Likelihood analysis based on ITS and LSU sequences of *Gongronella* conducted in RAxML in the CIPRES science gateway (Miller *et al.* 2010). Confidence values for ML-BS ≥ 70 % (RAxML) and BPP ≥ 0.90 are included near the nodes. Bayesian inference (BI) was conducted in MrBayes on XSEDE v. 3.2.7a (Ronquist *et al.* 2012). The substitution model GTR+G+I was used for the alignment in the ML and GTR +G in the BI analyses. The species obtained in this study is in **bold**. Ex-type strains are marked with an asterisk (*) and GenBank accession numbers (superscript; ITS/LSU) are indicated for all species. The tree was rooted to *Absidia californica* (FSU 4747) and *Absidia glauca* (CBS 101.608). The final alignment was deposited in Figshare.com (doi: 10.6084/m9.figshare.27183696).

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Hygrocybe mirabilis

Fungal Planet 1752 MycoBank MB 854067

Hygrocybe mirabilis Lodge, T.J. Baroni, Boertm. & Læssøe, ***sp. nov.***

Etymology: *mirabilis* – astonishing, for startling contrast of red lamellae and yellow pileus.

Classification: *Hygrocybaceae*, *Agaricales*, *Agaricomycetes*.

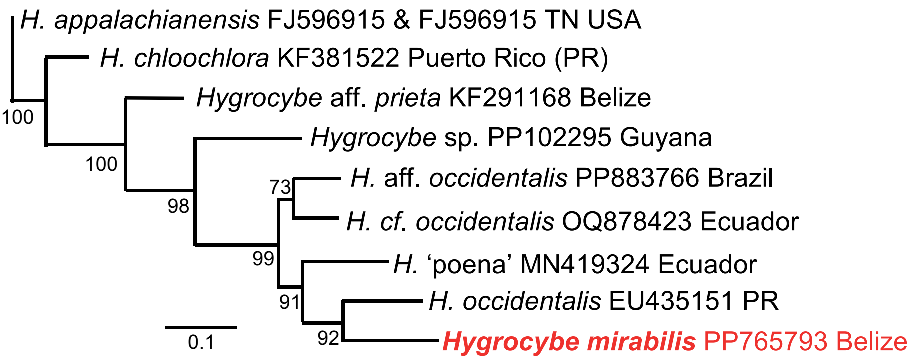
Pileus 38 mm diam, broadly convex, slightly depressed and perforated at centre; Spectrum Yellow at centre, Orange Yellow (Smithe 1975) on outer half, translucent-striate 2/3 to centre with pale red striae corresponding to lamellae below; surface smooth, shiny and viscid; *context* thin, yellow. *Lamellae* adnate with decurrent tooth, reaching the pileus margin, 5 mm broad, distant, 1–>1 mm apart at margin, Flame Scarlet, Orange Yellow near attachment to pileus. *Stipe* 40 × 6–7 mm, slightly clavate, Flame Scarlet above, Orange Yellow at base. *Basidiospores* dimorphic. *Macrospores* 14.7 ± 1.3 × 8.3 ± 0.64 µm, range 12.0–16.0 × 6.8–8.8 µm, mean Q 1.61 ± 0.19, range 1.4–1.9, ellipsoid. *Microspores* 5.2–6.4 × 3.2–4.8 µm, ovoid or lacrymoid, few mature. *Basidia* dimorphic. *Macrobasidia* 60–70.4 × 8.8–14 µm. *Microbasidia* 24–30 × 4.8–6.4 µm. *Lamellar trama* regular, consisting of long cells, 165–199 µm long, tapered at both ends. *Pileipellis* a thin repent cutis, hyphae 36–120 × 9.6–12 µm, with large *clamp connections*.

Habitat and habit: Solitary in humus of broadleaved evergreen tropical cloud forest.

Typus: **Belize**, Doyle's Delight, Chiquibul National Park, 16°30'N, 89°3'W, 1 080 m a.s.l., on soil, 15 Aug. 2004, coll. *T.J. Baroni*, CFMR BZ-3867, ledger *D.J. Lodge*, DJL-BZ-65 (**holotype** NY, ITS sequence GenBank PP765793); *idem*., **isotype** BRH.

Additional material examined: **Ecuador**, Napo Province, Cuyabeno, 00°35'S, 76°11'W, 205 m a.s.l., 8 Nov. 1993. coll. *T. Læssøe*, DJL-EC-166 (CFMR).

Notes: *Hygrocybe mirabilis* is related to *H. occidentalis* in sect. *Pseudofirmae* based on morphology and a megablast search in NCBI's GenBank nucleotide sequence database but differs by the striking red lamellae contrasting with the yellow pileus and 18.5 % divergence in ITS sequences (31.5 % in alignment). The closest GenBank hit was *H. poena* from the Ecuadorian cloud forest (95.3 %, GenBank OQ211589) but its pileus was dry and red rather than yellow and viscid. The ITS of a Brazilian specimen resembling *H. mirabilis* except for a thin fringed pileus margin and yellow stipe (GenBank PP883766) was only 82 % similar. An un-sequenced Ecuadorian collection by TL (DJL-EC-166) differed from *H. mirabilis* in the shape of macrospores.



Phylogenetic tree inferred from ITS sequences of *Hygrocybe* with at least 83 % identity and cover with *H. mirabilis* in a megablast search of GenBank nucleotides, and that were aligned using the CLUSTAL plugin and edited manually in Geneious Prime v. 2024.0.5. The phylogeny was made using the Maximum Likelihood plugin PhyML in Geneious v. R9 (Kearse *et al*. 2012) and rooted with *H. appalachianensis* based on the LSU phylogeny in Lodge *et al.* (2014). Bootstrap support values from 100 replicates are given below branches. *Hygrocybe* species, GenBank accession number, and country of origin are shown. The alignment and tree (doi: /10.6084/m9.figshare.25953991) and metadata for sequences used (doi: 10.6084/m9.figshare.25908742) were deposited in Figshare.

Colour illustrations: Belize cloud forest (Photo credit B. Holtz). Basidiome; basidia; basidiospores (Photos by T.J. Baroni, drawing by D.J. Lodge). Scale bars: basidiomes = 1 cm; others = 20 µm.

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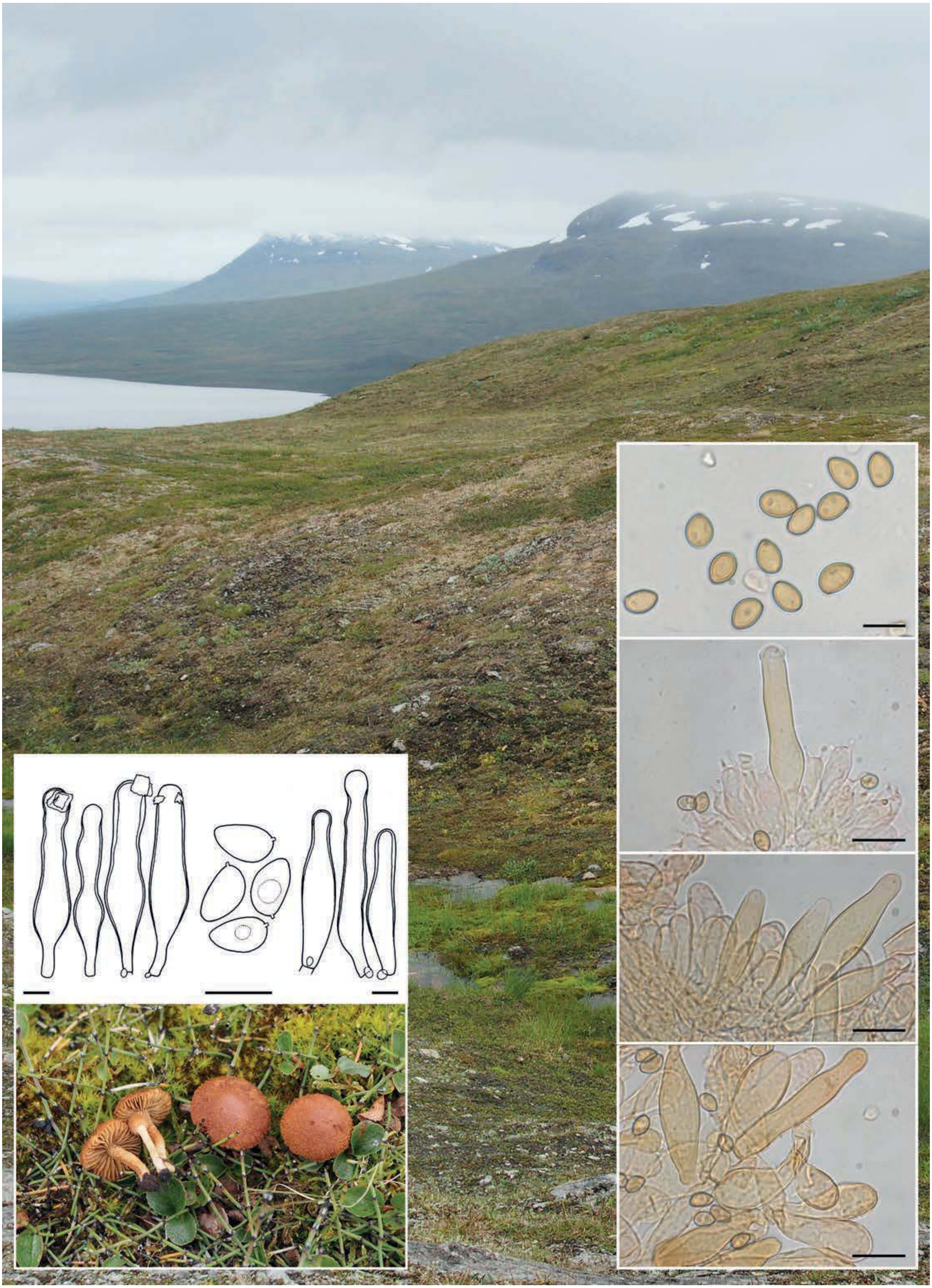


Fungal Planet 1753 MycoBank MB 855744

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

Etymology: Refers to the Sami name of the National Park Padjelanta/Badjelánnda in Sweden where the type was collected.

Classification: *Inocybaceae*, *Agaricales*, *Agaricomycetes*.

Pileus 4–18 mm diam, conical to convex, sometimes umbonate with and an obtuse and broad umbo, later plano-convex to plane with or without a broad umbo, as young with slightly incurved margin, dry, rather uniformly coloured yellowish ochraceous brown to brown, fibrillose to finely scaly, with age breaking up to be scaly, cortina whitish, visible in young basidiomata, soon disappearing. *Lamellae* up to 3 mm broad, distant to moderately crowded, interspersed with lamellulae, L = 20–30, adnate to adnexed, first buff white with a yellowish tint, later pale ochraceous brown to brown, edge concolourous or somewhat paler. *Stipe* 5–22 × 1.5–3 mm, cylindrical with a slightly rounded base, first pale white fibrillose, with age yellowish ochraceous brown with white stipe base, pruinose in the upper part, also fibrillose to finely scaly over the entire length. *Smell* spermatic. *Basidiospores* (7.7–)8.3–*8.8*–9.7(–10.1) × (5.0–)5.3–*5.7*–6.1(–6.7) µm, n = 110, Q = 1.42–1.66, Q av. = 1.56, smooth, ellipsoid, ovoid to subamygdaliform, often with an apical papilla, small apiculus, pale ochraceous brown. *Basidia* 29–*31*–36 × 8–*9*–11 µm, n = 25, clavate, 4-spored, a few 2-spored, hyaline, sterigmata 5.5–6.4 µm long. *Pleurocystidia* 57–*70*–87 × 9–*14*–22 µm, Q mean = 4.9, n = 70, cylindrical, slender fusiform to clavate, some mucronate capitate, pedicellate, thin-walled mainly without crystals, only a few are crystalliferous, some with wall up to 1.5 µm thick, hyaline to pale yellowish brown in KOH. *Cheilocystidia* 37–*57*–86 × 11–*16*–24 µm, n = 35, similar to pleurocystidia but more variable and on average shorter, mixed with hyaline pyriform to subglobose paracystidia 17–*25*–35 × 10–*16*–20 µm, n = 37. *Caulocystidia* over the entire length, at stipe apex similar to pleurocystidia, 28–*58*–83 × 11–*15*–22 µm, n = 40, hyaline or pale yellowish brown in KOH solution, few in the lower part, more fusiform to cylindrical, thin-walled and without crystals. *Cauloparacystidia* 16–40 × 9–20 µm, n = 30, clavate to pyriform and cylindrical, intermixed with hyphoid elements. *Clamp connections* frequent.

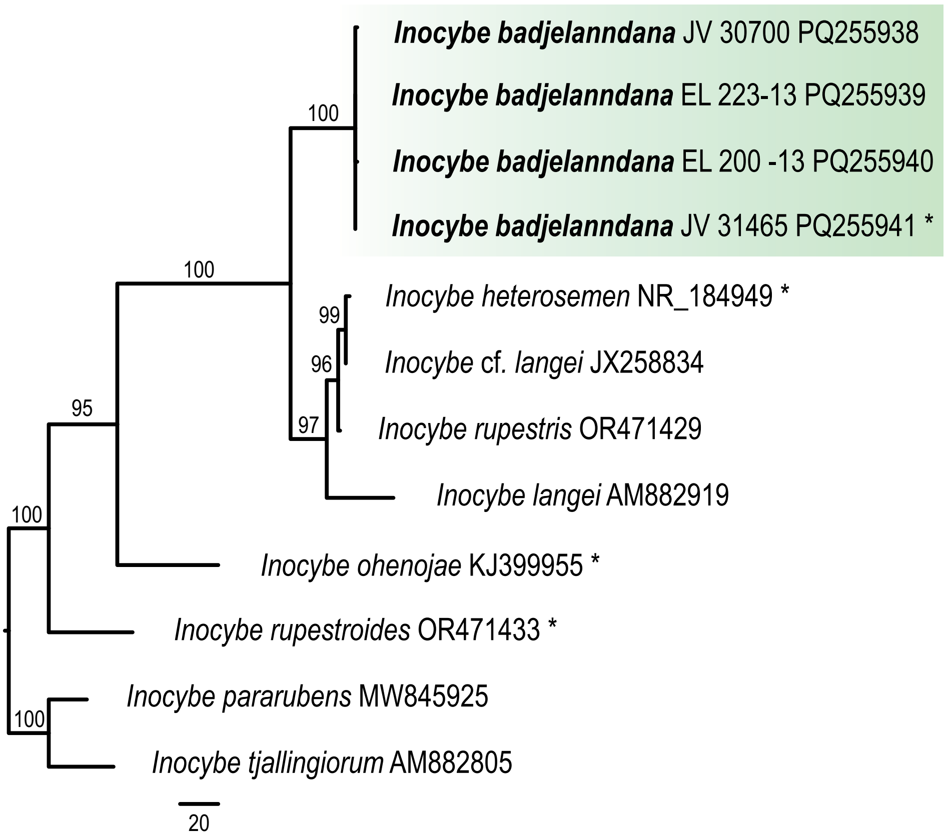
Ecology and distribution: The species occurs from the subalpine to the alpine zones, growing in moist more rich habitats, often on calcareous soils associated with *Salix lanata*, *S. phylicipholia*, *S. herbacea*, *S. polaris* and *S. reticulata,* sporulating from mid-August to September. Known from Sweden, Finland and Norway. Blast search of NCBIs GenBank and the UNITE database recovered no additional data.

Colour illustrations: *Inocybe badjelanndana* habitat in the alpine zone from the type locality, Árranoajvve, Padjelanta NP, Sweden. *In situ* basidiomata of the holotype (TUR-A 204571); photos of the hymenium with pleurocystidia, cheilocystidia, caulocystidia and basidiospores; drawing of pleurocystidia (left), basidiospores, caulocystidia (right). Scale bars: pleuro, caulo- and cheilocystidia = 20 µm; spores and drawing = 10 µm.

Typus: **Sweden**, Lule lappmark, Jokkmokk, Padjelanta National Park, Árranoajvve, (N67°29’57”, E16°37’9”) on North side of lake Vastenjaure, in alpine zone near small brook with *Salix reticulata* and *S. herbacea* on calcareous soil, 11 Aug. 2016, *J. Vauras*, JV31465 (**holotype** TUR-A 204571; ITS sequence GenBank PQ255941); *ibid*., **isotype** GB-0207686.

Additional materials examined: **Finland**, Enontekiön Lappi, Enontekiö, Kilpisjärvi, W slope of Korkeajehkas, SE of Jehkasjärvi, low alpine slope with brooks near *Betula nana* and *Salix* spp., 24 Aug. 2014, *J. Vauras*, JV30700 (TUR-A 171009, GB-0207688; ITS-LSU sequence GenBank PQ255938). **Norway**, Troms, Helligskogen, near the main road and the river Galgojokkaq, subalpine zone, old sandpit area near *Salix* spp. and *Betula pubescens* subsp. *czerepanovii*, *ca*. 325 m a.s.l., 30. Aug 2013, *J. Vauras*, JV30070F (TUR-A 198859); *ibid*., 20. Aug 2017, *J. Vauras*, JV32140F (TUR-A 204943). **Sweden**, Torne lappmark, Jukkasjärvi, Abisko, along river Rakkasjokka, moist subalpine habitat with *Betula pubescens*, *Salix lanata* and *S. phylicipholia*, in mosses with *Salix herbacea and Bistorta vivipara*, 23 Aug. 2013, *E. Larsson*, EL200-13 (GB-0207687; ITS-LSU sequence GenBank PQ255940); *ibid*., in mosses with *Salix polaris,* 24 Aug. 2013, *E. Larsson*, EL223-13 (GB-0207689; ITS-LSU sequence GenBank PQ255939); *ibid*., spring-fed slope with *Betula nana*, *B. pubescens* subsp. *czerepanovii*, *Salix herbacea*, *S. reticulata*, *S. lanata* and *S. phylicifolia*, *ca*. 600 m a.s.l., 23 Aug 2013, *J. Vauras*, JV29990F (TUR-A 199051).

Notes: *Inocybe badjelanndana* is a small yellowish ochraceous brown to brown species with tomentose to finely squamulose pileus, and often fibrillose to finely scaly stipe, found in moist alpine and subalpine habitats fruiting in mosses and mainly found associated with *Salix*. The closest match when blasting the ITS sequence in GenBank is with *I. rupestris* (91.9 % similarity; GenBank OR471429). *Inocybe rupestris* (Favre 1955) is similar in macromorphology to *I. badjelanndana* and the two can co-occur, but *I. rupestris* fruits usually on more calcareous soil in drier habitats on gravely ground. It differs from *I. badjelanndana* by having distinct shorter and thick-walled crystalliferous pleurocystidia. *Inocybe rupestroides* (Crous *et al.* 2023) is another similar alpine species associated with dwarf *Salix* but differs from *I. badjelanndana* by having a smooth more ochraceous brown pileus and on average longer spores, 9.6 µm *vs* 8.6 µm. Two other species that show similarity when blasting the ITS sequence in GenBank is *I. heterosemen* (GenBank NR_184949; Carteret & Reumaux 2012) and *I. langei* (GenBank AM882919; Heim 1931). Both are larger species and described from deciduous forests in France and do not occur in the alpine zone (Bandini *et al.* 2022).



Phylogram obtained using PAUP v. 4.0a (Swofford 2003) based on ITS and LSU data showing the position of *I. padjelantae* among its closest relatives. 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. *Inocybe badjelanndana* is marked in bold and holotypes are indicated with an asterisk (*). The alignment and tree were deposited in figshare.com, (doi: 10.6084/m9.figshare.27206190).

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Inocybe complutensis

Fungal Planet 1754

MycoBank MB 855478

Inocybe complutensis Esteve-Rav., Pancorbo & Altés, ***sp. nov.***

Etymology: Named after "*complutum*", the Latin name of the city of Alcalá de Henares (Spain), where the species was collected.

Classification: *Inocybaceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata agaricoid and stipitate. *Pileus* 15–35(–40) mm, initially hemispherical to paraboloid, then convex to plano-convex, finally applanate or shallowly and broadly umbonate; margin straight to hardly inflexed, often wavy, not or exceptionally reflexed with age; generally uniform in colour, bay, fulvous, snuff brown to umber brown (Mu 7.5YR 4/3–6, 5/4–8; Munsell 1994); surface dry, finely smooth fibrillose to subtomentose in some specimens, often broken or lacerated in old specimens when the veil is persistent, not hygrophanous. Velipellis very distinct in young specimens, especially in the centre, often rather persistent as an arachnoid silky dirty whitish to greyish patch, sometimes agglutinating soil debris. *Lamellae* moderately crowded (L = 36–40); l = 1–2(–3), 4–6 mm wide, adnexed to narrowly adnate, ventricose, long-time pale, initially whitish, becoming pale grey, then pale brown ochraceous, finally pale brown; edge white or paler, fimbriate to finely crenulate. *Stipe* 20–35(–40) × 5–10(–12) mm, firm, straight or sometimes curved towards the base, cylindrical to hardly enlarged towards the base; colour initially white to dirty white, in some specimens with a pale pink ochraceous tone or reflection especially towards the apex; surface uniform, finely white fibrillose longitudinally, subfloccose-fibrillose at the extreme apex. *Cortina* present in very young specimens only, very ephemeral. *Context* firm, fibrous, whitish to pale ochraceous at pileus and stipe base, sometimes pale pinkish ochraceous at the upper stipe cortex. *Smell* spermatic when cut. *Spores* (8.4–)9.1–*10.1*–11.0(–11.8) × (5.1–)5.6–*6.1*–7.0(–7.4) µm, (1.28–)1.44–*1.60*–1.82(–2.11) (n = 405 / N = 3), smooth, variable in shape, subovoid to subamygdaliform; apex rounded to subacute, sometimes showing a pseudopore or callus and then slightly thick walled. *Basidia* (24.7–)25.2–*29.6*–34.1(–37.4) × (9.2–)9.6–*11.1*–12.5(–13.3) µm, Q: (2.13–)2.22–*2.60*–3.11(–3.14) (n = 30 / N = 1), 4-spored, rarely 2-spored, clavate, sterigmata 3–6 µm long. *Lamellar edge* sterile, composed of numerous protruding cheilocystidia mixed with hyaline, thin-walled claviform paracystidia. *Pleurocystidia* (40.3–)47.7–*60.9*–79.1(–89.6) × (11.3–)12.3–*15.8*–20.2(–23.3) µm, Q: (1.98–)2.61–*3.90*–5.67(–6.91), (n = 164/ N = 3), polymorphous and often irregular, with a certain subfusiform tendency, often provided with a short or distinct pedicel, crystalliferous at the apex, sometimes with pale yellowish-brown intracellular contents, exceptionally one-two septate; walls (0.87–)1.04–*1.40*–1.97(–2.68) µm thick, faintly yellowish in aqueous ammonia solutions. *Cheilocystidia* (54.0–)57.1–*73.0*–89.6(–94.7) × (9.4–)12.2–*14.3*–17.7(–22.9) µm, Q: (3.18–)3.76–*5.10*–7.02(–8.06) (n = 32 / N = 2), longer and narrower than pleurocystidia, variable in shape, mostly subfusiform, but also ventricose or narrowly fusiform to subutriform, often with a brownish-ochre to yellowish content. *Stipitipellis* a cutis of parallel hyphae 5–10 µm wide, with parietal to encrusting yellowish pigment. *Caulocystidia* present in the extreme apex of the stipe, metuloid (sub)cylindrical to long fusiform cystidia only near the insertion zone, (36.2–)39.2–*62.5*–85.9(–101.5) × (7.6–)8.8–*14.3*–21.9(–23.8) µm, Q: (2.22–)2.69–*4.70*–8.96(–9.21) (n = 22 / N = 2) becoming caulocystidioid hairs downwards, sometimes with long broad subfusiform terminal cells, and with a thin zebra-like epiparietal pigment. *Clamp connections* abundant.

Habitat and distribution: Always found in association with the Aleppo pine (*Pinus halepensis*). It is often found in large numbers under this tree in the parks and gardens around the external campus of the University of Alcalá de Henares (Spain). It grows in limestone soils, with a sandy component.

Typus: **Spain**, Community of Madrid, Alcalá de Henares, Campus Universitario externo, Faculty of Science Building, 40°30'17.53"N, 3°20'14.95"W, 597 m a.s.l., among grass and fallen needles of *Pinus halepensis* (*Pinaceae*) in garden, in calcareous loamy soil, 7 Nov. 2023, *F. Esteve-Raventós & A. Altés* (**holotype** AH 36384; ITS and LSU sequences GenBank PQ226170 and PQ226167).

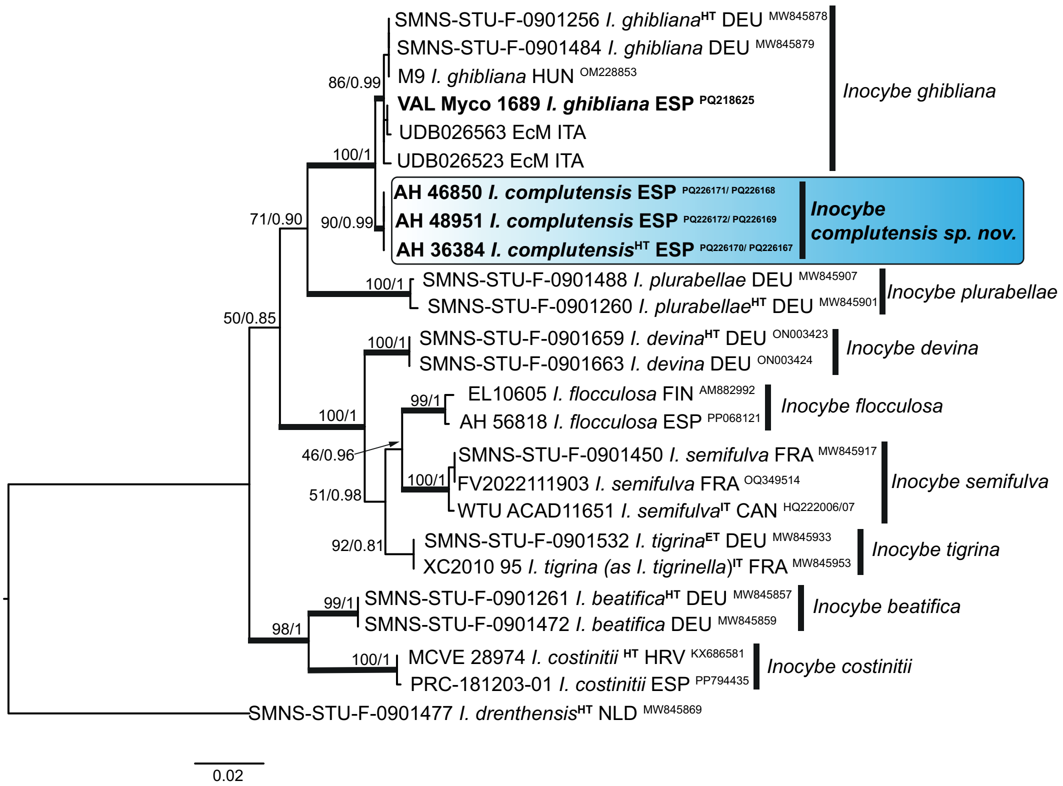
Additional materials examined: **Spain**, Community of Madrid, Alcalá de Henares, Campus Universitario externo, close to the Genetics Unit Building, 40°30'32"N, 3°20'38"W, 608 m a.s.l., among grass and fallen needles of *P. halepensis* in garden, in calcareous loamy soil, 16 Oct. 2008, *G. Moreno & J. Picado* (AH 46850; ITS and LSU sequences GenBank PQ226171 and PQ226168); Community of Madrid, Alcalá de Henares, Campus Universitario externo, Faculty of Science Building, 40°30'17.53"N, 3°20'14.95"W, 597 m a.s.l., among grass and fallen needles of *P. halepensis* in garden, in calcareous loamy and sandy soil, 15 Mar. 2018, *J. Picado* (AH 48951; ITS and LSU sequences GenBank PQ226172 and PQ226169).

Notes: Terminology follows Vellinga (1988) and Kuyper (1986). *Inocybe complutensis* is morphologically and genetically very similar to *I. ghibliana*. The two species are sister in the obtained phylogram and, together, they might constitute a species complex. *Inocybe ghibliana* is considered by Bandini *et al*. (2021, 2023) to be a thermotolerant species, with xerophilic preferences and distributed in Central Europe (Germany, Estonia), recently also found in urban areas in Budapest, Hungary (Czismar *et al*. 2022); besides, it seems to be present throughout the Mediterranean belt (France, Greece, Iran, Israel, Italy, Morocco) and Asia (Kyrgyzstan), according to species hypothesis SH0998501.10FU from the UNITE database, mostly from ectomycorrhizae and probably related to the presence of *Cistus.* Interestingly, *I. ghibliana* has also been found in Spain in the Valencian Community (VAL Myco 1689) in *Cistus albidus* communities, on limestone soils. *Inocybe complutensis* grows under *P. halepensis*, the Aleppo pine, without the presence of *Cistaceae*, in calcareous and slightly sandy soils, and differs from *I. ghibliana* in its phylogenetic characters (ITS with 97.99 %

Colour illustrations. Inocybe complutensis habitat in gardens surrounding the Faculty of Sciences in Alcalá de Henares, Spain, the type locality. *In situ* basidiomata of the holotype (AH 36384); from bottom to top: photos of basidiospores; pleurocystidia; cheilocystidia; caulocystidia in the upper part of the stipe. Scale bars: basidiomata = 10 mm; cystidia = 50 µm; spores = 10 µm.

similarity), and morphologically by the more robust growth habit (the stipe can reach –10 mm diam), darker colour of the pileus, less distant lamellae, the presence of a very abundant and persistent diagnostic greyish veil, slightly larger and more elongated spores and slightly narrower cystidial walls.

Phylogenetically close to *I. complutensis* and *I. ghibliana* is *I. plurabellae*, a species of continental distribution fruiting under *Picea*; it differs clearly from both in the appearance of the basidiomata, with a typically tomentose to squamulose pileus, without or with a transient velipellis and with more ventricose cystidia (Bandini *et al*. 2021). From their morphological characters, *Inocybe griseovelata* (= *I. subvirgata*), *I. psammobrunnea* (= *I. griseotarda*) and *I. dagamae* could be reminiscent of *I. complutensis*. Although these three species are phylogenetically related to each other, they are in turn very distant from *I. complutensis* and *I. ghibliana* (Bandini *et al*. 2022, 2023). *Inocybe griseovelata* (Kühner 1955, Bandini *et al*. 2022, 2023) initially shows a well-developed greyish veil, and is a species often associated with deciduous trees in gardens and parks (Czismar *et al*. 2022), with very elongated and progressively attenuated cystidia apically. *Inocybe psammobrunnea* (Bon 1990), whose epithet has priority over *I. griseotarda* (Bandini *et al*. 2021), as well as *I. dagamae* (Fachada *et al*. in Crous *et al*. 2023), show a preference for sporulating under *Pinus* in sandy soils and warm, mild climates; both are morphologically similar, the latter differing in its preference for calcareous soils and smaller spores. They also have a well-developed arachnoid dirty white to ochraceous velipellis, and the cystidia are subcylindrical to subfusiform and lack a well-defined neck.



Most likely tree of the Maximum Likelihood analysis of smooth-spored species of *Inocybe* inferred from the ITS and LSU regions generated by IQ-TREE web server (Trifinopoulos *et al.* 2016) using 1 000 bootstrap replicates. Maximum Likelihood bootstrap values (ML-BS) ≥ 70 % and Bayesian posterior probabilities (BPP) ≥ 0.95 are shown on the thick branches and ordered as ML-BS/BPP. The Bayesian Inference analysis was performed with MrBayes v. 3.2.7a (Ronquist & Huelsenbeck 2003). Voucher numbers and the nucleotide accession numbers are indicated for all species retrieved from GenBank and generated in this study, as well as country ISO alpha3 code abbreviations. Type collections are indicated in superscript by their initials: HT = holotype, ET = epitype and IT = isotype. The tree was rooted to *Inocybe drenthensis* (SMNS-STU-F-0901477). The new species described here is embedded in the coloured rectangle. The sequences generated in this study are highlighted in **bold**. The scale bar represents the expected number of nucleotide changes per site. The alignments were deposited in Figshare.com (doi: 10.6084/m9.figshare.26809750).

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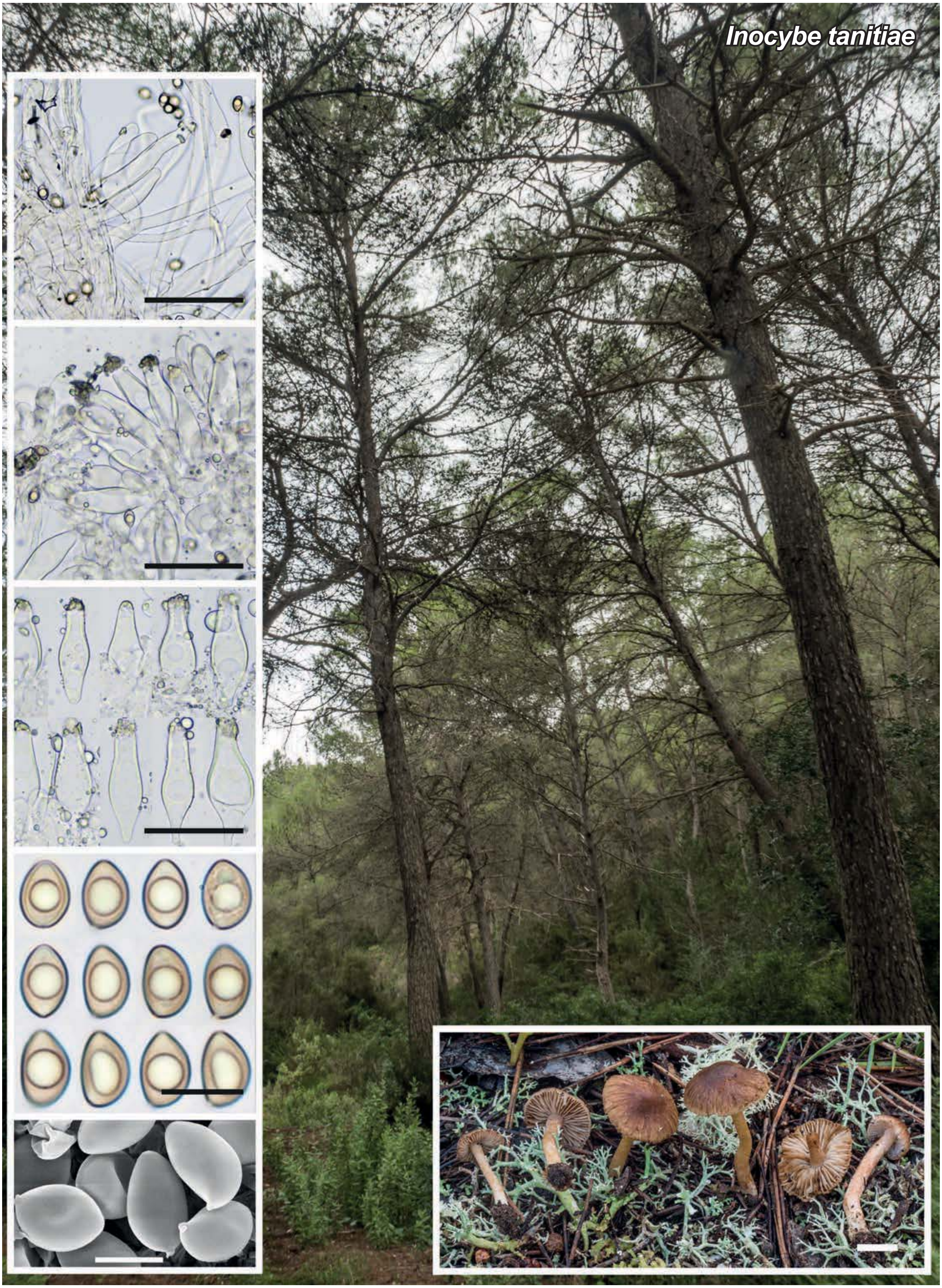

Inocybe tanitiae

Fungal Planet 1755 MycoBank MB 855479

Inocybe tanitiae Pancorbo & Esteve-Rav., *sp. nov.*

Etymology: Name in reference to Tanit, the Phoenician goddess of the moon and protector of Ibiza (Eivissa).

Classification: *Inocybaceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata agaricoid and stipitate, small and slender. *Pileus* 8–15 mm, initially hemispherical to paraboloid, then convex to plano-convex, subumbonate; margin straight to slightly deflexed, quite regular; colour uniform to slightly darker towards the centre, fulvous to snuff brown or hazel brown (Mu 7.5YR 5/3–6, 4/4–6; Munsell 1994); surface dry, often smooth to finely fibrillose, but in some specimens scurfy fibrillose, often radially fibrous in adpressed bands towards the margin (rimulose appearance), not or hardly hygrophanous. Velipellis not distinct or quite ephemeral and arachnoid in young specimens. *Lamellae* subdistant to moderately crowded (L = 32–36); l = 1–2, 3–5 mm wide, adnexed to narrowly adnate, rather ventricose with age, initially whitish, becoming beige, pale grey to clay yellowish, then pale brown ochraceous, edge white, fimbriate to finely crenulate. *Stipe* 20–30 × 2–4(–5) mm, firm, straight or curved at the base, cylindrical or progressively enlarged towards the base, not bulbous; colour initially dirty white, soon pale ochraceous, showing a slight pinkish tinge in young specimens, but often becoming uniformly ochraceous with age; surface coated in young specimens with whitish fibrils along the entire length, soon sub-smooth, floccose-fibrillose in the upper ¼ zone. *Cortina* present in young specimens. *Context* fibrous, concolourous to the surface. *Smell* spermatic to subspermatic. *Spores* (7.3–)7.9–*8.7*–9.5(–9.9) × (4.6–)5.2–*5.6*–6.2(–6.5) µm; Q: (1.31–)1.38–*1.50*–1.70(–1.86) (n = 275 / N = 2) smooth, ovoid in frontal view, subamygdaloid in profile and with a subacute apex, sometimes with a callus or pseudopore. *Basidia* (25.0–)26.1–*31.2*–36.5(–38.0) × (7.2–)8.5–*10.8*–12.9(–13.9) µm; Q: (2.06–)2.42–2.*90*–3.54(–4.06) (n = 54 / N = 2), 4-spored, rarely 2-spored, clavate, sterigmata 4–7 µm long. *Lamella edge* almost sterile, composed of numerous protruding hyaline cheilocystidia mixed with abundant mostly hyaline, thin-walled, clavate to pyriform paracystidia (17.4–)17.7–*21.9*–26.0(–26.2) × (9.0–)9.6–*12.4*–14.9(–16.4) µm, (n = 40 / N = 1). *Pleurocystidia* (39.5–)43.9–*54.7*–63.3(–65.2) × (11.9–)12.8–*15.9*–19.4(–23.8) µm; Q: (2.5–)2.7–*3.4*–4.5(–4.6) (n = 61 / N = 2), subfusiform, to subutriform mostly hyaline, but some with ochre to ochre-greyish intracellular contents, base sometimes pedicellate, mainly crystalliferous at the apex, walls (1.13–)1.23–*1.50*–1.94(–2.05) µm thick, faintly yellowish in ammonia solutions. *Cheilocystidia* (30.5–)37.7–*46.1*–54.7(–56.7) × (11.3–)12.7–*15.8*–19.2(–22.1) µm; Q: (1.9–)2.2–*3.0*–3.9(–4.8) (n = 96 / N = 2), similar in shape to pleurocystidia but usually shorter. *Stipitipellis* a cutis of parallel hyphae 2.5–7.5 µm, with parietal to encrusting brownish pigment. *Caulocystidia* present at extreme apex only and then similar to cheilocystidia but longer and narrower, (38.2–)42.2–*61.4*–81.0(–96.3) × (7.8–)8.2–*11.3*–14.8(–16.3) µm; Q: (2.5–)3.4–*5.6*–9.4(–11.2) (n = 65 / N = 2), mixed with clavate to subcylindrical hyaline paracystidia, soon forming a narrow intermediate zone of rather undifferentiated caulocystidioid hairs. *Hymenophoral trama* of parallel hyphae constricted at the septa, 7–9 µm broad, hyaline. *Clamp connections* abundant.

Habitat and distribution: So far only known from the type locality in the island of Ibiza (Eivissa), in thermo-mediterranean machia with *Pinus halepensis*, *Quercus coccifera*, *Cistus albidus*, *Pistacia lentiscus* and *Juniperus phoenicea*. It occurs in calcareous soils.

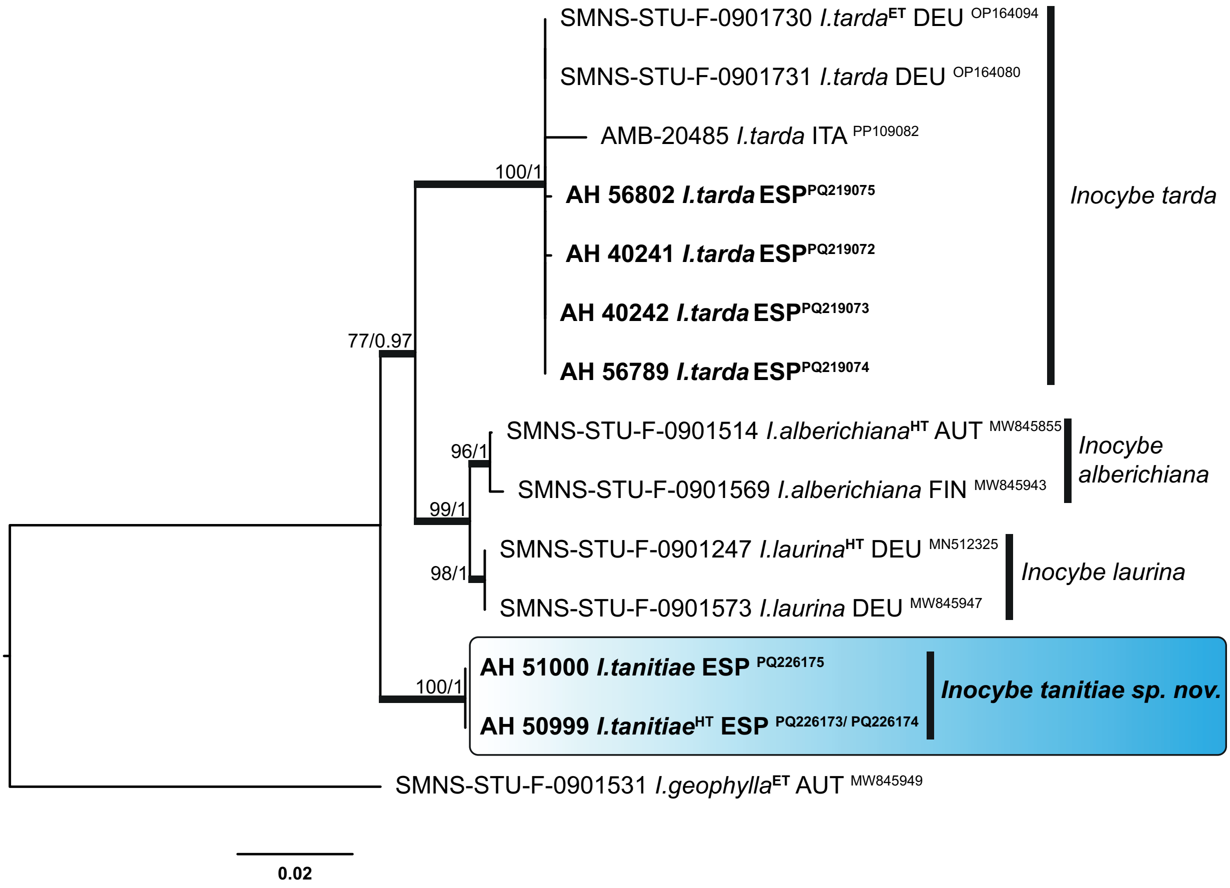
Typus: **Spain**, Illes Balears, Ibiza (Eivissa), Sant Antoni de Portmany, Planes den Frencolí, 39°01’25”N, 01°21’46”E, 156 m a.s.l., mixed Mediterranean forest (machia) with *Pinus halepensis* (*Pinaceae*), *Cistus albidus* (*Cistaceae*), *Quercus coccifera* (*Fagaceae*) and *Pistacia lentiscus* (*Anacardiaceae*), in calcareous sandy soil, 5 Dec. 2018, *F. Pancorbo*, *A. Altés*, *J.L. Siquier*, *J.C. Salom*, *J. Llistosella* & *F. Esteve-Raventós* (**holotype** AH 50999; ITS and LSU sequences GenBank PQ226173 and PQ226174).

Additional material examined: **Spain**, Illes Balears, Ibiza (Eivissa), Sant Antoni de Portmany, Planes den Frencolí, 39°01’25”N, 01°21’46”E, 156 m a.s.l., mixed Mediterranean forest (machia) with *P. halepensis*, *C. albidus*, *Q. coccifera* and *P. lentiscus*, in calcareous sandy soil, 5 Dec. 2018, *F. Pancorbo*, *A. Altés*, *J.L. Siquier*, *J.C. Salom*, *J. Llistosella* & *F. Esteve-Raventós* (AH 51000; ITS-LSU sequence GenBank PQ226175).

Notes: Terminology follows Vellinga (1988) and Kuyper (1986). *Inocybe tanitiae* belongs to a phylogenetic clade corresponding to section *Tardae*, subsection *Tardinae*, after the taxonomic scheme proposed by Bon (1997). According to the Mediterranean biogeographical region and the habitat in which it grows, it could be confused with *I. tarda* and *I. pinophila*, which at first sight have more robust or larger basidiomata. *Inocybe tarda* occurs in the Balearic Islands in the same environments and is very common under Aleppo pine in calcareous sandy soils; it differs in its cystidia with a clear subcylindrical to subfusiform tendency, with wide necks, generally not very differentiated, as well as its larger and amygdaliform spores (Kühner 1955, Bandini *et al*. 2021, 2022, 2023). *Inocybe pinophila* is very similar in appearance to *I. tarda*, its habitat is also associated with *Pinus* on sandy soil and it is only known from Mediterranean environments (France, Italy, and Spain, this last unpublished). *Inocybe pinophila* differs from *I. tanitiae* by its much more robust

Colour illustrations: *Inocybe tanitiae* habitat in Ibiza, Spain, the type locality. *In situ* basidiomata of the holotype (AH 50999); from bottom to top: basidiospores (SEM, MO); pleurocystidia; cheilocystidia; caulocystidia in the upper part of the stipe. Scale bars: basidiomata = 10 mm; cystidia = 50 µm; spores (MO) = 10 µm; spores (SEM) = 2 µm.

appearance, more reddish stipe, its well-developed velipellis, its unremarkable odour and spore morphology without ovoid-amygdaliform tendency (Cervini *et al*. 2024). These three species are well separated genetically (see Phylogenetic Tree). Other species phylogenetically close to *I. tanitiae* have been described recently, all from milder or colder climates in Europe: *I. alberichiana* (ITS with 92.63 % similarity) has long cystidia with a wavy neck, and fruits under *Picea* and *Pinus* in montane, subalpine or boreal regions (Bandini *et al*. 2021); *Inocybe laurina* is small in size and with well-developed velipellis, lives in continental and boreal Europe, associated with *Pinus* and *Picea* in sandy and gravelly soils (Bandini *et al*. 2020); *Inocybe astraiana* is also associated with *Pinus*, shows a more robust growth habit with a hygrophanous and often bicoloured pileus, has lageniform and ventricose cystidia, and is phylogenetically closer to *Inocybe nemorosa* (Bandini *et al*. 2020); finally, *Inocybe clandestina* shows a very dark and finely tomentose pileus, very elongated cystidia and a completely reddish stipe (Bandini *et al*. 2021).



Most likely tree of the Maximum Likelihood analysis of smooth-spored species of *Inocybe* inferred from the ITS and LSU regions generated by IQ-TREE web server (Trifinopoulos *et al.* 2016) using 1 000 bootstrap replicates. Maximum Likelihood bootstrap values (ML-BS) ≥ 70 % and Bayesian posterior probabilities (BPP) ≥ 0.95 are shown on the branches and ordered as ML-BS/BPP. The Bayesian Inference analysis was performed with MrBayes v. 3.2.7a (Ronquist & Huelsenbeck 2003). Voucher numbers and the nucleotide accession numbers are indicated for all species retrieved from GenBank and generated in this study, as well as country ISO alpha3 code abbreviations. Type collections are indicated by their initials encircled: HT = holotype, ET = epitype. The tree was rooted to *Inocybe geophylla* (SMNS-STU-F-0901531). The new species described here is embedded in the coloured rectangle. The sequences generated in this study are highlighted in **bold**. The scale bar represents the expected number of nucleotide changes per site. The alignments were deposited in FigShare.com (doi: 0.6084/m9.figshare.26806753).

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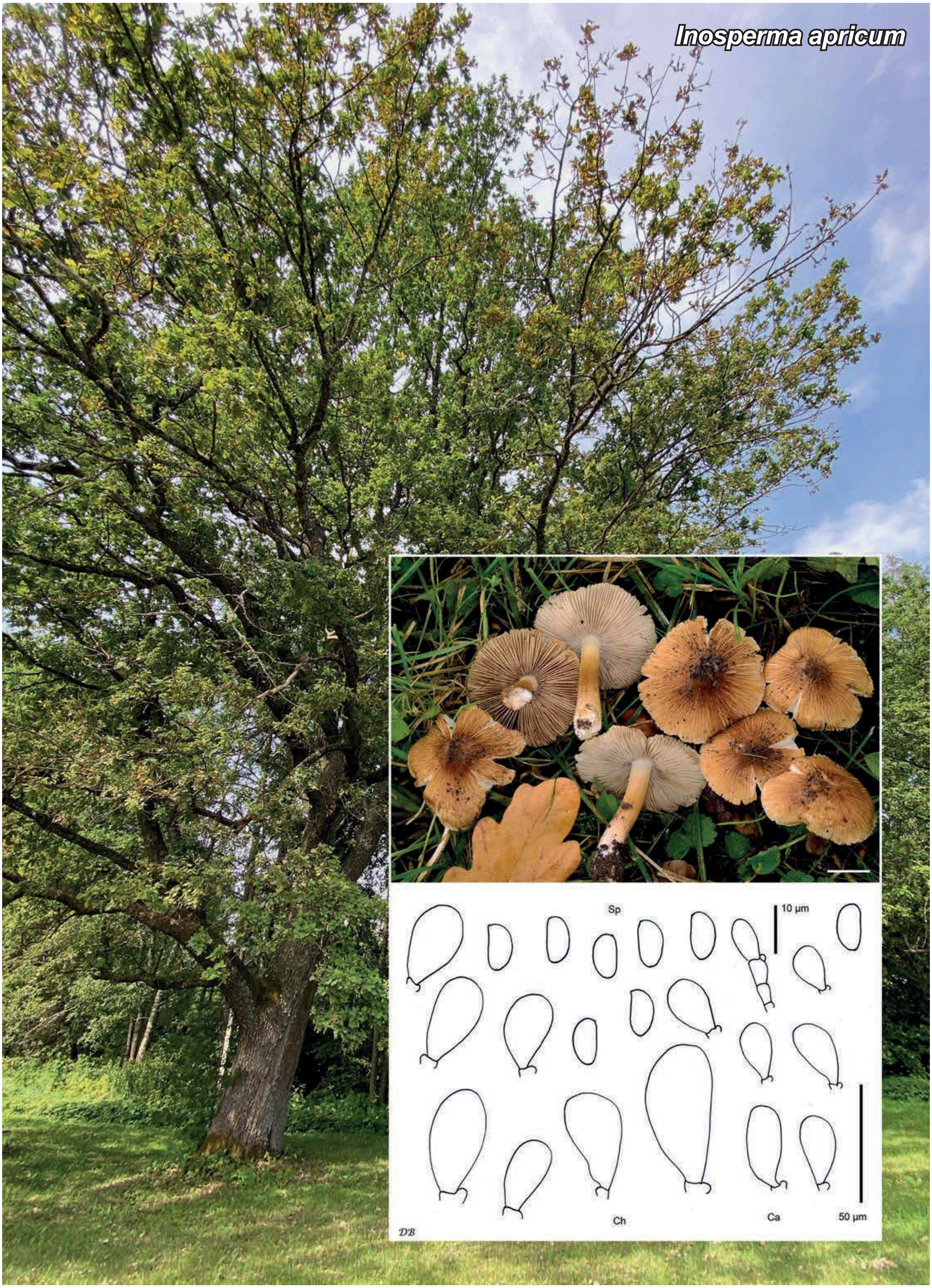

Inosperma apricum
Sp
10 µm
Ch
Ca
50 µm
DB

Fungal Planet 1756 MycoBank MB 854826

Inosperma apricum Bandini & I. Saar, *sp. nov*.

Etymology: From Latin *aprica* = sunny, because of the sunny pileus colour.

Classification: *Inocybaceae*, *Agaricales*, *Agaricomycetes*.

Pileus 20–50 mm wide, at first subcampanulate or subconical, later conico-convex to almost expanded, at first without, later with more or less pronounced large umbo, margin at first slightly incurved, later decurved to straight or even uplifted, and then pileus depressed around the umbo; young basidiomata with faint and fugacious remnants of a pale velipellis; at first pale yellow-ochraceous with faint orange reddish tinges at the centre, then bicoloured with bright orange-reddish-brownish fibres on paler ones (7.5YR 7/8, 6/6–6/8, 5/6–5/8; 4/4–4/6; 10YR 7/6–7/8; Munsell 2009); surface at first almost smooth, later distinctly rimose with fine diverging fibres, partly showing the whitish context beneath; sometimes slightly sticky and therefore sullied with soil particles, young basidiomata with remnants of a whitish cortina. *Lamellae* moderately crowded to crowded (*ca*. 45–60), adnate with tooth, even to subventricose, at first whitish, later dingy whitish, whitish greyish to pale ochraceous with greyish hue; edge fimbriate, whitish. *Stipe* 30–60 × 3–6 mm, straight or curved, when young covered with whitish tomentum, soon glabrous, at first whitish, then yellowish-ochraceous, and then in parts, especially in the middle, greyish brownish, remaining whitish near the apex; sparely pruinose only near the extreme apex. *Context* at first whitish in pileus and stipe, with age getting partially pale greyish. *Smell* indistinct. Dry basidiomata: pileus brownish (Mu 10YR 6/4–6/6, 5/4–5/6), lamellae and stipe concolourous or a little lighter in colour, no darkening or blackening on drying. *Basidiospores* 8.6–10.9 µm × 4.7–6.3 µm, av. 9.5 (SD 0.4) × 5.3 µm, (SD 0.3), Q = 1.6–2.0, $Q_{av.}$ = 1.8 (SD 0.1), n = 80 of two collections, smooth, subcylindrical to subphaseoliform, without or with faint suprahilar depression, apex obtuse. *Basidia* 25–32 × 7–11 µm, generally 4-spored. *Cheilocystidia* 26–56 µm × 11–34 µm, av. 39 µm (SD 7) × 19 µm (SD 6), Q = 1.4–3.9, $Q_{av.}$ = 2.2 (SD 0.5), n = 30 of two collections, subclavate, subovoid or balloon-shaped, rarely subcylindrical, colourless and thin-walled. *Caulocystidia* only near the apex of the stipe, 20–40 × 8–15 µm, mostly subclavate, colourless and thin-walled.

Habitat and distribution: Solitary or gregarious, in gardens, parks and woodland. The holotype was found under *Quercus robur*, the paratype from Germany was found next to an old beech tree, with *Picea abies* in some distance. So far known in Europe (Estonia, Germany, Latvia) and Western Asia (Iran, Turkey) based on soil DNA data and ectomycorrhizal samples (UNITE: SH0565703.10FU), possibly growing with a wide range of host trees: *Alnus incana*, *Betula pendula*, *Corylus avellana*, *Fagus sylvatica*, *Picea abies*, *Populus* spp., *Quercus robur*, *Salix* spp., *Tilia cordata*.

Typus: **Estonia**, Võru county, Antsla commune, Karula Nature Park, Ähijärve, 57.71192°N, 26.50483°E, garden, under *Quercus robur*, 7 Sep. 2012, *V. Liiv* (**holotype** TUF118505; ITS sequence UNITE UDB017942).

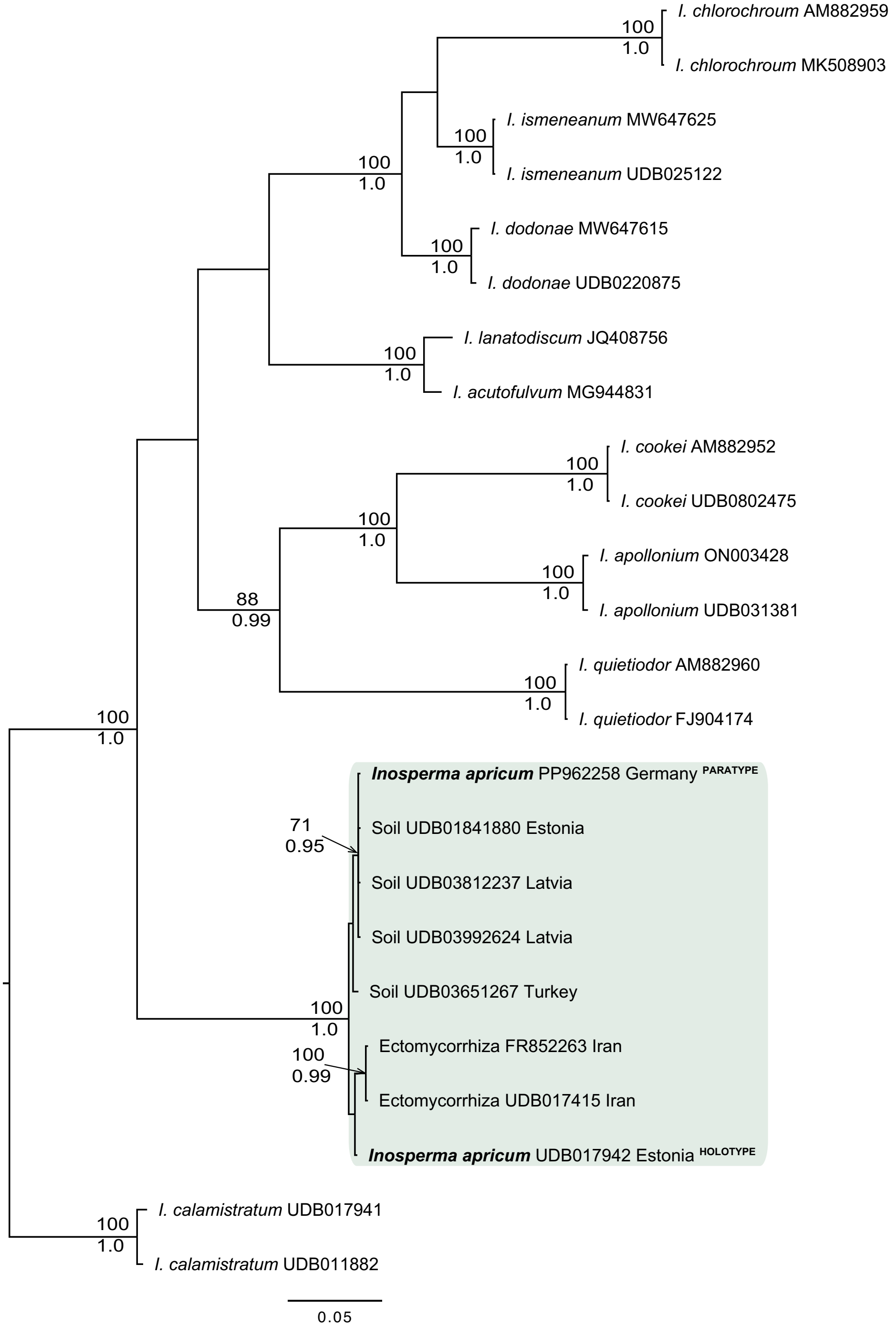
Additional material examined: **Germany**, Bayern, Ostallgäu, Füssen, TK25 8430/1, alt. 795 m, *Fagus sylvatica*, in some distance *Picea abies*, 10 Aug. 2021, *D. Bandini* DB10-8-21-3 (SMNS-STU-F-0901844; ITS sequence GenBank PP962258).

Notes: *Inosperma apricum* has with age a bicoloured pileus with bright orange brownish fibres on paler ones, up to distinctly rimose pileus surface, smooth spores, size on av. 9.5 × 5.3 µm, mostly subclavate to balloon-shaped thin-walled cheilocystidia, measuring on average 39 × 19 µm, and mostly subclavate caulocystidia. It grows on acid and calcareous soils with deciduous and coniferous (*Picea abies*) trees. It can be recognised by the combination of the above characters and differs in its ITS sequence from other species, such as *Inosperma apollonium*.

Inosperma apollonium differs from *I. apricum*, *e.g*., by less bright and paler pileus colour with age, only finely rimose pileus surface, smell sweetly aromatic, and on av. smaller cheilocystidia, often with undate walls (Bandini *et al*. 2022), and *I. cookei e.g*., by usually not bicoloured, with age much paler and more yellow pileus, smaller basidiospores and cheilocystidia, and smell like honey (Bresadola 1881–1892). *Inocybe quietiodor* differs, *e.g*., by usually not bicoloured, with age much paler and more yellow pileus, radially scattered abundant whitish velipellis, smell intensely like bugs, and on av. smaller cheilocystidia (Bon 1976), and *I. lanatodiscum* has a more reddish pileus colour and on av. smaller basidiospores (Kauffman 1918).

Based on a blastn search of NCBI's GenBank nucleotide database, the closest hits of the ITS sequence of the holotype are *Inosperma ismeneanum* [GenBank MW647625; Identities = 654/712 (92 %), 18 gaps (2 %)] and *Inosperma dodonae* [GenBank MW647615; Identities = 655/715 (92 %), 18 gaps (2 %)].

Colour illustrations: Collection site of the holotype of *Inosperma apricum*, Estonia. Holotype *in situ*; basidiospores (Sp), caulo- (Ca) and cheilocystidia (Ch) in KOH. Scale bars: basidiomata = 10 mm; cystidia = 50 µm; basidiospores = 10 µm.



Bayesian inference (BI) analysis was performed with MrBayes v. 3.2.6 (Ronquist *et al*. 2012) with 5 M generations, applying default values of other prior settings. The first 500 K generations without a stable likelihood score were discarded. Maximum likelihood (ML) analysis was performed with RAxML-HPC2 on ACCESS v. 8.2.12 (Stamatakis 2014) with 1 000 bootstrap replicates, at the CIPRES Science Gateway (Miller *et al*. 2010; http://www.phylo.org/). The best tree of the BI analysis is presented. The novel species is highlighted in a light green box, types are in **bold**. The scale bar indicates the expected number of substitutions per site, and bootstrap support values of the ML analyses (≥ 70 %) and Bayesian Posterior Probabilities (≥ 0.95) are above and below branches, respectively. The tree was rooted to the sequences of *Inosperma calamistratum*, the type of the genus. The alignment was deposited in the PlutoF web platform (doi: 10.15156/BIO/2959353) and Figshare.com (doi: 10.6084/m9.figshare.27169395).

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Leuconeurospora bharatiensis

Fungal Planet 1757 MycoBank MB 855707

Leuconeurospora bharatiensis N. Jiya, R. Avchar, G. Rawat & A. Sharma, ***sp. nov.***

Etymology: The name reflects the Indian research station Bharati in Antarctica, where the sediment sample was collected.

Classification: *Pseudeurontiaceae*, *Thelebolales*, *Leotiomycetidae*, *Leotiomycetes*.

Mycelium consisting of unbranched, septate, hyaline, smooth-walled hyphae, 0.7–3.01 µm diam. *Conidiophore cells* are nearly cylindrical, produced in chain or pairs on the supporting branch. *Conidiophores* are 3.6–7 µm long, gradually elongating to 12.7 µm and 1.4–5 µm diam. *Conidia* light greyish green after 4 wk of incubation, obovate and truncate at the point of attachment. Yeast-like structures were observed after incubation at 15 °C for 21 d. The reverse colony morphology exhibited a pinkish appearance. The optimum growth temperature was 10–15°C.

Culture characteristics: Colonies flat, smooth, reaching 31 mm diam after 3 wk of incubation on yeast peptone dextrose agar (YEPD) at 15 °C. Colonies circular, raised at the centre and cream to foam-coloured at centre, and pastel red at margin on YEPD. On MEA, the colony was dry, raised at centre and obtained a diameter of 28 mm after 21 d of incubation. It was cream to foam-coloured at centre, and white towards the margin. The margins were entire on both media.

Habitat and distribution: *Leuconeurospora bharatiensis* was isolated from accumulated snow sediment from Larsemann Hills, near the Indian research station Bharati, Antarctica.

Typus: **Antarctica**, Larsemann Hills, near the Indian Station Bharati, 69°22’29.0”S, 76°08’29.0”E, from accumulated snow sediment sample, Feb. 2019, *A. Sharma* [**holotype** MCC 10126 preserved as a metabolically inactive culture at the National Centre for Microbial Resource (formerly Microbial Culture Collection; MCC) - National Centre for Cell Science, Pune, India, culture ex-type MCC 10126; ITS and LSU sequences GenBank PQ304642 and PQ304641].

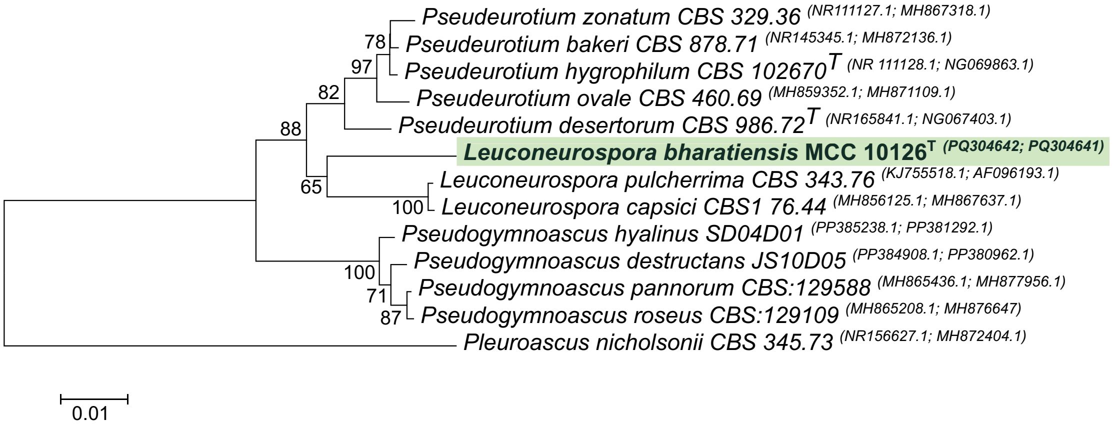
Notes: The ascomycetous genus *Leuconeurospora* belongs to the class *Leotiomycetes*. The three species described under this genus include *L. capscici*, *L. polypaeciloides* and *L. pulcherrima*. *Leuconeurospora pulcherrima* represents the type species (Malloch & Cain 1970), the strains of which have been isolated from alpine and polar northern regions like Canada, Switzerland, Scandinavia and Japan (von Arx 1978). However, *L. capsici* and *L. polypaeciloides* have been isolated from bats and substrata of the humid and cold caves in New Brunswick, Canada (Malloch *et al*. 2016). A few *Leuconeurospora* isolates exhibiting the yeast-like fungus morphology have also been identified from Antarctica (Kochkina *et al*. 2014). Based on the phylogenetic analyses of the ITS region and D1/D2 domain of the 28S nrRNA gene (LSU), a new species in the genus *Leuconeurospora* is proposed and positioned in the clade with *L. pulcherrima* and *L. capsici*. It represents the fourth species in the genus *Leuconeurospora*. The LSU sequence of *L. polypaeciloides* was unavailable for comparison, hence it has been excluded from the phylogenetic analysis.

On the basis of a megablast search on the NCBI’s GenBank nucleotide database, the phylogenetically closest hits using the **LSU** sequence of *L. bharatiensis* (MCC 10126) were found to be *Leuconeurospora capscici* [strain CBS 176.44, GenBank MH867637.1; Identities = 844/858 (98 %), one gap (0 %)], *Leuconeurospora pulcherrima* [strain CBS 343.76, GenBank AF096193.1; Identities = 844/859 (98 %), two gaps (0 %)] and *Pseudeurotium desertorum* [strain CBS 986.72, GenBank NG_067403.1; Identities = 837/858 (98 %), one gap (0 %)]. Using the **ITS** sequence of *L. bharatiensis* (MCC 10126), the closest hits were *Leuconeurospora* sp. [strain T17Cd1, GenBank JQ857040.1; Identities = 544/545 (99 %), one gap (0 %)], *Leuconeurospora* sp. [strain M20-22C-6, GenBank KU145522.1; Identities = 539/541 (99 %), no gaps] and *Leuconeurospora* sp. [strain T11Cd2, GenBank JQ857041.1; Identities = 531/534 (99 %), no gaps] (Carrasco *et al*. 2012, Troncoso *et al*. 2017). However, these sequences were not included in the phylogenetic tree construction due to the absence of their corresponding LSU sequences in the database.

Since the ITS region is not very informative in the genus *Leuconeurospora*, more confident identification was achieved by sequencing the LSU gene, in association with morphological characterisation (Malloch *et al*. 2016). Therefore, strains for which both the LSU and ITS sequences were available on the NCBI database were compared for phylogenetic analysis by constructing a concatenated tree.

Supplementary material: doi.10.6084/m9.figshare.27193395.v1

Colour illustrations: Accumulated snow sediment from Larsemann Hills, near the Indian research station Bharati, Antarctica (type locality). Colony on YEPD medium; septate hyphae of the strain MCC 10126; conidia on YEPD medium. Scale bars: chlamydospores = 20 µm; hyphae = 10 µm.



The placement of *Leuconeurospora bharatiensis* based on a concatenated alignment of the ITS region and the D1/D2 of LSU rRNA gene sequences. The tree was constructed using Maximum Likelihood (ML) analysis by applying the GTR+F+I+G4 model in IQ-TREE v. 1.6.12 (Nguyen *et al.* 2015). The scale bar indicates the expected number of substitutions per site. The numbers provided on the branches are frequencies with which a given branch appeared in 1 000 bootstrap replications. The tree was rooted with *Pleuroascus nicholsonii* CBS 345.73 as the outgroup. The new species proposed in the present study is highlighted and indicated in bold text. The alignment and tree were deposited in figshare.

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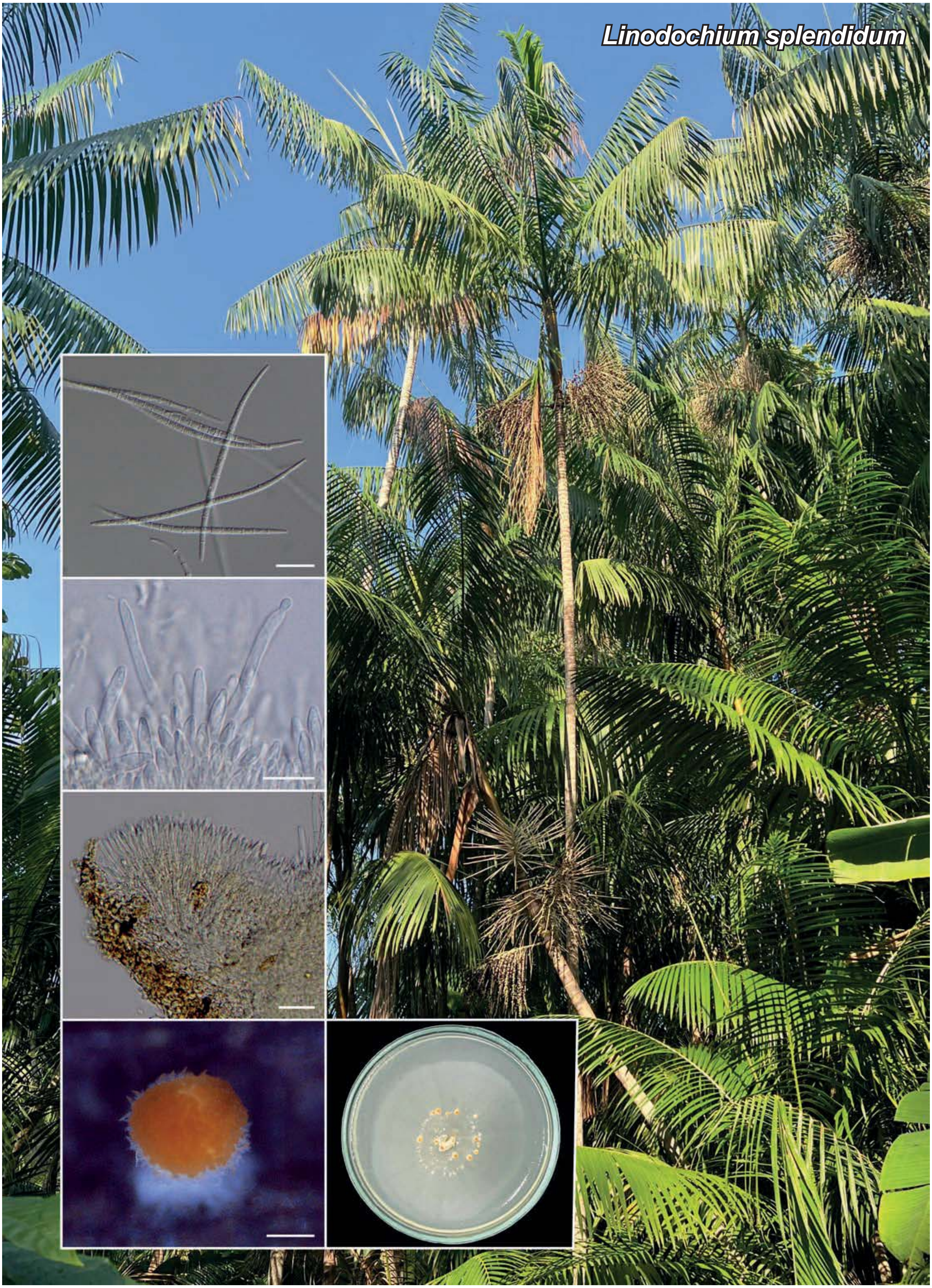

Linodochium splendidum

Fungal Planet 1758 MycoBank MB 855743

Linodochium splendidum Miglio, R.F. Castañeda & Gusmão, *sp. nov.*

Etymology: Named after the distinct appearance of its conidiomata.

Classification: *Bionectriaceae*, *Hypocreales*, *Sordariomycetes.*

Conidiomata on the natural substrate sporodochial, cupulate or pulvinate, scattered, orange to sienna, ≤ 700 µm diam. *Stroma* superficial, *textura intricata*. *Mycelium* composed of septate, branched, smooth, hyaline hyphae, 1–1.5 µm diam. *Conidiophores* distinct, unbranched, erect or flexuous, strongly geniculate above, numerous, tightly aggregated, 1–2-septate, smooth, hyaline, 30–40 × 1–2 µm. *Conidiogenous cells* monoblastic, discrete, terminal, determinate, elongated, hyaline, 16–26 × 2–3 µm. Conidial secession schizolytic. *Conidia* solitary, acerose to vermiform, truncated at the base, (5–)11–16-septate, hyaline, smooth-walled, 33–40 × 1.5–2 µm

Culture characteristics: On corn-meal and carrot agar (CMCA), colonies reaching 39.7 mm diam after 2 wk at 25 °C, flat, with a circular form, entire margin, with moderate aerial and hyaline mycelium, sporulating in culture; sporodochia superficial, scattered, solitary, with saffron to orange conidial masses (Rayner 1970).

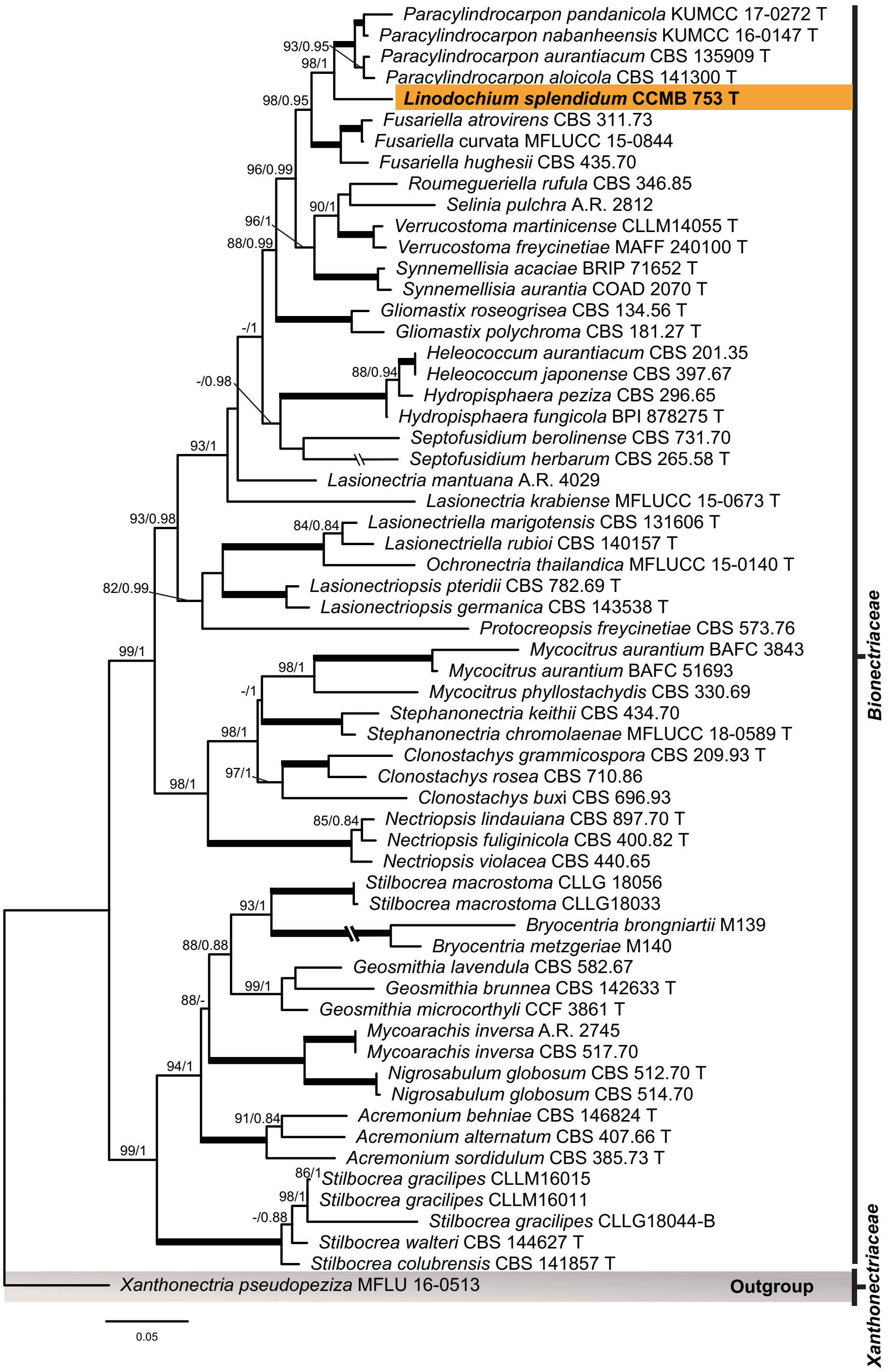
Typus: **Brazil**, Pará, Belém, Ilha do Combu, 1°28’33”S, 48°28’06”W, on decaying sheath of *Euterpe oleracea* (*Arecaceae*), 21 Jan. 2024, *B.V. Miglio*, Miglio-246 (**holotype** HUEFS 276556, culture ex-type CCMB 753 = CCLAMIC20/24; ITS and LSU sequences GenBank PQ325261 and PQ325262).

Colour illustrations: *Euterpe oleracea* in Ilha do Combu, Brazil. Conidia; monoblastic conidiogenous cells; detail of a section of the conidiomata by freezing microtome; conidiomata on natural substrate; colony on CMCA. Scale bars: conidiomata on natural substrate = 0.2 mm; conidia and conidiomata = 20 µm; conidiogenous cells = 10 µm.

Notes: *Linodochium splendidum* is morphologically similar to *L. formosum*, primarily due to the presence of numerous septa in its conidia. However, the main differences between these two species lie in the branched conidiophores and sympodial development of the conidiogenous cells of *L. formosum* (Minter & Holubová-Jechová 1981). No sequences are currently available for any species in this genus, making the new species introduced here the first to be sequenced. Phylogenetic analyses indicate that this genus belongs to the *Bionectriaceae*, with *Paracylindrocarpon aloicola* being the closest related species.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Paracylindrocarpon aloicola* [strain CBS 141300, GenBank NR_154346; Identities = 543/582 (93 %), eight gaps (1.3 %)], *Paracylindrocarpon nabanheense* [strain KUMCC 16-0147, GenBank NR_168196; Identities = 487/525 (92 %), seven gaps (1.3 %)]. Closest hits using the **LSU** sequence are *Hydropisphaera saulensis* [strain BRFM 3053, GenBank NG_088113; Identities = 857/877 (97 %), two gaps (0.2 %)], and *Verrucostoma freycinetiae* [strain MAFF 240100, GenBank NG_059924; Identities = 843/857 (98 %), one gap (0.1 %)].

Supplementary material: doi: 10.6084/m9.figshare.27018109 (Table of GenBank accession numbers); 10.6084/m9.figshare.27018112 (phylogenetic tree); 10.6084/m9.figshare.27018166 (alignment).



The phylogenetic tree was inferred from ITS and LSU sequences of *Linodochium splendidum* (CCMB 753) and related species from *Bionectriaceae*, rooted with *Xanthonectria pseudopeziza* (MFLU 16-0513) as outgroup. Maximum likelihood bootstrap support values > 80 % obtained in MEGA 7 and Bayesian posterior probability (BPP) values > 0.80 conducted using the CIPRES portal are shown at the nodes, respectively, with a dash ('–') indicating lack of statistical support (Kumar *et al.* 2016, Miller *et al.* 2010, http://www.phylo.org/). The scale bar represents the expected number of changes per site. Full statistical support (MLBS = 100 % and BPP = 1.0) is highlighted by thickened branches. The newly generated sequence from the new species is in **bold** and the ex-type strains are marked with a 'T' after the culture number. The tree and alignment are available in Figshare.com (doi: 10.6084/m9.figshare.27018112 and 10.6084/m9.figshare.27018166, respectively).

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Monosporascus solitarius

Fungal Planet 1759

MycoBank MB 855626

Monosporascus solitarius G. Delgado & Maciá-Vicente, ***sp. nov.***

Etymology: Named after the isolated phylogenetic position of the fungus within the genus *Monosporascus*.

Classification: *Diatrypaceae*, *Xylariales*, *Sordariomycetes.*

Root endophyte isolated on culture media from surface-sterilised roots of living plants. *Mycelium* composed of branched, septate, smooth, hyaline, thin-walled hyphae, 1.5–4 µm wide, becoming brown to dark brown, verruculose to verrucose, constricted at some septa, thick-walled with age, 3–6(–7) µm wide.

Culture characteristics: Colonies on potato dextrose agar (PDA) fast growing, reaching 38–45 mm diam after 1 wk at 24 °C, cottony around the centre, floccose and less dense toward the edges, white, margin diffuse, reverse dull white. On malt extract agar (MEA) reaching 36–43 mm diam, velvety, flat, somewhat cottony toward the edges, white, margin diffuse, reverse dull white; aerial mycelium turning off-white with age and forming pale brown or cream superficial spots together with the production of pale-yellow exudates, the immersed mycelium forming a thick, dark brown to blackish brown dense layer of tightly packed darkened hyphae turning the reverse dull black after 2 mo. Cultures sterile.

Habit, habitat and distribution: Root endophyte. Presently known only from Greece.

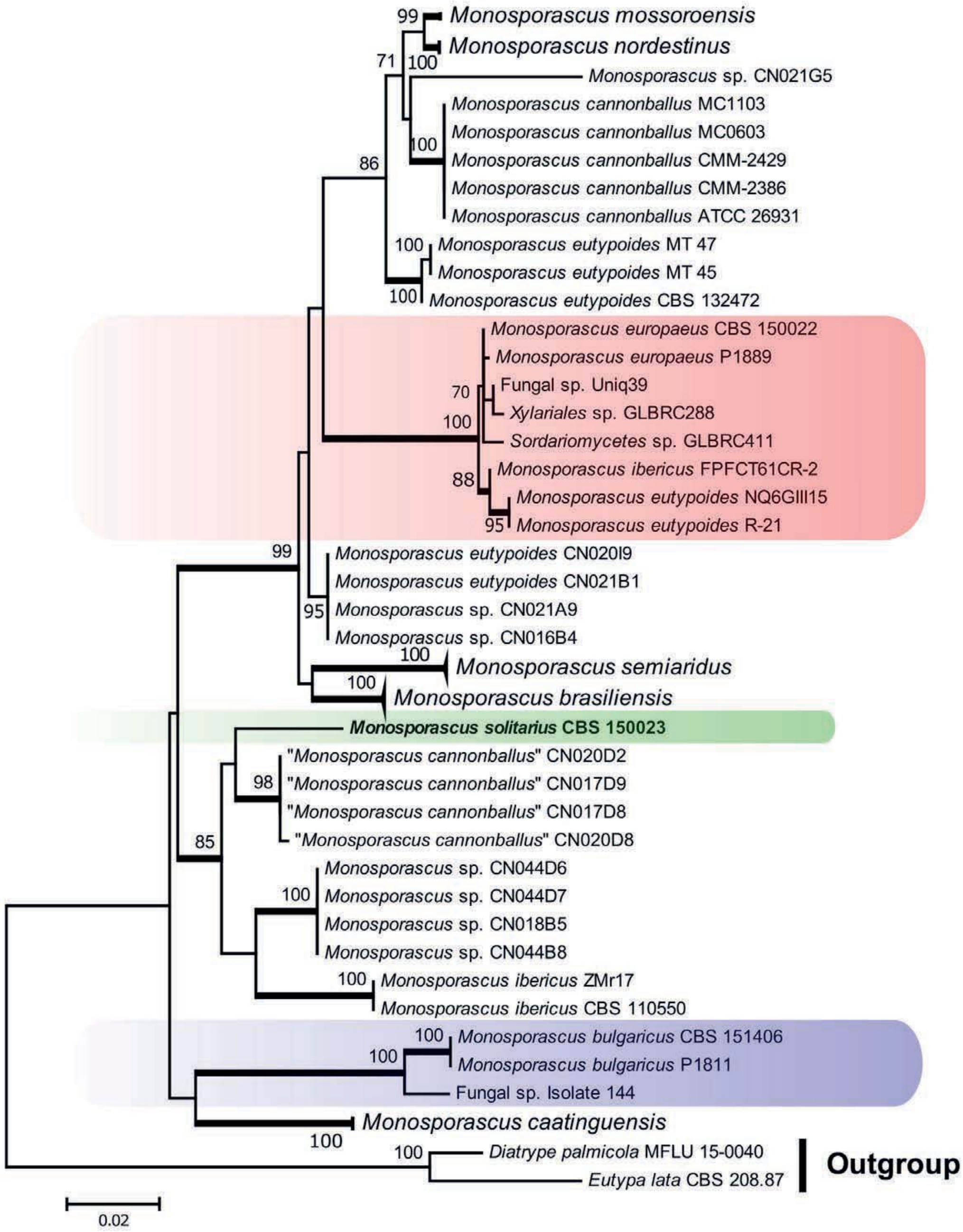
Typus: **Greece**, Evrytania, near Karpenissi, 38°54’25.6”N, 21°49’31.6”E, 912 m a.s.l., isolated from surface-sterilised, asymptomatic roots of *Microthlaspi perfoliatum* (*Brassicaceae*), 28 May 2013, coll. *K. Glynou* & *J.G. Maciá-Vicente*, isol. *K. Glynou*, P2549 (**holotype** permanently preserved in a metabolically inactive state CBS 150023, culture ex-type CBS 150023; ITS, LSU, and *tub2* sequences GenBank KT269777, PP454708, and PQ140140).

Notes: In recent years, several culturable, phylogenetic and phylogenomic studies have revealed that the diatrypaceous genus *Monosporascus* includes a hidden diversity still awaiting to be discovered and described (Negreiros *et al*. 2019, Robinson *et al*. 2020). Many strains with sequences available in GenBank and named *M. cannonballus* or *M. eutypoides*, both significant plant pathogens causing root rot and vine decline primarily of cucurbits, apparently represent novel species and account for a rich source of unexplored biodiversity. During an extensive sampling for root endophytic fungi across Europe (Glynou *et al*. 2016) several isolates of *Monosporascus* were obtained. Surprisingly, two culturally and phylogenetically distinct species were collected as root endophytes on the same host, *M. perfoliatum* (*Brassicaceae*), at the same location in Bulgaria on the same day but different plant individuals and newly described as *M. bulgaricus* and *M. europaeus* (Crous *et al*. 2024). *Monosporascus solitarius* is a third species also obtained from roots of the same brassicaceous host but in Greece and represented by a single isolate. A comparison with the previously described two taxa shows differences in culturable features. The three of them form white, fast-growing, sterile colonies on culture media but on MEA, for example, *M. bulgaricus* produces a dull-white and flat concentric ring around the umbonate, cottony centre whereas colonies of *M. europaeus* are cottony with scarce aerial mycelium around the centre and those of *M. solitarius* are velvety, flat, and somewhat cottony toward the edges. Phylogenetically, they were distantly related, and our novel species forms an isolated lineage sister to a group of strains named “*M. cannonballus*” without support. These strains are endophytes isolated from tissues of the grass *Stipagrostis ciliata* (*Poaceae*) collected at the so called “fairy circles” in the Namibian desert (van Vuuren 2022). They are distant from ATCC 26931, the ex-type strain of *M. cannonballus*, and represent an undescribed species. Moreover, megablast searches in GenBank of the ITS region of *M. solitarius* did not retrieve any close related strains from previous ecological or phylogenetic studies as happened for *M. bulgaricus* or *M. europaeus*. Despite the limitations and risks of describing singleton-based species (Cazabonne *et al*. 2024), *M. solitarius* is well supported by cultural, ecological and molecular evidence, and the emerging interest in the hyperdiverse *Monosporascus* will likely generate additional data in the future to corroborate its phylogenetic status and taxonomic validity.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Sordariomycetes* sp. [strain HTCR20, GenBank MK809935.1; Identities = 509/526 (97 %), 12 gaps (2 %)], *Monosporascus cannonballus* [strain CN020D2, GenBank ON074870.1; Identities = 544/574 (95 %), 11 gaps (1 %)], and *Monosporascus cannonballus* [strain CN017D9, GenBank ON074839.1; Identities = 544/574 (95 %), 11 gaps (1 %)]. Closest hits using the **LSU** sequence are *Monosporascus europaeus* [strain CBS 150022; GenBank PP454705.1; Identities = 1 317/1 350 (98 %), five gaps (0 %)], *Monosporascus europaeus* [isolate P1889, GenBank PP454706.1; 1 219/1 251 (97 %), five gaps (0 %)], and *Monosporascus bulgaricus* [strain CBS 151406, GenBank PP454707.1; Identities = 1 278/1 319(97 %), six gaps (0 %)]. Closest hits using the ***tub2*** sequence are *Monosporascus* sp. [isolate SCUA-Nem-KH34, GenBank MN635677.1; Identities = 404/436 (93 %), six gaps (1 %)], *Monosporascus bulgaricus* [strain CBS 151406, GenBank PP460994.1; Identities = 416/452 (92 %), five gaps (1%)], and *Monosporascus ibericus* [strain CBS 110550, GenBank JQ973833.1; 406/442 (92 %), six gaps (1 %)].

Supplementary material: doi: 10.6084/m9.figshare.26881174 (Alignments, table and trees).

Colour illustrations: Collection site in Greece. Colonies on PDA and MEA (after 1 wk at 24 °C) on surface view; mycelium with hyaline hyphae; immersed mycelium with brown hyphae. Scale bars = 5 µm.



Maximum likelihood phylogenetic tree obtained from the concatenated ITS, LSU and *tub2* sequences of *Monosporascus* (*Diatrypaceae*, *Sordariomycetes*) showing the position of *M. solitarius* within the genus. The dataset of Crous *et al*. (2024) was used for analyses with additional sequences obtained from closest hits after megablast searches in GenBank. Alignments were performed using MAFFT v. 7.511 on the online server (Katoh *et al*. 2019) with the final dataset consisting of 61 strains and a total of 1 934 positions, 533 from the ITS alignment, 686 from the LSU and 715 from the *tub2*. Maximum likelihood and Bayesian Inference phylogenetic analyses were run in 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, following the settings of Crous *et al*. (2021a). The best-fit substitution model for the concatenated ITS-LSU-*tub2* dataset according to the Bayesian Information Criterion obtained in MEGA v. 6 (Tamura *et al*. 2013) was K2+G. *Diatrype palmicola* MFLU 15-0040 and *Eutypa lata* CBS 208.87 were used as outgroups. Bootstrap support values ≥ 70 % are shown at the nodes and Bayesian posterior probabilities ≥ 0.95 are indicated by thickened branches. Each root endophytic *Monosporascus* species isolated from the brassicaceous host *Microthlaspi perfoliatum* is highlighted in a color box: blue for *M. bulgaricus*, red for *M. europaeus* and lime for *M. solitarius* with the novel strain in bold. Some strongly supported clades were collapsed to facilitate layout. Alignments and trees are deposited in figshare.com (doi: 10.6084/m9.figshare.26881174).

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Mycena subfragosa

Fungal Planet 1760

MycoBank MB 855757

Mycena subfragosa M. Villarreal, Couceiro & Traba, ***sp. nov.***

Etymology: Name reflects its similarity to *Mycena fragosa*.

Classification: *Mycenaceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata gregarious. *Primordia* 0.1–0.3 mm, hemispheric to obtusely conic, initially very dark brown to slightly greyish brown, densely hirsute overall. *Pileus* 1–2.5 mm diam, initially paraboloid to hemispheric or convex, flattening with age, without umbo, the disc flattened to shallowly depressed, surface minutely white-pubescent, partially to entirely glabrescent with age, dry, devoid of a separable gelatinous pellicle, sulcate-striate with striations distinctly darker than the rest of the pileus, disc and striations pale greyish brown initially and light grey elsewhere, hygrophanous, fading with moisture loss to watery white to pale grey and with or without brown tones. *Lamellae* ascending, narrowly adnate, distant to subdistant, 7–12 reaching stipe, with 1–3 series of lamellulae, moderately broad 0.2–0.4 mm, very pale grey to white; the edges paler, not separable as a gelatinous, elastic-like thread. *Stipe* 12–33 × 0.2–0.6 mm, cylindrical, central, hollow, straight to flexuous, the base broader at the point of attachment with a small pubescent basal disc; watery grey to watery white, surface entirely covered with minute white-pubescence, glabrescent towards the apex and more densely pubescent at the base. *Context* very thin, whitish; *odour* and *taste* absent. *Basidiospores* (7.2–)8.1–10.8(–13.0) × (3.2–)3.5–4.3(–4.8) µm; Q = (1.8–)2.1–2.7(–3.0); N = 100; Me = 9.5 × 3.9 µm; Qe = 2.4; narrowly ellipsoid to cylindrical, smooth, hyaline, strongly amyloid in Melzer´s reagent, thin-walled. *Basidia* 11.8–16 × 5.4–8.3 µm, generally 4-spored but some 2-spored present at the same lamellae, clavate, stout, with sterigmata up to 5.5 µm long; basidioles similar. *Cheilocystidia* 15.5–27 × 9–13 µm, claviform to subclaviform, rarely smooth, with 2–7 short to long apical excrescences, 1.5–9.6 × 0.7–1.4 µm, sometimes forked, forming a sterile band. *Pleurocystidia* absent. *Pileipellis* an ixocutis with dermatocystidia composed of narrow hyphae, 1–7 µm, diverticulated with simple excrescences 3–12 × 1.5–2.9 µm; terminal cells at the margin of the pileus claviform to irregular shaped, 8.5–16 × 6–9 µm, densely diverticulated. *Dermatocystidia* 15–125 µm long, protruding, ampullaceous, cylindrical to lageniform. *Hypodermium* composed of inflated, globose to ellipsoid cells, 8.5–17 µm broad, thin-walled, brownish-vinescent in Melzer's reagent. *Stipitipellis* a cutis composed of narrow and smooth hyphae, 2.5–4.5 µm diam. *Caulocystidia* 18–85 × 2–6 µm, flagelliform, simple to forked, usually with one or several thick protrusions at the base, smooth, all over the stipe. *Cystidia* of the basal disc utriform, cylindrical to lageniform. *Clamp connections* present in all tissues.

Colour illustrations: Coastal and hygrophilous wetlands of The Ría de Ortigueira, Spain. Basidiocarps; dermatocystidia; basidiospores, cheilocystidia; hyphae of the pileipellis; caulocystidia. Scale bars: basidiomes = 1 mm and 1 cm, respectively; all others = 10 µm.

Habitat and distribution: Gregarious, on fallen leaves of *Salix atrocinerea*, during spring and summer. Known from only one locality, where it is very frequent under willows.

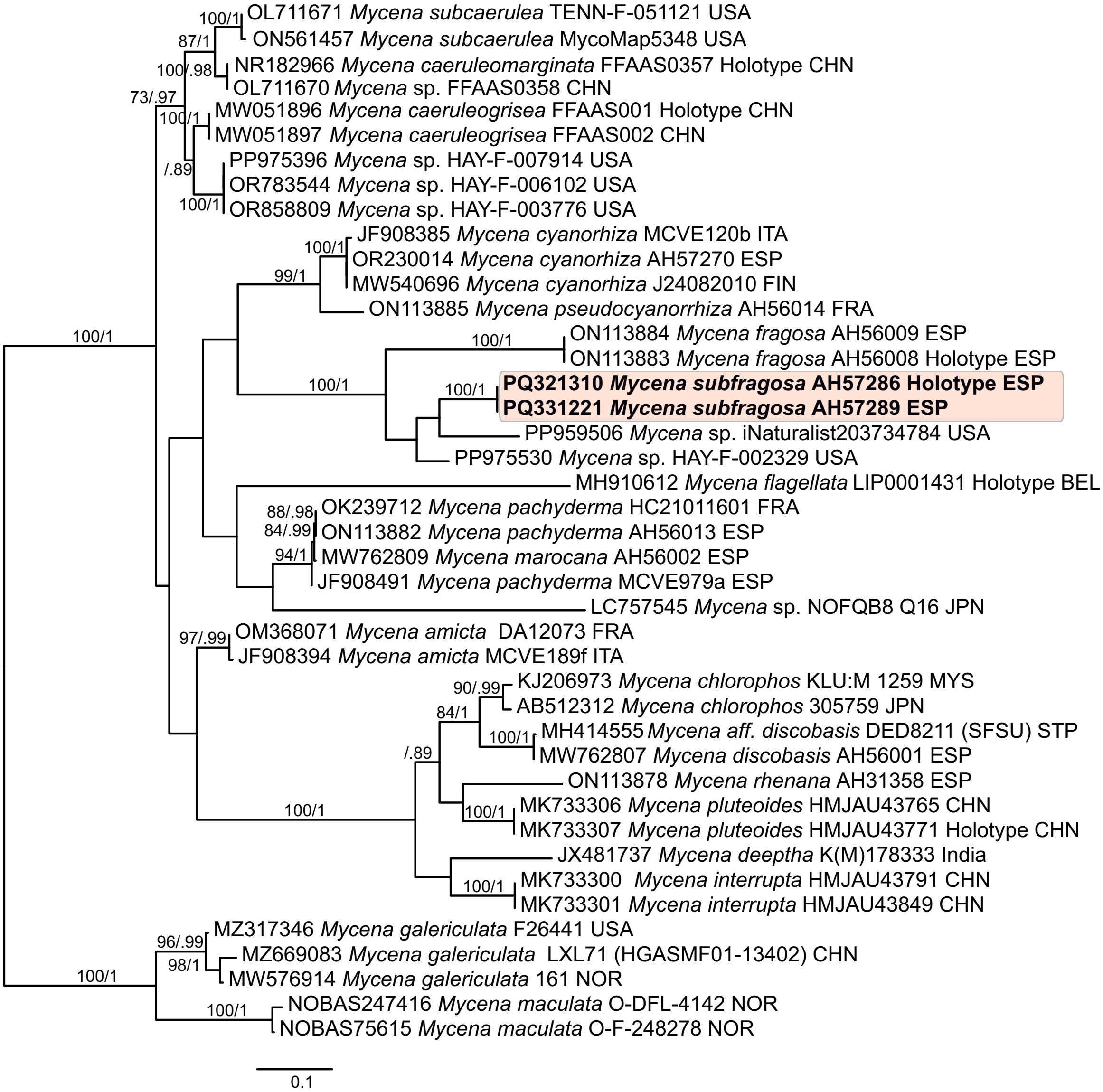
Typus: **Spain**, A Coruña**,** Ortigueira, Playa de Morouzos, 43º42'52"N 8º11'98"W, 9 m a.s.l., on dead leaves of *Salix atrocinerea* (*Salicaceae*), 15 Apr. 2022, *A. Couceiro, M. Saavedra, J.M. Traba & M. Villarreal* (**holotype** AH57286; ITS sequence GenBank PQ321310).

Additional material examined: **Spain**, A Coruña, Ortigueira, Playa de Morouzos, 43º42'52"N 8º11'98"W, 9 m a.s.l., on dead leaves of *S. atrocinerea*, 26 Apr. 2022, *A. Couceiro, M. Saavedra, J.M. Traba & M. Villarreal*, AH57287; *ibid.*, 8 Apr. 2023, *A. Couceiro & M. Villarreal*, AH57288; *ibid.*, 19 Apr. 2023, *A. Couceiro & M. Villarreal* (AH57289, ITS sequence GenBank PQ331221).

Notes: *Mycena subfragosa* is the second described species with a basal disc belonging to *Mycena* sect. *Viscipelles*. It is characterised by its tiny size, pale colours of the pileus, presence of a basal disc and gregarious basidiocarps growing on *Salix* dead leaves. The new species group with the recently described *M. fragosa* (Villarreal *et al*. 2023), from which it is macroscopically difficult to distinguish, except that the new species is generally paler in colour, and unlike *M. fragosa*, which is a mainly autumnal species, *M. subfragosa* has only been collected during spring or early summer. Microscopically, the new species differs from *M. fragosa* in having slightly larger and more elongated spores, cheilocystidia rarely smooth and with somewhat more elongated apical excrescences.

Based on the results of a Blastn search of NCBIs GenBank nucleotide database using the ITS sequence, *M. subfragosa* differs from the holotype of *M. fragosa* by 80 bp in the ITS1 and 28 bp in the ITS2 region (82 % blast similarity) [voucher AH56008, GenBank ON113883; Identities = 511/623 (82 %), fifty gaps (8 %)].

A phylogenetic analysis based on internal transcribed spacer sequences derived from two *M. subfragosa* collections clearly showed that they cluster together with *M. fragosa* and other unidentified *Mycena* species in a well-supported branch, being phylogenetically distinct from the closest species within *Mycena* sect. *Viscipelles*.



Phylogenetic relationships in *Mycena* sect. *Viscipelles* and sect. *Exornatae* reconstructed from an unpartitioned ITS dataset. Maximum Likelihood (ML) analyses were performed using IQ-TREE v. 2.2.0 (Nguyen *et al*. 2015). Branch support was assessed through 1 000 replicates of standard non-parametric bootstrapping (Felsenstein 1985). Bayesian Interference (BI) analyses were carried out in MrBayes v. 3.2.7 (Ronquist *et al*. 2012) and included two runs that will stop automatically when the standard deviation falls below 0.01 or the generation number reaches 5 000 000, with a sample frequency of 500 and a burn-in value of 25 %. The ML bootstrap support values and Bayesian posterior probabilities are indicated above the branches. The tree was displayed with FigTree v. 1.4.4 (Rambaut 2018) and edited with Inkscape. All tips are labelled with database accession number, taxon name, collection number and origin. *Mycena subfragosa* is marked in bold and the holotype is indicated. Scale bar on the tree indicates the expected number of changes per site. The tree was rooted to *M. galericulata* and *M. inclinata*. The alignment was deposited at Figshare.com (doi: 10.6084/m9.figshare.27188328).

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Phakopsora sageretiae

Fungal Planet 1761 MycoBank MB 855498

Phakopsora sageretiae Y.P. Tan, T.Y. Chi & R.G. Shivas, ***sp. nov.***

Etymology: Named after the host genus *Sageretia*.

Classification: *Phakopsoraceae*, *Pucciniales*, *Pucciniomycetes.*

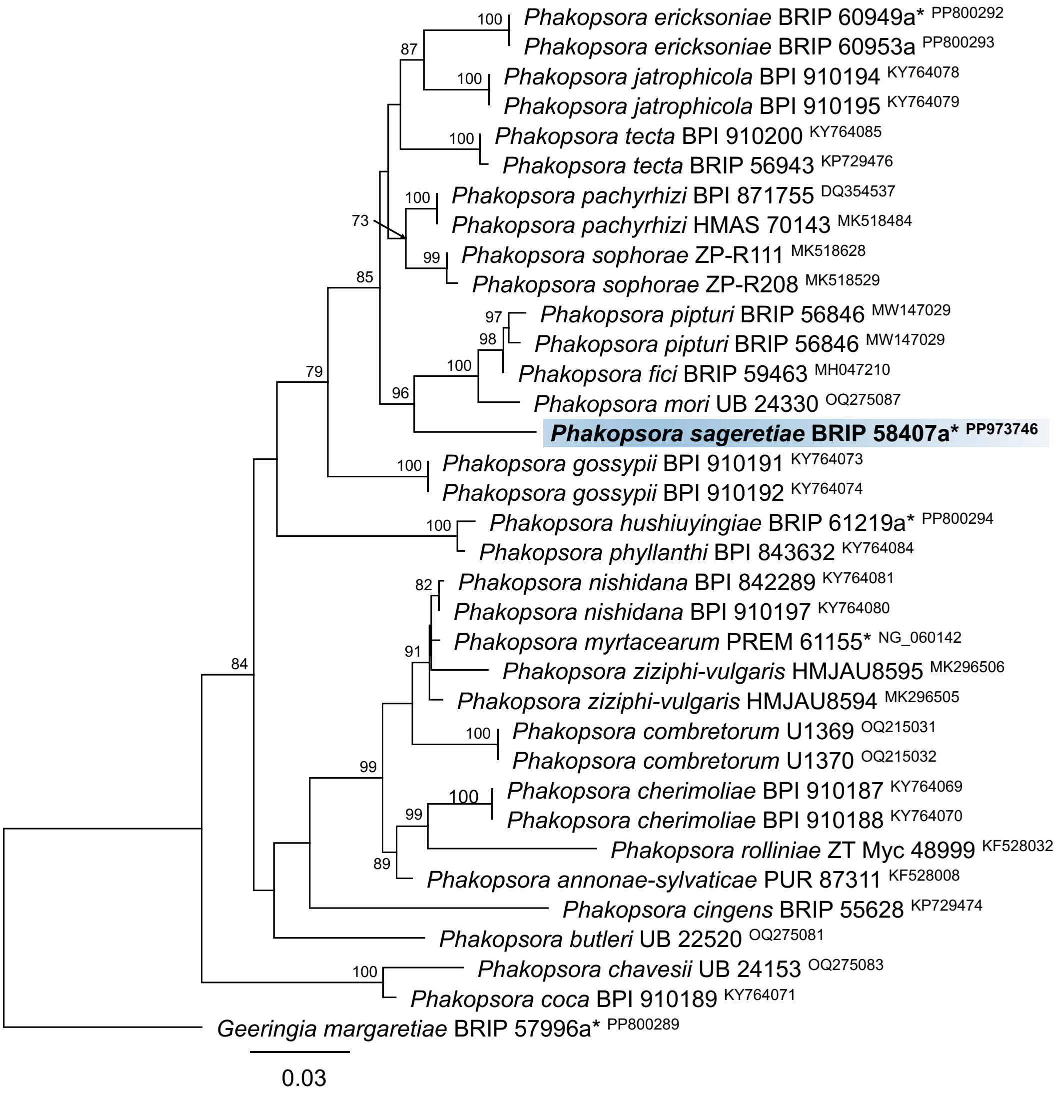
Uredinia on leaves of *Sageretia theezans*, mostly hypophyllous, blister-like with an indistinct opening, 100–250 µm diam, reddish brown, solitary or in small groups. *Paraphyses* subhyaline to yellowish brown, straight or slightly curved, cylindrical to clavate, 10–30 × 8–12 µm; wall smooth, 1–2 µm wide at sides, 3–5 µm wide at apex. *Urediniospores* ellipsoidal or obovoid, 20–30 × 14–18 µm, pale yellowish brown; wall even, 1–1.5 µm wide, yellowish brown, moderately echinulate. *Telia* not seen.

Typus: **Vietnam**, Tam Dao, Vinh Phuc Province, leaf rust on *Sageretia theezans* (*Rhamnaceae*), 27 Dec. 2012, *T.Y. Chi, A.R. McTaggart, T.S. Marney, M.A. Shivas, M.D.E Shivas & R.G. Shivas*, VND074 (**holotype** specimen BRIP 58407a; LSU sequence GenBank PP973746).

Colour illustrations: Thác Bạc Tam Đảo, Vietnam. Uredinia on lower leaf surface of *Sageretia theezans*; uredinia; paraphyses; urediniospores (equatorial view, bottom left; surface view, bottom right). Scale bars: lower leaf surface = 2 mm; uredinia = 1 mm; all others = 10 µm.

Notes: In the phylogenetic analysis, *P*. *sageretiae* was not closely related to any known species of *Phakopsora* that infect hosts in the *Rhamnaceae*. This may indicate an evolutionary host jump from another plant family (Maier *et al*. 2015, McTaggart *et al*. 2016). The host plant, *Sageretia theezans*, is native to the region in Vietnam where *P*. *sageretiae* was collected.

Based on a Blastn search of the NCBI GenBank nucleotide database, the closest relevant hits with the LSU region of *P. sageretiae* were *Cerotelium fici* [specimen voucher BRIP 56890, GenBank MH047209; Identities = 559/591 (95 %), ten gaps (1 %)], *P. jatrophicola* [specimen voucher BPI 910194, GenBank KY764078; Identities = 554/590 (94 %), seven gaps (1 %)], *P. mori* [specimen voucher UB 24330, GenBank OQ275087; Identities = 509/538 (95 %), 11 gaps (2 %)], *P. pachyrhizi* [specimen voucher BPI 910200, GenBank KY764085; Identities = 505/531 (95 %), four gaps (0 %)], *P. pipturi* [specimen voucher BRIP 56846, GenBank MW147029; Identities = 540/573 (94 %), nine gaps (1 %)], and *P. tecta* [specimen voucher BRIP 56943, GenBank KP729476; Identities = 511/538 (95 %), four gaps (0 %)].



Phylogenetic tree of selected *Phakopsora* species based on maximum likelihood analysis of the LSU region. The phylogenetic analysis was performed with the IQ-TREE web server (Trifinopoulos *et al.* 2016) based on the GTR substitution model with gamma-distribution rate variation. *Geeringia margaretiae* (holotype specimen BRIP 57996a) was used as the outgroup. GenBank accession numbers are indicated (superscript LSU). Novel taxon is shown in **bold**. Type specimens are marked by an asterisk (*). The alignment and phylogeny are publicly available in Zenodo (doi: 10.5281/zenodo.13231529).

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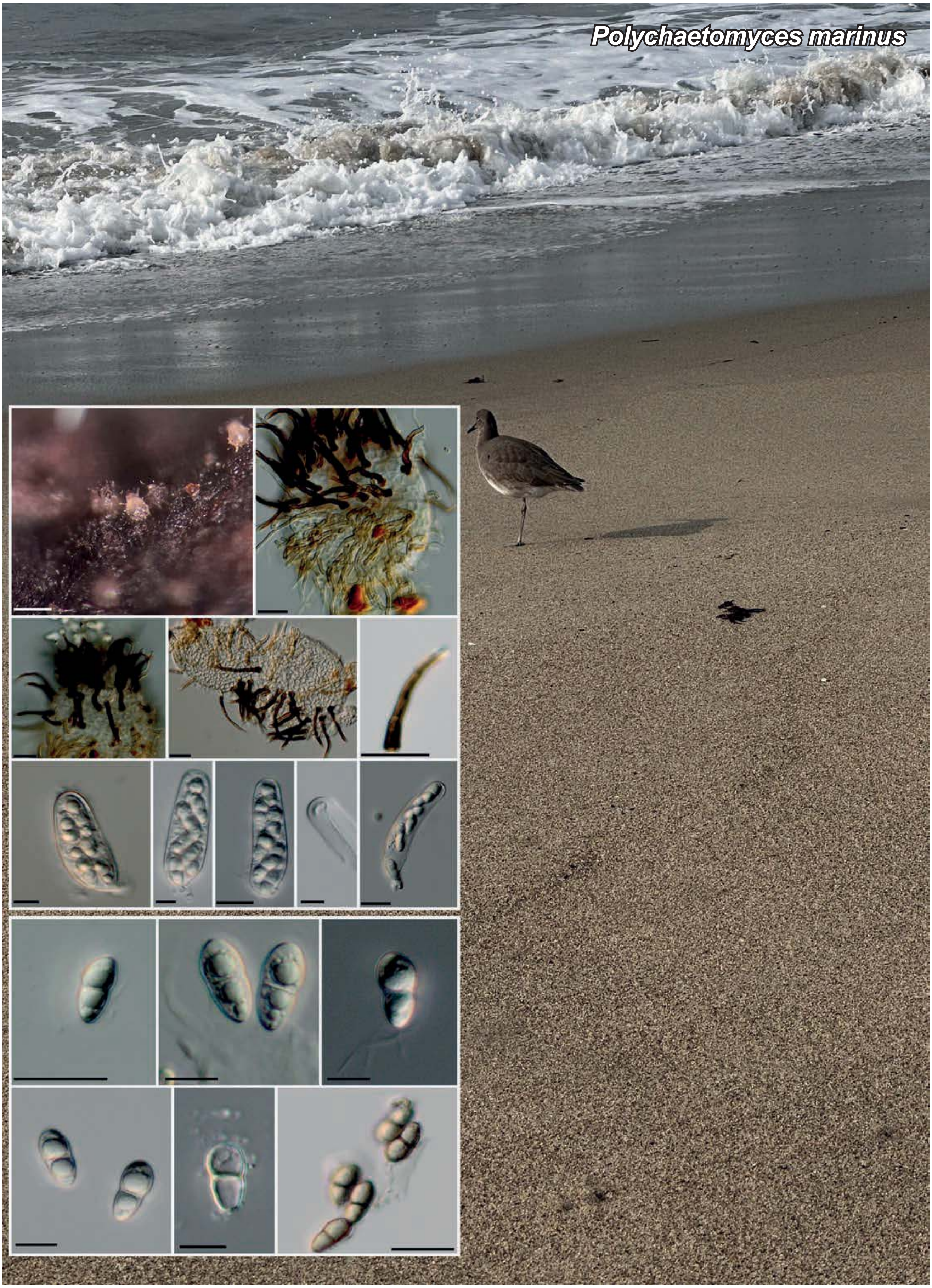

Polychaetomyces marinus

Fungal Planet 1762 MycoBank MB 856054

Polychaetomyces Raja, Fryar, D.E.A. Catches. & Oberlies, ***gen. nov.***

Etymology: "*Polychaet*" is Latin for "many setae"; "*myces*" in Latin which means fungus.

Classification: *Incertae sedis*, *incertae sedis*, *Dothideomycetes*.

Ascomata on wood, superficial to partially immersed, scattered or gregarious, globose to subglobose, ostiolate, papillate, subiculate or not, bearing numerous dark flexuous setae around the papilla. *Ascomal wall* membranous. *Pseudoparaphyses* mostly evanescent or absent. *Asci* 8-spored, bitunicate, fissitunicate, usually broadly clavate to obclavate, pedicel knob-like, ungulate or absent. *Ascospores* hyaline, with or without amorphous gelatinous sheath, 1-septate, thick-walled, verruculose or not, symmetrical or asymmetrical becoming brown with age.

Type species: *Polychaetomyces marinus* Raja, Fryar, D.E.A. Catches. & Oberlies

MycoBank MB 856055

Polychaetomyces marinus Raja, Fryar, D.E.A. Catches. & Oberlies, ***sp. nov.***

Etymology: Latin *marinus* in reference to the marine habitat (Pacific Ocean) from which the fungus was isolated in California, USA.

Saprobic on decaying wood in marine habitats. *Ascomata* solitary to gregarious, scattered, superficial to partially immersed, hyaline to light brown, membranous, subglobose to obpyriform, ostiolate, setose, subiculate or not, with hyaline to light brown, 1–3-septate hyphae attached to the upper two-thirds of the ascoma, 106–148 × 80–109 µm. Numerous, dark brown, 3–4-septate, straight to slightly flexuous setae all over the ascoma, but concentrated around the short papilla. *Setae* dark brown, bulbous towards the base, hyaline, and tapering towards apices, 27–50 × 3–4 µm. *Peridium* single layered, thick-walled, *textura angularis* in surface view. *Hamathecium* mostly evanescent and almost absent. *Asci* 8-spored, bitunicate, fissitunicate, thick-walled, in a gelatinous matrix, with ocular chamber, usually broadly clavate to obclavate, pedicel knob-like or ungulate, sometimes absent, 48–70 × 10–23 µm (mean and SD = 60 ± 7 × 17 ± 3 µm, n = 20). *Ascospores* 1-septate; septum thick-walled with one large guttule in each cell, biseriate, symmetrical or asymmetrical; when asymmetrical, upper cell broader than lower cell, hyaline when young, becoming brown with age, verruculose, thick-walled; in older ascomata, ascospores accumulating in a mass around the ostiole, 12–22 × 5–8 µm (mean and SD = 16 ± 2 × 6 ± 1 µm, n = 100). Sheath not persistent, sometimes amorphous, gelatinous sheath seen in water mounts, disappearing in lactic acid and glycerin.

Habit, habitat and distribution: Submerged wood, marine (Pacific Ocean), California, USA.

Colour illustrations: Redondo Beach, California, USA (photo credit: Sara Oberlies Brown). *Polychaetomyces marinus* from holotype. Ascomata on wood, note dark setae; squash mount of ascoma showing dark setae around the short papilla of the ascoma and brown hyphae attached to the upper two-thirds of the ascoma; note, ascospores accumulating in a mass around the ostiole; squash mount of the ascomata showing dark brown setae and *textura angularis* cells in surface view; septate seta, dark brown at the base and hyaline at the apex; clavate to obclavate asci; ocular chamber; ascus extending in water; ascospores with one guttule in each cell, note amorphous sheath; old ascospores with thick-wall and becoming brown with age. Scale bars: Ascomata = 100 µm; ascoma and setae = 20 µm; asci and ascospores = 10 µm.

Typus: **USA**, California, Los Angeles County, South Redondo, Redondo Beach, 33°49'59.0"N, 118°23'26.0"W, 19 m a.s.l., on submerged driftwood collected during high tide in sea water, 29 Dec. 2023, *N.H. Oberlies* (**holotype** ILLS00122906; ITS and partial 28S nrRNA sequences GenBank PQ427269 and PQ427270).

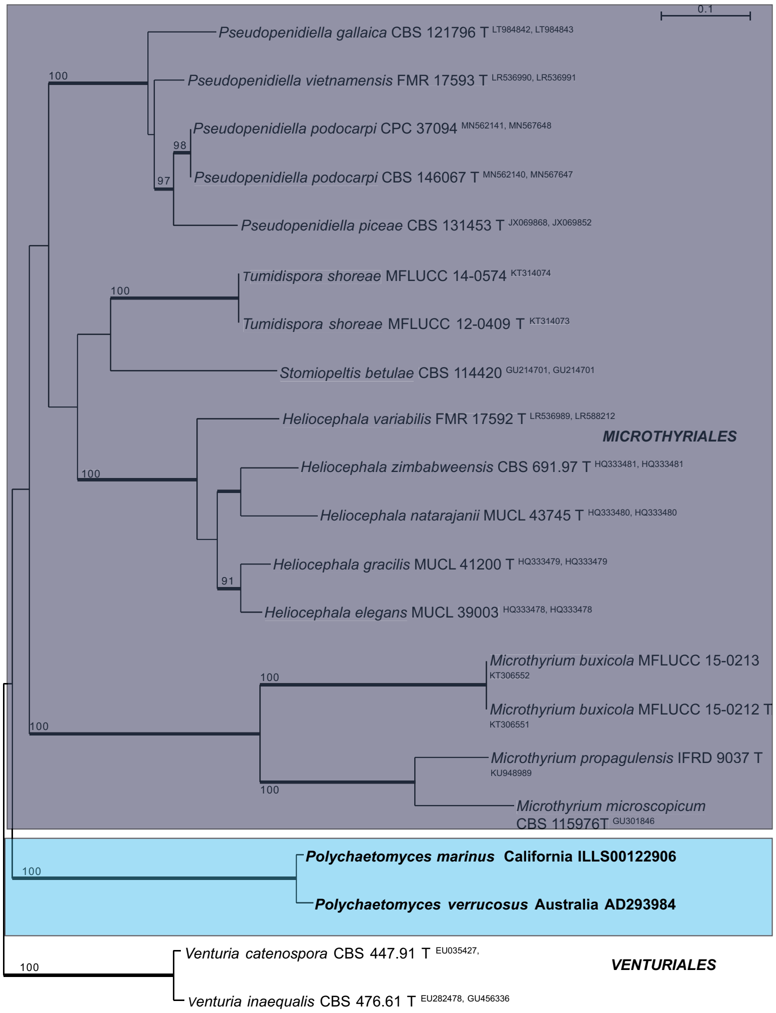
Notes: Based on ecological and morphological characteristics such as saprophytic habitat, ascomata that are superficial to partially immersed with numerous dark setae around the short papilla, evanescent pseudoparaphyses, 8-spored, bitunicate, obclavate asci, and hyaline 1-septate, asymmetrical ascospores, the new genus could be classified in the *Venturiales,* an order within the class *Dothideomycetes* (Zhang *et al.* 2011, Hyde *et al.* 2013, Shen *et al.* 2020). To date, three genera, *Septonema, Scolecobasidiumm* and *Proventuria* have been documented from marine habitats in the *Venturiales* (Jones *et al.* 2019). None of the above taxa have any morphological similarity to the new genus being introduced herein. The new genus and species, *Polychaetomyces marinus*, is characterised by its small, hyaline, membranous ascomata, dark brown straight to flexuous, septate setae, and obclavate asci found in a gelatinous matrix along with asymmetrical, 1-septate ascospores, with or without an amorphous gelatinous material, represent a unique combination of features not hitherto observed in previously described marine ascomycetes (Jones *et al.* 2019). Through the NCBI BLAST search it was found that the ITS region of this new genus shows sequence homology of 80–87 % with members of the *Venturiales,* an order that is closely related to the *Microthyriales*, *Natipusillales,* and *Asterinales* within the *Dothideomycetes* (Hyde *et al*. 2013). To determine the ordinal position of the new genus and species, we included selected members from the above orders in our maximum likelihood phylogenetic analysis. The analysis of the combined ITS and partial 28S nrRNA gene regions, as well as the separate analysis of partial 28S nrRNA gene region (Supplementary material), revealed that *Polychaetomyces marinus* forms a distinct clade. It shows phylogenetic relatedness with *Microthyriales*, *Natipusillales*, and *Venturiales,* and exhibits a sister group relationship with these orders. Based on our analysis of the ITS and partial 28S nrRNA gene regions, we classify *Polychaetomyces marinus* as *Dothideomycetes incertae sedis.*

Also, refer to notes of another new species described elsewhere in this publication, *Polychaetomyces verrucosus* (FP

1763), which was described and isolated from submerged wood in sea water in Coorong National Park, South Australia. Both *P. marinus* and *P. verrucosus* co-occur in a strongly supported clade (≥95 % ultrafast bootstrap support and ≥ 0.95 Bayesian posterior probability).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cylindrosympodium lauri* [strain CBS 240.95, GenBank EU035414; Identities = 303/371(82%) 22 gaps (5 %)], *Cylindrosympodium variabile* [strain CBS 563.82, GenBank MH861528; Identities = 289/356 (81%) 21 gaps (5 %)], and *Fagicola fagi* [strain CBS 621.84, GenBank EU035431; Identities = 312/389 (80%) 31 gaps (7 %)]. Closest hits using the partial **28S nrRNA** sequence are *Pseudoanungitea syzygii* [strain CBS:520.93, GenBank MH107957; Identities = 514/604 (85%) 16 gaps (2 %)], *Sympodiella acicola* [strain CBS 487.82, GenBank KY853530; Identities = 512/603 (85%) 14 gaps (2 %)], and *Pseudoanungitea vaccinii* [strain CBS 143164, GenBank MH107958; Identities = 503/593(85%) 16 gaps (2 %)].

Supplementary material: The alignments and Expanded Phylogenetic tree were deposited in FigShare.com, https://figshare.com/s/4847e33fb2c4ed7cb78e



Phylogram of the most likely tree (-lnL = 8431.601) from an IQ-TREE analysis v2.2.0 (Nguyen *et al.,* 2015) of 21 taxa based on ITS and partial 28S nrRNA gene data (1 454 bp) under Edge-linked partition model for 5000 ultrafast bootstraps using (Minh *et al.,* 2013) using PhyloSuite v.1.2.3 (Xiang *et al.,* 2023). Numbers refer to UFBoot support values ≥ 90 % based on 5 000 replicates. Nodes ≥ 95 % are considered strongly supported. Thickened branches indicate significant Bayesian posterior probabilities ≥ 95 %. Bayesian analysis was calculated using Mr. Bayes v. 3.2 (Ronquist *et al.,* 2012) under GTR+G model for ITS region and GTR+I+G model for partial 28S nRNA gene region using PartitionFinder2 (Lanfear *et al.,* 2017). ClipKit (https://dev-clipkit.genomelybio.com/#/) (Steenwyk *et al.,* 2020) was used to remove ambiguous characters from the alignment The new taxa are highlighted in **bold** and a blue box. Scale bar indicates the expected number of nucleotide substitutions per site. Taxon sampling was performed as per (Iturrieta-González *et al.,* 2020). GenBank numbers of ITS and LSU data are indicated as superscript.

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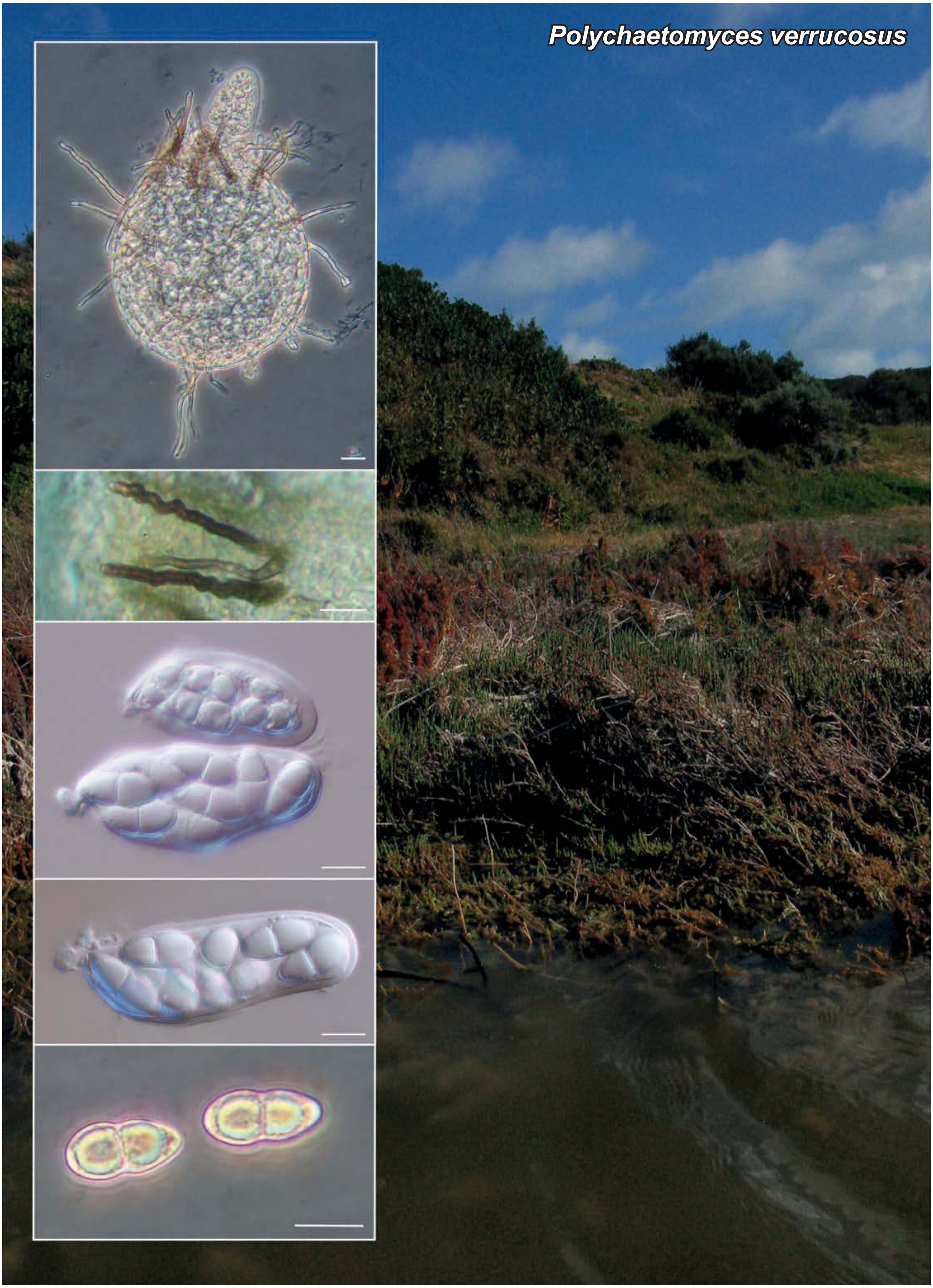
Polychaetomyces verrucosus

Fungal Planet 1763

MycoBank MB 856064

Polychaetomyces verrucosus Fryar, D.E.A. Catches., Oberlies & Raja, *sp. nov.*

Etymology: Name refers to the fine verrucose ornamentation on the ascospores.

Classification: Incertae sedis, incertae sedis, Dothideomycetes.

Ascomata hyaline, globose, papillate, superficial, solitary or gregarious, ostiolate, with a ring of dark brown setae at the base of the short papilla, 65–100 × 87.5–125 µm. *Setae* hyaline to dark brown, sinuate, tapered, wider at the base, often with a bulb at the base, 17.5–47.5 × 2.5–5.5 µm, walls thinner at the apex, 3–4-septate. *Peridium* hyaline, single-layered, membranous, *textura angularis* in surface view, stains bright orange in Melzers. *Hamathecium* not present. *Asci* obclavate to broadly cylindrical, saccate, 8-spored, bitunicate, fissitunicate, thick-walled, rupturing at the apex in water, sometimes pedicellate, staining bright orange in Melzers, 47.5–75 × 15–22.5 µm (mean and SD = 64 ± 9.5 × 20 ± 2 *µm*, n = 13), in a gelatinous matrix, ocular chamber absent. *Ascospores* hyaline, finely verrucose, 1-septate, constricted at septa, with one large guttule in each cell, asymmetrical, rounded upper cell broader than acute lower cell, sheath and appendages absent, 16–22.5 × 6–10 µm (mean and SD = 19 ± 1.5 × 8.5 ± 1 *µm*, n = 22).

Typus: **Australia**, South Australia, Coorong National Park, 35°54'S, 139°24'E, on unidentified submerged decaying wood in sea water, Sep. 2013, *S.C. Fryar* (**holotype** AD293984; ITS and LSU sequences GenBank PQ406469 and PQ406470).

Colour illustrations: Coorong National Park, South Australia, Australia. *Polychaetomyces verrucosus* from holotype. Ascoma; setae; asci; ascospores. Scale bars = 10 *µm.*

Notes: Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Hydropunctaria* sp. [strain KH-2020B, GenBank LC547493; Identities = 149/154 (97%), no gaps], *Bacidia friesiana* [strain KBA-L-0001910, GenBank ON352609; Identities = 148/153 (97%), no gaps], and *Bacidia friesiana* [strain KBA-L-0001913, GenBank ON352610; Identies = 148/153, no gaps] Closest hits using the **LSU** sequence are *Stomiopeltis betulae* [strain CBS 114420, GenBank OQ694459, Identities = 830/953 (87%), 11 gaps (1%)], *Agyrium rufum* [strain Wedin 7931 (UPS), GenBank EF581826, Identities = 823/945 (87%), 17 gaps (1%)], and *Heliocephala elegans* [strain MUCL 39003, GenBank HQ333478, Identities 829/952 (87%), 13 gaps (1%)].

The novel genus *Polychaetomyces* was introduced elsewhere in this publication to accommodate *Polychaetomyces marinus* (FP 1762) from submerged driftwood in California, USA. *Polychaetomyces verrucosus* represents a second species for this genus. The ITS sequences of *P. marinus* and *P. verrucosus* are 95 % similar, indicating that they are separate species. They are morphologically similar in nearly all characters but can be distinguished by their setae and ascospores. *Polychaetomyces verrucosus* has distinctive sinuate setae with a bulb at the base, whereas those of *P. marinus* are straighter and more numerous. The ascospores of *P. marinus* have a sheath, which is absent in *P. verrucosus.* While the ascospores of the two species have similar ranges in dimensions, those of *P. verrucosus* on average are longer and wider than those of *P. marinus*.

For phylogenetic tree, see *Polychaetomyces marinus* (FP 1762).

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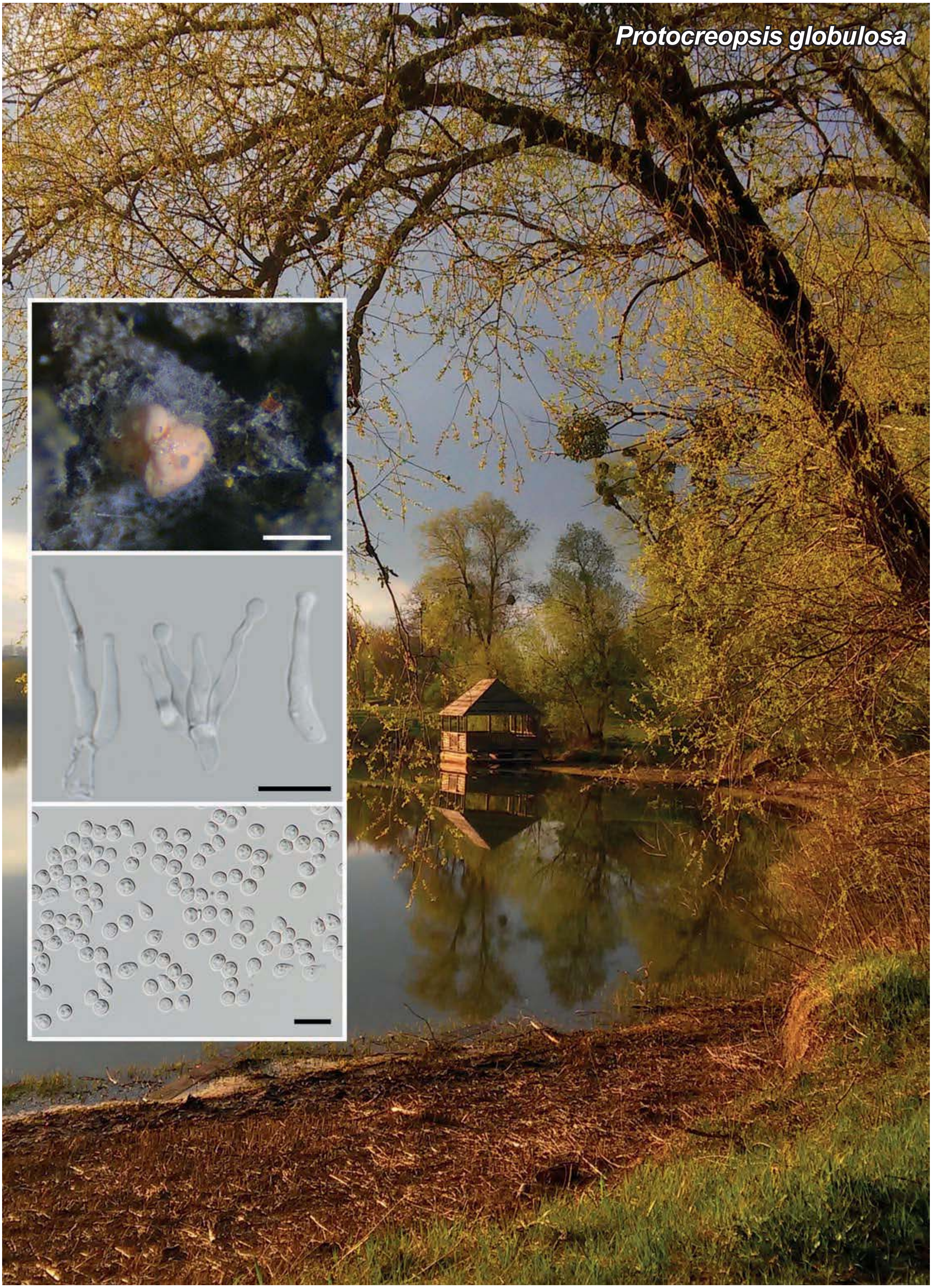

Protocreopsis globulosa

Fungal Planet 1764

MycoBank MB 855752

Protocreopsis globulosa **Darmostuk, *sp. nov.***

Etymology: Named after its globose conidia.

Classification: *Bionectriaceae*, *Hypocreales*, *Sordariomycetes*.

Sexual morph not observed. *Asexual morph* sporodochia-like agglomerated conidiophores, developing on a tiny arachnoid subiculum on the host thallus, pale pink to orange, convex, up to 0.5 mm diam. *Conidiophores* solitary or aggregated in clusters, forming sporodochia with mucoid, pale orange spore masses; conidiophores branched, septate, subcylindrical, up to 100 µm tall, 3–4 µm diam. *Conidiogenous cells* integrated, terminal and intercalary, phialidic, hyaline, smooth-walled, subcylindrical to aculeiform, straight to flexuous with a slightly apical taper, 2–2.5 µm diam at the apex, with periclinal thickening and cylindrical collarette, 1–2 µm long, (14.0–)15.2–20.8(–25.8) × (2.0–)2.4–2.8(–3.4) *µm* (n = 30). *Conidia* solitary, aseptate, hyaline, smooth-walled, globose to subglobose, with attenuated apex, base truncate, 1.5–2 µm, (3.6–)4.0–4.8(–5.8) µm diam (n = 50).

Habit, habitat and distribution: *Protocreopsis globulosa* is known from the type locality in the Kharkiv region of Ukraine, where it was found growing on *Lecania cyrtella* on *Populus* bark.

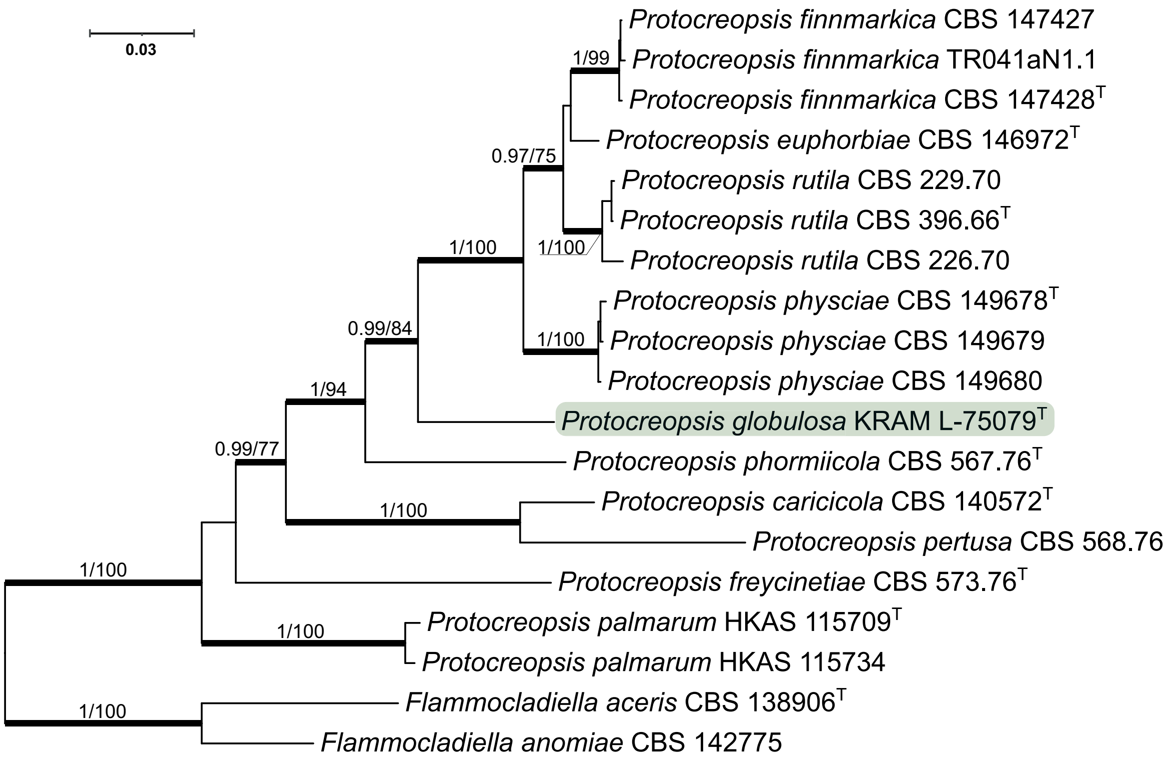
Typus: **Ukraine**, Kharkiv region, Derhachivskyi district, near Luzhok village, 50.08313°N, 36.10139°E, 130 m a.s.l., mixed forest on the bottom of the ravine, on bark of *Populus* sp. (*Salicaceae*), on thallus and apothecia of *Lecania cyrtella* (*Ramalinaceae*), 30 Apr. 2021, *V. Darmostuk 1049* (**holotype** KRAM L-75079; ITS, LSU and *tef1* sequences GenBank PQ284592, PQ284593 and PQ301172); *ibid*., **isotype** KRAM L-75080.

Colour illustrations: Ukraine, Kharkiv region, mixed forest near a lake (photo credit O. Sira). Habits of the sporodochia-like colony; conidiogenous cells; conidia. Scale bars: habits = 250 µm; all others = 10 µm.

Notes: The genus *Protocreopsis*, with the type species *Protocreopsis fusigera*, comprises 19 species, mostly associated with the leaves of monocotyledonous plants, although some have been isolated from other substrates (*e.g*., wood, lichens). These fungi are characterised by ascomata completely enclosed in long, white to tan or green, flexuous hyphal stroma, thick ascomatal walls, typically striate ascospores, and acremonium-like asexual morphs (Rossman *et al.* 1999, Hou *et al*. 2023). Molecular data for the type species is not available, so the genus circumscription still requires further study. *Protocreopsis physciae* was recently described as a lichenicolous species on *Physcia caesia* from the Netherlands (Visagie *et al*. 2024). However, it can be distinguished from *P. globulosa* by its larger, ellipsoid conidia, (9–)11–13(–15) × (5–)5.5–6(–7) µm [*vs*. (3.6–)4.0–4.8(–5.8) µm diam in *P. globulosa*].

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Acremonium psychrophilum* [voucher J. Etayo 31294, GenBank OP883927; Identities = 90.59 %, eight gaps (1 %)], *Protocreopsis euphorbiae* [strain CBS 146972, GenBank OK664700; Identities = 90.17 %, 12 gaps (2 %)], and *Protocreopsis finnmarkica* [strain CBS 147428, GenBank OQ429801; Identities = 89.6 %, 12 gaps (2 %)]. Closest hits using the **LSU** sequence are *Protocreopsis euphorbiae* [strain CBS 146972, GenBank OK663739; Identities = 98.32 %, no gaps], and *Protocreopsis rutila* [strain CBS 396.66, GenBank HQ232124; Identities = 98.20 %, no gaps]. Closest hits using the ***tef1*** sequence are *Pseudosynnemellisia favida* [strain CGMCC 3.22477, GenBank OQ809058; Identities = 91.76 %, no gaps], and *Acremonium guizhouense* [strain SQT06, GenBank OP757292; Identities = 91.45 %, two gaps (0 %)].

Supplementary material: doi: https://doi.org/10.6084/m9.figshare.27015514 (Table)



Phylogenetic relationships of *Protocreopsis globulosa* (highlighted with a coloured block) inferred from Bayesian Inference analysis (BI) of a combined ITS, LSU and *tef1* data set. *Flammocladiella aceris* and *F. anomiae* were used as the outgroup. Thickened branches represent either Bayesian posterior probabilities ≥ 0.97 and/or bootstrap support values ≥ 75 %. Maximum likelihood analyses were carried out using a heuristic search as implemented in IQ-TREE v. 2.1.2 on XSEDE (Nguyen *et al*. 2015) and 100 bootstrap interactions on 1 000 replicates to estimate branch support. Bayesian inference of the phylogenetic relationships was calculated using the Markov chain Monte Carlo (MCMC) approach as implemented in MrBayes v. 3.2.6 on XSEDE (Ronquist *et al.* 2012). Sequences from material with a type status are indicated by superscript T. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.27015532).

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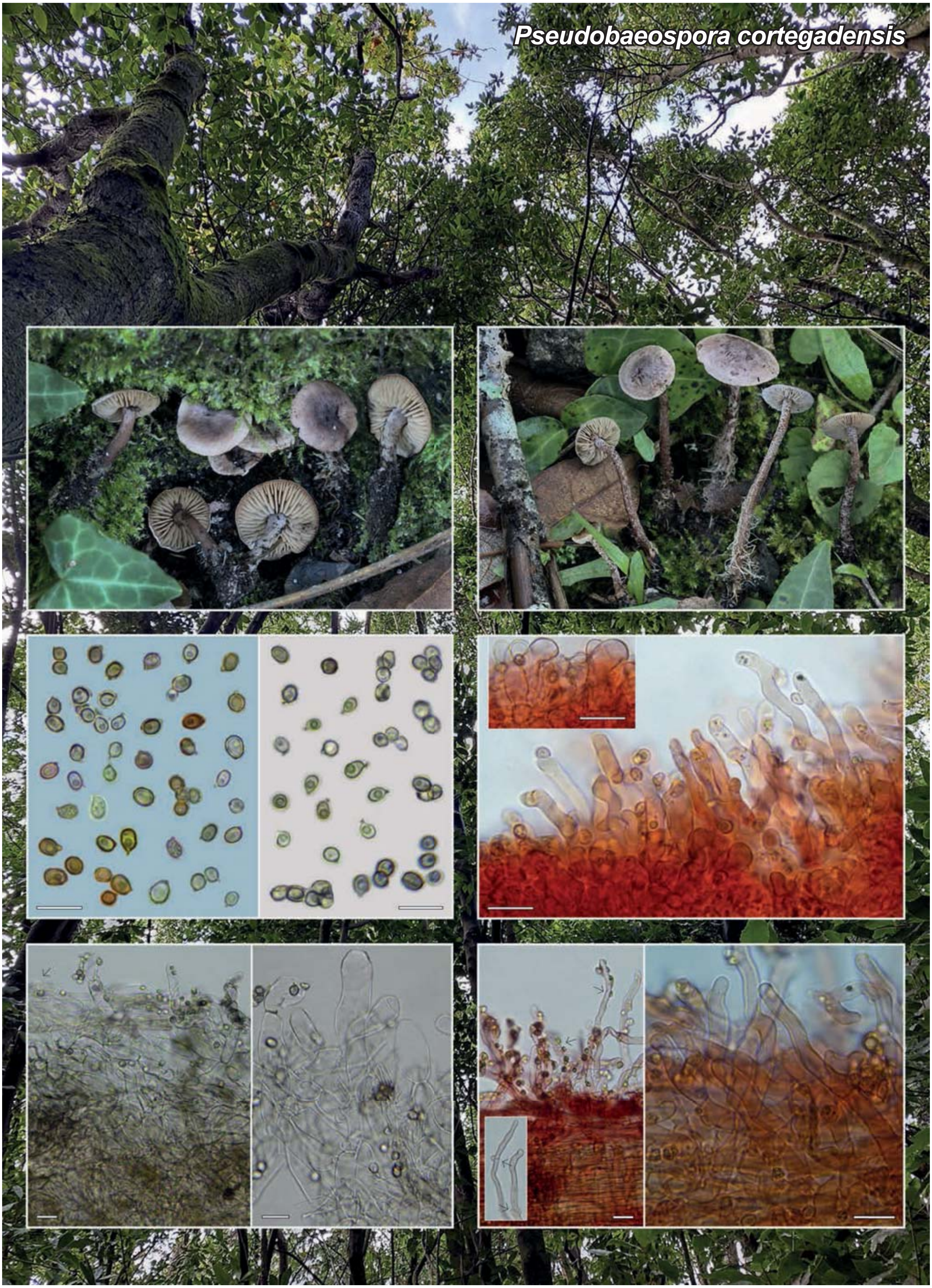

Pseudobaeospora cortegadensis

Fungal Planet 1765

MycoBank MB 855549

Pseudobaeospora cortegadensis De la Peña-Lastra & A. Mateos, ***sp. nov.***

Etymology: The epithet refers to the place where it was found (Illa de Cortegada, Parque Nacional Marítimo-Terrestre de las Islas Atlánticas, Galicia, Spain).

Classification: *Tricholomataceae*, *Agaricales*, *Agaricomycetes*.

Pileus 7–10 mm diam, convex, flat-convex or flattened, generally with obtuse mamelon when young, then obtuse-flattened and at the end somewhat depressed; cuticle somewhat granular or wrinkled and even with a concentric annular zone, purple-violet in the centre (Ség. 633 or somewhat mixed with Ség. 644; Séguy 1936), brownish violet (Ség. 12) with pinkish margin, paler towards the margin, where it is cream or beige, with fleshy tints. *Lamellae* moderately spaced, with abundant lamellulae (L = 24–30; l = 3–5 lam), emarginate, shortly adnate to almost free, sometimes somewhat bifurcate at margin, thick, ventrate at maturity, intervening on face and the background, cream, then beige, whitish pubescent on ridge. *Stipe* 12–26 × 1.0–1.5 mm, cylindrical, straight or somewhat sinuous, widening towards base, claviform (up to 2 mm), lower half of stipe length strigose, densely covered with whitish hairs or rhizoids hairs, the rest whitish pruinose, aboveground, which is subcoloured to the pileus, brownish purple. *Context* sparse on the pileus, fistulous on the stipe, beige, on the pileus cortex concolorous to the cuticle purple, faint fungal *odour*, rather bitter *taste*. *Macrochemical reactions*: KOH (5 %) very dark green (Ség. 416) and soon blackish in flesh, emerald green on cuticle (Ség. 406). *Basidiospores* (3.3–)3.5–*4*–4.4(–4.8) × (2.6–)2.8–*3*–3.4(–3.5) µm, Q = (1.1–)1.2–*1.3*–1.4(–1.5); n = 30; Ve = 20 μm^3, ellipsoid, broadly ellipsoid, ovoid or subspherical, with prominent apiculum, smooth, unigutulate, at first thin-walled non-amyloid, at maturity thick-walled and somewhat dextrinoid, congophilous and cyanophilous; adherent by their slimy texture in tetrads to the hyphae of the caulopellis and pileipellis (Voto 2019). *Basidia* (38.3–)40.1–*42.9*–45.3(–45.9) × (6.9–)7.4–*8.6*–9.7(–10.2) µm; cylindrical, claviform, fibulate at base, tetrasporic or rarely bisporic, with sterigmata 3.6–8 µm high. *Lamellar edge* with short, grouped or isolated cystidiod elements, 11–24 × 4.5–9.2 µm, fusiform, claviform or pyriform, thick-walled and *cheilocystidia* long 17–57 *× 3*–5 µm forming dense clusters on a heterogeneous edge, cylindrical with rounded apex, filiform, claviform or narrowly lageniform, irregularly sinuous, sometimes with excrescences or lobed. *Lamellar trama* subregular, with cylindrical or somewhat thickened elements up to 10 µm. *Pileipellis* consisting mainly of a suprapellis with a cutis of equal hyphae 3.4–7.5 µm diam, and chains of cells 41.2–50.4 × 5.1–10.3 µm, hyaline, with erect, cylindrical, claviform, cystidioid terminal elements, thus appearing as a trichoderm, often septate and fibulate; subpellis consisting of chains of thickened cells 20.9–43.8 × 8.5–16 µm, irregularly arranged with pseudoparenchymatous appearance, distinctly bluish green in 5 % KOH; with frequent intracellular pigment and smooth, sometimes moderately encrusting parietal pigment. *Pileus trama* consisting of interwoven hyphae, often in short segments, cylindrical inflated to globose, hyaline. *Stipitate trama* banal, consisting of longitudinally parallel hyphae, often septate, widening inwards. *Caulocystidia* 25.7–72.3 × 2.6–4.2 µm; filiform, cylindrical sinuous with rounded apex, less frequently lobed or branched, septate and clamped, thick-walled. *Clamp connections* frequent in all tissues.

Distribution: Currently known only from the type location in northwestern Spain.

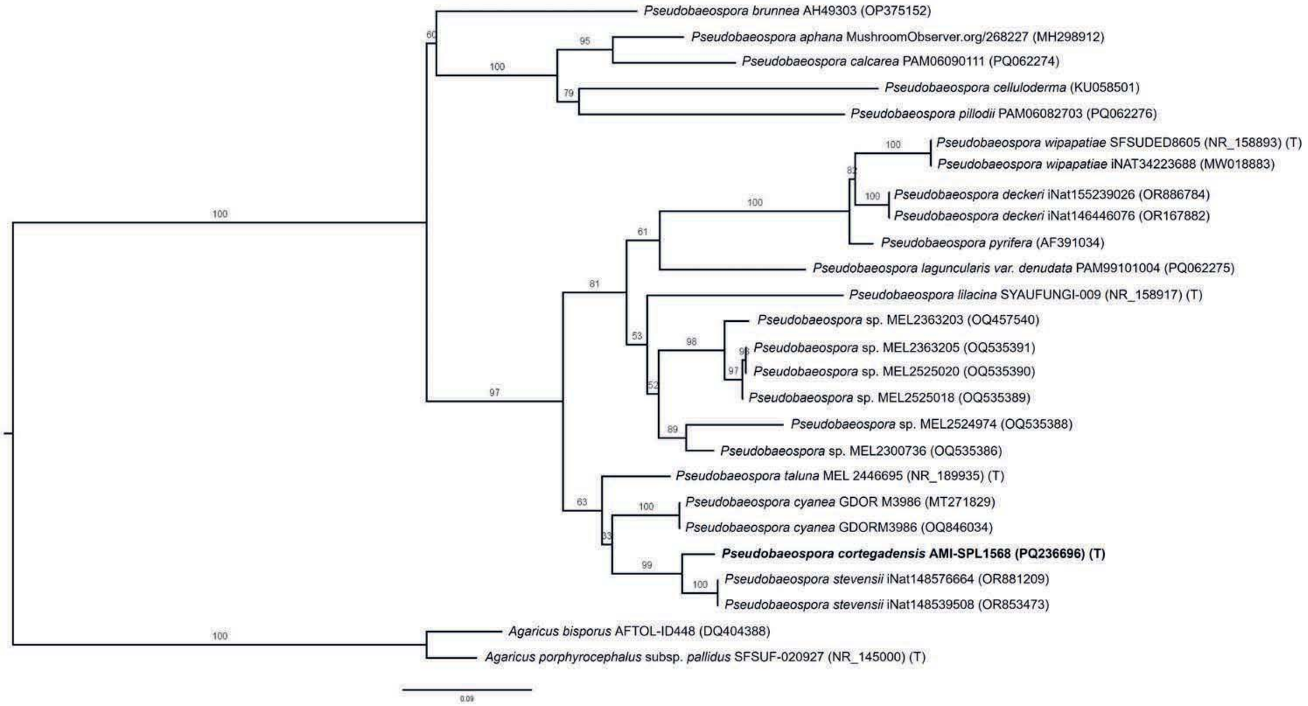
Typus: **Spain**, Galicia, Pontevedra, Parque Nacional de las Islas Atlánticas de Galicia, Illa de Cortegada, N42°37’13.3”, W8°47’13.7”, 3 m a.s.l., gregarious in laurel forests, 10 Nov. 2022, *A. Mateos* & *S. De la Peña-Lastra* (**holotype** AMI-SPL1568; ITS1 and LSU sequences GenBank PQ236696 and PQ236697).

Additional material examined. **Spain**, Galicia, Pontevedra, Parque Nacional de las Islas Atlánticas de Galicia, Illa de Cortegada, N42°37’13.3”, W8°47’13.7”, 3 m a.s.l., gregarious in laurel forests, 27 Nov. 2020, *S. De la Peña-Lastra* (AMI-SPL557).

Notes: *Pseudobaeospora cortegadensis* belongs to sect. *Pseudobaeospora*, subsect. *Pseudobaeospara sensu* Voto (2009) and Bas (2002, 2003), although it has recently been shown by Gisotti *et al.* (2021) and Craig *et al*. (2023) that the infrageneric structure based on morphology (Voto 2009, 2015, 2021), does not coincide with the phylogeny. *Pseudobaeospora laguncularis* is very similar but differs morphologically by the somewhat different colour of the pileus, wine brown or reddish instead of violet brown, with caulo- and cheilocystidia red to red-brown incrusted in KOH, has a distinct pileipellis, with abundant erect pileocystidia of cylindrical or sublageniform shape with thinned termination, and the reaction of the pileipellis to KOH

Colour illustrations: Spain, Pontevedra, P. Nacional Illas Atlánticas de Galicia, Illa de Cortegada, forest of *Laurus nobilis*, where the holotype of *Pseudobaeospora cortegadensis* was collected. Right column: basidiomata in upper photo correspond with the holotype (AMI-SPL1568); middle photo corresponds with cheilocystidia (RC); and the bottom photo caulocystidia and stipitipellis (H_2O). Left column: basidiomata in upper photo correspond with AMI- SPL557; middle photo corresponds to basidiospores (H_2O in right, RC in left), and the bottom photo is pileipellis (H_2O). Scale bars = 10 µm.

is brownish with greenish staining (Voto 2009, 2021), very pale, brownish with greenish, yellowish or reddish (Bas 2003), although Arauzo (2011) indicates that it is greenish (ITS BLAST 88.26 % match). *Pseudobaeospora brunnea* is distinguished by having somewhat larger spores [(4.8–)5.3–6.0(–6.6) × 3.2–4.0 µm], and long ellipsoid to subcylindrical (Qm = 1.54); the pileipellis is immutable in KOH and has more abundant and differently shaped terminal elements (Arauzo 2011, Moyne & Montgeon 2018, Rubio & Palazón 2019, Bañares & Moreno 2022). *Pseudobaeospora taluna* differs in having citrine-yellow or olive green lamellae, spores are more subglobose (Qm = 1.14), with pleurocystidia present, has a distinct pileipellis, a loose disrupted trichoderm, never in cutis (Craig *et al*. 2023) (ITS BLAST 90.65 % match). *Pseudobaeospora cyanea* has larger basidiomata, variable colour, similar to *P. cortegadensis* when purplish grey, but different when bluish purple, slightly larger spores [4.0–5.5(–6.5) × 3.3–4.0 µm], cheilocystidia less slender and sparser, pileipellis is to trichodermium, never with suprapellis in uniform cutis (Arnolds *et al*. 2003, Arauzo 2011, Gisotti *et al*. 2021) (ITS BLAST 91.65 % match). *Pseudobaeospora stevensii*, a North American species that is well differentiated by the pileus which is reddish brown, striated-sulcate in the margin at maturity and the spores which are subglobose (Qm = 1.14) (Desjardin 2004, Wood & Stevens 2021) (ITS BLAST 92.57 % match). *Pseudobaeospora pallidifolia* differs by the violaceous brown pileus, the mealy odour, with larger spores [(4.2–)4.4–6.4(–6.9) × (2.7–)3.0–4.4(–4.8) µm], with absence of cheilocystidia and the pileipellis in the form of a strict cutis (Bas *et al*. 1997, Bas 2003, Muñoz 2020).



The most probable maximum likelihood (ML) tree calculated with IQ-TREE v. 2.1.3 (Nguyen *et al.* 2015) using the UltraFast method from the ITS sequence alignment (GenBank accession numbers in brackets in the tree), showing on the branches the ML bootstrap support values (ML-BS; 1 000 replicates and ≥ 95 % were considered significant). Sequences from type material are indicated with a T and the novel species is indicated in **bold** font. The alignment and tree were deposited in Figshare.com (doi: 10.6084/m9.figshare.27186642).

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Pseudocercospora quetri

Fungal Planet 1766 MycoBank MB 855030

Pseudocercospora quetri G.H. Ramirez, *sp. nov.*

Etymology: The name derives from the term “quetri”, used by the native Mapuche people to refer to the arrayán tree (*Luma apiculata*), from which this fungus was isolated.

Classification: *Mycosphaerellaceae*, *Capnodiales*, *Dothideomycetes*.

Leaf spots amphigenous, circular to irregular, up to 7 mm diam, grey to pale brown in middle, sometimes with concentric rings, with raised purple border. *Ascomata* pseudothecial, epiphyllous, semi-immersed, globose, dark brown, up to 130 µm wide, unilocular, with central ostiole 10–20 µm wide; wall consisting of 2–4 layers of brown *textura angularis*. *Asci* fasciculate, bitunicate, cylindric-clavate, straight to slightly curved, 8-spored, with apical chamber, hyaline, 40–60 × 8–12 µm. *Ascospores* biseriate, fusoid-ellipsoidal with obtuse ends, straight to slightly curved, 1-septate, slightly constricted at septum, widest in middle of apical cell, tapering towards both ends, more prominently towards the lower end, thin-walled, smooth, hyaline, (14–)15–21(–22) × 3–4 µm. *Mycelium* subhyaline to pale brown, smooth, septate, branched, 2–4 µm diam hyphae. *Sclerotia* formed on sterile pine needles, cylindrical, dark brown, up to 300 × 100 µm. *Asexual morph* observed only on artificial cultures (potato dextrose agar; PDA, malt extract agar; MEA, and oatmeal agar; OA). *Conidiophores* reduced to conidiogenous cells, indistinguishable from the vegetative hyphae. *Conidia* solitary, subcylindrical, apex obtuse to subobtuse, base obconically truncate to truncate, straight to geniculate, smooth, subhyaline, 0–8-septate, (24–)32–96(–108) × 2.5–3.5(–4) µm; hila neither thickened nor darkened-refractive, with marginal frill.

Culture characteristics (in darkness, 20 °C, 14 d): Colonies round, raised surface, velvety, with entire margin, reaching 11 mm diam. On MEA and PDA surface greyish sepia, reverse olivaceous. On OA surface smoke grey, reverse greyish sepia.

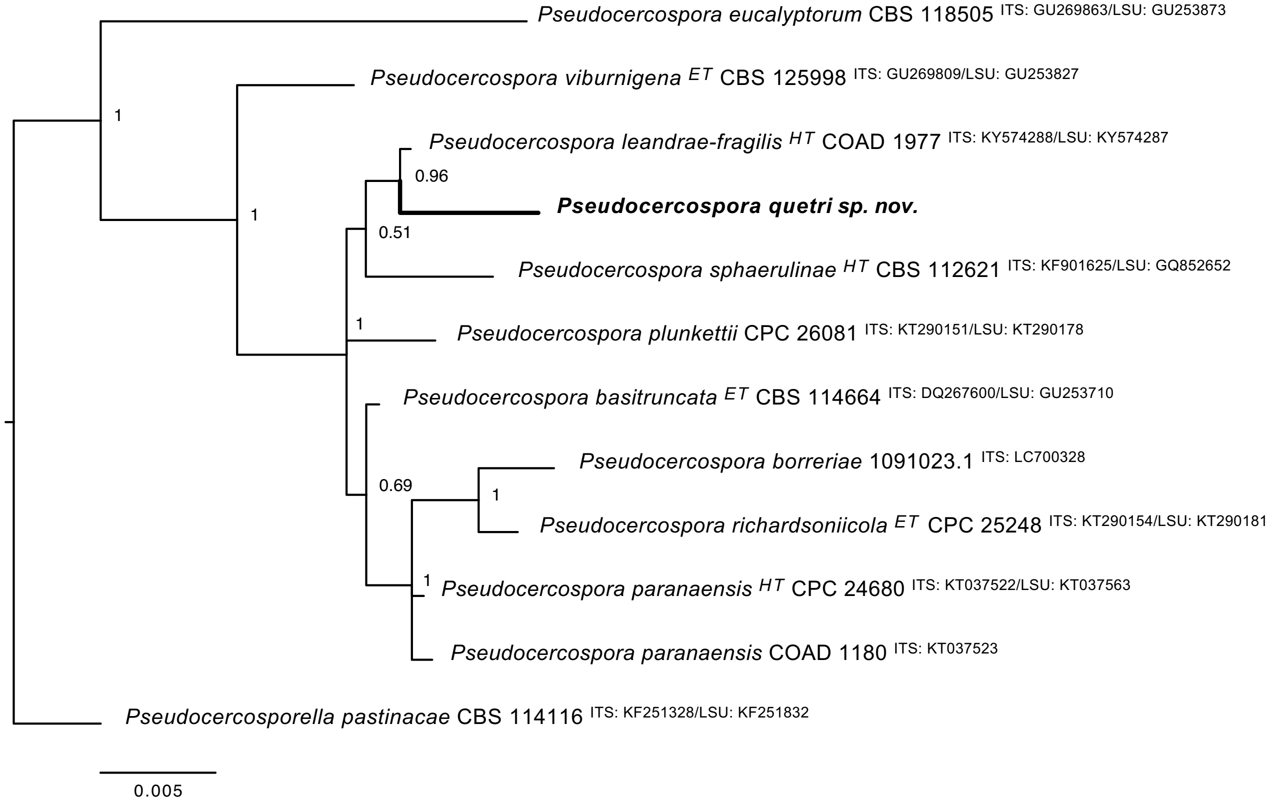
Typus: **Argentina**, Neuquén Province, Villa la Angostura, 40°47’S, 71°39’W, on leaf spots of *Luma apiculata* (*Myrtaceae*), 21 Jan. 2024, *G.H. Ramírez* (**holotype** BBB:GR-LUM-03, culture ex-type BBB:GR-PSE-03; ITS and LSU sequences GenBank PQ111801 and PQ111802).

Colour illustrations: *Luma apiculata* in Villa la Angostura, Argentina. Foliar symptoms; detail of leaf spot with semi-immersed ascomata; asci; ascospores; conidia; sclerotium. Scale bars = 10 µm.

Notes: The occurrence of *Mycosphaerella* and its asexual morphs on *Myrtaceae* has been extensively documented (*e.g.* Crous 1999, Aptroot 2006). Among these species, *Amomyrtus luma* is frequently misidentified as *Luma apiculata* due to their overlapping distribution. *Mycosphaerella lumae* was originally described on leaves of *A. luma* (Sydow 1928). Despite the lack of molecular data for *M. lumae*, it has notable differences from *Pseudocercospora quetri*, such as the morphology and location of the ascomata (hypophyllous, densely clustered in groups, and often aggregated in a stroma in *M. lumae*).

Molecular phylogenetic analysis places *Pseudocercospora quetri* within a monophyletic clade, being closely related to *P. leandrae-fragilis* and *P. sphaerulinae*. Although the absence of a known sexual morph of *P. leandrae-fragilis* to compare with, its conidial size (80–164.5 × 4–5 µm) is notably larger than those from *P. quetri*. In contrast, while the conidia of *P. sphaerulinae* (70–100 × 2–3 µm) are similar to those of *P. quetri*, it can be distinguished by its 3-septate ascospores. *Pseudocercospora quetri* represents the first recorded species of *Pseudocercospora* with a sexual morph occurring on *Luma apiculata*.

Based on a search in GenBank database, the closest hits using the **ITS** sequence had highest similarity to *Pseudocercospora basitruncata* [CBS 114664, GenBank DQ267600; Identities = 497/505 (98 %), three gaps], *P. paranaensis* [CPS 24680, GenBank NR_147289; Identities = 495/505 (98 %), three gaps] and *P. plunkettii* [CPC 26081, GenBank KT290151.1; Identities = 484/494 (98 %), four gaps]; closest hits using the **LSU** sequence had highest similarity to *P. paranaensis* [CPC 24680, GenBank NG_069294; Identities = 804/811 (99 %), no gaps], *P. rhabdothamni* [CBS 114872, GenBank NG_069099; Identities = 804/811 (99 %), no gaps] and *P. cyatheicola* [CBS 129520, GenBank MH878060; Identities = 804/811(99 %), no gaps].



Bayesian inference phylogenetic tree of concatenated ITS and LSU sequences using MrBayes v. 3.2.7, illustrates the relationship of *Pseudocercospora quetri* to closely related species. The species included in this analysis belong predominantly to clade 5 *sensu* Groenewald *et al*. (2024), with the exception of *P. eucalyptorum*, which belongs to clade 7. *Pseudocercosporella pastinacae* was used as outgroup. Sequences derived from material with a type status are indicated with a superscript HT [from (ex-)type] and ET [from (ex-)epitype]. Bayesian posterior probability values are shown at the nodes. The coloured block comprises Clade 5, and the novel species is indicated in **bold**. The alignment and tree were deposited at figshare.com, (doi: 10.6084/m9.figshare.27173130.v1).

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Pseudotricholoma pusillum

Fungal Planet 1767 MycoBank MB 854495

Pseudotricholoma pusillum Reschke & T.A. Hofm., ***sp. nov.***

Etymology: *pusillus* (Latin) = very small, tiny; referring to the small size of the basidiocarps.

Classification: *Tricholomataceae*, *Agaricales*, *Agaricomycetes*.

Basidiocarps small tricholomatoid. *Pileus* 9–14 mm diam, hemispherical to convex, with initially deflexed to incurved, later straight margin, dark brown grey to almost black, slightly velvety to almost smooth, not translucently striate, not hygrophanous. *Lamellae*, L = 30–40, l = 1–3, often with some anastomoses, medium to rather narrowly spaced, emarginate to adnate or slightly decurrent, segmentiform to ventricose, pale greyish cream with concolourous edges, staining reddish grey and eventually black after touch. *Stipe* 13–20 × 3.5–4.0 mm, cylindrical or slightly broadening towards base, sometimes with tapering base, longitudinally fibrillose and finely pruinose all over, brownish grey to grey. *Basal mycelium* white, finely tomentose, without conspicuous rhizomorphs. *Odour* farinaceous, *taste* not tested. *Basidiospores* 4.5–6.0 × 3.0–4.0 µm, av. 5.1–5.3 × 3.3–3.4 µm, Q = 1.40–1.75, Qav 1.55–1.60, ellipsoid, thin-walled, hyaline, smooth to slightly uneven, distinctly amyloid. *Basidia* cylindrical when young, becoming narrowly clavate upon maturity, then 22.5–30.5(–33.5) × (4.5–)5.0–6.5(–7.0) µm, hyaline, 4-spored, with up to 4 µm long sterigmata. *Lamella edge* sterile, with abundant cheilocystidia. *Cheilocystidia* (13–)14.5–25.5(–32) × (4–)4.5–8.0(–9.5) µm, subcylindrical, clavate to fusiform, more rarely somewhat lageniform, with rather dark brown, parietal pigment. *Hymenophoral trama* regular, made up of cylindrical hyphae, 2.5–4.5 µm wide, hyaline. *Pileipellis* an irregular cutis with transitions to a trichoderm, composed of densely packed, interwoven, cylindrical to somewhat inflated hyphae, (2.5–)3.5–17 µm wide, with frequent erect trichodermal elements with subcylindrical to clavate terminal cells, 17–37 × (4.5–)6.0–10.5 µm, pigment parietal and in addition often encrusting, especially at rather broad hyphae. *Pileitrama* composed of parallel, cylindrical hyphae, 3.5–8.0 µm wide, hyaline. *Stipitipellis* a cutis composed of long and narrow cylindrical hyphae, 3.0–7.0 µm wide, pigment encrusting and in addition parietal, with abundant tufts of caulocystidia. *Caulocystidia* narrowly clavate, (17.5–)24–46 × (5.0–)6.0–9.0 µm, with brown, parietal pigment. *Clamp connections* abundant in all parts of the basidiocarp. Refractive content abundant in all parts, especially the trama, microscopic sections emitting a viscous fluid.

Colour illustrations: Sendero Culebra in tropical montane forest in Panama, holotype location. Basidiocarps of KaiR466 (holotype); caulocystidia; cheilocystidia; basidiospores; lamella cross-section emitting viscous fluid (all from holotype). Scale bars: basidiocarps = 10 mm; lamella cross-section = 50 µm; caulocystidia and cheilocystidia = 10 µm; basidiospores = 5 µm.

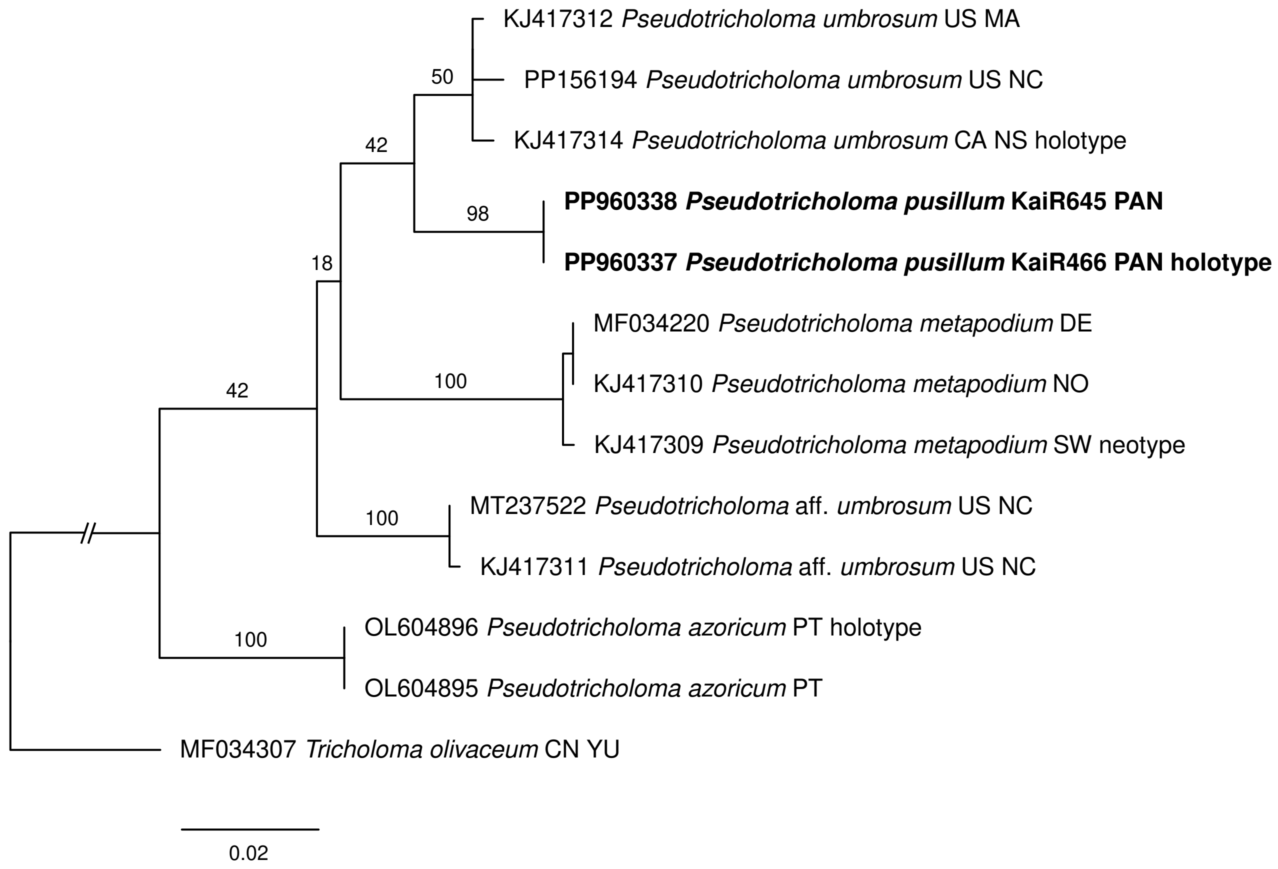
Habitat and distribution: Sporulating in small groups of basidiocarps on soil at steep embankments of a washed-out path through tropical montane *Quercus*-dominated forest in Panama.

Typus: **Panama**, near Boquete, Sendero Culebra, N08°51’13.7’’, W82°29’01.2’’, 1 850 m, tropical montane forest dominated by *Quercus* spp. (*Fagaceae*), 9 Jun. 2017, *K. Reschke*, KaiR466 (**holotype** in UCH: 12326; ITS sequence GenBank PP960337); *ibid*., **isotype** in M.

Additional material examined: **Panama**, near Boquete, Sendero Culebra, N08°51’22.3’’, W82°29’03.3’’, 1 880 m, tropical montane forest dominated by *Quercus* spp., 22 Jun. 2017, *K. Reschke, J. Rodriguez & B. Wergen*, KaiR645 (in UCH: 9230; ITS sequence GenBank PP960338).

Notes: *Pseudotricholoma pusillum* is distinctive by its small tricholomatoid basidiocarps with reddish and eventually black staining reaction, its abundant cheilocystidia, and small, amyloid basidiospores. It is phylogenetically relatively close to *P. umbrinum* (p-distances of ITS 2.5–3.0 %). However, this species has much larger basidiocarps, longer basidiospores and no differentiated cheilocystidia (Smith & Walters 1943). The basidiocarps of *P. pusillum* are in general distinctly smaller than those of the other three species of *Pseudotricholoma*. The pilei of *P. azoricum*, the species with the second smallest basidiocarps, are 20–50 mm diam (Iglesias *et al*. 2021). In addition to that, the basidiospores of *P. pusillum* are at most 6 µm long, while the basidiospores of the other species in the genus are at the minimum 6 µm long.

Pseudotricholoma was relatively recently elevated to generic rank, the species therein being treated in *Porpoloma s. l.* before (Sanchez-Garcia *et al*. 2014). No species similar to *P. pusillum* were found among the species of *Porpoloma* in the wide, traditional sense.



Phylogenetic tree derived from a Maximum Likelihood analysis based on nrITS1-5.8S-ITS2 sequence data aligned with MAFFT v. 7 (Katoh & Standley 2013) using the E-INS-i model. Analysis was performed in RAxML v. 8.2.11 (Stamatakis 2014) using the GTRGAMMA model with 35 per site rate categories, and 500 rapid bootstrap replications. The ML bootstrap support values are shown at the branches. GenBank accession numbers are given before the species names, country codes after ISO-3166-1 and 3166-2 for large countries are given after the species names. The novelty described here is indicated in **bold** font. Scale bar = estimated changes/nucleotide. The alignment was deposited at figshare.com (doi: 10.6084/m9.figshare.26121859).

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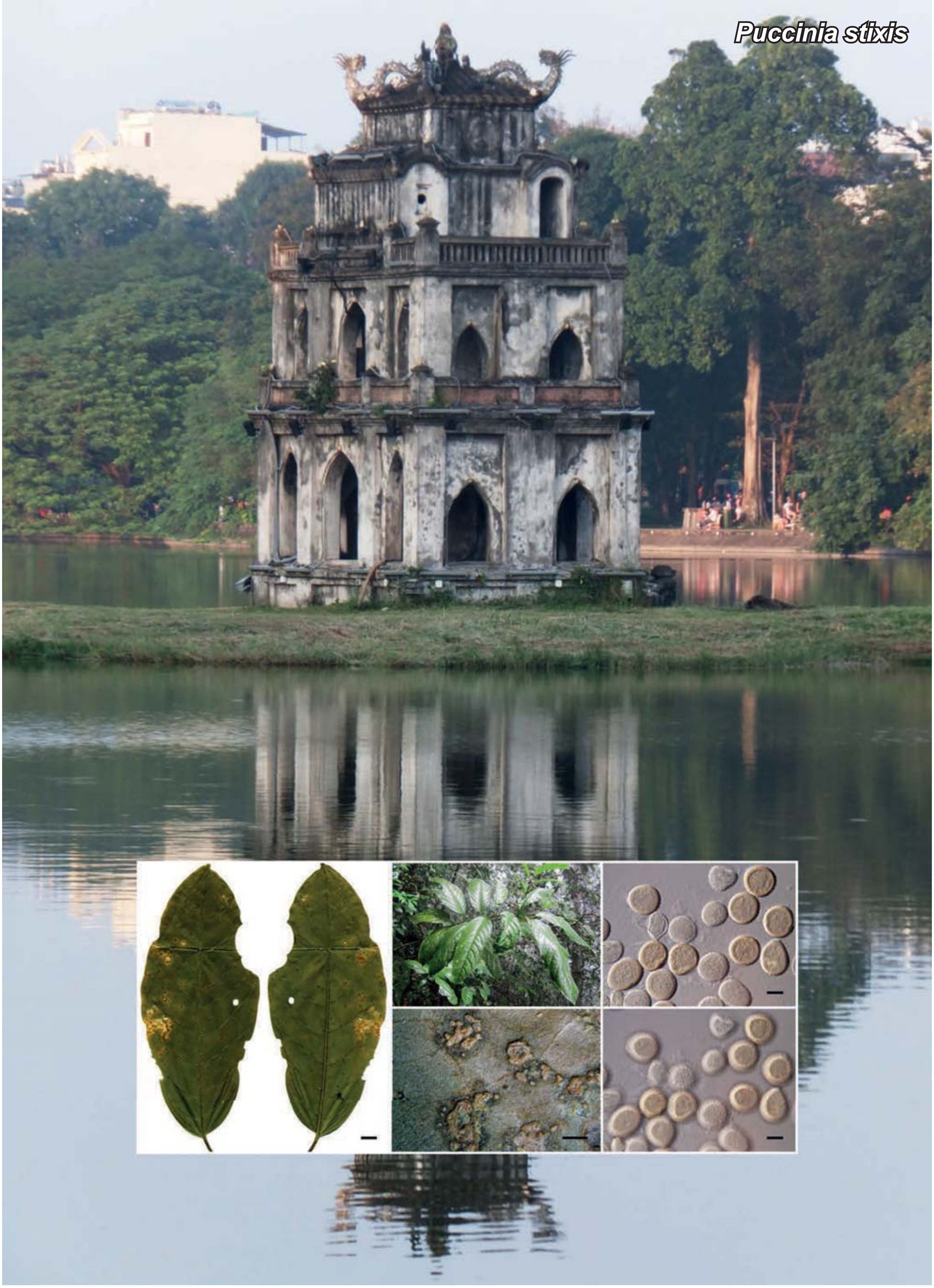

Puccinia stixis

Fungal Planet 1768

MycoBank MB 855520

Puccinia stixis Y.P. Tan, T.Y. Chi & R.G. Shivas, ***sp. nov.***

Etymology: Named after the host genus *Stixis*.

Classification: *Pucciniaceae*, *Pucciniales*, *Pucciniomycetes.*

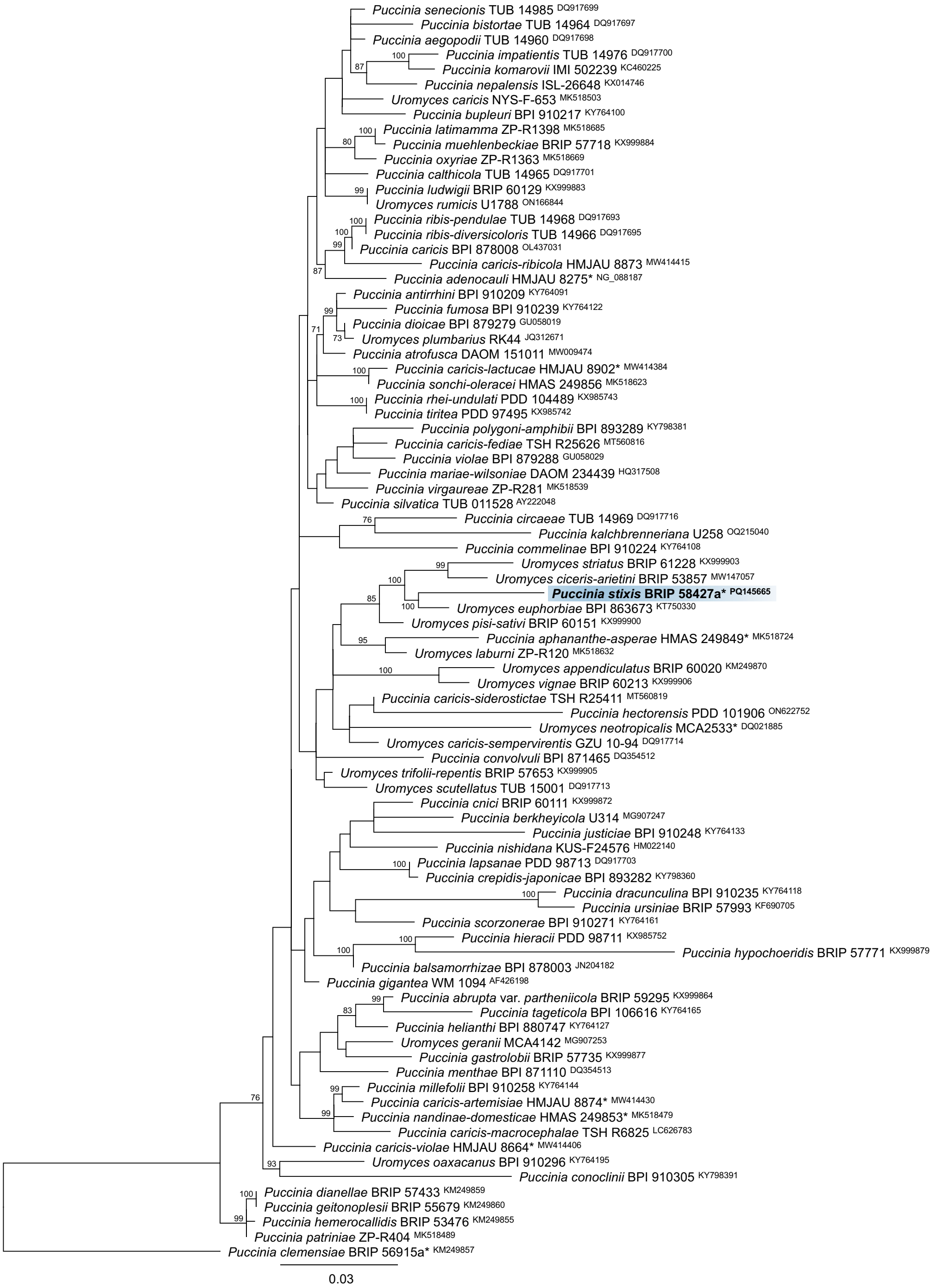
Uredinia on leaves of *Stixis scandens*, mostly amphigenous with corresponding pale chlorotic irregular lesions 2–20 mm wide with diffuse margins on upper leaf surface, occasionally epiphyllous, solitary or aggregated in groups, scattered, erumpent, pulverulent, subglobose to ellipsoidal, 50–600 µm diam, pale yellowish brown. *Urediniospores* subglobose to broadly ellipsoidal, 19–25 × 15–23 µm, subhyaline to pale yellowish brown; wall 2–4.5 µm wide, pale yellowish brown, sparsely and finely echinulate. *Telia* not seen.

Typus: **Vietnam**, Ha Tay Province, Ba Vi National Park, leaf rust on *Stixis scandens* (*Resedaceae*), 29 Dec. 2012, *T.Y. Chi, A.R. McTaggart, T.S. Marney, M.A. Shivas, M.D.E. Shivas & R.G. Shivas*, VND095 (**holotype** specimen BRIP 58427a; LSU sequence GenBank PQ145665).

Notes: *Puccinia stixis* is only known from the uredinial stage seen on leaves of *Stixis scandens* in the type specimen. The genus *Stixis* is endemic to Southeast Asia, and its systematic placement was long considered enigmatic and controversial (Su *et al*. 2012). This is the first record of rust on species of either *Stixis* or its close relative *Tirania*, both in the family *Resedaceae*.

Based on a megablast search of the NCBI GenBank nucleotide database, the closest relevant hits with the LSU region of *P. stixis* were *Uromyces galegae* [GenBank DQ250133; Identities = 1 015/1 039 (98 %), seven gaps (0 %)], *U. orientalis* [specimen voucher BRIP 60934, GenBank KX999899; Identities 1 007/1 038 (97 %), seven gaps (0 %)], *U. pisi-sativi* [specimen voucher BRIP 60151, GenBank KX999900; Identities 1 003/1 028 (98 %), seven gaps (0 %)], *U. striatus* [specimen voucher DAOM 240966, GenBank HQ317512; Identities 1 001/1 029 (98 %), 11 gaps (1 %)], and *U. trifolii-repentis* [specimen voucher BRIP 57653, GenBank KX999905; Identities 1 009/1 038 (97 %), nine gaps (0 %)].

Colour illustrations: Tháp Rùa, Hồ Hoàn Kiếm, Hanoi, Vietnam. Uredinia on leaf surfaces of *Stixis scandens* (upper, far left; lower, right); branch of host plant at type location; uredinia; urediniospores (equatorial view, upper right; surface view, bottom right). Scale bars: leaf surface = 1 cm; uredinia = 1 mm; all others = 10 µm.



Phylogenetic tree of selected *Puccinia* species based on maximum likelihood analysis of the LSU region. The phylogenetic analysis was performed with the IQ-TREE web server (Trifinopoulos *et al.* 2016) based on the substitution model with gamma-distribution rate variation. *Puccinia clemensiae* (holotype specimen BRIP 56915a) was used as the outgroup. GenBank accession numbers are indicated (superscript LSU). Novel taxon is shown in **bold**. Type specimens are marked by an asterisk (*). The alignment and phylogeny are publicly available in Zenodo (doi: 10.5281/zenodo.13363385).

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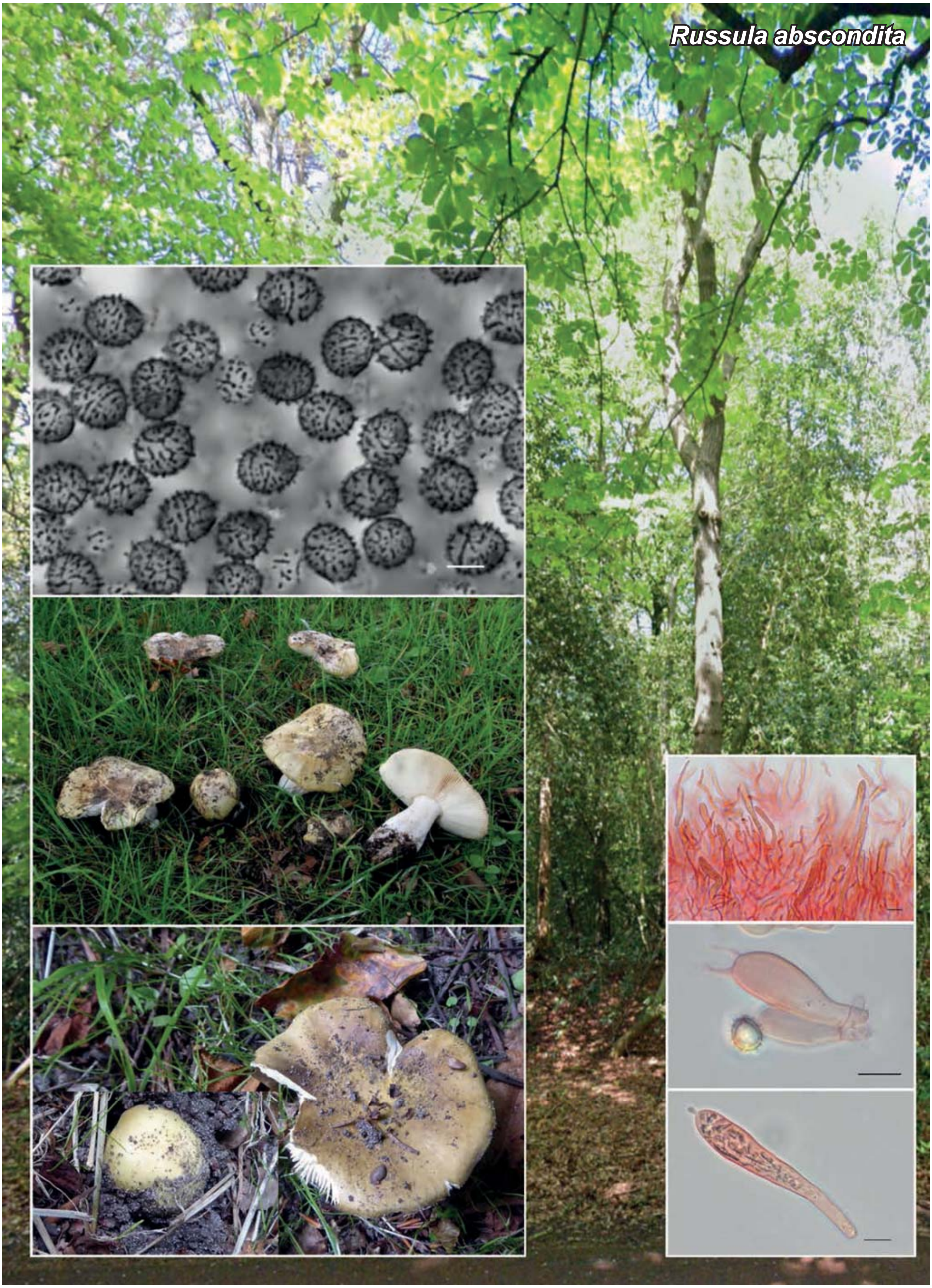

Russula abscondita

Fungal Planet 1769

MycoBank MB 855760

Russula abscondita G.M. Jansen, ***sp. nov.***

Etymology: From Latin *abscondita*, refers to the hidden place in the *Violaceinae*.

Classification: *Russulaceae*, *Russulales*, *Agaricomycetes*.

Basidiomata medium to large sized. *Pileus* 70(–140) mm, convex then expanding to applanate with depressed centre, margin smooth but also slightly sulcate, dull to slightly shiny, when wet sticky, colour at centre olive brown to cream, brown with some pinkish hue near margin never with violet colours, peeling 1/4–3/4 of the radius. *Lamellae* L = 100, l = 0, adnexed, emarginate, normally spaced to rather crowded, occasionally with short gills, few forking, brittle, cream, greyish seldom white, rarely with ochreous staining, edge entire, concolorous. *Stipe* 40–75 × 14–20 mm, cylindrical, clavate, cylindrical, longitudinally rugulose, spongy, soft, white, greying after handling, stains grey, sordid brown. *Macro chemical reactions* FeSO4 on stem light salmon pink. Guaiac on stem and gills slowly weakly (strong) blue. KOH no reaction on flesh or gills, occasionally yellowish on stem. *Taste* acrid but not strong, occasionally mild or longer lasting acrid, *smell* fruity–pelargonium, reminiscent of *R. fellea*, fish-like on ageing. *Spore print* light cream, colour code Romagnesi Ia–IIc(–IId). *Basidiospores* 7.2–8.2–9.3 × 5.9–6.8–7.7 µm (sl = 0.5 µm, sw = 0.5 µm), Q = 1.08–1.21–1.35 (sQ = 0.07) (n = 106 from 6 collections); ornamentation subreticulate, amyloid, 0.7 µm high. *Basidia* 35–40–46 × 9–12–14 µm, Qav. = 3.50, clavate, 4-spored, sterigmata 6–11 µm. Hymenial cystidia on the lamellae 41–47–60 × 7.5–9.5–12.5 µm, clavate, cylindrical with blunt apex, lanceolate, occasionally with appendiculate apex. *Hymenial cystidia* on lamellae edge, 32–46–60 × 7–9.5–11.5 µm, clavate, fragile, content crystalline, not much above the basidioles, deeply embedded, abundant. Lamellae edges heterogeneous. *Pileipellis* near centre ortho chromatic in cresyl blue, delimited from the underlying context, 130–180 µm thick, two–-layered; subpellis 90–140 µm deep, composed of more or less densely intermixed, horizontally oriented hyphae and dispersed pileocystidia; suprapellis an ixo-palisade, 40–60 µm thick, mainly composed of ascending thin-walled hyphen and pileocystidia; near margin delimited from the underlying context, 200–220 µm thick, two-layered; subpellis 150–160 µm deep, composed of more or less densely intermixed, horizontally oriented hyphae and dispersed pileocystidia; suprapellis an ixo-palisade, 45–55 µm thick, mainly composed of ascending thin walled hyphen and pileocystidia. *Hyphal terminations* near centre, 14–40 × 2.5–3.5 µm, cylindrical with blunt apex; near margin 8–32 × 2.0–5.5 µm, cylindrical, partially somewhat tapering, with blunt apex. *Pileocystidia* near margin 45–71–120 × 5.5–7.5–11 µm, contents crystalline; near centre 20–56–92 × 4–7–10 µm, occasionally branched in the basal segment, contents crystalline. Blackening in sulphovanillin. *Clamp connections* absent.

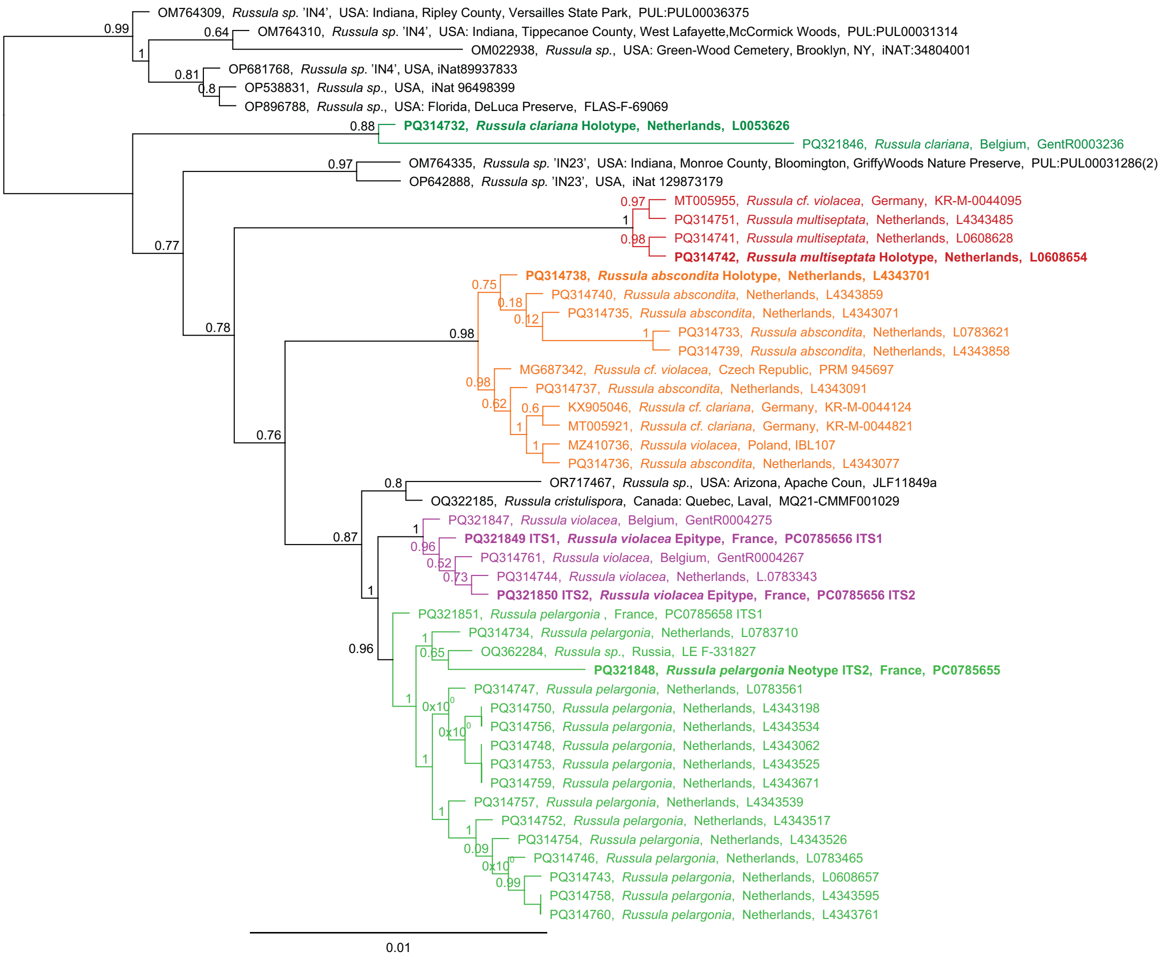
Colour illustrations. The Netherlands, Eeuwigelaan, Bergen, in verge of dry rich avenue, type locality. Left top then anticlockwise: spores in Melzer's reagent; basidiomata *in situ* (L.4343077. Photo E. Arnolds), basidiomata (holotype) *in situ* (L.4343701. Photo F. de Buijzer); hymenial cystidium; basidium; pileipellis near centre in Congo red. Scale bars: all microscopic structures = 10 µm; spores = 5 µm.

Habitat and distribution: Never grows with *Populus* but mainly with *Quercus* species in dry avenues and parks, fruits later in the season mainly in October, occasionally in September. Widespread in The Netherlands, known from Belgium, Czech Republic, Germany, Poland and Romania, common. Soil samples are known from Bolivia, Bulgaria, Estonia, Italy and Turkey.

Typus: **Netherlands**, Noord-Holland province, Bergen, Eeuwigelaan, on rich calcareous soil in verge of dry avenue, 52.6671, 4.6911, 6 Sep. 2021, *F. de Buijzer* (**holotype** L.4343701; ITS sequence GenBank PQ314738).

Additional materials examined: **Germany**, Karlsruhe, Beierheimer Allee, 48.9958, 8.3964, 21 Oct. 2015, *T. Bernhauer* (KR–M–0044124; ITS sequence GenBank KX905046); Karlsruhe, Schlossgarten Richtung W. Brandt Allee, approx. 49.014, 8.400, 20 Oct. 2016, *A. Schneider* (KR–M–0044821; ITS sequence GenBank MT005921). **Netherlands**, Utrecht Province, Amerongen, Kolland, 51.9945, 5.4298, 4 Sep. 2004, *R. Chrispijn* (L.0783621; ITS sequence GenBank PQ314733); Groningen Province, Zevenhuizen, Commissiebos, 51.106, 6.354, 18 Oct. 2019, *I. Somhorst*, IS19151 (L.4343091; ITS sequence GenBank PQ314737); Overijssel Province, N348, Raalte, 52.3642, 6.2601, 10 Oct. 2021, *R. Chrispijn* (L.4343859; ITS sequence GenBank PQ314740); Drenthe Province, Aalden, 52.8017, 6.6955, 3 Oct 2019, *E. Arnolds* (L.4343077; ITS sequence GenBank PQ314736); Overijssel Province, N748 P 3.4 Vriezenveen, NL 52.4211, 6.6882, 4 Oct. 2021, *R. Chrispijn* (L.4343858; ITS sequence GenBank PQ314739); Drenthe Province, Assen, Witterveld 52.947, 6.5093, 30 Oct. 2019, *E. Arnolds*, 19–79 (L.4343071; ITS sequence GenBank PQ314735); Utrecht Province, Zeist, 22 Aug. 1993, *B. Tolsma* (L.4376096).

Notes: GenBank and UNITE were queried using the BLAST algorithm. The comparison of the generated holotype sequence with the closest BLAST results from GenBank revealed a greater than 97 % identity match with eight sequences from *Russula* species, either unidentified or identified as *R. violacea, R. cf. violacea,* or *R. cf. clariana.* These sequences originated from Romania, Germany, Poland and the Czech Republic. Querying UNITE with species hypothesis SH0956392.10FU with a 1.5 % distance threshold yielded 74 sequences associated with the ecology of *Quercus robur* (1), *Quercus* sp. (2), and *Populus* sp. (1). However, that single sequence (GenBank OR511608) from a root tip of *Populus* sp. shows, once trimmed to ITS1, 5.8S, ITS2, 17 nt differences with the consensus sequence of the /abscondita clade. Romagnesi (1967) distinguishes the section *Violaceinae* from *Atropurpurinae* by its *R. fellea* smell, *R. pseudointegra* spores, and cream-coloured spore print and includes the following three species: *R. clariana*, *R. pelargonia s.s.* Romagn. and *R. violacea s.s.* Romagn. *Russula abscondita* forms a well-supported clade in the /violaceinae. It differs from *R. violacea* by its sub reticulate basidiospore ornamentation. *Russula pelargonia* and *R. clariana* sporulate with *Populus*. *Russula multiseptata* generally has violet cap colours and more septated pileocystidia.



Phylogenetic tree of the /violaceinae with FastTree support values based on nrITS1–5.8S–ITS2 sequence data for /violaceinae using a maximum likelihood analysis with FastTree v. 2.1.12 (Price *et al*. 2009, 2010) following a MAFFT alignment (MAFFT G–INS–i, v. 7.490 (Katoh *et al.* 2002, Katoh & Standley 2013). The alignment and tree were deposited on Figshare.com: (doi: 10.6084/m9.figshare.27170076).

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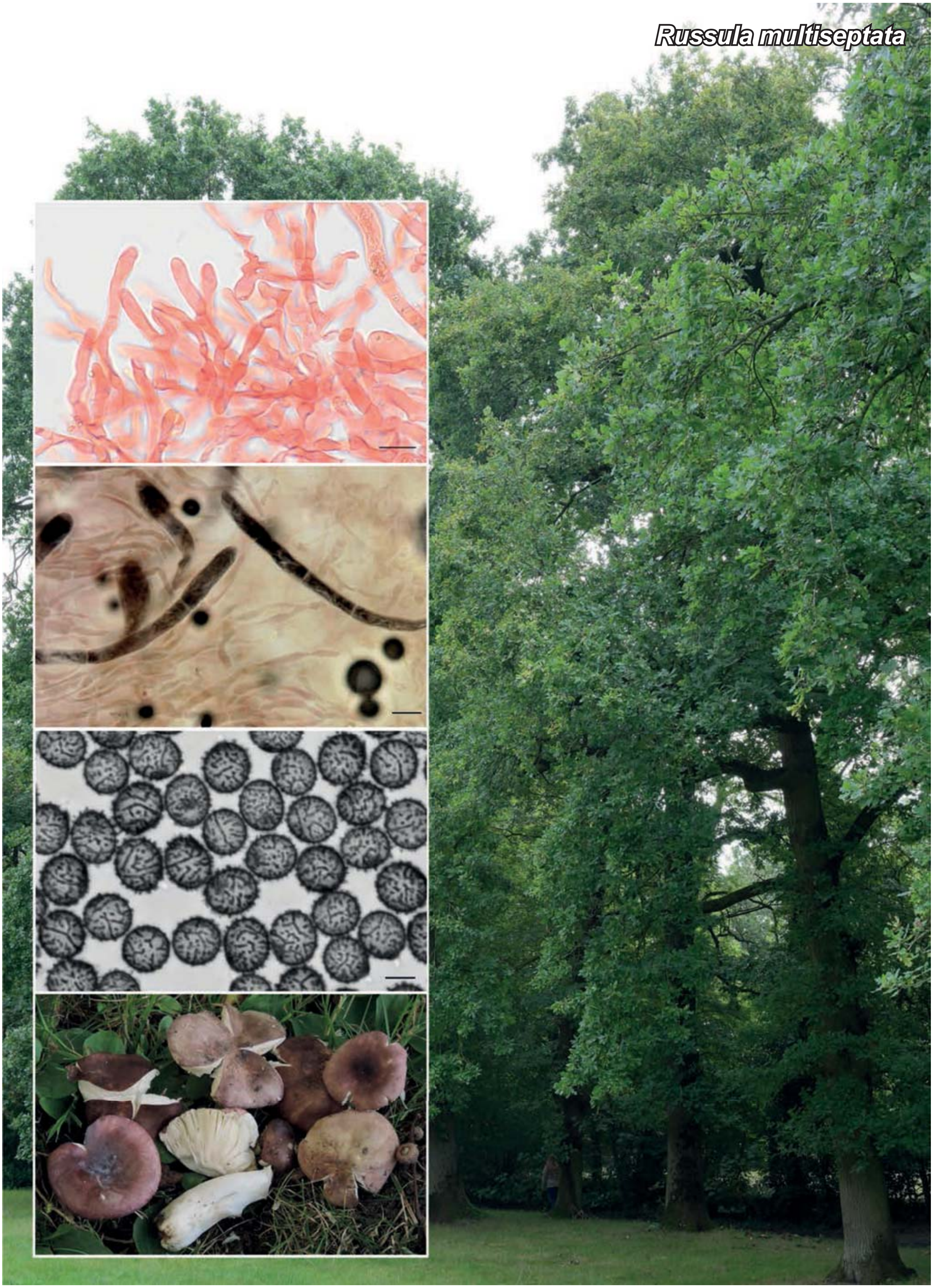
Russula multiseptata

Fungal Planet 1770

MycoBank MB 855758

Russula multiseptata G.M. Jansen & Wisman ***sp. nov.***

Etymology: From the Latin *multi septa* referring to the multiseptated pileocystidia.

Classification: *Russulaceae*, *Russulales*, *Agaricomycetes*.

Basidiomata medium sized. *Pileus* 40–70 mm, convex then expanding to applanate with depressed centre, margin slightly sulcate on ageing, dull to slightly shiny, colours violet turning greenish towards centre at ageing, greyish green, ochre greenish, peeling 2/3 of the radius. *Lamellae* emarginate, normally spaced, without short gills, obtuse, no forking, white then light cream, edge entire, concolorous. *Stipe* 30–75 × 7–9 mm, tapering toward apex, irregular wrinkled, white, then at places slightly grey, occasionally staining yellow. *Macro chemical reactions* $FeSO_4$ on stem pale pink to deep orange, salmon orange. Guaiac on stem and gills slow, at first light later more intense blue. *Taste* acrid, short lasting, *smell* normal to strongly pelargonium or like *R. fellea*. *Spore print* colour code Romagnesi Ib–IIb. *Basidiospores* 7.5–8.7–10.0 × 6.2–7.3–8.3 µm (sl = 0.6 µm, sw = 0.5 µm), Q = 1.1–1.21–1.31 (sQ = 0.05) (n = 82 from 5 collections); ornamentation with ridges and few isolated warts, little reticulate, amyloid, 0.8 µm high. *Basidia* 33–41–40 × 9–11–13 µm, clavate, subclavate, sterigmata in average 6–7(–11) µm, 4-spored. Lamellae edges heterogeneous or sterile. *Hymenial cystidia* on lamellae edges 40–60–78 × 8–10–12 µm lanceolate with obtuse-rounded apex, some with apical appendix, content finely crystalline turning grey black with sulphovanillin. Marginal cells are similar. *Hymenophoral trama* composed of sphaerocytes in average 25–35 µm wide and a few hyphal elements. *Pileipellis* with pileocystidia; near centre cylindrical, flexuous, multi septate, similar to the margin but somewhat smaller; near margin 55–116–175 × 3.5–9–12.5 µm, flexuous, cylindrical, obtuse apex, with crystalline content, (0–)1–3-septate. *Hyphal terminations* 1.5–6.5 µm wide, cylindrical with blunt apex, a few branched. *Clamp connections* absent.

Habitat and distribution: Never grows with *Populus* but mainly with *Quercus* species on clay in parks, fruits generally early in the season August and September. Widespread in the Netherlands, Flanders and Germany, common. Soil samples are known from the Russian Federation, Morocco, Italy, Kyrgyzstan, Turkey and Iran.

Colour illustrations: The Netherlands, Appingedam, Ekenstein park, type locality. From top: Pileipellis near centre in Congo red; pileocystidia in sulphovanillin; basidiospores in Melzer's reagent; basidiomata (holotype) *in situ*. Scale bars: all microscopic structures = 10 µm; spores = 5 µm.

Typus: **Netherlands**, Groningen Province, Appingedam, Ekenstein, on soil, clay, rich, 53.31911, 6.80714, 27 Aug. 2013, *J. Wisman* (**holotype** L.0608654; ITS sequence GenBank PQ314742).

Additional materials examined: **Belgium**, Brussels, Park Tervuren, 26 Aug. 2014, *F. Hampe* (FH_Rus_14082606). **Netherlands**, Overijssel Province, Zwolle, Groot Wezenland, 52.510365, 6.099450, 28 Oct. 2020, *E. Arnolds*, 20–26 (L.4343485; ITS sequence GenBank PQ314751); Utrecht Province, Breukelen, Gunterstein, 52.1717, 5.0105, 30 Sep. 2013, *S. v.d. Haar* (L.0608628; ITS sequence GenBank PQ314741); Overijssel Province, Wijhe, Eikenlaan bij landgoed, 18 Oct. 1988, *P.J. Keizer*, 88078 (L.4397409); Utrecht Province, Breukelen, Nijenrode, 13 Oct. 1991, *P.J. Keizer*, 91020 (L.4376091).

Notes: GenBank and UNITE were queried using the BLAST algorithm. The comparison of the generated holotype sequence with the closest BLAST results from GenBank and UNITE revealed a 100 % match with two sequences from *Russula cf. violacea* originating from Germany (GenBank MT005955 = KX905042) and *Russula* sp. from ectomycorrhizal mantle of *Quercus ilex* in Italy (GenBank HE601889). Querying UNITE with species hypothesis SH0956496.10FU with a 1.5 % distance threshold yielded 65 additional sequences from soil samples originating from Russian Federation, Morocco, Italy, Kyrgyzstan, Turkey and Iran. Romagnesi (1967) distinguishes the section *Violaceinae* from the *Atropurpurinae* by its *R. fellea* or pelargonium smell, *R. pseudointegra* spores, and cream coloured spore print and includes the following three species: *R. clariana*, *R. pelargonia*, *ss.* Romagn., *R. violacea ss*. Romagn. *Russula multiseptata* forms a well-supported clade in the /violaceinae. It differs from *R. violacea* by its subreticulate basidiospore ornamentation. *Russula pelargonia* and *R. clariana* are restricted to sporulate with *Populus*. *Russula abscondita* generally is devoid of violet cap colours and has few septated pileocystidia.

For phylogenetic tree, see *Russula abscondita* (FP 1769).

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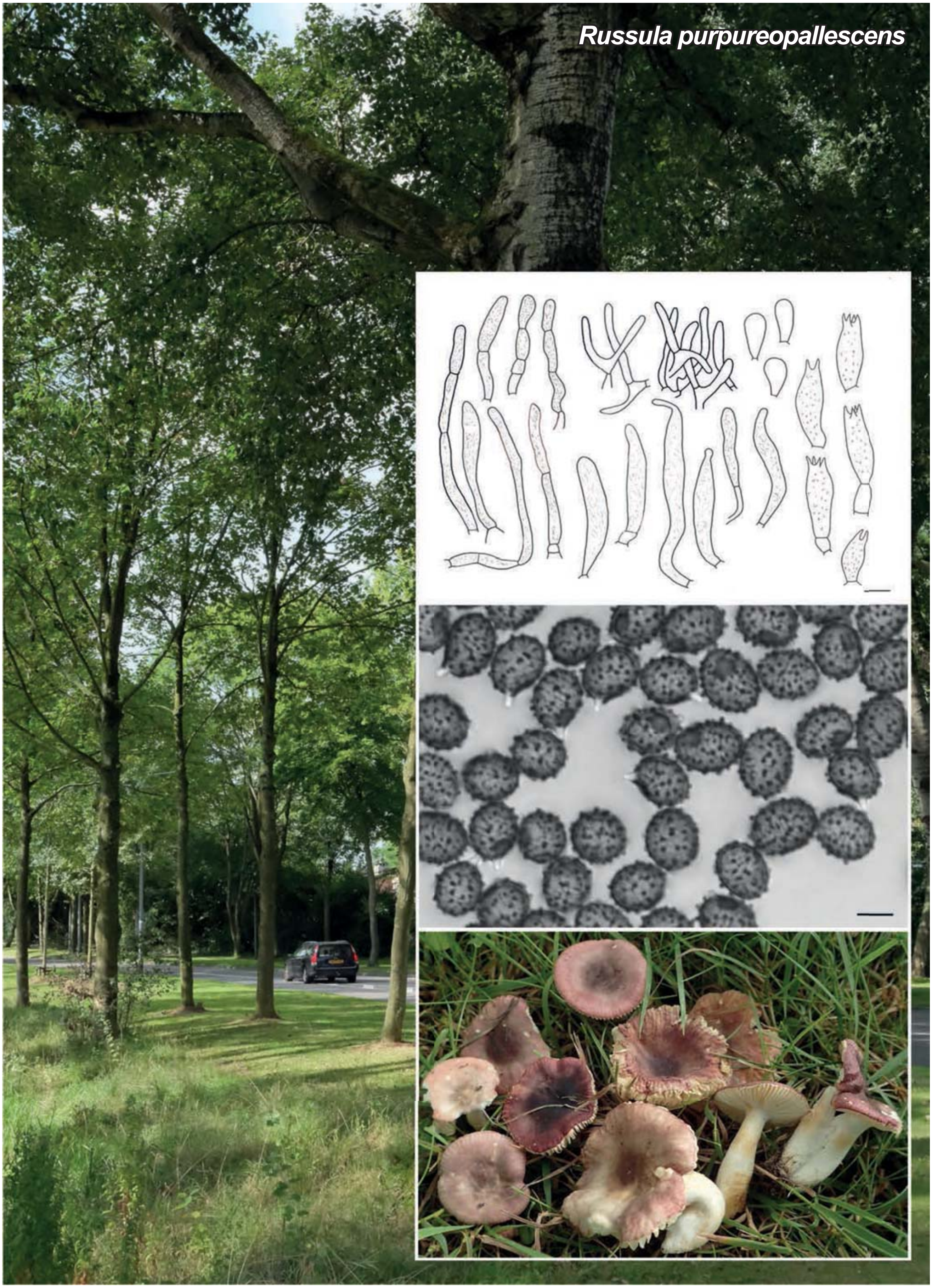

Russula purpureopallescens

Fungal Planet 1771 MycoBank MB 855671

Russula purpureopallescens G.M. Jansen, K. Raangs, Somhorst & Wisman, *sp. nov.*

Etymology: Refers to the purple pileus colours fading towards the margin.

Classification: *Russulaceae*, *Russulales*, *Agaricomycetes*.

Basidiomata small to medium-sized. *Pileus* 15–40(–50) mm, when young hemispherical, convex then applanate, centre depressed; with a sulcate margin, with purple colours, more intense at centre, occasionally fading to almost colourless at margin; when wet sticky, when dry matt; peeling 1/4–3/4; context mild. *Lamellae* L = 70–90, l = (0–)1–3, intermediate gills absent to few, few forking gills; brittle; young white, then cream, staining ochre yellow after 5 min or not staining; edge even not serrate; acute to bluntly attached to margin; *taste* mild or slightly prickling. *Stipe* 30–45 × 5–10 mm, cylindrical, enlarged towards the base, firm, brittle, soft, spongy, chambered, white, stains ochre in 5 min. *Smell* weak, indistinct, fruity. *Macro chemical reactions* Sulphovanillin on context no reaction, on lamellae no reaction, on stipe no reaction, FeSO4 on stipe salmon pink, KOH/ammonia on context yellow, on stipe yellow, Guaiac on lamellae medium blue, on stem intense blue within 5 s. *Spore print* colour code Romagnesi IIc(–IId). *Basidiospores* 7.4–8.6–9.9 µm × 6.0–6.7–7.5 µm (sl = 0.6 µm, sw = 0.4 µm); Q = 1.15–1.28–1.39 (sQ = 0.06) (n = 100 from 5 collections); broadly ellipsoid, ornamentation amyloid; isolated and subridged warts, thin partial reticulum, not exceeding 0.7–0.9 µm in height; suprahilar plage blackish to black; hilar appendix distinct, inamyloid. *Basidia* 28–48 × 9–15 µm, clavate, sub clavate, sterigmata in average 5–8 µm, (2–)4-spored. Lamellae edges heterogeneous. *Hymenial cystidia* on lamellae sides 26–105 × 6–14.5 µm, subclavate with obtuse rounded apex, fusiform, some mucronate, content finely crystalline turning grey black with sulphovanillin. Hymenial cystidia on the lamellae edges 46–69 × 10–12 µm, clavate, some mucronate, content finely crystalline turning grey black with sulphovanillin, arising 10–15 above the basidioles. Lamellae edges heterogeneous. *Hymenophoral trama* composed of sphaerocytes in average 10–25 µm wide and a few hyphal elements. *Pileipellis* near centre in cresyl blue orthochromatic, delimited from the underlying context, 145–270 µm thick, two-layered; subpellis 80–180 µm deep, composed of more or less densely intermixed, horizontally oriented hyphae and dispersed pileocystidia; suprapellis an ixo-palisade, 63–82 µm thick, mainly composed of ascending thin-walled hyphen and pileocystidia. Pileipellis near margin orthochromatic in cresyl blue, delimited from the underlying context, 195–210 µm thick, two-layered; subpellis 120–135 µm deep, composed of more or less densely intermixed, horizontally oriented hyphae and dispersed pileocystidia; suprapellis an ixo-palisade, 60–120 µm thick, mainly composed of ascending thin-walled hyphen and pileocystidia. *Pileocystidia* near centre 57–94 × 4–7.5 µm, cylindrical, subclavate, multi septate; near margin (22–)47–73(–120) × 3–7.5 µm, clavate, subclavate, obtuse apex, with crystalline contents, (0–)multiseptate. *Hyphal terminations* near centre 11–60 × 3–4 µm, cylindrical, with blunt apex. Near margin 8–43 × 3–4.5 µm, cylindrical, with blunt or slightly enlarged apex. *Clamp connections* absent.

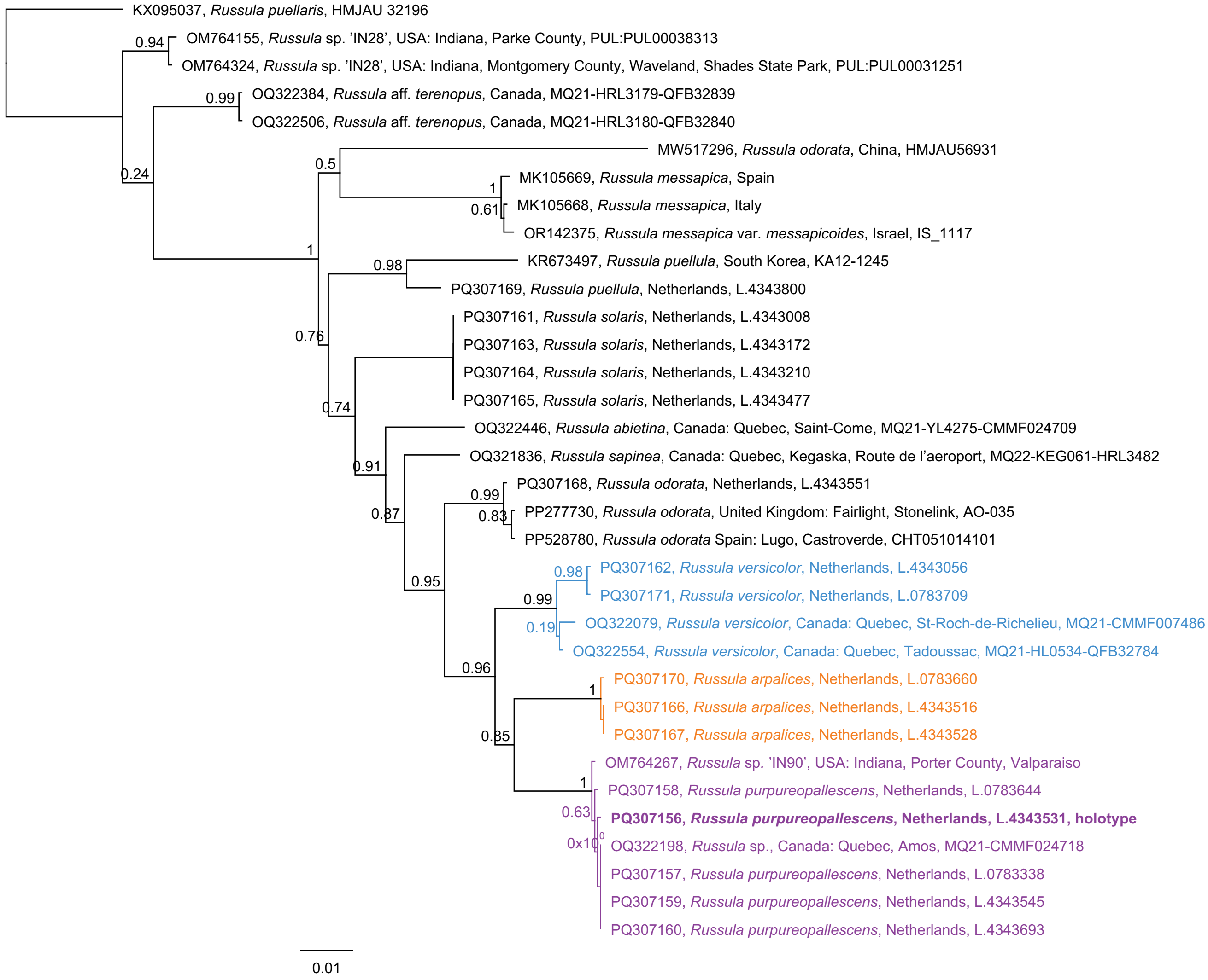
Habitat and distribution: Solitary or gregarious on soil that is low in humus and exclusively with *Populus.* Known from Netherlands, Belgium, Estonia, Latvia, Canada and USA. Widespread in Europe and Northern America, uncommon.

Typus: **Netherlands**, Groningen Province, Lewenborg, in verge of dry rich soil, 53.23641, 6.63126, 30 Jul. 2020, *K. Raangs & I. Somhorst*, IS20026 (**holotype** L.4343531; ITS sequence GenBank PQ307156).

Additional materials examined. **Netherlands**, Noord Holland Province, Zandvoort, dunes poor grassland, 52.3361, 4.5398, 20 Jul. 2021, *F. de Buijzer* (L.4343693; ITS sequence GenBank PQ307160); Noord Holland Province, Zandvoort, dunes poor grassland, 52.3361, 4.5398, 26 Jul. 2020, *F. de Buijzer* (L.4343545; ITS sequence GenBank PQ307159); Groningen Province, Baflo, rich lawn, 53.3604, 6.5092, 12 Aug. 2011, *K. Raangs* (L.0783644; ITS sequence GenBank PQ307158); Friesland Province, Noordbergum, Rijksstraatweg 63, 53.2217, 6.0151, 5 Nov. 2016, *J. Wisman* (L.0783338; ITS sequence GenBank PQ307157).

Notes: GenBank and UNITE were queried using the BLAST algorithm. The comparison of the generated holotype sequence with the closest BLAST results from GenBank revealed a 100 % match with two sequences from unidentified *Russula* species originating from the USA (GenBank OM764267) and Canada (GenBank OQ322198). Querying UNITE with species hypothesis SH1831890.10FU with a 1.5 % distance threshold yielded 14 additional sequences of unidentified *Russula* species that showed a connection with *Populus tremula* originating from Estonia and Latvia. *Russula purpureopallescens* belongs to the section *Tenellae* where it forms with *R. arpalices* and *R. versicolor* the /versicolor clade. *Russula arpalices* forms sporocarps in The Netherlands with *Populus* but has a much darker spore print (IIIc *vs* IIb for *R. purpureopallescens*) and does not react with FeSO4, whereas *R. purpureopallescens* turns salmon pink. Sometimes *R. purpureopallescens* is mistaken for *R. versicolor* but that species associates with *Betula*. Also confused with *R. puellaris*, but those spores are subglobose (*vs* broadly ellipsoid for *R. purpureopallescens*) and it is not known to associate with *Populus* (*vs R. purpureopallescens* growing exclusively with *Populus*). *Russula terenopus* possesses echinulate spores, has a distinct smell that reminds of *R. fellea* or pelargonium. *Russula versatilis* has ochre echinulate spores that are subglobose, with Qav. = 1.15, and does not associate with *Populus.*

Colour illustrations. The Netherlands, Groningen, Lewenborg, verge of dry rich avenue, type locality. Line drawing by J. Wisman (all structures from holotype) clockwise from top left: from centre of the pileus: pileocystidia, hyphal terminations; basidioles; basidia; hymenial cystidia. Basidiospores in Melzer's reagent. Basidiomata (holotype) *in situ*. Scale bars: drawing = 10 µm; spores = 5 µm.



Phylogenetic tree of part of the *Tenellae* with FastTree support values based on nrITS1-5.8S-ITS2 sequence data for *Russula purpureopallescens* using a maximum likelihood analysis with FastTree v. 2.1.12 (Price *et al.* 2009, 2010) following a MAFFT alignment (MAFFT G–INS–i, v. 7.490 (Katoh *et al.* 2002, Katoh & Standley 2013). The alignment and tree were deposited on Figshare.com: (doi: 10.6084/m9.figshare.27171810).

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Sebacina spongicarpa

Fungal Planet 1772 MycoBank MB 852960

Sebacina spongicarpa A. Thomas & T.K.A. Kumar, *sp. nov.*

Etymology: Name refers to the spongy nature of the basidiocarp.

Classification: *Sebacinaceae*, *Sebacinales*, *Agaricomycetes*.

Basidiocarp 55–98 × 3–13 mm, resupinate, coriaceous, spongy, with a gelatinous texture on upper surface, lobed, undulate, dull white to cream when fresh, turning to yellowish brown when dry. *Tramal hyphae* 2–4 µm wide, thick-walled, gelatinous, agglutinated, densely packed, yellow to yellowish brown, septate, without clamp connections. Densely packed hyphae are interspersed with air spaces. *Hymenium* 58–200 µm wide, gelatinous, composed of basidia and hyphidia. *Hyphidia* 58–200 × 2–3 µm, numerous, branched, cylindrical, hyaline to pale grey, thin-walled, without *clamp connections*, projecting beyond basidia. *Basidia* 10–19 × 8–18 µm, globose to ellipsoid, 2–4-celled, longitudinally septate, thin-walled, guttulate, hyaline. *Basidiospores* 9–12 × 5–6 µm (Q = 1.58–2.1 Qm = 1.88) ellipsoid, broadly ellipsoid, ovoid, hyaline, thin-walled, smooth, guttulate. *Spore print* not observed.

Habit, habitat and distribution: On soil, incrusting twigs, stones, leaf bits and on base of plants.

Typus: **India**, Kerala State, Malappuram District, Nilambur, 11°16’45.96”N, 76°14’23.23”E, 23.22 m a.s.l., on soil, incrusting twigs, stones, leaf bits and on base of plants, 23 Oct. 2021, *A. Thomas* (**holotype** ZGCAT302; ITS and LSU sequences GenBank OQ918288 and OQ918308).

Additional material examined: **India**, Kerala State, Malappuram District, Nilambur, on soil, incrusting twigs, stones, leaf bits, 23 Oct. 2021, *A. Thomas*, ZGCAT301; ITS sequence GenBank PP388210.

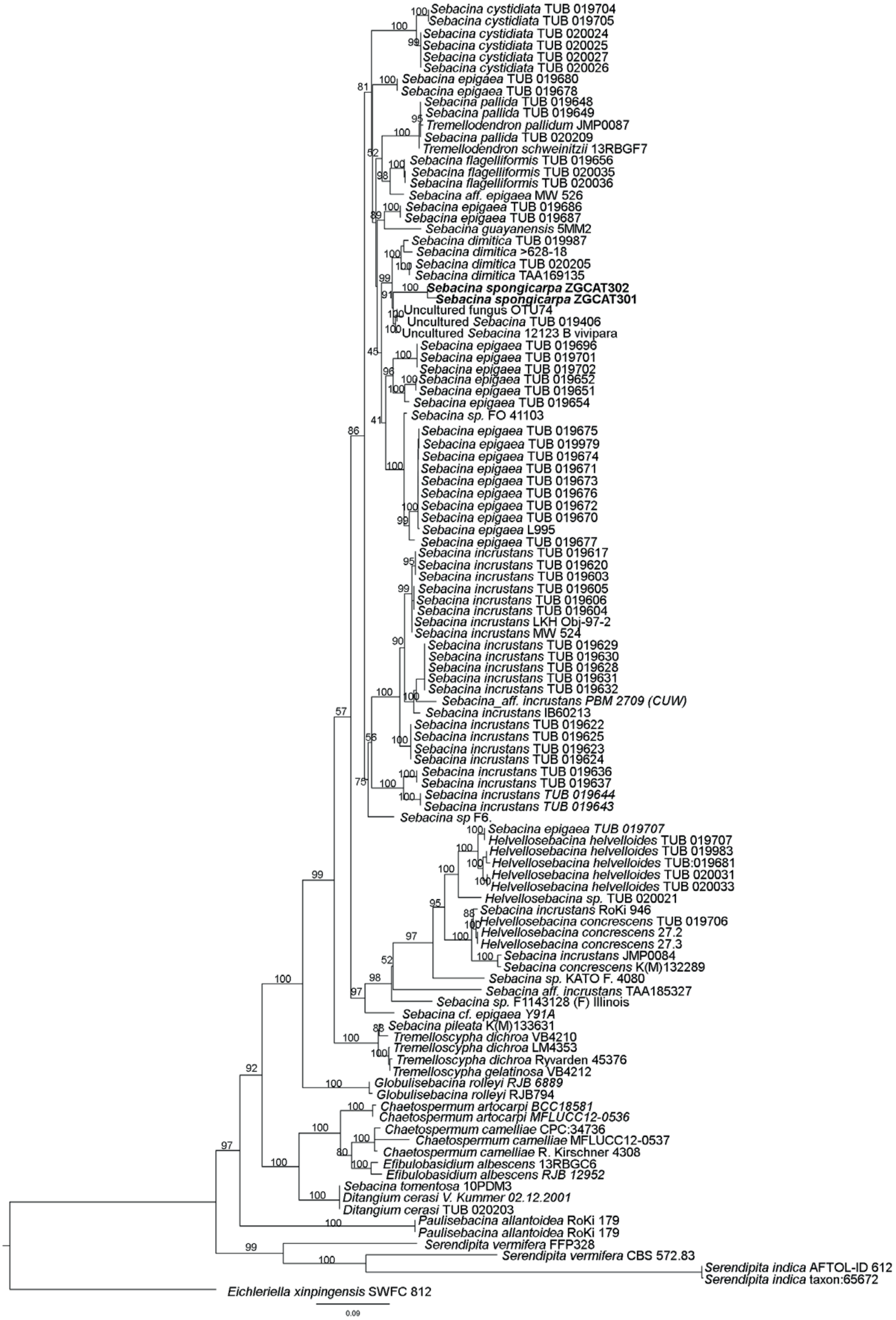
Notes: *Sebacina spongicarpa* has thick-walled tramal hyphae, which are agglutinated and densely packed, with well-defined cavity-like spaces resulting in a spongy texture. The hymenium is compactly arranged, gelatinous, with thin-walled basidia and occasionally branching, thin-walled hyphidia. *Sebacina spongicarpa* is morphologically related to *S. epigaea* and *S. incrustans* with the incrusting and terricolous nature (Riess *et al.* 2013, Oberwinkler *et al.* 2014). According to Riess *et al.* (2013), the basidiocarps of *S. epigaea* are opalescent, becoming membraneous when drying, and has thin-walled hyphae. However, *S. spongicarpa* has thick-walled tramal hyphae, densely packed with gaps which results in a spongy texture of the basidiocarp. In addition, *S. epigaea* has an irregularly branching short hyphidia (up to 60 µm) in the hymenial region (McNabb 1966). *Sebacina spongicarpa* has dense, occasionally branching, cylindrical, long (58–200 × 2–3 µm) hyphidia, which projects beyond the basidial zone. *Sebacina incrustans* has an incrusting and terricolous nature, with unchanging cream to ochre coloured basidiocarp, similar to *S. spongicarpa*. But the former has irregularly branching hyphidia, and larger basidiospores, 10–20 × 6–10 um (Burt 1915, Henkel *et al*. 2004, Riess *et al*. 2013) compared with short basidiospores (9–12 × 5–6 µm) of *S. spongicarpa*. In addition, *S. incrustans* has a 2–3 mm thick basidiocarp with loosely intertwined tramal hyphae, whereas *S. spongicarpa* has a 3–13 mm thick basidiocarp and agglutinated, densely packed tramal hyphae with gaps in the tramal region.

In the BLAST search (https://blast.ncbi.nlm.nih.gov/), the newly generated ITS sequences of ZGCAT301 (GenBank PP388210) and ZGCAT302 (GenBank OQ918288) showed 92.65 % and 93.13 % similarity with an uncultured *Sebacina* isolate (HQ154314) as first hit. Subsequent hits are also uncultured *Sebacina* clones (GenBank JQ890308, Identity = 92.65 %; GenBank KM247668, Identity = 93.16 %; GenBank KU924635, Identity = 93.63 %; GenBank KF000529, Identity = 93.14 %). The closest hit of LSU sequence of ZGCAT302 (GenBank OQ918308) are *Tremellodendron* sp. (GenBank AY745701, Identity = 98 %) as first hit, and uncultured *Sebacina* clones as the subsequent hits (GenBank FJ207491, Identity = 98.38 %; GenBank FJ207513, Identity = 98.38 %).

Phylogenetically, *S. spongicarpa* is distinct from *S. epigaea* and *S. incrustans.* In the phylogenetic tree constructed with the combined ITS and LSU sequences, the accessions of *S. spongicarpa* clustered with accessions of uncultured *Sebacina* species with a 91 % bootstrap support value, and together they form a sister clade to *S. dimitica* with a 99 % bootstrap support value. *Sebacina spongicarpa* differs from *S. dimitica* by the absence of dimitic hyphal system (Duenas 2005).

Supplementary material: doi: 10.6084/m9.figshare.27193362 (Table, alignment and phylogram).

Colour illustrations: India, Kerala state, Malappuram district, Nilambur, type locality. Upper left insets show fresh basidiocarps; upper right inset show dried basidiocarp; middle insets show basidia (left), and basidiospores (right); lower insets show arrangement of tramal hyphae and hyphidia in cross-section (left), and deeply embedded basidia within hyphidia (right). Scale bars: basidiocarps = 10 mm; lower insets = 100 µm; middle insets = 10 µm.



Maximum Likelihood tree generated from the combined nrITS and nrLSU sequences of *Sebacinales* members. IQ-TREE (IQ-TREE Web Server: Fast and accurate phylogenetic trees under maximum likelihood; univie.ac.at) (Nguyen *et al.* 2015) was used to generate the phylogenetic tree. Parameters such as autodetecting the substitution model, ultrafast bootstrap analysis with 1000 bootstrap alignments, and Shimodaira–Hasegawa (SH)-like approximate likelihood-ratio test (SHaLRT) were set for constructing the phylogram (Nguyen *et al*. 2015, Kalyaanamoorthy *et al.* 2017, Hoang *et al.* 2018). New species and its voucher numbers are indicated in bold black letters. The alignment and tree were deposited in figshare.com (10.6084/m9.figshare.27193362).

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Sporisorium enterogonipteri

Fungal Planet 1773 MycoBank MB 853716

Sporisorium enterogonipteri R. Knop., Hammerb. & T. Bose, ***sp. nov.***

Etymology: A single isolate of this fungus was recovered from the gut of *Gonipterus* sp. n. 2 (*Eucalyptus* snout beetle).

Classification: *Ustilaginaceae*, *Ustilaginales*, *Ustilaginomycetes*.

Thallus usually unicellular, infrequently bi-cellular with a single horizontal septum; cell surface smooth; cell wall thicker in non-budding cells while thin in actively budding cells; cells globose to ellipsoid in shape measuring 2.02–4.87(–5.33) × 2.22–4.74(–4.74) µm, sometimes oblong measuring 5.16–7.42(–8.3) × 3.36–4.56(–5.19) µm; cells often with prominent bud scars, if bud scars present in both apices cells frequently have a limoniform appearance; cells are 1–4 nucleate, usually binucleate; often with multiple inconspicuous storage bodies; hyphae or pseudohyphae absent; buds are globose to ellipsoid in shape, 1.73–2.43(–3.44) × 2.23–3.31(–3.54) µm, rarely pyriform measuring 2.18–3.4(–7.5) × 3.22–3.45(–3.56) µm; buds sometimes remain attached on a short pedicel measuring 1.23–2.14(–2.33) × 1.19–1.34(–1.44) µm. *Sexual morph* not observed.

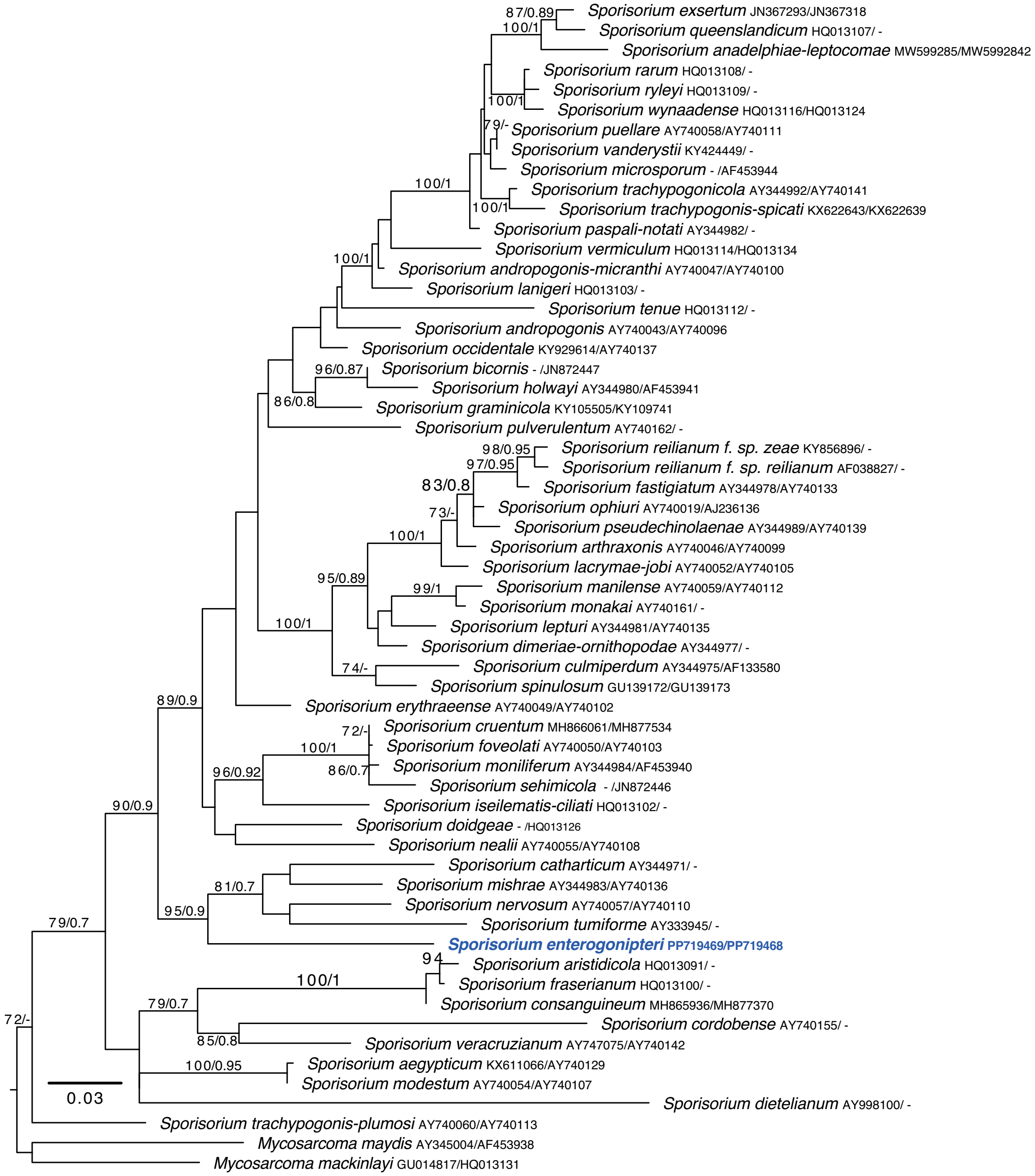
Culture characteristics: On potato dextrose agar (PDA), 2 % malt extract agar (MEA), and yeast peptone dextrose agar (YPD) colony cream yellow (top and reverse; Rayner 1970). Colony circular, margin entire, elevation umbonate. The optimal growth temperature was 25 °C on all three tested microbial growth media. However, the colony density after 7 d at 25 °C was greater on PDA compared to MEA and YPD.

Typus: **South Africa**, Gauteng Province, Pretoria, Blue Gum Valley Shooting Range, isolated from the gut of *Gonipterus* sp. n. 2 (*Eucalyptus* snout beetle), Jan. 2024, *R. Knoppersen* [**holotype** PRU(M): 4599, culture ex-type CMW 64171 = CMW-IA 6966; ITS and LSU sequences GenBank PP719469 and PP719468].

Notes: In the pairwise sequence similarity analysis using BLAST, the ITS sequence of *Sporisorium enterogonipteri* exhibited affinity with *Anthracocystis mexicana* (AY998101), *Anthracocystis bothriochloae* (HQ013092.1), *Sporisorium mishrae* (JN367294), and *Sporisorium panici-leucophaei* (AY998102), though with relatively low percentage identities of 94.24 %, 94.13 %, 93.86 %, and 93.82 %, respectively. In contrast, the LSU sequence demonstrated closer similarity to *Sporisorium pseudanthistiriae* (JN367320.1), *Sporisorium walkeri* (JN367322), *Cintractia sorghi-vulgaris* (AY745726), and *Sporisorium sorghi* (KR014151), with percentage identities of 96.13 %, 95.12 %, 94.67 %, and 94.66 %, respectively. In the phylogenetic analyses of ITS and concatenated datasets, *S. enterogonipteri* emerged as the sister to the clade that included *S. catharticum*, *S. mishrae*, *S. nervosum* and *S. tumiforme.* However, in the LSU tree, *S. enterogonipteri* was sister to *S. consanguineum* and *S. veracruzianum.*

Sporisorium includes mycelial fungi that are plant pathogens affecting various grasses (Stoll *et al*. 2005). Among them, *S. enterogonipteri*, described here, stands out as the only known species with a yeast-like unicellular thallus morphology, recovered from the gut of *Gonipterus* sp. n. 2. Unlike other *Sporisorium* species, *S. enterogonipteri* can be successfully grown on a variety of microbial media but does not develop any mycelial or pseudomycelial thalli even after 60 d. Despite multiple attempts, no further isolates of this fungus could be recovered from the gut of *Gonipterus* sp. n. 2, suggesting it may not be a typical inhabitant of their gut. Thus, it is plausible that the particular *Gonipterus* sp. n. 2 harbouring this fungus in its gut acquired it while feeding on *Eucalyptus* leaves at the collection site.

Colour illustrations: *Gonipterus* sp. n. 2 on *Eucalyptus* leaves. 7-d-old colonies of *Sporisorium enterogonipteri* on three different microbial media, PDA, MEA, and YPD (left to right top row). Yeast-like unicellular thalli of *S. enterogonipteri*; bud with pedicel; bud scars on both apices giving cells a limoniform appearance; various budding cells (bottom row). Scale bars: thalli = 10 µm; all others = 5 µm.



The maximum likelihood (ML) tree of fungal species from the genus *Sporisorium* for which ITS and/or LSU sequences were available. The tree was constructed with IQ-TREE v. 1.6.12 (Minh *et al*. 2020) using the concatenated dataset (ITS and LSU) with 1 000 bootstrap replicates. Bayesian analysis of the dataset was done using MrBayes v. 3.2.7a (Huelsenbeck & Ronquist 2001). *Mycosarcoma maydis* and *Mycosarcoma mackinlayi* served as the outgroup taxa. Branch labels indicate ML bootstrap support values / Bayesian posterior probabilities. Only bootstrap support values ≥ 70 % and posterior probability above ≥ 0.80 are shown. Isolates recovered in this study are in **bold** and blue font. GenBank accession numbers are listed as suffixes after each taxon (ITS/LSU). The alignment and tree were deposited in Mendeley Data (doi: 10.17632/xjpbk78wx9.1)

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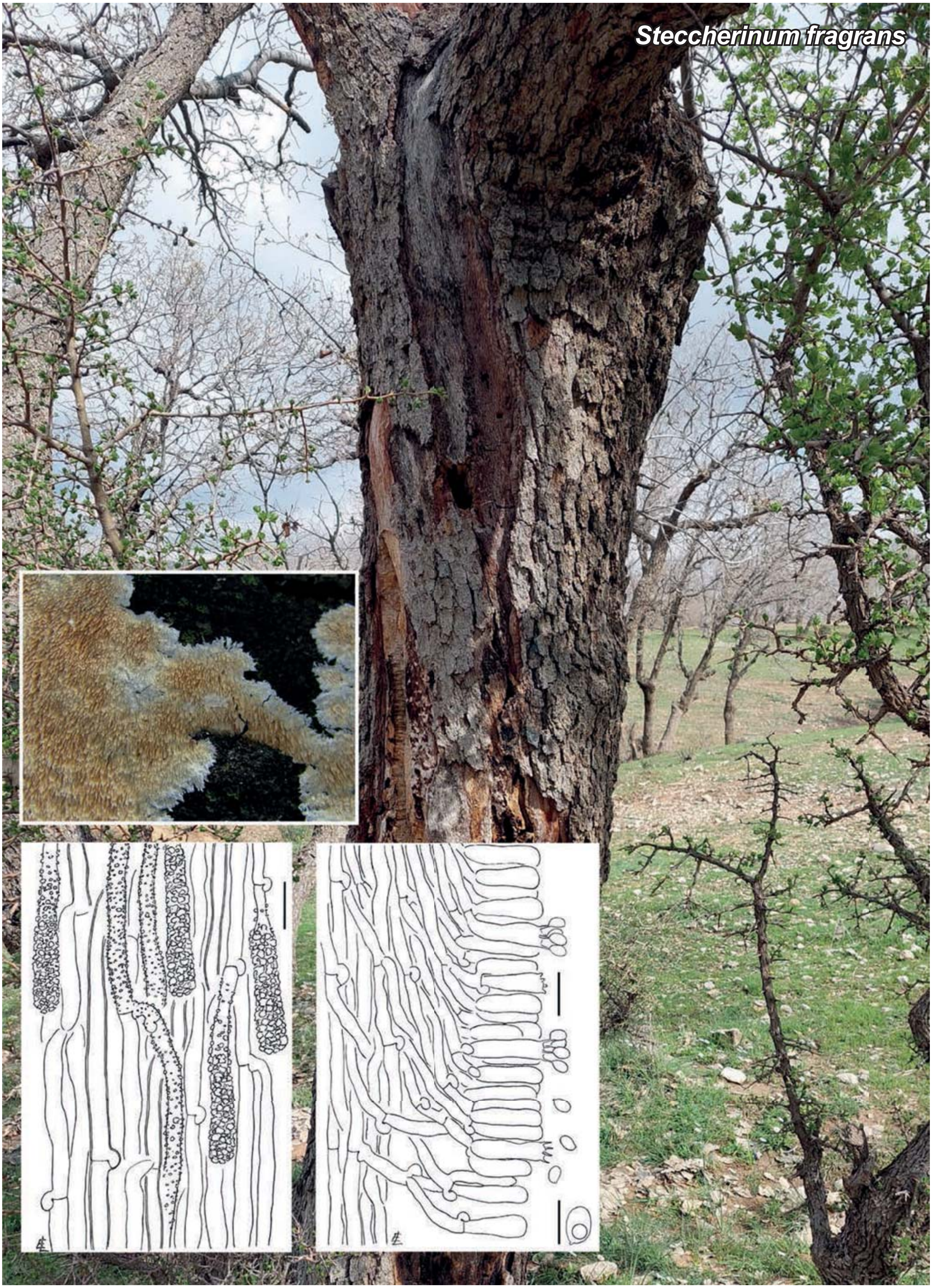

Steccherinum fragrans

Fungal Planet 1774

MycoBank MB 854213

Steccherinum fragrans Ghobad-Nejhad & Langer, ***sp. nov.***

Etymology: Referring to the fragrant basidiomata of the new species.

Classification: *Steccherinaceae*, *Polyporales*, *Agaricomycetes*.

Basidiomata annual, resupinate, subceraceous, becoming fragile when dried, creamish ochraceous to straw-coloured, no colour change upon drying, with a mild, pleasant, sweet *smell* when fresh or wet. *Hymenophore* raduloid, aculei obtuse, mostly flattened, occasionally conical, crowded, 2–5 per mm at base, concolourous, (2–)3–5 mm long; margin distinct, cottony to fimbriate, white. *Hyphal system* pseudodimitic, loosely interwoven, texture soft, negative in Melzer's reagent, moderately cyanophilous in Cotton Blue; generative hyphae dominate, moderately branched, 2.5–3.5(–4) µm wide, width even, with clamp connections, hyaline, walls thin but distinct. *Skeletocystidia* embedded in trama, hyaline, thick-walled, with clamp connections, 3.7–5 µm wide, encrusted with fine, amorphous crystals apically or entirely. *Basidia* clavate, more or less flexuous, mature basidia finely guttulate, with four sterigmata and a basal clamp connection, (18–)24–26 × 4–5 µm; basidioles dominate, similar in shape to basidia, but slightly smaller. *Basidiospores* broadly ellipsoid, hyaline, usually with one large guttule, thin-walled, smooth, negative in Melzer's reagent, cyanophilous in Cotton Blue, with a small apiculus, 3.5–4 × 2.5–2.8(–3) µm, L = 3.8 µm, W = 2.6 µm, Q = 1.45.

Habit, habitat and distribution: Collected so far in a riverside area in the eastern USA, and in open oak woodland in western Iran. Isolated from hardwood, in winter and early spring.

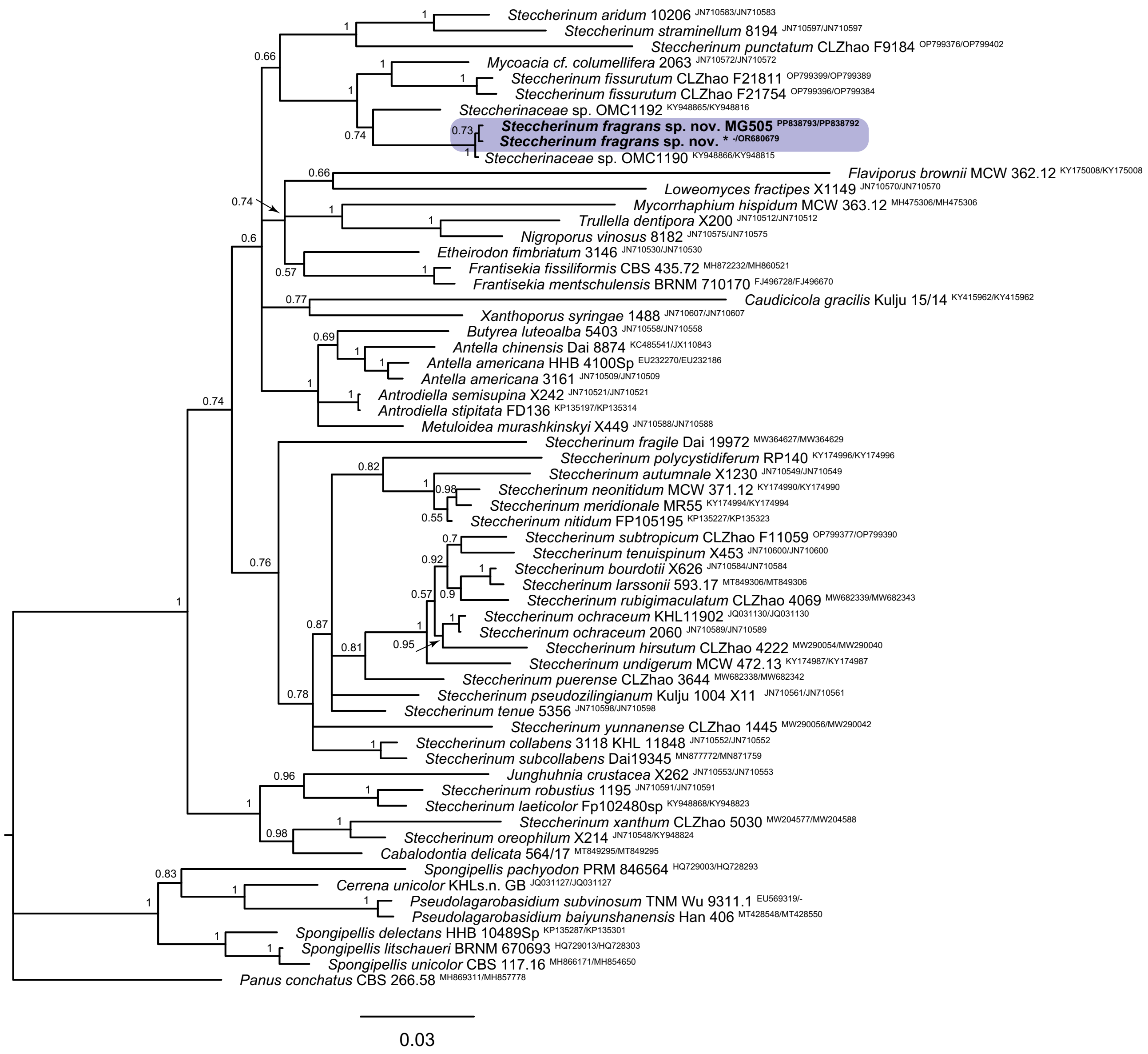
Typus: **USA**, New Jersey, Burlington Co., Delran, 40.0358N, 74.9819W, on hardwood fallen on the beach, 24 Nov. 2022, *M. Patino*, iNaturalist #143236601 (**holotype** KAS-ACD0690, ITS sequence GenBank OR680679).

Additional material examined (paratype): **Iran**, Lorestan Prov., Khorramabad-Andimeshk highway, 70 km to Khorramabad, 33.1212 E, 48.4724 N, on rotten trunk of *Quercus* sp. (*Fagaceae*), 23 Mar. 2023, *M. Ghobad-Nejhad*, 4686, isolate MG505, Ghobad-Nejhad reference collection, ITS and LSU sequences GenBank PP838792 and PP838793.

Notes: *Steccherinum fragrans* is distinguished by its resupinate, straw-coloured basidiomata with a mild, sweet smell, raduloid hymenophore with flattened aculei, the presence of skeletocystidia, and broadly ellipsoid, cyanophilous spores measuring 3.5–4 × 2.5–2.8(–3) µm. Phylogenetically, its closest species is *S. fissurutum* described from China, which however has grandiniod hymenophore and cylindrical basidiospores measuring 4.5–6 × 2.5–3 (Dong *et al.* 2023). *Steccherinum robustius* resembles *S. fragrans* in resupinate, rather ochraceous basidiomata, flattened aculei, distinct marginal zone, and ellipsoid basidiospores; however, the former has firm skeletal hyphae and conspicuous, heavily encrusted metuloid cystidia extending above the hymenial layer. Moreover, the two species are nested completely apart in the phylogenetic tree. *Steccherinum laeticolor*, sometimes synonymised with *S. robustius*, differs by shorter aculei 0.5–1.5 mm long, and narrowly ellipsoid to subcylindrical basidiospores (Eriksson *et al.* 1984). The isolate *Steccherinaceae* sp. OMC1190 clusters closely to the new species; we could not closely examine it, but based on the phylogeny, it appears to belong to *S. fragrans*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence from the paratype had the highest similarity to *Steccherinaceae* sp. [strain Maricel Patino iNaturalist #143236601, GenBank OR680679.1; Identities = 656/661 (99 %), no gaps], *Steccherinaceae* sp. [strain OMC1190, GenBank KY948815.1; Identities = 650/655 (99 %), no gaps], and *Steccherinaceae* sp. [strain OMC1192, GenBank KY948816.1; Identities = 525/605 (87 %), 29 gaps (4 %)]. Closest hits using the **LSU** sequence are *Mycoacia cf. columellifera* [strain 2063, GenBank JN710572.1; Identities = 603/612 (99 %), no gaps], *Steccherinaceae* sp. [strain OMC1190, GenBank KY948866.1; Identities = 587/588 (99 %), no gaps], and *Antrodiella americana* [strain 3161, GenBank JN710509.1; Identities = 601/612(98 %), no gaps].

Colour illustrations: Rotten trunk of *Quercus* sp. from which the paratype was isolated (photo credit M. Ghobad-Nejhad). Basidioma from the holotype (photo credit M. Patino); a section from the trama of the holotype with skeletocystidia; a section from the hymenium of the holotype with basidia and basidiospores. Scale bars: trama and hymenium = 10 µm; the large basidiospore = 5 µm.



Phylogenetic tree of *Steccherinaceae* species obtained from a Bayesian analysis of the combined alignment (LSU and ITS, 62 taxa, 1 872 characters including alignment gaps). Bayesian inference was performed using MrBayes v. 3.2.6 (Ronquist *et al*. 2012). The new species is indicated in **bold**. The ex-type sequence is indicated with an asterisks (*). Numbers before nodes indicate Bayesian posterior probability values (BPP). *Panus conchatus* was used as an outgroup. The scale bar represents the expected number of changes per site. The alignment was deposited at figshare.com (doi: 10.6084/m9.figshare.25912639).

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Torula kanvae

Fungal Planet 1775 MycoBank MB 855674

Torula kanvae G. Gore, R. Avchar, D. Shelke, H. Sonawane & D. Dhotre, *sp. nov.*

Etymology: The name honours the ancient Indian sage Rishi Kanva, who provided early evidence of microbes, or Jeevanu, in the Hindu Vedas.

Classification: *Pseudeurotiaceae*, *Thelebolales*, *Pleosporomycetidae*, *Leotiomycetes.*

Mycelium immersed or superficial, branched, and septate, with subhyaline to pale brown, smooth-walled hyphae, measuring 0.7–2.8 µm diam. The reverse colony morphology exhibits a dark grey colour with a white margin. The optimum growth temperature ranges between 25–28 °C. *Conidiophores* are 15–17 µm long and 3–5 µm diam, macronematous, mononematous, solitary, and erect, with thick walls, consisting of two distinct cells. The first cell, which is pale brown to subhyaline, is wider at the base and narrower at the apex. The second cell, which is pale brown to brown, differs in shape from the first cell. It is cylindrical to subcylindrical at the base and globose to subglobose at the apex. The conidiophore arises from a prostrate hypha. *Conidiogenous cells* are 12–20 µm long and 3–8 µm diam, monoblastic, and terminal, dark brown to black, verruculose, thick-walled, ellipsoid, paler or subhyaline at the apex, and dark to black at the base. *Conidia* are 3–6 µm long and 3–8 µm wide, solitary to catenate, acrogenous, moniliform, phragmosporous, and dark brown, with the apical cell often pale brown, minutely verruculose, often 3–4-septate, rounded at both ends, composed of subglobose cells, and slightly constricted at some septa. Immature conidia are subhyaline to pale brown and arise at multiple angles from mature conidia.

Culture characteristics: After 20 d at 28 °C, the colony reached 48 mm diam on potato dextrose agar (PDA). The colonies on PDA had mycelium that spread with a raised and undulate margin, superficial and slightly effuse, with a nearly circular appearance. From the top, the colony was dark grey in the centre with a moss-green margin; from below, it was dark brown to black in the centre with a whitish margin. No pigmentation was observed in the culture.

Habitat and distribution: *Torula kanvae* was isolated from the gut of a *Copris signatus* beetle feeding on organic waste in Pune, Maharashtra, India.

Typus: **India**, Maharashtra, Pune district, N19°22.338', E73°88.218' from the gut of *Copris signatus* beetle, 18 Aug. 2022, *G. Gore* [**holotype** MCC 10010, preserved in a metabolically inactive state at the National Centre for Microbial Resource (NCMR), Pune India, culture ex-type MCC 10010; ITS, LSU, SSU, *tef1* and *rpb2* sequences GenBank PQ248154, PQ248155, PQ248153, PQ287916, and PQ284948].

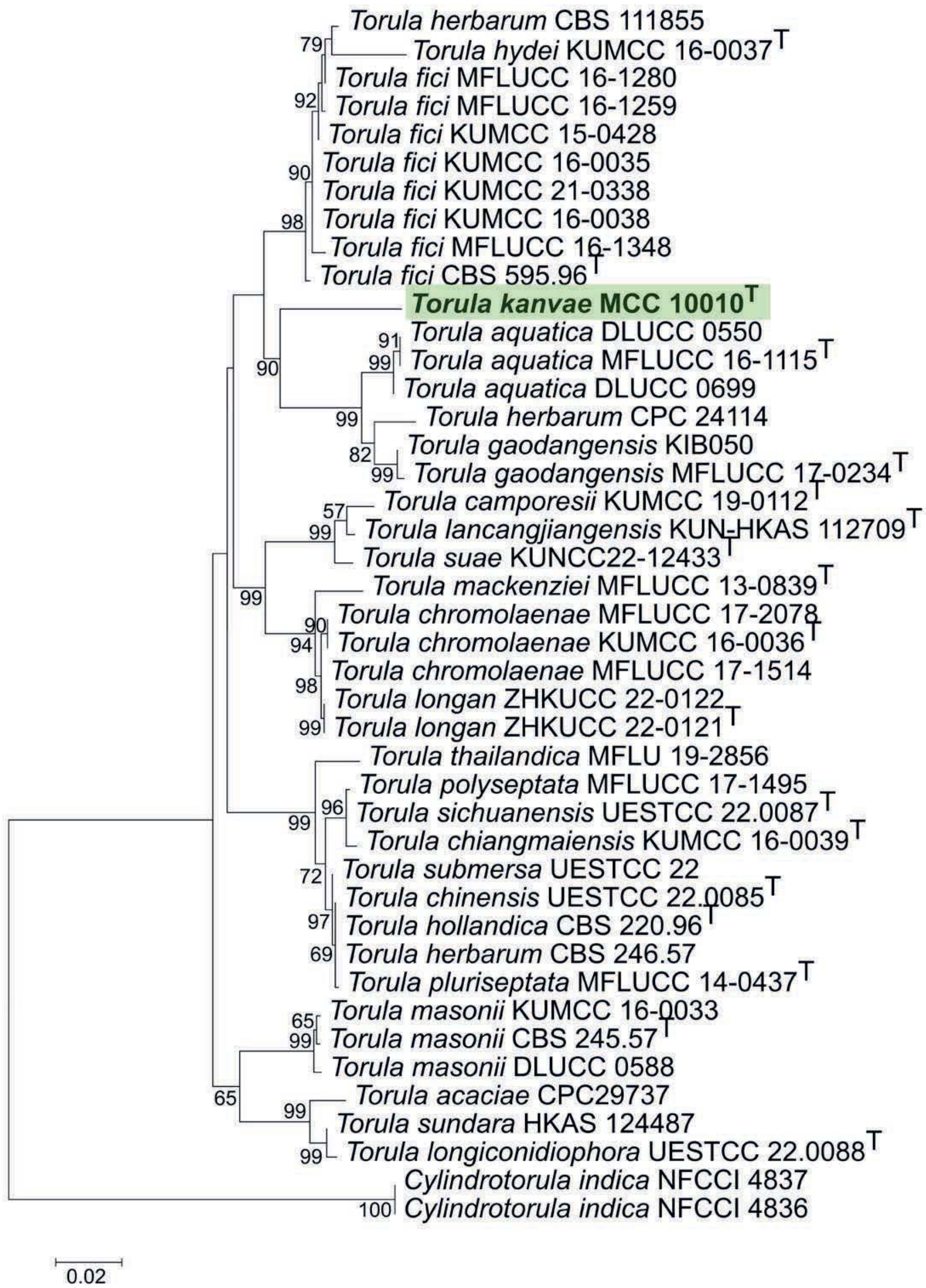
Colour illustrations: Cow dung at the type locality, Lenyadri (Chandipura), Maharashtra, India. The host (*Copris signatus*) of *Torula kanvae*; colony on PDA medium; septate hyphae of the strain MCC 10010; conidiogenous cells with conidia; catenate conidia; solitary conidia. Scale bars = 10 µm

Notes: Persoon (1795) established the genus *Torula* (*Torulaceae*), typified by *T. herbarum*. Most *Torula* species have been reported from terrestrial habitats. Nine species have been documented in freshwater habitats, and four species, *viz*. *T. masonii, T. fici, T. mackenziei*, and *T. gaodangensis*, have been found in both freshwater and terrestrial habitats (Su *et al.* 2018, Hyde *et al.* 2020, Tian *et al*. 2023). Index Fungorum (August 2024) lists more than 540 epithets, while Species Fungorum (2024) lists more than 250 records of *Torula*. Because there are not many morphological distinctions between *Torula* species, DNA sequence data have become the primary method for species identification in recent years.

Through morphological and phylogenetic analyses based on the sequences of the ITS rDNA region, D1/D2 domain of the 28S rRNA gene (LSU), SSU, *tef1*, and the *RPB2* gene, we introduce a new species within the genus *Torula* and position *Torula kanvae* near *T. auatica* (Crous *et al.* 2015a).

Based on a megablast search of the NCBI GenBank nucleotide database, the closest hits using the **ITS** sequence of *Torula kanvae* (MCC 10010) showed the highest similarity to *Torula camporesii* [strain KUMCC 19-0112, GenBank: NR_168226; Identities = 498/546 (91 %), twelve gaps (2 %)], *Torula herbarum* [strain CBS 140066, GenBank NR_132929; Identities = 501/553 (91 %), 13 gaps (2 %)], *Torula fici* [strain CBS 595, GenBank NR_171060; Identities = 456/494 (92 %), 11 gaps (2 %)] Closest hits using the **LSU** sequence of *Torula kanvae* (MCC 10010) are *Torula herbarum* [strain CBS 140066, GenBank NG_058184; Identities = 832/841 (99 %), one gap (0 %)], *Torula gaodangensis* [strain MFLUCC 17-0234, GenBank NG_059827; Identities = 831/841 (99 %), one gap (0 %)], and *Torula acaciae* [strain CPC 29737, GenBank NG_059764; Identities = 827/837 (99 %), one gap (0 %)]. The closest hits using the **SSU** sequence of *Torula kanvae* (MCC 10010) are *Torula gaodangensis* [strain MFLUCC 17-0234, GenBank NG_063641; Identities = 727/728 (99 %), no gaps], *Torula fici* [strain CBS 595.96, GenBank NG_073498, Identities = 726/728 (99 %), no gaps] and *Torula lancangjiangensis* [strain HKAS 112709, GenBank NG_078759, Identities = 724/728 (99 %), no gaps (0 %)]. Closest hits using the ***tef1*** sequence of *Torula kanvae* (MCC 10010) are *Torula camporesii* [strain KUMCC:19-0112, GenBank MN507403; Identities = 394/415 (95 %), no gaps (0 %)], *Pseudophaeosphaeria rubi* [strain MFLUCC 14-0259, GenBank MG520934; Identities = 391/413 (95 %), no gaps (0 %)], and *Torula calceiformis* [strain HKAS 125551, GenBank OQ630512; Identities = 393/416 (94 %), two gaps (0 %)]. Closest hits using the ***rpb2*** sequence of *Torula kanvae* (MCC 10010) are *Torula fici* [strain CBS 595.96, GenBank KF443395; Identities = 760/874 (87 %), one gap (0 %)], *Torula longan* [strain ZHKUCC 22-0121, GenBank OR228535; Identities = 729/866 (84 %, one gap (0 %)], and *Torula calceiformis* [strain HKAS 125551, GenBank OQ630510; Identities = 711/846 (84 %), one gap (0 %)].

Supplementary material: doi: 10.6084/m9.figshare.27179391.



The placement of *Torula kanvae* using a maximum-likelihood (ML) analysis of the combined ITS nrDNA, D1/D2 domain of the 28S nrRNA gene, SSU, *tef1,* and the *RPB2* gene sequences employing the TIM2e+I+G4 model in IQ-TREE v. 1.6.12 (Nguyen *et al.* 2015). The scale bar indicates the expected number of substitutions per site. The numbers provided on branches are frequencies with which a given branch appeared in 1 000 bootstrap replications. The tree was rooted with *Cylindrotorula indica*. The new species proposed in the present study is highlighted and indicated in bold text. Strains with a type status are indicated with a superscript T. The alignment and tree were deposited in figshare.

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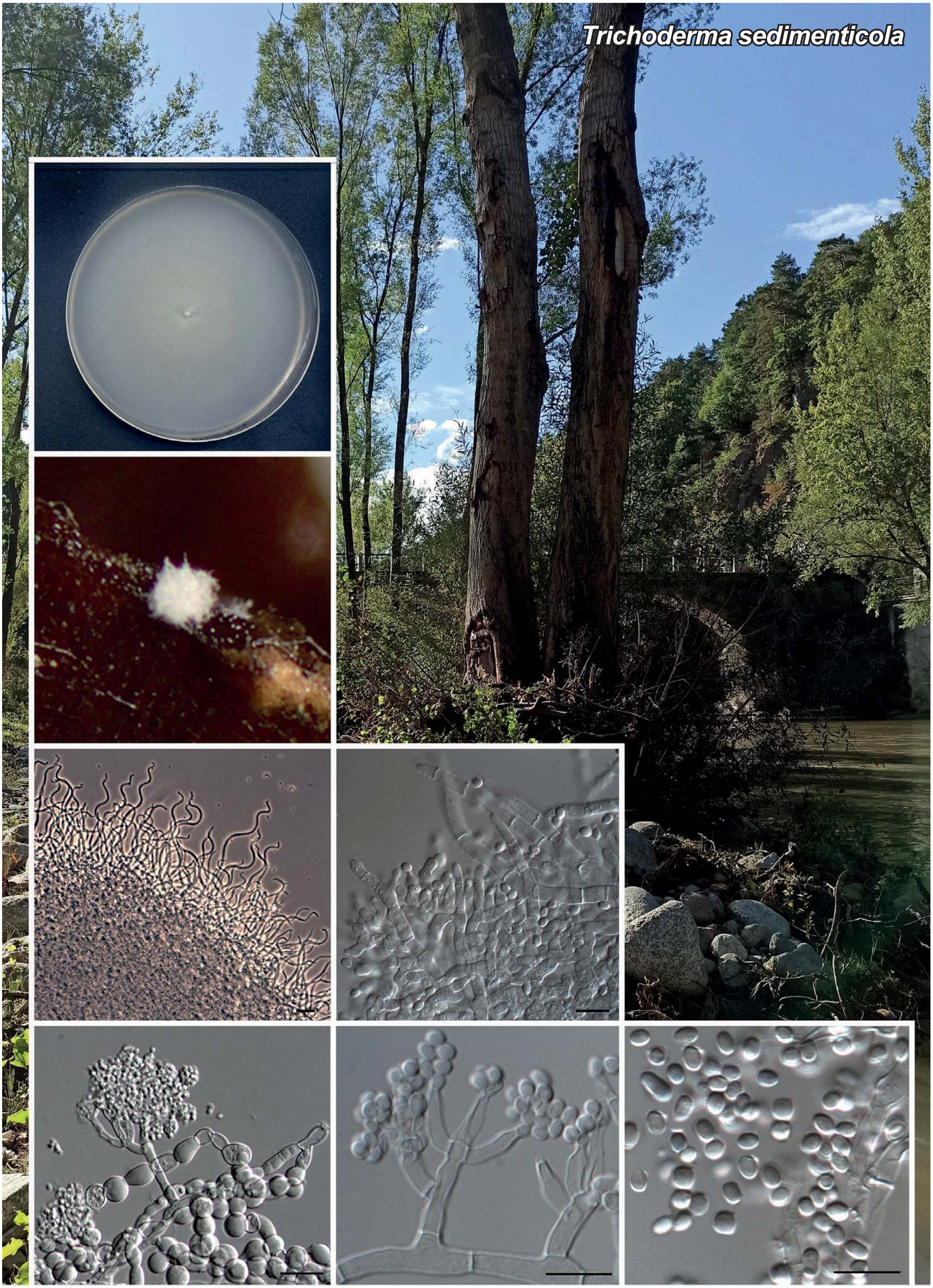

Trichoderma sedimenticola

Fungal Planet 1776

MycoBank MB 856135

Trichoderma sedimenticola Torres-Garcia, Kolarczyková, Hernández-Pérez & Gené, ***sp. nov.***

Etymology: Name refers to the substrate from which the fungus was isolated, freshwater sediments.

Classification: *Hypocreaceae*, *Hypocreales, Sordariomycetes.*

Mycelium composed of branched, hyaline, smooth-walled, septate, 2.5–5.5 µm wide hyphae. Conidiation only on potato carrot agar (PCA) with sterile plant material at 25 °C, developing conidiophores aggregated in tufts or pustules, up to 3 mm diam, surrounded by unbranched, hyaline, smooth or asperulate, sinuose, septate, 3–4.5 µm wide, sterile hyphae. *Conidiophores* irregularly branched in a somewhat dendriform structure, with branches at right angles or slightly inclined upward; branches with phialides born solitary and lateral on the main axis, or in small terminal whorls of 2–3 divergent phialides. *Phialides* smooth, hyaline, lageniform or ampulliform, straight or curved, 5.5–11(–15.5) × 1.5–3 µm. *Conidia* aseptate, smooth, hyaline to subhyaline, globose, subglobose to ellipsoidal, 2–4.5 × 1.5–2.5 µm. *Chlamydospores* abundant, commonly in chains composed of smooth, thick-walled, hyaline, globose to subglobose or barrel-shaped cells, 5.5–13 × 5.5–10.5 µm. *Sexual morph* not observed.

Culture characteristics at 25 °C after 1 wk: Colonies on potato dextrose agar (PDA), reaching 85 mm diam, cottony, flattened, yellowish white (4A2) (Kornerup & Wanscher 1978) at centre, colourless towards periphery, margin entire, sporulation absent; reverse yellowish grey (3B2) at centre. On carrot agar (PCA), reaching 80 mm diam, slightly velvety, flattened, yellowish white (1A2) at centre, white (1A1) towards periphery, margin slightly fimbriate, sporulation absent; reverse yellowish white (1A2) at centre. On synthetic nutrient poor agar (SNA), reaching 77 mm diam, near glabrous, yellowish white (1A2) at centre, colourless towards periphery, margin slightly fimbriate, sporulation absent; reverse yellowish white (1A2) at centre. On cornmeal agar (CMA), reaching 81 mm diam, flattened, with immersed mycelium at centre to semi-immersed towards periphery, white (1A1), sporulation absent; reverse colourless. Diffusible pigment absent in all culture media tested.

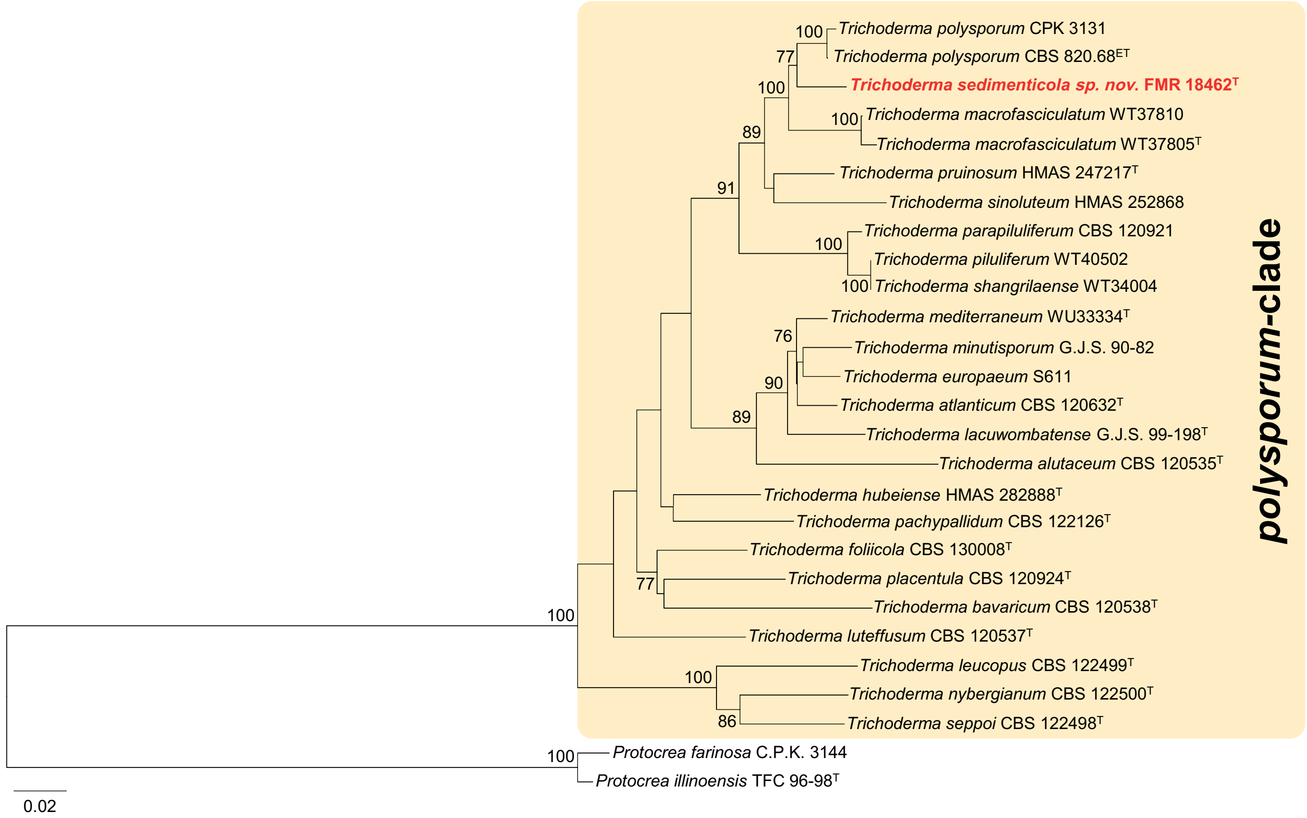
Cardinal temperatures for growth: Maximum 30 °C, optimum 25 °C, minimum 5 °C.

Colour illustrations: Ter River, Sant Joan de les Abadesses, Catalonia, Spain. Colony on PCA after 7 d at 25 °C; pustules, conidiophores, phialides, chlamydospores and conidia after 7–14 d at 25 °C. Scale bars = 10 µm (microscopic structures in PCA).

Typus: **Spain**, Catalonia, Sant Joan de les Abadesses, Ter River, isolated on dichloran rose bengal chloramphenicol agar, from fluvial sediments, Sep. 2020, *D. Torres-Garcia* & *J. Gené* (**holotype** FMR H-18462, culture ex-type FMR 18462, ITS, LSU, *rpb2* and *tef1-α* sequences GenBank OQ271407, OQ271416, OQ291215, and OQ298916).

Notes: *Trichoderma sedimenticola* is included in the well-defined *polysporum*-clade (Jaklitsch & Voglmayr 2015). Regarding our multi-locus phylogenetic analyses, the novel species formed a single branch into a fully supported clade placed distant from the representatives of *T. polysporum* and *T. macrofasciculatum*. All three species are morphologically similar and characterized by forming large and white fertile pustules in culture (Lu *et al.* 2004, Zhang *et al*. 2022). However, the phialides and conidia in *T. sedimenticola* tend to be larger than those of its counterparts [phialides up to 11(–15.5) µm long *vs.* 7.8(–8.8) µm in *T. macrofasciculatum*, and 6.7(–13.5) µm in *T. polysporum*; conidia 2–4.5 µm *vs.* 2.6–3.6 µm in *T. macrofascitulatum*, and 1.2–3.5(–5.5) µm in *T. polysporum*] (Lu *et al*. 2004, Zhang *et al*. 2022). Moreover, *T. macrofasciculatum* also differs in the absence of chlamydospores and sterile hyphae associated with the pustules (Zhang *et al.* 2022). *Trichoderma sedimenticola* and *T. polysporum* can also be distinguished by the arrangement and the morphology of their chlamydospores; in the novel species they are in chains, with cells smaller (5.5–13 × 5.5–10.5 µm) and smooth, while in *T. polysporum* are solitary, with cells larger (3–23 × 2.8–16 µm) and smooth to spinulose (Lu *et al*. 2004). Of note is that *T. polysporum* produces the sexual morph in nature (Lu *et al*. 2004), which has not been observed for the other two species.

Based on a megablast search of NCBIs GenBank database, the ***rpb2*** sequence of *T. sedimenticola* showed a similarity of 97.72 % (770/778) and 97.27 % (821/844) with sequences of *T. polysporum* strains*,* CBS 820.68 (GenBank DQ87238) and CPK 3131 (GenBank FJ860558), respectively, and of 97.16 % (820/844) with the sequences of *T. macrofasciculatum* strains, WT 37810 (GenBank MH287494) and WT 37805 (GenBank MH287493). Whereas the similarity using ***tef1-α*** sequences was 94.95 % (339/357) and 91.35 % (264/289) with the two sequences (GenBank AF400989, GenBank FJ860661) of the *T. polysporum* strains mentioned above, and a similarity of 88.78 % (261/294) and 87.41 % (257/294) with the two sequences of *T. macrofasciculatum* strains*,* WT 37810 (GenBank MH287510) and WT 37805 (GenBank MH287509), respectively. The similarity of the **ITS** sequences ranged from 97.63 % (577/591) with *T. polysporum* (CBS 820.68; GenBank MH859230) to 98.81 % (581/588) and 98.80 % (578/585) with those of *T. macrofasciculatum* strains, WT 37810 (GenBank MH287488) and WT 37805 (GenBank MH287487), respectively.



Phylogenetic tree based on Maximum likelihood analysis obtained by RAxML using the combined ITS, *rpb2,* and *tef1-α* sequences of *Trichoderma* species belonging to the *polysporum*-clade. Bootstrap support values above 70 % are indicated on the nodes. The alignment included 2 905 bp and was performed using Kimura 2-parameter with Gamma distribution and Invariant sites (K2+G+I) as the best nucleotide substitution model. The tree was rooted with *Protocrea illinoensis* TFC 96-98 and *Protocrea farinosa* CPK 3144. Both the alignment and the tree were 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 and ET denotes ex-type and epitype strains.

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Ustilaginoidea cookiorum

Fungal Planet 1777

MycoBank MB 855550

Ustilaginoidea cookiorum Y.P. Tan & R.G. Shivas, ***sp. nov.***

Etymology: Named after Anita and Keith Cook, who established the Iron Range Research Station where this fungus was found.

Classification: *Clavicipitaceae*, *Hypocreales*, *Sordariomycetes*.

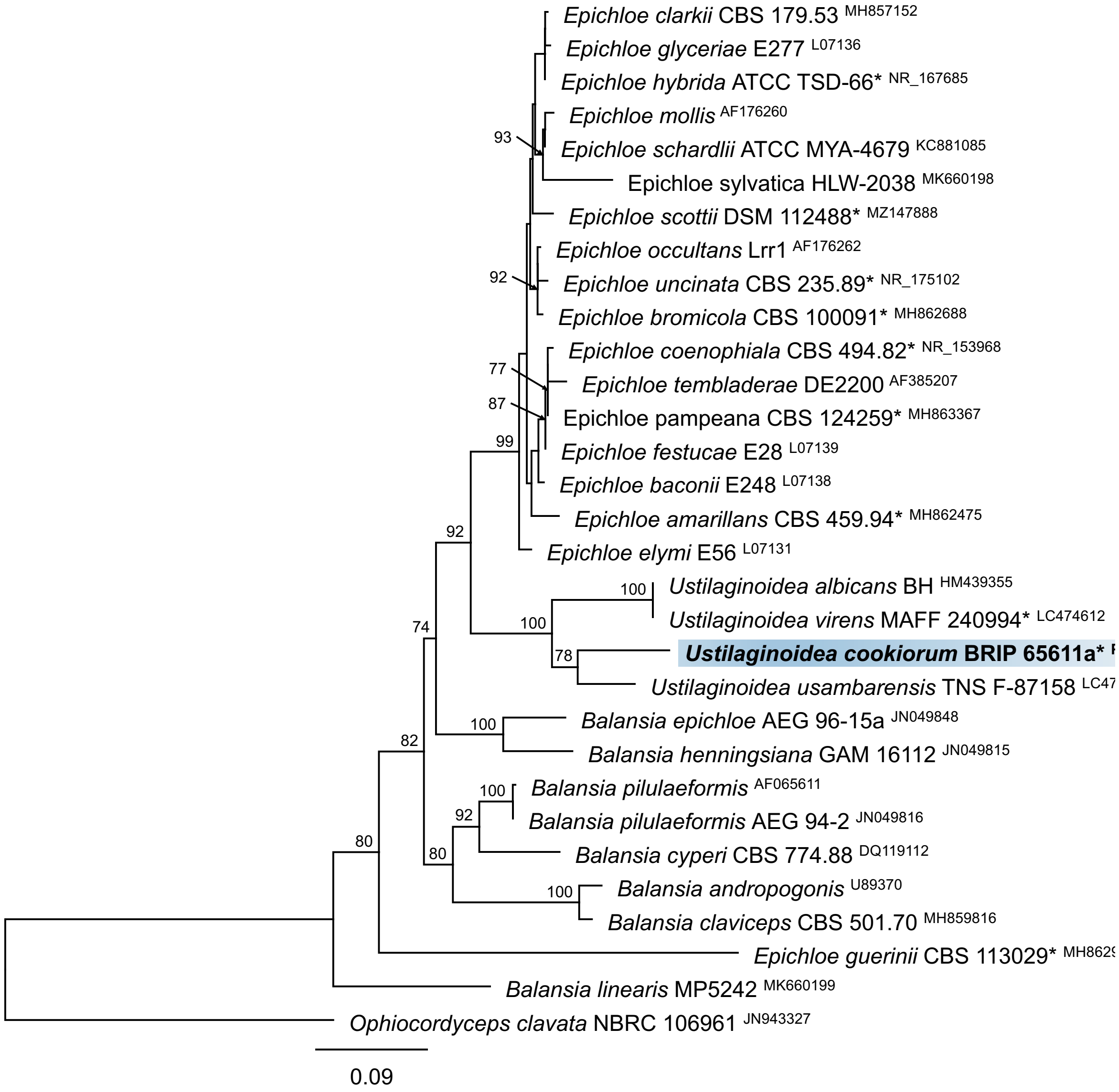
Stromata composed of masses of powdery conidia mixed with irregular extracellular orange particles replace seeds of *Scleria levis*, each stroma comprised of three layers - a white central part of compact *textura prismatica* with hyaline septate hyphae 3–5 µm wide, a luteus middle fibrous layer with abundant subhyaline to pale yellow conidiogenous cells and immature conidia, and an outer layer initially yellow becoming olivaceous green and dark brown to black at maturity. *Conidiophores* reduced to conidiogenous cells, intercalary, hyaline, monoblastic and polyblastic, with inconspicuous denticles, scars inconspicuous to slightly raised and apically truncate. *Conidia* globose to subglobose, olivaceous brown, 7–9 µm diam; wall irregularly and densely verruculose.

Typus: **Australia**, Queensland, Iron Range, on *Scleria levis* (*Cyperaceae*), 1 Apr. 2017, *R.G. Shivas*, *M.D.E. Shivas*, *A. Cook & K. Cook* (**holotype** BRIP 65611a; ITS, LSU and SSU sequences GenBank PQ145668, PQ145667, and PQ145666).

Notes: There are 23 species of *Ustilaginoidea*, most of which are pathogens of seeds of grasses (*Poaceae*). Two species have been reported as pathogens of sedges (*Cyperaceae*), namely *U. dichromenae* [type on *Rhynchospora* (*Dichromena*) *pubera*, Brazil] (Hennings 1904) and *U. flavonigrescens* (as *Ustilago flavonigrescens*, type on *Scleria* sp., Cuba) (Berkeley 1868). *Ustilaginoidea cookiorum* has spores with a larger diameter than given in the original diagnoses of *U. dichromenae* (5–7 µm) and *U. flavonigrescens* (0.00028 inch = 7 µm). Zhang *et al*. (2014) found phylogenetic evidence that the plant pathogenic *Ustilaginoidea* was closely related to the entomopathogenic genus *Metarrhizium*, indicating a host jump across kingdoms. The species boundaries in *Ustilaginoidea* have yet to be comprehensively challenged by sequence data, although some data are available *e.g. U. virens* (Bashyal *et al.* 2004).

Based on a blastn search of the NCBI GenBank nucleotide database, the closest relevant hits with the **LSU** sequence are *Epichloe uncinata* [strain CBS 235.89, GenBank MH873858; Identities = 853/879 (97 %), one gap (xxx %)], *U. dichromenae* [specimen voucher MRL IB9228, GenBank JQ257010; Identities = 860/881 (98 %), three gaps (xxx %)], and *U. usambarensis* [specimen voucher TNS:F-87158, GenBank LC474613; Identities = 841/865 (97 %), two gaps (xxx %)]. The closest relevant hits with the **ITS** region are *E. brachyelytri* [strain E1124, GenBank CP097977; Identities = 598/679 (88 %), 30 gaps (4 %)], *E. gansuensis* [strain e7080, GenBank CP098284; Identities = 602/683 (88 %), 38 gaps (5 %)], and *E. uncinata* [strain NBRC 32642, GenBank AB102783; Identities = 599/679 (88 %), 32 gaps (4 %)]. The closest relevant hits with the **SSU** sequence are *Cordyceps ochraceostromata* [strain ARS 5691; GenBank AY245660; Identities 1 027/1 037 (99%), two gaps (0 %)], *C. roseostromata* [strain ARS 4870; GenBank AY245662; Identities 1 027/1 037 (99%), two gaps (0 %)], *Keithomyces acicularis* [ex-type strain JCM 33284; GenBank NG_067656; Identities 1 027/1 037 (99 %), two gaps (0 %)], *K. carneus* [ex-type culture CBS 239.32; GenBank MH855304; Identities 1 027/1 037 (99%), two gaps (0 %)], *Metarhizium viride* [ex-type strain CBS 248.65; GenBank NG_062608; Identities 1 027/1 037 (99%), two gaps (0 %)], *M. granulomatis* [ex-type strain UAMH 11028; GenBank NG_064956; Identities 1 027/1 037 (99%), two gaps (0 %)], *Tolypocladium inflatum* [ex-type strain NBRC 31668; GenBank AB103381; Identities 1 027/1 037 (99%), two gaps (0 %)], and *U. virens* [epitype MAFF 240994; GenBank LC474618; Identities 1 029/1 038 (99%), three gaps (0 %)].

Colour illustrations. *Ustilaginoidea cookiorum* on *Scleria levis* at Iron Range (background); sori; sorus in section; soral matrix; extacellular particles; conidiogenous cells and immature conidia; mature conidia. Scale bars: sori and sorus section = 1 mm; all others = 10 µm.



Phylogenetic tree of selected *Clavicipitaceae* species based on maximum likelihood analysis of the ITS region. Analyses were performed on the IQ-TREE webserver (Trifinopoulos *et al.* 2016) based on the GTR substitution model with gamma-distribution rate variation (1 000 bootstrap replicates). Bootstrap support values greater than 70 % are given at the nodes. *Ophiocordyceps clavata* (strain NBRC 106961) was used as the outgroup. GenBank accession numbers are indicated (superscript ITS). Novel taxon is indicated in **bold**. Ex-type strains are indicated with asterisks (*). The alignment and phylogeny are publicly available in Zenodo (doi: 10.5281/zenodo.13231703).

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Verrucohypha endophytica

Fungal Planet 1778 MycoBank MB 854563

Verrucohypha J.A. Oliveira & O.L. Pereira, ***gen. nov.***

Etymology: The name refers to the verruculose-walled hyphae produced by the fungus.

Classification: *Latoruaceae*, *Pleosporales*, *Dothideomycetes.*

Dark septate endophyte (DSE) isolated on culture media from surface-sterilized healthy roots of living plants. *Mycelium* immersed to superficial, composed of branched, septate, hyaline to dark brown, predominantly dark brown, thin-walled to verruculose *hyphae*, with a predominance of verruculose hyphae in older cultures, brown bubbles of mucilage associated to hyphae laterally commonly observed.

Type species: *Verrucohypha endophytica* J. A. Oliveira & O. L. Pereira

MycoBank MB 854564

Verrucohypha endophytica J.A. Oliveira & O.L. Pereira, ***sp. nov.***

Etymology: The epithet refers to the endophytic habitat associated with macaw palm roots.

Dark septate endophyte (DSE) isolated on culture media from surface-sterilised roots of macaw palm. *Mycelium* immersed to superficial, composed of branched, septate, hyaline to dark brown, predominantly dark brown, thin-walled to verruculose *hyphae*, 2–3 µm wide of thin hyphae, and 2.5–5 µm wide of verruculose hyphae, with predominance of verruculose hyphae in older cultures, sometimes brown bubbles of mucilage associated to hyphae laterally up to 8 µm wide are formed.

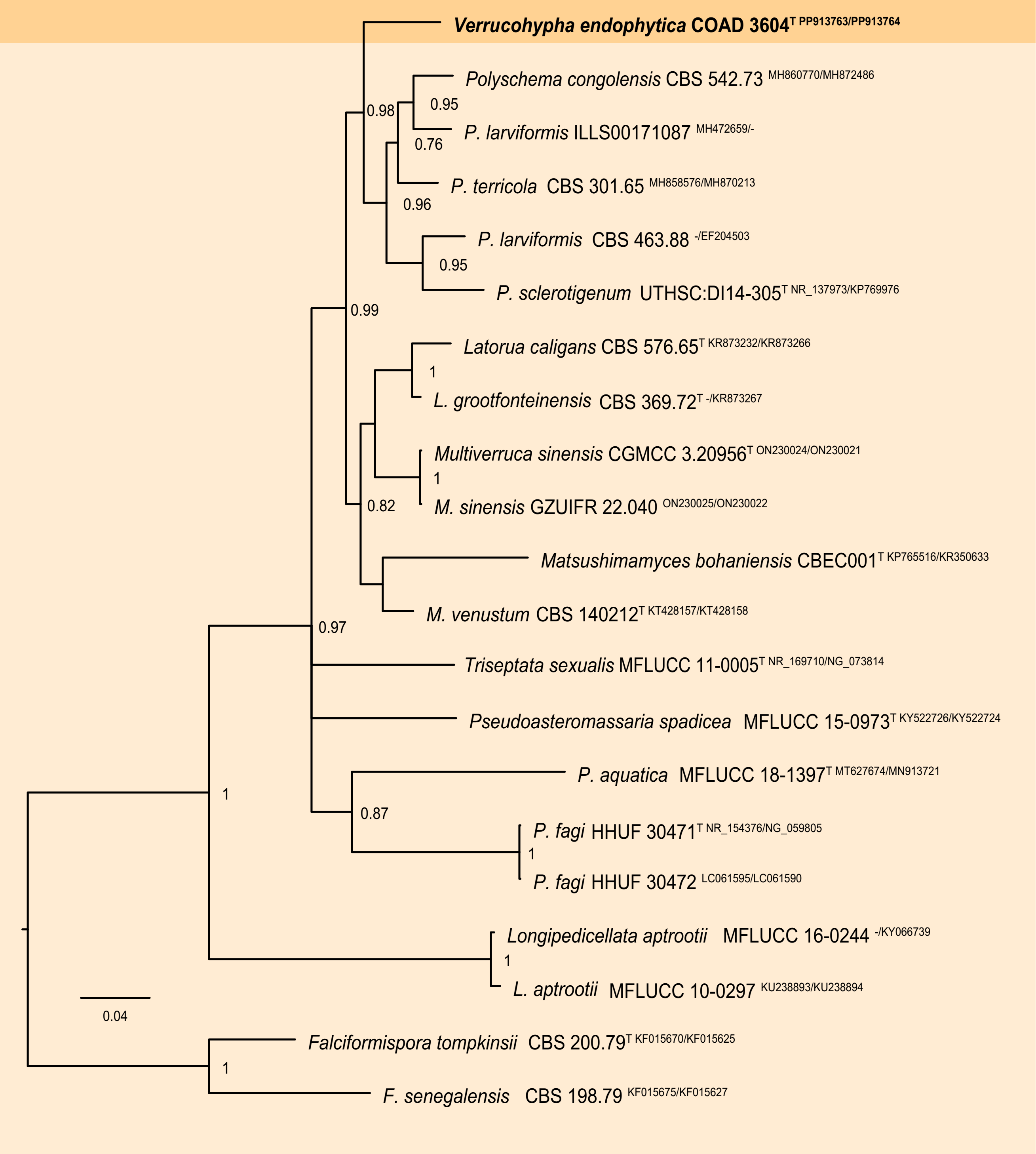
Culture characteristics: Colonies on potato dextrose agar (PDA) umbonate with entire edge, aerial mycelium moderate, cottony, dense, fawn colour in the centre to smoke grey, colourless on the periphery surface, umber on reverse (Rayner 1970), reaching 27 mm diam after 2 wk at 25 °C with a photoperiod of 12 h. Colonies on malt extract agar (MEA) raised with entire edge, aerial mycelium moderate, cottony, dense, vinaceus buff colour in the centre to smoke grey, colourless on the periphery surface, reverse dark brick, reaching 27 mm diam after 2 wk at 25 °C with a photoperiod of 12 h. Colonies on oatmeal agar (OA) flat with entire edge, aerial mycelium moderate, cottony, dense, greyish sepia colour in the centre to smoke grey, colourless periphery surface, reverse brown vinaceous, reaching 20 mm diam after 2 wk at 25 °C with a photoperiod of 12 h. Colonies on synthetic nutrient-poor agar (SNA) flat with fimbriate edge, aerial mycelium scarce to moderate, greyish sepia colour in the centre to olivaceous buff periphery surface, reverse iron grey, reaching 23 mm diam after 2 wk at 25 °C with a photoperiod of 12 h. Cultures sterile.

Colour illustrations: Macaw palm growing in an experimental field located at the João Pinheiro, Minas Gerais state, Brazil (photo credit P. Hilst). Colonies (top to bottom on PDA, MEA, OA, and SNA); verruculose-walled hyphae with bubbles of mucilage on MEA; verruculose-walled hyphae on MEA; verruculose-walled hyphae on MEA; thin-walled hyphae on OA. Scale bars = 20 µm.

Typus: **Brazil**, Minas Gerais, João Pinheiro, 17°59'18.597"S, 45°57'30.597"W, isolated from healthy roots of *Acrocomia aculeata* (*Arecaceae*), Dec. 2021, *M.N.S. Santos* (**holotype** VIC 49511, culture ex-type COAD 3604; ITS and LSU sequences GenBank PP913763 and PP913764).

Notes: The family *Latoruaceae* established by Crous *et al*. (2015a) presently includes six formally described genera associated with plant leaves, soil, decaying wood material, and human clinical specimens (Ariyawansa *et al*. 2015, Crous *et al*. 2015b, Wang *et al*. 2023). To our knowledge, this is the first report on the family as root endophytes. The morphological characteristic of *V. endophytica* is similar to other genera belonging to *Latoruaceae*, with verruculose hyphae and a predominance of dark brown colour. *Verrucohypha endophytica* is a root endophyte with dark septate hyphae, which refers to dark septate endophytes (DSE) and the first DSE report in *Latoruaceae*. *Verrucohypha endophytica* formed a new and distinct lineage closest to the clade formed by the genus *Polyschema*. Compared to the type species *P. terricola*, *V. endophytica* has 88 % identity and 62 polymorphisms including gaps for the ITS region, and 96 % identity with LSU and 34 polymorphisms including gaps. *Acrocomia aculeata* is a native Brazilian palm of great economic importance with an associated microbiota that is still poorly described.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had the highest similarity to 'uncultured *Pleosporales'* isolate from the soil in Republic of Benin (Africa) [clone d6a48ffd, GenBank HG996244.1; Identities = 589/610 (97 %), 11 gaps (1 %)], 'uncultured fungus' isolate from soil [ASV_776, GenBank LR994093.1; Identities = 587/610 (96 %), nine gaps (1 %)], and 'uncultured fungus' isolate from soil [ASV_732, GenBank LR994049.1; Identities = 582/615 (95 %), sixteen gaps (2 %)]. Closest hits using the **LSU** sequence are 'uncultured fungus' from soil [ASV_776, GenBank LR994093.1; Identities = 944/955 (99 %), two gaps (0 %)], 'uncultured *Pleosporales'* from soil [clone d6a48ffd, GenBank HG996244.1; Identities = 942/954 (99 %), three gaps (0 %)], and 'uncultured fungus' from soil [ASV_732, GenBank LR994049.1; Identities = 943/957 (99 %), three gaps (0 %)].



Bayesian inference tree obtained by phylogenetic analyses of ITS sequences conducted in MrBayes v. 3.2.7a on XSEDE in the CIPRES science gateway. Bayesian posterior probability values > 0.70 are indicated at the nodes. Strains with an ex-type status are indicated with a superscript 'T'. The new species is shown in **bold** face. *Falciformispora tompkinsii* (CBS 200.79) and *Falciformispora tompkinsii* (CBS 198.79) were used as outgroups. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.26099149.v1).

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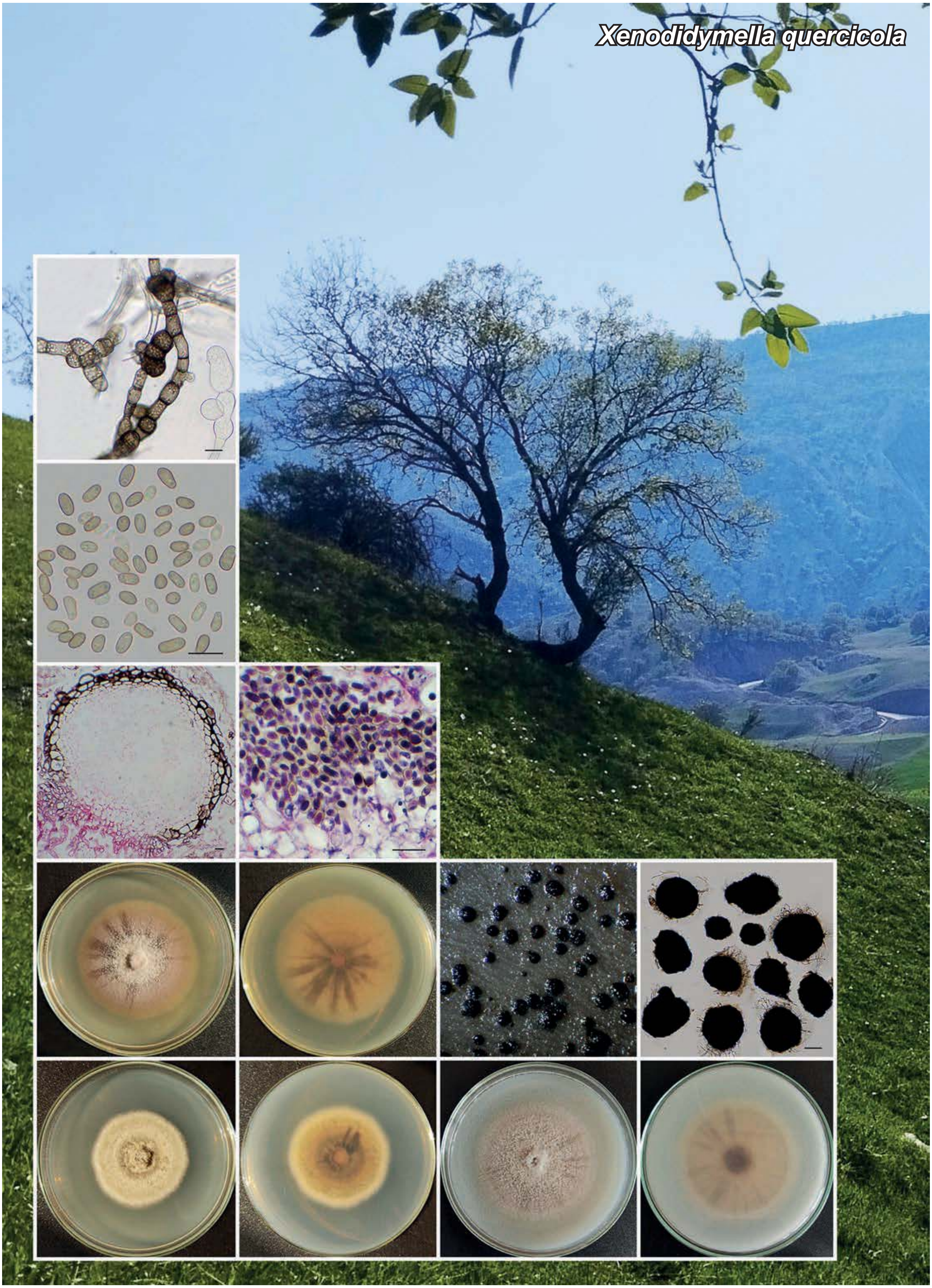

Xenodidymella quercicola

Fungal Planet 1779

MycoBank MB 854800

Xenodidymella quercicola Eisvand & M. Mehrabi-Koushki, ***sp. nov.***

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

Classification: *Didymellaceae*, *Pleosporales*, *Dothideomycetes*.

Morphology on oatmeal agar (OA): *Conidiomata* pycnidial, solitary or aggregated in small groups, semi-immersed to immersed in the agar, globose, subglobose or ellipsoidal, ostiolate or non-ostiolate, occasionally with a short neck, non-papilate, dark brown or black, glabrous or with some hyphal outgrowths, 81–260(–375) × 75–235(–353) µm, 95 % confidence limits = 162–183 × 131–151 µm, (av. ± SD = 172 ± 52.5 × 141 ± 51 µm, n = 100). *Pycnidial wall* pseudoparenchymatous, 3–12 layered, composed of more or less oblong to isodiametric cells, outer layer pigmented. *Conidiogenous cells* phialidic, hyaline, smooth, ampulliform or doliiform, (2.7–)3.7–5.8(–7.5) × (2.2–)2.7–4.8(–6.2) µm, 95 % confidence limits = 4.5–5.2 × 3.3–4 µm, (av. ± SD = 4.9 ± 1 × 3.7 ± 0.8 µm, n = 30). *Conidia* ellipsoidal to sub-cylindrical, rarely sub-globose, straight or very slightly curved, smooth- and thin-walled, aseptate, guttulate, rounded at both ends, pale brown, 3.5–8.8(–11.3) × 2.2–5.3(–6.6) µm, 95 % confidence limits = 5.8–6 × 3.4–3.6 µm, (av. ± SD = 5.9 ± 1 × 3.5 ± 0.62 µm, n = 240). *Conidial matrix* whitish to buff. *Chlamydospores* unicellular or multicellular, solitary or in chain, intercalary or terminal, smooth, grey, pale brown to brown, variable in shape and size.

Culture characteristics: Colonies on oatmeal agar (OA) reaching 59 mm diam after 9 d of incubation at 25 ± 0.5 °C, and 54 mm diam at 30 ± 0.5 °C, circular with filiform margin, pinkish white, floccose; reverse pinkish grey with paler margin and brown sectors. Colonies on potato dextrose agar (PDA) reaching 43 mm diam after 9 d of incubation at 25 ± 0.5 °C, and 50 mm diam at 30 ± 0.5 °C, circular with filiform margin, pinkish to pale green, floccose, reverse greenish to grey with pale brown centre and lighter margin. Colonies on malt extract agar (MEA) reaching 55 mm diam after 9 d of incubation at 25 ± 0.5 °C, and 47 mm diam at 30 ± 0.5 °C, circular with regular margin, pale rosy pink with cream centre and brown sectors, floccose; cream to pink.

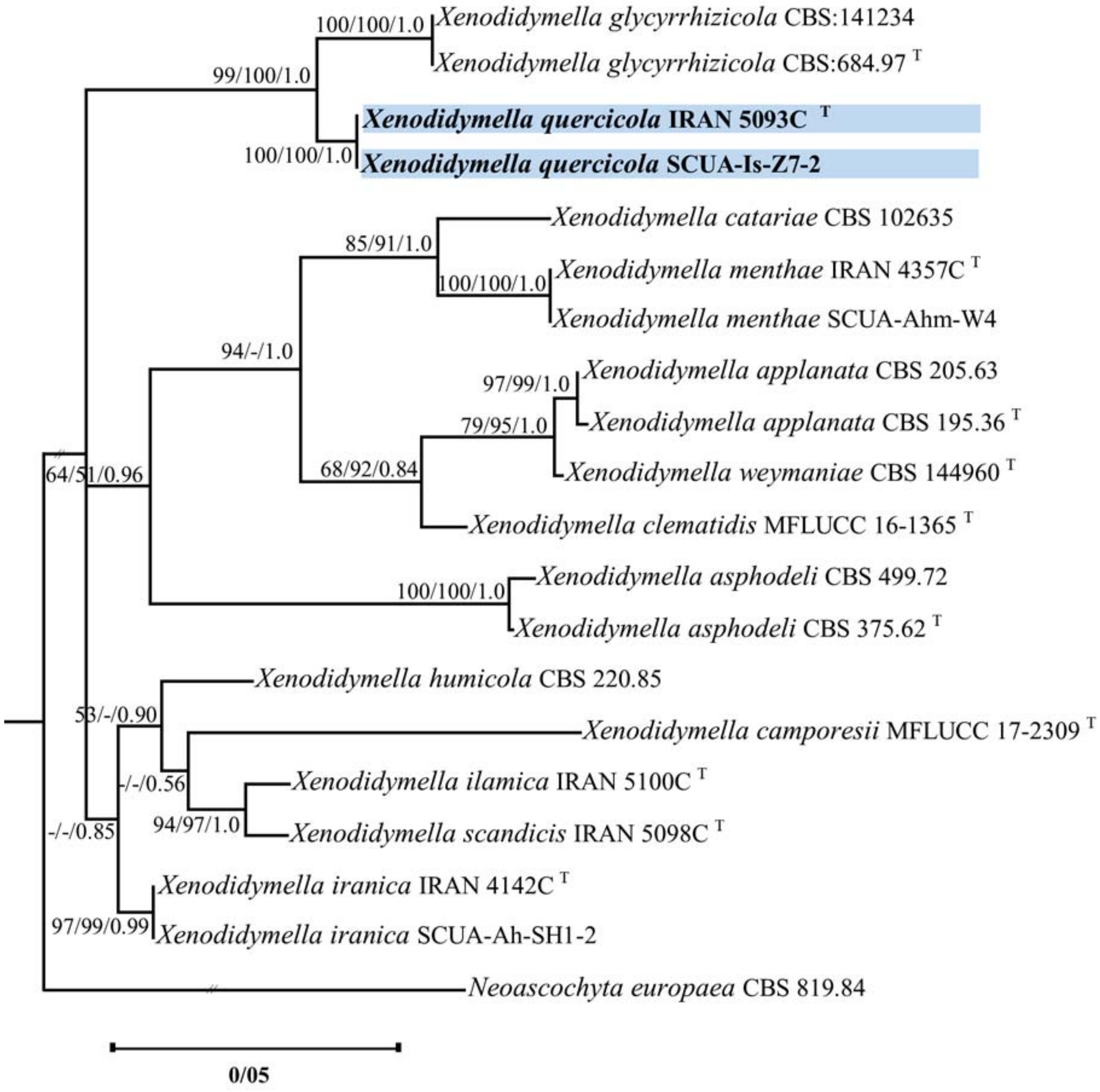
Colour illustrations: *Quercus brantii* in the Zagros mountain forest steppe of Dehdez, Iran. From bottom to top: First row: 9-d-old colonies on PDA (left) and OA (right) in top and reverse sides, respectively; Second row: 9-d-old colonies on MEA in top and reverse sides and pycnidia; Third row: section of pycnidia and conidiogenous cells; Fourth row: conidia; Fifth row: chlamydospores. Scale bars: pycnidia = 70 mm; all others = 10 µm.

Typus: **Iran**, Khuzestan Province, Dehdez, isolated from leaf spot of *Quercus brantii* (*Fagaceae*), Apr. 2022, *P. Eisvand* (**holotype** IRAN 18533F, culture ex-type IRAN 5093C = SCUA-Is-Z7; ITS, *tub2* and *rpb2* sequences GenBank PQ037109, PQ037570 and PQ037568).

Additional material examined: **Iran**, Khuzestan Province, Dehdez, isolated from leaf spot of *Q. brantii*, Apr. 2022, *P. Eisvand*, culture SCUA-Is-Z7-2; ITS, *tub2* and *rpb2* sequences GenBank PQ037110, PQ037571 and PQ037569.

Notes: In BLASTn search, the closest match for the ITS, *tub2* and *rpb2* sequences of *Xenodidymella quercicola* IRAN 5093C was *Xenodidymella glycyrrhizicola* strain CBS 684.97 (ITS: GenBank MN973606.1, identities = 99 %; *tub2*: GenBank MT005717.1, identities = 98%; rpb2: GenBank MT018283.1, identities = 96 %). *Xenodidymella quercicola* is phylogenetically closely related to species *X. glycyrrhizicola* (MLBS 99 %, MPBS 100 %, BPP 1.0). This new species and the ex-type strain of *X. glycyrrhizicola* (CBS 684.97) showed 4 bp difference (1 %) across 410 nucleotides of the ITS region, 6 bp difference (2.5 %) across 240 nucleotides of the *tub2* region, and 21 bp difference (3.8 %) across 552 nucleotides of the *rpb2* region. Morphologically, *X. quercicola* can be distinguished from *X. glycyrrhizicola* by more elongated conidia and smaller non-papilate pycnidia [81–260(–375) × 75–235(–353) *vs* 270–465 × 215–340 µm; Hou *et al.* 2020]. *Xenodidymella glycyrrhizicola* was introduced with the description of isolates obtained from *Glycyrrhiza* spp., causing leaf spot on *Glycyrrhiza* in Iran and New Zealand (Hou *et al.* 2020), while the strains of *X. quercicola* were isolated from a different host, *Quercus brantii*.

Supplementary material: doi: 10.6084/m9.figshare.27212565 (Table).



RAxML phylogenetic tree constructed from a maximum likelihood analysis based on the combined ITS, *tub2* and *rpb2* sequences of *Xenodidymella* species. The tree was rooted to *Neoascochyta europaea* strain CBS 819.84. Bootstrap support values (MLBS, MPBS, respectively) obtained in maximum likelihood (ML, GTR + G + I) and maximum parsimony (MP) analyses > 50% and Bayesian posterior probability values (BPP) ≥ 0.5 are shown at the nodes, respectively. (software used: ML: raxmlGUI 2.0 beta, Edler *et al.* 2019; MP: MEGA v. 7, Tamura *et al.* 2013; BI: jModelTest 2 and MrBayes v. 3.2.6, Darriba *et al.* 2012, Ronquist *et al.* 2012). Taxa obtained newly from Iran are indicated in **bold**.

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Xylaria guardiae

Fungal Planet 1780

MycoBank MB 855627

Xylaria guardiae B. Raphael, M.J. Lynch, E.J. Whiteside & Dearnaley, ***sp. nov.***

Etymology: Named after F.E. Guard, a friend and mentor, who shared extensive knowledge of the property from where this species was collected.

Classification: *Xylariaceae*, *Xylariales*, *Sordariomycetes*.

Conidiomata solitary, upright or occasionally prostrate, cylindrical, unbranched, 0.5–1.5 cm long × 1–2 mm diam, surface roughened, externally black with white interior, swollen and hairy at the base. *Conidiophores* formed directly on hyphae, mostly reduced to conidiogenous cells. *Conidiogenous cells* hyaline, smooth, (4.4–)6.5–7.5(–12.34) × (3.8–)4.5–5.5(–6.1) µm, with denticular cells (1.2–)1.5–1.8(–2.1) × (1.0–)1.2–1.3(–1.6) µm. *Conidia* solitary, aseptate, hyaline to pale brown, smooth, and ovoid to obclavate, (5.8–)6–7(–7.6) × (3.3–)3.5–4.1(–5) µm. *Sexual morph* not observed.

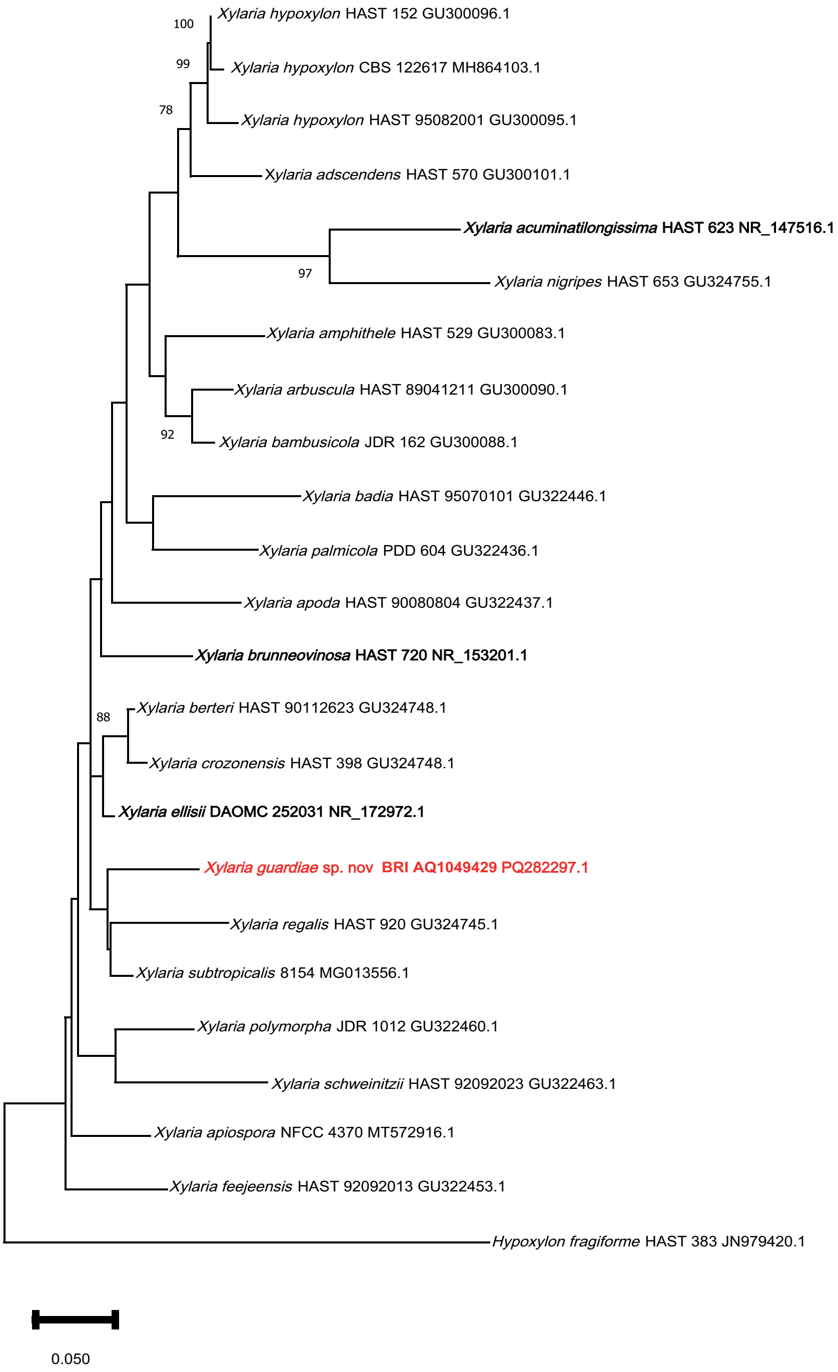
Culture characteristics: Colonies are textured, spreading, with smooth circular margins; abundant aerial hyphae; initially white in colour, developing dark sheath from 4 wk; reaching 85 mm diam after 2 wk dark incubation at 22 °C on potato dextrose agar (PDA).

Typus: **Australia**, Queensland, Dilkusha Nature Refuge, 26°44’13’’S, 152°53’31’’E, 3 m a.s.l., isolated as an endophyte from healthy leaves of *Macaranga tanarius* (*Euphorbiaceae*), 6 Jul. 2022, *B. Raphael BR001*, (**holotype** stroma lodged in herbarium BRI AQ1049429, culture ex-type BRI AQ1049429 = MT2.8; ITS and LSU sequences GenBank PQ282297 and PQ282298).

Colour illustrations: *Macaranga tanarius* growing at Dilkusha Nature Refuge, Maleny, Queensland, Australia. Colony of *Xylaria guardiae* on PDA; stroma of *X. guardiae* growing from sterilised grapevine twigs on synthetic-nutrient poor agar; conidiogenous cells with denticles; conidia. Scale bars: colony = 1 cm; stroma = 5 mm; all others = 5 µm.

Notes: *Xylaria guardiae* was collected as an endophyte from the foliage of *Macaranga tanarius*. *Xylaria* spp. are characterised as cosmopolitan, wood decaying fungi that develop “club-shaped” or “finger-like” stroma. *Xylaria guardiae* produces a “finger-like” stroma, similar to that of *X. polymorpha* (Hsieh *et al.* 2010), although stromata of *X. guardiae* are narrower. Blast2 searches aligning the ITS of *X. guardiae* with the sequence of *X. polymorpha* (GenBank MH860591.1) resulted in a similarity index of 92.13 % GenBank MH860591.1 Identities = 351/381, 5/381 gaps (1 %).

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Xylaria ellisii* [strain DAOMC 252031, GenBank NR_172972.1; Identities = 363/379 (95.78 %), three gaps (0 %)], *Xylaria subtropicalis* [strain 8154, GenBank MG013556.1; Identities = 361/380 (95 %), three (0 %)], and *Xylaria apiospora* [strain NFCC-4370, GenBank MT572916.1; Identities = 352/372 (94.62 %), two gaps (0 %)]. Closest hits using the **LSU** sequence are *Astrocystis bambusicola* [MFLUCC 17-0127, GenBank NG_066199.1; Identities = 717/729 (98.35 %), no gaps], *Hypocropa zeae* [MFLU 18-0809, GenBank NG_081508.1; Identities = 717/729 (98.35 %), no gaps], and *Wawelia amuloasca* [LE F-334908, GenBank OP687953.1; Identities = 713/729 (97.81 %), no gaps]. A range of standard *RPB2* and beta-tubulin primers and PCR cycling parameters for *Xylariaceae* were trialled. However, none were successful in product amplification.



Maximum Likelihood tree produced from an analysis of nrDNA ITS sequences from *X. guardiae* (bold) and related *Xylaria* species in GenBank. Phylogenetic analysis was conducted in MEGA v. 11 (Tamura, Stecher, and Kumar, 2021) following a MAFFT Q-NSI-i alignment (Waterhouse et al. 2009), Kimura 2 parameters, Gamma distribution with invariant sites and 1 000 bootstrap re-samplings were used to build the tree. Bootstrap values less than 70 % are not shown, and *Hypoxylon fragiforme* (*Hypoxylaceae*) was used as an outgroup to root the tree. The taxon described here is bold and in red font. Other type species in the tree are bold in black font. Species are also labelled with the accession numbers for the sequences used in the tree. The alignment for the ITS phylogeny tree was deposited in figshare.com (doi: 10.6084/m9.figshare.27185886).

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Conflict of interest: The authors declare that there is no conflict of interest.

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