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RESEARCH ARTICLE

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Fungal Planet description sheets: 1550–1613

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Key words

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Abstract Novel species of fungi described in this study include those from various countries as follows: **Argentina**, *Neocamarosporium halophilum* in leaf spots of *Atriplex undulata*. **Australia**, *Aschersonia merianiae* on scale insect (*Coccoidea*), *Curvularia huamulaniae* isolated from air, *Hevansia mainiae* on dead spider, *Ophiocordyceps poecilometigena* on *Poecilometis* sp. **Bolivia**, *Lecanora menthoides* on sandstone, in open semi-desert montane areas, *Sticta monlueckiorum* corticolous in a forest, *Trichonectria epimegalosporae* on apothecia of corticolous *Megalospora sulphurata* var. *sulphurata*, *Trichonectria puncteliae* on the thallus of *Punctelia borreri*. **Brazil**, *Catenomargarita pseudocercosporicola* (incl. *Catenomargarita* gen. nov.) hyperparasitic on *Pseudocercospora fijiensis* on leaves of *Musa acuminata*, *Tulasnella restingae* on protocorms and roots of *Epidendrum fulgens*. **Bulgaria**, *Anthracoidea umbrosae* on *Carex* spp. **Croatia**, *Hymenoscyphus radicis* from surface-sterilised, asymptomatic roots of *Microthlaspi erraticum*, *Orbilia multiserpentina* on wood of decorticated branches of *Quercus pubescens*. **France**, *Calosporella punctatispora* on dead corticated twigs of *Acer opalus*. **French West Indies (Martinique)**, *Eutypella lechatii* on dead corticated palm stem. **Germany**, *Arrhenia alcalinophila* on loamy soil. **Iceland**, *Cistella blauvikensis* on dead grass (*Poaceae*). **India**, *Fulvifomes maritimus* on living *Peltophorum pterocarpum*, *Fulvifomes natarajanii* on dead wood of *Prosopis juliflora*, *Fulvifomes subazonatus* on trunk of *Azadirachta indica*, *Macrolepiota bharadwajii* on moist soil near the forest, *Narcissea delicata* on decaying elephant dung, *Paramyrothecium indicum* on living leaves of *Hibiscus hispidissimus*, *Trichoglossum syamviswanathii* on moist soil near the base of a bamboo plantation. **Iran**, *Vacuiphoma astragalicola* from stem canker of *Astragalus sarcocolla*. **Malaysia**, *Neoeriomycopsis fissistigmae* (incl. *Neoeriomycopsidaceae* fam. nov.) on leaf spots on flower *Fissistigma* sp. **Namibia**, *Exophiala lichenicola* lichenicolous on *Acarospora* cf. *luederitzensis*. **Netherlands**, *Entoloma occultatum* on soil, *Extremus caricis* on dead leaves of *Carex* sp., *Inocybe pseudomytiliodora* on loamy soil. **Norway**, *Inocybe guldeniae* on calcareous soil, *Inocybe*

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rupestroides on gravelly soil. **Pakistan**, *Hymenagaricus brunneodiscus* on soil. **Philippines**, *Ophiocordyceps philippinensis* parasitic on *Asilus* sp. **Poland**, *Hawksworthiomyces ciconiae* isolated from *Ciconia ciconia* nest, *Plectosphaerella vigrensis* from leaf spots on *Impatiens noli-tangere*, *Xenoramularia epitaxicola* from sooty mould community on *Taxus baccata*. **Portugal**, *Inocybe dagamae* on clay soil. **Saudi Arabia**, *Diaporthe jazanensis* on branches of *Coffea arabica*. **South Africa**, *Alternaria moraeae* on dead leaves of *Moraea* sp., *Bonitomyces buffelskloofinus* (incl. *Bonitomyces* gen. nov.) on dead twigs of unknown tree, *Constrictochalara koukolii* on living leaves of *Itea rhamnoides* colonised by a *Meliola* sp., *Cylindromonium lichenophilum* on *Parmelina tiliacea*, *Gamszarella buffelskloofina* (incl. *Gamszarella* gen. nov.) on dead insect, *Isthmosporiella africana* (incl. *Isthmosporiella* gen. nov.) on dead twigs of unknown tree, *Nothoeucasphaeria buffelskloofina* (incl. *Nothoeucasphaeria* gen. nov.), on dead twigs of unknown tree, *Nothomicrothyrium beaucarneae* (incl. *Nothomicrothyrium* gen. nov.) on dead leaves of *Beaucarnea stricta*, *Paramycosphaerella proteae* on living leaves of *Protea caffra*, *Querciphoma foliicola* on leaf litter, *Rachicladosporium conostomii* on dead twigs of *Conostomium natalense* var. *glabrum*, *Rhamphoriopsis synnematosa* on dead twig of unknown tree, *Waltergamsia mpumalanga* on dead leaves of unknown tree. **Spain**, *Amanita fulvogrisea* on limestone soil, in mixed forest, *Amanita herculis* in open *Quercus* forest, *Vuilleminia beltraniae* on *Cistus symphytifolius*. **Sweden**, *Pachyella pulchella* on decaying wood on sand-silt riverbank. **Thailand**, *Deniquelata cassiae* on dead stem of *Cassia fistula*, *Stomiopeltis thailandica* on dead twigs of *Magnolia champaca*. **Ukraine**, *Circinaria podoliana* on natural limestone outcrops, *Neonematogonum carpinicola* (incl. *Neonematogonum* gen. nov.) on dead branches of *Carpinus betulus*. **USA**, *Exophiala wilsonii* water from cooling tower, *Hygrophorus aesculeticola* on soil in mixed forest, and *Neocelosporium aereum* from air in a house attic. Morphological and culture characteristics are supported by DNA barcodes.

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Amanita fulvogrisea

Fungal Planet 1550 – 30 December 2023

Amanita fulvogrisea Illescas, *sp. nov.*

Etymology. From the Latin adjectives *fulvus* (brownish, tawny) and *griseus* (grey), in reference to its basidiomatal colours.

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

Basidiomata with isolated to gregarious growth, medium-sized, with stipe base deeply inserted in the substrate. *Pileus* 60–80 mm diam, initially conical-convex, later convex, finally flat-convex, without umbon, smooth, not viscid in dry weather, grey (5Y 6/1), bistre (10YR 5/2), or tan (10YR 7/4) (Munsell 2009), usually with the umbon and the marginal zone slightly darker, presenting large patches of general veil; margin strongly striate, occupying 1/7 to 1/4 of the radius of the pileus, and strongly cleft at several points. *Lamellae* white to cream (7.5Y 9/2), moderately crowed, free, arcuate, sometimes bifurcate, with edges crenulate, concolourous or slightly darker; lamellulae numerous to very numerous, truncate at right angles, or reduced to a denticle at margin. *Stipe* cylindrical, slightly broadened towards the base, 80–100 × 9–15 mm, striated at the junction with the lamellae, white or whitish, sub-smooth or more frequently with floccose, and brownish to greyish remains of the partial veil along almost its entire length, forming meandering bands. *Volva* adherent (type III; Fraiture 1993), membranous but fragile, externally spotted with brown well as the pileus veil. *Context* whitish, with banal fungal *odour*. *Spore deposit* white. *Basidiospores* (8–)9–12(–13.5) × (8–)8.5–10.5(–11.5) µm (av. = 10.4 × 9.6; Q = 1.00–1.16; Qm = 1.09), globose, subglobose or broadly ellipsoid, with rounded, slightly prominent apicula, thin-walled, hyaline, inamyloid; in fresh material with abundant vacuolar content, in dry material agglutinated forming a large guttule. *Basidia* claviform, tetrasporic, rarely bisporic or monosporic, 47–68 × 12–15 µm, thin-walled, with frequently curved sterigmata up to 8 µm long, and abundant yellow-green vacuolar content. *Lamellar edge* partially sterile, especially in young specimens. *Marginal cells* spherical, sphaeropedunculate or ellipsoid, with somewhat thickened wall, 25–42 × 21–31 µm. *Lamellar trama* bilateral, irregularly divergent, 150–250 µm wide. *Subhymenium* predominantly ramose, composed of cylindrical to truncated cone-shaped cells, some with lateral projections, and frequently cellular at the base of the basidia, 9–16 × 6–10 µm, Qm = 1.6. *Mediostratum* composed of almost parallel, septate hyphae, 3–7.5 µm wide, sometimes with thickened walls, showing some physaloid elements. *Hymenopodium* formed by chains of prismatic or subspherical cells, with terminal elements frequently very thick-walled, up to 4 µm, and irregularly sharp ends, 24–45 × 10–22 µm, and presence of some sphaeropedunculate acrophysalids, diverging diagonally to the lamina axis, 25–50 × 16–28 µm. *Pileipellis* 420–525 µm wide. *Suprapellis* with a first layer in cutis 110–125 µm wide, with gelatinised hyphae 1.3–3.4 µm wide, and a lower layer with greenish yellow pigmented hyphae, parallel in the first layers, then progressively more interwoven, 2.6–5.3 µm wide. *Subpellis* with some physaloid and intricate elements, less pigmented hyphae, 3.7–9.7 µm wide. *Context* under cuticle with hyphae similar to subcutis but wider, with intraparietally and extraparietally pigmented physaloid elements, and some spherocytes, 25–36 × 15–21 µm. *Volva* 375–550 µm wide, with an outer layer consisting of septate hyphae, mostly parallel to the stipe surface on the outer side, intertwined and wider on the inner side, 4.0–7.3 µm wide, with sparse spherocytes, 28–52 × 17–41 µm. *Stipitipellis* formed by parallel hyphae, 4.2–7.5 µm wide, showing some emergent elements, replaced towards the interior of the context by thick-walled, yellow-pigmented, physaloid elements. *Oleiferous hyphae* ramificate, 12–17.5 µm wide, mostly present on the pileipellis and volva. *Clamps* absent in all examined structures.

Habit, Habitat & Distribution — Collected so far only in two nearby locations in the Baetic System, in mid-mountain areas, in early October (although it probably also appears in late spring), growing in small groups on limestone soils in forests of *Quercus rotundifolia*, *Quercus faginea* and *Pinus nigra* subsp*. salzsmanii*, probably in association with *Quercus* spp.

Typus. Spain, Hornos, N38°13' W02°10', 1310 m a.s.l., on limestone soil, in mixed forest of *Quercus faginea*, *Quercus rotundifolia* and *Pinus nigra* subsp. *salzmanii*, 5 Oct. 2019, *T. Illescas & C. Morente* (holotype in Herbarium of the Junta de Andalucía: JA-Cussta 9346; ITS and LSU sequences GenBank OR420077 and OR416232; MycoBank MB 849798).

Additional material examined. Spain, Hornos, N38°14' W02°39', 1325 m a.s.l., on limestone soil, in mixed forest of *Quercus rotundifolia*, *Pinus nigra* subsp. *Salzmanii* and *Quercus faginea*, 5 Oct. 2019, *T. Illescas & C. Morente*, JA-Cussta 9345, ITS and LSU sequences GenBank OR420078 and OR416233.

Notes — *Amanita fulvogrisea* is characterised by a robust habit such as *Amanita fulvoides* basidiomata, but with possible greyish colouration, subglobose spores, an almost exclusively filamentous veil, and especially their characteristic hymenopodium cells. It forms a subclade with good support (0.98/99), forming together with the *A. exilis* sister subclade, an independent clade within *Amanita* stirps *Lividopallescens*, also well supported (1/100). *Amanita fulvogrisea* has an affinity of 98.1 % with the phylogenetically closest species, *A. exilis*, comparing the ITS+LSU sequences obtained from their respective holotypes. However, this species produces "tall and slender basidiomata usually with a stipe twice as long as the width of the pileus" and ellipsoid spores (Crous et al. 2021c). Another difference with *A. fulvogrisea* would be its epicutis in trichoderm. *Amanita lividopallescens* is a robust species like *A. fulvogrisea* that could grow in the same habitats, but in its more typical forms, differs in its cream to ochraceous pileus, spores usually with Qm 1.2–1.3, fertile lamellar edge and volva usually broad and membranous (Tulloss 1994, Vizzini et al. 2016). Our phylogenetic analysis includes an *Amanita* not yet described in the *A. lividopallescens* clade, which we have given the working name *Amanita tigrinipes* nom. prov., and which appeared as *Amanita lividopallescens* subclade 'A' in Loizides et al. (2018); we have collected this species growing in Mediterranean *Quercus* forests, with or without *Cistus* spp., and it has darker brown and grey colourations than *A. lividopallescens*, as well as a very marked zigzag banding decoration on the stipe and concolourous to that of the pileus, which makes it morphologically very similar to *A. fulvogrisea*.

(Notes continued on Supplementary page)

Colour illustrations. Holotype collection area at Hornos. Holotype collection JA-Cussta 9346; collection JA-Cussta 9345; basidiospores; hymenopodium cells; hyphae of the inner layer of the volva. Scale bars = 50 mm (specimens in situ), 10 µm (microscopy).

Supplementary material

FP1550 Phylogenetic tree.

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Amanita herculis

Fungal Planet 1551 – 30 December 2023

Amanita herculis Plaza & Illescas, *sp. nov.*

Etymology. Herculis, genitive of Hercules, in reference to the robustness of most of its specimens and to the mythological character who opened the Strait of Gibraltar, 'columns of Hercules', where some of these specimens were found.

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

Basidiomata medium to large sized. *Pileus* 47–115 mm diam, ash grey (10P 8/1), silver grey (10RP 7/1), greyish brown (5RP 8/1) or bistre (2.5Y 5/2), often with a brownish border (5R 5/1) at margin (Munsell 2009), convex to planoconvex, sometimes depressed at centre with maturity; usually without umbon. Striated margin between 1/5 and 1/3 of the radius of the pileus, often with broad patches of general veil remnants, white with ferruginous macules. *Lamellae* dense, not very thick, some bifurcate, with numerous lamellulae, white to light cream, with crenulate edge greyish brown pigmented at maturity. *Stipe* 73–170 × 10–28 mm, cylindrical, widening towards the base, although in adult specimens it may narrow slightly at the centre, without annulus; longitudinally striated surface even along its entire length, with slightly differentiated remnants of the partial veil, which may take on shades of the pileus at maturity, and form a slight scaly band at the point of junction with the volva. *Volva* thick and membranous, externally white with numerous ferruginous spots, and internally whitish or with slight tints of the colour of the pileus, up to 90 × 50 × 6 mm, usually type IV (Fraiture 1993), irregularly shaped with few lobes. *Context* white, cavernous in the stipe, with agreeable fungal *odour* and *taste*. *Spore deposit* white. *Basidiospores* (8.9–)10.2–12.8(–14.8) × (8.6–)9.5–12.2(–14.4) µm (av. = 11.5 × 10.8; Q = 1.01–1.14; Qm = 1.07), globose to subglobose, with rounded or troncoconic, slightly prominent apicula, often sublateral; thin-walled, hyaline, inamyloid; in fresh material with abundant vacuolar content, in dry material agglutinated forming a large guttule. *Basidia* claviform, tetrasporic, rarely mono- or bisporic, 50–70 × 14–19 µm, thin-walled, with sterigmata 3–12(–15.5) µm length, and abundant yellow-green vacuolar content. *Lamellar edge* sterile. *Marginal cells* spherical or sphaeropedunculata, with slightly thickened wall, 22–48 × 16–35 µm. *Lamellar trama* bilateral, irregularly divergent. *Subhymenium* cellular, ramose in primary branches (Bas 1969), composed by cylindrical cells widened at the top, truncated cone-shaped or rounded cells, often with lateral projections, 8–19 × 5–10 µm. *Mediostratum* composed of nearly parallel hyphae, 4–12 µm wide, with frequent inflated articles. *Hymenopodium* with subspherical or broadly claviform terminal elements, with thickened wall, disorderly disposed, 21.5–54 × 14.5–27 µm. *Suprapellis* with a first layer in cutis, with gelified hyphae, 1.7–4.3 µm wide, and a lower layer with greenish yellow pigmented hyphae with a slightly thickened wall, usually parallel to the surface of the pileus, 3.3–8.0 µm wide. *Subpellis* formed by similar but more intertwined hyphae. *Volva* with an outer layer formed by hyphae parallel to the stipe axis, with slightly thickened wall, 3.7–9.0 µm wide; a visually distinguishable intermediate layer consisting of interwoven hyphae with abundant greenish yellow intracellular pigment, and an inner layer with the side next to the stipe slightly gelified, consisting of laxly interwoven hyphae of variable thickness; in the last two layers interspersed, with relative abundance, physaloid elements and globose to broadly claviform spherocytes, 34–65 × 21–49 µm. *Stipitipellis* formed by parallel hyphae, the outer layer thinner, 1.2–6.4 µm wide, replaced towards the interior of the context by thick-walled, yellow-pigmented, physaloid elements. *Oleiferous hyphae* mainly present on the pileipellis and volva. *Clamps* absent in all examined structures.

Habit, Habitat & Distribution — Isolated to gregarious fruitlets located in several provinces of Andalusia at low altitudes, in acid or neutral soils, always under the influence of *Quercus* spp. Collected mostly in late spring, with high temperatures, although also in early autumn

Typus. Spain, La Puebla de los Infantes, N37°49' W05°24', 272 m a.s.l., on sandy soil, in open *Quercus rotundifolia* forest with *Cistus* spp., 15 May 2022, *T. Illescas & C. Morente* (holotype in the Fungarium of the Junta de Andalucía: JA-Cussta 9355; ITS and LSU sequences GenBank OR427365 and OR428566; MycoBank MB 849920).

Additional materials examined. Spain, Castellar de la Frontera, La Almoraima, in *Quercus suber* forest, 21 May 2022, *M. Plaza & C.M. Jiménez*, JA-Cussta 9357, ITS and LSU sequences GenBank OR427366 and OR428567; ibid., 25 May 2022, JA-Cussta 9358, ITS sequence GenBank OR501895; Córdoba, Conejeras, in *Quercus suber*, *Quercus rotundifolia* and *Pinus pinea* mixed forest, 9 Oct. 2021, *T. Illescas*, JA-Cussta 9353, ITS and LSU sequences GenBank OR427363 and OR428564; ibid., 19 June 2023, JA-Cussta 9356; La Puebla de los Infantes, La Goyorita, under *Quercus rotundifolia* with *Cistus* spp., 24 Apr. 2022, *C. Morente & T. Illescas*, JA-Cussta 9354, ITS and LSU sequences GenBank ITS OR427364 and OR428565.

Notes — Species of *Amanita* sect. *Vaginatae* with a large to medium-sized sacciform and membranous volva (type IV) are phylogenetically all found, for the most part, in clade 1 of the Section (Hanss & Moreau 2020). Among the European species of this clade, *A. herculis* is characterised by its robust habit, relatively short stipe, silver-grey or bistre coloured and occurrence in thermophilous *Quercus* spp. forests. *Amanita calida*, the phylogenetically closest species (97.4 % identity in the combined ITS+LSU matrix of their holotypes), which may share the same spots and times of occurrence, has much lighter colourations with a mixture of light brownish and greyish tones, a distinct umbon and a much more stylised habit (Illescas & Plaza 2022). *Amanita praelongipes* differs from the previous two species as it has no marginal cells on the lamellar edge (Kärcher 1988, Kärcher & Contu 1999); in addition, the partial ITS sequence of its typus is only 90 % identical to the same region of the holotype of *A. herculis*. These three species are characterised by having the smallest spores within the clade (Lm < 12 µm), but whereas *A. calida* and *A. praelongipes* have globose spores, *A. herculis* has subglobose spores. In a sister clade to *A. herculis* and *A. calida* are two species typical of Eurosiberian coniferous or mixed forests, of large size, also with broad, membranous volva: *Amanita magnivolvata*, which has a grey pileus with an olive tinge, darker at the margin, and broadly ellipsoid spores, with Qm = 1.2 (Aalto 1974), and *Amanita pachyvolvata*, with ochraceous to yellowish ochraceous tones in the pileus, initially olivaceous (Bon 1978, Tulloss 1994).

(Notes continued on Supplementary page)

Colour illustrations. Holotype collection area at La Puebla de los Infantes. Collections JA-Cussta 9354, JA-Cussta 9355 (holotype), JA-Cussta 9357, JA-Cussta 9356; basidiospores; subhymenium; hyphae of the outer layer of the volva. Scale bars = 20 mm (specimens in situ), 10 µm (microscopy)

Supplementary material

FP1551 Phylogenetic tree.

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Anthracoidea umbrosae

Fungal Planet 1552 – 30 December 2023

Anthracoidea umbrosae T. Denchev, Denchev, Begerow & Kemler, *sp. nov.*

Etymology. The epithet is derived from the host plant, *Carex umbrosa*.

Classification — *Anthracoideaceae*, *Ustilaginales*, *Ustilaginomycetes*.

Infection local. *Sori* in some female flowers, around aborted nuts as subglobose to ovoid hard bodies, 1.5–2.0 × 1.2–1.8 mm, initially covered by a thin, greyish peridium that later flakes away exposing a black spore mass, powdery on the surface. *Spores* small-sized, flattened, in plane view irregularly rounded, suborbicular, broadly elliptical, elliptical or ovate in outline, (14.5–) 15.5–20.5(–22) × (13–)14–17.5(–18.5) (17.9 ± 1.1 × 15.9 ± 1.0) µm (n/$_6$ = 600), in side view 10–13 µm thick, medium to dark reddish brown; wall unevenly thickened, 1.0–2.0(–2.3) µm thick, sometimes with 1–2, usually inconspicuous internal swellings, light refractive areas rarely present, protuberances absent; minutely verruculose to almost smooth, spore profile not affected. In scanning electron microscopy (SEM), warts up to 0.2 µm high, sometimes partly confluent, forming short rows or small groups. *Spore germination* unknown.

Host & Distribution — On *Cyperaceae*: *Carex*, Rhomboidales-Mitrata Clade of *C.* subg. *Carex*: *C. umbrosa* subsp. *umbrosa*, *C. umbrosa* subsp. *huetiana*, and hybrids of *C. umbrosa* subsp. *huetiana*; Europe (Andorra, Austria, Bulgaria, Czechia, Spain) and Asia (Armenia, Georgia).

Typus. Bulgaria, Mt Vitosha, below Golyam Rezen Peak, near the trail Aleko Chalet – Kupena Chalet, N42°33'25.4" E23°17'50.5", 1983 m a.s.l., on *Carex umbrosa* subsp. *huetiana* (*Cyperaceae*), 6 July 2016, *C.M. Denchev & T.T. Denchev*, 1643 (holotype SOMF 30500; LSU sequence GenBank OQ801120; MycoBank MB 848431).

Additional materials examined. ***Anthracoidea caryophylleae***: Austria, Steiermark, Graz, Bezirk Mariatrost, bei Bildunghaus Mariatrost SSE unterhalb der Basilika, N47°06'19" E15°29'30", 450 m a.s.l., on *C. caryophyllea*, 13 May 2013, *C. Scheuer*, s.n. (GZU 000306019, LSU sequence GenBank OQ801115). – Bulgaria, Sredna Gora Mts, Mt Lozenska Planina, above St. Spas Monastery, N42°35'08.8" E23°31'11.1", 1043 m a.s.l., on *C. caryophyllea*, 1 June 2016, *T.T. Denchev & C.M. Denchev*, 1611 (SOMF 30791, LSU sequence GenBank OQ801116); Mt Konyavska Planina, above Tsarvenyano village, Kyustendil Province, N42°21'12.2" E22°47'55.4", 863 m a.s.l., on *C. caryophyllea*, 5 June 2021, *T.T. Denchev & C.M. Denchev*, 2122 (SOMF 30792, LSU sequence GenBank OQ801113); the Rhodopes, near Trigrad, Smolyan Province, N41°35'14.8" E24°24'04.8", 1300 m a.s.l., on *C. caryophyllea*, 23 June 2021, *T.T. Denchev & C.M. Denchev*, 2129 (SOMF 30793, LSU sequence GenBank OQ801114). — ***Anthracoidea umbrosae***: Andorra, Circo de Pessons, en bosques subalpinos, 2000–2600 m a.s.l., on *C. umbrosa* subsp. *huetiana*, 21 July 1986, *C. Gómez*, *M. Luzeño & P. Vargas*, 10138 GL (paratype MA-Fungi 37689). – Armenia, Shirak Province, Ashotsk District, near the border to Georgia, NE of Bavra, SE from former village Saragyugh, unnamed mountain, S of Mt Akchala, N of top, 3065 m a.s.l., on *C. umbrosa* subsp. *huetiana*, N41°08'24" E43°57'19", 1 Sept. 2005, *M. Oganesyan*, *H. Ter-Voskanyan & E. Vitek*, 05-2290 (paratype W 2006-0011768). – Bulgaria, Mt Vitosha, above Goli Vrah Lift Station, N42°35'19.9" 23°17'16.1", 1845 m a.s.l., on *C. umbrosa* subsp. *huetiana*, 31 July 2021, *T.T. Denchev & C.M. Denchev*, 2146 (paratype SOMF 30794, LSU sequence GenBank OQ801117); Mt Vitosha, SE of Cherni Vrah Peak, N42°33'36.7" E23°17'03.0", 2240 m a.s.l., on *C. umbrosa* subsp. *huetiana*, 1 Aug. 2021, *T.T. Denchev & C.M. Denchev*, 2150 (paratype SOMF 30796, LSU sequence GenBank OQ801119); Mt Vitosha, below Golyam Rezen Peak, near the trail Aleko Chalet – Kupena Chalet, N42°33'15.5" 23°17'57.1", 2230 m a.s.l., on *C. umbrosa* subsp. *huetiana*, 6 July 2016, *T.T. Denchev & C.M. Denchev*, 1646 (paratype SOMF 30501); Mt Vitosha, below Golyam Rezen Peak, near the trail Kupena Chalet – Cherni Vrah Peak, N42°33'14.4" E23°17'46.6", 2097 m a.s.l., on *C. umbrosa* subsp. *huetiana*, 6 July 2016, *T.T. Denchev & C.M. Denchev*, 1644 (paratype SOMF 30797); Mt Vitosha, above Kumata Chalet, 1800 m a.s.l., on *C. umbrosa* subsp. *huetiana*, 7 July 1985, *C.M. Denchev*, s.n. (paratype SOMF 18498); Mt Vitosha, above Kumata Chalet, N42°35'13.3" E23°14'49.6", 1792 m a.s.l., on hybrid of *C. umbrosa* subsp. *huetiana*, 12 July 2019, *T.T. Denchev & C.M. Denchev*, 1942 (paratype SOMF 30795, LSU sequence GenBank OQ801118); Rila Mts, below Ribno Yakoruda Lake, N42°06'04.5" E23°35'48.7", 2149 m a.s.l., on *C. umbrosa* subsp. *huetiana*, 3 Aug. 2021, *T.T. Denchev*, 2154 (paratype SOMF 30798).

Notes — *Anthracoidea* species are restricted to host plants belonging to the same or closely related sections of *Carex* (Kukkonen 1963, Vánky 1979). *Carex umbrosa* has been traditionally included in *Carex* sect. *Mitratae* (Chater 1980, Egorova 1999). For this reason, the smut fungus on *Carex umbrosa* was referred to *A. caryophylleae* (Vánky 1994, 2011). *Anthracoidea caryophylleae* on *C. umbrosa* subsp. *umbrosa* has been previously reported from Austria (Zwetko & Blanz 2004) and Czech Republic (Vánky 1985), and on *C. umbrosa* subsp. *huetiana* – from Andorra (Almaraz 2002), Bulgaria (Denchev 2001), Georgia (Karatygin & Simonyan 1985) and Spain (Almaraz 2002). Currently, the hosts of *A. caryophylleae* are reduced to carices in *C.* sect. *Mitratae*, in its traditional circumscription (Denchev et al. 2013). A recently proposed classification of *Carex* places *C. umbrosa* within the Rhomboidales-Mitrata Clade of *Carex* subg. *Carex* (Roalson et al. 2021). The aim of the present study was to clarify the taxonomic status of the *Anthracoidea* species on *C. umbrosa*. A combined approach, using host specialisation, comparative morphology, and molecular data, revealed that the smut fungus on *C. umbrosa* is a distinct species from *A. caryophylleae*. *Anthracoidea umbrosae* can be distinguished from *A. caryophylleae* by having a thinner spore wall (up to 3 µm thick for *A. caryophylleae*). The phylogeny inferred from the nLSU sequences demonstrated that the new species *A. umbrosae* is not closely related to *A. caryophylleae* but is sister group to a clade containing *A. hallerianae*, *A. pamiroalaica*, *A. rupestris*, *A. baldensis*, *A. caricis-albae*, *A.* cf. *rupestris*, *A. globularis*, *A. irregularis* and *A. caricis*. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **LSU** sequence are *A. hallerianae* (voucher SOMF 30201, GenBank MT628657; Identities = 95.93 %, 10 gaps (0.9 %)), *A. hallerianae* (strain SOMF 30199, GenBank MT628660; Identities = 95.93 %, 11 gaps (0.9 %)) and *A. hallerianae* (strain SOMF 30000, GenBank MT628661; Identities = 95.98 %, 11 gaps (1 %)).

Colour illustrations. Mount Vitosha, near Sofia City – habitat. Habit; spores in LM; spores in SEM. Scale bars = 0.2 cm (sori), 10 µm (spores in LM), 5 µm (spores in SEM).

Supplementary material

FP1552-1 Phylogenetic tree.
FP1552-2 Table.

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Arrhenia alcalinophila

Fungal Planet 1553 – 30 December 2023

Arrhenia alcalinophila Karich, Krisai & Klofac, *sp. nov.*

Etymology. Named after its base-rich habitat.

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

Basidiomata omphalinoid. *Pileus* 4–15 mm wide, when fresh greyish cream and translucently striate with brownish striation, centrally small umbilicate and brownish, hygrophanous, becoming light grey when drying, glabrous, margin straight to somewhat wavy and slightly involute. *Lamellae* slightly to strongly decurrent, developed normally, sometimes slightly thickish, not clearly anastomosing, greyish, lighter than fresh pilei and darker than dried ones. *Stipe* central, sometimes slightly eccentric, 10–25 mm long, 1–2 mm wide, concolorous to pileus, smooth, slightly pruinose at apex. *Smell* inconspicuous, occasionally pelargonium-like when drying; *taste* not tested. *Spore print* white. *Basidia* 2-spored 26–33 × 7–8 µm. *Sterigmata* 6–8 µm. *Basidiospores* variable in size and shape (n = 67, 2 collections, 3 basidiomata): 9.0–12.0(–14.0) × (4.5–)5.0–6.5(–7.5) µm, Q = (1.4–)1.5–2.4(–2.9), Q_{AV} = 1.8–2.1, subglobose to broadly ellipsoid or (sub)lacrymoid to pyriform and then centrally constricted. *Hymenophoral trama* subirregular, consisting of 2–8 µm wide hyphae, indistinctly incrusted. *Pileipellis* a cutis of (sub)parallel 3–13 µm wide hyphae. *Pileipellis* and *pileitrama* hyphae distinctly incrusted. *Stipitipellis* hyphae 2–9 µm wide, incrusted. *Stipititrama* hyphae not incrusted. *Cystidia* absent. *Clamp connections* abundant in all tissues.

Sociability, Habitat & Distribution — Basidiomata growing solitary or in small clusters on the ground in unimproved grassland on loamy to calcareous soil. Known from Germany, Austria, France and the USA (from one environmental sample).

Typus. Germany, Mittelherwigsdorf, 'Katzenlehne', N50°55,51' E14°44,71', 280 m a.s.l., orchard meadow in unimproved grassland on loamy soil, 2 Oct. 2022, *A. Karich* (holotype GLM-F135687; ITS and LSU sequences GenBank OR258065 and OR258067; MycoBank MB 849350).

Additional materials examined. Austria, Lower Austria, Pyhra: Hinterholz-Schauching, N48°8.65' E15°39.65', mapping grid square 7859/4, 400 m a.s.l., in meadow, 10 Nov. 2012, *W. Klofac*, WU-Myc 32560, ITS sequence GenBank MW113705. – Germany, Zittau, 'Kaiserfelder', N50°52.44' E14°47.58', 283 m a.s.l., on bare soil in a sheep pasture, 10 Oct. 2021, *A. Karich*, GLM-F135688, ITS and LSU sequences GenBank OR258064 and OR258066.

Colour illustrations. Orchard meadow at the holotype location. Basidiomata of holotype and GLM-F135688 (photo credit A. Karich); line drawings of spores from holotype (top) and GLM-F135688 (bottom) and two-spored basidia from holotype (drawing A. Karich). Scale bars = 1 cm (basidiomata), 10 µm (line drawings).

Notes — A recent study showed high morphological and molecular genetic diversity in the *Arrhenia acerosa* complex (Voitk et al. 2020). This species complex includes pleurotoid species, e.g., *A. acerosa* and *A. glauca*, as well as species with omphalinoid habit. *Arrhenia alcalinophila* was treated as 'G-3' in Voitk et al. (2020). Due to the limited number of specimens and the limited information about the specimens available the authors decided not yet to describe 'G-3' as new species. In a phylogenetic tree based on ITS-sequences, *A. alcalinophila* belongs to a separate clade within the *acerosa*-complex and is quite distant from another species with omphalinoid habit, i.e., 'G-2'. In contrast to *A. alcalinophila*, however, all examined specimens of 'G-2' have four-spored basidia, while the spore size is roughly in the same range (Voitk et al. 2020). Phylogenetically, *A. acerosa* s.str. is the closest species, but has pleurotoid basidiomata, at least, when young.

From a look at the morphological descriptions of *A. griseopallida* in the literature (Quelét 1886, Bas et al. 1995, Ludwig 2001) it is obvious that it could be confused with *A. alcalinophila*. However, according to Kühner & Lamoure (1972), *A. griseopallida* can develop pleurotoid basidiomata and has four-spored basidia. Furthermore, the colour of fresh basidiomata of *A. griseopallida* is dark greyish brown and therefore seems to represent another group within the *acerosa*-complex (Clemençon 1982, Ludwig 2001). Persoon (1828), who examined Desmazière's original material of *Agaricus griseopallidus*, mentions an upright pileus margin, thicker lamellae and a slightly reddish colouration when drying. All these features were not observed in specimens of *A. alcalinophila*. Lutzoni (1997) published an ITS/LSU sequence of *Phaeotellus griseopallidus* (= *A. griseopallida*) generated of a specimen which had been approved by Lamoure (GenBank U66436). It can be concluded that this specimen represents *A. griseopallida* s.str.

Supplementary material

FP1553 Phylogenetic tree.

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Aschersonia merianiae

Fungal Planet 1554 – 30 December 2023

Aschersonia merianiae Y.P. Tan, Marney, Abell & R.G. Shivas, *sp. nov.*

Etymology. Named after Maria Sibylla Merian (1647–1717), who was a German naturalist and artist. Maria Merian made several trips to South America from the sale of her illustrations of plants and insects, in an age when science was largely the pursuit of wealthy men. Maria Merian documented the nature of metamorphosis with illustrated life cycles for nearly 200 species of insects and amphibians.

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

Hosts are scale insects (*Hemiptera*: *Coccoidea*) attached to upper and lower leaf surfaces in tropical and sub-tropical rainforests. *Mycelium* covers host, orange, with a membranous yellow to orange hypothallus. *Stromata* 1–3 mm diam, luteus, globose to nodular, with several ostioles visible as brown dots, outer tissue composed of thin-walled collapsed cells, internal tissue composed of thick-walled *textura epidermoidea*. *Perithecia* immersed in stroma, obpyriform, 350–450 × 125–160 µm. *Asci* cylindrical, 130–160 × 5–10 µm, capitate, 8-spored. *Ascospores* pale yellow, smooth, filiform, multiseptate; part-ascospores disarticulate at septa, doliiform to subcylindrical, 6–10 × 2–3 µm. *Conidiomata* scattered in stroma, cavities or convolutions, exude luteus conidial masses. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous* cells phialides, cylindrical, 15–25 × 2–2.5 µm, narrowed at the apex, lateral on hyphae or densely crowed on the hymenium. *Paraphyses* not seen. *Conidia* fusoid, 7.5–10 × 2.5–3 µm, straight, smooth-walled, hyaline to pale yellow.

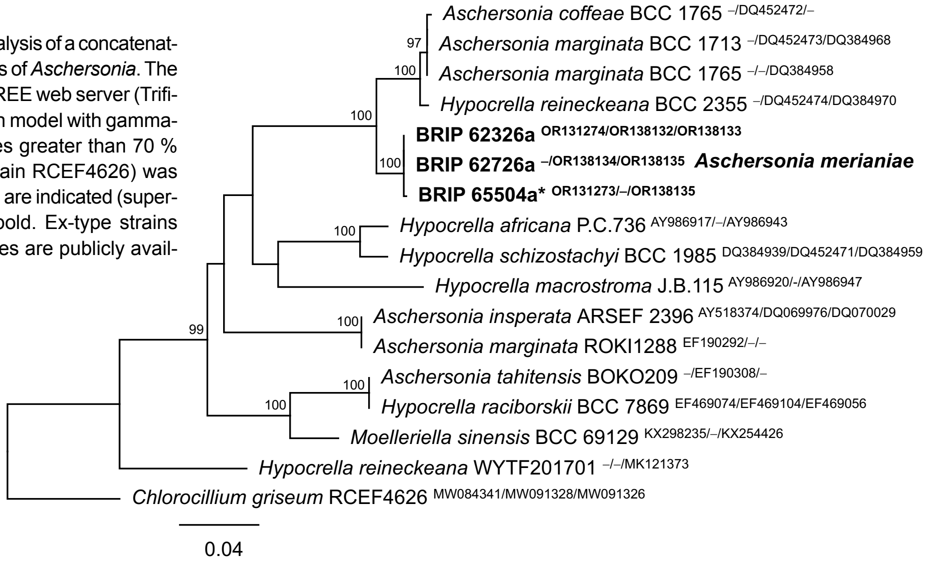
Culture characteristics (25 °C, 4 wk, in darkness) — On potato dextrose agar (PDA) colonies 7–10 mm diam and 2 mm high, compact, partly immersed, low convex, luteus coloured due to abundant conidial ooze, with a distinct sienna to rust-coloured slightly undulating margin 1–2 mm wide; reverse sienna becoming paler towards the margin. In densely spread-plate cultures colonies less than 1 mm diam, luteus to orange, coral in reverse; after 8 wk colonies 15–18 mm diam.

Typus. Australia, Queensland, Lacey Creek, on scale insect (*Coccoidea*), Mar. 2017, *S.E. Abell*, *Y.P. Tan*, *M.D.E. Shivas & R.G Shivas* (holotype preserved as metabolically inactive culture BRIP 65504a; ex-type culture BRIP 65504a; LSU and *tef1* sequences GenBank OR131273 and OR138131; MycoBank MB 850245).

Additional materials examined. Australia, Queensland, Babinda, on scale insect (*Coccoidea*), 5 Apr. 2015, *T.S. Marney*, *S.E. Abell*, *M.D.E. Shivas & R.G Shivas*, culture BRIP 62326a, LSU, *rpb2* and *tef1* sequences GenBank OR131274, OR138132 and OR138133; Lacey Creek, on scale insect (*Coccoidea*), 7 June 2015, *T.S. Marney*, *S.E. Abell*, *M.D.E. Shivas & R.G Shivas*, culture BRIP 62726a, *rpb2* and *tef1* sequences GenBank OR138134 and OR138135.

Notes — *Aschersonia merianiae* was found on scale insects on leaves of unidentified trees in a lowland rainforest in northern Queensland. The stromata from specimens collected in the field contained perithecia. Pure cultures were generated from mycelium taken internally from the stromata. These cultures were very slow-growing and produced abundant conidial ooze after 4 wk.

Based on a megablast of NCBIs GenBank nucleotide database, the closest relevant hits using the **LSU** sequence are *Hypocrella reineckeana* (strain ZZHBL201707, GenBank MK121374, Identities 832/834 (99 %)), *Moelleriella sinensis* (culture CGMCC 3.18912, GenBank KT963554, Identities 824/826 (99 %)) and *M. epiphylla* (strain I93-813, GenBank EU392583, Identities 795/838 (95 %), 11 gaps). The closes hits using the ***rpb2*** sequence are *H. reineckeana* (strain BCC 2355, GenBank DQ452474, Identities 832/866 (96 %)), *A. marginata* (strain BCC 1713, GenBank DQ452473, Identities 801/835 (96 %)) and *A. coffeae* (strain BCC 1765, Identities 792/828 (96 %)). The closest hits using the ***tef1*** sequence are *H. reineckeana* (strain ZZHBL201707, GenBank MK121375, Identities 879/905 (97 %)), *Aschersonia marginata* (strain BCC 1713, GenBank DQ384968, Identities 862/902 (96 %)) and *M. sinensis* (culture CGMCC 3.18912, GenBank KT987415, Identities 794/815 (97 %)).



Phylogenetic tree based on a maximum likelihood analysis of a concatenated alignment (*rpb2*, *tef1* and LSU) of selected species of *Aschersonia*. The maximum likelihood analysis was done on the IQ-TREE web server (Trifinopoulos et al. 2016) based on the GTR substitution model with gamma-distribution rate variation. Bootstrap support values greater than 70 % are given at the nodes. *Chlorocillium griseum* (strain RCEF4626) was used as the outgroup. GenBank accession numbers are indicated (superscript LSU/*rpb2*/*tef1*). Novel taxon is shown in bold. Ex-type strains indicated with asterisks (*). The alignment and trees are publicly available in Zenodo (doi: 10.5281/zenodo.8046093).

Colour illustrations. Dirt track through tropical rainforest, northern Queensland. Stromata; spread-plate culture after 4 wk on PDA; colony after 4 wk on PDA; conidiophores and conidia; conidia; part-ascospores. Scale bars (top to bottom) = 1 mm, 1 cm, 1 mm, all others 10 µm.

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Calosporella punctatispora

Fungal Planet 1555 – 30 December 2023

Calosporella punctatispora Voglmayr & Mombert, *sp. nov.*

Etymology. The name refers to the punctate ascospore wall due to its verruculose ornamentation.

Classification — *Sydowiellaceae*, *Diaporthales*, *Sordariomycetes*.

Pseudostromata c. 0.5–1.5 mm diam, corticolous, immersed, inconspicuous, elevating and rupturing the bark, pustulate in face view, circular to elongate, without a black line, containing up to 15 perithecia. *Ectostromatic disc* 0.2–1 mm diam, erumpent, reduced, fusoid to circular, brownish, containing 1–15 distinctly protruding black ostioles. *Entostroma* inconspicuous, reduced, crumbly, brownish. *Ostioles necks* 140–200 µm long, 90–130 µm diam, erumpent, cylindrical, black, rounded at tips. *Perithecia* black, 350–500 µm diam. *Asci* broadly fusoid, 55–75 × 14–25 µm, containing four obliquely biseriate to irregularly arranged ascospores, with an indistinct, not congophilic, inamyloid apical apparatus. *Ascospores* 21–29.5 × 7–9.5 µm, hyaline, fusoid to oblong, straight to slightly curved, uniseptate, distinctly constricted at septum, inequilateral with one cell commonly wider, 2–4 guttulate, with broadly subacute to rounded ends and hyaline tapering appendages at both ends projecting for 6–11 µm, with distinctly verruculose ascospore wall ornamentation in water and Congo red, appearing smooth in 3 % KOH. *Asexual morph* unknown.

Culture characteristics (22 °C after 4 wk) — Colonies on 2 % cornmeal dextrose agar (CMD) reaching 50 mm diam, first dull yellowish, in centre turning umber with age, floccose in centre, smooth at margins, margins irregular, indistinct; reverse umber in centre, dull yellowish towards margin.

Ecology & Distribution — On thin (1.5–4.5 mm diam) dead corticated twigs of *Acer opalus* still attached to the trees; only known from eastern and southern France.

Typus. France, Jura (39), Port-Lesney, Bélvedère Edgar Faure, on dead corticated twigs of *Acer opalus* still attached to the tree, N47.003502° E5.808043°, 348 m a.s.l., 11 Apr. 2020, *A. Mombert*, AM2004111 (holotype WU-MYC 0050080; ex-type culture D336 = CBS 149660; ITS-LSU sequence GenBank OR143132; MycoBank MB 850243).

Additional materials examined. France, Doubs (25), Quingey, on dead twigs of a young *Acer opalus* still attached to the tree, N47.095852° E5.85464°, 495 m a.s.l., 13 Apr. 2020, *A. Mombert*, AM2004134 (WU-MYC 0050081); Doubs (25), Chassagne-st-Denis, Les Dents du Léri, on dead twigs of *Acer opalus* still attached to the tree, N47.079621° E6.104152°, 9 Jan. 2021, *A. Mombert*, AM2101092 (WU-MYC 0050082); Alpes-de-Haute-Provence (04), Le Castellard-Mélan, near to the grotte St-Vincent, on dead twigs of *Acer opalus* still attached to the tree, N44.220441° E6.125649°, 1511 m a.s.l., 24 June 2023, *A. Mombert*, AM2306241 (WU-MYC 0050583).

Colour illustrations. *Acer opalus* forest in spring, where the holotype was collected. Overview and detail of dead corticated twig showing brownish ectostromatic disks and ostioles; pseudostroma in vertical section; pseudostroma in horizontal section; four-spored ascus (in Congo red); ascospore with appendages (in water); ascospore with verruculose wall and appendages (in Congo red); ascospore with apparently smooth wall (in 3 % KOH); culture on CMD after 4 wk. Scale bars = 500 µm (pseudostromata), 5 µm (ascus and spores).

Notes — Nucleotide BLAST searches of the ITS and LSU at the NCBI GenBank nucleotide database revealed species of *Sydowiellaceae* (*Diaporthales*) as closest matches; the ITS sequence had highest similarity to *Calosporella innesii* (strain AR 3831, GenBank JF681964.1, Identities = 486/524 (92.75 %), 13 gaps), strain AR 3639, GenBank JF681965.1, Identities = 485/524 (92.56 %), 13 gaps), followed by *Alborbis galericulata* (strain AR 3890, GenBank JF681967.1, Identities = 434/506 (85.77 %), 33 gaps) and *Paragnomonia fragariae* (e.g., strain CBS 146.64, EF212844.1, Identities = 375/428 (87.62 %), 20 gaps) while the LSU sequence again had highest similarity to *Calosporella innesii* (e.g., strain AR 3639, EU683071.1, Identities = 846/852 (99.30 %), no gaps), followed by *Rossmania ukurunduensis* (strain AR 3484, EU683075.1, Identities = 839/852 (98.47 %), no gaps) and then various species from *Sydowiellaceae* (all with Identities = 836/852 (98.12 %), no gaps), e.g., *Cainiella johansonii* (voucher Kruys 731, JF701920.1), *Paragnomonia fragariae* (e.g., strain F133.1, MK524450.1), *Sillia ferruginea* (e.g., strain CBS 125581), *Sydowiella centaureae* (e.g., strain MFLU 16-2858, KY52350.1), *Sydowiella depressula* (strain CBS 813.79, MK524445.1) and *S. fenestrans* (e.g., strain CBS 125530, MK524444).

The phylogeny inferred from a matrix of ITS and nLSU sequences of *Sydowiellaceae* revealed a highly supported sister group relationship of the new species *Calosporella punctatispora* with the generic type of *Calosporella*, *C. innesii* (100 % ML and MP BS). Morphologically, *C. punctatispora* and *C. innesii* share similar pustulate stromata with reduced crumbly entostroma, broadly fusoid asci with an indistinct apical apparatus and hyaline, guttulate ascospores with distinct tapering appendages at each end; ecologically, they share occurrence on dead corticated thin twigs of the same host genus, *Acer* (Voglmayr & Jaklitsch 2014). However, *C. punctatispora* differs markedly from *C. innesii* by four-spored (vs eight-spored) asci, 1-septate, strongly constricted, inequilateral, straight to curved ascospores with verruculose walls (vs 3-septate, not to slightly constricted, equilateral, straight ascospores with smooth walls) (Voglmayr & Jaklitsch 2014). While *C. innesii* is only known from *Acer pseudoplatanus*, *C. punctatispora* appears to be restricted to *Acer opalus*. The verruculose ascospore walls and ascospore appendages in *C. punctatispora* are only evident in water and Congo red; they disappear in 3 % KOH.

Supplementary material

FP1555-1	Table.
FP1555-2	Phylogenetic tree.

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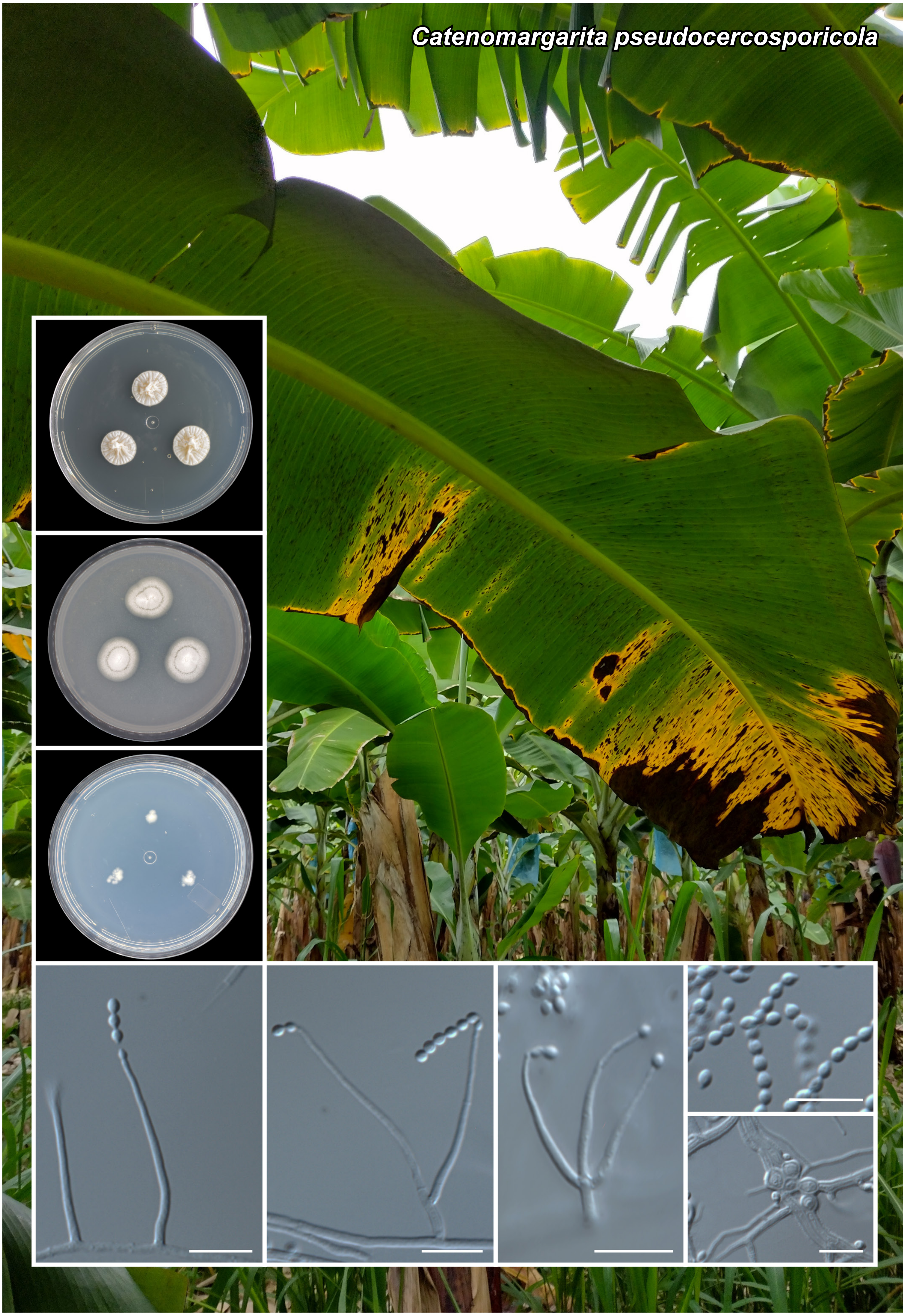
Catenomargarita pseudocercosporicola

Fungal Planet 1556 – 30 December 2023

Catenomargarita F.A. Custódio & O.L. Pereira, *gen. nov.*

Etymology. Name derived from the combination of *catena* and *margarita*, meaning chain and pearls, respectively, in Latin, referring to the long conidial chains produced by the fungus.

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

Mycelium septate, branched, smooth- or rough-walled, forming bundles, hyaline. *Conidiophores* erect, cylindrical straight or flexuous, arising from hyphae or the from ropes formed by the mycelium, unbranched, poorly branched, septate, sometimes reduced to conidiogenous cells, hyaline. *Conidiogenous cells* monophialidic, terminal or intercalary, smooth-walled, cylindrical to subulate, flexuous, hyaline. *Conidia* limoniform, papillated, thin- and smooth-walled, formed in long basipetal chains, aseptate, hyaline. *Chlamydospores* ellipsoid, globose, thick- and smooth-walled, intercalated, hyaline. *Sexual morph* was not observed.

Type species. *Catenomargarita pseudocercosporicola* F.A. Custódio & O.L. Pereira
MycoBank MB 850039.

Catenomargarita pseudocercosporicola F.A. Custódio & O.L. Pereira, *sp. nov.*

Etymology. Name refers to *Pseudocercospora*, the fungal genus from which this fungus was isolated.

Mycelium septate, branched, smooth- or rough-walled, forming bundles, hyaline, 0.85–2.8 µm diam hyphae. *Conidiophores* solitary or aggregated, erect, arising from hyphae, with 1–3 septa, sometimes reduced to conidiogenous cells, unbranched, poorly branched, bearing 1–3 phialides, flexuous, hyaline, (18–)28.5–52.5 × (1.3–)1.5–2.0 µm. *Conidiogenous cells* monophialidic, terminal or intercalary, smooth-walled, cylindrical to subulate, flexuous, hyaline, (12–)16.5–33(–40) × 1–2 µm. *Conidia* limoniform, papillate, thin- and smooth-walled, aseptate, hyaline, 2.0–2.9 × 1.5–2.0(–2.5) µm, with a germ pore, arranged in dry chains. *Chlamydospores* ellipsoid, globose, thick- and smooth-walled, intercalated, hyaline, 3.5–6.2 × 3.2–5.3 µm.

Culture characteristics — Colonies on potato dextrose agar (PDA) umbonate, radially striate with lobate edge, aerial mycelium scarce to moderate, dense, cottony, buff colour (45) (Rayner 1970) in the centre to white on the periphery surface, buff on reverse, reaching 16 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, aerial sporulation, white to vinaceous buff (86) surface, reverse buff, reaching 22 mm diam after 2 wk at 25 °C with a photoperiod of 12 h. Colonies on synthetic nutrient-poor agar (SNA) flat, fimbriate, aerial mycelium scarce, buff surface and reverse, reaching 6 mm diam after 2 wk at 25 °C with a photoperiod of 12 h.

Typus. Brazil, Maranhão, Itinga do Maranhão, hyaline hyperparasite on *Pseudocercospora fijiensis* growing on leaves of *Musa acuminata* (*Musaceae*), 15 Dec. 2021, *F.A. Custódio* (holotype VIC 49479; culture ex-type COAD 3662; ITS, LSU, SSU, *rpb2* and *tef1-α* sequences GenBank OR558367, OR558365, OR558366, OR557609 and OR557608; MycoBank MB 850040).

Notes — The LSU and SSU sequences of *Catenomargarita pseudocercosporicola* have similarity with sequences of *Niessliaceae* and *Clavicipitaceae*. Phylogenetic analyses indicate that the genus belongs to *Niessliaceae*, with *Trichosphaerella ceratophora* being the closest species. *Catenomargarita* differs from *Trichosphaerella* by producing monophialidic conidiogenous cells and smooth-walled conidia. The family includes acremonium-like fungi that produce monophialides and hyaline conidia, such as the genera *Acremoniopsis*, *Collarina*, *Monocillium* and *Niesslia* (Hou et al. 2023). *Catenomargarita* differs from the other *Niessliaceae* genera by producing conidial chains, branched conidiophores and chlamydospores. *Niesslia catenata* and *N. indica* produce conidial chains but differs from *Catenomargarita pseudocercosporicola* in the absence of branched conidiophores and chlamydospores (Gams et al. 2019).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to the sequence of an ‘uncultured fungus’ hyperparasitic of *Hemileia vastratrix* in Puerto Rico (OTU 79, GenBank KT328841; Identities = 545/546 (99 %), one gap (0 %)), ‘*Colletotrichum* sp.’ (strain PT0920, GenBank ON155281; Identities = 611/640 (95 %), 10 gaps (1 %)) and *Trichoderma longibrachiatum* (strain 0501G, GenBank MF276664; Identities = 595/644 (92 %), 19 gaps (2 %)). Closest hits using the **LSU** sequence are *Eucasphaeria capensis* (strains CBS 120027 and CBS 120028, GenBank EF110619 and EF110618; Identities = 1 028/1 059 (97 %), one gap (0 %)), *Keithomyces* cf. *carneus* (strain CBS 126563, GenBank MT078856; Identities = 980/1 009 (97 %), three gaps (0 %)) and ‘*Clavicipitaceae* sp.’ (strain MEXU 26354, GenBank JQ811556; Identities = 1 005/1 036 (97 %), four gaps (0 %)). Closest hits using the **SSU** sequence has highest similarity to an ‘uncultured fungus’ (strain nco61b01c1, GenBank KC672415; Identities = 934/939 (99 %), one gap (0 %)), ‘*Hypocreales* sp. MR-2023e’ (strains CGMCC 3.22396 and CGMCC 3.22401, GenBank OQ758192 and OQ758191; Identities = 925/939 (99 %), one gap (0 %)). For the sequences of *rpb2* and *tef1-α* on a megablast search of NCBIs GenBank nucleotide database, no significant hits were obtained.

Colour illustrations. Black Sigatoka disease symptoms on *Musa acuminata* (*Musaceae*) in Itinga do Maranhão, state of Maranhão, Brazil. Colony on PDA after 2 wk at 25 °C; colony on OA after 2 wk at 25 °C; colony on SNA after 2 wk at 25 °C; conidiophores and conidiogenous cells giving rise to conidia; conidia in chains; chlamydospores. Scale bars = 10 µm.

Supplementary material

FP1556 Phylogenetic tree.

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Circinaria podoliana

Fungal Planet 1557 – 30 December 2023

Circinaria podoliana Szczepańska, Rodr. Flakus, Urbaniak & Śliwa, *sp. nov.*

Etymology. The epithet refers to the geographical region of Ukraine where the species was first collected.

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

Thallus lichenised, saxicolous, crustose, squamulose-areolate, contiguous rarely divided into small groups, 300–600 µm thick. Squamules thick, flexuose, irregular, (0.4–2.0 mm diam), partially erected and overlapping, less often rounded and slightly convex. *Prothallus* absent. *Upper surface* smooth, olive brown to chocolate brown, mat, pruinose on the margins. *Upper cortex* 30–50 µm thick, hyaline, with a thin, brown epinecral layer, 7–20 µm thick; *medulla* hyaline, with many tiny crystals, partially dissolving in N, not dissolving in K. *Photobiont* green, chlorococcoid, cells 7–16 µm diam; photobiont layer 50–70 µm thick, continuous but uneven in some parts. *Apothecia* immersed, rounded to irregular, 1 per areole, 0.3–1.2 mm diam; *thalline margin* not apparent, formed by radially cracked and white pruinose thalline areole; *disc* flat, circular to irregular, black, densely white pruinose; *proper margin* indistinct; *hymenium* hyaline, 150–170 µm high, I+ greenish blue; *paraphyses* septate and anastomosing, thin at the base, c. 2 µm wide, swollen at tips; submoniliform (2–3 globose apical cells), *epithecium*, c. 20 µm high, olive brown, N+ clearly green, K+ orange brown (Caesiocinerea-green pigment; Meyer & Printzen 2000), with a thin, uneven crystal layer, c. 10 µm thick (crystals colourless, dissolving in N and not dissolving in K); *hypothecium* hyaline, 40–50 µm high, I+ blue. *Asci* cylindrical in an immature state, 110–120 × 20–25 µm, clavate when mature, *Aspicilia*-type, *ascospores* 4–6 per ascus, hyaline, subglobose to broadly ellipsoid (20–)24–28(–32) µm diam (n = 20). *Pycnidia* immersed, c. 200 µm diam, rounded, ostiolar region projected, rounded, white pruinose. *Conidia* filiform, straight, 6–10 × 1 µm (n = 30). Chemistry. Spot tests: cortex K–, C–, P–, medulla K–, C–, P–. TLC (solvent A and C): all of the analysed samples contained aspicilin as a secondary metabolite.

Habit, Habitat & Distribution — *Circinaria podoliana* grows on natural limestone outcrops in open area, rarely on artificial substrata (mortar), in sunny, warm and exposed places.

Typus. Ukraine, Podilya Upland, Khmelnytskyi Oblast (province), Podil's'ki Tovtry National Park, Kitaygorod village, 15 km SE of Kamyanets' Podil's'kyi, canyon of Ternava River, N48°38'25" E26°46'59", 140 m a.s.l., limestone outcrops on south and southwest facing slope with *Crataegus* sp., *Rosa* sp. and young trees of *Juglans regia*, *Morus* sp. and *Populus* sp., 24 June 2003, *L. Śliwa*, 1878 (holotype KRAM L-49384; ITS and *mcm7* sequences GenBank OR436503 and OR441081; MycoBank MB 849796).

Additional materials examined. Ukraine, Podilya Upland, Khmelnytskyi Oblast (province), Podil's'ki Tovtry National Park, Ustya village at the junction of Smotrich River and the Dniester, N48°33'54" E26°39'24", 200 m, 26 June 2003, *L. Śliwa*, 1981 (KRAM L-49477; ITS, mtSSU and *mcm7* sequences GenBank OR436500, OR436507 and OR441080); Privorot'e near Makiv village, 10 km N of Kamyanets' Podil's'kyi, N48°47'27" E26°38'41", 223 m, 25 June 2003, *M. Kukwa*, 1880 (KRAM L-48743; ITS and mtSSU sequences GenBank OR436501 and OR457667); Chotyry Kavalery near Verbka village (Tovtra Verbets'ka nature reserve), 13 km N of Kamyanets' Podil's'kyi, N48°48'24" E26°35'54", 289 m, 26 June 2003, *A. Zalewska* (KRAM L-49261; ITS sequence GenBank OR436502); Kitaygorod village, 15 km SE of Kamyanets' Podil's'kyi, canyon of Ternava River, N48°38'25" E26°46'59", 140 m, 24 June 2003, *K. Czyżewska* (KRAM L-48907; ITS and mtSSU sequences GenBank OR436505 and OR436509, KRAM L-48920; ITS and mtSSU sequences GenBank OR436504 and OR436508); Chernivtsi Oblast (province), right bank of the Dniester River in Khotyn city, the Khotyn Fortress, 15 Aug. 2005, *J. Kiszka* (KRAP; ITS, mtSSU and *mcm7* sequences GenBank OR436506, OR436510 and OR441082).

Colour illustrations. Podilya Upland in Ukraine, canyon of Ternava River near Kitaygorod village (*locus classicus*). A habit of thallus with ascomata (holotype, KRAM L-49384); cross-section through thallus and apothecium with mature spores. Scale bars = 2 mm (a habit), 50 µm (apothecium), 100 µm (thallus).

Notes — *Circinaria* is heteromorphic genus, including crustose, subfruticose and subfoliose species (Sohrabi et al. 2013). Currently, there are 13 taxa of the genus known to occur in Ukraine (Kondratyuk et al. 2021). The new species, *C. podoliana*, is a member of *Circinaria contorta/calcarea* complex and presents typical features of the genus, such as: broadly ellipsoid spores reduced to four or six per ascus, short conidia and the presence of aspicilin. Specimens of *C. podoliana* were housed in fungaria under the current name *Circinaria contorta* (Nordin et al. 2010). *Circinaria contorta* is a very common and widely distributed lichen, occurring on calcareous rocks and other base-rich substrata (Fletcher et al. 2009, Wirth et al. 2013). The species has a crustose thallus consisting of separate or partly aggregated, white pruinose, rounded, slightly convex areoles with immersed crater-like apothecia (Rico 1999, Owe-Larsson et al. 2007). The main feature that distinguishes *C. podoliana* from *C. contorta* is the habit of the thallus, which is distinctly thicker and composed of overlapping, flexuose, olive brown to chocolate brown squamules that are pruinose only on the margins. Some specimens of the new species were labelled as *C. hoffmanniana* (Roux et al. 2016), which is also a common species occurring on calcareous rocky substrates. The most characteristic features of *C. hoffmanniana* are: grey to brownish grey, thin, cracked-areolate but continuous thallus producing immersed to sessile, prominent apothecia. *Circinaria podoliana* can be distinguished from the species mainly by a thicker and clearly squamulose-areolate thallus. A third calcareous lichen that may be confused with *C. podoliana* is *C. calcarea*. However, the latter species differs in having circular, chalk-white, smooth, cracked-areolate thallus and a grey prothallus.

In our analyses *C. podoliana* is nested within *Megasporaceae* and forms a distinct and highly supported lineage within the *Circinaria* as a sister to the *C. contorta* clade. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the **ITS** sequence had highest similarity to *Circinaria* sp. (voucher *Leavitt* 19096 (SL-2021a), GenBank MZ922119; Identities = 92.80 %, nine gaps (1 %)). The closest hit using the **mtSSU** sequence is *Aspicilia calcarea* (voucher *Wedin* 6500 (UPS), GenBank AY853310; Identities = 96.89 %, three gaps (0 %)). The closest hit using the ***mcm7*** sequence is *Aspicilia contorta* (voucher *Wetmore* (MIN 808806), GenBank GU980989; Identities = 99.42 %, no gaps).

Supplementary material

FP1557-1 Phylogenetic tree.
FP1557-2 Table.

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Curvularia huamulaniae

Fungal Planet 1558 – 30 December 2023

Curvularia huamulaniae Y.P. Tan & R.G. Shivas, *sp. nov.*

Etymology. Named after Hua Mulan, a legendary folk heroine from the period of Chinese history called the Northern and Southern Dynasties (386–581 AD).

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

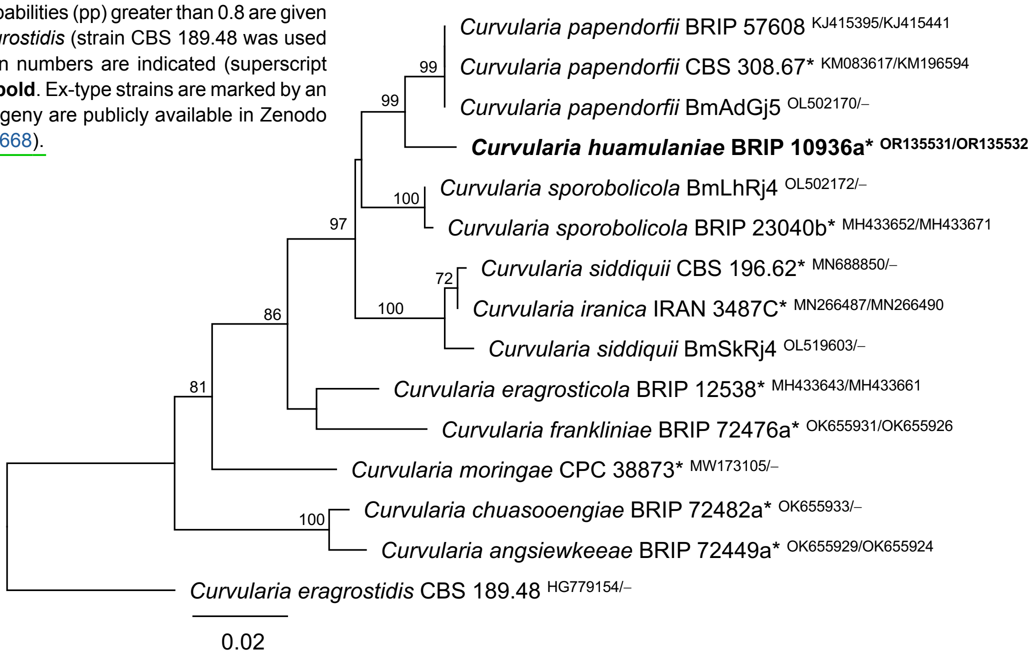
Asexual morph abundant on wheat straw agar after 2 wk at 25 °C in the dark. *Conidiophores* single, erect, straight to flexuous, with many geniculations, brown, cylindrical, smooth, 70–150 µm long, 6–8 µm wide, septate, with prominent scars, unbranched or sparingly branched. *Conidiogenous cells* intercalary and terminal, brown, smooth, with darkened scars. *Conidia* straight to slightly curved on one side and strongly curved on the other, hemispherical to obpyriform, 28–42 × 14–22 µm, rounded at the apex and flattened to rounded at the base, 3–4-distoseptate, reddish brown, smooth.

Typus. Australia, Queensland, Brisbane, isolated from air, 12 Feb. 1964, *R.G. Rees* (holotype BRIP 10936a permanently preserved in a metabolically inactive state; culture ex-type BRIP 10936a; ITS, *gapdh* and *tef1* sequences GenBank OR130931, OR135531 and OR135532; MycoBank MB 849552; isotype IMI 108517).

Notes — *Curvularia huamulaniae* is morphologically indistinguishable from *C. papendorfii* (Van der Aa 1967). *Curvularia huamulaniae* differs from *C. papendorfii* (ex-type strain CBS 308.67) by sequence comparison of the ITS region (GenBank KJ909774; Identities 647/653 (99 %), three gaps; unique nucleotide at positions 188(C), 258(T), 512(T)), *gapdh* (GenBank KM083617; Identities 414/430 (96 %); unique nucleotide at positions 25(T), 28(T), 37(G), 47(G), 49(T), 54(T), 65(C), 78(G), 177(T), 189(C), 273(T), 291(A), 297(T), 348(C), 375(C), 426(C)), and *tef1* (GenBank KM196594; Identities 895/899 (99 %); unique nucleotide at positions 156(C), 276(T), 366(C), 393(C)).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest relevant hits using the **ITS** sequence are *C. papendorfii* (strain CBS 308.67, GenBank KJ909774, Identities 647/653 (99 %), three gaps), *C. sporobolicola* (strain BRIP23040b, GenBank MH414908, Identities 646/652 (99 %), two gaps) and *C. siddiquii* (strain CBS 196.62, Identities 580/590 (98 %), six gaps). The closest relevant hits using the ***gapdh*** sequence are *C. papendorfii* (strain CBS 308.67, GenBank KM083617, Identities 414/430 (96 %)), *C. sporobolicola* (strain BRIP23040b, GenBank MH433652, Identities 423/446 (95 %)) and *C. siddiquii* (strain CBS 196.62, GenBank MN688850, Identities 431/461 (93 %)). The closest relevant hits using the ***tef1*** sequence are *C. papendorfii* (strain CBS 308.67, GenBank KM196594, Identities 895/899 (99 %)), *C. eragrostidis* (isolate CD15, GenBank MK886803, Identities 966/989 (98 %)) and *C. dactyloctenicola* (strain M0307, GenBank OM714560, Identities 922/944 (98 %)).

Phylogenetic tree based on maximum likelihood analysis of the alignment of the combined *gapdh* and *tef1α* sequences from species of *Curvularia*. Analyses were performed on the Geneious Prime 2023 platform using RAxML v. 8.2.11 and MrBayes v. 3.2.6, both based on the GTR substitution model with gamma-distribution rate variation. Bootstrap support (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). *Curvularia eragrostidis* (strain CBS 189.48 was used as the outgroup. GenBank accession numbers are indicated (superscript *gapdh*/*tef1*). Novel taxon is shown in **bold**. Ex-type strains are marked by an asterisk (*). The alignment and phylogeny are publicly available in Zenodo (https://doi.org/10.5281/zenodo.8042668).



Colour illustrations. Moonrise on Sunrise Beach, Queensland, Australia. Colony on wheat straw agar; conidiophores; conidia. Scale bars = 100 µm (colony), 10 µm (others).

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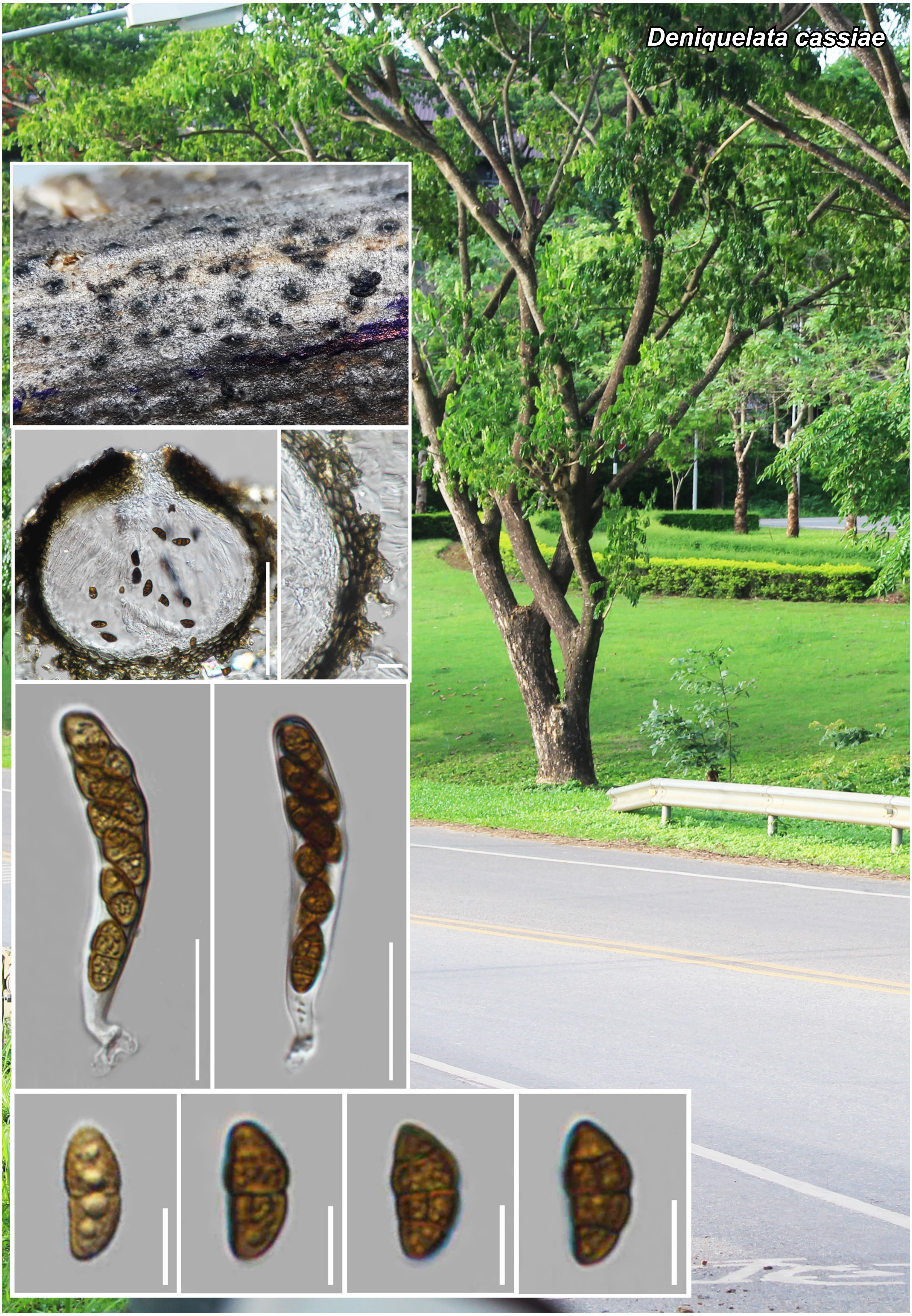
Deniquelata cassiae

Fungal Planet 1559 – 30 December 2023

Deniquelata cassiae Tennakoon & Suwannar., *sp. nov*.

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

Classification — *Didymosphaeriaceae*, *Pleosporales*, *Dothideomycetes*.

Ascomata separate, immersed to semi-immersed, partly erumpent, solitary or scattered, globose to sub-globose, unilocular, dark brown to black, 200 µm diam, with central papillate ostiole; wall of 3–4 layers of brown, darkly pigmented cells of *textura angularis*. *Pseudoparaphyse*s cellular, hyaline, smooth, branched, septate, anastomosing, 1–2 µm diam. *Asci* bitunicate, 8-spored, cylindrical-clavate, fissitunicate, slightly curved, rounded apex, with low ocular chamber, 1–3 µm diam, 1–2 µm high (visible only in young asci), with a short pedicel, 60–80 × 10–12 µm. *Ascospores* bi- to tri-seriate, ellipsoidal to fusoid, widest in middle of second cell from apex, developing a central septum and then becoming muriformly septate, slightly constricted at the septa, straight to curved, hyaline when immature and reddish brown at maturity, guttulate, 14–16 × 6–8 µm.

Typus. Thailand, Chiang Rai, on dead stem of *Cassia fistula* (*Fabaceae*), 12 Aug. 2021, *D.S. Tennakoon*, CMD012A (holotype CMUB 40013, isotype CMUB 40015; ITS, LSU, SSU and *tef1* sequences GenBank OR500092–OR500093, OR500088–OR500089, OR500090–OR500091 and OR501827–OR501828; MycoBank MB 849873).

Notes — *Deniquelata* was introduced by Ariyawansa et al. (2013) to accommodate *D. barringtoniae* as the type species. Subsequently, *D. hypolithi*, *D. macphersoniae*, *D. quercina*, *D. vittalii* and *D. yunnanensis* were added by various researchers (Devadatha et al. 2018, Alidadi et al. 2019, Crous et al. 2021a, Lu et al. 2022, Tan & Shivas 2022). *Deniquelata* species have been reported as pathogens, saprophytes, and endophytes (Ariyawansa et al. 2013, Crous et al. 2021a, Tan & Shivas 2022). The phylogeny inferred from the ITS, LSU, SSU and *tef1* sequences demonstrated that the new species *D. cassiae* nested in the *Deniquelata* clade and forms an independent lineage sister to *D. yunnanensis* with 80 % statistical support. *Deniquelata cassiae* differs from *D. yunnanensis* in their ellipsoidal to fusoid ascospores, whereas *D. yunnanensis* has ellipsoidal to oblong ascospores (Lu et al. 2022). Furthermore, *D. cassiae* can be distinguished from *D. macphersoniae* based on ITS nucleotide differences (14/698 bases). *Deniquelata cassiae* can be distinguished from *D. quercina* in the distinct size differences of asci (85–155 × 13–18 µm vs 60–80 × 10–12 µm) and ascospores (9–11 × 18–21 µm vs 14–16 × 6–8 µm) (Alidadi et al. 2019). In addition, *D. cassiae* differs from *D. vittalii* and *D. barringtoniae* in the distinct size differences in asci (68–80 × 10–15 µm and 75–135 × 10–19 µm) and ascospores (14–16 × 5–7 µm and 18–26 × 7.5–13.5 µm) (Ariyawansa et al. 2013, Devadatha et al. 2018).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Deniquelata yunnanensis* (strain ZHKUCC:22-0198, GenBank OP297803; Identities = 785/794 (98.86 %), two gaps (0.8 %)), *D. yunnanensis* (strain ZHKUCC:22-0199, GenBank OP297804; Identities = 802/813 (98.64 %), two gaps (0.2 %)), *D. macphersoniae* (strain BRIP 72538b, GenBank NR_182616; Identities = 839/847 (99.1 %), one gap (0.1 %)), *Didymosphaeriaceae* sp. (strain A1S3-D34, GenBank KJ780753; Identities = 709/745 (95.1 %), 12 gaps (1.6 %)). Closest hits using the **LSU** sequence are *D. yunnanensis* (strains ZHKUCC:22-0199 and ZHKUCC:22-0198, GenBank OP297774 and OP297773; Identities = 916/919 (99.78 %), two gaps (0.2 %)), *D. macphersoniae* (strain BRIP 72538b, GenBank OP598061; Identities = 890/890 (99.6 %), one gap (0.1 %)), *Neokalmusia arundinis* (strain MFLUCC 14-0222, GenBank KX954400; Identities = 948/953 (4.2 %), seven gaps (0.1 %)), *Phaeodothis winteri* (strain AFTOL-ID 1590, GenBank DQ678073; Identities = 947/953 (99.4 %), six gaps (0.1 %)), *Bimuria novae-zelandiae* (strain CBS 107.79, GenBank OM337538; Identities = 1702/1707 (99.7 %), four gaps (0.1 %)).

Colour illustrations. Holotype collection area in Chiang Rai, Thailand. Appearance of ascomata on dead stem of *Cassia fistula*; vertical section of ascoma; peridium; asci; ascospores. Scale bars = 100 µm (section), 10 µm (peridium), 30 µm (asci), 8 µm (ascospores).

Supplementary material

FP1559-1 Phylogenetic tree.
FP1559-2 Table.

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Diaporthe jazanensis

Fungal Planet 1560 – 30 December 2023

Diaporthe jazanensis Alhudaib & A.M. Ismail, *sp. nov.*

Etymology. The name refers to the collection locality (Jazan, Saudi Arabia).

Classification — *Diaporthaceae*, *Diaporthales*, *Sordariomycetes*.

Conidiomata pycnidial, mostly solitary, pale to dark brown, deeply embedded in potato dextrose agar (PDA) erumpent, irregular globose or sub-globose to depressed, exuding dark brown to black conidial masses, when aged bordered with thick-walled cells of *textura angularis*. *Conidiophores* hyaline, smooth, densely aggregated. *Conidiogenous cells* densely phialidic, hyaline, terminal, sub-cylindrical, tapered towards the apex. *Paraphyses* not observed. *Alpha conidia* hyaline, smooth, fusoid or ellipsoidal, straight to curved, aseptate, tapered at both ends, 7.0–9.8 × 2.5–3.3 µm (av. = 8.4 ± 0.69 × 2.9 ± 0.19 µm). *Beta conidia* spindle-shaped, smooth, acute at apex, slightly truncate at base, frequently curved, 20.9–36.3 × 0.7–2.2 (av. = 30.6 ± 4.3 × 1.6 ± 0.41 µm). *Gamma conidia* not observed.

Culture characteristics — Colonies covered the dish after 10 d at 25 °C. Colony on PDA at the beginning white to beige becoming pale brown, flattened, distinctly imbricated like tree branches. Reverse side pale brown, turning dark brown with age.

Typus. Saudi Arabia, Jazan Region, N17°23'07.9" E43°09'01.5", on branches of *Coffea arabica* (*Rubiaceae*), 12 Oct. 2022, *A.M. Ismail* (holotype KSA-28R-2023; culture ex-type PPDU28R; ITS, *tef1* and *tub2* sequences GenBank OQ586408, OR137582 and OR137586; MycoBank MB 849121).

Additional materials examined. Saudi Arabia, Jazan Region, N17°23'07.9" E43°09'01.5", on branches of *C. arabica*, 12 Oct. 2022, *A.M. Ismail*, culture PPDU28S, ITS, *tef1* and *tub2* sequences GenBank OQ586409, OR137583 and OR137587; ibid., culture PPDU28U, ITS, *tef1* and *tub2* sequences GenBank OQ586410, OR137584 and OR137588; ibid., culture PPDU28Z, ITS, *tef1* and *tub2* sequences GenBank OQ586411, OR137585 and OR137589.

Colour illustrations. *Coffea arabica* in coffee plantation in the Jazan Region, Saudi Arabia. Colony morphology and sporulation on PDA medium; alpha and beta conidia. Scale bars = 10 µm.

Notes — *Diaporthe jazanensis* is phylogenetically closely related but well-separated from *D. caatingaensis* CBS 141542 and *D. brasiliensis* CBS 133183. Furthermore, *D. jazanensis* can be distinguished by its somewhat wider alpha conidia (2.5–3.3 µm) than those of *D. caatingaensis* (1.5–2.5 µm) (Crous et al. 2016) and *D. brasiliensis* (2–3 µm) (Gomes et al. 2013). Additionally, beta conidia are present in *D. jazanensis*, but absent in *D. caatingaensis* and *D. brasiliensis*. Colonies of *D. jazanensis* on PDA covered the entire surface of Petri dishes after 10 d, which is faster than observed in *D. caatingaensis* (14 d) and *D. brasiliensis* (14 d) at 25 °C. Moreover, the colony morphology of *D. jazanensis* is white to beige, becoming pale brown with age, flattened, distinctly imbricated like a tree branch while, the colonies of *D. caatingaensis* have white, fluffy aerial mycelium and colonies of *D. brasiliensis* are flat, with an entire edge, dense, felty and buff, grey olivaceous.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *D. caatingaensis* (strain 11, GenBank OP955669; Identities = 513/513 (100 %), no gaps), *D. caatingaensis* (strain 21, GenBank OP959918; Identities = 513/514 (99 %), one gap (0 %)) and *D. caatingaensis* (strain 16, GenBank OP956980; Identities = 513/514 (99 %)), no gaps (0 %)). Closest hits using the ***tef1*** sequence are *D. caatingaensis* (strain URM7486, GenBank KY115603; Identities = 336/347 (97 %), three gaps (0 %)), *D. brasiliensis* (strain CBS 133183, GenBank KC343768; Identities = 321/345 (93 %), one gap (0 %)) and *D. brasiliensis* (strain LGMF926; GenBank KC343769; Identities = 321/346 (93 %), one gap (0 %)). Further, the closest hits using the ***tub2*** gene sequence are *D. brasiliensis* (strain CBS 133183, GenBank KC344010; Identities = 353/359 (98 %), no gaps (0 %)), *D. caatingaensis* (strain URM7486, GenBank KY115600; Identities = 374/385 (97 %), four gaps (1 %)) and *D. monospora* (strain CFCC 55362, GenBank MZ577286; Identities = 409/444 (92 %), two gaps (0 %)).

Supplementary material

FP1560-1	Table.
FP1560-2	Phylogenetic tree.

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Entoloma occultatum

Fungal Planet 1561 – 30 December 2023

Entoloma occultatum M. van der Vegte & G.M. Jansen, *sp. nov.*

Etymology. Refers to the easily overlooked hidden basidiomata.

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

Basidiomata small-sized. *Pileus* 2–6 mm, hemispherical, centre slightly depressed; young: not striate, a little micaceous, tomentose with little scales at the centre, white; mature: striate for 3/4 of the radius, smooth, light cream, more beige towards the centre, margin involute. *Lamellae* L = 8–12, l = 1–3, intermediate gills present, adnate with decurrent tooth, ventricose, pallid white; edge entire, concolorous. *Stipe* 13–40 × 0.5–0.6 mm, cylindrical, smooth; pallid, pale cream with lengthwise paler fibres. *Smell* inconspicuous. *Spores* 7.5–10.8 × 5.9–7.7 µm (av. 8.6 × 6.6 µm), Q = 1.1–1.5 (Qav = 1.27) (n = 97 from three collections), heterodiametrical, 5–6 angled. *Basidia* 24–41 × 6.5–11 µm, clavate, 4-spored, clamped. *Lamellae edge* fertile. *Pleurocystidia* not seen. *Cheilocystidia* not seen. *Caulocystidia* not seen. *Pileipellis* cutis with a transition to a trichoderm, terminal cells clavate up to 85 µm long and 6–13 µm wide, intracellular pigment hardly visible (somewhat granular pigment in the terminal hyphen at centre, incrusted pigment not seen. *Stipititrama* cylindrical hyphen 7–10.5 µm wide, intracellular pigment. *Trama* hyphen rather short 50–100 × 10–11 µm. *Clamps* all tissues with clamps. All measurements in 5 % KOH.

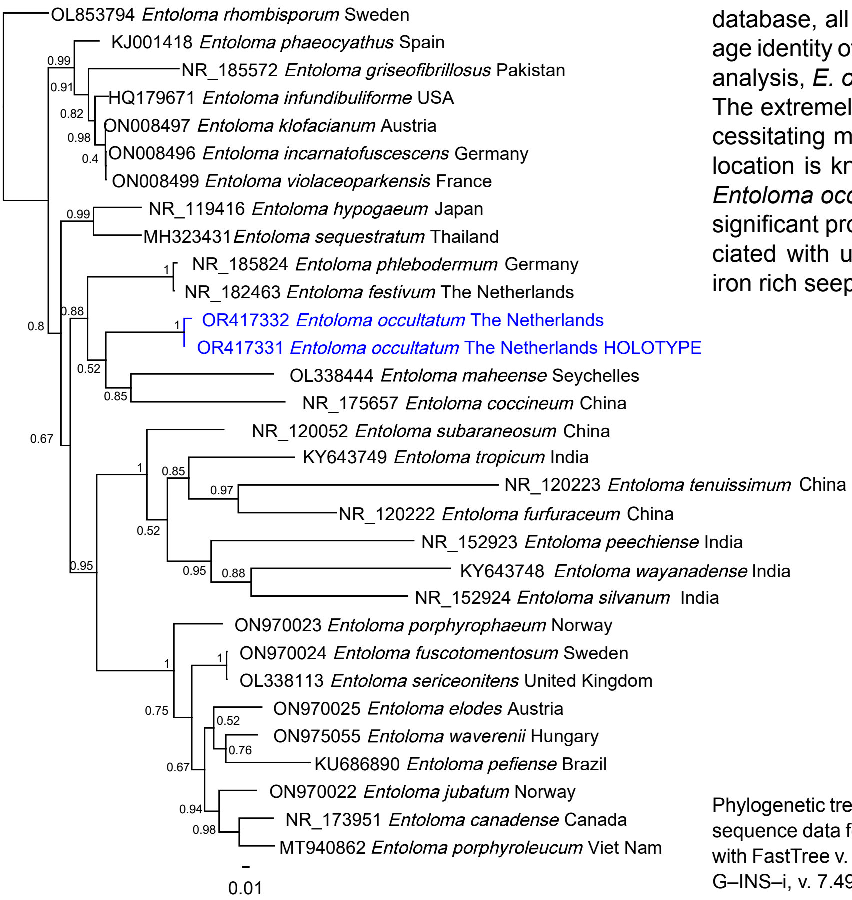
Habitat & Distribution — Gregarious between mosses on peaty soil, unfertilised hayfield on loamy ground with calcareous and iron rich seepage. So far only known from the type location.

Typus. The Netherlands, Gelderland Province, Groesbeek, De Bruuk, 51.762 5.958, 22 July 2019, *M. van der Vegte* (holotype L 0608197; ITS sequence GenBank OR417331; MycoBank MB 849735).

Additional materials examined. The Netherlands, Gelderland Province, Groesbeek, De Bruuk, 51.761 5.957, 25 Sept. 2022, *M. van der Vegte* (L 4343915, ITS sequence GenBank OR417332); ibid., 51.762 5.958, 23 Aug. 2019, *M. van der Vegte* (L 4343928, not sequenced).

Notes — This minute fungus thrives inconspicuously amidst mosses, its diminutive stature making it prone to being easily disregarded. It bears a resemblance to *Hemimycena* or *Mycena* species. However, under microscopic observation, the significant portion of pentagonal spores stands out. Superficially, *E. occultatum* exhibits similarities to *E. olorinum*, a species that is also small but substantially less petite in its growth habit. Another species, *E. percandidum*, bears some resemblance but differs in having spores with 6–10 angles in side view. Additionally, *E. cephalotrichum* comes close in resemblance, but it can be distinguished by its larger spores and pileipellis and stipitipellis both featuring capitate terminal elements and lacking clamps.

Based on a megablast search of NCBIs GenBank nucleotide database, all hits using the ITS sequence showed a percentage identity of less than 85 %. Interestingly, in the phylogenetic analysis, *E. occultatum* shows an isolated position in the tree. The extremely minute basidiomata are easily overlooked, necessitating meticulous and close examination even when the location is known, to locate these diminutive fruiting bodies. *Entoloma occultatum* is characterised by its small size, with a significant proportion of pentagonal spores, and is likely associated with uncultured hay land featuring a calcareous and iron rich seepage.



Phylogenetic tree with FastTree support values based on nrITS1-5.8S-ITS2 sequence data for *Entoloma occultatum* using maximum likelihood analysis with FastTree v. 2.1.12 (Price et al. 2009, 2010); MAFFT alignment (MAFFT G–INS–i, v. 7.490 (Katoh et al. 2002, Katoh & Standley 2013).

Colour illustrations. The Netherlands, Groesbeek, de Bruuk, unfertilised hayfield, type locality. Spores, pileipellis, (all from holotype); basidiomata in situ. Scale bars = 10 µm (pileipellis), 5 µm (spores).

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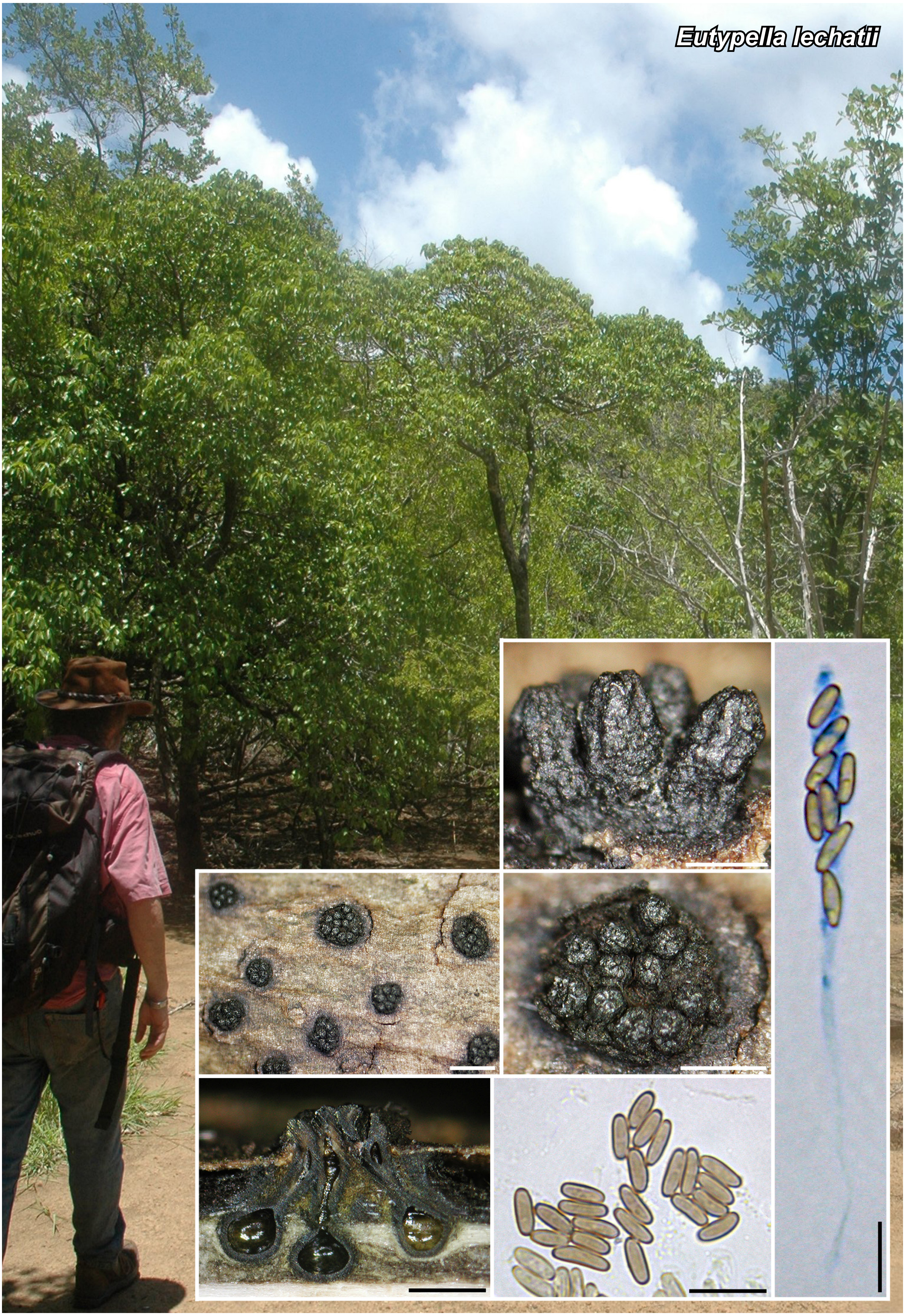

Eutypella lechatii

Fungal Planet 1562 – 30 December 2023

Eutypella lechatii J. Fourn. & A.N. Mill., *sp. nov.*

Etymology. Name refers to our friend Christian Lechat († 7 January 2022) who first collected this species.

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

Stromata corticolous, pustulate, not raising the periderm individually, regularly scattered, rarely in contact or coalescent, broadly conical with flat base, 1–1.7 mm diam at base, containing 5–15(–25) perithecia, appearing on host surface as discoid to ellipsoid structures 0.5–1.5 mm diam, roughened by prominent clusters of ostioles. Ectostroma black, well-developed around stromata, 150–350 µm thick, flaky to crumbly, loosely prosenchymatous and spreading horizontally between stromata, not reaching the woody host tissues. Entostroma present above perithecia between ostiolar necks, composed of yellowish to olivaceous yellow necrotic host tissue. *Perithecia* subglobose to depressed-spherical, 350–480 µm diam, with strongly convergent ostiolar necks 400–550 µm long. *Ostioles* collectively erumpent, more or less shiny black, tightly packed, slightly diverging above the disk, 300–850 µm high, 150–325 µm diam, cylindrical to most often attenuated at apex, coarsely sulcate lengthwise, apically rounded to flattened and reticulately-cracked. *Paraphyses* copious, hyphal, hyaline, remotely septate, obscurely guttulate, 4–5 µm wide at base, gradually tapering to 1 µm wide above asci, embedded in a dense gelatinous matrix. *Asci* long-pedicellate, 8-spored, the spore-bearing part spindle-shaped at maturity with ascospores 2–3-seriate in central part, 32–42 × 4.5–6 µm, stipes 40–50 µm long; ascus apex poorly differentiated, without visible apical ring, not bluing in Melzer's reagent after 3 % KOH pre-treatment. *Ascospores* (5.2–)5.8–7.6(–8.7) × (1.9–)2.2–2.6(–2.8) µm, Q = (2.0–)2.3–3.2(–4.3) µm, N = 180 (Me = 6.5 × 2.4 µm, Qe = 2.8), pale brown, narrowly ellipsoid to oblong, with broadly rounded ends, occasionally faintly bent, smooth-walled. The three collections CLL7200, MJF07029 and MJF10154 respectively feature ascospores 6.5 × 2.3 µm, 6.8 × 2.4 µm and 6.3 × 2.4 µm on average.

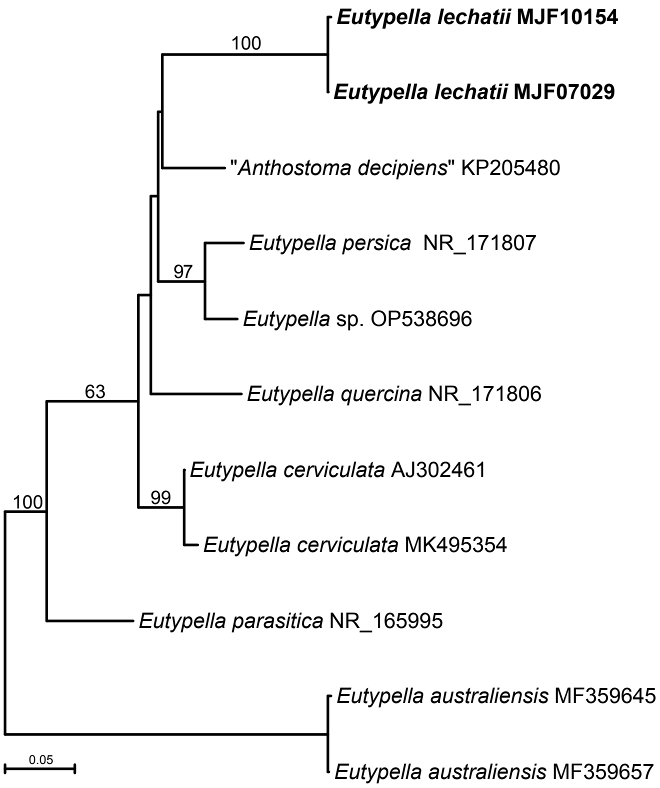
Habitat & Distribution — Coastal meso- to xerophilic forest. Known only from Martinique.

Typus. French West Indies, Martinique, Les Anses d'Arlet, Anse Noire, N14.5263 W61.0839, costal meso- to xerophilic forest, on dead corticated palm stem, 22 Aug. 2007, *J. Fournier*, MJF07029 (holotype ILLS00122397 (ILLS); ITS sequence GenBank OR616540; MycoBank MB 850272).

Additional materials examined. French West Indies, Martinique, La Trinité, Caravelle peninsula, Pointe-Rouge, N14.7605 W60.9344, costal meso- to xerophilic forest, on dead corticated palm stem, 12 Aug. 2007, *C. Lechat* (CLL7200, ILLS00122398), ITS2 sequence GenBank OR616541; N14.7189 W60.9318W, costal meso- to xerophilic forest, on dead corticated palm stem, 26 Aug. 2010, *J. Fournier* (MJF10154, ILLS00122399), ITS sequence GenBank OR616542.

Colour illustrations. Christian Lechat entering a dry coastal forest in Caravelle peninsula, La Trinité, Martinique, French West Indies (photo credit P.-A. Moreau). Ostioles; stromatic discs on host surface; stroma in vertical section; ascospores in water; ascus in diluted blue ink. Scale bars = 1 mm (ostioles), 500 µm (stromatic disks, stroma section), 250 µm (stromatic disk), 10 µm (ascospores and ascus) (photos J. Fournier).

Notes — This diatrypaceous fungus features the main characters of the genus *Eutypella* in having small pustulate stromata with ostiolar necks converging and protruding through a common disc (Rappaz 1987). It is characterised by rounded, separate stromata piercing the persistent periderm, long, stout ostioles that are deeply sulcate, a thick layer of blackened host tissue above the deeply immersed perithecia, olivaceous entostromatic tissue between the ostiolar necks and perithecia, inconspicuous and inamyloid apical ring and light brown, narrowly ellipsoid to occasionally suballantoid ascospores, 6.5 × 2.4 µm on average. It is morphologically distinct from the three north temperate species *E. grandis*, *E. parasitica* and *E. phaeospora*, which possess similar dark-coloured and mostly straight ascospores, by an olivaceous entostroma vs white for the two former and absent for the latter (Rappaz 1987, Fournier & Lechat 2011). Ascospores of *E. grandis* and *E. parasitica* are larger, respectively 8.5–11.2 × 3.0–3.2 µm and 6.8–11.2 × 2.2–2.5 µm, whereas those of *E. phaeospora* are more broadly ellipsoid, 6–7.5 × 3.4–4 µm. Although *Anthostoma decipiens* could likewise be considered because of its pale brown ascospores, (5–)6–9(–10) × (2.5–)2.8–4 µm, it differs by its widely spread diatrypoid to eutypoid stromata with an abundant brownish grey entostroma and shorter ostioles (Rappaz 1992). None of the ITS sequences of *A. decipiens* in GenBank originate from a verifiable sexual morph and are better assigned to *Eutypella* sp.



Maximum Likelihood tree generated using PhyML in SeaView v. 5.0.4 (Gouy et al. 2010). *Eutypella lechatii* is in bold. Numbers above branches refer to bootstrap support values from 1 000 bootstrap replicates. GenBank accession numbers for the ITS region are given after taxon names. The alignment and trees are publicly available in TreeBASE (study ID: TB2: S30694).

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Exophiala wilsonii

Fungal Planet 1563 – 30 December 2023

Exophiala wilsonii Jurjević, Torres-Garcia, Gené & Hubka, *sp. nov.*

Etymology. Named in honour of David Merl Wilson for his significant contribution to Mycotoxin and Plant Pathology science.

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

Micromorphology (on malt extract agar; MEA): *Hyphae* light olive brown, moniliform, smooth-walled, septate, 2–3 µm diam. *Conidiophores* poorly differentiated from vegetative hyphae, micronematous or short erect. *Conidiogenous cells* variable in shape, cylindrical, flask-shaped, ovoid to elongate. *Conidia* obovoid to cylindrical, usually aseptate, smooth, 3.5–7 × 2–4 µm diam. *Yeast-like budding cells* not observed. *Chlamydospores* not observed. *Sexual morph* unknown.

Culture characteristics — (in darkness, 25 °C after 14 d): Colonies MEA 10–12 mm diam, floccose, mycelium smoke grey to dark greyish olive in the centre (R46; Ridgway 1912), abruptly rising 3–4 mm, margins submerged (3–5 mm broad zone), good sporulation, soluble pigments absent, reverse olivaceous black (R46). Colonies on Czapek yeast autolysate agar (CYA) 7–9 mm diam, floccose to velvety, mycelium greyish olive to dark greyish olive (R46), centrally crateriform, poor sporulation, soluble pigments absent, reverse deep greyish olive to dark greyish olive (R46). Colonies on potato dextrose agar (PDA**)** 11–12 mm diam, floccose to slightly funiculose centrally, mycelium smoke grey to greyish olive (R46), poor sporulation, soluble pigments absent, reverse dark greyish olive (R46). Colonies on oatmeal agar (OA**)** 10–11 mm diam, floccose, mycelium dark greyish olive (R46), heavy sporulation, soluble pigments absent, reverse dark greyish olive (R46). Colony diam (in mm after 14 d) at 20 °C / 30 °C / 35 °C; MEA 9–10 / 11–12 / germinate; CYA 5–6 / 8–9 / no growth; PDA 5–8 / 12–13 / 2–3; OA 7–9 / 10–12 / no growth; no growth at 37 °C on MEA, CYA, PDA and OA.

Typus. USA, Indiana, water from cooling tower, 28 Jan. 2015, *Ž. Jurjević* (holotype CBS H-25008, culture ex-type CCF 5674 = CBS 142811 = EMSL 2678; ITS, LSU, SSU, *mcm7*, *tub2* and *RPB1* sequences GenBank OR552118, OR555859, OR555748, OR581281, OR581282 and OR581283; MycoBank MB 843824).

Notes — A BLAST analysis of the **ITS** sequence of *E. wilsonii* showed the greatest similarity with sequences derived from the ex-types of *Cladophialophora nyingchiensis*, *Capronia acutiseta* and *Capronia rubiginosa* with similarities ranging from 88.9–89.8 %. The **LSU** region showed greater similarity with *Capronia fungicola*, *Capronia kleinmondensis* and *Exophiala dermatitidis* with similarities ranging from 97.8–98.1 %, while the **SSU** region was most similar to *Exophiala halophila*, *Cladophialophora devriesii* and *Rhinocladiella phaeophora* with similarities ranging from 99.2–99.3 %. The similarities of *mcm7*, *tub2* and *RPB1* to known taxa were < 85 %.

In the phylogeny based on combined data from the ITS and LSU regions of the nrDNA, *E. wilsonii* most closely clustered with *Exophiala alcalophila* and *Valentiella maceioensis.* These species differ from *E. wilsonii* by having slimy, smooth colonies and by the shape of their conidia which are spherical, ellipsoidal to slightly reniform in *E. alcalophila*, and ellipsoid, subglobose to globose in *V. maceioensis*.

The phylogeny of the family *Herpotrichiellaceae* (black yeasts and allies) has been analysed repeatedly using sets of different genes; however, the statistical support of the backbone of the trees is minimal (Quan et al. 2020), similar to our phylogeny. Many morphologically defined genera appear to be polyphyletic, but the re-definition of generic limits is postponed until a more complete overview of species and a better-supported phylogeny is obtained. For this reason, we temporarily describe our new species in the genus *Exophiala* based on morphological similarities. At the same time, it is highly probable that it will be reclassified in the future, as evidenced for instance by very high genetic distances from its closest relatives and a high phylogenetic distance from the type species of the genus *Exophiala*, *E. salmonis*.

Colour illustrations. Cooling tower where the novel species was collected. Fourteen-day-old cultures of *Exophiala wilsonii* on MEA (top to bottom 20, 25, 30 and 35 °C); conidia and conidiophores on MEA. Scale bars = 10 µm.

Supplementary material

FP1563 Phylogenetic tree.

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Fulvifomes maritimus

Fungal Planet 1564 – 30 December 2023

Fulvifomes maritimus V. Vasan, N. Chellappan & M. Kaliyaperumal, *sp. nov.*

Etymology. The species epithet '*maritimus*' derived from Latin word representing the coastal area.

Classification — *Hymenochaetaceae*, *Hymenochaetales*, *Agaricomycetes.*

Basidiomata perennial, solitary, pileate, sessile, hard when fresh, and light in weight when dry. *Pilei* applanate, projecting up to 8 cm in length, 13.5 cm wide and 6.5 cm thick near attachment. *Pileal surface* greyish brown (6F3; Kornerup & Wanscher 1978) near the margin to greyish brown (6F2) towards the attachment, crusted, azonate, meagerly cracked, scrupose. *Margin* greyish brown (6F2), acute to obtuse, 4 mm in thickness. *Pore surface* brown (6D7). *Pores* regular, round, 5–7 per mm. *Context* brown (6E6) homogenous, 2.5 cm thick. *Tube layer* brown (6D7), 3.7 cm, stratified, each stratum up to 5 mm. *Hyphal system* dimitic; tissue darkening in KOH without hyphal swelling. *Context* generative hyphae thin- to thick-walled, pale yellow to brown, simple septate, rarely branched, 3.1–4.9 µm; skeletal hyphae, thick-walled with narrow to wide lumen, pale yellow, aseptate, unbranched, 3–4.2 µm wide. *Trama* generative hyphae thin- to thick-walled, hyaline to dark brown, simple septate, rarely branched, 2.8–4.6 µm wide. Skeletal hyphae thick-walled with narrow to wide lumen, brown, aseptate, unbranched, 3.4–4.6 µm. *Setae* and *cystidioles* absent. *Basidia* clavate to broadly clavate, with four sterigmata, 8–12.9 × 5–9 µm. *Basidioles* clavate, 3–10 × 3.5–5 µm. *Basidiospores* smooth, subglobose to broadly ellipsoid, thick-walled, pale yellow to golden yellow in water, turning golden brown to brown in KOH, (4.9–)5.2–5.4(–5.7) × (4.4–)4.6–4.9(–5.2) µm (n = 30/2), Q = 1.12 (Q range 1.1–1.17), CB$^-$, IKI$^-$.

Typus. India, Tamil Nadu, Chennai district, Besant Nagar, E80°26'28.31" N13°00'08.34", on living *Peltophorum pterocarpum* (*Fabaceae*), 8 Sept. 2022, *V. Vasan* (holotype MUBL1095; ITS and LSU sequences GenBank OR520888 and OR512084; MycoBank MB 849926).

Notes — *Fulvifomes maritimus* is a typical species of *Fulvifomes*. Phylogenetic analysis inferred from ITS and LSU sequence data indicates that *F. maritimus* forms a distinct lineage with *F. grenadensis*, *F. thailandicus*, *F. aurantiacus* and three Indian species viz., *F. malaiyanurensis*, *F. thiruvannamalaiensis* and *F. jawadhuvensis* (63 % ML, 1.00 BPP). *Fulvifomes maritimus* is similar to *F. jawadhuvensis* and *F. malaiyanurensis* in having homogenous context, dimitic hyphal system, absence of cystidioles but varies in basidiome and basidiospore characters. *Fulvifomes maritimus* resembles *F. thiruvannamalaiensis* and *F. grenadensis* in having a cracked basidiome, homogenous context and dimitic hyphal system, but our Indian specimen differs microscopically in the absence of cystidioles and basidiospore size (Ryvarden 2004, Jayawardena et al. 2022).

Fulvifomes maritimus and *F. thailandicus* have a similar dimitic hyphal system and crusted pileus, but differ significantly in other morphological features (Zhou 2015). Our Indian species, *F. aurantiacus* and *F. hainanensis* have a dimitic hyphal system and lack cystidioles. Nevertheless, *F. maritimus* differs in having a meagerly cracked crusted pilear surface, a homogenous context and smaller spores (Zhou 2014, Fathima et al. 2023).

Fulvifomes maritimus differs from *F. caligoporus*, *F. cedrelae*, *F. coffeatoporus*, *F. dracaenicola*, *F. eleodendri* and *F. subindicus* in having a dimitic hyphal system, compared to the mono-dimitic hyphal system in the other species (Hattori et al. 2014, Salvador-Montoya et al. 2018, Tchoumi et al. 2020, Du et al. 2021, Wu et al. 2022).

Based on a BLAST search of NCBI (GenBank nucleotide database), the closest hits using the ITS sequence had highest similarity with *Phellinus* sp. (YD-2015 isolate NZ13, GenBank KP658515; Identities = 641/642 (99 %), no gaps), *Phellinus* sp. (YD-2015 isolate KP31, GenBank KP658591; Identities = 640/642 (99 %), no gaps) and *Phellinus* sp. (YD-2015 isolate NZ7, GenBank KP658510; Identities = 640/642 (99 %), no gaps). Closest hits using the LSU sequence are *Fulvifomes jawadhuvensis* (SKM-JMR5, GenBank MW048886; Identities = 862/864 (99 %), no gaps), *Fulvifomes thailandicus* (LWZ 20140731-1, GenBank NG068761; Identities = 858/864 (99 %), no gaps) and *Fulvifomes thailandicus* (LWZ 20140731-1, GenBank KR905665; Identities = 858/864 (99 %), no gaps).

Colour illustrations. Holotype collection area, Besant Nagar, Chennai district. Habitat; pilear surface; pore surface; transverse section of basidiomata; camera lucida drawing of holotype: contextual hyphae, tramal hyphae; basidioles; basidia and basidiospores. Scale bars = 5 µm.

Supplementary material

FP1564-1	Table.
FP1564-2	Phylogenetic tree.

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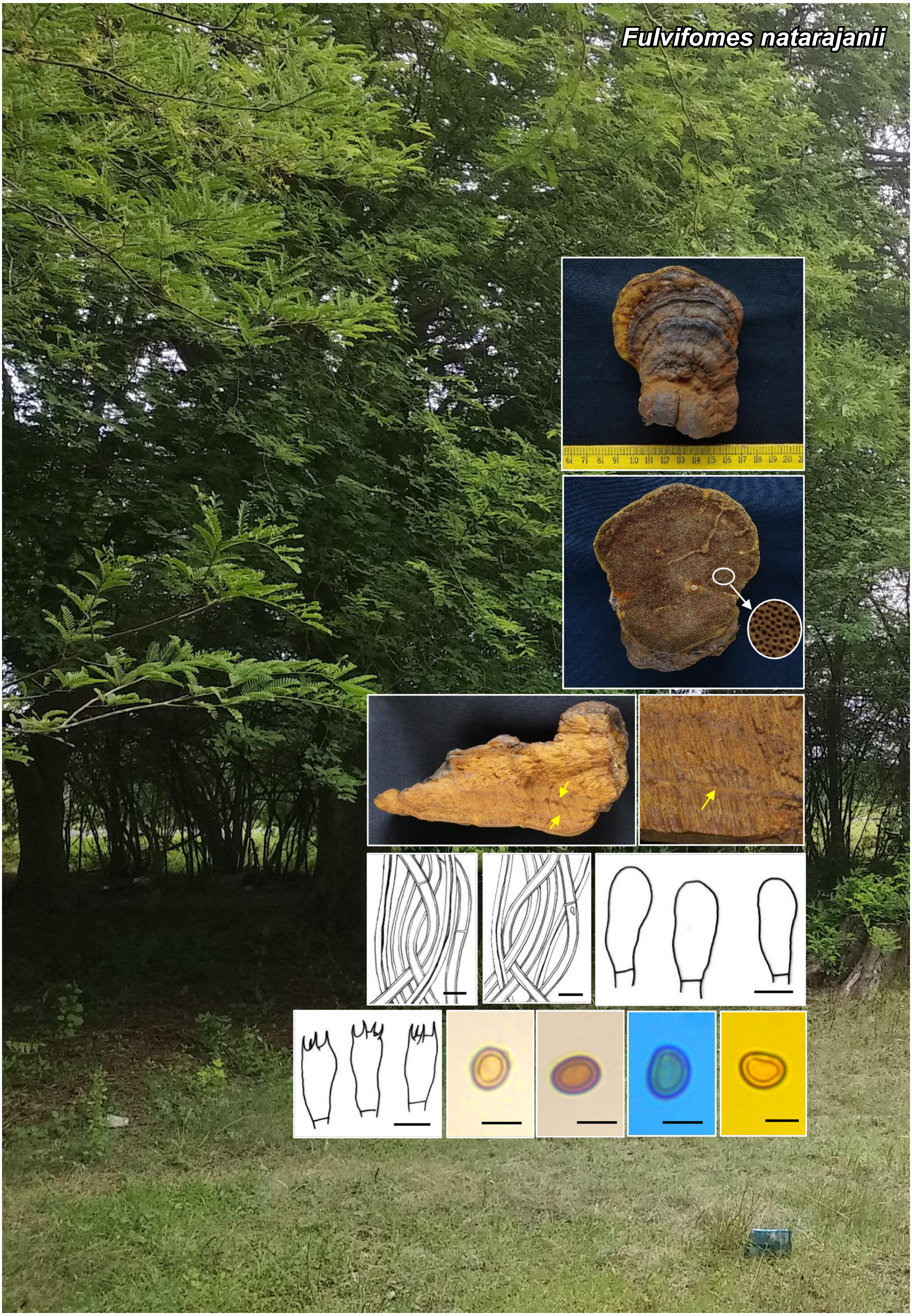
Fulvifomes natarajanii

Fungal Planet 1565 – 30 December 2023

Fulvifomes natarajanii E. Arumugam, S. Gunaseelan, & M. Kaliyaperumal, *sp. nov.*

Etymology. The species epithet '*natarajanii*' refers to the Indian mycologist, Krishnamoorthy Natarajan, in recognition for his contributions to Indian mycology, especially on taxonomic studies in *Agaricomycetes*.

Classification — *Hymenochaetaceae*, *Hymenochaetales*, *Agaricomycetes.*

Basidiomata perennial, solitary, pileate, applanate to meagrely ungulate, sessile, woody hard when fresh, light in weight when dry. *Pileus* dimidiate, projecting up to 9.5 cm, 7 cm wide and 3.6 cm thick near the base. *Pilear surface* brown (6E7; Kornerup & Wanscher 1978) to greyish brown (6F3) near the attachment, glabrous, narrowly zonate, with a few irregular cracks and without any distinct crust. *Margin* brown (6D7), entire, obtuse, 3 mm in thickness. *Pore surface* dark brown (6F7). *Pores* round to angular, regular, 4–6 per mm. *Context* brown (6D7), homogenous, zonate, up to 3 cm in thickness. *Tube* brown (6E7), distinctly stratified with intermittent context layers, each stratum up to 5 mm long. *Hyphal system* dimitic, tissue darkening in KOH without hyphal swelling. *Context* generative hyphae thin- to thick-walled, pale yellow to brown, simple septate, frequently branched, 3–4.6 µm wide, skeletal hyphae, thick-walled with narrow to wide lumen, pale yellow, aseptate, unbranched, 3–4.2 µm wide. *Trama* generative hyphae thin- to thick-walled, hyaline to dark brown, simple septate, rarely branched, 2.6–4.7 µm wide, skeletal hyphae, thick-walled with narrow to wide lumen, pale yellow to brown, aseptate, unbranched, 3.0–4.4 µm wide, *Cystidioles* and *setae* absent. *Basidioles* clavate, 5–18 × 3–7 µm. *Basidia* clavate to broadly clavate, with four sterigmata, 6–17 × 3–8 µm. *Basidiospores* smooth, thick-walled, subglobose to broadly ellipsoid, pale yellow to golden yellow in water, turning golden brown to brown in KOH, (5.4–)6.0–6.5(–6.8) × (4.9–)5.2–5.4(–5.7) µm (n = 30/2), Q = 1.14; (Q range 1.10–1.25), CB$^-$, IKI$^-$.

Typus. India, Tamil Nadu, Villupuram district, Nedimozhiyanur, N12°12'74.45" E78°73'28.05", on dead wood of *Prosopis juliflora* (*Fabaceae*), 14 Sept. 2021, *E. Arumugam* (holotype MUBL1047; LSU sequence GenBank OQ608722; MycoBank MB 847912).

Additional material examined. India, Tamil Nadu, Villupuram district, Nedimozhiyanur, N12°12'74.45" E78°73'28.05", on dead wood of *P. juliflora*, 14 Sept. 2021, *E. Arumugam* (paratype MUBL1048, LSU sequence GenBank OQ608723).

Notes — *Fulvifomes natarajanii* is similar to *F. malaiyanurensis* (Jayawardena et al. 2022) in sharing a zonate pilear surface, dimitic hyphal system, stratified tube layer and in the absence of cystidioles. However, the former varies by having an applanate basidiome, glabrous pilear surface, tube layer with intermittent context and in the size of its basidiospores (5.4–6.8 × 4.9–5.7 µm), whereas *F. malaiyanurensis* is distinct by having ungulate to triquetrous basidiomata, a velutinate pilear surface and 4.2–5.7 × 3.9–5.2 µm basidiospores. *Fulvifomes jawadhuvensis* is similar to *F. natarajanii* in having a stratified tube layer with a thin layer of context in between the stratum, a dimitic hyphal system and the absence of cystidioles, but the former varies in having meagrely warted pilei and in its basidiospore size (4.8–6.9 × 4.1–5.2 µm) (Jayawardena et al. 2022). *Fulvifomes thiruvannamalaiensis* resemblances *F. natarajanii* by sharing a glabrous pilear surface with a stratified tube layer and dimitic hyphal system, yet *F. thiruvannamalaiensis* differs in having a radially sulcate pilear surface with round to obtuse margin, the presence of cystidioles and in its basidiospore size (5.3–6.9 × 4.6–5.5 µm) (Jayawardena et al. 2022). The Maximum Likelihood (ML) and Bayesian Inference (BI) analyses revealed that *F. natarajanii* formed a distinct lineage (100 % ML, 1.0 BI) from other Indian *Fulvifomes* spp. (*F. jawadhuvensis*, *F. malaiyanurensis* and *F. thiruvannamalaiensis*) with 82 % ML, 0.9 BI.

Fulvifomes natarajanii is similar to *F. thailandicus* (Zhou 2015) in sharing distinctly stratified tube layers with intermittent context layers, a dimitic hyphal system and in the absence of cystidioles, but the latter differs in having nodulose, concentrically sulcate, uncracked basidiomes with a duplex context, smaller pores (8–9 per mm) and cyanophilic basidiospores (4.4–5.3 × 3.5–4.5 µm). *Fulvifomes natarajanii* shares similar characteristics with *F. grenadensis* by having a homogeneous context, lacking cystidioles and stratified tubes with intermittent context, but the latter differs by having sulcate, cracked basidiomes, and in basidiospore size (4–6 × 3–4 µm) (Ryvarden 2004).

Fulvifomes natarajanii shares similar microscopic characters with *F. hainanensis* by having a dimitic hyphal system and in the absence of cystidioles, but the latter differs in the presence of an uncracked pilear surface, duplex context, larger pores (3–4 / mm) and slightly smaller spores (5–6.4 × 4–5.1 µm) (Zhou 2014). *Fulvifomes natarajanii* is similar to *F. elaeodendri* and *F. yoroui* in having triquetrous to ungulate basidiomata, and number of pores per mm, but differs in other characters (Olou et al. 2019, Tchoumi et al. 2020).

Fulvifomes natarajanii varies from *F. caligoporus*, *F. cedrelae*, *F. coffeatoporus*, *F. dracaenicola*, *F. elaeodendri*, *F. floridanus*, *F. robinae*, *F. siamensis*, *F. squamosus* and *F. subindicus* in having a dimitic hyphal system, whereas the other species have a mono-dimitic hyphal system (Hattori et al. 2014, Salvador-Montoya et al. 2018, Tchoumi et al. 2020, Du et al. 2021, Wu et al. 2022).

Based on a BLAST search of NCBI (GenBank nucleotide database), the closest hits using the **LSU** sequence had highest similarity with *Fulvifomes thailandicus* IFP (LWZ 20140731-1, GenBank NG_068761; Identities = 857/870 (99 %), one gap (0 %)), *Fulvifomes thailandicus* (LWZ 20140731-1, GenBank KR905665; Identities = 857/870 (99 %), one gap (0 %)) and *Phellinus robiniae* (CBS 211.36, GenBank AY059038; Identities = 853/871 (98 %), two gaps (0 %)).

Colour illustrations. Holotype collection area. Habitat; pilear surface; pore surface; transverse section of basidiomata; microscope illustrations and camera lucida drawing of holotype: contextual hyphae, tramal hyphae; cystidioles; basidioles; basidia and basidiospores: basidiospore in water; basidiospore in KOH; basidiospore in cotton blue; basidiospore in Melzer's reagent. Scale bars = 5 µm.

Supplementary material

FP1565-1 Table.
FP1565-2 Phylogenetic tree.

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Fulvifomes subazonatus

Fungal Planet 1566 – 30 December 2023

Fulvifomes subazonatus R. Murugadoss, S. Gunaseelan & M. Kaliyaperumal, *sp. nov.*

Etymology. The species epithet '*subazonatus*', signifies the close phylogenetic relationship with *Fulvifomes azonatus*.

Classification — *Hymenochaetaceae*, *Hymenochaetales*, *Agaricomycetes.*

Basidiomata perennial, resupinate to pileate, applanate, sessile, broadly attached to the substrate by the whole width, wood corky when dry. *Pilei* dimidiate, projecting up to 10.3 cm, 22 cm wide and 9 cm thick at the base. *Pilear surface* yellowish brown (5E8; Kornerup & Wanscher 1978), velutinate when fresh, smooth, azonate, lacks crust, at maturity turning brownish grey (7F2). *Margin* yellowish brown (5E6), round to obtuse, 4.2 mm thick. *Pore surface* yellowish brown (5F7). *Pores* regular, round, smooth, 3–5 per mm. *Context* dark brown (6F6), duplex with discontinuous black line, up to 6 mm thick. *Tube layer* brown (6E6), stratified with intermittent context, each stratum up to 0.3 cm thick. *Hyphal system* mono-dimitic; tissue darkening in KOH without hyphal swelling. *Context*, monomitic with thin-walled generative hyphae frequently septate, branched, pale yellow to brown 2.6–3.9 µm wide; thick-walled generative hyphae rarely septate, brown, 4.6–5.7 µm wide. *Trama* dimitic, hyphae loosely interwoven, generative hyphae dominant, thin- to thick-walled, rarely septate, infrequently branched, thick-walled generative hyphae rarely encrusted, 2.8–5.2 µm wide. Skeletal hyphae golden yellow, narrow lumen, unbranched, aseptate 2.8–3.4 µm wide. *Setae* and *cystidioles* absent. *Basidioles* clavate, 9–12 × 3.2–3.7 µm. *Basidia* clavate with four sterigmata, 10–12 × 3.2–4 µm. *Basidiospores* smooth, thick-walled, globose to broadly ellipsoid, golden yellow (5.2–)5.4–5.7(–5.9) × 4.6–4.9(–5.2), Q = 1.08, (n = 30/2), Q = 1.0–1.17, CB⁻, IKI⁻.

Typus. India, Tamil Nadu, Chennai district, Guindy, N13°00'45.65" E80°14'10.90", basal trunk of *Azadirachta indica* (*Meliaceae*), 20 Oct. 2021, *R. Murugadoss* (holotype MUBL1046; ITS and LSU sequences GenBank OQ608642 and OQ608643; MycoBank MB 847919).

Additional material examined. India, Tamil Nadu, Chennai district, Guindy, N13°00'45.65" E80°14'10.90", basal trunk of *A. indica*, 15 Oct. 2021, *R. Murugadoss* (paratype AT03, ITS and LSU sequences GenBank OR502858 and OR502859).

Colour illustrations. Holotype collection area, Guindy, Chennai district. Habitat; pilear surface; pore surface; transverse section of basidiomata; camera lucida drawing of holotype: contextual hyphae, tramal hyphae; basidioles; basidia and basidiospores. Scale bars = 5 µm.

Notes — *Fulvifomes subazonatus* resembles *F. azonatus* in having an azonate pilear surface, and duplex context, but differs in having larger pores (3–5 / mm), a mono-dimitic hyphal system, in the absence of cystidioles and larger basidiospore size. The phylogenetic analysis inferred from ITS and LSU reveal that *F. subazonatus* formed a sister clade to *F. azonatus* and *F. nonggangensis* (92 % MLBS, 1 BI). *Fulvifomes subazonatus* differs from *F. nonggangensis* in basidiome characters, hyphal system, absence of cystidioles and larger basidiospores (*F. subazonatus*, 5.4–5.7 × 4.6–4.9 µm vs *F. nonggangensis*, 4.2–5.5 × 3.1–4.2 µm) (Zheng et al. 2021).

Although *F. subazonatus* is similar to *F. dracaenicola*, *F. elaeodendri*, *F. floridanus*, *F. robiniae*, *F. siamensis*, *F. squamosus*, *F. subindicus* and *F. wrightii* in having a mono-dimitic hyphal system, it differs significantly in its morphological characters (Hattori et al. 2014, Salvador-Montoya et al. 2018, Tchoumi et al. 2020, Du et al. 2021, Wu et al. 2022, Martinez et al. 2023). *Fulvifomes subazonatus* differs significantly from other *Fulvifomes* spp. having a dimitic hyphal system (*F. aurantiacus*, *F. centroamericanus*, *F. costaricense*, *F. fastuosus*, *F. hainanensis*, *F. halophilus*, *F. imazekii*, *F. imbricatus*, *F. inermis*, *F. jouzaii*, *F. krugiodendri*, *F. merrillii*, *F. nakasoneae*, *F. thailandicus*, *F. tubogneratus* and *F. xylocarpicola* (Hattori et al. 2014, 2022, Zhou 2014, 2015, Ji et al. 2017, Zheng et al. 2021, Fathima et al. 2023).

Based on a BLAST search of NCBI (GenBank nucleotide database), the closest hits using the ITS sequence had highest similarity with *Fulvifomes nonggangensis* (GXU2254, GenBank MT571503; Identities = 662/693 (96 %), 11 gaps (1 %)), *Fulvifomes azonatus* (Dai 17470, GenBank MH390418; Identities = 661/693 (95 %), ten gaps (1 %)) and *Fulvifomes azonatus* (Cui 8452, GenBank MH390417; Identities = 661/693 (95 %), ten gaps (1 %)). Closest hits using the LSU sequence are *Fulvifomes azonatus* (Dai 17203, GenBank MH390397; Identities = 825/857 (96 %), eight gaps (0 %)), *Fulvifomes nonggangensis* (GXU1127, GenBank MT571502; Identities = 824/857 (96 %), eight gaps (0 %)) and *Fulvifomes nonggangensis* (GXU2254, GenBank MT571501; Identities = 824/857 (96 %), eight gaps (0 %)).

Supplementary material

FP1566-1	Table.
FP1566-2	Phylogenetic tree.

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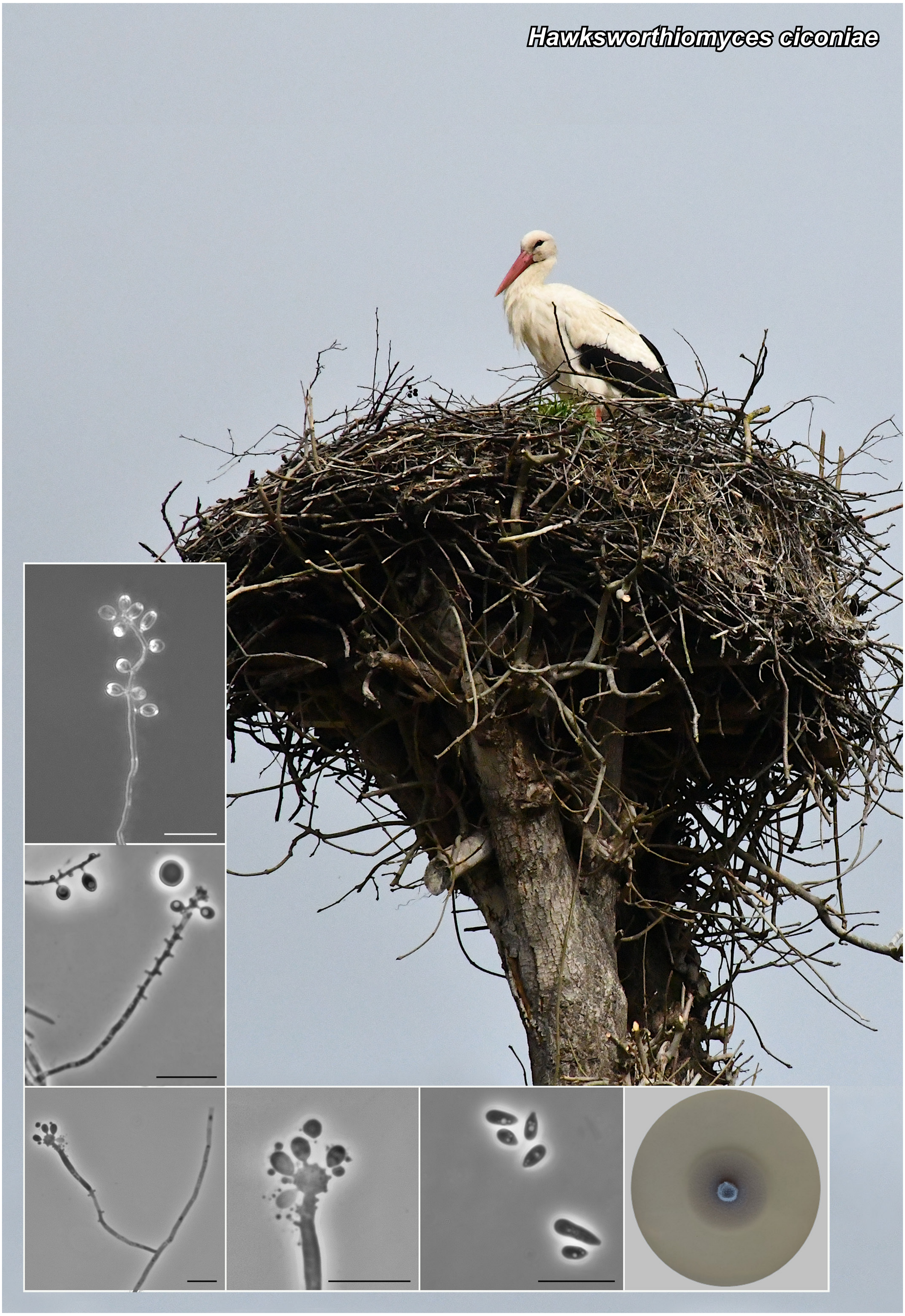
Hawksworthiomyces ciconiae

Fungal Planet 1567 – 30 December 2023

Hawksworthiomyces ciconiae R. Jankowiak, *sp. nov.*

Etymology. Name refers to the *Ciconia ciconia* nest where the ex-type strain was collected.

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

Sexual morph not observed. *Conidiophores* hyaline, mononematous, micronematous or semi-macronematous, cylindrical, straight or flexuous, unbranched, smooth-walled, reduced to conidiogenous cells. *Conidiogenous cells* polyblastic, integrated or discrete, terminal or intercalary, cylindrical, straight or curved, sympodial with multiple apical and subapical denticles, (2–)17–59(–121) µm long, (0.5–)1–1.5(–1.5) µm wide at base. Swollen apical part with denticles (1.5–)2–4(–6.5) µm long and (2–)2.5–4(–5) µm wide. *Conidia* subhyaline to slightly pigmented, aseptate, diverse in shape varying from slightly pyriforme, broadly ellipsoidal to subglobose, tapering towards the base, base truncate, sometimes formed singly on denticles directly emerging from vegetative hyphae, (2.5–)3.5–5(–7.5) × (1–)1.5–3.5(–4.5) µm.

Culture characteristics — Colonies with optimal growth at 25 °C on 2 % malt extract agar (MEA), reaching 31 mm (± 0.52 mm) diam in 14 d, with a radial growth rate of 1.12 (± 0.02) mm/d. Colonies flattened, brownish grey (4D2; Kornerup & Wanscher 1978) to greyish beige (4C2) towards the margin, surface slightly velvet, margin smooth, reverse brownish grey (4D2). Hyphae submerged in agar with little aerial mycelium, yellowish white (2A2), smooth, (0.5–)1–2(–3.5) µm wide.

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

Typus. Poland, north-eastern Poland, isolated from *Ciconia ciconia* nest, Góra Stokowa, Oct. 2018, *R. Jankowiak* (holotype O-F-261729; culture ex-type CBS 147964 = CMW = 57296; ITS, LSU, *βT*, *CAL* and *TEF1-α* sequences GenBank OR195108, OR195108, OR195095, OR195096 and OR195097; MycoBank MB 849341).

Colour illustrations. *Ciconia ciconia* nest, northern-eastern Poland. Conidiogenous cells and conidia; colony on MEA. Scale bars = 10 µm.

Notes — Phylogenetically, *H. ciconiae* resides in a strongly supported clade in the genus *Hawksworthiomyces*. In a multigene phylogeny of the ITS and LSU gene regions, *H. ciconiae* differs from *H. hibbettii* (CMW 37663) by 11.94 %, *H. riparius* (FMR 19083) by 13.29 %, *Hawksworthiomyces* sp. (INBio_4506O) by 6.03 %, and from *Hawksworthiomyces* sp. (INBio_4506N) by 6.04 %.

The genus *Hawksworthiomyces* established by De Beer et al. (2016) presently includes six formally described species that are associated with decaying wood or other plant material, and/or soil. Similarly, *H. ciconiae* was found in a White Stork nest that was built with decaying organic matter, e.g., leaf litter or wood debris (Błońska et al. 2021). In addition, a recently described species, *H. riparius* has been found in fluvial sediments in Spain (Tan et al. 2022). Members of the *Hawksworthiomyces* are characterised by mononematous conidiophores with integrated or discrete, polyblastic, and apically denticulate conidiogenous cells, and hyaline, aseptate, ellipsoidal to cylindrical conidia (De Beer et al. 2016). In addition, *H. riparius* produces synnemata in culture (Tan et al. 2022). *Hawksworthiomyces ciconiae* is like other *Hawksworthiomyces* species in the conidial dimensions and shape, except *H. riparius* that has distinctly smaller conidia (2.5–3.5 × 1–2.5 µm). The new *Hawksworthiomyces* species differs from other species in having conidiogenous cells with apical as well as subapical denticles. In addition, *H. ciconiae* does not produce secondary conidia as *H. crousii* and does not form synnemata as seen in *H. riparius*. Furthermore, the optimum growth temperature for *H. hibbettii* and *H. crousii* is 30 °C (De Beer et al. 2016), while in *H. ciconiae* it is 25 °C. *Hawksworthiomyces riparius* grows at an optimum temperature of 25 °C, to a maximum of 37 °C, while *H. ciconiae* is unable to grow above 25 °C.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit of *H. ciconiae* (CBS 147964) using the **ITS** sequence is *Hawksworthiomyces* sp. (INBio4515N, GenBank KM242369, from beetle gut, Costa Rica; identities = 392/422 (93 %), eight gaps (1 %)). The closest hits using the **LSU** sequence are *Sporothrix stylites* (CBS 118848, GenBank MH874594, from pine utility poles, South Africa, identities = 869/896 (97 %), one gap (0 %)) and *S. narcissi* (CBS 138.50, GenBank NG_067354, from *Narcissus* sp., Netherlands, Identities = 865/893 (97 %), one gap (0 %)). The closest hits using the ***βT***, ***CAL*** and ***TEF1-α*** sequences are different members of the *Ophiostomatales*, as there are no protein-coding sequence data in GenBank for *Hawksworthiomyces* species.

Supplementary material

FP1567-1	Phylogenetic tree.
FP1567-2	Table.

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Hevansia mainiae

Fungal Planet 1568 – 30 December 2023

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

Etymology. Named after Barbara York Main (1929–2019), an Australian arachnologist who became an expert on the taxonomy, biogeography and ecology of trapdoor and funnel-web spiders. Barbara Main collected specimens across Australia and described 34 species and seven new genera of arachnids. Barbara Main was awarded the Medal of the Order of Australia in 2011 for her service to science, conservation, and to the community of Western Australia, as a researcher and educator in the field of arachnology. The genera *Bymainiella* and *Mainosa* (spiders), as well as *Barbarella* (pseudoscorpion) were named in her honour.

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

Hosts are spiders attached to lower leaf surfaces in tropical rainforests. *Mycelium* covers host, off-white, comprised of hyphae 1.5–3 µm wide, smooth, hyaline and septate. *Synnemata* numerous, simple, filiform, 3–5 mm long and 50–150 µm wide, composed of *textura porrecta*. *Conidiophores* abundant on middle and upper portions of synnemata, reduced to conidiogenous cells, lateral or terminal on hyphae. *Conidiogenous cells* phialidic globose to lageniform or obovoid, 4–11 × 4–6 µm, with a short cylindrical neck 2.5–5 × 1 µm, hyaline, thin-walled. *Conidia* cylindrical to fusoid, rounded at apex, narrowed near the base, with a minute refractive hilum, 7–12 × 1.5–2 µm, hyaline.

Culture characteristics (25 °C, 4 wk, in darkness) — On potato dextrose agar (PDA) up to 3 cm diam, white, flat, with abundant synnemata at the centre, powdery due to abundant sporulation, growth sparse at margin, pale pink pigment produced in the agar; reverse vinaceous at centre, rosy vinaceous towards the margin.

Typus. Australia, Queensland, Kuranda, on dead spider, 6 June 2015, *T.S. Marney*, *K.L. Bransgrove*, *M.D.E. Shivas* & *R.G. Shivas* (holotype BRIP 62570a permanently preserved in a metabolically inactive state; culture ex-type BRIP 62570a; LSU, SSU, *rpb2* and *tef1α* sequences GenBank OQ025237, OQ025232, OQ054472 and OQ054473; MycoBank MB 849551).

Additional materials examined. Australia, Queensland, Julatten, on dead spider, 4 Apr. 2015, *T.S. Marney*, *S.E. Abell*, *M.D.E. Shivas* & *R.G. Shivas*, culture BRIP 62358a, LSU, SSU, *rpb2* and *tef1α* sequences GenBank OQ025236, OQ025231, OQ054470 and OQ054471; ibid., on dead spider, 6 June 2015, *T.S. Marney*, *M.D.E. Shivas & R.G. Shivas*, culture BRIP 62738a, *rpb2* and *tef1α* sequences GenBank OR161069 and OR161070; Kuranda, on dead spider, 5 June 2015, *T.S. Marney*, *K.L. Bransgrove*, *M.D.E. Shivas* & *R.G. Shivas*, culture BRIP 62571a, SSU, *rpb2* and *tef1α* sequences GenBank OQ025233, OQ054474 and OQ054475; ibid., on dead spider, 5 June 2015, *T.S. Marney*, *K.L. Bransgrove*, *M.D.E. Shivas* & *R.G. Shivas*, culture BRIP 62587a, SSU, *rpb2* and *tef1α* sequences GenBank OQ025234, OQ054476 and OQ054477; Mission Beach, on dead spider, 8 June 2015, *T.S. Marney*, *S.E. Abell*, *M.D.E. Shivas* & *R.G. Shivas*, culture BRIP 62590a, SSU, *rpb2* and *tef1α* sequences GenBank OQ025235, OQ054478 and OQ054479; ibid., on dead spider, 8 June 2015, *T.S. Marney*, *S.E. Abell*, *M.D.E. Shivas* & *R.G. Shivas*, culture BRIP 62591a, LSU, *rpb2* and *tef1α* sequences GenBank OQ025238, OQ054480 and OQ054481; ibid., on dead spider, 8 June 2015, *T.S. Marney*, *S.E. Abell*, *M.D.E. Shivas* & *R.G. Shivas*, culture BRIP 62592a, *rpb2* and *tef1α* sequences GenBank OQ054482 and OQ054483; Tully, 29 Apr. 2021, *T.S. Marney*, *Y.P. Tan*, *K.L. Bransgrove*, *M.J. Ryley*, *S.M. Thompson*, *M.D.E. Shivas* & *R.G. Shivas*, culture BRIP 72771a, LSU, *rpb2* and *tef1α* sequences GenBank OR140733, OR161071 and OR161072.

Notes — *Hevansia mainiae* is the tenth species described in this genus of spider infecting fungi (Mongkolsamrit et al. 2022). *Hevansia mainiae* is known only as an asexual morph from several Australian specimens that are morphologically indistinguishable from the description of the holotype of *Akanthomyces novoguineensis* collected in Papua New Guinea (Samson & Brady 1982). *Akanthomyces novoguineensis* was transferred to *H. novoguineensis* (Kepler et al. 2017) as a consequence of the ending of the dual nomenclatural system for pleomorphic fungi in 2011. *Hevansia* was established for the least inclusive genus-level clade that includes *H. novoguineensis* and *H. nelumboides*, with *H. novoguineensis* as the type species (Kepler et al. 2017). In our phylogenetic analysis, *H. mainiae* was sister to the ex-type strain (CBS 610.80) of *H. novoguineensis*. Based on a megablast search of NCBIs GenBank nucleotide database, the closest relevant hits using the **LSU** sequence are *H. novoguineensis* (strain EPF020, GenBank JX192737, Identities 803/803 (100 %)), *H. nelumboides* (strain BCC 41864, GenBank JN201873, Identities 803/803 (100 %)) and *A. arachnophilus* (strain BCC 17655, GenBank GQ249977, 803/803 (100 %)). The closest relevant hits using the **SSU** sequence are *A. arachnophilus* (strain BCC 17655, GenBank GQ249949; Identities 473/473 (100 %)), *H. novoguineensis* (strain EPF020, GenBank JX192767, Identities 472/473 (99 %)) and *H. nelumboides* (strain BCC 2190, GenBank MF416584, Identities 471/472 (99 %)). The closest relevant hits using the ***rpb2*** sequence are *H. novoguineensis* (ex-type strain CBS 610.80, GenBank MH521844, Identities 887/895 (99 %)), *H. nelumboides* (strain BCC 2093, GenBank MF416437, Identities 878/889 (99 %)) and *H. minuta* (strain MY06537.02, GenBank MZ707834, Identities 794/820 (97 %)). The closest relevant hits using the ***tef1α*** sequence are *H. novoguineensis* (strain EPF046, GenBank JX192799, Identities 911/918 (99 %)), *H. nelumboides* (strain BCC41864, GenBank JN201867, Identities 896/910 (98 %)) and *Jenniferia cinerea* strain EPF155, GenBank JX192812, Identities 876/918 (95 %)).

Colour illustrations. Creek running through tropical rainforest, northern Queensland. On infected spider in tropical rainforest (top and middle left); on PDA (middle right); synnema with conidiophores; conidia; colonies on PDA (upper surface and reverse). Scale bars = 1 mm (macromorphology), 10 µm (micromorphology), 1 cm (colonies on PDA).

Supplementary material

FP1568 Phylogenetic tree.

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Hygrophorus aesculeticola

Fungal Planet 1569 – 30 December 2023

Hygrophorus aesculeticola Lebeuf, Thorn & M.E. Sm., *sp. nov.*

Etymology. From the Latin noun *aesculetum*, an oak grove, and adjectival suffix *-icola* (not declined), dweller.

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

Pileus 30–70 mm broad, hemispherical to convex and eventually plane, covered with a thick (1–2 mm deep) clear yellow-brown gluten over a yellowish brown to deep brown surface, in one older basidiome the gluten receding to the centre, leaving 8–10 mm of the margin glabrous, grey-brown; margin at first incurved, then slightly upturned, acute. *Lamellae* subdistant, from arcuate to segmentiform, white to cream, or pale yellow especially near pileus margin, waxy, sometimes partly forked or laterally attached, with 1–2 tiers of lamellulae. *Stipe* 40–70 × 8–20 mm, equal or tapering to apex from clavate base, solid, sheathed from base to 10–15 mm below apex with brown fibrils overlain with clear, yellow-brown glutinous universal veil, in upper part covered with pale yellow squamules turning brown in exsiccata, on a white, dry background. *Context* white in stipe. *Odour* absent. *Basidiospores* (128 spores, 3 basidiomata, 2 collections) 7–10(–10.5) × 4–5.5(–6.0) µm, av. 8.5 × 4.9 µm, Q = 1.54–2.25, Qav = 1.75, ellipsoid, oblong, amygdaliform, inamyloid, smooth; also present were infrequent larger basidiospores, variable in shape (ellipsoid, heart-shaped, triangular), measuring 12.5–16 × 5.5–7.5 µm, borne on 1- or 2-spored basidia. *Basidia* 48–63 × 7–10.5 µm, mostly 4-spored, also 1-, 2- or 3-spored, narrowly clavate. *Hymenial cystidia* absent. *Lamellar trama* divergent, made of thin-walled, interwoven, cylindrical hyphae 3–8 µm broad. *Pileipellis* a thick ixotrichoderm, 600–800 µm thick in KOH, filled with abundant pale yellow to yellowish brown extracellular crystals (granular, rod-shaped, ellipsoid), free in matrix or adhering to the hyphae, and less abundant small to large amorphous crystals, dark blue in KOH, always adhering to the hyphae. Upper hyphae ± repent to interwoven, branched, colourless or with intracellular pale yellow pigment or intraparietal amber-like pigment, 2–4.5 µm diam. Lower hyphae ascending, branched, colourless or with intracellular pale yellow pigment, 2–4(–7) µm diam, rather compact below, more loose above. *Pileitrama* hyphae subparallel to interwoven, smooth, colourless, 2–8 µm diam. *Stipitipellis* a mostly thick gelatinous matrix 100–1 000 µm wide, filled with abundant extracellular pale yellow crystals (granular, ellipsoid, rod-shaped), free or adhering to the hyphae, and less abundant small to large amorphous crystals, dark blue in KOH, always adhering to the hyphae. Hyphae in matrix repent, interwoven or ascending, branched, cylindrical, 3–7 µm broad, colourless or with a spirally-incrusting or intracellular pale yellow pigment. *Stipititrama* of parallel, cylindrical or slightly inflated hyphae 2–12 µm wide. *Upper stipe squamules* made of compact masses of erect, branched, parallel, cylindrical hyphae, colourless or with a yellowish brown intracellular pigment, 3–5 µm wide; terminal hyphae cylindrical, mostly rounded at apex, also narrowly clavate, tapered or rostrate, measuring 26–90 × 3–8 µm. *Clamp connections* present in all tissues, including frequent medallion clamps in pileipellis and stipitipellis.

Habitat & Distribution — Solitary or gregarious under *Quercus*, in late fall (Ontario) or mid-winter (Florida). Known from Ontario, in Canada, and from Florida, in the USA. Also found on root samples collected in Mississippi, in the USA.

Typus. USA, Florida, Putnam County, Ordway-Swisher Biological Station, N29.705482° W81.967156°, in a mixed forest dominated by *Quercus* (mostly *Q. virginiana* and *Q. laurifolia*) with some *Pinus* mixed in (*P. elliottii* and *P. palustris*) near the classroom, 5 Feb. 2018, *M.E. Smith*, MES-3095 (holotype DAOM 984968, isotype FLAS-F-62822; ITS sequence GenBank MK020098; MycoBank MB 849951).

Additional material examined. Canada, Ontario, Wallaceburg, Walpole Island First Nation, approx. N42.635° W82.500°, on soil in oak savannah with *Quercus alba* and *Sassafras albidum*, 3 Nov. 2013, *S.N. Allan*, RGT131109/02 (UWO-F-3092, ITS sequences GenBank MN752314, MN752315).

Notes — *Hygrophorus aesculeticola* was first recognised as an undescribed species in section *Limacini* by Bellanger et al. (2021, as *Hygrophorus* sp. 3). It is characterised by its medium size, yellowish brown to dark brown glutinous pileus and stipe, upper part of stipe dry, covered with pale yellow squamules turning brown in dried specimens, and growth with *Quercus*. Microscopically, the presence of very large variously-shaped spores borne on 1- or 2-spored basidia and the abundant crystals seen in the pileipellis, particularly the amorphous crystals turning dark blue in KOH, are distinctive. *Hygrophorus glutinifer* is very similar macroscopically and also produces extracellular pigments, some of them turning blue-green in alkali, but the gluten on the stipe forms dark brown bands or spots on a whitish background when drying, its basidia are 4-spored, sometimes 2-spored, and it is restricted to Europe (Arnolds 1990, Candusso 1997, Bellanger et al. 2021). *Hygrophorus paludosoides*, described from Michigan, in the USA, is also similar, but it differs in its paler pileus and association with *Fagus* (Hesler & Smith 1963). Even though spores are said by Hesler & Smith to measure 7–9 × 5–5.5 µm, in the Quebec collection sequenced by Bellanger et al. (2021), they measured 9.2–11.5 × 6–6.5 µm. The pileipellis of that collection also contained extracellular crystals turning blue in KOH (Y. Lamoureux, pers. comm.).

Colour illustrations. Collection site of the holotype in Florida. Lower inserts show holotype (left) and collection RGT131109/02 (right). Middle inserts show spores (left) and floccules at stipe apex (right). Upper insert shows pileipellis hyphae incrusted with amorphous crystals turning blue in KOH. Scale bars = 20 mm (basidiomata), 10 µm (all others).

Supplementary material

FP1569 Phylogenetic tree.

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Hymenagaricus brunneodiscus

Fungal Planet 1570 – 30 December 2023

Hymenagaricus brunneodiscus M. Asif, Saba & M. Raza, *sp. nov.*

Etymology. The name refers to the brown disc on the pileus of the specimen.

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

Basidiomata large in size. *Pileus* 2.8–4.3 cm diam, plane to convex, light-grey (10YR8/1; Munsell 1975) to brownish grey (10YR4/1), slightly umbo, covered with very dark brown (7.5YR2/3), rarely depressed around umbo, thin context, initially covered with villose or velvety threads, later greyish brown patches (7.5YR6/2), crowded at centre, scattered towards margins, dry and dull, margins appendiculate or hairy, raptured radially at maturity. *Lamellae* greyish brown (5YR4/2), crowded, free to adnex, narrow, edges even, margins entire, lamellulae present in 3 tiers of different lengths and alternating with lamellae. *Stipe* 3.5–8.6 × 0.5–0.9 cm, greyish white (N8/0), centrally attached, tapering upwards, curved from the middle or upper half, reddish brown (5YR2/4) on bruising, cylindrical, hollow, thin whitish context, covered with whitish cottony flacks, dry and shiny, base slightly bulbous with pseudorrhiza. *Annulus* present, pendant, whitish, superior, disappear at maturity. *Volva* absent. *Smell* and *taste* are not recorded. *Basidiospores* (50/2/2), (4.1–)5.1–6.2(–6.4) × (3.0–)3.3–3.9(–4.0) µm, avl × avw = 5.6 × 3.6 µm; Q = 1.3–1.8; Qav = 1.6; ellipsoid to oblong or subcylindrical, rarely lacrymoid, thick-walled, smooth, apiculate, hyaline in 5 % KOH, non-dextrinoid, congophilous. *Basidia* (12.2–)13.4–16.1(–18.2) × (5.7–)6.0–6.9(–7.3) µm, avl × avw = 13.8 × 6.1 µm, clavate to broadly clavate, frequently bisporic, rarely tetrasporic, rarely with long sterigmata up to 5 µm, thick-walled, congophilous. *Cheilocystidia* (9.1–)9.5–14.1(–15.4) × (4.7–)4.8–6.2(–6.4) µm, avl × avw = 12.2 × 5.5 µm, clavate to broadly clavate or rarely sphaeropedunculate, thick-walled, tiny oil droplets present. *Pleurocystidia* absent. *Pileipellis* a trichoderm, made up of cylindrical and long and irregular hyphae with 1.6–3.3 µm diam, avw = 2.2 µm, thick-walled, septate, rarely constricted at septa, smooth, rarely branched. *Pileocystidia* absent. *Stipitipellis* made up of long, narrow cylindrical hyphae with 1.4–2.5 µm diam, avw = 2 µm, thick-walled, septate, regularly arranged. *Caulocystidia* absent. *Clamp connections* are absent in all tissues.

Habitat — Saprotrophic, caespitose (in clusters), or connate (fused at base), rarely in solitary, on fallen leaf debris in nutrient-rich loamy soil under mixed angiospermic vegetation dominated by *Eucalyptus*.

Typus. Pakistan, Punjab, Pirowal Reseve Forest, District Khanewal N30°34' E71°98', 136 m a.s.l., in nutrient-rich soil on fallen leaves of mixed angiospermic vegetation dominated by *Eucalyptus* (*Myrtaceae*), 27 July 2022, *M. Asif*, SP38 (holotype LAH37956; ITS and LSU sequences GenBank OR510862 and OR510864; MycoBank MB 849872); Fungi of Pakistan FOP: UPID_0008. Figshare: 10.6084/m9.figshare.24211023.

Additional material examined. Pakistan, Punjab, Pirowal Reserve Forest, Distruct Khanewal N30°34' E71°98', 136 m a.s.l., in nutrient-rich soil on fallen leaves of mixed angiospermic vegetation dominated by *Eucalyptus*, 27 July 2022, *M. Asif*, SP40 (isotype LAH37955; ITS and LSU sequences GenBank OR510863 and OR510865).

Colour illustrations. Pakistan, Punjab, District Khanewal, Pirowal Reserve Forest, in nutrient-rich soil on fallen leaves of mixed angiospermic vegetation dominated by *Eucalyptus* (photo credit M. Asif). Basidiomata of *Hymenagaricus brunneodiscus* in natural habitat; line drawings of basidia, basidiospores, cheilocystidia, pileus, and stipe elements; basidiospores in 5 % KOH, Melzer's reagent, and Congo red. Scale bars = 1 cm (basidiomata), 10 µm (micromorphology).

Notes — Previously, 21 species of the genus *Hymenagaricus* have been reported globally (Index Fungorum, accessed 3 Sept. 2023) including only one species (*H. pakistanicus*) from Pakistan (Syed et al. 2023). Here, we describe a new species named *H. brunneodiscus*, growing in nutrient-rich soil on fallen leaves of *Eucalyptus*, and is characterized by its large basidiomata (up to 9 cm diam), dark-brown disc, velvety threads on the surface, raptured margins, stipe pseudorrhiza, rarely lacrymoid basidiospores, clavate to sphaeropedunculate cheilocystidia, and pileipellis made of cylindrical and long hyphae. In the phylogenetic analyses, based on nrITS and combined nrITS-LSU datasets, *H. brunneodiscus* belongs to a well-supported clade of *Hymenagaricus* and is closely related to *H. pakistanicus* (GenBank OP082406), *H. saisamornae* (GenBank MW345912), and *H. ardosiicolor* (GenBank KM360160), with a strong bootstrap and Bayesian posterior probability value (100 % / 1). Apart from nrITS and LSU (28S) sequences, *H. pakistanicus* differs from *H. brunneodiscus* by its small basidiomata, striate margins, dark-olive black squamules, absence of annulus, subglobose basidiospores, and parallel interwoven pileal cells (Syed et al. 2023). *Hymenagaricus saisamornae* differs due to its unique combination of morpho-anatomical features such as smaller hemispherical pileus (up to 2.5 cm diam), pinkish white surface, stipe turned pastel red when bruised, broadly ellipsoidal to elongate basidiospores, various forms of cheilocystidia, and pileipellis made up of radially parallel hyphae (Kumla et al. 2021). *Hymenagaricus ardosiicolor* has medium-sized basidiomata, convex pileus, brown scales, and incurved margins (Tibuhwa & Mwanga 2014).

Hymenagaricus brunnodiscus is also closely allied to *Heinemannomyces splendidissimus* (Watling 1998). However, both genera show noticeable differences in their morphological characters, as *Heinemannomyces splendidissimus* has a pileus surface with woolly-arachnoid veil remnants composed of cylindrical hyphae; lamellae that are dark blue to bluish grey, and delicate and fugacious annulus (Watling 1998, Hosen et al. 2017).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had the highest similarity to *Hymenagaricus* cf. *kivuensis* (voucher BR6089, GenBank KM982454; Identities = 615/674, (90 %), nine gaps (1 %), *Heinemannomyces splendidissimus* (voucher Q. Zhao 2591, GenBank KY039571; Identities = 612/667 (90 %), ten gaps (1 %)) and *Hymenagaricus* sp. (voucher Q. Zhao 2591, GenBank KM982450; Identities = 613/668 (90 %), nine gaps (1 %)). The closest hits using the **LSU** sequence are *Hymenagaricus* sp. (voucher SDBR-CMUWP038, GenBank OP836600; Identities = 945/968 (96 %), three gaps (0 %)) and *Hymenagaricus* sp. (voucher SDBR-CMUNK1508, GenBank OP836385; Identities = 950/965 (98 %), four gaps (0 %).

Supplementary material

FP1570-1	Table.
FP1570-2	Phylogenetic ITS tree.
FP1570-3	Phylogenetic ITS-LSU tree.

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Hymenoscyphus radicis
POTATO DEXTROSE AGAR, USP

Fungal Planet 1571 – 30 December 2023

Hymenoscyphus radicis G. Delgado & Maciá-Vicente, *sp. nov.*

Etymology. Named after the isolation source of the fungus, plant roots.

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

Root endophyte isolated on culture media from surface-sterilised roots of living plants. *Mycelium* composed of branched, septate, smooth, hyaline, thin-walled *hyphae*, 1.5–3(–3.5) µm wide, brown to dark brown in mass, sometimes aggregated in tightly packed, brown cords, up to 27 µm wide; spherical or subspherical, brown blobs of mucilage 6–10 µm diam and produced terminally or intercalary were present in older cultures.

Culture characteristics — Colonies on potato dextrose agar (PDA) moderately slow growing, reaching 12–15 mm diam after 2 wk at 23–24 °C, velvety, flat, cream colour, darker and slightly raised at the centre, with one white concentric ring toward the edge, margin entire, reverse brown, paler brown around the edge. On malt extract agar (MEA) reaching 8–11 mm diam, velvety, cream colour, convex and raised 3–4 mm, margin entire, reverse dull yellow. Cultures sterile.

Habitat & Distribution — Root endophyte. Known so far from Croatia, Germany and France.

Typus. Croatia, Zadar, Novigrad, Karinsko more, N44°11'26.3" E15°30'58.1", 0 m a.s.l., isolated from surface-sterilised, asymptomatic roots of a plant of *Microthlaspi erraticum* (*Brassicaceae*), 4 May 2013, coll. *T. Ali*, isol. *K. Glynou*, P1180 (holotype and culture ex-type permanently preserved in a metabolically inactive state CBS 147105; ITS, LSU, *tef1* and *RPB2* sequences GenBank KT268497, OR398665, OR400762 and OR400761; MycoBank MB 849824).

Additional materials examined. Croatia, Zadar, Jasenice, N44°14'30.1" E15°32'08.0", 35 m a.s.l., isolated from surface-sterilised, asymptomatic roots of a plant of *M. perfoliatum*, 4 May 2013, coll. *T. Ali*, isol. *K. Glynou*, P1539, ITS sequence GenBank KT268833. – France, Lorraine, Fleisheim, N48°48'0.0" E7°10'48.0", 310 m a.s.l., isolated from surface-sterilised, asymptomatic roots of a plant of *Brassica napus* (*Brassicaceae*), 26 May 2014, coll. *K. Glynou* & *J.G. Maciá-Vicente*, isol. *K. Glynou*, P6332, ITS sequence GenBank MH063617. – Germany, Baden-Württemberg, Buchen, N49°31'12.0" E9°24'00.0", 380 m a.s.l., isolated from surface-sterilised, asymptomatic roots of a plant of *Capsella bursa-pastoris* (*Brassicaceae*), 26 May 2014, coll. *K. Glynou* & *J.G. Maciá-Vicente*, isol. *K. Glynou*, P6291, ITS sequence GenBank MH063781.

Notes — *Hymenoscyphus* is a large helotiaceous genus which members were previously considered saprotrophic decomposers or non-pathogenic endophytes until *H. fraxineus*, the causal agent of the ash dieback and a harmless leaf endophyte in its native Asia, devastated the populations of European ash trees across the continent (Coker et al. 2019, Hietala et al. 2022, Rafiqi et al. 2023). However, despite its extensive diversity and importance, reports of *Hymenoscyphus* species as root endophytes are practically non-existent (Rashmi et al. 2019). The novel species introduced in this work, *H. radicis*, was isolated in two distinct studies focusing on root endophytic fungi of *Brassicaceae* across Europe (Glynou et al. 2016, 2018). The recovered isolates did not produce any of the structures observed in culture for other members of the genus, including apothecial ascomata or chalara-like phialides with conidia, and they remained sterile in all the media used. Intraspecific pairwise comparisons of the ITS sequences belonging to the four strains of *H. radicis* show they are identical except for one A-G transition between the pairs CBS 147105/P6291 and P1539/P6332 at position 73 of their 462 aligned positions, and one C-A transversion between CBS 147105 and the remaining strains at position 75. Phylogenetically, the four strains of *H. radicis* grouped together in a strongly supported monophyletic clade (100 % BS/1 BPP) sister to two strains of *H. peruni* without support. They were placed within the strongly supported '*Hymenoscyphus*' 1 clade (100 % BS/1 BPP) of Lebeuf et al. (2021) which includes several terrestrial species such as *H. aurantiacus*, *H. calyculus*, *H. menthae*, *H. repandus* and the cleistothecial, strictly marine fungus *Amylocarpus encephaloides* (Hagestad et al. 2021). This varied group is distant from the species-rich *Hymenoscyphus* s.str. lineage containing a representative strain of the generic lectotype *H. fructigenus*. We momentarily retain our root endophyte species within *Hymenoscyphus* s.lat. as the taxonomy of the genus is clearly in need of revision and members of this clade distant from *Hymenoscyphus* s.str. will be most likely rearranged in a new or another genus in the future.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Hymenoscyphus aurantiacus* (strain HMAS 264143, GenBank NR_154907.1; Identities = 486/508 (96 %), five gaps (0 %)), *H. peruni* (voucher H.B. 9329, GenBank OQ940286.1; Identities = 486/510 (95 %), four gaps (0 %)) and *H. menthae* (strain HB_5846, GenBank KM114537.1; Identities = 443/476 (93 %), six gaps (1 %)). Closest hits using the **LSU** sequence are *Hymenoscyphus peruni* (voucher H.B. 9329, GenBank OQ940286.1; Identities = 749/765 (98 %), eight gaps (1 %)), *H. aurantiacus* (strain HMAS 264143, GenBank NG_059509.1; Identities = 770/789 (98 %), eight gaps (1 %)) and *H. repandus* (voucher H.B. 9057, GenBank KT876975.1; Identities = 770/789 (98 %), eight gaps (1 %)). Closest hits using the ***rpb2*** sequence are *Amylocarpus encephaloides* (strain TRa-018bII, GenBank OL634969.1; Identities = 614/682 (90 %), no gaps), *Tricladium obesum* (strain CCM F-14598, GenBank MK241440.1; Identities = 554/690 (80 %), 10 gaps (1 %)) and *Mycofalcella calcarata* (strain CCM F-10289, GenBank MK241439.1; Identities = 548/687 (80 %), four gaps (0 %)). No significant hits were obtained using the ***tef1*** sequence.

Colour illustrations. Rapeseed field verge near Buchen, Germany, where one of the specimens studied was isolated. Colonies on PDA surface and reverse views; mycelium with hyphae and cords; blob of mucilage encasing hypha. Scale bars = 10 µm (hyphal cords), 5 µm (blob of mucilage).

Supplementary material

FP1571-1	Table.
FP1572-2	Phylogenetic tree.

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Inocybe dagamae

Fungal Planet 1572 – 30 December 2023

Inocybe dagamae Fachada, Beja-Pereira & Vila-Viçosa, *sp. nov.*

Etymology. Named after Sebastião da Gama, poet and ecologist who dedicated his life to promote and preserve the mountain range harbouring this species.

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

Basidiomata stocky, solitary or in small groups. *Pileus* 10–27 mm, first hemispherical later becoming hemispheric-convex to plano-convex, retaining incurved margin, without or with inconspicuous low umbo, cuticle silky-fibrillose to finely tomentose (especially at sub-appendiculate margin), colour pale hazelnut-brown with yellowish ochraceous hues (7.5YR 5/8, 5YR 5/8; Munsell 1919) to darker caramel-brown (5YR 3/6, 4/8), streaked or mottled radially from fibrillosity, often developing a dark brown centre (5YR 1/2, 2/2), abundant greyish white velipellis when young often remaining until late stages. *Cortina* visible in young specimens, remaining as appendiculate margin, and eventually lost. *Lamellae* crowded (L = 50–70; l = 1) whitish beige, adnate to broadly adnexed, sinuose, edge entire to finely fimbriate. *Stipe* 10–20 × 5–7 mm, cylindrical, straight, and rarely curved, slightly enlarged at the base, whitish beige to pale ochraceous pink (especially in upper third), longitudinally lined with whitish fibrils, pruinose only in the upper third. *Context* whitish beige. *Smell* spermatic. *Taste* indistinctive. *Basidiospores* (6.1–)7.8–*8.9*–9.9(–11.0) × (5.2–)5.8–*6.6*–7.4(–8.3) µm, Q = (1.1–)1.2–*1.4*–1.6(–1.7) (n = 125; N = 2), smooth, highly variable in shape and between basidiomata, short-ovoid (mostly from 4-spored basidia) to elongated-ellipsoid (mostly from 2-spored basidia), rarely subamygdalyform, apex often subconical, rarely obtuse. *Basidia* 20–34 × 8–11 µm, Q = 2.4–4 (n = 23; N = 2), clavate, 2- and 4-spored. *Pleurocystidia* (45–)54–*61*–68(–77) × (11–)13–*16*–19(–24) µm, Q = (2.4–) 2.9–*4.0*–4.8(–6.5) (n = 32; N = 2), common to somewhat scarce, rather variable in shape but mostly of fusiform tendency with rather short pedicel and neck, occasionally subcylindrical, subutriform, subclavate or ventricose, rarely sublageniform, often with rounded and enlarged apex, sometimes subcapitate, mucronation common and often strong but easily lost, walls most often thin (< 2 µm), sometimes moderately thick at neck (2–3 µm), rarely thicker, very slightly greenish yellow in KOH 4 %. *Cheilocystidia* (38–)43–*55*–68(–71) × 12–*16*–19 µm, Q = (2.1–)2.7–*3.9*–5.0(–5.3) (n = 16; N = 2), common to abundant, similar to pleurocystidia but shorter and yellower, in contents and walls, sometimes sided by clavate paracystidia. *Caulocystidia* (28–)39–*49*–60(–67) × (10–)12–*15*–21(–67) µm, Q = (1.9–)2.5–*3.3*–4.0(–5.3) (n = 61; N = 2), abundant in very apex, rare or absent elsewhere, mostly shaped like hymenial cystidia but often more contorted and with a more clavate-utriform tendency, accompanied by numerous clavate paracystidia. *Pileipellis* a intertwined cutis with slight incrustating brown pigment (especially in subpellis made of short, inflated cells < 15 µm thick), suprapellis made of thinner (3 < 10 µm thick) and more hyaline hyphae. *Lamellar trama* subregular, made of inflated hyaline cells, most often < 15 µm, thick. *Clamp connections* present in all tissues.

Habitat & Distribution — On clay soil above limestones. Likely associated with *Pinus halepensis* and/or *Cistus monspeliensis*, sometimes having *Quercus coccifera* and *Juniperus turbinata* close by. Only known from two localities in Serra da Arrábida, mainland Portugal. No similar ITS sequences were found in GenBank or UNITE.

Typus. Portugal, Sesimbra, Serra da Achada, Parque Natural da Arrábida, WGS84: 38.440402, -9.082391, 214 m a.s.l., on clay-limestone, near *Juniperus turbinata* and *Cistus monspeliensis*, with *Pinus halepensis* in the area, 27 Dec. 2020, *V. Fachada*, VF271220IS1 (holotype PO-F2611; ITS sequence GenBank OR439020; MycoBank MB 849790).

Additional material examined. Portugal, Sesimbra, Serra da Achada, Parque Natural da Arrábida, WGS84: 38.445083, -9.085083, 203 m a.s.l., on clay over limestone, near *Pinus halepensis*, *Quercus coccifera* and *Salvia rosmarinus*, 16 Dec. 2022, *V. Fachada*, VF171222IS1, PO-F2740, ITS+LSU sequence GenBank OR439021.

Notes — Our ITS+LSU analysis shows that *Inocybe dagamae* has strong support (ufb = 0.96, pp = 1) within the *Inocybe psammobrunnea* group (Bandini et al. 2021). Although the *psammobrunnea/griseotarda* complex may hide several cryptic species, *I. dagamae* is well separated from the latter with at least 20 stable base pair differences (~2.6 %) in the ITS region. Correspondingly, *I. dagamae* is morphologically very close to *I. psammobrunnea* and equally as polymorphic (Bon 1990, Poirier 2002, Bandini & Huijser 2017, Bizio et al. 2017). However, its habitat in calcareous clay together with the shorter and wider spores on average (much lower Q value), set it apart from *I. psammobrunnea*.

Colour illustrations. Atlantic cliffs of the karstic and clayey Serra da Arrábida, Portugal. Pleurocystidia; cheilocystidia; caulocystidia; basidiospores; basidiomata (PO-F2611, PO-F2740). Scale bars = 10 mm (basidiomata), 20 µm (micrographs). Photography & micrography by Vasco Fachada.

Supplementary material

FP1572 Phylogenetic tree.

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Inocybe guldeniae

Fungal Planet 1573 – 30 December 2023

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

Etymology. In honour of Gro Gulden, Norway, for her contributions to the knowledge of fungi in the arctic and alpine zones.

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

Pileus 8–32 mm diam, as young hemisphaerical, later plano-convex, not umbonate or indistinctly umbonate, margin inflexed, pale brown to brown, often with abundant whitish velipellis, subtomentose-smooth around centre, towards margin coarsely fibrillose to subsquamulose. *Cortina* pale greyish, rather abundant in young basidiomata. *Lamellae* moderately crowded, interspersed with lamellulae, up to 7 mm broad, ventricose, adnexed to narrowly adnate, first pale greyish brown, then pale brown to brown, edge fimbriate, whitish to concolorous. *Stipe* 20–50 × 2–6 mm, equal to subbulbous, base often tapering, pale brown, greyish brown, brown, not pruinose, woolly-fibrillose. *Context* in pileus yellowish to brownish white, in stipe pale brown. *Smell* indistinct. *Basidiospores* (10.8–)11.3–*12.6*–14.4(–15.8) × (5.6–)6.0–*7.1*–8.4(–9.5) µm, Q = (1.4–)1.45–2.15(–2.2), Q mean = 1.77, n = 80, smooth, subamygdaloid, subellipsoid, subboletoid, some somewhat angular, with obtuse apex, often with suprahilar depression, dark yellowish brown. *Basidia* (27–)29–35(–36) × 10–13(–14) µm, n = 40, subclavate to clavate, 4-spored, hyaline to pale yellow-brown. *Pleurocystidia* (54–)60–*69*–82(–94) × (11–)13–*19*–23(–26) µm, Q mean = 3,7, n = 60, mainly fusiform, crystalliferous at apex, crystals often abundant, thick-walled, wall up to 2 µm thick, yellowish. *Cheilocystidia* (42–)44–*64*–88(–90) × (12–)13–*16*–17(–18) µm, n = 40, rather variable, some mucronate, often yellow-brown. *Paracystidia* 12–*21*–30 × 8–*11*–14 µm, n = 40, oval to pyriform, rather scarce. *Caulocystidia* only at extreme apex of stipe, (44–)48–*64*–86(–100) × (11–)12–*16*–20(–21) µm, n = 40, oblong to misshaped subfusiform, *cauloparacystidia* 14–*20*–31 × 8–*11*–15 µm, n = 30, intermixed with hyphoid elements. *Clamp connections* frequent.

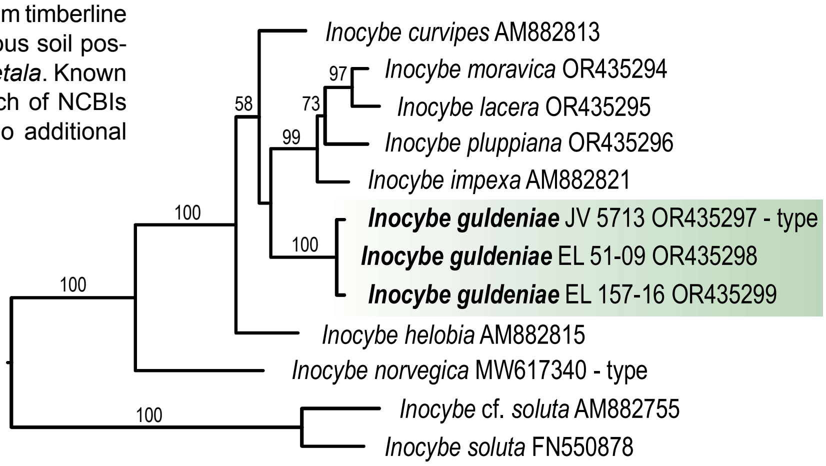
Ecology & Distribution — The species occurs from timberline to the arctic and alpine zone growing on calcareous soil possibly with *Salix* spp., *Betula* spp. and *Dryas octopetala*. Known from Sweden, Norway and Svalbard. Blast search of NCBIs GenBank and the UNITE database recovered no additional data.

Colour illustrations. *Inocybe guldeniae* habitat in the subalpine zone, the type locality in Norway, Oppdal and Dovre area. Basidiomata of the holotype (TUR-A171545); photos of pleuro-, caulo-, cheilocystidia and basidiospores; drawing of pleurocystidia (left), basidiospores, caulocystidia (right). Scale bars = 10 µm (spores and drawing), 20 µm (pleuro, caulo- and cheilocystidia).

Typus. Norway, Sør-Trøndelag, Oppdal commune, S of Kongsvoll, NNW of the mountain Hjerkinnhö, SSW of Grønbakken, between Dovrevegen and the river Svone, alluvial site, near *Betula pubescens* subsp. *czerepanovii*, *B. nana* and *Salix* spp., on calcareous soil, about 950 m a.s.l., 10 Aug. 1991, *J. Vauras*, 5713F (holotype TUR-A 171545, isotype GB-0207672; ITS-LSU sequence GenBank OR435297; MycoBank MB 849874).

Additional material examined. Svalbard and Jan Mayen, Svalbard, near Longyearbyen, with *Salix polaris*, *Dryas octopetala* and *Bistorta vivipara*, 12 Aug. 2009, *G. Gulden* & *E. Larsson*, EL51-09, GB-0207671, TUR-A 209467, ITS-LSU sequence GenBank OR435298. – Sweden, Lule lappmark, Jokkmokk, Padjelanta NP, Unna Duvgge, moist site on calcareous soil near *Betula nana* and *Salix* spp., 15 Aug 2016, *G. Gulden*, EL157-16, GB-0207670, TUR-A 209468, ITS-LSU sequence GenBank OR435299.

Notes — *Inocybe guldeniae* belongs in the *I. lacera* group that earlier was treated as a smooth-spored species (Kuyper 1986, Stangl 1989), but molecular phylogenetic analyses show that it is closely related with species in section *Cortinatae* (e.g., Ryberg et al. 2010), characterised by nodulose spores and caulocystidia only at extreme apex of stipe or not at all, and by having a cortina at early stages of basidiocarp development. Some species in the *I. lacera* group have clearly nodulose to angular spores as *I. curvipes* and *I. polytrichi-norvegici*, but other species have somewhat undulating spores as *I. helobia* and *I. pluppiana*, and others have more boletoid to smooth ellipsoid spores as *I. lacera*, *I. moravica*, *I. impexa*, *I. norvegica*, and *I. guldeniae*. Like *I. impexa*, *I. guldeniae* has rather large and dark spores. It is a medium-sized species characterised by ochraceous brown plano-convex pileus, having a whitish velipellis when young, on average broader spores (av. Q 1.77) and longer pleurocystidia than the other ± smooth-spored species of the *I. lacera* group. A blast search of the **ITS** sequence in NCBIs GenBank nucleotide databae shows about 95 % similarity of *I. guldeniae* with *I. impexa*, *I. curvipes* and *I. moravica*.



Phylogram obtained using PAUP v. 4.0a (Swofford 2003) based on ITS and LSU data showing the position of *I. guldeniae* within the *I. lacera* group. Heuristic searches with 1000 random-addition sequence replicates and tree bisection-reconnection (TBR) branch swapping were performed. Relative robustness of clades was assessed by the bootstrap method using 1000 heuristic search replicates with 100 random taxon addition sequence replicates and TBR branch swapping. Bootstrap support values are indicated on branches. *Inocybe guldeniae* is marked in **bold** and a green box, the holotype indicated. The tree and alignment were deposited in TreeBASE.

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Inocybe pseudomytiliodora

Fungal Planet 1574 – 30 December 2023

Inocybe pseudomytiliodora G.M. Jansen, *sp. nov.*

Etymology. *pseudomytiliodora*, not the real mytiliodora.

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

Basidiomata small-sized. Pileus surface and stipe surface darkening after collection. *Pileus* 8–25(–40) mm, when young hemispherical, convex then flattened, centre with wide low umbo; with a strongly in-rolled margin, ochreous or pale yellow which may change to brownish; covered with brown scales or radially fibrillose covering forming concolorous non-erect scales, which change towards the margin in brown fibrils. *Veil* pale yellowish brownish silky. *Lamellae* intermediate gills present, narrowly adnate, young pale yellow, then yellowish to brownish, edge whitish then partially brownish in older specimen. *Stipe* 20–40 × 2–4 mm, cylindrical, slightly enlarged towards the base, concolorous with the cap, paler to whitish at the apex, covered with distinctly brown squamules in irregular girdles. *Smell* like rotten mushrooms, fish or mussels, not pleasant; exsiccati still with unpleasant smell after 2 yr. *Spores* 7.6–10.1 µm (av. 8.8 µm, sd. 0.6 µm) × 4.4–5.7 µm (av. 5.1 µm, sd. 0.3 µm); Q = 1.5–2.0 (Qav = 1.75, sd. 0.15) (n = 60 from 4 collections); ellipsoid, amygdaloid, smooth, thick-walled. *Basidia* 24–38 × 6.5–9.5 µm, clavate, 4-spored, clamped. *Lamellae edges* composed of cheilocystidia and colourless and occasionally brown, (sub)clavate, thin-walled paracystidia. *Pleurocystidia* 29–48 µm (av. 38 µm, sd. 5 µm) × 12–22 µm (av. 17 µm, sd. 2 µm) (n = 61 from 3 collections), clavate, pyriform, narrowly utriform with crystals, walls 1.25–2.0 µm thick. *Cheilocystidia* 22–71 µm (av. 47 µm, sd. 12 µm) × 9–23 µm (av. 16 µm, sd. 3.5 µm) (n = 66 from 4 collections), clavate, narrowly utriform with crystals (sometimes a few without crystals), thin-walled, walls 0.7–1.4 µm thick. *Caulocystidia* present or not, if present narrowly utriform, intermixed with pseudocaulocystidia clavate. *Pileipellis* cylindrical hyphen 2–16 µm, yellow brown intracellular pigment in addition finely incrusted pigment, subpellis cylindrical hyphen 2.5–10 µm wide, pigment hardly visible. *Clamps* all tissues with clamps. All measurements in 5 % KOH.

Habit & Distribution — Solitary or gregarious with deciduous trees such as *Tilia*, *Fagus*, *Quercus* or *Betula* on loamy soil. Basidiomata known from the Netherlands and Estonia. The ITS sequences obtained from soil samples available in the public databases, further indicate the presence of *I. pseudomytiliodora* mycelium in Latvia, Georgia and Iran.

Typus. Netherlands, Gelderland Province, Vorden, Estate Wildenborgh, unpaved path with *Tilia* on loamy soil, 52.121, 6.384, 11 Oct. 2020, *M. Gotink*, MG481 (holotype L 4343913; ITS sequence GenBank OR387050; MycoBank MB 849561).

Additional materials examined. Estonia, Hiiumaa, Sarve Nature Reserve (FL 2 1, Grid 27° E: 653:27), 16 Sept. 2001, *J. Vauras* (TUR 156412, GenBank OR387052). – The Netherlands, South Holland Province, Rotterdam, Kralingen, 16 Sept. 2017, *T. de Graaf-Matulessy* (L 4343914, GenBank OR387056); Gelderland Province, Rheden, Graveyard Heiderust, 30 Aug. 2021, *M. Plekkenpol* (L 4343844, GenBank OR387051).

Colour illustrations. *Inocybe pseudomytiliodora* habitat in *Tilia* lane on loamy soil on the estate Wildenborch, The Netherlands, Gelderland Province, Vorden. In situ basidiomata of the holotype (Photo M. Gotink); studio photo of the holotype (L43443913) collection (Photo M. Gotink); gill edge with cheilocystidia collection L4343914; cheilocystidia above and pleurocystidia below from holotype; spores from holotype. Scale bars = 5 µm (spores), 10 µm (cystidia), 20 µm (gill edge).

Notes — Initially, all the studied collections of *I. mytiliodora* and *I. pseudomytiliodora* were identified as *I. mytiliodora* based on the characteristic smell resembling mussels or fish, the presence of thin-walled cystidia, and the absence of caulocystidia. However, upon studying the collections, it became evident that both the presence and absence of caulocystidia varied within and between collections. Additionally, caulocystidia were found in some basidiomata of the isotype material of *I. mytiliodora* (L 0054127; ITS sequence GenBank OR387053). Therefore, the presence or absence of caulocystidia proved to be an unreliable distinguishing feature. Fortunately, the difference in spore sizes and Qav can be helpful to separate *I. mytiliodora* and *I. pseudomytiliodora*, but the limited number of sequenced collections available do not allow for a highly reliable differentiation. If Qav ≈ 1.75, it indicates *I. pseudomytiliodora*, whereas Qav ≈ 1.6 indicates *I. mytiliodora*. Spores of *I. mytiliodora* from two collections including the isotype show Qav = 1.6, sd. 0.14; n = 65). The sequences of *I. pseudomytiliodora* and *I. mytiliodora* form two sister branches in the /Ochroalba clade. Their ITS1-5.8S-ITS2 sequences differ at 7 indels and 22 point mutations.

Another closely related species is *I. pedemontana*. Morphological examination of the syntype (TUR190735; ITS sequence GenBank OR387049) revealed few distinguishing traits separating it from *I. mytiliodora*. Hobart & Henrici (2011) provide an overview of the naming history of *I. pedemontana* and, based on morphological descriptions, conclude that *I. pedemontana* is synonymous with their collection identified as *I. mytiliodora*. All collections of *I. pedemontana* including the syntype, from which the ITS sequence was obtained, cluster with *I. appendiculata* in the /Ochroalba clade. Based solely on morphological traits, Kuyper (1986) considers *I. ovoideicystis* (nom. inval.), *I. pedemontana* and *I. piricystis* as synonyms of *I. appendiculata*. Despite the absence of the ITS type sequence from *I. appendiculata*, it seems reasonably certain to consider *I. pedemontana* as a synonym of *I. appendiculata*. The identity of the Scottish collection by Hobart & Henrici remains uncertain. Considering the Qav = 1.75 of that collection, *I. pseudomytiliodora* could potentially be the correct name.

The main traditional differences between *I. appendiculata* and the *I. mytiliodora* – *I. pseudomytiliodora* complex lie in the presence of an appendicular veil and distinct odours, more like rotten flesh, but spermatic when cut or bruised in *I. appendiculata* and resembling mussels or fish in *I. mytiliodora* – *I. pseudomytiliodora*. However, it is important to note that mycologists may perceive odours differently. All *I. pedemontana* collections had a distinctive mussel-fish smell apparently very different from *I. appendiculata*, however, that difference turned out to be incorrect to separate those collections from *I. appendiculata.* Both *I. mytiliodora* and *I. pseudomytiliodora* are species that rarely produce basidiomata. The studied collections were all found in association with deciduous trees, whereas *I. appendiculata* has a preference for coniferous trees.

Supplementary material

FP1574 Phylogenetic tree.

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Inocybe rupestroides

Fungal Planet 1575 – 30 December 2023

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

Etymology. Refers to the similarity with *Inocybe rupestris*.

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

Pileus 8–35 mm diam, conical to convex, umbonate with obtuse to broad umbo, later plano-convex to plane with or without a broad umbo, as young with slightly incurved margin, dry, rather uniformly coloured ochraceous brown, darker brown with age, smooth to matted fibrillose, with age breaking up to fibrillose scaly at the centre and rimose towards the margin, cortina absent, velipellis thin, fugacious, white, visible in young basidiomata at pileus margin, soon disappearing. *Lamellae* moderately crowded, interspersed with lamellulae, L = 30–40, adnexed to almost free, first buff white, later ochraceous brown, edge concolourous to dark ochraceous brown. *Stipe* 10–40 × 3–5 mm, cylindrical with a slightly rounded base, first pale ochraceous brown, white fibrillose, with age dark ochraceous brown with white stipe base, pruinose for the entire length. *Context* in pileus pale ochraceous brown, in stipe ochraceous brown, base white. *Smell* spermatic. *Taste* indistinct. *Basidiospores* (7.8–)9.0–*9.6*–10.0(–11.2) × (4.6–)5.1–*5.3*–5.6(–6.4) µm, n = 140, Q = 1.68–*1.80*–1.84, smooth, subamygdaliform, sometimes with an apical papilla and/or suprahilar depression, distinct apiculus, ochraceous brown. *Basidia* 26–*28*–32 × 7–*9*–10 µm, n = 20, clavate, 4-spored, hyaline, sterigmata 5.0–7.3 µm. *Pleurocystidia* 52–*66*–85 × 11–*14*–17 µm, n = 60, lageniform to utriform to fusiform with short pedicel, thick-walled 2.5–4.5 µm, hyaline to slightly yellow in KOH solution, with crystals. *Cheilocystidia* similar to pleurocystidia but somewhat shorter, 38–*57*–65 × 11–*15*–22 µm, n = 60, with short pedicel or rounded base, thick-walled 2.0–3.5 µm, ochraceous-brown in mature specimens, mixed with clavate to pyriform paracystidia. *Caulocystidia* over the entire length, dense at stipe apex and few in the lower part, similar to pleurocystidia but longer at stipe apex, fusiform to cylindrical, with crystals, less so in the lower part, 43–*70*–87 × 11–*15*–26 µm, n = 54, thick-walled 1.5–3.5 µm, hyaline to slightly yellow in KOH solution. Cauloparacystidia 23–44 × 9–20 µm, n = 30, clavate to pyriform and cylindrical, abundant at apex. *Pileipellis* a cutis of cylindrical to inflated hyphae with 5–15 µm wide, encrusted, yellowish brown pigmented. *Clamp connections* present.

Ecology & Distribution — Occurs in the alpine and subalpine zone growing in moist areas on gravelly ground associated with *Salix lanata*, *S. reticulata*, *S. herbacea*, *Betula pubescens* and *B. nana*. Collections known from Sweden, Norway and Finland, but Blast search of NCBIs GenBank and the UNITE database recovered one ITS sequence (GenBank AB669653) from ectomycorrhiza of *Pyrola* sp. on Hokkaido, Japan, suggesting the species to have a wider distribution.

Colour illustrations. *Inocybe rupestroides* habitat in the subalpine zone, the type locality in Norway, Troms, 2 km west of Helligskogen. Basidiomata of the holotype (GB-0207662); photos of pleuro-, caulo-, cheilocystidia and basidiospores; drawing of pleurocystidia (left), basidiospores, caulocystidia (right). Scale bars = 10 µm (spores and drawing), 20 µm (pleuro, caulo- and cheilocystidia).

Typus. Norway, Troms, Storfjord, 2 km west of Helligskogen, in subalpine area on gravelly soil with *Salix* spp., *Betula pubescens* subsp. *czerepanovii* and *B. nana* amongst mosses and lichens, 21 Aug. 2017, *E. Larsson* & *J. Vauras*, EL198-17 (holotype GB-0207662, isotype TUR-A 206599; ITS-LSU sequence GenBank OR471433; MycoBank MB 849999).

Additional materials examined. Finland, Ostrobotnia ultima, Rovaniemi, Sinettä around Bear Lodge, in sand under *Salix* spp. and *Betula pubescens*, 3 Sept. 2013, *M. Sasa* & *E. Larsson*, EL359-13, GB-0207663 (ITS-LSU sequence GenBank OR471434). – Norway, Troms, Storfjord, 2 km west of Helligskogen, in subalpine area on gravelly soil with *Salix* spp., *Betula pubescens* subsp. *czerepanovii* and *B. nana*, 20 Aug. 2017, *E. Larsson* & *J. Vauras*, EL186-17, GB-0207664 (ITS-LSU sequence GenBank OR471432); Nordland, Tysfjord, along roadside under *Salix* spp. and *Betula pubescens*, 12 July 2006, *E. Larsson*, EL2-06, GB-0207665 (ITS-LSU sequence GenBank OR471436); ibid., EL3-06, GB-0207666 (ITS-LSU sequence GenBank FN550900). – Sweden, Torne lappmark, Jukkasjärvi, Latnjavagge in alpine zone with *Salix reticulata*, 11 Aug. 2007, *E. Larsson*, EL85-07, GB-0207667; Lule lappmark, Jokkmokk, Padjelanta, Arralåbbdå in alpine zone with *Salix reticulata* and *S. herbacea*, 11 Aug. 2016, *E. Larsson*, EL45-16, GB-0207668 (ITS sequence GenBank OR471437); Lycksele lappmark, Tärna, Laisaliden in alpine zone with Salix spp. and *Betula nana*, 19 Aug. 2015, *E. Larsson*, EL113-15, GB-0207669 (ITS-LSU sequence GenBank OR471435); Pite Lappmark, Arjeplog, Gabsjetjåhkkå in alpine zone with *Salix* spp., 13 Aug. 2018, *J. Vauras*, JV32512, TUR-A 208243 (ITS-LSU sequence GenBank OR471431).

Notes — *Inocybe rupestroides* is characterised by the ochraceous brown fibrose pileus with obtuse broad umbo, first with pale buff lamella that become dark ochraceous-brown in mature specimens, rather thick-walled hyaline to slightly yellow pleuro- and caulocystidia and brown cheilocystidia. Both *I. rupestroides* and *I. rupestris* are found in alpine ecosystems on gravelly ground and they often co-occur, however *I. rupestris* seems to be favoured by more calcareous ground and was described associated with *Salix reticulata* and *Dryas* (Favre 1955). In macro-morphology they are both rather variable species and since Favre (1955) described *I. rupestris* it has also been described by Kühner (1988) as *I. auricomella* and by Ferrari (2010) as *I. iseranensis*. *Inocybe rupestris* has in general smaller basidiomata with a fine scaly convex pileus, a yellowish ochraceous tone in both pileus, stipe and the lamellae, where *I. rupestroides* become dark ochraceous brown. Also, *I. rupestris* has less dense lamellae (L = 25–30) than *I. rupestroides* (L = 30–40). In micro-morphology *I. rupestroides* can be discriminated by having on average longer spores than *I. rupestris*, 9.6 µm vs 8.7 µm (n = 100). Also, *I. rupestroides* has lageniform cystidia and brown cheilocystidia and *I. rupestris* has more cylindrical cystidia. Another smooth-spored reddish brown species that can be found in the alpine zones on gravelly ground is *I. tjallingiorum* (Kuyper 1986), that differs from *I. rupestroides* by having slightly shorter and ovoid to subamygdaliform spores with almost obtuse apex, no lageniform pleurocystidia and only slightly yellowish cheilocystidia.

Blast searches of the **ITS** and **LSU** sequences in NCBIs GenBank show 94 % similarity of *I. rupestroides* with *I. tjallingiorum*; the genetic difference to *I. rupestris* is larger.

Supplementary material

FP1575 Phylogenetic tree.

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Lecanora menthoides

Fungal Planet 1576 – 30 December 2023

Lecanora menthoides Mazur, *sp. nov.*

Etymology. The epithet refers to the unique colour of the thallus (*mentha* = mint, *-ides* = suffix meaning similarity).

Classification — *Lecanoromycetes*, *Lecanorales*, *Lecanoraceae.*

Thallus mint-green, olive or yellowish, conspicuous, thick, areolate, irregular in the outline, and without pruinosity; surface areolate, areoles undulate and irregular (0.1–0.9 mm diam) without vegetative propagules; *prothallus* not visible or present, black or inky, with filamentous structure; *photobiont* green, *Trebouxia* clade C (Medeiros et al. 2021), cells 7–12 µm diam, abundant, photobiont layer 60–75 µm thick, continuous but uneven in some parts; a*pothecia* scarce to abundant, scattered, adnate or sessile, 0.4–1.5 mm diam, circular and densely pruinose, discs concave or convex, brown grey, inky, blue grey or yellow, without blackness; *apothecium margin* concolourous with thallus, continuous, prominent, below disc level or level with the disc; *amphithecium* 120–150 µm high, with large crystals (insoluble in K and N); *amphithecial cortex* amorphous, not well delimited; *parathecium* not visible; *epihymenium* brown (HCl–, K–, N–); *hymenium* hyaline, 80–95 µm high; *hypothecium* hyaline, pigmented yellow-orange, 280–300 µm high; *subhymenium* not visible; *paraphyses* simple, septate, robust, and unthickened at the top – apical and basal parts measure 5 µm; *asci* clavate with 8 spores; *ascospores* simple, hyaline, broadly ellipsoid, (11.0–)11.9–13(–13.3) length (L) × (7.0–)7.4–8(–8.2) µm width (W), and spores ratio L/W = 1.6 µm (n = 40); *pycnidia* present. TLC (A and C solvents) revealed two chemotypes: only zeorin present (AF 27602, AF 27515); atranorin, zeorin, usnic acid, and traces of an unknown substance (AF 27192, AF 27119).

Habit, Habitat & Distribution — *Lecanora menthoides* grows on sandstone, in open semi-desert montane areas, open areas with *Asteraceae*, *Puya*, table mountains of sandstone and rocks, as well as in windy and foggy places (on the fringes of cloud forest).

Typus. Bolivia, Tarija (department), Burnet O'Connor (province), la Cumbre close to the gas pipeline, old road between Entre Ríos and Tarija, S21°26'11" W64°24'42", 2769 m a.s.l., on sandstone, open area with shrubs and sandstone rocks, 1 Aug. 2015, leg. *A. Flakus 27515* (holotype KRAM, isotype LPB; mycobiont ITS, mtSSU and *rpb2* sequences GenBank OL603991, OL604072 and OK665590, photobiont ITS OL625036; MycoBank MB 850007).

Additional materials examined. See supplementary page.

Colour illustrations. Bolivia, Tarija, Burnet O'Connor, la Cumbre close to the gas pipeline, old road between Entre Ríos and Tarija (*locus classicus*) (photo credit A. Flakus). A habit of the thallus (*Flakus 9288*); the holotype (*Flakus 27515*); cross-section of apothecium in standard and polarized light (*Flakus 27515*). Scale bars = 1 cm (a habit), 1 mm (thallus), 100 µm (apothecium).

Notes — *Lecanora* (Acharius 1810) is placed in the *Lecanoraceae* and is the most extended genus in the family, including approximately 550 species worldwide. The genus *Lecanora* s.lat. includes taxa with lecanorine apothecia, crustose, rarely lobate thallus containing green-algal photobionts of the genus *Trebouxia*. It is characterised by hyaline, aseptate ascospores, and *Lecanora*-type asci. Thallus may be adnate, areolate, crustose, granular, placodioid, or peltate, rarely immersed in the substratum. Prothallus is usually blackish brown, whitish to whitish grey, or not visible. Isidia and cephalodia are absent; soredia are present or absent (Lumbsch & Elix 2004). The tropics are poorly explored in the context of crustose lichens, especially of problematic genera, as is *Lecanora* in its broad sense. The first studies on the genus in the neotropical part of the zone, undoubtedly one of the wealthiest areas in biodiversity, date back to the 19th century. However, only a single or up to dozens of species of the genus have been recorded in particular countries of South America (e.g., 26 in Bolivia). *Lecanora menthoides* presents typical features for the genus, which are lecanorine apothecia and clavate asci containing eight simple hyaline ascospores. A distinguishing feature of a new species is the colour of the thallus – fresh material is in a mint colour, and with time it fades to shades of olive and yellow (sand) tint. The geographical location – the Andes –, and the substrate – sandstone – are also characteristic for the new species. The species cannot be confused with any of the known saxicolous lecanoroid lichens due to the composition of morphological characters such as the structure of the thallus, pruinosity of apothecia, and chemistry in addition to the colour of the thallus. The closely related species *L. fulvastra* is epiphytic and differs in the thalli structure, the colour of apothecia and the chemistry.

In the conducted phylogenetic analyses *Lecanora menthoides* is nested in the clade incorporating the species *L. flavidomarginata*, *L. fulvastra*, *L. pangerangoensis*, *L. ulrikii* and *L. wilsonii*. The new species forms a distinct and highly supported lineage as a sister clade to *L. fulvastra*. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **mtSSU** sequence are *L. flavidomarginata* (Flakus 28943, GenBank OL604077, identities = 96.9 %, 13 gaps (1 %)); *L. fulvastra* (Flakus 26717, GenBank OL604089, identities = 96.5 %, nine gaps (0 %)); *L. saxigena* (Landemer 49057, GenBank NC_042183, identities = 92.0 %, 38 gaps (2 %)). The closest hits using **ITS** sequence had the highest similarity to *L. barkmaniana* (Vondrak 24669, GenBank OQ717893, identities = 91.60 %, eight gaps (1 %)); *L. fulvastra* (Sakata 3591, GenBank LC269720, identities = 90.1 %, 11 gaps (1 %)); *L. flavidomarginata* (Flakus 28943, GenBank OL603996, identities = 85.16 %, 16 gaps (2 %)). The closest hits using the ***rpb2*** sequence are *L. flavidomarginata* (Flakus 29951, GenBank OK665640, identities = 90.4 %, four gaps (0 %)); *Palicella glaucopa* (PRF 3174, GenBank KJ152497, identities = 82.0 %, four gaps (0 %)); *L. rupicola* (Flakus 29527, GenBank OK665608, identities = 81.0 %, no gaps).

Supplementary material

FP1576-1	Phylogenetic tree.
FP1576-2	Table.

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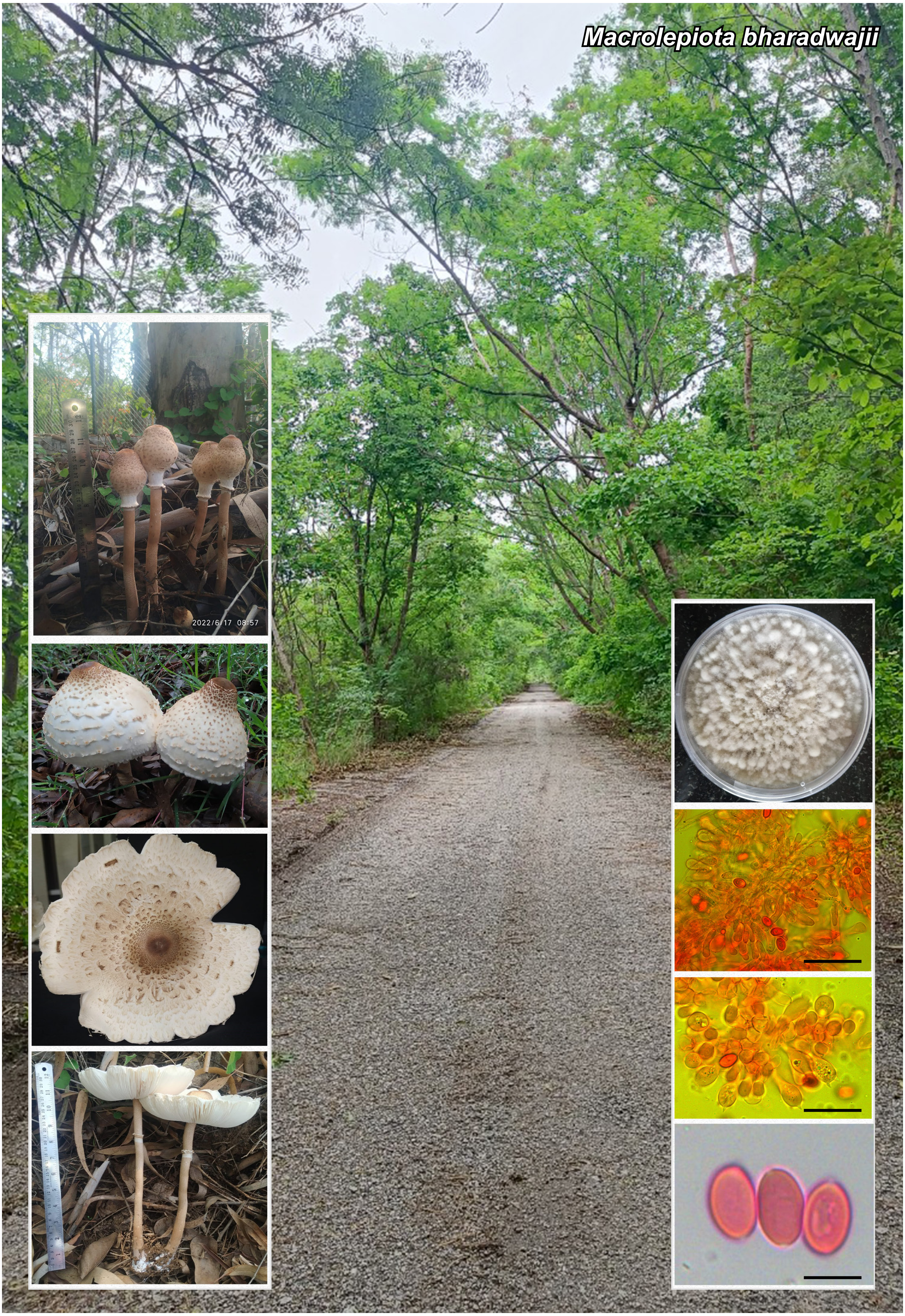
Macrolepiota bharadwajii
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Fungal Planet 1577 – 30 December 2023

Macrolepiota bharadwajii Sarma, C. Danteswari, Mahadevak., Chandran. & A.R. Podile, *sp. nov.*

Etymology. Name refers to Pullabhotla Bharadwaja Sarma, who collected the holotype specimen and provided it for further scientific investigation.

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

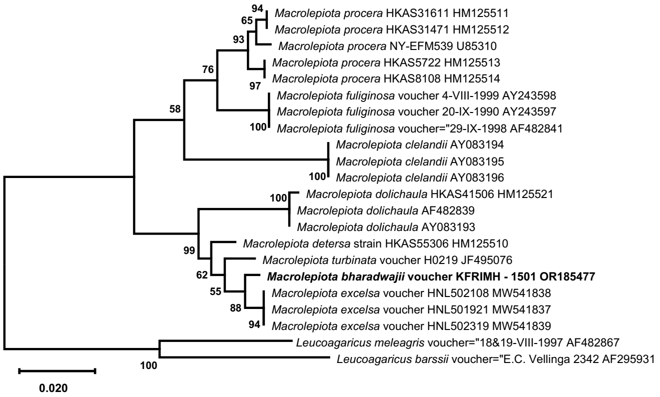
Basidiomata medium sized to large, up to 32 cm tall, pileus 12.8–28.3 cm diam, globose to subglobose, expanding to campanulate when young, and convex at maturity; umbo is distinct and acute; as the pileus expands the umbo slightly flattens, whitish, covered with brownish squamules concentrated towards the centre, becoming minute and sparse towards margin; margins incurved, hymenophore lamellate, lamellulae intercalated when young, margin brownish to whitish. *Pileus* covered with brownish granular squamules. *Cheilocystidia* (20–)33 × 11(–15) µm clavate to broadly clavate, hyaline, thin-walled. *Pleurocystidia* not observed. *Squamules* on pileus composed of a short chain of palisade cells, and frequently branched, subcylindrical to subfusiform, 8–17 µm diam, hyaline or with yellowish vacuolar pigment, thin- to slightly thick-walled. *Clamp connections* frequent at the base of basidia and cheilocystidia. *Stipe* cylindrical (7–)28 × 1.2(–2.9) cm, attenuating upwards, slightly widening towards the base, completely covered with brown tomentose-velvety light brown to brown covering which breaks open into small fine horizontal bands, hollow with central white cottony strand protruding into pileus. *Annulus* ascending, simple, whitish, membranous. *Context* whitish, sometimes becoming orange at the base of the stipe when cut. *Basidia* (28–)33 × 12(–16) µm, clavate, thin-walled, hyaline, four-spored, sterigmata reaching up to 5.2 µm tall. *Basidiospores* (8.7–)12.2 × (7.4–)11.8 µm, ellipsoid to oblong, slightly thick-walled, smooth, hyaline, with a germ pore caused by an interruption in the episporium on the rounded apex and covered with a hyaline cap.

Culture characteristics — Colonies on potato dextrose agar (PDA) reaching 54 mm diam after 7 d at 28 °C. Surface velvety, with wavy margin, circular. Reverse cream yellowish to pale and buff towards the centre. Sporulation not observed.

Typus. India, Telangana, Hyderabad, on the Campus of University of Hyderabad, Gachibowli, associated with leaf litter under *Eucalyptus* tree, basidiomata growing solitary on moist soil near the forest region of Hyderabad Central University Campus, 17 June 2022, *P.B. Sarma* (holotype KFRIMH1501; ITS and LSU sequences GenBank OR185477 and OR238483; MycoBank MB 845642).

Colour illustrations. University of Hyderabad Campus, mushroom rock road through eastern campus where the holotype specimen was collected. Left panel: immature basidiomata before opening of pileus; basidiocarp showing party expanded pileus; mature basidiocarp with fully expanded pileus; side view of full expanded basidiocarp showing the convex nature of expanded pileus; right panel: pure culture of *Macrolepiota bharadwajii*; basidium with sterigmata with immature basidiospores; basidium with sterigmata and spores; and basidiospores. Scale bars = 20 µm.

Notes — *Macrolepiota bharadwajii* closely resembles *M. excelsa* morphologically and phylogenetically. Morphologically, *M. bharadwajii* is distinct since *M. excelsa* has a distinct basidiocarp colour (completely brown to dark brown) and its basidiospores are larger in size compared to *M. bharadwajii*. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of KFRIMH1501 had highest similarity to *Macrolepiota excelsa* (vouchers HNL502108 & HNL501921; GenBank MW541838 & MW541837; Identities = 634/636 (98.39 %), one gap (0 %)), *Macrolepiota excelsa* (voucher HNL502108, GenBank MW541838; Identities = 615/623 (98.72 %), two gaps (0 %)), *Macrolepiota* sp. (H-603, GenBank GQ254066; Identities = 621/635 (97.80 %), seven gaps (1 %)), *M. detersa* (MFLU121784, GenBank MN128538; Identities = 619/634 (97.63 %), seven gaps (1 %)) and *M. detersa* (voucher CCMSSC04769, GenBank MT658754; Identities = 616/631 (97.62 %), eight gaps (1 %)). Further, the closest hits using the **LSU** sequence of KFRIMH1501 had highest similarity to *Macrolepiota procera* (voucher TAA147834, GenBank AM946456; Identities = 811/814 (99.63 %), two gaps (0 %)), *M. procera* (voucher GLM45957, GenBank AY207233; Identities = 811/814 (99.63 %), two gaps (0 %)), *M. turbinata* (voucher FBT2105H, GenBank OL652992; Identities = 810/814 (99.51 %), two gaps (0 %)) and *M. fuliginosa* (voucher MF-IS2, GenBank OM238168; Identities = 810/814 (99.51 %), two gaps (0 %)) respectively.



Phylogenetic tree of *Macrolepiota bharadwajii* constructed using MEGA v. X (Kumar et al. 2018)of the ITS-nrDNA sequence alignment by Neighbour-Joining Method (Saitou & Nei 1987). Thepercentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 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 27 nucleotide sequences. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There were 811 positions in the final dataset. The phylogenetic position of *Macrolepiota bharadwajii* is indicated in **bold**. The trees and alignment were deposited in 10.6084/m9.figshare.24216099.

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Narcissea delicata

Fungal Planet 1578 – 30 December 2023

Narcissea delicata K.G.G. Ganga, Manim. & K.P.D. Latha, *sp. nov.*

Etymology. Name refers to its delicate basidiocarps.

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

Basidiocarps very small, fragile. *Pileus* < 1 mm diam when young, finally 2–4 mm diam at maturity, initially ellipsoid to cylindrical, becoming broadly convex to conical, sometimes with a shallow central depression at maturity; surface light brown (6D6; Kornerup & Wanscher 1978) to yellowish brown (5D6) all over when young, becoming brown (6D7) to dark brown (5F5) at the centre, grey (6C1) elsewhere when mature, initially completely covered with a powdery veil, which later becomes granulose with erect, conical flocks at the centre, plicate-striate towards the margin, deliquescent; margin incurved, crenate. *Lamellae* adnate to adnexed, L = 18–19, subdistant to distant, initially white, becoming grey (6A5) with age, with lamellulae in 1 tier; edge even to the naked eye, finely pruinose under a lens, concolourous with the sides. *Stipe* 6–10 × 0.1–0.4 mm, central, terete, equal, filiform, hollow; surface translucent, smooth, often with a minute inferior annulus; base slightly enlarged. *Odour* and *taste* not distinctive. *Pleurocystidia* 40–57 × 18–27 µm, abundant, subcylindrical, lageniform or rarely clavate to sphaeropedunculate, hyaline, thin-walled. *Lamella-edge* heterogeneous. *Cheilocystidia* 20–26 × 10–12 µm, abundant, lageniform or clavate with cylindrical apical branches, hyaline, thin-walled. *Pileipellis* an undifferentiated cutis overlaid with scattered or chains of ellipsoid to subglobose velar elements; hyphae 6–20 µm wide, hyaline, thin-walled; velar elements 25–76 × 6–26 µm, thin-walled, with a pale brown plasmatic pigment and hyaline, granular encrustations dissolving in 3 % KOH. *Stipitipellis* a cutis rarely with scattered velar elements; hyphae 20–25 µm wide, hyaline, slightly thick-walled; velar elements 10–52 × 4–7 µm, cylindrical, hyaline, thin-walled. *Clamp connections* not observed on any tissues. *Basidia* 11–24 × 6–8 µm, clavate or pedicellate-clavate, hyaline, slightly thick-walled, surrounded by 3–5(–6) pseudoparaphyses, 4-spored; sterigmata up to 3 µm long. *Basidiospores* 6–8.5 × 6–8 × 4–5 µm, on an average 7.18 × 6.92 × 4.5 µm, Q_1 = 0.85–1.16, Q_{1avg} = 1.09, Q_2 = 1.2–2.0, Q_{2avg} = 1.52, lenticular, rounded-pentagonal often with an apical projection in face view, oblong or ellipsoid or rarely subcylindrical in side view, dark brown to black, thick-walled, with a central germ-pore up to 1.5 µm wide.

Habit, Habitat & Distribution — In small groups, on decaying elephant dung. Known only from the type locality in Kerala State, India.

Typus. India, Kerala State, Kozhikode District, on decaying elephant dung, substratum collected from Kakkayam forest and incubated in the lab at the University of Calicut, N11°33'04.7" E75°55'33.6", 27 Oct. 2016, *K.G.G. Ganga* (holotype G124 at CALI; ITS and LSU sequences GenBank OR420069 and OR420071; MycoBank MB 849770).

Colour illustrations. India, Kerala State, Kozhikode District, Kakkayam forest, type locality. Basidiocarps, basidiocarp showing lamellae; photos of basidiospores; basidia, pseudoparaphyses; cheilocystidia; pleurocystidia; pileipellis; velar hyphae on pileipellis; stipitipellis. Scale bars = 5 mm (basidiocarps), 20 µm (basidiospores, basidia, cheilocystidia, velar elements on the pileipellis), 50 µm (all others).

Additional materials examined. India, Kerala State, Kozhikode District, on decaying elephant dung, substratum collected from Kakkayam forest and incubated in the lab at the University of Calicut, N11°33'04.7" E75°55'33.6", 7 Oct. 2016, *K.G.G. Ganga*, G111 (ITS sequence GenBank OR420068); ibid., 8 Oct. 2016, *K.G.G. Ganga*, G112 (ITS sequence GenBank OR420070).

Notes — *Narcissea delicata* is characterised by tiny basidiocarps; a broadly convex to conical pileus with erect, conical velar flocks and plicate-striations; adnate to adnexed lamellae; a stipe with a minute inferior annulus; rounded-pentagonal basidiospores with an apical projection; a hymenium with abundant pleurocystidia; a lamella-edge with lageniform to clavate cheilocystidia with cylindrical apical branches; an undifferentiated cutis-type pileipellis with velar elements and a cutis-type stipitipellis with cylindrical velar elements.

Narcissea cordispora, a species originally described from England as *Coprinus cordisporus* (Gibbs 1908) and also reported from the Hawaiian Islands and India (Keirle et al. 2004, Amandeep et al. 2015), resembles *N. delicata* in having fragile basidiocarps with granular velar remnants on the pileus, basidiospores of somewhat similar size and shape, a pileipellis with scattered or chains of ellipsoid to subglobose velar elements and the absence of clamp connections. However, *N. cordispora* can be distinguished from *N. delicata* in having larger basidiocarps (pileus > 4 mm diam and stipe 35–50(–75) × 0.5–2 mm) with greater number (> 20) of lamellae, a stipe with a pseudovolva, a lamella-edge with lageniform cheilocystidia and a pileipellis with smooth velar elements. *Narcissea cardiaspora*, a German species originally described as *Coprinus cardiasporus* (Enderle et al. 1986) and also recorded from the Netherlands (Uljé 2005), seems to be close to *N. delicata* in having delicate basidiocarps with granular velar remnants on the pileus, a translucent stipe with a slightly enlarged base, each basidium surrounded by 3–6 pseudoparaphyses and a pileipellis with encrusted velar elements. *Narcissea cardiaspora*, however, differs from *N. delicata* in having larger basidiocarps (pileus 10 mm diam and stipe 15–35 × 0.8–1.5 mm), a stipe devoid of an inferior, complete or incomplete annulus, triangular to heart-shaped and narrow basidiospores (6–8.4 × 4–4.7 × 5.3–6(–6.5) µm) and a lamella-edge with subglobose to utriform cheilocystidia.

Narcissea patouillardii, a species originally described as *Coprinus patouillardii* from France (Orton & Watling 1979), shares a few characters such as delicate basidiocarps with granular velar remnants on the pileus, a translucent stipe with a slightly enlarged base and a pileipellis with granular, encrusted velar elements. However, *N. patouillardii* has larger basidiocarps (pileus 10–30 mm diam, and stipe 40–70 × 1–2 mm), a stipe devoid of an annulus, lageniform to globose cheilocystidia devoid of cylindrical apical branches and a habitat on vegetable refuse. Except for the description of *N. patouillardii* based on a collection from Germany (Enderle et al. 1986), any other descriptions available on *N. patouillardii*, including the description from the type material, do not mention the apical branches of cheilocystidia.

(Notes continued on Supplementary page)

Supplementary material

FP1578 Phylogenetic tree.

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Neocamarosporium halophilum

Fungal Planet 1579 – 30 December 2023

Neocamarosporium halophilum R.M. Sánchez & Bianchin., *sp. nov.*

Etymology. Name refers to the high salinity of the environment where the fungus occurs.

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

Sexual morph not observed. *Conidiomata* solitary to aggregated, pycnidial, 200–600 µm diam, brown to black, immersed, papillae becoming erumpent, globose with papillate apex and central ostiole, up to 160 µm diam; wall of 3–6 layers of brown *textura angularis*. *Paraphyses* sometimes present, up to 113 µm long, 3–6 septate, with a barrel to globose basal cell 6–10 × 8.5–15.5 µm. *Conidiophores* reduced to cubic or barrel, hyaline, smooth cells 5–9 × 3–8 µm. *Conidiogenous cells* lining the inner layer of conidioma, separate, sometimes alternating with paraphyses, hyaline, smooth, ampulliform, 4–12.5 × 3–11 µm; proliferating several times percurrently. *Conidia* solitary, initially hyaline, aseptate, thick-walled, developing a central septum and then becoming muriformly septate, shape variable from globose to obovoid to irregularly ellipsoid, brown, smooth, (12–)13.5–22(–24) × 7–12(–13.5) µm.

Culture characteristics — Colonies after 2 wk at 25 °C, flat, spreading, with moderate aerial mycelium and folded surface. On potato dextrose agar (PDA) surface with a white centre of 50–60 mm and an outer ring umber to greyish sepia (Rayner 1970), reverse black, reaching 60–70 mm diam. On oatmeal agar (OA) surface greyish sepia to olivaceous, reverse black, reaching 55 mm diam. On malt extract agar (MEA) surface pale olivaceous grey to pale mouse grey, reverse black, 20 mm diam.

Habit, Habitat & Distribution — Pathogenic on *Atriplex undultata*, a halophyte plant found in saline soils from the northwestern region of Patagonia Argentina to the centre of the country. Currently known only from the type location in southwest of Buenos Aires province, Argentina.

Typus. Argentina, Buenos Aires, Villarino, Salitral de la Vidriera, S38°44' O62°33', 1 m a.s.l., in necrotic spots on leaves of *Atriplex undulata* (*Chenopodiaceae*), 16 Sept. 2019, *R.M. Sánchez*, M4-2019 (holotype BBB:Atr4-19; culture ex-type BBB:RMS70; ITS, LSU and *TEF1* sequences GenBank OR242722, GenBank OR242721 and OR289930; MycoBank MB 849420).

Additional material examined. Argentina, Buenos Aires, Villarino, Salitral de la Vidriera, S38°44' O62°33', 1 m a.s.l., on leaves of *A. undulata*, 16 Sept. 2019, *R.M. Sánchez*, M1-2019, BBB:Atr1-19, cultures BBB:RMS56, ITS, LSU and *TEF1* sequences GenBank OR297949, OR297951, OR339880 and BBB:RMS57, ITS, LSU and *TEF1* sequences GenBank OR297950, OR297952 and OR339881.

Colour illustrations. *Atriplex undulata* growing in Salitral de la Vidriera, south of Buenos Aires province, Argentina. Foliar symptom with visible conidiomata; portion of peridium with conidiogenous cells alternating with paraphyses; paraphyses; percurrent conidiogenous cell; conidia. Scale bars = 0.5 cm (foliar symptom), 10 µm (all others)

Notes — *Neocamarosporium halophilum* is the first species of the genus found in Argentina and on this host. Phylogenies inferred from concatenated ITS and LSU sequences place the fungus in a clade along with *N. aestuarinum*, *N. aquaticum*, and *N. jorjanensis*, all species characterised for being found in saline environments. *Neocamarosporium halophilum* was found causing necrotic spots on living halophyte plants near the sea coastline, *N. aestuarinum* growing in sea water or endophytic in a halophyte plant of the *Amaranthaceae*, *Halimiones portulacoides* (Portugal), *N. aquaticum* was found on lignocellulosic debris of the shoreline (England) and *N. jorjanensis* in soils of saline lakes (Iran). The new species differs from *N. aestuarinum* (12.1 ± 2 × 10.7 ± 2.5 µm) and *N. jorjanensis* (9–12(–13) × 4–8 µm) in having darker, smooth and larger conidia. Besides, it has the largest conidiomata of the four species here mentioned and it is the only one with differentiated conidiophores. Furthermore, *N. aquaticum* and *N. halophilum* have a similar conidial length but they are much wider in the former species (18–24 × 14–19 µm) and as *N. aestuarinum*, both also differ from the new species by the absence of paraphyses. On the other hand, the paraphyses in *N. jorjanensis* (up to 30 µm long) are much shorter than those of *N. halophilum* (Papizadeh et al. 2018, Gonçalves et al. 2019, Prematunga et al. 2023).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *N. aquaticum* (strain MFLUCC:22-0063, GenBank OP730890; Identities = 503/521 (97 %), three gaps (0 %)), *N. aestuarinum* (strain CMG4, GenBank MH397366; Identities = 504/525 (96 %), six gaps (1 %)) and *Neocamarosporium* sp. (strain CF-287455, GenBank MG065836; Identities = 503/522 (96 %), four gaps (0 %)). Closest hits using the **LSU** sequence are *N. aquaticum* (strain MFLUCC:22-0062, GenBank OP730886; Identities = 845/848 (99 %), one gap (0 %)), *N. aquaticum* (strain MFLUCC:22-0063, GenBank OP730885; Identities = 845/848 (99 %), one gap (0 %)) and *N. chichastianum* (strain IBRC-M:30126, GenBank KP004483; Identities = 845/848 (99 %), one gap (0 %)). Closest hits using the ***TEF1*** sequence are *Pleosporaceae* sp. (strain M303, GenBank KJ443210; Identities = 896/921 (97 %), one gap (0 %)), *N. halimiones* (strain AFTOL-ID 1240, GenBank DQ677895; Identities = 926/958 (97 %), one gap (0 %)), *N. phragmitis* (strain MFLUCC 17-0756, GenBank MG844351; Identities = 894/926 (97 %), one gap (0 %)), *N. salsolae* (strain MFLUCC 17-0826, GenBank MF434456; Identities = 893/925 (97 %), one gap (0 %)) and *Pleosporaceae* sp. (strain M305, Genbank KJ443212; Identities = 889/921 (97 %), one gap (0 %)).

Supplementary material

FP1579-1	Table.
FP1579-2	Phylogenetic tree.

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Ophiocordyceps philippinensis

Fungal Planet 1580 – 30 December 2023

Ophiocordyceps philippinensis Piskorski, Kisło & Ruszk.-Mich., *sp. nov.*

Etymology. The epithet refers to the Philippines, where the specimen was collected.

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

Sexual morph capitated. Stromata 5–6 mm long × 1–2 mm diam, several from the host, stipitate, branching, ochre to brown. Stipe 4–5 mm long × 0.5–0.6 mm diam, cylindrical, dark brown, with a fertile head. Head 2–3 mm long × 2–2.5 mm diam, ochre to brown, single, hemispherical to allantoid. *Perithecia* 236–256 × 98.5–113 µm, immersed, thick-walled, ovate to elongated pear-shaped, set upright with ostioles on the upper surface of the head. *Peridium* hyaline, of *textura oblita* to *textura intricata* to *textura angularis*. *Asci* immature, 140–160 × 3–4.5 µm, hyaline, filiform, with a thick apex; apical cap 4–4.5 × 5 µm, thick, with a small channel in the centre. *Ascospores* immature. *Asexual morph* undetermined.

Typus. Philippines, Mindanao Island, Northern Mindanao region, Lanao del Norte province, Iligan City, Mount Agad-Agad, vegetation on the banks of a mountain stream, N08°13'12.4" E124°16'04.080", parasitic on *Asilus* sp. (*Asilidae*), 28 Jan. 2022, *D.A. Acal* (holotype LOD PF 4565, specimen preserved in ethanol; ITS, LSU, SSU and *tef1* sequences GenBank OQ641807, OQ641808, OQ660303, OQ641806; MycoBank MB 848172).

Notes — The genus *Ophiocordyceps* was first described in 1931 as a taxon grouping parasites of invertebrates and having ascospores that do not disintegrate into part-spores (Petch 1931). Disarticulation of ascospores was thereafter not considered a crucial character, and the molecular data were prioritised in the generic delimitation (Sung et al. 2007). Species in this genus are characterised by darkly pigmented, tough to supple stromata that are present in *O. philippinensis* (stromata branched, dark brown, with hemispherical to allantoid and ochre to brown fertile heads). Phylogenetically, *O. philippinensis* is closely related to *Ophiocordyceps* sp. reported from China (GenBank MT248272.1; 3 bp ITS differences), *O. globiceps*, and *O. dipterigena*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence are *Ophiocordyceps* sp. (culture MFLU 20-0264, GenBank MT248272.1; Identities 200/203 (99 %), one gap), *O. globiceps* (culture CBS 756.96, GenBank MN431394; Identities 646/652 (99 %), two gaps) and *O. globiceps* (culture MFLU:22-0267, GenBank OM100734; Identities 169/170 (99 %), one gap). The closest hits using the **LSU** sequence are *Ophiocordyceps* sp. (culture FY-2020a, GenBank MT248289.1; Identities 542/568 (95 %), two gaps), *O. globiceps* (culture MFLUCC 18-0495, GenBank NG_068274; Identities 500/565 (88 %), 15 gaps) and *O. globiceps* (culture MFLUCC 18-0495, GenBank NG_068274; Identities 502/568 (88 %), 15 gaps). The closest hits using the **SSU** sequence are *O. globiceps* (strain MFLU 18-0661, GenBank MH725812.2; Identities 959/963 (99 %), no gaps), *O. globiceps* (strain MFLUCC 18-0495, GenBank MH725811.2; Identities 959/963 (99 %), no gaps) and *O. globiceps* (isolate MFLUCC 18-0495, GenBank NG_068397.1; Identities 959/963 (99 %), no gaps). The closest hits using the ***tef1*** sequence are *O. globiceps* (culture MFLU:18-066, GenBank H727388.2; Identities 552/571 (97 %), no gaps), *O. globiceps* (culture MFLUCC:18-0495, GenBank MH727387.1; 544/563 (97 %), no gaps) and *O. globiceps* (culture MFLU:22-0267, GenBank OQ186383.1; Identities 542/561 (97 %), no gaps).

Ophiocordyceps philippinensis is best distinguished from two related species (*O. globiceps* and *O. dipterigena*) by DNA data (*tef1*, LSU and ITS). From *O. globiceps*, it differs in some morphological features of the stromata. They are single, unbranched, and cinnamon to yellow in *O. globiceps* (Xiao et al. 2019), while in *O. philippinensis*, as many as three ochre to brown stipes grow from the host. Differences are also observed in dimensions: *O. globiceps* stromata are shorter than in *O. philippinensis* (4–8 mm long × 0.5–1 mm diam vs 5–6 mm long × 1–2 mm diam). It is visible also in both parts of the stromata: in specimens of *O. globiceps* the stipe is shorter (3.5–7.5 mm long × 0.2–0.5 mm diam vs 4–5 mm long × 0.5–0.6 mm diam), and the head is smaller (2–3 mm long × 2–2.5 mm diam vs 1–1.5 mm long × 1–1.2 mm diam) than in *O. philippinensis*. The comparison of *O. philippinensis* and *O. dipterigena* is greatly limited due to the incomplete original species description (Berkeley & Broome 1873) and the characteristics given in the subsequent reports (cf. Xiao et al. 2019).

The ecological data on the host spectrum of *O. globiceps* and *O. philippinensis* also support separating the two species. Both species attack insects from the order *Diptera* but from different families: *O. globiceps* parasitises true big flies of *Muscidae* (Xiao et al. 2019), and *O. philippinensis* was collected on a robberfly of *Asilidae*. The third species, *O. dipterigena*, was reported on diverse dipteran taxa (e.g., *Agromyzidae*; *Asilidae*; *Muscidae*; Salgado-Neto et al. 2018, Chhetri et al. 2019, Tasanathai et al. 2019). Most probably, *O. dipterigena* is a species complex that is also expressed by the location of sequences from its specimens on the phylogenetic tree, and some of its records may represent *O. philippinensis.*

Colour illustrations. Sampling site at Mount Agad-Agad, Philippines. Stromata emerging from infected robberfly; fertile head and details of the upper surface with perithecial apices; single perithecium; asci; apical cap. Scale bars = 10 µm.

Supplementary material

FP1580 Phylogenetic tree.

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Ophiocordyceps poecilometigena

Fungal Planet 1581 – 30 December 2023

Ophiocordyceps poecilometigena Y.P. Tan, Marney, Abell & R.G. Shivas, *sp. nov.*

Etymology. Named after the insect host, *Poecilometis* sp. (*Hemiptera*: *Pentatomidae*).

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

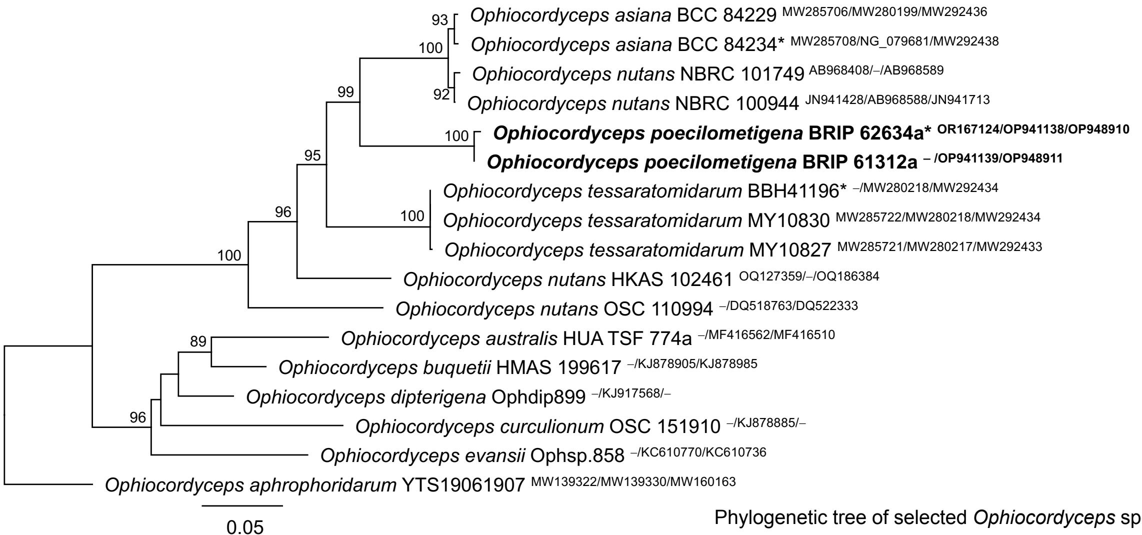
Hosts are adult stinkbugs (*Poecilometis* sp.) on leaf litter in tropical rainforest. *Stromata* stipitate, solitary, arising from between the head and thorax of host, filiform, flexuous, 5–10 cm long × 1–1.5 mm wide, sometimes bifurcate in the apical part, black, with a pink to bright red cylindrical clava, 10–20 × 2–4 mm, hymenostilbe-like morph present in sub-apical part and perithecial morph in apical part of clava. *Conidiophores* 25–50 µm long, septate, branched at apex, basal cell 20–25 × 4–7 µm, narrower at the base, hyaline, in palisade layers, with 2–3 apical conidiogenous cells. *Conidiogenous cells* are phialides, subcylindrical, 14–25 × 3.5–6 µm, hyaline to pink, with 2–5 apical pegs. *Conidia* aseptate, tear-shaped, 7–10 × 3–4 µm, hyaline or with reddish granulations. *Perithecia* immersed, ovoid, 500–600 × 150–200 µm, ostiolate. *Asci* cylindrical, 8-spored, up to 550 × 5–7 µm, breaking into part spores 8–14 × 1.5–2 µm, with hemispherical apical caps, 5–6 × 4–5 µm.

Typus. Australia, Queensland, Mission Beach, on *Poecilometis* sp., 7 June 2015, *T.S. Marney*, *S. Abell*, *M.D.E. Shivas* & *R.G. Shivas* (holotype specimen BRIP 62634a; ITS, LSU, SSU and *tef1* sequences GenBank OR167124, OP941138, OP941140 and OP948910; MycoBank MB 849554).

Additional specimen examined. Australia, Queensland, Mission Beach, on *Poecilometis* sp., 7 July 2014, *T.S. Marney*, *M.A. Shivas*, *M.D.E. Shivas* & *R.G. Shivas*, voucher specimen BRIP 61312a, LSU, SSU and *tef1* sequences GenBank OP941139, OP941141 and OP948911.

Notes — *Ophiocordyceps poecilometigena* is a member of the *Ophiocordyceps nutans* species complex (Friedrich et al. 2018). Its discovery provides further evidence of cryptic speciation within this complex, along with the recent descriptions of *O. asiana* and *O. tessaratomidarum* (Khao-ngam et al. 2021). *Ophiocordyceps poecilometigena* has only been found at one location in northern Queensland on adult *Poecilometis* sp. DNA sequences were amplified from nucleic acids extracted directly from fresh stromata. Attempts to obtain the fungus into artificial culture medium were unsuccessful.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest relevant hits using the ITS region are *O. nutans* (strain UoO-113/78, GenBank AJ786583, Identities 346/413 (84 %), 35 gaps) and *O. asiana* (isolate MY11878, GenBank MW285719, Identities 207/215 (96 %), four gaps). The closest relevant hits using the **LSU** sequence are *O. myrmecophila* (strain BCC82258, GenBank MH028159, Identities 746/785 (95 %), six gaps), *O. sphecocephala* (strain 4169, GenBank AF327390, Identities 749/798 (93 %), six gaps) and *O. irangiensis* (strain 3450, GenBank AF327389, Identities 782/852 (92 %), 19 gaps). The closest relevant hits using the **SSU** sequence are *O. nutans* (strain NBRC 101749, GenBank JN941712, Identities 1030/1039 (99 %), one gap), *O. sphecocephala* (strain OSC 110998, GenBank DQ522551, Identities 1019/1039 (98 %), one gap) and *O. tricentri* (culture collection NBRC 106968, GenBank AB968393, Identities 1015/1039 (98 %), one gap). The closest relevant hits using the ***tef1*** sequence are *O. nutans* (strain OSC 110994, GenBank AB968588, Identities 940/978 (96 %), no gaps), *O. asiana* (isolate BCC84234, GenBank MW292438, Identities 814/850 (96 %), no gaps) and *O. tessaratomidarum* (isolate MY10829, GenBank MW292435, Identity 838/880 (96 %), no gaps).



Colour illustrations. *Ophiocordyceps poecilometigena* on adult *Poecilometis* sp., northern Queensland. Adult host with stroma emergent from between head and thorax; clava; conidiophores, phialides and conidia; vertical section through perithecia; ascus; ascospores. Scale bars = 1 cm (host), 1 mm (clava), 100 µm (vertical section), 10 µm (all others).

Phylogenetic tree of selected *Ophiocordyceps* species based on maximum likelihood analysis of the combined ITS, LSU, and *tef1* gene regions. Analyses were performed on the IQ-TREE web server (Trifinopoulos et al. 2016). Bootstrap support values greater than 70 % are given at the nodes. GenBank accession numbers are indicated (superscript ITS/LSU/*tef1*). *Ophiocordyceps aphrophoridarum* (voucher YTS19061907) was used as outgroup. Novel taxon is indicated in **bold**. Ex-type strains indicated with asterisk (*). The alignment and phylogeny are publicly available in Zenodo (doi: 10.5281/zenodo.8176474).

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Orbilia multiserpentina

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Orbilia multiserpentina Fuljer, Polhorský & Baral, *sp. nov.*

Etymology. The name refers to the 32-spored asci and the ascospores similar to *O. serpentina*.

Classification — *Orbiliaceae*, *Orbiliales*, *Orbiliomycetes*.

Apothecia rehydrated 0.1–0.4(–0.5) mm diam (av. 0.25 mm), 0.15–0.22 mm high, slightly translucent, bright to deep orange when dry, round, scattered to subgregarious; disc slightly concave or ± flat, margin smooth to finely rough, indistinct, 0–8 µm protruding; broadly sessile, superficial. *Asci* *(64–)73–97 (–113) × (6.8–)7.8–9.7(–10.2) µm {5}, †(63–)67–78(–87) × (6–)7–9(–10.8) µm {5}, 32-spored, cylindric-clavate, spores *3–4-seriate, lower spores inverted (usually mixed), pars sporifera *29–64 µm long; apex (†) slightly to medium truncate, sometimes laterally inflated, thin-walled; base with short to long, medium to thick flexuous stalk, T-, L- or Y-shaped. *Ascospores* *(5.8–)6.5–11.2(–12.5) × (2–)2.1–2.7(–3.1) µm {10}, †(5.5–)6.3–10.5(–10.9) × 1.9–2.5(–2.6) µm {2}, fusoid to fusiform (narrowly amygdaliform), also ellipsoid-fusoid or fusiform-clavate, apex subacute to acute (to acuminate), base very slightly up to strongly attenuated (rarely tail-like), straight to slightly inequilateral, often slightly to medium curved at base. *Spore bodies* *(3.3–)3.6–7.8(–8.5) × (0.4–)0.5–1.1(–1.3) µm {10}, vermiform to subulate (rarely curved below like an inverted question mark), base often slightly to medium inflated (bulbous), mostly slightly to strongly flexuous. *Paraphyses* apically slightly to strongly capitate-clavate, rarely spathulate or uninflated, terminal cells *(6.7–)8–22(–29) × (2–)2.7–6.5(–7) µm {6}, †(1.5–) 2.3–5.4 µm wide {2}, lower cells *(3.5–)6.5–20.5(–23) × (1.1–)1.3–2.6(–3) µm {6}, †(0.9–)1.2–1.9 µm wide {2}; sometimes branched near apex and anastomosing near base. *Medullary excipulum* pale orange, 30–40 µm thick in centre, of loose to dense *textura intricata*(*-globulosa*), at flanks sharply delimited from ectal excipulum. *Ectal excipulum* subhyaline to light orange, of irregularly oriented *textura angularis*, 25–65 µm thick, cells *(4.6–)5.7–16(–19.6) × (2.3–)4.3–12.2(–15.8) µm. *Anchoring hyphae* sparse to medium abundant, *(1.3–)1.7–3.7(–4.6) µm wide, walls 0.3–0.9 µm thick. *SCBs* abundant in paraphyses and ectal excipulum (from base up to margin), globose, faintly refractive, hyaline, and crystalloid, strongly refractive, rod- or ring- to keyhole-shaped {6}, subhyaline to pale orange, (1–) 2.5–4(–6) × (0.4–)1–4(–5.2) µm. *Exudate* over paraphyses 0.3–1 µm thick, granular, cloddy to cap-like, pale yellow-orange, at margin and flanks 1–2.3 µm thick, yellow-orange. *Asexual morph*: trinacrium-like (presumed, from natural substrate) {6}. *Conidiophores* not observed. *Conidia* Y-shaped, total size *(27–)28.9–45.3(–50) × (13–)14–30(–32) µm, stipe *(10.3–) 11–20 × (3.2–)3.8–5.1 µm, 1–2-septate (proximal septa not counted), arms medium to strongly tapering and lageniform, with obtuse ends, proximal arm cells often inflated and constricted at septa, *(15.8–)19–27(–32) × (3.6–)4.2–5.3(–6) µm, 2–4(–5)-septate (proximal septum counted).

Colour illustrations. Croatia, Pag Island, Nature Reserve of Dubrava – Hanzina, submediterranean forest with dominant oak (holotype locality; photo credit F. Fuljer). Top left to bottom right. Rehydrated apothecia (BRACR38487); conidium (BRACR38493); ascospores (from top to bottom BRACR38492, BRACR38499, BRACR38490); ectal excipulum with mainly crystalloid SCBs (BRACR38493); paraphyses with globose and crystalloid SCBs (BRACR38487) and asci (BRACR38492). All tissues mounted in H_2O and living. Scale bars = 100 µm (apothecia), 10 µm (all others).

Distribution & Habitat — Known from Croatia, probably more widespread but overlooked. Growing on rotten, periodically dry, decorticated xeric branches of *Quercus ilex* {4}, *Q. pubescens* {7}, *Morus nigra* {1}, *Myrtus communis* {1}, *Pistacia lentiscus* {1}, *Prunus mahaleb* {1} and *Vitex agnus-castus* {1}, typically in maquis vegetation or in oak forests. Desiccation tolerance: fully tolerant for at least 6 m. Altitude: 1–64 m a.s.l. Phenology: Jan., July–Aug. (probably throughout the year).

* = living state; † = dead state; SCBs = KOH-soluble cytoplasmic bodies.

Typus. Croatia, Pag Island, Pag town, Nature Reserve of Dubrava – Hanzina, 4.8 km NW of Pag town, 44.473000N 15.010041E, 20 m a.s.l., attached xeric branch of *Quercus pubescens* (*Fagaceae*), on wood, 17 July 2021, *F. Fuljer* (holotype BRACR38493; ITS and LSU sequences GenBank OR610771 and OR610774; Mycobank MB850242).

Additional materials examined. See supplementary page.

Notes — *Orbilia multiserpentina* is characterised by 32-spored asci, mainly fusoid to fusiform ascospores, vermiform to subulate spore bodies, abundant presence of crystalloid SCBs in ectal excipulum and paraphyses and occurrence on decorticated, superficially rotten, xeric deciduous branches in mesomediterranean, submediterranean and thermomediterranean thermophilous forests and maquis (north of Dalmatia). Although our records are only from Pag and Rab Islands, we assume, that it is a more widespread species across the islands and coastal areas in the Adriatic and Mediterranean Sea. A trinacrium-like asexual morph was repeatedly observed among the apothecia, but its connection to the sexual morph is only presumed. The remarkable shape of the conidia is unknown in any other orbiliaceous trinacrium-like asexual morphs: they show a constriction at the base of the two arms and partly also between the arm cells, with an often very short septum at the attachment to the stipe. They resemble tridentaria-like asexual morphs (e.g., *O. quaestiformis*), which are 3- or sometimes more-armed. Morphologically closest species are from series *Serpentinae* and *Ellipsospermae*. The very similar *O. serpentina* differs in 16-spored asci and in smaller trinacrium-like conidia, which are not constricted at the septa. The 32-spored *O. multidelphinus* with partly similar ascospore characteristics lacks crystalloid SCBs. The 32-spored *O. multicercocarpi* differs in shorter ascospores with rounded to obtuse ends. The phylogenetically closest species *O. multiurosperma* concurs in having 32-spored asci and in crystalloid SCBs, but differs in shorter and wider ascospores with shorter spore bodies and basally more curved tail-like ends. Another related taxon, *O. filiformis*, is somewhat similar in fusiform ascospores with acute apex and attenuated base and in long, sometimes subulate and flexuous spore bodies, but differs in 8-spored asci, absence of crystalloid SCBs in ectal excipulum, and in a more temperate distribution (Baral et al. 2020).

Supplementary material

FP1582 Phylogenetic tree.

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Pachyella pulchella

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Pachyella pulchella K. Hansen, *sp. nov.*

Etymology. Named for the beauty and small size of the apothecia.

Classification — *Pezizaceae*, *Pezizales*, *Pezizomycetes*.

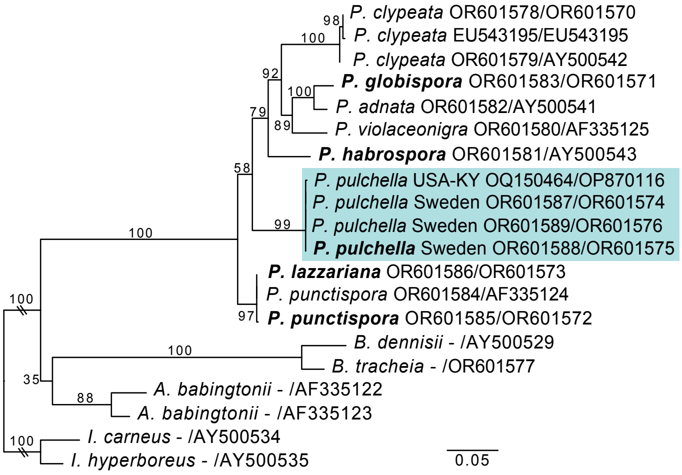
Apothecia gregarious, shallowly concave when young, soon flat, regularly disc-shaped, sessile, centrally attached to the substrate, flanks attached to the substrate or free, margin amply free, up to 7 mm diam when fresh, thick-fleshed; hymenium smooth, dark violet brown to dark violet (9F4 to 10F4, 11F4; Kornerup & Wanscher 1961) when fresh, becoming dark brown to almost black with violaceous tinge when dried; outside tuberculate to slightly tufted, light greyish yellow, pale violet when fresh, cream-coloured when dried, margin seen as a distinct line (sharp colour change). *Excipulum* c. 1 500 µm thick when fresh. *Ectal excipulum* of *textura globulosa* to *textura angularis*, c. 600 µm thick, four to seven cells wide at flanks, nine or more cells wide at the base; cells 13–41 × 8–26 µm (longer than wide), with the long axes perpendicular to the outside, with some terminal cells ending in short, ± interwoven, hyphoid hairs, 15–45 × 3–4.5 µm, forming a layer of few hyphae on the outer surface; without gelatinous matrix. *Medullary excipulum* of dense *textura intricata* with large inflated cells, lacking a clear boundary with ectal excipulum and subhymenium, cells towards (sub)hymenium less inflated. *Asci* distinctly, but diffusely amyloid, strong, but evenly blue over the apex, 350–400 × 18–20 µm, arising from croziers. *Ascospores* uniseriate, hyaline, thin-walled, (21.7–)22.2–25.9(–27.1) × (11.1–)11.4–13.9(–14.9) µm (n = 69), ellipsoid to slightly fusoid, Q = (1.6–)1.7–2.2, with very low, fine, rounded, irregular, cyanophilic warts, visible on the surface, not or barely seen in outline; cytoplasm slightly granular, with two large guttules c. 7.5 µm diam when fresh, often persisting in dried material, but sometimes fusing into a single large guttule; deBary bubbles sometimes present. *Paraphyses* simple, straight, 3–6 µm broad, in upper part gradually enlarged to 7.3–8.8 µm broad, clavate, septate, uppermost cells 75–90 µm long, exceeding the asci, some embedded in or covered with a thin gelatinous matrix; filled with amorphous, orange brown pigment when fresh, except at the very apex, when dry with large, not well-delimited brownish vacuoles, more abundant towards the apex and especially in the uppermost cell, only slightly darkening in Melzer's reagent.

Typus. Sweden, Medelpad, Höglandsbodarna, Mjällådalen Nature Reserve, river Mjällån, on sand-silt bank in the river, with *Salix*, *Betula* and *Alnus*, on water-soaked decaying deciduous wood, 14 Sept. 2014, *K. Hansen* & *I. Olariaga*, KH.14.72 (holotype S-F470616; ITS and LSU sequences GenBank OR601588 and OR601575; MycoBank MB 850276).

Additional material examined. Sweden, Hälsingland, Bergsjö, Bjästa, on branches of deciduous trees, laying on very moist soil at the edge of a stream, 14 Aug. 2018, *J. Myhrer* (UPS F-923036; ITS and LSU sequences GenBank OR601589 and OR601576); in the same place as the holotype, 13 Sept. 2014, *K. Hansen* & *S. Kyrk*, KH.14.66 (S-F470617; ITS and LSU sequences GenBank OR601587 and OR601574).

Colour illustrations. The type locality and habitat for *Pachyella pulchella* in Mjällådalen Nature Reserve in Sweden. In situ apothecia of the paratype (S-F470617); ectal excipulum, asci and paraphyses in MLZ (note the thin gel layer covering the hymenium) and ascospores of holotype (S-F470616). Scale bars = 20 µm (spores), 25 µm (excipulum, asci and paraphyses).

Notes — The placement of this new species in the genus *Pachyella* is supported by the diffusely blueing asci in Melzer's reagent, hymenial gel, large globose cells in the ectal excipulum, broadly clavate paraphyses filled with amorphous orange brown pigment, the occurrence on moist wood that is regularly inundated with flowing water, and molecular phylogenetic analyses. The genus *Pachyella* is, however, currently recognised by globose excipular cells which, on the outside, terminate in flexuous hyphoid hairs embedded in a gelatinous matrix, and often presence of a gel in the medullary excipulum (Pfister 1973, Pfister et al. 2008). Herewith, the circumscription of *Pachyella* is emended to also include species without excipular gel. In addition to lacking excipular gel, *P. pulchella* is distinguished from other species of *Pachyella* by the combination of small, perfectly disc-shaped, centrally attached, dark violet apothecia, and large, very finely warty spores. It naturally represents an early diverging lineage in the genus, together with *P. punctispora.* These two species are sisters to the rest of the *Pachyella* species (see ITS-LSU phylogram), i.e., *P. adnata*, *P. clypeata*, *P. globispora*, *P. habrospora* and *P. violaceonigra* that produce apothecia with hyphoid hairs forming a palisade layer at the base (Pfister & Candoussau 1981, Pfister 1995, Hosoya & Maruyama 2004). The apothecia of *P. punctispora* do not have a discrete palisade layer of hyphoid hairs, but have shorter outer excipulum hairs embedded in a gel and a gelatinous matter is present in the medullary excipulum. One additional species, *P. hydrophila*, produces small apothecia, 4–8 mm diam, with sparse excipular gel that are difficult to see in dried material (type studies by Pfister (1979) and Kristiansen (2011)). *Pachyella pulchella* differs clearly from *P. hydrophila* that has reddish brown apothecia, broader paraphyses, reaching a diam of 15 µm, and excipular gel.



Phylogram of a ML analysis of ITS and LSU rDNA sequences, showing the position of *P. pulchella* (highlighted with a coloured box). Two species of *Iodophanus* were used for rooting purpose. ITS sequences of *Adelphella*, *Boudiera* and *Iodophanus* were too divergent to be aligned, and only LSU rDNA sequences were used. The RAxML v. 7.2.6 search (Stamatakis 2006), used a GTR-GAMMA model, with all free model parameters estimated by the program and 1 000 bootstrap replicates (shown by the branches). The terminals originating from holo- or isotypes are marked in **bold**. The tree and alignment are available in TreeBASE, as no. S30801.

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Paramyrothecium indicum

Fungal Planet 1584 – 30 December 2023

Paramyrothecium indicum Sh. Kumar, Mufeeda, Raghv. Singh & Mahadevak., *sp. nov.*

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

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

Phytopathogenic, foliicolous, associated with leaf spots, amphigenous, circular to sub-circular, necrotic, brown, 5–20 µm, forming many sporodochia. *Colonies* amphigenous, brown to blackish in centre and whitish at periphery. *Sexual morph*: not found. *Asexual morph*: *Conidiomata* sporodochial, stromatic, superficial, cupulate, scattered or gregarious; outline oval or irregular in outline, 45–400 µm diam, 50–225 µm deep with a white setose fringe surrounding an olivaceous green to dark green slimy mass of conidia. *Setae* developing from sporodochia, thin-walled, hyaline, 1–3-septate, smooth, unbranched, straight to flexuous, 35–125 µm long, 2–3 µm wide, terminating in an acute rounded apex. *Conidiophores* developing from the basal stroma, consisting of a stipe and a penicillately branched conidiogenous apparatus, stipes unbranched, hyaline, septate, smooth, 15–38 × 2–3 µm, primary branches aseptate, unbranched, thin-walled, smooth, 10–20 × 2–2.5 µm; secondary branches aseptate, unbranched, smooth, 10–14 × 2–3 µm; terminating in a single whorl of 3–5 conidiogenous cells arising apically. *Conidiogenous cells* integrated, terminal, phialidic, cylindrical to sub-cylindrical, hyaline, smooth, straight to slightly curved, 10–15 × 2.5–3.5 µm, conspicuous collarettes and periclinal thickenings. *Conidia* solitary to catenate, acrogenous, simple, aseptate, hyaline, smooth, thin-walled, straight, conidia two types: cylindrical conidia abundant, 6–8 × 1.5–2.5 µm (av. 6 × 2 µm, n = 20); ellipsoidal conidia observed, 6–10 × 3–4 µm (av. 6 × 3.5 µm, n = 10), rounded at both ends, scars unthickened.

Culture characteristics — See supplementary page.

Typus. India, Kerala, Thrissur, Peechi, near Peechi-Vazhani Wildlife Sanctuary on living leaves of *Hibiscus hispidissimus* (*Malvaceae*), 27 July 2022, *S. Kumar* (holotype as voucher specimen KFRIMH 445; ex-type living culture KFRIMCC 445 as metabolically inactive culture; ITS, LSU, *cmdA*, *tub2* and *rpb2* sequences GenBank OR405967, OR419836, OR484298, OR484297 and OR484303; MycoBank MB 849844).

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of *Paramyrothecium indicum* (KFRIMH 445) had highest similarity to *Paramyrothecium roridum* (GenBank AB823653; Identities = 536/537 (99.81 %), one gap (0 %)), *Paramyrothecium* sp. (isolate MC-BHU36, GenBank ON620079, Identities = 533/533 (100 %), no gaps), *Paramyrothecium* sp. (isolate MC-BHU-32, GenBank OL505438, Identities = 536/537 (99.81 %)), one gap (0 %)), *Paramyrothecium* sp. (strain CRC143, GenBank MZ373255, Identities = 535/536 (99.81 %), one gap (0 %)) and *Paramyrothecium* sp. (strain CRC9, GenBank MZ373248, Identities = 535/536 (99.81 %), one gap (0 %)). The **LSU** sequence data of *P. indicum* had highest similarity to *P. roridum* (culture CBS 372:50, GenBank MH868182; Identities = 862/862 (100 %), no gaps), *Paramyrothecium* sp. (isolate TBRC, GenBank MT974029; Identities = 864/865 (99.8 %), no gaps), *P. cupuliforme* (culture CBS 127789, GenBank MH876139; Identities = 860/862 (99.77 %), no gaps), *Xenomyrothecium tongaense* (culture CBS 598.80, GenBank MH873062; Identities = 861/863 (99.77 %), two gaps (0 %)) and *P. foeniculicola* (culture CBS 331.51, GenBank MH868404; Identities = 860/862 (99.77 %), two gaps (0 %)). The ***cmdA*** gene sequence had highest similarity to *P. eichhorniae* (voucher CRC148, GenBank OM810415; Identities = 564/592 (95.27 %), five gaps (0 %)), *P. eichhorniae* (voucher CRC3, GenBank OM810411; Identities = 562/592 (94.93 %), five gaps (0 %)), *P. amorphophalli* (strain MFLUCC 22-0085, GenBank OP434479; Identities = 561/592 (94.76 %), six gaps (1 %)), *P. eichhorniae* (voucher CRC11, GenBank OM81416; Identities = 560/593 (94.44 %), six gaps (1 %)) and *P. foliicola* (strain MU9, GenBank MN593634; Identities = 540/570 (94.74 %), seven gaps (1 %)). The ***tub2*** gene sequence shared highest similarity to *P. amorphophalli* (strain MFLUCC 22-0085, GenBank OP434480; Identities = 262/266 (98.5 %), one gap (0 %)), *P. eichhorniae* (voucher CRC8, GenBank ON033772; Identities = 262/266 (98.5 %), one gap (0 %)), *P. eichhorniae* (voucher CRC148, GenBank ON033768; Identities = 262/266 (98.5 %), one gap (0 %)), *P. eichhorniae* (voucher CRC143, GenBank ON033769; Identities = 256/266 (96.24 %), one gap (0 %)), *P. foliicola* (strain 9_1, GenBank MH824737; Identities = 255/266 (95.86 %), one gap (0 %)) and *P. foliicola* (strain MU1, GenBank MN398051; Identities = 254/266 (95.49 %), one gap (0 %)). Further, the ***rpb2*** gene sequence shared highest similarity to *P. eichhorniae* (voucher CRC3, GenBank ON033781; Identities = 850/861 (98.72 %), no gaps), *P. eichhorniae* (voucher CRC8, GenBank ON033782; Identities = 849/861 (98.61 %), no gaps), *P. eichhorniae* (voucher CRC148, GenBank ON033783; Identities = 847/861 (98.37 %), no gaps), *P. amorphophalli* (culture MFLUCC 22-0085, GenBank OP434481; Identities = 688/694 (98.5 %), no gaps), *P. breviseta* (voucher CRC13, GenBank ON033774; Identities = 790/861 (91.75 %), no gaps) and *P. foliicola* (strain HS01, GenBank MW116070; Identities = 650/662 (98.19 %), one gap (0 %)). *Paramyrothecium indicum* is phylogenetically close to *P. amorphophalli* (MFLUCC 22 0085^{T}; Armand et al. 2023). Morphologically, *P. indicum* differs from *P. amorphophalli* in its longer conidiophores (up to 38 µm long). The conidia of *P. indicum* are slightly larger (cylindrical conidia 6–8 × 1.5–2.5 µm, ellipsoidal conidia 6–10 × 3–4 µm), than those of *P. amorphophalli* (cylindrical conidia 5–6.4 × 1.5–2 µm, ellipsoidal conidia 6–7 × 3–3.5 µm).

Colour illustrations. *Hibiscus hispidissimus* habit near Peechi-Vazhani Wildlife Sanctuary, Thrissur, Kerala. Left panel from top: upper and lower surface of infected leaves, enlarged view of symptoms showing fruiting bodies (sporodochia), top and reverse view of PDA plate; bottom from left: enlarged view of fungus culture showing sporodochia, sporodochia with embedded conidiophores and conidia, conidiophore attached with conidia, cylindrical and ellipsoidal conidia (in lactophenol-cotton blue mixture). Scale bars = 10 µm.

Supplementary material

FP1584-1 Phylogenetic tree.
FP1584-2 Table.

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Plectosphaerella vigrensis

Fungal Planet 1585 – 30 December 2023

Plectosphaerella vigrensis Piątek, Patejuk, Baturo-Cieśniewska, Stryjak-Bogacka & Pusz, *sp. nov.*

Etymology. Name refers to the Wigry National Park (from Latin *vigrensis* = Wigry), located in northeast Poland, where the fungus was collected.

Classification — *Trichosphaeriaceae* (syn. *Plectosphaerellaceae*), *Trichosphaeriales*, *Sordariomycetes*.

Hyphae branched, septate, hyaline, smooth, straight, thin-walled, with oil guttules, 1.5–3.0 µm wide, sometimes coiled. *Conidiophores* monophialidic, emerged laterally or terminally, subcylindrical or ampulliform, hyaline, smooth. *Conidiogeneous cells* subcylindrical, hyaline, smooth, 13.5–32 × 2–3.5 µm, with conspicuous cylindrical collarette at the conidiogenous locus. *Conidia* subcylindrical, with rounded apex and slightly truncate base, hyaline, smooth, aseptate or 1-septate, 6–13 × 2.5–3(–3.5) µm, single. *Sexual morph* not observed.

Culture characteristics — Colonies on malt extract agar (MEA) and potato dextrose agar (PDA) flat, membranaceous, buff white, reaching 55 mm (on MEA) or 45 mm (on PDA) diam after 2 wk growth at 25 °C; surface papillate, with sparse aerial mycelium, margin entire, fimbriate. Reverse yellowish buff.

Typus. Poland, Podlaskie Province, Suwałki County, Wigry National Park (between Nowa Wieś and Królówek), N54°07'11" E23°04'43", mixed forest, isolated from leaf spots on *Impatiens noli-tangere* (*Balsaminaceae*), 6 June 2021, *W. Pusz* (holotype KRAM F-59983; culture ex-type I-2 WPN = CBS 150722; ITS, LSU, *cmdA*, *rpb2*, *tef1* and *tub2* sequences GenBank OR539695, OR539696, OR553647, OR540198, OR540197 and OR553648; MycoBank MB 850291).

Notes — The genus *Plectosphaerella* includes 23 sequenced species of soilborne, plant pathogenic and endophytic fungi (e.g., Giraldo & Crous 2019, Giraldo et al. 2019, Zhang et al. 2019, Crous et al. 2021b, Yang et al. 2021, Tan & Shivas 2023). *Plectosphaerella vigrensis* is phylogenetically distinct from all previously described species. The most closely related species resolved in phylogenetic analyses are *Plectosphaerella nauculispora* and *P. verschoorii*. Morphologically, *P. vigrensis* is distinct from *P. nauculispora* in having longer conidia (conidia, both aseptate and 1-septate, 3–7 × 1–2 µm in *P. nauculispora*; Zhang et al. 2019). It differs from *P. verschoorii* in having somewhat longer conidia and common production of aseptate conidia. The conidia (both aseptate and 1-septate) in *P. verschoorii* are 3–11.5 × 2–3 µm while aseptate conidia are scarce (Giraldo et al. 2019). *Plectosphaerella vigrensis* was isolated from leaf spots occurring on native *Impatiens noli-tangere*. It was not observed on alien and invasive *Impatiens parviflora* occurring in the same area of Wigry National Park (Pusz et al. 2022).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence are *Plectosphaerella pauciseptata* (culture CBS 144924, GenBank LR590240; Identities = 469/475 (99 %), no gaps), *Plectosphaerella niemeijerarum* (culture GBC-Fungus 109, GenBank MN077480; Identities = 469/475 (99 %), no gaps) and *Plectosphaerella cucumerina* (culture Ppf5, GenBank EF495236; Identities = 469/475 (99 %), no gaps). The closest hits using the **LSU** sequence are *Plectosphaerella cucumerina* (culture HHAUF 210510, GenBank MZ209396; Identities = 962/965 (99 %), no gaps), *Plectosphaerella endophytica* (culture YMF 1.04701, GenBank MW024052; Identities = 960/966 (99 %), one gap (0 %)) and *Plectosphaerella plurivora* (culture GZUIFR-H26.5.2, GenBank MK880437; Identities = 955/965 (99 %), no gaps). The closest hits using the ***cmdA*** sequence are *Plectosphaerella plurivora* (culture CBS 131742, GenBank KY416922; Identities = 273/299 (91 %), eight gaps (2 %)), *Plectosphaerella ramiseptata* (culture CBS 131861, GenBank KY416915; Identities = 261/287 (91 %), seven gaps (2 %)) and *Plectosphaerella melonis* (culture CBS 489.96, GenBank KY416904; Identities = 262/303 (86 %), twelve gaps (3 %)). The closest hits using the ***rpb2*** sequence are *Plectosphaerella cucumerina* (culture JW:191043, GenBank LR594804; Identities = 555/563 (99 %), no gaps), *Plectosphaerella slobbergiarum* (culture NL1930002, GenBank MW890074; Identities = 553/569 (97 %), no gaps) and *Plectosphaerella cucumerina* (culture CBS 139.60, GenBank LR026200; Identities = 557/578 (96 %), no gaps). The closest hits using the ***tef1*** sequence are *Plectosphaerella cucumerina* (culture JW:62006, GenBank LR594776; Identities = 896/902 (99 %), no gaps), *Plectosphaerella melonis* (culture CBS 525.93, GenBank LR026508; Identities = 768/787 (98 %), no gaps) and *Plectosphaerella slobbergiarum* (culture NL1930002, GenBank MW890114; Identities = 806/527 (97 %), no gaps). The closest hits using the ***tub2*** sequence are *Plectosphaerella alismatis* (culture CBS 113362, GenBank KY421304; Identities = 182/202 (90 %), nine gaps (4 %)), *Plectosphaerella oligotrophica* (culture LC2510, GenBank KY421310; Identities = 183/209 (88 %), six gaps (2 %)) and *Plectosphaerella ramiseptata* (culture CBS 131861, GenBank KY421305; Identities = 183/210 (87 %), eight gaps (3 %)).

Colour illustrations. Leaves of *Impatiens noli-tangere* with leaf spots caused by *Plectosphaerella vigrensis*, Poland. Colony on MEA; hyphae with hyphal coil; conidiophores; conidia. Scale bars = 10 µm.

Supplementary material

FP1585 Phylogenetic tree.

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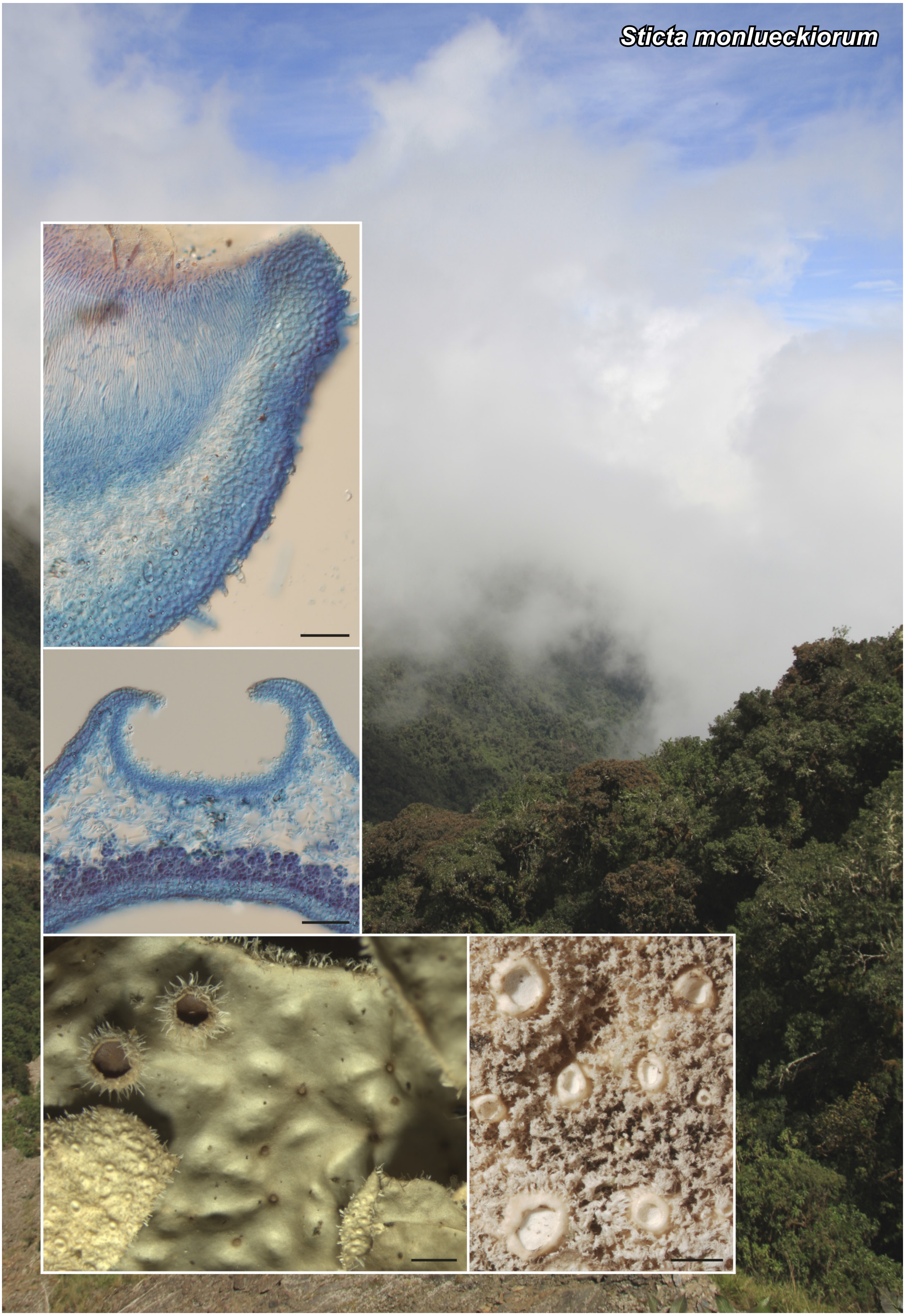
Sticta monlueckiorum

Fungal Planet 1586 – 30 December 2023

Sticta monlueckiorum Ossowska, Flakus & Rodr.Flakus, *sp. nov.*

Etymology. Named in honour of the lichenologists, Bibiana Moncada and Robert Lücking, for their important contributions to the taxonomy of the genus *Sticta*.

Classification — *Peltigeraceae*, *Peltigerales*, *Lecanoromycetes*.

Photobiont nostoc. *Stipe* absent. *Thallus* coriaceous, irregular to suborbicular, up to 10 cm diam, moderately branched, with 3–5 branches per 5 cm radius, branching anisotomous to polytomous; lobes laciniate to flabellate, adjacent to interspaced, canaliculate to involute, apices obtuse or truncate and involute, margins sinuous, slightly thickened; lobe internodes 5–20 mm long, 7–20 mm broad. *Upper surface* pitted to scrobiculate or rugose towards the centre, olive grey to brown with darker apices, glabrous; marginal cilia white to pale brown, fasciculate, up to 0.5 mm long, but also with extension of the lower tomentum. *Apothecia* principally laminal, dispersed, subpedicellate, with pronounced invagination on lower side, up to 1.5 mm diam; disc brown, shiny; margin entire to crenate, hirsute-ciliate, but in young apothecia glabrous, hairs usually white. *Pycnidia* visible as brown dots, immersed, up to 400 µm diam. *Lower surface* uneven, beige or yellowish to dark brown towards the centre; primary tomentum dense and scarce towards the margin, thick but thinner towards the margin, fasciculate in marginal part to spongy in central part of thalli, soft, white to dark brown; secondary tomentum absent. *Rhizines* absent. *Cyphellae* 41–60 per cm^2 towards the thallus centre and more than 100 per cm^2 towards the margin, scattered to aggregated, circular or elongated, urceolate with wide pore to cupuliform, prominent to sessile or suprasessile, in younger parts of thalli above the level of the primary tomentum, with the margin raised and involute, raised and circinate or erect in old cyphellae, beige to brown-coloured, with tomentum only in basal parts; pore (0.25–)0.5–1(–1.5) mm diam; basal membrane scabrous, beige, K–, C–, KC–, P–. Medulla compact, white, K–, C–, KC–, P–. Epihymenium K+ carmine-red. No substances detected by TLC. *Upper cortex* paraplectenchymatous, up to 40 µm thick. *Photobiont layer* up to 75 µm thick, cells 6–10 µm diam. *Medulla* up to 130 µm thick, very compact, without crystals. *Lower cortex* paraplectenchymatous, up to 40 µm thick. *Primary tomentum* up to 400 µm long, in fascicles of 12–20, unbranched or rarely sparsely branched in upper part of hyphae, with free apices. *Cyphellae cavity* up to 600 µm deep; cells of basal membrane very rarely with one papilla. *Apothecia* up to 650 µm high, without distinct stipe. *Excipulum* up to 200 µm broad, laterally with projecting hairs, up to 350 µm long, in lower part of excipular medulla with few photobiont cells. *Hymenium* up to 120 µm high. *Epihymenium* up to 5 µm high, orange brown, gelatinous upper layer present and with orange granules at top, granules K+ carmine-red dissolving. *Asci* 6–8-spored. *Ascospores* predominantly 1-septate, rarely 3-septate, 31–40 × 8–10 µm. *Conidia* 3.5–5 × 1 µm.

Colour illustrations. Camino de los Nubes Inca road in Yungas cloud forest, Nacional Park Carrasco, Cochabamba department, Bolivia (photo credit A. Flakus). Cross-section of apothecial margin (mounted in LPCB), cross-section of cyphellum (mounted in LPCB), a habit of thallus with ascomata, lower side of thallus with tomentum and cyphellae. Scale bars = 50 µm (exciple and cyphellum sections), 1 mm (a habit and lower side of thallus).

Habit, Habitat & Distribution — *Sticta monlueckiorum* is known from two localities in Parque Nacional Carrasco in Department Cochabamba, where it grows on tree bark at altitude 2220 m and 3520 m a.s.l.

Typus. Bolivia, Dept. Cochabamba, Prov. Tiraque, Parque Nacional Carrasco, Camino de los Nubes, Antenas Sillar-Villa Tunari old road, S17°12'32" W65°41'52", 3520 m a.s.l., upper montane Yungas cloud forest, Ceja de Monte Inferior (Altimontano), corticolous, 30 Nov. 2014, *M. Kukwa*, 15234 (holotype UGDA L-62116, isotype LPB; ITS sequence GenBank OR142412; MycoBank MB 849838).

Additional material examined. See supplementary page.

Notes — The new species is closely related to *Sticta bicellulata* and *S. pseudoimpressula*, as they all have a pitted to rugose upper surface and epihymenium reacting with K. However, those two species differ in having additional K positive reactions of the ring around the apothecial disc, medulla and membrane of the cyphellae, which in *S. monlueckiorum* is negative. The primary tomentum in *S. bicellulata* is white to dark brown and secondary tomentum is absent, in *S. pseudoimpressula* it is greyish brown to black and the secondary tomentum is present, whereas *S. monlueckiorum* has white to dark brown primary tomentum, but the secondary tomentum is absent. There are also differences in the shape of the cyphellae. In the new species they are circular to elongated, with raised and involute, raised and circinate or erect margins, whereas in *S. bicellulata* the cyphellae are rounded to irregular with raised and involute margins, and in *S. pseudoimpressula* irregular with erect margins (Ossowska et al. 2022a). Both species have recently been described from Bolivia, where they were found only in the Department La Paz (Ossowska et al. 2022a), while *S. monlueckiorum* is reported here from two localities in the Department Cochabamba.

Sticta monlueckiorum belongs to clade I sensu Widhelm et al. (2018) together with *S. sylvatica*, to which it is closely related. However, this species is characterised by different, undulate to slightly scrobiculate or faveolate, reddish brown upper surface, without true cilia, but with abundant laminal isidia. The density of cyphellae is lower than in *S. monlueckiorum* and is 1–10 per cm^2 towards the centre and 41–60 per cm^2 towards the margins, and they are rounded to irregular, cupuliform to urceolate with wide pore and with raised and involute margins (Moncada 2012). *Sticta sylvatica* is a common species (Magain & Sérusiaux 2015, Widhelm et al. 2018), although it has not yet been found in Bolivia (see also Ossowska 2021, Ossowska et al. 2022a, b).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Sticta sylvatica* (voucher Lg3837, GenBank KT281736; Identities = 512/517 (99 %), one gap (0 %)), *S. peltigerella* (voucher MON4410, GenBank MT132763; Identities = 509/517 (89 %), one gap (0 %)), *S. bicellulata* (voucher 14859, GenBank OP250129; Identities = 507/513 (99 %), no gaps) and *S. pseudoimpressula* (voucher 14752, GenBank OP250128; Identities = 480/484 (99 %), no gaps).

Supplementary material

FP1586 Phylogenetic tree.

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Stomiopeltis thailandica

Fungal Planet 1587 – 30 December 2023

Stomiopeltis thailandica N.I. de Silva & Lumyong, *sp. nov.*

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

Classification — *Phaeothecoidiellaceae*, *Mycosphaerellales*, *Dothideomycetes*.

Thyriothecia black, solitary, gregarious, superficial, rounded, 180–230 µm diam, easily removed from the host surface, ostiolate, wall of dark brown *textura angularis* cell layers, 40–60 µm thickness. Lacking *pseudoparaphyses*. *Asci* 8-spored, bitunicate, fissitunicate, oblong to subglobose, with a minute pedicel, apical region of asci usually with a thick opaque region, 45–55 × 11–14 µm. *Ascospores* uniseriate, hyaline, obovoid to ellipsoid, 1-septate, strongly constricted at the septum, with two different length cells, lower cell slightly broader, guttulate, 10–18 × 4–6 µm.

Typus. Thailand, Chiang Mai Province, on dead twigs of *Magnolia champaca* (*Magnoliaceae*), 5 Feb. 2021, *N.I. de Silva*, NI101 (holotype CMUB 40014; ITS and LSU sequences GenBank OR498908 and OR498907; MycoBank MB 849884).

Notes — The new collection CMUB 40014 resembles the genus *Stomiopeltis* in having superficial, orbicular, unilocular thyriothecia with pseudoparenchyma cell wall, bitunicate asci with hyaline ascospores with a transverse septum (Ajitomi et al. 2017, Jayasiri et al. 2019). *Stomiopeltis* species have been reported as pathogens on fruits (Mayfield et al. 2013, Ajitomi et al. 2017), as saprobes on decaying wild fruits (Jayasiri et al. 2019), and on leaves of *Syzygium cordatum* (Crous et al. 2019). *Stomiopeltis thailandica* forms a sister clade to *Stomiopeltis* spp. strains (GA3-23C2b, S1-2-G2, S1-10-G3, S1-14-G3 and S1-5-G4) with high statistical support (93 % ML, 0.99 BYPP). *Stomiopeltis thailandica* can be distinguished from *S. syzygii* in having 10–18 × 4–6 µm, hyaline, obovoid to ellipsoid ascospores that are strongly constricted at the septum. *Stomiopeltis syzygii* has 5 µm wide ascospores that become brown, verruculose, and are only slightly constricted at the septum (Crous et al. 2019). Furthermore, in terms of ascospore dimensions, *Stomiopeltis thailandica* differs from *S. sinensis* (19–21 × 5–7 µm) and *S. phyllanthi* (15–17 × 4–5 µm) (Jayasiri et al. 2019).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Stomiopeltis* sp. RS5.1 (strain GA3_23C2b, GenBank FJ438375.1; Identities = 463/517 (90 %), 12 gaps (2 %)), *Stomiopeltis* sp. RS5.2 (strain NC1_18C1d, GenBank FJ438376.1; Identities = 463/518 (89 %), 13 gaps (2 %)) and *Stomiopeltis syzygii* (CPC 36323, GenBank NR_166321.1; Identities = 494/567 (87 %), 26 gaps (4 %)). Closest hits using the **LSU** sequence are Fungal sp. RS3.2 (strain KY4_11.2F2b, GenBank FJ147161.1; Identities = 830/835 (99 %), no gaps), Fungal sp. (culture CBS 119228, GenBank MH874607.1; Identities = 828/836 (99 %), one gap (0 %)) and Fungal sp. (culture CBS 118941, GenBank MH874597.1; Identities = 828/836 (99 %), one gap (0 %)).

Colour illustrations. Flower of *Magnolia champaca* from which *Stomiopeltis thailandica* was isolated. Appearance of thyriothecia on host surface; squash mount of thyriothecium; section through thyriothecium; asci; ascospores. Scale bars = 100 µm (thyriothecia, section), 10 µm (asci), 5 µm (ascospores).

Supplementary material

FP1587-1	Table.
FP1587-2	Phylogenetic tree.

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Trichoglossum syamviswanathii

Fungal Planet 1588 – 30 December 2023

Trichoglossum syamviswanathii Mahadevak., Mufeeda, C. Danteswari, Sarma & Sh. Kumar, *sp. nov.*

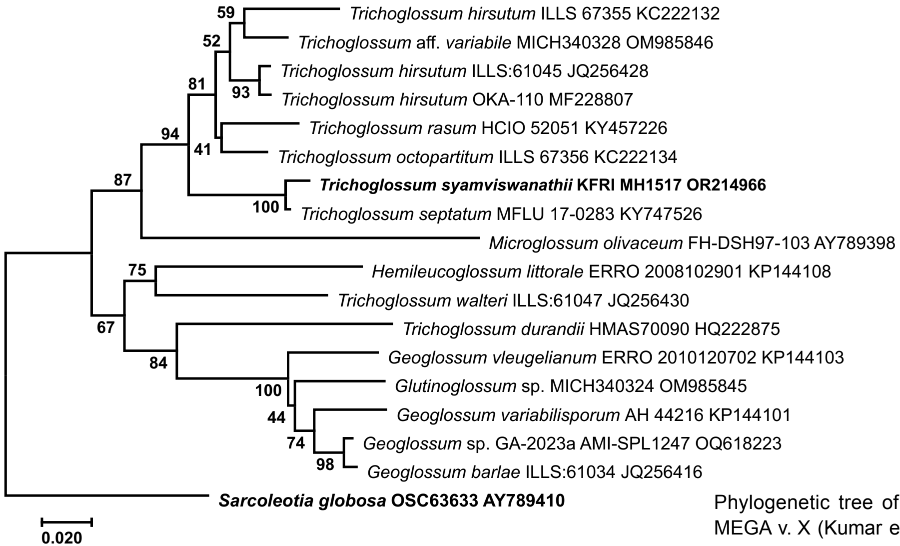
Etymology. Named in honour of Dr. Syam Viswanath, Director of the Kerala Forest Research Institute, for his outstanding contribution to the field of forestry in India.

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

Saprobic on soil. *Sexual morph*: *Apothecia* 25–40 mm in height, scattered, stipitate, slender, clavate – oval, hirsute, dry, shiny when wet, blackish, velvety, ascogenous portion and sterile portion are clearly distinguishable. Ascogenous portion flattened clavate and sometimes curved, black, densely hirsute with setae. Sterile portion cylindrical, densely hirsute from setae, concolourous with fertile part. Ascomatal core made up of brownish cells. *Hymenial setae* 350–550 × 12–20 µm, blackish brown, acuminate, tapered at the apex and base, thick-walled, septate, sometimes protruding above hymenium. *Paraphyses* 3–5 µm wide at the apices, numerous, filiform, septate, apically enlarged and curved, light brown at the base and darker at the apex, walls granulate. *Asci* (220–)265–310(–335) × (21–)24–38(–45) µm, unitunicate, consistently 8-spored, clavate, fusiform, with rounded apex, narrowed below. *Ascospores* (133–)156–191(–202) × (4–)6–7(–9) µm, guttulate, pale brown when young and greenish brown to dark brown at maturity, fusoid to fusoid-clavate, immature spores aseptate, mature spores with 7- or 15-septate; a single ascus can have spores with both variations in septation number.

Typus. India, Kerala, Thrissur, Palappilly, Field Research Station, Bambusetum, KFRI, basidiomata growing solitary on moist soil near the base of bamboo plantation, 29 June 2022, *S. Mahadevakumar* (holotype KFRI MH1517; ITS sequence GenBank OR214966; MycoBank MB 849768).

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of *T. syamviswanathii* (KFRIMH 1517) had the highest similarity to *T. septatum* (voucher MFLU 17-0283, GenBank KY747526; Identities = 530/547 (96.89 %), 10 gaps (1 %)), *T.* aff. *variabile* (voucher MICH340328, GenBank OM985846; Identities = 496/576 (86.11 %), 31 gaps (5 %)), *T. hirsutum* (voucher ILLS:61045, GenBank JQ256428; Identities = 501/593 (84.49 %), 40 gaps (6 %)), *Trichoglossum variabile* (isolate DM289, GenBank MT773330; Identities = 495/587 (84.33 %), 37 gaps (6 %)) and *Trichoglossum octopartitum* (voucher HKAS:82228, GenBank KY747525; Identities = 451/525 (85.90 %), 30 gaps (5 %)). *Trichoglossum syamviswanathii* is closely related to *T. septatum.* However, in *T. syamviswanathii* immature ascospores are hyaline whereas immature ascospores of *T. septatum* are pale brown and aseptate (Ekanayaka et al. 2017). Furthermore, they also differ in ascomata, asci, and ascospore size.



Colour illustrations. Bambusetum of FRC, Palappilly, KFRI. Left panel: apothecia; right panel: top – close view of hymenial setae, septate unbranched paraphyses; middle – immature, cylindrical asci (in KOH); bottom – elongated fusiform mature ascospores. Scale bars = 100 µm.

Phylogenetic tree of *Trichoglossum syamviswanathii* constructed using MEGA v. X (Kumar et al. 2018) of the ITS-nrDNA sequence alignment by Neighbour-Joining Method (Saitou & Nei 1987). The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 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 18 nucleotide sequences. All positions containing gaps and missing data were eliminated (complete deletion option). There were a total of 360 positions in the final dataset. The phylogenetic position of *Trichoglossum syamviswanathii* is indicated in **bold**. The tree and alignment were deposited in 10.6084/m9.figshare.24214410.

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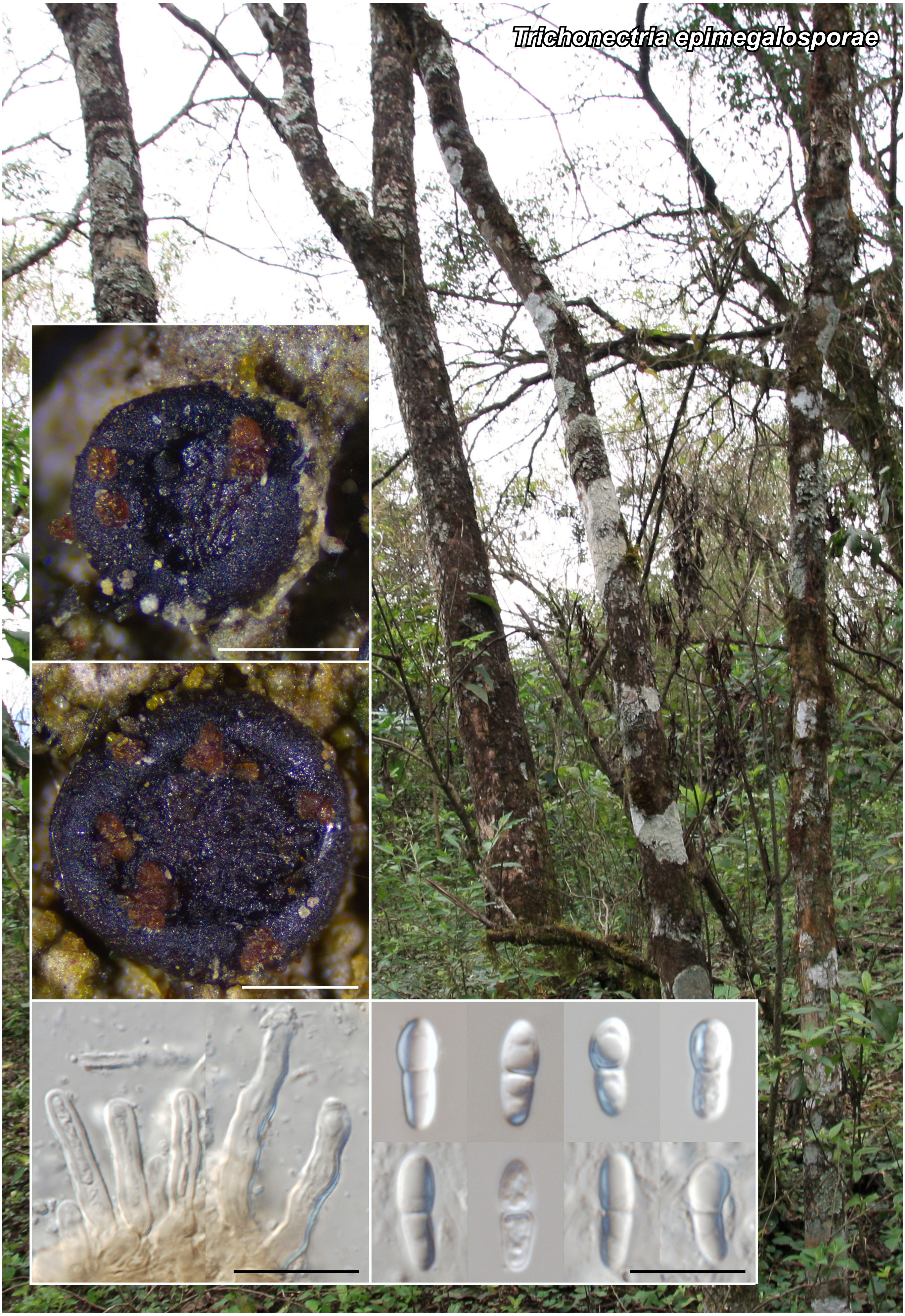
Trichonectria epimegalosporae

Fungal Planet 1589 – 30 December 2023

Trichonectria epimegalosporae Darmostuk, Etayo & Flakus, *sp. nov.*

Etymology. Named after the host, *Megalospora*.

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

Ascomata situated on the apothecial disk and margin or rarely on the host thallus, solitary or forming small groups, orange-brown, subglobose, sessile, irregularly collapsing when dry, with a central ostiole, (105–)110–125(–130) µm diam (n = 20), with tiny hyaline, thick-walled setae at the upper part of ascomata; setae (24–)28–32(–36) × (4.2–)4.5–5.5(–5.7) µm (n = 20). Ascomatal wall 10–12 µm thick, composed of several rows of radially compressed cells, with thin and hyaline cells inside to pale orange wall in external zones, superficially irregular cells with wall unevenly thickened and sinuose, 7–10 × 4–5 µm; outer part with some interwoven hyphae; ostiole central, 20–25 µm diam; periphyses 3–4 × 1.5–2 µm. *Asci* subcylindrical to narrowly clavate, (7.4–)8.2–9.8(–10.6) × (2.2–)2.5–3.5(–4.0) µm (n = 10), 8-spored. *Ascospores* biseriate, narrowly ellipsoid, smooth, without perisporium, straight to slightly curved, hyaline, with round ends, sometimes with broader upper cell, 1-septate, usually slightly constricted at the septum, (7.4–)8.2–9.8(–10.6) × (2.2–)2.5–3.5(–4.0) µm (n = 40). *Asexual morph* not observed.

Habit, Habitat & Distribution — *Trichonectria epimegalosporae* is known from a few specimens in the Boliviano-Tucumano forest, where it was found on the apothecia and rarely on the thallus of *Megalospora sulphurata* on tree bark.

Typus. Bolivia, Department Tarija, Burnet O’Connor Province, old road between Tarija and Entre Ríos, S21°27'35" W64°13'28", 1917 m a.s.l., Boliviano-Tucumano forest with *Podocarpus*, on apothecia of corticolous *Megalospora sulphurata* var. *sulphurata* (*Megalosporaceae*), 30 July 2015, *A. Flakus*, 27667 (holotype KRAM-L-74376, isotypes LPB; ITS, LSU, SSU, *tef1*, *rpb1* sequences GenBank OR514877, OR514879, OR517232, OR525298 and OR529405; MycoBank MB 849952).

Additional material examined. Bolivia, Department Tarija, Burnet O’Connor Province, close to gasoduct, old road between Tarija and Entre Ríos, S21°25'33" W64°19'13", 2256 m a.s.l., Boliviano-Tucumano forest with *Podocarpus* and *Alnus acuminata*, on corticolous *Megalospora sulphurata*, 1 Aug. 2015, *J. Etayo*, 32917 (LPB, hb. Etayo).

Colour illustrations. Boliviano-Tucumano vegetation, Tarija department, Bolivia (photo credit A. Flakus). Habits of the ascomata on the host apothecia; setae (mounted in water), ascospores (mounted in water). Scale bars = 500 µm (habits), 15 µm (setae), 5 µm (ascospores).

Notes — The genus *Trichonectria*, with the generic type *Trichonectria hirta*, comprises fungi associated with lichens and bryophytes. These fungi are characterised by superficial ascomata that collapse when dry, accompanied by thick-walled setae, and (0-)1-septate to multi-septate ascospores (Rossman 1983, Rossman et al. 1999). The hyphomycetous genus *Cylindromonium*, with the generic type *C. eugeniicola*, is often considered an asexual morph of *Trichonectria*, and this connection has been confirmed for a few species (Glenn et al. 1997, Ohmaki et al. 2023). However, molecular data for *Trichonectria hirta* is unavailable, and the circumscription of the genus remains unclear. Recent studies have indicated that *Cylindromonium* and *Trichonectria* form separate clades within *Hypocreales*, but their phylogenetic position remains unresolved and requires further sampling (Hou et al. 2023, Perera et al. 2023). The newly described species *T. epimegalosporae* is characterised by sessile, subglobose, orange-brown ascomata, (105–)110–125(–130) µm diam, with tiny hyaline hairs, 8-spored asci and 1-septate, ellipsoid ascospores (7.4–)8.2–9.8(–10.6) × (2.2–)2.5–3.5(–4.0) µm. Phylogenetically, the new species shows a well-supported sister relationship with *Trichonectria pertusariae*. The latter species was described on *Lepra ophthalmiza* (*Pertusariaceae*) from the Canary Islands and this fungus can be distinguished by having longer fusiform ascospores, (8–)10–11(–15) µm, and different host selection (Etayo & Van den Boom 2005). Morphologically, the new species resembles *Trichonectria australis*, which was described on *Usnea* sp. from Argentina and Chile. However, the latter species can be differentiated by its somewhat larger, 100–170 µm orange ascomata, ellipsoid ascospores without constriction at the septum, and different host selection (Etayo & Sancho 2008).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the **ITS** sequence had the highest similarity to *Cylindromonium lichenicola* (strain CBS 188.70, GenBank MH859549; Identities = 95 %, four gaps (0 %)). The closest hit using the **LSU** sequence is *C. lichenicola* (strain CBS 415.70A, GenBank MH871536; Identities = 99.06 %, two gaps (0 %)). The closest hit using the **SSU** sequence is *Neoacremonium vitellinum* (strain CBS 792.69, GenBank HQ232212; Identities = 93.56 %, 59 gaps (2 %)). The closest hit using the ***tef1*** sequence is *C. lichenicola* (strain CBS 188.70, GenBank OQ470834; Identities = 96.92 %, no gaps). The closest hit using the ***rpb1*** sequence is *Metapochonia bulbillosa* (strain JCM 18596, GenBank AB758663; Identities = 84.27 %, two gaps (0 %)).

Supplementary material

FP1589 & FP1590-1 Table.
FP1589 & FP1590-2 Phylogenetic tree.

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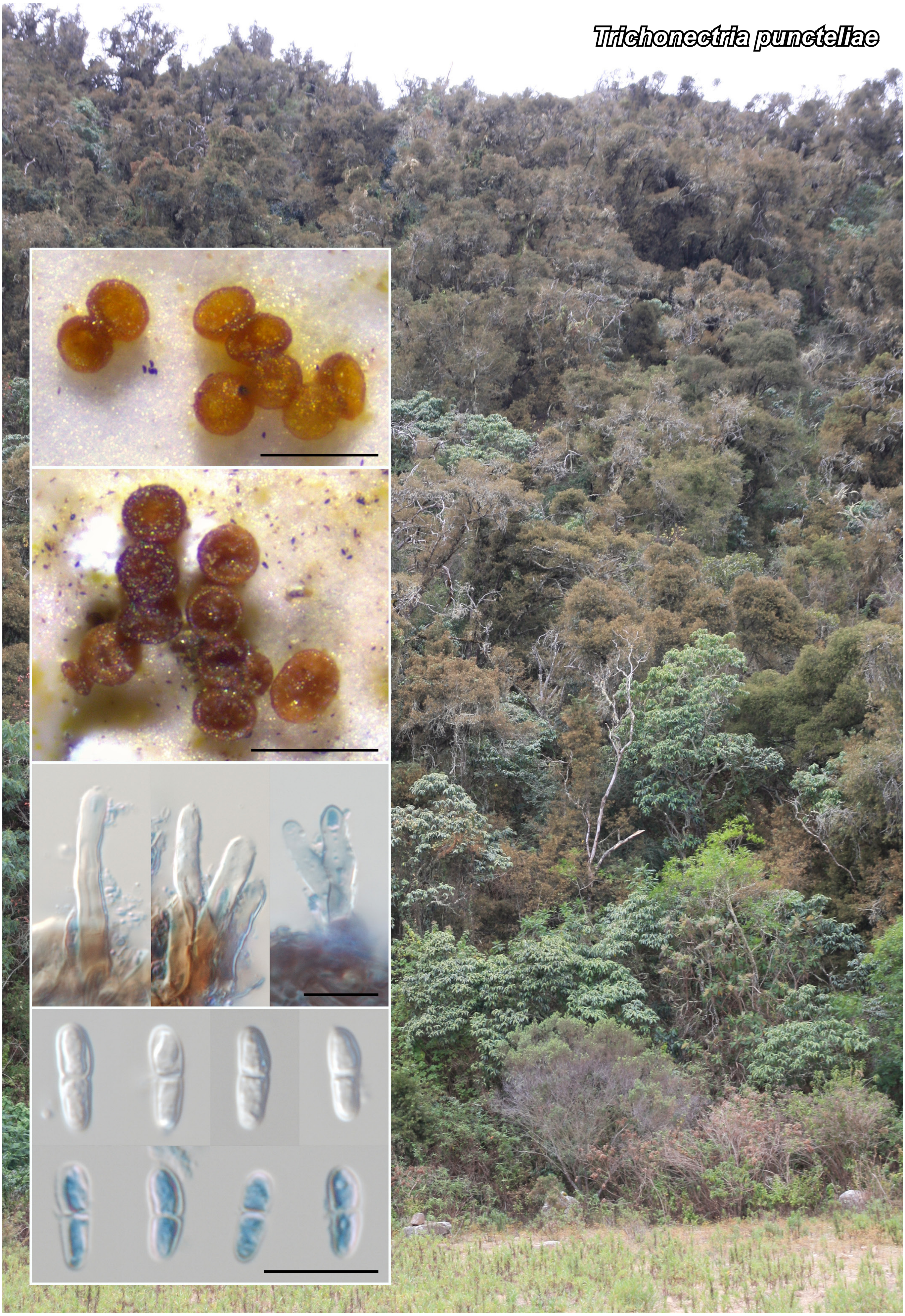
Trichonectria puncteliae

Fungal Planet 1590 – 30 December 2023

Trichonectria puncteliae Darmostuk, Etayo & Flakus, *sp. nov.*

Etymology. Named after the host lichen.

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

Ascomata situated on the upper surface of the host thallus, solitary or forming groups, brownish orange, subglobose, sessile, cup-like collapsing when dry, with a central ostiole, (100–)110–125(–135) µm diam (n = 15), with scattered hyaline setae at the upper part of ascomata; setae relatively thick-walled, (18–)20–22(–24) × (2.8–)3.0–3.5(–3.8) µm (n = 10). Ascomatal wall 11–13 µm thick, composed of several rows of radially compressed cells, with a thin and hyaline wall near the centrum and thicker and pale orange (KOH–), at the surface of the perithecial wall, superficially irregular cells with wall unevenly thickened and sinuose, 8.5–12 × 5–6.5 µm; outer part with some interwoven hyphae; ostiole central, 22–27 µm diam; periphyses 4–5 µm length. *Asci* subcylindrical to narrowly clavate, (26.4–)27.0–32.4(–34.8) × (5.8–)6.0–8.2(–9.5) µm (n = 10), 8-spored. *Ascospores* biseriate, narrowly ellipsoid, variable in shape, smooth, without perisporium, straight to slightly curved, hyaline, with round ends, 1-septate, sometimes slightly constricted at the septum, (7.4–)8.0–9.4(–10.8) × (2.2–)2.6–3.0(–3.5) µm (n = 60). *Asexual morph* not observed.

Habit, Habitat & Distribution — *Trichonectria puncteliae* is known from numerous specimens from the Boliviano-Tucumano forest with altitudinal range 1 535–2 560 m a.s.l., where it was found on the thallus of corticolous *Punctelia* species (*Punctelia borreri* and *P. subpraesignis*).

Typus. Bolivia, Department Tarija, Burnet O'Connor Province, old road between Tarija and Entre Ríos, S21°29'13" W64°11'42", 1 535 m a.s.l., Boliviano-Tucumano forest with *Podocarpus*, on the thallus of *Punctelia borreri* (*Parmeliaceae*), 31 July 2015, *A. Flakus*, 27667 (holotype KRAM-L-74377, isotypes LPB; ITS, LSU, SSU, *tef1*, *rpb1* sequences GenBank OR514876, OR514878, OR517231, OR525297 and OR529406; MycoBank MB 849953).

Additional materials examined. Bolivia, Department Chuquisaca, Hernando Siles Province, 15 km west of Monte Agudo, S19°48'57" W64°05'60", 1 815 m, subandino, disturbed Tucumano-Boliviano forest, on *Punctelia borreri*, 20 July 2015, *J. Etayo*, 30321 (LPB, hb. Etayo); Department Tarija, Burnet O'Connor Province, old road between Tarija and Entre Ríos, S21°27'35" W64°13'28", 1 917 m a.s.l., Boliviano-Tucumano forest with *Podocarpus*, on the thallus of *Punctelia* cf. *subpraesignis* (*Parmeliaceae*), 30 July 2015, *A. Flakus*, 27714 (KRAM-L-74378, LPB); ibid., S21°27'50" W64°12'51", 1 924 m a.s.l., Boliviano-Tucumano forest with epiphytes exposed NW, on *Punctelia* cf. *subpraesignis*, 30 July 2015, *A. Flakus*, 27675 (LPB); ibid., *J. Etayo* 29977 (LPB, hb. Etayo); ibid., 112 km from Tarija on the way to Entre Ríos, near San Diego, S21°26'28" W64°14'37", 1 620 m a.s.l., Tucumano-Boliviano montano forest, on corticolous *Punctelia constantimontium*, 9 Aug. 2012, *J. Etayo*, 28596 (LPB, hb. Etayo); Aniceto Arce Province, Reserva Nacional de Flora y Fauna Tariquía, between la Cumbre and camamento los Alisos, S22°00'41" W64°36'02", 2 560 m a.s.l., Boliviano-Tucumano forest with *Alnus acuminata* and *Polylepis*, on *Punctelia subpraesignis*, 22 July 2015, *A. Flakus*, 26992 (KRAM-L-74379, LPB); ibid., *J. Etayo*, 33000 (LPB, hb. Etayo).

Colour illustrations. Montane Boliviano-Tucumano forest, Tarija department, Bolivia (photo credit A. Flakus). Habit of the wet and dry ascomata on the host thallus; setae (mounted in LPCB), ascospores (mounted in water and LPCB (lower line)). Scale bars = 250 µm (habits), 10 µm (setae and ascospores).

Notes — *Trichonectria puncteliae* is characterised by brownish orange ascomata, that appear darker and cup-like when dry, 8-spored asci and relatively small ascospores, (7.4–)8.0–9.4(–10.8) × (2.2–)2.6–3.0(–3.5) µm. Based on our multi-gene phylogeny, it forms a well-supported sister relationship to recently described *Cylindromonium dirinariae*. Although, *C. dirinariae* is morphologically similar to *Trichonectria puncteliae*, it can be distinguished by its smaller pale-orange ascomata without setae, 80–100 µm, smaller asci, (21.4–)22.2–26.8(–29.1) × (3.9–)4.2–5.8(–6.5) µm, and different host selection (Ohmaki et al. 2023). *Trichonectria leptogiicola* is also characterised by relatively small ascospores, 8–10.5 × 3–4 µm, but it can be distinguished by bigger pink to orange coloured ascomata 150–200 µm, larger asci, 45–55 × 7–10 µm, and ascospores ornamented with line-like structure (Etayo 2001).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the **ITS** sequence had the highest similarity to *Cylindromonium lichenicola* (strain CBS 188.70, GenBank MH859549; Identities = 96.70 %, one gap (0 %)). The closest hit using the **LSU** sequence is *C. lichenicola* (strain CBS 415.70A, GenBank MH871536; Identities = 98.59 %, two gaps (0 %)). The closest hit using the **SSU** sequence is *Neoacremonium vitellinum* (strain CBS 792.69, GenBank HQ232212; Identities = 93.69 %, 48 gaps (2 %)). The closest hit using the ***tef1*** sequence is *C. lichenicola* (strain CBS 188.70, GenBank OQ470834; Identities = 96.18 %, no gaps). The closest hit using the ***rpb1*** sequence is *Metapochonia variabilis* (strain CGMCC:3.17926, GenBank KY883215; Identities = 83.51 %, two gaps (0 %)).

Supplementary material

FP1589 & FP1590-1 Table.
FP1589 & FP1590-2 Phylogenetic tree.

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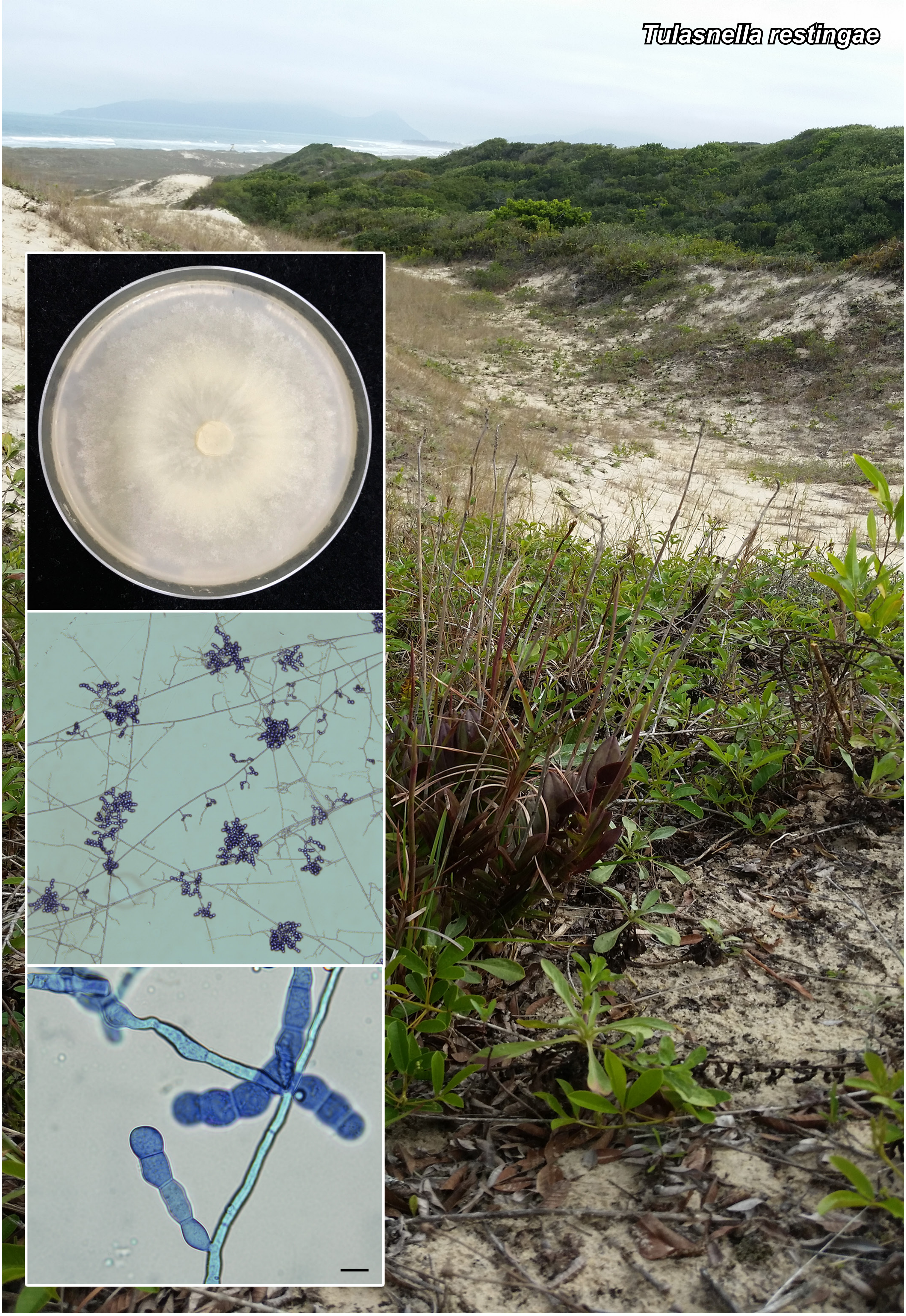

Tulasnella restingae

Fungal Planet 1591 – 30 December 2023

Tulasnella restingae Fritsche, M.E. Lopes, Zappelini, Ornellas, Stefenon & M.P. Guerra, *sp. nov.*

Etymology. Named after the vegetation of its host plant occurrence, the Restinga.

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

Hyphae hyaline, septate and thin-walled, lacking clamp connections; (1.9–)2.2–2.9(–3.2) µm in width. Hyphal anastomosis frequent. The septa often show slight constrictions, and the hyphae exhibit branching, typically at right angles. The base of a branch is frequently narrowed, and the terminal cells of the hyphae are long and often have a bulbous appearance. The monilioid cells are catenulate and arranged in clusters of up to eight cells. Each cell has a globose appearance, but the wall separating each monilioid cell is typically flat. The monilioid cells are (5.6–)6.9–10.0(–12.5) × (7.8–)8.8–13.9(–16.5) µm, and are produced abundantly in long ramified chains of 3–8 cells. No *sexual structures* have been observed.

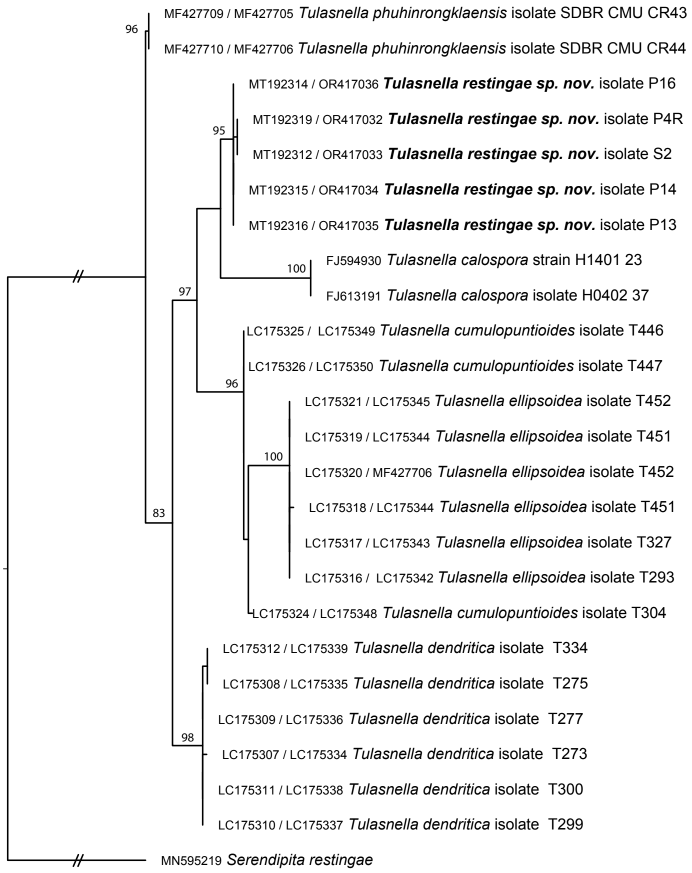
Culture characteristics — Colonies on potato dextrose agar (PDA) are cream-colored, with rapid growth rate (up to 6 cm diam after 1 wk of culture at 25 °C, in the dark), margins irregular and translucent with aerial mycelium mostly composed of chains of monilioid cells. On MMN medium colonies are white and produce much less aerial mycelium.

Typus. Brazil, Santa Catarina state, Florianópolis, S27°34'58.6" W48°30'18.7", at sea level, on *Epidendrum fulgens* (*Orchidaceae*) protocorms and roots, Sept. 2018, *Y. Fritsche* (holotype TRP4R, culture preserved in a metabolically inactive state at the LFDGV Collection from the Federal University of Santa Catarina, Florianópolis SC, Brazil; culture ex-type TRP4R; ITS and LSU sequences GenBank MT192319 and OR417032; MycoBank MB 849750).

Additional material examined. Brazil, Santa Catarina state, Florianópolis, from protocorms, seedling roots and adult plant roots of *E. fulgens*, 2018, *Y. Fritsche*, isolate TRS2, ITS and LSU sequences GenBank MT192312 and OR417033.

Colour illustrations. *Epidendrum fulgens* growing next to the Atlantic Ocean in the Restinga vegetation, at the Florianópolis Island. Colony on MMN medium; monilioid cells clusters and monilioid cell details. Scale bars = 10 µm.

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence are from an uncultured *Tulasnella* (GenBank KC478558; Identity (99 %)), obtained from *Phragmipedium longifolium* (*Orchidaceae*). The closest hit from type material was from *Tulasnella cumulopuntioides* (GenBank LC175323, Identity (93.89 %)), isolated from *Spiranthes sinensis* (*Orchidaceae*) in Japan (Fujimori et al. 2019). The closest hit using the **LSU** sequence had highest similarity to an uncultured *Tulasnella* sequence (GenBank EU909268; Identity (94.96 %)) obtained from the liverwort *Aneura pinguis*. The closest hit from type material was from *Tulasnella dendritica* (GenBank LC175335; Identity (97.35 %)), isolated from *Spiranthes sinensis* (*Orchidaceae*) in Japan. It differs from *Tulasnella dendritica* and *T. cumulopuntioides* by the size and shape of monilioid cells and also from producing them in mass clusters, which was not observed for these two species.



Maximum likelihood tree obtained using a maximum likelihood analysis with a general time reversible (GTR) substitution model on the complete ITS and partial LSU sequence alignment, as implemented in RAxML-NG v. 1.2.0 (Kozlov et al. 2019). Novel species are indicated in a **bold** font. The scale bar indicates the expected number of substitutions per site and the bootstrap (BS) support values (based on 1 000 replicates) are shown above each branch. Values less than 70 % are not shown. The tree was rooted to a sequence of *Serendipita restingae* (GenBank MN595219) and the alignment and tree were deposited in TreeBASE (study ID: TB2:S30664).

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Vacuiphoma astragalicola

Fungal Planet 1592 – 30 December 2023

Vacuiphoma astragalicola Eisvand & M. Mehrabi, *sp. nov.*

Etymology. Species epithet refers to the host genus *Astragalus* from which it was isolated.

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

Morphology on oatmeal agar (OA): *Hyphae* white to pale olivaceous grey, septate, branched. *Conidiomata* pycnidial, scattered, mostly solitary, occasionally aggregated to complex structures, immersed or partly immersed in the agar, rarely on aerial mycelium, pale brown to dark brown, with age becoming black, mostly globose to sub-globose but also ovoid or flask-shaped, glabrous but sometimes with some hyphal outgrowths, ostiolate, 61–393 × 50.5–329.5 µm, 95 % confidence limits = 192.5–220 × 155.5–180 µm, (av. ± SD = 206 ± 76.5 × 167.5 ± 69 µm, n = 100), sometimes developing 1(–3) short necks, 17 –118 × 27.5–102(–128) µm, 95 % confidence limits = 52.5–66 × 58.5–70 µm, (av. ± SD = 59 ± 24.5 × 64.5 ± 21.5 µm, n = 50). *Ostioles* 1–3(–4), papillate or non-papillate. *Pycnidial wall* pseudoparenchymatous, composed of oblong to isodiametric cells, 3–5 layers, 8–24 µm thick, outer 2–3 cell layers pigmented. *Conidiogenous cells* phialidic, hyaline, smooth, ampulliform to doliiform, 5–8 × 4–7 µm. *Conidia* smooth- and thin-walled, cylindrical to oblong, erect or sometimes slightly curved, rounded in both ends, 0-septate, guttulate, commonly with several scattered guttules, sometimes with two large polar guttules, 3.5–7(–8) × 1.3–3.1 µm, 95 % confidence limits = 5.1–5.4 × 1.96–2 µm, (av. ± SD = 5.3 ± 0.82 × 2 ± 0.4 µm, n = 100). *Conidial matrix* cream to buff. *Chlamydospores* unicellular or multicellular (pseudosclerotioid), solitary or in chain, intercalary or terminal, smooth, brownish grey to grey, where multicellular variable in shape and size.

Culture characteristics — Colonies on OA reaching 53–57 mm diam after 12 d of incubation at 25 ± 0.5 °C, and 20–24 mm diam at 30 ± 0.5 °C, circular with filiform margin, pale olivaceous grey, floccose, pycnidia abundant and scattered all over the colony except active-growing edge; reverse pale olivaceous. Colonies on potato dextrose agar (PDA) reaching 49–53 mm diam after 12 d of incubation at 25 ± 0.5 °C, and 15–19 mm diam at 30 ± 0.5 °C, circular with a regular and white-felted margin, white to pale olivaceous grey, floccose to cottony with abundant woolly aerial mycelium, pycnidia scattered abundantly all over the colony and covered partly by aerial mycelium, sometimes pycnidia obviously aggregated near the centre; reverse pale rosy buff with lighter margin, dark brown to black in zones with abundant pycnidia.

Colour illustrations. *Astragalus sarcocolla*. From bottom to top: colonies on OA (left) and PDA (right) in top and reverse views, respectively; pycnidia; section of pycnidium; conidia; chlamydospores. Scale bars = 70 µm (pycnidia), 20 µm (microscopic section and chlamydospores), 7 µm (conidia mounted in lactophenol cotton blue), 20 µm (conidia mounted in lactophenol).

Typus. Iran, Khuzestan Province, Dehdez, isolated from stem canker of *Astragalus sarcocolla* (*Leguminosae*), Apr. 2018, *P. Eisvand* (holotype IRAN 18301 F; culture ex-type IRAN 4859C = SCUA-Is-A8; ITS, *tub2* and *rpb2* sequences GenBank OR286122, OR286203 and OR286201; MycoBank MB 849478).

Additional material examined. Iran, Khuzestan Province, Dehdez, isolated from stem canker of *Astragalus sarcocolla* (*Leguminosae*), Apr. 2018, *P. Eisvand*, culture SCUA-Is-A8-2, ITS, *tub2* and *rpb2* sequences GenBank OR286123, OR286204 and OR286202.

Notes — *Vacuiphoma astragalicola* is introduced here as a new species based on molecular phylogeny, together with morphological features. In the phylogenetic tree, both strains of *V. astragalicola* clustered in a fully-supported clade (MLBS 100 %, MPBS 100 %, BPP 1.0), closely related to the species *V. bulgarica* and *V. ferulae* (MLBS 59 %, BPP 0.78). This new species and the ex-type strain of *V. bulgarica* (CBS 357.84) showed 8 bp difference (1.8 %) across 449 nucleotides of the ITS region, 18 bp difference (5.4 %) across 332 nucleotides of the *tub2* region, and 23 bp difference (5.3 %) across 433 nucleotides of the *rpb2* region. Morphologically, *V. bulgarica* was poorly characterised due to the production of sterile pycnidial conidiomata (Aveskamp et al. 2010). Moreover, *V. astragalicola* differs from *V. ferulae* (CBS 353.71) in 1.1 %, 6.3 % and 9.7 % nucleotide diversity in ITS, *tub2* and *rpb2*, respectively. *Vacuiphoma astragalicola* can be morphologically distinguished from *V. ferulae* by smaller aseptate conidia (3.5–7 × 1.3–3.1 vs 6.5–17 × 3.5–6.5 µm) lacking septa (Hou et al. 2020). *Vacuiphoma* was established by Valenzuela-Lopez et al. (2018) to accommodate both the new combination *V. bulgarica* (basionym *Phoma bulgarica*) and new species *V. oculihominis*, which formed a well-supported clade distinct from other genera in *Didymellaceae*, Later, two new species have been introduced, namely *V. ferulae* and *V. laurina* (Hou et al. 2020).

Supplementary material

FP1592-1 Table.
FP1592-2 Phylogenetic tree.

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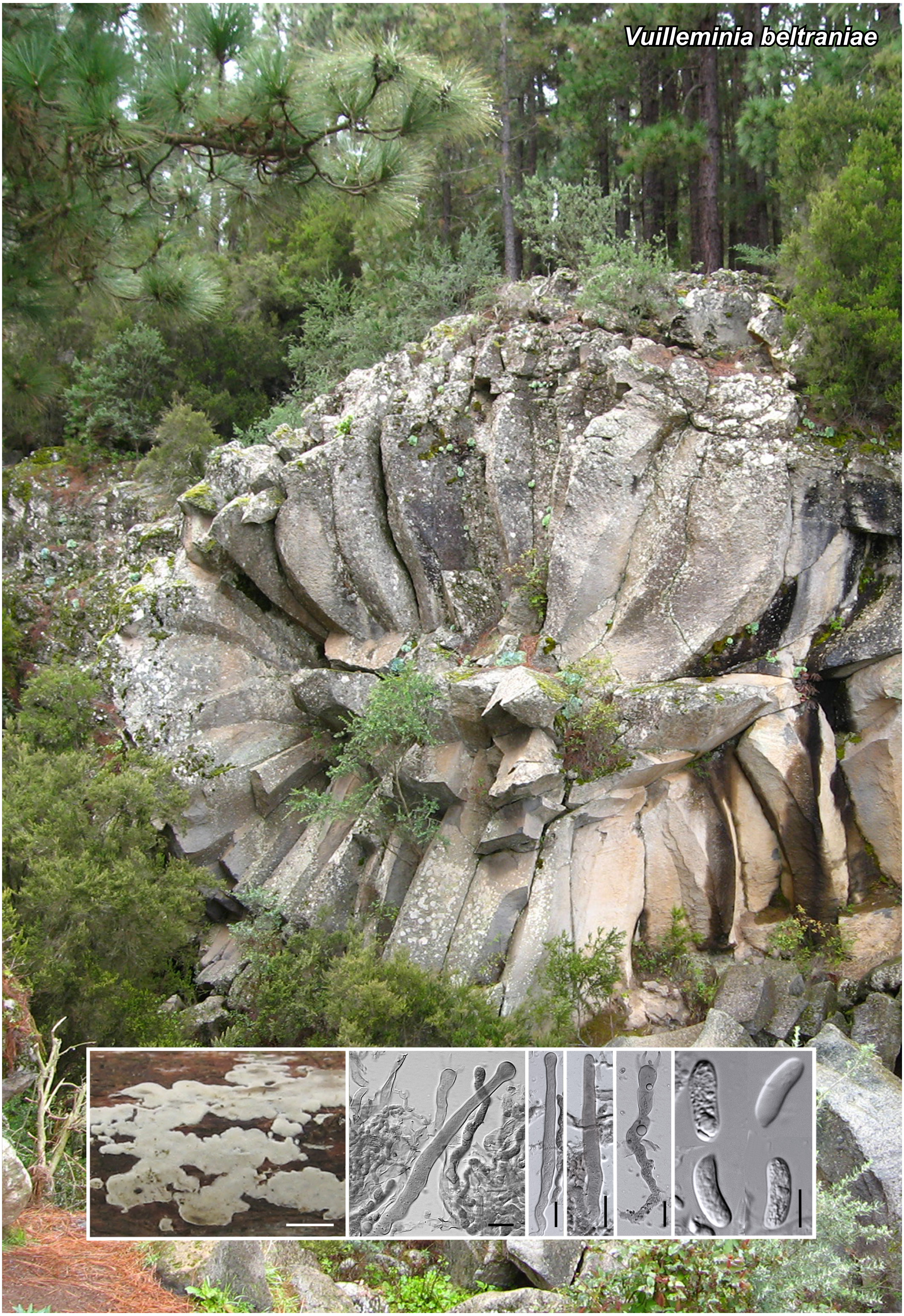
Vuilleminia beltraniae

Fungal Planet 1593 – 30 December 2023

Vuilleminia beltraniae M. Dueñas, Telleria & M.P. Martín, *sp. nov.*

Etymology. Named after Esperanza Beltrán-Tejera, mycologist, botanist, colleague and friend, for her contribution to the knowledge of Macaronesian mycobiota.

Classification — *Corticiaceae*, *Corticiales*, *Agaricomycetes*.

Basidioma resupinate, adnate, at first orbicular, forming small patches, then confluent and effused, crustaceous to ceraceous when dry; hymenophore smooth, pruinose under the lens, finely cracking in older parts, white to yellowish (86.l.Y; Kelly & Judd 1976), with age darker (83.brill. Y–82.V.Y); margin finely fibrillose in young specimens, later abrupt, not especially differentiated. *Hyphal system* monomitic; hyphae thin to thick-walled, richly branched, with clamps, 3–4 µm wide, those of the subiculum mostly horizontal, loosely interwoven, those of the subhymenium vertical, densely interwoven; abundant crystals especially in the old fruitbodies. *Hyphidia* numerous, sparsely branched, thin to thick-walled, encrusted with small crystals in the apex. *Cystidia* of two kinds: 1) tubular, capitate, thin- to moderately thick-walled, projecting in the hymenium, 70–130 × 9–13 µm; 2) cylindrical to fusiform cystidia, thin- to moderately thick-walled, normally included, 80–160 × (6–)8–14 µm. *Basidia* claviform, more or less pedunculated, sinuous, (55–)65–100 × 6–12 µm, with four sterigmata and basal clamp. *Spores* allantoid, adaxially concave, (12–)14–23 × (4.5–)5–7 µm, Q = 2.7, thin-walled, smooth, non-amyloid, non-cyanophilous, often with adventitious septa, with oil drops in the protoplasm.

Habitat & Distribution — Most of the specimens examined were found on species of *Cistus*. Studied samples are from France, Iberian Peninsula, Canary Islands, and Morocco.

Typus. Spain, Canary Islands, Tenerife, La Orotava, La Corona Forestal Natural Park, Caldera de Aguamansa, forest track to Chimoche, N28°21'18.01" W16°29'59.37", 1 240 m a.s.l., on *Cistus symphytifolius* (*Cistaceae*), 1 Feb. 2007, *M.T. Telleria*, 17205Tell. (holotype MA-Fungi 92857; ITS sequence GenBank OR146623; MycoBank MB 849062).

Additional material examined. France, Pyrénées-Orientales, Languedoc-Rosillon, Massif des Albères, Lavall, N42°30'27" E03°00'18", 225 m a.s.l., on *Cistus*, 5 Nov. 2008, *M.T. Telleria*, 17851Tell. (MA-Fungi 78451, ITS sequence GenBank OR127125). – Morocco, Marrakech-Tensift-El Haouz, Essaouira, Arganeraie Biosphere Reserve, R 301 road, N31°35'46.3" W09°39'09.4", 145 m a.s.l., on *Tetraclinis articulata*, 22 Apr. 2010, *M.T. Telleria*, 18884Tell (MA-Fungi 82460, ITS sequence GenBank JX892944); Marrakech-Tensift-El Haouz, N 9 road, Marrakech to Ouarzazate, next to Touflihte, N31°27'46.9" W07°24'19.9", 1 420 m a.s.l., on *C. monspeliensis*, 14 Apr. 2010, *M.T. Telleria*, 18400Tell. (MA-Fungi 92147, ITS sequence GenBank OR127123). – Spain, Ávila, Piedralaves, road to La Adrada, on unidentified twigs, 14 May 1984, *M.T. Telleria*, 5853Tell. (MA-Fungi 37129, ITS sequence GenBank ON972396); Cantabria, Potes, Monte Tolibes, 30TUN6878, 450 m a.s.l., on *C. salvifolius* burned, 1 Apr. 1985, *M. Dueñas*, 3639MD (MA-Fungi 11811, ITS sequence GenBank ON972400); ibid., 3605MD (MA-Fungi 11810, ITS sequence GenBank ON972398); Cantabria, Toyo, Naroba to Toyo road, ravine of Naroba, N43°06'57.7" W04°37'20.6", 605 m a.s.l., on *C. salvifolius*, 25 Apr. 2015, *M.T. Telleria*, 20616Tell. (MA-Fungi 98702, ITS sequence GenBank ON972399); Huelva, Doñana Biological Reserve, Laguna de Santa Olaya, next to gatehouse, 29 Apr. 1983, *M.T. Telleria*, 2513Tell. (MA-Fungi 23575, ITS sequence GenBank OR127128); Teruel, port of Noguera de Albarracín, N40°30'43.4" W01°39'52.6", 1 675 m a.s.l., on *Cistus*, 5 June 2019, *M. Dueñas*, 15702MD (MA-Fungi 98799, ITS sequence GenBank OR127124); Toledo, Almorox, 30TUK8641, 720 m a.s.l., on *C. ladanifer* twigs, 8 Mar. 2008, *J. Hernanz & J.C. Zamora* (MA-Fungi 75662, ITS sequences GenBank JX892942, JX892943); Toledo, Corral de Cantos, 30SUJ7282, 1 300 m a.s.l., on *Cistus*, 15 May 1988, *M. Dueñas*, 4651MD (MA-Fungi 23536, ITS sequence GenBank OR127119); Toledo, Marjaliza, Lituero Alto, 30SVJ1278, 870 m a.s.l., on *C. ladanifer*, 12 May 1988, *M. Dueñas*, 4485MD (MA-Fungi 23370, ITS sequence GenBank OR127120); Canary Islands, La Gomera, Degollada de Peraza, on *C. monspeliensis* twigs, 13 Jan. 1990, *M.P. Núñez García* (MA-Fungi 35477, ITS sequence GenBank ON972397); Canary Islands, Tenerife, La Orotava, La Corona Forestal Natural Park, Caldera de Aguamansa, forest track to Chimoche, N28°21'18.01" W16°29'59.37", 1 240 m a.s.l., on *C. symphytifolius*, 1 Feb. 2007, *M. Dueñas*, 11592MD (MA-Fungi 92820, ITS sequence GenBank OR127126).

Additional material examined of *Vuilleminia macrospora*. Morocco, Marrakech-Tensift-Al Haouz, road R 203, Tzi-n-Test, N30°54'53.9" W08°18'44.1", 1 875 m a.s.l., on *Quercus ilex* subsp. *ballota*, 16 Apr. 2010, *M. Dueñas*, 13038MD (MA-Fungi 98696, ITS sequence GenBank ON972398); ibid., 13042MD (MA-Fungi 98700, ITS sequence GenBank ON972393); ibid., 13048MD (MA-Fungi 98697, ITS sequence GenBank ON972391); ibid., 13049MD (MA-Fungi 98698, ITS sequence GenBank ON972392); ibid., on *Cistus albidus*, *M.T. Telleria*, 18429Tell. (MA-Fungi 98701, ITS sequence GenBank ON972395); ibid., 18435Tell. (MA-Fungi 98699, ITS sequence GenBank ON972394). – Poland, ad ramas *Cornus sanguinea*, *Eichler* 47, (type, F258095, herbarium S!). – Spain, Madrid, Aranjuez, road to Ontígola, 30TUK8969, 580 m a.s.l., on *Quercus coccifera*, 24 May 1994, *M. Dueñas*, 7553MD (MA-Fungi 41594, ITS sequence GenBank OR127117).

Notes — Analysis of combined ITS + LSU nrDNA previously published by Ghobad-Nejhad & Duhem (2014), grouped sequences of *Vuilleminia macrospora* in two clades. Phylogenetic analyses (ITS nrDNA), based on specimens of the MA-Fungi herbarium and previously published data confirm these results. Sequences of *Vuilleminia beltraniae* cluster together as the sister clade of nine sequences of *V. macrospora*, six from Morocco, and three from Spain, France and Sweden. Both species have capitate cystidia, but *V. beltraniae* also has cylindrical to fusiform cystidia, and spores, (12–)14–23 × (4.5–)5–7 µm, narrower than *V. macrospora*, 12–21 × 6–10.5 µm.

Bresadola (1903) described *Corticium acerinum* var. *macrospora* (= *V. macrospora*) based on Eichler's material on *Cornus sanguinea* from Poland, with spores 15–20 × 6–9 µm. Ghobad-Nejhad & Duhem (2014) noted that the type of *V. macrospora* was lacking and selected the specimen Bourdot 3786 (PC, France, Allier, Saint Priest, 19 Dec. 1904, on *Prunus spinosae*) as lectotype. We have studied the original specimen (F258095, herbarium S!) and we could not obtain a DNA sequence from it, but its spores agree with the Bresadola description, 17–20 × 7–9 µm. Ghobad-Nejhad & Duhem (2014) considered the specimens MA-Fungi 75662, 18884Tell. (MA-Fungi 82460) and Duhem 4860 (PC) as *V. macrospora*, but in this study we confirm that they belong to the new species *V. beltraniae*.

Colour illustrations. Canary Islands, Tenerife, La Corona Forestal Natural Park, Piedra La Rosa viewpoint, where the type was collected (photo credit: M.T. Telleria). From left to right: basidioma, hymenium with cystidia and basidia, capitate cystidia, cylindrical cystidia, basidium and spores (17205Tell., MA-Fungi 92857). Scale bars = 2 mm (basidiome), 20 µm (cystidia and basidia), 10 µm (spores).

Supplementary material

FP1593 Phylogenetic tree.

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Xenoramularia epitaxicola

Fungal Planet 1594 – 30 December 2023

Xenoramularia epitaxicola Piątek, Stryjak-Bogacka & Czachura, *sp. nov.*

Etymology. Name refers to the occurrence on the surface of *Taxus baccata* needles.

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

Mycelium composed of branched, septate, hyaline, straight to curved, thin-walled hyphae, 1.5–3 µm wide; hyphae disintegrate into arthroconidia. *Arthroconidia* subcylindrical, rarely ellipsoid, hyaline, smooth, aseptate or rarely 1-septate, 7.5–17 × 1.5–3.5 µm, sometimes constricted at septa, produced by fragmenting hyphae, intercalary or terminally, usually in chains.

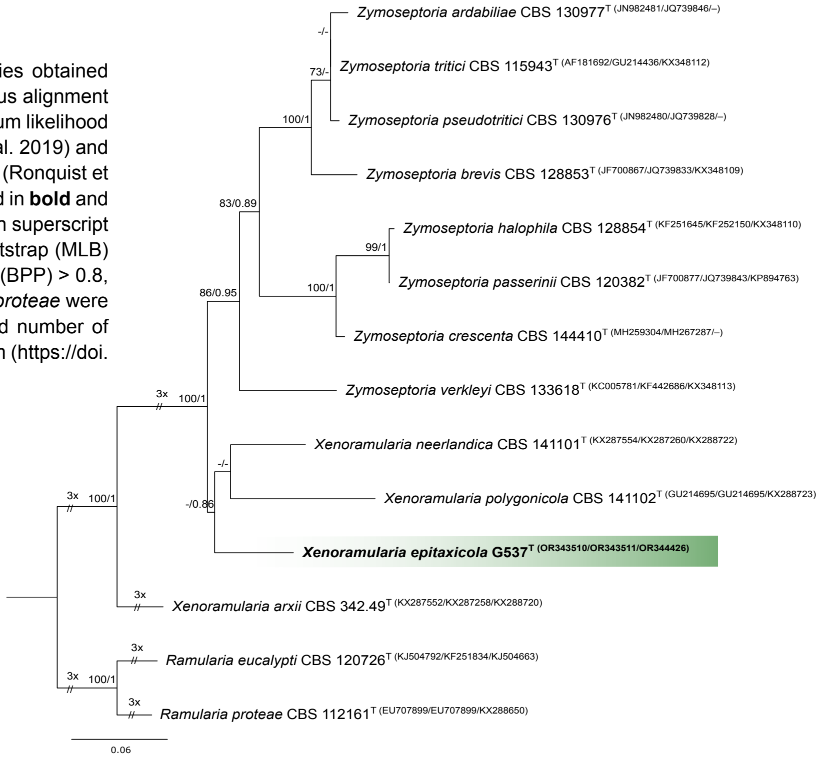
Culture characteristics — Colonies on malt extract agar (MEA) and potato dextrose agar (PDA) erumpent, spreading, pale grey, reaching 8 mm diam after 2 wk growth at 25 °C and 14 mm diam after 4 wk growth at 25 °C, surface cerebriform, with moderate aerial mycelium, margin smooth and entire (on MEA) or undulate (on PDA), rosaceous. Reverse dirty rosaceous.

Typus. Poland, Podkarpackie Province, Rzeszów County, Rzeszów-Kmity, municipal greenery, isolated from sooty mould community on *Taxus baccata* (*Taxaceae*) needles, 17 Sept. 2018, *M. Piątek*, *W. Bartoszek & P. Czachura* (holotype KRAM F-59982; culture ex-type G537 = CBS 150719; ITS, LSU and *rpb2* sequences GenBank OR343510, OR343511 and OR344426; MycoBank MB 850289).

Notes — The genus *Xenoramularia* accommodates ramularia-like hyphomycetes having hyaline, reduced and mostly solitary conidiophores and thickened but undarkened conidial hila and conidiogenous loci (Videira et al. 2016). Three already described species are phytopathogens on angiosperms: *X. arxii* on *Acorus calamus* (*Acoraceae*) in the Netherlands, *Xenoramularia neerlandica* on *Iris pseudoacorus* (*Iridaceae*) and *Sparganium ramosum* (*Typhaceae*) in the Netherlands and *Xenoramularia polygonicola* (type species) on *Polygonum* (*Polygonaceae*) in South Korea (Videira et al. 2016). *Xenoramularia epitaxicola* is phylogenetically related to *X. neerlandica* and *X. polygonicola* but differs in having only hyphae disintegrating into arthroconidia. No conidiophores and conidia were observed in cultures. This is the first member of *Xenoramularia* known on gymnosperms since it was isolated from the sooty mould community covering needles of *Taxus baccata* (*Taxaceae*).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence are *Zymoseptoria verkleyi* (culture SFC20220920-D398, GenBank OP598057; Identities = 493/498 (99 %), one gap (0 %)), *Xenoramularia neerlandica* (culture CBS 113615, GenBank KX287553; Identities = 517/529 (98 %), two gaps (0 %)) and *Zymoseptoria tritici* (culture StA161, GenBank KP852517; Identities = 534/548 (97 %), six gaps (1 %)). The closest hits using the **LSU** sequence are *Xenoramularia neerlandica* (culture CPC 18377, GenBank NG_066370; Identities = 879/881 (99 %), one gap (0 %)), *Xenoramularia polygonicola* (culture CPC 10853, GenBank KX287262; Identities = 874/880 (99 %), no gaps) and *Zymoseptoria verkleyi* (culture CBS 133618, GenBank NG_042756; Identities = 854/863 (99 %), three gaps (0 %)). The closest hits using the ***rpb2*** sequence are *Xenoramularia neerlandica* (culture CPC 18378, GenBank KX348108; Identities = 916/1045 (88 %), no gaps), *Zymoseptoria verkleyi* (culture CBS 133618, GenBank KX348113; Identities = 795/913 (87 %), three gaps (0 %)) and *Zymoseptoria tritici* (culture ST99CH_3D1, GenBank LT854276; Identities = 927/1070 (87 %), no gaps).

Phylogenetic tree of *Xenoramularia* and *Zymoseptoria* species obtained from a maximum likelihood analysis of the combined multi-locus alignment (2 232 characters, including gaps: ITS/LSU/*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 *Xenoramularia epitaxicola* is indicated in **bold** and marked by a coloured block. Ex-type cultures are indicated with superscript T. Numbers above branches indicate maximum likelihood bootstrap (MLB) support values > 70 % and Bayesian posterior probabilities (BPP) > 0.8, respectively (MLB/BPP). *Ramularia eucalypti* and *Ramularia proteae* were used as an outgroup. The scale bar represents the expected number of changes per site. The alignment was deposited at figshare.com (https://doi.org/10.6084/m9.figshare.23725806.v1).



Colour illustrations. Needles of *Taxus baccata* with sooty mould communities, Poland. Colony on MEA; hyphae and arthroconidia. Scale bars = 10 µm.

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Nothomicrothyrium beaucarneae

Fungal Planet 1595 – 30 December 2023

Nothomicrothyrium Crous, *gen. nov.*

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

Classification — *Microthyriaceae*, *Microthyriales*, *Dothideomycetes*.

Saprobic on dead leaves. *Hyphae* 2–3 µm diam, superficial, medium brown, septate. *Ascomata* thyrothecial, superficial, circular, medium brown, solitary, connected by hyphae, loose on host tissue; upper wall medium brown, composed of radiating rows of *textura prismatica*, slightly darker around the ostiole; margin smooth, lobate, slightly darker brown. *Hamathecium* consisting of asci arranged in a rosette from the rim towards the ostiole, with thin, branched, septate, cellular pseudoparaphyses. *Asci* 8-spored, bitunicate, fissitunicate, obovoid. *Ascospores* multiseriate, submedianly 1-septate, upper cell longer and wider than basal cell, not constricted at septum, guttulate, with 2 large guttules in upper cell, smooth-walled, upper cell with central perpendicular linear zone giving rise to flexuous hair-like appendages.

Type species. *Nothomicrothyrium beaucarneae* Crous
MycoBank MB 850600

Nothomicrothyrium beaucarneae Crous, *sp. nov.*

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

Saprobic on dead leaves. *Hyphae* 2–3 µm diam, superficial, medium brown, septate. *Ascomata* thyrothecial, 70–120 µm diam, superficial, circular, medium brown, solitary, connected by hyphae, loose on host tissue; upper wall medium brown, composed of radiating rows of *textura prismatica*, slightly darker around the ostiole, 5–15 µm diam; margin smooth, lobate, slightly darker brown. *Hamathecium* consisting of asci arranged in a rosette from the rim towards the ostiole, with thin, branched, septate, 2–2.5 µm diam cellular pseudoparaphyses. *Asci* 8-spored, bitunicate, fissitunicate, obovoid, apical chamber not well developed, 20–27 × 8–10 µm. *Ascospores* (9–)10–11(–12) × 3(–4) µm, multiseriate, submedianly 1-septate, upper cell longer and wider than basal cell, not constricted at septum, guttulate, with 2 large guttules in upper cell, smooth-walled, upper cell with central perpendicular linear zone giving rise to flexuous hair-like appendages, up to 16, 8–16 µm long.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 5 mm diam after 2 wk at 25 °C. On MEA surface and reverse isabelline, on PDA surface isabelline, reverse olivaceous grey, on OA surface olivaceous grey. Colonies forming spermatogonia in culture.

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-25289; culture ex-type CPC 45780 = CBS 150084, CPC 45781; ITS sequence GenBank OR680761.1; MycoBank MB 850601).

Notes — *Nothomicrothyrium* is morphologically similar to *Pseudomicrothyrium*, which was introduced as a new genus, distinguished from *Microthyrium* by having superficial, brown thyrothecia with slightly darker ostioles, a reticulate hyphal network, and ascospores with 2–4 apical appendages (Hongsanan et al. 2020). *Pseudomicrothyrium* is monotypic, with *P. thailandicum* characterised in having ascospores that are larger than those of *N. beaucarneae*, 13–15 × 4–5 µm, and having apical appendages. *Nothomicrothyrium beaucarneae* is phylogenetically distinct, and can be morphologically distinguished from *Pseudomicrothyrium* and *Microthyrium* in that it has numerous ascospore appendages, which and are arranged in a central perpendicular linear zone.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity mainly to the 5.8S nrDNA of *Triscelophorus* cf. *acuminatus* (strain denovo61, GenBank OM987014.1; Identities = 160/163 (98 %), no gaps), *Microthyrium macrosporum* (strain VUL.460, GenBank MG844147.1; Identities = 188/195 (96 %), two gaps (1 %)) and *Triscelophorus monosporus* (strain TOMO 185-1686, GenBank KX858630.1; Identities = 186/194 (96 %), one gap (0 %)).

Colour illustrations. *Beaucarnea stricta* in Stellenbosch Botanical Garden, South Africa. Superficial thyrothecial ascomata; ascoma with central ostiole; ascoma with internal rosette of asci; pseudoparaphyses and asci; ascospores with flexuous hair-like appendages (note attachment in central perpendicular linear zone). Scale bars: ascomata = 100 µm, 60 µm, all others = 10 µm.

Supplementary material

FP1595 Phylogenetic tree.

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Exophiala lichenicola

Fungal Planet 1596 – 30 December 2023

Exophiala lichenicola Crous, *sp. nov.*

Etymology. Name refers to its habitat, dwelling on lichens.

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

Mycelium consisting of olivaceous brown, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* solitary, creeping on agar surface, up to 160 µm tall, 2–3 µm diam, branched, septate, constricted at septa, olivaceous brown, smooth, with tuft-like terminal conidiogenous apparatus, but also with lateral branches, with conidiogenous cells. *Conidiogenous cells* olivaceous brown, smooth, ellipsoid to fusoid-ellipsoid, polyblastic, 3–10 × 2.5–4 µm. *Conidia* aseptate, ellipsoid, olivaceous brown, smooth, remaining attached in long, branched chains, loci flattened, not darkened nor thickened, 1–1.5 µm diam, becoming swollen, subglobose, or disarticulating off, ellipsoid, 3–6 × 2–3 µm; older conidia globose, dark red-brown, thicker walled, 5–7 µm diam.

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

Typus. NAMIBIA, Gobabeb-Namib Research Institute, salt pan, lichenicolous on *Acarospora cf. luederitzensis* lichen growing on a rock, 4 Apr. 2022, *P.W. Crous*, HPC 3888 (holotype CBS H-25268; culture ex-type CPC 43306 = CBS 150055; ITS and LSU sequences GenBank OR680762.1 and OR717018.1; MycoBank MB 850602).

Notes — The *Herpotrichiellaceae* accommodates more than 180 species, including the polyphyletic genera *Exophiala* and *Cladophialophora*, which are common in the anthropogenic environment but apparently rarely found in nature (Quan et al. 2023). *Exophiala lichenicola* represents such a rare species, which is lichenicolous, occurring on a lichen growing on a rock adjacent to a salt pan in the Namib desert, where it was isolated together with *Fusariella atrovirens* (Crous et al. 2023). Phylogenetically, *E. lichenicola* appears distinct from other presently known species in the genus.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Chaetothyriales* sp. (strain G4.5E1d, GenBank KP400576.1; Identities = 528/535 (99 %), two gaps (0 %)), *Exophiala crusticola* (strain CCCT 19.109, GenBank MT137541.1; Identities = 475/536 (89 %), 33 gaps (6 %)) and *Exophiala capensis* (strain SM, GenBank MW361315.1; Identities = 477/539 (88 %), 21 gaps (3 %)). Closest hits using the **LSU** sequence are *Chaetothyriales* sp. (strain TRN 30, GenBank FJ358252.1; Identities = 873/873 (100 %), no gaps), *Exophiala crusticola* (strain CBS 119970, GenBank MH874623.1; Identities = 873/890 (98 %), two gaps (0 %)) and *Minimelanolocus asiaticus* (strain MFLUCC 15-0237, GenBank NG_070384.1; Identities = 851/874 (97 %), one gap (0 %)).

Colour illustrations. Lichenicolous growth on rock at Gobabeb-Namib Research Institute. Colony on SNA; hyphae giving rise to conidial chains; immature conidia; older, red-brown, globose conidia. Scale bars = 10 µm.

Supplementary material

FP1596 Phylogenetic tree.

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Alternaria moraeae

Fungal Planet 1597 – 30 December 2023

Alternaria moraeae Crous, *sp. nov.*

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

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

Mycelium consisting of branched, septate, hyaline to brown, smooth, 3–4 µm diam hyphae. *Conidiophores* solitary, erect, subcylindrical, brown, smooth, 2–6-septate, 50–150 × 7–10 µm; unbranched or with lateral branches. *Conidiogenous cells* terminal and intercalary, subcylindrical to clavate, straight to geniculate, polytretic, scars thickened, darkened, refractive, 2.5–3 µm diam, 20–60 × 6–10 µm. *Conidia* solitary, or in short chains (2–3), medium brown, surface finely roughened, thick-walled, 3–7-distoseptate, fusoid, tapering to obtuse apex and subtruncate base; hilum thickened, darkened and refractive, 3–4 µm, (38–)50–70(–80) × (11–)12–14(–15) µm.

Culture characteristics — Colonies erumpent, spreading, with abundant, woolly aerial mycelium and smooth, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse apricot; on PDA and OA surface dirty white, reverse salmon with patches of olivaceous.

Typus. South Africa, Western Cape Province, Clanwilliam, on dead leaves of *Moraea* sp. (*Iridaceae*), Sept. 2022, *M.J. Wingfield*, HPC 4019 (holotype CBS H-25269; culture ex-type CPC 45031 = CBS 150056; ITS, LSU, *gapdh* and *rpb2* sequences GenBank OR680763.1, OR717019.1, OR683708.1 and OR683721.1; MycoBank MB 850603).

Notes — Woudenberg et al. (2013) introduced *Alternaria* section *Embellisioides* to accommodate species with conidia solitary or in short chains, obovoid to ellipsoid, with transverse and longitudinal septa, thus fitting the morphology of *Alternaria moraeae*, which represents the first species of *Alternaria* described from *Moraea*. However, a literature search revealed a New Zealand culture, ICMP 15785, which might be the same, or another taxon with similar morphology (from *Moraea ramosissima*, New Zealand).

Alternaria moraeae clustered adjacent to '*Bipolaris iridis*' (CBS 226.66, CBS 503.73), which represents another species of *Alternaria* in section *Embellisioides*. The name *Alternaria iridis* (based on CBS 101.26) was used by Lawrence et al. (2013), but represents an unpublished name, also not recognised by Simmons (2007) or Woudenberg et al. (2013). Other *Alternaria* species occurring on *Iris* are *A. iridiaustralis* (Luo et al. 2018) and *A. iridicola* (section *Alternaria*; see Nishikawa & Nakashima 2020), although these taxa are morphologically distinct. A new combination is thus proposed for '*Bipolaris iridis*' below, which causes 'ink disease' of *Iris* in Europe.

Alternaria iridis (Oudem.) Crous, *comb. nov.* — MycoBank MB 850604

Basionym. *Clasterosporium iridis* Oudem., Hedwigia 37: 318. 1898.

Synonyms. *Bipolaris iridis* (Oudem.) C.H. Dickinson, Trans. Brit. Mycol. Soc. 49: 578. 1966.

Drechslera iridis (Oudem.) M.B. Ellis, Dematiaceous Hyphomycetes (Kew): 423. 1971.

(See FP1597-2)

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Bipolaris iridis* (strain CBS 127222, GenBank MH864475.1; Identities = 529/549 (96 %), two gaps (0 %)), *Alternaria botryospora* (strain CBS 478.90, GenBank MH862228.1; Identities = 524/550 (95 %), four gaps (0 %)) and *Alternaria hyacinthi* (strain CBS 498.71, GenBank MH860234.1; Identities = 522/549 (95 %), three gaps (0 %)). Closest hits using the **LSU** sequence are *Bipolaris iridis* (strain CBS 127222, GenBank MH875907.1; Identities = 877/878 (99 %), no gaps), *Alternaria planifunda* (strain CBS 537.83, GenBank NG_070597.1; Identities = 877/882 (99 %), no gaps) and *Alternaria oblongo-obovoidea* (strain CBS 127670, GenBank MH876050.1; Identities = 873/880 (99 %), no gaps). Closest hits using the ***gapdh*** sequence had highest similarity to *Bipolaris iridis* (strain CBS 127223, GenBank LT715867.1; Identities = 564/585 (96 %), three gaps (0 %)), *Alternaria proteae* (strain CBS 475.90, GenBank KC584161.1; Identities = 548/574 (95 %), no gaps) and *Embellisia planifunda* (strain CBS 537.83, GenBank FJ266492.1; Identities = 547/574 (95 %), no gaps). Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Bipolaris iridis* (strain CBS 226.66, GenBank LT715735.1; Identities = 756/782 (97 %), no gaps), *Alternaria botryospora* (strain CBS 478.90, GenBank KC584461.1; Identities = 825/863 (96 %), one gap (0 %)) and *Alternaria tumida* (strain CBS 539.83, GenBank KC584466.1; Identities = 827/866 (95 %), one gap (0 %)).

Colour illustrations. *Moraea* sp. growing in the Clanwilliam area, South Africa. Colony on SNA; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Supplementary material

FP1597-1 Phylogenetic tree.

FP1597-2 Conidiophores and conidia of *Alternaria iridis.*

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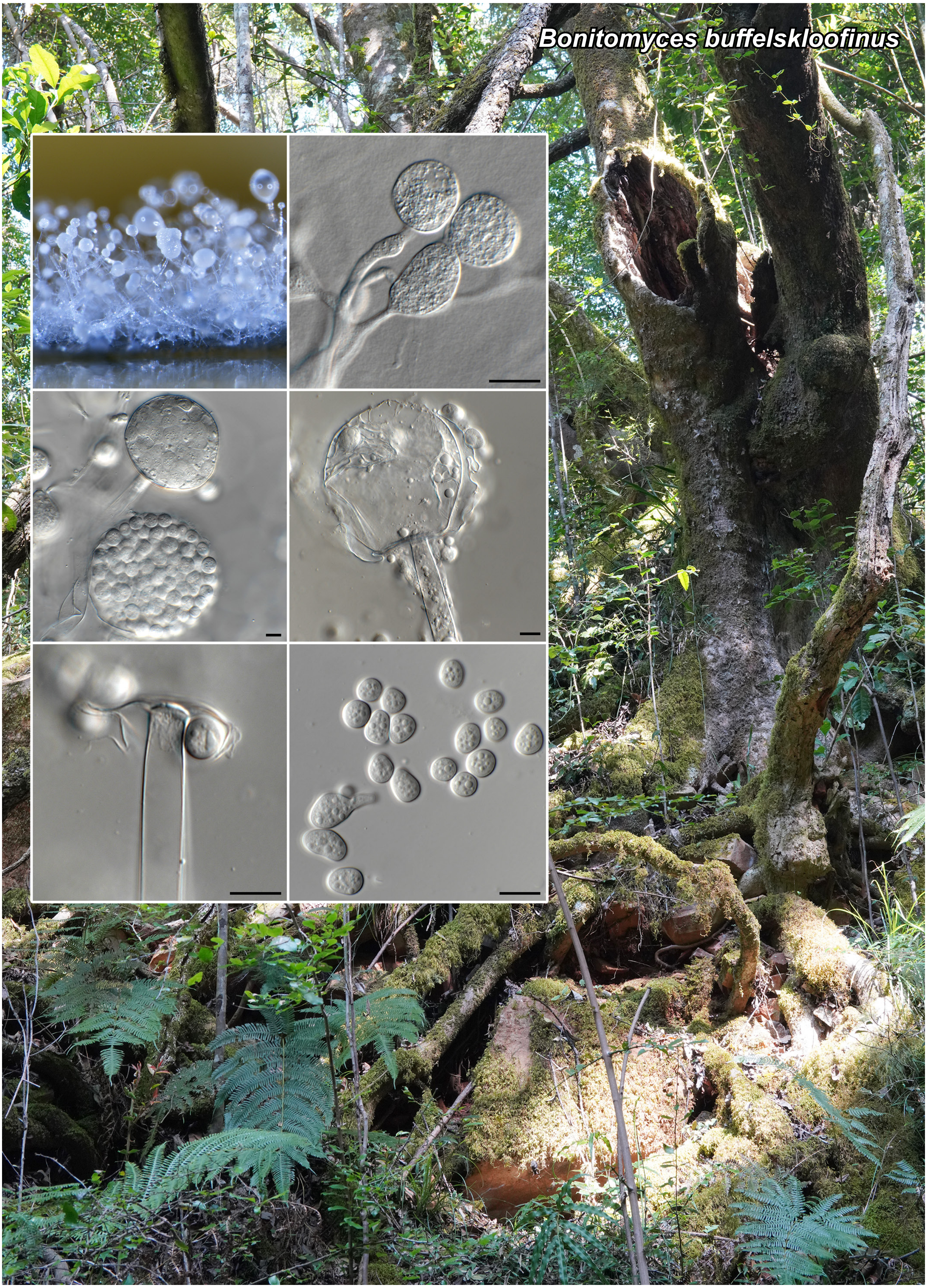
Bonitomyces buffelskloofinus

Fungal Planet 1598 – 30 December 2023

Bonitomyces Crous, *gen. nov.*

Etymology. Named for the American mycologist, Gregory Bonito, in recognition of his contribution to *Mortierellaceae* systematics.

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

Sporangiophores in clusters, erect, base lacking rhizoids, unbranched, hyaline, smooth, up to 1 200 µm tall. *Sporangia* globose, multi-spored; after spore liberation with pronounced columella and collarette. *Sporangiospores* hyaline, smooth-walled, globose to ellipsoid or reniform, aseptate. *Chlamydospores* abundant, globose, thick-walled.

Type species. *Bonitomyces buffelskloofinus* Crous
MycoBank MB 850605

Bonitomyces buffelskloofinus Crous, *sp. nov.*

Etymology. Name refers to Buffelskloof, Mpumalanga Province, South Africa, where it was collected.

Sporangiophores in clusters, erect, base lacking rhizoids, unbranched, hyaline, smooth, up to 1 200 µm tall, 30–45 µm diam at base, 7–8 µm diam below columella. *Sporangia* globose, 50–70 µm diam, multi-spored; after spore liberation with pronounced columella and collarette. *Sporangiospores* hyaline, smooth-walled, globose to ellipsoid or reniform, aseptate, 8–18 × 7–11 µm. *Chlamydospores* abundant, globose, thick-walled, 12–20 µm diam.

Culture characteristics — Colonies with moderate aerial mycelium, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse white to cream.

Typus. South Africa, Mpumalanga Province, Buffelskloof Nature Reserve, on dead twigs of unidentified tree, 5 Aug. 2022, *P.W. Crous*, HPC 3971 (holotype CBS H-25270; culture ex-type CPC 45055 = CBS 150057; ITS and LSU sequences GenBank OR680764.1 and OR717020.1; MycoBank MB 850606).

Notes — *Bonitomyces buffelskloofinus* is related to *Dissophora globulifera*. Vandepol et al. (2020) report that all *Dissophora* species have been isolated from forest litter and soil, which fits with the ecology of *B. buffelskloofinus*. Furthermore, it also produces ‘tufts’ of sporangiophores, similar to that reported for *D. globulifera* by Vandepol et al. (2020) but appears to represent a genus between *Dissophora* and *Benniella*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to ‘Uncultured eukaryote’ from soil (clone 2512, GenBank MF570869.1; Identities = 425/425 (100 %), no gaps), *Dissophora globulifera* (strain CBS 858.70, GenBank NR_077211.1; Identities = 533/646 (83 %), 47 gaps (7 %)) and *Mortierella echinula* (strain CBS 282.71, GenBank JX975948.1; Identities = 536/651 (82 %), 42 gaps (6 %)). Closest hits using the **LSU** sequence are *Mortierella echinula* (strain CBS 282.71, GenBank MH871899.1; Identities = 912/955 (95 %), eight gaps (0 %)), *Linnemannia exigua* (strain CBS 655.68, GenBank MH870921.1; Identities = 905/952 (95 %), six gaps (0 %)) and *Mortierella exigua* (strain CBS 655.68, GenBank HQ667406.1; Identities = 902/949 (95 %), six gaps (0 %)).

Colour illustrations. Forest at Buffelskloof Nature Reserve. Colony sporulating in culture; conidiophores and conidiogenous cells giving rise to conidia on SNA; chlamydospores; sporangia; columella; sporangiospores. Scale bars = 10 µm.

Supplementary material

FP1598 Phylogenetic tree.

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Cistella blauvikensis

Fungal Planet 1599 – 30 December 2023

Cistella blauvikensis Crous & Thines, *sp. nov.*

Etymology. Name refers to Blávík, Iceland, where it was collected.

Classification — *Incertae sedis*, *Helotiales*, *Leotiomycetidae*, *Leotiomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* reduced to hyphal pegs on hyphae, subcylindrical, smooth, erect, 10–20 × 1.5–2 µm, or reduced to conidiogenous loci, 1–1.5 µm diam, proliferating sympodially; loci not thickened nor darkened. *Conidia* occurring in branched chains, hyaline, smooth, (0–)3–6-septate, (8–)10–20(–45) × 2(–3) µm; hila truncate, 1–1.5 µm diam, not thickened nor darkened.

Culture characteristics — Colonies flat, spreading, surface folded, with moderate aerial mycelium and smooth, even margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse ochreous; on PDA surface and reverse dirty white; on OA surface pale luteous.

Typus. ICELAND, Fáskrúðsfjörður, Blávík, surf-spray-influenced meadow, near the scarp to the rocky beach, on dead grass (*Poaceae*), 4 Oct. 2022, *M. Thines*, HPC 4045 (holotype CBS H-25271; culture ex-type CPC 45252 = CBS 150058; ITS, LSU and *rpb2* sequences GenBank OR680765.1, OR717021.1 and OR683722.1; MycoBank MB 850607).

Notes — Species of *Cistella* (*Hyaloscyphaceae*) occur on diverse substrates, including soil, to plant litter (Quijada et al. 2015, Johnston et al. 2019). Although no asexual morph has been confirmed for *Cistella*, the present collection is phylogenetically linked to it, and thus appropriate to name it as a new species of *Cistella*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cistella* sp. (strain F-232, GenBank OM670130.1; Identities = 482/483 (99 %), no gaps), *Leohumicola minima* (strain SD-61, GenBank MF467895.1; Identities = 466/480 (97 %), one gap (0 %)) and *Cistella albidolutea* (voucher KUS-F52678, GenBank JN033429.1; Identities = 489/511 (96 %), two gaps (0 %)). Closest hits using the **LSU** sequence are *Cistella albidolutea* (voucher KUS-F52678, GenBank JN086732.1; Identities = 775/788 (98 %), no gaps), *Incrupila aspidii* (voucher SBRH909, GenBank OM218632.1; Identities = 791/813 (97 %), no gaps) and *Vandijckella johannae* (strain CBS 143182, GenBank NG_075222.1; Identities = 805/828 (97 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Cistella albidolutea* (voucher KUS-F52678 GenBank JN086872.1; Identities = 638/752 (85 %), six gaps (0 %)), *Hyaloscypha melinii* (strain CBS 143705, GenBank MH018952.1; Identities = 630/787 (80 %), 18 gaps (2 %)) and *Arachnopeziza trabinelloides* (voucher GJO0071771, GenBank MT228664.1; Identities = 637/797 (80 %), 21 gaps (2 %)).

Colour illustrations. Research station at Blávík, Iceland, with grass in the foreground. Hyphae giving rise to conidial chains; conidia. Scale bars = 10 µm.

Supplementary material

FP1599 Phylogenetic tree.

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Neonematogonum carpinicola

Fungal Planet 1600 – 30 December 2023

Neonematogonum Crous & Akulov, *gen. nov.*

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

Classification — *Incertae sedis*, *Helotiales*, *Leotiomycetes*.

Conidiophores erect, unbranched, subcylindrical, pale brown, granular, straight, flexuous, base lacking rhizoids; 3–6-septate, terminating in clavate vesicles, with several flattened lateral loci, unthickened, not darkened, giving rise to short conidial chains. *Conidia* in unbranched chains, aseptate, pale brown, smooth, granular; primary conidia obovoid, with protruding hilum; secondary conidia in short chains, attached to primary conidia, ellipsoid to globose; basal hilum inconspicuous to slightly protruding.

Type species. *Neonematogonum carpinicola* Crous & Akulov
MycoBank MB 850608

Neonematogonum carpinicola Crous & Akulov, *sp. nov.*

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

Conidiophores erect, unbranched, subcylindrical, pale brown, granular, straight, flexuous; base 10–12 µm diam, lacking rhizoids, 3–6-septate, 280–400 µm tall, terminating in clavate vesicles, 17–20 µm diam, with several flattened lateral loci, 1.5–2 µm diam; unthickened, not darkened, giving rise to short conidial chains. *Conidia* in unbranched chains, aseptate, pale brown, smooth, granular; primary conidia obovoid, 16–18 × 13–15 µm with protruding hilum, 1.5–2 µm diam; secondary conidia in short chains (–8), attached to primary conidia, ellipsoid to globose, 8–12 × 8–9 µm; basal hilum inconspicuous to slightly protruding, 1 µm diam.

Culture characteristics — Colonies erumpent, with sparse aerial mycelium and smooth, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse ochreous with patches of umber.

Typus. Ukraine, Ternopil region, Zalischyky district, National Nature Park, Dniester Canyon, forest near Dzhuryn waterfall, on dead branches of *Carpinus betulus* (*Betulaceae*), 13 Aug. 2022, *A. Akulov*, HPC 4043 = CWI (Myc) AS 8430 (holotype CBS H-25272; culture ex-type CPC 45250 = CBS 150059; ITS, LSU, *rpb2* and *tub2* sequences GenBank OR680766.1, OR717022.1, OR683723.1 and OR683717.1; MycoBank MB 850609).

Notes — *Neonematogonum* resembles *Nematogonum* in morphology (Crous et al. 2018b), except that the latter has nodose conidiophores, and is obligately fungicolous, not growing in culture without the host fungus (Seifert et al. 2011). Phylogenetically *Neonematogonum* is related to genera in *Helotiales*, from which it is morphologically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cadophora* sp. from Atlantic Ocean driftwood in Norway (strain 066aW1.2, GenBank KY061160.1; Identities = 524/527 (99 %), no gaps), *Rhexocercosporidium senecionis* (voucher MFLU 17-1635, GenBank NR_170001.1; Identities = 445/473 (94 %), eight gaps (1 %)) and *Cadophora luteo-olivacea* (strain DI-116, GenBank OP961971.1; Identities = 442/473 (93 %), eight gaps (1 %)). Closest hits using the **LSU** sequence are *Cadophora* cf. *orchidicola* (strain P1615, GenBank MN339366.1; Identities = 827/841 (98 %), no gaps), *Cadophora neoregeliae* (strain CBS 146821, GenBank NG_076727.1; Identities = 833/849 (98 %), no gaps) and *Heterosphaeria linariae* (voucher MFLU 19-2866, GenBank MT183474.1; Identities = 832/849 (98 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Rhynchobrunnera orthospora* (strain CBS 698.79, GenBank MW297445.1; Identities = 676/802 (84 %), nine gaps (1 %)), *Neospermospora avenae* (strain CBS 388.64, GenBank MW297370.1; Identities = 679/808 (84 %), five gaps (0 %)) and *Rhynchobrunnera lolii* (strain 15lp11, GenBank KU844339.1; Identities = 681/811 (84 %), seven gaps (0 %)). No significant hits were obtained when the ***tub2*** sequence was used in blastn and megablast searches.

Colour illustrations. National Nature Park, Dniester Canyon, Ukraine. Conidiophores and conidiogenous cells giving rise to conidia on pine needle agar; clavate vesicles giving rise to conidia; conidiophore foot cell; vesicles forming conidia; conidia. Scale bars = 10 µm.

Supplementary material

FP1600 Phylogenetic tree.

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Rachicladosporium conostomii

Fungal Planet 1601 – 30 December 2023

Rachicladosporium conostomii Crous, *sp. nov.*

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

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

Conidiophores solitary, erect, subcylindrical, flexuous, unbranched, lacking rhizoids, medium brown, smooth, 3–5-septate, 50–100 × 5–6 µm. *Conidiogenous cells* integrated, terminal, smooth, medium brown, 10–25 × 3–4 µm, with several sympodial terminal loci, thickened, darkened and refractive, 1 µm diam. *Conidia* occurring in branched chains, medium brown, smooth, subcylindrical to fusoid; secondary ramoconidia 0–1-septate, 10–13 × 2.5–3 µm; intercalary and terminal conidia aseptate, 7–9(–11) × 2(–3) µm; loci thickened, darkened, somewhat refractive, 1 µm diam.

Culture characteristics — Colonies erumpent, spreading, folded, with moderate aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface pale olivaceous grey, reverse iron grey.

Typus. South Africa, Mpumalanga Province, Buffelskloof Nature Reserve, on dead twigs of *Conostomium natalense* var. *glabrum* (*Rubiaceae*), 5 Aug. 2022, *P.W. Crous*, HPC 3980 (holotype CBS H-25273; culture ex-type CPC 45059 = CBS 150060; ITS, LSU and *rpb2* sequences GenBank OR680767.1, OR717023.1 and OR683724.1; MycoBank MB 850610).

Notes — *Rachicladosporium conostomii* resembles *R. pini* (from needles of *Pinus monophylla*, the Netherlands; terminal conidia (5–)6–7(–8) × 2–2.5(–3) µm; Crous et al. 2011), *R. cboliae* (from twig debris, USA; terminal conidia (6–)7–8(–10) × (2–)2.5(–3) µm; Crous et al. 2009) and *R. corymbiae* (on leaf spots of *Corymbia citriodora*, Ghana; forming ascomata and conidiophores; terminal conidia (8–)9–10(–12) × 2(–2.5) µm; Crous et al. 2018a) but is morphologically and phylogenetically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Rachicladosporium pini* (strain CPC 16770, GenBank JF951145.1; Identities = 544/559 (97 %), two gaps (0 %)), *Ochrocladosporium adansoniae* (strain CPC 21227, GenBank KF777176.2; Identities = 448/462 (97 %), two gaps (0 %)) and *Rachicladosporium cboliae* (clone LMGI 112/21, GenBank OQ324707.1; Identities = 471/486 (97 %), three gaps (0 %)). Closest hits using the **LSU** sequence are *Rachicladosporium pini* (strain CBS 129525, GenBank MH876826.1; Identities = 830/832 (99 %), no gaps), *Rachicladosporium luculiae* (strain CPC 11407, GenBank EU040237.1; Identities = 830/832 (99 %), no gaps) and *Rachicladosporium paucitum* (strain CCFEE 5458, GenBank KF309988.1; Identities = 739/741 (99 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Rachicladosporium pini* (strain CPC 16770, GenBank LT799764.1; Identities = 730/835 (87 %), no gaps), *Rachicladosporium cboliae* (strain CPC 14034, GenBank LT799763.1; Identities = 750/866 (87 %), no gaps) and *Toxicocladosporium protearum* (strain CPC 15254, GenBank LT799786.1; Identities = 727/910 (80 %), 26 gaps (2 %)).

Colour illustrations. *Conostomium natalense* var. *glabrum* at Buffelskloof Nature Reserve, South Africa. Conidiophores and conidiogenous cells giving rise to conidia on SNA; conidia. Scale bars = 10 µm.

Supplementary material

FP1601 Phylogenetic tree.

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Nothoeucasphaeria buffelskloofina

Fungal Planet 1602 – 30 December 2023

Nothoeucasphaeria Crous, *gen. nov.*

Etymology. Name refers to its similarity to *Eucasphaeria*, from which it is morphologically distinct.

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

Ascomata superficial, perithecial, smooth-walled, with central periphysate ostiole, separate or in clusters, globose, pale orange, not changing colour in KOH+, collapsing when dry, situated on a basal stroma; wall of two regions, outer region of *textura angularis*, inner region of flattened *textura angularis*, straining darker in Melzer's reagent than outer region. *Asci* subcylindrical to narrowly fusoid, apex bluntly rounded with apical mechanism, not straining blue in Melzer, 8-spored, stipitate. *Ascospores* hyaline, smooth, guttulate, fusoid-ellipsoid, slightly curved, ends subobtuse, septate, becoming slightly constricted at septa. *Mycelium* consisting of hyaline, smooth, branched, septate hyphae, frequently forming hyphal coils. *Conidiophores* solitary or in clusters, erect, subcylindrical, smooth, hyaline, mostly unbranched, rarely with a lateral branch, 1–2-septate, frequently reduced to *conidiogenous cells*, with inconspicuous collarette. *Conidia* solitary, hyaline, smooth, aseptate, guttulate, subcylindrical with obtuse ends, aggregating in mucoid mass.

Type species. *Nothoeucasphaeria buffelskloofina* Crous
MycoBank MB 850611

Nothoeucasphaeria buffelskloofina Crous, *sp. nov.*

Etymology. Name refers to Buffelskloof, Mpumalanga Province, South Africa, where the specimen was collected.

Ascomata superficial, perithecial, 250–350 µm diam, smooth-walled, with central periphysate ostiole, separate or in clusters, globose, pale orange, not changing colour in KOH+, collapsing when dry, situated on a basal stroma, 80–130 µm diam; wall of two regions, outer region 50–70 µm diam, of *textura angularis*, inner region 15–20 µm diam, of flattened *textura angularis*, straining darker in Melzer's reagent than outer region. *Asci* subcylindrical to narrowly fusoid, apex bluntly rounded with apical mechanism, not straining blue in Melzer, 8-spored, stipitate, 60–100 × 10–12 µm. *Ascospores* hyaline, smooth, guttulate, fusoid-ellipsoid, slightly curved, ends subobtuse, 3-septate, becoming slightly constricted at septa, (20–)25–26(–30) × (3.5–)4–5 µm. *Mycelium* consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae, frequently forming hyphal coils. *Conidiophores* solitary or in clusters, erect, subcylindrical, smooth, hyaline, mostly unbranched, rarely with a lateral branch, 1–2-septate, frequently reduced to *conidiogenous cells*, 35–50 × 2–2.5 µm, apex 1–1.5 µm diam, with inconspicuous collarette. *Conidia* solitary, hyaline, smooth, aseptate, guttulate, subcylindrical with obtuse ends, aggregating in mucoid mass, (3–)4–5(–6) × 1.5(–2) µm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with sparse aerial mycelium and smooth, lobate margin, reaching 25 mm diam after 2 wk at 25 °C. On MEA surface dirty white with patches of pale olivaceous grey, reverse saffron with patches of olivaceous grey; on PDA surface and reverse saffron; on OA surface saffron.

Typus. South Africa, Mpumalanga Province, Buffelskloof Nature Reserve, on dead twigs of unidentified tree, 5 Aug. 2022, *P.W. Crous*, HPC 3983 (holotype CBS H-25274; culture ex-type CPC 45066 = CBS 150061; ITS, LSU, *actA*, *rpb2*, *tef1* (first part), *tef1* (second part) and *tub2* sequences GenBank OR680768.1, OR717024.1, OR683704.1, OR683725.1, OR683710.1, OR683714.1 and OR683718.1; MycoBank MB 850612).

Notes — *Eucasphaeria* was introduced for *E. capensis*, a fungus occurring on *Eucalyptus* leaf litter in South Africa, characterised by immersed ascomata, and fusoid-ellipsoid, curved, 1-septate ascospores. Conidiomata are acervuloid (sporodochial in culture), giving rise to hyaline, falcate, aseptate to septate conidia in mucoid saffron masses (Crous et al. 2007). *Eucasphaeria* is presently known from three species (Crous et al. 2016, 2020). *Rosasphaeria* was introduced for *R. moravica* (on dead twigs of *Rosa canina*, Europe), having immersed, subglobose ascomata and cylindrical asci with 1-septate, fusiform to cylindrical ascospores, inamyloid asci, hamathecium with periphyses and apical papaphyses, and septate, hyaline ascospores; conidiomata are pycnidial, with cylindrical, hyaline, 1-septate conidia (Jaklitsch & Voglmayr 2012). *Nothoeucasphaeria* is closely related to *Eucasphaeria*, *Neoeucasphaeria* and *Rosasphaeria* in *Niessliaceae*. It is distinct in having superficial, pale orange perithecia that collapse when dry, 3-septate ascospores, and an acremonium-like asexual morph (Hou et al. 2023). Although *Nothoeucasphaeria buffelskloofina* clusters among asexual species of '*Niesslia*', the latter genus is linked to ascomata that are tiny, superficial, dark brown to black, shiny, and typically covered in spines (Gams et al. 2019).

(Notes continued on Supplementary page)

Colour illustrations. Forest at Buffelskloof Nature Reserve, South Africa. Conidiophores and conidiogenous cells giving rise to conidia on SNA; ascomata on twig; asci; ascospores. Scale bars = 300 µm (ascomata), 10 µm (all others).

Supplementary material

FP1602 Phylogenetic tree.

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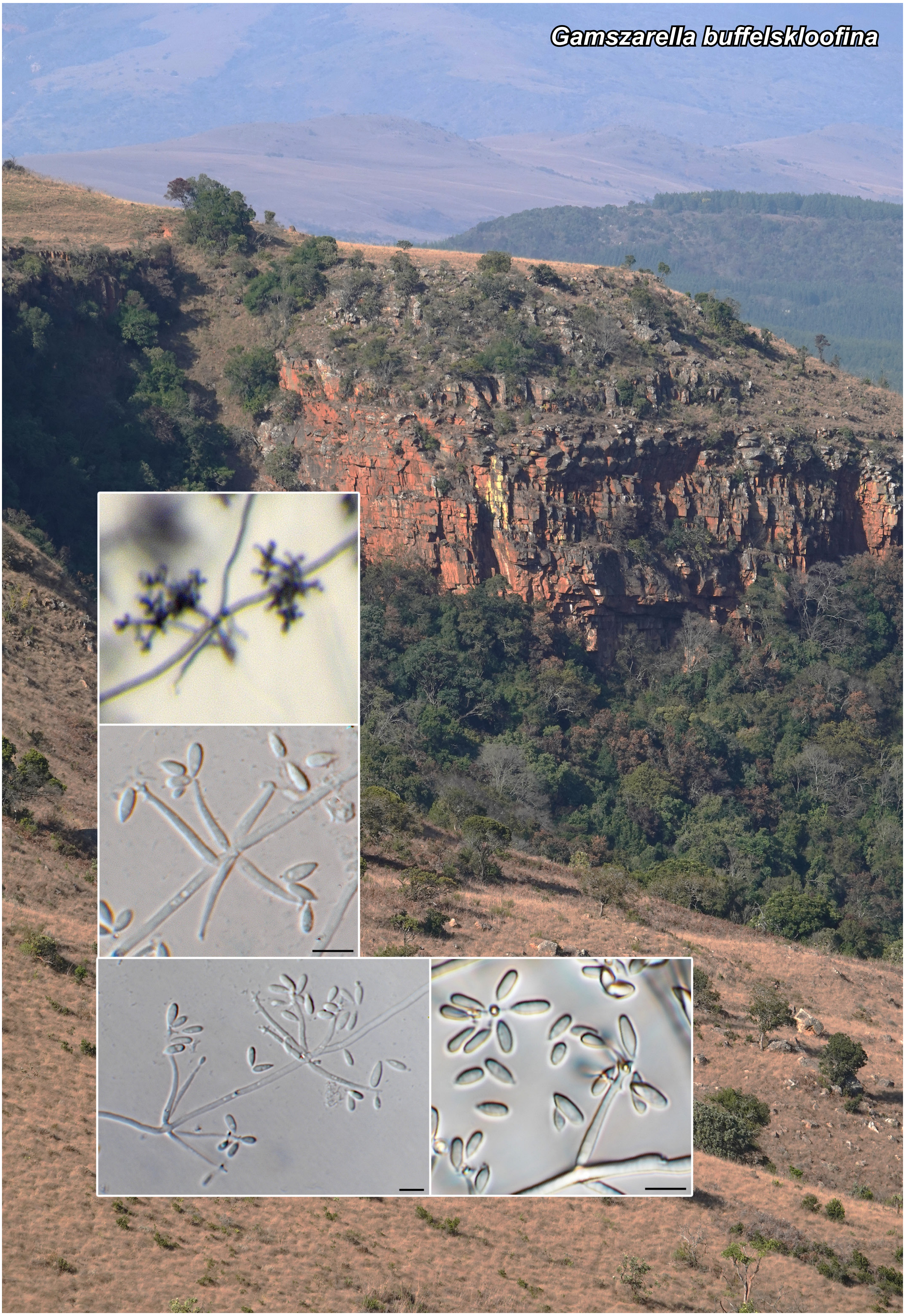
Gamszarella buffelskloofina

Fungal Planet 1603 – 30 December 2023

Gamszarella Crous, *gen. nov.*

Etymology. Named in honour of the mycologists W. Gams and R. Zare, who originally introduced the genus *Lecanicillium*, some species of which are now accommodated in *Gamszarella*.

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

Mycelium consisting of hyaline, smooth, branched, septate hyphae. *Conidiophores* arranged in whorls, reduced to conidiogenous cells or with a supporting cell, giving rise to a whorl of conidiogenous cells. *Conidiogenous cells* hyaline, smooth, subcylindrical with apical taper, terminating in a cluster of denticles, not thickened nor darkened. *Conidia* hyaline, smooth, guttulate, aseptate, subcylindrical, apex obtuse, tapering in basal region to truncate hilum.

Type species. *Gamszarella buffelskloofina* Crous
MycoBank MB 850613

Gamszarella buffelskloofina Crous, *sp. nov.*

Etymology. Name refers Buffelskloof, Mpumalanga Province, South Africa, where it was collected.

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* arranged in whorls, reduced to conidiogenous cells or with a supporting cell, giving rise to a whorl of conidiogenous cells. *Conidiogenous cells* hyaline, smooth, subcylindrical with apical taper, 7–22 × 1.5–2 µm, terminating in a cluster of denticles, 1–3 × 1 µm, not thickened nor darkened. *Conidia* hyaline, smooth, guttulate, aseptate, subcylindrical, apex obtuse, tapering in basal region to truncate hilum, 0.5 µm diam, (3–)4–6(–10) × 2 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 dirty white, reverse ochreous; on PDA surface dirty white, reverse pale luteous; on OA surface dirty white.

Typus. South Africa, Mpumalanga Province, Buffelskloof Nature Reserve, on dead insect on leaf litter of unidentified tree, 5 Aug. 2022, *P.W. Crous*, HPC 3987 (holotype CBS H-25275; culture ex-type CPC 45071 = CBS 150062; ITS, LSU, *rpb2* and *tef1* (second part) sequences GenBank OR680769.1, OR717025.1, OR683726.1 and OR683715.1; MycoBank MB 850614).

Gamszarella antillana (R.F. Castañeda & G.R.W. Arnold) Crous, *comb. nov*. — MycoBank MB 850615

Basionym. *Verticillium antillanum* R.F. Castañeda & G.R.W. Arnold, Feddes Repert. Spec. Nov. Regni Veg. 98: 411. 1987.
Synonym. *Lecanicillium antillanum* (R.F. Castañeda & G.R.W. Arnold) Zare & W. Gams, Nova Hedwigia 73: 34. 2001.

Gamszarella magnispora (Z.F. Zhang & L. Cai) Crous, *comb. nov*. — MycoBank MB 850616

Basionym. *Lecanicillium magnisporum* Z.F. Zhang & L. Cai, Fungal Diversity 106: 103. 2020.

Notes — *Lecanicillium* (based *L. lecanii*) was established to accommodate entomogenous and fungicolous verticillium-like asexual morphs (Gams & Zare 2001). Species of *Lecanicillium* have been found infecting various hosts such as arthropods, nematodes, plants and fungi, but are largely recognised as insect pathogens (Goettel et al. 2008). However, because the congeneric genus *Akanthomyces* represents an older name than *Lecanicillium*, *L. lecanii* is now treated as *A. lecanii*. Furthermore, *Lecanicillium* is polyphyletic (see Kepler et al. 2017), with three species treated here as belonging to the new genus *Gamszarella*. *Gamszarella buffelskloofina* was isolated from a dead insect on leaf litter at Buffelskloof Nature Reserve, South Africa. It is phylogenetically closest to *G. magnispora* (conidia fusoid, falcate, 9–16 × 2–3 µm; Zhang et al. 2021), but distinct in having smaller conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Lecanicillium magnisporum* (strain CGMCC 3.19304, GenBank NR_172833.1; Identities = 509/529 (96 %), nine gaps (1 %)), *Lecanicillium antillanum* (strain CBS 350.85, GenBank NR_111097.1; Identities = 522/548 (95 %), seven gaps (1 %)) and *Lecanicillium fusisporum* (strain SW381, GenBank MH469503.1; Identities = 545/582 (94 %), 15 gaps (2 %)). Closest hits using the **LSU** sequence are *Lecanicillium antillanum* (strain MUT<ITA> 3468, GenBank MG980404.1; Identities = 831/837 (99 %), no gaps), *Lecanicillium magnisporum* (strain FZ2632, GenBank MK329008.1; Identities = 833/841 (99 %), no gaps) and *Lecanicillium fungicola* var. *fungicola* (strain CBS 440.34, GenBank MH867107.1; Identities = 853/862 (99 %), one gap (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Lecanicillium magnisporum* (strain LC12468, GenBank MK335985.1; Identities = 787/865 (91 %), no gaps), *Lecanicillium antillanum* (strain CBS 350.85, GenBank DQ522450.1; Identities = 721/818 (88 %), no gaps) and *Hevansia websteri* (strain BCC36541, GenBank MH521849.1; Identities = 755/871 (87 %), one gap (0 %)). Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Lecanicillium primulinum* (strain JCM 18525, GenBank LC557125.1; Identities = 862/915 (94 %), two gaps (0 %)), *Flavocillium bifurcatum* (strain YFCC 6101, GenBank MN576951.1; Identities = 882/939 (94 %), three gaps (0 %)) and *Flavocillium subprimulinum* (strain KUMCC 17-0148, GenBank MG585317.1; Identities = 843/898 (94 %), no gaps).

Colour illustrations. Buffelskloof Nature Reserve, South Africa. Conidiophores and conidiogenous cells giving rise to conidia on SNA. Scale bars = 10 µm.

Supplementary material

FP1603 Phylogenetic tree.

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Cylindromonium lichenophilum

Fungal Planet 1604 – 30 December 2023

Cylindromonium lichenophilum Crous, *sp. nov.*

Etymology. Name refers to the fact that it was collected growing on a lichen.

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

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–3 µm diam hyphae. *Conidiophores* solitary, erect, flexuous, subcylindrical, hyaline, smooth, base lacking rhizoids, unbranched, 1–3-septate, 90–160 × 3(–3.5) µm. *Conidiogenous cells* integrated, terminal, subcylindrical, 80–140 × 2.5–3 µm; apex 1.5 µm diam, with slightly flared collarette. *Conidia* hyaline, smooth, aseptate, cylindrical with obtuse ends, granular to guttulate, with obtuse ends, aseptate, (11–)13–16(–18) × (2.5–)3(–3.5) µm.

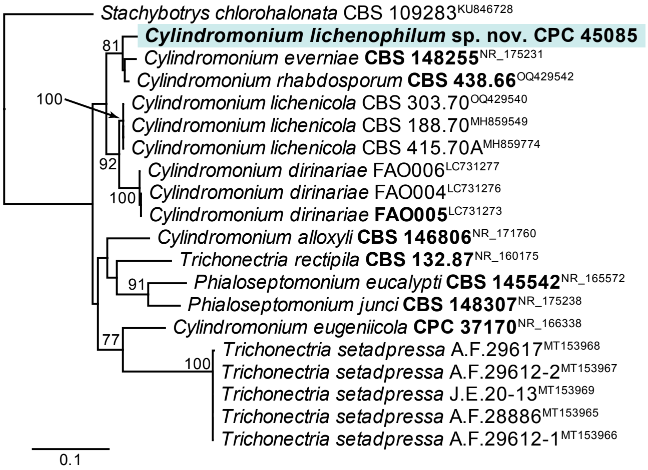
Culture characteristics — Colonies flat, spreading, with folded surface and sparse to moderate aerial mycelium and smooth, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface saffron, reverse ochreous; on PDA surface and reverse dirty white; on OA surface dirty white.

Typus. South Africa, Mpumalanga Province, Buffelskloof Nature Reserve, on *Parmelina tiliacea* (*Parmeliaceae*) thallus with dieback, 5 Aug. 2022, *P.W. Crous*, HPC 3985 (holotype CBS H-25276; culture ex-type CPC 45085 = CBS 150063; ITS, LSU, *actA*, *rpb2* and *tef1* (first part) sequences GenBank OR680770.1, OR717026.1, OR683705.1, OR683727.1 and OR683711.1; MycoBank MB 850617).

Notes — *Cylindromonium* (based on *C. eugeniicola*, on leaf litter of *Eugenia capensis*, South Africa) includes species that are lichenicolous, mycophilic or saprophytic (Gams 1971, Hou et al. 2023), that are acremonium-like in morphology, with cylindrical, 1-septate conidia (Crous et al. 2019), and nectria-like sexual morphs (Ohmaki et al. 2023). Species of *Cylindromonium* are intermixed with those tentatively named in *Trichonectria* (based on *T. hirta*), which could represent the sexual morph of *Cylindromonium*. However, as the type species of the latter (on decaying rails, associated with *Lecidia uliginosa*; England, Twycross, Leicesterhire) is not known from DNA or culture, the question remains unresolved. *Cylindromonium rhabdosporum* (conidia 15–16 × 2.2–2.4 µm; Gams 1971) and *Cylindromonium everniae* (conidia 8–19 × 3–4 µm; Crous et al. 2021c) are closely related to *C. lichenophilum*, but distinct based on morphology and phylogeny.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cylindromonium rhabdosporum* (strain CBS 438.66, GenBank MH858850.1; Identities = 566/579 (98 %), no gaps), *Cylindromonium everniae* (strain CBS 148255, GenBank NR_175231.1; Identities = 532/548 (97 %), no gaps) and *Cylindromonium lichenicola* (strain CBS 188.70, GenBank MH859549.1; Identities = 556/585 (95 %), 10 gaps (1 %)). Closest hits using the **LSU** sequence are *Cylindromonium rhabdosporum* (strain CBS 438.66, GenBank HQ232120.1; Identities = 807/810 (99 %), no gaps), *Cylindromonium everniae* (strain CBS 148255, GenBank NG_081339.1; Identities = 790/794 (99 %), no gaps) and *Cylindromonium dirinariae* (strain FAO006, GenBank LC744401.1; Identities = 827/838 (99 %), no gaps). The closest hit using the ***actA*** sequence had highest similarity to *Cylindromonium everniae* (strain CPC 40760, GenBank OK651129.1; Identities = 673/749 (90 %), 30 gaps (4 %)). Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Cylindromonium rhabdosporum* (strain CBS 438.66, GenBank OQ453929.1; Identities = 717/759 (94 %), no gaps), *Cylindromonium everniae* (strain CPC 40760, GenBank OK651171.1; Identities = 748/815 (92 %), no gaps) and *Cylindromonium dirinariae* (strain FAO006, GenBank LC744392.1; Identities = 737/868 (85 %), no gaps). The closest hit using the ***tef1*** (first part) sequence had highest similarity to *Cylindromonium everniae* (strain CPC 40760, GenBank OK651192.1; Identities = 376/441 (85 %), 32 gaps (7 %)). A comparison to the *tef1* sequence of *Cylindromonium rhabdosporum* (strain CBS 438.66) generated in this study (GenBank OR683713.1) revealed a similarity of 366/412 (89 %, including 17 gaps).

Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy et al. 2017, Minh et al. 2020) of the *Cylindromonium* ITS nucleotide alignment. Bootstrap support values (> 74 % are shown) from 1 000 non-parametric bootstrap replicates are shown at the nodes. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Stachybotrys chlorohalonata* (CBS 109283; GenBank KU846728) and the novelty described here is highlighted with a coloured block and **bold** font. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 20 strains including the outgroup; 571 characters including alignment gaps analysed: 195 distinct patterns, 108 parsimony-informative, 50 singleton sites, 413 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.23447342).



Colour illustrations. Lichens (note dieback) growing on tree trunk at Buffelskloof Nature Reserve, South Africa. Conidiophores and conidiogenous cells giving rise to conidia on SNA; conidia. Scale bars = 10 µm.

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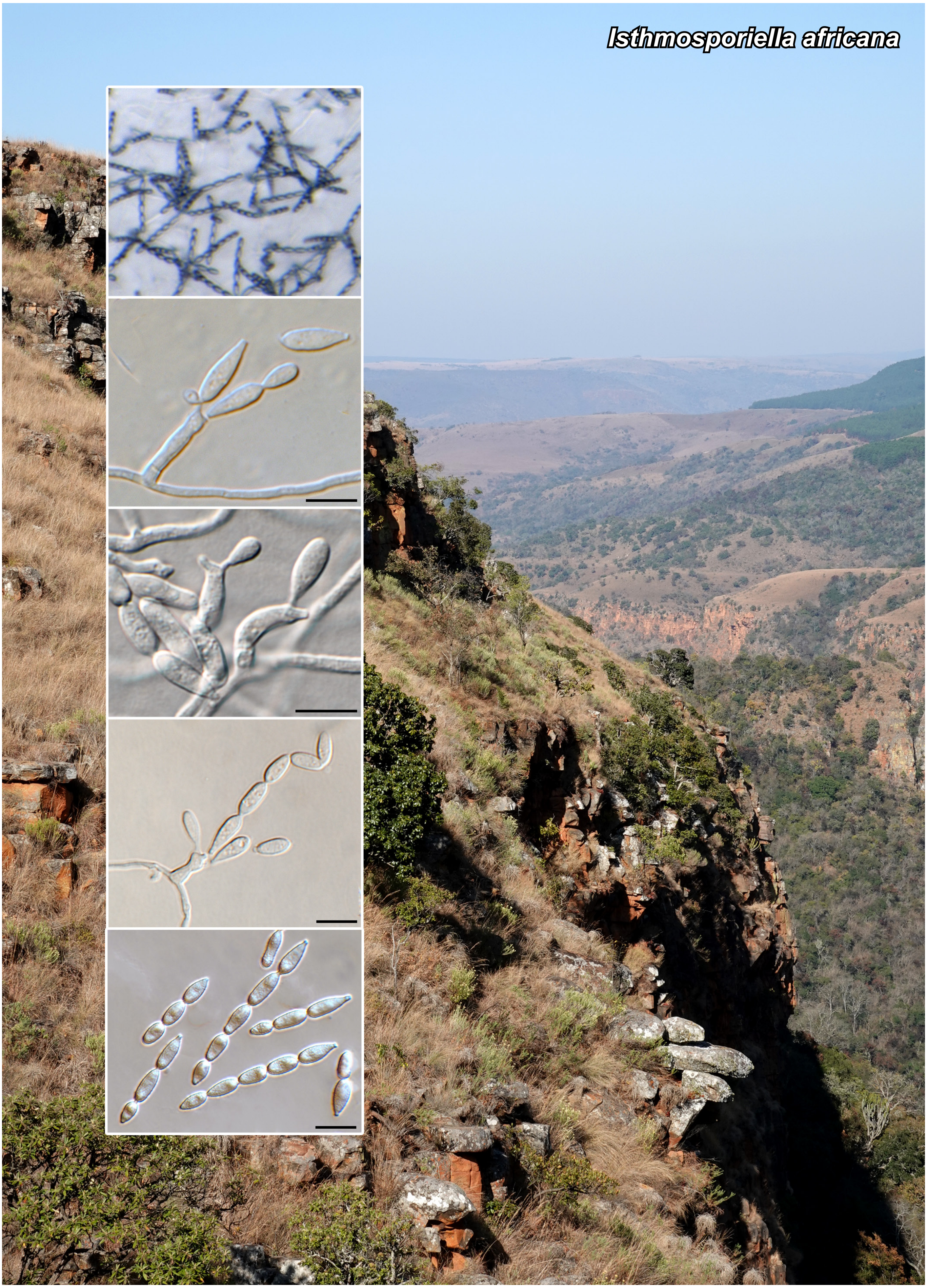
Isthmosporiella africana

Fungal Planet 1605 – 30 December 2023

Isthmosporiella Crous, *gen. nov.*

Etymology. Name refers to its morphological similarity to *Isthmolongispora* and *Isthmomyces*.

Classification — *Hyaloscyphaceae*, *Helotiales*, *Leotiomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate, hyphae. *Conidiophores* reduced to conidiogenous cells on hyphae, erect, solitary, hyaline, smooth, subcylindrical, terminating in a whorl of several, sympodial, polyblastic denticles, subcylindrical, not thickened nor darkened. *Conidia* arranged in unbranched acropetal chains, 4–8, fusoid-ellipsoid to clavate, linked by a narrow isthmus, mostly remaining attached until maturity, when they disarticulate into aseptate cells, hyaline, smooth, guttulate.

Type species. *Isthmosporiella africana* Crous
MycoBank MB 850618

Isthmosporiella africana Crous, *sp. nov.*

Etymology. Name refers to the African continent where it was collected.

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells on hyphae, erect, solitary, hyaline, smooth, subcylindrical, 5–15 × 2–3 µm, terminating in a whorl of several, sympodial, polyblastic denticles, subcylindrical, 1–2 × 1 µm, not thickened nor darkened. *Conidia* arranged in unbranched acropetal chains, 4–8, fusoid-ellipsoid to clavate, linked by a narrow isthmus, mostly remaining attached until maturity, when they disarticulate into aseptate cells, hyaline, smooth, guttulate, 5–15 × 3–4 µm.

Culture characteristics — Colonies erumpent, folded, with moderate aerial mycelium and smooth, lobate margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white, reverse pale luteous.

Typus. SOUTH AFRICA, Mpumalanga Province, Buffelskloof Nature Reserve, on dead twigs of unidentified tree, 5 Aug. 2022, *P.W. Crous*, HPC 3971 (holotype CBS H-25277; culture ex-type CPC 45125 = CBS 150064; ITS, LSU and *rpb2* sequences GenBank OR680771.1, OR717027.1 and OR683728.1; MycoBank MB 850619).

Notes — *Isthmosporiella* is phylogenetically related to *Nagrajchalara* and *Hyaloscypha* (*Monodictys* and *Pseudaegerita* asexual morphs) and *Eupezizella* (Kosonen et al. 2021), but is morphologically distinct, resembling *Isthmolongispora*, based on *Ia. intermedia* (2–3-septate conidia), and *Isthmomyces*, based on *Is. oxysporus* (*Microthyriaceae*). However, *Isthmolongispora* is polyphyletic (Qiao et al. 2021), and the type species is not known from culture or DNA. *Isthmolongispora* is characterised by denticulate, sympodial conidiogenous cells and isthmospore conidia consisting of 2–3-septate conidia, with cells connected by narrow isthmuses. There are no obvious morphological differences between *Isthmolongispora* and *Isthmomyces* other than conidial septation, and the South African collection adds another phylogenetically distinct lineage with a similar morphology, distinguishable only by the fact that the conidial chains disarticulate into single, aseptate conidial propagules.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Nagrajchalara jonesii* (strain NN076451, GenBank ON994073.1; Identities = 426/451 (94 %), three gaps (0 %)), *Hyaloscypha spinulosa* (strain JAC10151, GenBank MK432695.1; Identities = 501/553 (91 %), 17 gaps (3 %)) and *Hyaloscypha spiralis* (strain BHI-F214a, GenBank MF161204.1; Identities = 499/551 (91 %), 12 gaps (1 %)). Closest hits using the **LSU** sequence are *Hyaloscypha monodictys* (voucher TNS-F5013, GenBank JN086756.1; Identities = 794/806 (99 %), one gap (0 %)), *Hyaloscypha spinulosa* (strain CBS 479.67, GenBank MH870748.1; Identities = 822/835 (98 %), one gap (0 %)) and *Hyaloscypha vraolstadiae* (strain UAMH 10111, GenBank NG_068557.1; Identities = 796/809 (98 %), one gap (0 %)). Interestingly, the LSU sequence of *Nagrajchalara jonesii* (strain NN076451, GenBank OP173693.1) is only 94 % similar (781/834, including seven gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Hyaloscypha albohyalina* (voucher TNS F31133, GenBank LC425010.1; Identities = 613/708 (87 %), no gaps), *Hyaloscypha desmidiacea* (strain NBRC 109736, GenBank LC333294.1; Identities = 742/865 (86 %), eight gaps (0 %)) and *Hyaloscypha intacta* (voucher TK7111, GenBank MT228678.1; Identities = 740/863 (86 %), four gaps (0 %)).

Colour illustrations. Buffelskloof Nature Reserve, South Africa. Conidiophores and conidiogenous cells giving rise to conidia on SNA; conidia. Scale bars = 10 µm.

Supplementary material

FP1600 Phylogenetic tree.

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Waltergamsia mpumalangana

Fungal Planet 1606 – 30 December 2023

Waltergamsia mpumalangana Crous, *sp. nov.*

Etymology. Name refers to the province where it was collected, Mpumalanga, South Africa.

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

Mycelium consisting of hyaline, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* solitary, erect, flexuous, subcylindrical with apical taper, hyaline, smooth, reduced to conidiogenous cells, rarely branched at basal septum. *Conidiogenous cells* phialidic, 450–90 × 2–3.5 µm; apex 1.5 µm diam, lacking visible collarette. *Conidia* hyaline, smooth, guttulate, aseptate, fusoid, curved, apex subobtuse, base subtruncate, (7–)8–10(–12) × (2.5–)3(–3.5) µm.

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

Typus. South Africa, Mpumalanga Province, Buffelskloof Nature Reserve, on dead leaves of unidentified tree, 5 Aug. 2022, *P.W. Crous*, HPC 3987 (holotype CBS H-25278; culture ex-type CPC 45131 = CBS 150065; ITS, LSU, *rpb1*, *rpb2* and *tef1* (second part) sequences GenBank OR680772.1, OR717028.1, OR683709.1, OR683729.1 and OR683716.1; MycoBank MB 850620).

Notes — *Waltergamsia mpumalangana* is treated here as a phylogenetic distinct species (see Hou et al. 2023), together with two other taxa, for which a new combination in *Waltergamsia* is introduced for one, and a new synonymy for the other.

Waltergamsia mali (G.Y. Sun & Y.M. Hou) Crous, *comb. nov.* — MycoBank MB 850621

Basionym. Acremonium mali G.Y. Sun & Y.M. Hou, Pl. Dis. 103: 1895. 2019.

A blast2 comparison between the ITS, LSU and *tub2* sequences of the ex-type cultures of *Acremonium mali* (ACCC 39305; GenBank MF987658, NG_088063 & MF987667) and *Waltergamsia pilosa* (CBS 124.70; GenBank OQ429949, OQ430199 & HF680249) revealed a single nucleotide difference on ITS, no differences on LSU and nine differences (561/570 nucleotides similar) on *tub2*.

Waltergamsia zeylanica (Petch) L.W. Hou et al., Stud. Mycol. 105: 145. 2023

Basionym. Cephalosporium zeylanicum Petch, Trans. Brit. Mycol. Soc. 16: 236. 1932. 1931.

New synonym. Acremonium isabellae Y.P. Tan et al., Index of Australian Fungi 15: 5. 2023.

A blast2 comparison between the ITS and LSU sequences of the ex-type culture of *Acremonium isabellae* (BRIP 75819a; GenBank OR527519.1 & OR527527.1) and the representative culture of *Waltergamsia zeylanica* (CBS 746.73; GenBank OQ429951.1 & OQ430201.1) revealed no differences between the two cultures.

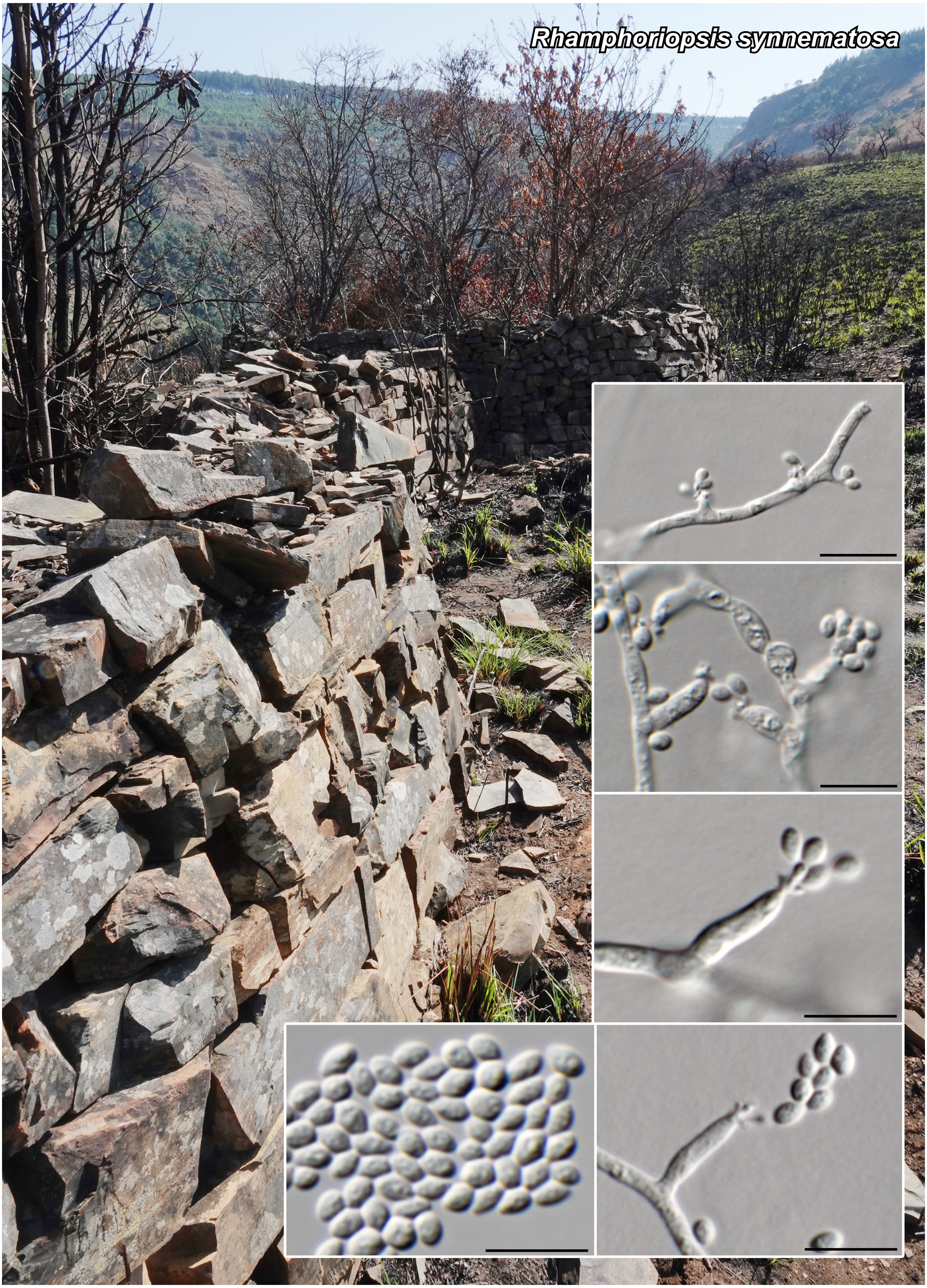
Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Geosmithia pulverea* (strain 18162, GenBank MW222409.1; Identities = 508/592 (86 %), 31 gaps (5 %)), *Geosmithia lavendula* (strain CCF4336, GenBank KF808300.1; Identities = 508/594 (86 %), 33 gaps (5 %)) and *Geosmithia pallida* (strain IHEM 25458, GenBank OW987450.1; Identities = 505/591 (85 %), 31 gaps (5 %)). Closest hits using the **LSU** sequence are *Waltergamsia fusidioides* (as *Acremonium fusidioides*; strain CBS 191.60, GenBank MH869501.1; Identities = 822/846 (97 %), one gap (0 %)), *Acremonium mali* (strain ACCC 39305, GenBank NG_088063.1; Identities = 806/832 (97 %), one gap (0 %)) and *Waltergamsia parva* (as *Acremonium alternatum*; strain CBS 381.70A, GenBank HQ231986.1; Identities = 792/818 (97 %), three gaps (0 %)). No significant hits were obtained when the ***rpb1***, ***rpb2*** and ***tef1*** (second part) sequences were used in blastn and megablast searches.

Colour illustrations. Buffelskloof Nature Reserve, South Africa. Conidiophores and conidiogenous cells giving rise to conidia on SNA; conidia. Scale bars = 10 µm.

Supplementary material

FP1602 Phylogenetic tree.
FP1606 Phylogenetic tree.

P.W. Crous, M.M. Costa, H. Kandemir, L. Zhao & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl, m.costa@wi.knaw.nl, h.kandemir@wi.knaw.nl, l.zhao@wi.knaw.nl & e.groenewald@wi.knaw.nl


Rhamphoriopsis synnematosa

Fungal Planet 1607 – 30 December 2023

Rhamphoriopsis synnematosa Crous, *sp. nov.*

Etymology. Name refers to the characteristic synnematous conidiophores observed in nature.

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

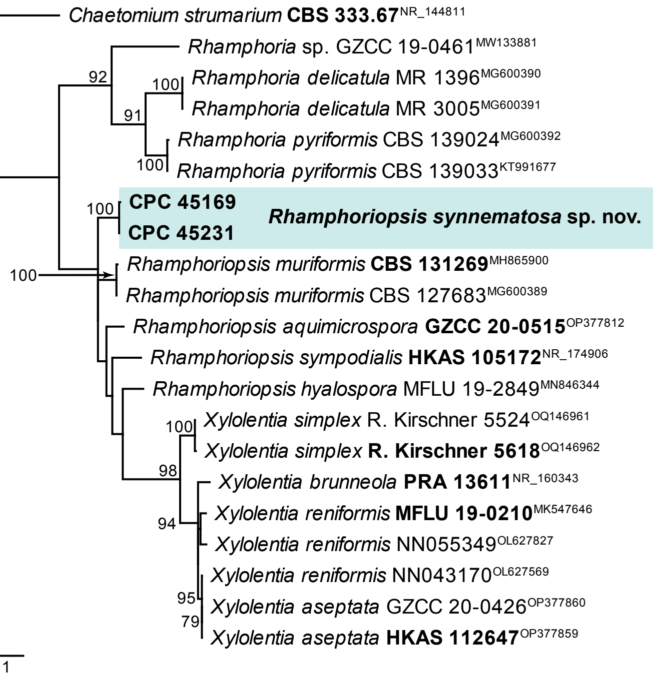
Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* dimorphic; micronematous conidiophores in loose tufts on hyphae, subcylindrical, base pale brown, smooth, multiseptate, 15–60 µm tall; macronematous conidiophores synnematal, consisting of tufts of red-brown, smooth, cylindrical conidiophores, erect, synnemata 10–30 µm diam at base, 70–300 µm tall, with terminal cells giving rise to clusters of conidiogenous cells, subcylindrical, pale brown, smooth, 15–35 × 2–2.5 µm, with several terminal denticles, 1–6 µm tall, 1–1.5 µm diam, with terminal and lateral sympodial, polyblastic loci, somewhat darkened. *Conidia* solitary, dry, ellipsoid, hyaline, smooth, aseptate, 2.5–3 × 1.5–2 µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 6 mm diam after 2 wk at 25 °C. On MEA surface amber with patches of umber, reverse sienna; on PDA surface sienna in middle, outer region pale luteous, reverse grey olivaceous; on OA surface ochreous.

Typus. South Africa, Mpumalanga Province, Buffelskloof Nature Reserve, on dead twig of unidentified tree, 5 Aug. 2022, *P.W. Crous*, HPC 3975 (holotype CBS H-25279; cultures ex-type CPC 45231, CPC 45169 = CBS 150066; ITS, LSU and *rpb2* sequences GenBank OR680773.1 (CPC 45231) & OR680774.1 (CPC 45169), OR717029.1 (CPC 45231) and OR683730.1 (CPC 45231); MycoBank MB 850622).

Notes — *Rhamphoriopsis* was introduced for a lichenicolous perithecial ascomycete with a phaeoisaria-like asexual morph (Réblová & Štěpánek 2018). The genus is presently known from four species, of which two, *R. muriformis* (conidia 3.5–5.5 × 1.5–2 µm; Réblová & Štěpánek 2018) and *R. sympodialis* (conidia 1.9–4 × 1.4–2.2 µm; Hyde et al. 2020) are closely related. *Rhamphoriopsis synnematosa* has smaller conidia in culture, and is phylogenetically distinct from all known species in the genus.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 45169 had highest similarity to *Rhamphoriopsis muriformis* (strain CBS 127683, GenBank MG600389.1; Identities = 461/494 (93 %), six gaps (1 %)), *Rhamphoriopsis sympodialis* (strain HKAS 105172, GenBank NR_174906.1; Identities = 482/521 (93 %), nine gaps (1 %)) and *Rhamphoria buxi* (strain CBS 127683, GenBank MH864677.1; Identities = 511/553 (92 %), 13 gaps (2 %)). The ITS sequences of CPC 45169 and CPC 45231 only differ with four gaps in repeat rich areas. Closest hits using the **LSU** sequence of CPC 45231 are *Rhamphoriopsis muriformis* (strain CBS 131269, GenBank NG_063952.1; Identities = 812/823 (99 %), no gaps), *Rhamphoriopsis sympodialis* (voucher HKAS 105172, GenBank NG_079672.1; Identities = 811/822 (99 %), one gap (0 %)) and *Rhamphoria buxi* (strain CBS 127683, GenBank MH876114.1; Identities = 828/841 (98 %), one gap (0 %)). Closest hits using the ***rpb2*** of CPC 45231 sequence had highest similarity to *Rhamphoriopsis muriformis* (strain CBS 131269, GenBank MG600400.1; Identities = 738/843 (88 %), no gaps), *Linkosia multiseptum* (voucher HKUCC 10825, GenBank DQ435091.1; Identities = 703/844 (83 %), no gaps) and *Raffaelea lauricola* (strain Raff. sp.570, GenBank OM631614.1; Identities = 692/844 (82 %), two gaps (0 %)).



FP1607 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy et al. 2017, Minh et al. 2020) of the *Rhamphoriopsis* and related genera ITS nucleotide alignment. Bootstrap support values (> 74 % are shown) from 1 000 non-parametric bootstrap replicates are shown at the nodes. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Chaetomium strumarium* (CBS 333.67; GenBank NR_144811) and the novelty described here is highlighted with a coloured block and **bold** font. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 21 strains including the outgroup; 579 characters including alignment gaps analysed: 251 distinct patterns, 175 parsimony-informative, 80 singleton sites, 324 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.23447342).

Colour illustrations. Buffelskloof Nature Reserve, South Africa. Conidiophores and conidiogenous cells giving rise to conidia on SNA; conidia. Scale bars = 10 µm.

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Neoeriomycopsis fissistigmae

Fungal Planet 1608 – 30 December 2023

Neoeriomycopsidaceae Crous, *fam. nov.*

Etymology. Name refers to the genus *Neoeriomycopsis*.

Classification — *Neoeriomycopsidaceae*, *Pararamichloridiales*, *Sordariomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate, hyphae. *Conidiophores* solitary or forming sporodochia, with slimy conidial masses; subcylindrical, erect, flexuous, branched, septate. *Conidiogenous cells* terminal and intercalary, subcylindrical, hyaline, smooth, polyblastic, with several sympodial denticles, not thickened nor darkened. *Conidia* hyaline, septate, thin-walled, smooth, fusoid, slightly curved, tapering toward the apex with unbranched appendage.

Type species. *Neoeriomycopsis aristata* (B. Sutton & Hodges) Crous & M.J. Wingf.
MycoBank MB 850623

Neoeriomycopsis fissistigmae Crous, *sp. nov.*

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

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* solitary on aerial mycelium or forming sporodochia on SNA, with slimy conidial masses; subcylindrical, erect, flexuous, branched, septate, up to 100 µm tall, 3–4 µm diam. *Conidiogenous cells* terminal and intercalary, subcylindrical, hyaline, smooth, 10–50 × 3–4 µm, polyblastic, with several sympodial denticles, 1–2 × 1 µm, not thickened nor darkened. *Conidia* (20–)23–26(–35) × (2.5–)3 µm (excluding appendage), hyaline, 1–3-septate, thin-walled, smooth, fusoid, slightly curved, tapering toward the apex with unbranched appendage, (4–)5–6(–8) µm long; conidia undergoing microcyclic conidiation in culture; hila unthickened, 1 µm diam.

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

Typus. Malaysia, growing on other fungi (mycophylic?) on leaf spots on flower *of Fissistigma* sp. (*Annonaceae*), July 2022, *M.J. Wingfield*, HPC 4020 (holotype CBS H-25282; culture ex-type CPC 45225 = CBS 150069; ITS and LSU sequences GenBank OR680775.1 and OR717030.1; MycoBank MB 850624).

Neoeriomycopsis acutispora (Matsush.) Crous, *comb. nov*. — MycoBank MB 850625

Basionym. *Phaeodactylium acutisporum* Matsush., Matsush. Mycol. Mem. 7: 59. 1993.
Synonym. *Guarroa acutispora* (Matsush.) Heredia & R. F. Castañeda, Mycol. Progr. 19: 23. 2020.

Colour illustrations. *Fissistigma* flower, Malaysia. Conidiophores and conidiogenous cells giving rise to conidia on SNA. Scale bars = 10 µm.

Notes — *Phaeobotrys* M. Calduch, Gené & Guarro, based on *P. acutisporus*, was established as a monotypic genus by Calduch et al. (2002) for a saprobic fungus occurring on plant debris in Nigeria and Peru. Because the name was already occupied (*Phaeobotrys* H. Ettl 1966; *Algae*), a new name, *Guarroa*, was introduced by Heredia et al. (2020). *Guarroa* is characterised by having flexuous, brown, septate conidiophores, denticulate conidiogenous cells, and 0–3-septate fusoid, hyaline conidia with an apical appendage.

Neoeriomycopsis, based on *N. aristata*, was introduced for a fungus occurring on *Eucalyptus* leaves in South America. The genus was characterised by forming sporodochia in culture, loose conidiophores on host tissue, and having hyaline structures. Phylogenetically however, the present collection, and *N. aristata*, cluster with *Guarroa acutispora*, suggesting that *Guarroa* (2020) and *Neoeriomycopsis* (2015) are congeneric. The distinguishing features of conidiophore pigmentation and sporodiochial formation are therefore not informative at generic level.

Morphologically *N. fissistigmae* resembles *N. aristata*, although the latter has conidia with a shorter median range, (10–)17–26(–32) × (2.5–)3(–3.5) µm, and shorter conidiogenous cells, 5–15 × 2–3 µm (Crous et al. 2015). *Neoeriomycopsis acutispora* on the other hand, has much shorter conidia, 5–11 × 1.5–2.5 µm (Calduch et al. 2002).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neoeriomycopsis aristata* (strain CBS 139913, GenBank NR_154231.1; Identities = 474/549 (86 %), 27 gaps (4 %)) and *Guarroa acutispora* (strain CBS 101302, GenBank MH862730.1; Identities = 463/542 (85 %), 23 gaps (4 %)). Closest hits using the **LSU** sequence are *Neoeriomycopsis aristata* (strain CBS 139913, GenBank NG_058170.1; Identities = 777/790 (98 %), no gaps), *Guarroa acutispora* (strain CBS 101302, GenBank MH874337.1; Identities = 771/815 (95 %), no gaps) and *Pararamichloridium verrucosum* (strain CBS 128.86, GenBank MH873621.1; Identities = 769/821 (94 %), three gaps (0 %)).

Supplementary material

FP1602 Phylogenetic tree.

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Neocelosporium aereum

Fungal Planet 1609 – 30 December 2023

Neocelosporium aereum Crous & Jurjević, *sp. nov.*

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

Classification — *Neocelosporiaceae*, *Neocelosporiales*, *Dothideomycetes*.

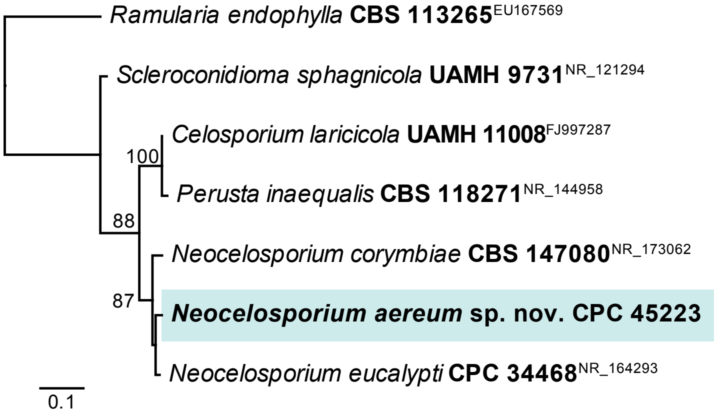
Mycelium consisting of branched, septate, thick-walled, dark brown, verruculose, 5–7 µm diam hyphae, becoming constricted at septa, encased in mucoid sheath. *Conidiophores* reduced to conidiogenous cells, intercalary on hyphae; loci phialidica, inconspicuous, 2 µm diam. *Conidia* solitary, initially hyaline, smooth, fusoid-ellipsoid, aseptate, 6–8 × 3–4 µm, becoming medium brown, 0–2-septate, subcylindrical, verruculosa, enclosed in mucoid sheath, 9–16 × 4–6 µm.

Culture characteristics — Colonies erumpent, folded, with sparse aerial mycelium and smooth, lobate margin, reaching 6 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse leaden black.

Typus. USA, New Jersey, Sparta, air from house attic, 30 Sept. 2022, *Z. Jurjević*, 5757 (holotype CBS H-25283; culture ex-type CPC 45223 = CBS 150070; ITS sequence GenBank OR680776.1; MycoBank MB 850626).

Notes — *Neocelosporium*, based on *N. eucalypti*, is characterised by having hyaline conidia that primarily arise on the surface of pigmented hyphae. The genus presently contains two species, *N. eucalypti* (conidia 5–12 × 3–5 µm; Crous et al. 2018a) and *N. corymbiae* (conidia (8–)10–11(–13) × (3.5–)4(–5) µm; Crous et al. 2021a) to which *N. aereum* is closely related, but morphologically and phylogenetically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neocelosporium eucalypti* (strain CBS 145086, GenBank NR_164293.1; Identities = 559/576 (97 %), four gaps (0 %)), *Neocelosporium corymbiae* (strain CBS 147080, GenBank NR_173062.1; Identities = 549/573 (96 %), four gaps (0 %)) and *Celosporium laricicola* (strain 19E084, GenBank ON430568.1; Identities = 477/514 (93 %), five gaps (0 %)).



Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy et al. 2017, Minh et al. 2020) of the *Neocelosporium* and related genera ITS nucleotide alignment. Bootstrap support values (> 74 % are shown) from 1000 non-parametric bootstrap replicates are shown at the nodes. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Ramularia endophylla* (CBS 113265; GenBank EU167569) and the novelty described here is highlighted with a coloured block and **bold** font. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: seven strains including the outgroup; 535 characters including alignment gaps analysed: 115 distinct patterns, 49 parsimony-informative, 93 singleton sites, 393 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+I. 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.23447342).

Colour illustrations. House attic in New Jersey, USA. Colony on synthetic nutrient-poor medium; hyphae and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

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Querciphoma foliicola

Fungal Planet 1610 – 30 December 2023

Querciphoma foliicola Crous, *sp. nov.*

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

Classification — *Leptosphaeriaceae*, *Pleosporineae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*.

Conidiomata pycnidial, sporulating on aerial mycelium on MEA (sterile on other media); pycnidia separate, brown, globose, 150–250 µm diam, with 1–2 papillate necks, and central ostioles; necks dark brown, up to 40 µm tall, 25–35 µm diam; wall 4–6 µm diam, of 3–4 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining inner cavity, hyaline, smooth, doliiform to ampulliform, phialidic, 3–4 × 3–3.5 µm. *Conidia* solitary, hyaline, smooth, aseptate, ellipsoid to subcylindrical with obtuse ends, 3–5 × 2 µm.

Culture characteristics — Colonies spreading, with moderate to abundant aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white with patches of pale olivaceous grey and luteous; in reverse luteous with patches of olivaceous grey.

Typus. South Africa, Mpumalanga Province, Buffelskloof Nature Reserve, on leaf litter, Aug. 2022, *P.W. Crous*, HPC 4015 (holotype CBS H-25172; culture ex-type CPC 45029 = CBS 150071; ITS and LSU sequences GenBank OR680777.1 and OR717031.1; MycoBank MB 850627).

Notes — *Querciphoma*, based on *Q. minuta*, was introduced for a phoma-like genus with eustromatic, uni- to multi-locular conidiomata and conidia that become brown and verruculose with age (Crous & Groenewald 2017). The genus has since been linked to a sexual morph (Gao et al. 2022), while the type species, *Q. minuta*, was shown to be a canker pathogen of *Platanus* in Germany (Boldt-Burisch & Douanla-Meli 2023). *Querciphoma foliicola* is phylogenetically closely related to *Q. minuta* (conidia (3.5–)4–5(–6) × 3(–3.5) µm; Crous & Groenewald 2017), but has smaller conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Querciphoma carteri* (strain CBS 105.91, GenBank KF251209.1; Identities = 539/565 (95 %), 13 gaps (2 %)), *Ochrocladosporium frigidarii* (strain CBS 103.81, GenBank MH861307.1; Identities = 463/482 (96 %), six gaps (1 %)) and *Ochrocladosporium elatum* (strain CBS 146.33, GenBank EU040233.1; Identities = 463/482 (96 %), six gaps (1 %)). Closest hits using the **LSU** sequence are *Paraleptosphaeria dryadis* (strain CBS 643.86, GenBank MH873696.1; Identities = 769/776 (99 %), two gaps (0 %)), *Sclerenchymomyces clematidis* (strain MFLUCC 17-2180, GenBank MT214558.1; Identities = 768/775 (99 %), no gaps) and *Querciphoma carteri* (strain CBS 105.91, GenBank GQ387594.1; Identities = 767/774 (99 %), no gaps).

Colour illustrations. Buffelskloof Nature Reserve, South Africa. Papillate pycnidium; ostiolar region; conidiogenous cells; conidia. Scale bars: pycnidia = 125 µm, all others = 10 µm.

Supplementary material

FP1610 Phylogenetic tree.

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Extremus caricis

Fungal Planet 1611 – 30 December 2023

Extremus caricis Crous, *sp. nov.*

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

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

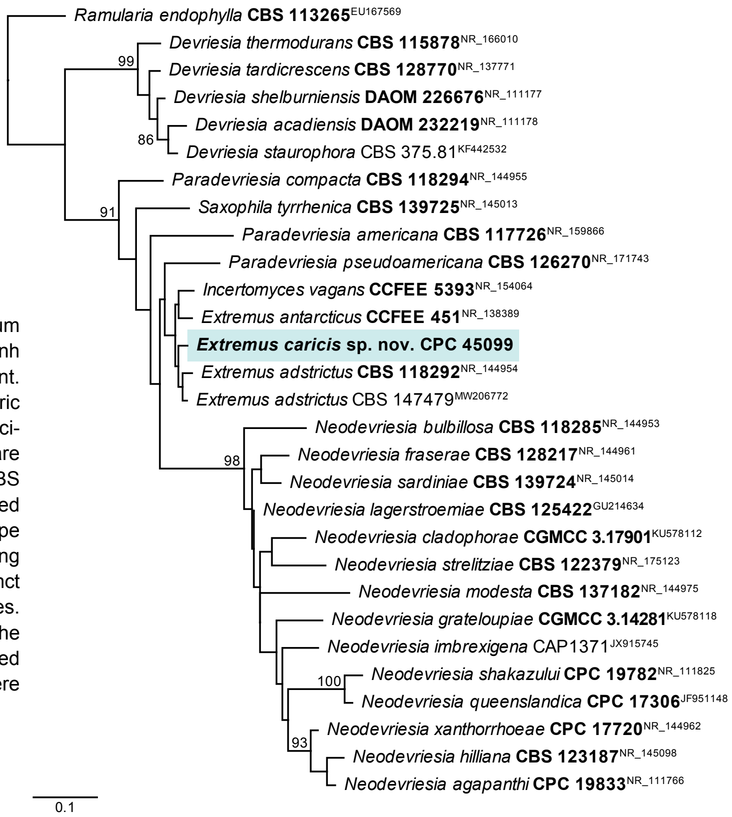
Ascomata separate, immersed in leaf tissue, becoming erumpent, globose, brown, 70–150 µm diam with central ostiole, 10–15 µm diam, lined with hyaline periphyses; wall of 3–4 layers of brown *textura angularis. Asci* stipitate, arranged in a rosette, subcylindrical to obovoid, bitunicate, 8-spored with visible apical chamber, 1.5–2 µm diam, 35–50 × 8–10 µm. *Ascospores* multiseriate, fusoid-ellipsoid, straight, medianly 1-septate, widest in middle of apical cell; each cell with two large, prominent guttules, hyaline, smooth, not constricted at septum, (11–)12–14(–17) × 3(–3.5) µm; ascospores germinating irregularly, spores becoming constricted as median septum, and verruculose, 6–7 µm diam.

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

Typus. Netherlands, Utrecht Province, Bilthoven station, on dead leaves of *Carex* sp. (*Cyperaceae*) (tip blight symptoms), 17 Sept. 2022, *P.W. Crous*, HPC 4031 (holotype CBS H-25286; culture ex-type CPC 45099 = CBS 150073; ITS, LSU, *rpb2* and *tub2* sequences GenBank OR680778.1, OR717032.1, OR683731.1 and OR683719.1; MycoBank MB 850628).

Notes — *Extremus* is known from two species (Egidi et al. 2014, Quaedvlieg et al. 2014), which are characterised by brown, subcylindrical to ellipsoid conidiogenous cells, catenate, subcylindrical to ellipsoid conidia with hyaline to slightly darkened hila. Both species are rock-inhabiting fungi. *Extremus caricis* is the first species of the genus reported from a plant host, and exhibiting a sexual morph.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Extremus adstrictus* (strain CBS 118292, GenBank NR_144954.1; Identities = 452/463 (98 %), one gap (0 %)), *Extremus antarcticus* (strain CCFEE 451, GenBank NR_138389.1; Identities = 446/460 (97 %), one gap (0 %)) and *Incertomyces vagans* (strain CCFEE 5393, GenBank NR_154064.1; Identities = 449/466 (96 %), two gaps (0 %)). Closest hits using the **LSU** sequence are *Extremus adstrictus* (strain TRN96, GenBank KF310022.1; Identities = 755/764 (99 %), no gaps), *Extremus antarcticus* (strain CCFEE 5312, GenBank KF310020.1; Identities = 782/792 (99 %), no gaps) and *Paradevriesia pseudoamericana* (strain CBS 126270, GenBank NG_064229.1; Identities = 796/816 (98 %), two gaps (0 %)). No significant hits were obtained when the ***rpb2*** sequence was used in blastn and megablast searches. Closest hits using the ***tub2*** sequence had highest similarity to *Extremus adstrictus* (strain TRN96, GenBank KF546783.1; Identities = 247/290 (85 %), seven gaps (2 %)) and *Rachicladosporium alpinum* (strain CCFEE 5395, GenBank KF546736.1; Identities = 296/350 (85 %), 17 gaps (4 %)).



Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy et al. 2017, Minh et al. 2020) of the *Extremus* and allied genera ITS nucleotide alignment. Bootstrap support values (> 74 % are shown) from 1 000 non-parametric bootstrap replicates are shown at the nodes. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Ramularia endophylla* (CBS 113265; GenBank EU167569) and the novelty described here is highlighted with a coloured block and **bold** font. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 29 strains including the outgroup; 555 characters including alignment gaps analysed: 292 distinct patterns, 168 parsimony-informative, 72 singleton sites, 315 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.23447342).

Colour illustrations. *Carex* sp. at Bilthoven train station, the Netherlands. Ascomata on leaf tissue; broken ascoma; asci and ascospores; germinating ascospores. Scale bars: ascomata = 150 µm, 75 µm, and all others = 10 µm.

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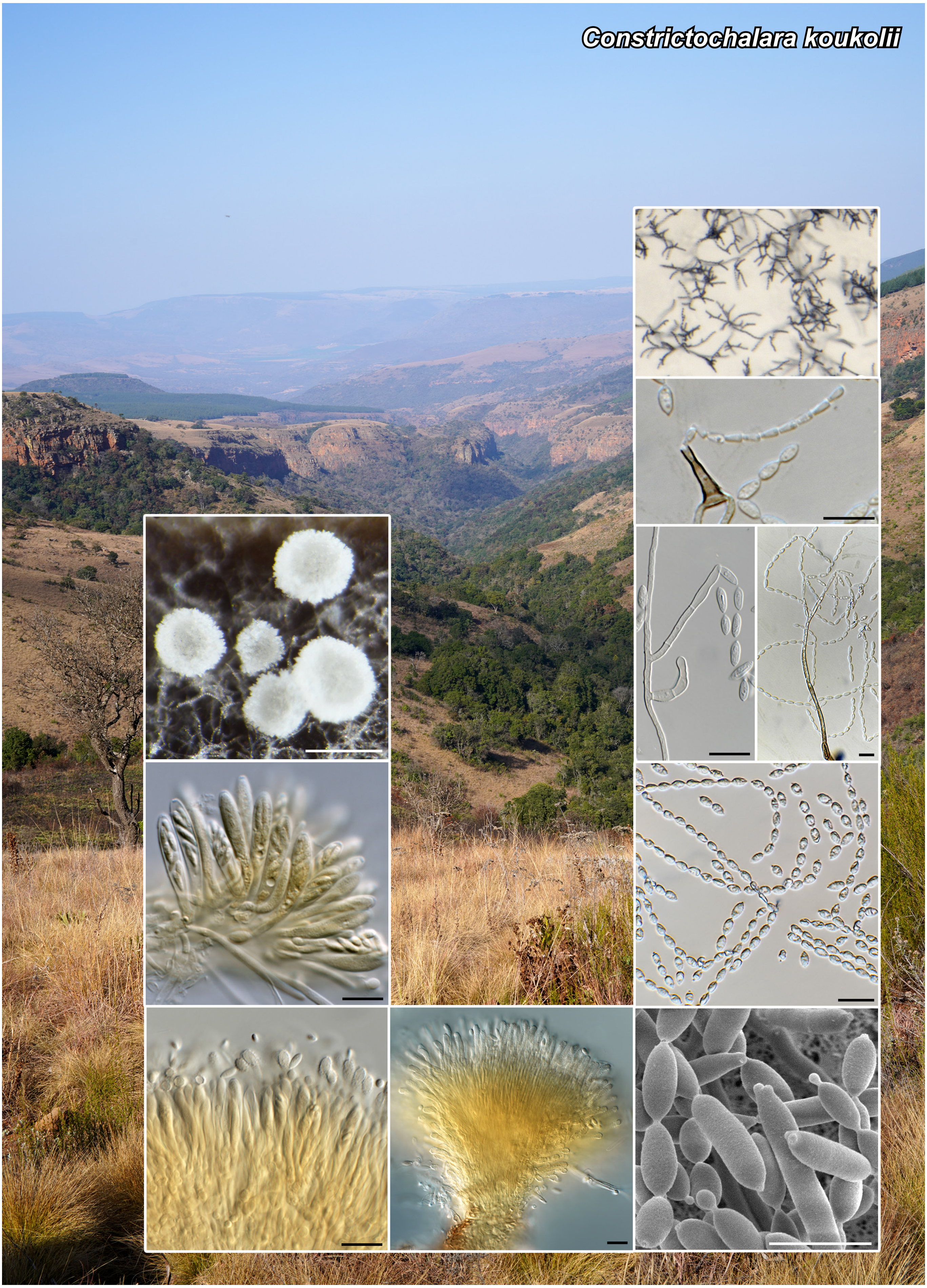
Constrictochalara koukolii

Fungal Planet 1612 – 30 December 2023

Constrictochalara koukolii Crous, *sp. nov.*

Etymology. Named in honour of Ondřej Koukol, Department of Botany, Faculty of Science, Czech Republic, in recognition for his contribution to the taxonomy of *Chalara* and allied genera.

Classification — *Hamatocanthoscyphaceae*, *Helotiales*, *Leotiomycetes*.

Ascomata apothecia, sessile, gregarious, cup-shaped, white, covered in white hairs; apothecial disc 100–250 µm diam, base 50–60 µm diam, apothecia 150–170 µm tall; hairs subcylindrical, slightly clavate, apex verruculose, 2.5–3 µm diam. *Paraphyses* intermingled among asci, hyaline, smooth, sparsely septate, 1.5–2 µm diam. *Asci* cylindrical, unitunicate, base truncate, apex bluntly rounded, apical mechanism with weak reaction in Melzer's reagent, 25–30 × 4–5 µm. *Ascospores* multiseriate, hyaline, smooth, aseptate, fusoid-ellipsoid, 4–5 × 1.5–2 µm. *Asexual morph* dimorphic. Ramularia-like morph: *Conidiophores* erect, subcylindrical on SNA, hyaline, smooth, septate, on MEA becoming brown and verruculous, up to 120 µm tall, 2.5–3 µm diam. *Conidiogenous cells* integrated, terminal, subcylindrical, hyaline, smooth, 15–25 × 2–2.5 µm; scars slightly darkened and thickened, 1 µm diam. *Conidia* in branched chains, hyaline, smooth, guttulate, aseptate; primary ramoconidia subcylindrical, 12–22 × 2–2.5 µm; secondary ramoconidia fusoid-ellipsoid, 10–15 × 2.5–3 µm; intercalary and terminal conidia fusoid-ellipsoid, 5–6(–7) × 2.5–3 µm; hila slightly darkened and thickened, 0.5–1 µm diam. *Infundichalara* morph (sparsely formed): *Conidiophores* 0–2-septate, subcylindrical, erect, up to 40 µm tall, commonly reduced to conidiogenous cells, brown, smooth, phialidic, 10–15 × 2.5–3.5 µm, with cylindrical venter, slightly flared, 3–4 µm long, 2 µm diam. *Conidia* occurring in unbranched chains, hyaline, smooth, guttulate, wedge-shaped, 3–4 × 1.5 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse ochreous; on PDA surface dirty white, reverse olivaceous grey; on OA surface dirty white.

Typus. South Africa, Mpumalanga Province, Buffelskloof Nature Reserve, on living leaves of *Itea rhamnoides* (*Escalloniaceae*) colonised by a *Meliola* sp., 5 Aug. 2022, *P.W. Crous*, HPC 3977 (holotype CBS H-25298; culture ex-type CPC 45057 = CBS 150640; ITS, LSU, *rpb2* and *tub2* sequences GenBank OR680779.1, OR717033.1, OR683732.1 and OR683720.1; MycoBank MB 850629).

Colour illustrations. Buffelskloof Nature Reserve, South Africa. Left column: apothecia, asci with paraphyses and ascospores; right column: colony sporulating on SNA; conidiogenous cell giving rise to infundichalara-like morph; conidial chains and conidia of ramularia-like morph; scanning electron microscope photo of ramularia-like morph. Scale bars: apothecia = 250 µm, all others = 10 µm.

Notes — The genus *Chalara* was recently treated by Wu & Diao (2023), and segregated into several genera based on DNA phylogeny and morphology. *Constrictochalara koukolii* resembles the genus *Infundichalara*. *Infundichalara* is based on *Chalara microchona* (conidia wedge-shaped with truncate base, 3.5–5 × 1.3–2.5 µm; Gams & Holubová-Jechová 1976), which Réblová et al. (2011) regarded as atypical of *Chalara* based on its funnel-shaped collarette and shallow-seated conidiogenous locus, for which they then introduced *Infundichalara*. At the time of description, no sexual or synasexual morph was known. Koukol (2012) introduced a second species, *I. minuta* (conidia wedge-shaped, 3–4(–5) × 2–3 µm) which in culture predominantly formed a ramularia-like synasexual morph (conidia subcylindrical, (5–)7–9.5(–11.5) × 1.5–2.5 µm), similar to that observed in the South African collection, where the ramularia-like morph was also dominant. *Constrictochalara koukolii* is, however, morphologically different, and phylogenetically distinct, and also has a cistella-like sexual morph which forms in culture. The genus *Discocistella* (based on *D. fugiens*) could represent an older, competing name for *Constrictochalara*, but cultures and additional loci will be required to resolve this issue, as the LSU gene is not informative in this clade.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cistella acuum* (strain CBS 302.58, GenBank MH857792.1; Identities = 721/806 (89 %), 16 gaps (1 %)), *Chalara holubovae* (strain Cha6, GenBank ON921297.1; Identities = 497/504 (99 %), three gaps (0 %)) and *Infundichalara microchona* (strain C33, GenBank KF156300.1; Identities = 494/509 (97 %), four gaps (0 %)). Closest hits using the **LSU** sequence are *Constrictochalara clavatospora* (as *Chalara constricta*; strain CBS 248.76, GenBank FJ176256.1; Identities = 784/787 (99 %), no gaps), *Leptodontidium beauverioides* (strain CBS 672.76, GenBank MH872794.1; Identities = 788/792 (99 %), no gaps) and *Tricladium caudatum* (strain CCM F-13498, GenBank GQ477318.1; Identities = 788/792 (99 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Hamatocanthoscypha laricionis* (voucher TNS-F24336, GenBank JN086905.1; Identities = 614/756 (81 %), two gaps (0 %)), *Infundichalara microchona* (strain CBS 175.74, GenBank KR859318.1; Identities = 681/857 (79 %), 11 gaps (1 %)) and *Pezicula eucalyptigena* (strain RBG7255, GenBank OP066957.1; Identities = 674/864 (78 %), 23 gaps (2 %)). No significant hits were obtained when the ***tub2*** sequence was used in blastn and megablast searches.

Supplementary material

FP1600 Phylogenetic tree.

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Paramycosphaerella proteae

Fungal Planet 1613 – 30 December 2023

Paramycosphaerella proteae Crous, *sp. nov.*

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

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

Conidiomata solitary, erumpent, globose, pycnidial, 200–300 µm diam, exuding a crystalline conidial cirrhus; wall of 3–6 layers of brown *textura angularis. Conidiophores* reduced to *conidiogenous cells* lining the inner cavity, ampulliform to doliiform, medium brown, verruculous, proliferating percurrently, 5–7 × 3–7 µm. *Conidia* solitary, subcylindrical to fusoid-ellipsoid, aseptate, hyaline, smooth, guttulate, thick-walled, straight, apex subobtuse, base truncate with minute marginal frill, (6–)7–8(–10) × 2.5–3 µm.

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

Typus. South Africa, Mpumalanga Province, Buffelskloof Nature Reserve, on living leaves of *Protea caffra* (*Proteaceae*) exhibiting leaf spots, 5 Aug. 2022, *P.W. Crous*, HPC 3967 (holotype CBS H-25290; culture ex-type CPC 45121 = CBS 150085; ITS, LSU, *actA*, *cmdA*, *rpb2* and *tef1* (first part) sequences GenBank OR680780.1, OR717034.1, OR683706.1, OR683707.1, OR683733.1 and OR683712.1; MycoBank MB 850630).

Notes — *Paramycosphaerella* is based on *P. brachystegia*, which occurs on *Brachystegia* sp. (*Fabaceae*) from Zimbabwe (Crous et al. 2013). Most species form mycosphaerella-like sexual morphs, although some form zasmidium- or pseudocercospora-like asexual morphs (Videira et al. 2017). *Paramycosphaerella proteae* is peculiar in the sense that it forms a phoma-like morph in culture, similar to *P. pterocarpi* and *P. watsoniae*, suggesting that the genus could be heterogeneous.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Paramycosphaerella pterocarpi* (strain CBS 147071, GenBank NR_173059.1; Identities = 502/522 (96 %), three gaps (0 %)), *Paramycosphaerella watsoniae* (strain CPC 37392, GenBank NR_166341.1; Identities = 507/529 (96 %), four gaps (0 %)) and *Paramycosphaerella sticheri* (strain COAD 1422, GenBank NR_155660.1; Identities = 481/518 (93 %), one gap (0 %)). Closest hits using the **LSU** sequence are *Paramycosphaerella pterocarpi* (strain CBS 147071, GenBank MZ064506.1; Identities = 851/855 (99 %), no gaps), *Paramycosphaerella brachystegiae* (strain CBS 136436, GenBank NG_058048.1; Identities = 849/855 (99 %), no gaps) and *Paramycosphaerella watsoniae* (strain CPC 37392, GenBank NG_068339.1; Identities = 839/845 (99 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Paramycosphaerella watsoniae* (strain CBS 146064, GenBank MN556790.1; Identities = 560/599 (93 %), 10 gaps (1 %)), *Paramycosphaerella pterocarpi* (strain CPC 39035, GenBank MZ078154.1; Identities = 541/581 (93 %), seven gaps (1 %)) and *Paramycosphaerella marksii* (strain CBS 110750, GenBank KF903404.1; Identities = 498/543 (92 %), four gaps (0 %)). Closest hits using the ***cmdA*** sequence had highest similarity to *Paramycosphaerella intermedia* (strain CBS 114356, GenBank KF902579.1; Identities = 258/283 (91 %), no gaps), *Paramycosphaerella marksii* (strain CBS 110963, GenBank KF902583.1; Identities = 257/283 (91 %), no gaps) and *Paramycosphaerella intermedia* (strain CBS 114415, GenBank KF902580.1; Identities = 257/283 (91 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Paramycosphaerella watsoniae* (strain CBS 146064, GenBank MN556814.1; Identities = 720/793 (91 %), no gaps) and *Paramycosphaerella pterocarpi* (strain CPC 39035, GenBank MZ078208.1; Identities = 773/862 (90 %), no gaps). No significant hits were obtained when the ***tef1*** (first part) sequence was used in blastn and megablast searches.

Colour illustrations. *Protea caffra* at Buffelskloof Nature Reserve, South Africa. Symptomatic leaves; colony sporulating on malt extract agar; conidiogenous cells; conidia. Scale bars = 10 µm.

Supplementary material

FP1613 Phylogenetic tree.

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