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Fungal Planet description sheets: 1868–1920

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Abstract: Novel species of fungi described in this study include those from various countries as follows: **Australia**, *Marasmius ballator* on leaf litter in subtropical rainforest, *Marasmius carbinensis* on litter and twigs of *Hyptis suaveolens*, *Marasmius clocca* on leaf litter of regenerating subtropical rainforest. **Bolivia**, *Aggregatorygma saraanense* on trunk of *Trichilia inaequilatera*. **Brazil**, *Arthropolymorpha endophytica* (incl. *Arthropolymorpha gen. nov.),* from healthy roots of *Coffea arabica*, *Didymella digitariae* on *Digitaria insularis*, *Geastrum baseiae* on soil, *Magnibotryascoma souzamottae* as endophyte from cladodes of *Tacinga inamoena*, *Neoleptosporella agapanthi* from stalks of *Agapanthus praecox*, *Penicillifer endoradicis* as endophyte from roots of *Musa acuminata*, *Sirastachys cavernicola* from leaf litter, *Toxicocladosporium atratum* as root endophyte of *Cattleya locatellii*. **China**, *Fasciatispora citri* on dead twig of *Citrus maxima*. **Denmark**, *Inocybe leucantheana* on wet ground with *Alnus*, *Betula* and *Picea*. **Ecuador (Galapagos Islands)**, *Fusarium cristobalense* on *Scalesia gordilloi*, *Fusarium scalesiae* on *Scalesia pedunculata*. **Finland**, *Inocybe ranaria* on mull soil, near *Betula pendula* and *Abies* sp. **France**, *Bullatosporium pinophilum* on the bark of *Pinus nigra* subsp. *nigra*, *Dialonectria eutypellicola* on *Eutypella prunastri*, on branches of *Prunus spinosa, Mycobernardia involucriformis* on dead *Bambusa* sp., *Pseudocosmospora perforaticola* on dead stromata of *Hypoxylon perforatum* on *Fraxinus*, *Stylonectria colleeniae* on *Trimmatostroma scutellare,* with *Lophium mytillinum*, on dead branch of *Larix decidua*. **French Guiana**, *Neocosmospora duolechatii* on dead bark of *Bauhinia* sp. **Germany**, *Inocybe giovannii* on soil under *Abies alba*, *Fagus sylvatica* and *Picea abies*, *Triseptosporium fallopiae* (incl. *Triseptosporium gen. nov.*) on *Fallopia japonica*. **India**, *Phylloporia bharatavarsa* on living tree of *Phyllanthus emblica*. **Iran**, *Fusarium phoenicis* on roots of *Phoenix dactylifera*. **Italy**, *Inosperma confusum* on soil under *Quercus ilex* and *Pinus halepensis*, *Inosperma subinodorum* on calcareous soil in *Picea abies* forest. **Madagascar**, *Oudemansiella viscida* on dead wood or branches. **Netherlands**, *Colletotrichum urticicola* from leaf spots on *Urtica dioica.* **Pakistan**, *Agrocybe punjabensis* on soil on fallen remains of *Saccharum officinarum*. **Panama**, *Ijuhya panamaensis* and *Sarcopodium panamaense* on twig litter of angiosperm. **Poland**, *Cytospora tatrensis* from dead stems of *Pinus mugo*, *Myxotrichum flavum* on resin of *Picea abies*, *Symphoricola tarnoviensis* (incl. *Symphoricola gen. nov.*) from sooty mould community on *Symphoricarpos albus*. **Portugal**, *Hypoxylon azoricum* on fallen branch of *Laurus azorica*, *Tuber honstrassii* in clayey and calcareous soil under *Quercus rotundifolia* and *Arbutus unedo.* **South Africa**, *Paraphaeosphaeria*

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Abstract: *andropogonicola* on leaves of *Andropogon eucomus*, *Talaromyces armstrongii* from soil. **Spain**, *Geoglossum martinae* on soil under *Quercus ilex* and *Cistus ladanifer*, *Inocybe percastanea* on sandy, acidic soils under *Cistus ladanifer* and *Pinus pinaster*, *Lamproderma stephensonii* on twigs of *Pinus sylvestris*, *Ramariopsis alboviolacea* on soil under *Prunus lusitanica* subsp. *lusitanica*, *Russula olivaceopinetorum* on acidic sandy soil among *Pinus sylvestris* needles, *Scolecobasidium endophyticum* from root-associated soil collected in a grassland, *Tuber danielis* in acidic soil beneath *Cistus ladanifer*, *Quercus ilex*, and *Genista scorpius*. **Sweden**, *Inocybe adusticans* on soil, in snow bed area with *Salix herbacea* and *Bistorta vivipara*, *Inosperma friesii* on soil in mixed deciduous forest. **Switzerland**, *Stylonectria stoeckliana* on *Cytospora* sp. on twigs of *Salix* sp. **Thailand**, *Neoleptosporella camporesiana* on dead branch of unidentified plant. **Uganda**, *Bjerkandera ugandensis* on a rotting log. **UK (Scotland)**, *Narcissea scotica* on decaying dung of *Lagopus scotica*. Morphological and culture characteristics are supported by DNA barcodes.

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Declaration on conflict of interest The authors include members of the Editorial Board of Persoonia. They were not involved in the journal's review of, or decisions related to, this manuscript.


Aggregatorygma saraanense

Fungal Planet 1868 MB 860662

Aggregatorygma saraanense Darmostuk, Plata, Rodr. Flakus & Flakus, ***sp. nov.***

Etymology: The epithet is derived from the collection site, located in the vicinity of the Sara Ana Agroecological Experimental Station, Bolivia.

Classification: *Diploschistaceae*, *Ostropales*, *Lecanoromycetes*.

Thallus epiperidermal, crustose, continuous, cracked, not corticate, dull, greenish to slightly pale bluish green, up to 5–7 cm diam., 70–100 µm thick, not surrounded by a prothallus. *Photobiont* trentepohlioid, cells globose, 8–10 µm diam. *Isidia* pale bluish green to sometimes greenish, pruinose, not corticate, round to ovoid, disc-shaped, flat, connected with the thallus by hyphae at the central part, sometimes irregularly attached by margin when younger, easily breaking from the thallus, 300–320 µm diam. and 70–100 µm thick. *Thallus* and *isidia* UV–, K–, P–. *Ascomata* and *pycnidia* not observed.

Habit, habitat and distribution: *Aggregatorygma saraanense* is known only from its type locality in sub-Andean seasonal evergreen forests of the southwestern Amazon, where it was found growing corticolous on the trunk of *Trichilia inaequilatera*.

Typus: **Bolivia**, La Paz department, Alto Beni province, near the Sara Ana Agroecological Experimental Station, 15.46081°S, 67.47788°W, 440 m.a.s.l., the primary sub-Andean Amazon forest, on trunk of *Trichilia inaequilatera* (*Meliaceae*), 27 Nov. 2024, *A. Flakus & O. Plata*, 30163 (**holotype** KRAM L-75219, **isotype** LPB; LSU and mtSSU sequences GenBank PX353698 and PX353699).

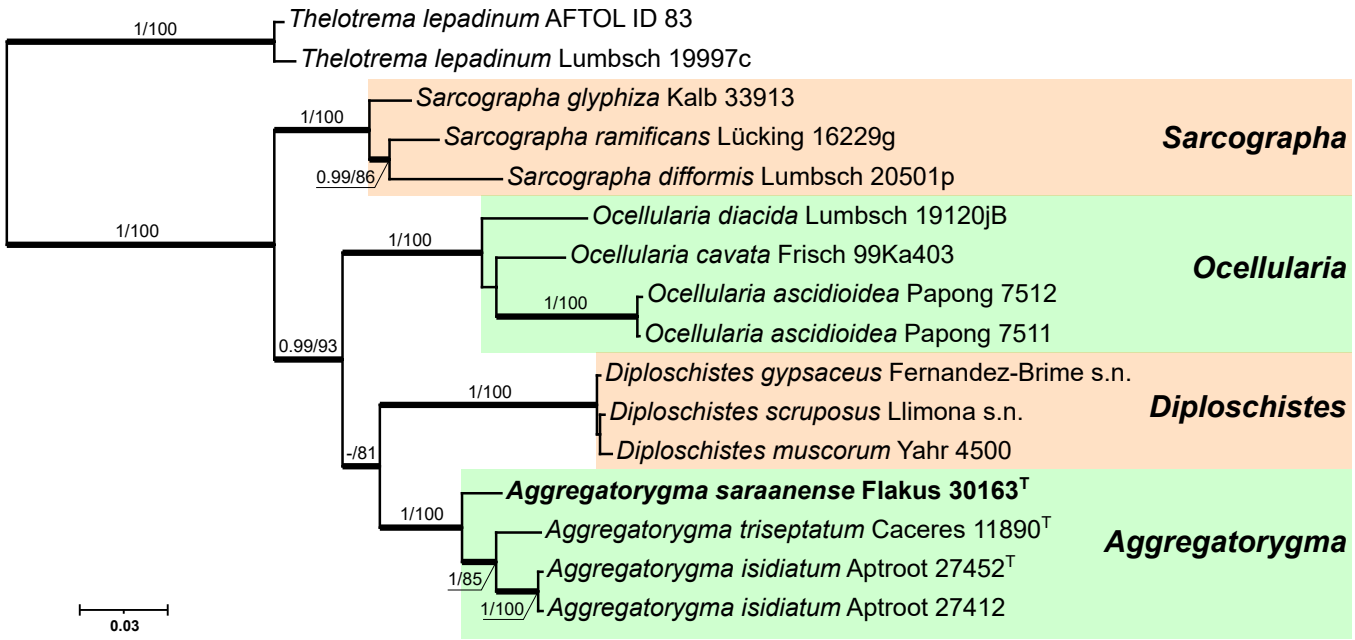
Notes: The genus *Aggregatorygma* was introduced by Cáceres *et al.* (2014) to accommodate a corticolous lichen with a continuous, ecorticate, pale thallus with a minutely farinose surface, a trentepohlioid photobiont, aggregated and branched lirellate apothecia, and hyaline, 3-septate, ellipsoidal ascospores. The generic concept was later expanded through the inclusion of additional species with submuriform ascospores or sterile thalli, bringing the total number of currently recognized species in the genus to four (Aptroot & Feuerstein 2020, Aptroot *et al.* 2022, Manawasinghe *et al.* 2025). Within the genus, another sterile species with ecorticate isidia, *Aggregatorygma isidiatum*, can be distinguished from the new species by its pale cream-white thallus, the presence of irregularly globose isidia, and confluentic acid as a secondary metabolite (Manawasinghe *et al.* 2025).

Phylogenetic analyses based on the mtSSU and LSU regions resolved the specimen of *Aggregatorygma saraanense* in a well-supported sister relationship to *A. isidiatum* and *A. triseptatum*. The genus *Aggregatorygma* was recovered as a moderately supported sister group with the genus *Diploschistes*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **LSU** sequence had highest similarity to *Acanthothecis aurantiaca* (voucher Kalb 33945, GenBank DQ431929; Identities = 91.32 %, 11 gaps), *Acanthothecis fontana* (voucher Lendemer 49537, GenBank MK110675; Identities = 90.71 %, 11 gaps), *Deltopyxis triangulispora* (voucher Marson 2017-12-26.1, GenBank OK625308; Identities = 90.67 %, six gaps), Closest hits using the **mtSSU** sequence are *Aggregatorygma isidiatum* (voucher Aptroot 27412, GenBank OR759507; Identities = 96.57 %, six gaps), *Aggregatorygma isidiatum* (voucher Aptroot 27452, GenBank OR759506; Identities = 95.45 %, seven gaps), and *Aggregatorygma triseptatum* (voucher Cáceres 11890, GenBank KJ440979; Identities = 96.02 %, 11 gaps).

Supplementary material: doi: 10.6084/m9.figshare.30094186 (alignment and phylogenetic tree); doi: 10.6084/m9.figshare.30102898 (table).

Colour illustrations: Bolivia, La Paz department, Alto Beni province, primary sub-Andean Amazon forest. Habit of the lichen thallus with isidia; two isidia; cross section through isidium (in lactophenol cotton blue and water). Scale bars: habit = 1 mm; isidia = 0.5 mm, section = 50 µm.



Phylogenetic relationships of *Aggregatorygma saraanense* (highlighted with **bold** font) inferred from Bayesian Inference analysis (BI) of a combined mtSSU and LSU data set. Two specimens of *Thelotrema lepadinum* were used as the outgroup. Thickened branches represent either Bayesian posterior probabilities ≥ 0.97 and/or bootstrap support values ≥ 70 %. Maximum likelihood analyses were carried out using a heuristic search as implemented in IQ-TREE v. 2.1.2 on XSEDE (Nguyen *et al*. 2015) and 100 bootstrap interactions on 1000 replicates to estimate branch support. Bayesian inference of the phylogenetic relationships was calculated using the Markov chain Monte Carlo (MCMC) approach as implemented in MrBayes v. 3.2.6 on XSEDE (Ronquist *et al.* 2012). Sequences from material with a type status are indicated by superscript T.

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Agrocybe punjabensis

Fungal Planet 1869 MB 854655

Agrocybe punjabensis W. Akram, Saba & Asif, ***sp. nov.***

Etymology: The epithet "*punjabensis*" refers to Punjab, a province of Pakistan, from where the type specimen was collected.

Classification: *Strophariaceae*, *Agaricales*, *Agaricomycetes.*

Basidiomata small to medium-sized. *Pileus* 0.7–3 cm diam., conic at early age becoming plane to convex at maturity, greyish yellow (25YR6/2) at younger age becoming bright yellowish brown (25YR7/6) with age; (Munsell 2009), umbo absent, slightly depressed at maturity, surface smooth, shiny at early age becoming dull at maturity, dry, margins smooth at younger age becoming undulating at maturity. *Lamellae* dull yellow orange (10YR6/3) at younger age becoming brownish black (7.5YR3/1) with age, subdistant, free, approximate, with entire margins, become eroded with age, lamellulae in 2–3 tiers of different lengths, alternating with lamellae. *Stipe* 1–6 × 0.2–0.4 cm, pale yellow (25YR8/4) at early age becoming dull yellowish at maturity (25YR6/4), whitish (2.5Y8/1) towards the base, central, cylindrical, strigose, equal, solid, dry and dull, bulbous base. *Annulus* absent. *Volva* absent. *Odour* and *taste* not recorded. *Basidiospores* (50/2/2) (8.1–)12.1–14.5(–17.2) × (6.9–)7.8–9.4(–10.2) µm, avl × avw = 13.3 × 8.6 µm; Qav = 1.6. ellipsoid to oblong, amygdaliform from side view, with central prominent germ pore of 1.53 µm wide, thick-walled, smooth, hyaline in 5 % KOH, dark reddish brown (5YR3/4) in Congo Red. *Basidia* (25.7–)26.6–31.3(–32.3) × (9.3–)10.0–11.7(–12.1) µm, avl × avw = 29.4 × 10.8 µm, clavate to broadly clavate, with median constriction, frequently 4-spored, sterigmata 4–6 µm long, thin-walled, hyaline in 5 % KOH, congophilous. *Cheilocystidia* (6.7–)12.6–14.2(–16.2) × (5.9–)6.5–9.0(–11.6) µm, avl × avw = 12 × 8.2 µm, lageniform to narrowly lageniform, thin-walled, no internal content present, hyaline, congophilous. *Pleurocystidia* (22.7–)26.5–33.3(–36.6) × (8.6–)9.5–12.9(–25.2) µm, avl × avw = 30.5 × 12.3 µm; clavate, cylindrical, utriform to narrowly utriform with median constriction, thin-walled, hyaline in 5 % KOH, congophilous. *Pileipellis* euhymeniderm to irregular trichoderm made up of long and regular hyphae with 4–8 µm diam, avw = 6 µm wide, hyaline, thin-walled, septate, smooth, narrow, hyaline in 5 % KOH, congophilous. *Stipitipellis* 2–4 µm diam., avw = 2.6 µm, cylindrical, regular, septate, parallel made up of long, narrow hyphae thick-walled, rarely constricted at septa, congophilous. *Caulocystidia* absent. *Clamp connections* present.

Habitat: Saprotrophic, gregarious, or scattered on decaying leaves of shrubs and grasses under the tree *Dalbergia sissoo*, associated with *Pennisetum setaceum*, on fallen remains of *Saccharum officinarum.*

Colour illustrations: Pakistan, Punjab Province, District Mandi Bahauddin, canal view park, on nutrient-rich soil on fallen leaves and other grasses (photo credit M. Asif). Basidiomata; basidiospores; basidia; cheilocystidia; pleurocystidia; pileipellis; stipitipellis. Scale bars: basidiomata = 1 cm; micromorphology = 5 µm.

Typus: **Pakistan**, Punjab Province, Mandi bahauddin District, 33°58'81"N, 73°49'73"E, 204 m.a.s.l., surrounded by tall grasses (*Pennisetum setaceum*), on borderline of rice field, 13 Jul. 2022, *W. Akram, W-06* (**holotype** LAH38146; ITS and LSU sequences GenBank PP386164 and PQ678707).

Additional material examined: **Pakistan**, Punjab Province, Mandi Bahauddin District, near Shaheedanwali, in nutrient-rich soil on bark of dead tree, 33°58'81"N, 73°49'73"E, 204 m.a.s.l., 8 Jul. 2023, *W. Akram, W07* (LAH30147; ITS and LSU sequences GenBank PP386165, and PQ678708).

Notes: Previously, only eight species of the genus *Agrocybe* have been reported from Pakistan (Ahmad *et al.* 1997, Aman *et al.* 2022, Crous *et al.* 2024a). Here, we describe a new species named *A. punjabensis*, growing on fallen remains of *Saccharum officinarum* in nutrient-rich soil. *Agrocybe punjabensis* is characterized by its conic to plano-convex, greyish yellow pileus with uplifted margins, dull yellow orange lamellae, ellipsoid to oblong, or amygdaliform basidiospores, clavate basidia with medial constriction, narrowly lageniform cheilocystidia, and narrowly utriform pleurocystidia,

In the phylogenetic analysis based on ITS and LSU sequence data, *A. punjabensis* is found to be a close relative of *A. auriolus* (GenBank PP431557) reported from Pakistan (Crous *et al.* 2024a), *A. arvalis* (GenBank MH615058) and *A. pediades* (GenBank MH615058) with strong bootstrap support and Bayesian posterior probability values (100 %/1). *Agrocybe auriolus* can be distinguished from *A. punjabensis* by a combination of morpho-anatomical characteristics such as light golden and centrally depressed pileus with crisped wavy margins, light orange lamellae, yellow orange and smaller basidiospores (6.3–9.1 × 3.8–5.9 µm vs 8.1–17.2 × 6.9–10.2 µm in *A. punjabensis*, and 2-spored basidia vs 4-spored in *A. punjabensis*), relatively larger cheilocystidia and pleurocystidia, and absence of clamp connections (Crous *et al*. 2024a).

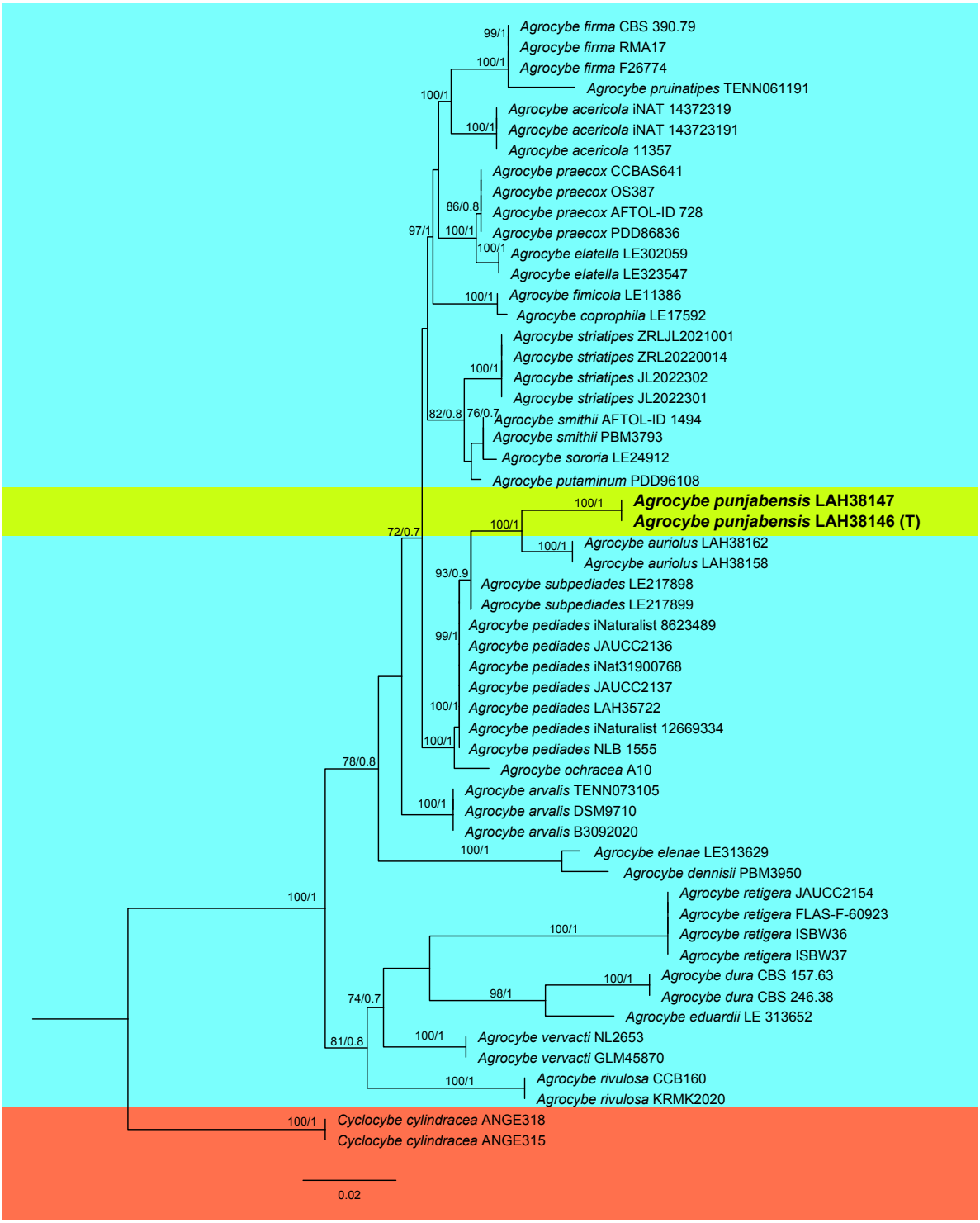
Agrocybe arvalis differs from *A. punjabensis* by its velvety, dark yellow brown to dark brown, sometimes olivaceous, smooth pileus, and cheilocystidia with characteristic finger like projections (Nauta *et al*. 2003). *Agrocybe ochracea* shares key traits with *A. punjabensis*, but stands out with its ochraceous-yellow pileus, thick context, wide basidiospores, and utriform cheilocystidia. Its pileipellis is an irregular hymeniderm, unlike the *A. punjabensis* trichoderm (Nauta 2004).

Agrocybe pediades is also phylogenetically close but differs from *A. punjabensis*, due to its ochraceous, glabrous and applanate pileus, brown and ventricose lamellae, fragile stipe, ellipsoid and smaller basidiosores (6.3–9.1 × 3.8–5.9 µm vs 8.1–17.2 × 6.9–10.2 µm in *A. punjabensis*), cheilocystidia with capitate to subcapitate apex, and absence of pleurocystidia (Niveiro *et al*. 2020). *Agrocybe subpediades* is also recognized as synonym of *Agrocybe pediades* (Malysheva & Kiyashko 2011).

Based on a BLAST search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had the highest similarity 96 % with *Agrocybe pediades* (voucher

iNat31900768, GenBank OK346364), 96 % *Agrocybe pediades* (voucher iNaturalist 12669334, GenBank OP549271), 95 % *Agrocybe pediades* (voucher NLB 1555, GenBank MT571662) and 95 % with *Agrocybe* sp. (voucher 151_A07, GenBank MK627487), while the **LSU** sequences showed 97 % similarity with *A. auriolus* (GenBank PP431558) from Pakistan and 93 % similarity with *A. smithii* (GenBank DQ484058) from Canada. The combined **ITS-LSU** dataset has a total of 55 sequences out of which 53 are of the genus *Agrocybe*, including *Cyclocybe cylindracea* (ANGE315 & ANGE318) as an outgroup taxon (Li *et al.* 2023, Crous *et al.* 2024). The combined ITS-LSU alignment file consists of 2421 sites including gaps, from which 1859 sites were conserved, and 538 were variables.

Supplementary material: doi: https://doi.org/10.6084/m9.figshare.26781079 (table); TreeBASE ID: S31648 (alignment and phylogenetic tree).



Molecular phylogenetic tree inferred from the combined ITS-LSU sequence alignment. The phylogenetic analysis was conducted using RAxML-HPC2 v. 8.1.11 on CIPRES, using Maximum Likelihood (ML) and Bayesian Inference (BI) methods (Stamatakis 2014). The tree was rooted to *Cyclocybe cylindracea* (ANGE315 & ANGE318). The new species is shown in **bold**.

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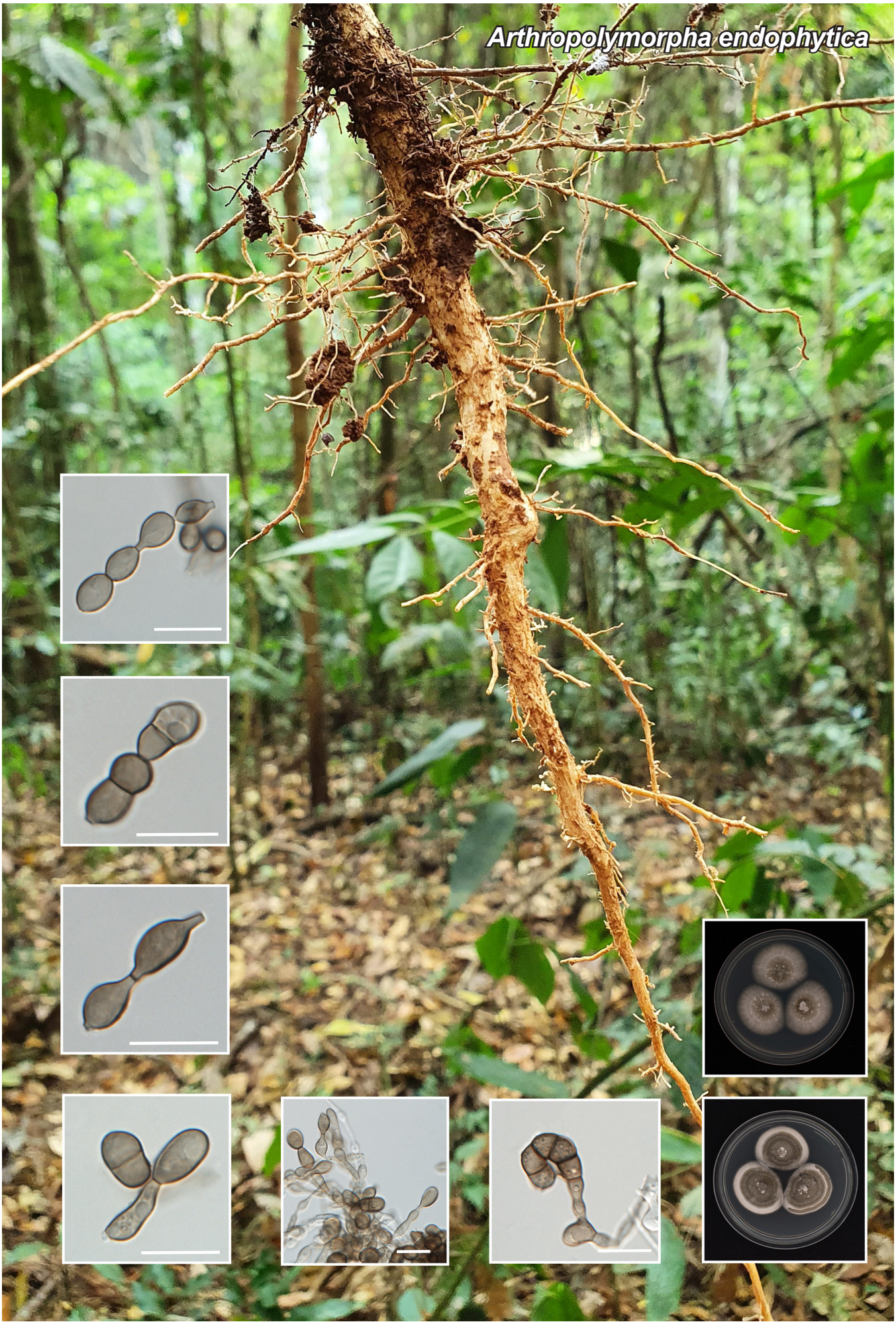

Arthropolymorpha endophytica

Fungal Planet 1870 MB 860425

Arthropolymorpha J.A. Oliveira, R. F. Castañeda-Ruiz & O.L. Pereira, ***gen. nov.***

Etymology: Referring to a kind of conidiogenesis involving hyphal fragmentation, resulting in the formation of morphologically diverse conidia.

Classification: *Muyocopronaceae*, *Muyocopronales*, *Dothideomycetes.*

Dark septate endophyte (DSE) isolated on culture media from surface-sterilized healthy roots of living plants. *Mycelium* consisting of hyaline to pigmented, smooth-walled, septate hyphae. *Conidiogenous hyphae* range from hyaline to darkly pigmented, with a predominance of dark, thick-walled hyphae involved in spore formation. *Conidiogenesis* arthro-thallic, typically retrogressive. *Conidia* are frequently pigmented, with smooth walls, 0–1-septate, and vary in shape from globose to ellipsoidal, clavate to ovoid, constricted doliiform, pyriform, to limoniform.

Type species: *Arthropolymorpha endophytica* J.A. Oliveira, R.F. Castañeda-Ruiz & O.L. Pereira

MB 860426

Arthropolymorpha endophytica J.A. Oliveira, R.F. Castañeda-Ruiz & O.L. Pereira, ***sp. nov.***

Etymology: The epithet refers to the endophytic habitat associated with coffee plant roots.

Dark septate endophyte (DSE) isolated on culture media from surface-sterilized roots of healthy coffee plant. *Mycelium* consisting of hyaline to pigmented, smooth-walled, septate hyphae. *Conidiogenous hyphae* range from hyaline to darkly pigmented, with a predominance of dark, thick-walled hyphae involved in conidial formation. *Conidiogenesis* arthro-thallic, typically retrogressive, with conidia exhibiting increased pigmentation at the distal end. *Conidia* are frequently pigmented, with smooth walls, 0–1-septate, and vary in shape from globose to ellipsoidal, 14.5–6.5 × 16–7.5 µm, clavate with truncate base to obovoid, 7–8 × 19–9 µm, doliiform, septate with median constriction, 18–20 × 5–9.5 µm, pyriform, 21.5–8 × 20–5.5 µm, and limoniform, 22–11 × 11–5 µm. *Chlamydospores* trichocladium-like, commonly curved or folded, observed on potato dextrose agar (PDA). *Sexual morph* was not observed.

Culture characteristics: Colonies on PDA umbonate with undulate edge, profuse aerial mycelium, dark brick grey colour in the centre to rosy buff periphery on surface, reverse fuscous black colour in the centre to rosy buff periphery (Rayner 1970), reaching 39 mm diam. after 2 wk at 25 °C in the dark. Colonies on malt extract agar (MEA) umbonate with entire edge, profuse aerial mycelium, vinaceous buff in the centre to fawn at periphery on surface, reverse fuscous black colour in the centre to rosy buff periphery, reaching 40 mm diam. after 2 wk at 25 °C in the dark. Colonies on oatmeal agar (OA) umbonate with entire edge, profuse aerial mycelium, olivaceus grey colour in the centre to pale olivaceous grey surface, purplish grey buff, reaching 38 mm diam. after 2 wk at 25 °C in the dark.

Typus: **Brazil**, Minas Gerais, Viçosa, Mata do Paraíso, 20°41'20''S, 42°49'36''W, isolated from healthy roots of *Coffea arabica* (*Rubiaceae*), Oct. 2024, *O.L. Pereira* & *J.A. Oliveira* (**holotype** VIC 49702, culture ex-type COAD 4165; ITS, LSU, *rpb2*, and *tef* sequences GenBank PV935328, PV935329, PV941788 and PV941789).

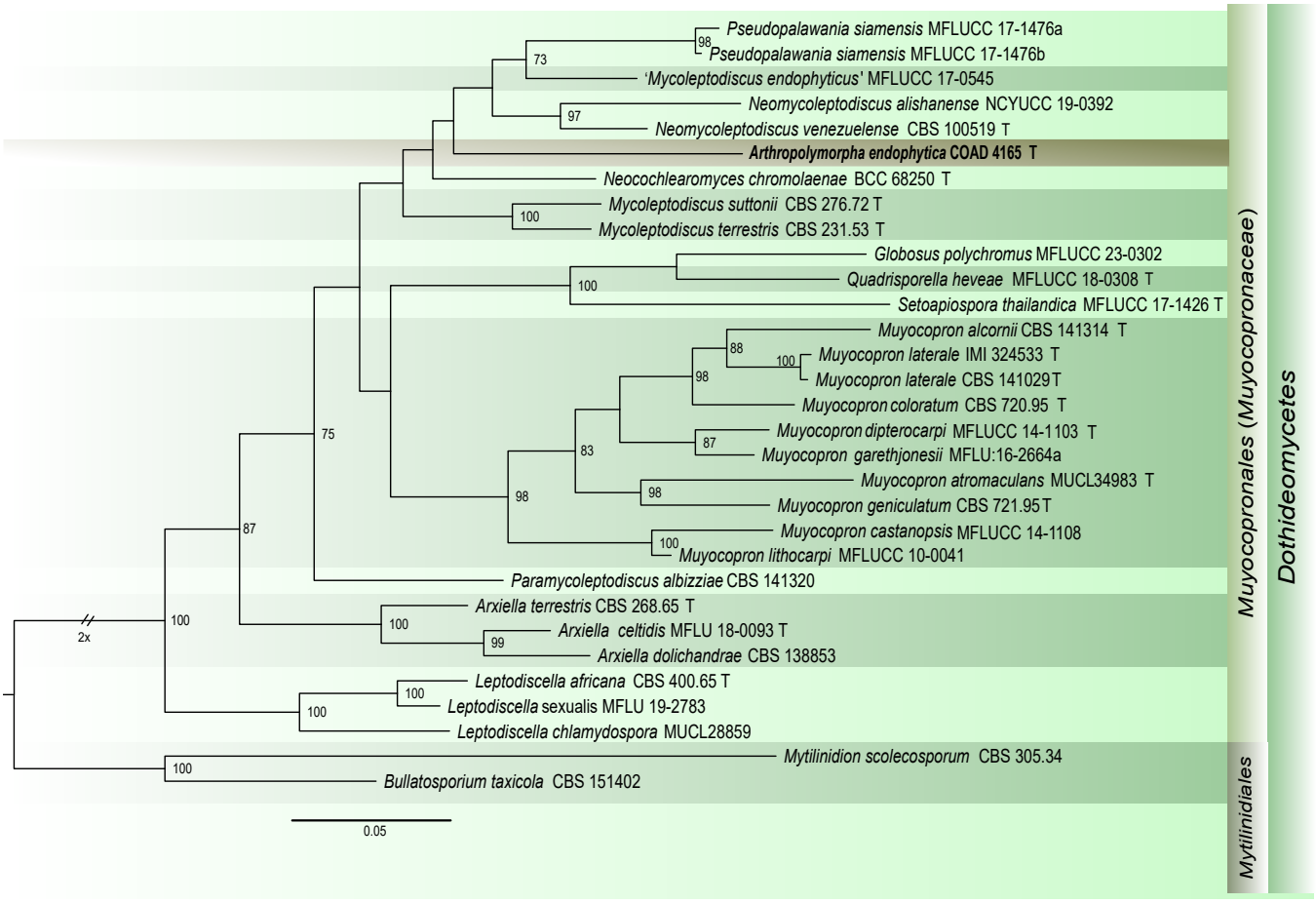
Notes: Muyocopronaceae is a monotypic family introduced by Luttrell (1951) and formally validated by Hyde *et al*. (2013). Based on phylogeny and morphological characteristics, Mapook *et al*. (2016) established the order *Muyocopronales* to include the family *Muyocopronaceae*. *Muyocopron* was the first genus described within the family, introduced by Spegazzini (1881). Hernández-Restrepo *et al*. (2016) reorganized the group by excluding and reassigning several species and formally incorporated *Mycoleptodiscus* into *Muyocopronaceae.* Currently, with the addition of *Arthropolymorpha endophytica*, the family comprises 12 formally described genera. Hernández-Restrepo *et al*. (2016) also showed that *Mycoleptodiscus endophyticus* forms a separate lineage, outside all other established genera in the family, aligning with the results of the current study. The lack of distinct morphological features was the reason for not formally establishing a new genus; therefore, the species is still listed in our phylogeny as '*Mycoleptodiscus endophyticus'*. The genera within *Muyocopronaceae* have previously been associated with blastic asexual morphs, including *Muyocopron*, *Mycoleptodiscus*, *Neocochlearomyces*, *Neomycoleptodiscus*, and *Paramycoleptodiscus*. However, none exhibit thallic ontogeny as observed in *A. endophytica*, a distinctive morphological feature that distinguishes *Arthropolymorpha* from the other genera. Additionally, members of *Muyocopronaceae* have been reported from a wide range of habitats and geographic regions, with diverse lifestyles, reflecting the cosmopolitan

Colour illustrations: Roots of young coffee plants growing in the undergrowth of a forest reserve called Mata do Paraíso at Universidade Federal de Viçosa, Viçosa, Minas Gerais state, Brazil (photo credit O.L. Pereira). Top to bottom conidia morphology variation: globose, pyriform, doliiform, limoniform arthroconidia produced by disarticulation; conidiogenous hyphae; chlamydospore; colonies on BDA and MEA. Scale bars = 20 µm.

distribution and ecological plasticity of this taxonomic group. *Arthropolymorpha endophytica* represents the second reported instance of a DSE in coffee roots worldwide, following the recent proposition of *Polyschema endophytica* (Crous *et al*. 2025). The distinctive morphological features of *A. endophytica* compared to other known DSE fungi indicate a largely unexplored diversity within this community of root endophytes.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Dothideomycetes* sp. [strain OGPBioA5, GenBank JX243875.1; Identities = 698/699 (99 %), no gaps], *Dothideomycetes* sp. [strain OGPBioA9, GenBank JX243878.1; Identities = 697/699 (99 %), no gaps], and 'uncultured fungus' [clone PDB11GadID, GenBank JN890322.1; Identities = 692/699 (99 %), one gap (0 %)]. Closest hits using the **LSU** sequence are *Dothideomycetes* sp. [strain OGPBioA5, GenBank JX243875.1; Identities = 626/626 (100 %), no gaps], 'uncultured fungus' [clone PDB11GadID, GenBank JN890322.1; Identities = 628/630 (99 %), no gaps], and *Mycoleptodiscus endophyticus* [strain MFLUCC 17-0545, GenBank NG_064487.1; Identities = 606/628 (96 %), seven gaps (1 %)]. Closest hits using the ***rpb2*** sequence are *Muyocopron atromaculans* [strain MUCL_34983, GenBank MK492713.1; Identities = 582/739 (79 %), two gaps (0 %)], *Muyocopron geniculatum* [strain CBS 721.95, GenBank MK492715.1; Identities = 517/651 (79 %), six gaps (0 %)], and *Muyocopron chromolaenae* [strain MFLUCC:17-1513, GenBank MT136761.1; Identities = 486/606 (80 %), four gaps (0 %)]. Closest hits using the ***tef*** sequence are *Bagnisiella examinans* [strain CBS 551.66, GenBank GU349056.1; Identities = 693/765 (91 %), five gaps (0 %)], *Pteridiospora javanica* [strain MFLUCC 11-0195, GenBank KJ739606.1; Identities = 691/766(90 %), seven gaps (0 %)], and *Pteridiospora javanica* [strain MFLUCC 11-0159, GenBank KJ739605.1; Identities = 691/766 (90 %), seven gaps (0 %)].

Supplementary material: https://figshare.com/s/c341ff292b8f759b1044 (database table and alignment).



Maximum likelihood tree obtained by phylogenetic analyses of ITS, LSU, *rpb2*, and *tef* sequences conducted with IQ-TREE v. 2.4.0 (Minh *et al*. 2020). Bootstrap support values are shown at the nodes (> 70 % are shown). The bootstrap was computed using the Ultrafast Bootstrapping (UFBoot) method (Hoang *et al.* 2018) with 1000 replicates. Model testing for each partition was conducted using the ModelFinder tool (Kalyaanamoorthy *et al*. 2017) implemented in IQ-TREE according to the Bayesian Information Criterion (BIC). Strains with an ex-type status are indicated with a T. The new species is shown in **bold** and brown colour. *Mytilinidion scolecosporum* (CBS 305.34) and *Bullatosporium taxicola* (CBS 151402) were used as outgroups.

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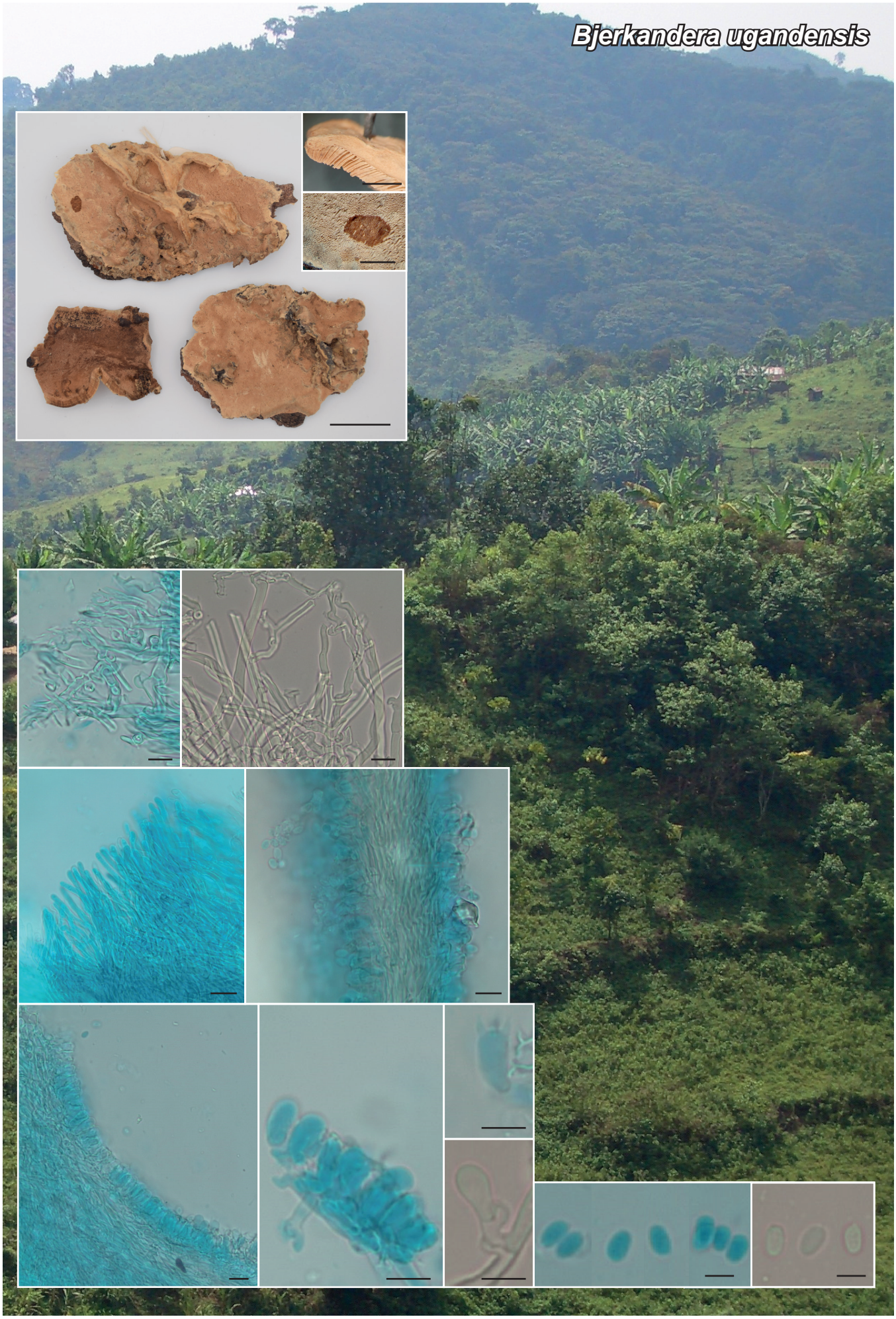

Bjerkandera ugandensis

Fungal Planet 1871 MB 860755

Bjerkandera ugandensis Ghobad-Nejhad, ***sp. nov.***

Etymology: Referring to Uganda, the country where it was collected.

Classification: *Phanerochaetaceae*, *Polyporales*, *Agaricomycetes*.

Basidiomata annual, resupinate with some projected pilei, adnate, soft corky, dried basidiomata 4–8 × 2.5–5 cm, with a mild sweet smell, pilei up to 1 cm projecting, 3 cm wide, and 1 cm thick at the base. *Pileal surface* buff ochraceous, glabrous, azonate, pileal margin blunt, becoming more or less dark grey, margin in resupinate parts of basidiomata distinct. *Hymenophore* poroid, pore surface buff ochraceous, darkened in bruised parts and upon touch with KOH, pores more or less round, (2–)4–5 per mm. *Context* buff cream, soft fibrous, 1–2 mm thick in pilei, with a thin dark line between tubes and context. *Tubes* concolourous with the pore surface and context, corky, up to 1–2 mm long. *Hyphal system* monomitic, generative hyphae with clamp connections, smooth, hyaline to light yellow, moderately cyanophilous in cotton blue, negative in Melzer's reagent. *Generative hyphae* in context thick-walled, interwoven, moderately branched, width uneven, 4.5–6.5 µm diam., walls up to 1 µm thick. Generative hyphae in tubes up to 2.5 µm diam., width even, walls thin but distinct, interwoven, subparallel along the tubes; hymenium entire, sporadic rhomboid to polyhedral, hyaline crystals present, basically aggregated in tube trama and occasionally extending into hymenium, 9–23 × 6–15 µm. Hyphae in dissepiments thin, smooth, entire, cyanophilous, without characteristic crystals or swellings. *Cystidia,* cystidioles, and dendrohyphidia absent. *Basidia* short clavate to barrel-shaped, with four sterigmata and a basal clamp connection, 10–12.8 × 4.5–5.5 µm. *Basidiospores* short cylindrical to ellipsoid, with a very small apiculus, walls hyaline, thin, smooth, non-cyanophilous, negative in Melzer's reagent, contents homogenous, 5.0–6.2(–6.5) × (2.7–)3–4 µm, L = 5.55 µm, W = 3.36 µm, Q = 1.67 (n = 30/1).

Habit, habitat and distribution: Presently known from a mature mixed forest in southern Uganda. Isolated in June from rotting log of an undetermined tree.

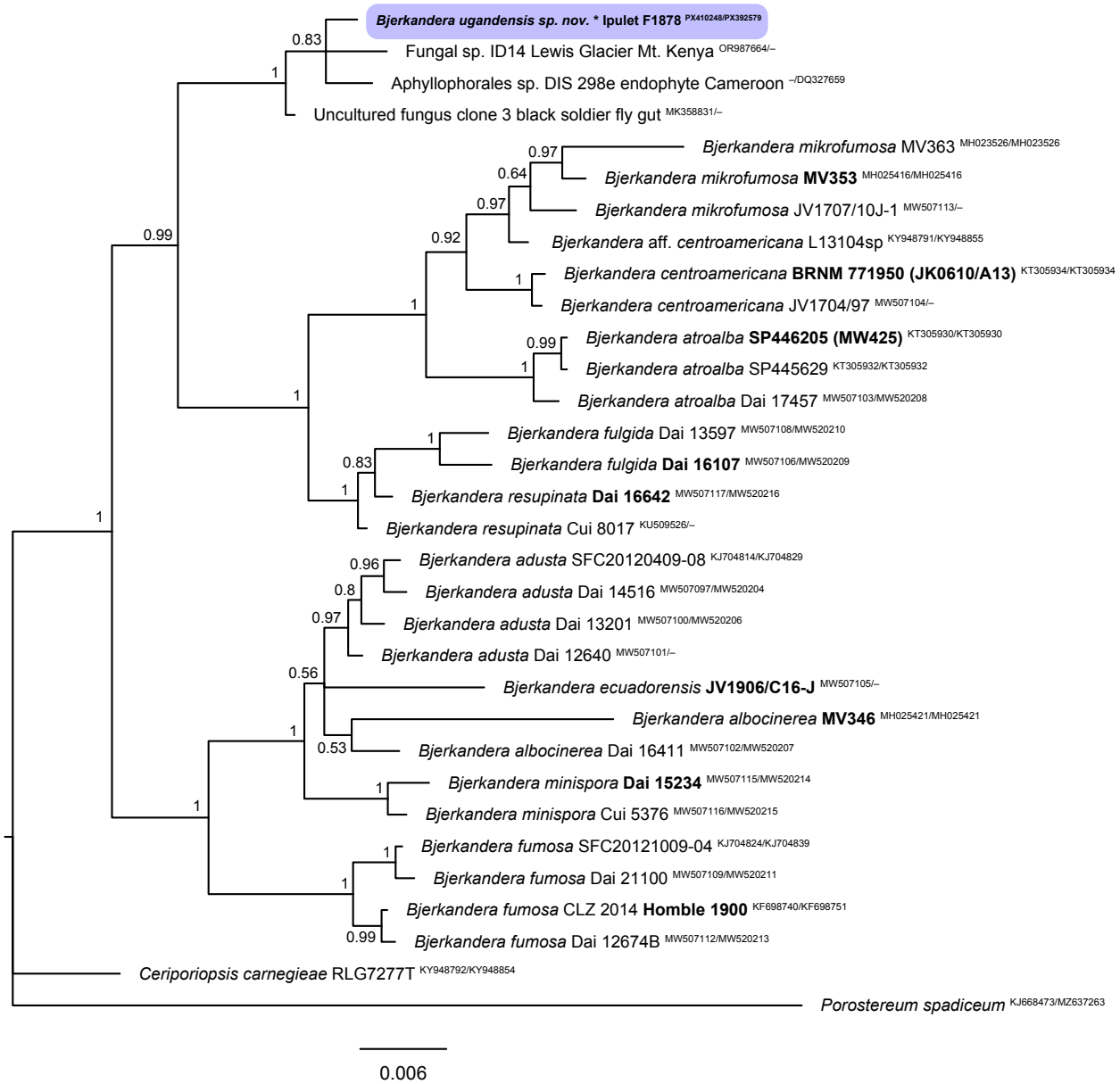
Typus: **Uganda**, Kabale, Bwindi Impenetrable National Park, Ruhija, mature mixed forest, on a rotting log, 2 Jun. 2003, *P. Ipulet*, F1878 (**holotype** O-F-918590, **isotype** K-M000130450; ITS, LSU, *rpb1*, *rpb2*, *tef1*, and nSSU sequences GenBank PX410248, PX392579, PX400459, PX400460, PX400458, and PX392578).

Notes: *Bjerkandera ugandensis* is distinguished by its buff ochraceous, resupinate to pileate basidiomata with 4–5 pores/mm, a thin dark line between tubes and context, sporadic crystals in hymenium, and short cylindrical to ellipsoid basidiospores, 5.0–6.2(–6.5) × (2.7–)3–4 µm. The smell of its basidiomata somewhat reminds that of *Evernia prunastri*. In the ITS-LSU-based phylogeny, *Bjerkandera ugandensis* forms a highly supported monophyletic clade (BPP = 1) with other unidentified isolates from Kenya and Cameroon. This clade is the sister (BPP = 0.99) of a clade that contains *B. mikrofumosa*, *B. atroalba*, and *B. resupinata*, among others. *Bjerkandera ugandensis* resembles *B. atroalba* and *B. mikrofumosa* in having effused basidiomata and ellipsoid basidiospores. However, *B. atroalba* has white to cream basidiomata and shorter (4–5 µm) basidiospores, and was described from the Neotropics (Westphalen *et al.* 2015). Unlike *B. ugandensis*, no crystals have been mentioned for *B. atroalba*. *Bjerkandera mikrofumosa* also forms crystals on hyphae but has a pale, golden brown pileal surface, smaller and angular pores (7–9/mm), and smaller basidiospores, 3.5–4.8 × 2.3–3 µm (Motato-Vásquez *et al.* 2020). *Bjerkandera resupinata* described from Thailand has resupinate basidiomata and the size of its pores and basidiospores are more or less similar to *B. ugandensis*, but its basidiomata are strictly resupinate without pileate parts, and it lacks crystals on the hymenium. Moreover, the two species are phylogenetically nested distantly from each other. *Bjerkandera ugandensis* showed the highest similarity with *B. minispora* based on the ITS megablast search, but the ITS-LSU-based phylogeny resolved a more distant relationship with *B. minispora* compared to the species mentioned above. *Bjerkandera minispora* differs from *B. ugandensis* by its flabelliform basidiomata, smaller pores (6–9/mm) and smaller basidiospores (3.1–4.2 × 2–2.8 µm) (Wang *et al.* 2021).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had the highest similarity to an uncultured fungus isolated from gut of black soldier fly (from Kenya?) [strain clone 3, GenBank MK358831; Identities = 444/454 (98 %), no gaps], Fungal sp. isolated from Lewis Glacier Mt. in Kenya [strain ID14, GenBank OR987664; Identities = 431/455 (95 %), 19 gaps (4 %)], and *Bjerkandera minispora* [voucher Cui_5376, GenBank MW507116; Identities = 429/461 (93 %), 10 gaps (2 %)]. Closest hits using the nuclear **LSU** sequence are *Aphyllophorales* sp. isolated as endophyte of *Theobroma cacao* from Cameroon [strain DIS 298e, GenBank DQ327659.1; Identities = 459/461 (99 %), no gaps], *Bjerkandera resupinata* [strain BJFC 022752, GenBank NG_088197.1; Identities = 457/461 (99 %), no gaps; other version is MW520216.1], and *Bjerkandera fulgida* [strain Dai_13597, GenBank MW520210.1; Identities = 456/461 (99 %), no gaps]. Closest hits using the ***rpb1*** sequence are *Ceriporiopsis carnegieae* [voucher RLG7277T, GenBank KY948935.1; Identities = 1052/1176 (89 %), no gaps], *Bjerkandera adusta* [voucher Cui 16682, GenBank

Colour illustrations: Photo of Bwindi Impenetrable National Park where the holotype was isolated, reproduced from Wikimedia Commons under the Creative Commons Attribution-Share Alike 3.0 IGO license (https://en.wikipedia.org/wiki/File %3ABwindi_ Impenetrable_National_Park-112358.jpg). Dried basidiomata from the isotype; insets showing a section through pilei with a thin dark line between tubes and context, and a dark spot on the hymenium after touch with KOH. Microscopy photos from the isotype showing the hyphae from context in cotton blue and in KOH; dissepiments; tube trama with a crystal on hymenium; hymenium and subhymenium; basidioles and basidia in cotton blue and in KOH; basidiospores in cotton blue and in KOH. Scale bars: basidiomata = 2 cm; insets = 0.5 cm; all microscopy photos except for basidiospores = 10 µm; basidiospores = 5 µm.

ON688461.1; Identities = 1054/1180 (89 %), 16 gaps (1 %)], and *Bjerkandera adusta* [voucher Cui 16670, GenBank ON688460.1; Identities = 1052/1179 (89 %), 13 gaps (1 %)]. Closest hits using the ***rpb2*** sequence are *Bjerkandera adusta* [voucher HHB-12826-Sp, GenBank KP134913.1; Identities = 971/1099(88 %), no gaps], *Bjerkandera adusta* [voucher Cui 16670, GenBank ON688481.1; Identities = 980/1112(88 %), no gaps], and *Bjerkandera adusta* [voucher Cui 16682, GenBank ON688482.1; Identities = 963/1104(87 %), no gaps]. Closest hits using the ***tef1*** sequence are *Bjerkandera adusta* [voucher Cui 16670, GenBank ON688502.1; Identities = 493/547 (90 %), 12 gaps (2 %)], *Bjerkandera* sp. isolated from *Lolium* seed [strain HMCC-23, GenBank MK051163.1; Identities = 491/547 (90 %), 14 gaps (2 %); this sequence is apparently *B. adusta*, see Robledo *et al.* (2021)], and *Ceriporiopsis carnegieae* [voucher CFMR:RLG-7277, GenBank OL405699.1; Identities = 486/542 (90 %), 11 gaps (2 %)]. Closest hits using the nuclear **SSU** sequence are *Bjerkandera adusta* [strain DAOM 215869, GenBank DQ060084.1; Identities = 1017/1041(98 %), no gaps], *Bjerkandera* sp. isolated as endophyte from unknown source [strain CPCC 480726, GenBank FJ515313.1; Identities = 1017/1041 (98 %), no gaps], and *Bjerkandera* sp. collected on *Thuja* in USA [isolate FP133581, GenBank OR464335.1; Identities = 1017/1041 (98 %), no gaps].



Phylogenetic trees of *Bjerkandera* species obtained from a Bayesian analysis of the combined alignment of ITS and LSU (32 taxa, 1606 characters including alignment gaps), and the combined alignment of Bayesian inference was performed using MrBayes v. 3.2.7a (Ronquist *et al*. 2012) implemented in CIPRES Science Gateway (Miller *et al.* 2010). The new species is indicated in **bold** font and in the blue box. The ex-type sequence is indicated with an asterisk (*). Strains from material with a type status are indicated in **bold** font. Numbers before nodes indicate Bayesian posterior probability values (BPP). *Porostereum spadiceum* was used as an outgroup. The scale bar represents the expected number of changes per site. The alignments and the 6-gene tree [ITS, LSU, *rpb1*, *rpb2*, *tef1*, and nSSU (8 taxa, 4953 characters including alignment gaps)] were deposited at figshare.com (https://doi.org/10.6084/m9.figshare.30168871.v1).

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Bullatosporium pinophilum

Fungal Planet 1872 MB 860992

Bullatosporium pinophilum Gardiennet, ***sp. nov.***

Etymology: The epithet refers to the host genus, *Pinus* (*Pinaceae*).

Classification: *Mytilinidiaceae*, *Mytilinidiales*, *Dothideomycetes*.

Ascomata hysterioid, superficial, scattered or somewhat gregarious, lying sinuously (rarely straight) in various directions on the substrate, occasionally coalescing or overlapping, rarely triangular in shape, approximately 370–880 µm long, 180–275 µm wide, 150–200 µm high, longitudinally striated in appearance, with an apex presenting a longitudinal ostiolar slit, clearly marked at maturity. *Peridium* 20–47 µm thick (n = 20), composed of small cells, 1–2.5 µm diam., mostly globular, with thick, dark brown walls, 1.5–3 µm wide. *Ostiolar canal* periphysate. *Hamathecium* composed of pseudoparaphyses, 1–2.5 µm wide, septate, with segments that may swell, hyaline, slightly sinuous, possibly branched. *Asci* bitunicate, cylindrical to clavate, short-stipitate, (71.6–)77.1–103.9(–109.4) × 12.8–16.0(–18.2) µm, containing eight obliquely to irregularly biseriate ascospores. *Ascospores* (20.8–)22.6–25.7(–27.7) × (5.9–)6.5–7.5(–8.5) µm, l/w = (2.9–)3.2–3.7(–4.1) (n = 60), rarely long-ellipsoid, generally heteropolar and slightly curved, 5–7-septate, mostly 7-septate (on 70 fully mature spores: 4 = 2.9 %; 5 = 30 %; 6 = 18.6 %; 7 = 44.3 %; 8 = 4.3 %), slightly constricted at the septa, hyaline when immature, pale brownish yellow to brown when senescent, smooth.

Culture characteristics: Colonies on potato dextrose agar (PDA) at 25 °C, slow-growing, reaching 1 cm diam. after 3 wk, 3.5–4.5 cm diam. after 2 mo; quickly turning brown, darker in the centre, covered with a white grey aerial mycelium (top). No odour detected.

Ecology and distribution: *Bullatosporium pinophilum* has been observed mainly on *Pinus nigra* subsp. *nigra*, but also on *Pinus sylvestris* (only twice among several hundred trees examined), on living or dead trees with a diameter of at least 35 cm, generally on trunk, but also on branches (holotype), usually occurring precisely along the edges of bark scales, on non-lichenised trees. It appears to be widely distributed in France, from the plains to the mountains, on trees in open locations (isolated trees, roadside trees or in thinned forests).

Typus: **France**, Côte-d'Or (21), Brochon, Champ Sement, (R.N.N. Combe Lavaux-Jean-Roland) 47.242343°N, 4.959544°E, 404 m.a.s.l., on the bark of a horizontal branch of a living black pine (*Pinus nigra* subsp. *nigra*) (*Pinaceae*), 11 Oct. 2022, *A. Gardiennet*, AG22062 (**holotype** LIP-AG22062, culture ex-type CBS 154572; ITS and LSU sequences GenBank PX119173 and PX111781).

Additional materials examined: **France**: Alpes-Maritimes (06), Tende, Castérino, 44.098776°N, 7.510289°E, 1577 m.a.s.l., on the bark of a horizontal fallen Scots pine trunk (*Pinus sylvestris*), 18 Jun. 2023, *A. Gardiennet*, AG23135 (LSU-PX127642; ITS-PX131014); Alpes-Maritimes (06), Valdeblore, La Colmiane, 44.07266°N, 7.224498°E, 1539 m.a.s.l., on the bark of a living Scots pine trunk (*P. sylvestris*), 18 Jun. 2023, *A. Gardiennet*, AG23137; Côte-d'Or (21), Brochon, Champ Sement, 47.24406°N, 4.953009°E, 453 m.a.s.l., on the bark of a cut black pine tree (*P. nigra* subsp. *nigra*), 30 Oct. 2023, *A. Gardiennet*, AG23236; Côte-d'Or (21), Brochon, Champ Sement, 47.242183°N, 4.96041°E, 394 m.a.s.l., on bark of a living black pine trunk (*P. nigra* subsp. *nigra*), 29 Nov. 2024, *A. Gardiennet*, AG24105 (LSU-PX127643; ITS-PX131015); Côte-d'Or (21), Véronnes, Fontaine-Française road (plot 0124), 47.538688°N, 5.24119°E, 289 m.a.s.l., on the bark of a living black pine trunk (*P. nigra* subsp. *nigra*), 11 Jan. 2025, *A. Gardiennet*, AG25003 (LSU-PX127644; ITS-PX131016); Véronnes, Fontaine-Française road (plot 0124), 47.538688°N, 5.24119°E, 289 m.a.s.l., on the bark of a living black pine trunk (*P. nigra* subsp. *nigra*), 11 Jan. 2025, *A. Gardiennet*, AG25003; Jura (39), Thésy, towards Maison-le-Franc, 46.905278°N, 5.92311°E, 703 m.a.s.l., on the bark of a living black pine trunk (*P. nigra* subsp. *nigra*), in a row along the D65 roadside, soc. *Poetschia buellioides,* 12 Apr. 2025, *A. Gardiennet*, AG25033 (LSU-PX127645) ; Côte-d'Or (21), Brochon, start of the Brochon valley, 47.240798°N, 4.96352°E, 335 m.a.s.l., on the bark of an old fallen black pine tree (*P. nigra* subsp. *nigra*), 24 May 2025, *A. Gardiennet*, AG25041; Saône-et-Loire (71), Tournus, Les Perrières, Lycée Horticole et du Paysage, 46.566069°N, 4.893252°E, 214 m.a.s.l., on the bark of a living black pine tree (*P. nigra* subsp. *nigra*), 30 Jun. 2025, *A. Gardiennet*, AG25055; Côte-d'Or (21), Saulx-le-Duc, Butte de Saint-Siméon, 47.538638°N, 5.01729°E, 447 m.a.s.l., on the bark of a living black pine trunk (*P. nigra* subsp. *nigra*).

Colour illustrations: *Pinus nigra* on which the holotype was collected, in an isolated site on limestone grassland within the R.N.N. Combe Lavaux-Jean-Roland in Brochon, France (photo credit A. Gardiennet). Overview of a small colony of ascomata on the substrate; scanning electron micrograph of coalescing ascomata; ascus (in water); ascospores (in water). Scale bars: colony = 200 µm; scanning electron micrograph = 100 µm; ascus and ascospores = 10 µm.

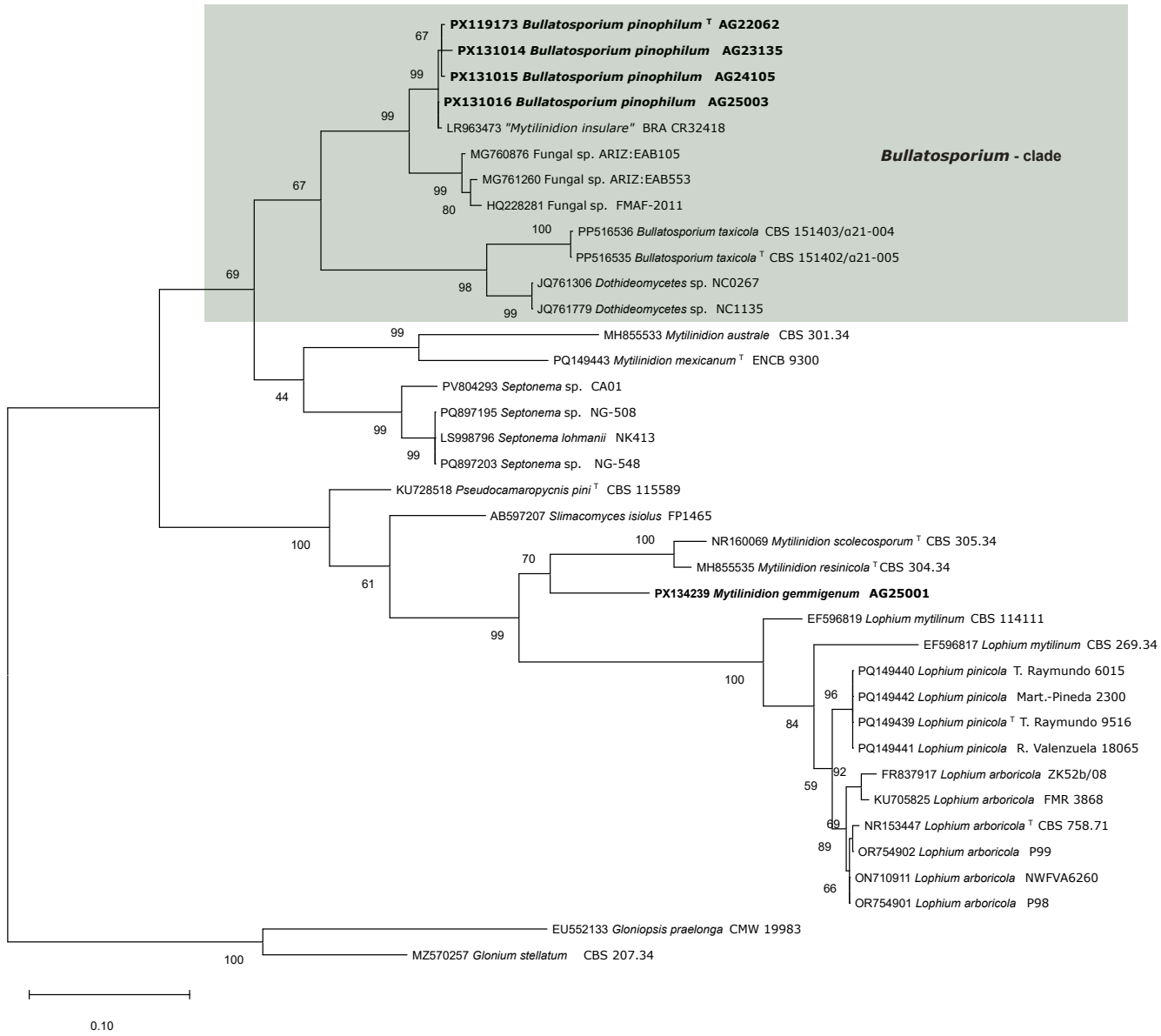
Notes: The genus *Bullatosporium* was recently introduced within the family *Mytilinidiaceae* (*Mytilinidiales*) to accommodate *B. taxicola*, a species collected on dead wood of *Taxus baccata* in western Norway. Molecular data (ITS, LSU & *TEF1α* markers) supported *Bullatosporium* as a monospecific clade, sister to *Mytilinidion* (Andreasen *et al.* 2024).

The new species *B. pinophilum* introduced here adds a second species to the genus and confirms the robustness of the *Bullatosporium* clade (bootstrap value > 0.97 on ITS and LSU phylogenies) within the *Mytilinidiaceae* lineage, of which it seems to represent the most basal clade. Pairwise comparisons between *B. pinophilum* and *B. taxicola* sequences exclude a conspecificity, with 84.3 % of identity on ITS between *B. pinophilum* (AG22062, GenBank PX119173) and *B. taxicola* [strain CBS 151402/a21-005, GenBank PP516535: 626 positions, 27 gaps; GenBank BLAST: 89.9 % identity] and 98.4 % of identity on LSU (strain CBS 151402/a21-005, GenBank PP516534: 714 positions, 0 gap; GenBank BLAST: 98.5 %). BLAST results identify **LSU** sequences of *B. taxicola* as the most similar to *B. pinophilum* (a paratype sequence PP516533 has only 95.7 % identity; main differences with the holotype sequence PP516534 consists of 6 substitutions concentrated within the 200 first nucleotides), followed by various species of *Lophium*, *Mytilinidion*, *Quasiconcha* and *Halokirschsteiniothelia* (91.3–95.9 %) representing other clades within *Mytilinidiaceae*. In BLAST results of **ITS** sequences, *B. taxicola* (89.9 %) is superseded by unidentified endophyte sequences scoring 93.4–96.5 % identity; phylogenetic analyses confirm (bootstrap value 99 %) that these sequences also cluster in the *Bullatosporium*-clade and likely represent as yet unnamed North American species.

The morphology of *B. pinophilum* indicates closest proximity with *B. taxicola*. Both species share similar spore size range, although length-to-width (l/w) ratio data are not available for the latter, and the ratio appears to differ slightly. Ascospores of *B. pinophilum* are (3–)5–7-septate, mostly 7-septate, and this occurs relatively early in the asci (vs 4–7-septate, typically 5-septate in *B. taxicola*), and they are also paler in colour, yellow brown to pale brown (vs brown to dark brown). Furthermore, the asci of *B. pinophilum* are significantly shorter, measuring (71.6–)77.1–103.9(–109.4) × 12.8–16.0(–18.2) µm (vs (91–)98–126(–146) × (10–)12–14.5(–16) µm). Our revision of an original collection of *B. taxicola* (OF270953, cited as a paratype) revealed that the spores of these specimens were striate when mature (vs smooth in *B. pinophilum*). Regrettably, despite careful observations in various media, we could not observe the 'bullate epispore' in either *B. pinophilum* or in the paratype collection of *B. taxicola*, although this feature was considered distinctive enough by Andreasen *et al.* (2024) to inspire the genus name. Ecologically, the two species differ in their niches: *B. pinophilum* fruits along the edges of pine bark scales, whereas *B. taxicola* mainly grows on yew wood. Despite repeated surveys on old yew trees in France, *B. taxicola* has never been observed, suggesting that their geographical distributions may also not overlap.

In the ITS phylotree, one sequence from Slovakia (strain BRA CR32418, GenBank LR963473; 99.31 % identity, no gaps) also clusters in the *B. pinophilum*-clade and is very likely conspecific with *B. pinophilum*. The authors of that sequence (Koukol *et al.* 2023) revived for it the name *Mytilinidion insulare*, a species discovered on blackened pine wood in Sardinia in 1866 by Dr Marcucci, and later described by Saccardo in Barbey (1885). Koukol *et al.* (2023) based their identification on Saccardo's brief morphological description, which they found compatible with their observations of a species on the stripped trunk of *Pinus sylvestris*. Previously, Zogg (1962) in his authoritative monograph of *Hysteriaceae* and *Lophiaceae* had concluded that "der Pilz mit *Mytilidion gemmigenum* Fuckel identisch ist" (i.e. the *Mytilinidion insulare* Sacc., is identical to *Mytilinidion gemmigenum* Fuckel) The curator of PAD (Padua, Italy) kindly provided us images of Saccardo's unpublished drawings of *M. insulare* and elements of H. Zogg's revision. Specifically, Saccardo's drawings show well mussel-shaped ascomata, superficial on the substrate and a vertical section of an ascoma reminiscent of species of the genus *Mytilinidion* such as *M. gemmigenum*. Furthermore, the spore shapes (l/w) in the drawing are similar to those of the latter. Zogg's conclusion, accompanied by a revision of the range of spore dimensions, leaves little doubt: *Mytilinidion insulare* Sacc., is identical to *Mytilinidion gemmigenum* Fuckel. We also agree with Zogg (1962) that *M. insulare* is indistinguishable from *M. gemmigenum*. Therefore, we do not consider that the name *M. insulare* is applicable to our species. Moreover, we provide molecular evidence that *M. gemmigenum* does not belong to the *Bullatosporium*-clade (phylotree, GenBank ITS sequence: PX134239).

Supplementary material: (Phylogenetic tree based on LSU sequences and two tables).
https://doi.org/zenodo.17425721
https://doi.org/zenodo.17425588
https://doi.org/zenodo.17425948



The ITS phylogeny was inferred using the Maximum Likelihood method and Tamura-Nei (1993) model (Tamura & Nei 1993) of nucleotide substitutions and the tree with the highest log-likelihood (-4481.91) is shown. The percentage of replicate trees in which the associated taxa clustered together (500 replicates) is indicated next to the branches (Felsenstein 1985). The initial tree for the heuristic search was selected by choosing the tree with the superior log-likelihood between a Neighbour-Joining (NJ) tree (Saitou & Nei 1987) and a Maximum Parsimony (MP) tree. The NJ tree was generated using a matrix of pairwise distances computed using the p-distance (Tamura & Nei 1993). The MP tree had the shortest length among 10 MP tree searches, each performed with a randomly generated starting tree. The analytical procedure encompassed 37 nucleotide sequences with 553 positions in the final dataset. Evolutionary analyses were conducted in MEGA v. 12 (Kumar *et al.* 2024), using up to three parallel computing threads.

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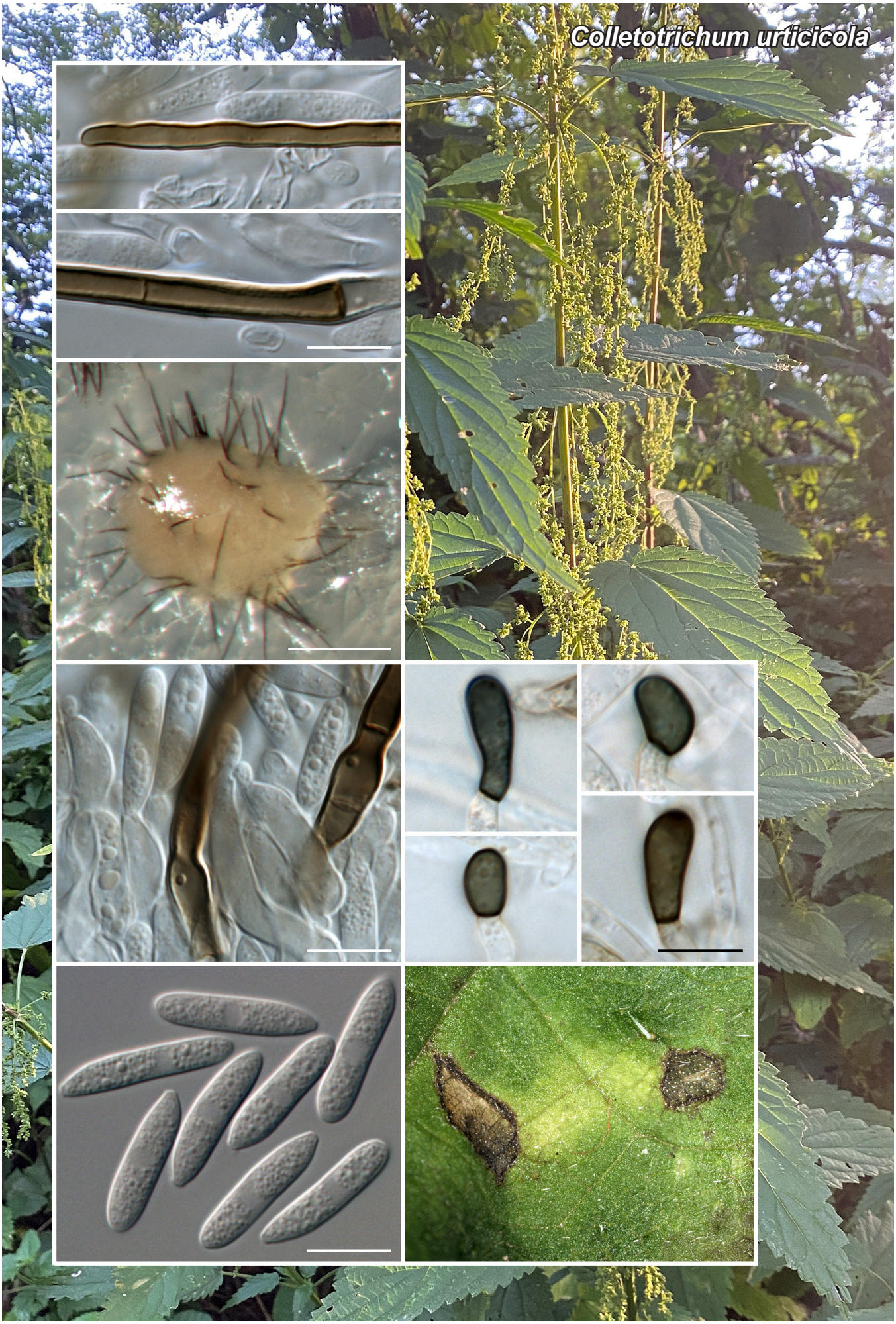

Colletotrichum urticicola

Fungal Planet 1873 MB 860676

Colletotrichum urticicola Damm, ***sp. nov.***

Etymology: Named after the host plant genus, *Urtica*.

Classification: *Glomerellaceae*, *Glomerellales*, *Sordariomycetes*.

Sexual morph not observed. *Asexual morph* on synthetic nutrient-poor agar medium (SNA; Nirenberg 1976). *Vegetative hyphae* 1–6 µm diam., hyaline, smooth-walled, septate, branched. *Chlamydospores* not observed. *Conidiomata* reduced to conidiophores and setae that are formed directly on hyphae. *Setae* pale to medium brown, smooth-walled, 40–220 µm long, 1–5-septate, base cylindrical, 3.5–5.5 µm diam., tip rounded. *Conidiophores* hyaline, smooth-walled, septate, branched, up to 50 µm long. *Conidiogenous cells* hyaline, smooth-walled, cylindrical, 11–25 × 3–5.5 µm, opening 1.5–2.5 µm diam., collarette ≤ 0.5 µm long, periclinal thickening observed, sometimes distinct. *Conidia* hyaline, smooth-walled, aseptate, straight or slightly curved, cylindrical, clavate to fusiform, with one end round and the other truncate, (14.5–)16.5–19.5(–21) × 3.5–4.5(–5) µm, mean ± SD = 18.0 ± 1.5 × 4.1 ± 0.3 µm, L/W ratio = 4.4. *Appressoria* single, pale to dark brown, smooth-walled, clavate to ellipsoidal in outline, with an entire margin, (6–)8–12(–14.5) × (2–)4–6(–6.5) µm, mean ± SD = 10.0 ± 2.2 × 5.0 ± 0.9 µm, L/W ratio = 2.0. *Asexual morph* on double-autoclaved *Anthriscus* stem. *Conidiomata* acervular, conidiophores and setae formed on a base of hyaline to pale brown, smooth-walled, angular cells, 3–7 µm diam. *Setae* pale to medium brown, smooth-walled, 55–200 µm long, 1–4-septate, base cylindrical, 5–7 µm diam., tip rounded. *Conidiophores* hyaline to pale brown, smooth-walled. *Conidiogenous cells* hyaline to pale brown, smooth-walled, cylindrical to ampulliform, 7–19 × 3–5 µm, opening 1 µm diam., collarette ≤ 0.5 µm long, periclinal thickening visible. *Conidia* hyaline, smooth-walled, aseptate, straight, sometimes ± curved, cylindrical, clavate to fusoid, with one end round and the other truncate, (13.5–)16–21(–24) × 4–4.5 µm, mean ± SD = 18.3 ± 2.5 × 4.2 ± 0.2 µm, L/W ratio = 4.4.

Culture characteristics (near UV, 12 h photoperiod, 20 °C after 10 d; colours according to Rayner 1970): Colonies on SNA: flat with entire margin, hyaline to nearly white, agar medium covered with felty white aerial mycelium and salmon acervuli, reverse same colours; growth 4–5 mm in 7 d (8.5–10.5 mm in 10 d). Colonies on oatmeal agar (OA; Crous *et al.* 2019b): flat with entire margin; greenish olivaceous, with a buff margin, aerial mycelium lacking, reverse olivaceous buff to olivaceous grey, growth 3–5.5 mm in 7 d (7–9.5 mm in 10 d). *Conidia in mass* salmon.

Colour illustrations: *Urtica dioica* flowering near Görlitz, Germany. Tip and base of setae; conidioma; setae; conidiogenous cells giving rise to conidia and bases of setae; conidia; appressoria (all microscopic structures from SNA culture of ex-holotype strain CBS 135938); symptom on host leaf. Scale bars: conidioma = 100 µm; all others = 10 µm.

Typus: **Netherlands**, Gelderland Province, Ede, Otterlo, Weversteeg, 52°06'05.9"N, 5°46'45.4"E, 77 m.a.s.l., from leaf spots on *Urtica dioica* (*Urticaceae*), 8 Jul. 2013, *W. Quaedvlieg* (**holotype** CBS H-21911, culture ex-holotype CBS 135938; ITS, *act*, *chs-1*, *his3*, *gapdh*, *tub2* and LSU sequences GenBank PX337220, PX376050, PX363481, PX376052, PX376054, PX363483 and PX352780, respectively).

Additional materials examined: **Netherlands**, Gelderland Province, Ede, Otterlo, Weversteeg, 52°06'05.9"N, 5°46'45.4"E, 77 m.a.s.l., from leaves of *Urtica dioica* (*Urticaceae*), Jul. 2013, *W. Quaedvlieg*, culture CBS 136878; ITS, *act*, *chs-1*, *his3*, *gapdh*, *tub2* and LSU sequences GenBank PX337221, PX376051, PX363482, PX376053, PX376055, PX363484 and PX352781, respectively. **USA**, Wisconsin, Madison, Dane County, University of Wisconsin Arboretum, from leaf spots on *Urtica gracilis*, 1 Jul. 1952, *H.C. Green* (**isotype** of *C. urticae* BPI 399628).

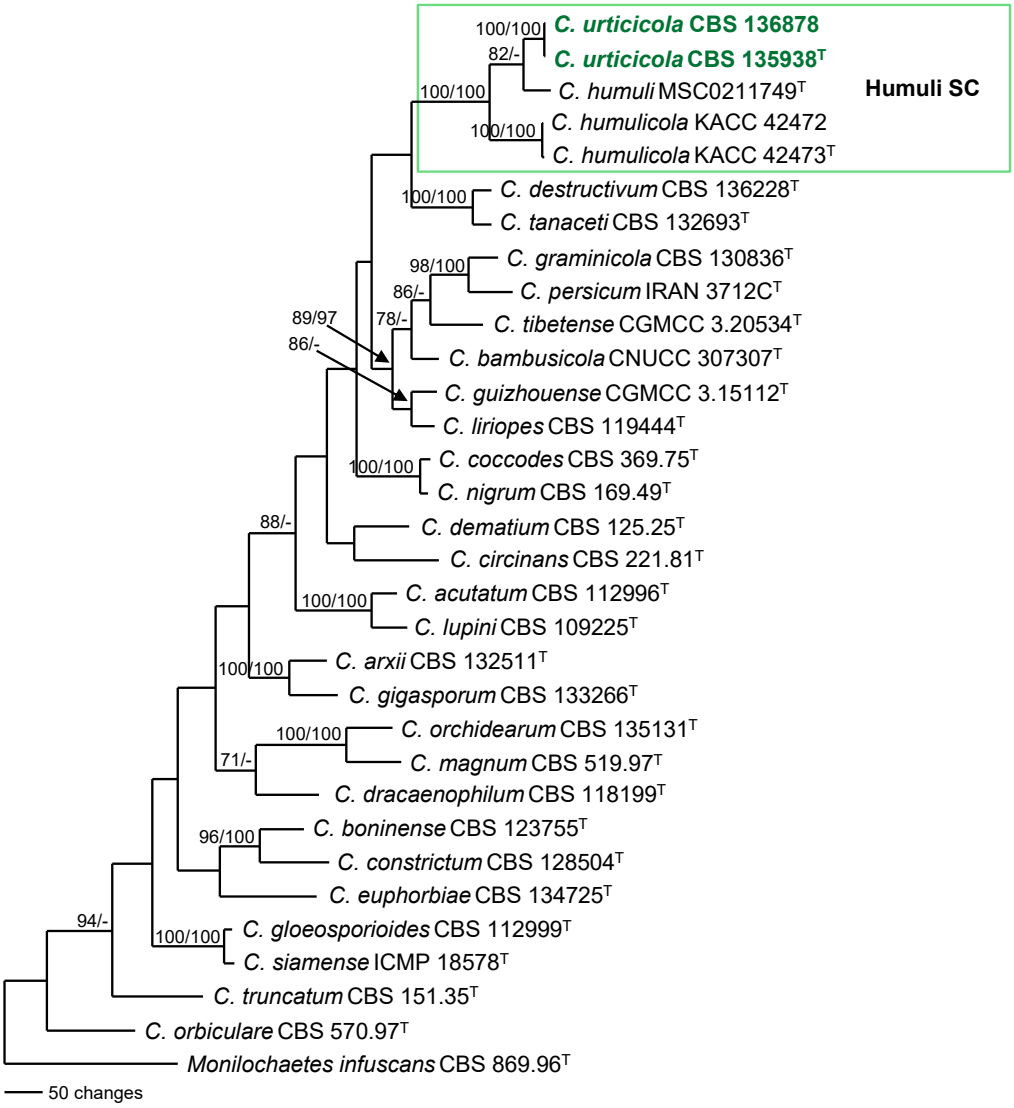
Notes: *Urtica dioica* (*Urticaceae*) is a herbaceous perennial flowering plant (weed and medicinal plant) that is native to Europe, most of Asia and NW Africa. It has also been introduced to many American and some African countries (Anonymous 2025). Although this plant is very common, reports of *Colletotrichum* associated with *U. dioica* are rare and only refer to *C. urticae*. This species was described from *Urtica gracilis* in Wisconsin, USA (Greene 1953) and also reported from *Urtica dioica* (Greene 1960). *Colletotrichum urticae* forms straight, fusoid or subfusoid, hyaline conidia, measuring 17–20 × 4–5 µm, on short, thin, almost obsolete conidiophores as well as slender, sinuous, brown, aseptate setae with an obtuse apex, measuring 45–70 × 4–4.5 (Greene 1953). Conidia of BPI 399628, which is regarded as isotype specimen ("Ex-Type" on BPI specimen label; holotype in Wisconsin State Herbarium, Fungi, WIS-F-0011313, not seen), are mostly straight and fusoid with both ends acute to truncate, measuring (17.5–)18.5–22.5(–23.5) × 4.5–5(–5.5) µm, mean ± SD = 20.5 ± 1.9 × 4.9 ± 0.3 µm, L/W ratio = 4.2. Conidia of *C. urticicola* are smaller (av. 18.0 × 4.1 µm on SNA) and have a different shape; they are often slightly curved with one end round and the other truncate, and the setae are septate and longer than those of *C. urticae*. Moreover, the two species originate from different continents and, *C. urticae* was originally described from a different host species, although later also observed on *U. dioica*. There are no cultures or sequences available of *C. urticae.*

Furthermore, there are two unpublished reports of *Colletotrichum* from *U. dioica* in Germany. One of them represents the so far only *Colletotrichum* sequence from *Urtica* available in NCBI GenBank, the ITS sequence of *C. lupini* strain BBA 71330 (AJ301975) submitted by Nirenberg *et al.* (2002), however not included in the respective paper itself. A blastn search confirmed the strain as belonging to clade 1 of the *C. acutatum* species complex (Damm *et al.* 2012); thus the fungus is not closely related to the species described here. There is also a report of *C. dematium* in the database www.pilze-deutschland.de (Dämmrich *et al.* 2025). Although the identification was probably based on morphology, it is

most likely a different species as well, because the conidia of *C. dematium* are distinctly curved (Damm *et al*. 2009).

Closest matches with the **ITS** sequence of *C. urticicola* resulted in *C. humulicola* strains, including its ex-type KACC 42473 with 93 % identity (GenBank PV034415; Thao *et al.* 2025). With the *act*, *chs-1*, *gapdh*, *his3* and *tub2* sequences there were no strains closer than 90 % (*C. humuli*, MSC0211749, PV054790; Thao *et al.* 2025), 95 % (*C. guizhouense*, CGMCC 3.15112, MZ799321; Liu *et al.* 2022), 81 % (*C. humuli*, MSC0211749, PV054787), 90 % (*C. liriopes*, HZ-1, MK644099; Yang *et al.* 2020 and *C. arxii*, CBS 169.59, KF687846; Liu *et al.* 2014) and 90 % (*C. humulicola*, KACC 42473, PV054784), respectively. Thus the closest matches of four loci, were strains of *C. humuli* or *C. humulicola*, belonging to the recently established Humuli species complex (Thao *et al.* 2025); while the closest matches of further two loci were species from the Spaethianum and Gigasporum complexes. The multilocus phylogeny confirmed *C. humulicola* to belong to the Humuli complex, in which the two strains formed a distinct clade, sister to *C. humuli*. As there is no closely related species, *C. urticicola* can be identified with all loci sequenced.

Supplementary material: doi: 10.6084/m9.figshare.30121930 (table, alignment and tree).



The first of two equally most parsimonious trees obtained from a heuristic search of the combined ITS, *chs-1*, *his3*, *act*, *tub2* sequence alignment of the Humuli (green box) and other species complexes in PAUP v. 4.0b10 (Swofford 2003), using the heuristic search option with 100 random sequence additions and tree bisection and reconstruction as the branch-swapping algorithm. Alignment gaps were treated as missing, and all characters were unordered and of equal weight. Additionally, a maximum likelihood (ML) analysis was calculated online using IQ-TREE v. 1.6 (http://iqtree.cibiv.univie.ac.at; Nguyen *et al*. 2015; Trifinopoulos *et al.* 2016) with model testing under the Bayesian information criterion (BIC) (Kalyaanamoorthy *et al*. 2017). Bootstrap support values (10000 replications, using fast-stepwise addition algorithm; Hillis & Bull 1993) of the MP analysis > 70 % and of the ML analysis (5000 replicates of ultrafast bootstrap; Hoang *et al*. 2018; Minh *et al*. 2013) > 95 % (Guindon *et al*. 2010) are shown at the nodes. *Monilochaetes infuscans* (CBS 869.96) was used as outgroup. Culture collection numbers of the species are listed in the tree; GenBank accession numbers are in the supplementary table. Numbers of ex-type strains are indicated by a superscript T. Isolates of the novelty described are shown in green **bold** font.

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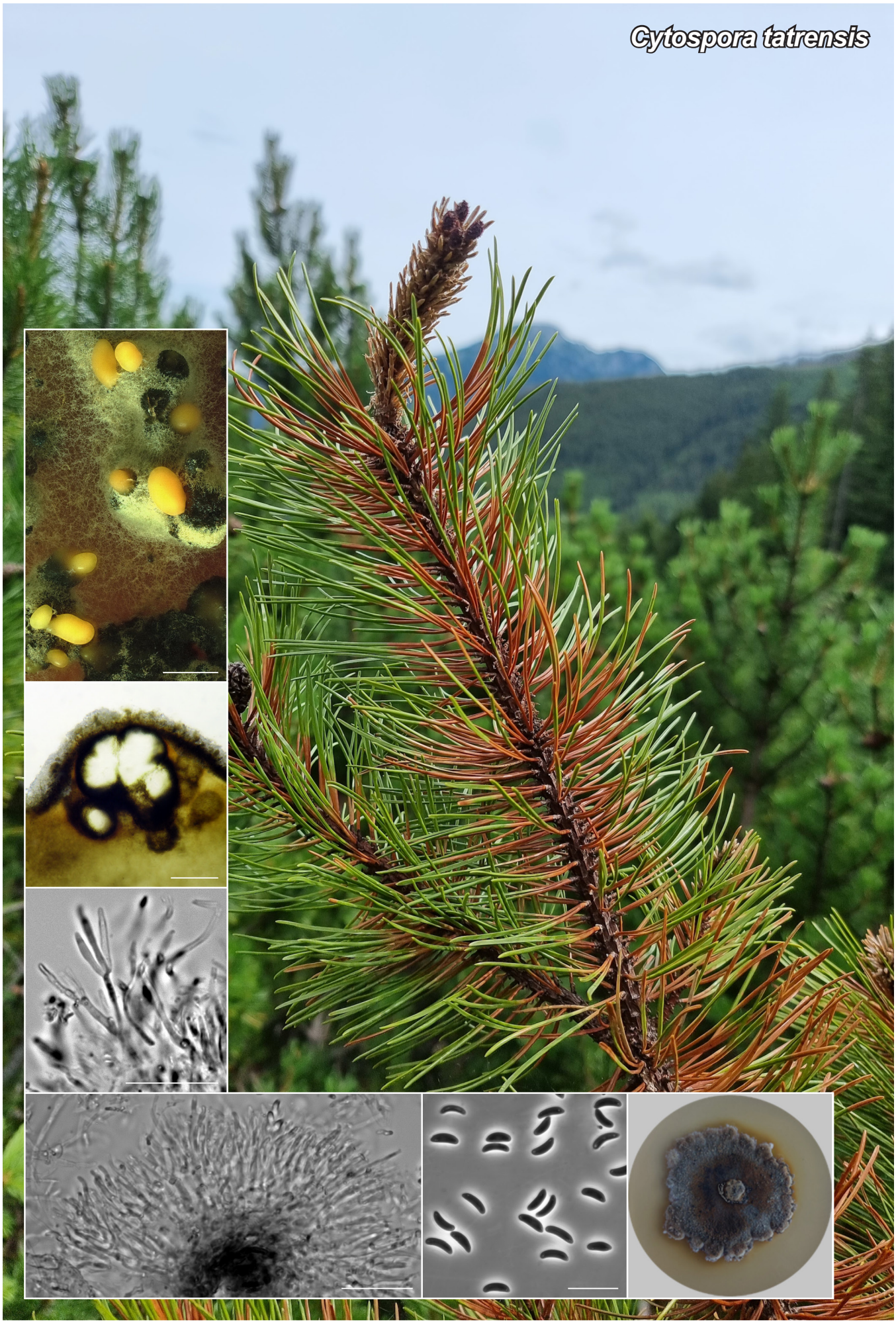

Cytospora tatrensis

Fungal Planet 1874 MB 860581

Cytospora tatrensis Jankowiak & Stępniewska, ***sp. nov.***

Etymology: Named after its occurrence in the Tatra Mountains within the Western Carpathians.

Classification: *Cytosporaceae*, *Diaporthales*, *Sordariomycetes*.

Sexual morph not observed. *Conidiomata* on potato dextrose agar (PDA) pycnidial, mostly aggregated, sometimes solitary, many with cream-coloured conidial exudate, globose (549–)682–1285(–1653) µm, with multiple, irregular locules sharing common walls. *Conceptacle* absent. *Locules* numerous, irregular, subdivided frequently by invaginations with common walls, (122–)168–326(–452) µm diam. *Conidiophores* smooth-walled, hyaline, branched at the base, in the middle, or unbranched, (5–)16.4–16.5(–46.8) × (1.4–)1.7–2.6(–3) µm, sometimes reduced to conidiogenous cells. *Conidiogenous cells* enteroblastic, phialidic, sub-cylindrical to cylindrical, (2.8–)8.5–14.1(–16.9) × (0.7–)1.1–2.2(–3.0) µm, tapering towards apices. *Conidia* hyaline, allantoid, smooth, eguttulate, aseptate, thin-walled, (4.1–)4.4–6.0(–8.1) × (0.8–)1.1–1.4(–1.7) µm.

Culture characteristics: Colonies after 7 d at 25 °C on PDA average 42.2 (± 0.4) mm, no growth at 5 °C on PDA, strongly dentate, dark grey outer margin (1F1, Kornerup & Wanscher 1978), and greyish yellow (B4) inner margin with centre of the colony becoming yellowish brown (D5) with age. *Hyphae* hyaline, smooth, straight, branched, and septate.

Typus: **Poland**, South Poland, Tatry Mts. isolated from dead *Pinus mugo* (*Pinaceae*) stem, Jul. 2023, *Cz. Bartnik* (**holotype** KRAM F 60043, culture ex-type CBS 152107; ITS, LSU, *ACT1, RBP2, TEF1,* and *TUB2* sequences GenBank PX260479, PX260479, PX254870, PX254872, PX254874 and PX254876).

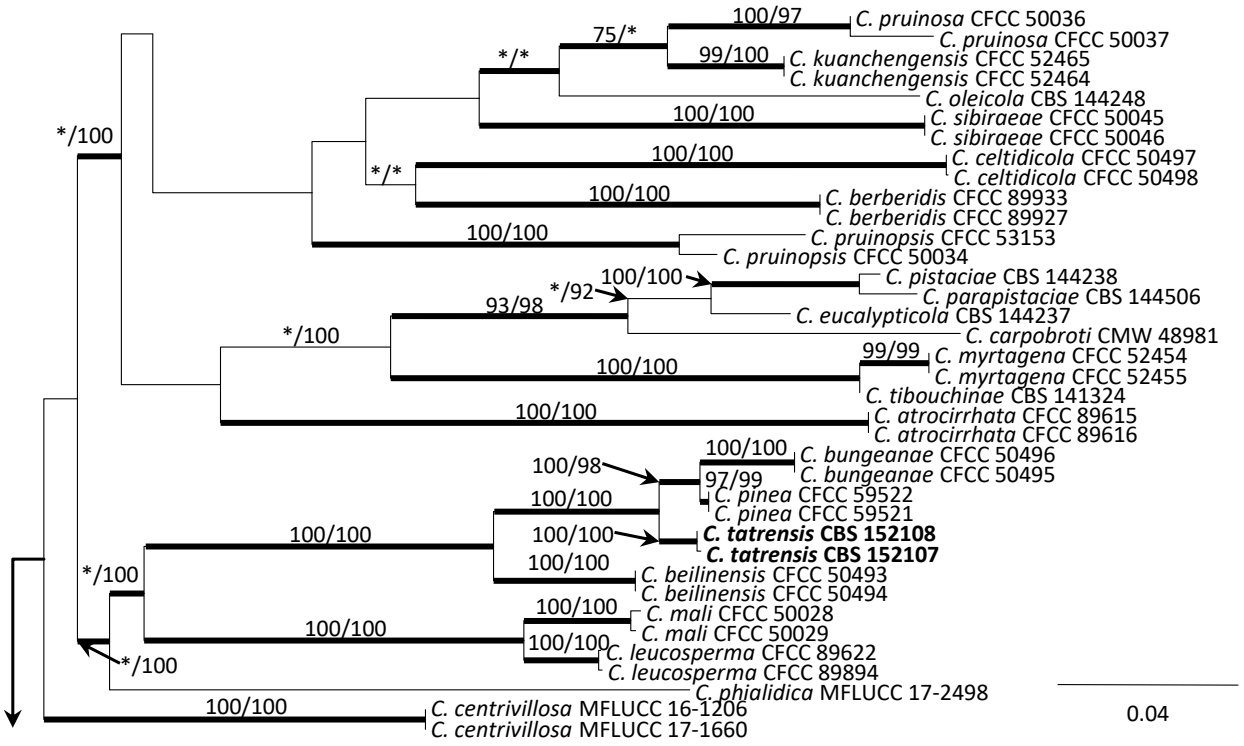
Additional materials examined: **Poland**, South Poland, Tatry Mts. isolated from dead *Pinus mugo* stem, Jul. 2023, *Cz. Bartnik* (culture CBS 152108; ITS, LSU, *ACT1, RBP2, TEF1*, and *TUB2* sequences GenBank PX260480, PX260480, PX254871, PX254873, PX254875 and PX254877).

Colour illustrations: Shoot dieback of *Pinus mugo* in the Tatra Mountains, Poland; pycnidia; transverse section through conidioma; conidiogenous cells; conidiophores; conidia; seven-day-old PDA culture. Scale bars: pycnidia = 1000 µm; section = 250 µm; conidiophores = 25 µm; conidia = 10 µm.

Notes: Similar to many members of the genus *Cytospora*, *C. tatrensis* is associated with woody host plants. *Cytospora tatrensis* was isolated from shoots with the symptom of dieback in the Polish Tatra Mountains (Jankowiak *et al.* 2024). The concatenated multilocus tree from the five-marker data set showed that the ex-type isolate of *C. tatrensis* together with the four other isolates formed a well-supported lineage and grouped closely with *C. bugeanae* and *C. pinea* that have been described from diseased branches of *Pinus bungeana* in China (Fan *et al.* 2020, Jia *et al.* 2024). *Cytospora tatrensis* is similar to *C. bungeanae* and *C. pinea* in terms of forming the multiple locules without conceptacle but differs in having larger conidiophores, conidiogenous cells and conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cytospora bugeanae* [strain CFCC 50495, GenBank NR 171063; Identities = 497/499 (99 %), no gaps], *Cytospora pinea* [CFCC 59521, GenBank OR826181; Identities = 486/488 (99 %), no gaps], and *Cytospora beilinensis* [strain CFCC55816, GenBank OR029655; Identities = 498/506 (98 %), two gaps (0 %)]. Closest hits using the **LSU** sequence are *Cytospora* sp. [strain RGM_3390, GenBank OR036922; Identities = 1285/1287(99 %), no gaps], *Cytospora mali* [isolate ARI-15-US, GenBank PP976972; Identities = 1298/1303(99 %), two gaps (0 %)] and *Cytospora mali* [isolate ARI-23-GW , GenBank PP976971 Identities = 1293/1299(99 %), no gaps]. Closest hits using the ***ACT1*** sequence had highest similarity to *Cytospora euonymicola* strain [CFCC 50499, GenBank MH933535; Identities = 244/247(99 %), no gaps], and *Cytospora beilinensis* [CFCC 50493, GenBank MH933527; Identities = 235/248(95 %), five gaps (2 %)]. Closest hits using the ***RPB2*** sequence had highest similarity to *Cytospora bugeanae* [strain CFCC 50495, GenBank MH933593; Identities = 720/727 (99 %), no gaps], and *Cytospora pinea* [strain CFCC 59521, GenBank OR832036; Identities = 719/726(99 %), no gaps]. Closest hits using the ***TEF1*** sequence had highest similarity to *Cytospora bugeanae* [strain CFCC 50495, GenBank MH933497; Identities = 559/582 (96 %), four gaps (0 %)], *Cytospora pinea* [CFCC 59521, GenBank OR832058; Identities = 456/481 (95 %), five gaps (1 %)], and *Cytospora beilinensis* [strain CFCC 50493, GenBank MH933495; Identities = 513/589 (87 %), 20 gaps (3 %)]. Closest hits using the ***TUB2*** sequence had highest similarity to *Cytospora bugeanae* [strain CFCC 50495, GenBank MH933563; Identities = 472/492 (96 %), eight gaps (1 %)], *Cytospora pinea* [CFCC 59521, GenBank OR832078; Identities = 460/480 (96 %), eight gaps (1 %)], and *Cytospora beilinensis* [strain CFCC 50493, GenBank MH933561; Identities = 444/503 (88 %), 17 gaps (3 %)].

Supplementary materials: doi: 10.6084/m9.figshare.30350317 (table, tree); TreeBASE ID S32320 (alignment and tree).



Phylogram from Maximum Likelihood (ML) analyses of the combined datasets of ITS, LSU, *ACT1*, *RPB2*, *TEF1* and *TUB2* genes for species of the genus *Cytospora*. The ML analysis was performed using PhyML v. 3.0 (Guindon *et al.* 2010) under the GTR+I+G substitution model with 1000 bootstrap replicates. Maximum Parsimony (MP) analyses were conducted with PAUP v. 4.0b10 (Swofford 2003), also using 1000 bootstrap replicates. Bayesian Inference (BI) analyses were carried out with MrBayes v. 3.1.2 (Ronquist & Huelsenbeck 2003) employing Markov Chain Monte Carlo (MCMC) methods for 13 M generations. The novel species is shown in **bold** face. The bootstrap support values (≥ 75 % for ML and MP analyses) are presented at nodes as follows: ML/MP. Bold branches indicate posterior probabilities ≥ 0.95 obtained from BI analyses. * indicates bootstrap support values < 75 %. The tree is drawn to scale (see bar) with branch lengths indicating the expected number of substitutions per site. *Diaporthe vaccinii* was used as outgroup taxon. The tree is a subset of the supplementary tree.

Maximum Parsimony (MP) analyses were conducted with PAUP v. 4.0b10 (Swofford 2003), also using 1000 bootstrap replicates. Bayesian Inference (BI) analyses were carried out with MrBayes v. 3.1.2 (Ronquist & Huelsenbeck 2003) employing Markov Chain Monte Carlo (MCMC) methods for 13 million generations.

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Didymella digitariae

Fungal Planet 1875 MB 860725

Didymella digitariae B.S. Vieira, E.M. Inokuti, A.L. Firmino, J.G. Rodrigues & D.R. Mendes, ***sp. nov.***

Etymology: The name refers to the host genus *Digitaria* from which it was isolated.

Classification: *Didymellaceae*, *Pleosporales*, *Dothideomycetes*.

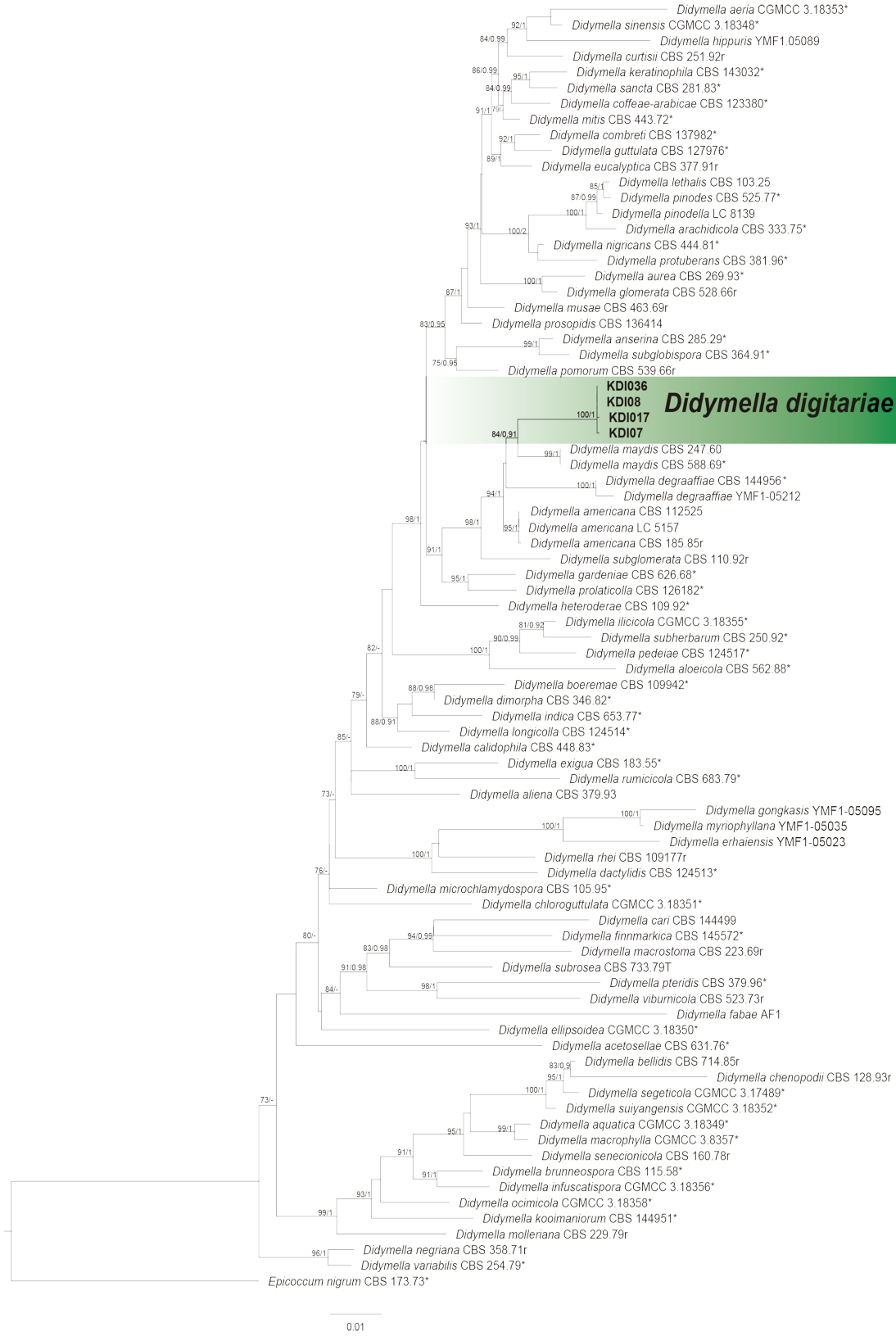
Conidiomata are pycnidial, produced on the surface or semi-immersed in the culture medium, usually solitary and scattered, but occasionally confluent (2–3 aggregated). *Pycnidia* are predominantly pyriform to subglobose, brown to dark brown, 29.5–79.5 × 27.1–79 µm, with relatively thin walls and a central ostiole. The pycnidial wall is composed ranging for pseudoparenchymatous tissue formed by pigmented, oblong to isodiametric cells, with a thickness of 3.7–12.5 µm. *Conidia* are hyaline, smooth, 0–1-septate, and typically allantoid, fusoid to limoniform, with one end rounded and the other end truncate, 4.1–7.6 × 1.2–1.8 µm. *Chlamydospores* formed in hyphal cells, globose to spherical, solitary, mostly catenulate, pale to dark brown, 8.5–10.5 µm.

Culture characteristics: Colonies showed rapid growth after 7 d at 25 °C, reaching 64.92 mm diam. on potato dextrose agar (PDA), 66.47 mm on malt extract agar (MEA), and 64.22 mm on oatmeal agar (OA). On PDA, the colonies were dense and exhibited uniform mycelial growth covering the entire plate. The texture ranged from velvety to floccose, with abundant aerial mycelium and a homogeneous olivaceous to glaucous-green coloration. On MEA, the colonies exhibited distinct concentric rings with colour gradients from darker centres to lighter margins, including shades of olivaceous, honey, yellow, isabelline, dark mouse-grey, honey, and fuscous black. On OA, the colonies were pulverulent to velvety, with a colour transition from olivaceous-yellow at the centre to glaucous-green at the margin, with abundant sporulation forming dark spots or patches, mainly concentrated at the colony's centre.

Typus: **Brazil**, Minas Gerais, São Gotardo, São Jerônimo dos Poções, on *Digitaria insularis* (*Poaceae*), 4 Dec. 2021, *B.S. Vieira & A.L. Firmino*, KDI036 [**holotype** dried specimen deposited in VIC, Fungarium of the Universidade Federal de Viçosa, Department of Plant Biology (VIC 49445); ex-type culture deposited in the Coleção Octavio de Almeida Drummond (COAD) of the Universidade Federal de Viçosa, Department of Plant Pathology COAD 3600 = KDI036; ITS, LSU, *rpb2* and *tub2* sequences GenBank PV830646, PV830650, PV835324 and PV835328]; ibid., culture KDI07; ITS, LSU, *rpb2* and *tub2* sequences GenBank PV830643, PV830647, PV835321 and PV835325, culture KDI08; ITS, LSU, *rpb2* and *tub2* sequences GenBank PV830644, PV830648, PV835322 and PV835326, and culture KDI017; ITS, LSU, *rpb2* and *tub2* sequences GenBank PV830645, PV830649, PV835323 and PV835327.

Notes: The fungus is a necrotrophic pathogen associated with leaf spots and stem necrosis in *Digitaria insularis*. *Didymella digitariae* is phylogenetically closely related to *D. maydis* (neotype CBS 588.69). The sexual-asexual connection of *D. maydis* was first established by Mukunya & Boothroyd (1973). This species was later recombined as *Peyronellaea zeae-maydis* by Aveskamp *et al.* (2010) and subsequently corrected to *Peyronellaea maydis* by Crous *et al.* (2014). Chen *et al.* (2015) reclassified the species based on its asexual morph and introduced the currently accepted name *Didymella maydis*. Although *D. digitariae* and *D. maydis* form a well-supported clade in multilocus phylogenetic analyses (ITS, LSU, *tub2* and *rpb2*), they differ in host and substrate association. *Didymella maydis* was isolated from dead tissue of *Zea mays*, while *D. digitariae* was collected from living leaves of *D. insularis*. These differences, along with subtle morphological (smaller pycnidia and conidia) and cultural distinctions, support the recognition of *D. digitariae* as a distinct species within the genus *Didymella*.

Colour illustrations: *Digitaria insularis* growing next to the roadside in São Gotardo, Brazil. Necrotic spots caused by *Didymella digitariae* on living leaves of *D. insularis*; pycnidia on PDA; cross section of the pycnidia; conidiogenous cells and aseptate conidia; conidia hyaline, 0–1-septate, allantoid, fusoid to limoniform; chlamydospores globose to spherical, mostly catenulate. Scale bars = 10 µm.



Phylogenetic relationships of *Didymella digitariae* (highlighted with a coloured block and bold font) inferred from Bayesian Inference analysis (BI) of a combined ITS, LSU, *rpb2* and *tub2* data set. *Epicoccum nigrum* was used as the outgroup. Bayesian inference of the phylogenetic relationships was calculated using the Markov chain Monte Carlo (MCMC) approach as implemented in MrBayes v. 3.2.6 on XSEDE (Ronquist *et al.* 2012). Culture or collection numbers are indicated for all species. Sequences from material with a type status are indicated in asterisk.

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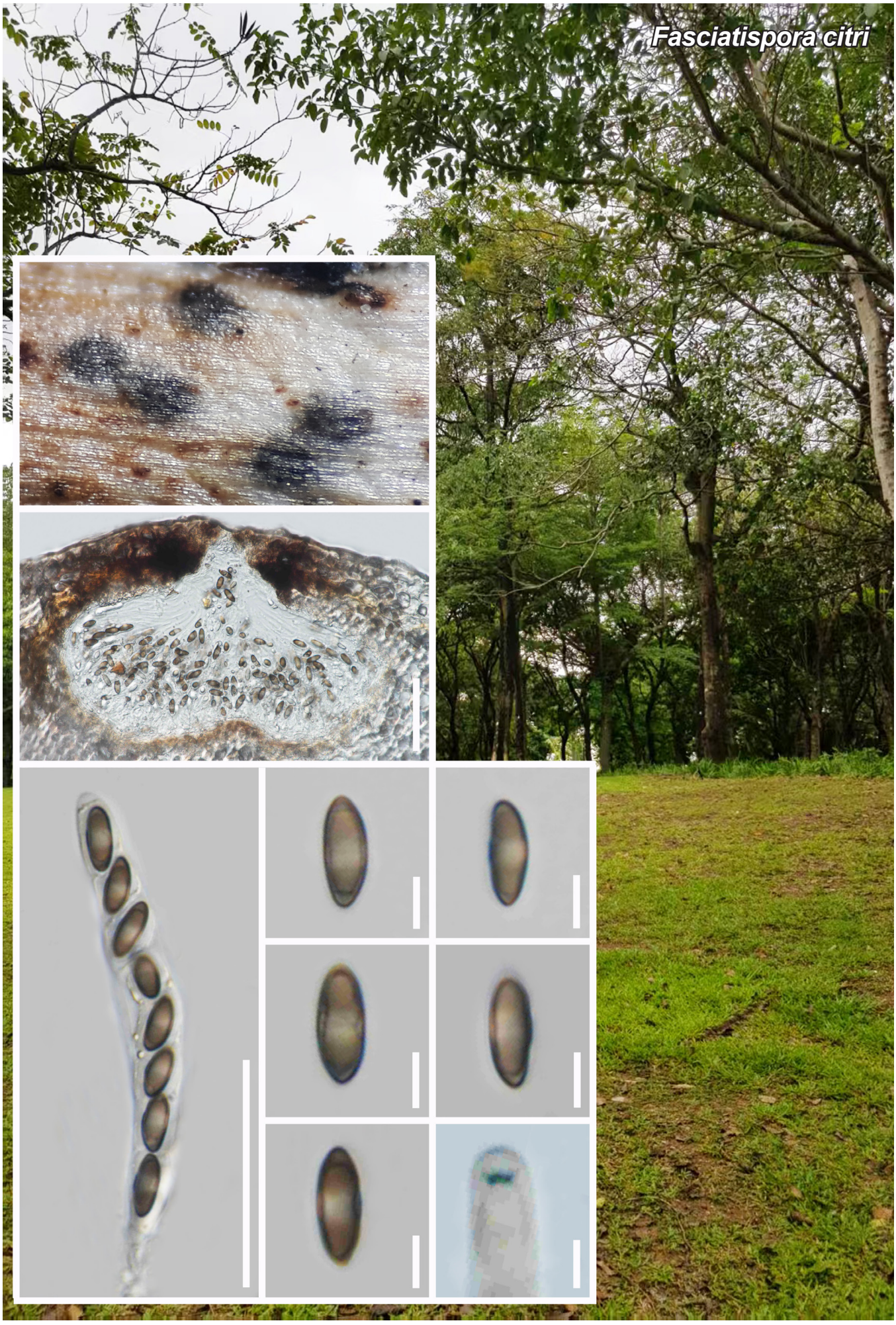

Fasciatispora citri

Fungal Planet 1876 MB 860996

Fasciatispora citri Tennakoon, N.I. de Silva & S. Hongsanan, ***sp. nov.***

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

Classification: *Fasciatisporaceae*, *Xylariales*, *Sordariomycetes*.

Ascomata forming as black dots on the host surface, solitary or aggregated into small groups, immersed beneath the clypeus, subglobose-globose, coriaceous, ostiole central or slightly protruding outside, ostiolar canal periphysate, 250–280 × 150–170 µm. *Peridium* multi-layered, outer layer comprising brown, thick-walled cells of *textura angularis*, inner layer composed of hyaline, thin-walled cells of *textura angularis*, 10–15 µm wide. *Paraphyses* hyaline, filamentous, flexuous, numerous, septate. *Asci* 8-spored, unitunicate, cylindrical, apically rounded, short-pedicellate, with a J+, subapical ring, 60–70 × 7–9 µm. *Ascospores* uniseriate, unicellular, initially hyaline, olivaceous brown when mature, with wide equatorial pallid band, ellipsoidal to fusoid, without a mucilaginous sheath and lacking a germ slit, guttulate, smooth-walled, 8–10 × 4–4.5 µm.

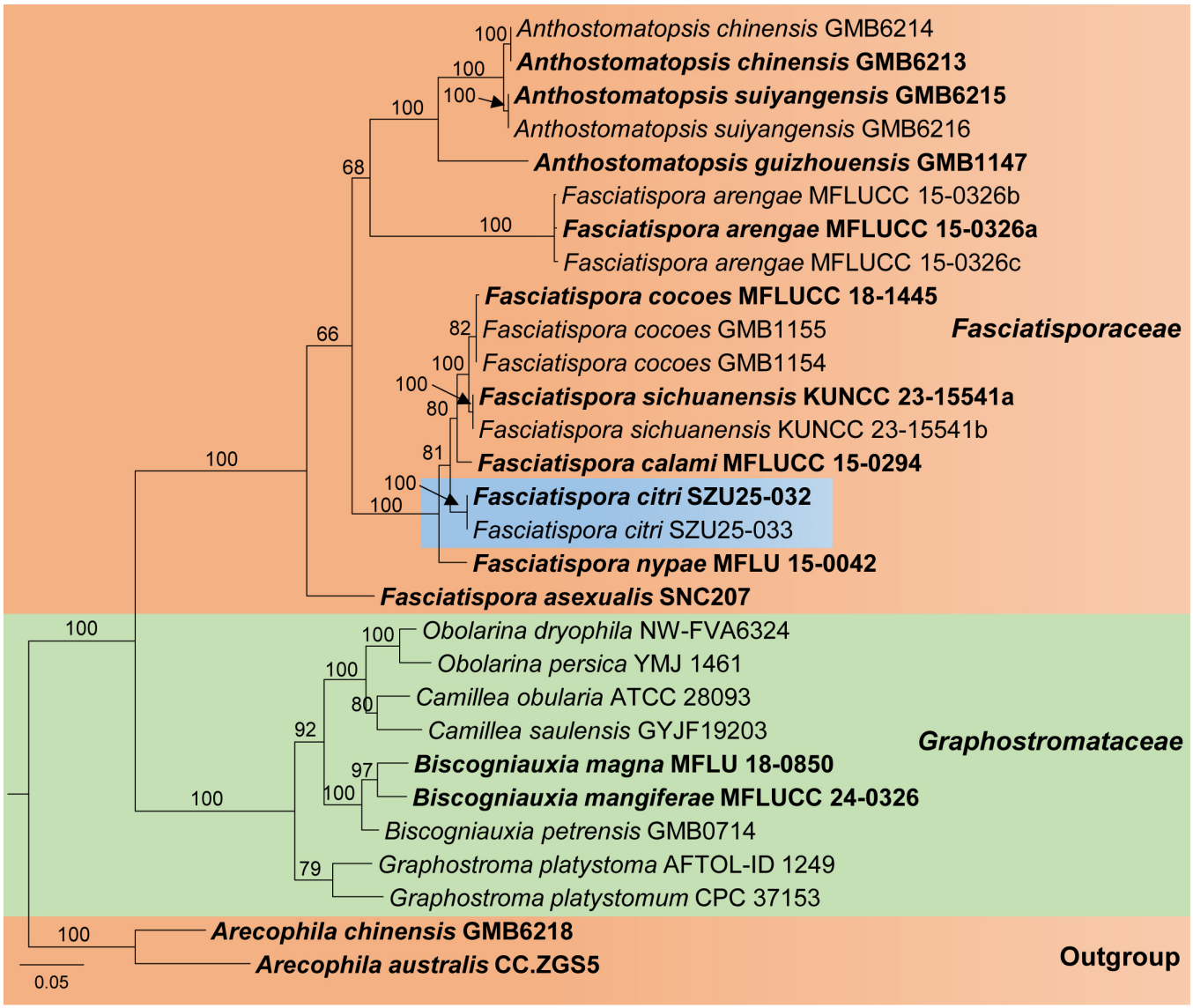
Typus: **China**, Jiangxi Province, Nanchang, on dead twig of *Citrus maxima* (*Rutaceae*), 25 Feb. 2024, *D.S. Tennakoon*, DS028A (**holotype** SZU25-032, **isotype** SZU25-033; ITS, LSU, *tef* and *rpb2* sequences GenBank PV845194-PV845189-PV853879-PV853881 and PV845195-PV845190-PV853880-PV853882).

Notes: *Fasciatispora* was introduced by Hyde (1991) to accommodate *F. nypae* as the type species. This genus is characterized by having unicellular, brown ascospores with a unique central pallid band (Hyde 1991, Alias *et al*. 1994, Hidayat *et al*. 2007, Hyde *et al*. 2019, Dissanayake *et al*. 2024, Habib *et al*. 2025). *Fasciatispora* species have been reported as saprobes on palms and other monocotyledons in terrestrial and coastal habitats (Hyde *et al*. 2019, Dissanayake *et al*. 2024). The phylogeny inferred from the LSU, ITS, *tef* and *rpb2* sequences demonstrated that the new species *F. citri* nested with the clade containing *F. calami* (MFLUCC 15-0294), *F. cocoes* (MFLUCC 18-1445, GMB1154 and GMB1155), and *F. sichuanensis* (KUNCC 23-15541a and KUNCC 23-15541b) with 81 % statistical support. In particular, it forms an independent lineage between *F. nypae* (MFLU 15-0042) and *F. calami* (MFLUCC 15-0294). *Fasciatispora citri* can be distinguished from *F. calami* and *F. nyphae* in their ellipsoidal to fusoid, smaller ascospores (8–10 × 4–4.5 µm vs 12–13 × 5–6 µm vs 11–18 × 5–8 µm) and lacking a mucilaginous sheath (Hyde 1991, Hyde *et al*. 2017). In addition, there are 17 base pair differences across 526 nucleotides (3.23 %) of the ITS (+5.8S) region between *F. citri* (SZU 25-032) and *F. nyphae* (MFLU 15-0042).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Fasciatispora cocoes* [strain MFLU 19-2143, GenBank MW240618.1; Identities = 545/583 (93 %), 19 gaps (3 %)], *F. cocoes* [strain SNT331, GenBank PP592397.1; Identities = 505/528 (96 %), four gaps (0 %)], and *Xylariomycetidae* sp. [strain FL0915, GenBank JQ760548.1; Identities = 520/556 (94 %), 19 gaps (3 %)]. Closest hits using the **LSU** sequence are *F. cocoes* [strain MFLUCC 18-1445, GenBank NG_068663.1; Identities = 1231/1266 (97 %), 16 gaps (1 %)], *F. calami* [strain MFLUCC 15-0294, GenBank MF459055.1; Identities = 1229/1264 (97 %), 16 gaps (1 %)], and *F. sichuanensis* [strain KUNCC 23-15541, GenBank PV578340.1; Identities = 1199/1228 (98 %), 14 gaps (1 %)]. Closest hits using the ***tef*** sequence are *F. sichuanensis* [strain KUNCC 23-15541, GenBank PV608846.1; Identities = 926/947 (98 %), no gaps], *F. cocoes* [strain MFLU 19-2143, GenBank MW759499.1; Identities = 939/969 (97 %), no gaps], *F. cocoes* [strain SNT331, GenBank PP740433.1; Identities = 912/936 (97 %), no gaps], and *F. cocoes* [strain SNC62A, GenBank PP740429.1; Identities = 917/945 (97 %), no gaps]. Closest hits using the ***rpb2*** sequence are *F. sichuanensis* [strain KUNCC 23-15541, GenBank PV595326.1; Identities = 1026/1065 (96 %), one gap (0 %)], *F. cocoes* [strain SNC01, GenBank PP761058.1; Identities = 1023/1063 (96 %), one gap (0 %)], *F. cocoes* [strain SNC137, GenBank PP780215.1; Identities = 1023/1065 (96 %), one gap (0 %)], and *F. cocoes* [strain SNC57, GenBank PP780212.1; Identities = 1004/1044 (96 %), one gap (0 %)].

Supplementary material: doi: 10.6084/m9.figshare.30352027 (table); TreeBASE study ID: S32200 (matrix and resulting tree).

Colour illustrations: Holotype collection area in Jiangxi, China. Appearance of ascomata on dead twig of *Citrus maxima*; vertical section of ascoma; asci; ascospores; J+ reaction of apical ring in Melzer's reagent. Scale bars: section = 50 µm; asci = 30 µm; ascospores and apex of the ascus = 5 µm.



Phylogenetic analysis for *Fasciatispora citri* inferred from a maximum likelihood analysis of ITS/LSU/*tef*/*rpb2* sequences. The analysis was performed with RAxML v. 8.2.12 (Stamatakis 2014) using the rapid bootstrapping and search algorithm, with GTR+GAMMA nucleotide substitution model, and 1000 bootstrap replicates. Maximum likelihood support values > 65 % are indicated on the branches. The tree is rooted with *Arecophila australis* (CC. ZGS5) and *A. chinensis* (GMB6218). Ex-type strains are in **bold**. The novel species is indicated in a blue box. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Scale bar on the tree indicates the expected number of changes per site.

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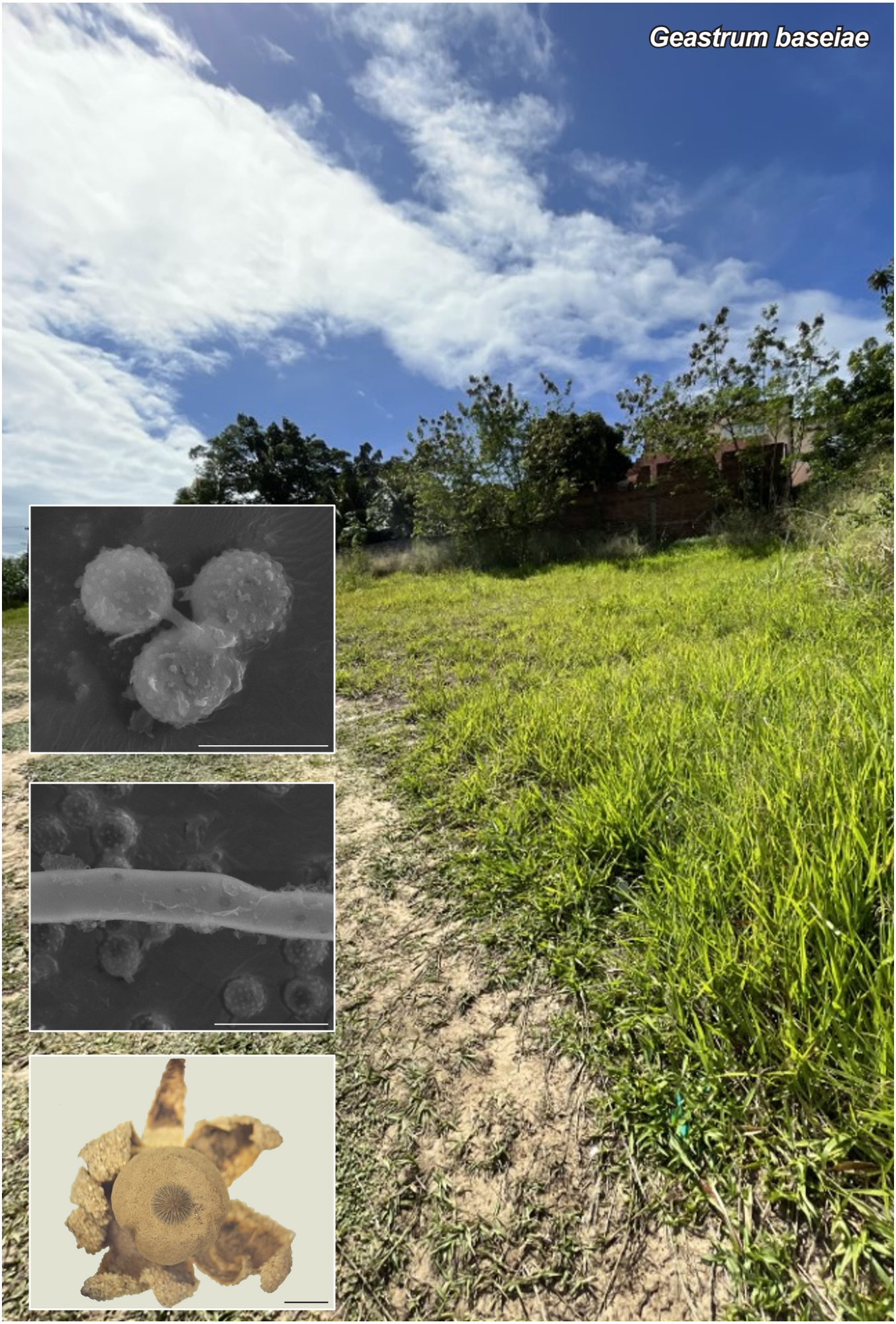

Geastrum baseiae

Fungal Planet 1877 MB 860341

Geastrum baseiae R.J. Ferreira, Monteiro, J.A.S. Silva, S.R. Lacerda & A.A. Lima, ***sp. nov.***

Etymology: Named for Dr. Iuri G. Baseia, in recognition of his pioneering studies on earthstar fungi (*Geastrales*, *Geastraceae*) in South America.

Classification: *Geastraceae*, *Geastrales*, *Phallomycetidae*, *Agaricomycetes*, *Agaricomycotina.*

Unexpanded basidiomata absent. Expanded *basidiomata* arched, 12.8–16.8 mm tall (including peristome) × 19.5–27.3 mm wide. *Exoperidium* splitting into 9–10 planar to revolute, triangular and irregular rays. *Mycelial layer* single, completely encrusted with sand at the base, cottonose, persistent, brownish grey (KW5F2; Kornerup & Wanscher 1978), formed by hyaline hyphae in 5 % KOH, branched, 1.3–2.7 µm wide, lumen evident, mostly straight walls, and 0.3–0.8 µm thick. *Fibrous layer* papery, beige (KW4C3), < 1 mm thick when fresh, formed by hyaline hyphae in 5 % KOH, 2.1–4.3 µm wide, lumen evident, unbranched, straight walls, and 0.6–1.2 µm thick. *Pseudoparenchymatous layer* peeling off in irregular patches, non-rimose, glabrous, brownish orange (KW5C3) to brown (KW5E5), absent of collar, formed by globose to pyriform cells, 15.6–61.1 µm high × 13.7–31.8 µm wide, hyaline in 5 % KOH, straight walls, 0.4–1.5 µm thick. *Endoperidial body* globose, 6.1–7.3 mm high × 9.1–13.5 wide, stalked, with protruding hyphae, non-pruinose, brownish grey (KW5C2 to 5E2), and apophysis absent. *Peristome* regularly plicate, 22–35 folds, mammiform, brownish grey (KW5E2 to 5F2), 0.9–1.2 mm high, and non-delimited. *Mature gleba* powdery and brown (KW6F4). *Eucapillitium* 2.4–4.8 µm wide, branched, encrusted, verrucose, lumen evident, hyaline to light brown in 5 % KOH, straight walls, 0.9–1.9 µm thick. *Basidiospores* globose, 5.4–6.1 × 4.9–6.1 µm [av. = 5.7 ± 0.15 × 5.41 ± 0.19, Qm = 1.05, n = 20), pale brown in 5 % KOH, covered by columnar warts with truncate apex, 0.4–0.9 µm tall.

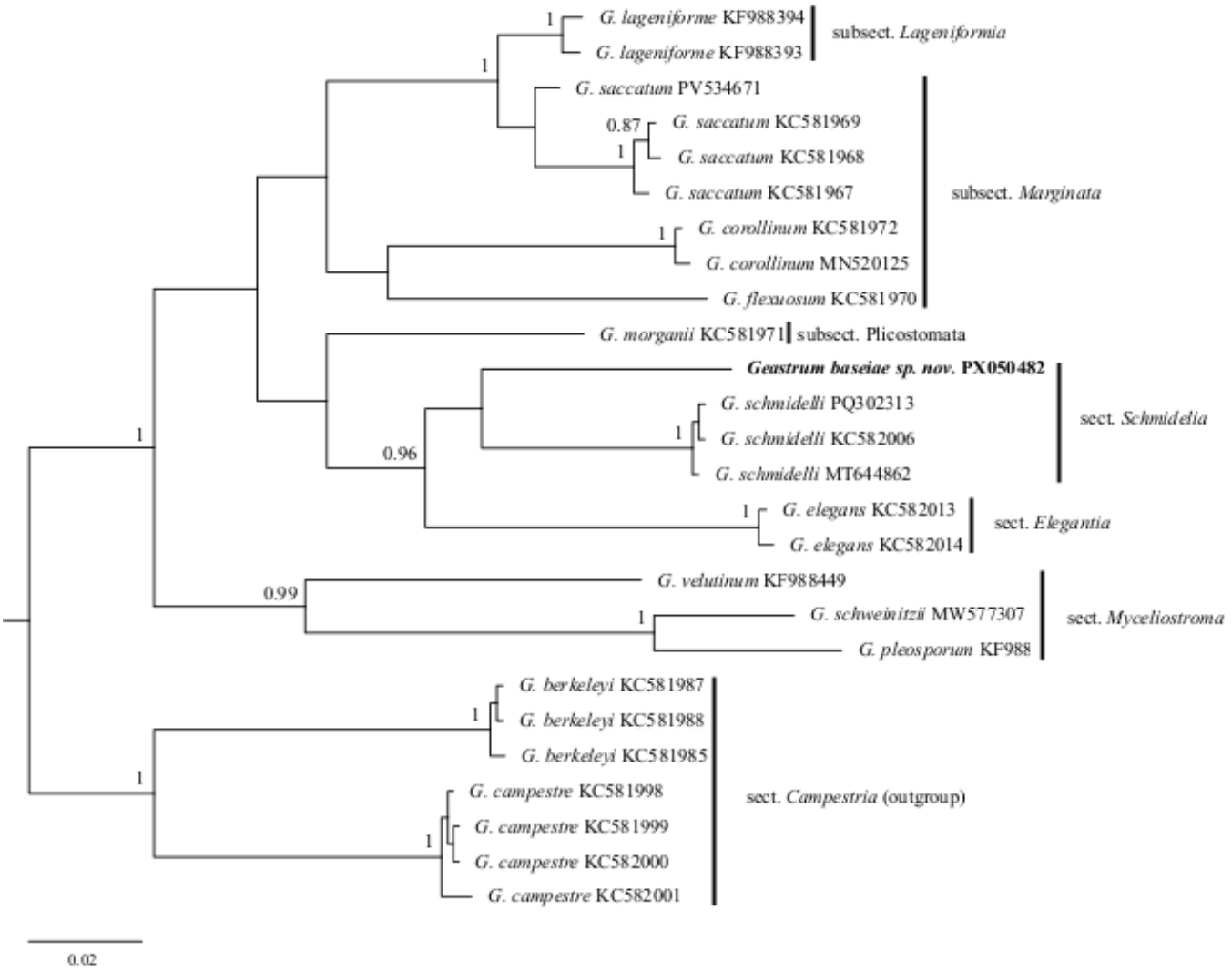
Habit and habitat: Basidiomata growing on soil.

Typus: **Brazil**, Rio Grande do Norte, Natal, 35°12'S, 05°51'W, 30 m.a.s.l., on soil, 28 Jul. 2017, *R.J. Ferreira* (**holotype** HCDAL-Fungos 253, ITS sequence GenBank PX050482).

Notes: Based on morphological and molecular characters, *Geastrum baseiae sp. nov.* has shown similarities to *G. schmidelii*, *G. elegans*, *G. morganii*, *G. violaceum*, and *G. lloydianum*, whose occurrences were registered for the Brazilian northeastern region and with whom it shares the sulcate peristome feature (Zamora *et al*. 2014a, b). Although those could be confused at first sight there are remarkable differences such as *G. schmidelii* and *G. elegans* having a conical peristome, glabrous endoperidium and basidiospores measuring 4–7 µm wide (Vittadini 1842, Zamora *et al*. 2014a, b). *Geastrum morganii* is distinct due to its saccate shape, a smooth mycelial layer not encrusted to furfuraceous, sessile and glabrous endoperidium, with a conical peristome, and basidiospores measuring 3–4 µm wide (Jeppson *et al*. 2013). *Geastrum violaceum* has a vibrant violet basidiomata with a non-encrusted mycelial layer, sessile and glabrous endoperidium, collar on the pseudoparenchymatous layer and basidiospores measuring 2.7–3 µm wide (Sousa *et al*. 2014). Lastly *G. lloydianum* has sessile to substipitate basidiomata with a noticeable apophysis when dried and a conical peristome (Trierveiler-Pereira & Silveira 2012). Therefore, morphological and molecular data (ITS nrDNA) provide strong support for considering *Geastrum baseiae sp. nov.* a new species.

Supplementary material: TreeBASE study: S32330 (alignment and trees).

Colour illustrations: Collection site located in an anthropic setting, Natal, Rio Grande do Norte, Brazil (photo credit: A.A. Lima). Basidiospores on scanning electron microscope (SEM); capillitium on SEM; dried basidiomata. Scale bars: basidiomata = 5 mm; capillitium = 10 µm; basidiospores = 5 µm.



ITS and LSU nrDNA phylogenetic tree obtained with MrBayes v. 3.2.7a (Huelsenbeck & Ronquist 2001) under T92+G model for 2M generations. The new species is highlighted in **bold**. The posterior probabilities greater than 0.85 are indicated on the branches. The species *G. berkeleyi* and *G. campestre* (sect. *Campestria*) were included as outgroup. Figtree v. 1.4.4 and Inkscape v. 1.4.2 software were used to edit the final tree.

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Geoglossum martinae
50 µm

Fungal Planet 1878 MB 859685

Geoglossum martinae M. Romero & P. Alvarado, ***sp. nov*.**

Etymology: Named after Martina Romero Peña, granddaughter of one of the authors.

Classification: *Geoglossaceae*, *Geoglossales*, *Geoglossomycetes*.

Ascomata growing in groups at various developmental stages, some deeply buried in the soil or moss, measuring 1–3.5 × 0.4–1.8 cm. *Clava* represents 40–60 % of the total ascoma height (0.4–2.2 cm); matte black with a dry surface that becomes shiny when wet, finely granular, somewhat wrinkled with age, showing irregular shapes including laterally compressed lanceolate forms, cylindrical ones with longitudinal twisted grooves, irregularly club-shaped, or spatulate with broader centers and narrowed, irregularly ridged upper zones. *Stipe* 0.6–1.5 cm, cylindrical, tapering and curving at the base, dark brown black, glabrous surface, smoother than the clava; spatulate forms have a short, soil-adhered stipe; lanceolate or cylindrical forms have longer, thinner, and more distinct stipes emerging among high moss. *Spores* hyaline and multiguttulate when young, becoming dark brown in water and blackish brown in Melzer's reagent, forming rows of larger guttules before disappearing in maturity; cylindrical, slightly curved, sharp at ends, mostly 7-septate, (49.5–)51.9–69.9(–74.0) × (5.9–)6.2–7.8(–8.1) µm; Q = (7.1–)7.4–10.1(–11.4); N = 25; Me = 61.1 × 6.9 µm; Qe = 8.9. *Asci* 170–200 × 17–20 µm, fusoid with rounded apex, 8-spored, euamyloid; tips turn dark green to bluish green in Melzer's. *Paraphyses* slender (3–4 µm diam.), forming a network above the asci, with dark brown parietal/incrusting pigment, blackish in Melzer's, septate with increasing septum density toward the apex; most end in hooked, capitate (5.5–9 µm) or irregularly dilated forms. *Medullary excipulum*: cylindrical cells, 8–18 × 6–10 µm. *Hypothecium*: pseudoparenchymatous tissue with ovoid, ellipsoid, and subangular cells, 4–7 µm diam. *Ectal excipulum*: chains of 50–75 µm made of 3–5 elements, 8–15 × 3–4 µm, final element elongate-pyriform, 5–8 µm diam.

Habitat and distribution: Found between January and April, growing in groups in Mediterranean forest, among moss under *Quercus ilex*, with *Cistus ladanifer* and *Genista scorpius* or in acidic pastures with *Retama sphaerocarpa* and *Tuberaria guttata*, in southwestern Iberian Peninsula.

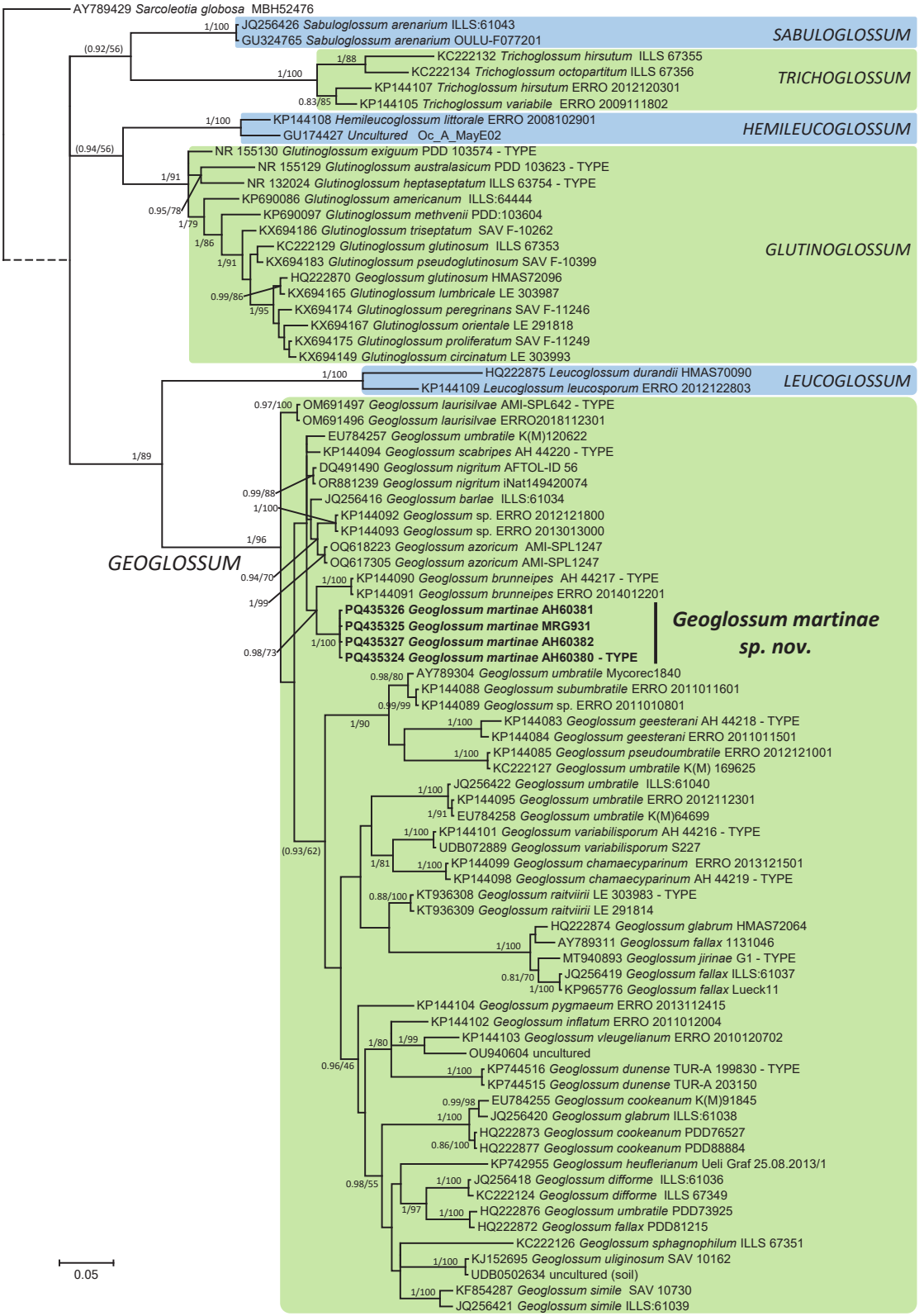
Typus: **Spain**, Extremadura, Valle de la Serena, Sierra de Utrera trail, Mediterranean forest under *Quercus ilex* and *Cistus ladanifer*, 8 Mar. 2024, *M. Romero*, MRG923 (**holotype** AH60380, ITS sequence GenBank PQ435324).

Additional materials examined: **Spain**, Andalucia, Cádiz, Castellar de la Frontera, 4 Jan. 2025, *M. Romero*, MRG980 (ITS sequence GenBank PV984495); Extremadura, Badajoz, Sierra de Agalla, 29 Mar. 2018, *M. Romero*, MRG766 (**paratype** AH60381, ITS sequence GenBank PQ435326); Extremadura, Badajoz, Magacela, Las Torralbas estate, 25 Mar. 2024, *M. Romero*, MRG927 (**paratype** AH60382, ITS and LSU sequences GenBank PQ435327, PQ427317); Extremadura, Badajoz, Valle de la Serena, Sierra de Utrera trail, 15 Mar. 2024, *M. Romero* (**paratype** MRG931); Extremadura, Badajoz, Benquerencia de la Serena, Mediterranean forest under *Quercus ilex*, *Cistus ladanifer* and *Genista scorpius*, 15 Mar. 2024, *M. Romero*, MRG931 (ITS and LSU sequences GenBank PQ435325 and PQ427316).

Notes: *Geoglossum martinae* is distinguished by its medium-sized ascomata, matte black clava with variable forms, a glabrous, sinuous, dark stipe, fusoid euamyloid asci, cylindrical 7-septate spores, and predominantly hooked paraphyses. It differs from similar species in size, clava form, stipe texture, ascus amyloidity, and paraphyses morphology. *Geoglossum brunneipes* (Arauzo & Iglesias 2014) differs from *G. martinae* by having larger apothecia, ranging from 30 to 79 mm in height, and a differently shaped clava, from clavate to elliptic-lanceolate; the stipe ranges from subcylindrical to laterally compressed; ascus apical pore hemiamyloid in IKI; paraphyses with a terminal element moderately to strongly thickened, straight or slightly curved, not hook-shaped. *Geoglossum azoricum* (Crous *et al.* 2023) differs from *G. martinae* by having much larger and slenderer apothecia, the ascus apical pore is hemiamyloid, ascospores are longer and narrower, and it grows in laurel forests (laurisilva). *Geoglossum barlae* (Boudier 1889) differs from *G. martinae* by having significantly larger ascomata; the clava is also larger and of different shapes, lanceolate or subcylindrical, typically with only one longitudinal groove; the paraphyses have straight terminal elements of similar diameter, the last one being slightly wider with septal constrictions, and few are hook-shaped. *Geoglossum scabripes* (Arauzo & Iglesias 2014) has smaller apothecia, a rough stipe, and a small clava making up 1/3 of the total ascoma, shaped from cylindrical to clavate; its asci are hemiamyloid and pseudoparaphyses are present. *Geoglossum umbratile* (Saccardo 1878) differs from *G. martinae* by having larger ascomata with a clava ranging from ellipsoid to compressed or lanceolate in shape, with a central groove running along the entire apothecium; paraphyses have a terminal element that is cylindrical, clavate, or fusiform; ascospores are larger. Finally, *G. laurisilvae* (Crous *et al*. 2022) differs from *G. martinae* by having larger ascospores, a brown stipe with scaly ornamentation, and a different habitat – laurel forest.

Supplementary material: doi: 10.6084/m9.figshare.30354598 (table, alignment and tree figure).

Colour illustrations: Spain, Extremadura, Quintana de la Serena. Mediterranean forest habitat where the holotype was found, with *Quercus ilex*, *Cistus ladanifer*, and *Genista scorpius*. Column (top to bottom, left to right): apical pores of asci in Melzer's reagent ×1000; paraphyses in KOH ×1000; asci and paraphyses in water ×400; spores in Melzer's reagent ×1000; ascomata of MRG927; ascomata of the type. Scale bars: third image of the column = 50 µm; all others = 20 µm.



An ITS consensus phylogram (50 % majority rule) of selected species of *Geoglossum* (*Geoglossaceae*, *Geoglossales*) and related genera (with *Sarcoleotia globosa* as outgroup) obtained using MrBayes v. 3.2.6 (Ronquist *et al*. 2012) from 8475 sampled trees. Nodes were annotated if they were supported by ≥ 0.95 Bayesian posterior probability (left) or ≥ 70 % maximum likelihood bootstrap proportions (right) obtained in RAxML v. 8.2.12 (Stamatakis 2014). Non-significant support values are presented inside parentheses. Sequences newly generated in this study are in **bold**.

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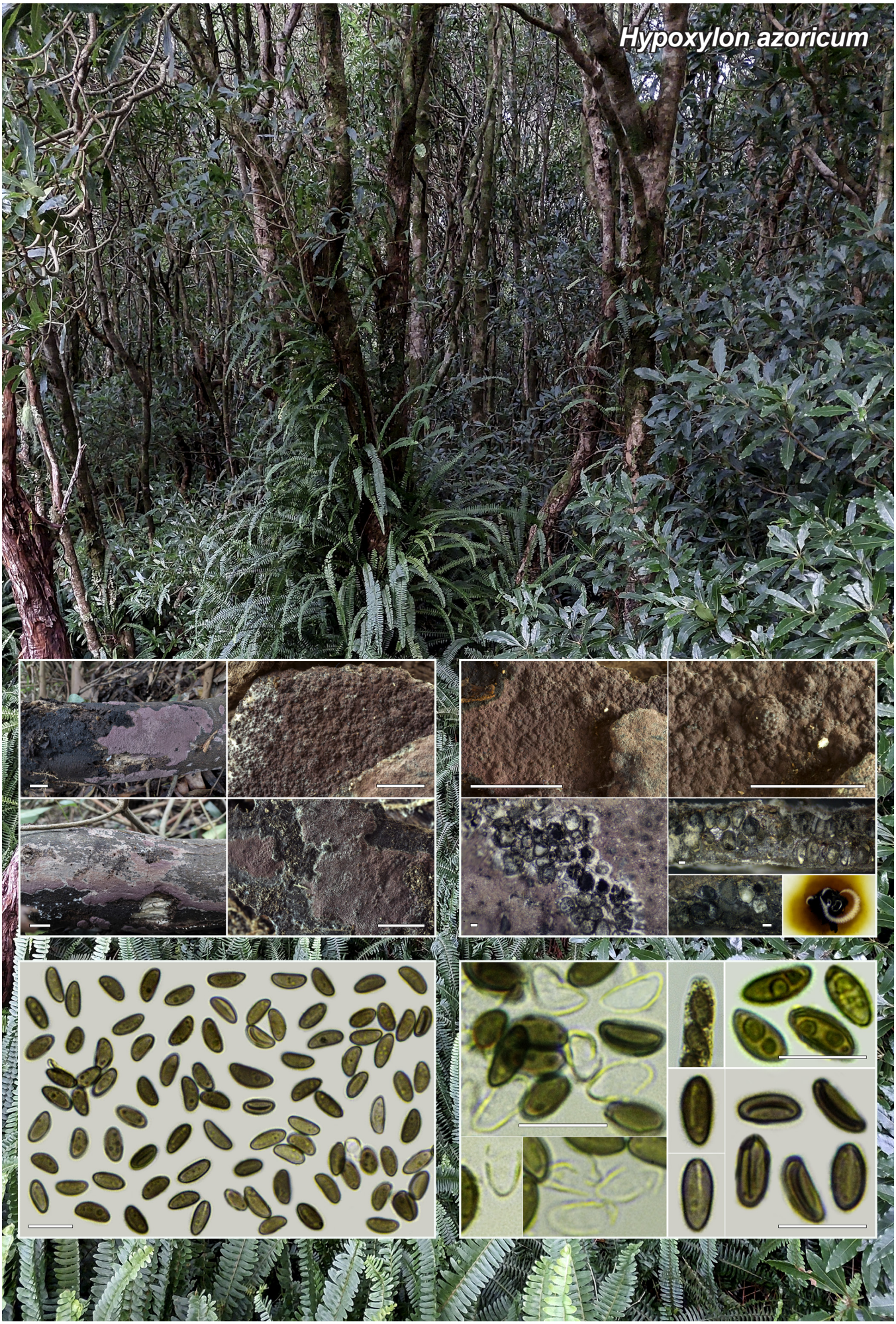

Hypoxylon azoricum

Fungal Planet 1879 MB 855548

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

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

Classification: *Hypoxylaceae*, *Xylariales*, *Sordariomycetes*.

Stromata effused to effused-pulvinate, corticolous, 28–60 mm long × 13–28 mm broad × 0.5–1.2 mm thick, with abrupt to effused concolourous margin, very thin when immature; surface lilacinose at first (Ség. 7, 8; Séguy 1936), dark deep raspberry (Ség. 36, 42) when mature, tending to mahogany red or henna-coloured (Ség. 81, 101) on maturing, finally carbonaceous black; sometimes with very visible perithecial mounds, generally with rough appearance (conspicuous), plane to slightly undulate, velvety, matt, with black ostiolar areas, black immediately beneath surface and between perithecia, tissue below perithecial layer inconspicuous, with rust granules (Ség. 151), stromata with amber (Ség. 158, 160) to ochre (Ség. 196, 211) extractable pigments in 10 % KOH, subperithecial tissue inconspicuous 0.2–0.3 mm thick. *Perithecia* spherical to obovoid, sometimes ellipsoid, 0.15–0.30 mm × 0.15–0.25 mm, the fertile perithecial layer may be seated on two up to three layers of old and empty perithecia. *Ostioles* higher than the stromatal surface, black, minutely umbilicate, rarely surrounded by a white substance. *Asci* 8-spored, total length 105–160 µm, the spore-bearing parts 60–80 µm long × 6–7 µm broad, the stipes 25–40 µm long, with apical apparatus discoid, 0.5–1 µm high × 2–2.5 µm broad, bluing in IKI 2 solution (potassium iodide 6 g; resublimated iodine 2 g; distilled water, up to 100 mL). *Ascospores* brown to dark green, ellipsoid-inequilateral to often slightly crescentic, (6.4–)7.0–*7.6*–8.2(–9.4) × (3.0–)3.2–*3.5*–3.7(–3.9) µm, Q = (1.8–)2.0–*2.2*–2.5(–2.8), N = 100, with a faint, straight, spore-length germ slit on the more convex side; perispore dehiscent in 10 % KOH, smooth.

Distribution: Currently known only from the type location in the Azores Islands.

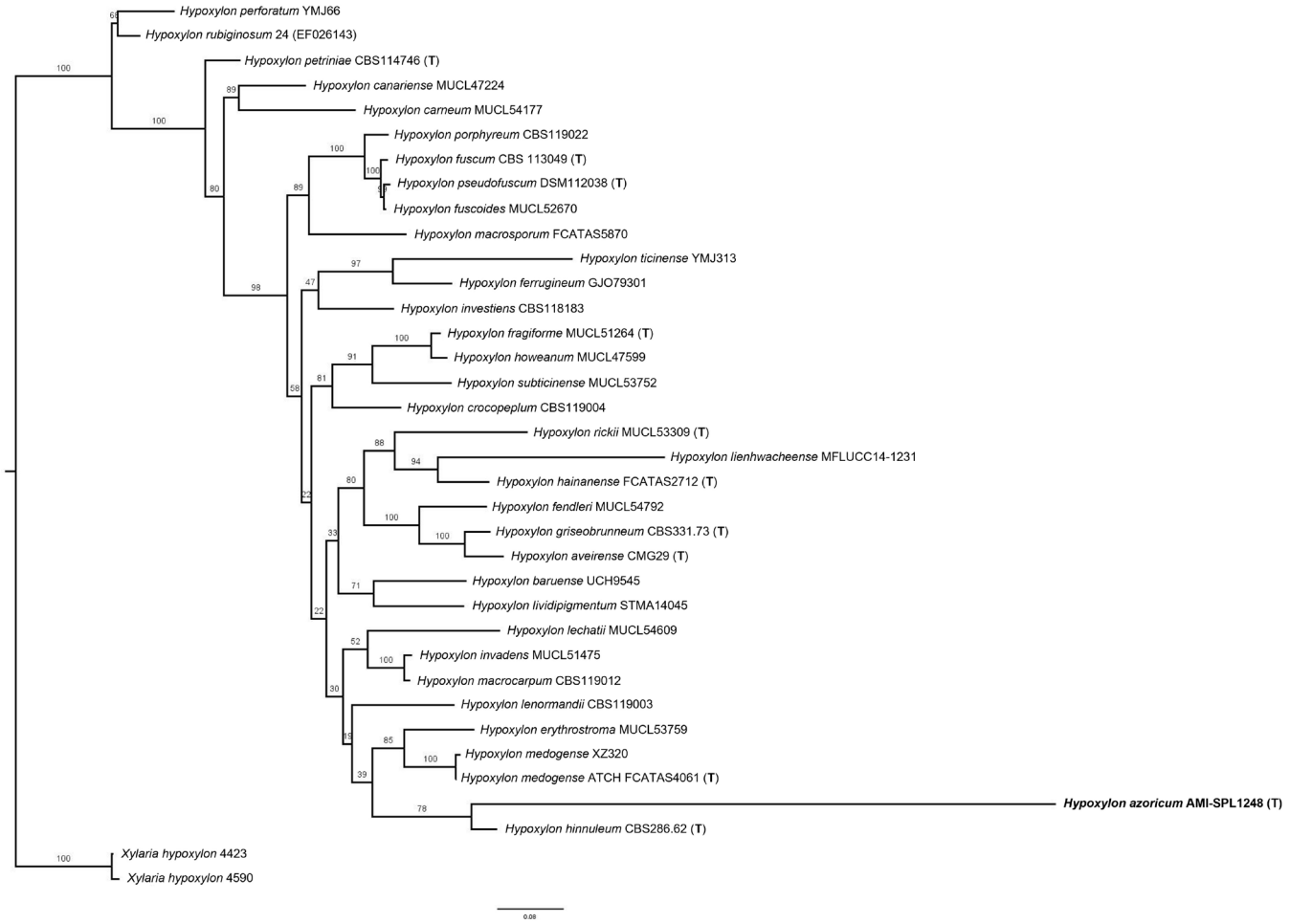
Typus: **Portugal**, Azores, Terceira, Praia da Vitória, Fontinhas, Largo São João, N38º45'17.9", W27º07'30.2", 0 m.a.s.l., on fallen branch of *Laurus azorica*, 14 Jan. 2022, *A. Mateos* & *S. De la Peña-Lastra* (**holotype** AMI-SPL1248; ITS, LSU and *RPB2* sequences GenBank PQ236694, PQ236695 and PX373527).

Colour illustrations: Portugal, Azores, Terceira, Fontinhas, Largo São João, laurel forest, where the holotype of *Hypoxylon azoricum* was collected. Left column: in upper photo, stromata on bark correspond with the holotype (two pictures left, immature), (two pictures right, mature); and the bottom photo corresponds to ascospores (*H_2O). Right column: in upper photo, stromata overmature (two pictures), stromata in horizontal section with the perithecia, stromata in vertical section, KOH extractable pigments after 1 min of incubation; and the bottom photo ascospores with perispores dehiscing in 10 % KOH (three pictures left); in upper photo, asci (*IKI 2); upper right, ascospores (*IKI 2); and the bottom photo is ascospores with germ slits (three pictures *H_2O). Scale bars: stromata immature and overmature left = 10 mm; stromata mature and overmature detail right = 5 mm; stromata section = 0.1 mm; all ascospores = 10 µm.

Notes: The molecular studies of Sánchez-Ballesteros *et al*. (2000), Triebel *et al*. (2005) and Pelaez *et al*. (2008) with internal transcribed spacer region (ITS), the studies of Hsieh *et al*. (2005) based on the protein-coding genes alpha-actin (*ACT*) and beta-tubulin (*TUB2*), as well as those of Tang *et al*. (2009) with a multigene phylogeny derived from a combination of rRNA and protein-coding genes, as well as others such as Jaklitsch *et al*. (2014), Kuhnert *et al*. (2014), Daranagama *et al*. (2015, 2016), Wendt *et al*. (2018) and Cedeño-Sanchez *et al*. (2024) using multigene phylogeny have served to develop a family genealogy, create new genera and resolve hypoxyloid clades.

Hypoxylon azoricum has umbilicate ostioles and lacks disks, which are typical characters of the genus *Hypoxylon*, not present in related genera. Its most distinctive character is a multilayered stromata with perithecial mounds with moderate to strong relief, also typical of several species of the *H. rubiginosum* complex (Anderson 2008), with which it has other analogies such as the similar colour of the stromal surface and the spherical or subovoid perithecia forming multilayers. The morphologically most similar *H. perforatum* has a similar surface colour, as well as the colour of the KOH-extractable pigments, but differs in the ostioles which are surrounded by a ring of white substance and has larger spores [9.7–11.5 × 4.7–5.3 µm (av. = 10.9 × 4.9 µm)] (Anderson 2008, Fournier *et al*. 2010) (ITS similarity 80.14 %). *Hypoxylon rubiginosum* is distinct by its rust or sienna coloured surface, orange to rust KOH-extractable pigments, larger perithecia (300–650 µm × 450–800 µm) and larger ascospores [8.8–11(–12) × 4–5.5 µm (av. = 10.1 × 4.4 µm)] (Anderson 2008, Fournier *et al*. 2010) (ITS similarity 81.99 %). *Hypoxylon petriniae* is distinguished by its black, linear stromal margins, orange to rust-coloured KOH-extractable pigments, larger perithecia (250–380 µm × 250–500 µm), white-ringed ostioles, and much larger ascospores [8.8–11.5 (–13) × 4.8–6 µm (av. = 10.7 × 5.1 µm)] (Anderson 2008, Fournier *et al*. 2010). All three of the above species may have perithecial multilayers. *Hypoxylon fuscum* differs from *H. azoricum* in having ostioles with white substance ring, much larger spores [11–16 × 5–8 µm (av. = 13.2 × 5.8 µm)] and with sigmoid germination cleft (ITS similarity 77.23 %). *Hypoxylon carneum* differs in dark purple or dark vinous stromatic colour and livid violet KOH extractable pigments, ostioles surrounded by a ring of white substance and somewhat larger spores [8.8–11 × 4–4.8 µm (av. = 9.8 × 4.6 µm)] (Fournier *et al*. 2010) (ITS similarity 68.48 %). *Hypoxylon macrocarpum, H. macrosporum* and *H. porphyreum* (ITS similarity 74.35, 80.21 and 78.14 %, respectively) have olivaceous KOH-extractable pigments and larger ascospores (Fournier *et al*. 2010).

Supplementary material: doi: 10.6084/m9.figshare.30090295 (alignment and table).



The most probable maximum likelihood (ML) tree obtained from a concatenated dataset of the ITS-LSU-*RPB2* (GenBank accession numbers in supplementary material). The tree was inferred using IQ-TREE v. 2.1.3 (Nguyen *et al*. 2015) under the best-fit substitution model selected by ModelFinder (Kalyaanamoorthy *et al*. 2017). Branch support was assessed with 1000 ultrafast bootstrap (UFBoot) replicates (Minh *et al*. 2013), and ML bootstrap values ≥ 70 % were considered significant.

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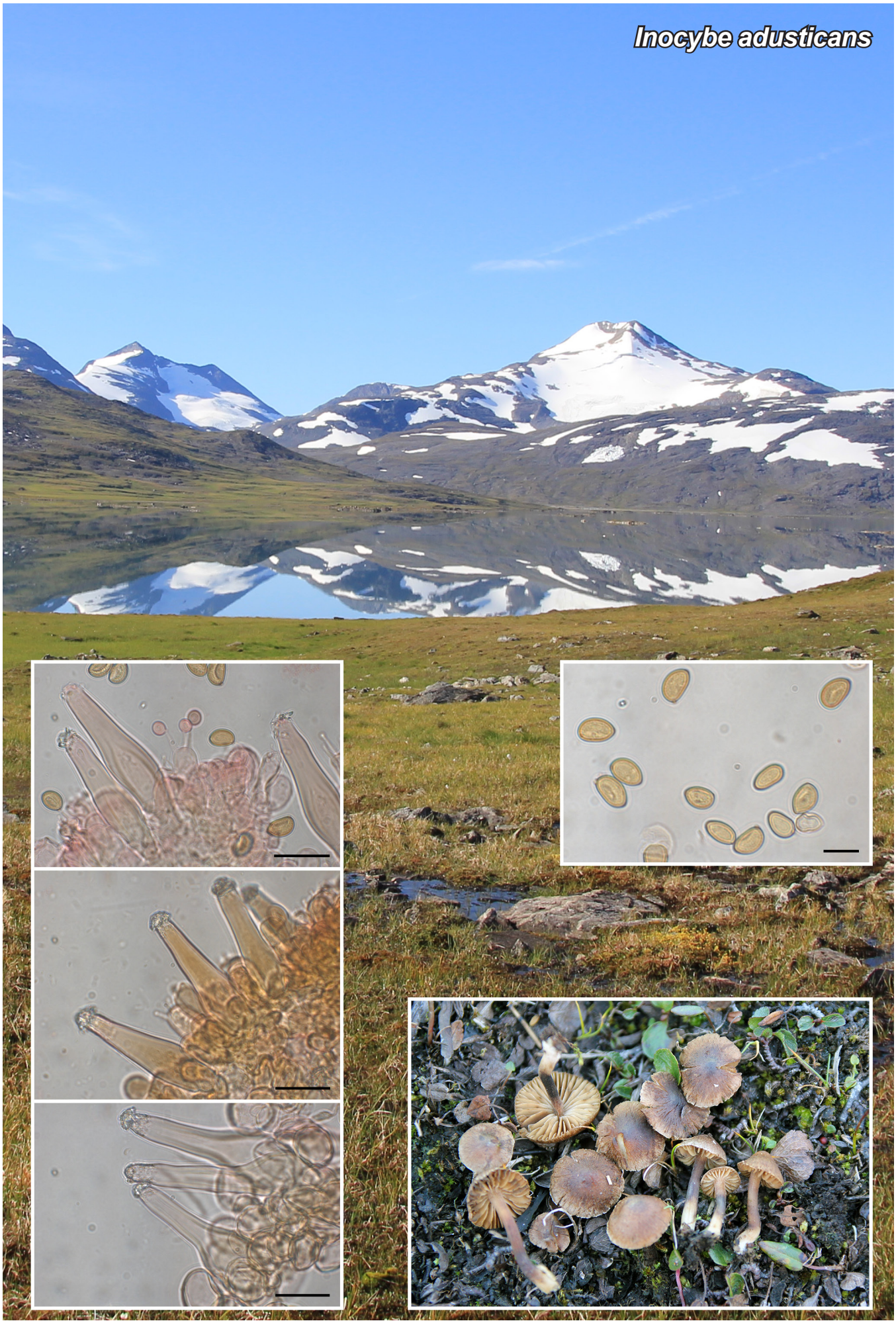

Inocybe adusticans

Fungal Planet 1880 MB 860686

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

Etymology: Refers to the fact that the species becomes dark brown with age, like scorched.

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

Pileus 5–20 mm diam., first conical to convex, later plano-convex to applanate, mostly with an obtuse broad umbo, margin deflexed, later straight to somewhat uplifted, as young rather uniformly ochraceous brown to dark brown, with age often blackish brown at centre and paler brown at margin, first smooth to finely fibrillose with age radially fibrillose to rimose, when young with whitish velipellis, fugacious, later often visible white remnants at pileus margin, cortina not observed. *Lamellae* up to 3 mm broad, distant to moderately crowded, interspersed with lamellulae, L = 20–30, adnate, adnexed to emarginate, first pale beige, later ochraceous brown to brown, edge fimbriate, first concolourous or somewhat paler, with age ochraceous brown. *Stipe* 8–22 × 1.5–2.5 mm, equal cylindrical, often bending, slightly bulbous base, first pale ochraceous brown, then soon dark ochraceous brown, with age even blackish brown, stipe base pale whitish, pruinose over the entire length, glabrous. Context whitish in pileus and stipe. *Smell* indistinct to weakly spermatic. *Basidiospores* (8.4–)9.1–*9.7*–10.7(–11.3) × (5.2–)5.5–*6.2*–6.3(–6.4) µm, Q = 1.41–1.88, Q av. = 1.56 (n = 60), smooth, subamygdaliform to amygdaliform, some almost ovoid, apex subobtuse, with small distinct apiculus, pale ochraceous brown. *Basidia* 26–*32*–36 × 9–*10*–12 µm (n = 20), clavate, 4-spored, a few 2-spored, hyaline, sterigmata 4.9–7.1 µm long. *Pleurocystidia* 59–*66*–76 × 11–*14*–16 µm, Q mean = 4.9 (n = 50), lageniform, utriform to fusiform, with truncate base or pedicel, thick-walled, wall up to 3.5 µm thick, hyaline to pale yellowish in KOH solution, with crystals and microcrystals under the crown of crystals. *Cheilocystidia* 45–*55*–66 × 10–*13*–17 µm (n = 40), similar to pleurocystidia but more variable, with rounded or truncate base, thick-walled, first hyaline, with age becoming ochraceous brown, mixed with clusters of pyriform to globose paracystidia 15–*19*–26 ×10–*12*–17 µm (n = 25), somewhat thick-walled, first hyaline and with age becoming ochraceous brown pigmented. *Caulocystidia* over the entire length, similar to pleurocystidia but more variable, 37–*51*–92 × 13–*14*–18 µm (n = 40), hyaline. *Cauloparacystidia* 14–*19*–25 × 10–*13*–17 µm (n = 35 / N = 2), pyriform to globose, somewhat thick-walled, first hyaline, with age becoming ochraceous brown pigmented. *Clamp connections* frequent.

Colour illustrations: *Inocybe adusticans* habitat in the alpine zone from the type locality close to Sårjåsávrre, Padjelanta National Park, Sweden. In situ basidiomata of the holotype (GB-0207768); photos of the hymenium with pleurocystidia, cheilocystidia, caulocystidia and basidiospores. Scale bars: pleuro, caulo- and cheilocystidia = 20 µm; spores = 10 µm.

Ecology and distribution: So far only known from one collection originating from Sweden and the alpine zone, in reindeer grazed area on calcareous ground. Found sporulating in mid-August, in snow bed area likely associated with *Salix herbacea*, but *Bistorta vivipara* was also present. Blast search of NCBI's GenBank nucleotide database and the UNITE database gave 100 % matches with two ITS sequences from Fairbanks, Alaska. One was isolated from ectomycorrhiza of *Dryas integrifolia* (GenBank JX630788), the other from a soil sample (GenBank KC966045), suggesting the species to have a wide intercontinental distribution range in the arctic and alpine zones, but seems to be rare.

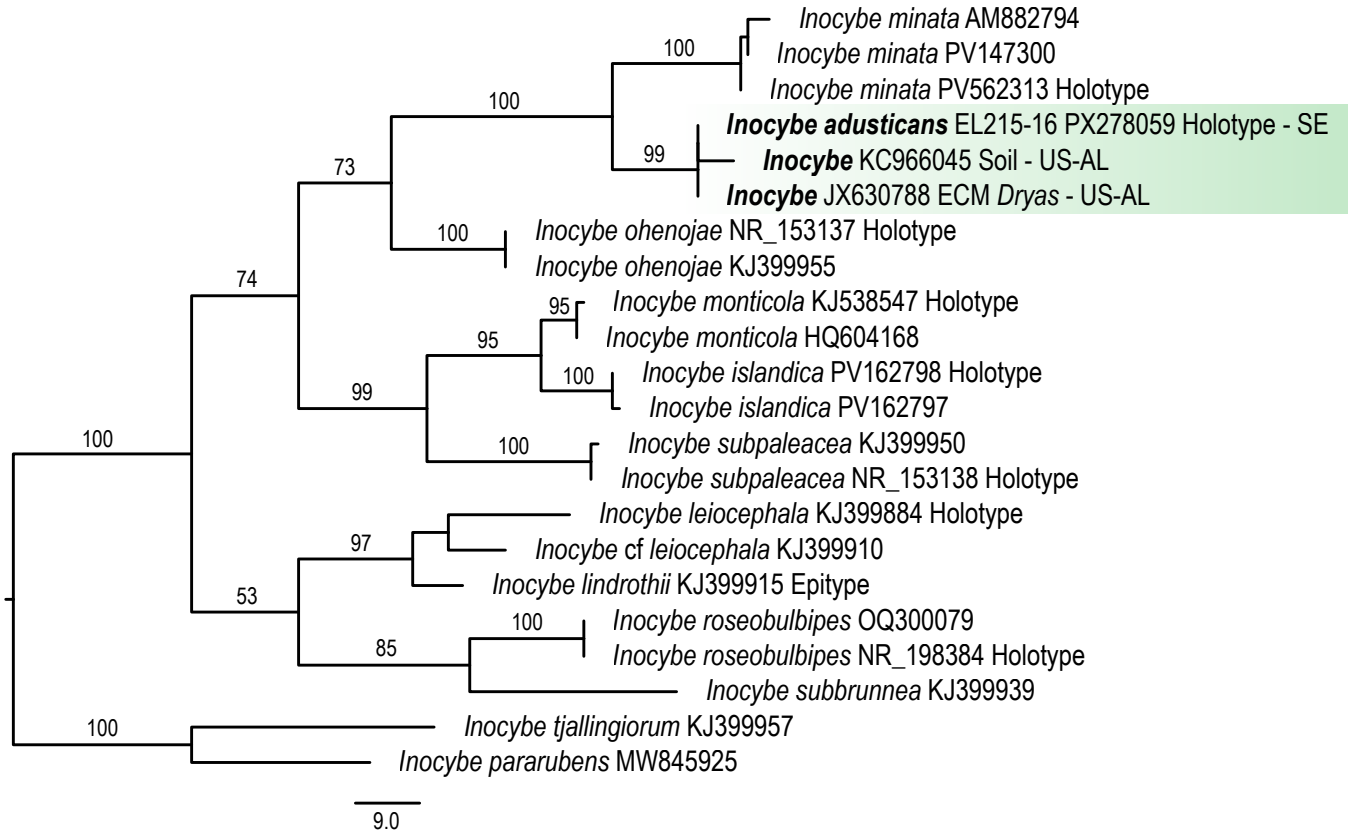
Typus: **Sweden**, Lule lappmark, Jokkmokk, Padjelanta NP, close to Sårjåsjávrre, N67°14´21", E16°25´39", mosaic alpine vegetation on calcareous soil, in snow bed area with *Salix herbacea* and *Bistorta vivipara*, 17 Aug. 2016, *E. Larsson*, EL215-16 (**holotype** GB-0207768; ITS-LSU sequence GenBank PX278059; **isotype** TUR-A 217630).

Collections studied for comparison: *Inocybe minata*. **Finland**, Etelä-Häme, Orivesi, Yröskulma, S side of the river Yrösjioki, 61.7563N, 24.3046E, 120 m.a.s.l., N slope in moist, fairly rich spring-fed forest with *Betula*, *Alnus incana*, *Picea abies*, *Salix* spp. and *Populus tremula*, 15 Sep. 1999, *J. Vauras*, JV15556 (TUR 178213; ITS sequence GenBank PV147301); Etelä-Häme, Ruovesi, Nature Reserve Runeberginlähde, 61,9904N, 24.0663E, 99 m.a.s.l., 8 Sep. 2005, *E. Larsson*, EL108-05 (GB-0248104; ITS-LSU sequence GenBank AM882794; TUR-A 208299); Kainuu, Paltamo, Melalahti, Nature Reserve Ellukanlahden lehto, near the end of Ellukka bay, 64.39406N, 27.67443E, 123 m.a.s.l., 26 Aug. 2011, *J. Vauras*, JV28393 (TUR-A195577; ITS sequence GenBank PV147302). Kainuu, Paltamo, Melalahti, Nature Reserve Ellukanlahden lehto, near the end of Ellukka bay, middle boreal zone in forest close to lake shore, on moist somewhat calcareous soil, near *Salix caprea*, *Alnus incana*, *Picea abies*, *Pinus sylvestris* and *Betula*, 1 Sep. 2018, *J. Vauras*, JV32664 (TUR-A 208003; ITS-LSU sequence GenBank PV147300). *Inocybe ohenojae*. **Canada**, Northwest Territories, District of Franklin, Melville Penisula, Repulse Bay, on hummock in *Dryas integrifolia* and *Salix* sp. vegetation, 2 Aug. 1974, *E.* & *M. Ohenoja* (OULU **holotype**; ITS-LSU sequence GenBank NR_153137). **Svalbard and Jan Mayen**, Svalbard, Nordenskiöld Land, Revneset, arctic tundra with *Salix polaris*, 12 Aug. 2015, *E. Larsson*, EL72-15 (ITS-LSU sequence GenBank PV167069).

Notes: *Inocybe adusticans* is an arctic alpine small ochraceous brown species characterized by becoming dark ochraceous brown, to even blackish brown with age on the pileus and stipe. It has a totally pruinose stipe, smooth spores, thick-walled pleurocystidia with microcrystals under the crown of crystals, suggesting it belongs in sect. *Splendentes*. In the phylogeny it clusters as a sister species to the recently described *I. minata* (Crous *et al*. 2025), and the two show 95.2 % similarity in ITS data. In micromorphology the two have rather similar measurements of spores and

cystidia. However, *I. adusticans* can be separated by the cheilo- and caulocystidia that turn clearly dark brown with age. Also, *I. minata* is a boreal species found in moist to wet habitats associated with *Salix* spp., *Betula pendula* and *Alnus incana*. Other alpine species in the group with similar micromorphology are *I. ohenojae* described by Larsson *et al*. (2014) based on a specimen from the arctic tundra in Canada associated with *Dryas*, and the recently described *I. islandica* (Crous *et al.* 2025) described from Iceland associated with *Dryas*. *Inocybe ohenojae* differs from *I. adusticans* by having dirty grey brown pileus and somewhat larger significantly thick-walled spores, and *I. islandica* differs by the yellowish ochraceous brown pileus and stipe, which do not turn dark brown. *Inocybe badjelanndana* is another small ochraceous brown alpine species growing associated with *Salix* in moist habitats (Crous *et al.* 2024b). It differs from *I. adusticans* by having slender, fusiform to clavate, rather thin-walled cheilo- and pleurocystidia with no or few crystals. *Inocybe monticola* belongs in the group and comes out as the sister species to *I. islandica*. It was described by Kropp *et al*. (2010) from a subalpine fir, lodgepole pine and aspen community in Utah and seems to be restricted to North America, is so far not found in Europe.

Supplementary material: doi: 10.6084/m9.figshare.30121528 (alignment and tree).



Phylogram obtained using PAUP v. 4.0b10 (Swofford 2003) based on ITS and LSU data showing the position of *I. adusticans* among its closest relatives. 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 adusticans* is marked in **bold** and a coloured block, the holotype is indicated.

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Inocybe percastanea

Fungal Planet 1881 MB 860457

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

Etymology: *per* (Lat.) = resembling, referring to the likeness with *Inocybe castanea.*

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

Pileus 10–50 mm diam., as young conical to campanulate, later becoming plano-convex to expanded, with broad obtuse umbo, margin at first inflexed, later deflexed to somewhat uplifted to wavy, colour somewhat variable depending on the degree of humidity, usually chestnut brown, sometimes orange brown or paler, even ochre brown or yellowish brown, darker around centre, outwards paler (Mu 7.5YR 3/4, 4/3–6, 5/4–8, Mu 10YR 6/6–8; Munsell 1994), velipellis greyish white, conspicuous in young individuals, often persistent in central parts and at pileus margin, surface dry, smooth, glabrous, more or less lubricous when moist, fibrous, with age finely squamulose to fibrillose and margin breaking up. *Cortina* absent. *Lamellae* up to 5 mm broad, moderately crowded, interspersed with lamellulae, L = 38–44, adnexed to emarginate, subventricose, first pale beige to cream, with age yellowish ochre to olive brown or reddish olive brown, edge uneven, fimbriate, concolourous to pale. *Stipe* 15–40 × 3–6 mm, firm, cylindrical, often bended, with subbulbous base, (5–8) mm, base occasionally covered with abundant whitish tomentum, ochre cream (Mu 7.5YR 6/3–4) with a pink tone when young (Mu 5YR 6/3–4), with age becoming pale brownish, longitudinally striate, pruinose over the entire length. *Context* in pileus whitish to pale ochraceous brown, in stem pale to pinkish ochraceous. *Smell* slightly spermatic.

Basidiospores (5.0–)6.8–*7.7*–8.6(–10.0) × (4.4–)4.7–5.3–6.2(–6.8) µm, n = 300 / N = 8, Q = 1.20–1.64, Q mean = 1.42, variable angular-nodulose, with rounded obtuse nodules (5–)6–8(–9) and a small apiculus, pale ochraceous brown. *Basidia* 22–*26*–31 × 7–*8*–9 µm, n = 20, clavate to subcylindrical, 4-spored, some 2-spored, hyaline, sterigmata 3–6 µm long. *Pleurocystidia* 45–*60*–*75* × 12–*15*–20 µm, Q mean = 3.9, n =175, subfusiform to lageniform with a widened or rounded base, sometimes with a thick septum towards mid-length, thick-walled, 1.6–*2.0*–2.4 µm, walls at apex up to 4 µm, crystalliferous with abundant microcrystals, hyaline to pale yellowish in KOH and ammonium solutions. *Cheilocystidia* similar to pleurocystidia, 46–*58*–74× 11–*16*–22 µm, n = 70, lamella edge heterogeneous, fertile in some places, cheilocystidia solitary or in fascicles deeply embedded in the lamella trama, intermixed with thin-walled, hyaline, subcylindrical, clavate to pyriform paracystidia, 7–*13*–17 × 7–*8*–12 µm, n = 35. *Caulocystidia* over the entire length, less frequent in the lower part, similar to pleurocystidia but more variable, 36–*60*–100 ×11–*14*–22 µm, n = 80, intermixed with thin-walled, hyaline, clavate to pyriform paracystidia, 7–*16*–26 × 5–*10*–17 µm, n = 45. *Stipitipellis* a cutis of parallel interwoven hyphae 3–9(–15) µm wide, encrusted, with pale yellowish-brown pigments. *Pileipellis* a cutis with repent cylindrical hyphae 3–7 µm wide, hyaline, terminal end cells not differentiated. Below parallel interwoven hyphae 6–16 µm wide, hyaline. Subpellis, chains of inflated, long and rounded cells, 31–*56*–112 × 13–*22*–38 µm, n = 40, encrusted with pale yellowish-brown pigments. *Clamp connections* frequent.

Ecology and distribution: *Inocybe percastanea* is commonly found in south-western Europe in warm mediterranean ecosystems associated with *Pinus pinaster*, *Quercus ilex*, *Cistus ladanifer* and *C. laurifolius*, in sandy areas mostly on acidic soils, but also in stabilised coastal sand dunes. In Northern Europe *I. percastanea* is rather rare but found in mixed deciduous dominated forests on more rich soils under *Corylus avellana*, *Betula pendula* and *Fagus sylvatica*. A blast search of NCBIs GenBank and the UNITE database gave matches of ITS data from environmental sample in Italy (GenBank DQ054548) and Georgia (UNITE UDB01956970), from ECM of *Quercus rotundifolia* in Portugal (GenBank FJ897196) and *Quercus robur* in Italy (GenBank HF565071), from basidiomata associated with *Pinus pinea* in Spain (UNITE UDB0754131). In addition, from soil samples in Bolivia (UNITE UDB02157142) and Morocco (UNITE UDB03826303) confirming our findings that *I. percastanea* is common in mediterranean ecosystems and has a broad distribution in Europe, and the soil data suggest that it also occurs in South America and Northern Africa.

Typus: **Spain**, Castilla-La Mancha, Guadalajara, Tamajón, Los Navazales, 3°13´33”W, 40°59´02”N, 1006 m.a.s.l., in sandy, acidic soils under *Cistus ladanifer* (*Cistaceae*) and *Pinus pinaster* (*Pinaceae*), 28 Nov. 2014, *J.C. Campos* (**holotype** AH 45158, ITS-LSU sequences GenBank PX093724; **isotype** GB-0207767).

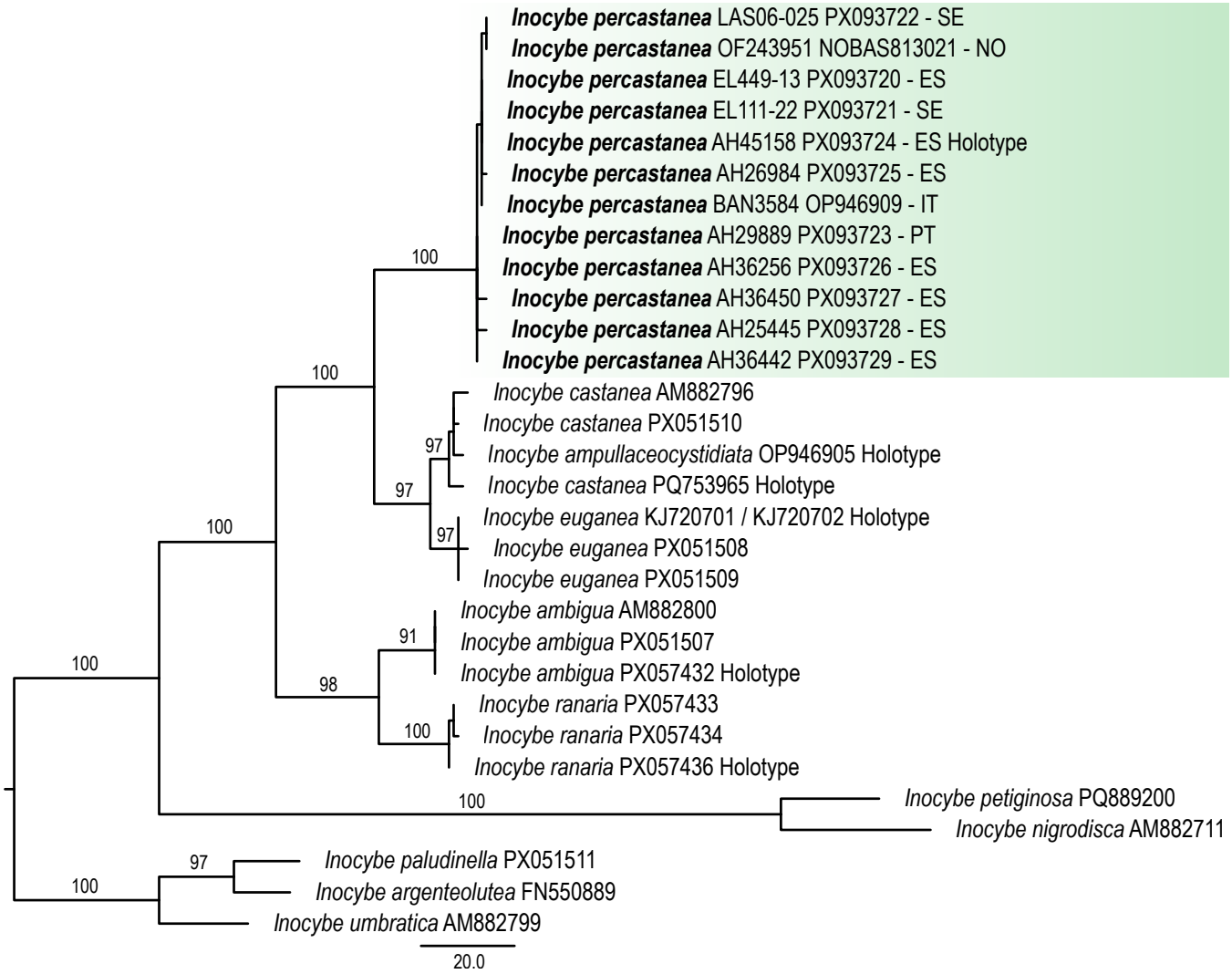
Colour illustrations: Habitat of *Inocybe percastanea* under *Cistus ladanifer* and *Pinus pinaster* in Tamajón, Spain at 1006 m altitude, the type locality. *In situ* basidiomata of the holotype (AH 45158); from bottom to top: photos of SEM basidiospores (AH 29889); OM basidiospores; pleurocystidia; cheilocystidia; caulocystidia. Scale bars: basidiomata = 10 mm; cystidia = 50 µm; OM spores = 10 µm; SEM spores = 2 µm.

Additional materials examined: **Italy**, Tuscany, Castiglion Fiorentino, Cantalena, with *Castanea sativa,* 19 Oct. 2017, *M. Dondl*, DB19-10-17 (STU-F-0901756, ITS-LSU sequence GenBank OP946909). **Germany**, Sachsen-Anhalt, Harz, nature reserve Münchenberg, TK25 4232/4, *Quercus*, 15 Jun. 2013, *H. Schubert*, DB15-6-13-1. **Norway**, Møre og Romsdal, Skodje, Lia, Skodje, in forest with *Corylus*, *Betula* and *Pinus*, 15 Oct. 2008, *P. Larsen* (OF-243951, ITS sequence NOBAS 813021). **Portugal**, Leiría, Marinha Grande, Fonte Santa, 39°45'4.02"N, 9°1'18.03"W, 72 m.a.s.l., under *P. pinaster* in dunes, acidic soil, 9 Nov. 2000, *F. Esteve-Raventós* (AH 29889, ITS sequence GenBank PX093723); ibid., AH 29890. **Spain**, Castilla-La Mancha, Guadalajara, Tamajón, 40°56'36.13"N, 3°16'9.32"W, 1015 m.a.s.l., in *P. pinaster* forest with *C. ladanifer*, in acidic soils, 23 Apr. 1989, *M. Heykoop & F. Esteve-Raventós* (AH 26984, ITS sequence GenBank PX093725); Castilla-La Mancha, Guadalajara, Tamajón, Sacedoncillo, 40°59'32.06"N, 3°13'6.57"W, 1005 m.a.s.l., under *P. pinaster* and *C. ladanifer* on acidic soil, 30 Oct. 2013, *E. Larsson, M. Jeppson* & *F. Esteve-Raventós*, EL449-13 (GB-0207765, ITS-LSU sequence GenBank PX093720); Castilla-León, Burgos, Hontoria del Pinar, 1100 m.a.s.l., in mixed forest of *P. pinaster* and *P. sylvestris*, 13 Apr. 2007, *A. Caballero,* AC3510 (AH 36256, ITS-LSU sequence GenBank PX093726); La Rioja, Cidamón, 42°29'21.50"N, 2°52'19.34"W, 580 m.a.s.l., in *P. pinaster* forest with some *Quercus ilex* subsp. *ballota*, 21 Nov. 1992, *C.E. Hermosilla*, CEH 0142-Na76 (AH 25410); ibid., 20 Nov. 1999, CEH 04519 (AH 25445, ITS sequence GenBank PX093728); ibid., 27 Nov. 1999, CEH 04564 (AH 25425); ibid., 27 Nov. 1999, CEH 04565 (AH 25446); ibid., 1 Dec. 1999, CEH 04571 (AH 25447); La Rioja, Villarroya, encinar de Villarroya, 42°7'25.38"N, 2°2'38.18"W, 820 m.a.s.l., in *Q. ilex* subsp. *ballota* forest, 18 Jun. 1992, *A. Caballero*, AC 1645 (AH 36104); ibid., 2 May 2008, AC 3800 (AH 36442, ITS sequence GenBank PX093729); ibid., 18 May 2008, AC 3821 (AH 36447); ibid., 1 Jun. 2008, AC 3833 (AH 36450, ITS sequence GenBank PX093727). **Sweden**, Dalsland, Färgelanda, Ödeborg, NO Ögården, Kroppefjälls sydsluttning, in mixed forest on rich soil, 10 Sep. 2006, *L.* & *A. Stridvall*, LAS06/025 (GB-0064634, ITS-LSU sequence GenBank PX093722); Skåne, Kiaby, Ivö Klack, under *Fagus sylvatica*, 30 Sep. 2022, *F. Esteve-Raventós & F. Pancorbo*, EL111-22 (AH60453, ITS-LSU sequence GenBank PX093721).

Collections studied for comparison: *Inocybe ambigua*. **Finland**, Varsinais-Soumi, Koski Tl, Vähä-Sorvasto, Sulkalammi, in moist forest near a spring pond, close to *Betula pubescens*, *Picea abies*, *Pinus sylvestris* and *Salix* spp., 19 Jul. 1991, *M-L Heinonen*, *P. Heinonen* & *J. Vauras*, JV5555 (GB-0207740, ITS-LSU sequence GenBank PX051507). **Sweden**, Värmland, Övre Ullerud, Butorp, in *Picea* forest close to small brook on calcareous ground, 30 Jul. 1991, *B. Jansson* (GB-0182144, ITS-LSU sequence GenBank AM882800). *Inocybe euganea*. **Norway**, Oppland, Lesja, Lesjaverken kyrkje, 20 Aug. 2022, *S. Kholsa*, (EL49-22, ITS-LSU sequence GenBank PX051509). **Sweden**, Värmland, Fryksände, Gultberget, 25 Aug. 1991, *L. Bood* (GB-0207766, ITS-LSU sequence GenBank PX051508). *Inocybe castanea*. **Finland**, Tavastia australis, Ruovesi, Juupajoki, in moist coniferous forest, 5 Sep. 2005, *E. Larsson* (GB-0248076, ITS-LSU sequence GenBank AM882796). **Sweden**, Medelpad, Timrå, Indalsälvens delta NR, moist mixed forest with *Picea abies*, *B. pubescens*, and *Salix* spp., 12 Sep. 2014, *T. Læssøe* & *E. Larsson* (EL144-14, ITS-LSU sequence GenBank PX051510).

Notes: Inocybe percastanea would traditionally be placed in sect. *Petiginosae* (Heim 1931) but recent phylogenetic studies show that the *I. castanea* clade belongs in the new sect. *Umbraticae* (Chen *et al.* 2024). *Inocybe percastanea* is similar in morphology to *I. euganea*, *I. castanea*, *I. ambigua* and *I. ranaria* (described here in the same FP volume). In the phylogeny it clusters with *I. castanea* (Peck 1904) as closest relative, and it is the closest match with a described species when blasting the ITS sequence in GenBank (94.3 % similarity). We identify *I. ampullaceocystidiata* (Shchukin 1985) to be a synonym of *I. castanea* according to morphology and ITS data obtained from the holotype (TAA122532, GenBank OP946905) that is identical with that of the holotype of *I. castanea* (NYSf676, GenBank PQ753965). *Inocybe percastanea* is very similar in macro- and micromorphology to *I. castanea* and was treated under that name by Esteve-Raventós & Caballero Moreno (2009), and the two have chestnut brown pileus and about the same spore and cystidial measurements. But *I. percastanea* can be discriminated by the distinct velipellis that usually is persistent, by the lamella edge that is heterogeneous, fertile in some places, with cheilocystidia solitary or in fascicles deeply embedded in the lamella trama, and paracystidia that are hyaline, subcylindrical, clavate to pyriform, 7–*13*–17 × 7–*8*–12 µm. In *I. castanea* the cystidia occur regularly along the edge intermixed with larger pyriform to globose paracystidia that in mature specimens develop yellowish brown incrustations, 18–*24*–39 × 10–*16*–22 µm. *Inocybe percastanea* has its main distribution in dry mediterranean ecosystems, whether *I. castanea* is usually found in temperate moist coniferous dominated mixed forests up to the subalpine zone (Peck 1904, Jacobsson & Larsson 2018). *Inocybe euganea* (Giliberto *et al.* 2018) was described from Italy in mossy *Castanea* forest, it can be discriminated by having a warmer yellowish brown pileus colour. The cystidia in *I. percastanea*, *I. euganea* and *I. castanea* all have rich microcrystals below the top crown of crystals, whether *I. ambigua* and *I. ranaria* have no or only few microcrystals. *Inocybe ambigua* can be identified by having only angular outline of the spores (Romagnesi 1979, all other known species in the group have distinct obtuse nodulose spores.

Supplementary material: doi: 10.6084/m9.figshare.30009073 (alignment and tree).



Phylogram obtained using PAUP v. 4.0b10 (Swofford 2003) based on ITS and LSU data showing the position of *Inocybe percastanea* among its closest relatives in the *Inocybe castanea* clade. 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 percastanea* is marked in **bold** and a coloured block, the holotype is indicated.

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Inocybe ranaria

Fungal Planet 1882 MB 860551

Inocybe ranaria E. Larss., Vauras & Bandini, ***sp. nov.***

Etymology: *Rana* = frog, refers to the moist habitat of the species, close to brooks and lakes.

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

Pileus 8–30 mm diam., as young conical to campanulate, later becoming plano-convex to expanded, with broad obtuse umbo, margin at first inflexed, later deflexed to somewhat uplifted, warm ochraceous-brown, darker around centre, outwards paler, velipellis whitish, fugacious, visible in young basidiomata and at pileus margin, surface dry, silky shiny, smooth, fine felted, later finely squamulose to fibrillose, rimose and margin breaking up. *Cortina* absent. *Lamellae* up to 5 mm broad, moderately crowded, interspersed with lamellulae, L = 30–40, adnexed to almost free, first pale beige, with age grey brown to brown, edge uneven, concolourous to pale. *Stipe* 20–60 × 1.5–4 mm, equal, with slightly subbulbous base, often bended, solid, pale brown, pale yellow brown, pale greyish brown, yellow brown, red brown, greyish red, longitudinally striate, pruinose over the entire length. *Context* in pileus whitish, in stem whitish, pale brown to reddish-brown, shiny. *Smell* slightly spermatic. *Basidiospores* (7.1–)7.7–*8.2*–8.7(–9.6) × (4.8–)5.2–*5.6*–6.4(–7.1) µm, n = 150, Q = 1.38–1.66, Q mean = 1.47, variable angular-nodulose, with rounded obtuse nodules and a small apiculus, pale ochraceous brown. *Basidia* 24–*27*–29 × 7–*8*–9 µm, n = 20, clavate to subcylindrical, 4-spored, hyaline, sterigmata 4.2–5.1 µm long. *Pleurocystidia* 48–*58*–67 × 12–*15*–21 µm, Q mean = 3.8, n =125, fusiform to sublageniform, rounded base or truncate, crystalliferous at apex, thick-walled, wall up to 3.5 µm, hyaline to pale yellowish in KOH. *Cheilocystidia* similar to pleurocystidia but on average shorter, with rounded base or truncate, with crystals, thick-walled, wall up to 3 µm, hyaline in KOH solution 39–*47*–55 × 11–*14*–19 µm, n = 50. *Cheiloparacystidia* hyaline, rather abundant, ovoid, pyriform to clavate, 13–*20*–24 × 7–*9*–13 µm, n = 25. *Caulocystidia* over the entire length, less frequent in the lower part, similar to pleurocystidia, 33–*55*–66 × 11–*14*–20 µm, n = 25, intermixed with thin-walled, hyaline, clavate to pyriform paracystidia, 15–*20*–26 × 9–*12*–15 µm, n = 25. *Stipitipellis* consists of parallel interwoven hyphae 3–9 µm wide, encrusted, with pale yellowish-brown pigments. *Pileipellis* a cutis with repent cylindrical hyphae 3–7 µm wide, hyaline, terminal end cells not differentiated. Below parallel interwoven hyphae 6–16 µm wide, hyaline. Subpellis, chains of inflated, long and rounded cells, 22–*62*–110 × 14–*24*–35 µm, n = 40, encrusted, with pale yellowish-brown pigments. *Clamp connections* frequent.

Colour illustrations: *Inocybe ranaria* habitat in the northern boreal zone from the locality Oulanka National Park, Kuusamo, Finland. In situ basidiomata of the holotype (TUR-A 216819); photos of the hymenium with pleurocystidia, cheilocystidia, caulocystidia and basidiospores; drawing of pleurocystidia (left), basidiospores, caulocystidia (right). Scale bars: pleuro, caulo- and cheilocystidia = 20 µm; drawing (short bar for cystidia, long bar for spores) and spores = 10 µm.

Ecology and distribution: *Inocybe ranaria* is ectomycorrhizal (ECM), most often collected in mixed moist forests likely associated with *Betula* and *Salix* spp., but other trees noted close by were also *Alnus*, *Populus* and *Picea*. It is known from Finland and Sweden, found from the southern boreal zone up to subalpine forests of the northern boreal zone, sporulating from late July to September on both acid and richer soils. a blast search of the ITS sequence of *I. ranaria* in NCBIs GenBank and the UNITE nucleotide databases gave no matches or further information.

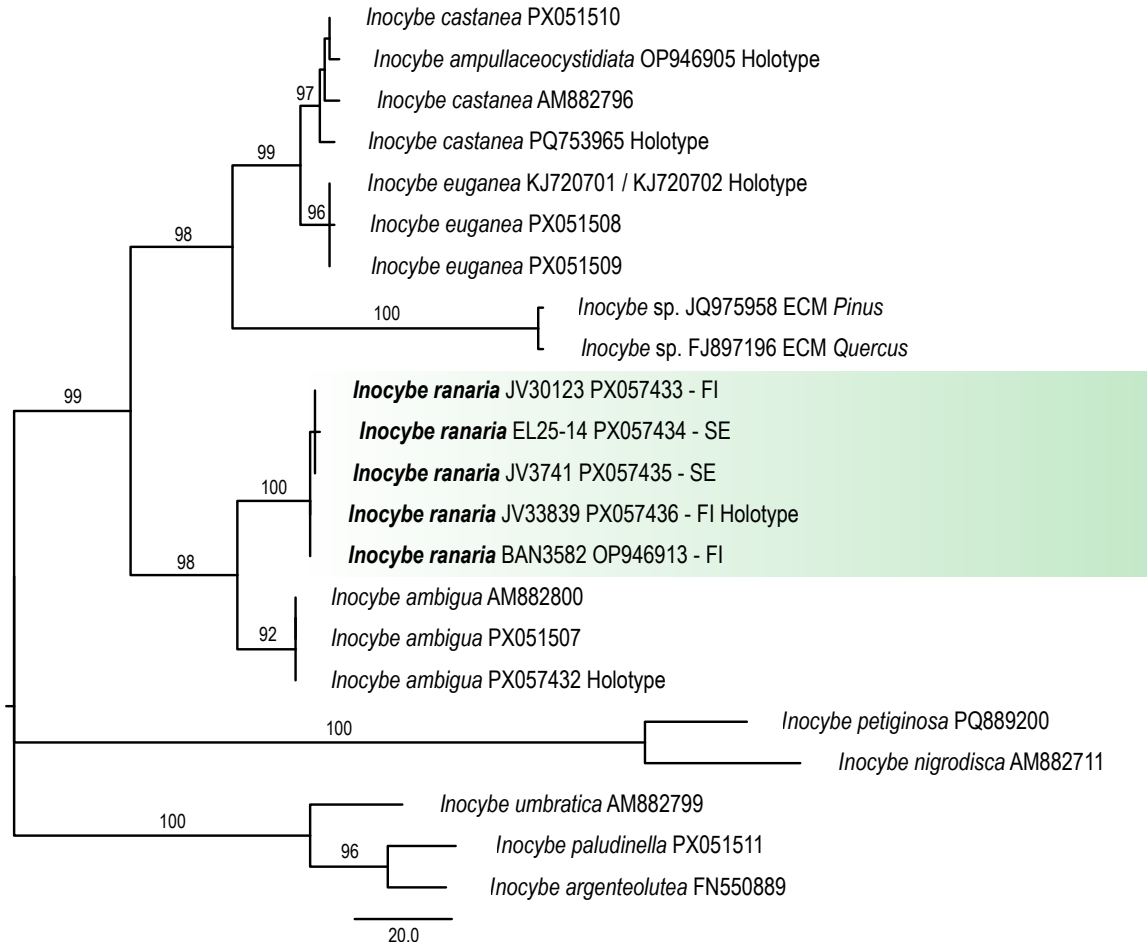
Typus: **Finland**, Satakunta, Hämeenkyrö, Tuokkola, the cemetery Vanha hautausmaa, WGS84: 61.6319, 23.1956, 64 m.a.s.l., margin of lawn near *Betula pendula* and *Abies* sp., on mull soil, 8 Sep. 2023, *T. Siuvatti* & *J. Vauras*, JV33839 (**holotype** TUR-A 216819, ITS-LSU sequence GenBank PX057436; **isotype** GB-0207738).

Additional materials examined: **Finland**, Kuusamo, Oulanka National Park, Päähkänänkallio – Venäänniemi, moist depression of *Salix* scrub, *Picea abies* and *Betula* sp. also nearby, 21 Aug. 2015, *D. Bandini, B. Oertel* & *J. Vauras*, JV31113 (TUR-A 203468); ibid., JV31114 (TUR-A 203544); ibid., JV31115 (TUR-A 203545); Perä-Pohjanmaa, Rovaniemi, Pisavaara, NE corner of the Strict Nature Reserve, brookside forest with *Betula* and *Picea abies*, 4 Sep. 2013, *J. Vauras*, JV30123 (TUR-A 198950, GB-0207739, ITS-LSU sequence GenBank PX057433). **Sweden**, Lycksele lappmark, Tärna, Hemavan Portbron vid Jobäcken, moist herb-rich subalpine *Betula pubescens* forest with *Salix* spp., 27 Jul. 2014, *E. Larsson*, EL25-14 (GB-0207761, ITS-LSU sequence GenBank PX057434); Medelpad, Borgsjö, Erikslund, near the river Ljungan, rather moist mixed forest with *Picea abies*, *Betula*, *Populus tremula*, *Salix* and *Alnus incana*, 1 Sep. 1989, *J. Ruotsalainen* & *J. Vauras*, JV3741 (TUR-A 175807, GB-0207740, ITS-LSU sequence GenBank PX057435).

Collections studied for comparison: *Inocybe ambigua*. **Finland**, Varsinais-Soumi, Koski Tl, Vähä-Sorvasto, Sulkalammi, in moist forest near a spring pond, close to *Betula pubescens*, *Picea abies*, *Pinus sylvestris* and *Salix* spp., 19 Jul. 1991, *M-L Heinonen*, *P. Heinonen* & *J. Vauras*, JV5555 (GB-0207740, ITS-LSU sequence GenBank PX051507). **Sweden**, Värmland, Övre Ullerud, Butorp, in *Picea* forest close to small brook on calcareous ground, 30 Jul. 1991, *B. Jansson* (GB-0182144, ITS-LSU sequence GenBank GenBank AM882800). *Inocybe euganea*. **Norway**, Oppland, Lesja, Lesjaverken kyrkje, 20 Aug. 2022, *S. Kholsa*, (EL49-22, ITS-LSU sequence GenBank PX051509). **Sweden**, Värmland, Fryksände, Gultberget, 25 Aug. 1991, *L. Bood* (GB-0207766, ITS-LSU sequence GenBank PX051508). *Inocybe castanea*. **Finland**, Tavastia australis, Ruovesi, Juupajoki, in moist coniferous forest, 5 Sep. 2005, *E. Larsson* (GB-0248076, ITS-LSU sequence GenBank AM882796). **Sweden**, Medelpad, Timrå, Indalsälvens delta NR, moist mixed forest with *Picea abies*, *Betula pubescens*, and *Salix* spp., 12 Sep. 2014, *T. Læssøe* & *E. Larsson* (EL144-14, ITS-LSU sequence GenBank PX051510).

Notes: *Inocybe ranaria* would traditionally be placed in sect. *Petiginosae* (Heim 1931), but recent phylogenetic studies show that the *I. castanea* clade belongs in the new sect. *Umbraticae* (Chen *et al*. 2024). It is similar in morphology to *I. ambigua*, *I. euganea* and *I. castanea*. In the phylogeny *I. ranaria* clusters with *I. ambigua* as closest relative, and it is the closest match when blasting the ITS sequence in GenBank (95.2 % similarity). *Inocybe ranaria* differ from *I. ambigua* by having on average somewhat broader spores 5.2–6.4 µm, vs 4.5–5.7 µm (Romagnesi 1979, Stangl 1989, own observations) with distinct obtuse nodules, *I. ambigua* has only an angular outline of the spores. The two species have no or only few microcrystals under the top crown of crystals. Further, both species favour moist and richer soils. *Inocybe ambigua* was described from France by Romagnesi (1979) but occurs also in the boreal zone of Fennoscandia (Jacobsson & Larsson 2018). Both *I. euganea* (Gilberto *et al.* 2018) and *I. castanea* (Peck 1904, Jacobsson & Larsson 2018) have about the same spore measurements as *I. ranaria,* and they also occur in boreal to subalpine ecosystems in Fennoscandia but in general on drier localities. *Inocybe euganea* was described from Italy and mossy *Castanea* forest. It can be discriminated by having a warmer yellowish brown pileus colour and no distinct longitudinally striate stipe. *Inocybe castanea* was described from a coniferous forest of North America, it can be discriminated by having a darker chestnut colour of the pileus, on average longer pleurocystidia, lack of a distinct persistent velipellis and is most often collected in coniferous dominated forests, but can also be found in subalpine *Betula* forests. Both *I. euganea* and *I. castanea* usually have abundant microcrystals under the top crown of crystals. We identify *I. ampullaceocystidiata* (Shchukin 1985) to be a synonym of *I. castanea* according to morphology and ITS data obtained from the holotype (TAA122532, GenBank OP946905) that is identical with that of the holotype of *I. castanea* (NYSf676, GenBank PQ753965).

Supplementary material: doi:10.6084/m9.figshare.29994781 (alignment).



Phylogram obtained using PAUP v. 4.0b10 (Swofford 2003) based on ITS and LSU data showing the position of *Inocybe ranaria* among its closest relatives in the *Inocybe castanea* clade. 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 ranaria* is marked in **bold** and a coloured block, the holotype is indicated.

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Inocybe giovannii
Pa
Cpa
Sp
Ch
Pl
Ca
DB

Fungal Planet 1883 MB 860606

Inocybe giovannii Bandini, B. Oertel & U. Eberh., ***sp. nov.***

Etymology: Named after Giovanni Bandini for his unfaltering moral and practical support of D. Bandini's *Inocybe* research.

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

Pileus 15–40 mm wide, at first (sub)campanulate, soon broadly convex or expanded, without or with rather low large umbo, rarely with more prominent umbo, margin at first slightly incurved to decurved, later straight or even uplifted, and then pileus depressed around the centre; young basidiomata usually covered with abundant, often cobweb-like remnants of a whitish velipellis, vanishing soon or visible even later at the centre; colour ochraceous to (sometimes speckled) ochraceous-brownish (Mu 10YR 5/6–5/8, 6/6–6/8, 7/8; 7.5YR 5/4–5/6, 6/6; Munsell 2009), often paler to yellow towards the margin, sometimes with faint orange to orange-reddish hue at the centre; surface at first tomentose, then tomentose-lanose, lanose to subsquamulose or even squarrose at the centre with small to larger fibre bundles, often areolate-diffracted at the centre and tomentose-fibrillose towards the margin; no remnants of a cortina observed. *Lamellae* moderately crowded to subdistant (ca 30–45), somewhat thickish, adnate to broadly adnate, (sub)ventricose, at first strikingly white, later ochraceous to ochraceous with greyish or brownish hue, sometimes with rusty blots; edge often uneven, fimbriate, whitish. *Stipe* 20–60 × 2–5 mm, straight or curved, sometimes widening towards the base, base sometimes somewhat thickened, when young usually covered with a thick layer of whitish tomentum, later longitudinally striate or glabrous, at first whitish to pale flesh-coloured or yellowish, later often entirely with more or less intense reddish tinge, at the apex always with pinkish hue or more or less intensely pinkish-reddish; roughly pruinose, as if strewn with salt, on the entire length. *Context* whitish in the pileus, in the stipe at first whitish then with reddish tinge or reddish at least in the (cortex near the) apex. *Smell* spermatic, at least when cut. *Colour of exsiccata* pileus brown in different intensities with or without reddish hue (Mu 10YR 5/8, 4/4–4/6; 7.5YR 5/4–5/6, 4/4–4/6), lamellae and stipe concolourous or a little lighter, no darkening or blackening on drying. *Basidiospores* 7.4–10.4 µm (av. 8.9 µm, SD 0.5 µm) × 5.0–7.1 µm (av. 5.5 µm, SD 0.3 µm); Q = 1.4–1.9 (av. 1.6, SD 0.1) (n = 120 of 3 coll.), usually broadly (sub)amygdaloid, mostly without, rarely with faint suprahilar depression, apex mostly (sub)acute, sometimes subobtuse, often with indistinct pseudoporus. *Basidia* 25–31 × 7–10 µm, generally 4-spored, rarely also 2-spored and then spore length up to 11.5 µm. *Pleurocystidia* 39–80 µm (av. 61 µm, SD 11 µm) × 9–20 µm (av. 14 µm, SD 3 µm); Q = 2.8–6.7 (av. 4.4, SD 0.9) (n = 45 of 3 coll.), mostly (sub)utriform, also (sub)fusiform, very often transition between bulge and neck clearly demarcated, usually with short or longer neck, sometimes without neck, with short or longer pedicel, apex usually crystalliferous, walls up to 3.0 (3.5) µm thick at the apex, wall thickness can vary within the same collection, intensely yellow-green with 3 % KOH. *Cheilocystidia* more variable in size and shape; intermixed with numerous colourless, (sub)clavate to (sub)cylindrical, thin-walled paracystidia. *Caulocystidia* on entire length of the stipe, 40–90(–100) × 8–15 µm, mostly (sub)utriform or (sub)lageniform, often with rather long and somewhat wavy (undate) neck and without or with short pedicel, apex usually crystalliferous, walls up to 1.5(–2.5) µm thick at the apex, intensely yellow green with 3 % KOH; intermixed with numerous colourless (sub)clavate to subglobose, thin-walled cauloparacystidia.

Habit, habitat and distribution: Most often collected under conifers, sometimes with *Picea abies* as the only tree present, but sometimes no conifers noted. The species grows on calcareous, often somewhat humid soil, at low to subalpine elevations. Based on ITS data (UNITE database: SH0955436.10FU; Kõljalg *et al*. 2013), the species occurs in Europe, Asia and North Africa.

Typus: **Germany**, Baden-Württemberg, Alb-Donau-Kreis, Ehingen, Briel, TK25 7623/4, alt. 675 m, *Abies alba*, *Fagus sylvatica*, *Picea abies*, 1 Oct. 2021, *D. Bandini & J. Christan* (**holotype** STU SMNS-STU-F0007565, **isotype** personal collection *D. Bandini* DB1-10-21-19; ITS-LSU sequence GenBank PX281927).

Additional materials examined (selection): **Austria,** Tirol, Reutte, Bichlbach-Lähn, ÖK25V 2215-Ost, alt. ca 1140 m, *Picea abies*, 16 Oct. 2017, *B. Oertel* (pers. coll. *D. Bandini* DB16-10-17-1b). **France**, Alsace, département du Bas-Rhin (67), commune de Mothern, UTM 32N: 0439405/5421255, *Quercus* sp., *Carpinus betulus*, *Fagus sylvatica*, *Corylus avellana*, 8 Oct. 2021, *J.-M. Trendel* (pers. coll. *D. Bandini* DB8-10-21-1-Trendel). **Germany**, Baden-Württemberg, Rhein-Neckar-Kreis, Wiesenbach, TK25 6618/2, alt. ca 180 m, *F. sylvatica*, 16 Oct. 2011, *D. Bandini* (pers. coll. DB16-10-11-2; ITS sequence GenBank MW856432); ibid., at some distance, alt. ca 160 m, *F. sylvatica*, 23 Sep. 2014, *D. Bandini* (STU SMNS-STU-F-0900985, pers. coll. DB23-9-14-2; ITS-LSU sequence GenBank MW845931); Baden-Württemberg, Alb-Donau-Kreis, Ehingen, Briel, TK25 7623/4, alt. ca 680 m, *Abies alba*, *F. sylvatica*, *P. abies*, 1 Oct. 2021, *D. Bandini* & *J. Christan* (STU SMNS-STU-F-0901914, pers. coll. *D. Bandini* DB1-10-21-17; ITS sequence Genbank PX281928); ibid., at some distance, alt. c. 680 m, *F. sylvatica*, *Quercus robur*, *A. alba*, *P. abies*, 2 Oct. 2021, *D. Bandini*, *J. Christan*, *B. Oertel* & *U. Eberhardt* (STU SMNS-STU-F-0901915, pers. coll. *D. Bandini* DB2-10-21-11; ITS sequence GenBank PX281924); Bayern, Ostallgäu, Halblech, near nature reserve "Ammergebirge", Kenzenhütte, TK25 8431/1/3, alt. ca 1200 m, *P. abies*, 17 Sep. 2018, *H.* & *E. Huijser* (pers. coll. *D. Bandini* DB17-9-18-3); ibid., Pfronten, TK25 8429/1, alt. ca 900 m, *Alnus incana*, *P. abies*, *C. avellana*, 12 Aug. 2021, *D. Bandini* (pers. coll. DB12-8-21-23); ibid., Pfronten, Breitenberg, TK25 8429/3, alt. ca 1800 m, *P. abies*, 13 Sep. 2021, *D. Bandini* (STU SMNS-STU-F-0901916, pers. coll. DB13-9-21-11; ITS

Colour illustrations: Germany, Baden-Württemberg, Alb-Donau-Kreis, Ehingen, Briel, mixed forest. Type collection in situ; Drawing: spores (Sp), caulocystidia (Ca), cheilocystidia (Ch), cauloparacystidia (Cpa), cheiloparacystidia (Pa) and pleurocystidia (Pl) (photos and drawing credit: D. Bandini). Scale bars: all others = 50 µm; spores = 10 µm.

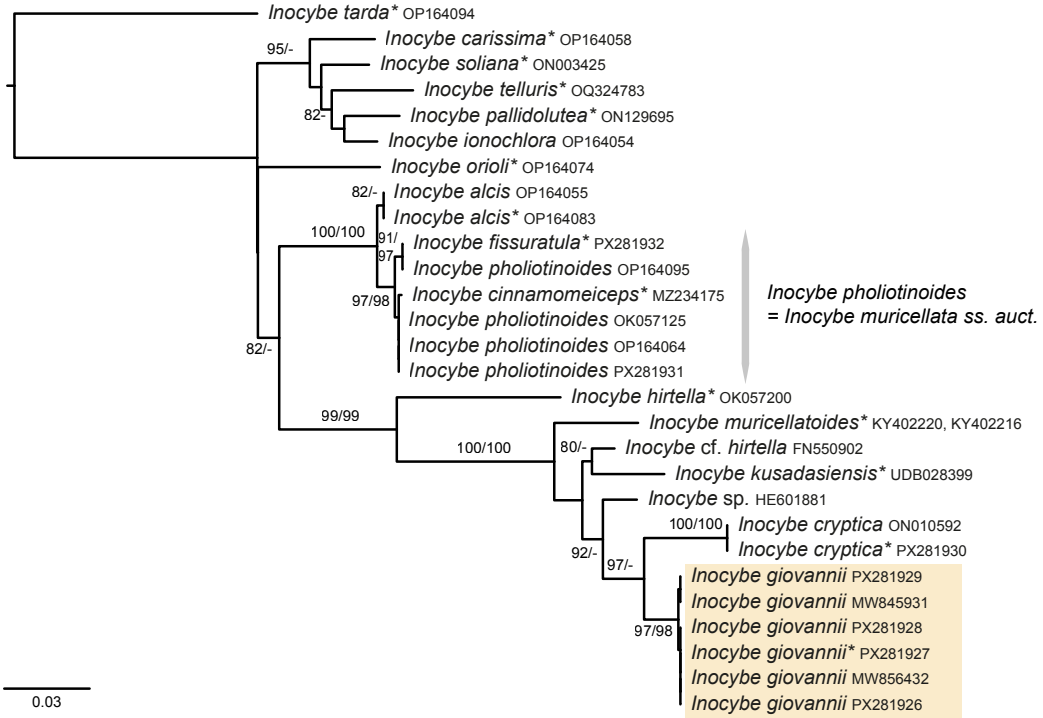
sequence GenBank PX281925); ibid., Pfronten, Achtal, TK25 8429/1, alt. ca 980 m, *P. abies*, *F. sylvatica*, 21 Sep. 2021, *D. Bandini* (STU SMNS-STU-F-0901913, pers. coll. DB21-9-21-8; ITS-LSU sequence GenBank PX281926); Rheinland-Pfalz, Rhein-Pfalz-Kreis, Böhl-Iggelheim, TK25 6615/4, alt. ca 110 m, *Q. robur*, *Alnus glutinosa*, *C. avellana*, *P. sylvestris*, 6 Sep. 2014, *D. Bandini* (pers. coll. DB6-9-14-9).

Notes: *Inocybe giovannii* is characterized by the ochraceous to ochraceous brownish pileus colour, up to squarrose pileus surface, whitish velipellis, at first strikingly white lamellae, with age pinkish-reddish stipe at least near the apex and a rather rough salt-grain-like pruina on the entire length. Confusion can most easily occur with the other ingroup species included in the tree figure, but, apart from macroscopic differences, either spores or cystidia or both differ in dimensions.

In earlier publications we treated *I. giovannii* as *I. muricellata* (e.g. Bandini *et al.* 2021a, 2022a, c). As additional collections became available, it became clear that spore size and cystidia shapes consistently differed from the original description of *I. muricellata* (Bresadola 1905). A recent morphological examination of the holotype (S-F14463) (for micromorphology see Supplementary Fig. 1; no sequence data available) confirmed that the older name *I. muricellata* may indeed be synonymous with the species we referred to as *I. pholiotinoides* in the past. Given the number of similar species in this clade, we hesitate to synonymize *I. muricellata* and *I. pholiotinoides* without molecular support. However, the recently described *I. cinnamomeiceps* (holotype M-0216701) and *I. fissuratula* (holotype M-0216731) (Ludwig 2017) are shown here to cluster with and are treated as synonyms of *I. pholiotinoides*. *Inocybe scabelliformis* (Malençon & Bertault 1970), considered by Kuyper (1986) as another synonym of *I. pholiotinoides* and *I. muricellata*, differs from *I. giovannii* by e.g., darker and less yellow pileus colours, less strikingly, more dingy coloured lamellae when young, distinctly longer spores and cystidia that are more fusiform and thick-walled down to the base of the cells, without demarcation between bulge and neck (see Supplementary Fig. 2 for micromorphology of holotype MPU312226; no sequence data available).

Based on a megablast search of NCBI's GenBank nuc-core database accessed 2 Sep. 2025, the closest **ITS** sequence hit ordered by Max Score of the holotype of *I. giovannii* was from an unidentified sequence, a *Quercus ilex* ectomycorrhiza sequence from Sardegna, Italy (Genbank HE601881, Unite SH0151512.10FU, 93 %). The most similar identified sequences are from *I. kusadasiensis* (Unite SH0955440.10FU, ca 92 %). For the **LSU**, the closest hits were 98.7 % for "*I.* cf. *hirtella*" EL707 from Spain (GenBank FN550902), which is not *I. hirtella*, followed by sequences from *I. somae* and *I. mycenoides* with 96.3 % similarity (see Bandini *et al.* 2022c). *Inocybe giovannii* (as *I. muricellata*) was also included in more extensive trees in Bandini *et al.* (2021a, 2022a, c). Allı *et al.* (2024) mistook *I. giovannii* for *I. subporospora*; however, morphology and type sequence refer *I. subporospora* to *I. tjallingiorum* (see Bandini *et al.* 2021a). The BLAST results and the tree figure show clearly that *I. giovannii* is different from all sequenced species.

Supplementary material: doi: 10.57754/FDAT.034my-8s396 (supplementary figures, alignment and tree).



Maximum Likelihood phylogram obtained from a MAFFT v. 7.526 (Katoh *et al.* 2019) alignment and analysed by IQ-TREE v. 1.6.12 (Trifinopoulos *et al.* 2016, Kalyaanamoorthy *et al.* 2017, Hoang *et al.* 2018) based on ITS and LSU data of the clade including *Inocybe giovannii*. *Inocybe tarda* was used as outgroup. Sequences are identified by GenBank accession numbers resp. UNITE numbers. Support values were obtained from 1000 replicates of SH-like approximate likelihood ratio tests (SH-aLRT) and ultrafast bootstrap (ufb). Support values ≥ 80 % were given for SH-aLRT and ≥ 95 % for ufb; * indicates type sequences or sequences that matched the respective type sequence in ≥ 99 % similarity BLAST searches. For species names without *, we were not aware of published type sequences. The clade of the new species is indicated in yellow.

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Inocybe leucantheana
Pa
Sp
10 µm
Cpa
Ch
Pl
Ca
50 µm
DB

Fungal Planet 1884 MB 861135

Inocybe leucantheana Bandini, Kehlet & Heilm.-Claus., ***sp. nov.***

Etymology: Named based on its similarity to *Inocybe bellidiana*, as the flowers of members of the plant genus *Leucantheanum* share the combination of yellow and white colours with the flowers in *Bellis.*

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

Pileus 10–25 mm wide, at first conico-convex, soon expanded, without or with a more or less prominent broad umbo, margin decurved to straight or even uplifted, and then pileus depressed around the umbo; young basidiomata with faint remnants of a fugacious whitish velipellis; colour white, whitish, dingy whitish to ivory or cream-coloured (Mu 10YR 8/1–8/4; Munsell 1975), often yellowish in the centre, with age suffused in different intensities with yellowish, orange to orange reddish tinges, especially at the centre; surface smooth to minutely rimulose or minutely innately fibrillose towards the margin; young basidiomata with faint remnants of a pale cortina. *Lamellae* moderately crowded (ca 24–50), almost free to emarginate adnate, (sub)ventricose, at first pale whitish greyish, with age brown(ish) with greyish to faintly reddish hue; edge fimbriate, whitish to concolourous. *Stipe* 25–60 × (1–)2–5(–7) mm, straight or curved, when young covered with whitish tomentum, later longitudinally striate or (almost) glabrous, at first watery whitish to pale yellowish, later flesh-coloured to clay pink in different intensities; pruinose only near the apex. *Context* whitish in the pileus, and at first in the stipe, later sometimes with somewhat flesh-coloured tinge. *Smell* spermatic, at least when cut. *Colour of exsiccata* pileus brown with reddish hue (Mu 7.5YR 5/4–5/6, 4/6), lamellae and stipe concolourous or a little lighter in colour, apparently getting somewhat reddish on drying. *Basidospores* 7–9.5 µm (av. 8.3–8.5 µm, SD 0.5 µm) × 4.3–5.8 µm (av. 5.1 µm, SD 0.2 µm); Q = 1.4–2.0 (av. 1.6, SD 0.1) (n = 60 of 2 coll.), smooth, (sub)amygdaloid to (sub)ellipsoid, without or with only faint suprahilar depression, apex (sub)obtuse to subacute. *Basidia* 22–28 × 7–10 µm, generally 4-spored. *Pleurocystidia* 45–80 µm (av. 55–59 µm, SD 7 µm) × 11–21 µm (av. 14–17 µm, SD 2 µm); Q = 3.4–5.6 (av. 4.3, SD 0.5) (n = 15 of 1 coll.), mostly (sub)utriform or (sub)fusiform, also subcylindrical or (sub)lageniform, without or with short or longer neck, with short or without pedicel, apex crystalliferous or not, walls up to 1.5(–2.5) µm thick at the apex, yellow green with 3 % KOH. *Cheilocystidia* similar to cheilocystidia but somewhat more variable in size and shape; intermixed with numerous colourless, (sub)clavate, to subovoid, thin-walled paracystidia. *Caulocystidia* only near the apex of the stipe, 35–80 × 8–15 µm, oblong and narrow, mostly somewhat deformed, near the apex often somewhat bent or bulging or subcapitate, mostly no distinct neck visible, without or with only short pedicel, apex without or with only very few and very small crystals, walls up to 1.0(–1.5) µm thick, yellow green with 3 % KOH; intermixed with some colourless, (sub)clavate to subovoid, thin-walled cauloparacystidia.

Ecology and distribution: *Inocybe leucantheana* occurs with both deciduous and coniferous hosts in forests on somewhat calcareous ground. The type locality is a moist mixed forest dominated by *Alnus glutinosa*, but with scattered individuals of *Betula pubescens* and *Picea abies*, and a very rich presence of members of *Entoloma* subgenus *cyanula* (including *E. anatinum*, *E. callipygmaeum*, *E. erhardtii*, *E. queletii* and *E. phaeosdiscum.* The Dutch records are from mixed forests on sandy soil, with *Betula* and *Quercus* as stable hosts. Finally, the Estonian collection represented by a sequence in UNITE (TUF118879) was collected in a *Picea abies* stand. Based on sequences (mainly from soil samples) deposited in UNITE, *I. leucantheana* (SH1700693.10FU) is widespread in Estonia, but with specimens also from Finland and matching environmental sequences also from Latvia and Japan. The GlobalFungi database contain further matching sequences from Russia, Belarus and the Netherlands, suggesting a wide distribution in the temperate region.

Typus: **Denmark**, Zealand, Helvigstrup Skov, 55.5667711°N, 11.8870930°E, with *Alnus*, *Betula* and *Picea* in moist forest on wet ground, 22 Sep. 2022, *P. Schilling & T. Kehlet*, coll. DMS-10293008 (**holotype** C, NHMD001862572, ITS sequence GenBank PX585991).

Additional materials examined: **Denmark,** Zealand, Helvigstrup Skov, 55.5667711°N, 11.8870930°E, with *Alnus*, *Betula* and *Picea* in moist forest on wet ground, 19 Aug. 2021, *T. Kehlet*, DMS-10199254. **Netherlands**, Drenthe, Hoogeveen, Stuifzand, alt. 23 m, *Quercus robur*, *Betula* sp., 17 Oct. 2022, *D. Bandini* (DB17-10-22-16); ibid., at some distance from former location, alt. 23 m, *Quercus robur*, *Betula* sp., 17 Oct. 2022, *D. Bandini* (DB17-10-22-20); Drenthe, Eursinge, alt. 22 m, *Quercus robur*, *Betula* sp., *Pinus sylvestris*, 19 Oct. 2022, *D. Bandini* (DB19-10-22-3); ibid., at some distance from former location, alt. 22 m, *Quercus robur*, *Betula* sp., *Pinus sylvestris*, 19 Oct. 2022, *D. Bandini* (DB19-10-22-7).

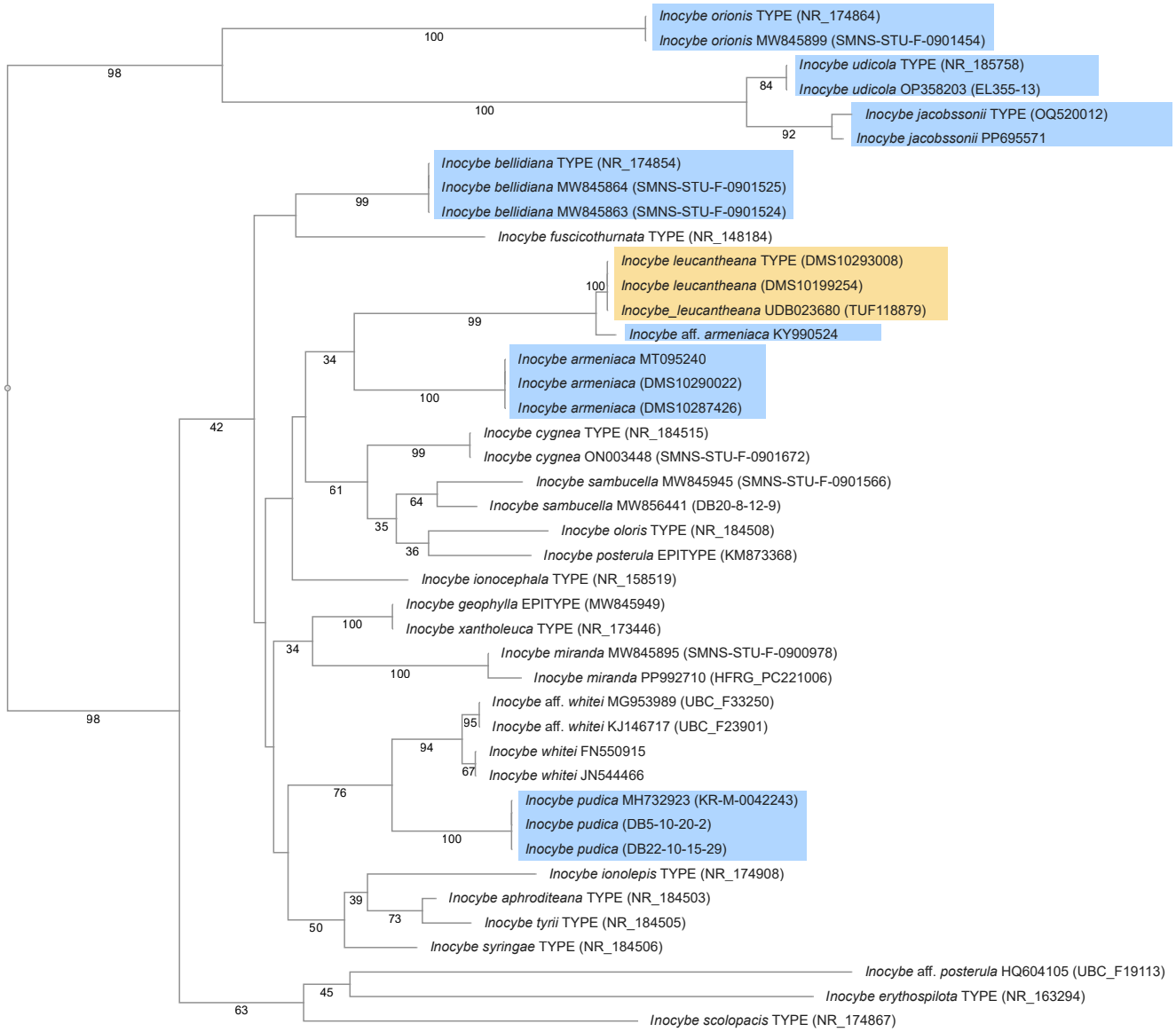
Notes: *Inocybe leucantheana* is a typical member of the *I. geophylla*-clade, characterized by the almost smooth pileus with predominantly whitish colours and a stipe that is only pruinose near the apex. Based on ITS sequence data, it is most closely related to other taxa with reddening flesh, i.e. *I. whitei*, *I. pudica* and *I. armeniaca*. The reddening reaction is, however, sometimes quite weak in *I. leucantheana* and was not noted in the type collection, which was first identified as *I. bellidiana* due to the gracile whitish sporocarps, with distinct buff colours at the cap umbo. The two species further share a preference for rich, somewhat humid soils, but preliminary

Colour illustrations: *Inocybe leucantheana* habitat in mixed woodland on rich, moist soil; Helvigstrup Skov, Denmark, the type locality. *In situ* basidiomata of the holotype (DMS-10293008) (photo credits: T. Kehlet). Drawing: spores (Sp), caulocystidia (Ca), cheilocystidia (Ch), cauloparacystidia (Cpa), cheiloparacystidia (Pa) and pleurocystidia (Pl) (drawing credit: D. Bandini). Scale bars: all others = 50 µm; spores = 10 µm.

evidence suggests that *I. bellidiana* is ectomycorrhizal only with deciduous hosts, while conifers have been present in many but not all known growing sites of *I. leucantheana.* The lack of a (faint) reddening reaction in *I. bellidiana* should further help separate the two species in the field, while differences in spore and cystidia shape separate the two species in the microscope: In *I. bellidiana* the spores tend to have a characteristic bulgy dorsal side and the hymenial cystidia are predominantly subfusiform to subcylindrical, without a well-differentiated neck (Bandini *et al*. 2021a).

Among the reddening taxa, *I. armeniaca* is the most similar taxon, based on the often only faintly reddening flesh. It differs by a usually acute umbo on the cap, distinctly shorter and on av. somewhat wider, at most short-necked pleurocystidia, and only faint reaction of walls with KOH. *Inocybe pudica*, another species with reddening context, has stockier basidiomata, on av. longer spores, on av. shorter but wider pleurocystidia, often with long curved pedicel, and the reaction of walls of hymenial cystidia with KOH is weaker. Other similar taxa include *I. orionis*, *I. jacobssonii* and *I. udicola*, which all differ by more brownish colours towards the cap centre and a lack of a reddening reaction in the flesh and cap cuticle. The north American sequence KY990524 comes close but differs in two substitutions and one indel in the ITS region of the DNA and may represent a separate species.

Supplementary material: doi 10.6084/m9.figshare.30448190 (alignment, raw tree)



Neighbour-Joining phylogram obtained from a MAFFT v. 7.526 (Katoh *et al.* 2019) alignment, analysed and visualised by Archaeopteryx.js v. 2.0 (Zmasek & Zhang 2022) based on 128 gap-free sites on the ITS2 region, showing the position of *Inocybe leucantheana* within the *I. geophylla* clade. Support values are bootstrap values obtained from 1000 replicates. Sequences are mostly identified by type status and GenBank accession numbers, supplemented by my fungarium numbers if available. DMS-numbers refer to sequences obtained from collections from the Danish Fungal Atlas (Frøslev *et al.* 2025) available through GBIF. The clade of the new species is indicated in yellow. Names of species discussed as similar are indicated in blue.

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Inosperma confusum

Fungal Planet 1885 MB 860618

Inosperma confusum Ferisin, Esteve-Rav., Pancorbo & Dovana, ***sp. nov.***

Etymology: From Latin '*confusus*', which refers to the difficulty in distinguishing it from other similar species within *Inosperma cervicolor* group.

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

Pileus 20–35 mm diam., at first campanulate, later convex, distinctly to barely obtusely umbonate; margin involute when young often fibrillose and often showing traces of veil; surface tomentose to appressed fibrillose, initially covered by a conspicuous whitish veil fully coating the light brown to greyish brown or ochre brown surface, usually persisting at the margin. *Lamellae* subdistant, adnate, subventricose, greyish brown; edge thick, undulate to crenate, white to light brown, paler than sides. *Stipe* 30–70 × 4–6 mm, cylindrical, regular, sometimes slightly thickened towards the base; whitish to pale brown, strongly fibrillose, tomentose-flocculose towards apex; often reddening in places when touched or with age. *Context* brownish to reddish in pileus and at stipe base. *Odour* initially aromatic with a sweet note, becoming earthy at maturity. *Taste* indistinct. *Basidiospores* (10.5–)12.7–*13.7*–14.9(–17.0) × (6.5–)7.2–*7.7*–8.2(–9.0) µm, Q = (1.41–)1.63–*1.80*–1.97(–2.23) (n = 90); smooth, light brown, ellipsoid to subphaseoliform, apiculus not very distinct, usually with a large internal guttule, without germ pore; wall up to 0.8 µm thick. *Basidia* 40–47 × 10–15 µm, clavate, 4-spored; sterigmata up to 8 µm long; not very abundant on gill edge and intermingled with cheilocystidia. *Hymenophoral trama* regular, made of cylindrical-ellipsoid elements 10–16 µm wide, with brownish walls; subhymenium of elements up to 100 × 7–13 µm. *Cheilocystidia* abundant, (30–)40–50(–55) × 8–12(–15) µm, hyaline to pale reddish brown, thin-walled, mostly cylindrical with rounded apex, sometimes narrowly subclavate, with a wavy profile, sometimes constrained in the middle. *Caulocystidia* similar but often longer, 50–60(–65) × (9–)10–14 µm. *Pileipellis* undifferentiated, of ascending terminal elements tending towards a trichoderm, cylindrical, 50–110 × 7–14 µm. *Clamp connections* present.

Habitat and distribution: On soil, gregarious to subcaespitose, in the Mediterranean region, found in calcareous soils, with evergreen oak (*Quercus ilex*, *Fagaceae*) and Aleppo pine (*Pinus halepensis*, *Pinaceae*). Known so far only from Italy and Spain.

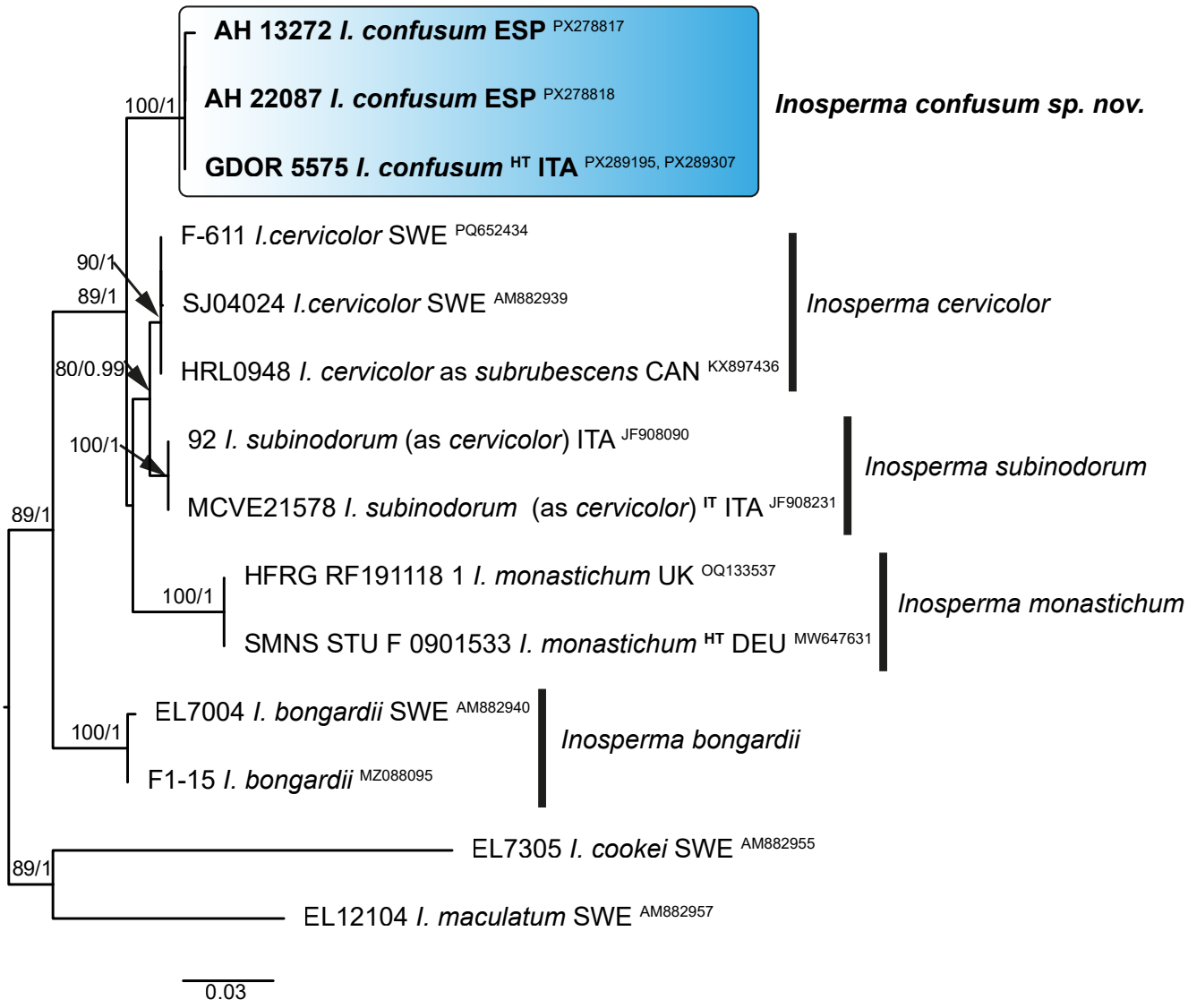
Typus: **Italy**, Friuli-Venezia Giulia, Grado, under *Quercus ilex* and *Pinus halepensis*, 3 Nov. 2020, *G. Ferisin* (**holotype** GDOR 5575; ITS, LSU and *RPB2* sequences GenBank PX289195, PX289307 and PX317238).

Colour illustrations: *Inosperma confusum* habitat from the type locality in Grado, Italy. *Inosperma confusum* basidiomata in typical habitat (on the left, holotype GDOR 5575 from Italy, Grado; on the right AH 22087 from Spain, Mallorca). Microscopy pictures from top to bottom: cheilocystidia and basidia, cheilocystidia, basidiospores. Scale bars: basidiomata = 10 mm; cheilocystidia and basidiospores = 10 µm.

Additional materials examined: **Spain**, Balearic Islands, Mallorca, Artà, in calcareous soil under *Arbutus unedo* (*Ericaceae*), *Quercus ilex* and *Pinus halepensis*, 28 Oct. 1996, *J.L. Siquier* (AH 22087; ITS-LSU sequence GenBank PX278818); Castilla-La Mancha, Guadalajara, Tamajón, Ciudad Encantada, in calcareous soil under *Quercus ilex* subsp. *ballota* and *Juniperus thurifera* (*Cupressaceae*), 26 Apr. 1991, *M. Heykoop* (AH 13272; ITS-LSU sequence GenBank PX278817).

Notes: The terminology follows that of Vellinga (1988) and Kuyper (1986). *Inosperma confusum* is a species of the Mediterranean maquis, which seems to be associated with *Quercus ilex* and *Pinus halepensis* on calcareous soils, and probably also *Cistaceae*. Its size and general appearance resemble those of *Inosperma cervicolor*, which is also its closest genetic relative. *Inosperma confusum* is characterised by its medium size; its light brown to brown pileus surface, covered in youth by a tomentose-woolly whitish velipellis; also, its cylindrical to narrowly subclavate, often undulate, cheilocystidia; and its comparatively large basidiospores, often reaching 13.5–14 µm in length. The ITS+LSU sequence of *I. confusum* shows 94.17 % similarity to that of *I. cervicolor* (voucher SJ04024; GenBank AM882939) when blasted in GenBank. Beyond its genetic distinction, *I. cervicolor* differs morphologically in having a squamulose to squamose, rough pileus with contrasting scales at maturity, and in producing a strong, earthy or DDT-like odour when cut (Kuyper 1986, Bon 1997). Its cystidia are somewhat broader at the apex and often subcapitate, and its spores are smaller, rarely exceeding 13 µm in length and 7.5 µm in width. In our experience, *Inosperma cervicolor* is occasionally found in humid Mediterranean ecosystems with evergreen oaks, but it more typically occurs in moister continental habitats in association with coniferous, frondose or mixed forests (*Pinaceae* and *Fagaceae*) on basic soils. The larger species *Inosperma bongardii* and *I. pisciodorum* exhibit a distinctive initial odour: the former fruity (orange, Muscari-like) or floral, the latter tending towards a fishy or pelargonium-like smell. *Inosperma monastichum* is distinguished by its small size, smooth to slightly fibrillose pileus, much smaller spores, an odour ranging from aromatic to faintly unpleasant (Bandini *et al*. 2021b). The ITS+LSU sequence of *I. confusum* shows 90.78 % similarity to that of *I. monastichum* (holotype) when blasted in GenBank. Finally, *Inosperma subinodorum*, a new species also described in this *Fungal Planet* contribution, is a species typically associated with *Picea* in the Alps. It possesses a distinctly squamulose pileus and lacks any characteristic odour. The ITS+LSU sequence of *I. confusum* shows 91.94 % similarity to that of *I. subinodorum* (holotype) when blasted in GenBank.

Supplementary material: doi:10.6084/m9.figshare.29767040 (alignment).



The 50 % majority rule consensus tree resulting from the Bayesian analysis of the ITS and LSU regions. Bootstrap values ≥ 75 % and posterior probabilities ≥ 0.80 are shown above the branches. The maximum likelihood (ML) analyses were performed using IQ-TREE v. 2.4.0 (Minh *et al.* 2020). The partitioning scheme and model parameters were estimated by the partition merging option and ModelFinder (Kalyaanamoorthy *et al*. 2017) as implemented in IQ-TREE, with two partitions corresponding to the ITS and LSU DNA regions. Ten ML searches were performed, retaining the best likelihood tree. Node support was assessed using 1000 standard non-parametric bootstrap replicates (significant when ≥ 75 %). Bayesian inference (BI) was conducted with MrBayes v. 3.2.7 (Ronquist *et al*. 2012) using the same partitioning scheme. Voucher numbers and GenBank accession numbers are provided for all sequences, including those generated in this study, as well as country ISO alpha3 code abbreviations. Type collections are indicated in superscript: HT = holotype, IT = isotype. The tree was rooted with sequences of *Inosperma maculatum* and *I. cookei*. The new species described is highlighted in the coloured rectangle. Sequences newly generated are indicated in **bold**. The scale bar represents the expected number of nucleotide changes per site.

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Inosperma friesii

Fungal Planet 1886 MB 860225

Inosperma friesii E. Larss., Esteve-Rav. & Pancorbo, ***sp. nov.***

Etymology: Named in honour of the Swedish mycologist, Elias Fries.

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

Pileus 20–50 mm diam., as young conical, conical-convex or campanulate, later becoming plano-convex to expanded, with indistinct low to a broad obtuse umbo, margin inflexed when young, later deflexed, becoming straight and often wavy, straw-yellow to ochraceous yellow, rather uniformly coloured, surface sericeous smooth, radially fibrillose, fibrils often diverging towards the margin, becoming rimulose, velipellis whitish, often distinct forming a velar patch around the centre. *Lamellae* rather crowded, interspersed with lamellulae, L = 48–56, up to 5 mm broad, subventricose, adnate-submarginate, first whitish to pale beige with a greyish tone, then grey-ochraceous to light tobacco brown, without olive tinges, margin white, fimbriate. *Stipe* 30–55 × 3–8 mm, equal cylindrical to subcylindrical, base clavate to moderately or distinctly bulbous, white, cream white to pale yellowish, with age yellowish ochraceous, finely subflocculoose at apex, smoother or sparsely fibrillose towards the base. *Cortina* present in young basidiomes, soon disappearing. *Context* in pileus and stem initially whitish, becoming pale yellow-ochraceous in some mature specimens. *Smell* aromatic rather unpleasant reminding of *Lactarius quietus*. *Taste* as smell. *Basidiospores* (6.7–)7.1–*8.0*–8.8(–9.8) × (3.5–)4.0–*4.6*–5.2(–5.8) µm, Q = (1.37–)1.51–*1.7*–1.97(–2.21), (n = 357/5), smooth, phaseoliform to subphaseoliform, ellipsoid to subovoid, very pale yellowish brown. *Basidia* 26–*31*–38 × 7–*8*–10 µm, Q = 3.0–*3.6*–4.5 clavate, mainly 4-spored, pale yellowish, some with intracellular brown greenish pigments. *Pleurocystidia* absent. *Cheilocystidia* (22.0–)25.7–*33.1*–40.7(–48.1) × (6.9–)7.8–*10.2*–13.4(–14.3) µm, Q = (2.7–)2.8–*3.6*–4.7(–5.0), (n = 171/4), thin-walled, pale yellowish, clavate to subclavate, subcylindrical with rounded apex, in some substrangled towards the middle of its length, often with two or three septa at the base. *Caulocystidia* (25.7–)29.7–*47.6*–69.7(–77.5) × (8.1–)8.6–*11.8*–17.0(–17.3) µm, Q = (2.4–)2.7–*4.0*–6.5(–6.8), present near stipe apex, similar in shape to cheilocystidia, but in general longer, multiseptate, irregularly shaped. *Clamp connections* present.

Ecology and distribution: The species is ectomycorrhizal (ECM), most often collected in mixed deciduous forests likely associated with *Corylus avellana* (*Betulaceae*), *Fagus sylvatica* and *Castanea sativa* (*Fagaceae*), but several other potential host trees were also observed as *Populus tremula* (*Salicaceae*) and *Abies alba* (*Pinaceae*). It is known from the hemiboreal and nemoral zones in Europe, sporulating from late July to October on both acid and rich soils. Blast searches of NCBIs GenBank and the UNITE database gave matches to ITS data from a soil sample in Germany (GenBank GQ219881), ECM of *Abies alba* in Slovenia (GenBank MN265550, MN265551, MN265552, MK820084) and basidiomata from Austria (GenBank UDB07676179, UDB0802475), suggesting the species to have broad host preferences and a wide distribution in Europe.

Typus: **Sweden**, Västra Götalands, Långared, Östad säteri, Djurgården, 57°57'10.70"N, 12°24'30.69"E, 75 m.a.s.l., in mixed deciduous dominated forest with *Corylus avellana*, *Populus tremula*, *Quercus robur*, *Fagus sylvatica* and *Pinus sylvestris*, on rich soil, 18 Sep. 2014, *E. Larsson*, EL161-14 (**holotype** GB-0207737; ITS-LSU sequence GenBank PV962265; **isotype** AH 59983).

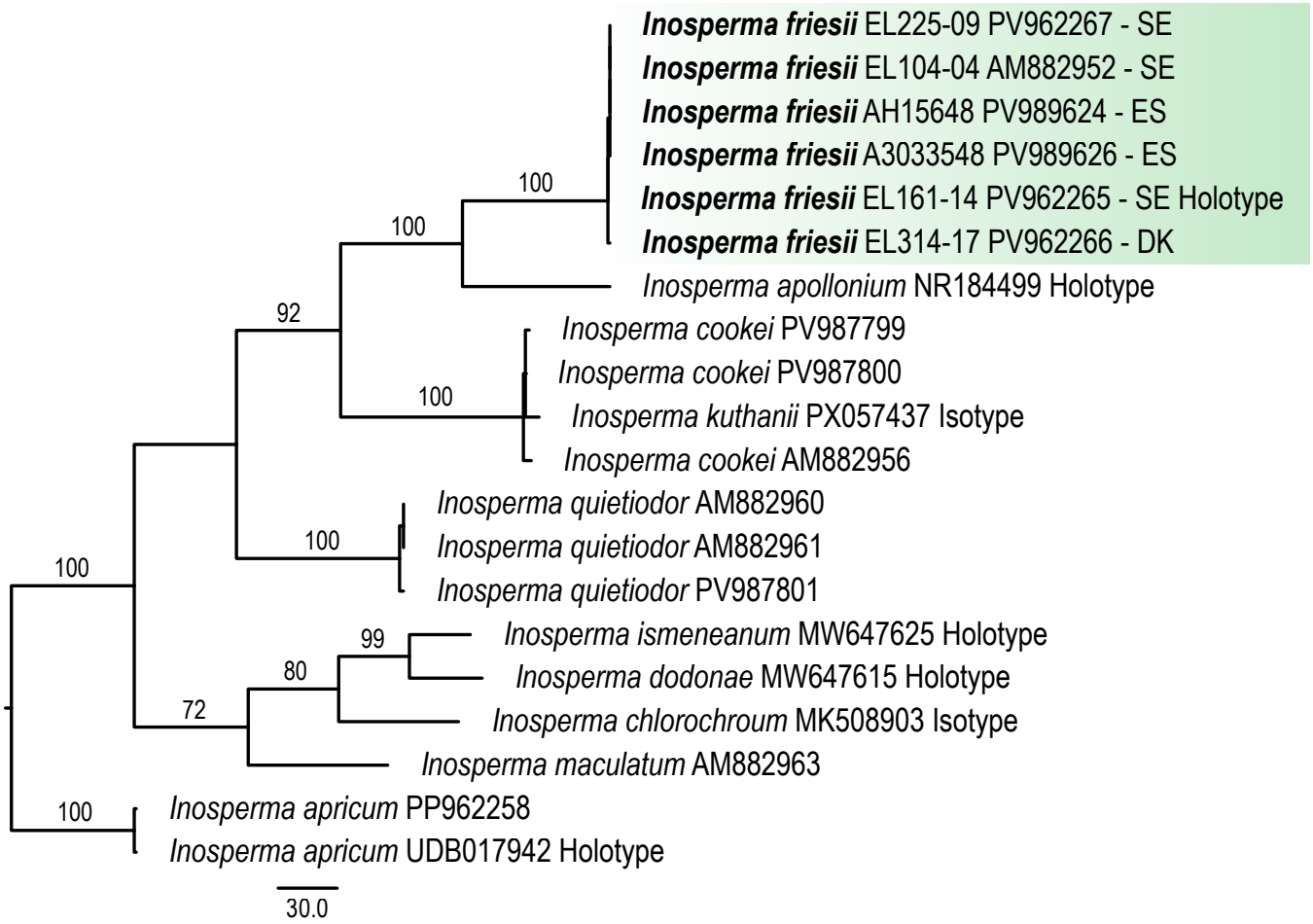
Additional materials examined: **Spain**, Castilla-León, Salamanca, Linares de Riofrío, fuente del Cántaro, 40°34'3"N, 5°54'49" W, 990 m.a.s.l., in *Castanea sativa* and *Alnus glutinosa* forest in acidic soil, 26 Sep. 1991, *F. Esteve-Raventós* & *A. Altés* (AH 15648; ITS and LSU sequences GenBank PV989624 and PV989625); País Vasco, Gipuzkoa, Aia-Sagastizabal 43°13'58"N, 02°10'30"W, 609 m, in mixed forest litter under *Fagus sylvatica* and *Picea abies*, 15 Oct. 2011, *J. Teres* (A3033548-2; ITS and LSU sequences GenBank PV989626 and PV989627). **Denmark**, Jylland, Vejle, Barrit, Staksrode Skov, in forest with *Fagus sylvatica* on sandy and clay soil, 20 Sep. 2017, *E. Larsson*, EL314-17 (GB-0207735; ITS-LSU sequence GenBank PV962266). **Sweden**, Västragötaland, Långared, Östad, Ekedalen, 57°57'58"N, 12°24'16"E, 78 m, in mixed deciduous forest under *Corylus avellana*, 26 Jul. 2004, *E. Larsson*, EL104-04 (GB-0240782; ITS-LSU sequence GenBank AM882952; AH 59984); Småland, Femsjö, Femsjö kyrkoreservat, in mixed forest under *Corylus avellana*, 19 Sep. 2009, *E. Larsson & A. Molia*, EL225-09 (GB-0207736; ITS-LSU sequence GenBank PV962267).

Collections studied for comparison: *Inosperma cookei*. **Sweden**, Bohuslän, Tanum, Greby kleva, mixed deciduous forest on calcareous ground, under *Corylus*, 6 Sep. 2016, *E. Larsson* (EL299-16; ITS-LSU sequence GenBank PV987799); Västergötland, Horla, Yxnås, meadow area with *Populus*, *Betula* and *Quercus*, 28 Sep. 2014, *E. Larsson* (EL192-14; ITS-LSU sequence GenBank PV987800). *Inosperma quietiodor*. **Sweden**, Västergötland, Östeplana, Östeplana hed, grazed meadow area with *Quercus*, *Corylus* and *Tilia*, 27 Sep. 2004, *E. Larsson* (EL115-04; ITS-LSU sequence GenBank AM882960); Västergötland, Medelplana, Råbäcks munkängar, mixed deciduous forest on calcareous ground, 10 Sep. 1994, *L. & A. Stridvall* (GB-0127900; ITS-LSU sequence GenBank AM882961). *Inosperma kuthanii*. **Czechoslovakia**, Moravica, Starý Podvorov, near Hodonin, *Kuthan*, 26 Sep. 1975, (M0020326, isotype; ITS-LSU sequence GenBank PX057437).

Colour illustrations: *Inosperma friesii* habitat in the boreo-nemoral zone in Sweden, Småland, Femsjö, Fries-minnet, the place where Elias Fries grew up and started to study mycology and where this species has been found. *In situ* basidiomata of the holotype (GB-0207737); photos from bottom to top, SEM basidiospores, OM basidiospores, cheilocystidia, caulocystidia from the upper part of the stipe. Scale bars: basidiomata = 1 cm; cystidia = 50 µm; OM spores = 10 µm; SEM spores = 2 µm.

Notes: Inosperma friesii is similar in morphology to *I. cookei*, *I. apollonium* and *I. quietiodor* and they can also co-occur on the same locality. In the phylogeny *I. friesii* clusters with *I. apollonium* as closest relative, and *I. apollonium* is also the closest match with a described species when blasting the ITS sequence in GenBank (84.3 % similarity). *Inosperma cookei* differs from *I. friesii* by the strong smell of honey and distinctly claviform to pyriform cheilocystidia (Bresadola 1892, Kuyper 1986, Larsson *et al*. 2009). Both *I. apollonium* and *I. friesii* have narrowly claviform and smaller cheilocystidia. In *I. apollonium*, the cheilocystidia show a typically wavy outline (Bandini *et al*. 2022b) and the spores are on average larger than in *I. friesii* (9.7–5.2 vs 8.0–4.6 µm). *Inosperma kuthanii* (Stangl & Veselsky1979) turns out to be a synonym of *I. cookei* according to ITS data obtained from the isotype (M0020326) that is identical with that of *I. cookei*. The similarity in morphology was already noticed by Kuyper (1986) who regarded it as a variety, *I. cookei* var. *kuthanii*. *Inosperma friesii* seems to have a smell that reminds of *I. quietiodor*, and two of our collections were initially determined to be *I. quietiodor*. But *I. quietiodor* differs by having larger spores with and ellipsoid or barely reniform profile (Bon 1976, Kuyper 1986). Terminology follows Vellinga (1988) and Kuyper (1986).

Supplementary material: doi: 10.6084/m9.figshare.30001117 (alignment and tree).



Phylogram obtained using PAUP v. 4.0b10 (Swofford 2003) based on ITS and LSU data showing the position of *I. friesii* among its closest relatives in *Inosperma*. 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. *Inosperma friesii* is marked in **bold** and a coloured block, the holotype is indicated.

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Inosperma subinodorum

Fungal Planet 1887 MB 860077

Inosperma subinodorum Bizio, Esteve-Rav. & Pancorbo, ***sp. nov.***

Etymology: From Latin '*sub*' = under, below or beneath, and '*inodorus*, *a*, *um*' = odourless, without smell; referring to the faint or indistinct odour of this species.

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

Pileus 15–40 mm, conical-convex to flat-convex, shallowly to indistinctly umbonate when expanded; surface typically covered with rust-brown scales around the centre (lepiotoid appearance), more sparsely arranged towards the margin, contrasting with the light brownish background colour; margin fimbriate, veil apparently absent or not observed. *Lamellae* adnate, submarginate, broad to subventricose, initially beige or light brown, then brownish with a slight olive tinge, tending to become rust-coloured in damaged or altered spots; margin wavy, whitish fibrillose. *Stipe* 20–50 × 2–5 mm, subcylindrical or slightly attenuated, light brown, gradually lighter towards the base, subflocculose at the apex, smoother towards the base, sometimes with whitish fibrils, tending to redden slightly in damaged areas or with age. *Context* initially whitish in the pileus and at the base of the stipe, later concolourous to brownish along the stipe, reddening in broken or damaged areas; *smell* absent or weak, sometimes slightly mouldy, somewhat unpleasant; *taste* sweetish. *Basidiospores* (10.5–)11.5–*13.0*–14.8(–16.0) × (6.2–)6.5–*7.3*–8.0(–9.6) µm, Q = (1.5–)1.6–*1.8*–2.0(–2.2), (n = 216/4), smooth, ellipsoid, subphaseoliform, yellowish ochraceous. *Basidia* 33.5–*40.8*–44.8 × 6.5–*11.6*–14.5 µm, narrowly clavate, mainly 4-spored, hyaline, some with intracellular brown pigment. *Pleurocystidia* absent. *Cheilocystidia* (23.8–)30.1–*43.1*–61.2(–87.4) × (6.3–)6.9–*9.6*–14.1(–17.2) µm, Q = (1.9–)3.0–*4.6*–6.3(–7.5), (n = 111/4), subcylindrical with round apex, subclavate, subcapitate, hyaline, thin-walled, some with brown contents. *Caulocystidia* (37.2–)41.4–*60.0*–81.3(–97.1) × (7.6–)8.9–*13.1*–22.3(–25.6) µm, Q = (1.8–)2.6–*4.9*–7.3(–7.9), (n = 35/2), present near apex, similar in shape to cheilocystidia, generally larger, irregularly shaped, often with a T-shaped apex, abundant. *Clamp connections* present.

Habitat and distribution: Ectomycorrhizal (ECM) in montane coniferous forests in the Alps, sometimes mixed with deciduous, and associating with *Picea abies* and *Larix decidua*, likely with a preference for acidic or acidified soils in calcareous ground. Known from Italy and Switzerland, but probably widespread in the Alps and central Europe, at an altitude of 1250–1750 m.

Typus: **Italy**, Belluno, Falcade, Tabiadon di Val, 46°22'04"N, 11°53'12"E, 1270 m.a.s.l., in *Picea abies* forest on calcareous ground, 26 Aug. 1997, *E. Bizio* (**holotype** AH 56188; ITS-LSU sequence GenBank PX046529; **isotype** MCVE21578; ITS sequence GenBank JF908231).

Additional materials examined: **Italy**, Belluno, Falcade, Tabiadon di Val, 46°21'17"N, 11°52'59"E, 1137 m.a.s.l., in *Picea abies* forest, 16 Dec. 1992, *E. Bizio,* MCVE19921 (ex MCVE92; ITS sequence GenBank JF908090; Trento, Moena, Passo S. Pellegrino, 46°22'37"N, 11°49'33"E, 1750 m.a.s.l., in *Picea abies* forest on acid igneous rock, 5 Sep. 1999, *E. Bizio* EB19990905, AH 56192; Belluno, Falcade, Tabiadon di Val, 46°22'04"N, 11°53'12"E, 1270 m.a.s.l., in *Picea abies* forest on calcareous ground, 27 Aug. 2002, *E. Bizio*, EB20020827, AH 56189; Belluno, Falcade, Centrale Elettrica Cavia, 46°22'01"N 11°50'05"E 1535 m.a.s.l., in *Picea abies* forest on acid igneous rock, 4 Sep. 2003, *E. Bizio*, EB20030904, AH 56190, ITS-LSU sequence GenBank PX046530; Belluno, Falcade, Centrale Elettrica Cavia, 46°22'01"N, 11°50'05"E, 1535 m.a.s.l., in *Picea abies* forest on acid igneous rock, 16 Aug. 2005, *E. Bizio* EB20050816, AH 56191, ITS-LSU sequence GenBank PX046531; Belluno, Malga Framont, Agordo, 46°18′53″N 12°03′13″E, 1595 m.a.s.l., in *Picea abies* forest on calcareous ground, 15 Aug. 2019, *E. Bizio* EB20190815, AH 46964. **Switzerland**, Grisones, Scuol, Ftan, God Chauols, 46°47′40.62″N, 10°14′29.45″E, 1720 m.a.s.l., in forest with *Picea excelsa* and *Larix decidua*, 11 Sep. 1995, *G. Moreno*, *E. Horak* & *F. Esteve-Raventós*, AH 46862, ITS sequence GenBank PX046532.

Notes: The terminology follows that of Vellinga (1988) and Kuyper (1986). This species is characterised by its typically squamous pileus with more or less erect and dark scales, especially in the centre, which contrast with a paler background (lepiotoid appearance at maturity); a flattened, obtusely umbonate pileus in mature specimens; caulocystidia larger than cheilocystidia; and, notably, its faint earthy to hardly distinctive odour and habitat. It appears to form an ectomycorrhizal association with conifers at montane elevations in the Alps (central Europe), particularly spruce (*Picea abies*), on acidic soils (quartz porphyry), and occasionally on acidified calcareous (Werfen) soils. *Inosperma bongardii* and *I. pisciodorum* exhibit a distinctive aromatic odour: the former is fruity (orange, Muscari-like) or floral, while the latter tends to develop a fishy or pelargonium-like smell. Both species have a nearly smooth and pale pileus when young, which sometimes breaks into flat, slightly contrasting scales as they develop or under certain environmental conditions. Their cystidia are clavate and larger than in *I. subinodorum*, and usually exhibit distinct reddish contents upon maturation. *Inosperma cervicolor*, the species phylogenetically closest to *I. subinodorum*, is characterised by a clear, strong and unpleasant odour, reminiscent of damp earth, or mould, sometimes compared to the smell of dry sausage or insecticide (Bon 1997). The cap exhibits a

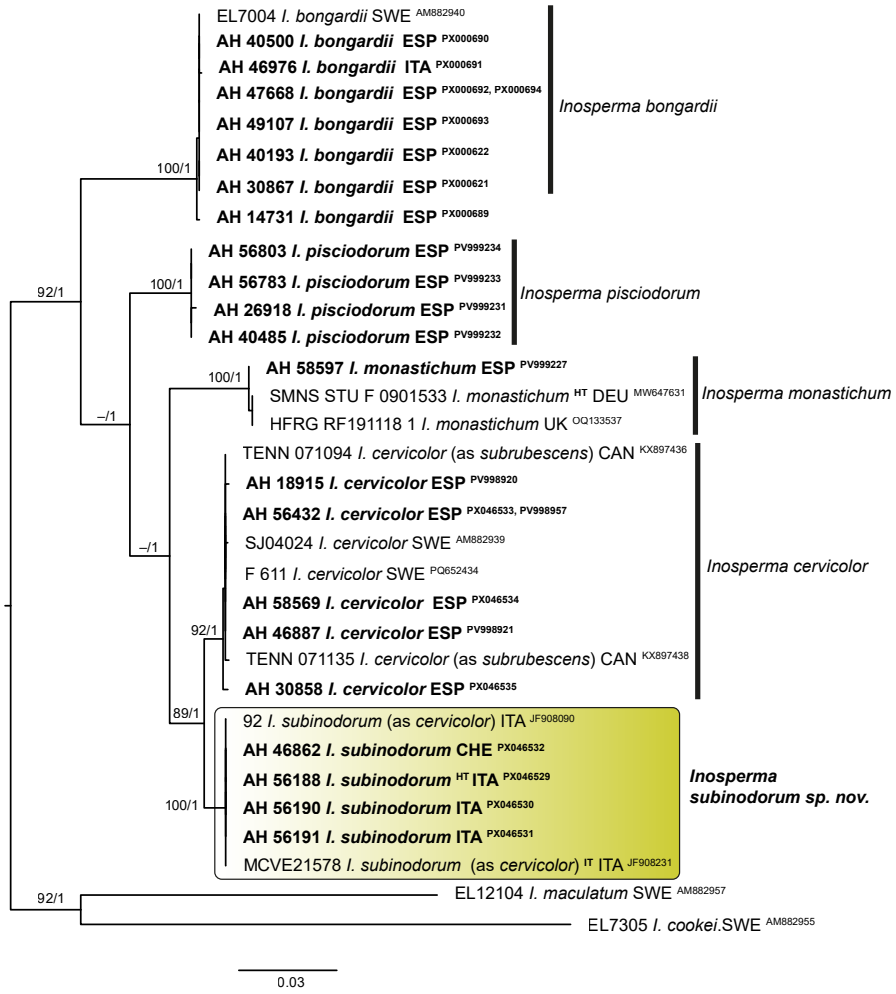
Colour illustrations: Habitat of *Inosperma subinodorum* in *Picea abies* forest in Tabiadon di Val, Italy, at 1270 m.a.sl. (type locality). *In situ* basidiomata of the holotype (AH 56188); from bottom to top: SEM basidiospores; OM basidiospores; cheilocystidia; caulocystidia (AH 46862) in the upper part of the stipe. Scale bars: basidiomata = 10 mm; cystidia = 50 µm; OM spores = 10 µm; SEM spores = 2 µm.

typically scaly appearance with background-coloured scales, and the cystidia are claviform to often subcapitate (Kuyper 1986, Stangl 1989 Bon, 1997). Finally, *I. monastichum* is distinguished by its small size, smooth or slightly fibrillose cap; smaller spores; cylindrical, non-capitate cystidia; and an odour ranging from aromatic to slightly unpleasant (Bandini *et al.* 2021b).

According to the description, habitat, iconography, and distribution provided by Ferrari (2007, 2010) for the *f. inolens* of *Inosperma cervicolor*, it can be assumed that this may correspond to *I. subinodorum*, although molecular studies of Ferrari's collections of this odourless form have not yet been conducted.

The phylogenetic analysis revealed that the species most closely related to *Inosperma subinodorum* is *I. cervicolor*, with strong support [bootstrap value (BS) = 89 %, Bayesian posterior probability (BPP) = 1] and a similarity range of 96–97.5 % with the holotype collection (AH 56188). More distantly related taxa with unresolved relationships include *I. monastichum*, *I. pisciodorum* and *I. bongardii*, which show 91.75 %, 92.76 %, and 84.4–84.8 % similarity to the holotype collection, respectively.

Supplementary material: doi: 10.6084/m9.figshare.29598851 (alignment).



Majority rule (50 %) consensus tree resulting from the Bayesian analysis of the ITS and LSU regions. Bootstrap values ≥ 75 % and posterior probabilities ≥ 0.80 are shown above the branches. ML analyses were performed using IQ-TREE v. 2.4.0 (Minh *et al.* 2020). The partitioning scheme and model parameters were estimated by the partition merging option and ModelFinder (Kalyaanamoorthy *et al.* 2017) as implemented in IQ-TREE, with two partitions corresponding to the ITS and LSU DNA regions. Ten ML searches were performed, retaining the best likelihood tree. Node support was assessed using 1000 standard non-parametric bootstrap replicates (significant when ≥ 75 %). Bayesian inference (BI) was conducted with MrBayes v. 3.2.7 (Ronquist *et al.* 2012) using the same partitioning scheme. Voucher numbers and GenBank accession numbers are provided for all sequences, including those generated in this study, as well as country ISO alpha3 code abbreviations. Type collections are indicated in superscript: HT = holotype, IT = isotype. The tree was rooted with sequences of *Inosperma maculatum* and *I. cookei*. The new species described is highlighted in the coloured rectangle. Sequences newly generated are indicated in **bold**. The scale bar represents the expected number of nucleotide changes per site.

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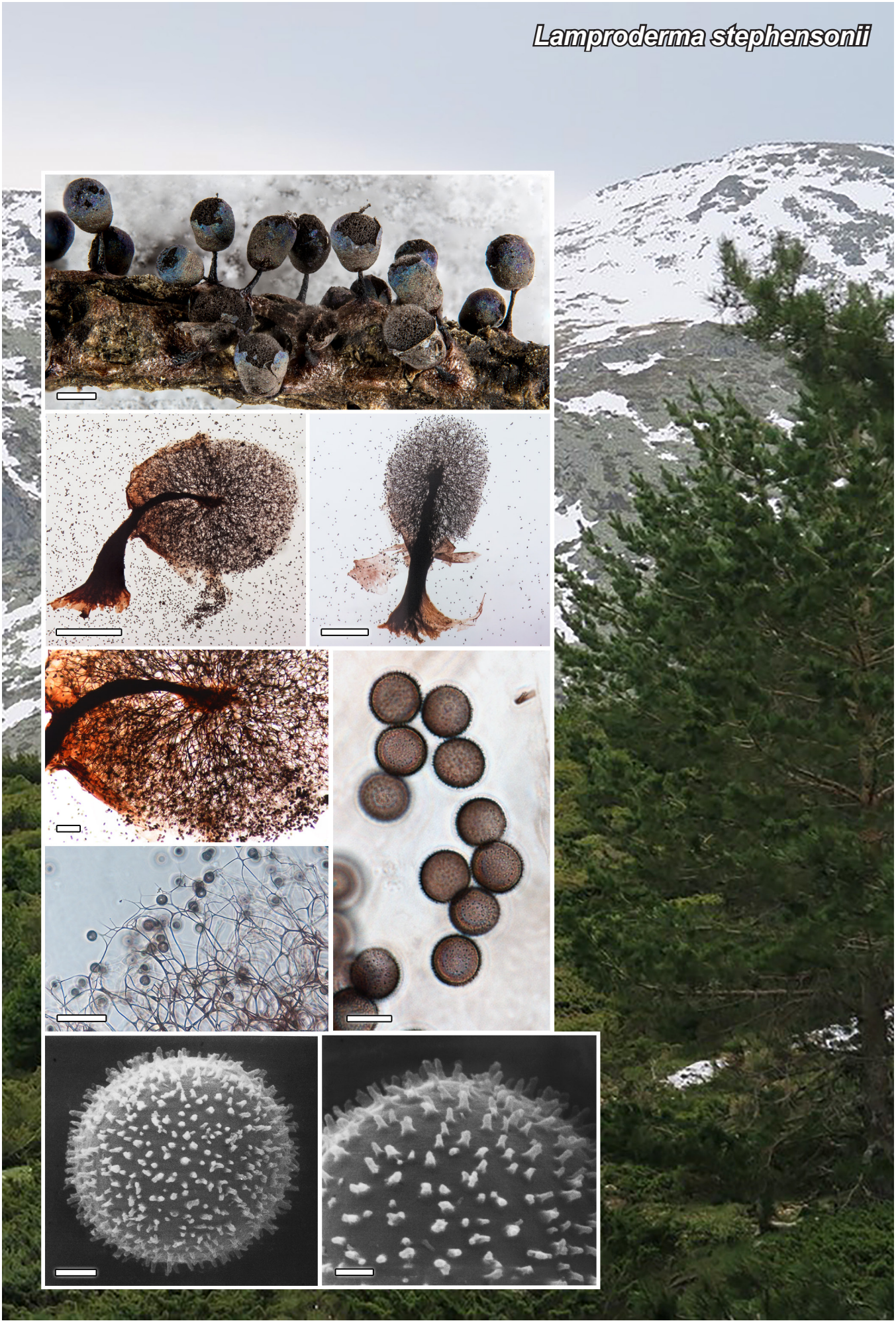

Lamproderma stephensonii

Fungal Planet 1888 MB 858841

Lamproderma stephensonii G. Moreno, López-Vill., & A. Sánchez, ***sp. nov.***

Etymology: *stephensonii* in honour of Steven L. Stephenson, for his work in the field of *Myxomycetes*.

Classification: *Lamprodermataceae*, *Physarales*, *Myxomycetes*.

Sporocarps abundant, densely aggregated, stalked, 2–3 mm tall. *Sporotheca* obovoid or broadly cylindrical, 1.0–2.1 × 0.9–1.2 mm, with an obtuse apex, blackish. *Peridium* membranous, greyish with a violet iridescence, persistent mainly in the lower half of the sporotheca. *Stalk* cylindrical, widened towards the base, solid, brownish black, inner fibers thick and dark reddish brown, up to 1 mm long, 1/2–1/3 of the height of the sporotheca. *Columella* a continuation of the stalk, reddish brown, reaching 2/3 the height of the sporotheca. *Capillitium* very dense, anastomosed, sinuous, emerging along the columella, reddish brown, paler towards the periphery, with elongated, free, spiny tips. *Hypothallus* membranous, reddish brown. *Spores* globose to subglobose, black in mass, uniformly violaceous brown under transmitted light, 11–13.5 µm in diam, av. 12.32 × 12.32 µm, Qav = 1 (n = 25), with spines. Under SEM the spore ornamentation is formed by bacula, densely and regularly distributed, reaching 0.5 µm in height. *Plasmodium* unknown.

Habitat and distribution: This is a nivicolous species occurring in groups on various coniferous substrates, including twigs and needles of *Abies alba* and *Pinus sylvestris*. Rare in the areas studied.

Typus: **Spain**, Segovia, Pto. de Navafría, twigs of *Pinus sylvestris*, 20 Mar. 2001, *A. Sánchez* (**holotype** AH 30037; nSSU, mtSSU and *EF1A* sequences GenBank PV535322, PV535326 and PV550373).

Additional material examined: **Italy**, Cuneo, Pratolungo-Roviera N44°14'26.05", E7°10'31.55", 1570 m.a.s.l., on living twigs and needles of *Abies alba*, 2 May 2019, *E. Richard & F. Hairie* (**paratype**, AH 50591, duplicate in MM40311; nSSU, mtSSU and *EF1A* sequences GenBank PV535323, PV535327 and PV550374). **Spain**, Segovia, Navafría mountain pass, twigs of *Pinus sylvestris*, 19 Mar. 2001, *A. Sánchez* (**paratype** AH 29308; nSSU, mtSSU, *EF1A* and *COI* sequences GenBank PV535320, PV535325, PV550371 and PV550376); ibid., 1770 m.a.s.l., 24 Mar. 2001 (**paratype** AH 28551; nSSU, mtSSU, *EF1A* and *COI* sequences GenBank PV535319, PV535324, PV550370 and PV550375); ibid., 1800 m.a.s.l. (**paratype** AH 49190); ibid., 27 Mar. 2001 (**paratype** AH 30036; nSSU, *EF1A* and *COI* sequences GenBank PV535321, PV550372 and PV550377).

Colour illustrations: Spain, Segovia, Navafría mountain pass, where the holotype was collected. Sporocarps; sporocarp; capillitium and columella; tips of the capillitium; spores by LM; spore by SEM (holotype). Scale bars: sporocarps = 1 mm; sporocarps under LM = 0.5 mm; capillitium and columella = 100 µm; capillitium = 50 µm; spores under LM = 10 µm, spores under SEM = 2 µm.

Notes: *Lamproderma stephensonii* is characterised by its densely aggregated sporocarps, noticeable large in size, with a persistent peridium mainly in the lower part of the sporotheca, a solid stalk formed by reddish brown inner fibres, a reddish brown capillitium, whitish towards the periphery, and spinose, relatively large (11–13.5 µm diam.) spores.

Lamproderma stephensonii can be confused with other species of *Lamproderma* in the *ovoideum* complex. It was originally described as *L. ovoideoechinulatum* var. *microsporum*. Indeed, *L. ovoideoechinulatum* is the closest species both macro- and microscopically. *Lamproderma ovoideoechinulatum* can be distinguished by its shorter stalk (up to 1/3 of the height of the sporotheca), and larger spores 12.5–15(–16) µm in diam, with irregularly distributed spines (Poulain & Meyer 2005) and a paler area that is absent in the new species.

Lamproderma ovoideum has a darker capillitium as viewed under transmitted light and larger spores (13–16 µm diam.) with very subtle, dense, and regularly distributed ornamentation (Moreno *et al.* 2002). Under SEM the spores are ornamented by short pila.

Lamproderma cucumer is characterized by very short stalks (sometimes it even appears to be sessile), and its spores are warted under transmitted light and shortly pilated under SEM.

Lamproderma piriforme has large spores (15–20 µm in diam) and the spore ornamentation is similar to that of *L. ovoideum*.

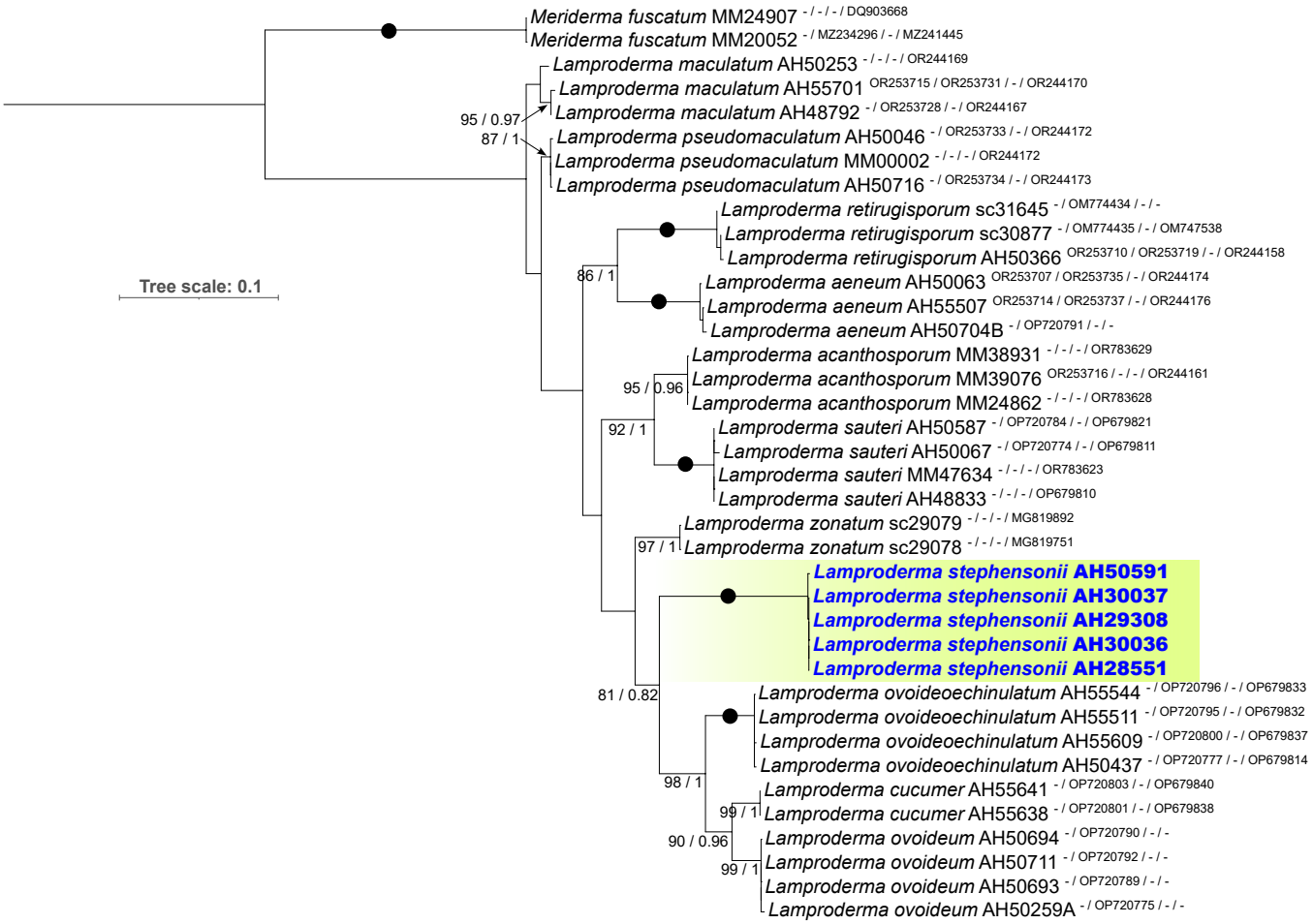
The presence of fibres in the stalk of this *Lamproderma* reminds one of the genus *Comatricha*. However, members of the latter genus develop the fibres on the outer surface of the stalk. In addition, nivicolous species of *Comatricha* usually retain remnants of the peridium attached to the sporotheca. These species are *Comatricha fusiformis*, and *C. pseudoalpina*.

Comatricha fusiformis differs by its long, fusiform sporotheca retaining remnants of the peridium and spores 12–14 µm in diam. By SEM, the ornamentation is formed by dense, regularly distributed stellate baculae (Singer *et al.* 2005). An instructive macrograph of the species is available in Poulain *et al*. (2011).

Comatricha nivalis is characterized by its small, globose, brownish sporocarps, scattered or clustered, with abundant remnants of the silver peridium, especially in the lower half of the sporotheca. The columella reaches up to 2/3 the height of the sporotheca. The capillitium has spiny free ends which are sometimes dichotomous or trichotomous and attached to remnants of the peridium. Spores verrucose, 10–12 µm diam (Moreno *et al.* 2012).

Comatricha pseudoalpina differs by its strongly aggregated sporocarps, very short stalk, the long and broad sporotheca, a persistent peridium at maturity that has irregular scales or patches where the spores remain attached (Moreno *et al.* 2004). Excellent macrographs of this species are available in Moreno *et al*. (2010) and Poulain *et al.* (2011).

Supplementary material: The alignment in fasta format and phylogenetic tree in pdf format are deposited at figshare.com (doi: 10.6084/m9.figshare.30340141).



Phylogram obtained from maximum likelihood (ML) analysis based on a combined *COI* / *EF1A* / mtSSU / nSSU alignment in IQ-TREE 1.6.12 (Nguyen *et al.* 2015). The ML analysis with 1000 ultrafast bootstrap replicates (Minh *et al.* 2013) which gave a best tree with a final likelihood value of −7304.0992 is presented. The best-fit model identified for the entire alignment in IQ-TREE using ModelFinder (Kalyaanamoorthy *et al.* 2017) was SYM+G4. Two specimens of the genus *Meriderma* were selected as the outgroup. In total, 38 sequences were included in the analyses, which comprise 2592 characters including gaps. The values on the branches represent ≥ 75 % ultrafast bootstrap support / ≥ 0.75 approximate Bayes test; black dots represent full support (100/1). The scale bar shows the expected number of nucleotide substitutions per site. The new species is indicated in **bold** and blue, and it is surrounded by a coloured rectangle.

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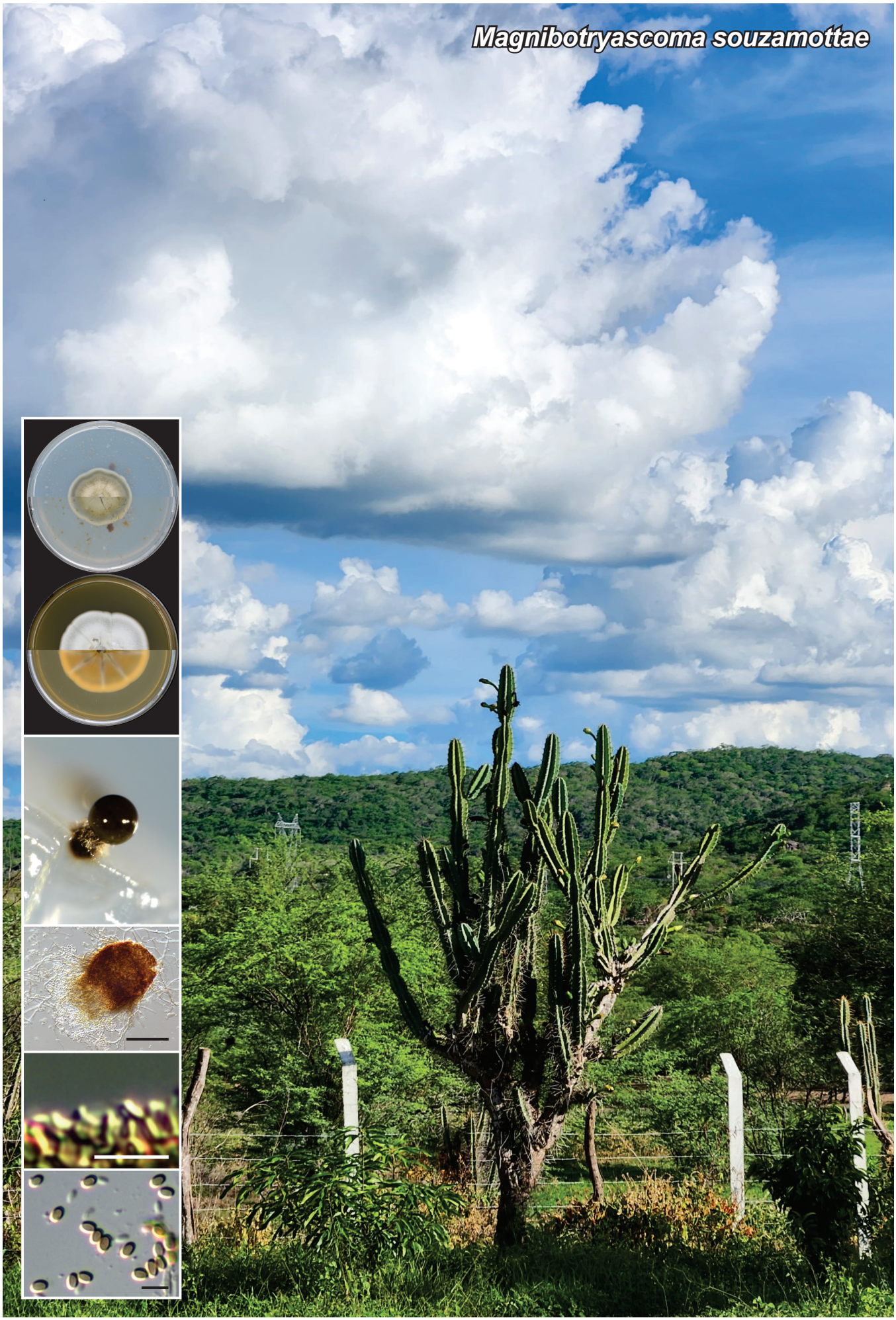

Magnibotryascoma souzamottae

Fungal Planet 1889 MB 859664

Magnibotryascoma souzamottae G.G. Barreto, G.M.R. Albuquerque, L.O. Ferro, P.H.F. Oliveira & J.D.P. Bezerra, ***sp. nov.***

Etymology: Named in honour of Prof. Dr Cristina Maria de Souza Motta for her contribution to fungal taxonomy at the URM culture collection of the Universidade Federal de Pernambuco (Recife, Brazil).

Classification: *Teichosporaceae*, *Pleosporales*, *Dothideomycetes*.

Hyphae septate, smooth, thin-walled, hyaline when young, becoming pale brown at maturity, 1.5–4 µm wide. *Conidiomata* solitary to aggregated, pycnidial, uniloculate, superficial on culture media and occasionally immersed, globose to subglobose, brown to dark brown, ostiolate, (65–)83.5–297(–418) × (45–)73.5–297(–418) µm. *Pycnidia wall* of brown textura angularis. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* enteroblastic, phialidic, discrete, cylindrical to oblong, hyaline, pale brown, 4–7(–13) × 1.5–2 µm. *Conidia* globose to subglobose, hyaline when young and pale brown at maturity, aseptate, smooth-walled, (3.5–)4–4.5(–5.5) × (2.5–)3–3.5 µm. *Sexual morph* not observed.

Culture characteristics: On PDA surface velvety, greenish brown, reverse greenish brown, reaching 36 mm diam. after 2 wk at 25 °C. On MEA surface velvety, white to greyish, reverse brownish, reaching 52 mm diam. after 2 wk at 25 °C.

Typus: **Brazil**, Pernambuco state, Itaíba municipality, Curral Velho farm, 9°08′53″S, 37°12′04″W, isolated as an endophyte from cladodes of *Tacinga inamoena* (*Cactaceae*), Sep. 2013, *J.D.P. Bezerra* (**holotype** UFG 54426, culture ex-type URM 8863 = CBS 141534 = FCCUFG 187; ITS, LSU, *tef-1*, and *rpb2* sequences GenBank PV424206, PV424210, PV432749, and PV432752).

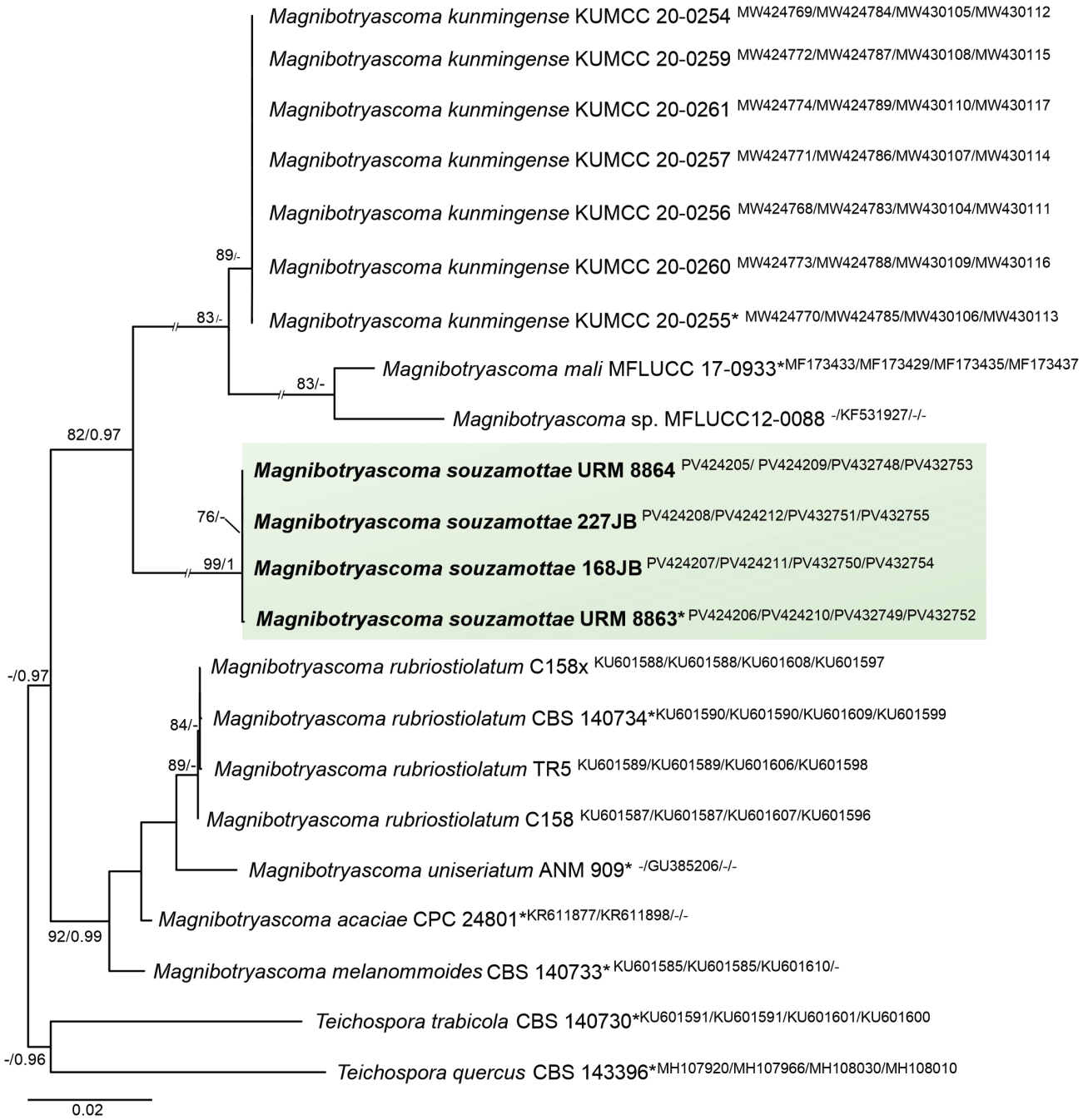
Additional material examined: **Brazil**, Pernambuco state, Buíque municipality, Catimbau National Park, 8°36′35″S, 37°14′40″W, isolated as an endophyte from cladodes of *T. inamoena*, Sep. 2013, *J.D.P. Bezerra*, isolates URM 8864 = CBS 141533 = FCCUFG 188; ITS, LSU, *tef-1*, and *rpb2* sequences GenBank PV424205, PV424209, PV432748, and PV432753; Itaíba municipality, Curral Velho farm, 9°08′53″S, 37°12′04″W, isolated as endophytes from cladodes of *T. inamoena*, Sep. 2013, *J.D.P. Bezerra*, isolate 168JB; ITS, LSU, *tef-1*, and *rpb2* sequences GenBank PV424207, PV424211, PV432750, and PV432754; ibid., isolated as an endophyte from cladodes of *Pilosocereus gounellei* (*Cactaceae*), isolate 227JB; ITS, LSU, *tef-1*, and *rpb2* sequences GenBank PV424208, PV424212, PV432751, and PV432755.

Notes: Studying endophytic fungi associated with cacti in Brazil, some isolates presented morphological features and phylogenetic relationships with *Magnibotryascoma* (*Teichosporaceae*) species. *Magnibotryascoma souzamottae sp. nov.* is morphologically and phylogenetically related to *M. kunmingense* and *M. mali*, differing in the size of pycnidia (150–180 × 250–380 µm in *M. kunmingense* and 136–186 × 173–316 µm in *M. mali*) (Hyde *et al.* 2017, Mortimer *et al.* 2021) and by having pale brown conidiogenous cells and the absence of guttules in globose to subglobose conidia of *M. souzamottae*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hit using the **LSU** sequence is *M. mali* [MFLUCC 17-0933, GenBank NG_059830; Identities = 785/789 (99 %), no gaps], best hit using the **ITS** sequence had highest similarity to *M. melanommoides* [CBS 140733, GenBank NR_154632; Identities = 437/485 (90 %), 21 gaps (4 %)], the closet hit using ***tef-1*** sequence is *Teichospora trabicola* [CBS 140730, GenBank KU601601; Identities = 689/721 (96 %), no gaps], and the closet hit using ***rpb2*** sequence is *M. rubriostiolatum* [CBS 140734, GenBank KU601599; Identities = 799/893 (89 %), no gaps].

Supplementary material: doi: 10.6084/m9.figshare.28697189 (alignment)

Colour illustrations: Caatinga dry forest, Brazil. Colony on PDA and MEA media; pycnidium on PDA medium; pycnidium; conidiogenous cells and conidia; conidia. Scale bars: pycnidium = 50 µm; all others = 10 µm.



Phylogenetic tree derived from a Maximum Likelihood (ML) analysis based on LSU, ITS, *tef-1* and *rpb2* sequences of *Magnibotryascoma* conducted in IQ-TREE v. 1.6.12 software (Nguyen *et al.* 2015) involving 5000 bootstrap replications and the ultrafast bootstrap (UFboot2) method was used to calculate branch support (Hoang *et al.* 2018). Bayesian inference (BI) was conducted in MrBayes on XSEDE v. 3.2.7a (Ronquist *et al.* 2012). The substitution models GTR+I (LSU and *tef-1*), HKY+G (ITS) and GTR+G (*rpb2*) were used for both analyses. Confidence values for ML-BS ≥ 70 % (IQ-TREE) and BPP ≥ 0.95 are included near the nodes. The species obtained in this study are in bold. Ex-type strains are marked with an asterisk (*) and GenBank accession numbers (superscript; ITS/LSU/*tef-1*/*rpb2*) are indicated for all species. The tree was rooted to *Teichospora quercus* (CBS 143396) and *Teichospora trabicola* (CBS 140730).

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Marasmius ballator

Fungal Planet 1890 MB 860455

Marasmius ballator F.E. Guard, J.D.W. Dearnaley & T. Lebel, ***sp. nov.***

Etymology: The epithet *'ballator'* is Latin for dancer, the basidiomata resembling of a group of ballet dancers in tutus. It is a noun in apposition.

Classification: *Marasmiaceae*, *Agaricales*, *Agaricomycetes.*

Basidiomata small to medium, collybioid. *Pileus* 7–15(–35) mm diam., parabolic as juvenile, convex-campanulate, opening to almost applanate on maturity, central disc umbonate, pileus deeply striate-sulcate, with shallow half-striations alternating with full sulci. Pileal disc thick, off-white (78; Royal Botanic Garden Edinburgh 1969), pileus greyish white (78), with vinaceous grey (80) to livid vinaceous (77) striations [dark violet (83) in juvenile pilei]. *Lamellae* creamy-white, non-marginate, distant, 8–12 with 0–1 tier shallow *lamellulae*, free to adnexed and occasional low cross-venations. *Stipe* 40–60 × 0.5–2 mm, cartilaginous, cylindrical, reddish brown bay (19) base, grading to apricot (47), then buff (52) upper half and white apex, non-insititious insertion and strigose hairs at base with thin cream mycelial mat binding substrate leaves and twigs. *Basidiospores* mean 20.5 ± 0.98 × 4.7 ± 0.22 µm, Qm = 4.42 ± 0.29, range 19.1–22.4 × 4.3–5.1 µm, Qmin = 3.76, Qmax = 5.12, n = 20, smooth, inamyloid, clavate. *Basidia* 4-spored, 28–37 × 8.5–10 µm. *Basidioles* long, cylindrical to narrowly clavate, 30–40 × 6–9 µm. *Cheilocystidia Globulares*-type cells, 13–22 × 6.5–10 µm, oblong, clavate, pyriform, thin-walled inamyloid. *Pleurocystidia* absent. *Lamellar trama* hyphae 3.5–4.5 µm diam., thin-walled, weakly dextrinoid. *Pileipellis* a hymeniderm of *Globulares*-type cells, 16–27 × 8–13 µm, subglobose to broadly clavate, inamyloid, thin-walled. *Pileal trama* hyphae 5–6.5 µm diam., interwoven, dextrinoid. *Caulocystidia* absent. *Clamp connections* present in all tissues.

Habit, habitat and distribution: Gregarious on leaf litter in subtropical rainforest. *Marasmius ballator* has been found in one area of central New South Wales, Australia.

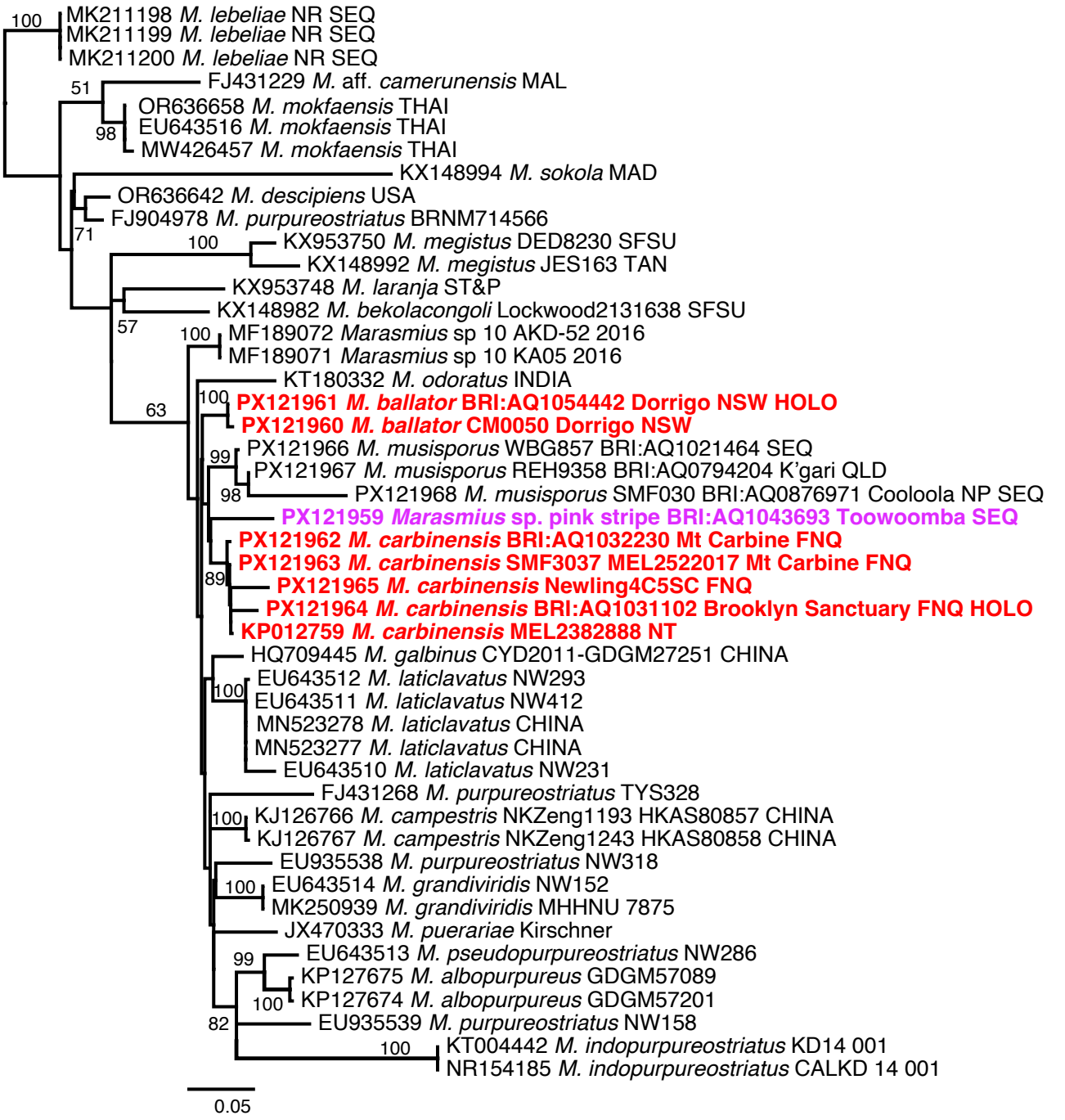
Typus: **Australia**, New South Wales, Dorrigo National Park, The Glades, S30°22'18.14", E152°43'32.16", in leaf litter and twigs, 20 Mar. 2025, *K. Millichamp*, F2025008 (**holotype** BRI AQ1054442; ITS and LSU sequences GenBank PX121960 and PX121952).

Additional material examined: **Australia**, New South Wales, Dorrigo National Park, The Glades, S30°22'20.64", E152°43'31.16", in leaf litter and twigs, 20 Mar. 2025, *C. Marciniak,* CM0050, DAR87346; ITS and LSU sequences GenBank PX121961 and PX121958.

Notes: *Marasmius ballator* is characterised by its moderately robust stature, striped, sulcate pileus, *Globulares*-type cells in pileipellis and elongate basidiospores. It is in sect. *Globulares,* subsect. *Atrorubentes,* ser. *Purpureostriati* (Oliveira *et al.* 2020). *Marasmius ballator* is part of a large clade of (mostly Asian) morphologically similar species including *M. purpureostriatus* and *M. grandiviridis* from Thailand, *M. galbinus* from China, *M. musisporus* from Papua New Guinea and Australia, *M. carbinensis sp. nov*. and one other undescribed species from Australia. They differ in pileal size, length of basidiospores and colour of striations. Molecularly, it is sister with low support to *M. galbinus*, *M. musisporus* and *M. carbinensis.*

Supplementary material: doi: 10.6084/m9.figshare.30389791 (alignment).

Colour illustrations: Understory of subtropical rainforest in Dorrigo National Park, Australia, showing *Marasmius ballator* in situ. Basidiomata with mycelial mat and details of pileal upper surface and lamellae. (Images by K. Millichamp). Illustration: upper row basidium, basidiospores and basidioles; lower row cheilocystidia and pileipellis *Globulares*-type cells (Illustration by F.E. Guard). Scale bars: basidiomata with mycelial mat and details of pileal upper surface and lamellae = 10 mm; illustration = 10 µm.



Phylogenetic tree of series *Purpureostriati* inferred from a Maximum Likelihood (RAxML) analysis of the ITS region (ITS1, 5.8S rDNA and ITS2) with 1500 bootstrap iterations using Geneious Prime v. 2023.2.1. (https://www.geneious.com) software. The ML bootstrap proportions > 50 % are shown at the nodes. *Marasmius* sequences in red font are of *M. ballator sp. nov*. and *M. carbinensis sp. nov*. also described elsewhere in this paper. *Marasmius lebeliae* (ser. *Crinipes*) is used as the outgroup.

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Marasmius carbinensis

Fungal Planet 1891 MB 860454

Marasmius carbinensis F.E. Guard, J.D.W. Dearnaley & T. Lebel, ***sp. nov.***

Etymology: The epithet *carbinensis* refers to the region, Mt Carbine, in far north Queensland, where the holotype and other collections of this species were made.

Classification: *Marasmiaceae*, *Agaricales*, *Agaricomycetes.*

Basidiomata small to medium, collybioid. *Pileus* 8–25 mm diam., parabolic, convex to plano-convex, with flat to slightly depressed central disc, deeply sulcate-striate remainder of pileus with alternating shorter, shallow sulci, corresponding with the lamellae and lamellulae, off-white to straw (50; Royal Botanic Garden Edinburgh 1969), dry surface, sulci and central disc blood red (41) in juveniles to clay pink (30) to fawn (29) in mature pilei. *Context* very thin, white, translucent. *Lamellae* distant, 12–16, free to adnexed, cream, non-marginate, with 1–2 tiers *lamellulae*. *Stipe* cartilaginous, central, hollow, 30–80 × 1.5–3 mm, smooth, cylindrical, occasionally flattened with vertical crease, pinkish fawn lower half ± whitish bloom, pale apex, and strigose base with a small mycelial mat binding the substrate. May have a strong *odour* of spring onions. *Spore print* white. *Basidiospores* 21–23.5 × 5–6.2 µm, Q = 3.39–4.36, (mean 22.5 ± 0.74 × 5.5 ± 0.34 µm, Qm = 3.96 ± 0.30), n = 30 from 3 specimens. *Basidia* 4-spored, 30–43 × 10–11.5 µm. *Basidioles* 26–30 × 8–11 µm, narrowly clavate to cylindrical. *Cheilocystidia* sparse *Globulares*-type cells, smooth, sub-globose, pyriform, broadly clavate, occasionally bifid, 12.5–19.5 × 6–13 µm. *Pleurocystidia* absent. *Lamellar trama* weakly dextrinoid, hyphae 4.5–6.5 µm diam. *Pileipellis* a hymeniderm of *Globulares*-type cells, commonly broadly clavate, rarely bluntly bifurcate, irregular, 15–25 × 7.5–14 µm. *Pileal trama* weakly dextrinoid, hyphae 3.5–5 µm diam. *Stipe* hyphae parallel, cortex hyphae 5–8 µm diam., medulla hyphae 6–10 µm diam., no *caulocystidia. Clamp connections* present in all tissues.

Habit, habitat and distribution: Gregarious in well-vegetated monsoonal savannah woodland, riparian *Melaleuca* swamp forest and managed grassy parkland under *Acacia melanoxylon* and *Eucalyptus* (iron bark) species. *Marasmius carbinensis* occurs across the tropical monsoon forests of northern Australia, including Northern Territory and Queensland.

Typus: **Australia**, Queensland, Mt Carbine District, Brooklyn AWC Wildlife Sanctuary, by a track south of main road in savannah woodland S16°34'15.1", E145°6'59.7" in litter and twigs of horehound (*Hyptis suaveolens*), 6 Mar. 2018, *S.J. McMullan-Fisher & F.E. Guard*, SMF3046 (**holotype** BRI AQ1031102, **isotype** MEL 2522022; ITS and LSU sequences GenBank PX121964 and PX121951).

Additional materials examined: **Australia**, Queensland, Mt Carbine Caravan Park, Mt Carbine, in grassy understory of open ironbark and black wattle woodland, 5 Mar. 2018, *F.E. Guard, M.D. Barrett & S.J. McMullan-Fisher*, SMF3037, MEL 2522017; ITS and LSU sequences GenBank PX121963 and PX121950; ibid., Brooklyn Wildlife Sanctuary, Mt Carbine, south of Station Creek, east of highway in *Melaleuca* riparian forest, on leaf litter, 8 Mar. 2018, *F.E. Guard & S.J. McMullan-Fisher*, SMF3057, BRI AQ1032230; ITS and LSU sequences GenBank PX121962 and PX121948; ibid., Cairns, 1 Jan. 2018, *P. Newling*, NEWLING4C5 SC, envt; ITS and LSU sequences GenBank PX121965 and PX121949; ibid., Northern Territory, Fogg Dam, black wattle and *Melaleuca* forest, on roadside embankment in leaf litter, 24 Jan. 2014, *G.M. Bonito, C.N. Barrett, M.D. Barrett & T. Lebel*, GMB543, MEL 2382888; ITS sequence GenBank KP012759.

Notes: *Marasmius carbinensis* with its deeply sulcate, striped pileus, long basidiospores, *Globulares*-type cheilocystidia and pileipellis cells and absence of pleurocystidia is one of a number of *Marasmius* species in Australia and overseas that are in ser. *Purpureostriati* (Oliveira & Moncalvo 2020), in subsect. *Atrorubentes* (Oliveira *et al.* 2024) of sect. *Globulares* (Oliveira *et al.* 2024). It is morphologically similar to *M. musisporus,* (Desjardin & Horak 1997) but lacks the greyish lilac tones and has much shorter basidiospores (mean length 22 µm c.f. 35 µm). It is also very similar to *M. campestris* (Liang *et al.* 2017), but has slightly shorter, narrower basidiospores and no caulocystidia. Phylogenetically it forms a well-supported clade (89/1.0) in the series *Purpureostriati,* with *M. musisporus* (Australia and PNG) and an undescribed species, *Marasmius* sp. "pink stripe" from southeast Queensland as its sisters with low support.

For phylogenetic tree, see *Marasmius ballator* (FP 1890).

Supplementary material: doi: 10.6084/m9.figshare.30389791 (alignment).

Savannah woodland on Brooklyn Wildlife Sanctuary near Mt. Carbine, Australia, where the holotype was found. Basidiomata on substrate; insets showing lamellae and upper surface of pileus. Illustration: upper row basidiospores, basidium, basidioles, middle row pileipellis *Globulares*-type cells, bottom row cheilocystidia *Globulares*-type cells. Scale bars: basidiomata, lamellae and upper surface of pileus = 10 mm; illustration = 10 µm.

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Marasmius clocca

Fungal Planet 1892 MB 860283

Marasmius clocca F.E. Guard, J.D.W. Dearnaley & T. Lebel, ***sp. nov.***

Etymology: The epithet *clocca* is Latin for 'bell or cloche-shaped cap' and refers to the shape of the pileus. It is a noun in apposition.

Classification: *Marasmiaceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata small, marasmioid. *Pileus* 3–9(–12) mm diam., parabolic, campanulate with slightly flared margin, apricot (47; Royal Botanic Garden Edinburgh 1969), orange (48) to sienna (11), pileal margin paler, central disc and inner third smooth, dry, outer two-thirds shallowly sulcate. Juveniles darker pilei - apricot (47) to rust (13), parabolic. *Flesh* white, very thin. *Lamellae* white, margin ± concolorous with pileus, free to occasionally adnexed, 11–15 with 0–1 tier *lamellulae*, occasional peripheral bifurcations and low cross-lamellae. *Stipe* central, filiform, hollow, (15–)25–40(–50) × 0.2–0.5 mm, glabrous, purplish chestnut base (21), rusty-tawny mid-stipe (14) with cream apex, insertion non-insititious, with tiny cream basal disc. Juvenile stipe paler with lower half rusty tawny and upper half white. *Spore print* white. *Basidiospores* 14.7–17 × 3.5–4 µm, Q = 3.64–4.64, (mean 16 ± 0.65 × 3.7 ± 0.22 µm, Qm = 4.25 ± 0.25, n = 20), smooth, inamyloid, clavate, slightly curved in profile. *Basidia* 4-spored, 22–24 × 8 µm. *Basidioles* narrow fusoid to clavate 20–27 × 5–7 µm. *Cheilocystidia Siccus*-type cells, cylindric, narrowly clavate, ovoid, main body 9–17 × 5.5–10.5 µm, with thin- to thick-walled, multiple apical setules, 2–4 × 0.5–1 µm, occasionally bifid. *Lamellar trama* faintly dextrinoid, hyphae 3.5–4.5 µm diam. *Pileal trama* dextrinoid, hyphae 5–7 µm diam. *Pileipellis* a hymeniderm of *Siccus*-type cells, cylindric, clavate, occasionally branching, main body 11–17.5 × 5.5–12.5 µm, multiple, apical setules 2–4 × 0.5 µm, occasionally bifid. *Pleurocystidia* absent. *Stipe* parallel hyphae, medulla hyphae 3.5–6 µm diam., thin-walled, cortex hyphae 4–6 µm diam., thick-walled. *Caulocystidia* absent. *Clamp connections* present in all tissues.

Habit, habitat and distribution: Gregarious, often in large numbers, in leaf litter by roadsides in rainforest from tropical north Queensland to subtropics of mid-coast New South Wales in Australia; occasionally on well-rotted bark.

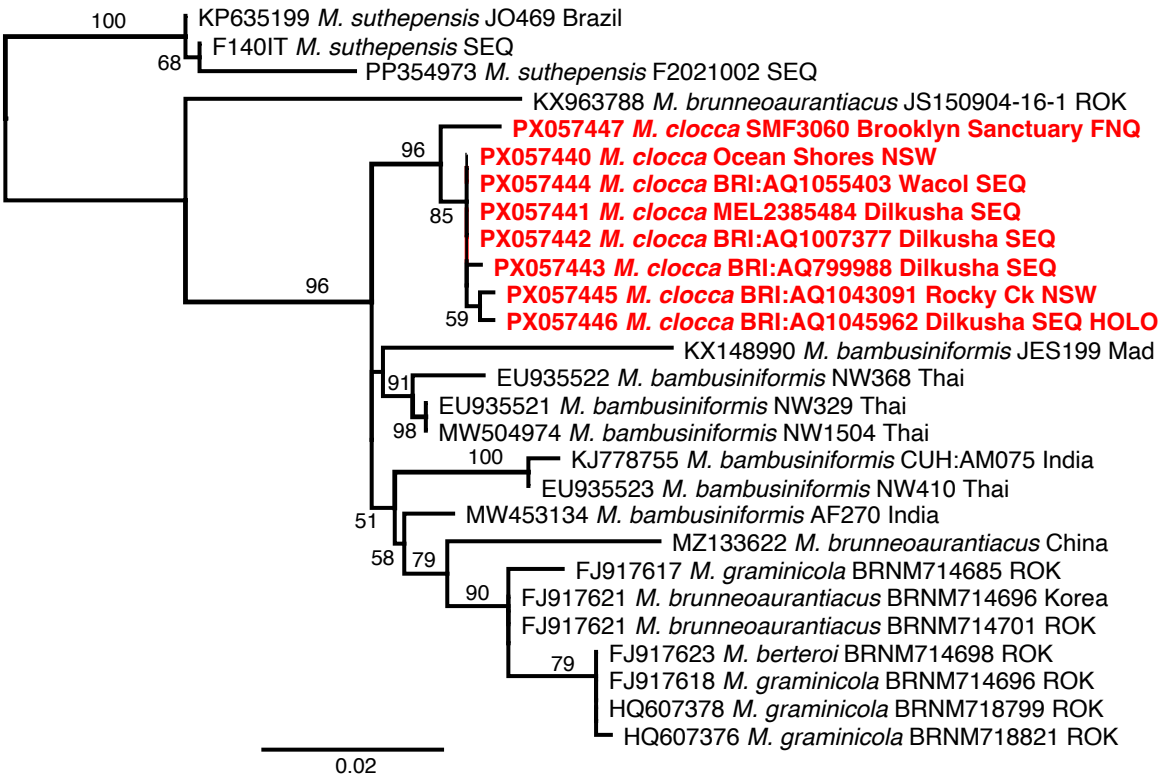
Typus: **Australia**, Queensland, Dilkusha Nature Refuge, S26°44'23.8", E152°53'35.3" in leaf litter of regenerating subtropical rainforest, road verge above Lot 3, 13 Jan. 2024, *F.E. Guard*, F2024010 (**holotype** BRI AQ 1045962; ITS and LSU sequences GenBank PX057446 and PX121953).

Additional materials examined: **Australia**, Queensland, Brisbane, Wacol, Pooh Corner, 27 Jan. 2012, *N.A. Fechner*, NAF27012012 (BRI AQ 1055403; ITS sequence GenBank PX057444); Dilkusha Nature Refuge, road verge near Elsie's Grove, 3 Feb. 2018, *F.E. Guard*, F2018013 (BRI AQ799988; ITS sequence GenBank PX057443); Dilkusha Nature Refuge, road verge near carpark corner, 1 May 2019, *F.E. Guard*, F2019035 (BRI AQ1007377; ITS sequence GenBank PX057442); New South Wales, Big Scrub, Rocky Creek Dam Loop, road verge in subtropical rainforest, 20 Feb. 2022, *F.E. Guard*, F2022010 (BRI AQ1043091; ITS and LSU sequences GenBank PX057445 and PX057448); Ocean Shores, Binya Place, suburban garden mulch, 24 Feb. 2022, *F.E. Guard*, F2022029 (BRI AQ1041079; ITS and LSU sequences GenBank PX057440 and PX057449).

Notes: *Marasmius clocca* is characterised by its small, orange sienna, plicate parabolic to bell-shaped pileus, subdistant lamellae and smooth non-insititious stipe. It has moderately long spores (14.7–17 × 3.5–4 µm) and lacks pleurocystidia and caulocystidia. Morphologically it is very similar to *M. bambusiniformis* Singer (1976), *sensu* Wannathes *et al*. (2009) and Tan *et al.* (2009) but across eight collections the mean of the spore means is 15.2 × 4.0 µm vs 16.2 × 3.2 µm and 16.9 × 3.4 µm respectively. DNA analysis shows *M. bambusiniformis* is not a monophyletic clade and there are probably several species within the series. *Marasmius clocca* is sister to the *M. bambusiniformis* collections from Thailand, with strong support (96/1.0). It is in sect. *Globulares*, subsect. *Leonini*, ser. *Bambusiniformis* (Oliveira *et al.* 2024). There are other morphologically similar, but molecularly distinct, species in Australia, which have not yet been described.

Supplementary material: doi: 10.6084/m9.figshare.30389791 (alignment).

Colour illustrations: Road verge in regenerating subtropical rainforest, Queensland, Australia, holotype site. Basidiomata in situ and illustrating lamellae. Illustration: upper row: basidium, basidioles, cheilocystidia *Siccus*-type cells; lower row: basidiospores, pileipellis *Siccus*-type cells. Scale bars: basidiomata = 10 mm; illustration = 10 µm. All images by F.E. Guard.



Phylogenetic analysis of series *Bambusiniformis* inferred from Maximum Likelihood (RAxML) analysis of the ITS region (ITS1, 5.8S rDNA and ITS2) using Geneious Prime v. 2023.2.1 (https://www.geneious.com) software. The ML bootstrap proportions (from 1500 replications) are shown at the nodes. *Marasmius* sequences in red font are of *M. clocca sp. nov*. *Marasmius suthepensis* (ser. *Graminicolae*) is used as outgroup.

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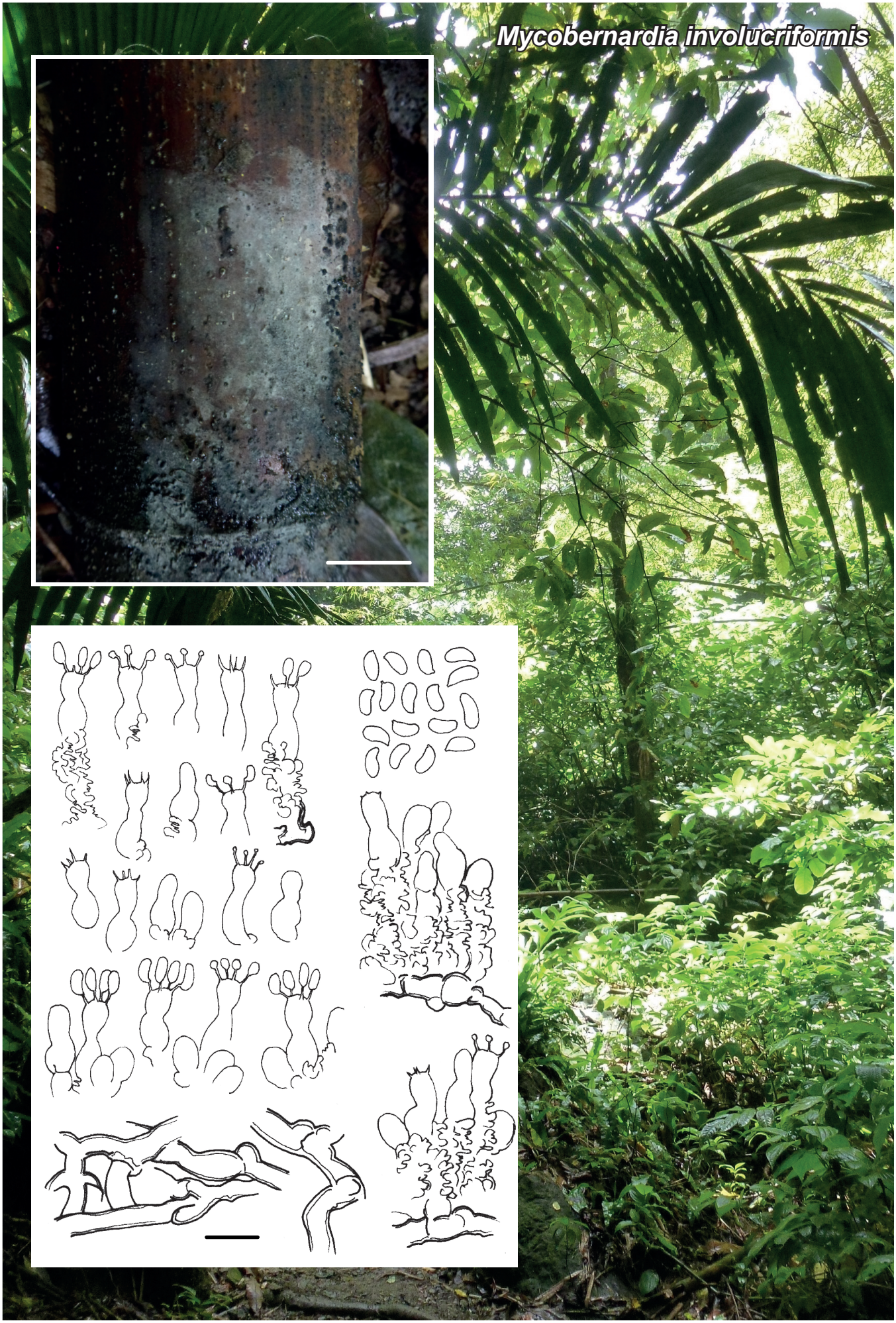

Mycobernardia involucriformis

Fungal Planet 1893 MB 860678

Mycobernardia involucriformis G. Gruhn & Ghobad-Nejhad, ***sp. nov.***

Etymology: Referring to the involucre-like layer of collapsed basidia.

Classification: *Corticiaceae*, *Corticiales*, *Agaricomycetes*.

Basidiomata annual, resupinate, adnate, patches 10 × 5 cm, very thin, 20–60 µm, ceraceous, continuous and cream in the field, strongly porulose and visible like a greyish bloom when dry. Margin indistinct, concolourous. *Hyphal system* monomitic, hyphae hyaline, smooth, with clamps, arranged perpendicularly in a comb-like pattern, negative in Melzer's reagent; hymenium formed on an involucre-like layer of collapsed basidia; tramal hyphae thin-walled, 2 µm diam.; basal hyphae with slightly thickened walls, 10–12 µm long, 2.5–5 µm wide, frequently anastomosing, refractive in KOH–phloxine. *Cystidia,* cystidioles, and dendrohyphidia absent. *Basidia* initially ovoid, later pleural to urniform, clamped, with 4 sterigmata (exceptionally 6 in two observations), sparsely arranged, repetitive, with collapsed basidia at the base forming an involucre-like layer, 11.0–13.4 × 4.2–4.7 µm (width measured at the basal swelling). *Basidiospores* moderately allantoid, smooth, hyaline, thin-walled, negative in Melzer's reagent, 4.5–5.5 × 1.8–2.3 µm, L = 4.7 µm, W = 2 µm, Q = 2.37.

Habit, habitat and distribution: Collected in a very rainy place in the Caribbean Island Martinique, in an old and forgotten plantation of cacao, on a bamboo log fallen in the river.

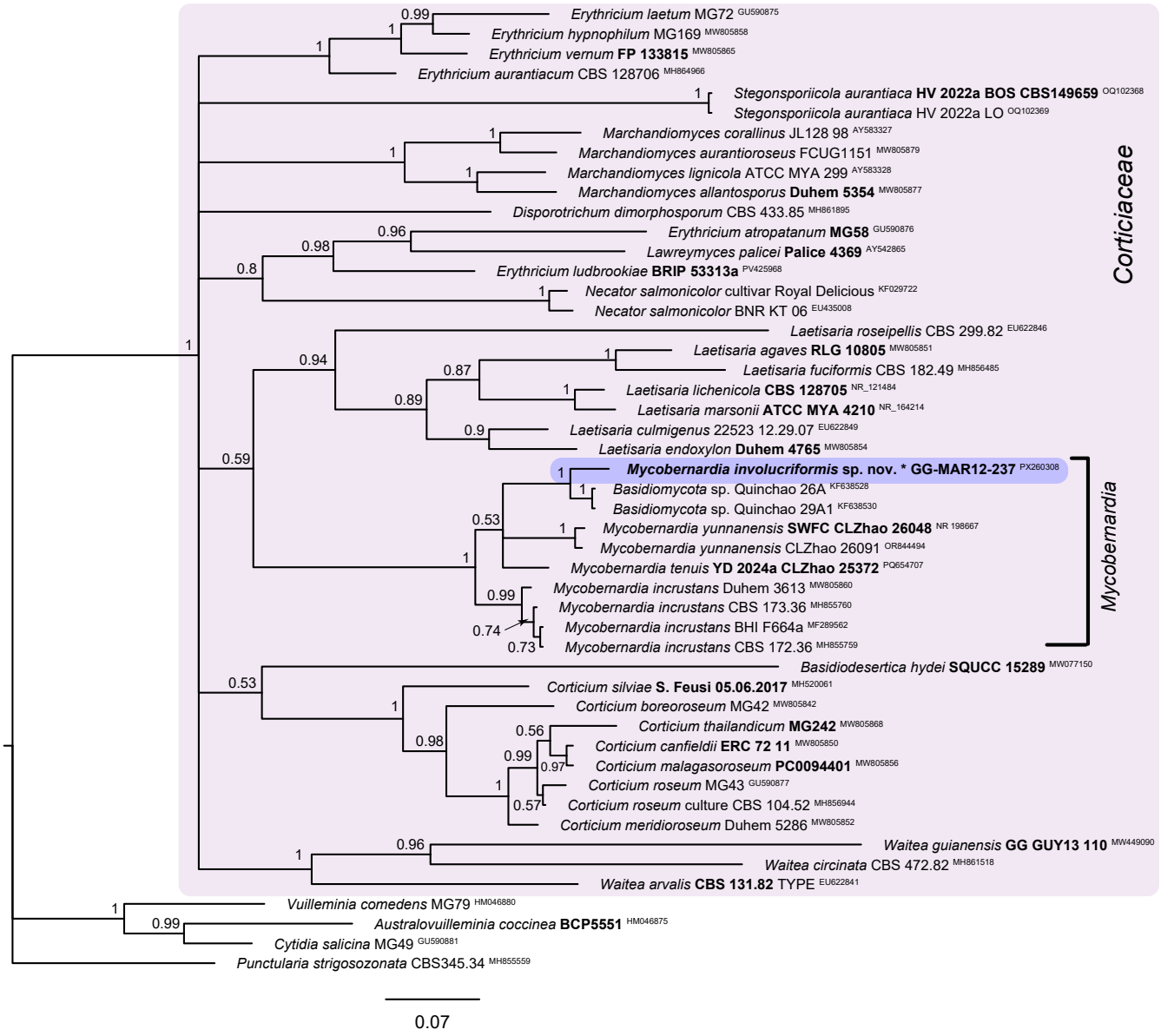
Typus: **France**, Martinique, Commune of Le Prêcheur, Anse Couleuvre, trail to the Couleuvre River waterfall, 30 m.a.s.l., on dead *Bambusa* sp. (*Poaceae*), 9 Aug. 2012, *G. Gruhn*, GG-MAR12-237 (**holotype** LIP, ITS sequence GenBank PX260308); **isotype** K-M001447196.

Notes: The genus *Mycobernardia,* typified with *M. incrustans*, was established by Ghobad-Nejhad *et al.* (2021) to accommodate *Galzinia incrustans.* Two additional species were described in the genus from China viz., *M. yunnanensis* (Li *et al.* 2024) and *M. tenuis* (Wang *et al.* 2025). *Mycobernardia involucriformis* is distinguished by its thin, ceraceous basidiomata, monomitic hyphal system with clamps, pleural to urniform basidia with new ones formed on an involucre-like layer of collapsed basidia, and moderately allantoid basidiospores measuring 4.5–5.5 × 1.8–2.3 µm. Basidia basal clamps are difficult to discern due to the abundance of collapsed basidia. The new species differs from *M. incrustans* by its urniform basidia (vs subcylindrical to suburniform; Eriksson & Ryvarden 1975) and its basidiomata being porulose in dry state and lacking a rose tint. Compared to *M. involucriformis*, *M. yunnanensis* has membranaceous and olivaceous basidiomata, subcylindrical to subclavate basidia, and larger basidiospores measuring 4.8–6 × 2–3 µm (Li *et al.* 2024). *Mycobernardia tenuis* differs from *M. involucriformis* by its subcylindrical to subclavate basidia and larger basidiospores measuring 6–8.5 × 2–3.5 µm (Wang *et al.* 2025). Among the four species currently in *Mycobernardia*, two species show some sort of basidia repetition: the generic type *M. incrustans* and the new species *M. involucriformis.* The involucre-like sheath of collapsed basidia in *M. involucriformis* reminds of *Basidiodendron* which however is a heterobasidiomycete producing phragmobasidia. The two environmental sequences KF638528 and KF638530 deposited in GenBank as *Basidiomycota* sp. and isolated from historic wood in Chile are nested together with the new species *M. involucriformis* in a distinct clade. Moreover, the GenBank sequence MF289562 deposited as *Galzinia* sp. (isolated from a polypore in Boston, USA) is nested well within the *M. incrustans* clade and represents *M. incrustans*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had the highest similarity to *Mycobernardia incrustans* [strain Duhem 3613, GenBank MW805860; Identities = 538/578 (93 %), no gaps], *Basidiomycota* sp. isolated from historic wood in Chile [strain Quinchao 26A, GenBank KF638528; Identities = 493/509 (97 %), no gaps], and *Galzinia* sp. isolated from a polypore in Boston, USA [strain BHI-F664a, GenBank MF289562; Identities = 518/549 (94 %), no gaps].

Supplementary material: doi: 10.6084/m9.figshare.30016612.v1 (alignment).

Colour illustrations: Photo of trail to the Couleuvre River waterfall where the holotype was isolated. Basidioma from the holotype (photo credit: G. Gruhn); line-drawing (by G. Gruhn) from a section through the basidioma of the holotype with basidia, basidiospores, and basal hyphae. Scale bars: basidioma = 2 cm; line-drawing = 10 µm.



Phylogenetic tree of *Corticiaceae* species obtained from a Bayesian analysis of the ITS alignment (49 taxa, 580 characters including alignment gaps). Bayesian inference was performed using MrBayes v. 3.2.7a (Ronquist *et al.* 2012) implemented in CIPRES Science Gateway (Miller *et al.* 2010). The new species is indicated in **bold** font and in the blue box. The ex-type sequence is indicated with an asterisk (*). Strains from material with a type status are indicated in **bold** font. Numbers before nodes indicate Bayesian posterior probability values (BPP). *Punctularia strigosozonata* was used as an outgroup. The scale bar represents the expected number of changes per site.

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Myxotrichum flavum

Fungal Planet 1894 MB 861008

Myxotrichum flavum Czachura & Piątek, ***sp. nov.***

Etymology: Name refers to the vivid yellow colour of fungal colonies in culture.

Classification: *Myxotrichaceae*, *Helotiales*, *Leotiomycetes*.

Mycelium composed of branched, septate, hyaline or subhyaline, yellow in mass, smooth vegetative hyphae, 1.5–2.5 µm wide, which develop into fertile hyphae. *Fertile hyphae* branched, densely septate, hyaline or subhyaline, 1.5–2.5 µm wide, disarticulate into arthroconidia. *Arthroconidia* intercalary or terminal, hyaline, smooth, aseptate, thin-walled, cylindrical, subglobose, globose or doliiform, sometimes curved, truncate at both ends (intercalary arthroconidia) or bullet-shaped (terminal arthroconidia), 2.5–4.5 × 2.0–2.8(–3.0) µm, often with visible connections between disarticulating arthroconidia. *Sexual morph* undetermined.

Culture characteristics: Colonies on malt extract agar (MEA) slightly umbonate with undulate, fimbriate margin, radially folded from the colony centre toward the margin, vivid yellow with a thin whitish edge, reaching 16 mm diam. after 2 wk at 15 °C and 18 mm diam. after 2 wk at 25 °C, reverse hazel or olivaceous with whitish edge. Colonies on potato dextrose agar (PDA) concave with raised undulate, fimbriate margin, radially folded from the colony centre toward the margin, vivid yellow with a thin whitish edge, reaching 17 mm diam. after 2 wk at 15 °C and at 25 °C, reverse hazel or olivaceous with whitish edge. Colonies on oatmeal agar (OA) convex with slightly undulate margin, vivid yellow, reaching 15 mm diam. after 2 wk at 15 °C and at 25 °C, reverse hazel. Colonies on synthetic nutrient-poor agar (SNA) flat with slightly undulate margin, whitish to pale yellow, reaching 18 mm diam. after 2 wk at 15 °C and 16 mm diam. after 2 wk at 25 °C, reverse whitish.

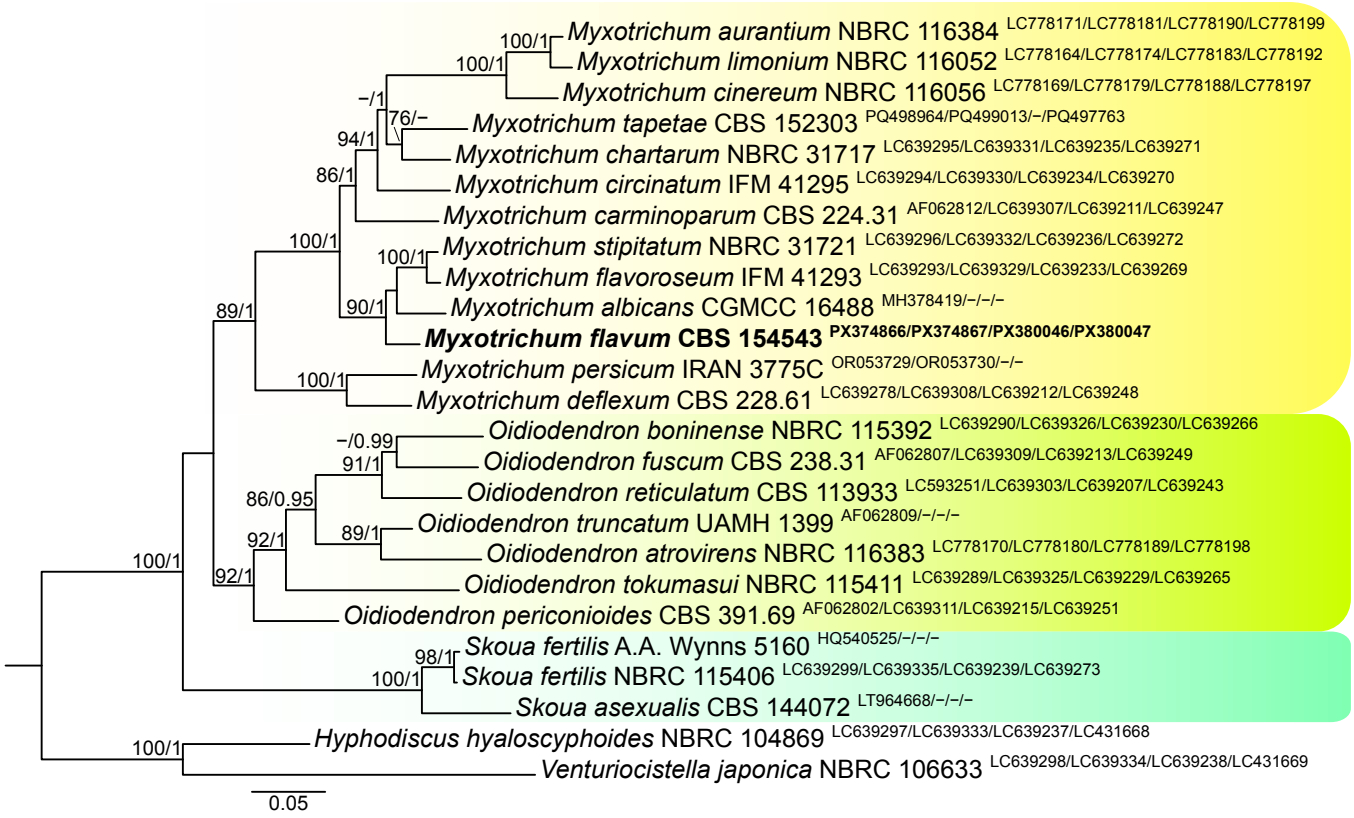
Typus: **Poland**, Świętokrzyskie Province, Kielce County, the Świętokrzyski National Park, the strict protection area Psarski Dół, on resin of *Picea abies* (*Pinaceae*), 16 Oct. 2020, *P. Czachura* (**holotype** KRAM F-60051, culture ex-type: CBS 154543 = P0027; ITS, LSU, *MCM7* and *rpb1* sequences GenBank: PX374866, PX374867, PX380046 and PX380047).

Notes: The genus *Myxotrichum* comprises 57 names, but most of them have been reallocated to other genera (Index Fungorum 2025). Recent phylogenetic studies included 12 species in the *Myxotrichum* s. str. clade (Liang *et al.* 2019, Mehrabi *et al.* 2024, Okubo *et al.* 2025). *Myxotrichum flavum* is phylogenetically closely related to *M. albicans*, *M. flavoroseum* and *M. stipitatum*. It produces a malbranchea-like asexual morph, similar to *M. albicans*, from which it differs in having vivid yellow colonies and cylindrical, subglobose, globose or doliiform arthroconidia. *Myxotrichum albicans* has white colonies and cylindrical arthroconidia (Liang *et al.* 2019). *Myxotrichum flavoroseum* forms both sexual and malbranchea-like asexual morphs but it has creamy white, yellow or rose pink colonies, depending on the agar medium (Sigler & Carmichael 1976, Mehrabi *et al.* 2024). *Myxotrichum stipitatum* mostly forms a sexual morph, with its asexual morph being rarely observed (Orr *et al.* 1963). Although *M. flavum* can therefore not be compared morphologically to *M. stipitatum*, it is phylogenetically distinct. Ecologically, *M. flavum* differs from other members of *Myxotrichum*, which were isolated from cardboard, carpet, forest litter, honey, soil, wood pulp or as endophytes (Mehrabi *et al.* 2024, Okubo *et al.* 2025). *Myxotrichum flavum* is the first representative of the genus isolated from conifer resin. However, what is noteworthy is that previously another *Myxotrichum* species, *M. resinae,* has been described from the resin of *Picea abies* in Sweden (Fries 1832). This species is now accommodated in the genus *Phaeoblastophora*, as *P. resinae* (Partridge & Morgan-Jones 2002), but its exact systematic position remains unknown (Hyde *et al*. 2024). Nevertheless, *P. resinae* is undoubtedly different from *M. flavum* since it has black colonies (in vivo) and a pigmented cladosporium-like asexual morph (Fries 1832, Ellis 1971, Partridge & Morgan-Jones 2002, Zhang *et al.* 2012).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits of the named species using the **ITS** sequence are *Myxotrichum flavoroseum* (as [*Malbranchea*] *flavorosea*) [strain ATCC 34529, GenBank MH037298; Identities = 422/438 (96 %), five gaps (1 %)], *Myxotrichum stipitatum* [culture CBS 393.62, GenBank MH858191; Identities = 505/526 (96 %), one gap (0 %)] and *Myxotrichum circinatum* (as [*Malbranchea*] *circinata*) [strain IFM 41295, GenBank LC639294; Identities = 514/536 (96 %), three gaps (0 %)]. The closest hits of the named species using the **LSU** sequence are *Myxotrichum albicans* [strain SGSF041, GenBank MH971222; Identities = 824/834 (99 %), no gaps], *Myxotrichum stipitatum* [culture CBS 393.62, GenBank MH869789; Identities = 871/884 (99 %), one gap (0 %)] and *Myxotrichum setosum* [culture CBS 260.52, GenBank MH868555; Identities = 870/883 (99 %), no gaps]. The closest hits using the ***MCM7*** sequence are *Myxotrichum stipitatum* [strain NBRC 31721, GenBank LC639236; Identities = 557/596 (93 %), no gaps], *Myxotrichum flavoroseum* (as [*Malbranchea*] *flavorosea*) [strain IFM 41293, GenBank LC639233; Identities = 557/596 (93 %), no gaps] and *Myxotrichum chartarum* [strain NBRC 31717, GenBank LC639235; Identities = 532/597 (89 %), one gap (0 %)]. The closest hits using the ***rpb1*** sequence are *Myxotrichum stipitatum* [strain NBRC 31721, GenBank LC639272; Identities = 637/686 (93 %), three gaps (0 %)], *Myxotrichum flavoroseum* (as [*Malbranchea*] *flavorosea*) [strain IFM 41293, GenBank LC639269; Identities = 615/663 (93 %), three gaps (0 %)] and *Myxotrichum cinereum* [strain NBRC 116056, GenBank LC778197; Identities = 597/694 (86 %), five gaps (0 %)].

Supplementary material: https://doi.org/10.6084/m9.figshare.30218332.v1 (alignment).

Colour illustrations: Spruce forest in the Świętokrzyski National Park, Poland. Colonies on MEA; hyphae; fertile hyphae; arthroconidia. Scale bars = 10 µm.



Maximum likelihood tree of representatives of the family *Myxotrichaceae* obtained from the combined multi-locus alignment (2667 characters: ITS: 541, LSU: 821, *MCM7*: 598, *rpb1*: 707, including gaps). Maximum likelihood analysis was performed using RAxML-NG v. 1.1.0 (Kozlov *et al.* 2019) and Bayesian inference was performed using MrBayes v. 3.2.6 (Ronquist *et al.* 2012). The position of *Myxotrichum flavum* is indicated in **bold**. Numbers above branches indicate maximum likelihood (MLB) support values ≥ 70 % and Bayesian posterior probabilities (BPP) ≥ 0.9, respectively (MLB/BPP). *Hyphodiscus hyaloscyphoides* and *Venturiocistella japonica* were used as an outgroup. The scale bar represents the expected number of changes per site.

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Narcissea scotica

Fungal Planet 1895 MB 860823

Narcissea scotica Drumm.-Herdman & L. Nagy, ***sp. nov.***

Etymology: The specific epithet "*scotica*" (Latin) refers to Scotland, the country from which this species is described.

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

Common name: Moorland inkcap.

Basidiomata small to tiny, solitary or in small groups. *Pileus* 2.0–8.1 mm diam. at maturity, initially convex-paraboloid to subcylindrical, becoming convex, broadly convex or plane with maturity; surface with a moderately thick granulose covering, interspersed with pale irregular flocks, plicate from margin to the edge of the disk when mature, with radial ridges organised in sets of two, slightly apart at the margin and joining at the disk; orange to light brown as primordia, turning mouse grey with maturity but staying orange to light brown on the peaks of the ridges (reflecting veil distribution), orange to light brown colouration concentrated at the disk. *Veil on pileus* composed of two different types: type (a) numerous small to very small white granules; and (b) indistinct fibrillose elements concentrated at the margin. Both clumps and granules of veil cover the entire surface before the pileus splits, after which they are concentrated on the raised parts of the resulting ridges. *Lamellae* free, close, delicate; white at first, turning black with maturity, edge white, non-deliquescent but quickly collapsing. *Stipe* 6.7–39 mm long and 0.2–1 mm wide when mature, translucent, fibrillous, completely covered in fibrils when immature, predominantly pruinose or glabrous when mature, apart from base; surface lined with faint vertical striations that fade with maturity; with a slightly swollen base (0.6–1 mm across) which retains a pale brown hue through all stages of maturity. *Odour* and *taste* not observed. *Basidiospores* [119/3/5] (7.3–)8.0–9.3(–9.8) × (6.0–)7.0–8.1(–8.6) × (4.3–)4.7–5.6(–5.9) µm, av. 8.6 × 7.5 × 5.1 µm, Q 1.05–1.24, Qav 1.15, subglobose, cordate, subangular or subrhomboid in face view, oblong-elliptic or ovate in side view, lenticular, germ pore 1.8–3 µm diam., central or slightly eccentric, often accompanied by 1–3 smaller germ pores, reddish brown in KOH. *Basidia* 16.7–26.1 × 7.4–9.2 µm, 4-spored, dimorphous, (1) clavate or broadly clavate; and (2) pedicellate-clavate or pedicellate-subcylindrical, pedicle often tapered to a slightly broader base. *Cheilocystidia*: of two morphologies, (1) lageniform and 17.4–21.7 × 7.8–11.0 µm, moderately variable in shape, neck 6.0–9.7 × 2.8–4.1 µm, often slightly or moderately flexuous and tapering to a subcapitate apex, joining the clavate base either centrally or eccentrically; and (2) globose, subglobose, broadly clavate or sphaeropedunculate and 16.4–25.4 × 15.6–22.2 µm. *Pleurocystidia*: absent. *Caulocystidia* 18.8–25.2 × 7.2–11.5 µm, lageniform, more variable than cheilocystidia, solitary or in small groups, sparse or almost non-existent in some specimens, sometimes accompanied by 1–3 small, globose elements, hyaline or encrusted. *Pileipellis*: a thin, fleeting layer of hyphal suprapellis composed of hyphae 4.4–9.0 µm broad, typically cylindrical to subcylindrical elements, occasionally narrowly ellipsoid or fusoid elements, width often unequal with one or two marginally broader parts, hyaline or slightly encrusted; subpellis composed of shorter and broader subcylindrical, limoniform elements mixed with irregularly shaped cellular or subangular elements. *Stipitipellis*: a cutis composed of hyphae 2.7–7.4 µm broad, often with intermittent small nodules and protrusions close to the ends of the hyphae. *Veil on pileus*: type (a) (granular elements) highly variable, globose, subglobose, subpentagonal or otherwise subangular, or broadly limoniform or elliptical, hyaline or pigmented elements, sometimes encrusted, 17.4–33.4 × 13.2–28.5 µm; type (b) (fibrillose elements) subcylindrical, cylindrical-fusoid, cigar-shaped elongate elements, 27.4–49.3 × 8.2–14 µm, not as common as type a, typically found in bunches. *Veil on stipe*: chains of subcylindrical elongate elements, similar in shape to type (b) elements on the pileus, but typically longer, 20.5–59.6 × 7.9–11.8 µm; concentrated at the base but present on the entire stipe. *Clamps* not observed.

Habit, habitat and distribution: On dung of red grouse, mountain hare and red deer in *Ericaceae* dominated moorland, heathland and adjoining acidic grassland, in the uplands of central Scotland and the Highlands.

Typus: **Scotland**, Midlothian, Pentland Hills, 55.88000, -3.24100, 430 m.a.s.l., on decaying dung of *Lagopus scotica* (Phasianidae) incubated in a damp chamber indoors, 25 Nov. 2024, *A. Drummond-Herdman*, NG7 (**holotype** E01515780; ITS and LSU sequences GenBank PX399543 and PX399661).

Additional materials examined: **Scotland**, Midlothian, Pentland Hills, 55.88862, -3.22601, 323 m.a.s.l., on decaying dung of *Lagopus scotica* incubated in a damp chamber indoors, 27 Sep. 2024, *A. Drummond-Herdman*, NG4 (ITS sequence GenBank PX369868); Midlothian, Pentland Hills, 55.88507, -3.22670, 423 m.a.s.l., on decaying dung of *Lagopus scotica* incubated in a damp chamber indoors, 30 Aug. 2024, *A. Drummond-Herdman*, NG6 (ITS sequence GenBank PX373609); Midlothian, Pentland Hills, 55.88702, -3.22696, 345 m.a.s.l., on decaying dung of *Lagopus scotica* incubated in a damp chamber indoors, 2 Mar. 2025, *A. Drummond-Herdman*, NG9 (ITS sequence GenBank PX376896); Highland, Càrn Dearg (Monadhliath), 57.09761, -4.25262, 784 m.a.s.l., on decaying dung of *Lepus timidus* (Leporidae) incubated in a damp chamber indoors, 24 Feb. 2025, *A. Drummond-Herdman*, NH1; Aberdeenshire, Old Military Road, 56.95546, -3.40623, 391 m.a.s.l., on decaying dung of *Lepus timidus* incubated in a damp chamber indoors, 7 Apr. 2025, *A. Drummond-Herdman*, NH2 (ITS and LSU sequences GenBank PX376897 and PX399662); Aberdeenshire, Sron nan Gabhar, 56.95551, -3.40186, 457 m.a.s.l., on decaying dung of *Lepus timidus*

Colour illustrations: Mixed moorland in the Pentland Hills, Scotland. Anticlockwise: basidiomata at various stages of maturity; basidiospores of holotype; line drawings of microstructures. Microstructures, from top-down: basidia and lageniform cheilocystidia, subglobose-broadly clavate cheilocystidia, pileipellis, caulocystidia. Scale bars: line drawings = 20 µm; spores = 10 µm.

incubated in a damp chamber indoors, 14 Apr. 2025, *A. Drummond-Herdman*, NGG2; Aberdeenshire, Sron nan Gabhar, 56.95551, -3.40186, 457 m.a.s.l., on dung of *Cervus elaphus* (Cervidae) incubated in a damp chamber indoors, 25 Mar. 2025, *A. Drummond-Herdman*, NRD1 (ITS sequence GenBank PX376898).

Notes: *Narcissea scotica* differs from all currently described species of *Narcissea* by having caulocystidia. As well as this, *N. scotica* differs from *N. cordispora* by lacking pleurocystidia; from *N. ephemeroides* by lacking an annulus, having lageniform cheilocystidia and lacking pleurocystidia; from *N. delicata* by lacking apical branches on the cheilocystidia and lacking pleurocystidia; and from *N. patouillardii, N. cardiaspora* and *N. lahorensis* by growing on dung, having lageniform cheilocystidia and lacking pleurocystidia.

Although caulocystidia have not been recorded in previous descriptions of *Narcissea* species (or taxa that would now be classified as *Narcissea*), Uljé & Noordeloos (1993) mention caulocystidia in their discussion of *Coprinus cordisporus*. The authors note that lageniform cheilocystidia with apical branches were found in two collections of *C. cordisporus*. They then add 'also on the stipe similar caulocystidia have been found, mixed with globose velar elements'. On the former point, if the authors are referring to lageniform caulocystidia with apical branches, it is possible that this represents some yet undescribed species. On the latter point, the caulocystidia of *N. scotica* are often accompanied by 1–3 small, globose elements. It is possible that these are the same sort of elements that Uljé & Noordeloos refer to.

The ecology and habitat of *N. scotica* is noteworthy. Given the complete lack of records of *N. scotica*-like species to date, it is possible that this species occupies a specialised ecological niche. It should be noted that macro *Basidiomycota* of heather moorland habitats remain comparatively understudied, particularly in the context of phylogenetic work.

Keirle *et al.* (2004) noted (in the context of the *C. cordisporus* / *C. cardiasporus* complex) that "substrate specificity may be an important taxonomic tool". Redhead *et al.* (2001) stated that "taxonomic characters [of *Coprinus* s.l.] previously considered not to be generically significant gain importance when correlated with molecular evidence". It is becoming increasingly clear that substrate, habitat and ecology are important taxonomic features for members of the genus *Narcissea*, as Keirle *et al*. suggest, and this is demonstrated by *N. scotica*'s unique ecology combined with its novel status.

All of our collections are from dung of upland, heath–moorland herbivores – red grouse, mountain hare and red deer – in the Pentland Hills and in the Cairngorm and Monadhliath mountain ranges in Scotland, where the prevailing vegetation is heath and acid grassland, dominated by shrubby *Ericaceae* species, such as heather (*Calluna vulgaris*) and bilberry (*Vaccinium myrtillus*). Therefore, the species appears to occupy a specialised, moorland coprophilous ecological niche. However, as with all new species, they first become known from isolated habitats, and more collections may broaden our understanding of the ecological niche of this species.

First, the dung composition from animals grazing in these habitats is not the same as typical grassland-based herbivore dung. Richardson's (2001) extensive study of dung chemistry found that deer, hare and red grouse dung contains higher levels of lignin than other samples, reflecting the moorland plant composition.

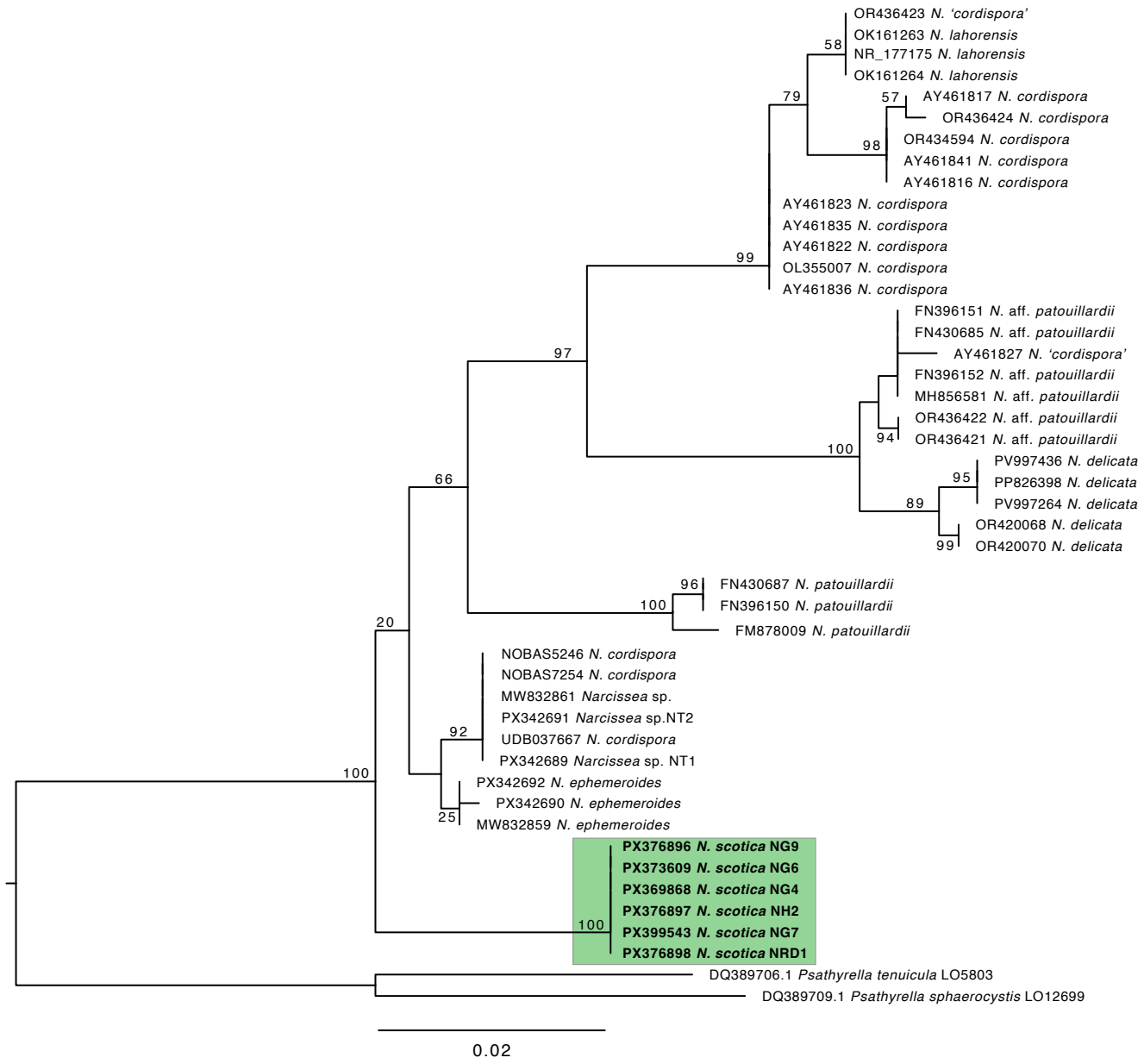
In terms of ecology, it might seem peculiar that a species with such small and delicate basidiocarps grows in a windy, open habitat that is often subject to dry periods. This species appears to be adapted to grow in sheltered dips and shallow holes between clumps of heather and other shrubs where a bryophyte layer (with other low flora and damp soil) retains moisture and provides shelter from wind. This is supported by the hypothesis of Nagy *et al*. (2011) that many coprinoid fungi are adapted to exposed habitats with fluctuating water availability.

Furthermore, the dung of these animals typically forms small pellet heaps that partly coalesce with age and weathering, creating a more contiguous substrate that allows for inter–pellet colonisation by the mycelium, prolonging hydration. The mycelium may be colonising the soil–bryophyte layer immediately surrounding the pellets to further expand its size and reach additional moisture, keeping the organism active during dry periods. This may be supported by our observations of the species growing in culture: basidiocarps grown from pellets on a layer of damp perlite would occasionally grow a few cm away from the dung, on the perlite granules.

Therefore, we hypothesise that *N. scotica* may be specially adapted to the dung from moorland–grazing upland herbivores in cool, exposed, acidic conditions. As there is currently no evidence of it growing in any other habitat, it is possible that it is restricted to this particular ecological niche, but further phylogenetically supported studies are needed before this hypothesis is developed.

Phylogenetic analyses of nuclear ribosomal ITS sequences support that *N. scotica* represents a novel species. *Narcissea scotica* branches as a basal clade in the genus *Narcissea* (ML bootstrap: 100 %), close to the two *Psathyrella* species used as outgroups. It should be noted that, because even the closest related *Psathyrella* spp. (and hence used here) are quite distant, the placement of the root is somewhat uncertain. Nevertheless, *N. scotica* is distinct from all other species in the genus, branching, on our tree, closest to *N. ephemeroides* and a clade of sequences labelled as *N. cordispora*.

Supplementary material: doi: 10.6084/m9.figshare.25406335 (table); TreeBASE study 32329 (alignment and trees); Time-lapse footage: https://youtu.be/3dAtDGxY1W8.



Maximum likelihood phylogram demonstrating the distinct phylogenetic position of *N. scotica* relative to other *Narcissea* species. The tree was inferred based on ITS sequences using RAxML v. 8.0.2 (Stamatakis 2014), under the Jukes-Cantor model of sequence evolution with gamma-distributed rate heterogeneity. Support values are based on 1000 non-parametric bootstrap replicates. Sequences were aligned using MAFFT v. 7.490 with the L-INS-I algorithm (Katoh *et al.* 2013).

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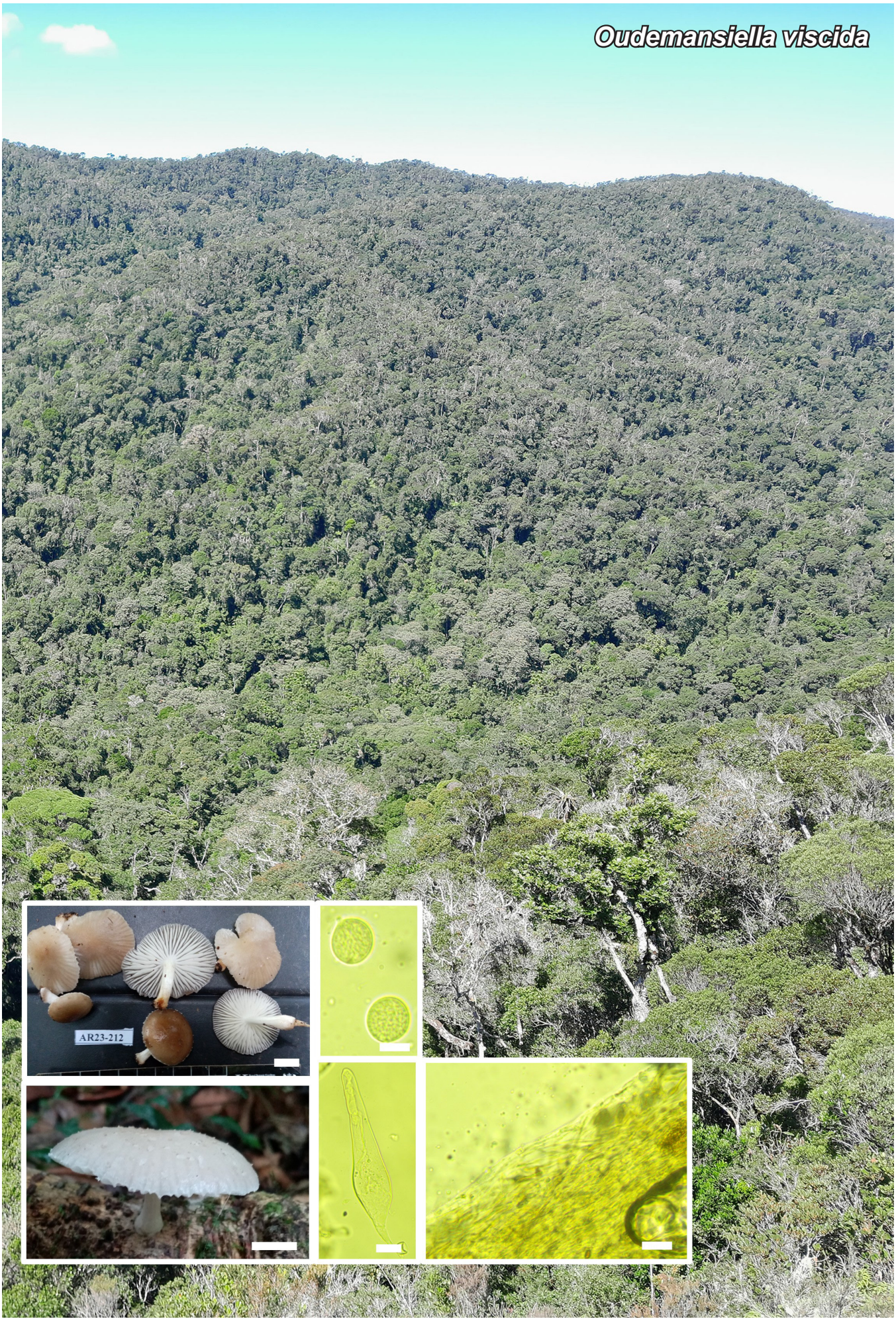

Oudemansiella viscida
AR23-212

Fungal Planet 1896 MB 860619

Oudemansiella viscida Ralaiv. & Niskanen, ***sp. nov.***

Etymology: Named after the sticky cap of the species and its occurrence in various humid forests across Madagascar.

Classification: *Physalacriaceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata usually gregarious in small clusters, with small to large size. *Pileus* 1–6 cm diam., hemispherical-convex when young, then plano-convex to almost plane when mature, viscid, up to 2/3 pellucid-striate, with appressed scales when mature, white, off-white to greyish brown, with a white margin. *Lamellae* adnate, white, medium-spaced to distant with lamellulae. *Stipe* up to 3 cm long, cylindric, some with a small bulb at the base, white, yellow brown at the base with age. *Odour* beef meat-like or indistinct. *Basidiospores* (14.5–)15.5–21 × (14.5–)15–20.5 µm (n = 20), Q = 0.99–1.28, Qav = 1.05, apiculate 0.5–1 µm, globose to subglobose, hyaline in Melzer's and KOH. *Basidia* 63–81 × 18–25 µm, 4-spored, rarely 2-spored, sterigmata 5–13.5 µm, clavate, hyaline in Melzer's and KOH, not clamped. *Pleurocystidia* 91.5–194 × 17–55 µm, lageniform, thick-walled. *Pileipellis* ixocutis, not clamped. *ITS regions* (GenBank PX278759, holotype) distinct from the other members of the genus *Oudemansiella* and deviating from the sister species *O. canarii* by 3.96 % (> 30 substitutions and indels).

Habitat and distribution: In tropical humid forest, on dead wood or branches. Basidiomata only known from Madagascar: North, East and Southeast.

Typus: **Madagascar**, Antsiranana, Montagne d'Ambre National Park, on branch, 24 Mar. 2023, *A. Ralaiveloarisoa*, AR23-085 (**holotype** in Royal Botanic gardens Kew Fungarium: K-M 1445916; ITS and LSU sequences GenBank PX278759 and PX262456).

Additional materials examined: **Madagascar**, Antsiranana, Montagne d'Ambre National Park, on branch, 24 Mar. 2023, *A. Ralaiveloarisoa*, AR23-084 (K-M 1445915; ITS and LSU sequences GenBank PX278760 and PX262455); Fianarantsoa, Ranomaana National Park, on dead tree, 17 Aug. 2023, *A. Ralaiveloarisoa*, AR23-178 (K-M 1445917; ITS and LSU sequences GenBank PX278761 and PX262457); Fianarantsoa, Ranomaana National Park, on dead tree, 19 Aug. 2023, *A. Ralaiveloarisoa*, AR23-212 (K-M 1445918; ITS and LSU sequences GenBank PX278762 and PX262458); Toamasina, Maromizaha Natural Resources Reserve, on dead *Ficus*, 1 Sep. 2023, *A. Ralaiveloarisoa*, AR23-302 (K-M 1445919; ITS and LSU sequences GenBank PX278763 and PX262459)

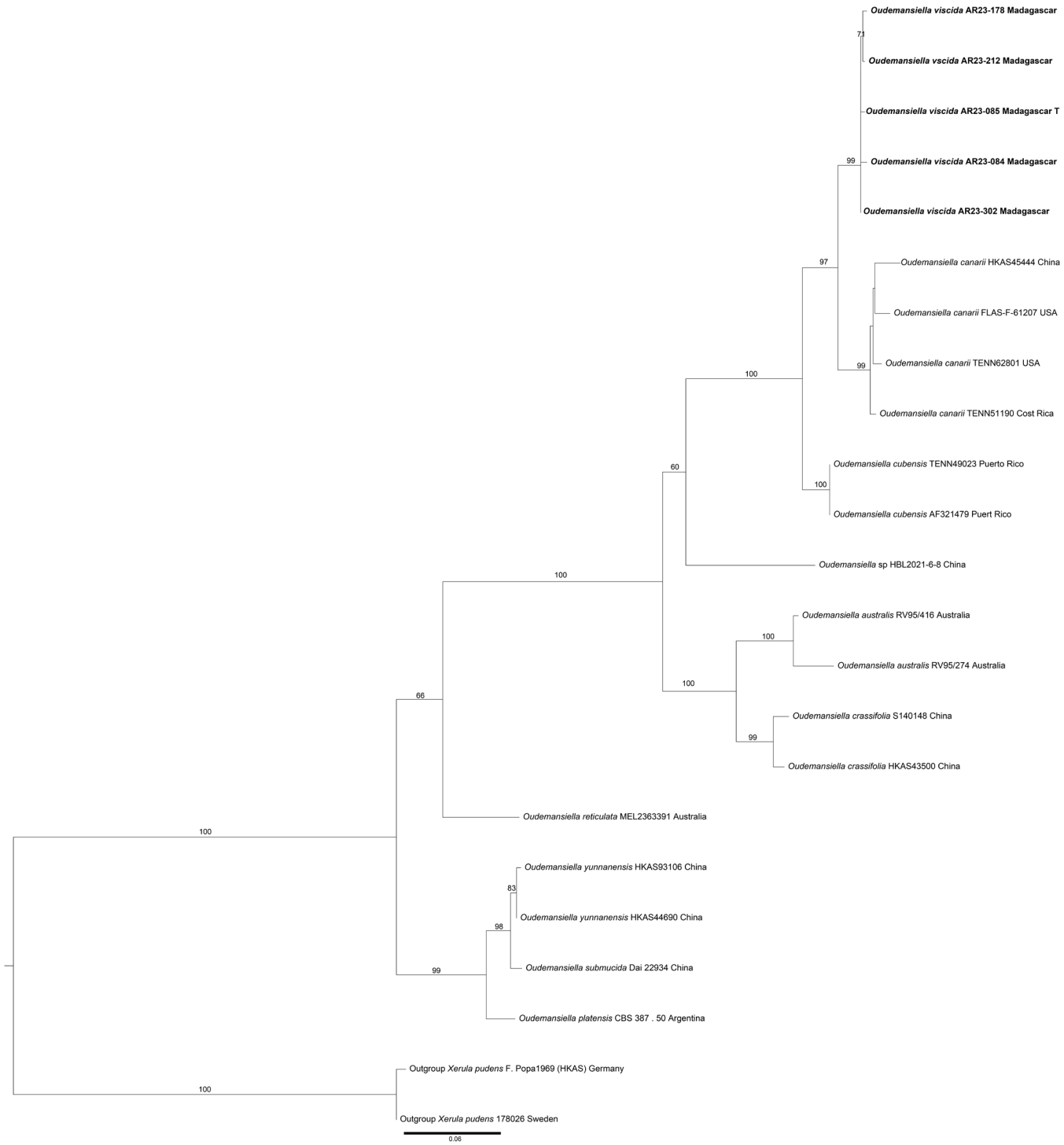
Notes: *Oudemansiella* is taxonomically a complex genus. Over time, species initially placed within this genus have been reclassified or synonymized with closely related genera such as *Hymenopellis*, *Mucidula*, *Paraxerula*, and *Xerula*. In our phylogenetic analysis based on ITS and LSU sequences, the specimens under study cluster within the *Oudemansiella* clade, including the type species of the genus *O. platensis* (GenBank MH856674) from Argentina, with strong bootstrap support (BS = 100 %).

The five *Oudemansiella* specimens collected from Madagascar form a distinct, well-supported clade (BS = 99 %) within the genus. These specimens exhibit low intraspecific variation in the ITS region (0.52 %, corresponding to four substitutions and indels) and no variation in the LSU region. Based on these results, all five specimens are considered conspecific and are here described as a new species, *Oudemansiella viscida*. Phylogenetically, *Oudemansiella viscida* is sister (BS = 97 %) to *O. canarii*, which is known from the southern United States (Florida, Mississippi) and China.

Oudemansiella viscida represents the first species of the genus described from Madagascar, and the second species reported from the African continent, according to the Fungus Flora of Tropical Africa (https://www.ffta-online.org/genera/). Typical characteristics of the species are white to off-white or grayish-brown, pellucid-striate, viscid pileus, and a short stipe.

Supplementary material: doi: 10.6084/m9.figshare.30061429 (table, excel file); TreeBASE study 32317 (alignment and trees).

Colour illustrations: Humid forest of the Maromizaha Natural Resources Reserve, Toamasina, Madagascar. Basidiomata showing young and mature fruit bodies; basidiomata of the holotype; microscopic features: smooth, rounded basidiospores; lageniform pleurocystidia; ixocutis pileipellis. Scale bars: basidiomata = 1 cm; all others = 10 µm.



Maximum Likelihood (ML) analysis based on concatenated ITS and LSU sequences. Sequence concatenation was performed in Mesquite; the ML analysis was conducted in RAxML v. 8 (Stamatakis 2014) using the GTR+GAMMA substitution model with 1000 rapid bootstrap replicates. Bootstrap support values from the ML analyses (> 50 %) are shown above branches. Newly described species are indicated in **bold**. The tree was edited in FigTree v1.4.4.exe (Rambaut, 2018) and finalized in Adobe Illustrator 2025 (v. 29.6, Adobe Inc.).

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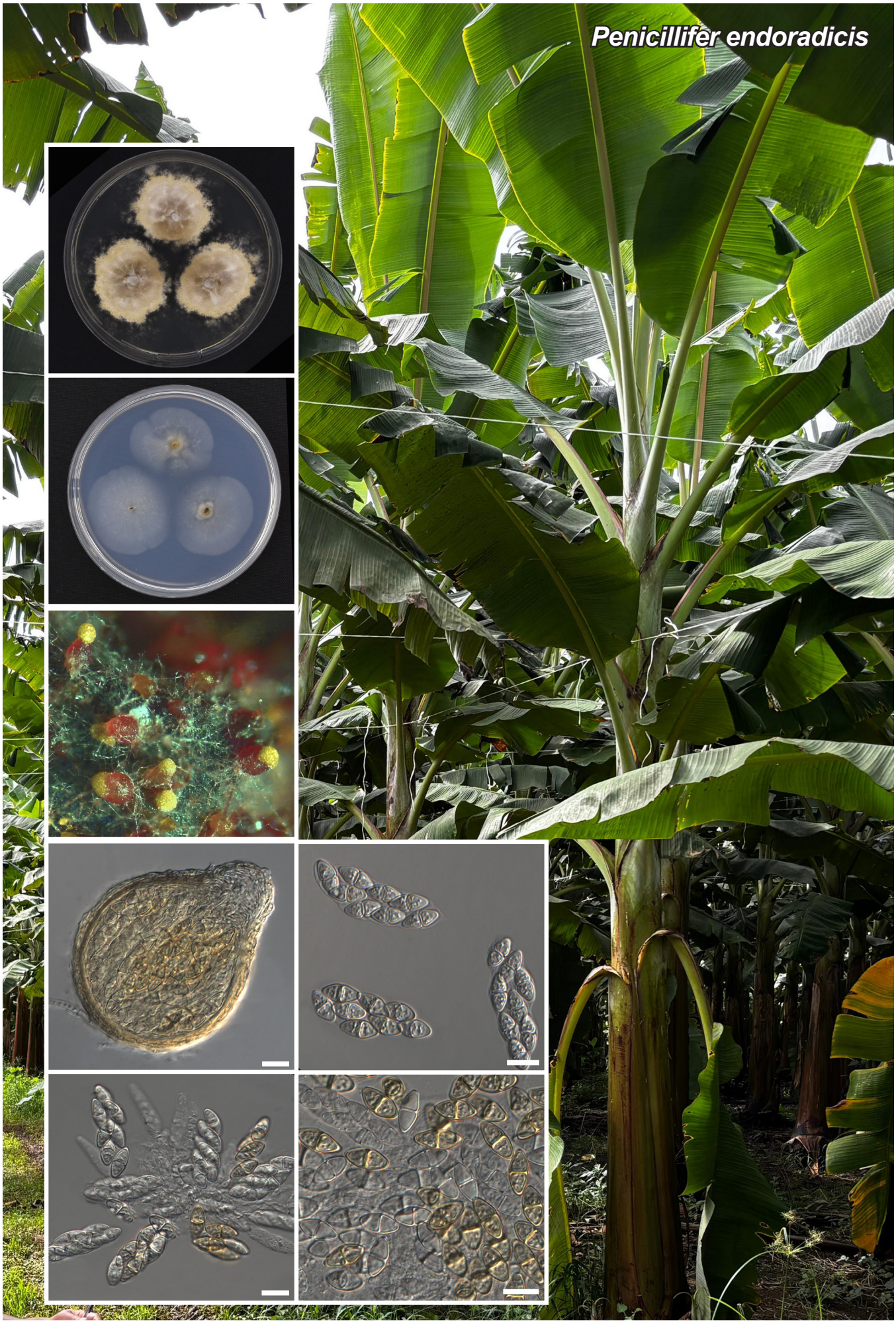

Penicillifer endoradicis

Fungal Planet 1897 MB 860653

Penicillifer endoradicis J.S. Santana, F.A. Custódio & O.L. Pereira, ***sp. nov*.**

Etymology: Name refers to the endophytic lifestyle of the fungus, occurring in roots.

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

Description on synthetic nutrient poor agar (SNA): *Ascomata* perithecial superficial or immersed in the medium, non-stromatic, abundant near the colony margin, commonly solitary or sometimes in groups of 3–4, ostiolate, obovoid to pyriform (181–)195–349(–363) × (133–)143–227(–252) *µm*, red to orangish red in culture, yellowish orange in lactoglycerol, red to red brownish in 5 % KOH, yellowish orange in lactic acid. *Ascomatal* wall smooth, 9–18 *µm thick, cells of* textura angularis. *Asci* unitunicate, clavate to fusoid, evanescent, (47–)51–85(–89) × (14–)18–27(–30) µm, 8-spored. *Ascospores* rhomboidal to fusoid, smooth thick-walled, 1-septate, often constricted at septum, hyaline when immature, becoming pale golden brown at maturity, 19–28 × 9–14 µm, covered by mucilage when immature, exuded en masse in a yellowish cirrus at maturity.

Culture characteristics: Colonies on potato dextrose agar (PDA) umbonate to sulcate, lobate edge, with aerial sporulation, moderate aerial mycelium, surface light brown (5D4; Kornerup & Wanscher 1978) in the centre to brownish orange (5C4) on the edge, reverse dark brown (6F8) in the centre to light brown (6D5) on the edge, reaching 59 mm diam. after 28 d at 25 °C under photoperiod of 12 h. Colonies on SNA flat or effuse, lobate edge, sparse to absent aerial mycelium, surface brownish orange (5C3) in the centre to pale grey (5B1) on the edge, reverse brownish orange (5C3) in the centre to pale grey (5B1) on the edge, reaching 48 mm diam. after 28 d at 25 °C under photoperiod of 12 h.

Habit, habitat and distribution: Endophytic fungus from roots of *Musa acuminata* (cv. Parata Anã) in Itinga do Maranhão, Maranhão, Brazil.

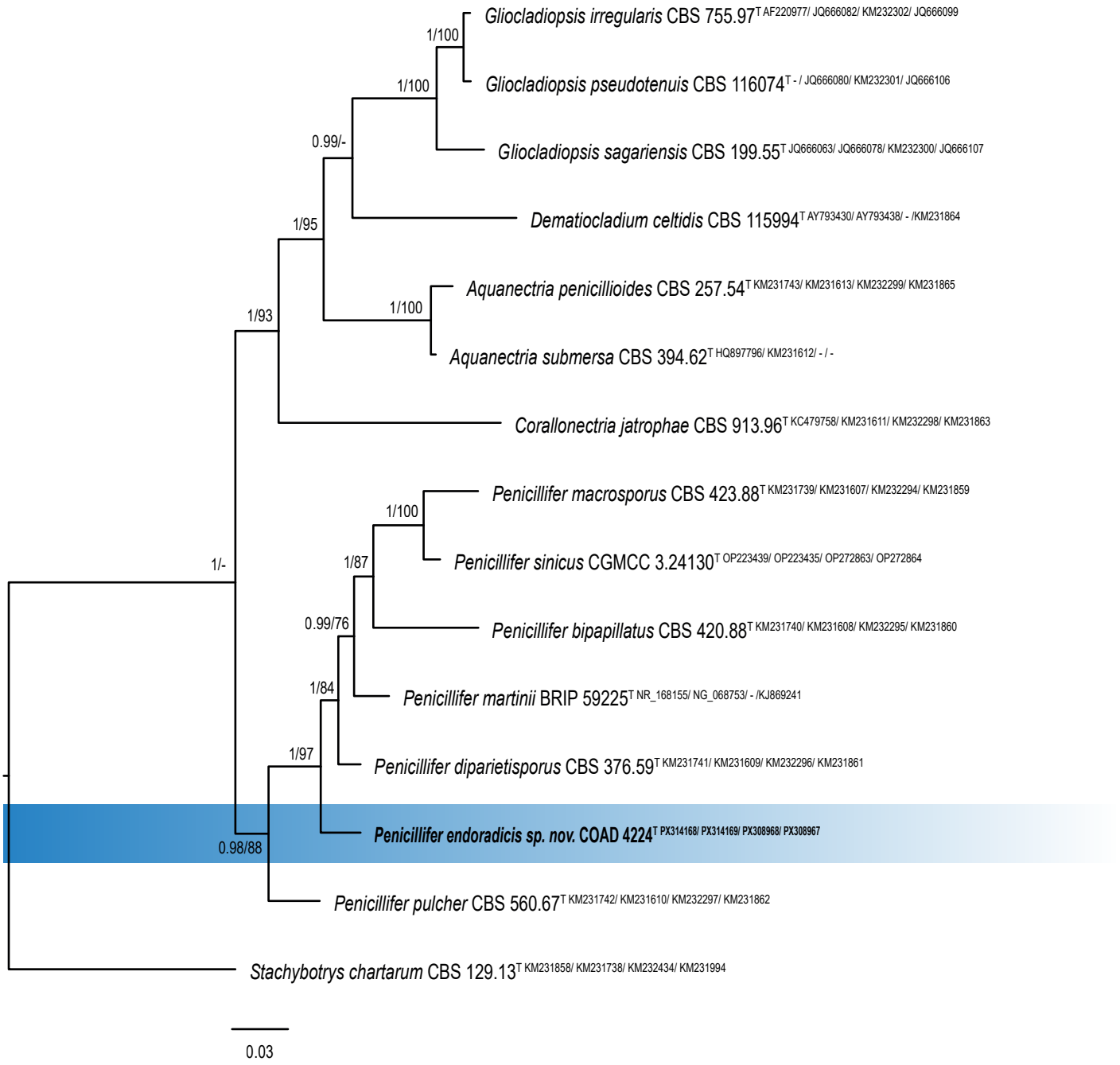
Typus: **Brazil**, Maranhão, Itinga do Maranhão, 52°03'N, 05°10'E, 1.5 m.a.s.l., isolated as endophyte from roots of *Musa acuminata* (*Musaceae*), 14 Dec. 2021, *F.A. Custódio* (**holotype** VIC 49760, culture ex-type COAD 4224; ITS, LSU, *rpb2* and *tef1-α* sequences GenBank PX314168, PX314169, PX308968 and PX308967).

Colour illustrations: Banana plants growing in a farm located in Itinga do Maranhão, Maranhão state, Brazil (photo credit: Fábio A. Custódio). Colonies after 28 d at 25 °C under photoperiod 12 h (top to bottom on PDA and SNA); perithecia on PDA; perithecium; immature asci; asci; ascospores. Scale bars = 20 µm.

Notes: *Penicillifer endoradicis* is a new endophytic species belonging to *Penicillifer*, and differs phylogenetically and morphologically from other species in this genus. The new species formed an independent lineage within the genus closest to *P. diparietisporus*, which differs morphologically mainly by the presence of ellipsoidal ascospores sometimes giving a roughened appearance (Polishook *et al.* 1991). On the other hand, *P. endoradicis* COAD 4224 produces smooth, rhomboidal to fusoid ascospores covered by mucilage when immature. Until the present study, there were nine described species in *Penicillifer*, of which six have both sexual and asexual morphs known, and the others are known only from asexual morphs (Van Emden 1968, Matsushima 1985, Samuels 1989, Polishook *et al.* 1991, Crous *et al.* 2014, Lombard *et al.* 2015, Zeng & Zhuang 2022). An asexual morph was not observed in cultures of *Penicillifer endoradicis* COAD 4224. *Penicillifer* species have been reported from different habitats such as soil, decaying plant material and diseased roots in different countries: Costa Rica, Venezuela, China, Japan and Korea (Van Emden 1968, Matsushima 1985, Samuels 1989, Polishook *et al*. 1991, Crous *et al.* 2014, Lombard *et al.* 2015, Zeng & Zhuang 2022). To the best of our knowledge, this is the first report of the genus *Penicillifer* in Brazil and its association with banana roots worldwide.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Sordariomycetes* sp. [strain VPS246 GenBank OR658621; Identities = 852/852 (100 %), no gaps], "Uncultured fungus" [strain clone: IU-FSC Fun07_FuA150, GenBank AB520271; Identities = 865/894 (97 %), eight gaps (0 %)], and "*Sordariomycetes* sp." [strain VPS452, GenBank OR658770; Identities = 798/799 (99 %), one gap (0 %)]. Closest hits using the **LSU** sequence are *Penicillifer diparietisporus* [strain TWS48Abf(a), GenBank MN393523; Identities = 937/942 (99 %), no gaps], *Penicillifer martinii* [strain BRIP:59225, GenBank KJ869225; Identities = 933/942 (99 %), no gaps], and *Penicillifer martinii* [strain BRIP 59225, GenBank NG_068753; Identities = 933/942 (99 %), no gaps]. Closest hits using the ***rpb2*** sequence are *Penicillifer diparietisporus* [strain TWS48(a), GenBank MN080532; Identities = 811/860 (94 %), no gaps], *Penicillifer diparietisporus* [strain CBS 376.59, GenBank KM232296; Identities = 809/858 (94 %), no gaps], and *Viridispora diparietispora* [strain CBS 102797, GenBank DQ522471; Identities = 780/830 (94 %), no gaps]. Closest hits using the ***tef1-α*** sequence are *Penicillifer diparietisporus* [strain CBS 376.59, GenBank KM231861; Identities = 406/428 (95 %), four gaps (0 %)], *Penicillifer diparietisporus* [strain KNU16:010, GenBank LC387601; Identities = 392/413 (95 %), four gaps (0 %)], and *Penicillifer sinicus* [strain 12496, GenBank OP272864; Identities = 390/422 (92 %), eight gaps (1 %)].

Supplementary material: doi: 10.6084/m9.figshare.30104356.v1 (alignment and tree).



Bayesian phylogenetic tree based on a dataset of ITS, LSU, *rpb2* and *tef1-α* sequences conducted in MrBayes v. 3.2.7a (Ronquist *et al*. 2012) on XSEDE in the CIPRES science gateway (Miller *et al.* 2015). The Maximum Likelihood analysis was conducted with IQ-TREE v. 2.2.0 (Minh *et al.* 2020), with 10000 ultrafast bootstrapping replicates (Hoang *et al*. 2018), and the best nucleotide substitution model for each region was defined using ModelFinder (Kalyaanamoorthy *et al*. 2017). Taxa obtained from banana roots in Brazil are highlighted in **bold**. Ex-type isolates are marked a superscript ''T''. Posterior probabilities (pp) ≥ 0.70 and ML bootstrap support values (mlbs) ≥ 75 % are shown at the branches (pp/mlbs). The tree is rooted with *Stachysbotrys chartarum* CBS 129.13.

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Phylloporia bharatavarsa

Fungal Planet 1898 MB 858360

Phylloporia bharatavarsa S. Ravikumar, E. Arumugam & M. Kaliyaperumal, ***sp. nov.***

Etymology: The species epithet "bharatavarsa" is a Sanskrit derived word for India.

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

Basidiomes annual, pileate, sessile, applanate, imbricate. *Pilear surface* semicircular, dark brown (6F6; Konerup & Wanscher 1978) to light brown (6D6), velutinous, tomentose, concentrically zonate, projecting up to 4.5 cm long, 6.5 cm wide and 4.7 cm thick at the base. *Margin* obtuse, incurved, yellow (3B8) to brownish orange (6C8). *Pore surface* glancing, light brown (6D4) to dull yellow (3B3). *Pores* circular, 7–11 / mm. *Context* duplex with thin black line between the upper tomentum and lower fibrous context; upper context brownish orange (6C8), fibrous, up to 4 mm thick, lower context brown (6D6), tightly interwoven, less than 1 mm thick. *Tube layer* light brown (6D4), up to 0.3 mm diam. *Hyphal system* mono-dimitic; tissue darkening in KOH; *Context* monomitic: *upper context* tomentum, generative hyphae turning golden brown to rusty brown in KOH, thick walled with a wide lumen, rarely branched, frequently septate, 3–5 µm diam.; *lower context* generative hyphae turning golden brown to rusty brown in KOH, thin- to thick-walled with a wide lumen, frequently branched, frequently septate, 2.2–4.2 µm diam. *Trama* dimitic, generative hyphae hyaline to pale yellow, thick-walled, occasionally branched, rarely septate, 3.8–4.4 µm diam.; skeletal hyphae thick-walled with narrow lumen, unbranched, aseptate, 3.0–3.6 µm diam. *Setae* absent. *Cystidioles* mostly fucoid, 8–21 × 4.9–5.9 µm. *Basidioles* clavate to broadly clavate, branched, simple septum at the base, 7–11 × 4.9–5.6 µm. *Basidia* clavate with four sterigmata 9–10.8 × 5.1–5.9 µm. *Basidiospores* hyaline to pale yellow, thin- to thick-walled, smooth, ellipsoid, weakly CN^+ to CN^-, IKI $^-$, (3.6–)3.8–4.1(–4.3) × (2.3–)2.8–3.1(–3.3) µm, Q = 1.4, Q = 1.2–1.8, (n = 30/2).

Typus: **India**, Tamil Nadu, Tenkasi, Navasolai, 9°20'N, 77°39'E, on living tree of *Phyllanthus emblica* (*Phyllanthaceae*), 6 Jan. 2025, *S. Ravikumar*, KM06 (**holotype** MUBL1230, ITS and LSU sequences GenBank PV243910 and PV242988).

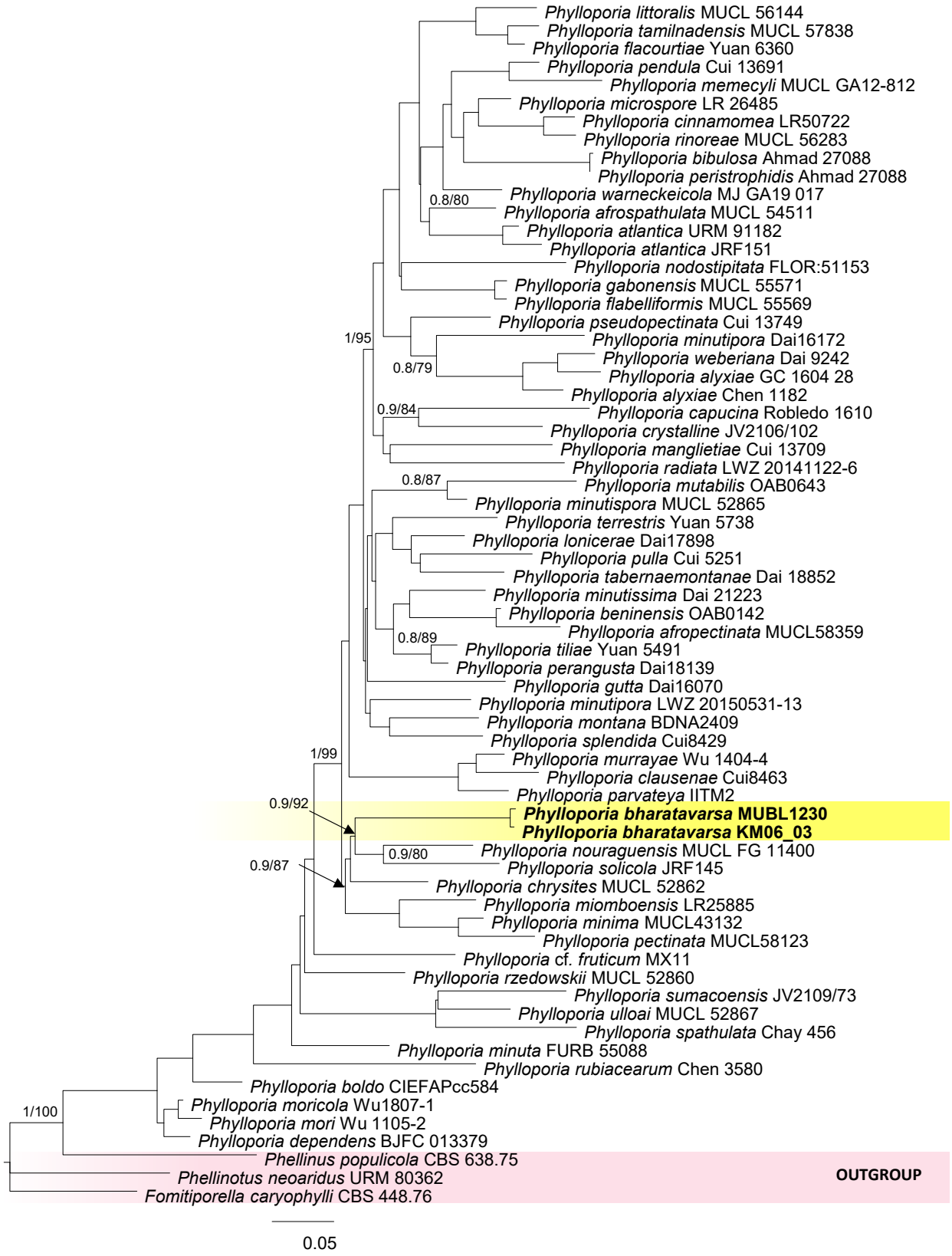
Additional material examined: **India**, Tamil Nadu, Tenkasi, Navasolai, 9°20'N, 77°39'E, on living tree of *P. emblica*, 6 Jan. 2025, *E. Arumugam*, KM06_03 (ITS and LSU sequences GenBank PV243911 and PV242989).

Notes: *Phylloporia bharatavarsa* clusters in a distinct lineage from the allied taxa *P. nouraguensis*, *P. solicola* (ML 92 %, 0.9 BPP) and P. parvateya (Crous *et al*. 2024a). *Phylloporia bharatavarsa* is characterized by annual, sessile, imbricate basidiomes with a duplex context separated by a thin black line, a mono-dimitic hyphal system, presence of fusoid cystidioles, and ellipsoid basidiospores measuring 3.8–4.1 × 2.8–3.1 µm. Indian *P. bharatavarsa* significantly differs from *P. nouraguensis* in having mono-dimitic hyphal system and larger basidiospores (*P. bharatavarsa* 3.8–4.1 × 2.8–3.1 µm vs *P. nouraguensis* 3.0–3.5 × 2.5–2.8 µm) (Decock *et al.* 2013). Basiomes of *P. bharatavarsa* is sessile and imbricate while *P. solicola* has stipitate basidiomes, monomitic hyphal system, lacks cystidioles with smaller spores (2.5–3.0 × 2.0–3.0 µm) (Wu *et al.* 2019). *Phylloporia chrysites* differs from *P. bharatavarsa* in having strictly monomitic hyphal system and subglobose spores (Wu *et al.* 2022). *Phylloporia bharatavarsa* resembles *P. miomboensis* in hyphal system and duplex context with a black line, but the latter has perennial turbinate basidiomes and smaller spores (*P. miomboensis* 3.0–3.5 × 2.2–2.6 µm vs *P. bharatavarsa* 3.8–4.1 × 2.8–3.1 µm; Jerusalem *et al.* 2025). Our Indian species differs from *P. minima* and *P. pectinata* by its larger ellipsoid spores while the latter two has smaller ovoid to broadly ellipsoid spores (Wu *et al.* 2022).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phylloporia* sp. [isolate PB-1692-324-D, GenBank PQ130483; Identities =437/504 (87 %), 29 gaps (5 %)], *Phylloporia radiata* [voucher Zhou20141122-6, GenBank MH151194; Identities = 666/839 (79 %) 73 gaps (8 %)] and *Phylloporia ephedrae* [voucher 13690, GenBank MH151184; Identities=425/493 (86 %), 27 gaps (5 %)]. Closest hits using the **LSU** sequence are *Phylloporia gutta* [voucher Dai16070 28S; GenBank MH165863; Identities =877/932 (94 %), 20 gaps (2 %)], *Phylloporia* sp. [FG10 321; GenBank KJ743277 Identities =874/930 (94 %), 13 gaps (1 %)], and *Phylloporia fontanesiae* [voucher Cui1 2356, GenBank MH165871 Identities =874/930 (94 %), 15 gaps (1 %)].

Supplementary material: doi: 10.6084/m9.figshare.30120244 (alignment and table).

Colour illustrations: *Phylloporia bharatavarsa* collection area, Kottaimalai Hills, Thenkasi, India. Habitat; pilear surface; enlarged transverse section of basidiome; camera lucida drawing of holotype: contextual hyphae, tramal hyphae; cystidioles; basidioles; basidia; basidiospores. Scale bars: basidiocarps = 5 cm; all other structures = 5 µm.



Phylogenetic analyses inferred from ITS and LSU of *Phylloporia bharatavarsa* (MUBL1230, holotype and KM06_03) and related species rooted with *Fomitiporella caryophylli* (CBS 448.76). The maximum likelihood (ML) analysis was performed using MEGA v. X (Kumar *et al*. 2018) and the same data were used for a Bayesian analysis using MrBayes v. 3.2.7 (Ronquist *et al*. 2012). Branches are labelled with ML bootstrap support and Bayesian posterior probabilities values (BPP). Novel species is in **bold** and red text.

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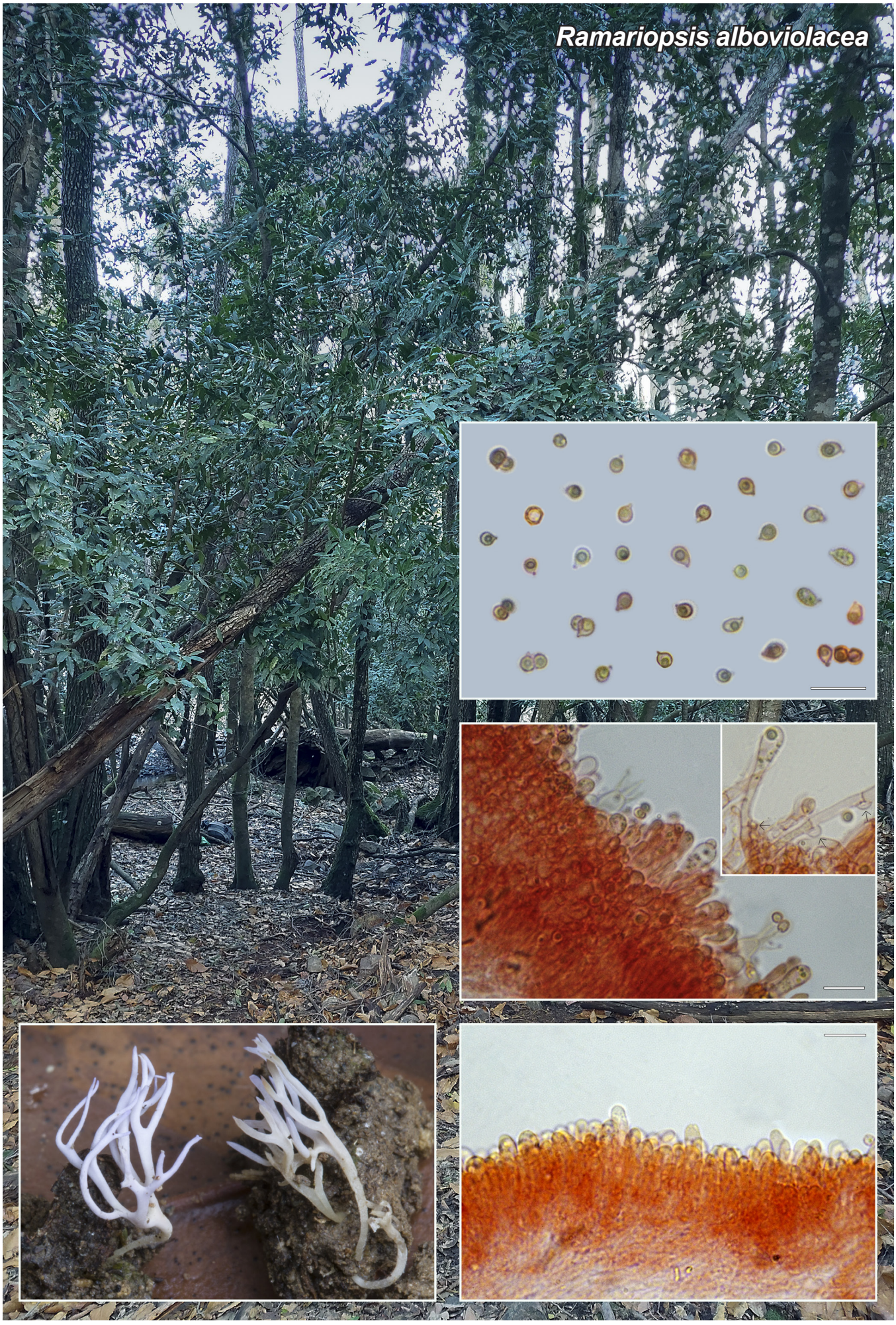

Ramariopsis alboviolacea

Fungal Planet 1899 MB 860656

Ramariopsis alboviolacea A. Mateos & De la Peña-Lastra, ***sp. nov*.**

Etymology: The epithet refers to the white to violet colouration of the basidiomata.

Classification: *Clavariaceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata branched, up to 10 mm high and 5 mm wide, isolated or gregarious. *Branches* few in number, thickness up to 0.2 mm, rounded in section, fragile, divergent and flexuous, branched twice in a dichotomous manner, in turn branched twice again, and ending in long pointed apices and sometimes short with two small obtuse tips in growth, with generally obtuse U-shaped angulations, some rare sharp V-shaped ones, smooth hymenophore surface, softly violet in colour, which tends to disappear when dehydrated, turning pale. The *stipe* is poorly developed, up to 4 mm high and up to 0.3 mm wide, cylindrical, straight or flexuous, with a hairy surface due to its mycelial residues, whitish cream in colour, turning translucent beige at maturity, distinguishable from the fertile part by its colour and pruinose surface. Creamy white context, fragile, hygrophane, with indistinct *taste* and *smell*. *Basidiospores* (2.4–)2.7–*3.0*–3.5(–3.9) × (2.1–)2.4–*2.6*–2.8(–3.3) µm; Q = (1.0–)1.1–*1.2*–1.3(–1.4); N = 35; Ve = 11 µm^3; globose, subglobose, to broadly ellipsoid, with a prominent apiculus 0.6–1 *µm* long, with a greenish, central large guttule, surface smooth or with some small irregularities, difficult to observe in a light microscope, hyaline, inamyloid, congophilous. *Basidia* (15.6–)16.1–*18.9*–21.8(–24.8) × (3.8–)4.8–*4.9*–5.3(–5.5) µm, 4-spored, clavate, with sterigmata up to 5 µm long, septate and basally clamped. *Branch apices* with claviform cystidioles, not exceeding the hymenophore palisade. *Hymenium* and *subhymenium* with abundant polymorphous crystallized deposits among hyphae, with irregular quadrangular shapes. *Hyphal system* monomitic, formed by parallel arranged to interwoven hyphae generative de 2.5–7 µm. *Basal tomentum* white, composed of sparse hyphae, cylindrical, slightly thick-walled, hyaline, clamped, 2–3 µm wide. *Clamp connections* present in all tissues.

Distribution: Currently known only from the type location in western Spain (Cáceres, Spain).

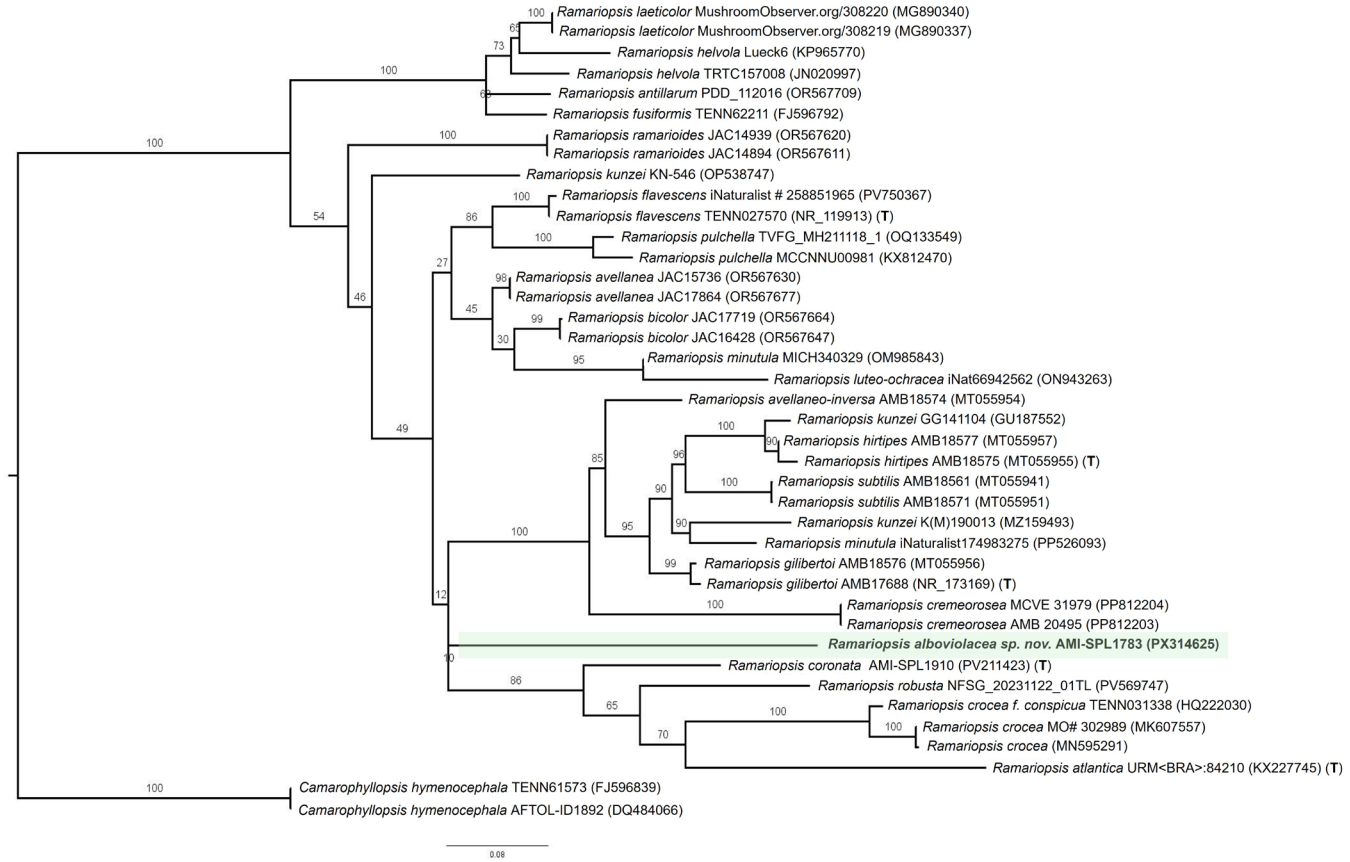
Typus: **Spain**, Extremadura, Cáceres, Villuercas-Ibores-Jara Geopark, Villar del Pedroso, Lorera del Mesto in the Mesto Gorge in the Hospital del Obispo Valley, N39°35'24", W5°19'35", 770 m.a.s.l., on slopes under *Prunus lusitanica* subsp. *lusitanica* (*Rosaceae*) laurel forests, 17 Jan. 2023, *A. Mateos* & *S. De la Peña-Lastra* (**holotype** AMI-SPL1783; ITS and LSU sequences GenBank PX314625 and PX314626).

Additional materials examined: **Spain**, Extremadura, Cáceres, Villuercas-Ibores-Jara Geopark, Villar del Pedroso, Lorera del Mesto in the Mesto Gorge in the Hospital del Obispo Valley, N39°34'23", W5°18'36", 770 m.a.s.l., on slopes under *Prunus lusitanica* subsp. *lusitanica* laurel forests, 17 Jan. 2023, *A. Mateos* & *S. De la Peña-Lastra* (AMI-SPL1782).

Notes: *Ramariopsis alboviolacea* has both macroscopically and microscopically the characteristics typical of the genus *Ramariopsis*, within the group that presents the Minutula-type (Pegler & Young 1985) with small and irregular roughness. The monomitic hyphal system with clamp connections on hyphae and subglobose ornamented basidiospores, present in *R. alboviolacea*, are also typical of *Ramariopsis* (Olariaga 2009, Franchi & Marchetti 2021, Crous *et al.* 2025). The most morphologically similar species in the genus is *Ramariopsis minutula* (PP526093; ITS 79.2 % match), also very small in size and with spores similar in shape (Q = 1.0–*1.2*–1.3), size (3.0–4.2 × 2.5–3.8 *µm)* and decoration, although its guttule is small and it also differs in having white or pale basidiomata rather than the delicate violet colour of *R. alboviolacea* (Franchi & Marchetti 2021). However, the same publication references the works of Oertel & Fuchs (2001) and Raillère-Burat & Gannaz (2010) (only a few keys), in which they cite unusual basidiomata with white purple or darker lilac branches at the ends; it is likely that these citations refer to different taxa, to be elucidated by sequencing, as they do not appear in the same publications. Another species with a similar appearance is *Ramariopsis subtilis* (MT055941; ITS 77.9 % match), which is much larger, with mainly acute angles, white, cream or beige in colour, with larger spores (4.2–6.1 × 3.2–4.2 *µm),* a different spore coefficient (Q = 1.3–*1.4*–1.6) and more evident warts (Franchi & Marchetti 2021). *Ramariopsis flavescens* (NR_119913; ITS 84.3 % match) and *Ramariopsis avellanea* (OR567630; ITS 85.2 % match) are the species with the closest phylogenetic relationship, but they differ significantly from *R. alboviolacea* in that they have larger basidiomes, a different colour (never violet), larger spores, and isolated excrescences (Pegler & Young 1985, Franchi & Marchetti 2021).

Supplementary material: doi: 10.6084/m9.figshare.30083938 (sequence alignment).

Colour illustrations: Spain, Cáceres, Lorera del Mesto, laurisilva of *Prunus lusitanica* subsp. *lusitanica*, where the holotype of *Ramariopsis alboviolacea* was collected. Left column: basidiomata corresponds with the holotype. Right column: upper photo corresponds with basidiospores (RC); middle photo corresponds is basidia and hymenophore, with detail clamp-connections (RC, indicated with arrows); and the bottom photo shows cistidioles at the tips of the branches (RC). Scale bars = 10 µm.



The most probable maximum likelihood (ML) tree calculated with IQ-TREE v. 2.1.3 (Nguyen et al. 2015) using the UltraFast method (Minh *et al.* 2013) from the ITS sequence alignment (GenBank accession numbers in brackets in the tree), showing on the branches the ML bootstrap support values (ML-BS; 1 000 replicates and ≥ 95 % were considered significant). Sequences from type material are indicated with a T and the novel species is indicated in **bold** font.

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Russula olivaceopinetorum

Fungal Planet 1900 MB 859436

Russula olivaceopinetorum G. Moreno, G. Sánchez-Dueñas & P. Alvarado, ***sp. nov.***

Etymology: Epithet derived from *olivaceo*—because of *Russula olivacea* (which is morphologically very similar)—, and *-pinetorum*, which refers to its habitat near *Pinus sylvestris*.

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

Basidiocarps annual, with a central stipe. *Pileus* 8.2–19.5 cm diam., convex, plano-convex, sometimes subapplanate, non-striate in mature basidiomata, with variable coloration: greenish hues interspersed with violet or purplish areas and yellowish-cream zones. *Lamellae* crowded, with lamellulae, adnate, ventricose, up to 0.5–1 cm broad, yellowish when mature, with concolourous edges or slightly violaceous near the pileus margin. *Stipe* 5.5–11 × 2.5–7.5 cm, robust, solid, variable in shape from cylindrical to clavate, white with more or less abundant pinkish tinges. *Odour* not distinctive. *Spore print* medium yellow (IVb to IVc on the Romagnesi scale). *Context* whitish, with a mild and sweet *taste*, not acrid; reacts fuchsia with phenol, orange with iron(II) sulfate, and gives an intense reaction with guaiac. *Basidia* 4-spored, 65–80 × 12–13 µm, sterigmata up to 8 µm long. *Spores* 9.9–13.1 × 8.1–11.2 µm, av. = 9.7–11.5 µm, Q av. = 1.2 (n = 30, holotype), yellowish, broadly ellipsoid, thick-walled, amyloid, ornamented with warts forming crests to subreticulate patterns, suprahilar plage rounded and well-defined, amyloid. *Cheilocystidia* and *pleurocystidia* abundant, fusiform with a long appendage, 80–110 × 11–16 µm. *Pileipellis* a trichoderm, lacking dermatocystidia and encrusted hyphae, composed of hairs formed by cylindrical hyphae, some diverticulate, 5–9 µm wide, thin-walled, septate, branched, with obtuse apices. *Clamp connections* absent.

Habitat and distribution: Growing gregariously on acidic sandy soil among *Pinus sylvestris* needles. Rare in the studied area.

Typus: **Spain**, Madrid, Las Dehesas de Cercedilla, Cercedilla, on acidic sandy soil among *Pinus sylvestris* needles, 21 Nov. 1996, *G. Moreno & J. Checa* (**holotype** AH 58330; ITS and LSU sequences GenBank PV581923 and PV581938).

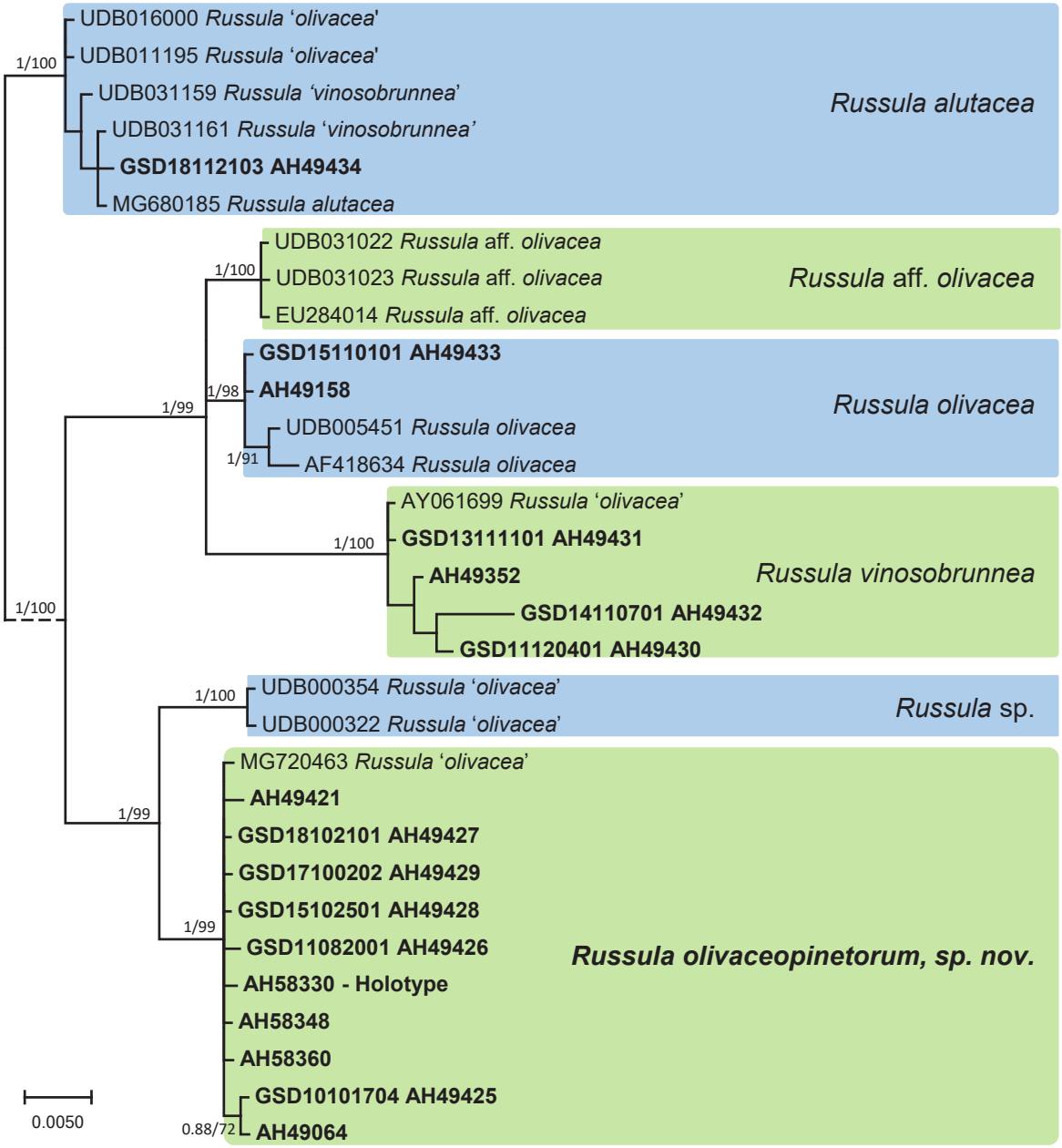
Additional materials examined: *Russula olivaceopinetorum*: **Spain**, Huesca, Selva de Oza, Hecho, under *Pinus sylvestris* and *Fagus sylvatica*, 13 Oct. 2023, *G. Sánchez Dueñas* (**paratype** AH 49421; ITS and LSU sequences GenBank PV581918 and PV581933); La Rioja, Canales de la Sierra, in humus of *Fagus sylvatica* and *Pinus sylvestris*, 13 Nov. 2024, *Á. Morales* (**paratype** AH 58360; ITS, LSU *RPB2* sequences GenBank PV581925, PV581940 and PV582987); Madrid, Rascafría, Arroyo Angostura, under *Pinus sylvestris*, 20 Aug. 2011, *L.M. Nieto & Dueñas* (**paratype** GSD11082001 at AH 49426; ITS and LSU sequences GenBank PV581922 and PV581937); Madrid, Umbría de Siete Picos, Parque Nacional de Guadarrama, under *Pinus sylvestris*, 2 Nov. 2017, *M. Lozano* (**paratype** AH 49064; ITS and LSU sequences GenBank PV581927 and PV581941); Segovia, Navafría, El Chorro, under *Pinus sylvestris*, 2 Oct. 2017, *L.M. Nieto* (**paratype** GSD17100202 at AH 49429; ITS and LSU sequences GenBank PV581920 and PV581935); Segovia, Valsaín, Las 7 Revueltas, acidic sandy soil among *Pinus sylvestris* needles, 15 Oct. 2010, *F. Prieto* (**paratype** GSD10101501 at AH 49424); ibid., 15 Oct. 2010, *J.C. Campos* (**paratype** GSD15102501 at AH 49428; ITS and LSU sequences GenBank PV581921 and PV581936); ibid., 17 Oct. 2010, *G. Sánchez Dueñas* (**paratype** GSD10101704 at AH 49425; ITS sequence GenBank PV581926); Teruel, Bronchales campsite, under *Pinus sylvestris*, 21 Oct. 2018, *A. Bernal* (**paratype** GSD18102101 at AH 49427; ITS and LSU sequences GenBank PV581919 and PV581934). *Russula vinosobrunnea*: **Spain**, Madrid, ascent to Puerto de Canencia, Bustarviejo, in humus of *Quercus pyrenaica*, 11 Nov. 2013, *G. Sánchez Dueñas* (GSD13111101 at AH 49431; ITS and LSU GenBank sequences PV581915 and PV581930); ibid., 7 Nov. 2014, *G. Sánchez Dueñas* (GSD14110701 at AH 49432; ITS and LSU GenBank sequences PV581916 and PV581931); Madrid, Prádena del Rincón, in humus of *Quercus ilex*, 10 Oct. 2024, *G. Sánchez Dueñas & J. Castillo* (GSD24101002 at AH49352; ITS GenBank sequence PV581914); Málaga, Cortes de la Frontera, leaf litter of *Quercus canariensis* and *Quercus suber*, 4 Dec. 2011, *G. Sánchez Dueñas* (GSD11120401 at AH 49430; ITS and LSU GenBank sequences PV581917 and PV581932). *Russula alutacea*: **Spain**, Madrid, Valgallegos, Torrelaguna, in humus of *Quercus faginea*, 21 Nov. 2018, *G. Sánchez Dueñas* (GSD18112103 at AH 49434; ITS and LSU sequences GenBank PV581911 and PV581928). *Russula olivacea*: **Spain**, Asturias, Hayedo de Valgrande, in humus of *Fagus sylvatica*, unknown date, *C. Traba* (CUT O40915142 at AH 49158; ITS and LSU GenBank sequences PV581913 and PV581929); Cantabria, Reinosa, in humus of *Fagus sylvatica*, 1 Nov. 2015, *C. Traba* (GSD15110101 at AH 49433; ITS sequence GenBank PV581912).

Notes: *Russula olivaceopinetorum* is characterized by its large pileus with variable colouration, yellowish lamellae, whitish stipe with pink tinges, sweet and non-spicy taste, spores with crested to subreticulate ornamentation, and its association with *Pinus sylvestris* forests. It belongs to sect./subsect. *Olivaceinae* (located inside the 'crown' clades of *Russula* s. str., Kong *et al.* 2015), whose species — particularly *Russula olivacea*— have often been confused with morphologically similar taxa (Kong *et al*. 2015). This species differs from *R. olivaceopinetorum* because it is associated with *Fagus sylvaticus*, and spores are ornamented with spines. In the present work, several specimens of *R. vinosobrunnea* and

Colour illustrations: Spain, Madrid, Las Dehesas de Cercedilla, acidic soil where the holotype was collected. Basidiomata (holotype); basidiomata flesh reaction to phenol (AH 49425); pileipellis (AH 49428 and holotype); cheilocystidia at the edge of the gills (holotype); spores (holotype). Scale bars: basidiomata = 10 cm; all others = 10 µm.

R. alutacea were also analysed. These species have also been confused with *R. olivacea* in the past, but differ from it because of their habitat, associated with broadleaved forests, and a different molecular profile.

Supplementary material: doi: 10.6084/m9.figshare.30354538 (table, alignment and tree figure).



A 50 % majority rule ITS rDNA-28S rDNA consensus phylogram of *Russula olivaceopinetorum* and related species (with *R. alutacea* as outgroup) obtained using MrBayes v. 3.2.6 (Ronquist *et al.* 2012) from 900 sampled trees. Nodes were annotated if they were supported by ≥ 0.95 Bayesian posterior probability (left) or ≥ 70 % maximum likelihood bootstrap proportions (right). Sequences newly generated in this study are in **bold**.

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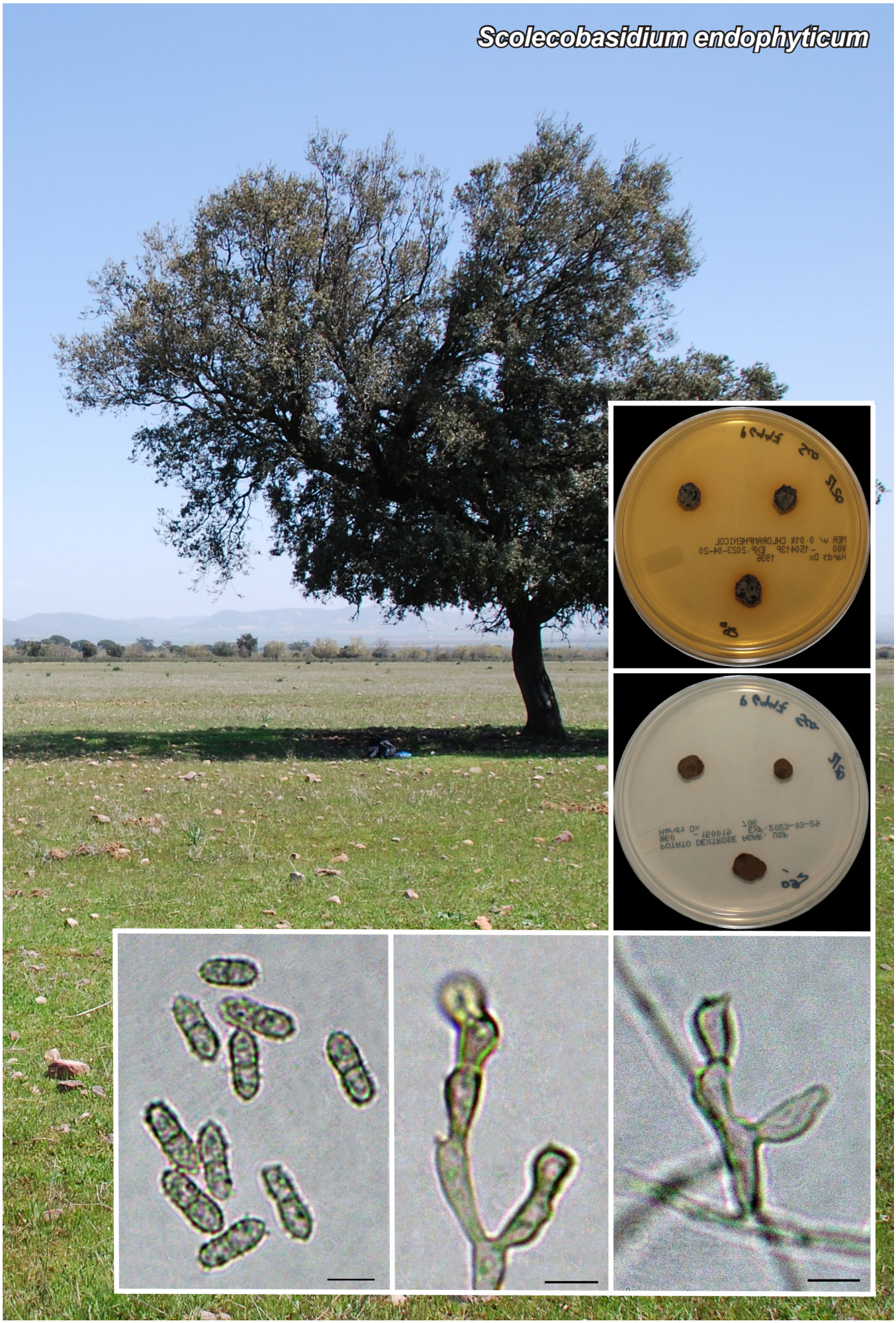

Scolecobasidium endophyticum

Fungal Planet 1901 MB 860647

Scolecobasidium endophyticum G. Delgado & Maciá-Vicente, ***sp. nov.***

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

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

Mycelium composed of branched, septate, smooth or finely verrucose, hyaline to subhyaline or pale brown, thin-walled *hyphae*, 1.5–3(–3.5) µm wide, single and dark reddish brown to blackish brown in mass or sometimes aggregated in tightly packed, brown cords up to 110 µm wide, immersed mycelium with swollen, thicker-walled cells 3.5–6 µm wide. *Conidiophores* micronematous to semi-macronematous, mononematous, terminal or intercalary and arising laterally from the hyphae, simple or sparingly branched, straight or flexuous, 0–1-septate, smooth, thin-walled, cylindrical to narrowly clavate, hyaline, subhyaline or pale brown, 5–10(–12) × 2–3 µm, often reduced to conidiogenous cells. *Conidiogenous cells* mono- or polyblastic, integrated, terminal or intercalary in conidiophores and hyphae, subcylindrical, clavate or rarely ampulliform, sympodial, straight or geniculate and with small shoulders resulting from sympodial extensions, 0-septate, denticulate, denticle sometimes visible on lateral shoulders, subhyaline to pale brown, 3–9 × 2–3(–3.5) µm, frequently emerging directly from the hyphae. *Conidial secession* rhexolytic. *Conidia* acropleurogenous, subcylindrical, 1-septate, slightly constricted at the septum, pale brown, minutely echinulate to verruculose, 6–9(–11) × 2–3(–4) *µm,* distal ends rounded, proximal ends slightly tapered and with minute frills. *Chlamydospores* present, globose, subglobose, ellipsoidal, elongated or irregularly-shaped, terminal or intercalary in the hyphae, forming long chains or in large, dense clusters, 0–1-septate, subhyaline to pale brown or brown to dark brown, smooth, (6–)7–13(–16) × (4–)5–11 *µm.*

Culture characteristics: Colonies on malt extract agar (MEA) reaching 5–10 mm diam. after 14 d at 26 °C, restricted, velvety, umbonate and raised 3–4 mm, black, somewhat membranaceous and with some dark grey felty patches on the surface, margin undulose to irregular, reverse dark brown, abundantly sporulated or sterile after 3 mo incubation depending of the isolate. Colonies on potato dextrose agar (PDA) reaching 5–11 mm diam. after 14 d at 26 °C, also restricted, velvety, chocolate brown, flat, slightly raised at the centre 1–2 mm, margin irregular or undulose, reverse dark brown, sterile but chlamydospores abundant.

Habit, habitat and distribution: Root endophyte isolated on culture media from surface-sterilised roots of living plants, known so far from Spain and The Netherlands.

Colour illustrations: Collection site in Spain. Colonies on MEA and PDA on surface view after 14 d at 26 °C; conidiophores and conidiogenous cells; conidia. Scale bars = 5 µm.

Typus: **Spain**, Ciudad Real, Cabañeros National Park, from root-associated soil collected in a grassland, 39°19’56.4”N, 4°21’41.2”W, 684 m.a.s.l., isolated from surface-sterilised, asymptomatic roots of an *Arabidopsis thaliana* (*Brassicaceae*) plant inoculated with soil and grown under controlled conditions, 19 Apr. 2018, *J.G. Maciá-Vicente*, P6447 (**holotype** stored in a metabolically inactive state CBS 149762, culture ex-type CBS 149762; ITS, LSU and *tef1* first and second part sequences GenBank MN365755, MN308484, PX047958 and PX047959).

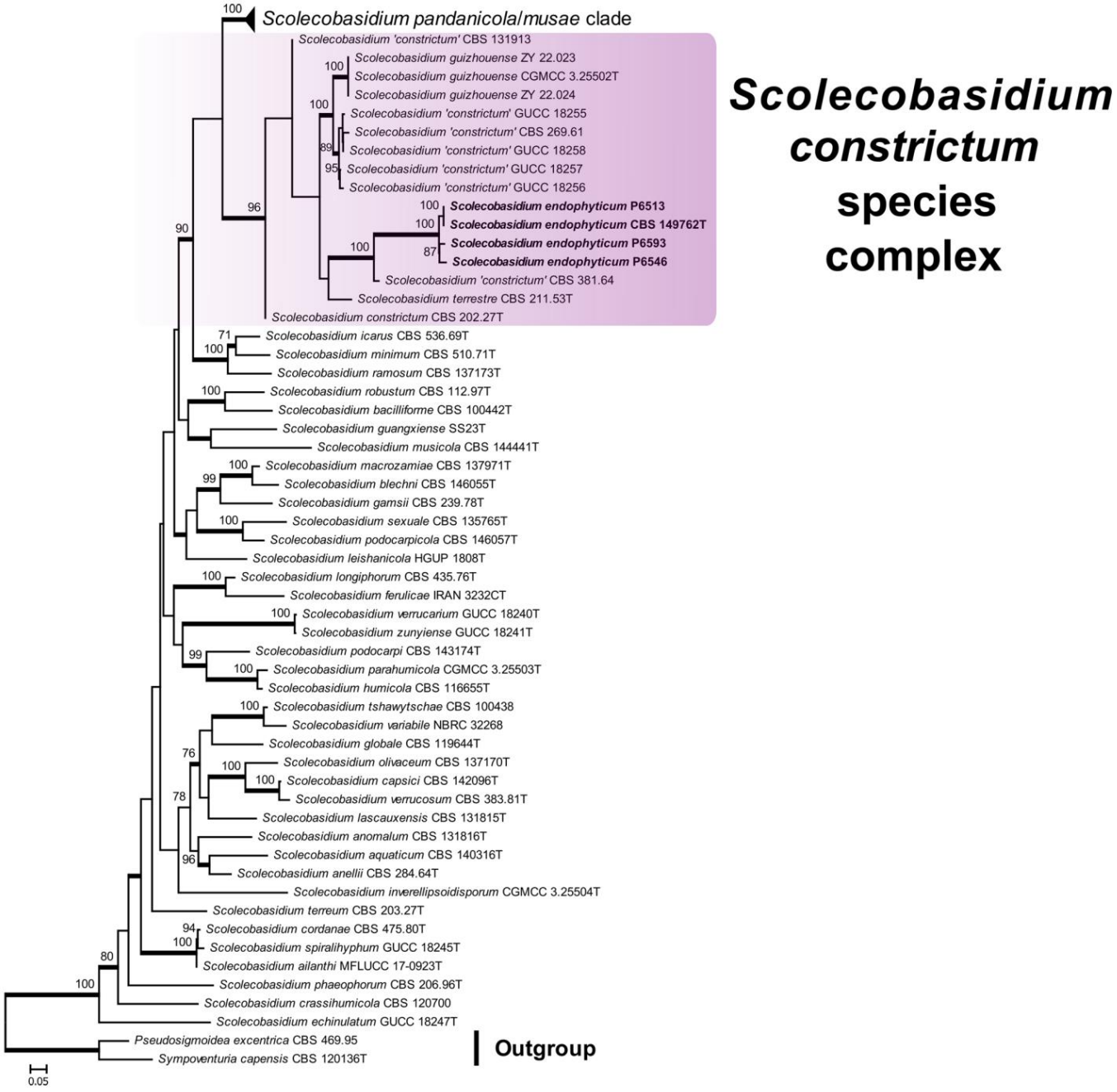
Additional materials examined: **Spain,** Cádiz, Los Alcornocales Natural Park, from root-associated soil, 36°30’47.2”N, 5°37’32.3”W, 832 m.a.s.l., isolated from surface-sterilised, asymptomatic roots of an *A. thaliana* plant inoculated with soil and grown under controlled conditions, 20 Apr. 2018, *J.G. Maciá-Vicente*, P6513, ITS and LSU sequences GenBank MN310232 and MN308537. **The Netherlands**, Gelderland Province, Veluwe region, Mossel, from root-associated soil, 52°04’27.8”N, 5°44’29.6”E, 28 m.a.s.l., isolated from surface-sterilised, asymptomatic roots of an *A. thaliana* plant inoculated with soil and grown under controlled conditions, 30 Apr. 2018, *J.G. Maciá-Vicente*, P6593, ITS, LSU and *tef1* sequences GenBank MN310276, MN308589 and PX047961; ibid., P6546, ITS, LSU and *tef1* sequences GenBank MN310251, MN308559 and PX047960.

Notes: *Scolecobasidium* is a large genus whose members exhibit a broad spectrum of lifestyles including endophytes, saprophytes, plant pathogens, and animal or human opportunistic pathogens (Wei *et al.* 2022). Among species reported as endophytes, *S. ferulica*, *S. humicola* and *S. tshawytschae* have been isolated from roots of a variety of plant hosts (Rashmi *et al.* 2019, Tazik *et al*. 2020). *Scolecobasidium constrictum*, on the other hand, is a widely distributed member of the genus often isolated from soil but also as a saprobe or a secondary invader on a variety of plant hosts (Kirk 1994). The fungus was originally described from cotton and sugar cane soils in Louisiana, USA, together with *S. terreum*, the type species of *Scolecobasidium* (Abbott 1927). Morphologically, it is distinct in having 1-septate, echinulate or verruculose, oblong conidia with rounded ends and slightly constricted at the septum. De Hoog & von Arx (1974) later introduced *Ochroconis*, a separate genus typified by *S. constrictum*, and retained *Scolecobasidium* for those species morphologically similar to *S. terreum* having two- to multi-celled, T- or Y-shaped or bilobate conidia. More recently, however, Shen *et al.* (2020) reduced *Ochroconis* to a synonym of *Scolecobasidium* after their ex-type strains grouped together in multigene phylogenetic analyses forming a strongly supported clade within *Sympoventuriaceae*, *Venturiales*. Subsequently, several species morphologically close but phylogenetically distinct to *S. constrictum* have been described from dead plant material or litter and soil (Wei *et al*. 2022, Zhang *et al*. 2024), suggesting a previously unrecognized diversity hidden within this species name. The isolates in this study were obtained during an extensive

sampling of root-associated fungi in semi-natural grasslands and heathlands across western Europe (Maciá-Vicente *et al.* 2022). Some of the recovered strains were first assigned to *S. constrictum* by comparing their ITS sequences with reference databases. However, phylogenetic analyses revealed that these isolates grouped distant from the ex-type strain of *S. constrictum* but within a strongly supported monophyletic lineage (100 BS, 1 BPP) treated here as the "*Scolecobasidium constrictum* species complex". This clade includes the ex-type strain of this fungus (CBS 202.27) and several others identified under that name as well as morphologically similar species such as *S. guizhouense* or *S. terrestre* (Atkinson 1952, Zhang *et al.* 2024). Remarkably, pairwise comparisons of the ITS region showed significant variability between strains of the novel *S. endophyticum*. Those obtained in Spain contain a long insertion of 139 bp in the ITS1 that is absent in strains from The Netherlands, whereas their ITS2 is considerably variable with several indels and gaps. This variability was also observed in culture where strains recovered from Spain sporulated and produced a scolecobasidium constrictum-like morphology after long term incubation, whereas those obtained in The Netherlands were sterile on both MEA and PDA. Furthermore, our strains were incubated at 26 °C for comparison with strains named '*S. constrictum'* isolated from dead branches, forest litter and soil in China (Wei *et al.* 2022). Similarly, they also exhibited slow growth but attained a larger diameter, 14–15 mm diam. after 14 d, on both culture media. In our ITS-LSU-*tef1* phylogeny, they form a distinct clade distant from our strains or the ex-type of *S. constrictum* and may represent a putative novel species within this species complex. A further assessment of ITS sequences available in GenBank and annotated as *S. constrictum* or its synonym *Ochroconis constricta* also provided clues on whether this fungus and its relatives, including the novel *S. endophyticum*, may actually represent a species complex. The ITS region is known to exhibit significant differences between *Scolecobasidium* species and some variability within species (Tazik *et al.* 2020). The ITS tree (not shown but deposited as supplementary material) reveals eight different strongly supported lineages that could eventually be recognized and named as new species as in the case of *S. endophyticum*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to '*Ochroconis*' *constricta* [strain CBS 381.64, GenBank HQ667517.1; Identities = 419/430 (97 %), eight gaps (1 %)], '*Ochroconis*' *constricta* [strain CBS 106.65, GenBank HQ667518.1; Identities = 418/430 (97 %), eight gaps (1 %)], and *Scolecobasidium* sp. [strain CCFEE 6388, GenBank MZ573466.1; Identities = 643/683 (94 %), 27 gaps (3 %)]. Closest hits using the **LSU** sequence are *Scolecobasidium* sp. [strain NH1682, GenBank LC469390.1; Identities = 544/552 (99 %), two gaps (0 %)], *Scolecobasidium* sp. [strain NH739, GenBank LC469385.1; Identities = 544/552 (99 %), two gaps (0 %)], and *Scolecobasidium* sp. [strain NH685, GenBank LC469383.1; Identities = 544/552 (99 %), two gaps (0 %]. Closest hits using the ***tef1*** sequence are *Verruconis* sp. [voucher BBH 49597, GenBank OQ116760.1; Identities = 870/926 (94 %), no gaps], *Verruconis hainanensis* [strain YMF1.04165, GenBank MK248272.1; Identities = 854/910 (94 %), no gaps], and *Verruconis gallopava* [strain CBS 437.64, GenBank XM_016361189.1; Identities = 876/949 (92 %), two gaps (0 %].

Supplementary material: doi: 10.6084/m9.figshare.30062794 (table, alignments and trees).



Best scoring RAxML phylogenetic tree based on a concatenated ITS-LSU-*tef1* dataset of the genus *Scolecobasidium* (*Sympoventuriaceae*, *Venturiales*) showing the placement of *S. endophyticum* within a putative *S. constrictum* species complex. The datasets of Song *et al.* (2023) and Zhang *et al.* (2024) were used for analysis, and the tree was rooted with *Pseudosigmoidea excentrica* CBS 469.95 and *Sympoventuria capensis* CBS 120136. The final dataset consisted of 67 strains and 2968 positions, 1242 from the ITS alignment, 859 from the LSU and 867 from the *tef1*. Alignments were implemented in MAFFT v. 7.511 on the online server (Katoh *et al.* 2019). Phylogenetic relationships were inferred by Maximum likelihood using RAxML v. 8.2.12 (Stamatakis 2014) on the CIPRES Science Gateway server (Miller et al. 2010) and Bayesian Inference (BI) using MrBayes v. 3.2.7a (Ronquist & Huelsenbeck 2003). The best fit-substitution model for BI was GTR+G selected using the Bayesian Information Criterion in MEGA v. 11.0 (Tamura *et al.* 2021). Bootstrap support (BS) values ≥ 70 % are shown at the nodes and Bayesian posterior probabilities (BPP) ≥ 0.95 are indicated by thickened branches. Strains with the epithet '*constrictum*' between quotation marks do not belong to the species sensu stricto but represent distinct lineages within the *S. constrictum* species complex. Those marked with a 'T' represent type strains. The *S. pandanicola*/*musae* clade was collapsed to facilitate layout. The uncollapsed tree is deposited as supplementary material.

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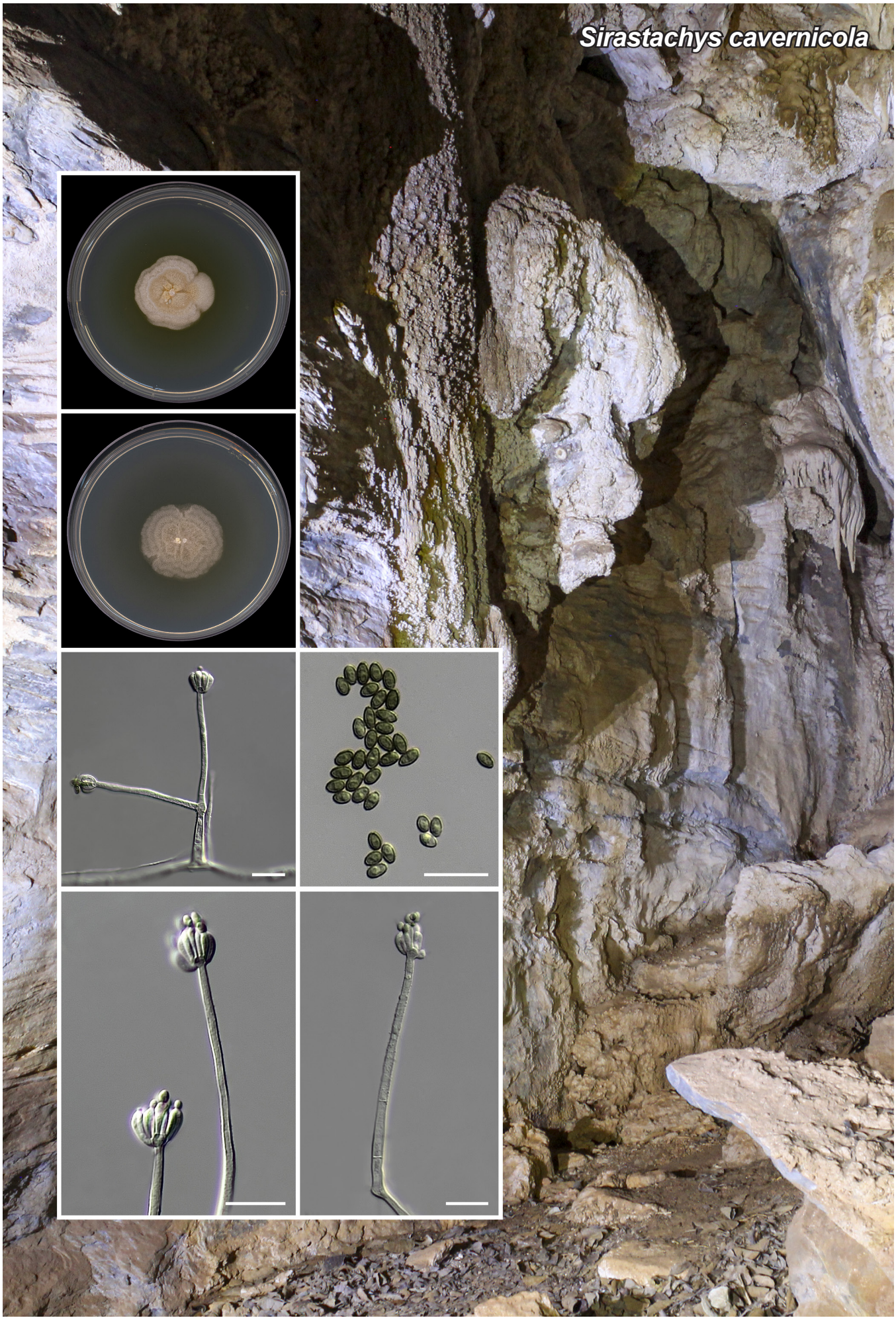

Sirastachys cavernicola

Fungal Planet 1902 MB 860687

Sirastachys cavernicola A.F. Leão, D.O. Ramos, F.A. Custódio, T.O. Condé & O.L. Pereira, ***sp. nov.***

Etymology: Named after the cave environment where the fungus was collected.

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

Conidiophores macronematous, at times laterally branched, hyaline, septate, straight or slightly flexuous, subcylindrical, smooth-walled to verrucose, bearing 3–6 conidiogenous cells, 44.1–68.4 × 2.1–3.5 µm. *Conidiogenous cells* phialidic, terminal, elongate doliiform to reniform, subhyaline to pale green, smooth-walled, 4.5–6.8 × 5.4–8.5 µm. *Conidia* acrogenous, ellipsoidal, aseptate, pale to dark olive, smooth-walled, 2.5–3.9 × 1.5–2.3 µm. *Sexual morph* not observed.

Culture characteristics: Colonies on potato dextrose agar (PDA) flat or effuse, aerial mycelium moderate, undulate edge, reaching 33 mm diam. after 2 wk at 25 °C. Colonies on malt extract agar (MEA) flat or effuse, aerial mycelium sparse to absent, undulate edge, reaching 35 mm diam. after 2 wk at 25 °C. Colonies on oatmeal agar (OA) umbonate, aerial mycelium moderate, entire edge, reaching 34 mm diam. after 2 wk at 25 °C. Colonies on cornmeal agar (CMA) flat or effuse, aerial mycelium sparse to absent, undulate edge reaching 33 mm diam. after 2 wk at 25 °C. On PDA surface (13B2) greyish magenta (Kornerup & Wanscher 1978), reverse (3C4) greyish yellow. On MEA surface (8C2) brownish grey, reverse (6A4) light orange. On OA surface (3C1) grey, reverse (3C3) greyish yellow. On CMA surface (8B3) dull red, reverse (4C3) greyish yellow.

Habit, habitat and distribution: Saprobic on leaf litter and animal dung from a cave. Known so far only from Brazil.

Typus: **Brazil**, Minas Gerais, Santana do Riacho, Teto de Seixos cave, from leaf litter, Feb. 2024, *A.F. Leão* (**holotype** VIC 49769, culture ex-type COAD 4244; ITS, LSU, *cal, tef1* and *tub2* sequences GenBank PX289351, PX314672, PX360293, PX317682 and PX360296).

Additional materials examined: **Brazil**, Minas Gerais, Santana do Riacho, Teto de Seixos cave, from leaf litter, Feb. 2024, *A.F. Leão* (living culture COAD 4245; ITS, LSU, *cal, tef1* and *tub2* sequences GenBank PX289350, PX314671, PX360291, PX317683 and PX360294); ibid., on animal dung, (living culture COAD 4246; ITS, LSU, *cal, tef1* and *tub2* sequences GenBank PX289349, PX314670, PX360292, PX317681 and PX360295).

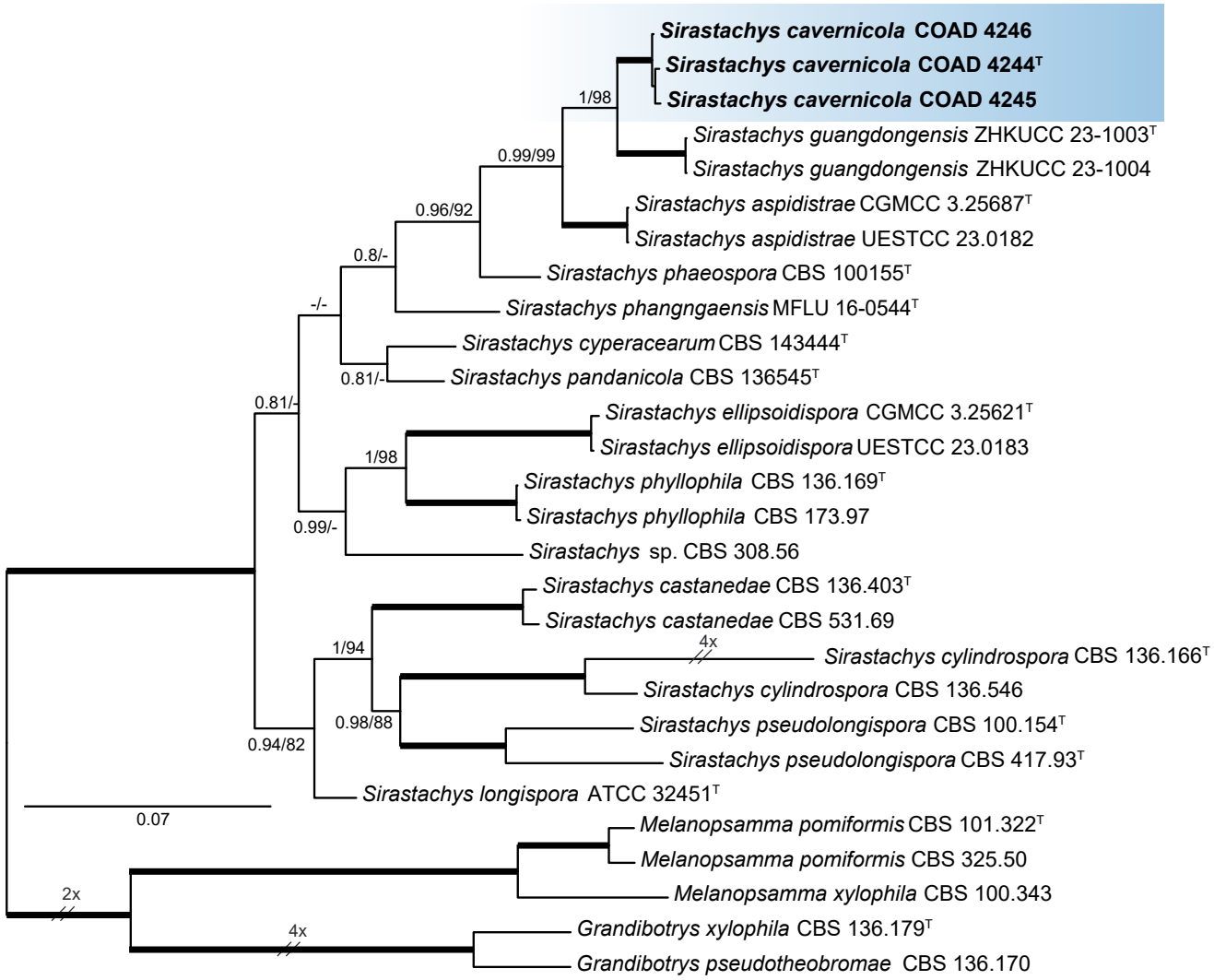
Colour illustrations: Teto de Seixos cave, Minas Gerais, Brazil. From left side top to bottom, colonies on PDA and MEA after 14 d at 25 °C, conidiophores and conidiogenous cells; from right side top to bottom, conidia and conidiophore. Scale bars = 10 µm.

Notes: *Sirastachys cavernicola* is a new species of the genus *Sirastachys*, distinct from the others both phylogenetically and morphologically. A multilocus phylogenetic analysis based on ITS, LSU, *cal*, *tef1*, *tub2*, and *rpb2* demonstrated that *S. cavernicola* forms a well-supported distinct branch (BS = 1.00; PP = 1.0), as a sister clade to *S. guangdongensis*. Species of *Sirastachys* have mainly been recorded from soil samples and as saprophytes on leaf litter and plant twigs (Lombard *et al*. 2016, Crous *et al*. 2018, Tibpromma *et al*. 2018, Du *et al*. 2025, Liao *et al*. 2025). *Sirastachys cavernicola* is the first species of the genus reported as saprophytic on leaf litter and animal faeces collected inside a cave, and it represents the second species of the genus described in Brazil (Lombard *et al*. 2016). Morphologically, *S. cavernicola* differs from *S. guangdongensis* by having smaller conidiophores (44.1–68.4 × 2.1–3.5 µm vs 105–170 × 3.5–7 µm) and a lower number of conidiogenous cells per conidiophore (3–6 vs 4–8) (Liao *et al*. 2025). Moreover, *S. cavernicola* produces branched conidiophores, a feature not observed in *S. guangdongensis* (Liao *et al*. 2025). The conidiogenous cells also differ: in *S. cavernicola* they are smaller (4.5–6.8 × 5.4–8.5 µm) and subhyaline to pale green, while in *S. guangdongensis* they measure 6.5–12.5 × 4–5 µm and vary from subhyaline to brown (Liao *et al*. 2025). Conidia of *S. cavernicola* are ellipsoidal, pale to dark olive, and 2.5–3.9 × 1.5–2.3 µm, contrasting with those of *S. guangdongensis*, which are obovoid, pale olivaceous brown to black, and larger (5–6 × 4–5 µm) (Liao *et al*. 2025).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Sirastachys phaeospora* [strain MFLU:23-0224, GenBank OR438399; Identities = 535/536 (99 %), no gaps], *Sirastachys phaeospora* [strain CPC 16093, GenBank KU846670; Identities = 533/534 (99 %), no gaps], and *Sirastachys guangdongensis* [strain ZHKUCC 23-1003, GenBank PP645734; Identities = 534/536 (99 %), no gaps]. Closest hits using the **LSU** sequence are *Sirastachys phaeospora* [strain CPC 16092, GenBank KU846782; Identities = 824/824 (100 %), no gaps], *Sirastachys phaeospora* [strain CBS 253.75, GenBank KU846778; Identities = 823/824 (99 %), no gaps], and *Sirastachys guangdongensis* [strain ZHKUCC 23-1003, GenBank PP683131; Identities = 823/824 (99 %), one gap (0 %)]. Closest hits using the ***cal*** sequence are *Sirastachys phaeospora* [strain CBS 136185, GenBank KU846562; Identities = 648/650(99 %), one gap (0 %)], *Sirastachys* sp. HZD-2024a [strain CGMCC 3.25687, GenBank PP838842; Identities = 643/651 (99 %), two gaps (0 %)], and *Sirastachys* sp. HZD-2024a [strain UESTCC 23.0182, GenBank PP838843; Identities = 641/649(99 %), two gaps (0 %)]. Closest hits using the ***tef1*** sequence are *Sirastachys guangdongensis* [strain ZHKUCC 23-1004, GenBank PP746520; Identities = 427/440 (97 %), no gaps], *Sirastachys guangdongensis* [strain ZHKUCC 23-1003, GenBank PP746519; Identities = 427/440 (97 %), no gaps], and *Sirastachys phaeospora* [strain CBS 136167, GenBank KU846996; Identities = 416/443 (94 %), no gaps]. Closest hits

using the ***tub2*** sequence are *Sirastachys phaeospora* [strain CBS 100155, GenBank KU847102; Identities = 266/274 (97 %), no gaps], *Sirastachys phaeospora* [strain MFLUCC 23-0122, GenBank OR538084; Identities = 264/274 (96 %), no gaps], and *Sirastachys phaeospora* [strain CBS 136185, GenBank KU847104; Identities = 264/274 (96 %), no gaps]. Closest hits using the *rpb2* sequence are *Sirastachys* sp. HZD-2024a [strain UESTCC 23.0182, GenBank PP855601; Identities = 714/727 (98 %), one gap (0 %)], *Sirastachys* sp. HZD-2024a [strain CGMCC 3.25687, GenBank PP855600; Identities = 714/727 (98 %), one gap (0 %)], and *Sirastachys phaeospora* [strain CPC 16092, GenBank KU846894; Identities = 683/693 (99 %), one gap (0 %)].

Supplementary material: doi: 10.6084/m9.figshare.30123019 (alignment, dataset and table with GenBank accession numbers).



Bayesian inference tree based on a dataset of ITS, LSU, *cal*, *tef1*, *tub* and *rpb2*. sequences conducted in MrBayes v. 3.2.7a (Ronquist *et al.* 2012) on XSEDE in the CIPRES science gateway (Miller *et al.* 2015) and Maximum Likelihood analysis were conducted in the IQ-TREE v. 2.2.0 (Minh *et al.* 2020), with 10 000 ultrafast bootstrapping replicates (Hoang *et al.* 2018), and the best nucleotide substitution model for each region was defined using ModelFinder (Kalyaanamoorthy et al. 2017). Bayesian posterior probabilities (pp) ≥ 0.80 and ML bootstrap values (mlbs) ≥ 80 % are indicated next to the nodes (pp/mlbs), lower values are indicated as "-". Bold lines mean support for analyses were 1 and 100 %. The tree was rooted with *Melanopsamma pomiformis* (CBS 101322 and CBS 325.50), *Melanopsamma xylophila* (CBS 100343), *Grandibotrys xylophila* (CBS 136179) and *Grandibotrys pseudotheobromae* (CBS 136170). Ex-type strains are marked with a superscript "T". Newly generated sequences are indicated **in bold**.

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Symphoricola tarnoviensis

Fungal Planet 1903 MB 861009

Symphoricola Piątek, Czachura & Stryjak-Bogacka, ***gen. nov.***

Etymology: Named after the host plant genus, *Symphoricarpos*.

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

Mycelium composed of branched, moderately or densely septate, subhyaline, pale brown or olivaceous-brown, finely verrucose, thick-walled, straight or twisted hyphae, sometimes constricted at septa. *Chlamydospores* in chains or in groups, subglobose, olivaceous or olivaceous-brown, finely verrucose, aseptate, 1-septate or muriformly septate, thick-walled, sometimes with endoconidia. *Endoconidia* subglobose or globose, hyaline, sometimes pale olivaceous in mass, smooth, aseptate, thin-walled.

Type species: *Symphoricola tarnoviensis* Piątek, Czachura & Stryjak-Bogacka

MB 861010

Symphoricola tarnoviensis Piątek, Czachura & Stryjak-Bogacka, ***sp. nov.***

Etymology: Named after Tarnów, a city in Poland, where the fungus was collected.

Mycelium composed of branched, moderately or densely septate, subhyaline, pale brown or olivaceous-brown, finely verrucose, thick-walled, straight or twisted hyphae, 2.5–5 µm wide, sometimes constricted at septa. *Chlamydospores* in chains or in groups, subglobose, olivaceous or olivaceous-brown, finely verrucose, aseptate, 1-septate or muriformly septate, thick-walled, (6–)7–16(–20) × 6–13.5(–17) µm, sometimes with endoconidia. *Endoconidia* subglobose or globose, hyaline, sometimes pale olivaceous in mass, smooth, aseptate, thin-walled, 3.5–6.5 × 3–5.5(–6) µm. [Description based on slide culture on malt extract agar (MEA)].

Cultures characteristics: Colonies on malt extract agar (MEA) erumpent, spreading, convex, dark olivaceous black, reaching 9 mm diam. after 4 wk at 15 °C, and 10 mm diam. after 4 wk at 25 °C, with strongly folded surface and sparse aerial mycelium, margin lobate. Reverse black. Colonies on potato dextrose agar (PDA) erumpent, spreading, convex, dark olivaceous black, reaching 12 mm diam. after 4 wk at 15 °C, and 9 mm diam. after 4 wk at 25 °C, with strongly folded surface and weak aerial mycelium, margin lobate. Reverse black.

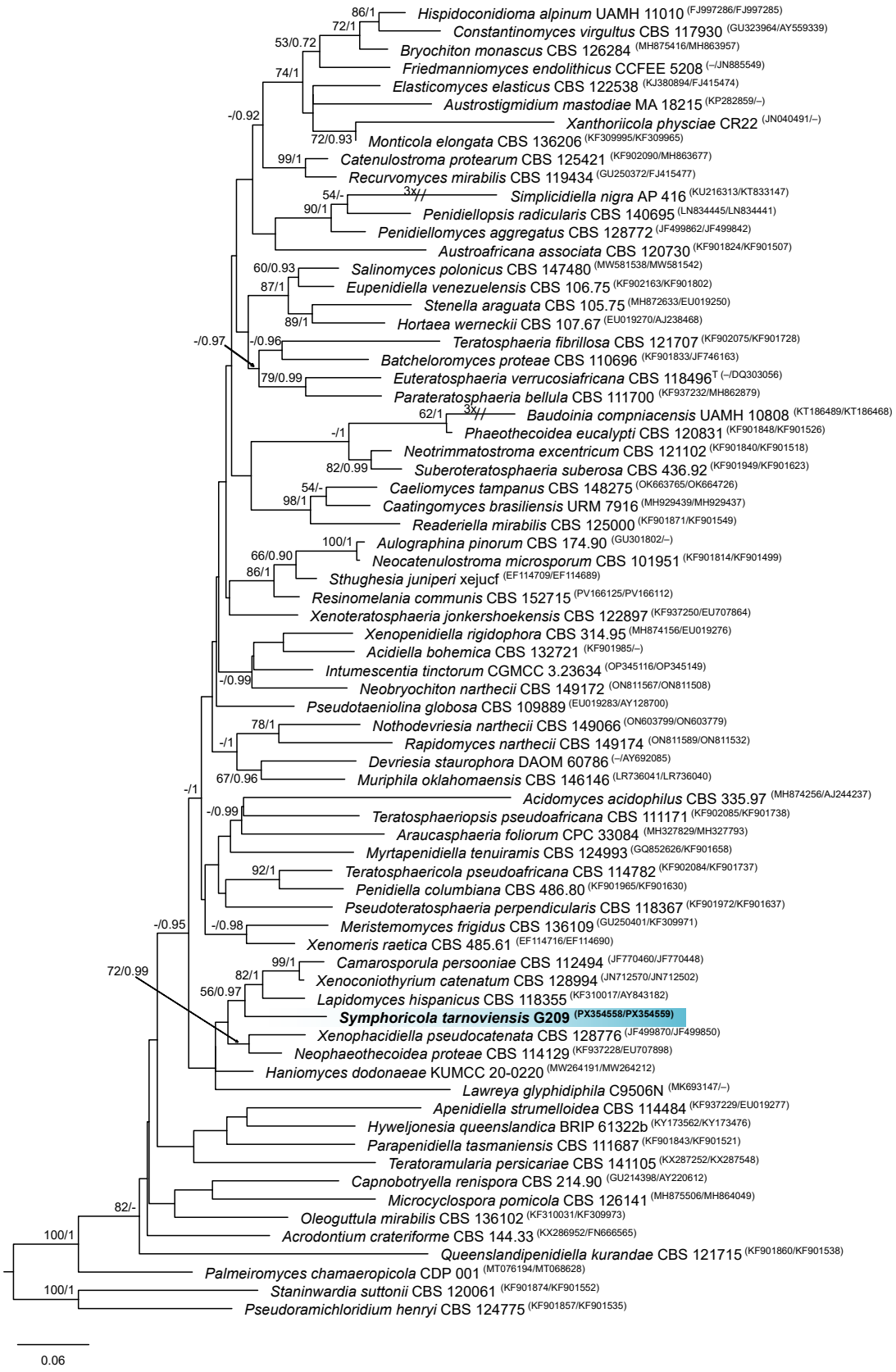
Typus: **Poland**, Małopolska Province, Tarnów County: Tarnów-Piaskówka, municipal greenery, isolated from sooty mould community on *Symphoricarpos albus* (*Caprifoliaceae*) leaves, 1 Oct. 2018, *M. Piątek, W. Bartoszek & P. Czachura* (**holotype** KRAM F-59997, culture ex type: G209 = CBS 152427; ITS and LSU sequences GenBank PX354559 and PX354558).

Notes: *Symphoricola* is another slow growing, melanized genus within the *Teratosphaeriaceae*. Morphologically, it produces only hyphae and chlamydospores with endoconidia. Phylogenetically, *Symphoricola* forms a distinct lineage within a clade that contains the genera *Camarosporula*, *Lapidomyces*, *Neophaeothecoidea*, *Xenoconiothyrium* and *Xenophacidiella*. They all develop asexual, coelomycetous or hyphomycetous morphs and *Camarosporula* additionally forms a sexual mycosphaerella-like morph (Crous & Groenewald 2011, Crous *et al.* 2011a, 2011b, 2019a, 2021a, 2023, Egidi *et al.* 2014, Quaedvlieg *et al.* 2014). Of these genera, *Neophaeothecoidea* is a genus most similar to *Symphoricola* since it forms endoconidia within hyphal cells. However, endoconidia in *Neophaeothecoidea* are medium to dark brown, verruculose to verrucose and 1-septate to multiseptate (Crous *et al.* 2008, Quaedvlieg *et al.* 2014) in contrast to the hyaline, smooth and aseptate endoconidia in *Symphoricola*, which are formed within chlamydospores.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits of the named species using the **ITS** sequence are *Neophaeothecoidea proteae* [strain CF-166084, GenBank PV835179; Identities = 492/530 (93 %), 13 gaps (2 %)], *Xenophacidiella pseudocatenata* [culture CBS 128776, GenBank MH865099; Identities = 482/521 (93 %), nine gaps (1 %)] and *Lapidomyces epipinicola* [voucher KRAM F-59827, GenBank NR_191225; Identities = 468/510 (92 %), seven gaps (1 %)]. The closest hits of the named species using the **LSU** sequence are *Phaeothecoidea melaleuca* [culture CPC 17223, GenBank HQ599595; Identities = 745/768 (97 %), no gaps], *Lapidomyces hispanicus* [culture CBS 118764, GenBank KF310016; Identities = 737/763 (97 %), two gaps (0 %)] and *Lapidomyces aloidendricola* [culture CBS 146968, GenBank MZ064493; Identities = 749/776 (97 %), two gaps (0 %)].

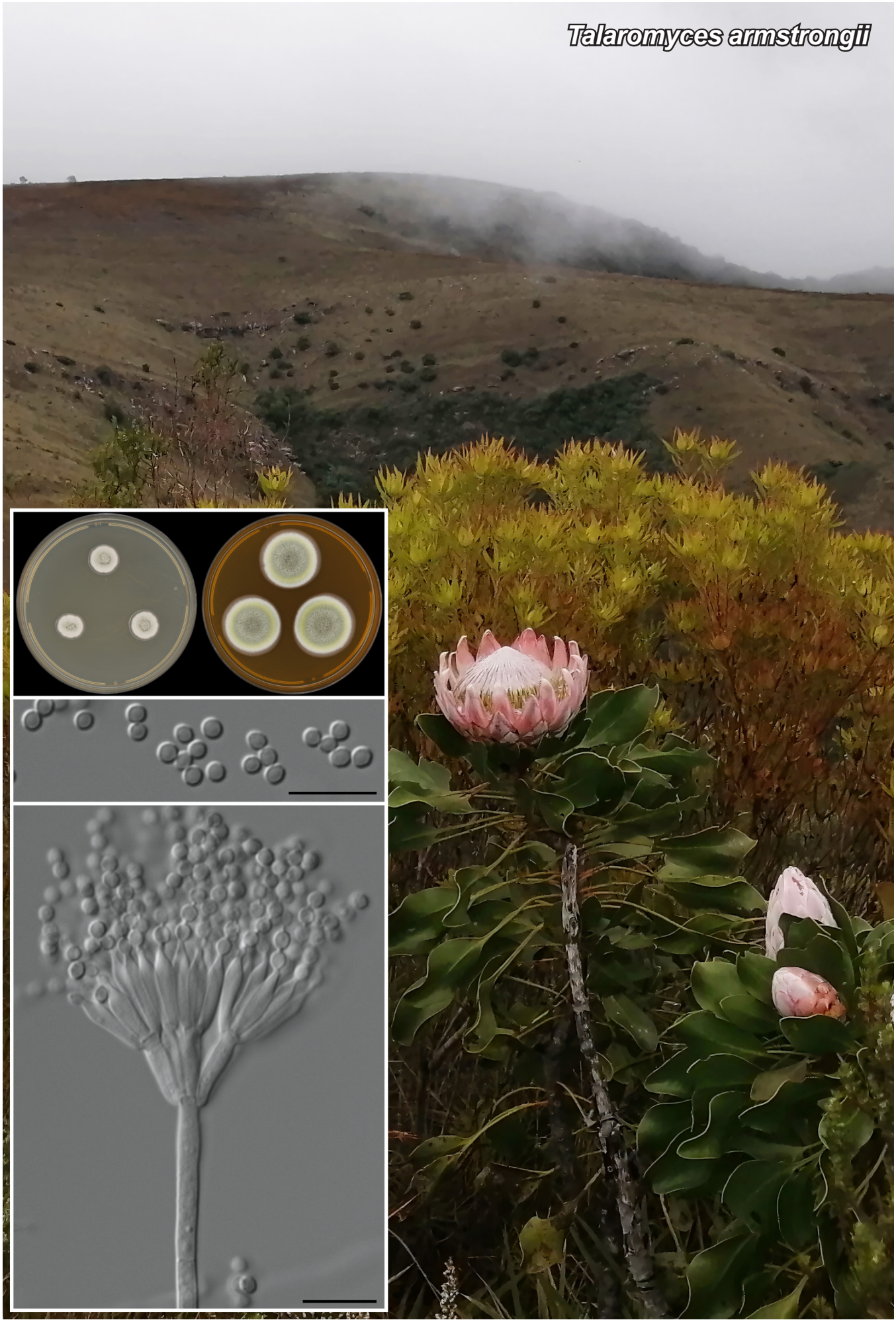
Supplementary material: https://doi.org/10.6084/m9.figshare.30111919.v1 (alignment).

Colour illustrations: Leaves of *Symphoricarpos albus* with patches of sooty mould communities, Poland. Colony on MEA; hyphae; chlamydospores; endoconidia. Scale bars = 10 µm.



Maximum likelihood phylogenetic tree of representatives of the family *Teratosphaeriaceae* obtained from a combined two-locus alignment (1336 characters, including gaps: LSU: 748, ITS: 588). The dataset for analyses contained LSU and ITS sequences of *Teratosphaeriaceae* genera used by Czachura & Piątek (2025), with slight modifications. The maximum likelihood analysis and the Bayesian inference were performed using RAxML-NG v. 1.1.0 (Kozlov *et al.* 2019) and MrBayes v. 3.2.6 (Ronquist *et al.* 2012), respectively. The position of *Symphoricola tarnoviensis* is indicated in **bold** and marked by coloured block. Numbers above branches indicate maximum likelihood (MLB) support values ≥ 50 % and Bayesian posterior probabilities (BPP) ≥ 0.9, respectively (MLB/BPP). *Pseudoramichloridium henryi* and *Staninwardia suttonii* were used as an outgroup. The scale bar represents the expected number of changes per site.

M. Piątek, P. Czachura & M. Stryjak-Bogacka, W. Szafer Institute of Botany, Polish Academy of Sciences, Lubicz 46, PL-31-512 Kraków, Poland; e-mail: m.piatek@botany.pl, p.czachura@botany.pl & m.bogacka@botany.pl


Talaromyces armstrongii

Fungal Planet 1904 MB 860993

Talaromyces armstrongii Van Vuuren, Harms & Visagie, ***sp. nov*.**

Etymology: Latin, *armstrongii*, named after Graham Armstrong, who was the Addo Elephant National Park warden in the period 1943–1960. He developed and built the elephant-proof fence in 1954 that helped to protect the Addo elephants.

Classification: *Trichocomaceae*, *Eurotiales*, *Eurotiomycetes.*

Conidiophores biverticillate; *stipes* smooth walled, 40–110 × 2.5–3.5(–4) µm; *metulae* 4–6 per stipe, appressed, 10–12(–13) × 2.5–3.5(–4) µm; *phialides* acerose, 4–6 per metula, (9–)10–12 × 2–3(–3.5) µm; *conidia* smooth, subglobose, 2–2.5 × 2–2.5 µm (2.37 ± 0.16 × 2.15 ± 0.14), average width/length = 0.89, n = 50.

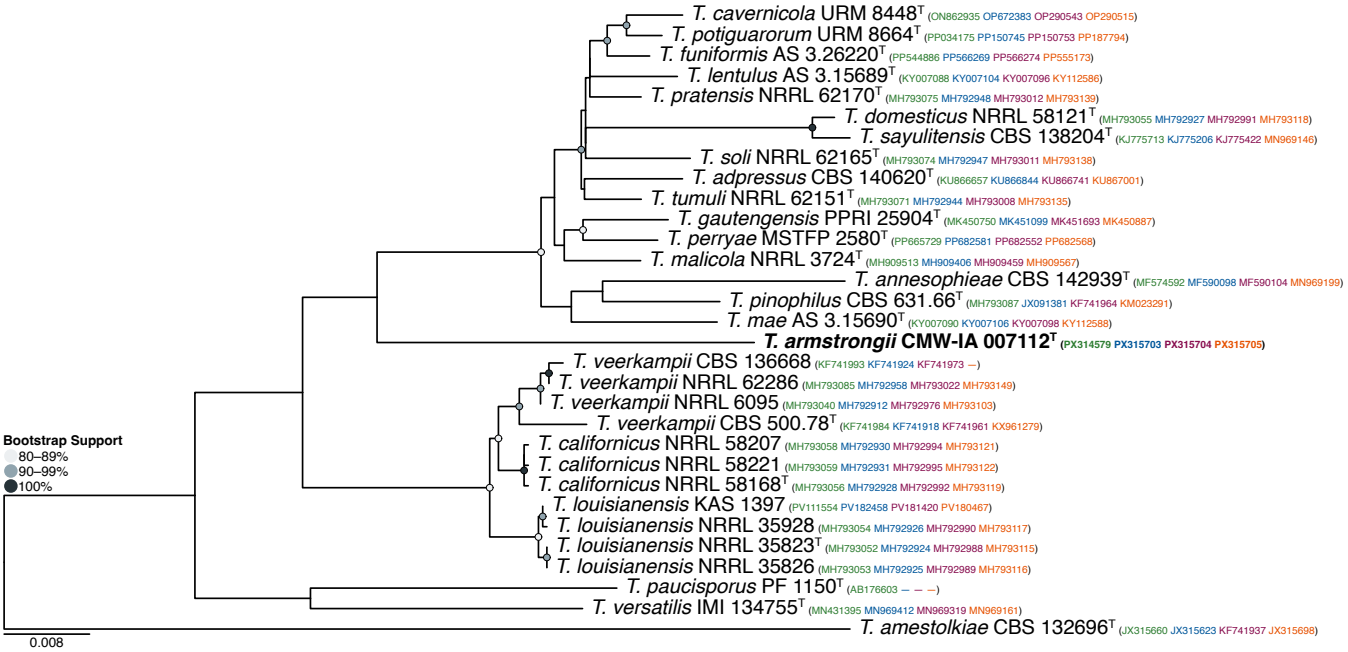
Culture characteristics (25 °C, 7 d): On Czapek yeast autolysate agar (CYA): Colonies moderately deep, slightly sulcate; margins low, narrow, entire; mycelia white; texture floccose; sporulation sparse to absent, conidia en masse greenish white (25A2; Kornerup & Wanscher 1967) to dull green (27D3); soluble pigments absent; exudates minute clear droplets; reverse dark yellow (4C8) to olive brown (4D8). On malt extract agar (MEA): Colonies plane, raised centrally, moderately deep, sulcate; margins low, wide, entire; mycelia white; texture floccose; sporulation moderately dense, conidia en masse greyish to dull green (27C3–D4); soluble pigments absent; exudates minute clear droplets; reverse brownish orange (5C4). On yeast extract sucrose agar (YES): Colonies similar to those on CYA. On dichloran 18 % glycerol agar (DG18): Colonies moderately deep, plane; margins low, narrow, entire; mycelia white; texture floccose, loosely funiculose; sporulation sparse, conidia en masse not determined; soluble pigments absent; exudates absent; reverse pale yellow (4A3–5). On oatmeal agar (OA): Colonies low, plane, granular appearance towards margins; margins low, wide, entire; mycelia white and yellow; texture velutinous; sporulation dense, conidia en masse deep green (29D8); soluble pigments absent; exudates clear. On creatine sucrose agar (CREA): Colonies weak growth, acid not produced. On creatine sucrose agar (CREA): Growth strong, no acid produced. Colony diam (in mm): CYA 10–13; CYA10C no growth; CYA15C 3–6; CYA20C 6–9; CYA30C 13–15; CYA37C 9–13; CYAS microcolonies; MEA 27–30; DG18 9–11; YES 15–18; OA 16–23; CREA 3–8.

Typus: **South Africa**, Eastern Cape Province, Addo Elephant National Park, Zuurberg (-33.348604323067654, 25.723075499909623), from soil, 19 Sep. 2023, coll. *N.I. van Vuuren*, isol. *J. Spraker* [**holotype** PRU(M):4627, culture ex-type CMW-IA 007112 = CMW 066565 = CBS 153398 = CN231B8 = iHX518104; ITS, *BenA*, *CaM* and *RPB2* sequences GenBank PX314579, PX315703, PX315704, PX315705].

Notes: *Talaromyces armstrongii* is resolved as a distinct species in the "*Talaromyces pinophilus* species complex" (Peterson & Jurjević 2019). Morphological differences observed between species in this group are considered superficial, with DNA sequence data essential for their identification (Peterson & Jurjević 2019, Visagie *et al.* 2024). Pairwise comparisons revealed that the new species has at least 3, 39, 28 and 38 bp differences from all other species based on ITS, *BenA*, *CaM* and *RPB2*, respectively.

Supplementary material: doi: 10.25403/UPresearchdata.30343939 (dataset, log files and trees).

Colour illustrations: The Zuurberg region of the Addo Elephant National Park, South Africa. Colonies on CYA and MEA; conidia; conidiophores. Scale bars = 10 µm.



A combined phylogeny of *Talaromyces armstrongii* and its close relatives based on ITS, *BenA*, *CaM* and *RPB2*, using the database of Visagie *et al.* (2025) available at https://doi.org/10.5281/zenodo.16605949. Each gene region was aligned in MAFFT v. 7.526 (Katoh & Standley 2013). These were then concatenated, and a Maximum likelihood tree calculate in IQ-TREE v. 2.3.4 (Minh *et al.* 2020). Each gene region was treated as a separate partition, and the most appropriate nucleotide substitution model selected using ModelFinder (Kalyaanamoorthy *et al.* 2017) built into IQ-TREE. A rapid-bootstrap analysis was performed with 10000 repeats (Hoang *et al*. 2018). The tree was rooted to *T. amestolkiae*. The new species is indicated by **bold** text, ^{T} = ex-type strain, and GenBank accession numbers are shown in a smaller font next to the culture accession number (ITS = green, *BenA* = blue, *CaM* = red, *RPB2* = orange).

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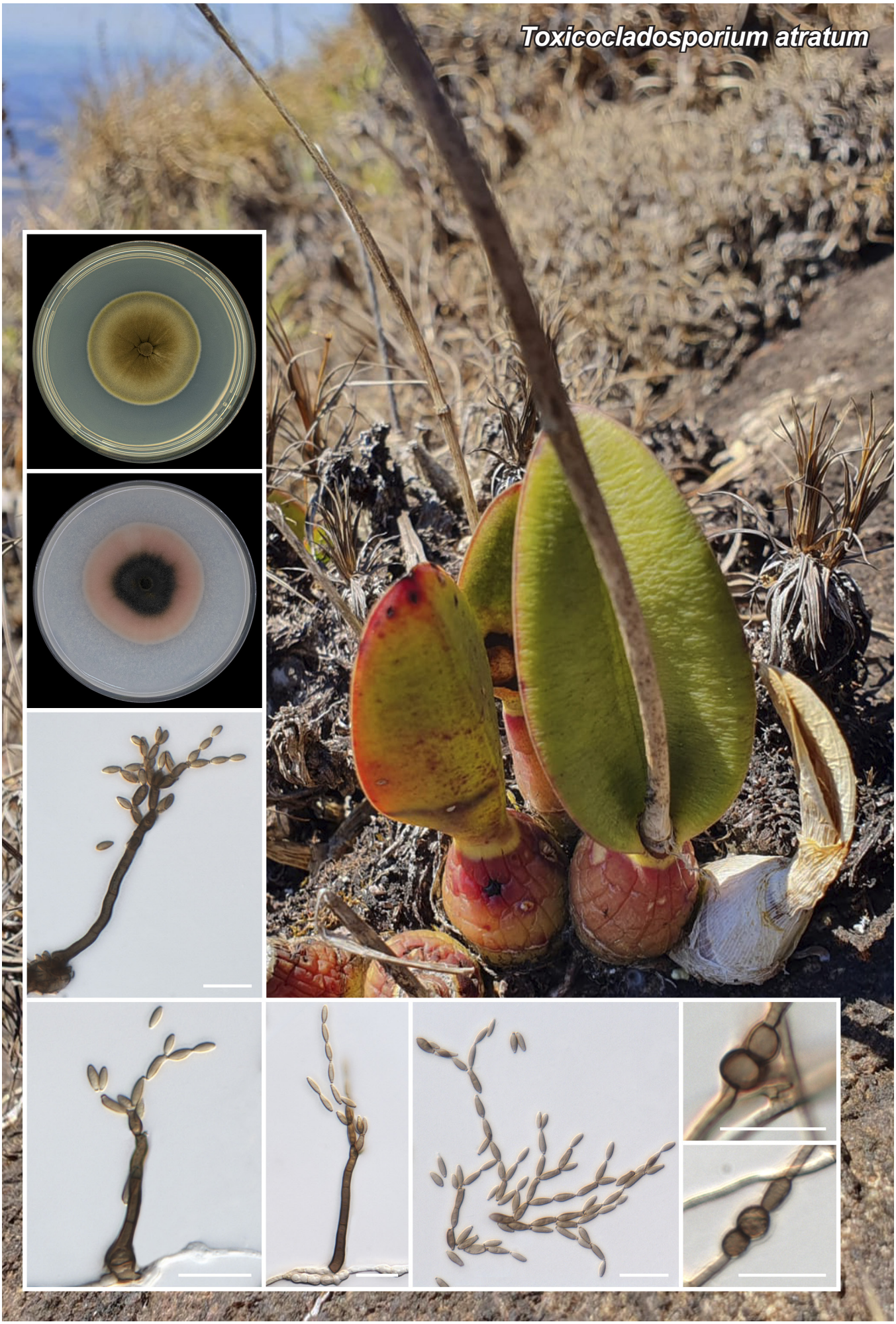

Toxicocladosporium atratum

Fungal Planet 1905 MB 860677

Toxicocladosporium atratum V.E.C. Batista, P.T.S. Nogueira, D.O. Ramos & O.L. Pereira, ***sp. nov.***

Etymology: Named after the dark colour of the conidiophores and conidia.

Classification: *Cladosporiaceae*, *Cladosporiales*, *Dothideomycetes*.

Mycelium consisting of pale brown to brown, smooth, septate, branched, 1.5–3.5 µm diam. hyphae, with abundant production of coiled hyphae on oatmeal agar (OA). *Conidiophores* erect to sinuous, sometimes arising from globose cells in superficial mycelium, 3–7-septate, dark brown, smooth, subcylindrical, unbranched, 50–120 × 2.5–4 µm. *Conidiogenous cells* integrated, smooth, dark brown, terminal or lateral, 8–12.5(–14) × 3–4.5 *µm*; scars truncate, thickened and darkened. *Primary ramoconidia* dark brown, smooth, 0–1-septate, subcylindrical, 8–12(–15) × 3–5(–6) µm. *Secondary ramoconidia* giving rise to branched chains of conidia, subcylindrical, polyblastic, brown to dark brown, 0–1-septate, (7–)9–14 × 2.5–4 µm. *Intercalary conidia* subcylindrical to fusoid-ellipsoidal, brown to dark brown, 7–10.5 × 2.5–4 µm. *Small terminal conidia* aseptate, fusoid-ellipsoid, smooth, pale brown, 6–9.5 × 2–3.5 µm. *Chlamydospores* subglobose to ellipsoidal occasionally doliiform, aseptate, smooth- and thick-walled, dark brown, solitary or small chains, intercalary or terminal on hyphae, 7–16 × 6–14.5 µm.

Culture characteristics: Colonies on potato dextrose agar (PDA) flat, radially striate with lobate edge, with moderate aerial mycelium, velvety, circular shape, reaching 49 mm diam. after 3 wk at 25 °C. Colonies on malt extract agar (MEA) flat, entire margin, with moderate aerial mycelium, velvety, circular shape, reaching 46 mm diam. after 3 wk at 25 °C. Colonies on synthetic nutrient-poor agar (SNA) flat, lobate margin, aerial mycelium absent, sporulating, circular shape, reaching 27 mm diam. after 3 wk at 25 °C. Colonies on OA flat, entire margin, aerial mycelium sparce to absent, sporulating, circular shape, reaching 51 mm diam. after 3 wk at 25 °C. On PDA surface honey to isabelline, reverse olivaceous grey and rosy buff at the margins. On MEA surface vinaceous buff to hazel, reverse olivaceous grey. On SNA surface honey to vinaceous buff, reverse hazel to vinaceous buff. On OA surface olivaceous black at the centre and peach at the margins, reverse peach and olivaceous black at the centre of the colony (colours according to Rayner 1970).

Habit, habitat and distribution: Root endophytic fungus of *Cattleya locatellii* (*Orchidaceae*). Known so far from Brazil.

Typus: **Brazil**, Minas Gerais, Araponga, isolated as root endophyte of *Cattleya locatellii* (*Orchidaceae*), 21 Nov. 2021, *O.L. Pereira* (**holotype** VIC 49515, dried culture, ex-type living culture COAD 3758; ITS, LSU, *actA*, *rpb2* and *tub2* sequences GenBank: PX314573, PX314572, PX314870, PX314869 and PX314871).

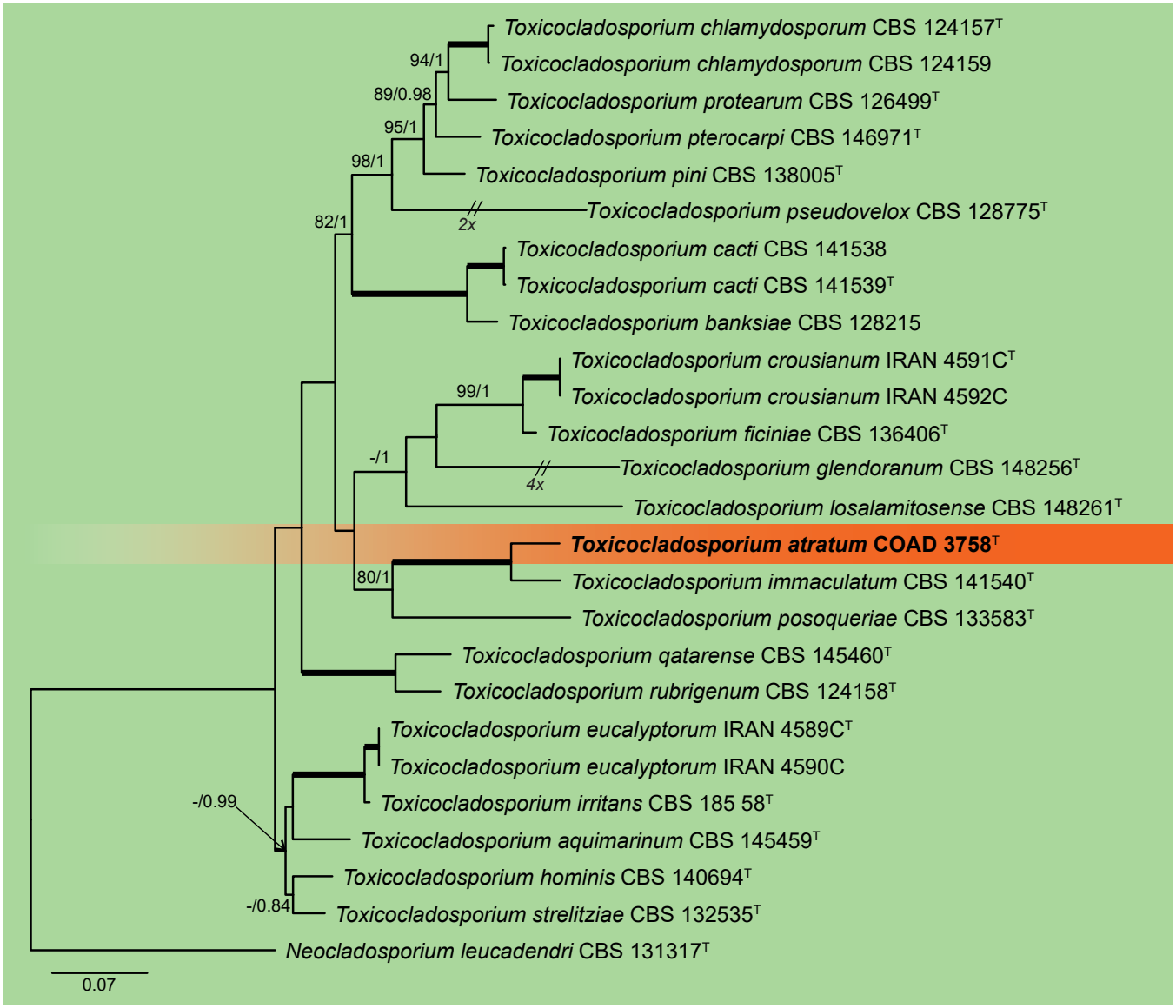
Notes: The genus *Toxicocladosporium* was proposed by Crous *et al.* (2007) to accommodate some cladosporium-like fungi. *Toxicocladosporium atratum* is phylogenetically related to *T. immaculatum* but differs from it by the production of chlamydospores, smaller primary ramoconidia [8–12(–15) × 3–5(–6) µm *vs.*14.5–22.5 × 2–4 µm], intercalary conidia (7–10.5 × 2.5–4 µm vs 11.5–13 × 2.5–3 µm), and terminal conidia [6–9.5 × 2–3.5 µm vs 8–10(–11) × 2–3 µm] (Bezerra *et al.* 2017). In addition, *T. atratum* did not produce pale brown to brown exudates on MEA and PDA and presented higher growth rates compared to *T. immaculatum*.

Toxicocladosporium immaculatum was described as an endophyte in a cactus in Brazil, while *T. atratum* was isolated as endophyte in an orchid, and is the first species of the genus to be reported on an *Orchidaceae* member worldwide.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Toxicocladosporium immaculatum* [strain CBS 141540, GenBank NR152377; Identities = 442/451 (98 %), no gaps], and *Toxicocladosporium posoqueriae* [strain CBS 133583, GenBank NR121555; Identities = 537/577 (93 %), 15/577 gaps (2 %)]. Closest hits using the **LSU** sequence are *T. immaculatum* [strain CBS 141540, GenBank NG058459; Identities = 803/804 (99 %), no gaps], and *T. posoqueriae* [strain CBS 133583, GenBank KC005803; Identities = 922/938 (98 %), no gaps]. Closest hits using the ***act*** sequence are *T. immaculatum* [strain CBS 141540, GenBank LT821370; Identities = 161/199 (81 %), eight gaps (4 %)], and *T. posoqueriae* [strain CBS 133583, GenBank LT821378; Identities = 150/196 (77 %), two gaps (1 %)]. Closest hits using the ***rpb2*** sequence are *T. immaculatum* [strain CBS 141540, GenBank LT799782; Identities = 690/754 (92 %), no gaps], and *T. posoqueriae* [strain CBS 133583, GenBank LT799785; Identities = 685/830 (83 %), no gaps]. Closest hits using the ***tub2*** sequence are *T. immaculatum* [strain CBS 141540, GenBank KY706596; Identities = 272/304 (89 %), eight gaps (2 %)], and *T. posoqueriae* [strain CBS 133583, GenBank KY706604; Identities = 247/304 (81 %), 13 gaps (4 %)].

Supplementary material: doi: 10.6084/m9.figshare.30104677 (table, alignments and tree).

Colour illustrations: *Cattleya locatellii* growing above rocks in Araponga, Minas Gerais, Brazil. From top to bottom, colonies on MEA, OA (after 3 wk at 25 °C) and conidiophores, respectively; From bottom left to right, conidiophores, ramoconidia, conidia, and chlamydospores. Scale bars = 20 µm.



Maximum likelihood tree of *Toxicocladosporium* obtained by combined dataset of ITS and LSU rDNA, *actA*, *tub2*, and *rpb2* sequences conducted in IQ-TREE v. 2.2.0 (Minh *et al.* 2020), with 10000 ultrafast bootstrapping replicates (Hoang *et al*. 2018), and the best nucleotide substitution model for each region was determined using ModelFinder (Kalyaanamoorthy *et al*. 2017). Bayesian inferences were conducted using MrBayes v. 3.2.7a (Ronquist *et al.* 2012) on XSEDE in the CIPRES science gateway (Miller *et al.* 2015), and the best nucleotide substitution model for each region was determined using jModelTest 2 (Darriba *et al*. 2012). The isolate obtained in this study is indicated in **bold** face. Bootstrap support values from Maximum Likelihood (ML-BS), and Bayesian posterior probabilities (BPP) above 80 % and 0.80, respectively, are indicated at the nodes. *Neocladosporium leucadendri* (CBS 131317) was used as outgroup. The best-fit substitution models, as determined by ModelFinder in IQ-TREE, were GTR+F+I+G4 for the ITS and LSU partitions, and TIM2+F+I+G4 for the *rpb2*, *actA*, and *tub2* partitions. For Bayesian inferences, the best-fit models identified were: ITS: SYM+I+G; LSU: GTR+I+G; *rpb2*: GTR+G; *actA* and *tub2*: HKY+I+G.

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Tuber danielis
20 µm

Fungal Planet 1906 MB 859816

Tuber danielis M. Romero, L. Möller & P. Alvarado, ***sp. nov.***

Etymology: Dedicated to Daniel Cabeza Romero, grandson of M. Romero.

Classification: *Tuberaceae*, *Pezizales*, *Pezizomycetes*.

Hypogeous *ascomata*, irregularly globose to tuberiform, firm in consistency, measuring 0.5–2 cm diam., slightly verrucose. Surface smooth to slightly pubescent, yellowish ochre in colour, becoming dark brown at maturity. Rhizomorphs, plant debris, and soil particles often adherent to the surface. *Peridium* thin, pale brown in section. *Gleba* smooth, with minute, punctiform locules discernible only under magnification when mature; fertile area dendriform, appearing elongate and greyish white when young, later turning dark brown; sterile zones located medially, somewhat elevated, short and broad, tapering toward the ends, pearly white in colour. *Odour* faint but pleasant. Peridium composed of a suprapellis 15–45 µm thick, formed of tightly interwoven, septate, cylindrical hyphae, 1–2.5 µm diam. Many terminal elements protrude as cystidia, often flattened due to pigmentation or arranged in a palisade; most exhibit concentric wall thickenings, either rounded or flattened, imparting a rosulate appearance. Underlying pellis 75–150 µm thick, formed of densely interwoven hyphae, 3.5–5 µm diam., exhibiting a pseudoparenchymatous appearance in the outer regions due to intersecting hyphae forming rounded to ovoid “cells”, and a prosenchymatous structure in the inner regions. *Asci* non-amyloid, mostly ellipsoid and occasionally pyriform, measuring 100 × 50 µm to 120 × 65 µm (excluding the neck). Neck 25–35 µm long, occasionally extending to 45–70 µm. Each ascus contains 1–2 (occasionally 3) spores. *Spores* dark brown in water when mature, reddish-brown in Melzer’s reagent, broadly ellipsoid to globose, with some oculiform elements. *Ornamentation* composed of spines 3–5 µm high, forming a complete reticulum with hexagonal to pentagonal meshes, 5–6 µm wide; typically 4–5 alveoli per spore in longitudinal section. Spore measurements were taken in water, including the ornamentation: (31.8–)34.1–41.8(–44.7) × (28.6–)31.6–36.3(–37.3) µm; Q = 1.0–1.2(–1.3); N = 25; Me = 37.3 × 33.7 µm; Qe = 1.1

Habitat and distribution: Growing hypogeously in small groups at shallow depth, beneath the litter of *Cistus ladanifer*, associated with *Quercus ilex* and *Genista scorpius*, in Mediterranean forest. Fruiting in late spring (April to May) in southwestern Spain.

Typus: **Spain**, Badajoz, Quintana de la Serena, Sierra del Vallejón, in acidic soil beneath *Cistus ladanifer*, *Quercus ilex*, and *Genista scorpius*, 14 Apr. 2021, *M. Romero*, MRG694 (**holotype** AH 60378, ITS and LSU sequences GenBank PQ435333 and PQ427318).

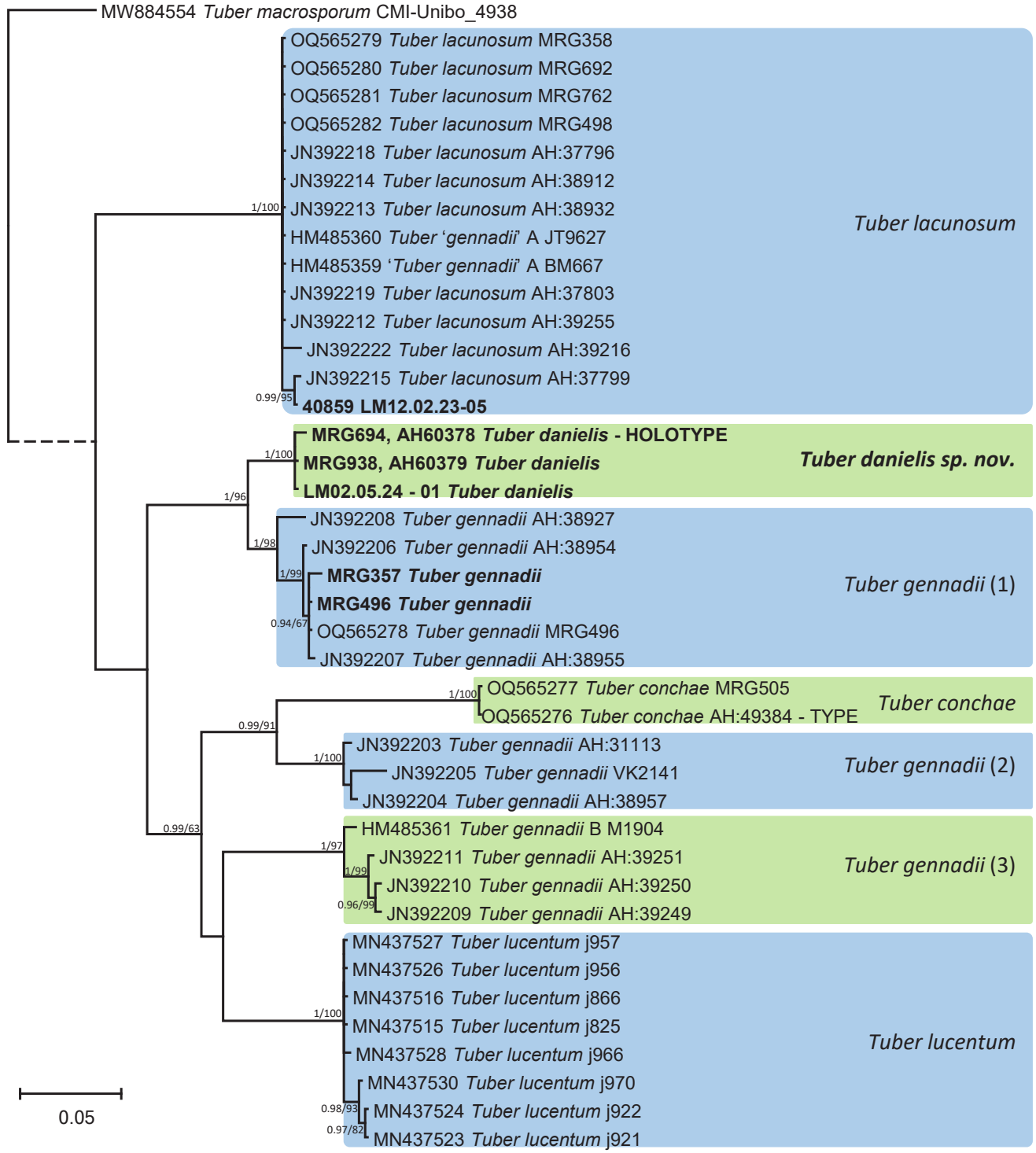
Additional materials examined: *Tuber danielis*. **Spain**, Badajoz, Quintana de la Serena, Sierra del Vallejón, in the same habitat, 16 Apr. 2024, *M. Romero*, MRG938 (**paratype** AH 60379; ITS and LSU sequences GenBank PQ435334 and PQ427319). **Portugal**, Carvoeiro, in sandy soil, *Pinus pinea*, directly with *Cistus salvifolius*, 2 May 2024, *L. Möller* (dog: Figo), LM 02.05.24 - 01 (ITS and LSU sequences GenBank PV871568 and PV856404). *Tuber gennadii*. **Spain**, Badajoz, Malpartida de la Serena, near *Tuberaria guttata*, *Quercus ilex*, *Genista scorpius,* 7 Apr. 2015, *M. Romero*, MRG357 (ITS and LSU sequences GenBank PV871569 and PV856405); idem., 7 May 2018, MRG496 (ITS and LSU sequences GenBank OQ565278 and PV856406). *Tuber lacunosum*. **Portugal**, Algarve, municipality of Salir, near *Pinus pinea* and *Cistus salvifolius*, soil slightly clayey (pH around 7.0), 12 Feb. 2023, *M. dos Santos* (dog: Nala), LM 12.02.23-05 (ITS sequence GenBank PV871570).

Notes: *Tuber danielis* is a white truffle belonging to the *Gennadii* clade, characterised by its occurrence in acidic soils in association with *Cistus ladanifer*. It forms small, non-verrucose, yellowish ochre ascomata covered with adherent debris. The gleba has very small, non-confluent locules that are only visible under magnification at maturity, and emits a faint but pleasant odour. The peridium is composed of a suprapellis with cystidia exhibiting symmetrical wall thickenings that give a rosulate appearance. The pellis is thin and formed by interwoven hyphae, appearing pseudoparenchymatous in the outer zones and prosenchymatous internally. Mature spores are dark brown in water and reddish brown in Melzer’s, globose to broadly ellipsoid, with some oculiform forms in immature asci. Asci are pyriform to ovoid, bearing (1–)2(–3) spores. *Tuber danielis* differs ecologically from *T. gennadii* (Chatin 1896, Montecchi & Sarasini 2000, Alvarado *et al.* 2012), because the latter typically occurs in habitats associated primarily with *Tuberaria guttata* instead of *Cistus*. Macroscopically, *T. gennadii* has a gleba with small locules that tend to become more or less interconnected at maturity; the odour is absent or undetected, and the pellis is composed of prosenchymatous tissue. Both species are otherwise very similar in size and both have some immature spores that look eye-shaped (oculiform). Compared to *T. conchae* (Crous *et al.* 2023), another white truffle with similar fruiting season and habitat, *T. danielis* has a smaller size (1–2 cm vs 1–4 cm), weakly verrucose surface, and faint odour. In contrast, *T. conchae* produces strongly verrucose ascomata with a pronounced goat-like odour, especially at maturity, golden-yellow ascospores in water, a compact marbled gleba without visible locules, and asci containing (1–)2–3(–4) spores. *Tuber lacunosum* (Mattirolo 1900) is also associated with *Tuberaria guttata*, has larger verrucose ascomata, and a reddish-brown gleba that is extremely fragile and breaks easily when cut, especially in young specimens. The locules

Colour illustrations. Spain, Extremadura, Quintana de la Serena, Mediterranean forest habitat dominated by *Cistus ladanifer*, *Quercus ilex*, and *Genista scorpius*. Top: peridium in water (×400); 2nd row left: detail of suprapellis in Congo red (×1000); 2nd row right: ascospores in Melzer (×1000); 3rd row left: ascus in water (×400); 3rd row right: spores in Melzer (×1000, inverted); 4th row: ascomata (holotype MRG938); bottom: ascoma (LM 02.05.24). Scale bars: peridium in water = 50 µm; all others = 20 µm.

in the gleba are larger and more abundant, but remain discrete. Fresh specimens emit a strong goat-like odour, which persists in dried material. Finally, *T. lucentum* (Crous *et al.* 2019c) is distinguished by its very small, rounded ascomata (approximately 1 cm), compact gleba lacking locules, and preference for calcareous soils, where it is found in association with *Helianthemum violaceum*, *H. syriacum*, and *Fumana thymifolia*.

Supplementary material: doi: 10.6084/m9.figshare.30354424 (table, alignment and tree figure).



A 50 % majority rule ITS rDNA consensus phylogram of *Tuber danielis* and related *Tuber* species of the Gennadii clade (with *T. macrosporum* as outgroup) obtained using MrBayes v. 3.2.6 (Ronquist *et al.* 2012) from 1650 sampled trees. Nodes were annotated if they were supported by ≥ 0.95 Bayesian posterior probability (left) or ≥ 70 % maximum likelihood bootstrap proportions (right) obtained in RAxML8.2.12 (Stamatakis 2014). Sequences newly generated in this study are in **bold**.

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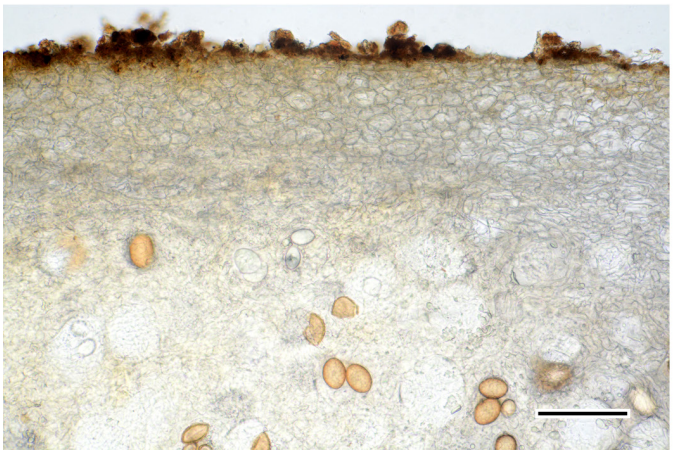
Tuber honstrassii



Fungal Planet 1907 MB 860902

Tuber honstrassii L. Möller & A. Paz, ***sp. nov.***

Etymology: Named for Prof. Didier Honstrass for dedicating his time and effort to teaching us about the world of hypogeal fungi.

Classification: *Tuberaceae*, *Pezizales*, *Pezizomycetidae*, *Pezizomycetes*.

Hypogeal *ascomata*, irregularly globose to tuberiform, with firm consistency, 0.8–1.6 cm diam., slightly cracked. *Surface* smooth to slightly pubescent, ochre-yellow in colour, turning dark brown at maturity. *Peridium* thin, light brown in section. Gleba compact, marbled, young specimens pinkish, maturing to brown-violet, with small sterile veins cream white. Peridium composed of two layers. External layer or exoperidium 15.5–55 µm thick, formed by subglobose or slightly elongated hyphae, 9.5–11 × 6–18 µm, with thick walls of 3–4 µm, pigmented with intense brown-reddish colour; interspersed with the bases of dermocystidia (or hairs), these are cylindrical, septate, 6 to 8.5 µm diam., some with incrustations and pigmented light brown, others hyaline and without incrustations, both with rounded terminations, very fragile, which are lost when cleaning the ascoma. Inner cap or endoperidium thicker, 130–155 µm thick, formed by subglobose hyphae with a wide range of sizes, from 7–34.5 × 5–26 µm, forming a pseudoparenchymatous structure. *Asci* not amyloid, mostly subglobose to ellipsoidal, measuring 75–110 × 58–80 µm with short stalk, 15–25 µm long. Each ascus contains between 1–4 (occasionally 5 and very rarely 6) spores. *Spores* ellipsoidal, dark brown when mature, ornamented with a complete reticulum, with very regular alveoli, hexagonal to pentagonal; in cross-section the spore has 7–9 alveoli along its length by 5–7 across, each alveolus averaging 8 × 5.5 µm, with a height not exceeding 2 µm. Spores measurements are highly variable, depending on the number of spores per ascus; asci with one spore measuring 43.5–55 × 26–32 µm; asci with two spores 31.5–39.5 × 24.5–26 µm; asci with three spores 28–34.5 × 20–24 µm; asci with four spores 26–30 × 17–18.5 µm; asci with five spores 23.5–26 × 14.5–16 µm. *Odour* initially chemical, gas, then mild, pleasant.

Habitat and distribution: Clayey and calcareous soil, under *Quercus rotundifolia* and *Arbutus unedo.* Species so far only known from the type locality in Portugal.

Typus: **Portugal**, Algarve, concelho de Loulé, Salir, 37°13’55.2’’N, 8°00’57.7’’O, 180 m, clayey and calcareous soil under *Quercus rotundifolia* and *Arbutus unedo,* 9 Apr. 2025, *N.-E. dos Santos* (dog Nala) & *L. Möller* (dog Figo) (**holotype** BCN-myc 3745, **isotype** IC09042501; ITS sequence GenBank PX444438).

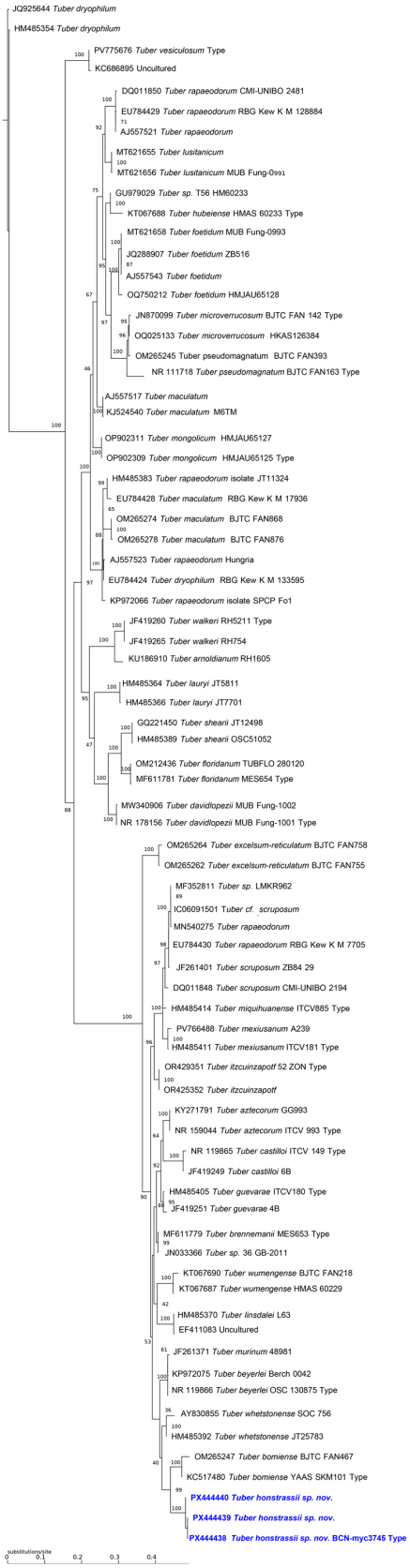
Additional materials studied **Portugal**, Algarve, concelho de Loulé, Salir, 37°13’55.2’’N, 8°00’57.7’’O, 181 m, in clayey and calcareous soil under *Quercus rotundifolia* and *Arbutus unedo,* 3 May 2024, *N.-E. dos Santos* (dog Nala) & *L. Möller* (dog Figo), IC03052407 **paratype**, ITS sequence GenBank PX444439; ibid., 19 May 2024, IC19052409 **paratype**, ITS sequence GenBank PX444440.

Notes: Phylogenetic studies indicate that *Tuber honstrassii* sits in the *T. maculatum* group and is in the same clade as the Chinese species *T. wumengense* and *T. bomiense*. Both differ from *T. honstrassii* by having verrucose surfaces on the ascomata and spore ornamentation with a network reticulation of greater height, up to 6 µm in depth (Su *et al*. 2013, Fan *et al.* 2016). Recently, in Cabero *et al*. (2025) a new species, *T. vesiculosum*, has been published within the *T. maculatum* group, but it differs because *T. vesiculosum* presents a pseudoparenchymatous peridial structure and a trama composed of swollen, vesicular cells.

Based on a Blast analysis of the ITS region for *T. honstrassii*, the following similarities were observed: *T. wumengense* GenBank KT067690: 92.55 %, *T. bomiense* GenBank KC517480 Type: 94.97 %, and *T. vesiculosum* GenBank PV775676 Type: 92.16 %.

Supplementary material: doi: 10.25664/ART-0412 (alignment and tree).

Colour illustrations: Portugal, Algarve, concelho de Loulé, Salir, where the specimens were collected. Mature ascomata; organisation of peridium hyphae (exoperidium and endoperidium) and gleba; ascospores under light microscope. All images are from the holotype. Scale bars: peridium = 100 µm; ascospores = 15 µm.



A 50 % majority rule ITS rDNA consensus phylogram of selected sequences of the maculatum clade of genus Tuber (*Tuber dryophilum* GenBank sequences JQ925644 and HM485354 was included as an outgroup) obtained using MrBayes from 18675 sampled trees. Nodes were annotated if they were supported by > 70 % maximum likelihood bootstrap proportions. The alignment was done with ClustalW and checked in BioEdit Sequence Alignment Editor v. 7.2.5 (12/11/2013) and then analysed with IQ-TREE v. 3.0.1 (May 5, 2025), "https://iqtree.github.io/". Gstree.exe and Adobe Acrobat Pro software was used to edit the final tree. The new species is shown in blue and **bold**. Terminals contain GenBank accession number, species name, voucher and type status where applicable.

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Neoleptosporella agapanthi

Fungal Planet 1908 MB 861171

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

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

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

Ascomata perithecial, separate, globose, up to 400 µm diam., dark brown, erumpent with papillate neck and central ostiole; wall of 4–6 layers of dark brown textura intricata; outer surface covered in brown conidiophores. *Asci* subcylindrical to narrowly subfusoid, slightly curved, apex subobtuse, unitunicate, apical mechanism not staining in Melzers regent, stipitate, 70–100 × 7–10 µm, 8-spored. *Paraphyses* intermingled among asci, hyphae-like, hyaline, smooth, septate, 3–5 µm diam. *Ascospores* spirally coiled in ascus, hyaline, smooth, guttulate, subcylindrical, ends obtuse to slightly swollen obtuse apex, 70–90 × 2–3 µm, mostly medianly 1-septate, but up to 3-septate ascospores observed. *Conidiophores* arising from ascomatal surface, subcylindrical, unbranched, straight to flexuous, dark brown, thick-walled, 4–6-septate, 100–160 × 3–5 µm. *Conidiogenous cells* terminal, integrated, brown, smooth-walled, subcylindrical with slight apical taper, phialidic with slightly flared collarette, 20–30 × 3–4 µm. *Conidia* solitary, hyaline, smooth, guttulate, aseptate, obclavate, widest in lower third, tapering to truncate hilum, 1 µm diam, apex subobtuse, 8–12(–15) × 1.5–2 µm.

Culture characteristics: Colonies erumpent, spreading with moderate fluffy aerial mycelium and even, lobate margin, reaching 50 mm diam. On MEA surface honey, reverse isabelline; on PDA surface and reverse isabelline; on OA surface isabelline.

Typus: **Brazil**, Minas Gerais, Viçosa experimental farm, from stalks of *Agapanthus praecox* (*Amaryllidaceae*), Feb. 2024, *P.W. Crous*, HPC 4392 (**holotype** CBS H-25749; culture ex-type COAD 4252 **=** CPC 47856; ITS, LSU, *tef1* (second part) and *tub2* sequences GenBank PX640123.1, PX640147.1, PX583896.1 and PX583897.1).

Notes: *Neoleptosporella*, based on *N. clematidis*, is characterised by being saprobic on stems of woody hosts, and having immersed ascomata, paraphyses, 8-spored unitunicate asci with a J- subapical ring, and fusoid, aseptate ascospores (Phukhamsakda *et al.* 2020). *Neoleptosporella agapanthi* is phylogentically related to *N. camporesiana*, but the latter has longer, 100–156 × 2.5–4 µm, aseptate ascospores (Hyde *et al.* 2000). This is also the first record of an asexual morph for the genus *Neoleptosporella*, and the first species with septate ascospores.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neoleptosporella camporesiana* (nom. inval.) [strain HLT9, GenBank PV649817.1; Identities = 533/558 (96 %), nine gaps (1 %)], *Ophiostoma karelicum* [strain VDLS8, GenBank MH305479.1; Identities = 484/501 (97 %), one gap (0 %)], and *Leptosporella cassiae* [strain NID17, GenBank PP327424.1; Identities = 503/537 (94 %), four gaps (0 %)]. Closest hits using the **LSU** sequence are *Neoleptosporella* sp. CFL-2021a [strain KUMCC 21-0014, GenBank OL473548.1; Identities = 708/713 (99 %), one gap (0 %)], *Neoleptosporella camporesiana* (nom. inval.) [strain ZHKUCC 22-0218, GenBank OP658918.1; Identities = 708/713 (99 %), one gap (0 %)], and *Neoleptosporella palmae* [strain SNC129, GenBank PP621056.1; Identities = 654/714 (92 %), five gaps (0 %)]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Neoleptosporella camporesiana* (nom. inval.) [strain ZHKUCC 22-0218, GenBank OP684008.1; Identities = 903/911 (99 %), no gaps], *Neoleptosporella palmae* [strain SNC129, GenBank PP740461.1; Identities = 852/918 (93 %), no gaps], and *Papiliomyces shibinensis* [strain YFCC 861.01, GenBank OR115231.1; Identities = 846/918 (92 %), two gaps (0 %)]. No significant hits were obtained when the ***tub2*** sequence was used in blastn and megablast searches.

The name *Neoleptosporella camporesiana* is invalid, as it was published before the generic name was introduced. It is therefore validated here:

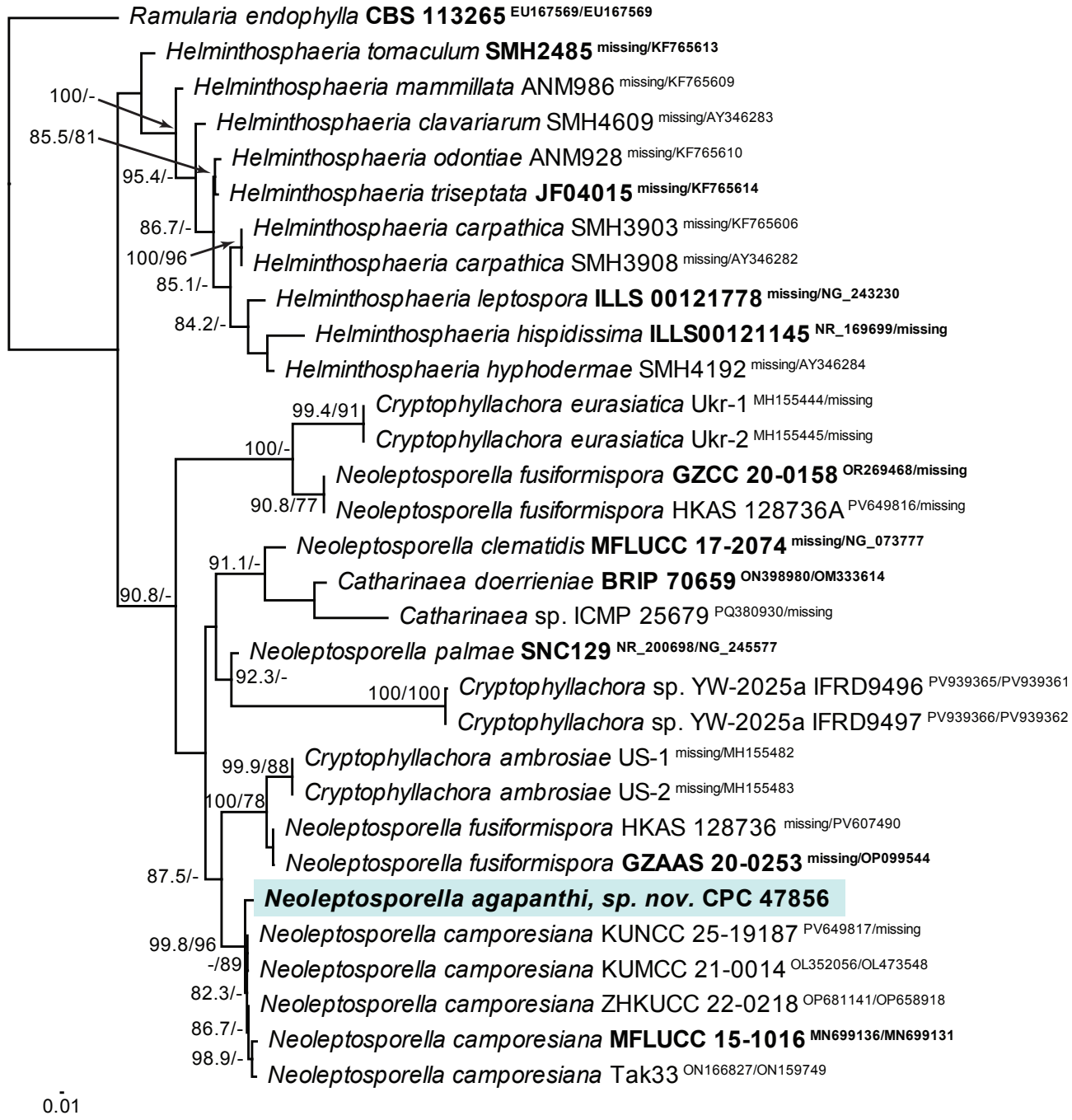
Neoleptosporella camporesiana R.H. Perera & K.D. Hyde, ***sp. nov.*** MB 861172
Synonym: *Neoleptosporella camporesiana* R.H. Perera & K.D. Hyde, *Fungal Diversity* **100**: 219. 2020. Nom. inval., Art. 35.1 (Shenzhen).

Description and illustration: Hyde *et al.* (2020).

Typus: **Thailand**, Chiang Rai Province, on dead branch of unidentified plant, 10 Jan. 2016, *R.H. Perera*, RHP 132 (**holotype** MFLU 19-0978, ex-type culture MFLUCC 15-1016, ITS and LSU sequences GenBank MN699136 and MN699131).

Supplementary material: doi: 10.6084/m9.figshare.30529955 (alignment and phylogenetic tree).

Colour illustrations: Flowers of *Agapanthus praecox*. Ascomata on OA; brown, septate conidiophores; conidiogenous cells; conidia; paraphyses; asci with ascospores. Scale bars: Ascomata = 400 µm, all others = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Neoleptosporella* ITS-LSU nucleotide alignment. Values > 74 % from the SH-aLRT test and bootstrap support values > 74 % 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. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Ramularia endophylla* (CBS 113265; GenBank EU167569/EU167569) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 31 strains including the outgroup; 1608 characters including alignment gaps analysed: 777 distinct patterns, 584 parsimony-informative, 186 singleton sites, 838 constant sites. The best-fit models identified in IQ-TREE using the TESTNEW option were: ITS (1-700): TIM+F+G4; LSU (701–1608): TN+F+G4. The scale bar shows the expected number of nucleotide substitutions per site.

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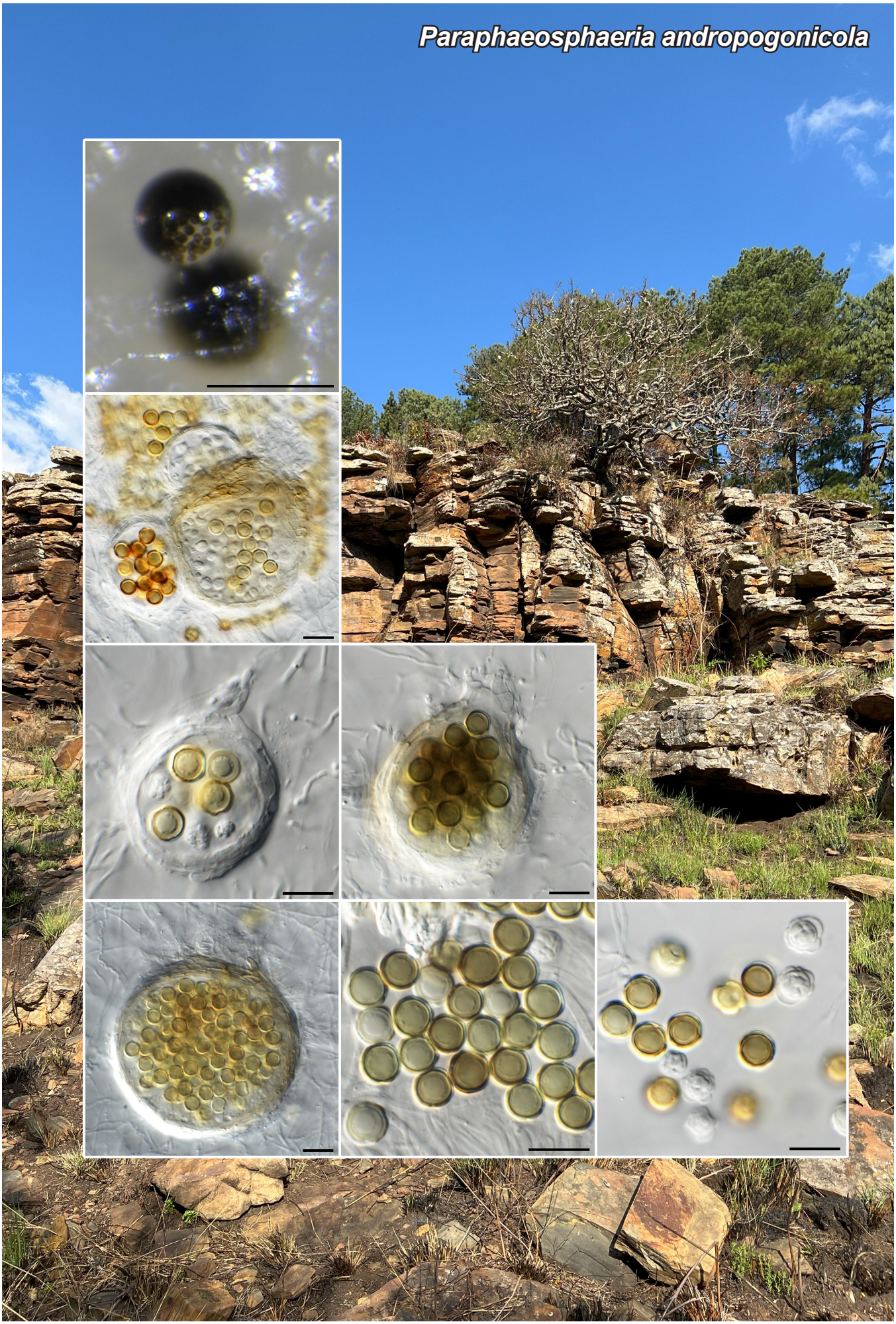

Paraphaeosphaeria andropogonicola

Fungal Planet 1909 MB 861173

Paraphaeosphaeria andropogonicola Crous & M.M. Costa, ***sp. nov.***

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

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

Conidiomata pycnidial, solitary, erumpent, globose, brown, 35–100 µm diam., becoming papillate with age; wall of 3–6 layers of pale brown textura angularis. *Conidiophores* reduced to *conidiogenous cells* lining inner cavity, hyaline, smooth, ampulliform, phialidic, 3–4 × 4–6 µm. *Conidia* solitary, aseptate, globose, becoming medium golden brown, guttulate, enclosed in lobed mucoid sheath giving conidia warty appearance with what appears to be several germ pores, conidia 6–7 µm diam.

Culture characteristics: Colonies flat, spreading, with sparse aerial mycelium, covering dish in 2 wk at 25 °C on all media except PDA. On MEA surface saffron with diffuse bay pigment, and reverse bay. On PDA surface and reverse pale luteous. On OA surface and reverse saffron.

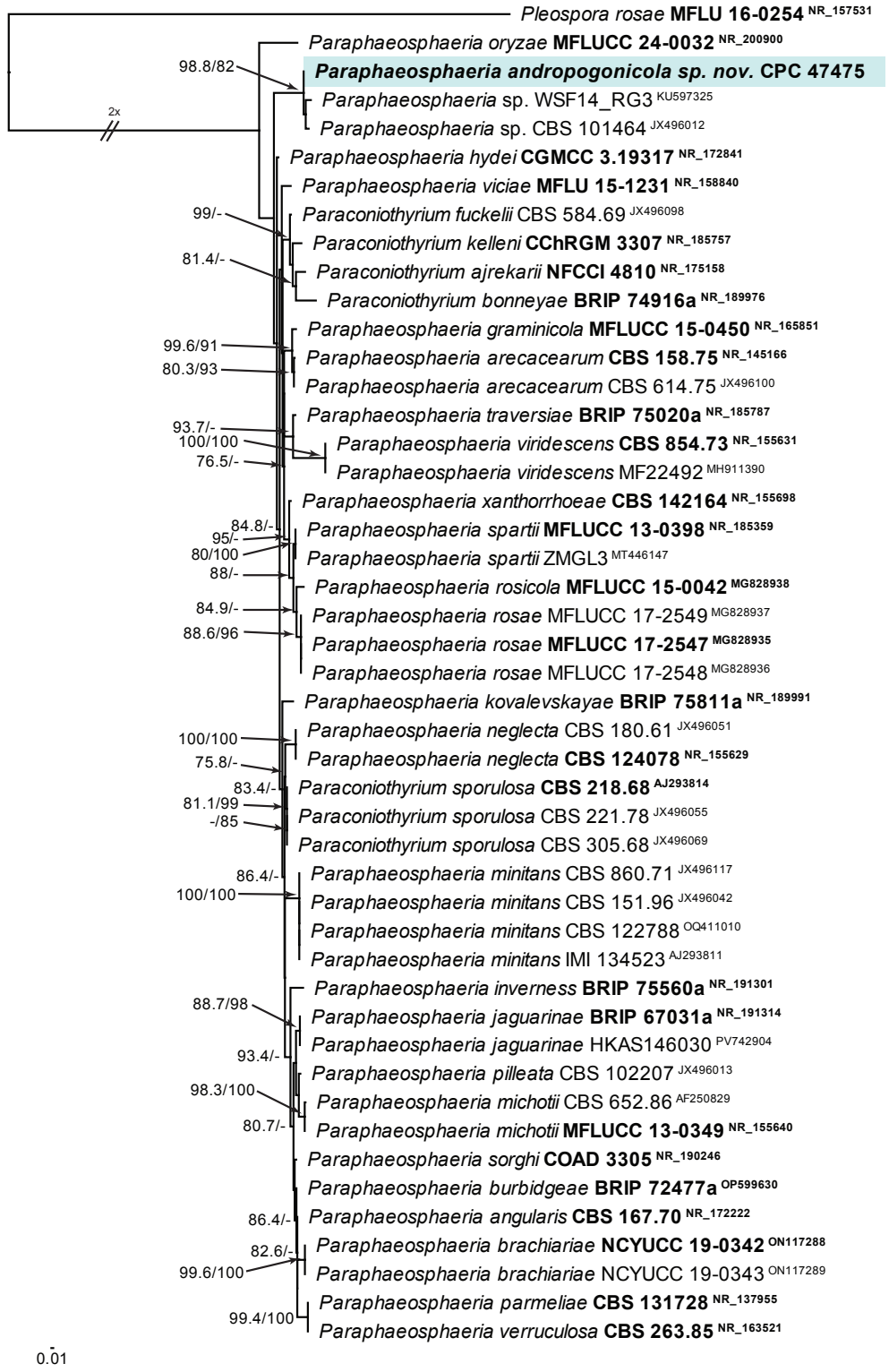
Typus: **South Africa**, Northern Province, Mpumalanga, Mbombela, Nelspruit, Buffelskloof Nature Reserve, on leaves of *Andropogon eucomus* (*Poaceae*), 5 Aug. 2022, *M.M. Costa* (**holotype** CBS H-25796, culture ex-type CPC 47475 = CBS 154455; ITS sequence GenBank PX640124.1).

Notes: *Paraphaeosphaeria* has immersed ascomata, bitunicate asci, and brown, multiseptate ascospores that frequently have a swollen cell below the primary septum, and coniothyrium-like asexual morphs (Verkley *et al.* 2004). No sexual morph is known for *P. andropogonicola*, which is distinct from other species in the genus based on its conidial dimensions, and having a warty appearance due to a lobed mucoid sheath.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Paraphaeosphaeria* sp. [strain CBS 101464, GenBank JX496012.1; Identities = 562/568 (99 %), no gaps], *Paraphaeosphaeria oryzae* [strain MFLUCC 24-0032, GenBank PQ374213.1; Identities = 455/466 (98 %), one gap (0 %)], and *Paraphaeosphaeria hydei* [strain CGMCC 3.19317, GenBank NR_172841.1; Identities = 457/469 (97 %), one gap (0 %)].

Supplementary material: doi: 10.6084/m9.figshare.30529955 (alignment and phylogenetic tree).

Colour illustrations: Rocky cliff with *Andropogon eucomus*. Conidioma with conidial droplet on OA; conidiomata with conidia; conidia. Scale bars: Upper conidioma 100 µm, all others = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Paraphaeosphaeria* ITS nucleotide alignment. Values > 74 % from the SH-aLRT test and bootstrap support values > 74 % 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. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Pleospora rosae* (MFLU 16-0254; GenBank NR_157531) and the novelty described here is highlighted with a coloured block and **bold** font. The root branch was shortened to facilitate layout. Alignment statistics: 47 strains including the outgroup; 606 characters including alignment gaps analysed: 240 distinct patterns, 113 parsimony-informative, 120 singleton sites, 373 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+I+R2. The scale bar shows the expected number of nucleotide substitutions per site.

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Triseptosporium fallopiae

Fungal Planet 1910 MB 861174

Triseptosporium Crous & Hülsewig, ***gen. nov.***

Etymology: Named after the its 3-septate conidia.

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

Mycelium consisting of hyaline, smooth, branched, septate hyphae. *Conidiophores* solitary, erect, flexuous, subcylindrical, unbranched. *Conidiogenous cells* terminal, hyaline, smooth, subcylindrical; apex phialidic with flared collarette. *Conidia* aggregating in mucoid mass, slightly curved, (1–)3-septate, fusoid, apex subobtuse, base truncate, widest in middle, tapering towards both ends.

Type species: *Triseptosporium fallopiae* Crous & Hülsewig

MB 861175

Triseptosporium fallopiae Crous & Hülsewig, ***sp. nov.***

Etymology: Named after the host genus it was isolated from, *Fallopia*.

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam. hyphae. *Conidiophores* solitary, erect, flexuous, subcylindrical, unbranched, up to 250 µm tall, 4–5 µm diam. *Conidiogenous cells* terminal, hyaline, smooth, subcylindrical, 90–120 × 4 µm; apex phialidic with flared collarette. *Conidia* aggregating in mucoid mass, slightly curved, (1–)3-septate, fusoid, apex subobtuse, base truncate, 3–4 µm diam., widest in middle, tapering towards both ends, (30–)34–38(–40) × (7–)8 µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and folded surface, reaching 20 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse pale luteous.

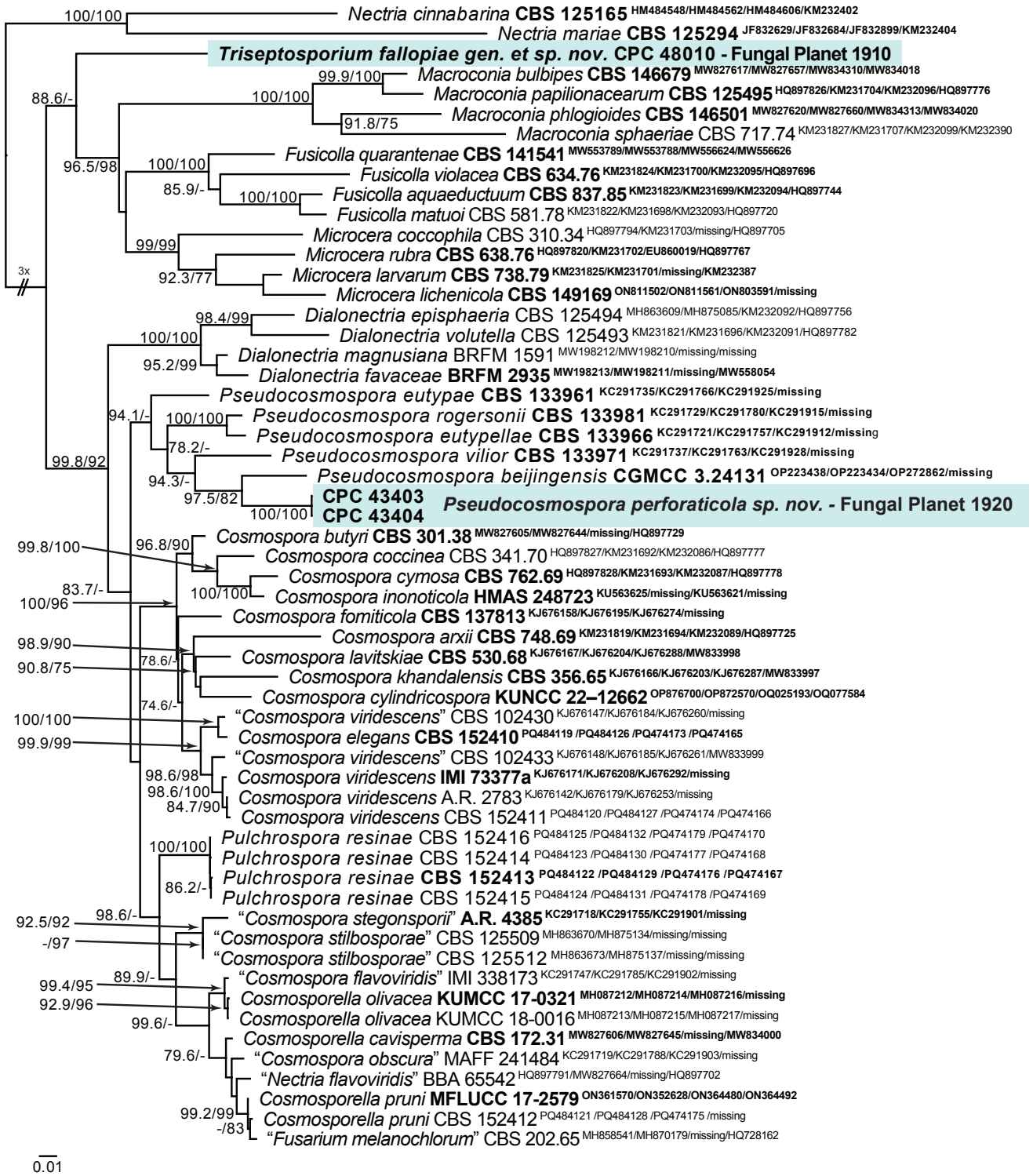
Typus: **Germany**, North Rhine-Westphalia, Witten, Recreation area Hohenstein, on rotten stems of on *Fallopia japonica* (*Polygonaceae*), 24 Feb. 2024, *T. Hülsewig*, Thorben 1195 = HPC 4416 (**holotype** CBS H-25799; culture ex-type CPC 48010 = CBS 153466; ITS, LSU, *rpb2* (first and second part), *tef1* (first part) and *tub2* sequences GenBank PX640125.1, PX640148.1, PX620759.1, PX583880.1 and PX583898.1).

Notes: The *Cosmospora* generic complex contains several nectrioid genera with acremonium-like or fusarioid asexual morphs, namely *Cosmospora*, *Cosmosporella*, *Dialonectria*, *Pseudocosmospora*, and *Pulchrospora* (Czachura & Janik 2025). *Triseptosporium* (presently only known from its asexual morph), adds yet another genus to this complex, characterised by acremonium-like conidiophores, but with fusoid, (1–)3-septate conidia having subobtuse apices and truncate bases.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cosmospora berkeleyana* [strain CBS 236.70, GenBank MH859582.1; Identities = 510/533 (96 %), eight gaps (1 %)], *Pseudocosmospora vilior* [strain CIRM-BRFM 3052, GenBank PV109356.1; Identities = 506/529 (96 %), five gaps (0 %)], and *Cosmosporella pruni* [strain MFLUCC 17-2579, GenBank NR_189388.1; Identities = 505/528 (96 %), five gaps (0 %)]. Closest hits using the **LSU** sequence are *Pulchrospora resinae* [as *Hypocreales* sp. PC-2024a; strain CBS 152415, GenBank PQ484131.1; Identities = 854/866 (99 %), no gaps], *Cosmospora berkeleyana* [strain CBS 121.70, GenBank MH871292.1; Identities = 857/870 (99 %), no gaps], and *Cosmospora coccinea* [strain CBS 342.70, GenBank MH871455.1; Identities = 857/870 (99 %), no gaps]. Closest hits using the ***rpb2*** (first part) sequence had distant similarity to *Cosmospora aquatica* [voucher MFLU 15-0072, GenBank MN194020.1; Identities = 671/777 (86 %), nine gaps (1 %)], *Cosmospora viridescens* [strain CBS 102433, GenBank HQ897712.1; Identities = 669/777 (86 %), nine gaps (1 %)], and *Cosmospora butyri* [strain IRAN 4322C, GenBank PP187011.1; Identities = 666/778 (86 %), 11 gaps (1 %)]. Closest hits using the ***rpb2*** (second part) sequence had distant similarity to *Cosmospora rishbethii* [strain CBS 496.67, GenBank HQ897714.1; Identities = 724/827 (88 %), two gaps (0 %)], *Cosmospora flavoviridis* [strain BBA 65542, GenBank HQ897702.1; Identities = 720/826 (87 %), two gaps (0 %)], and *Cosmosporella cavisperma* [strain BBA 64137, GenBank HQ897762.1; Identities = 718/826 (87 %), two gaps (0 %)]. Closest hits using the ***tef1*** (first part) sequence had distant similarity to *Cosmosporella pruni* [as *Cosmosporella* sp. RHP-2022a; voucher MFLU 17-0974, GenBank ON364467.1; Identities = 408/545 (75 %), 35 gaps (6 %)], *Fusicolla quarantenae* [strain 111JB, GenBank MW556625.1; Identities = 374/490 (76 %), 39 gaps (7 %)], and *Fusicolla violacea* [strain CBS 634.76, GenBank KM231956.1; Identities = 400/532 (75 %), 36 gaps (6 %)]. Closest hits using the ***tub2*** sequence had distant similarity to *Cosmospora lavitskiae* [strain 7976, GenBank KU563620.1; Identities = 475/549 (87 %), 21 gaps (3 %)], *Cosmospora viridescens* [strain 1802, GenBank PQ456771.1; Identities = 476/553 (86 %), 20 gaps (3 %)], and *Cosmospora cylindricospora* [voucher HKAS 125785, GenBank OQ025193.1; Identities = 505/587 (86 %), 21 gaps (3 %)].

Supplementary material: doi: 10.6084/m9.figshare.30529955 (alignment and phylogenetic tree).

Colour illustrations: Collection site in Germany. Sporulation on SNA; conidiogenous cells; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Nectriaceae* ITS-LSU-*tub2*-*rpb2* nucleotide alignment (Czachura & Janik 2025). Values > 74 % from the SH-aLRT test and bootstrap support values > 74 % from 1000 non-parametric bootstrap replicates are shown at the nodes. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript, following table in Czachura & Janik 2025) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Nectria cinnabarina* (CBS 125165; GenBank HM484548/HM484562/HM484606/KM232402) and *Nectria mariae* (CBS 125294; GenBank JF832629/JF832684/JF832899/KM232404) and the novelties described here are highlighted with coloured blocks and **bold** font. Two branches were shortened to facilitate layout. Alignment statistics: 57 strains including the outgroup; 3079 characters including alignment gaps analysed: 1356 distinct patterns, 790 parsimony-informative, 261 singleton sites, 2028 constant sites. The best-fit models identified in IQ-TREE using the TESTNEW option were: ITS (1–622): TIM2e+I+R2; LSU (623–1493): TIM+F+I+R3; *tub2* (1494–2206): TNe+I+G4; *rpb2* (2207–3079): TIM2e+I+G4. The scale bar shows the expected number of nucleotide substitutions per site.

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Sarcopodium panamaense

Fungal Planet 1911 MB 861176

Sarcopodium panamaense Crous, ***sp. nov.***

Etymology: Named after the country it was collected from, Panama.

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

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam. hyphae. Conidiophores and conidia dimorphic. *Verticillate conidiophores* solitary, subcylindrical, pale brown, smooth, septate, up to 300 µm tall, 3–4 µm diam. *Conidiogenous cells* hyaline to pale brown, smooth, subcylindrical with apical taper, intercalary and terminal, phialidic, 40–80 × 3–4 µm. *Conidia* aggregating in mucoid mass, fusoid-ellipsoid, hyaline, smooth, medianly 1-septate, apex subobtuse, hilum truncate, (9–)10–11(–13) × 3.5–4 µm. *Conidiomatal sporodochia* up to 300 µm diam., separate, yellowish with brown setae developing throughout sporodochia and extending above, visible under dissecting microscope. *Setae* separate, brown, prominently verruculose, septate, spirally curved, apex obtuse, up to 180 µm tall, widest in apical part, 5–6 µm diam. *Conidiophores* hyaline, smooth, septate, extensively branched, up to 80 µm tall, 3–4 µm diam. *Conidiogenous cells* terminal (rosette up to 6), and intercalary, subcylindrical, hyaline, smooth, phialidic, 15–20 × 2.5–3 µm. *Conidia* aggregating in mucoid mass, hyaline, smooth, 0–1-septate, fusoid-ellipsoid, (7–)8(–9) × 2.5–3 µm.

Culture characteristics: Colonies erumpent, spreading, with abundant aerial mycelium and folded surface, reaching 50 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse pale luteous.

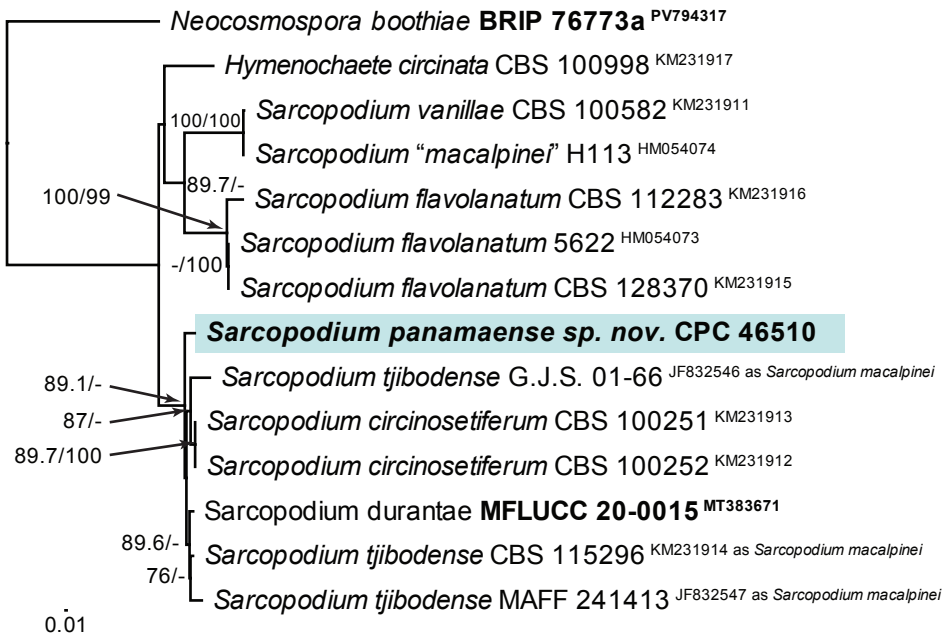
Typus: **Panama**, Colon Province, Soberania National Park, Pipeline Road, close to Gamboa, on twig litter of angiosperm, 6 Aug. 2023, *P.W. Crous*, HPC 4227 (**holotype** CBS H-25800; culture ex-type CPC 46510 = CBS 154456; ITS, *rpb1*, *rpb2* (first part), *tef1* (first part), and *tub2* sequences GenBank PX640126.1, PX620756.1, PX620760.1, PX583881.1 and PX583899.1).

Notes: The present collection was isolated from red, warty perithecia. Unfortunately, no material of the nectria-like sexual morph was retained, and hence only the asexual morph could be described. Lombard *et al.* (2015) presented DNA data to support the synonymy of *Actinostilbe* and *Kutilakesopsis* with *Sarcopodium*. *Sarcopodium panamaense* forms a distinct lineage between *S. flavolanatum* (asexual morph synnematous, conidia 10–17(–22) × 4–7 µm; Rossman *et al.* 1999), and *S. flocculentum* (as *S. macalpinei*, conidia cylindrical, 6–14 × 2.5–4.5 µm; Rossman *et al.* 1999) and is also morphologically distinct.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Sarcopodium circinosetiferum* [strain CBS 100252, GenBank KM231781.1; Identities = 552/552 (100 %), no gaps], *Sarcopodium tjibodense* [as *Lanatonectria flocculenta*; strain G.J.S. 01-66, GenBank JF832656.1; Identities = 473/473 (100 %), no gaps], and *Sarcopodium araliae* [strain ZH8-E2, GenBank FJ037741.1; Identities = 549/550 (99 %), one gap (0 %)]. Closest hits using the ***rpb1*** sequence are *Sarcopodium circinosetiferum* [strain CBS 100252, GenBank KM232196.1; Identities = 477/494 (97 %), four gaps (0 %)], *Sarcopodium macalpinei* [strain CBS 115296, GenBank KM232198.1; Identities = 479/497 (96 %), seven gaps (1 %)], and *Sarcopodium flavolanatum* [strain CBS 128370, GenBank KM232199.1; Identities = 438/497 (88 %), four gaps (0 %)]. Closest hits using the ***rpb2*** (first part) sequence are *Sarcopodium circinosetiferum* [strain CBS 100252, GenBank KM232355.1; Identities = 766/789 (97 %), five gaps (0 %)], *Sarcopodium flavolanatum* [strain CBS 112283, GenBank KM232358.1; Identities = 681/790 (86 %), seven gaps (1 %)], and *Chaetopsina penicillata* [strain CBS 608.92, GenBank HQ897709.1; Identities = 654/791 (83 %), nine gaps (1 %)]. Closest hits using the ***tef1*** (first part) sequence are *Sarcopodium tjibodense* [as *Sarcopodium macalpinei*; strain CBS 115296, GenBank KM231914.1; Identities = 461/485 (95 %), seven gaps (1 %)], *Sarcopodium circinosetiferum* [strain CBS 100251, GenBank KM231913.1; Identities = 454/483 (94 %), four gaps (0 %)], and *Sarcopodium durantae* [strain DN1, GenBank MT383671.1; Identities = 234/253 (92 %), one gap (0 %)]. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ***tub2*** sequence had highest similarity to *Sarcopodium tjibodense* [as *Sarcopodium macalpinei*; strain CBS 115296, GenBank KM232042.1; Identities = 561/574 (98 %), one gap (0 %)], *Sarcopodium durantae* [strain DN1, GenBank MT383672.1; Identities = 555/572 (97 %), two gaps (0 %)], and *Sarcopodium circinosetiferum* [strain CBS 100251, GenBank KM232041.1; Identities = 558/579 (96 %), six gaps (1 %)].

Supplementary material: doi: 10.6084/m9.figshare.30529955 (alignment and phylogenetic tree).

Colour illustrations: Jungle at Soberania National Park. Sporodochium; setate; verticillate conidiophores; conidiogenous cells and conidia; conidia. Scale bars: Sporodochium = 300 µm, all others = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Sarcopodium tef1* (first part) nucleotide alignment. Values > 74 % from the SH-aLRT test and bootstrap support values > 74 % 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. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Neocosmospora boothiae* (BRIP 76773a; GenBank PV794317) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 14 strains including the outgroup; 536 characters including alignment gaps analysed: 249 distinct patterns, 144 parsimony-informative, 92 singleton sites, 300 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TNe+G4. The scale bar shows the expected number of nucleotide substitutions per site.

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Ijuhya panamaensis

Fungal Planet 1912 MB 861177

Ijuhya panamaensis Crous, ***sp. nov.***

Etymology: Named after the country it was collected from, Panama.

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

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam. hyphae. *Conidiophores* separate, erect, aggregating on agar in a mucoid mass, subcylindrical with apical taper, base hyaline to pale brown, smooth to finely verruculose, 0–1-septate, 15–20 × (1.5–)2 µm. *Conidiogenous cells* integrated, terminal and intercalary, monophialidic, 15–18 × 1.5–2 µm. *Conidia* solitary, aggregating in mucoid mass, hyaline, smooth, aseptate, fusoid-ellipsoid, apex subobtuse, base truncate, (7–)9–10(–12) × (2.5–)3 µm.

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

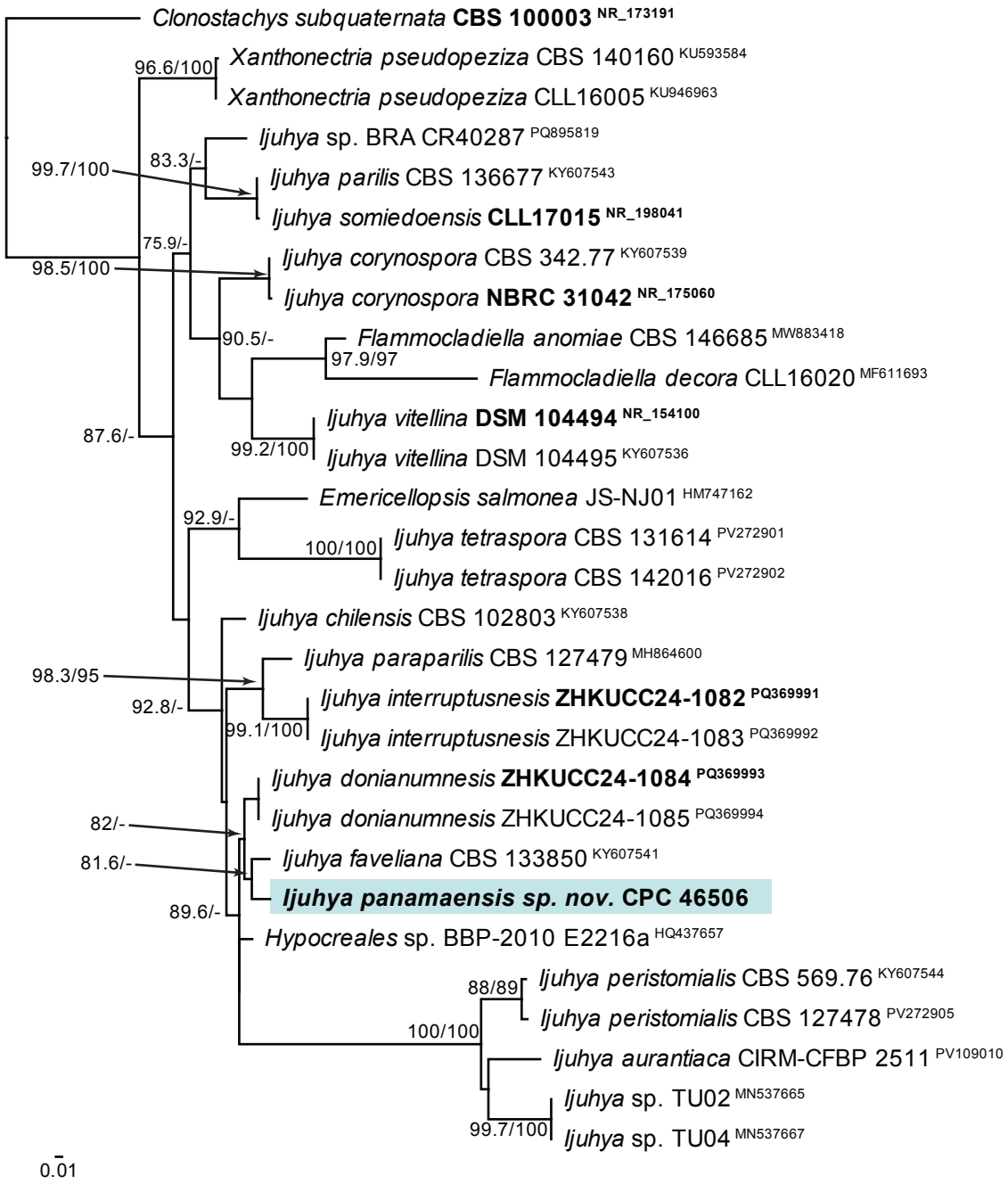
Typus: **Panama**, Colon Province, Soberania National Park, Pipeline Road, close to Gamboa, on twig litter of angiosperm, 6 Aug. 2023, *P.W. Crous*, HPC 4218 (**holotype** CBS H-25801; culture ex-type CPC 46506 = CBS 154460; ITS, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank PX640127.1, PX583903.1, PX583882.1 and PX583900.1).

Notes: *Ijuhya* is based on *I. peristomialis* (= *I. vitrea*), characterised by nectria-like perithecia with fasciculate hairs around the ascomatal apex (Rossman *et al*. 1999). Zhao *et al.* (2025) found *Ijuhya* to be polyphyletic. *Ijuhya panamaensis* is related to a sexual morph, *I. faveliana* (CBS 133850; Lechat & Fournier 2019) to which it cannot be compared morphologically. They are however distinct phylogenetically.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Ijuhya faveliana* [strain CBS 133850, GenBank KY607541.1; Identities = 541/558 (97 %), five gaps (0 %)], *Ijuhya* sp. CJ-2024b [strain ZHKUCC 24-1084, GenBank PQ369993.1; Identities = 478/499 (96 %), two gaps (0 %)], and *Ijuhya chilensis* [strain CBS 102803, GenBank PV272906.1; Identities = 517/553 (93 %), nine gaps (1 %)]. Closest hits using the ***rpb2*** sequence are *Kallichroma asperum* [strain CBS 141304, GenBank PV273467.1; Identities = 689/762 (90 %), no gaps], *Ijuhya chilensis* [strain CBS 102803, GenBank PV273466.1; Identities = 664/770 (86 %), nine gaps (1 %)], and *Ijuhya faveliana* [strain CBS 133850, GenBank PV273468.1; Identities = 662/772 (86 %), 11 gaps (1 %)]. No significant hits were obtained when the ***tef1*** (first part) sequence was used in blastn and megablast searches. Only *tef1* (second part) sequences are available for *Ijuhya* on GenBank. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ***tub2*** sequence had highest similarity to *Ijuhya faveliana* [strain CBS 133850, GenBank KY684190.1; Identities = 398/447 (89 %), three gaps (0 %)], *Ijuhya chilensis* [strain CBS 102803, GenBank KY684187.1; Identities = 458/520 (88 %), 10 gaps (1 %)], and *Ijuhya peristomialis* [strain CBS 569.76, GenBank KY684193.1; Identities = 369/420 (88 %), nine gaps (2 %)].

Supplementary material: doi: 10.6084/m9.figshare.30529955 (alignment and phylogenetic tree).

Colour illustrations: Jungle at Soberania National Park. Conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Ijuhya* ITS nucleotide alignment. Values > 74 % from the SH-aLRT test and bootstrap support values > 74 % 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. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Clonostachys subquaternata* (CBS 100003; GenBank NR_173191) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 29 strains including the outgroup; 777 characters including alignment gaps analysed: 280 distinct patterns, 181 parsimony-informative, 50 singleton sites, 546 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+I+G4. The scale bar shows the expected number of nucleotide substitutions per site.

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Dialonectria eutypellicola

Fungal Planet 1913 MB 861178

Dialonectria eutypellicola Mombert & Crous, *sp. nov.*

Etymology: Name refers to its ecology, occurring on *Eutypella* spp.

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

Ascomata crowded on live or dead stromata of *Eutypella prunastri*, in groups of 5–30, difficult to remove from substratum, subglobose to widely obpyriform, 220–360 µm high, 200–300 µm diam. (av. = 290 × 250 µm, n = 10), smooth, red to dark red, becoming purple in 5 % KOH and yellow in lactic acid, not collapsed or laterally pinched when dry. *Ascomatal surface* composed of cells of undefined shape, forming a textura epidermoidea. *Apex* obtuse, darker than perithecial venter, appearing nearly black when dry, composed of thick-walled, subglobose, ellipsoidal to narrowly clavate cells with orange wall. *Ascomatal wall* in vertical section 40–63 µm thick, of two regions; outer region 20–45 µm thick, composed of globose or subglobose to ellipsoidal, thick-walled cells with orange wall; inner region 10–18 µm composed of paler, flattened, thick-walled cells, gradually becoming thin-walled towards interior. *Asci* unitunicate, cylindrical to narrowly clavate, short-stipitate, 95–105 × 6.5–10 µm, 8-spored, attenuated at rounded to slightly flattened apex with a thickening, ascospores obliquely uniseriate; evanescent, narrowly moniliform paraphyses, interspersed between asci. *Ascospores* (10.4–)12.2–14.3(–15.1) × (5.7–)6.2–7.2(–7.8) µm (av. = 13.2 × 6.7 µm, n = 180), Q = (1.4–)2(–2.5), ellipsoidal, equally 1-septate, constricted at septum, thick-walled, hyaline at first, becoming pale golden brown at maturity, smooth, becoming verrucose. *Sporodochia* pale yellow to orange, giving rise to densely aggregated mycelium and chains of chlamydospores, subglobose, 8–12 µm diam. *Conidiogenous cells* solitary on hyphae, subcylindrical, hyaline, smooth, monophialidic, 5–40 × 2–3 µm, giving rise to micro- and macroconidia. *Macroconidia* hyaline, smooth, guttulate, slightly curved, 3(–7)-septate, apex subobtuse, basal cell obtuse, rarely with poorly developed foot-cell, (50–)58–65(–80) × (3–)3.5–4 µm; older conidia undergo microcyclic conidiation, giving rise to microconidia. *Microconidia* hyaline, smooth, subcylindrical, 0–1-septate, 5–30 × 2–3 µm. *Chlamydospores* solitary or in short chains, globose, hyaline to plate brown, but to 10 µm diam.

Culture characteristics: Colonies erumpent, spreading, with sparse aerial mycelium and folded surface with lobate margin, reaching 3 mm diam. after 2 wk at 25 °C. On MEA surface and reverse luteous. On PDA surface saffron to orange, reverse sienna. On OA surface pale luteous.

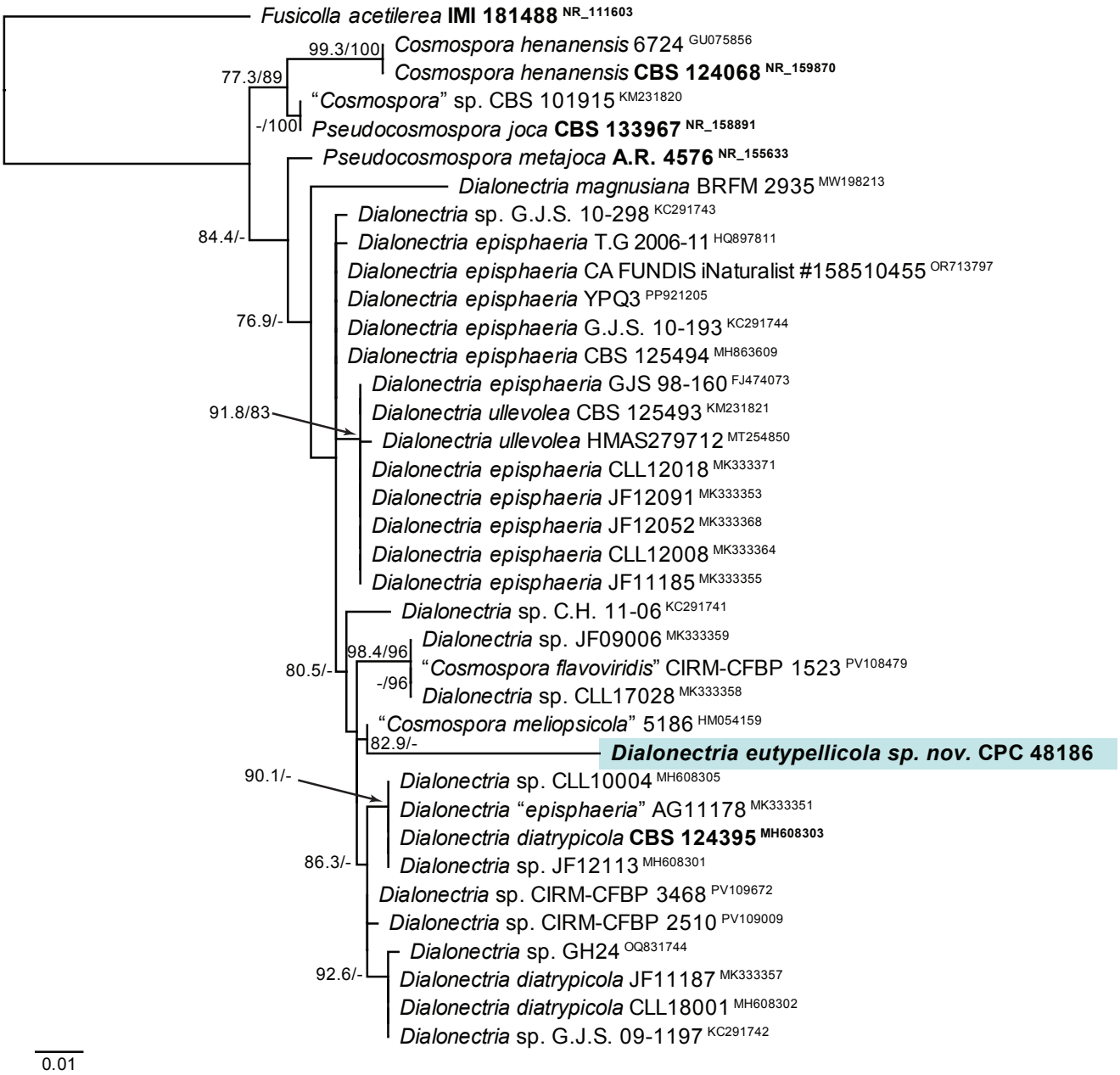
Typus: **France**, Côte d'Or, Marcilly-sur-Tille, étang de Marcilly, 47.51659°N, 5.14340°E, 269 m.a.s.l., on *Eutypella prunastri*, on branches of *Prunus spinosa,* 19 Mar. 2024, *A. Mombert*, CBNM0083 = HPC 4439 (**holotype** CBS H-25802, culture ex-type CPC 48186 = CBS 154477; ITS, LSU, *rpb1* and *tef1* (first part) sequences GenBank PX640128.1, PX640149.1, PX583879.1 and PX583883.1).

Notes: *Dialonectria* is a fungicolous genus in *Nectriaceae* that has fusarioid asexual morphs (Crous *et al.* 2021b). *Dialonectria eutypellicola* is phylogenetically closely related to *Dialonectria magnusiana* (BRFM 1591, on *Diatrypella* sp.), which has ascospores of similar dimensions, (12–)13–14(–15) × (5–)5.5–6.5(–7) µm, but shorter, 3-septate macroconidia, (26–)40–70 × 3–3.5 µm (Lechat *et al.* 2021a).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cosmospora meliopsicola* [strain 5186, GenBank HM054159.1; Identities = 498/527 (94 %), 10 gaps (1 %)], *Dialonectria episphaeria* [strain CBS 125494, GenBank MH863609.1; Identities = 497/527 (94 %), 10 gaps (1 %)], and *Dialonectria ullevolea* [strain CBS 125493, GenBank KM231821.1; Identities = 496/530 (94 %), 13 gaps (2 %)]. Closest hits using the **LSU** sequence are *Dialonectria magnusiana* [strain BRFM 1591, GenBank MW198210.1; Identities = 836/850 (98 %), no gaps], *Cosmospora meliopsicola* [strain 5186, GenBank HM042406.1; Identities = 836/851 (98 %), no gaps], and *Dialonectria episphaeria* [strain CBS 125494, GenBank KM231697.1; Identities = 814/829 (98 %), no gaps]. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ***rpb1*** sequence had highest similarity to *Dialonectria episphaeria* [strain G.J.S. 10-193, GenBank KC291892.1; Identities = 632/682 (93 %), one gap (0 %)], *Pseudocosmospora eutypae* [strain IMI 73016, GenBank KC291885.1; Identities = 601/685 (88 %), five gaps (0 %)], and *Cosmospora lavitskiae* [strain 7976, GenBank KU563622.1; Identities = 596/685 (87 %), five gaps (0 %)]. Based on a blastn search of NCBI's GenBank nucleotide database, the closest hits using the ***tef1*** (first part) sequence had highest similarity to *Cosmospora meliopsicola* [strain 5186, GenBank HM054068.1; Identities = 403/474 (85 %), 18 gaps (3 %)], *Dialonectria episphaeria* [strain CBS 125494, GenBank KM231953.1; Identities = 396/482 (82 %), 26 gaps (5 %)], and *Dialonectria ullevolea* [strain CBS 125493, GenBank KM231952.1; Identities = 391/477 (82 %), 24 gaps (5 %)].

Supplementary material: doi: 10.6084/m9.figshare.30529955 (alignment and phylogenetic tree).

Colour illustrations: Forest at Côte d'Or, Marcilly-sur-Tille. Conidiogenous cells giving rise to microconidia; microconidia; conidiogenous cells giving rise to macroconidia; macroconidia; chlamydospore; section through ascomata of *Eutypella prunastri*, with apical perithecia of *D. eutypellicola*; perithecia of *D. eutypellicola*; section through perithecial ascomatal wall; asci and ascospores. Scale bars: Section through ascomata of *E. prunastri* and *D. eutypellicola* = 300 µm, all others = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Dialonectria* ITS nucleotide alignment. Values > 74 % from the SH-aLRT test and bootstrap support values > 74 % 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. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Fusicolla acetilerea* (IMI 181488; GenBank NR_111603) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 37 strains including the outgroup; 504 characters including alignment gaps analysed: 100 distinct patterns, 36 parsimony-informative, 38 singleton sites, 430 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TNe+G4. The scale bar shows the expected number of nucleotide substitutions per site.

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Fusarium phoenicis

Fungal Planet 1914 MB 861179

Fusarium phoenicis Crous, Amirmijani & Pordel, ***sp. nov.***

Etymology: Named after the host genus on which it occurs, *Phoenix*.

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

Sporodochia on CLA pale yellow. *Sporodochial conidiophores* densely aggregated, irregularly and verticillately branched, typically producing dense whorls of 2–6 phialides; *sporodochial conidiogenous cells* monophialidic, subulate to doliiform, 9–12 × 4–5 µm, smooth- and thin-walled, with periclinal thickening and apical collarette. *Sporodochial conidia* falcate, widest in apical third, wedge-shaped, tapering toward the basal part; apical cell curved and papillate; basal cell foot-shaped, notch well developed, (3–)5-septate, hyaline, thin- and smooth-walled; 5-septate conidia (43–)45–50(–53) × 5–6 µm. *Chlamydospores* in chains, resembling hyphal swellings, ellipsoid, up to 8 µm diam, thick-walled, but subhyaline; older conidia also frequently developing swollen hyphal cells that appear chlamydospore-like.

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

Typus: **Iran**, Jiroft, roots of *Phoenix dactylifera* (*Arecaceae*), Oct. 2020, *A.R. Amirmijani & A. Pordel* (**holotype** CBS H-25803, culture ex-type IRJ47 = CPC 42150 = CBS 154466; ITS, *cmdA*, *rpb2* (first and second part) and *tef1* (first part) sequences GenBank PX640129.1, PX583872.1, PX583904.1 and PX583884.1).

Additional material examined: **Iran**, Manoojan, root of *P. dactylifera*, Nov. 2020, *A.R. Amirmijani & A. Pordel*, cultures IRJ42 = CPC 42106 = CBS 154464, IRJ03 = CPC 42145 = CBS 154465, IRJ50 = CPC 42153 = CBS 154468; Jiroft, root of *P. dactylifera*, Oct. 2020, *A.R. Amirmijani & A. Pordel*, culture IRJ49 = CPC 42152 = CBS 154467. ITS, *cmdA*, *rpb2* (first and second part) and *tef1* (first part) sequences GenBank PX640130– PX640133, PX583873– PX583876, PX583905– PX583908 and PX583885– PX583888.

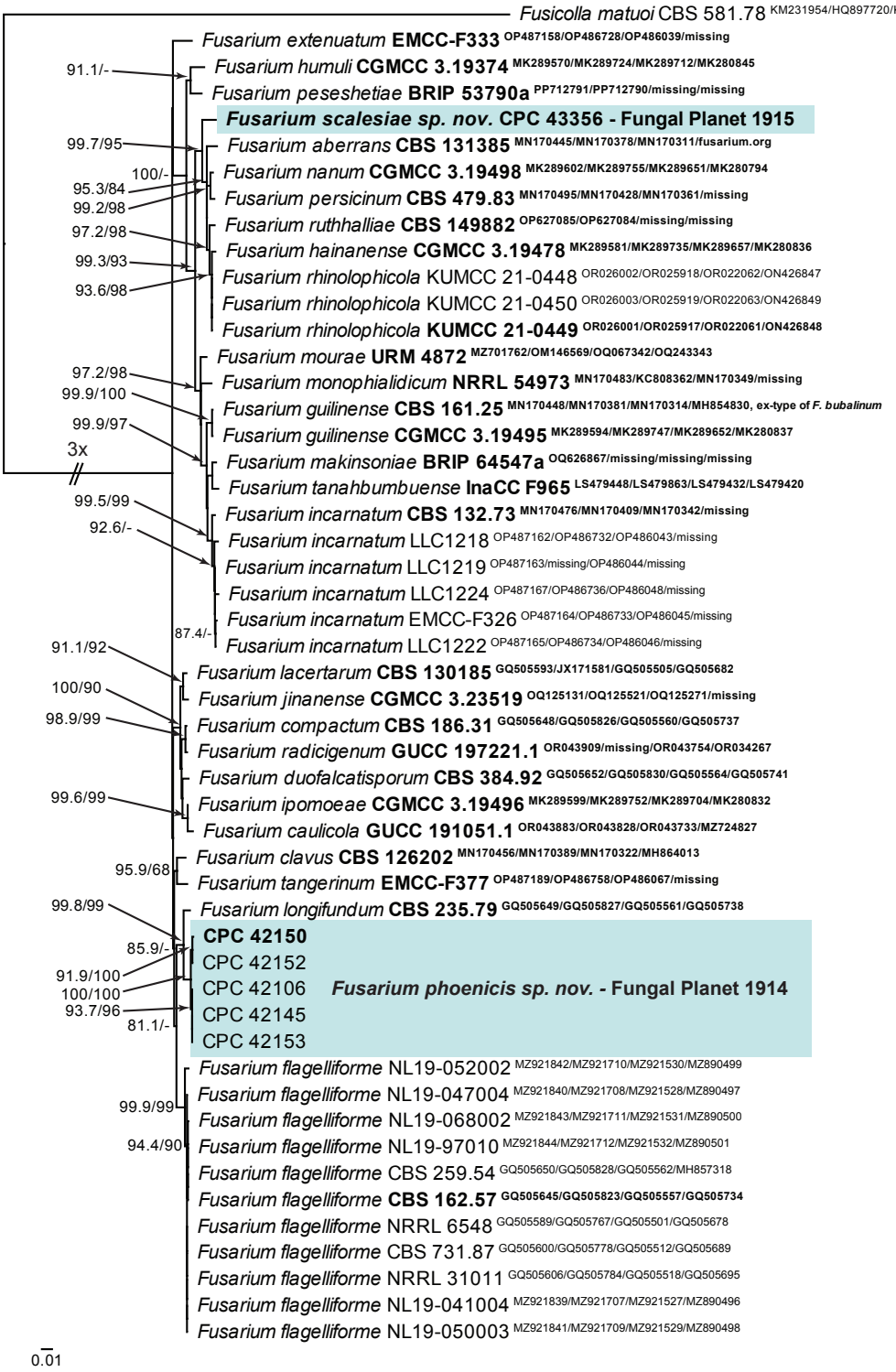
Notes: Fusarium wilt disease (or bayoud disease) is one of the most destructive diseases of date palm (*Phoenix dactylifera*) in the world, especially in date-producing countries in Africa, where it causes severe epidemics, and has killed millions of trees in the past century (Goudarzi 2023). Date palms are known to suffer from several *Fusarium* infections, including *F. oxysporum f. sp. albedinis* and *F. oxysporum f. sp. canariensis* (limited to xylem), while roots and leaves of declining date palms are linked to *F. annulatum* (as "*F. proliferatum*"; Yilmaz *et al.* 2021), and *Neocosmospora solani* (as *"F." solani*) (Mansoori & Kord 2006).

Fusarium phoenicis is yet another species linked to root disease of date palms. It represents a new species in the *Fusarium incarnatum-equiseti* species complex (FIESC), being closely related to *F. longifundum* (CBS 235.79), which has (3–)5(–6)-septate macroconidia (longer than in *F. phoenicis*) with elongated, or whip-like curved apical cells (more elongated than in *F. phoenicis*) and more prominently extended basal cells (Xia *et al.* 2019).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 42150 had highest similarity to *Fusarium equiseti* [strain CC1-3, GenBank MT428184.1; Identities = 525/525 (100 %), no gaps], *Fusarium incarnatum* [strain F361, GenBank MW995840.1; Identities = 525/525 (100 %), no gaps], and *Fusarium ipomoeae* [strain GZAX 312, GenBank ON961780.1; Identities = 525/525 (100 %), no gaps]. The ITS sequence of CPC 42150 differs 0–1 nucleotide from those of CPC 42106, 42145, 42152 and 42153. Closest hits using the ***cmdA*** sequence of CPC 42150 had highest similarity to *Fusarium* sp. [strain Feq 2_14 c6, GenBank MK937882.1; Identities = 556/557 (99 %), no gaps], *Fusarium longifundum* [strain NRRL 36372, GenBank GQ505561.1; Identities = 565/576 (98 %), no gaps], and *Fusarium brevicaudatum* [strain NRRL 43638, GenBank GQ505576.1; Identities = 561/576 (97 %), no gaps]. The *cmdA* sequence of CPC 42150 differs 0–5 nucleotides from those of CPC 42106, 42145, 42152 and 42153. Closest hits using the ***rpb2*** (first part) sequence of CPC 42150 had highest similarity to *Fusarium clavus* [as *Fusarium clavum*; strain 34, GenBank PP831790.1; Identities = 934/945 (99 %), no gaps], *Fusarium equiseti* [strain TP-001, GenBank PP266450.1; Identities = 908/919 (99 %), no gaps], and *Fusarium flagelliforme* [strain MFG 80215, GenBank OR727726.1; Identities = 930/945 (98 %), no gaps]. The *rpb2* (first part) sequence of CPC 42150 differs two nucleotides from those of CPC 42106, 42145, 42152 and 42153. Closest hits using the ***rpb2*** (second part) sequence of CPC 42150 had highest similarity to *Fusarium clavus* [as *Fusarium clavum*; strain EeR24, GenBank OP293705.1; Identities = 912/928 (98 %), no gaps], *Fusarium ipomoeae* [strain ZJUE1552, GenBank PX130440.1; Identities = 906/922 (98 %), no gaps], and *Fusarium lacertarum* [strain 21BY016, GenBank OR174777.1; Identities = 892/908 (98 %), no gaps]. The *rpb2* (second part) sequence of CPC 42150 differs one nucleotide from those of CPC 42106, 42145, 42152 and 42153. Closest hits using the ***tef1*** (first part) sequence of CPC 42150 had highest similarity to *Fusarium equiseti* [strain FSS6, GenBank ON381738.1; Identities = 529/529 (100 %), no gaps], *Fusarium longifundum* [strain QJ513112, GenBank PQ348091.1; Identities = 610/611 (99 %), no gaps], and *Fusarium neoscirpi* [as *Fusarium scirpi*; strain NRRL 26922, GenBank GQ505601.1; Identities = 593/611 (97 %), no gaps]. The *tef1* (first part) sequence of CPC 42150 differs 0–1 nucleotide from those of CPC 42106, 42145, 42152 and 42153.

Supplementary material: doi: 10.6084/m9.figshare.30529955 (alignment and phylogenetic tree).

Colour illustrations: Dying *Phoenix dactylifera* in Iran. Sporodochia on SNA; conidiogenous cells giving rise to conidia; conidia; chlamydospores. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Fusarium incarnatum-equiseti* species complex (FIESC) *tef1-rpb2-cmdA*-ITS nucleotide alignment. Values > 74 % from the SH-aLRT test and bootstrap support values > 74 % 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. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Fusicolla matuoi* (CBS 581.78; GenBank KM231954/HQ897720/KM231405/KM231822) and the novelties described here are highlighted with coloured blocks and **bold** font. The root branch was shortened to facilitate layout. Alignment statistics: 51 strains including the outgroup; 2723 characters including alignment gaps analysed: 673 distinct patterns, 254 parsimony-informative, 541 singleton sites, 1928 constant sites. The best-fit models identified in IQ-TREE using the TESTNEW option were: *tef1* (1–716): TIM2e+G4; *rpb2* (717–1553): K2P+I; *cmdA* (1554–2210): TNe+G4; ITS (2211–2723): JC. The scale bar shows the expected number of nucleotide substitutions per site.

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Fusarium scalesiae

Fungal Planet 1915 MB 861180

Fusarium scalesiae Crous, ***sp. nov.***

Etymology: Named after the host genus on which it occurs, *Scalesia*.

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

Sporodochia on CLA pale yellow, on MEA and OA orange. *Sporodochial conidiophores* densely aggregated, irregularly and verticillately branched, typically producing dense whorls of 2–6 phialides; *sporodochial conidiogenous cells* monophialidic, subulate to doliiform, 8–12 × 3–4 µm, smooth- and thin-walled, with periclinal thickening and apical collarette. *Sporodochial conidia* straight to falcate, tapering toward the basal part, moderately curved; apical cell subobtuse, curved; basal cell foot-shaped, notch poorly developed, (3–)5-septate, hyaline, thin- and smooth-walled; 3-septate conidia 30–36 × 3–3.5 µm; 5-septate conidia (37–)40–45(–47) × (3.5–)4(–5) µm. *Chlamydospores* not observed but hyphal swellings seen.

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

Typus: **Ecuador**, Galapagos Islands, San Cristobal Island, evergeen seasonal forest in the agricultural zone in the highlands, 423 m.a.s.l., on *Scalesia pedunculata* (*Asteraceae*), 20 May 2021, *D.A. Ortiz*, HPC 3918 = S13-HZ2 (**holotype** CBS H-25804; culture ex-type CPC 43356 = CBS 154472; ITS, *cmdA*, *rpb2* (first and second part) and *tef1* (first part) sequences GenBank PX640134.1, PX583877.1, PX583909.1 and PX583889.1).

Notes: *Fusarium scalesiae* is a new species in the *Fusarium incarnatum-equiseti* species complex, being closely related to *F. aberrans*, which is distinct in having mono- and polyphialides with aerial macroconidia (sporodochia not observed), (1–)3–5-septate macroconidia, and apical cells that are only slightly curved (Xia *et al.* 2019). Furthermore, colonies are also distinct, being pale yellow to yellow with yellow diffusible pigment (on PDA). *Fusarium scalesiae* is also related to *F. nanum* (macroconidia 3-septate, 20.5–32 × 3–5 µm, with bluntly rounded apical cell and poorly developed foot-shaped basal cell; Wang *et al.* 2019), and *F. persicinum* (macroconidia 3–5-septate, 3-septate conidia (26–)31–41(–44) × 4–6 µm, 5-septate conidia (39–)43–49(–54) × 5–6 µm, with conical to slightly papillate apical cell and a blunt to barely notched basal cell; Xia *et al.* 2019), from which it is morphologically and phylogentically distinct. Cultures of *F. scalesiae* formed purple-black ascomatal initials on MEA, but these remained sterile.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Fusarium aberrans* [strain IHEM 05042, GenBank OW983647.1; Identities = 511/511 (100 %), no gaps], *Fusarium equiseti* [strain U_13, GenBank OM899950.1; Identities = 511/511 (100 %), no gaps], and *Fusarium incarnatum* [strain IHEM 26632, GenBank OW987882.1; Identities = 511/511 (100 %), no gaps]. Closest hits using the ***cmdA*** sequence had highest similarity to *Fusarium hainanense* [strain LC13701, GenBank MW574193.1; Identities = 531/535 (99 %), no gaps], *Fusarium aberrans* [strain CBS 131385, GenBank MN170311.1; Identities = 531/535 (99 %), no gaps], and *Fusarium equiseti* [strain Indo161, GenBank LS479428.1; Identities = 531/535 (99 %), no gaps].Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Fusarium hainanense* [strain LC11638, GenBank MK289735.1; Identities = 715/721 (99 %), no gaps], *Fusarium incarnatum* [strain 174012-1, GenBank ON693004.1; Identities = 715/721 (99 %), no gaps], and *Fusarium sylviaearleae* [strain BRIP 76083a, GenBank PQ862372.1; Identities = 715/721 (99 %), no gaps]. Closest hits using the ***rpb2*** (second part) sequence had highest similarity to *Fusarium equiseti* [voucher URM 6776, GenBank LS398492.1; Identities = 775/784 (99 %), no gaps], *Fusarium guilinense* [strain LC12160, GenBank MK289747.1; Identities = 775/784 (99 %), no gaps], and *Fusarium tanahbumbuense* [strain NRRL 34005, GenBank GQ505807.1; Identities = 775/784 (99 %), no gaps]. Closest hits using the ***tef1*** (first part) sequence had highest similarity to *Fusarium hainanense* [strain 28C, GenBank MT239029.1; Identities = 624/652 (96 %), three gaps (0 %)], *Fusarium incarnatum* [strain F80MC4-21, GenBank PQ760394.1; Identities = 634/664 (95 %), three gaps (0 %)], and *Fusarium aberrans* [strain FC19c pod, GenBank OQ448930.1; Identities = 645/676 (95 %), five gaps (0 %)].

For phylogenetic tree, see *Fusarium phoenicis* (FP 1914).

Colour illustrations: San Cristobal Island. Sporodochia starting to form on SNA; conidiogenous cells giving rise to conidia; conidia; conidia and hyphal swellings. Scale bars = 10 µm.

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Fusarium cristobalense

Fungal Planet 1916 MB 861181

Fusarium cristobalense Crous, ***sp. nov.***

Etymology: Named after San Cristobal Island, where this species was collected.

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

Sporodochia on CLA pale yellow to orange. *Sporodochial conidiophores* densely aggregated, irregularly and verticillately branched, typically producing dense whorls of 2–4 phialides; *sporodochial conidiogenous cells* monophialidic, subcylindrical, 17–22 × 4(–5) µm, smooth- and thin-walled, with periclinal thickening and apical collarette. *Sporodochial conidia* falcate, tapering toward the basal part, moderately curved; apical cell hooked and papillate; basal cell foot-shaped, notch poorly to well developed, 3(–6)-septate, hyaline, thin- and smooth-walled; 3-septate conidia (45–)50–60(–65) × 5(–6) µm; 6-septate conidia up to 85 µm long. *Chlamydospores* occurring in chains, brown, subglobose, 10–15 µm diam.

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

Typus: **Ecuador**, Galapagos Islands, San Cristobal Island, on the volcanic cliffs close to shore at Via las Negritas towards Jardin de las Opuntias, on *Scalesia gordilloi* (*Asteraceae*), 17 m.a.s.l., 20 May 2021, *D.A. Ortiz*, HPC 3911 = S7-AZ1 (**holotype** CBS H-25805; culture ex-type CPC 43352 = CBS 154470; ITS, *cmdA*, *rpb2* (first and second part), *tef1* (first part) and *tub2* sequences GenBank PX640135.1, PX583878.1, PX583910.1, PX583890.1 and PX583901.1).

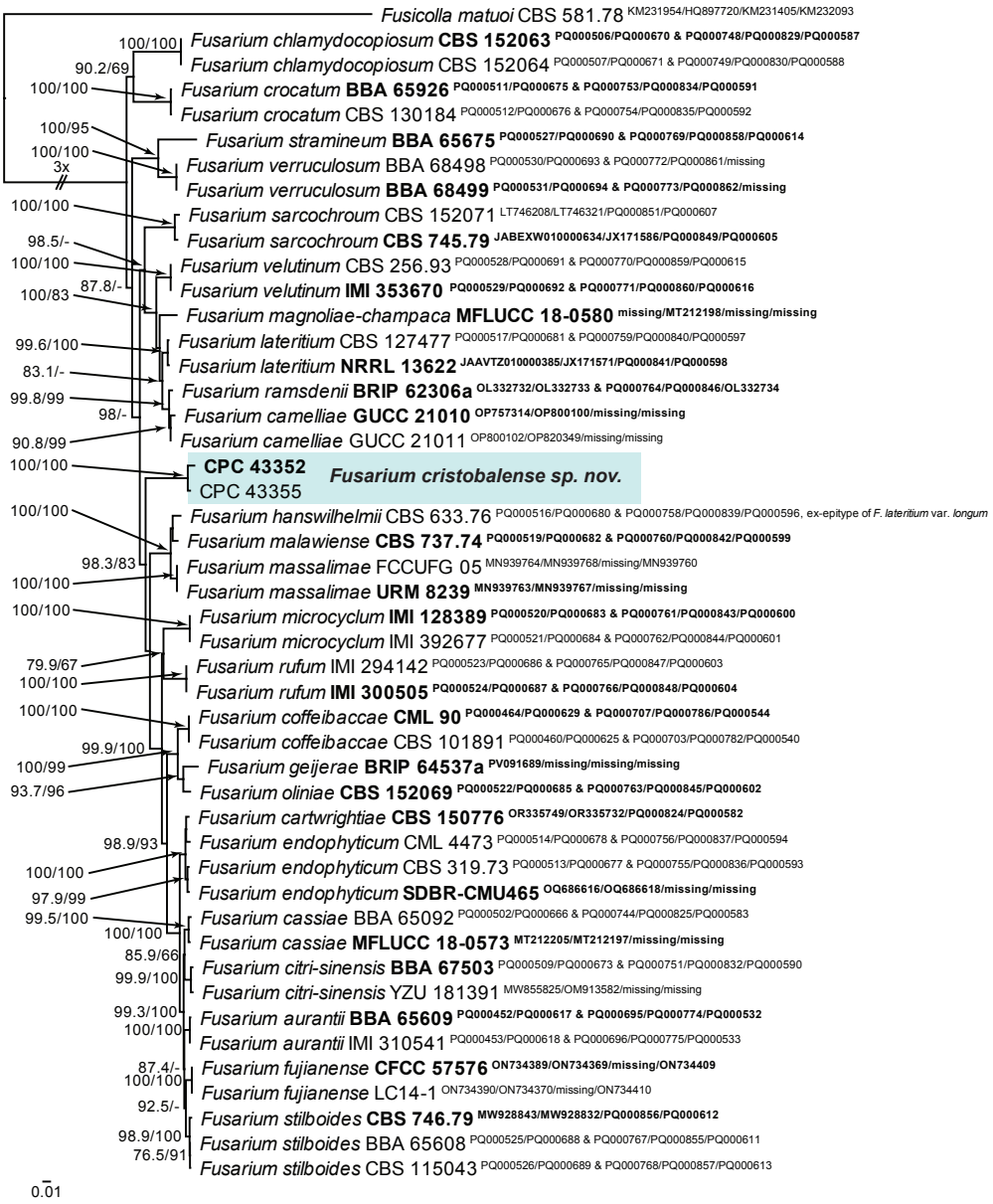
Additional material examined: **Ecuador**, Galapagos Islands, San Cristobal Island, mixed forest in the agricultural area in the highlands on *Scalesia pedunculata* (*Asteraceae*), 217 m.a.s.l., 20 May 2021, *D.A. Ortiz*, HPC 3913 = S9-HZ2 (culture CPC 43355 = CBS 154471; ITS, *rpb2* (first and second part), *tef1* (first part) and *tub2* sequences GenBank PX640136.1, PX583911.1, PX583891.1 and PX583902.1).

Notes: *Fusarium cristobalense* is a new species in the *Fusarium lateritium* species complex (FLSC). Species in the FLSC are known to have wide geographic distributions, broad host ranges, and vary from being plant pathogenic to endophytic. *Fusarium cristobalense* clusters as a separate lineage between the *F. lateritium* and *F. hanswilhelmii* subclades. The FLSC has recently been revised by Costa *et al.* (2024).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 43352 had highest similarity to *Fusarium lateritium* [strain FS138, GenBank OR538707.1; Identities = 516/533 (97 %), three gaps (0 %)], *Fusarium hanswilhelmii* [strain CBS 633.76, GenBank NR_197853.1; Identities = 516/534 (97 %), four gaps (0 %)], and *Fusarium citri* [strain JZB3110472, GenBank PQ363039.1; Identities = 513/533 (96 %), four gaps (0 %)]. The ITS sequences of CPC 43352 and 43355 are 99 % similar (529/531 nt, one gap). Closest hits using the ***cmdA*** sequence of CPC 43352 had highest similarity to *Fusarium malawiense* [strain CBS 737.74, GenBank PQ000842.1; Identities = 506/550 (92 %), nine gaps (1 %)], *Fusarium hanswilhelmii* [strain CBS 633.76, GenBank PQ000839.1; Identities = 505/550 (92 %), nine gaps (1 %)], and *Fusarium stilboides* [strain BBA 65608, GenBank PQ000855.1; Identities = 504/550 (92 %), 11 gaps (2 %)]. Closest hits using the ***rpb2*** (first part) sequence of CPC 43352 had highest similarity to *Fusarium lateritium* [strain QJ-B-4, GenBank OR237571.1; Identities = 822/889 (92 %), four gaps (0 %)], *Fusarium coffeibaccae* [as *Fusarium stilboides*; strain NRRL 20429, GenBank JX171582.1; Identities = 805/873 (92 %), no gaps], and *Fusarium sarcochroum* [strain NRRL 20472, GenBank JX171586.1; Identities = 803/874 (92 %), two gaps (0 %)]. The *rpb2* (first part) sequences of CPC 43352 and 43355 are 99 % similar (751/754 nt, no gaps). Closest hits using the ***rpb2*** (second part) sequence of CPC 43352 had highest similarity to *Fusarium ramsdenii* [strain CBS 150771, GenBank PQ000764.1; Identities = 761/797 (95 %), no gaps], *Fusarium velutinum* [strain CBS 256.93, GenBank PQ000770.1; Identities = 759/797 (95 %), no gaps], and *Fusarium lateritium* [strain CBS 127477, GenBank PQ000759.1; Identities = 758/797 (95 %), no gaps]. The *rpb2* (second part) sequences of CPC 43352 and 43355 are 99 % similar (866/868 nt, no gaps). Closest hits using the ***tef1*** (first part) sequence of CPC 43352 had highest similarity to *Fusarium malawiense* [strain CBS 737.74, GenBank PQ000519.1; Identities = 636/676 (94 %), nine gaps (1 %)], *Fusarium lateritium* [strain 121B PP2, GenBank OR553060.1; Identities = 643/685 (94 %), one gap (0 %)], and *Fusarium coffeibaccae* [strain CBS 178.31, GenBank PQ000458.1; Identities = 631/674 (94 %), one gap (0 %)]. The *tef1* (first part) sequences of CPC 43352 and 43355 are 99 % similar (676/684 nt, one gap). Closest hits using the ***tub2*** sequence of CPC 43352 had highest similarity to *Fusarium velutinum* [strain IMI 353670, GenBank PQ000616.1; Identities = 503/532 (95 %), nine gaps (1 %)], *Fusarium lateritium* [strain NRRL 13622, GenBank PQ000598.1; Identities = 499/532 (94 %), 12 gaps (2 %)], and *Fusarium ramsdenii* [strain BRIP 62306a, GenBank OL332734.1; Identities = 497/535 (93 %), 15 gaps (2 %)]. The *tub2* sequences of CPC 43352 and 43355 are identical (524/524 nt, no gaps).

Supplementary material: doi: 10.6084/m9.figshare.30529955 (alignment and phylogenetic tree).

Colour illustrations: *Scalesia pedunculata* on San Cristobal Island (photo credit Gonzalo Rivas). Sporodochia on SNA; conidiogenous cells giving rise to conidia; conidia; chlamydospores. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Fusarium lateritium* species complex (FLSC) *tef1-rpb2-cmdA-tub2* nucleotide alignment. Values > 74 % from the SH-aLRT test and bootstrap support values > 74 % 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. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Fusicolla matuoi* (CBS 581.78; GenBank KM231954/HQ897720/KM231405/KM232093) and the novelty described here is highlighted with a coloured block and **bold** font. The root branch was shortened to facilitate layout. Alignment statistics: 47 strains including the outgroup; 3515 characters including alignment gaps analysed: 1268 distinct patterns, 844 parsimony-informative, 373 singleton sites, 2298 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: *tef1* (1–706): TIM2e+G4; *rpb2* (707–2339): TNe+I+G4; *cmdA* (2340–2973): TNe+G4; *tub2* (2974–3515): TPM2+G4. The scale bar shows the expected number of nucleotide substitutions per site.

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Neocosmospora duolechatii

Fungal Planet 1917 MB 861182

Neocosmospora duolechatii J. Fourn. & Crous, ***sp. nov.***

Etymology: Name refers to Christian Lechat († 7 January 2022) who collected this species; duo- refers to the second *Neocosmospora* sp. on the same specimen.

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

Sporodochia on CLA pale yellow. *Sporodochial conidiophores* densely aggregated, irregularly and verticillately branched, typically producing dense whorls of 2–4 phialides; *sporodochial conidiogenous cells* monophialidic, subulate to subcylindrical, 13–25 × 4.5–6 µm, smooth- and thin-walled, with periclinal thickening and apical collarette. *Sporodochial conidia* falcate, sides parallel, moderately curved; apical cell slightly curved, subobtuse; basal cell obtuse to having a poorly developed foot cell, (4–)5-septate, hyaline, thin- and smooth-walled; 5-septate conidia (50–)55–60(–65) × 7(–8) µm. *Chlamydospores* not observed.

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

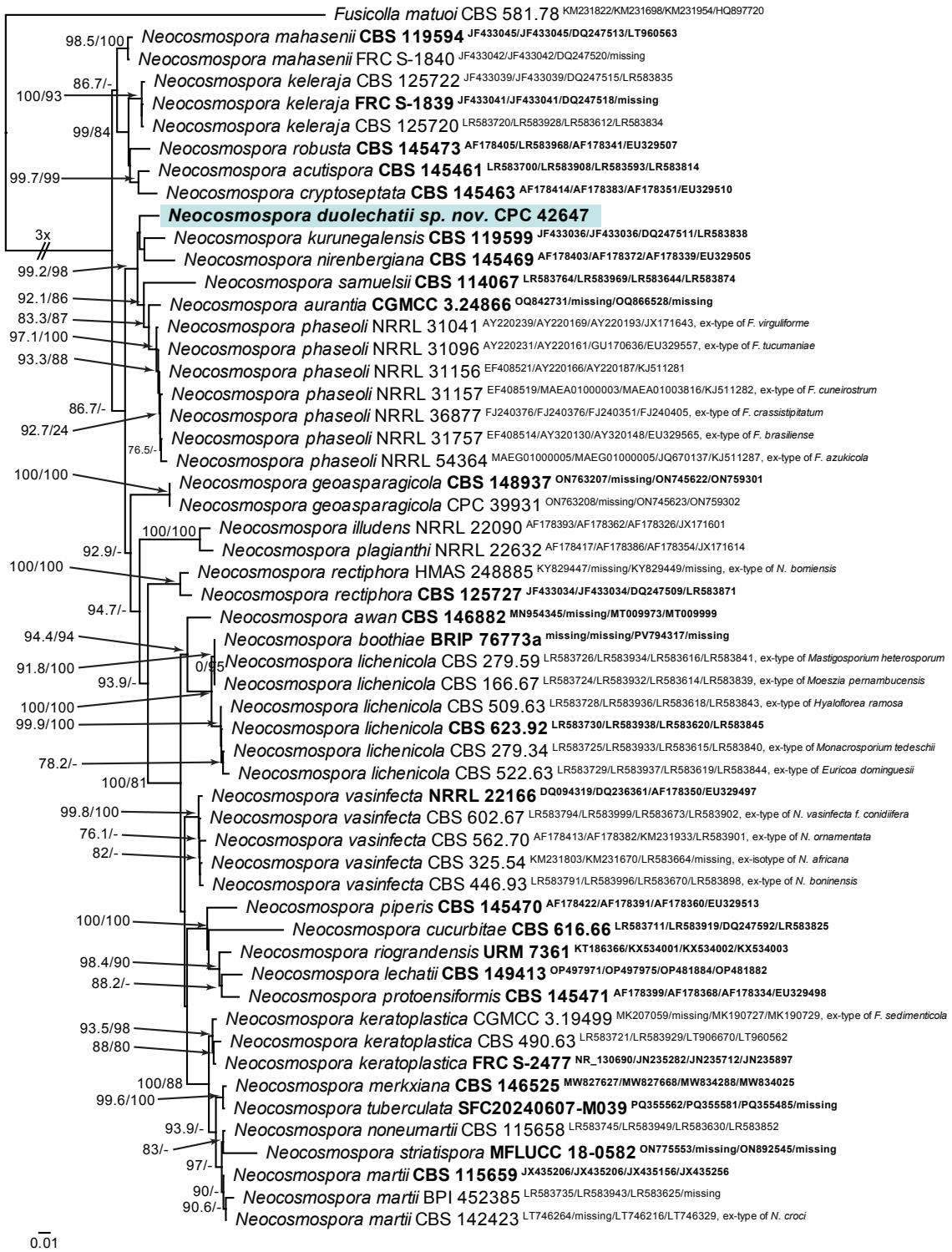
Typus: **French Guiana**, Saül, Gros Arbres trail, on dead bark of *Bauhinia* sp., 26 Mar. 2021, *C. Lechat* (**holotype** CBS H-25806, culture ex-type CLLG21056-b = CPC 42647 = CBS 154469; ITS, *rpb2* (first and second part) and *tef1* (first part) sequences GenBank PX640137.1, PX583912.1 and PX583892.1).

Notes: Sandoval-Denis *et al.* (2022) described *Neocosmospora lechatii* (CBS 149413 = CLLG21062 = CPC 42648) from a specimen collected in French Guiana. As it turns out, a second culture from the same specimen (CLLG21056-b = CPC 42647 = CBS 154469) represents a second new species, described here as *N. duolechatii*. *Neocosmospora lechatii* has falcate, gently dorsiventrally curved, 5–9-septate sporodochial conidia with well developed foot-cells, 0(1)-septate, ovoid to ellipsoid microconidia and chains of spherical chlamydospores (Sandoval-Denis *et al.* 2022). In contrast, the phylogenetically distinct *N. duolechatii* has falcate, moderately curved (4–)5-septate sporodochial macroconidia with parallel sides and poorly developed foot cells, and lacks chlamydospores and microconidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neocosmospora solani* [as *Fusarium solani*; strain MAL45, GenBank OM503007.1; Identities = 533/546 (98 %), three gaps (0 %)], *Neocosmospora phaseoli* [as *Fusarium virguliforme*; strain PPRI13434, GenBank KF648835.1; Identities = 533/546 (98 %), three gaps (0 %)], and *Neocosmospora acutispora* [as *Fusarium acutisporum*; strain NRRL 22574, GenBank NR_169884.1; Identities = 532/545 (98 %), two gaps (0 %)]. Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Neocosmospora cryptoseptata* [as *Fusarium cryptoseptatum*; strain NRRL 22412, GenBank EU329510.1; Identities = 773/808 (96 %), no gaps], *Neocosmospora aurantia* [strain 10053, GenBank OQ866523.1; Identities = 731/767 (95 %), no gaps], and *Neocosmospora robusta* [as *Fusarium venezuelense*; strain NRRL 22395, GenBank EU329507.1; Identities = 763/803 (95 %), no gaps]. Closest hits using the ***rpb2*** (second part) sequence had highest similarity to *Neocosmospora kurunegalensis* [as *Fusarium kurunegalense*; strain CBS 119599, GenBank LR583838.1; Identities = 752/770 (98 %), no gaps], *Neocosmospora phaseoli* [as *Fusarium phaseoli*; strain NRRL 22276, GenBank EU329500.1; Identities = 805/839 (96 %), no gaps], and *Neocosmospora phaseoli* [as *Fusarium tucumaniae*; strain NRRL 31096, GenBank GU170616.1; Identities = 805/839 (96 %), no gaps]. Closest hits using the ***tef1*** (first part) sequence had highest similarity to *Neocosmospora phaseoli* [as *Fusarium brasiliense*; strain F_16_38, GenBank MH541848.1; Identities = 609/627 (97 %), two gaps (0 %)], *Neocosmospora phaseoli* [as *Fusarium tucumaniae* strain NRRL 31776, GenBank AY320152.1; Identities = 652/673 (97 %), four gaps (0 %)], and *Neocosmospora phaseoli* [as *Fusarium virguliforme* strain PPRI13438, GenBank KF648847.1; Identities = 658/681 (97 %), four gaps (0 %)].

Supplementary material: doi: 10.6084/m9.figshare.30529955 (alignment and phylogenetic tree).

Colour illustrations: Jungle at Gros Arbres trail, French Guiana (photo credit Jacques Fournier). Sporodochia starting to form on SNA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Neocosmospora* ITS-LSU-*tef1*-*rpb2* nucleotide alignment. Values > 74 % from the SH-aLRT test and bootstrap support values > 74 % 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. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Fusicolla matuoi* (CBS 581.78; GenBank KM231822/KM231698/KM231954/HQ897720) and the novelty described here is highlighted with a coloured block and **bold** font. The root branch was shortened to facilitate layout. Alignment statistics: 55 strains including the outgroup; 2517 characters including alignment gaps analysed: 836 distinct patterns, 457 parsimony-informative, 284 singleton sites, 1776 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: ITS (1–548): TIM2e+R3; LSU (549–1032): TNe+I+R2; *tef1* (1033–1717): TIM2+F+I+R2; *rpb2* (1718–2517): TNe+I+G4. The scale bar shows the expected number of nucleotide substitutions per site.

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Stylonectria stoeckliana

Fungal Planet 1918 MB 861183

Stylonectria stoeckliana Mombert & Crous, ***sp. nov.***

Etymology: Named in honour of Elisabeth Stöckli, Swiss mycologist, for her contribution to the knowledge of ascomycetes, and for organizing the Ascomycete days in Tramelan (Jura, Switzerland), where the species was collected.

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

Ascomata perithecial, gregarious, in groups of 2–8, or solitary, erumpent to superficial with base remaining immersed in a hypostroma of fusarium-like sporodochia, arising from dead pseudostromata of *Cytospora* sp., broadly pyriform, 202–288 µm high, 156–208 µm wide. (av. 245 × 182 µm, n = 6), with a discoid papilla, red to dark red, becoming darker in 3 % KOH, yellow in lactic acid, collapsing when dry. *Ascomatal wall* smooth, 14–22 um thick, composed of two regions: outer region 11–14 µm thick, of irregularly shaped cells of textura intricata to textura epidermoidea; inner region 3–7 µm thick of thin-walled, flattened cells of textura prismatica to textura angularis. *Asci* unitunicate, subcylindrical, 74–88 × 5.5–8.5 µm, 8-spored, apices rounded and simple, uniseriate; evanescent, narrowly moniliform paraphyses, interspersed between asci. *Ascospores* ellipsoidal, 1-septate, often constricted at septum, (10.4–)11.4–13.1(–13.5) × (4.9–)5.1–5.8(–5.9) µm, (av. = 12.4 × 5.4 µm, n = 20), (Q = 1.9–2.3–2.6), smooth to faintly spinulose, ornamentation often inconspicuous, thick-walled, hyaline at first, becoming pale golden brown at maturity. *Sporodochia* on CLA pale yellow to orange, frequently erect, almost synnematal due to the intercalary conidiogenous cells. *Sporodochial conidiophores* densely aggregated, irregularly and verticillately branched, typically producing dense whorls of 2–4 phialides; *sporodochial conidiogenous cells* monophialidic, subulate to subcylindrical, 20–30 × 2.5–3 µm, smooth- and thin-walled, with periclinal thickening and apical collarette. *Sporodochial conidia* falcate, subcylindrical, moderately curved; apical cell subobtuse; basal cell subobtuse, rarely to having a poorly developed foot cell, 1-septate, hyaline, thin- and smooth-walled; 1-septate conidia (30–)40–46(–60) × (2.5–)3 µm. *Chlamydospores* not observed.

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

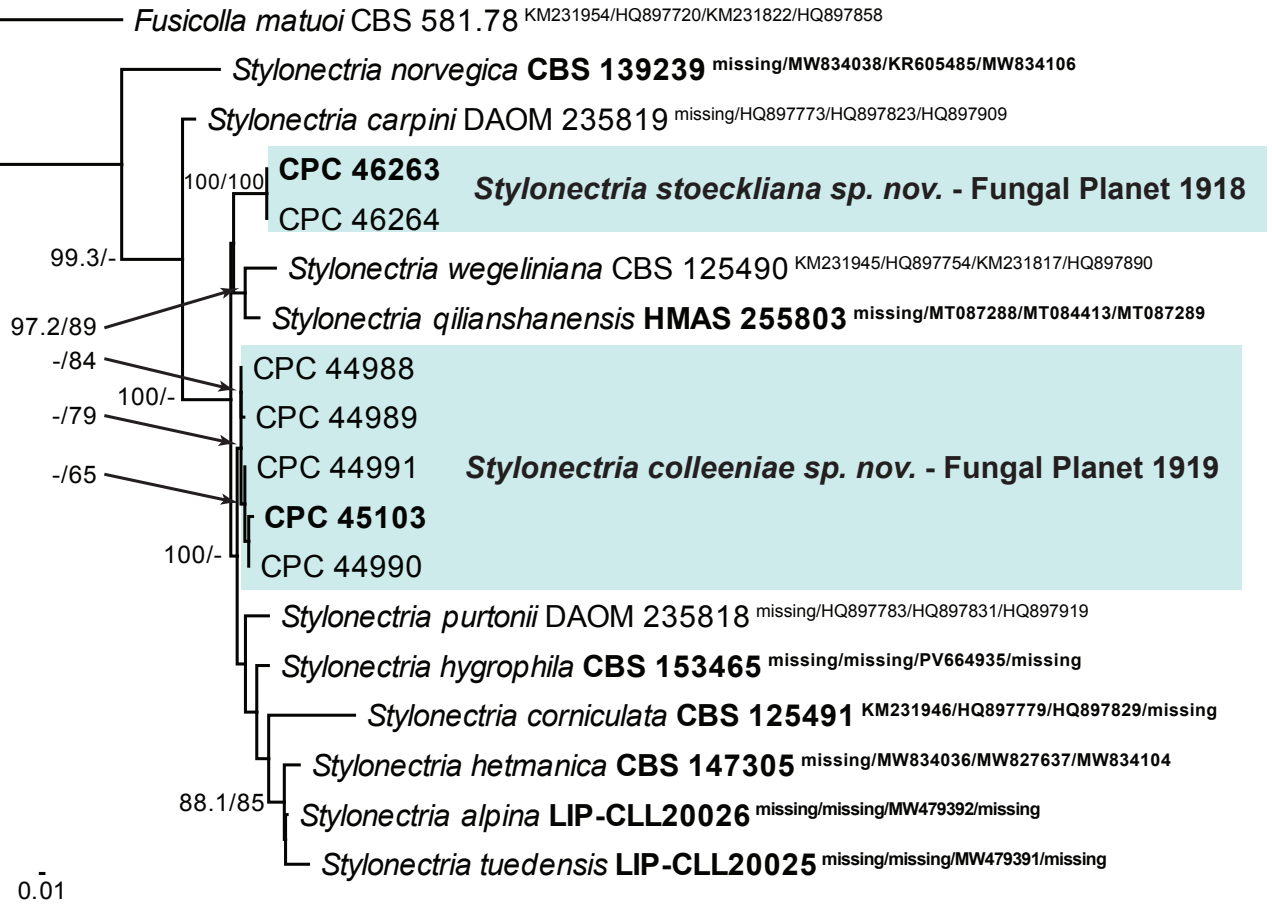
Typus: **Switzerland**, Canton of Jura, St-Brais, 47.288554°N, 7.104132°E, 835 m.a.s.l., on *Cytospora* sp. (sexual morph) on twigs of *Salix* sp. (*Salicaceae*), 3 Jun. 2023, *A. Mombert*, AM2306032 = HPC 4206 (**holotype** CBS H-25807, culture ex-type CPC 46263 = CBS 154475; ITS, *rpb2* (first and second part) and *tef1* (first part) sequences GenBank PX640138.1, PX583913.1 and PX583893.1); culture CPC 46264 = CBS 154476; ITS, *rpb2* (first and second part) and *tef1* (first part) sequences GenBank PX640139.1, PX583914.1 and PX583894.1.

Notes: Several fungicolous species previously assigned to *Cosmospora*, *Dialonectria*, and *Nectria* are presently accommodated in *Stylonectria* (based on *S. applanata*). *Stylonectria* is characterised by having nectria-like perithecia that occur on old stromata of black pyrenomycetes, and fusarioid asexual morphs. Species are regarded as host specific to the fungi on which they occur, which in turn may be specific to the plant host (Gräfenhan *et al.* 2011). *Stylonectria stoeckliana* is closely related to *S. wegeliniana* (CBS 125490), which produces both micro- and macroconidia in culture, has larger ascomata, 300–450 µm high, 250–350 µm wide, and larger ascospores, 15–18 × 7.5–9 µm (Lechat *et al.* 2021b).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to an uncultured fungus from irrigation water from a pond in Lithuania [clone 4248_279, GenBank MT236487.1; Identities = 535/535 (100 %), no gaps], *Stylonectria carpini* [strain DAOM 235819, GenBank HQ897823.1; Identities = 518/535 (97 %), five gaps (0 %)], and *Stylonectria qilianshanensis* [strain HMAS 255803, GenBank NR_173913.1; Identities = 496/513 (97 %), five gaps (0 %)]. The ITS sequences of CPC 46263 and 46264 are identical (517/517 nt, no gaps). Closest hits using the ***rpb2*** (first part) sequence had highest similarity to *Stylonectria qilianshanensis* [strain 12155, GenBank MT087288.1; Identities = 731/768 (95 %), no gaps], *Thelonectria applanata* [strain CBS 125489, GenBank HQ897739.1; Identities = 764/815 (94 %), no gaps], and *Stylonectria wegeliniana* [strain CBS 125490, GenBank HQ897754.1; Identities = 759/813 (93 %), no gaps]. The *rpb2* (first part) sequences of CPC 46263 and 46264 are identical (815/815 nt, no gaps). Closest hits using the ***rpb2*** (second part) sequence had highest similarity to *Stylonectria carpini* [strain DAOM 235819, GenBank HQ897773.1; Identities = 808/867 (93 %), no gaps], *Stylonectria purtonii* [strain DAOM 235818, GenBank HQ897783.1; Identities = 767/828 (93 %), no gaps], and *Stylonectria wegeliniana* [strain CBS 125490, GenBank HQ897754.1; Identities = 797/867 (92 %), no gaps]. The *rpb2* (second part) sequences of CPC 46263 and 46264 are identical (867/867 nt, no gaps). Closest hits using the ***tef1*** (first part) sequence had highest similarity in a blastn search to *Stylonectria wegeliniana* [strain CBS 125490, GenBank KM231945.1; Identities = 384/441 (87 %), four gaps (0 %)], *Neonectria obtusispora* [strain CBS 183.36, GenBank JF735796.1; Identities = 469/641 (73 %), 60 gaps (9 %)], and *Scolecofusarium ciliatum* [strain CBS 155.86, GenBank MW834295.1; Identities = 392/511 (77 %), 35 gaps (6 %)]. The *tef1* (first part) sequences of CPC 46263 and 46264 are identical (638/638 nt, no gaps).

Supplementary material: doi: 10.6084/m9.figshare.30529955 (alignment and phylogenetic tree).

Colour illustrations: Forest in Switzerland where the specimen was collected. Perithecia; section through perithecial wall; asci; ascospores; sporodochia starting to form on CLA; conidiophores and conidiogenous cells forming conidia; conidia. Scale bars: perithecia = 200 µm, all others = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Stylonectria tef1-rpb2*-ITS-*acl1* nucleotide alignment. Values > 74 % from the SH-aLRT test and bootstrap support values > 74 % 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. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Fusicolla matuoi* (CBS 581.78; GenBank KM231954/HQ897720/KM231822/HQ897858) and the novelties described here are highlighted with coloured blocks and **bold** font. Alignment statistics: 18 strains including the outgroup; 3990 characters including alignment gaps analysed: 1023 distinct patterns, 499 parsimony-informative, 729 singleton sites, 2762 constant sites. The best-fit models identified in IQ-TREE using the TESTNEW option were: *tef1* (1–727): HKY+F+G4; *rpb2* (728–2551): TNe+G4; ITS (2552–3078): TPM3+I+G4; *acl1* (3079–3990): TNe+G4. The scale bar shows the expected number of nucleotide substitutions per site.

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Stylonectria colleeniae

Fungal Planet 1919 MB 861184

Stylonectria colleeniae Mombert & Crous, ***sp. nov.***

Etymology: The name refers to Colleen Fleury, who discovered this species.

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

Ascomata perithecial, gregarious in groups of 2–50, or solitary, arising from dead ascomycetes, broadly pyriform, 188–292 µm high, 188–244 µm wide (av. 249 × 226 µm), with a discoid papilla, red to dark red, becoming dark purple in 5 % KOH, yellow in lactic acid, not collapsing or laterally pinched when dry. *Ascomatal wall* smooth, 33–47 um thick, composed of two regions: outer region 14–28 µm thick, of irregularly shaped thick-walled cells of textura intricata to textura epidermoidea; inner region 7.5–17 µm thick of thin-walled, flattened cells of textura prismatica to textura angularis. *Asci* unitunicate, subcylindrical, 56–90 × 4–8.5 µm, 8-spored, apices rounded and simple, uniseriate; evanescent, narrowly moniliform paraphyses, interspersed between asci. *Ascospores* ellipsoidal, 1-septate, often constricted at septum, (8.9–)9.1–10.4(–11.4) × (4.5–)4.8–5.7(–5.8) µm (av. = 9.8 × 5.2 µm, n = 49), Q = 1.6–1.9–2.3, smooth then spinulose, thick-walled, hyaline at first, becoming pale golden brown at maturity. *Mycelium* consisting of hyaline, smooth, branched, septate, 2–3 µm diam. hyphae. Orange to saffron *sporodochia* superficial on CLA, OA, MEA and PDA. *Conidiophores* solitary or aggregated in clusters to form sporodochia reduced to conidiogenous cells or 1–2-septate, branched, subcylindrical, hyaline, smooth, 30–60 × 2–3 µm. *Conidiogenous cells* hyaline, smooth, monophialidic, straight to curved, subcylindrical with apical taper, 8–35 × 2–2.5 µm, with inconspicuous collarette. *Conidia* solitary, aggregating in orange mucoid mass, hyaline, smooth, fusoid, apex subobtuse, curved, base tapered to truncate hilum, (0–)1-septate, (17–)20–23(–27) × 2(–2.5) µm; larger conidia develop a slight constriction in the basal cell, appearing as a poorly developed foot cell, but mostly absent, along with *chlamydospores* and *microconidia*.

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

Typus: **France**, Hautes-Alpes, Commune de Névache, lieu-dit Plampinet, sous la Pointe de pécé, 44.995144°N, 6.682309°E, 2215 m.a.s.l., on *Trimmatostroma scutellare,* with *Lophium mytillinum*, on dead branch of *Larix decidua* (*Pinaceae*), 11 Jul. 2022, *C. Fleury & A. Mombert*, HPC 4008 (**holotype** CBS H-25808, culture ex-type CPC 45103 = CBS 154478; ITS, *rpb2* (first and second part) and *tef1* (first part) sequences GenBank PX640140.1, PX583915.1 and PX583895.1).

Additional material examined: **Switzerland**, Canton of the Grisons, Pontresina, to the Bernina Pass, 46.45251°N, 9.94894°E, 2000 m.a.s.l., on unidentified ascomycete, with *Lophium mytillinum*, on recently cut branch of *Pinus cembra* (*Pinaceae*), 16 Aug. 2022, *C. Fleury & A. Mombert*, AM2208161 = HPC 3964, cultures CPC 44988–44991; ITS, *rpb2* (first part), *rpb2* (second part), and *tef1* (first part) sequences GenBank PX640141– PX640144, PX620761–PX620764 and PX620767– PX620770.

Notes: The confused taxonomic history of *Cucurbitaria pinastri*, which is in fact a *Stylonectria* growing on a *Valsa*, was discussed by Booth (1959), who designated a lectotype for *Sphaeria purtonii* (Scotland, on small branches of coniferous tree), which is the basionym of *Stylonectria purtonii* (Gräfenhan *et al.* 2011). Furthermore, Booth (1959) cited perithecia as yellow to red, 150–230 µm diam., with a characteristic flattened apex, ascospores as 1-septate, pale brown, 8–11 × 3.5–4.5 µm, and macroconidia as 1-septate, 20–24 × 1.5–2 µm. Samuels (1976) cited ascospores as (7–)9–11(–17) × 3–4(–5) µm, 1-septate, spinulose, and referred to the asexual morph as *Fusarium aquaeductuum*. Booth (1971) referred to conidia in nature being 9–16 × 2–2.5 µm, but in culture being 15–45 × 3–3.5 µm, which is rather atypical. *Fusicolla aquaeductuum* (ex-epitype CBS 837.85) was treated by Gräfenhan *et al.* (2011) and shown to be distinct from *Stylonectria purtonii* (DAOM 235818), for which no epitype has been designated to date. *Stylonectria colleeniae* has wider ascospores than those of *Stylonectria purtonii.*

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 45103 had highest similarity to *Stylonectria purtonii* [strain CA FUNDIS iNaturalist # 169302017, GenBank OR882768.1; Identities = 552/552 (100 %), no gaps], *Thelonectria applanata* [strain CBS 125489, GenBank HQ897805.1; Identities = 547/554 (99 %), two gaps (0 %)], *Stylonectria hetmanica* [strain 555J, GenBank PP524015.1; Identities = 544/554 (98 %), three gaps (0 %)], and *Stylonectria corniculata* [strain CBS 125491, GenBank NR_178095.1; Identities = 541/554 (98 %), three gaps (0 %)]. The ITS sequence of CPC 42150 differs 0–2 nucleotides from those of CPC 44988–44991. Closest hits using the ***rpb2*** (first part) sequence of CPC 45103 had highest similarity *Stylonectria carpini* [strain DAOM 235819, GenBank HQ897773.1; Identities = 785/825 (95 %), no gaps], *Stylonectria purtonii* [strain DAOM 235818, GenBank HQ897783.1; Identities = 769/825 (93 %), no gaps], and *Stylonectria wegeliniana* [strain CBS 125490, GenBank HQ897754.1; Identities = 767/824 (93 %), no gaps]. The *rpb2* (first part) sequence of CPC 42150 differs 1–2 nucleotides from those of CPC 44988–

Colour illustrations: Forest at Hautes-Alpes, Commune de Névache, lieu-dit Plampinet, France. Perithecia; section through perithecial wall; asci and ascospores; conidiophores and conidiogenous cells giving rise to conidia on SNA; conidia. Scale bars: Perithecia = 200 µm, wall section = 50 µm, all others = 10 µm.

44991. Closest hits using the ***rpb2*** (second part) sequence of CPC 45103 had highest similarity to *Stylonectria carpini* [strain DAOM 235819, GenBank HQ897773.1; Identities = 838/882 (95 %), no gaps], *Stylonectria wegeliniana* [strain CBS 125490, GenBank HQ897754.1; Identities = 837/894 (94 %), no gaps], and *Stylonectria purtonii* [strain DAOM 235818, GenBank HQ897783.1; Identities = 790/841 (94 %), no gaps]. The *rpb2* (second part) sequence of CPC 42150 differs 1–3 nucleotides from those of CPC 44988–44991. Closest hits using the ***tef1*** (first part) sequence of CPC 45103 had highest similarity to *Stylonectria wegeliniana* [strain CBS 125490, GenBank KM231945.1; Identities = 462/527 (88 %), 15 gaps (2 %)], and *Stylonectria* sp. [strain CBS 125491, GenBank KM231946.1; Identities = 439/540 (81 %), 30 gaps (5 %)]. The *tef1* (first part) sequence of CPC 42150 differs 0–5 nucleotides from those of CPC 44988–44991.

For phylogenetic tree, see *Stylonectria stoeckliana* (FP 1918).

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Pseudocosmospora perforaticola

Fungal Planet 1920 MB 861186

Pseudocosmospora perforaticola J. Fourn., Mombert & Crous, *sp. nov.*

Etymology: Name refers to *Hypoxylon perforatum* on which this species occurs.

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

Ascomata perithecial, solitary to gregarious, erumpent, almost superficial at maturity, difficult to remove without involving blackish host fragments, on a loose prosenchymatous stroma composed of thin-walled cells 2–4 µm wide originating from the ascomatal base, subglobose to obpyriform, 188–258 µm high, 162–234 µm wide (av. = 223 × 198 µm, n = 10), apically obtusely rounded to flattened, collapsing laterally when dry; wall glabrous, slightly roughened by protruding cells, orange red turning dark red at maturity, livid vinaceous in 3 % KOH, yellow in lactic acid. *Ostiole* inconspicuous to finely papillate, central, periphysate. *Ascomatal wall* 27–34 µm thick, composed of two regions of angular to prismatic cells, outwardly thick-walled with wall 2–3 µm thick and small lumina, intergrading inwardly into more flattened and thin-walled cells with wall 0.8–1 µm thick. *Asci* unitunicate, cylindrical, short-stipitate, 52–65 × 3.8–5.4 µm, containing 8 uniseriate ascospores, becoming narrowly clavate, with irregularly biseriate ascospores; evanescent, narrowly moniliform paraphyses, up to 7–12 µm wide, interspersed between asci. *Ascospores* (5.8–)6.3–7.4(–7.8) × (3.0–)3.1–3.6(–3.8) µm (av. = 6.9 × 3.4 µm, N = 60), Q = 1.7–2.0–2.5, ellipsoidal with broadly rounded ends, equally 1-septate, constricted at septum, hyaline, pale ochreous in mass, smooth, with one or two yellowish guttules in each cell (measurements from discharged mature ascospores). *Mycelium* consisting of hyaline, smooth, branched, septate, 2.5–3 µm diam. hyphae. *Conidiophores* solitary, but becoming aggregated in sporodochial mass that covers large areas of the plate; conidiophores hyaline, smooth, subcylindrical, septate, extensively branched, up to 120 µm tall, 2.5–3.5 µm diam. *Conidiogenous cells* hyaline, smooth, subcylindrical with apical taper, intercalary and terminal, phialidic, with flared collarettes, 25–50 × 2–3 µm. *Conidia* aggregating in mucoid mass, hyaline, smooth, guttulate, 0(–1)-septate, ellipsoid, (4–)6–7 × 2.5–3 µm.

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

Colour illustrations: Forest at Ariège, Rimont, Las Muros, France. Perithecia; section through perithecium; asci; ascospores; conidiophores and conidiogenous cells giving rise to conidia aggregated in mucoid masses. Scale bars: Perithecia = 200 µm; section though perithecial wall = 34 µm, all others = 10 µm.

Typus: **France**, Ariège (09), Rimont, Las Muros, 43.014816°N, 1.287797°E, 460 m.a.s.l., on dead stromata of *Hypoxylon perforatum* on *Fraxinus* excelsior. (*Oleaceae*), 11 Mar. 2022, *J. Fournier*, JF22002 (**holotype** CBS H-25809, cultures ex-type CPC 43403 = CBS 154459 and CPC 43404 = CBS 154458; ITS, LSU, *rpb1*, *rpb2* (first and second part) sequences GenBank PX640145 & PX640146, PX640150 & PX640151, PX620757 & PX620758 and PX583916 & PX583917).

Additional material examined: **France**, Ariège (09), Rimont, Las Muros, 43.014816°N, 1.287797°E, 460 m.a.s.l., on dead stromata of *Hypoxylon perforatum* on *Fraxinus excelsior*, 19 Apr. 2011, coll. *J. Fournier*, isol. *C. Lechat*, JF11042.

Notes: *Cosmospora* sensu lato is polyphyletic, and includes nectrioid fungi with small, reddish, smooth, thin-walled perithecia (Herrera *et al*. 2013). Several of these genera have in recent years been distinguished from *Cosmospora*, namely *Cosmosporella*, *Dialonectria*, *Pseudocosmospora* and *Pulchrospora* (Czachura & Janik 2025). Species of *Cosmospora* are mycoparasites, and commonly isolated from xylariaceous fungi (*Xylariaceae*). Herrera *et al*. (2016) found, however, that these species are highly host specific. *Pseudocosmospora perforaticola* is a cosmospora-like fungus that is fungicolous and specific on old stromata of *Hypoxylon perforatum*. It is characterised by erumpent perithecia, on a discrete prosenchymatous stroma, dark red at maturity, lacking a differentiated apex, ascospores small-sized and smooth-walled, and an acremonium-like asexual morph that forms large sporodochia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 43403 had highest similarity to *Cosmospora* sp. from *Hypoxylon* in France [strain CIRM-BRFM 1642, GenBank PV108591.1; Identities = 525/525 (100 %), no gaps], *Cosmospora butyri* [strain IRAN 4322C, GenBank PP153528.1; Identities = 496/528 (94 %), six gaps (1 %)], and *Cosmospora arxii* [strain ERD-9302, GenBank OP070951.1; Identities = 495/527 (94 %), seven gaps (1 %)]. The ITS sequences of CPC 43403 and CPC 43404 are identical (481/481 nt, no gaps). Closest hits using the **LSU** sequence of CPC 43403 are *Cosmosporella olivacea* [strain KUMCC 18-0016, GenBank MH087215.1; Identities = 844/874 (97 %), two gaps (0 %)], *Cosmosporella pruni* [strain MFLUCC 17-2579, GenBank NG_241985.1; Identities = 852/883 (96 %), two gaps (0 %)], and *Cosmospora stilbosporae* [strain CBS 125509, GenBank MH875134.1; Identities = 851/882 (96 %), one gap (0 %)]. The LSU sequences of CPC 43403 and CPC 43404 are identical (880/880 nt, no gaps). Closest hits using the ***rpb1*** sequence of CPC 43403 had highest similarity to *Cosmospora* sp. [strain IMI 362240, GenBank KJ676243.1; Identities = 548/610 (90 %), no gaps], *Cosmospora viridescens* [strain CBS 102430, GenBank KJ676221.1; Identities = 552/615 (90 %), no gaps], and *Pseudocosmospora eutypae* [strain IMI 73016, GenBank KC291885.1; Identities = 545/610 (89 %), no gaps]. The

rpb2 (first part) sequences of CPC 43403 and CPC 43404 are identical (852/852 nt, no gaps). The *rpb1* sequences of CPC 43403 and CPC 43404 are identical (616/616 nt, no gaps).Closest hits using the ***rpb2*** (first part) sequence of CPC 43403 had highest similarity to *Cosmospora aquatica* [voucher S-350, GenBank MN194021.1; Identities = 482/533 (90 %), no gaps], *Cosmospora coccinea* [strain NRRL 53583, GenBank JX171657.1; Identities = 755/860 (88 %), no gaps], and *Cosmospora viridescens* [strain CBS 152411, GenBank PQ474166.1; Identities = 766/873 (88 %), no gaps]. The *rpb2* (first part) sequences of CPC 43403 and CPC 43404 are identical (852/852 nt, no gaps). Closest hits using the ***rpb2*** (second part) sequence of CPC 43403 had highest similarity to *Cosmospora lavitskiae* [strain CBS 530.68, GenBank HQ897726.1; Identities = 635/707 (90 %), no gaps], *Cosmospora coccinea* [strain CBS 341.70, GenBank MH936717.1; Identities = 634/707 (90 %), no gaps], and *Cosmospora viridescens* [strain CBS 102433, GenBank HQ897712.1; Identities = 632/706 (90 %), no gaps]. The *rpb2* (first part) sequences of CPC 43403 and CPC 43404 are identical (706/706 nt, no gaps).

For phylogenetic tree, see *Triseptosporium fallopiae* (FP 1910).

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