Fungal Planet 1074 – 29 June 2020

Cylindrium magnoliae A. Pintos, M. González, P. Alvarado & E. Rubio, *sp. nov.*

Etymology. The epithet refers to *Magnolia grandiflora*, the host plant from which this fungus was originally collected.

Classification — *Cylindriaceae*, *Amphisphaeriales*, *Sordariomycetes*.

Asexual morph: *Mycelium* consisting of smooth hyaline hyphae, branched and septate, 1–5 µm diam. *Conidiomata* foliicolous, 150–400 wide and 100–250 µm tall, often in scattered groups, stromatic, immersed but erumpent when moist after pushing up a flap of host tissue and revealing a whitish jelly content. *Peridium* composed of a single subepidermal inner layer of brown cells arranged as *textura angularis*, presenting paler pigmentation towards the conidiogenous region. *Ostiole* absent. *Setae* dark brown, 90–200 × 3–5 µm (length/width), smooth, dichotomously branched at the base, with 3–7 transversal septa, tapered towards the apex. *Paraphyses* hyaline, scattered between setae and conidiophores. *Conidiophores* arising from lageniform or cylindrical cells with hyaline or brownish walls at the internal wall of the peridium, formed of 21–81 µm long cylindrical cells (tapered towards the apex), septate and branched. *Conidiogenous cells* integrated, hyaline, cylindrical (tapered towards the apex), lageniform, phialidic or percurrent, 10–25 × 1–2 µm (length/width). *Conidia* hyaline, smooth, falcate, wider in the middle, tapering towards the apex, truncate at the base, measuring 34–48 × 1.5–2.5 µm (length/width), completely filled with small droplets.

Culture characteristics — (day/light 25 °C, after 2 wk): Colonies slow-growing, with sparse aerial mycelium, rounded margins, reaching 12 mm in 2 wk. On malt extract agar and potato-dextrose agar white on surface, salmon in reverse.

Typus. Spain, Asturias, Gijón, Jardín Botánico Atlántico, on leaves of *Magnolia grandiflora* (*Magnoliaceae*), 13 Nov. 2019, *M. González* (holotype FCO-Fungi 14, culture ex-type CBS 146681; ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MT177212, MT177213, MT179311, MT179310 and MT179309, MycoBank MB834679; Isotype ERD-8142).

Additional materials examined. Spain, Asturias, Gijón, Isabel La Católica park, on leaves of *M. grandiflora*, V-2018; ibid., Gijón, Jardín Botánico Atlántico, on leaves of *M. grandiflora*, IX-2018; ibid., IX-2019. Gijón, urban street, on leaves of *M. grandiflora*, VI-2019; Asturias, Navia, Andés, on leaves of *M. grandiflora*, XI-2019.

Notes — On the basis of a combined phylogeny using ITS and 28S nrDNA data (available in MycoBank MB834679), *C. magnoliae* is probably related with *C. aeruginosum*, *C. algarvense*, and *C. purgamentum*. Lombard et al. (2015) proved that *C. aeruginosum* is phylogenetically related with the type species *C. elongatum*. Crous et al. (2018) created a new family, *Cylindriaceae* to accommodate this genus, proposing *C. algarvense* and *C. purgamentum*, and combining *C. syzygii*. Recently, the new species *C. grande* was added to the genus (Crous et al. 2019c). Morphologically, *C. magnoliae* differs from other species of *Cylindrium* because of its stromatic conidiomata, the specialised method of dehiscence, and the presence of setae and paraphyses. *Cylindrium magnoliae* does not produce a pigmented stipe or sympodial loci and lacks ramoconidia which are present in *C. purgamentum* (Crous et al. 2016). *Cylindrium grande* (Crous et al. 2019a) produces sympodial conidiogenous cells and solitary conidia, features not present in *C. magnoliae*.

Colour illustrations. Conidiomata on host. Section of conidioma with brown setae; conidiophore; conidiogenous cells with successive percurrent proliferations (annellations); conidiogenous cells giving rise to conidia. Scale bars = 100 µm (section of conidioma), 5 µm (others).

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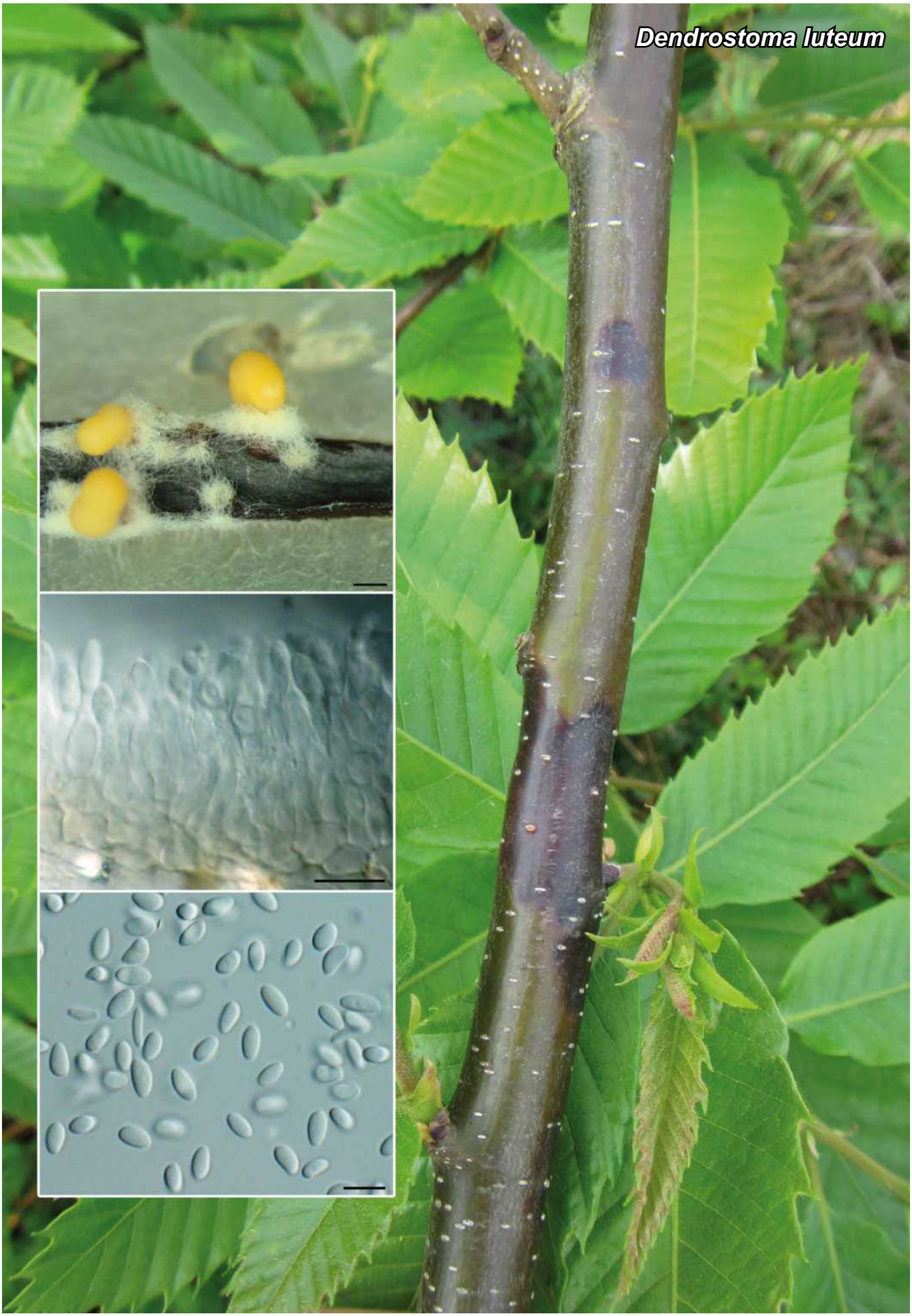

Dendrostoma luteum

Fungal Planet 1075 – 29 June 2020

Dendrostoma luteum L.A. Shuttlew., A.J. Lewis, C. Gorton, & Pérez-Sierra, *sp. nov.*

Etymology. Name refers to the colour of conidial masses produced by conidiomata in culture.

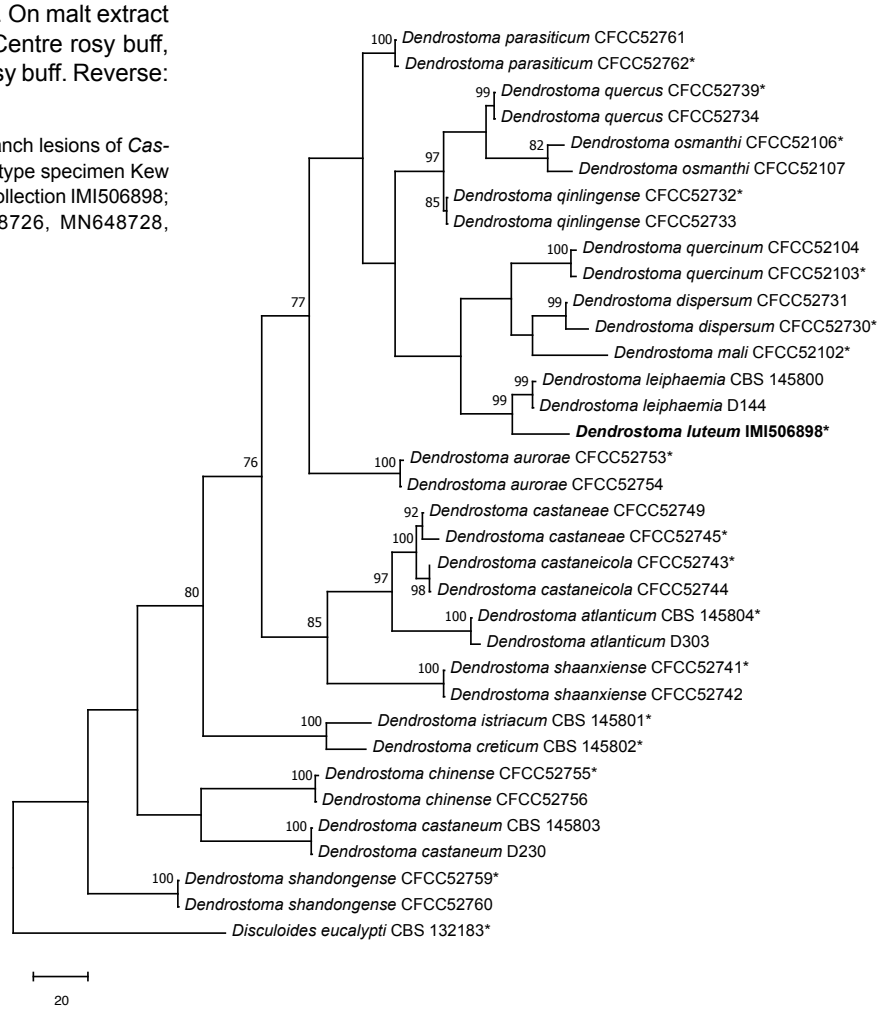
Classification — *Erythrogloeaceae*, *Diaporthales*, *Sordariomycetidae*, *Sordariomycetes*.

Conidiomata after 6 wk 14/10 h l/d cycles on *C. sativa* bark strips, pycnidial, separate, globose to subglobose, (407–)727(–965) × (368–)719(–869) µm with central ostiole, exuding a luteous, pale luteous to hyaline conidial mass. *Conidiophores* reduced to conidiogenous cells, ampulliform to doliiform with prominent taper towards narrow cylindrical apex, enteroblastic, (10–)11(–12) × (3–)4(–5) µm wide. *Conidia* aseptate, hyaline, smooth, ellipsoid, straight to curved, apex obtuse, smooth, thin-walled, guttules of varying sizes sometimes visible, (7–)9(–12) × (2–)4(–6) µm.

Culture characteristics — After 1 mo in the dark at 20 °C. Colours determined from Rayner (1970). Ex-type culture on potato dextrose agar 27.5 × 25.5 mm diam. Surface undulating, woolly to velvety in texture. Centre vinaceous buff, followed by dark mouse grey, hazel, fawn with an irregular pale vinaceous margin. Reverse: Centre sepia, extending to a 3 mm ring of fuscous black, extending to brick to dark brick. On malt extract agar 38 × 40 mm diam. Surface flat, woolly. Centre rosy buff, extending to buff, rosy buff, vinaceous, and rosy buff. Reverse: centre chestnut extending to flesh coloured.

Typus. UK, England, Hampshire, Fareham, from branch lesions of *Castanea sativa* (*Fagaceae*), 21 Aug. 2017, *H. Carter* (holotype specimen Kew Fungarium K(M)263346. Culture ex-type CABI culture collection IMI506898; ITS, LSU, and *tef1-a* sequences GenBank MN648726, MN648728, MN812768, MycoBank MB832934).

Notes — The genus *Dendrostoma* (*Erythrogloeaceae*, *Diaporthales*) was introduced by Fan et al. (2018) as a highly supported clade in the *Diaporthales* found on the host species *Quercus acutissima*, *Malus spectabilis*, and *Osmanthus fragrans* in China. Recently, Jaklitsch & Voglmayr (2019) described four new species of *Dendrostoma* from Europe, and also updated the description of *D. leiphaemia*. On the concatenated LSU, ITS, *tef1-a* tree, *D. luteum* was a strongly supported species (maximum parsimony bootstrap support 99 %), sister to *D. leiphaemia.* Morphologically, conidiomata of *D. luteum* are longer and wider than *D. leiphaemia*. *Dendrostoma luteum* was consistently associated with branch lesions, but pathogenicity testing on detached *C. sativa* branches (3 cm diam, 20 cm length, n = 12) did not produce lesions significantly longer than the control. Therefore *D. luteum* is currently considered as an endophyte of *C. sativa.*



Colour illustrations. Castanea sativa branch showing lesion from which *D. luteum* was isolated. Conidioma sporulating on *C. sativa* bark strips; conidiogenous cells and conidia. Scale bars = 500 µm (conidioma), 10 µm (others).

The concatenated phylogenetic tree was inferred using maximum parsimony. * indicates ex-type cultures, with taxonomic novelty in **bold**. Branch supports were determined using 1 000 maximum parsimony bootstrap replicates. Branch support values < 70 % were excluded. Scale bar on tree indicates number of changes.

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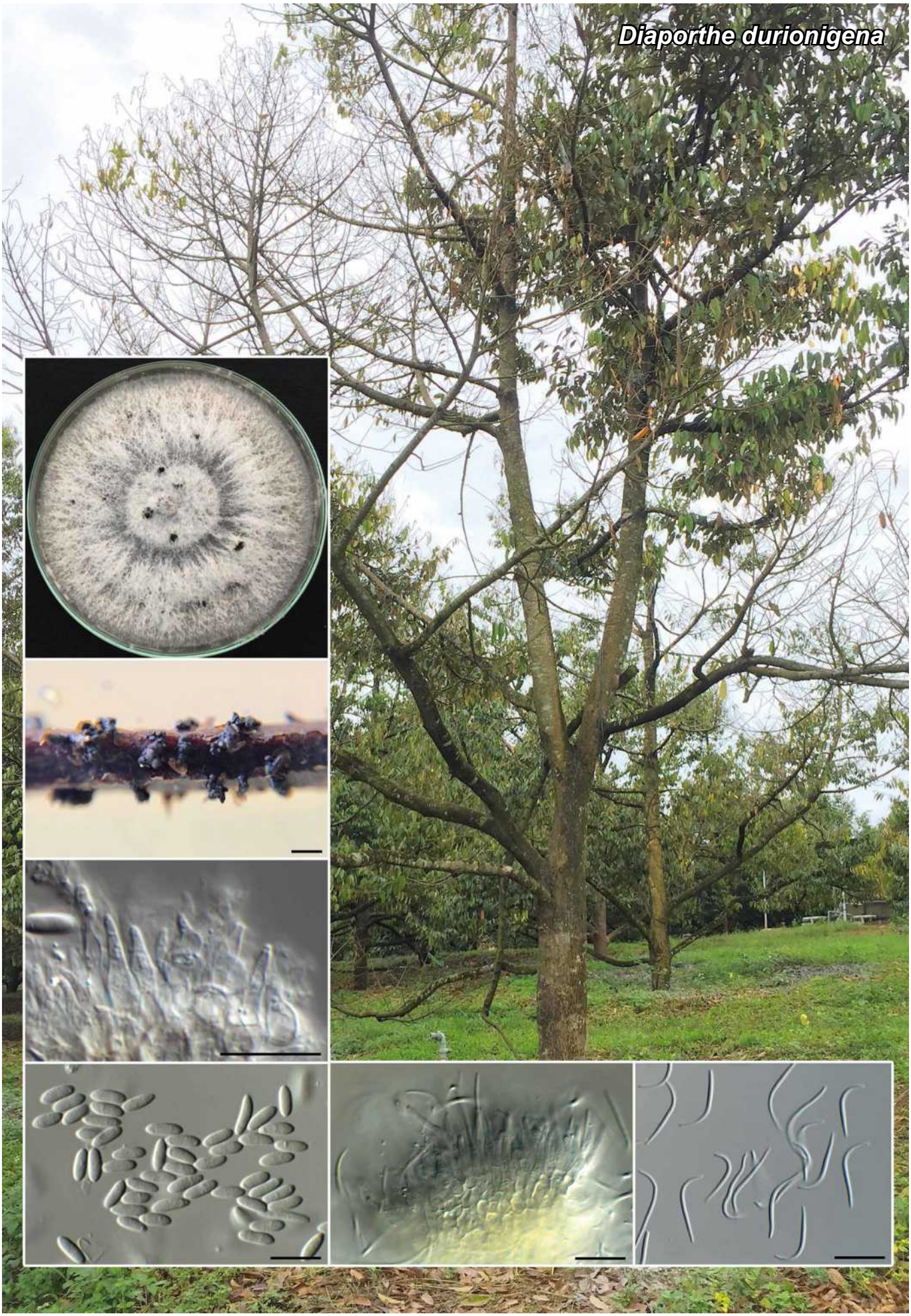

Diaporthe durionigena

Fungal Planet 1076 – 29 June 2020

Diaporthe durionigena L.D. Thao, L.T. Hien, N.V. Liem, H.M. Thanh & T.N. Khanh, *sp. nov.*

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

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

Conidiomata pycnidial, black, globose to subglobose, solitary or aggregated, embedded in tissue, 200–400 µm diam; forming up to six well-defined necks that can arise from a single conidioma. *Conidiophores* formed from the inner layer of the *conidiomatal* wall, reduced to conidiogenous cells, cylindrical, hyaline, 10–18 × 2.5–3.5 µm. *Alpha conidia* rare or absent in culture, hyaline, aseptate, biguttulate, ellipsoidal, smooth, (5.6–)6.1–7.5(–7.9) × (1.8–)2.1–2.7(–3) µm. *Beta conidia* abundant, hyaline, aseptate, hamate, (17.8–)20.3–26.1(–31.2) × 1.1–1.5(–1.7) µm.

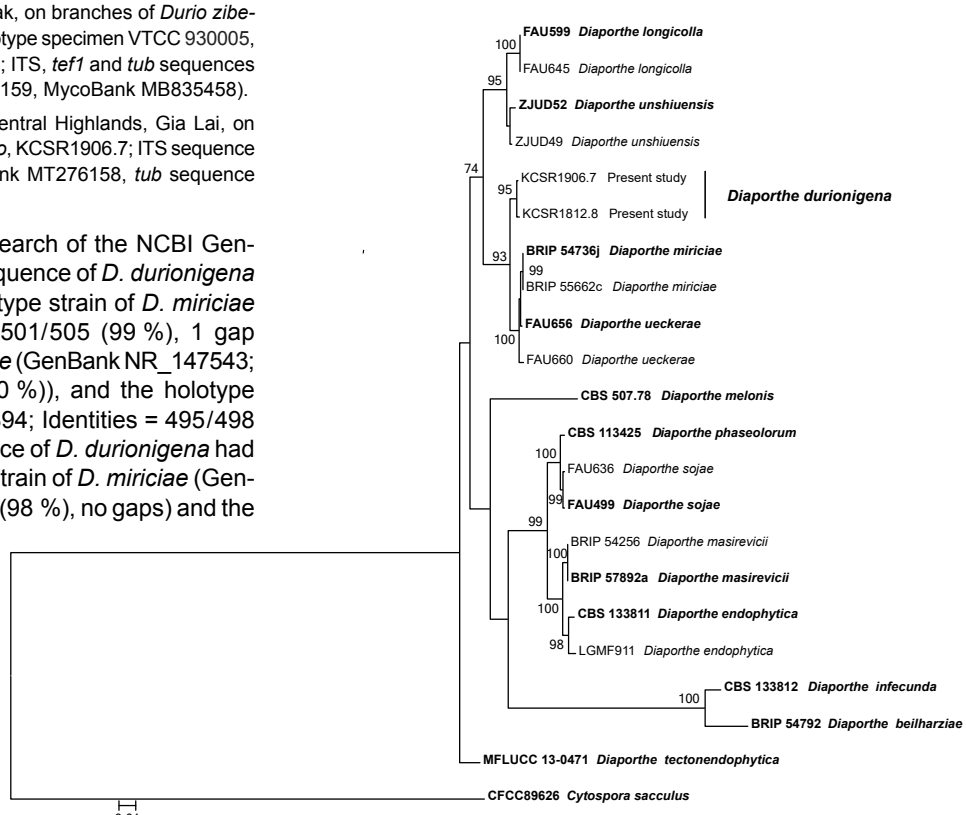
Culture characteristics — On potato dextrose agar (PDA), colonies white, fast-growing, covering dish after 10 d at 25 °C, surface buff with patches of purplish grey (Rayner 1970), reverse purplish grey, with patches of dirty white. On malt extract agar (MEA) with moderate aerial mycelium, and even, smooth margins; surface dirty white with patches of grey olivaceous, reverse dark mouse grey with patches of greyish sepia. On oatmeal agar (OA) surface dirty white with patches of dark mouse grey.

Typus. Vietnam, Central Highlands, Dak Lak, on branches of *Durio zibethinus* (*Malvaceae*), Dec. 2018, *L.D. Thao* (holotype specimen VTCC 930005, culture ex-type KCSR1812.8 = VTCC 930005; ITS, *tef1* and *tub* sequences GenBank MN453530, MT276157 and MT276159, MycoBank MB835458).

Additional material examined. Vietnam, Central Highlands, Gia Lai, on branches of *D. zibethinus*, June 2019, *L.D. Thao*, KCSR1906.7; ITS sequence GenBank MN453531, *tef1* sequence GenBank MT276158, *tub* sequence GenBank MT276160.

Notes — Based on a megablast search of the NCBI GenBank nucleotide database, the **ITS** sequence of *D. durionigena* had the highest similarities to the ex-type strain of *D. miriciae* (GenBank NR_147535; Identities = 501/505 (99 %), 1 gap (0 %)), the holotype strain of *D. ueckerae* (GenBank NR_147543; Identities = 501/506 (99 %), 1 gap (0 %)), and the holotype strain of *D. rosae* (GenBank MG828894; Identities = 495/498 (99 %), 1 gap (0 %)). The ***tef1*** sequence of *D. durionigena* had the highest similarities to the ex-type strain of *D. miriciae* (GenBank KJ197244; Identities = 304/310 (98 %), no gaps) and the holotype strain of *D. ueckerae* (GenBank KJ590747; Identities = 304/310 (98 %), no gaps). The ***tub*** sequence of *D. durionigena* had highest similarities to the ex-type strain of *D. miriciae* (GenBank KJ197262; Identities = 484/490 (99 %), no gaps), the holotype strain of *D. ueckerae* (GenBank KJ610881; Identities = 430/436 (99 %), no gaps), and the holotype strain of *D. rosae* (GenBank MG843878; Identities = 441/443 (99 %), no gaps).

The phylogenetic tree generated by RAxML from the combined sequences of three loci demonstrated that the isolates of this study, KCSR1812.8 and KCSR1906.7, grouped separately as a novel species. *Diaporthe ueckerae* on *Cucumis melo* has larger alpha conidia ((6–)6.4–8.2(–8.6) × (2–)2.3–3.0 µm), and lacks beta conidia (Udayanga et al. 2015). *Diaporthe miriciae* on *Helianthus annuus* has larger alpha conidia, 6–7.5(–9) × 2–2.5(–3) µm, and longer beta conidia (20–35 × 1.0–1.5 µm; Thompson et al. 2015). Previously, *Phomopsis durionis* (DNA data unavailable), was reported to be the causal agent of the durian leaf spot. However, the original description of *P. durionis* reports smaller conidioma, 120–130 µm diam, smaller alpha conidia (5–7.5 × 2–2.5 µm), with no beta conidia being observed (Sydow 1932). Based on the characteristically large conidiomata with multiple necks, the canker disease and dieback symptoms, the present collection is herewith introduced as a new species.



Phylogenetic tree constructed by RAxML from the combined sequences of ITS, *tef1* and *tub*. RAxML bootstrap > 70 % are presented at the nodes. Isolate numbers are listed in branches followed by the species name. The tree is rooted with *C. sacculus*. Ex-type, holotype and authentic strains are indicated in **bold**.

Colour illustrations. Dieback symptoms occurring on *Durio zibethinus* at Dak Lak, Central Highlands, Vietnam. Colony on PDA; conidioma on a durian twig on water agar; alpha conidia; conidiophores; beta conidia; conidiophores. Scale bars: twig = 1 mm, all others = 10 µm.

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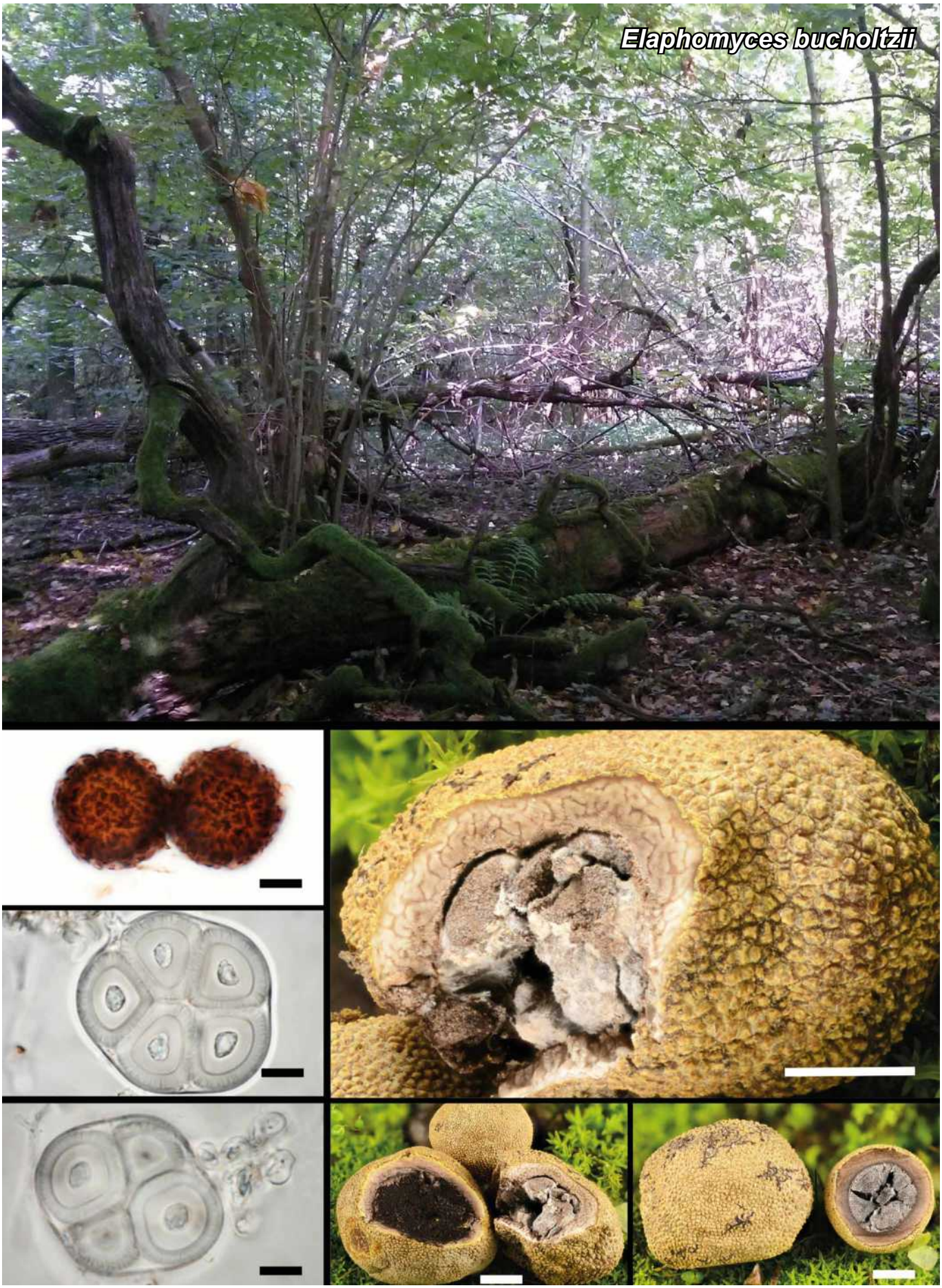
Elaphomyces bucholtzii

Fungal Planet 1077 – 29 June 2020

Elaphomyces bucholtzii Saitta, A. Paz, E. Otsing & Tedersoo, *sp. nov.*

Etymology. Dedicated to the Estonian mycologist Feodor Vladimirovic Bucholtz, for his contribution on taxonomy of hypogeous fungi.

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

Ascomata globose, 2–5 cm diam. *Peridial surface* with obtuse warts of various heights, pale yellow-brown, irregular at the base. Warts formed by very intertwined, sinuous, thick-walled hyphae, yellow pigmented, joined together by a series of layers of parallel hyphae, with very short segments, thin-walled, almost hyaline, guttulate. Base of the warts with transitional hyphae to the peridium. *Peridium* thick, distinctly marbled, forming elliptical irregular spots, paler on the outer part, darker in the middle towards gleba, lightly purple with cerebriform appearance, originating by the intense pigmentation in the walls of some hyphae. Peridium consisting of narrow hyphae, 2.2–4.5 µm wide, sinuous, interlaced with slight thickenings, slightly pigmented on the walls of the hypha towards the surface of the ascoma, accentuating towards the gleba, irregularly intercalated by layers of hyphae pigmented in all structures that intersect, giving the marmorised effect. *Asci* subglobose, 35–55 × 40–65 µm, with (1–)3–4(–5) spores. *Spores* globose, 21 25(–28) µm diam, ornamented by curved canes, 1.4 2.2 µm high, apices confluent and forming small irregular meshes.

Typus. Estonia, Viru-Jaagupi, Vinni, mixed forest of *Corylus avellana*, *Quercus robur* and *Tilia cordata*, 108 m asl, 59.291956, 26.434087, 9 Sept. 2016, *E. Otsing* (holotype TU 126183; ITS sequence GenBank MK685345, isotype in herb. pers. A. Paz, IC09091627, MycoBank MB832926).

Additional materials examined. Estonia, Polli, mixed forest of *Q. robur*, *Picea abies*, *T. cordata*, *C. avellana*, 76 m asl, 30 Aug. 2016, *E. Otsing* (TV126157, UDB032813, IC30081623); Pugritsa, mixed forest of *T. cordata*, *Q. robur*, *C. avellana*, *P. abies*, *Betula pendula*, *Salix caprea*, 78 m asl, 31 Aug. 2016, *E. Otsing* (TV126165, UDB032814, IC31081615); Järni, mixed forest of *T. cordata*, *Q. robur*, *C. avellana*, 129 m asl, 9 Sept. 2016, *E. Otsing* (TV126187, UDB032816, IC09091628). – Norway, Oppegård, mixed forest of *Quercus* sp. and *C. avellana*, 110 m asl, 13 Oct. 2011, *A. Molia* (AM153, IC13111117).

Notes — Macroscopically *Elaphomyces bucholtzii* closely resembles the *E. muricatus* group, being differentiated by the variable height of its cortex warts. Moreover, a section of the peridium is marbled, forming ellipsoidal (of cerebriform aspect) patches on a purple background, unlike the *E. muricatus* group that has a peridium marmorised in circles on a light background (white-cream), and the spores are decorated by thick, very curved sticks that usually form loops. A recently described European species *E. barrioi* (Paz et al. 2017) has a marmorised peridium in red-purple tones forming small ellipses, on a vinous background, a dark brown gleba with red tones and smaller spores than *E. bucholtzii*. Another species of the group is *E. decipiens*, but its cortex presents flat warts that are slightly oxidised after manipulation, a purple vinous peridium with cream-white veins arranged radially outward from the ascoma (Paz et al. 2017). *Elaphomyces violaceoniger* has a dark violet peridium and some spores decorated with canes that are joined at maturity by drawing plaits, that clearly distinguishes this species from all the others in the *E. muricatus* group (Paz et al. 2017). Macroscopically *Elaphomyces bucholtzii* can be placed in sect. *Elaphomyces* subsect. *Muricati*.

Phylogenetically *E. bucholtzii* is distinct from other species but grouped with two specimens: one from Spain, deposited as *Elaphomyces* sp. LM34 (GenBank KM576395), and one from the USA originally identified as *E.* cf. *decipiens* SE-2015 (GenBank KT275644). Analysing the percentage of similarity index of *E. bucholtzii* with other species of sect. *Muricati*, we obtained 95.24 % of similarity with *E. barrioi*; 92.87 % with *E. quercicola*; 92.71 % with *E. muricatus*; 91.65 % with *E. violaceoniger* and 91.64 % with *E. decipiens*.

Phylogenetic analyses were carried out online at http://phylogeny.lirmm.fr/ (Dereeper et al. 2008). Multiple sequence alignments were carried out with MUSCLE v. 3.7 (Edgar 2004). Phylogenetics analysis with the maximum likelihood (ML) was performed with PHyML v. 3.0 (Guindon et al. 2010). Trees were constructed using TreeDyn v. 198.3 (Chevenet et al. 2006) and edited with Adobe Photoshop and Inkscape v. 0.91 (https://inkscape.org/fr/). The alignment and tree are deposited in TreeBASE (study S25226).

Colour illustrations. *Elaphomyces bucholtzii*, habitat. Ascomata; ascospores, asci. Scale bars = 10 µm (ascospores and asci), 10 mm (ascomata).

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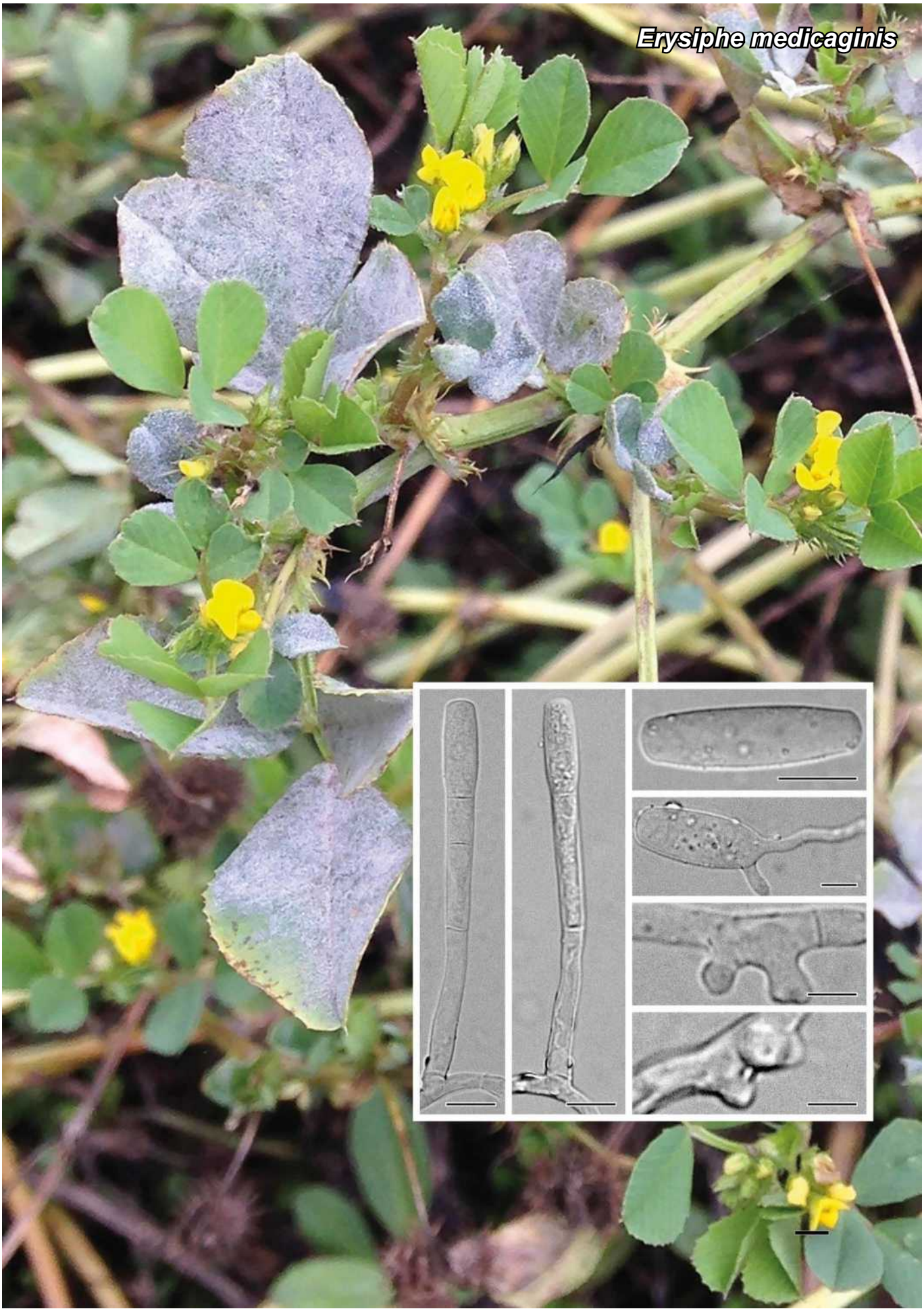

Erysiphe medicaginis

Fungal Planet 1078 – 29 June 2020

Erysiphe medicaginis L. Kiss, L. Kelly & Vaghefi, *sp. nov.*

Etymology. Name refers to the genus *Medicago*, from which this obligate biotrophic fungus was isolated.

Classification — *Erysiphaceae*, *Helotiales*, *Leotiomycetes*.

Mycelium on leaves, epiphytic, amphigenous, producing dense, white patches mostly on the upper leaf surfaces. *Hyphae* hyaline, thin-walled, 3–6 µm wide; *hyphal appressoria* mostly simple, nipple-shaped or knob-like, and rarely slightly lobed. *Conidiophores* erect, consisting of a *foot-cell*, straight or occasionally slightly curved-sinuous at the base, 35–48 × 5–7 µm, basal septum at the branching point, followed by (0–)1–2 cells up to the same length as the foot-cell. *Conidia* produced singly, mostly cylindrical or ellipsoid-cylindrical, and occasionally doliiform, 27–43 × 10–14 µm. *Germ tubes* terminal or subterminal, 1.2–3(–5) times longer than conidia (*longitubus* pattern when 5× longer), terminating in simple, often swollen, or rarely lobed appressoria. *Sexual morph* not observed.

Typus. Australia, Queensland, Toowoomba, -27.607396, 151.931924, on leaves of *Medicago polymorpha* (*Fabaceae*), 8 Aug. 2019, *L. Kiss* (holotype BRIP 70957; ITS and LSU sequences GenBank MT160214 and MT248412, MycoBank MB834939).

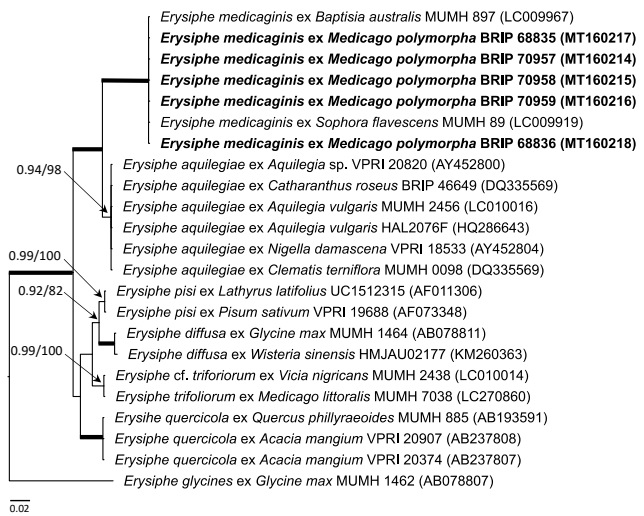
Additional material examined. Australia, Queensland, Tipton, -27.4403, 151.2465, on leaves of *M. polymorpha*, 19 Oct. 2017, *J.D.W. Dearnaley*, BRIP 68835; ITS sequence GenBank MT160217; Toowoomba, -27.5813, 151.9730, on leaves of *M. polymorpha*, 21 June 2018, *S. Takamatsu*, BRIP 68836; ITS sequence GenBank MT160218; Toowoomba, -27.534456, 151.928203, on leaves of *M. polymorpha*, 30 May 2019, *L. Kelly*, BRIP 70958; ITS and LSU sequences GenBank MT160215 and MT248413; Toowoomba, -27.556519, 151.932673, on leaves of *M. polymorpha*, 27 June 2019, *L. Kelly*, BRIP 70959; ITS and LSU sequences GenBank MT160216 and MT248414.

Notes — *Erysiphe* contains approximately 450 species of powdery mildew (Braun & Cook 2012), including many common, widespread, plurivorous taxa (Takamatsu et al. 2015). Some are taxonomically unresolved species complexes that are difficult to distinguish morphologically. These have similar or identical ITS sequences, and overlapping, or little-known, host ranges. An example is *E. aquilegiae* (Jankovics et al. 2008, Kovacs et al. 2011, Takamatsu et al. 2015). Powdery mildews with ITS sequences that were identical or highly similar to *E. aquilegiae* were recorded on diverse host plants in different parts of the world (Takamatsu et al. 2015), including Australia (Cunnington et al. 2004, Southwell et al. 2018), and belonged to the *E. aquilegiae* clade as defined by Takamatsu et al. (2015).

Phylogenetically, *E. medicaginis* belongs to a well-defined lineage that is sister to the *E. aquilegiae* clade. Morphologically, it differs from *E. aquilegiae*, and also from the asexual morphs of other taxa that had ITS sequences identical, or highly similar, to *E. aquilegiae*, by having mostly simple, and not lobed or multi-lobed hyphal appressoria.

The closest hits using the ITS sequence of *E. medicaginis* were two powdery mildew specimens from Japan, MUMH897 and MUMH89, collected from fabaceous hosts, *Baptisia australis* and *Sophora flavescens*, respectively. Their ITS sequences (GenBank LC009967 and LC009919) were identical to the five *E. medicaginis* specimens. These two specimens from Japan were recognised as representing a distinct lineage, sister to the *E. aquilegiae* clade, without being identified at the species level (Takamatsu et al. 2015).

Erysiphe medicaginis is commonly found on *M. polymorpha* in Queensland, Australia. Its host plant is a common weed globally, therefore it is likely that *E. medicaginis* is also widespread on *M. polymorpha* in different parts of the world, and likely on other fabaceous hosts, as indicated by the two specimens from Japan.



The majority rule consensus phylogram inferred from the internal transcribed spacer sequences of the nuclear ribosomal DNA and the intervening 5.8S nrDNA region using Bayesian Inference. The analysis was performed using MrBayes v. 3.2.4 (Ronquist et al. 2012) based on the GTR+G nucleotide substitution model selected using PAUP v. 4.0b10 (Swofford 2003) and MrModeltest v. 2.3. (Nylander 2009). A second measure of branch support was estimated through Maximum Likelihood analysis of the same alignment using RAxML v. 8 (Stamatakis 2014) in Geneious Prime (Biomatters Ltd.) based on the GTR substitution model with gamma-distribution rate variation. The tip labels in **bold** represent specimens sequenced in the current study. GenBank accession numbers are indicated in parentheses. Posterior Probability (PP) values > 0.90 and Bootstrap support (BS) values > 80 % are shown at the branches. Thickened lines indicate nodes with PP and BS values of 1.0 and 100 %, respectively. The tree is rooted to *Erysiphe glycines* MUMH 1462. The scale bar represents nucleotide substitutions per site.

Colour illustrations. *Medicago polymorpha* with powdery mildew-infected older leaves in a weedy area in Tipton, Queensland, Australia. Conidiophores; a non-germinating and a germinated conidium; and simple, nipple-shaped and knob-like hyphal appressoria of *Erysiphe medicaginis*. Micrographs were taken following rehydration of the powdery mildew mycelium by boiling small pieces of infected plant tissues in lactic acid. Scale bars = 10 µm (conidiophores, conidia), 5 µm (hyphal appressoria)

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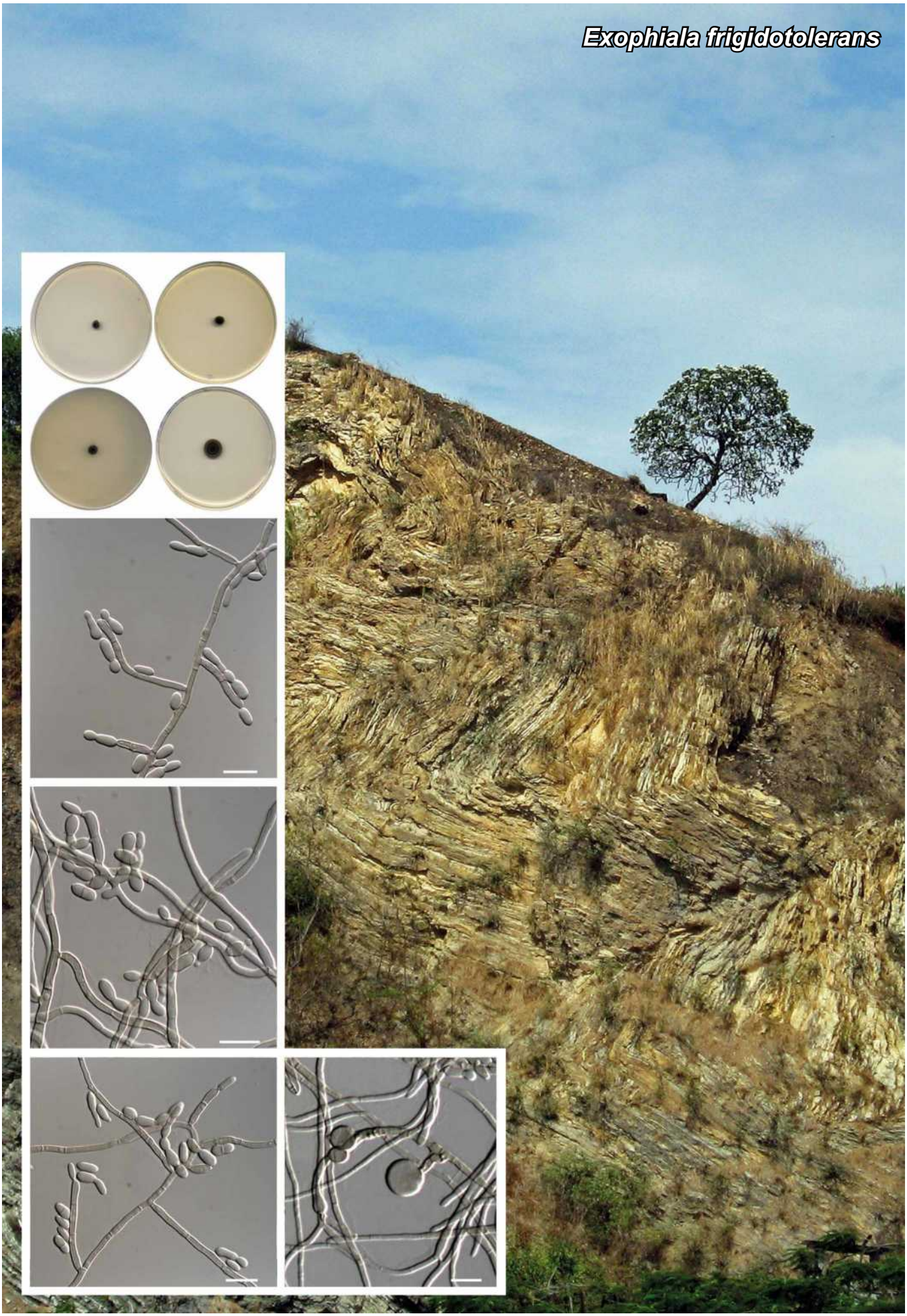

Exophiala frigidotolerans

Fungal Planet 1079 – 29 June 2020

Exophiala frigidotolerans Rodr.-Andr., Cano & Stchigel, *sp. nov.*

Etymology. From Latin *frigus*-, cold, and - *tolerans*, tolerant, referring to its ability to grow fast at lower temperatures than 20 °C.

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

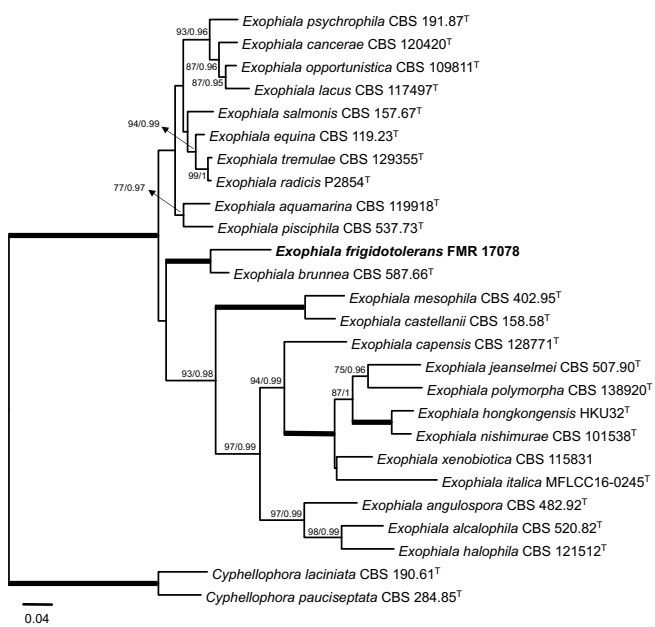
Mycelium composed of pale olivaceous brown, septate, branched, smooth- and thin-walled hyphae, 1–3 µm wide; older hyphae being more strongly pigmented. *Spirally twisted hyphae* present. *Moniliform cells* scarce, globose to ellipsoidal, in short chains (–5 cells). *Conidiophores* semi-micronematous, pale olivaceous brown, smooth- and thin-walled, mostly laterally disposed on the vegetative hyphae, sometimes terminally disposed, erect, rarely once branched near the base, cylindrical, with a rounded or pointed apex, 0–4-septate, with a terminal conidiogenous locus, sometimes with additional conidiogenous loci, 8–85 × 2–4 µm. *Conidiogenous cells* enteroblastic, mono- or polyblastic, integrated to the conidiophores, on vegetative hyphae or well-developed, in the latter case ellipsoidal, ovoid or flask-shaped, 5–11 × 2–3 µm, conidiogenous loci cylindrical or conic-cylindrical, with small percurrent proliferations. *Conidia* aseptate, occasionally 1-septate, pale olivaceous brown, smooth- and thin-walled, ellipsoidal to reniform, 4–7 × 2–4 µm, sometimes with a truncate base, solitary. *Budding cells* scarce, ellipsoidal, ovoid or barrel-shaped, 7–11 × 3–4 µm, in chains up to 5 elements. *Chlamydospores* scarce, olivaceous, globose, 5–15 µm diam.

Culture characteristics — *Colonies* on potato dextrose agar (PDA) reaching 5–6 mm diam after 2 wk at 25 °C, slightly raised, velvety, margins regular, brownish grey (M. 5E2; Kornerup & Wanscher 1978), sporulation absent, exudate absent; reverse brownish grey (M. 5E2), diffusible pigment absent. *Colonies* on oatmeal agar (OA) reaching 6–7 mm diam after 2 wk at 25 °C, morphologically similar to those on PDA, with sparse sporulation. *Colonies* on malt extract agar (MEA) reaching 5–7 mm diam after 2 wk at 25 °C, slightly raised, velvety, margins regular, olive brown (M. 4E4), sporulation absent, exudate absent; reverse olive brown (M. 4F3), diffusible pigment absent. *Colonies* on potato carrot agar (PCA) reaching 4–6 mm diam after 2 wk at 25 °C, slightly raised, velvety, margins regular, olive brown (M. 4E4), sparse sporulation, exudate absent; reverse brownish grey (M. 4F2), diffusible pigment absent. *Colonies* on PDA reaching 10–11 mm diam after 2 wk at 15 °C slightly raised velvety, margins regular, brownish grey (M. 5E2), sporulation absent, exudate absent; reverse brownish grey (M. 5E2), diffusible pigment absent. Minimum, optimal and maximum temperature of growth, 10 °C, 15 °C, and 25 °C, respectively.

Typus. Ecuador, Guayaquil, isolated from soil, Nov. 1996, *L. Zaror* (holotype CBS H-24326, cultures ex-type FMR 17078 = CBS 146539; ITS, LSU and *BenA* sequences GenBank LR699566, LR699567 and LR699568, MycoBank MB832466).

Notes — *Exophiala frigidotolerans* was recovered from a soil sample collected in Guayaquil, Ecuador. The genus *Exophiala* pertains to a group of fungi known as 'black yeasts', because of the production of yeast-like colonies and budding cells with dark, melanised cell walls. The genus *Exophiala* is characterised by an annellidic conidiogenesis and the production of solitary conidia grouping in slimy masses, and its phylogenetic affiliation to the ascomycete order *Chaetothyriales* (De Hoog et al. 2011). This genus contains numerous potential opportunists or pathogens of immunocompetent humans (Sudhadham et al. 2008, Li et al. 2008, 2009) and are isolated from a broad spectrum of substrata, environments and geographic areas (De Hoog et al. 2011, Ferrari et al. 2011). As in *E. psychrophila*, *E. frigidotolerans* exhibited the ability to grow at low temperatures. However, *E. frigidotolerans* presents more developed conidiophores than *E. psychrophila* (which are reduced to a unique discrete conidiogenous cell in this latter species), and produces shorter chains of moniliform cells (scarce and of up to 5 cells in the former species, and very abundant and of up to several hundred of cells in the latter).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the **ITS** sequence is the ex-type strain of *Exophiala brunnea* CBS 587.66 (GenBank JF747062; Identities = 539/560 (96 %), 6 gaps (1 %)); and using the **LSU** sequence the ex-type strain of *Exophiala brunnea* CBS 587.66 (GenBank MH870554; Identities = 868/876 (99 %), 1 gap (0 %)). The ITS-LSU-*BenA* phylogenetic tree corroborated the placement of our isolate as a new species of *Exophiala*, being located phylogenetically close to *E. brunnea*. *Exophiala brunnea* is easily distinguished from *E. frigidotolerans* by the production of 2-celled conidia (mostly 1-celled in *E. frigidotolerans*) and absence of budding cells (formed in *E. frigidotolerans*).



Maximum likelihood tree obtained from the ITS-LSU-*BenA* alignment of our isolate and sequences retrieved from GenBank. The tree was built by using RAxML CIPRES (http://www.phylo.org/sub_sections/portal/) and the analysis of probability was run in MrBayes v. 3.2.1 (Ronquist et al. 2012). Bootstrap support values ≥ 70 % and Bayesian posterior probability values ≥ 0.95 are presented at the nodes. Fully supported branches (100 % BS / 1 PP) are thickened. *Cyphellophora laciniata* CBS 190.61 and *Cyphellophora pauciseptata* CBS 284.85 were used as outgroup. The new species proposed in this study is indicated in **bold**. T represents the ex-type strains of the taxa employed in this analysis.

Colour illustrations. Guayaquil, Ecuador (image credit Doug Moyer). Colonies growing on different culture media (PCA, MEA, OA at 25 °C and PDA at 15 °C; upper pictures); conidiogenous cells, conidia, budding cells and inflated cells. Scale bars = 10 µm.

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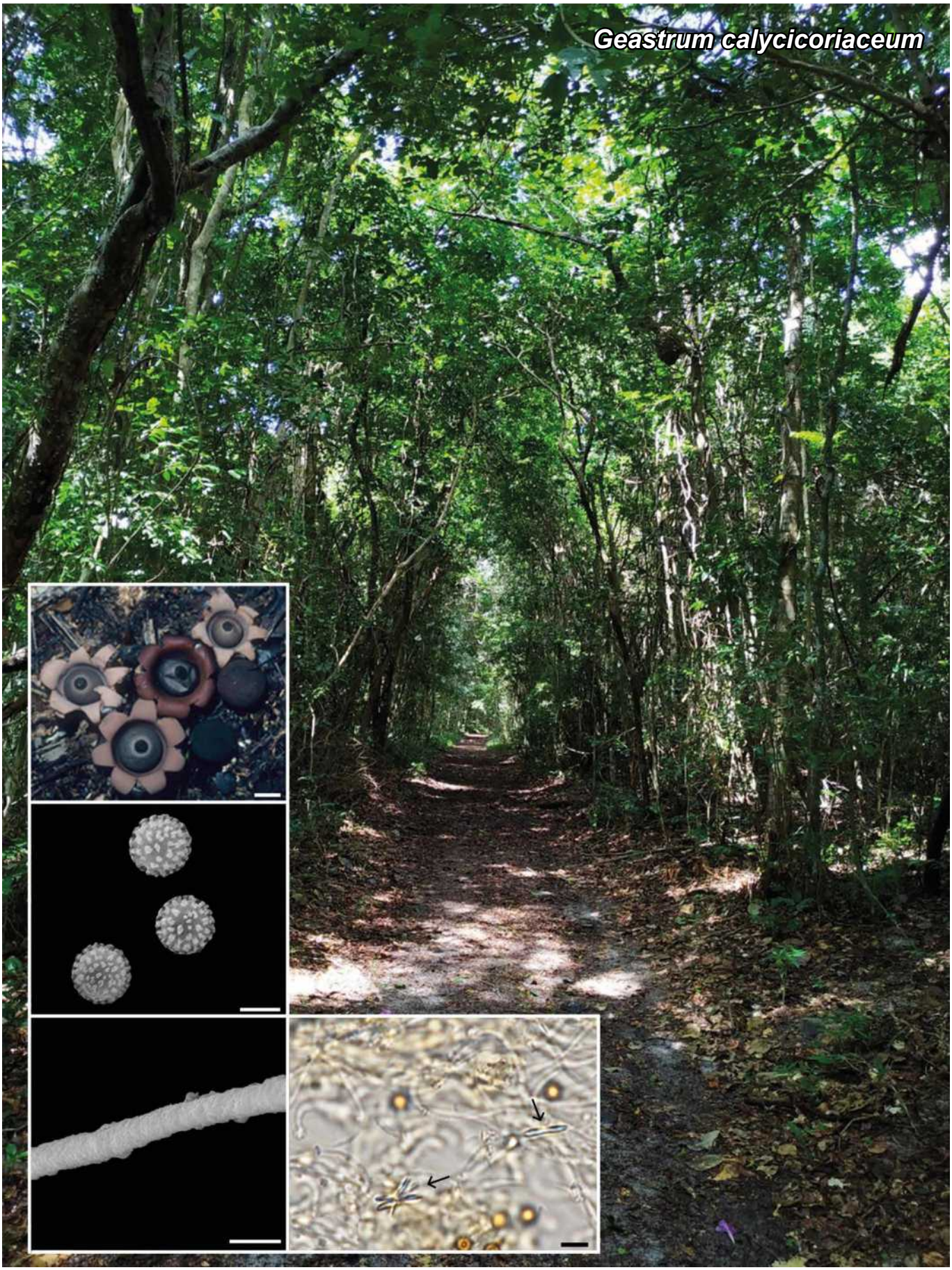
Geastrum calycicoriaceum

Fungal Planet 1080 – 29 June 2020

Geastrum calycicoriaceum Freitas-Neto, J.O. Sousa, Ovrebo, M.P. Martín & Baseia, *sp. nov.*

Etymology. From Latin *calyx* (cup) and *coriaceum* (leather). In reference to the coriaceous surface of mycelial layer, peeling-off to form a cup under basidiomata.

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

Unexpanded basidiomata epigeous, golden brown (5D7, Kornerup & Wanscher 1978) to brown (5E4; 5F4), subglobose to obpyriform, 11.5–15 × 12–20 mm, surface coriaceous, with little triangular processes when young, velutinous to papery with age, slightly encrusted with debris. *Subiculum* white (4A1). *Expanded basidiomata* saccate, 10–23 mm high (including peristome) × 11–32 mm wide. *Exoperidium* splitting into 5–9 triangular rays, revolute or sometimes involute, rolling up under basidiomata, non-hygroscopic. *Mycelial layer* honey yellow (5D6) to brown (5F5), non-persistent, ephemeral, peeling-off forming a cup under basidiomata, surface coriaceous, not encrusted. *Fibrous layer* greyish yellow (4B3) to white orange (5A2), coriaceous. *Pseudoparenchymatous layer* reddish (8E8) when fresh, brownish orange (5C4) to dark brown (6F4) when dried, rimose, persistent or peeling-off in irregular patches, with an inconspicuous collar. *Endoperidial* body greyish brown (6D3) to brownish orange (6C3), subglobose to pyriform, 5–18 × 9–21 mm, sessile, surface glabrous, non-pruinose. *Apophysis* absent. *Peristome* fimbriate, distinctly delimited by greyish brown (6E3) line, mammiform, lighter than endoperidium, < 2 mm high. *Gleba* greyish brown (6F3). *Basidiospores* brownish, globose to subglobose, 3.3–4.1 × 3.25–4.03 µm (x = 3.62 ± 0.2 × 3.55 ± 0.2 µm, Q_m = 1.02, n = 30), ornamentation conspicuous under LM. *Warts* cylindrical (0.3–0.5 µm high), sometimes with some confluent tips. *Apiculous* reduced. *Basidia* yellowish, oval, lageniform to clavate, thick walls (0.4–1.1 µm), 10.0–25.9 × 3.8–11.8 µm, 2–5 sterigmata. *Eucapillitium* pale brown hyphae, 2.8–6.4 µm diam, surface encrusted, covered by warts, thin walls (0.4–1.1 µm) and lumen evident. *Mycelial layer* composed of yellowish to hyaline, some sinuous and inflated hyphae, 1.9–3.3 µm diam, surface non-encrusted, some branched, thin-walled (0.3–0.75 µm) and lumen evident. *Fibrous layer* composed of yellowish to hyaline hyphae, 2.9–5 µm diam, surface non-encrusted, non-branched, thin-walled (0.5–1 µm) and lumen evident. *Pseudoparenchymatous layer* composed of yellowish, subglobose, oval to elongated cells, 21.2–69.8 × 10.1–47.9 µm, thick-walled (0.9–1.5 µm). *Rhizomorphs* composed of hyaline, thin hyphae, surface covered by acicular crystals, 3.8–11.6 × 1.1–1.9 µm, in an irregular arrangement.

Ecology & Distribution — The specimens were found in the Atlantic Rainforest of the state Rio Grande do Norte, Brazil, and the Lowland Tropical Moist Forest of Panama Province, Panama. Growing on wood and leaf litter, with forest cover and gregarious habit. The distribution of *G. calycicoriaceum* is restricted to Latin America, specifically Brazil, Panama and Peru.

Typus. Brazil, Rio Grande do Norte, Baía Formosa, Reserva Particular do Patrimônio Natural (RPPN) Mata da Estrela, S6°24'33" W34°59'25", on leaf litter, 26 June 2009, *B.D.B. Silva* et al. (holotype UFRN Fungos-1215; ITS and LSU sequences GenBank KJ127031 and JQ683663, MycoBank MB834940).

Additional materials examined. Panama, Panama Province, Gatun Lake, Buena Vista Peninsula, near Barro Colorado Island, N9°11'00" W79°49'34", on wood, 16 Aug. 1999, *C.L. Ovrebo* 3757 (paratype UFRN-Fungos 3002; ITS and LSU sequences GenBank MT183521 and MT183522). – Peru, Cuzco, Santa Maria, no date, *L. Papinutii*, *G. Rolól & J.C. Zamora* (paratype MA-Fungi 83787; ITS and LSU sequences GenBank KF988449 and KF988584).

Notes — *Geastrum calycicoriaceum* is characterised mainly by its ephemeral yellowish mycelial layer with coriaceous surface, peeling-off forming a cup under basidiomata and persistent rhizomorph with acicular crystals, also by distinct delimited peristome and basidiospores with 3.2–4.1 µm diam and small warts (up to 0.5 µm high). Our phylogenetic analyses (concatenate ITS and LSU) grouped *G. calycicoriaceum* in the *Mycelisotroma* section, *Velutina* subsection. This subsection comprises, until now, the species *Geastrum velutinum*, which has some features in common with *G. calycicoriaceum*: both have a yellowish mycelial layer, delimited and fimbriate peristome and presence of subiculum. However, *G. velutinum* has lighter colours in peridium layers (yellowish pseudoparenchymatous layer when fresh and pale brown endoperidium) than *G. calycicoriaceum*; moreover, *G. velutinum* lacks an ephemeral, coriaceous mycelial layer (Dissing & Lange 1962). *Geastrum javanicum* is another species which could be grouped in subsect. *Velutina* based on its morphological features. Presently there are no molecular data from the type to support *G. javanicum* as morphologically similar to *G. calycicoriaceum*, and it is distinct based on its smaller basidiospores (2.5–3.5 µm diam), conical peristome and felted endoperidium surface (Ponce de Leon 1968). *Geastrum argentinum* is another species morphologically close to *G. calycicoriaceum*. However, it has a non-delimited peristome, and larger basidiospores (4.8–5.6 µm diam) (Zamora et al. 2013).

Colour illustrations. Brazil, Rio Grande do Norte Baía Formosa, Reserva Particular do Patrimônio Natural (RPPN) Mata da Estrela, area of Atlantic Rainforest where the type species was collected; expanded basidiomata *in situ* (UFRN-Fungos 3002, paratype); basidiospores under SEM; eucapillitium under SEM; crystals of the rhizomorphs. Scale bars = 5 mm (basidiomata *in situ*), 2 µm (basidiospores under SEM), 5 µm (eucapillitium under SEM and crystals of the rhizomorphs under LM).

Supplementary material

FP1080 The tree was obtained after a Bayesian analysis (ITS nrDNA) in MrBayes v. 3.2.7a (Ronquist et al. 2012) using the settings indicated in Accioly et al. (2019), protocol deposited in protocols.io (https://doi.org/10.17504/protocols.io.wpdfdi6).

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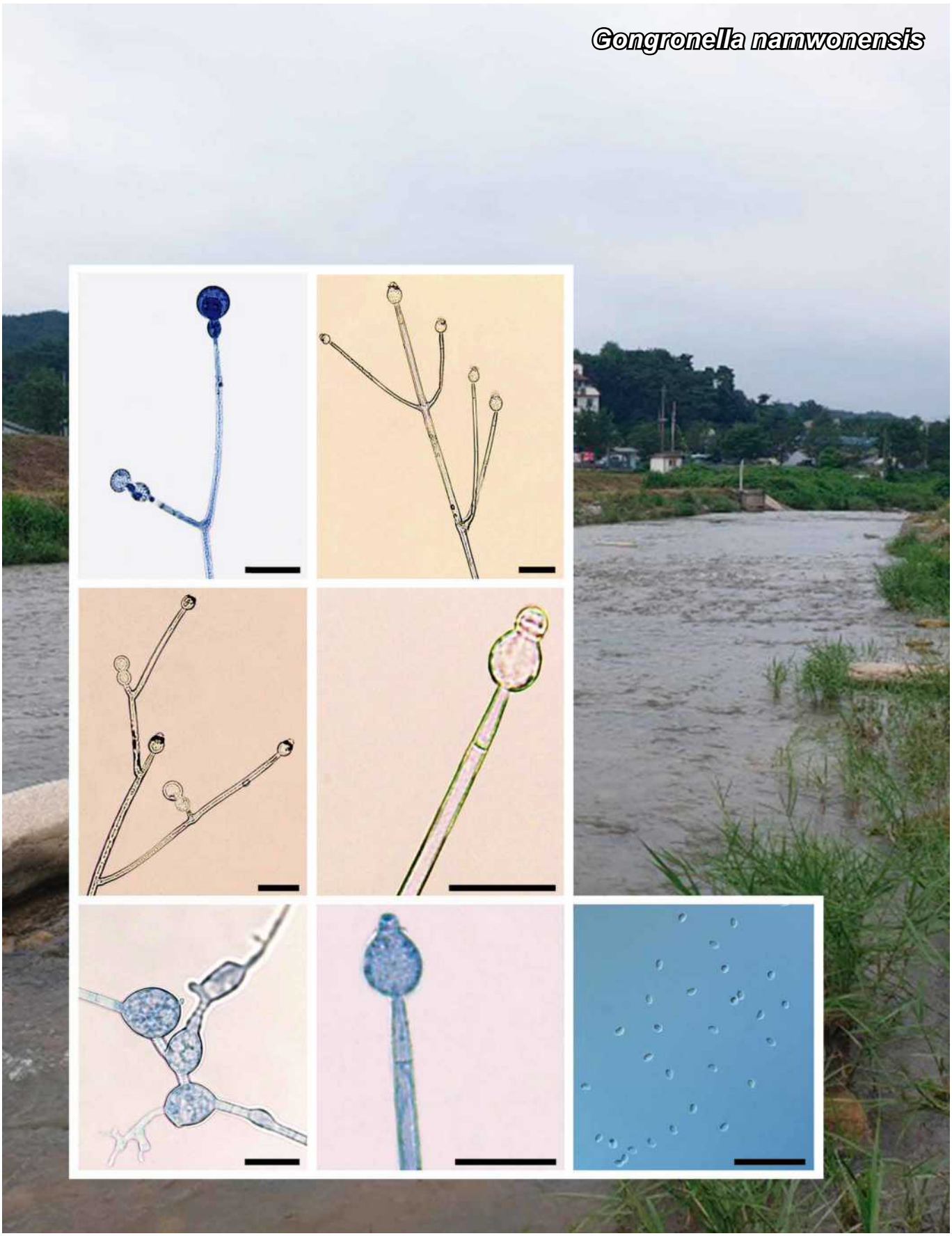

Gongronella namwonensis

Fungal Planet 1081 – 29 June 2020

Gongronella namwonensis Hyang B. Lee, A.L. Santiago & H.J. Lim, *sp. nov.*

Etymology. Name refers to the isolation site, Namwon city, from where the strain was first isolated.

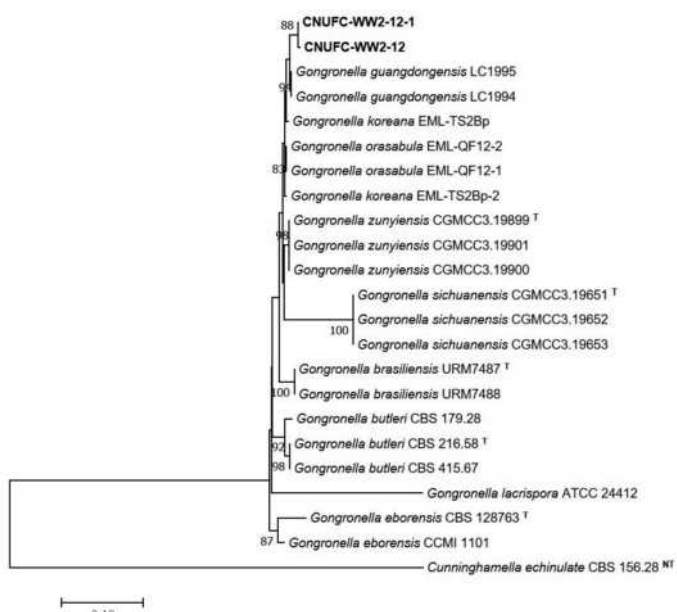
Classification — *Cunninghamellaceae*, *Mucorales*, *Mucoromycotina*, *Mucoromycota*, *Mucoromyceta.*

Mycelium hyaline. *Rhizoids* hyaline, coenocytic, branched; *stolons* hyaline, coenocytic, smooth-walled. *Sporangiophores* mostly arising from stolons or directly from aerial hyphae and stolon-like, erect or slightly recumbent, apophysate, simple or commonly sympodially and/or monopodially branched, smooth-walled, up to 1 mm in length and 5 µm diam, with up to 1 septum (majority) below the sporangium. Short and long branches may be found on the same sporangiophore at short or long distances from the main sporangium, and frequently rebranching. Branches in whorls of 2 or 3 may be found on some sporangiophores. *Apophyses* globose (2.5–)5–9.5(–12) µm, subglobose and ellipsoid, some with a truncated base, 7.5–14.5 × 5.5–12 µm, smooth-walled. *Sporangia* pale yellow, globose, wall transparent, deliquescent and smooth, up to 30 µm diam. Sometimes sterile sporangia are formed. *Columellae* hyaline, globose, subglobose, 3.5–7 µm diam, hemispherical, 1.8–5.5 × 2.5–8.5 µm, nipple-like, ellipsoidal, 2–3.8 × 2–5 µm. *Sporangiospores* hyaline, reniform, ellipsoidal, some ovoid, 2.5–3.5 × 1.7–2.5 µm, rarely irregular, up to 6 × 2.5 µm. *Giant cells* globose, subglobose and branched. *Chlamydospores* mostly globose and subglobose. *Zygosporangia* not observed.

Culture characteristics & Temperature tests — Colony white, reverse cream, low to moderate growth, taking the whole Petri dish (9 cm diam) after 5 d on malt extract agar (MEA) at 28 °C; odourless; at 5 °C – lack of growth; at 10 °C – slow growth (0.6 cm diam after 168 h); at 15 °C – slow growth (2.2 cm diam after 168 h); at 20 °C – slow growth (3.5 cm diam after 168 h), better than at 15 °C; at 25 °C – moderate growth (5.5 cm diam after 168 h); at 28 °C – optimum growth (9 cm diam after 120 h); at 30 °C – moderate growth (6 cm diam after 168 h); at 35 °C – slow growing (1.4 cm after 168 h). *Gongronella namwonensis* exhibited slightly better growth on MEA than on potato dextrose agar (PDA) at 20, 25, 28, 30 and 35 °C with similar growth at 10 and 15 °C. The growth was also slightly better on MEA than on synthetic mucor agar (SMA), except at 35 °C, where *G*. *namwonensis* grew 2.2 cm after 168 h in SMA.

Typus. South Korea, Namwon City, Jeonbuk Province, N35°24'27.66" E127°24'53.12", from freshwater samples, 24 July 2019, *H.B. Lee* (holotype CNUFC-WW2-12; ITS and LSU sequences GenBank MN658480 and MN658482, MycoBank MB833390).

Notes — *Gongronella namwonensis* differs from other species based on its morphological characters and the phylogenetic relationships established based on the ITS and LSU rDNA regions. Morphologically, *G. namwonensis* differs from the other species by producing concomitantly strongly sympodially and/or monopodially branched sporangiophores, some showing branches in whorls of 3, columellae varied (some nipple-like) and apophyses (some with a truncated basis), as well as giant cells. So far, giant cells had only been visualised in *G*. *brasiliensis*. Sporangiophores of *G. namwonensis* presents up to one septum below the sporangia and are long (up to 1 mm in length), different from the shorter (up to 320 µm in length) and with up to two septa sporangiophores of *G*. *brasiliensis*. The columellae of *G*. *brasiliensis* are globose, subglobose and conical-cylindrical, never hemispheric or nipple-like, as observed in *G. namwonensis.* Additionally, as observed in *G*. *brasiliensis*, our species produces sporangiospores varied in shape, but they are never falciform or ellipsoid to fusiform like the ones of the Brazilian species (Tibpromma et al. 2017). In the ITS and LSU rDNA trees (data not shown) *G. namwonensis* was placed in a well-supported clade separate from the other species. A more closely related species is *G*. *guangdonguensis*. Morphologically, both species can be easily distinguished by the shape of sporangiospores, being globose in *G*. *guangdonguensis*, as well the fact that it lacks rhizoids and stolons (AdAmčík et al. 2015), both structures which are present in *G. namwonensis.*



Phylogenetic tree of *Gongronella namwonensis* CNUFC-WW2-12 and CNUFC-WW2-12-1 based on maximum likelihood analysis of the internal transcribed spacer (ITS) nrDNA region. The numbers at the branches are bootstrap support value (≥ 50 %) from 1 000 replications. *Gongronella lacrispora* was used as the outgroup. Ex-type strains are indicated by T.

Colour illustrations. Woncheon stream, located in Namwon City, Jeonnam Povince, Republic of Korea. Once branched sporangiophore with fertile and sterile sporangium (branch); branched sporangiophore with two branches in whorls of two and columellae; sympodially branched sporangiophore with columellae and sterile sporangia; unbranched sporangiophore with apophysis and columella; giant cells; unbranched sporangiophore with apophysis and columella; sporangiospores. Scale bars = 20 µm.

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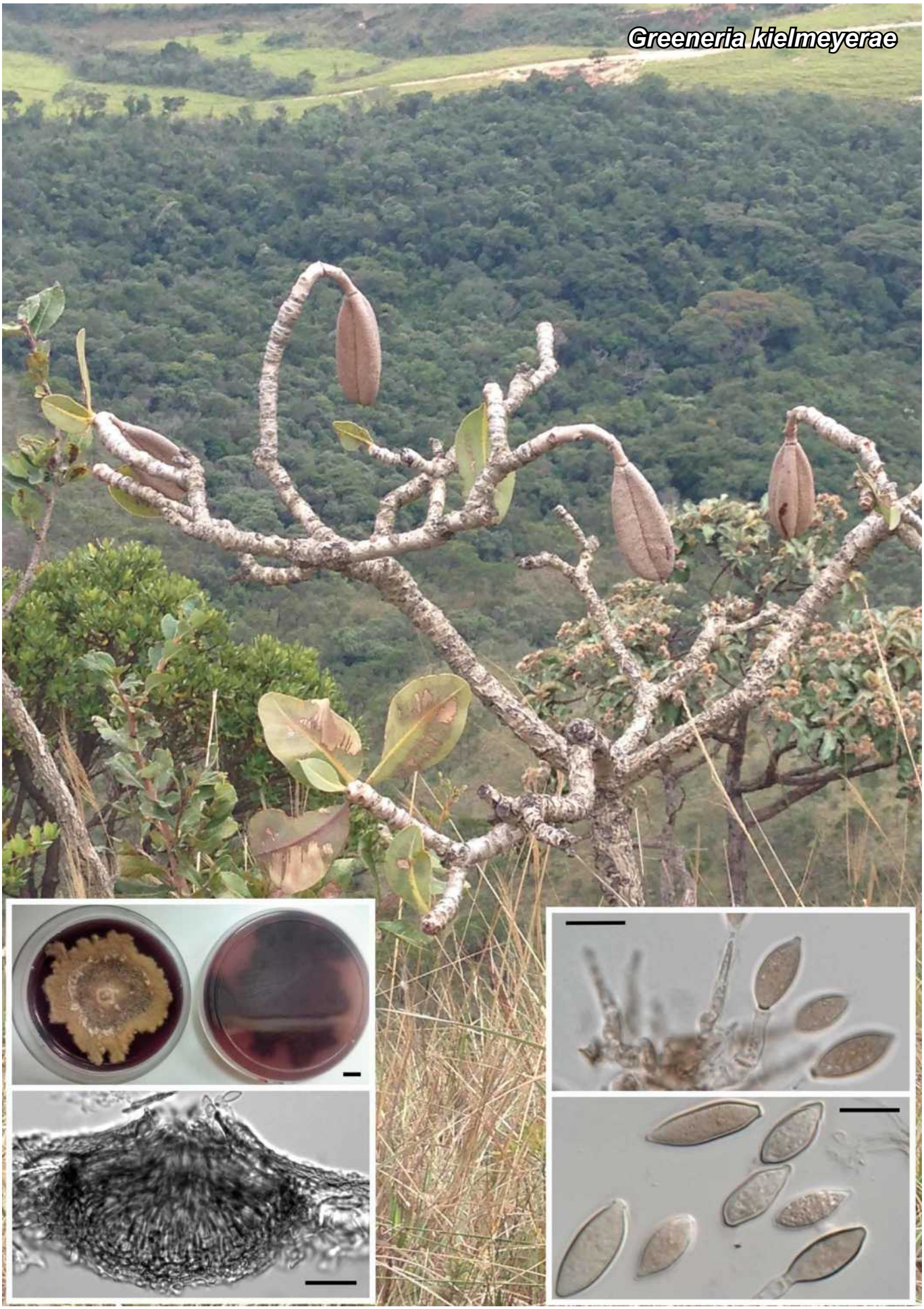

Greeneria kielmeyerae

Fungal Planet 1082 – 29 June 2020

Greeneria kielmeyerae C.P. Nicolli, F.S. Carmo, C.A. Inácio, P.A.S. Marbach, J.T. De Souza, *sp. nov.*

Etymology. *kielmeyerae*, named after the host genus, *Kielmeyera coriaceae* (*Calophyllaceae*).

Classification — *Melanconiellaceae*, *Diaporthales*, *Diaporthomycetidae*, *Sordariomycetes*.

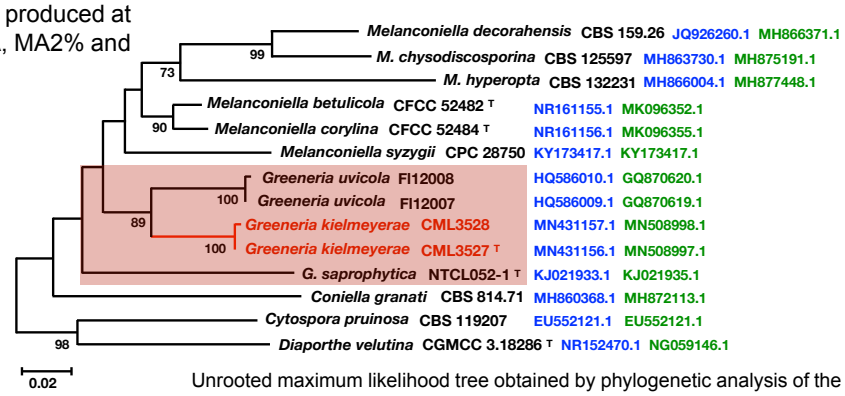
Pathogenic on leaves of *Kielmeyera coriacea*. *Leaf spots* up to 3 cm diam, rather irregular, sometimes confluent and covering almost the whole blade, often at the margins, amphigenous, showing small dark points of conidiomata at the upper side of the leaves. *Conidiomata* acervular at maturity, 175–300 µm diam, with brownish wall layers of *textura angularis*, subcuticular to intraepidermal, scattered. *Conidiophores* hyaline to pale brown, 5–10-septate, 11–25 × 2.5–5 µm, branched, smooth. *Vegetative hyphae* internal, hyaline to pale brown, smooth, intermingled with the host cells, branched, 1–3 µm diam. *Conidiogenous cells* hyaline, phialidic with a conspicuous collarette, 6–15 × 1–1.5 µm, percurrent proliferation with a serrate collarette. *Conidia* hyaline to pale brown, variable, sometimes elongate-fusoid, fusoid to ellipsoidal, aseptate, smooth and thick-walled, attenuate and papillate at the apex, truncate at the base, guttulate, 15–21 × 6–9 µm, 2–3 µm. Conidial cirrhi arising from conidiomata on the surface of infected leaves.

Culture characteristics — Colonies on potato dextrose agar (PDA), malt agar (MA2%) and oatmeal agar (OA) (near-UV light, 12 h photoperiod) with a pale brown centre surrounded by a greyish olivaceous ring containing dark spore masses, followed by a pale brown area with aerial feltose mycelium and irregular margins. A reddish to vinaceous pigment is produced in all media (either side of the plates), more intensely in PDA. Slow growth on all media, no growth at 10, 15, and 35 °C on PDA and MA2% and at 10, 15, 20 and 35 °C on OA. Growth / d at 20 °C on PDA was 0.9 and 0.5 mm (for isolates CML3527 and CML3528, respectively) while on MA2% it was 2.9 and 2.1 mm. Growth at 25 °C on PDA (1 and 1.6 mm), on MA2% (3.9 and 4.9 mm), on OA (4.5 and 5.2 mm). Growth at 30 °C on PDA was 0.7 mm for both isolates, on MA2% was 0.1 and 0.2 mm and on OA 0.3 and 0.1 mm. Conidia were produced at approximately 8, 10 and 14 d, respectively on OA, MA2% and PDA at 25 °C.

Typus. Brazil, DF, Brasilia, UNB campus, S15°53' W47°51', on leaf spots of *Kielmeyera coriacea* (*Calophyllaceae*), 20 May 2015, *J.T. De Souza* (holotype HURB 24682, dried culture on PDA, culture ex-type CML3527 = COAD2237; ITS, LSU and SSU sequences GenBank MN431156.1, MN508997.1 and MN508390.1, MycoBank MB834842).

Additional material examined. Brazil, Minas Gerais, Itutinga, from a leaf spot on *K. coriacea*, S21°18' W44°39', 20 Apr. 2016, *J.T. De Souza*, CML3528 = COAD2238; ITS, LSU and SSU sequences GenBank MN431157.1, MN508998.1 and MN508391.1.

Notes — *Greeneria kielmeyerae* is related to the other species of the genus, *G. uvicola* (Farr et al. 2001) and *G. saprophytica* (Tangthirasunun et al. 2014), but differs from these species in the production of a reddish to vinaceous pigment on plates, for having larger conidia (18 × 7.5 in *G. kielmeyerae*, 9.5 × 4.25 in *G. uvicola* and 12 × 5.5 in *G. saprophytica*) and a larger length to width ratio of the conidia (2.4 in *G. kielmeyerae*, 2.23 in *G. uvicola* and 2.18 in *G. saprophytica*). The closest phylogenetic relative of *G. kielmeyerae* CML3527^{T} (accession MN431156.1) with **ITS** sequences was *Melanconiella spodiaea* SPOD1 (GenBank JQ926301.1; 81.82 % identity), it had 80.1 % identity with the ITS sequence of *G. uvicola* FI12007 (GenBank HQ586009.1) and 77.93 % identity with the ITS of *G. saprophytica* NTCL052-1 (GenBank KJ021933.1). With **LSU** sequences the closest relative of *G. kielmeyerae* CML3527^{T} (GenBank MN508997.1) was *G. uvicola* USvitis (GenBank JN547723.1; 98.42 %) and it was 97.04 % identical to the LSU sequence of *G. saprophytica* NTCL052-1 (GenBank KJ021935.1). With **SSU** sequences, the closest relative of *G. kielmeyerae* CML3527^{T} (GenBank MN508390.1) was *Coryneum heveanum* MFLUCC17-0369 (GenBank NG_065764.1; 99.56 % identity), and had 99.33 % identity with the SSU sequence of *G. saprophytica* NTCL052-1 (GenBank KJ021934.1). The phylogenetic relationships of the genus *Greeneria* and closely-related genera are not well defined as observed by Tangthirasunun et al. (2014).



Unrooted maximum likelihood tree obtained by phylogenetic analysis of the combined ITS and LSU sequences from *Greeneria kiemeyerae* and phylogenetically related species performed in the software MEGA v. 6.06 (Tamura et al. 2013) employing the GTR+G model with 1 000 bootstrap re-samplings. Bootstrap support values > 70 % are presented. The new species is shown in red text (^{T} = ex-type) and the genus *Greeneria* is delimited in a pale red box. GenBank accession numbers are given after each strain (ITS = blue, LSU= green).

Colour illustrations. *Kielmeyera coriacea* with leaves showing symptoms of *Greeneria kielmeyerae* at the Bocaina hills in Lavras, Minas Gerais, Brazil. Fourteen-d-old colonies growing at 25 °C on PDA, both sides of a plate showing the reddish to vinaceous pigment produced by the fungus, immature conidioma, conidiophores showing the collarette and irregular percurrent proliferation, conidia. Scale bars = 1 cm (culture), 50 µm (conidioma) and 10 µm (other structures).

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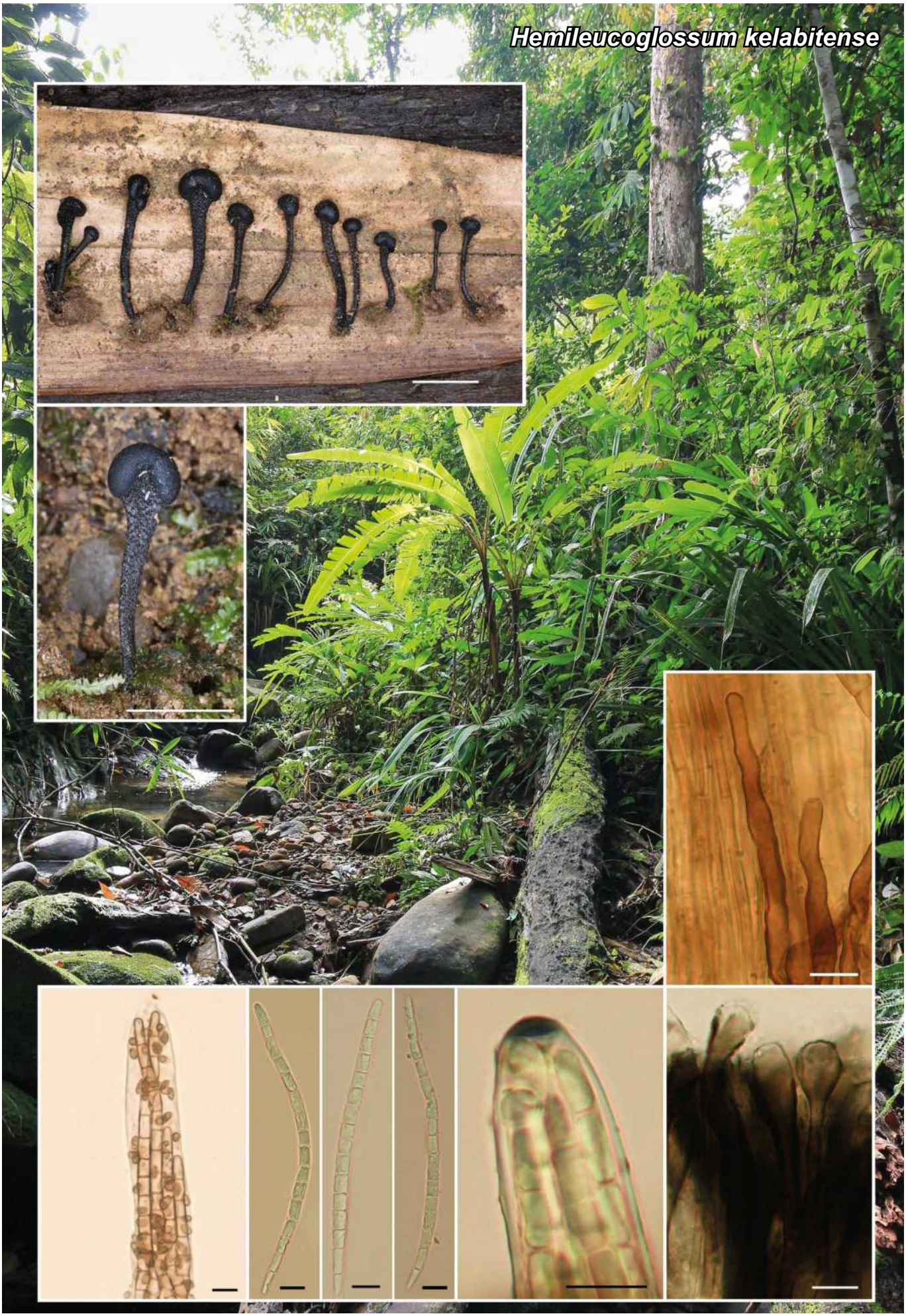

Hemileucoglossum kelabitense

Fungal Planet 1083 – 29 June 2020

Hemileucoglossum kelabitense V. Kučera, Fedosova & Sochorová, *sp. nov.*

Etymology. Name refers to the Kelabit Highlands where the fungus was collected.

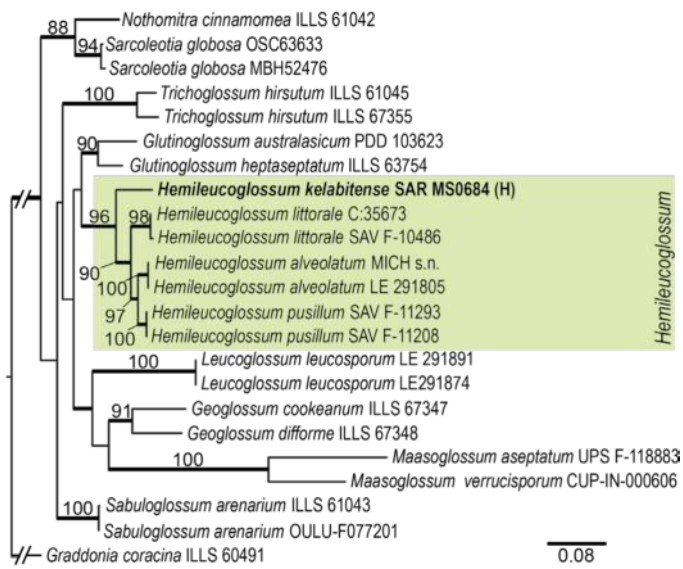
Classification — *Geoglossaceae*, *Geoglossales*, *Geoglossomycetes*.

Ascomata scattered to gregarious, capitate, stipitate, 6–22 × 1–6.7 mm, dry, black throughout. *Ascigerous part* capitate or broadly clavate, 1/7–1/4 of the total ascomata length, black, compressed or oval in cross section, sharply delimited from the stipe, smooth both in fresh and dry conditions. *Stipe* terete, cylindrical, oval in cross section, 5–17 × 0.6–4 mm, slender to robust, with dark brown setose hairs in tufts mainly at the upper part of the stipe, rough to squamulose. *Asci* cylindrical-clavate, (220–)223–245(–285) × 17.5–22 µm (all measurements of microscopic characters refer to rehydrated material in tap water), Q = 10.5–13.5, unitunicate, inoperculate, 8-spored, with euamyloid ascoapical apparatus and inamyloid wall in MLZ and IKI, arising from croziers. *Ascospores* elongate, ellipsoid baculiform, sometimes slightly curved, (110–)121–130(–135) × 5–5.7 µm, Q = (22–)24–27, hyaline, finally becoming brown, 15-septate at maturity, smooth. *Ascoconidia* ellipsoid, ovoid or dacryoid, 2.9–7.2 × 2.1–4.2 µm, Q = 1.2–2.5, brown, aseptate, formed already on ascospores inside the asci, smooth. *Paraphyses* straight, sparsely septate, 2–3 µm wide at lower part, hyaline at basal part to pale brown at the apex, agglutinated by dense brown amorphous matter. *Apical cells of paraphyses* usually inflated, clavate to capitate, sometimes constricted and proliferating, 22–60 × (4–)7–9(–12) µm. *Flesh of the fertile part* formed by grey cylindrical cells, 17–41 × 7–13 µm. *Flesh of the stipe* formed by grey cylindrical cells, 9–49 × 3–11 µm, oriented with their long axis in the same direction as the stipe. *Stipe surface* squamulose due to tufts of septate dark brown setose hairs, (100–)140–190(–220) × 7–10 µm at the middle part and 2–5 µm at the apical part, crumpled, sometimes bifurcated, thick-walled (0.5–1 µm), with rounded apex.

Habit, Habitat & Distribution — In small groups on soil among mosses. The species is known only from the type locality.

Typus. Malaysia, Borneo, Sarawak, Bario town surroundings, the Kelabit Highlands, N03°45'08" E115°26'16", elev. 1 130 m, on soil in a tropical rainforest, at a brook, 22 Jan. 2017, *Z. Egertová (Sochorová)* & *M. Sochor*, collection code: KH2017-1-22-01 (holotype SAR MS0684, isotype PRM 953086; ITS and LSU sequences GenBank MT021979 and MT021912, MycoBank MB834767).

Notes — Predominantly hyaline ascospores finally becoming brown, paraphyses agglutinated by a dense brown amorphous matter and setose hairs on the stipe (but lacking on the fertile part), as well as the genetic profile rank the new species with the genus *Hemileucoglossum* (Arauzo & Iglesias 2014). *Hemileucoglossum kelabitense* is characterised by the longest ascospores and asci within the genus. Morphologically, the most similar species is *H. alveolatum*, which is alike in number of septa (up to 15) in ascospores, but its ascospores are shorter and slightly thinner (60–95 × 4–5 µm). Moreover, *H. alveolatum* prefers very rotten wood and logs (Durand 1908). The remaining four species of the genus (*H. littorale*, *H. elongatum* and *H. pusillum* from Europe, and *H. intermedium* from North America) have significantly shorter ascospores with maximally 11 septa (Durand 1908, Nannfeldt 1942, Crous et al. 2017, Kučera & Fedosova 2017).



Maximum likelihood tree (RAxML v. 7.2.6; Stamatakis 2006) obtained from the ITS-LSU sequences dataset of *H. kelabitense* (H: holotype) and other *Geoglossaceae* species (TreeBASE study S25788). The Bayesian analysis (MrBayes v. 3.2.7; Ronquist & Huelsenbeck 2003) was performed for 1 M generations under SYM+I+G model for ITS and GTR+I+G model for LSU. Numbers above branches indicate Maximum likelihood bootstrap support values ≥ 85 %; thickened branches indicate Bayesian posterior probabilities ≥ 0.95. The scale bar represents the number of nucleotide changes per site.

Colour illustrations. Tropical rainforest in Bario town surroundings, the Kelabit Highlands. Macro- and microscopic structures of holotype: ascomata; ascospores (in tap water); ascospores germinating by ascoconidia inside the ascus (in tap water); amyloid reaction of the ascoapical apparatus (in IKI); paraphyses (in 3 % KOH); setose hairs of the stipe surface (in tap water). Rehydrated material was used for all photos of microscopic characters. Scale bars = 1 cm (ascomata), 10 µm (microscopic structures).

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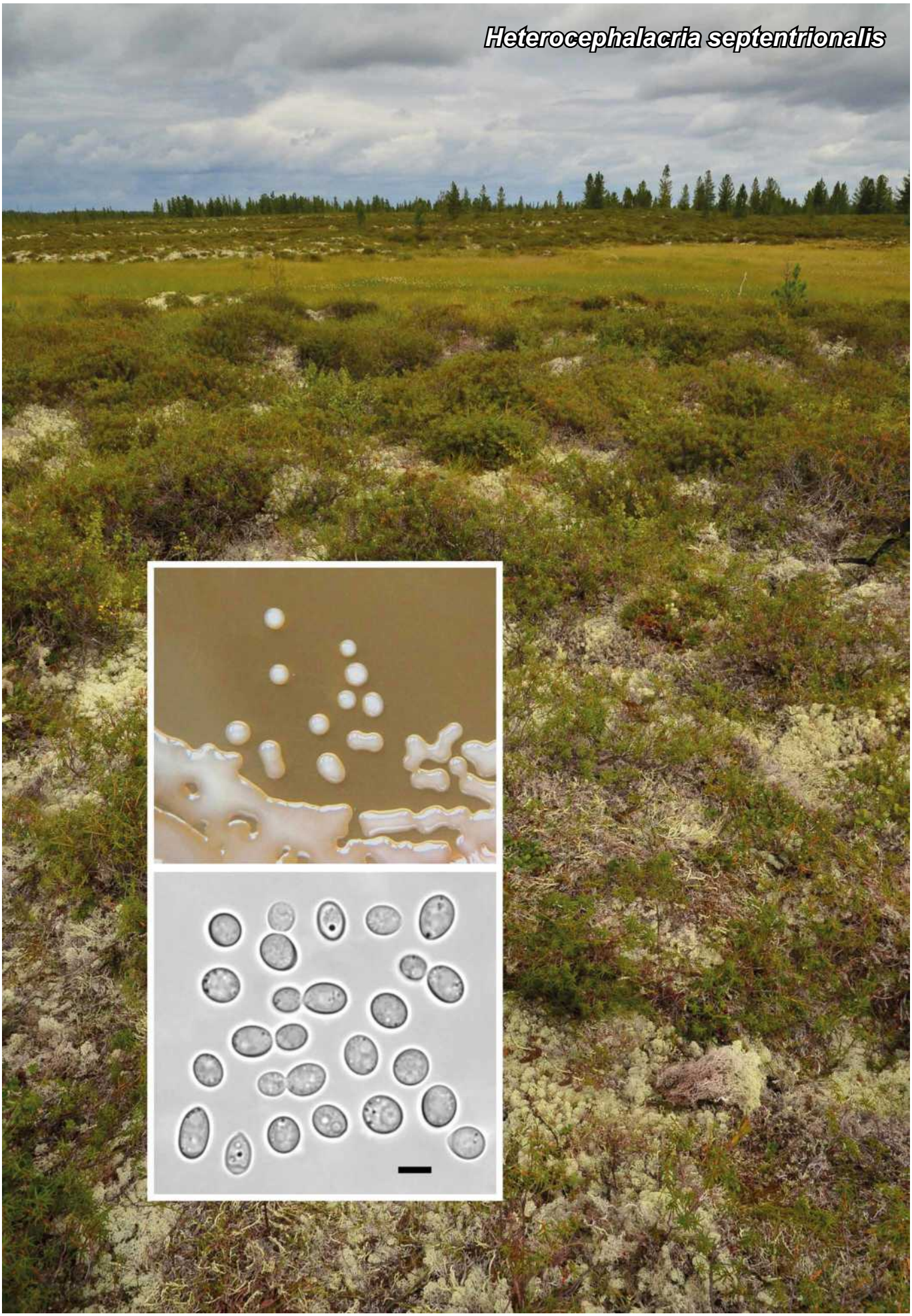

Heterocephalacria septentrionalis

Fungal Planet 1084 – 29 June 2020

Heterocephalacria septentrionalis Kachalkin, M.A. Tomashevskaya & T.A. Pankratov, *sp. nov.*

Etymology. The epithet refers to the species distribution in the northern regions of Russia.

Classification — *Filobasidiaceae*, *Filobasidiales*, *Tremellomycetes*.

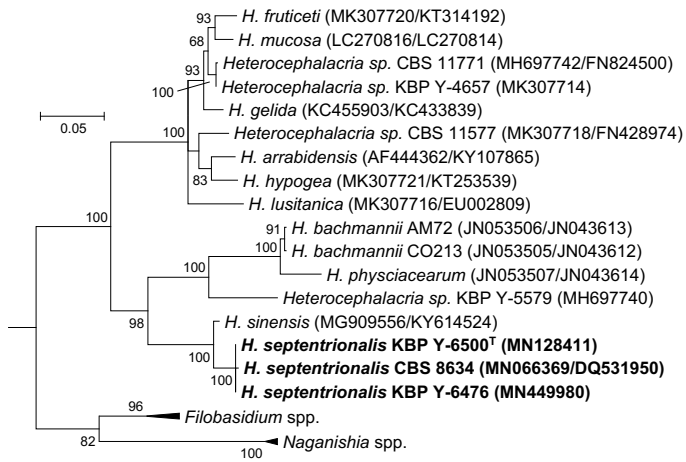
On glucose peptone yeast extract agar (GPYA) and 5 % malt extract agar (MEA), after 7 d at 20 °C, *streak* is cream-coloured, shiny and mucoid, with an entire margin, and flat profile. After a month, the colour of the streak is pinkish cinnamon. *Cells* are globose, ovoid to ellipsoid, 4–7 × 2.5–4 µm, occur singly or in pairs, dividing by polar and multilateral budding. *Sexual structures*, *pseudohyphae*, *true hyphae* and *ballistoconidia* have not been observed during 4 wk at 10 and 20 °C in culture (pure cultures and in mating test) grown on GPYA, MEA, potato dextrose agar (PDA), yeast nitrogen base with 0.5 % glucose (YNB) agar and cornmeal agar. Glucose is not fermented. Glucose, galactose, sucrose, maltose, cellobiose, trehalose, lactose, melibiose, raffinose, melezitose, soluble starch (variable and weak), D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, D-glucosamine (variable and weak), ethanol (weak), glycerol (weak), ribitol (weak), galactitol, D-mannitol, D-glucitol, methyl alpha-D-glucoside, salicin, D-gluconate, succinic acid, citric acid, 2-keto-D-gluconate, *myo*-inositol and arbutin are assimilated; no growth occurs on L-sorbose, inulin, erythritol, DL-lactic acid, methanol. Nitrogen compounds: ammonium sulfate, potassium nitrate, L-lysine (variable), D-glucosamine (variable), cadaverine (variable), creatinine (variable), creatine (variable) are assimilated, and no growth occurs on ethylamine. Growth on vitamin-free medium is variable. Growth on MEA with 10 % NaCl and on 50 % w/w glucose / yeast extract (0.5 %) agar is negative. Growth with 0.01 % and 0.1 % cycloheximide is variable. Starch-like compounds are produced. Diazonium blue B colour and urease reactions are positive. Maximum growth temperature is 22–24 °C.

Typus. Russia, Nadym, as endophyte from *Cladonia rangiferina* (*Cladoniaceae*), July 2017, *T.A. Pankratov & A.V. Kachalkin*, 1126v (holotype KBP Y-6500 preserved in a metabolically inactive state, ex-type cultures VKM Y-3042 = DSM 110122 = CBS 16173; SSU, ITS-D1/D2 domains of LSU nrDNA, *TEF1* and *RPB1* sequences GenBank MN449978, MN128411, LR702004 and LR702006, MycoBank MB833504).

Additional materials examined. Russia, Nadym, as endophyte from *C. stellaris*, July 2017, *T.A. Pankratov & A.V. Kachalkin*, KBP Y-6476; ITS-D1/D2 domains of LSU nrDNA and *TEF1* sequences GenBank MN449980 and LR702005; Kandalaksha, from *Empetrum nigrum*, Sept. 1994, *I.P. Bab eva & I.S. Reshetova*, KBP Y-3610 = CBS 8634; SSU, ITS and D1/D2 domains of LSU nrDNA sequences GenBank MN066371, MN066372 and DQ531950.

Colour illustrations. Russia, Nadym, forest-tundra zone of the Yamal Peninsula (photo provided by G.V. Matyshak). *Heterocephalacria septentrionalis* KBP Y-6500: growth of yeast colonies on MEA, yeast cells on MEA (after 7 d at 20 °C). Scale bar = 5 µm.

Notes — Analysis of the ITS-D1/D2 regions of the surveyed yeasts suggested that they were conspecific (2 subst. between strains from Nadym and Kandalaksha) and represented a hitherto undescribed species of *Heterocephalacria*. The genus *Heterocephalacria* comprises three sexual mycoparasites of lichens (*H. bachmannii* and *H. physciacearum*) and mushrooms (*H. solida*), and several asexual species of yeasts (Kachalkin et al. 2019, Kunthiphun et al. 2019, Li et al. 2019). Two new yeast strains were isolated as a minor component from *Cladonia* lichens whose thallus did not have basidioma-like structures. Although no sexual morph was discovered for new species, its mycoparasitic lifestyle cannot be excluded. Based on the NCBI GenBank database, the best hit using the **ITS** and **LSU** sequences is *H. sinensis* CBS 15417^{T} (**ITS** – GenBank MG909556; 96.21 % similar, 18 subst. and 3 gaps, **LSU** – GenBank KY614524; 98.01 % similar, 9 subst. and 2 gaps), using **SSU** it is *H. bachmannii* AM72 (GenBank JN043559; 99.34 % similar, 10 subst. and 1 gap), using ***TEF1*** and ***RPB1*** the number of nucleotide substitutions was considerable – without hits with *Heterocephalacria*. In compliance with a recent phylogenetic analysis of the genus (Kachalkin et al. 2019), the placement of the new species is demonstrated using the combined ITS and LSU rDNA phylogeny. *Heterocephalacria septentrionalis* can be differentiated from *H. sinensis* based on its ability to assimilate galactose, maltose, trehalose, melezitose, L-rhamnose, glycerol, D-mannitol, D-glucitol, citric acid, and negative growth on L-sorbose.



Maximum likelihood (ML) tree obtained from the combined analysis of ITS and LSU sequence data. Bootstrap support values above 55 % are shown at the nodes. The alignment included 980 bp and was performed with MAFFT v. 7 (Katoh et al. 2019). The General Time Reversible model (GTR) with Gamma distribution and invariant sites (G+I) was used as the best nucleotide substitution model. Phylogenetic analysis was conducted in MEGA v. 6 (Tamura et al. 2013). *Bullera alba* (AF444368/AF075500) was used as outgroup (hidden).

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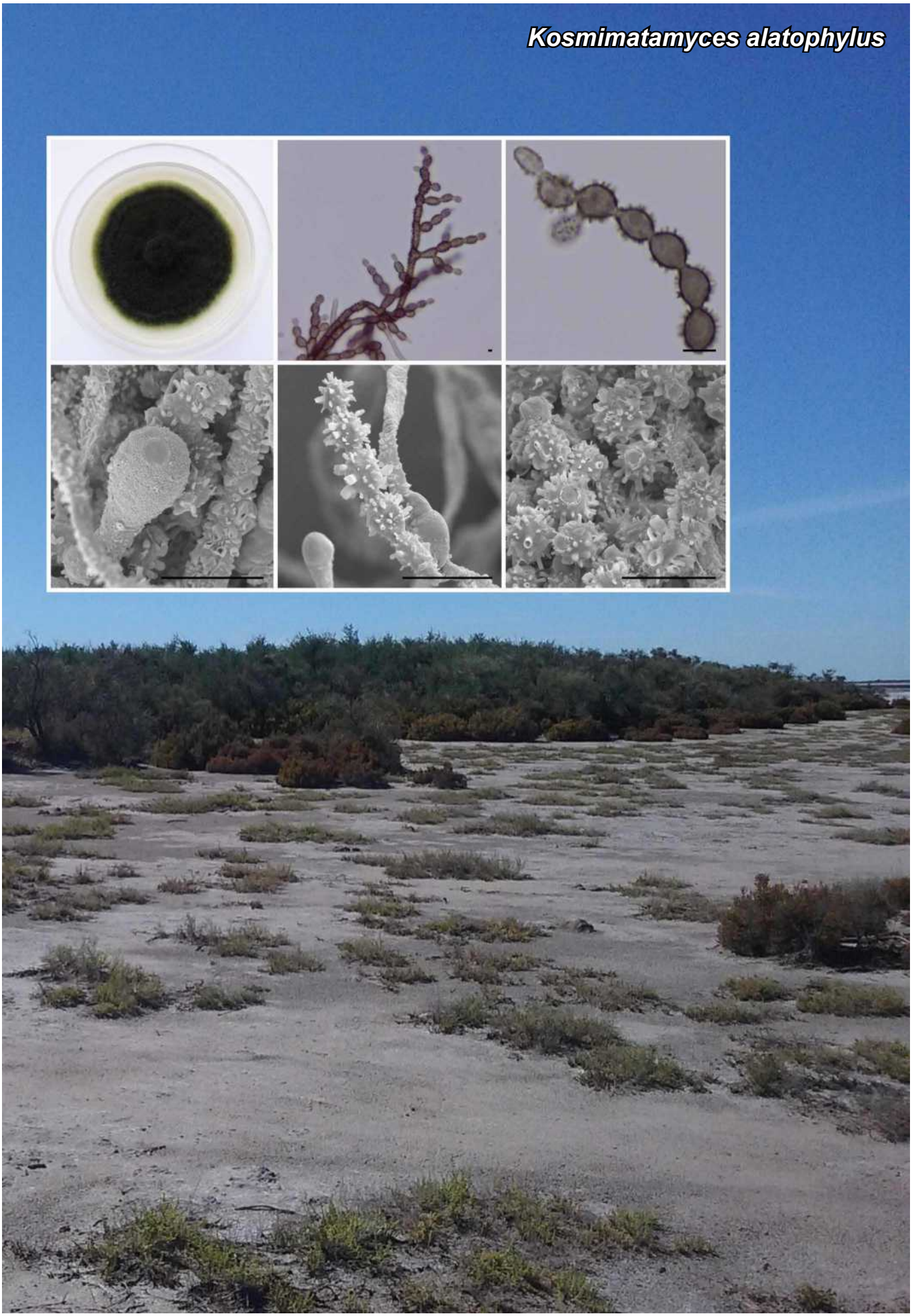
Kosmimatamyces alatophylus

Fungal Planet 1085 – 29 June 2020

Kosmimatamyces Bianchin., Reinoso F., Rodr.-Andr., Cano & Stchigel, *gen. nov*.

Etymology. From Greek *κοσμήματα-*, jewellery, and *-μύκης*, fungus, because of the microscopic look of the fungus.

Classification — *Capnodiaceae*, *Capnodiales*, *Dothideomycetidae*, *Dothideomycetes.*

Mycelium consisting of branched, septate, pale to dark brown, thick-walled hyphae, sometimes coarsely ornamented. *Conidiophores* solitary, macronematous or semimacronematous, erect, straight to flexuous, from hyaline to dark brown, thick- and smooth- to rough-walled, cylindrical, narrow, branched or not, branches terminal and lateral, in angles of 45 to 90°. *Conidiogenous cells* determinate, integrated, terminal and intercalary, mono- or polyblastic, pale to dark brown, verrucose, scars truncate. *Conidia* holoblastic, 0–1-septate, brown to dark brown, thick-walled, globose, ovoid or ellipsoid, ornamented with spines and crater-like warts, with dark scars at one or both ends, arranged in branching acropetal chains.

Type species. Kosmimatamyces alatophylus Bianchin., Reinoso F., Rodr.-Andr., Cano & Stchigel.

MycoBank MB833527.

Kosmimatamyces alatophylus Bianchin., Reinoso F., Rodr.-Andr., Cano & Stchigel, *sp. nov.*

Etymology. From Greek *αλατος-*, salt, and *-φιλος*, lover, because of the environment from which the fungus was recovered.

Mycelium consisting of branched, septate, thick-walled, 2.5–4.5 µm wide hyphae. *Conidiophores* solitary, macronematous or semimacronematous, erect, straight to flexuous, from hyaline to dark brown, thick- and smooth-walled to verrucose along its length, branched or unbranched, branches terminal or lateral, in an angle 45 to 90°, 13–100 × 3.5–6 µm. *Conidiogenous cells* determinate, integrated, terminal or intercalary, pale to dark brown, verrucose, mono- or polyblastic, 8–12 × 5–7.5 µm, scars truncate of 2–3.5 µm wide. *Ramoconidia* aseptate, pale to dark brown, thick- and smooth-walled to verrucose, subcylindrical, 8.5–25 × 3–6 µm. *Conidia* 0–1-septate, brown to dark brown, thick-walled, with a spinulose, digitate, pustulate to crater-like ornamentation, globose, limoniform to ovoid or ellipsoid, 6–11 × 5–10 µm, with one or more notorious scars, arranged in branching acropetal chains, of schizolytic secession.

Culture characteristics — (after 2 wk in darkness at 25 °C). Colonies on oatmeal agar (OA) up to 37 mm diam, flat, slightly dusty to floccose, greyish sepia (Rayner 1970), aerial mycelium scarce, margins entire, exudates as olivaceous brown; reverse black, diffusible pigments absent. Colonies on potato dextrose agar (PDA) up to 39 mm diam, flat, velvety, radiate and sulcate, greyish sepia at centre, greyish white to the borders, margins regular, scarce droplets of olivaceous exudates; reverse olive black to greyish sepia, diffusible pigments absent. On malt extract agar (MEA) up to 34 mm diam, velvety, zonate, radially folded and somewhat elevated, pale olivaceous grey, mostly consisting of vegetative mycelium, margins irregular; reverse greenish black, diffusible pigments absent. On potato carrot agar (PCA) up to 41 mm diam, floccose, olivaceous black, radiate, margin filamentous; reverse olivaceous black, diffusible pigments absent. On SNA up to 40 mm diam, flat, radiate, olivaceous at the centre and isabelline to the margins, margin entire; reverse olivaceous black at the centre, borders olive, diffusible pigments absent.

Typus. Argentina, Buenos Aires province, Salitral de la Vidriera, S38 44.816 W62 33.251, from soil collected in a saltmarsh, 28 Aug. 2015, *C.G. Reinoso Fuentealba & M.V. Bianchinotti* (holotype CBS H-24325, culture ex-type FMR 15091; ITS and LSU sequences GenBank LR588887 and LR588888, MycoBank MB833528).

Notes — *Kosmimatamyces* is a new genus that groups in the *Capnodiaceae*, a family whose members are known as sooty molds whose dark hyphae cover the surface of living leaves and twigs of many plants (Hughes 1976, Abdollahzadeh et al. 2020). Hypersaline soil represents a new ecological niche, reinforcing the hypothesis of Crous et al. (2009) and Chomnunti et al. (2011) that plant surfaces are not the only environmental niche for this group of fungi. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the **ITS** sequence was *Microxiphium theae* CBS 202.30 (GenBank MH855113; Identities = 475/514 (92 %), 11 gaps (2 %)), *Antennariella placitae* AS01 (GenBank MG583755; Identities = 472/511 (92 %), 11 gaps (2 %)), and *Leptoxyphium kurandae* MCC1085 (GenBank KF826942; Identities = 470/510 (92 %), 9 gaps (2 %)); using the **LSU** sequence the closest hit were *Capnodium coartatum* MFLUCC10-0066 (GenBank JN832613; Identities = 547/555 (99 %), no gaps), *Microxyphium aciculiforme* CBS 892.73 (GenBank GU301847; Identities = 547/555 (99 %), no gaps), and *Conidioxyphium gardeniorum* CPC 14327 (GenBank GU301807; Identities = 547/555 (99 %), no gaps). The LSU phylogenetic tree corroborated the placement of our isolate close to the genus *Leptoxyphium*. The species of *Leptoxyphium* are characterised by pycnidial conidiomata with a bulbous swollen base and cylindrical neck that expands at the apex to become funnel-shaped (Hughes 1976, Chomnunti et al. 2011), whereas *Kosmimatamyces* produces single conidiophores.

Colour illustrations. *Kosmimatamyces alatophylus*, Salitral de la Vidriera. Colony on OA at 2 wk; conidiophores, conidiogenous cells and conidia. Scale bar = 10 µm.

Supplementary material

FP1085 Maximum likelihood tree obtained from the LSU sequence of our isolate and those retrieved from GenBank.

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Lactifluus albopicri
JET 1203

Fungal Planet 1086 – 29 June 2020

Lactifluus albopicri T. Lebel & L. Tegart, *sp. nov.*

Etymology. Named for the colour and hot taste of the basidiomata, albo = white, picri- = hot.

Classification — *Russulaceae*, *Agaricales*, *Agaricomycetes.*

Basidiomata robust, lactarioid. *Pileus* 48–85(–120) mm diam, convex with decurved margin, planoconvex with depressed centre when mature; dry, smooth to very finely tomentose, white becoming very pale yellowish buff to pale honey cream with cream margin and slightly honey coloured centre; context solid, white becoming very pale cream coloured, no staining. *Lamellae* at first broadly adnate, then subdecurrent to decurrent, narrow (1.5 mm), close (c. 6–8 per cm) with some forking, and 2–3 rows lamellulae, concolourous with pileus or slightly paler. *Stipe* 20–50(–80) × 10–22(–30) mm, cylindrical or slightly tapered to base in older material, central, smooth, dry, whitish tinged with yellowish buff or hints of pale orange to pinkish buff; context firm, white, unchanging, dry, chalky. Basal mycelium white. *Latex* copious, white, unchanging, very hot and peppery. Spore deposit white. Phenol: rapidly wine red/pink; $FeSO_4$ – rapidly brown. *Spores* 6.2–7.65(–7.9) × 5.1–6.3 µm (n = 40, 7.22 ± 0.53 × 5.91 ± 0.39 µm), Q = 1.09–1.28, subglobose to broadly ellipsoid, hyaline, asymmetric; ornamentation and spore wall amyloid, up to 0.6–1 µm high, composed of isolated irregular warts that join together to variable degree in very fine lines to form a very partial reticulum, plage inamyloid. *Basidia* 29–40 × 5.5–11 µm, cylindrical to subclavate, 2–4-spored; sterigmata 3–5 µm long. *Pleuromacrocystidia* 25–60 × 5–9 µm, moderately common to abundant, cylindric to fusiform. *Pleuropseudocystidia* 32–48 × 7–12 µm, cylindrical, moderately abundant, apices occasionally mucronate. *Cheilomacrocystidia* 30–55 × 4–10 µm, cylindrical to subclavate with capitate apices, scattered. *Hymenophoral trama* predominantly composed of hyaline hyphae 3–6 µm diam, interwoven with abundant sinuous lactifers up to 12 µm broad; subhymenium cellular, 2–3 tiers of parenchymatous cells, 8–14 × 5–11 µm. *Pileipellis* a hyphoepithelium, 2-layered: subpellis up to 100 µm thick, composed of globose to subglobose cells 8–21(–32) µm diam; suprapellis 15–50 µm thick, composed of mostly upright thin-walled hyaline hyphae, 3–4(–5) µm diam, and abundant dermatocystidia 32–63 × 8–14 µm, cylindrical to clavate, with granular contents. *Pileus context* heteromerous, with abundant sinuous laticiferous hyphae, 6–11 µm diam.

Habit, Habitat & Distribution — Gregarious on soil amongst eucalypt leaf litter in wet sclerophyll forest. Widely distributed from cool temperate forest in southern Australia (Vic, Tas) with *Eucalyptus regnans* and *Nothofagus cunninghamii* dominant in canopy, scattered *Acacia dealbata* and *A. melanoxylon*, with ferny understorey of *Dicksonia antarctica*, *Blechnum watsii* and *Asplenium* sp., up to subtropical eucalypt and *Lophostemon* woodland in northern Australia (NT, QLD).

Typus. Australia, Victoria, Yarra State Forest, Big Creek Road, Ada Tree Walk, 25 Mar. 2005, *J.E. Tonkin* 1203 (holotype MEL 2297391; ITS and LSU sequences GenBank MN598874 and MN598855, MycoBank MB832708).

Notes — The overall diversity of *Lactifluus* in Australia is poorly known (May et al. 2004), perhaps in the order of 10–12 species, with only a few sections examined (i.e., *Gerardii*; Stubbe et al. 2012). The main characters used to distinguish species in *Lf.* sect. *Piperati* are the shape and ornamentation of the spores, the composition of the lamellar edge, the form of the cheilomacrocystidia and the hypoepithelium pileipellis that lacks thick-walled elements (Heilmann-Clausen et al. 1998, De Crop et al. 2014). The majority of other species in *Lactifluus* have pilei with thick-walled elements (Verbeken & Walleyn 2010). Two morphologically distinct species are recognised from Europe and an additional 10 or so Asian species remain to be morphologically documented and described (De Crop et al. 2014). Up until recently, no species of *Lf.* sect *Piperati* were known to occur in South America, Africa or Australasia.

Lactifluus albopicri is a widespread species in eastern Australia, from Tasmania up to subtropical Queensland and into the Northern Territory, occurring in wetter forests in association with *Eucalyptus* and *Nothofagus*. *Lactifluus albopicri* resembles many of the known species from *Lf.* sect. *Piperati*, in the robust, pale coloured basidiomata, hot peppery latex, and spores with fine, low ornamentation. *Lactifluus albopicri* differs from another Australian sect. *Piperati* species, *Lf. austropiperatus*, in the typically larger sporocarps, slightly darker yellowish to pale orange pileus and lamellae, larger and subglobose vs broadly ellipsoid spores with finer and lower ornamentation. *Lactifluus albopicri* sits in a well-supported clade with a single sequence from Thailand (GenBank KF220078), amongst other SE Asian clades.

Colour illustrations. Cool temperate rainforest dominated with *Eucalyptus regnans* and *Nothofagus cunninghamii* with scattered *Acacia* spp. and understorey of *Dicksonia antarctica* (photo G. Lay). Northern habitat of subtropical *Lophostemon* woodland; basidiomata; section through hypoepithelium pileipellis; SEM of spores. Scale bars: 10 mm; 20 µm; 5 µm.

Supplementary material

FP1086-1 Additional materials examined.

FP1086-2 Bayesian (MrBayes v. 3.2.6) 50 % majority-rule consensus tree of the ITS-nrDNA for a selection of *Lactifluus* species. Thickened lines indicate PP support > 0.95.

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Lactifluus austropiperatus

Fungal Planet 1087 – 29 June 2020

Lactifluus austropiperatus T. Lebel & L. Tegart, *sp. nov.*

Etymology. Named for its similarity to *Lactifluus piperatus* from the Northern Hemisphere and its distribution in Australia.

Classification — *Russulaceae*, *Agaricales*, *Agaricomycetes.*

Basidiomata robust, lactarioid. *Pileus* 30–50 mm diam, convex with decurved margin, planoconvex with depressed centre when mature; pileipellis dry, glabrous, azonate, whitish variously tinged with yellowish or hints of pale orange when younger, to pale-biscuit-buff overall in older specimens. *Lamellae* subdecurrent, close (c. 5–7 per cm) with some forking closer to margin, and 2–3 rows lamellulae, very pale orange, bruising a little darker with handling. *Stipe* 32–65 × 8–16 mm, cylindrical, whitish tinged with yellowish or hints of pale orange; context white, unchanging, taste hot and peppery. *Latex* copious, white, unchanging or barely yellowing slightly after 10–15 min, very hot and peppery. Spore print white. *Spores* (7.5–)8.5–9.5 × 6.8–8.4 µm (n = 40, 8.11 ± 0.55 × 7.28 ± 0.61), Q = 1.07–1.15 ± 0.03, barely globose to subglobose, asymmetric, hyaline; ornamentation amyloid, up to 0.4 µm high, composed of irregular warts that join together to variable degree in short thin fine lines; plage inamyloid. *Basidia* 32–45 × 6–11 µm, cylindrical to subclavate, 4-spored; sterigmata short, robust. *Pleuromacrocystidia* 35–60 × 4–7 µm, abundant, narrowly cylindrical to fusiform, with tapering apex. *Pleuropseudocystidia* similar size and shape to pleuromacrocystidia, moderately abundant, sometimes with irregular mucronate apices. *Cheilomacrocystidia* (29–)40–65(–75) × 4–6.5(–8) µm, cylindrical to filiform with acute or capitate apices, with crystalline contents, scattered, more obvious in younger specimens. *Hymenophoral trama* up to 70 µm wide, composed of interwoven hyaline hyphae of 3–6 µm diam and abundant sinuous lactifers up to 10 µm thick, sphaerocytes rare; subhymenium layer up to 25 µm thick, parenchymatous, cells 6–11 µm diam. *Pileipellis* a hyphoepithelium, 2-layered: subpellis up to 155 µm thick, composed of globose to subglobose cells 8–21 µm diam; suprapellis 31–50 µm thick, composed of mostly repent thin-walled hyphae, frequently septate, 2–4(–5) µm broad; context broad, composed of heteromerous tissue, sphaerocytes up to 35 µm diam interwoven with hyaline hyphae 3–7 µm diam, and scattered to abundant sinuous laticiferous hyphae of 5–12 µm diam.

Habit, Habitat & Distribution — In savanna eucalypt woodland with *Eucalyptus pilularis* or *E. delegatensis*, and *E. cypellocarpa* near creek lines with *Syzygium*, *Allocasuarina*, *Acacia* spp., with tall grass understorey, rarely in mixed *Nothofagus moorei* forest leaf litter; solitary but common.

Typus. Australia, Queensland, Yungaburra Rifle Range, 3 Apr. 1989, *N.L. Bougher* E4074, found in savanna woodland dominated by *Eucalyptus pilularis* and *Allocasuarina littoralis* (holotype PERTH 07550324; ITS and LSU sequences GenBank MN614115 and MN614111, MycoBank MB832709).

Additional material examined. Australia, Queensland, Tullawallal, 3 Apr. 2002, *A.M. Young* LNP551 & *N. Fechner* AQ 0808481 (ITS and LSU sequences GenBank MN614118 and MN614113); Northern Territory, Tiwi Islands, Melville Island, Conder Point, 27 Apr. 1989, *J.A. Curnow* 3148 MEL 2202701 (ITS sequence GenBank MN614117); New South Wales, Joys Creek Track near summit of Mt Jersey, 27 Mar. 2002, *Thiele* 2074, MEL 2150778 (ITS and LSU sequences GenBank MN614116 and MN614112).

Notes — *Lactifluus austropiperatus* morphologically closely resembles *Lf. subpiperatus*, described from Japan (Hongo 1964); unfortunately, no sequence data are currently available for comparison. *Lactifluus dwaliensis*, *Lf. allardii*, *Lf. glaucescens*, and *Lf. subpiperatus* grow respectively in association with species of oak in temperate deciduous forests in India, hardwood or pine-oak forests in central to southern USA, mixed deciduous forests in Europe, or deciduous oak forest in Japan (Das et al. 2003, Verbeken et al. 2012). *Lactifluus dwaliensis* is a rare all-white species with quite a long stipe, and context and tissue that slowly stains light greenish yellow, while *Lf. allardii* is stockier, with pinkish brown colours and flesh that stains purplish pinkish then green, and white copious latex that slowly turns greenish then brownish (Das et al. 2003, De Crop et al. 2014). *Lactifluus glaucescens* is an elegant, all-white species with densely crowded lamellae and latex that turns slowly olive to pastel green. All five species have smallish spores with low ornamentation under 0.5 µm high, as isolated warts with scattered connecting lines, grading into a partial reticulum. *Lactifluus subpiperatus* is morphologically most similar to *Lf. austropiperatus*, also having white then patchily pale ochraceous, somewhat stocky basidiomata, forked lamellae, and small subsphaerical spores (Hongo 1964). However, *Lf. austropiperatus* has sporocarps with more yellowish to pale orange tinges, flesh and latex that does not change colour or only very slowly and slightly, with no green tones, and pleuromacrocystidia are present (De Crop et al. 2014). *Lactifluus austropiperatus* grows in association with subtropical forest of *Eucalyptus*, and more rarely *Nothofagus*, in northern NSW and southern QLD, Australia.

In our analysis *Lf. austropiperatus* is in a strongly supported clade with a specimen from Thailand (GenBank KF220110, *H.T. Le* 376), however, at this time we maintain the Australian material as distinct until further collections from Thailand can be examined and sequenced. Preliminary morphological examination shows the spores of *H.T. Le* 376 to be slightly smaller, and the ornamentation to be slightly finer than the Australian material. *Lactifluus austropiperatus* is sister to *L. dwaliensis*, a specimen from Honduras (LMUNAH0073; no plant associate listed), and an environmental sample from Florida, USA associated with *Pinus clausa*.

Colour illustrations. Savanna eucalypt woodland dominated by *Eucalyptus pilularis* and *Allocasuarina littoralis* (photo F. Guard). Basidiomata; section through hyphoepithelium pileipellis; and spores in Melzer's reagent. Scale bars: 10 mm; 20 µm; 10 µm.

Supplementary material

FP1087 Bayesian (MrBayes v. 3.2.6) 50 % majority-rule consensus tree of the ITS-nrDNA for a selection of *Lactifluus* species. Thickened lines indicate PP support > 0.95.

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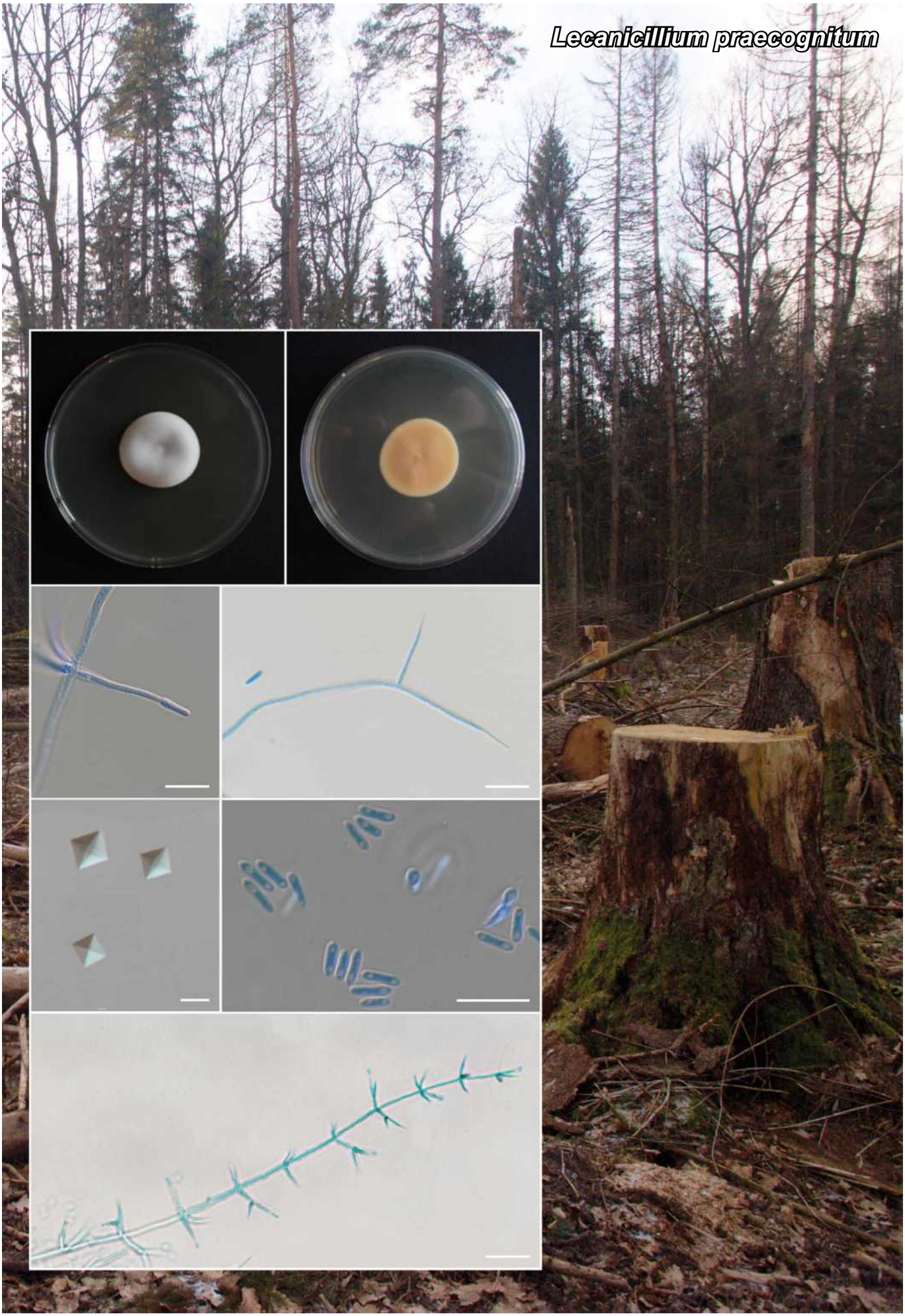

Lecanicillium praecognitum

Fungal Planet 1088 – 29 June 2020

Lecanicillium praecognitum Gorczak & Kisło, *sp. nov.*

Etymology. *prae* (Latin: before, ahead of) + *cognitum* (Latin: known, noted; neut. part. adj.); known before; referring to the fact that the species was noted several years before formal description.

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

On sabouraud dextrose agar (SDA): *Conidiophores* erect, mostly single, sometimes in whorls up to four. Unfrequently secondary phialides arise, sometimes in whorls up to three. *Phialides* 17.5–43.5 (av. = 28.5) µm long × 1.5–3 (av. = 2.3) µm wide. *Conidia* hyaline, smooth, granular, oblong to slightly fusiform, solitary or in small clusters, (3.5–)4–6.5(–7.5) (av. = 5.3) µm long × 1–2.5(–3) (av. = 1.8) µm wide, usually trice as long as wide, with one to two guttules. *Vegetative hyphae* smooth, hyaline, regularly septate, 1.5–3 (av. = 2.2) µm wide. *Crystals* octahedral, translucent, 10.5–20(–22.5) (av. = 16.5) µm long in medium, less regularly in substrate mycelium.

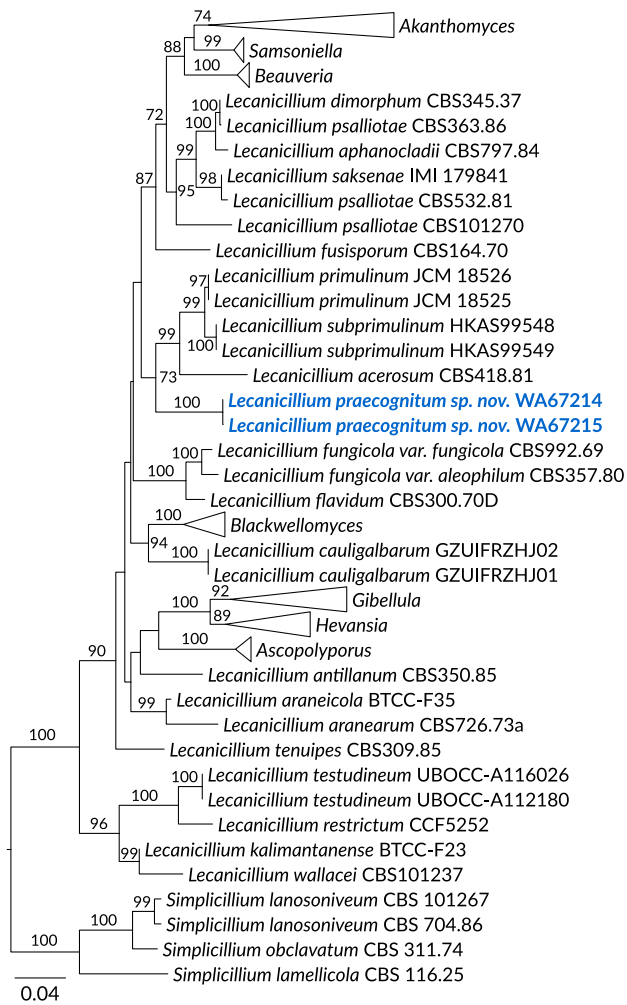
Culture characteristics — (in darkness, 20 ± 2 °C). Colonies cottony, margin even to slightly irregular, with dense and abundant aerial mycelium. On SDA and potato dextrose agar (PDA) averse white, reverse creamy to yellow, reaching 3 cm in 14 d, 5.5 cm in 21 d. Octahedral crystals produced in the medium and substrate mycelium. Sometimes yellowish droplets of exudate on the surface of older cultures. Growth is slow but not arrested in 4 °C.

Typus. Poland, Podlaskie Voivodeship, Białowieża Forest, forest division '210D–a', near Postołowo, on insects' frass beneath fallen bark of Norway spruce *Picea abies* previously infected with European spruce bark beetle *Ips typographus*, Nov. 2017, *M. Gorczak* (holotype WA0000067215, culture ex-type MGC 39; ITS, SSU, LSU, *TEF1-α* and *RPB2* sequences GenBank MT247058, MT247062, MT247060, MT267523 and MT267525, MycoBank MB834982).

Additional material examined. Poland, Pomorskie Voivodeship, Wierzchucino, Royal Fern Nature Reserve, on nematocerous fly exuvium in decaying *Fomes fomentarius* on *Betula pendula* log, July 2016, *M. Gorczak*, herbarium specimen WA0000067214, culture MGC 76; ITS, SSU, LSU, *TEF1-α* and *RPB2* sequences GenBank MT247059, MT247063, MT247061, MT267524 and MT267526.

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, four similar ITS sequences were found (98.9–99.8 % identity). Two of them belongs to strains isolated from wood: historic construction wood in Chiloé, Chile (GenBank KF675189.1) and *Picea abies* wood from Sweden (GenBank AY805597.1) and other two sequences were generated during research on mycorrhizae of *Ericaceae*: *Pyrola media* in Scotland, UK (GenBank FN565380.1) and *Epacris pulchella* in south-eastern Australia (GenBank AY627789.2). This variety suggests that the species have a global distribution and much wider ecological niche than known strains. However, if *L. praecognitum* can thrive on frass of minute arthropods as we observed, the actual substratum might have been overlooked in previous cases. No specimens are available from a 2004 study in Sweden (A. Menkis pers. comm.) or 2014 study in Chile (R. Blanchette pers. comm.).

Lecanicillium longisporum is morphologically most similar to *L. praecognitum*, but it has longer (up to 10.5 µm) and sometimes septate spores (Zare & Gams 2001). Other species with similar spores includes *Akanthomyces muscarius* (formerly *Lecanicillium*), which differs in size of conidia and more often has phialides in the whorls; *A. attenuatum*, which differs in phialide size and has at least some conidia with attenuate base; *L. flavidum* and *L. fungicola* which produce spores in slimy heads; *L. fusisporium* which produces characteristic broad conidia, and *L. nodulosum* which has characteristic swellings of hyphae. Related *L. acerosum* is most similar when it comes to size of phialides and conidia but it can be easily distinguished by its long, thin, acerose spores.



The best scoring maximum likelihood tree calculated from ITS, SSU, LSU rDNA and protein coding *TEF1-α*, *RPB1* and *RPB2* sequences shows the relationships within the family *Cordycipitaceae*. The tree was constructed with RAxML-NG (Kozlov et al. 2019) on a partitioned alignment based on the Zhou et al. (2018) dataset. The dataset contained 81 taxa and a total of 5 198 characters of which 2 050 were variable. Bootstrap support values at branches were obtained by generating 1 000 bootstrap replicates. Only bootstrap support values ≥ 70 % are shown. The tree is rooted with the genus *Simplicillium*.

Colour illustrations. Białowieża Primeval Forest logging site, Poland. Fourteen-day-old colonies of *L. praecognitum* on SDA at 20 °C, obverse (left) and reverse (right); solitary phialides; octahedral crystals in medium; conidia; apical hyphae with whorls of phialides and secondary phialides. Scale bars = 10 µm.

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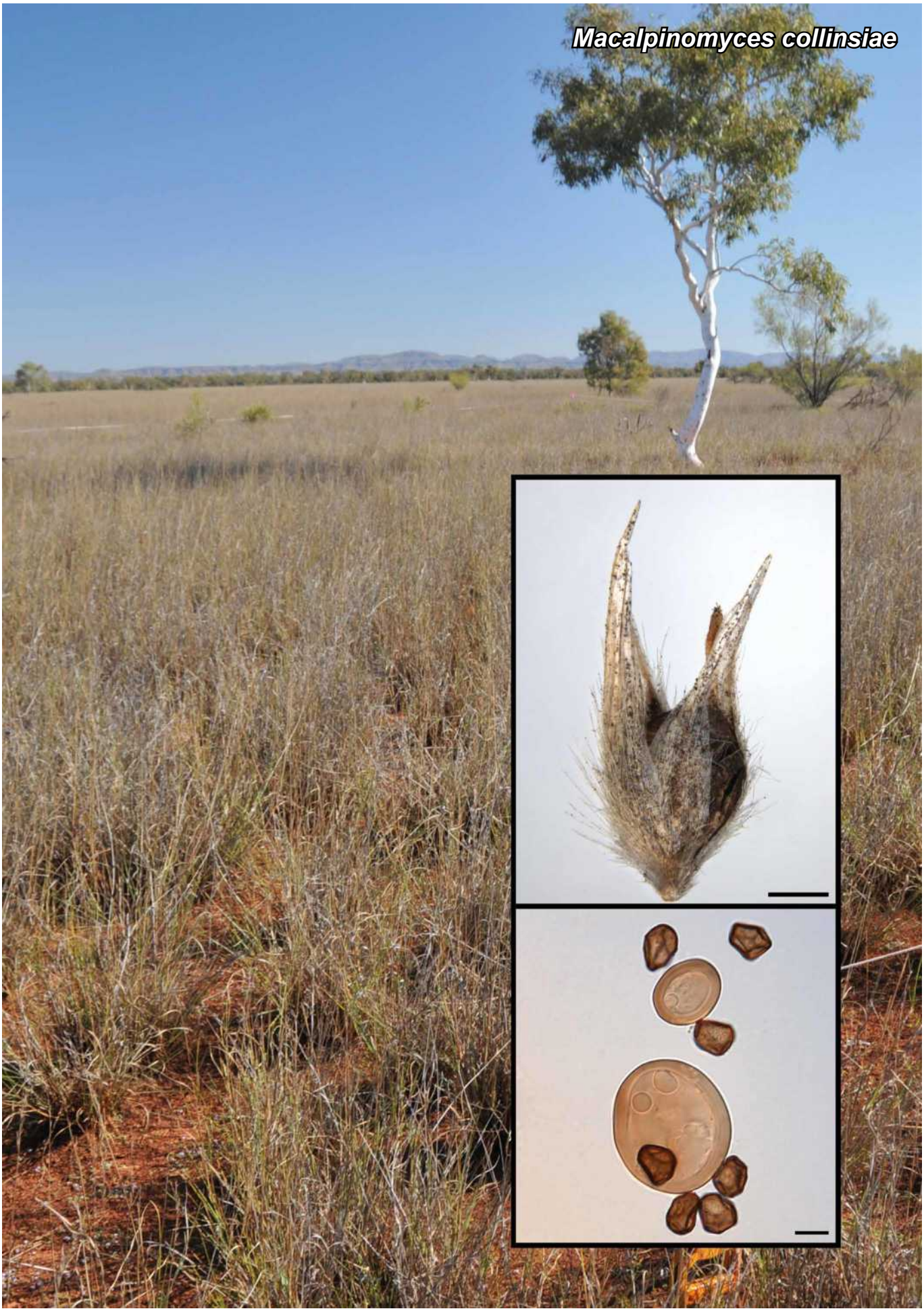

Macalpinomyces collinsiae

Fungal Planet 1089 – 29 June 2020

Macalpinomyces collinsiae J. Kruse, M.N. Lyons, McTaggart & R.G. Shivas, *sp. nov.*

Etymology. Named after Dr Margaret Thora Collins, a Western Australian botanist, conservation biologist and mycologist, for her role in the discovery of this fungus.

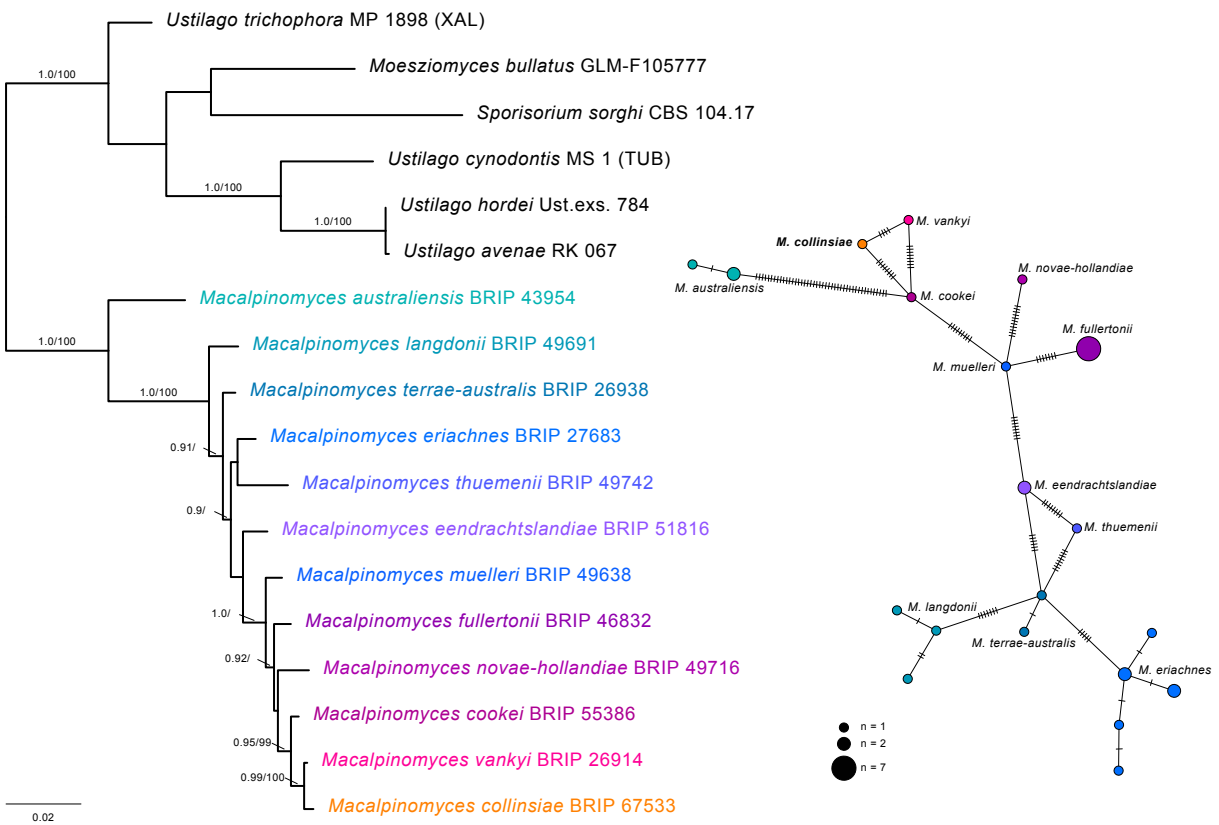
Classification — *Ustilaginaceae*, *Ustilaginales*, *Ustilaginomycetes*.

Sori ovoid, 1.5–2 × 2–3 mm, in all of the ovaries of *Eriachne benthamii*. *Spore mass* blackish brown, semi-agglutinated, comprised of spores and large giant sterile cells. *Spores* reddish brown, polyhedrally irregular, 11–15 × 8–10 µm; wall c. 1 µm wide, smooth. *Sterile cells* pale yellowish brown, globose to broadly ellipsoidal, 19–37 µm diam; wall 3–4 µm wide, smooth.

Typus. Australia, Western Australia, Pilbara Region, c. 17.5 km ENE of intersection of Great Northern Highway and Nanutarra-Munjina Road, 15 km WNW of Mulga Downs Outcamp, 1.4 km SSW of Bernie Bore, Mulga Downs Station, on *Eriachne benthamii* (*Poaceae*), 2 Aug. 2015, *M.N. Lyons & S.D. Lyons* (holotype BRIP 67533; ITS sequence GenBank MN855218, MycoBank MB833910; isotype PERTH 08981019).

Notes — Prior to this study, *Macalpinomyces* contained 11 host-specific species restricted to *Eriachne* (*Poaceae*) in Australasia (Li et al. 2017). *Macalpinomyces collinsiae* is the twelfth species, known only from the type specimen on *E. benthamii* in north-western Australia. All species of *Macalpinomyces* are morphologically similar and can only be reliably separated by host range and molecular phylogenetic analysis.

Based on a mega-BLAST search of species of *Macalpinomyces*, the ITS sequence of *M. collinsiae* differs from the sister species *M. vankyi* (GenBank KX686918; Identities = 730/746 (98 %), 9 gaps (1 %)), and from *M. cookei* (GenBank KX686942; Identities = 732/764 (96 %), 21 gaps (2 %)). The species of *Macalpinomyces* are further illustrated on the Smut Fungi of Australia Lucid Key (Shivas et al. 2014).



Phylogram obtained from a maximum likelihood analysis of the ITS region of rDNA in IQTree v. 1.7 beta (Nguyen et al. 2015) with a model test for each partition (command -m TEST -spp). aRLT values (≥ 90 %) (Guindon et al. 2010) and ultrafast bootstrap values (≥ 95 %) (Hoang et al. 2018) from 10 000 replicates above nodes. Minimum spanning network (Bandelt et al. 1999) sampled from all available ITS sequences of *Macalpinomyces* on GenBank. Hashes in network indicate number of parsimony informative sites in the alignment.

Colour illustrations. *Eriachne benthamii* tussock grassland, Mulga Downs Station, Pilbara region of Western Australia (Photo credit: M.N. Lyons). Floret of *Eriachne benthamii* infected with *Macalpinomyces collinsiae*; spores and sterile cells. Scale bars = 1 mm; 10 µm.

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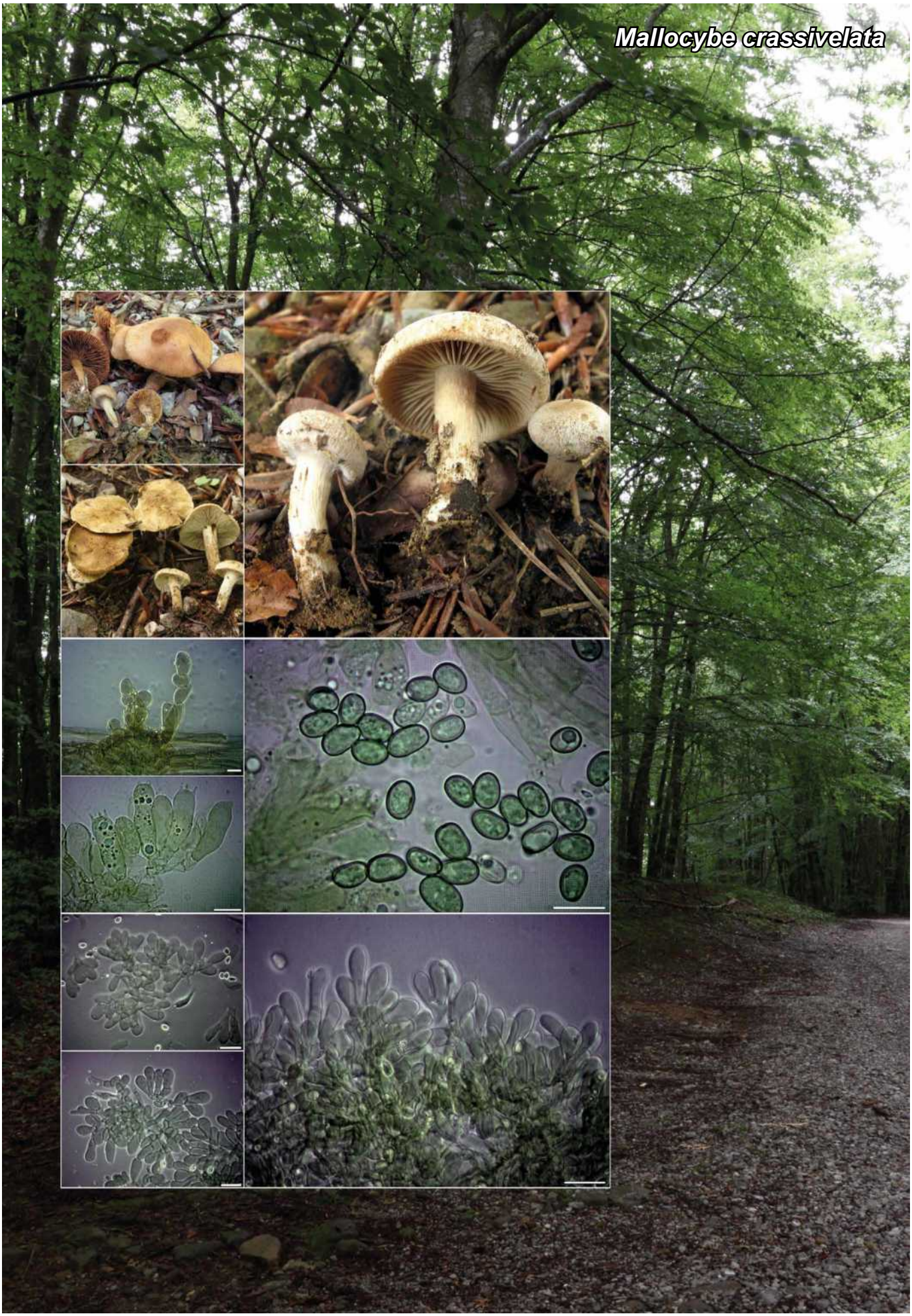
Mallocybe crassivelata

Fungal Planet 1090 – 29 June 2020

Mallocybe crassivelata Ferisin, Bizio, Esteve-Rav., Vizzini & Dovana, *sp. nov*.

Etymology. From the Latin *crassus* (thick) and *velatus* (with a veil), referring to the presence of a thick, abundant veil on the pileus surface.

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

Basidiomata stipitate. *Pileus* 20–40 mm diam, at first convex, then applanate to plano-convex, without umbo, with an inflexed margin when young, fibrillose-tomentose to woolly-tomentose, sometimes scaly, when moist almost smooth; initially ochraceous yellow (Mu 10YR 6/6) to ochraceous brown (Mu 7.5Y 8/4), brown with an olivaceous tinge when moist, sometimes fulvous orange (Mu 7.5YR 3/6) at disc; in young basidiomes with a thick, white velipellis. *Lamellae* rather crowded to crowded (L = 48–85), with lamellulae (l = 0–1), adnexed to arcuate, sometimes subdecurrent, initially pale ochraceous with a faint olivaceous hue, then brown; edge whitish to concolourous, crenulate. *Stipe* 25–40 × 3–6 mm, cylindrical, solid, then becoming fistulose, pale yellow to concolourous with pileus in aged basidiomes; surface fibrillose, white towards the base for the presence of a white velipellis; white cortina present in young basidiomes. *Context* yellowish in pileus, somewhat and ochraceous brownish in stipe. *Smell* earthy sometimes mixed with a subspermatic component. *Taste* indistinct. *Basidiospores* (7.7–)8.3–*8.7*–9.2(–11.4) × (3.9–)4.7–*5*–5.2(–5.9) µm, Q = (1.5–)1.67–*1.76*–1.85(–2.1), smooth, yellowish, very variable in shape, ellipsoid to subphaseoliform, sometimes amygdaliform in side view with obtuse or sub-ogival apex; presence of anomalous long spores (over 11 µm, probably discharged from bisporic basidia), walls up to 0.5 µm thick. *Basidia* (20–)22.7–26.3(–27) × (7.7–)8.2–9.4(–9.9) µm, clavate to cylindrical, 4-spored, sometimes 1–2-spored, with inner olivaceous guttulae and brown necropigment, sterigmata up to 3 µm long; sometimes they are rarely present on lamella edge. *Hymenophoral trama* regular, formed by cylindrical to ellipsoidal, 10–16 µm wide elements, with a brownish wall; subhymenium consisting of up to 100 µm long elements, 7–13 µm wide. *Cheilocystidia* very numerous, (14.3–)18–28.2(–32.6) × (6.1–)7.9–11.4(–14.7) µm, hyaline, usually thin-walled, very variable in shape, cylindrical, oblong to clavate, with a few septa; mixed with basidia. *Pleurocystidia* absent. *Caulocystidia* present at stipe apex (1/4), at least partly catenulate with terminal element as true cystidium, from ellipsoid to ovoid, up to 25 µm long. *Pileipellis* an undifferentiated cutis with some ascending hyphae; terminal elements cylindrical to subcylindrical, 50–110 × 7–14 µm, with ochraceous-brown parietal pigment. *Clamp-connections* present.

Habitat & Distribution — Gregarious in deciduous (*Fagaceae*) or coniferous (*Picea abies*, *Pinus sylvestris*) forests. So far known from Italy, Slovenia and Spain.

Typus. Slovenia, Pregarje, 710 m asl, under *Fagus sylvatica*, 28 June 2014, *G. Ferisin* (holotype MCVE 29561; ITS and LSU sequences GenBank MN536812 and MN537138, MycoBank MB832767).

Additional materials examined. Italy, Veneto, Belluno, Falcade, 1148 m asl, in *Picea abies* forest, 11 Oct. 2001, *E. Bizio*, MCVE 21499; ITS sequence GenBank MN536813. – Spain, Community of Galicia, Province of Orense, Cambela, 29TPG5280, 900 m asl, in *Castanea sativa* forest, 20 Oct. 1999, *F. Esteve-Raventós*, *M. Villarreal & F.D. Calonge*, AH 29788; ITS sequence GenBank MN536810; Community of Madrid, Rascafría, 24 June 1993, in mixed forest of *Quercus pyrenaica* and *Pinus sylvestris*, *A. Guerra & G. Moreno*, AH 46622; ITS sequence GenBank MN536811.

Notes — Terminology for descriptive terms is according to Kuyper (1986) and Vellinga (1988) and colour codes are taken from Munsell (1994). In our phylogeny *M. crassivelata* belongs to a well-supported clade (bootstrap support value = 88 %) together with *M. leucoloma*, *M. malenconii*, *M. myriadophylla* and three sequences of 'Uncultured *Inocybe* sp.' (GenBank JX630703, JX630710, JX630716) from the USA and associated with *Dryas integrifolia*. *Mallocybe crassivelata* shows, as major morphological features, a rather fleshy, predominately ochraceous basidioma, fibrillose-tomentose to woolly-tomentose pileus covered with a thick white velipellis, narrow subphaseoliform spores and an earthy smell (similar to that of *Inosperma cervicolor*) often associated to a subspermatic component, though in some collections (AH 29788) nearly indistinct. *Mallocybe leucoloma* differs from the new species mainly by a smaller and slender habit, different shape of cheilocystidia (often pyriform), sub-odourless context and being associated with dwarf *Salix* or *Dryas* (Kühner 1988). *Mallocybe malenconii* can easily be distinguished by its longer spores (9–12 × 4–5.5 µm) with mean Q-value of c. 1.95 (Vauras & Larsson 2011) and an indistinct smell (Heim 1931). Compared to *M. crassivelata*, *M. myriadophylla* has a pale grey cortina, very narrow and crowded lamellae (–4 mm wide), smell 'indistinct to somewhat fungoid and slightly metallic' and seems strictly associated with *Betula pendula* (Vauras & Larsson 2011). *Mallocybe hebeloomoides* is characterised by a smaller size, broadly elliptical to subovoid spores with Q =1.4–1.6 and habitat under dwarf *Salix* species (Kühner 1988). Finally, *M. pallidotomentosa*, so far known only from Germany, is morphologically quite close to *M. crassivelata*, but differs mainly in growing under *Populus tremula* and *Betula* sp. (Ludwig 2017) and by a different ITS sequence (Ditte Bandini, pers. comm.).

Colour illustrations. Pregarje, Slovenia, *Fagus sylvatica* forest. *Mallocybe crassivelata* basidiomata in habitat; basidiospores; caulocystidia; basidia and cheilocystidia. Scale bars = 10 µm.

Supplementary material

FP1090 Maximum-likelihood analysis of the combined *nrITS* and *nrLSU* regions was performed with RAxML v. 8.2.11 (Stamatakis & Alachiotis 2010) using the GTR+G model in Geneious v. 11.1.4.

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Marasmius vagus

Fungal Planet 1091 – 29 June 2020

Marasmius vagus Guard, M.D. Barrett & Farid, *sp. nov.*

Etymology. The Latin epithet *vagus*, wandering, refers to its widespread distribution in diverse habitats over a large area of monsoon tropical Australia, and its apparent recent dispersal and establishment in Florida, USA.

Classification — *Marasmiaceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata small to medium sized, collybioid. *Pileus* 10–40(–50) mm, initially hemispherical, convex, becoming plane at maturity, apricot (47; Flora of British fungi chart 1969), sometimes paler orange (48) margin, and darker sienna (11) centre, dry, smooth to finely matt, margin entire, not in-rolled. Pileus colours display much variation depending on weather, tending to wash out in rain, and increase in intensity in dry weather. Flesh thin, white. *Lamellae* white, margins white or concolourous with pileus, free to adnexed, close, 18–22, 3–4 mm deep, with 2–3 series of lamellulae, very fine shallow cross-anastomoses, mostly in outer half of cap, and not always present in juveniles. *Stipe* central, cartilaginous, 30–55 × 3–5 mm, white to cream full length of stipe, or occasionally yellowish brown lower half, smooth, hollow, cylindrical, sometimes bi-tubular; basal hyphae forming a white tuft. *Spore print* white. *Basidiospores* variable between collections, with holotype at lower end of range, (8.5–)9–10.5(–11.5) × (4.8–)5–6(–6.8) µm (av. 10 × 5.5 µm, Q = 1.47–2.04, Q_m = 1.76 ± 0.13, n = 50, s = 5 specimens), slightly curved ellipsoid to elongate, hyaline, inamyloid, with some granular contents. *Basidia* 22–30 × 8–9.5 µm, sterigmata short, rounded, 2–2.5 µm, 2–4-spored. *Basidioles* 22–23 × 5–8 µm, clavate. *Cheilocystidia* common, *Siccus*-type broom cells, with short to very long apical divergent projections, main body 9–20 × 4–11 µm, digits 4–12 × 1–2 µm, with 2–4(–8) digits, mostly thin-walled, with body also thin-walled except for outer 1/4 at base of projections; narrowly to broadly and irregularly cylindrical, clavate, occasionally branched; rare smooth, mucronate cheilocystidia also found, 24 × 8 µm. *Pleurocystidia* absent. *Pileipellis* consists of a hymeniderm of *Siccus*-type broom cells, main body 6–19(–27) × 3.5–10.5 µm, digits 2.5–11.5 × 1–2 µm, broadly clavate, cylindrical, ± branching with sparse to common digits, usually thin-walled at base, often thick-walled and refractive in upper two-thirds, and including the digits, which may be bifid; pileal hyphae 2.5–7 µm. *Caulocystidia* absent. *Stipitipellis* of parallel hyphae, 4.5–10 µm diam. *Clamp connections* present in all tissues. Melzer's reaction – pileal and lamellar trama inamyloid, stipe trama mildly dextrinoid.

Habit, Habitat & Distribution — Gregarious in habit and at times caespitose, it may also fruit in rings. A terrestrial saprotroph in accumulated leaf litter, the natural habitat in undisturbed sites varies from shaded microsites in tropical savanna woodland, to grassland and margins of tropical rainforest across more than 2000 km of northern Australia. For approximately 10 yr it has also been found growing in suburban lawns and highly disturbed habitats in Florida, USA.

Colour illustrations. Typical monsoon tropical habitat, Charnley River Station, Western Australia (Photo credit M. Barrett). Basidiomata Queensland (holotype); cheilocystidia of *Siccus*-type broom cells and basidiospores; coloured lamellar margins and cross-venations; basidiomata Florida (Farid 944, USF 300000). Scale bars = 10 mm (other) and 5 µm (microstructures).

Typus. Australia, Queensland, Mt Carbine, S16° 34'44.1" E145°11'13.7", in savanna grassland leaf litter, 7 Mar. 2018, *F. Guard & S. McMullan-Fisher SMF3041* (holotype AQ1008080; ITS and LSU sequences GenBank MT117839 and MT110674, MycoBank MB833552).

Notes — *Marasmius vagus* is characterised by a small to medium, orange to apricot, smooth pileus, close gills with cross-anastomoses and an all-white or pale cartilaginous stipe. These characters, with cheilocystidia of *Siccus*-type broom cells, in the absence of pleurocystidia and caulocystidia and a well-developed, non-collariate, non-instititious stipe place this species in sect. *Globulares* (group *Sicci*) subsect. *Siccini* ser. *Leonini*.

Marasmius vagus is sister to a well-supported *M. hypochroides*/*M. vladimiri* clade. *Marasmius hypochroides* (Berkeley & Broome 1875) described from Sri Lanka, but found across southern Asia, forms more robust, darker basidiomes (30–60 mm) with longer stipes (40–100 mm) that have dark reddish brown bases. *Marasmius vladimiri* (Crous et al. 2014) from India, is brighter in colour (orange scarlet with orange chestnut disc), has a coloured stipe with slightly shorter spores and larger basidia (36–40 µm). *Marasmius vagus* also bears a superficial resemblance to the Australian species *Marasmius elegans* (Grgurinovic 1997) that has bicoloured stipes (white above, brown below) and lacks cross-anastomoses in the lamellae. Our analyses of ITS data show that *M. elegans* and *M. vagus* are not genetically closely related.

Marasmius vagus is native to northern Australia where it is widely distributed amongst native vegetation in the monsoon tropics; it has been recorded there for more than 20 yr. However, it has also been found in lawns in the tourist mecca, Cairns, and several other towns in southeast Queensland. In Florida this species has been collected almost exclusively in suburban lawns and highly disturbed habitats, with the oldest known observation (Mushroom Observer, Obs. 106057) from 2012, suggestive of a recent introduction to Florida, USA. There are no records that this species was collected by Florida mycologists from previous generations, such as William Murrill (1859–1957) (Weber 1961) or James Kimbrough (1934–2017) (Smith & Healy 2019).

Supplementary material

FP1091-1 Additional materials examined.

FP1091-2 Phylogenetic tree. Bayesian (MrBayes v. 3.2.6) 50 % majority-rule consensus tree of the ITS-nrDNA for a selection of *Marasmius* species. Thickened lines indicate PP support > 0.95.

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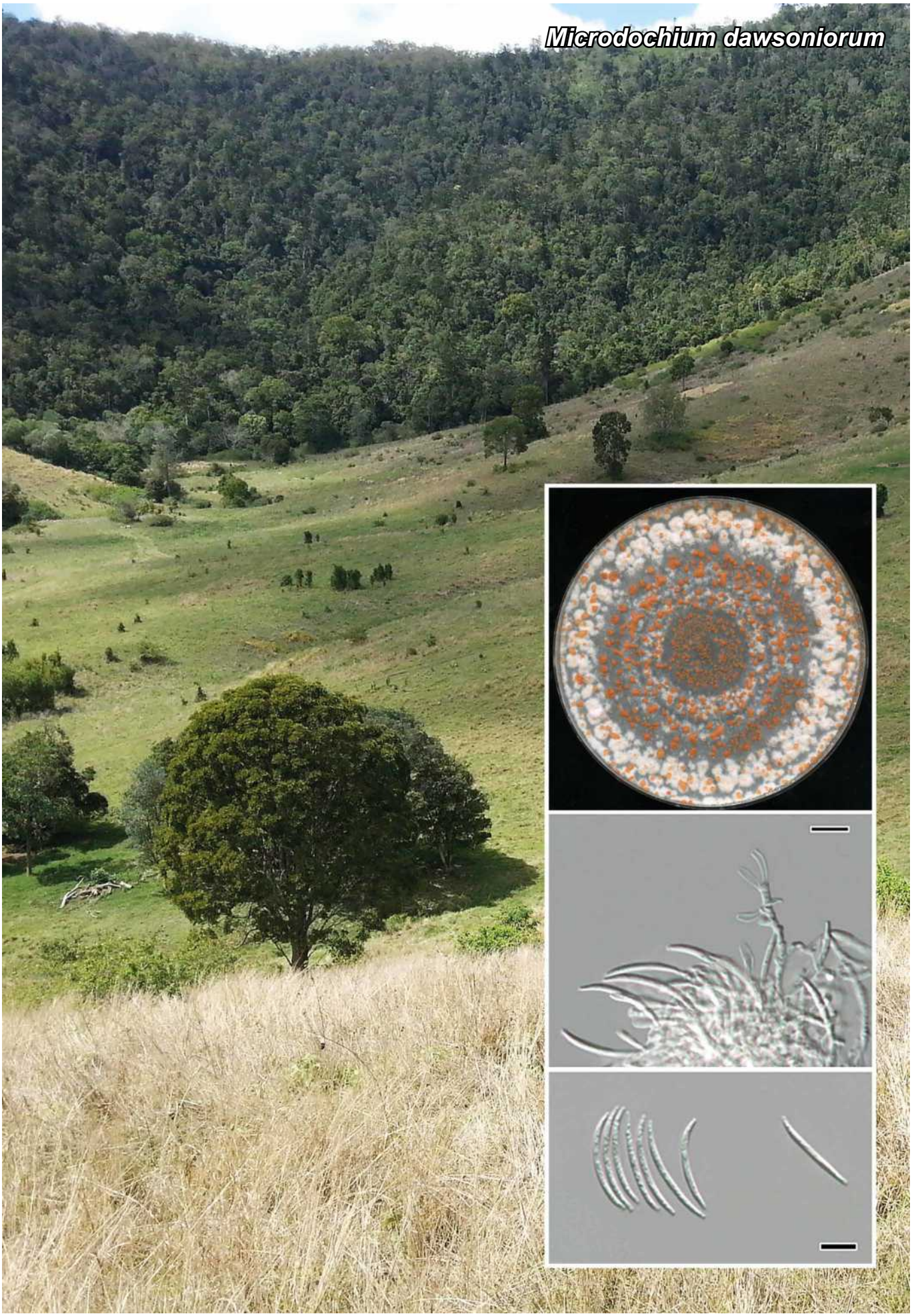

Microdochium dawsoniorum

Fungal Planet 1092 – 29 June 2020

Microdochium dawsoniorum C. Lock, Vitelli, Holdom, Y.P. Tan & R.G. Shivas, *sp. nov.*

Etymology. Named after the Dawson family from Taunton, Queensland, on whose property the fungus was first collected.

Classification — *Michrodochiaceae*, *Xylariales*, *Sordariomycetes*.

Conidiophores abundant in a dense compact layer, occasionally branched, mostly reduced to conidiogenous cells. *Conidiogenous cells* cylindrical to irregular, flexuous, 20–30 × 1–2 µm, narrowed towards the tip, hyaline, smooth. *Conidia* flexuous to falcate, 0–3-septate, sometimes with a geniculation, 25–75 × 1–2 µm, acute at the tip, narrow at the base. *Sexual morph* not seen.

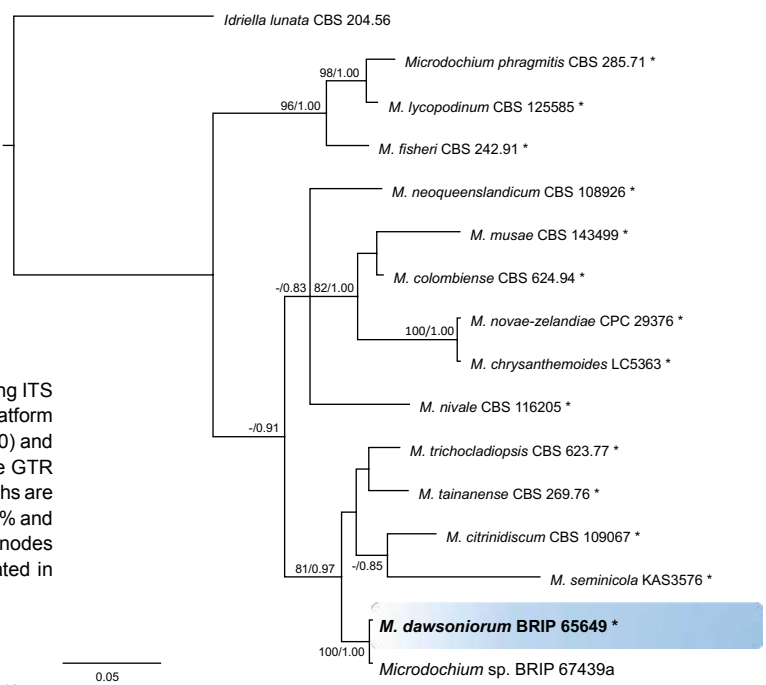
Culture characteristics — *Colonies* on oatmeal agar (OA) after 2 wk covering 9 cm diam plates, flat, mycelium in compact irregular to concentric scattered salmon tufts, with abundant slimy apricot sporodochia up to 3 mm arranged in irregular to concentric rings. Reverse pale saffron with sporodochia apparent as darker patches. *Mycelium* immersed or superficial, hyphae hyaline, septate, smooth.

Typus. Australia, Queensland, Taunton, Tableland Road, west side of road, S24°26'47.56" E151°47'13.27", isolated from leaves of *Sporobolus natalensis* (*Poaceae*), 8 Mar. 2017, *J. Vitelli* (holotype BRIP 65649, includes ex-type culture; ITS sequence GenBank MK966337, MycoBank MB831165).

Additional material examined. Australia, Queensland, Taunton, Tableland Road, east side of road, S24°26'51.98" E151°47'45.44", isolated from leaves of *S. elongatus*, 18 May 2018, *J. Vitelli*, BRIP 67439a; ITS sequence GenBank MN492650.

Notes — *Microdochium dawsoniorum* is sister to a clade that includes *M. citrinidiscum*, *M. seminicola*, *M. tainanense* and *M. trichocladiopsis*. Based on a mega-blast search of taxa within the sister clade, the ITS sequence of *M. dawsoniorum* differs from *M. citrinidiscum* (GenBank NR_155373; Identities = 529/556 (95 %), 9 gaps (1 %)), *M. seminicola* (GenBank KP859038; Identities = 488/541 (90 %), 34 gaps (6 %)), *M. tainanense* (GenBank NR_145248; Identities = 531/555 (96 %), 11 gaps (1 %)) and *M. trichocladiopsis* (GenBank KP858998; Identities = 536/557 (96 %), 13 gaps (2 %)). Morphologically, *M. dawsoniorum* has narrower conidia than *M. seminicola* (3–4.5 µm) and longer conidia than *M. citrinidiscum*, *M. tainanense* and *M. trichocladiopsis* (7–31 µm, 10–15 µm and 6–18 µm, respectively) (Hernández-Restrepo et al. 2016).

Microdochium dawsoniorum has only been found in Australia. Its close relatives include *M. citrinidiscum* from Peru; *M. seminicola* primarily from Canada and Switzerland; *M. tainanense* from Taiwan; and *M. trichocladiopsis* that has an unknown geographic origin (Hernández-Restrepo et al. 2016). *Microdochium dawsoniorum*, *M. tainanense* and *M. trichocladiopsis* have been isolated from the grasses *Sporobolus* spp., *Saccharum officinarum* and *Triticum aestivum*, respectively. *Microdochium seminicola* has been isolated from various grasses, including *T. aestivum*. *Microdochium citrinidiscum* has only been isolated from *Eichhornia crassipes* (*Pontederiaceae*) (Hernández-Restrepo et al. 2016). The origin of *M. dawsoniorum* is unclear as it has been isolated from both native Australian and established exotic *Sporobolus* spp.



Phylogenetic tree of *Microdochium* based on a Bayesian analysis using ITS sequences. Analyses were performed on the Geneious v. 11.1.2 platform (Biomatters Ltd.) using RAxML v. 8.2.11 (Stamatakis & Alachiotis 2010) and MrBayes v. 3.2.6 (Ronquist & Huelsenbeck 2003), both based on the GTR substitution model with gamma-distribution rate variation. Branch lengths are proportional to distance. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). *Idriella lunata* was used as outgroup. Novel taxon is indicated in **bold**. Ex-type strains are marked with an asterisk (*).

Colour illustrations. Forest trees close to collection site. Colony on 1/2 potato dextrose agar (PDA) after 2 wk; conidiomata on 1/2 PDA; conidiogenous cells; conidia. Scale bars = 200 µm (conidiomata) and 10 µm (conidiogenous cells and conidia).

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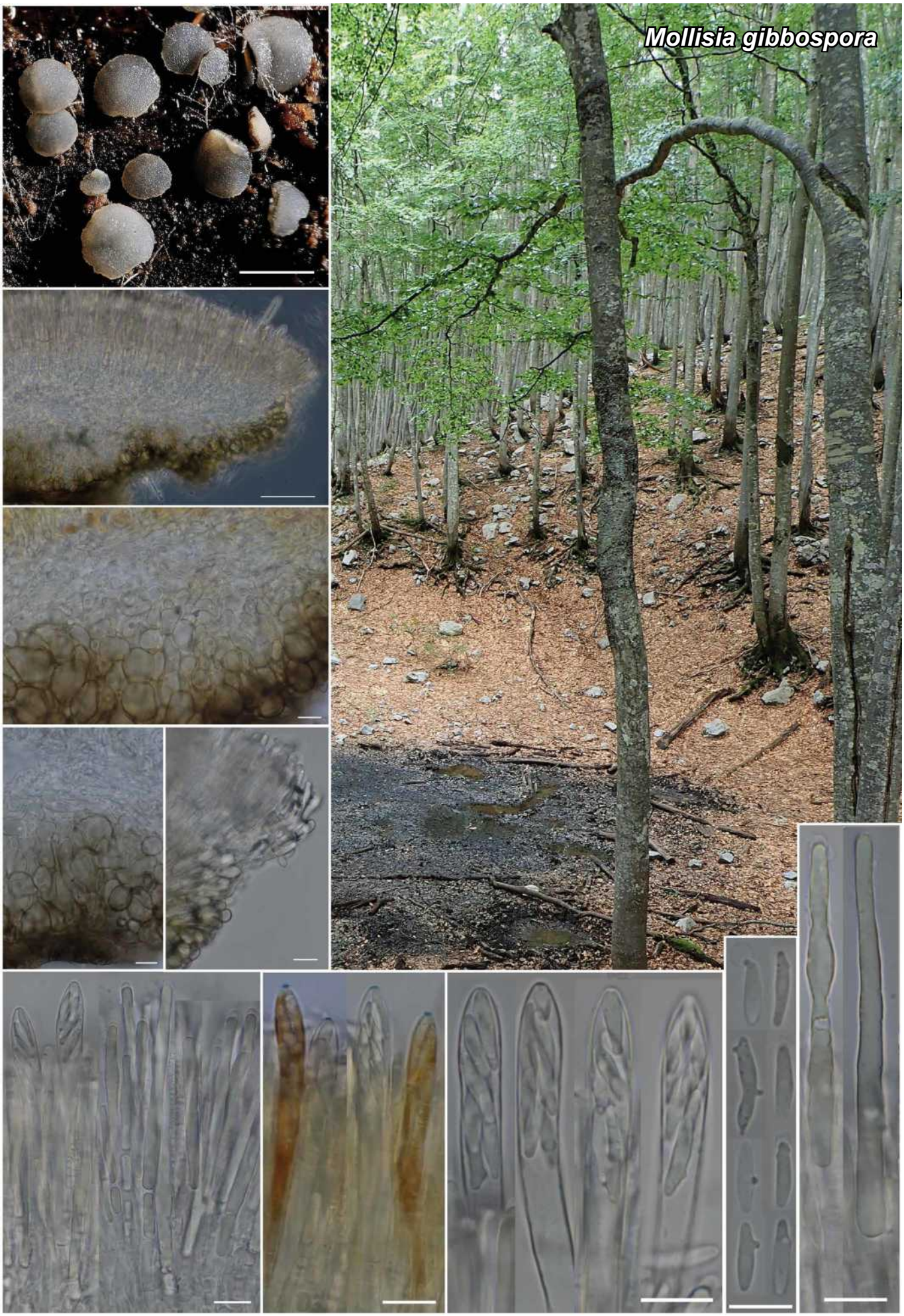
Mollisia gibbospora

Fungal Planet 1093 – 29 June 2020

Mollisia gibbospora I. Kušan, Matočec, Pošta, Tkalčec & Mešić, *sp. nov.*

Etymology. Named after the protuberances on living, mature ascospores.

Classification — *Mollisiaceae*, *Helotiales*, *Leotiomycetes*.

Ascomata apothecial, shallowly cupulate to plate-shaped when young, becoming sub-pulvinate to pulvinate when fully mature, superficial, sessile, ± circular from the top view, *0.4–1(–1.4) mm diam, solitary or gregarious (up to few apothecia). *Hymenium* whitish grey to pale lead-grey, not wrinkled but notably finely pruinose; margin slightly irregular, ± sharp, whitish, not concolourous with the hymenium, smooth, entire, finely wavy; excipular surface brownish from base to the upper flank, smooth. Basal hyphae macroscopically indistinguishable. *Asexual morph* not seen. *Hymenium* *80–95 µm thick. *Asci* cylindrical with conical-subtruncate apex, *67–89 × (5.8–)6.2–7.2 µm, *pars sporifera* *22–29 µm, 8-spored, of which 4–8 are gibbose, in living state protruding above ordinary paraphyses up to 17 µm, base cylindrical-truncate, arising from croziers, in Lugol's solution (IKI) apical ring of medium amyloidity (2bb) of *Calycina*-type. *Ascospores* subscutuloid, with rounded poles, majority of them having lateral or apical protuberation(s) already in *mature asci, 1-celled, *8.9–*11.3*–13.7(–14.7) × 2.2–*2.6*–3 µm, *Q = 3.3–*4.4*–5.7(–6.8), 1–2(–3) protuberations per spore, up to 1.4 µm high and 0.8–1.1 µm wide, hyaline, smooth, uninucleate, *sporoplasm with one to few non-refractive vacuoles, freshly ejected apically with sheath remnants persisting mostly around protuberations, biseriate inside *asci, lipid bodies scanty, overmatured partly with single septa; in IKI unstained, nucleus slightly contrasted, vacuoles hyaline and non-refractive. *Paraphyses* cylindric-obtuse, widest in the subapical or in the middle part, apical cell *28–57.5 × (2.8–)3.6–5.2 µm, some far projecting, exceeding living asci ('macroparaphyses'), *85–116 × 4.2–5.2 µm, straight, simple, *containing single cylindrical strongly refractive vacuolar body (VB), wall thin and hyaline; in KOH without yellow reaction; in IKI VBs not stained, soon collapse. *Subhymenium* *12–15.5 µm thick at the middle flank, hyaline, composed of densely packed epidermoid cells *3.5–7.1 µm wide. *Medullary excipulum* *24.5–31 µm thick at the middle flank, reaching 42 µm in the central part, hyaline, composed of *textura intricata*, cells *2.1–4 µm wide, at the border with ectal layer somewhat swollen, reaching 6.5 µm in width, thin-walled, KOH-soluble globules present, in IKI not stained, 1.3–3 µm wide, devoid of crystals. *Ectal excipulum* *36–54 µm thick at the middle flank, reaching 70 µm in the basal part, composed of *textura angularis*, cells *9.3–23.8 × 7.6–17.9 µm, upper flank and inner layers of lower flanks subhyaline and contain refractive KOH-soluble and IKI unstainable globules, while outer layer of lower flanks tobacco brown with cell walls *0.6–0.8 µm thick, most of the terminal clavate cells in the cortical layer of upper and middle flank contain single, hyaline and highly refractive VB. *Marginal tissue* very thin, *15–18.5 µm thick, composed of several cylindrical-clavate cells, *3.5–5.1 µm wide, thin-walled, each containing short cylindrical or elongated VB. *Subicular hyphae* confined to an apothecial base only, forming plaques, smooth, greyish brown, *2.4–3.3 µm wide, walls *0.4–0.6 µm thick. Asterisk (*) denotes living material. Ascus amyloidity is termed after Baral (1987) and spore shape after Kušan et al. (2014).

Distribution & Habitat — Sporogenous phases of the species are known so far from the type locality on Mt Velebit, Croatia, and (?)New Zealand (unpubl. data). Croatian collection is found on a decorticated fallen branch of *Fagus sylvatica* (originally a part of the trunk), lying in a moist litter at the edge of a natural karstic pond in a subalpine type of forest while New Zealand collection originates from decorticated wood.

Typus. Croatia, Lika-Senj County, Paklenica National Park, southern part of the Mt Velebit, Javornik area, 1170 m SW from Badanj peak (1638 m), 1360 m asl, N44°23'03" E15°27'22"; on fallen decorticated large branch of *Fagus sylvatica* (*Fagaceae*) in a virgin subalpine forest of *F. sylvatica*, 24 Oct. 2019, *N. Matočec* (holotype CNF 2/10951; ITS and LSU sequences GenBank MT179560 and MT178276, MycoBank MB834871).

Notes — Tanney & Seifert (2020) performed the first multigene analysis of the *Mollisiaceae* s.lat. A detailed polyphasic taxonomic analysis in this group is still missing. According to our analysis of ITS1-5.8S-ITS2 nrDNA data (see FP1093), *M. gibbospora* is conspecific with *Mollisia* sp. (GenBank MG195520) whose DNA sequence is derived from germinated ascospores of specimen PDD 58612 (unpublished) as well as with *Ascomycota* sp. (GenBank KC514847) isolated from wooden structures on Antarctica (Held & Blanchette 2017). Several other unidentified sequences from GenBank share identities higher than 99 % with *M. gibbospora* (Kauserud et al. 2005, Klaubauf et al. 2010). This group of isolates form the youngest phylogenetic lineage in *Mollisiaceae* among analysed sequences. It is evident that the mollisiaceous group comprises a number of generic representatives whose species, assigned to large genera such as *Mollisia* and *Pyrenopeziza* are mixed together thus clearly showing polyphyly in both genera. Numerous species attributed to some other genera, such as asexual *Acidomelania* and *Phialocephala* (cf. Crous et al. 2019a), sexual-aquatic *Loramyces* spp. and *Obtectodiscus aquaticus* form phylogenetic groups along with certain members ascribed to the genus *Mollisia*. Tanney & Seifert (2020) synonymised *Acidomelania* with *Mollisia*, while *Loramycetaceae* falls into synonymy with *Mollisiaceae*, which is supported in our analysis.

Until now, regularly present lateral and apical protuberations in fully mature, dormant and freshly ejected ascospores were not reported in the genus *Mollisia*. Even though *M. gibbospora* is macroscopically very much alike to a number of species in the genus (including its type *M. cinerea*), it is readily distinguishable according to the following microscopical differential characters: 1) living inner ectal excipular and some medullary excipular cells contain freely floating, hyaline and moderately refractive globules which are not stainable by CRB nor by IKI, and are soluble in KOH; 2) living mature asci containing four to eight gibbose ascospores; 3) ascospore sheath is fairly long-lived after spore ejection but retained around individual spore protuberations; and 4) some paraphyses are extremely long, far projecting above living mature asci, giving finely pruinose appearance of hymenial surface on living apothecia.

Colour illustrations. Croatia, Mt Velebit, subalpine beech forest in Javornik area - type locality. *Apothecia; vertical median section of the apothecium; upper excipular flank; lower exc. flank; margin; *asci and paraphyses, asci in IKI; mature ascospores in *asci; *ascospores; *'macroparaphyses'. Scale bars = 1 mm (apothecia), 50 µm (apothecial anatomy) and 10 µm (microscopic elements).

Supplementary material

FP1093 Maximum likelihood phylogenetic tree inferred from the dataset of ITS1-5.8S-ITS2 gene sequences from *Mollisia gibbospora* and related species.

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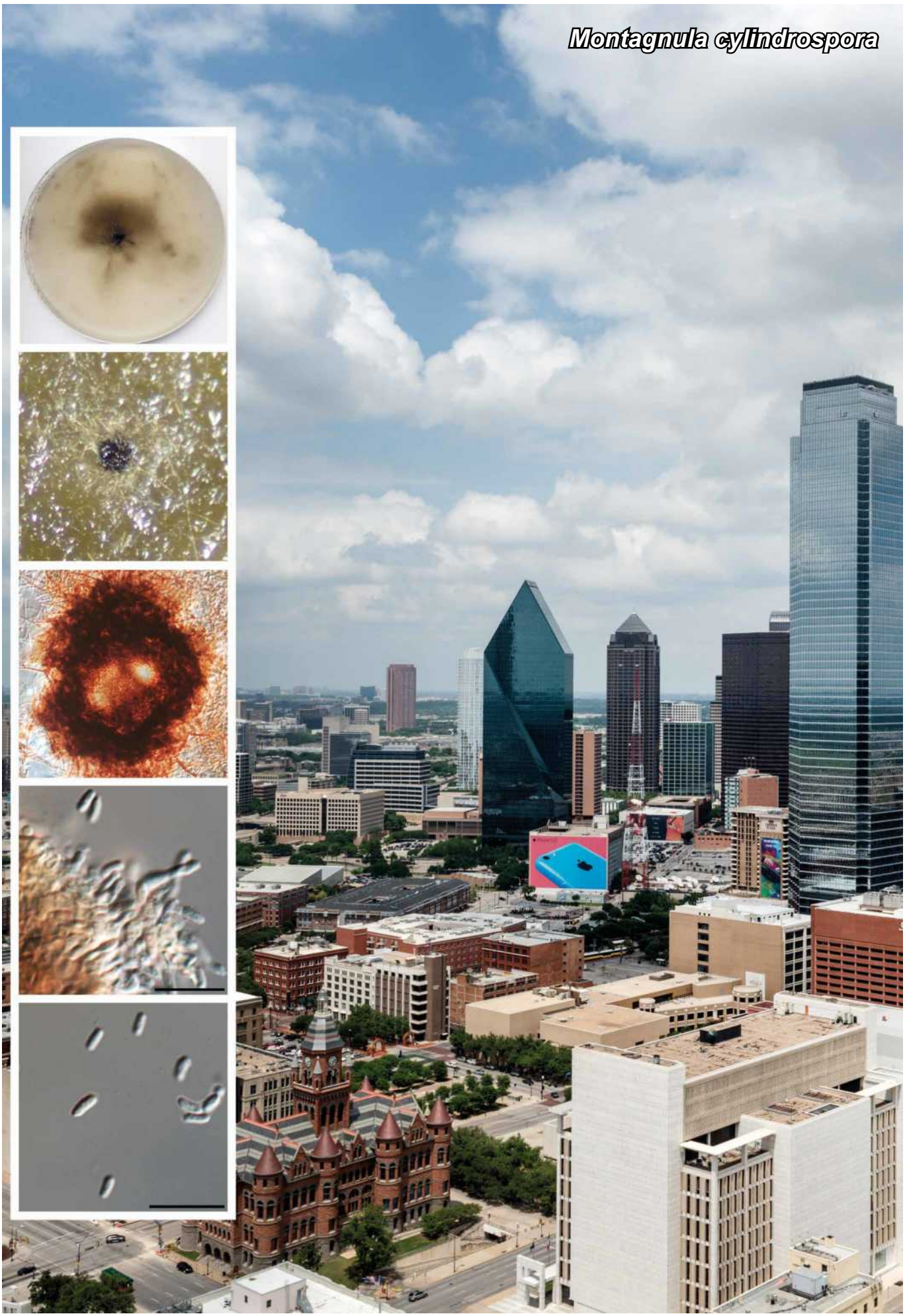

Montagnula cylindrospora

Fungal Planet 1094 – 29 June 2020

Montagnula cylindrospora Valenz.-Lopez, Cano, Guarro & Stchigel, *sp. nov.*

Etymology. From Latin *cylindratis*-, cylindrical, and *-sporarum*, spore, because of the shape of the conidia.

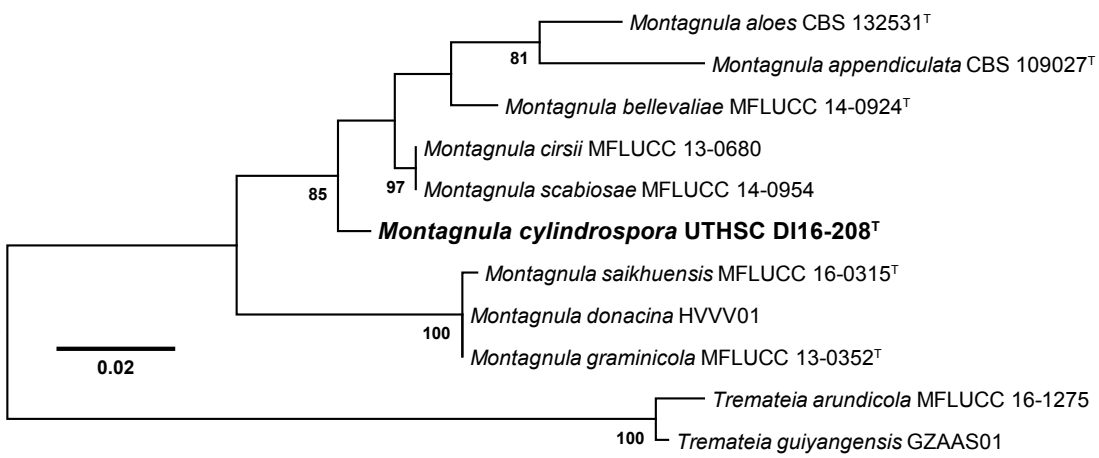
Classification — *Didymosphaeriaceae*, *Pleosporales*, *Dothideomycetes*.

Hyphae pale brown to brown, smooth- and thin-walled, septate, 2–5 µm wide. *Conidiomata* pycnidial, brown to dark brown, solitary, superficial (on oatmeal agar, OA), globose to subglobose, 160 × 110–150 µm, covered by brown, asperulate, septate setae of 33–65 µm long and 3.5–5 µm wide at the base, pycnidial wall of *textura angularis*, 2–4-layered, 15–40 µm thick, composed of brown to dark brown, flattened polygonal cells of 5–10 µm diam, neck absent, ostiolate. *Conidiogenous cells* phialidic, ampulliform to doliiform, hyaline, smooth-walled, 4 × 3.5 µm. *Conidia* aseptate, hyaline, smooth- and thin-walled, cylindrical, sometimes slightly curved, 3–5 × 1.5–2 µm, guttulate.

Culture characteristics — Colonies on OA reaching 50 mm diam after 7 d at 25 ± 1 °C, flattened, white (M. 5A1; Kornerup & Wanscher (1978) to dark blond (M. 5D4); reverse yellowish brown (M. 5E4). Colonies on malt extract agar (MEA) reaching 40 mm diam after 7 d at 25 ± 1 °C, floccose, white (M. 5A1) to brownish grey (M. 5C2); reverse orange white (M. 5A2) to brownish grey (M. 5C2). NaOH spot test negative. Crystals absent. Optimal, minimum and maximum temperatures were 25, 5 and 37 °C, respectively.

Typus. USA, Texas, Dallas, from a human skin sample, 2006, *D.A. Sutton* (holotype CBS H-24341, ex-type living cultures CBS 146572 = UTHSC DI16-208 = FMR 13698; ITS, LSU, *tub2*, *rpb2* and *tef1* sequences GenBank LT796834, LN907351, LT796914, LT796994 and LT797074, MycoBank MB834472).

Notes — This fungus differs from all known species of *Montagnula* by the *in vitro* formation of a coelomycetous asexual morph, and by the absence of a sexual morph (Tennakoon et al. 2016, Valenzuela-Lopez et al. 2017). Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the LSU sequence is *Montagnula cirsii* strain MFLUCC 13-0680 (GenBank KX274249; Identities = 876/879 (99 %), no gaps). Closest hit using ITS sequence is *Montagnula scabiosae* type strain MFLUCC 14-0954 (GenBank NR_155378; Identities = 502/520 (97 %), 6 gaps). The closest hit using the *tub2* sequence is *Montagnula saikhuensis* strain MFLUCC 16-0315 (GenBank KU743216; Identities = 418/478 (87 %), no gaps). The closest hit using the *rpb2* sequence is *Montagnula opulenta* strain AFTOL-ID 1734 (= CBS 168.34) (GenBank DQ677984; Identities = 869/947 (92 %), 4 gaps). The closest hit using the *tef1* sequence is *Bimuria novae-zelandiae* type strain AFTOL-ID 931 (= CBS 107.79) (GenBank DQ471087; Identities = 902/950 (95 %), 2 gaps).



Maximum likelihood (ML) tree obtained from ITS of our isolate and sequences retrieved from GenBank. Alignment and tree building were performed by MEGA v. 6.06 (Tamura et al. 2013). The ML bootstrap support values (≥ 70 %) are provided at the nodes. *Tremateia arundicola* MFLUCC 16-1275 and *Tremateia guiyangensis* GZAAS01 were used as outgroup. The new species proposed in this study is indicated in **bold**. Trepresents ex-type strains of the species used in this analysis.

Colour illustrations. Dallas, Texas, USA (image credit: Carol M. Highsmith); colony on OA after 14 d at 25 ± 1 °C, pycnidium under the dissecting microscope, pycnidium, conidiogenous cells, conidia. Scale bars = 10 µm.

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Muriphila oklahomaensis

Fungal Planet 1095 – 29 June 2020

Muriphila Jurjević, Čmoková & Hubka, *gen. nov.*

Etymology. Refers to the wall (*L. murum*) of distillery from where the species was repeatedly isolated.

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

Colonies slowly growing, velvety, dark olivaceous to black, convex, radially wrinkled to crateriform, colony margins entire, reverse dark. Hyphae septate, with smooth to verrucous walls, hyphal cells rectangular to asymmetrical, disintegrates into fragments at maturity. Sexual morph unknown.

Type species. Muriphila oklahomaensis Jurjević, Cmokova & Hubka. MycoBank MB834485.

Muriphila oklahomaensis Jurjević, Čmoková & Hubka, *sp. nov.*

Etymology. Name refers to the state in the USA where it was collected, Oklahoma.

Micromorphology (on MEA): *Hyphae* dark olivaceous, moderately thick, with smooth occasionally verrucous walls. *Hyphal cells* rectangular to sub-spherical, occasionally asymmetrical, 8–25(–45) × 4–11 µm diam, occasionally 1(–2) septa, at maturity hyphae falls apart into separate cells. *Sexual morph* unknown.

Culture characteristics — (in darkness, 25 °C after 21 d): Colonies on malt extract (Oxoid) agar (MEA) 13–15 mm diam, dark olivaceous to black, velvety, abruptly rising, 5–7 mm high, radially moderate deep to deep sulcate, crateriform; aerial mycelia absent; reverse black. Colonies on Czapek yeast autolysate agar (CYA) 6–8 mm diam, dark olivaceous black to black, smooth, abruptly rising approximately 3 mm high, radially moderate deep sulcate near wrinkled; reverse black. Colonies on potato dextrose agar (PDA) 13–14 mm diam, dark olivaceous black to black, velvety, approximately 3–4 mm high, radially moderate deep to deep sulcate; aerial mycelium absent; reverse black. Colonies on oatmeal agar (OA) 12–14 mm diam, black, smooth, abruptly rising approximately 3–4 mm, radially moderate deep to deep sulcate, crateriform; aerial mycelium absent; reverse black. Colony diam (in mm after 21 d) at 30 °C/32 °C: MEA 7–9/no growth (ng) to 4, CYA 5–6/ng, PDA 6–8/ng to 2, OA 8–10/ng to 2. No growth on MEA, CYA, PDA and OA at 35 °C.

Typus. USA, Oklahoma, McAlester, East side of building, outside wall, alcohol distillery, swab, 20 Jan. 2016, isol. *Ž. Jurjević* (holotype BPI 911212, culture ex-type CCF 5751 = CBS 146146 = EMSL 3307; ITS, LSU, SSU and β-tubulin sequences GenBank LR736040, LR736041, LR736042 and LR736049, MycoBank MB834486).

Additional materials examined. USA, Oklahoma, McAlester, East side of building, outside wall, alcohol distillery, swab, 20 Jan. 2016, *Ž. Jurjević* (culture CCF 5712 = CBS 142814 = EMSL 3308; ITS, LSU and SSU sequences GenBank LR736043, LR736044 and LR736045); South Carolina, outside wall, alcohol distillery, Oct. 2017, *Ž. Jurjević* (culture EMSL 4482; ITS sequence GenBank LR736046); ibid., (culture EMSL 4484; ITS sequence GenBank LR736047); ibid., (culture EMSL 4485; ITS sequence GenBank LR736048).

Notes — BLAST analysis with the **ITS** sequences of *M. oklahomaensis* showed low similarity with members of different genera, including *Austroafricana parva* (91.5–92 %), *Pseudotaeniolina globosa* (91.7 %) and *Camarosporula persooniae* (91.1 %), other taxa had similarity lower than 91 %. The **LSU** nrDNA sequence showed 94–95 % similarity to a wide variety of genera in the *Teratosphaeriaceae* with *Devriesia shelburniensis* having the highest degree of similarity (94.9 %). The position of *Muriphila* within *Teratosphaeriaceae* is unresolved. Neither LSU nor SSU phylogenetic analyses comprising *Teratosphaeriaceae* genera (Quaedvlieg et al. 2014) were able to resolve its position with satisfactory support. In the resulting phylogenetic trees, the genus *Muriphila* was most commonly placed close to genera *Batcheloromyces* and *Devriesia* (data not shown).

Muriphila oklahomaensis resembles morphologically meristematic rock-inhabiting fungi that are relatively common in *Teratosphaeriaceae* (Egidi et al. 2014). Namely, *Pseudotaeniolina* and *Meristemomyces* are the most closely related genera with similar ecology and morphology. *Muriphila oklahomaensis* produces on average larger hyphal cells, 8–25(–45) µm × 4–11 µm diam, compared to *Pseudotaeniolina globosa*, 8–15 × 6–7 µm diam.

Additionally, *M. oklahomaensis* hyphal cells are rectangular to asymmetrical, compared to *Meristemomyces frigidus* hyphal cells which are pyriform or reniform. Another morphologically and ecologically similar genus of *Teratophaeriaceaceae* is *Baudoinia* (Scott et al. 2016) that is, however, phylogenetically more distant (LSU similarity ~91–92 %, ITS similarity only ~84–85 %). The members of this genus frequently occur on outdoor surfaces near distilleries periodically exposed to ethanolic vapours, similarly to *M. oklahomaensis*. Interestingly, we were able to isolate *Baudoinia panamericana* strains (EMSL 4486 and EMSL 4487; identified by ITS rDNA) together with *M. oklahomaensis* from identical samples collected in South Carolina. The morphology of *Muriphila* and *Baudoinia* are very similar suggesting convergent evolution associated with adaptations to identical extreme environments. Reliable differentiation is possible only by means of molecular methods.

Colour illustrations. Barrels against outside wall, alcohol distillery. Twenty-one-day-old cultures at 25 °C of *Muriphila oklahomaensis*, from top to bottom on MEA, OA and PDA; hyphal structure on MEA. Scale bars = 10 µm.

Supplementary material

FP1095 A best scoring maximum likelihood tree based on the LSU region shows the relationships of *Muriphila* to selected genera of *Teratosphaeriaceae*.

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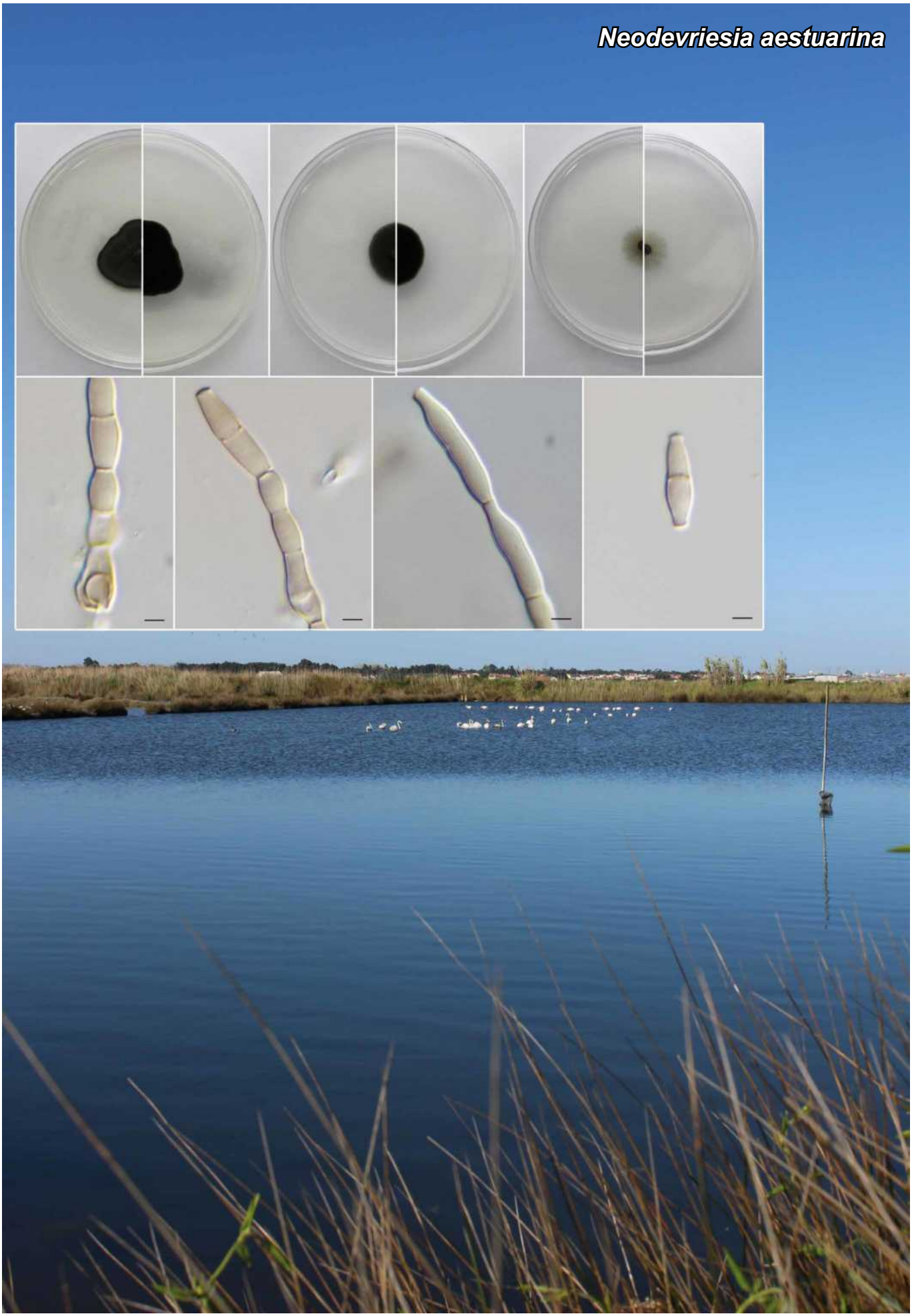

Neodevriesia aestuarina

Fungal Planet 1096 – 29 June 2020

Neodevriesia aestuarina M. Gonçalves & A. Alves, *sp. nov.*

Etymology. Named after the environment where the species was collected, namely an estuary.

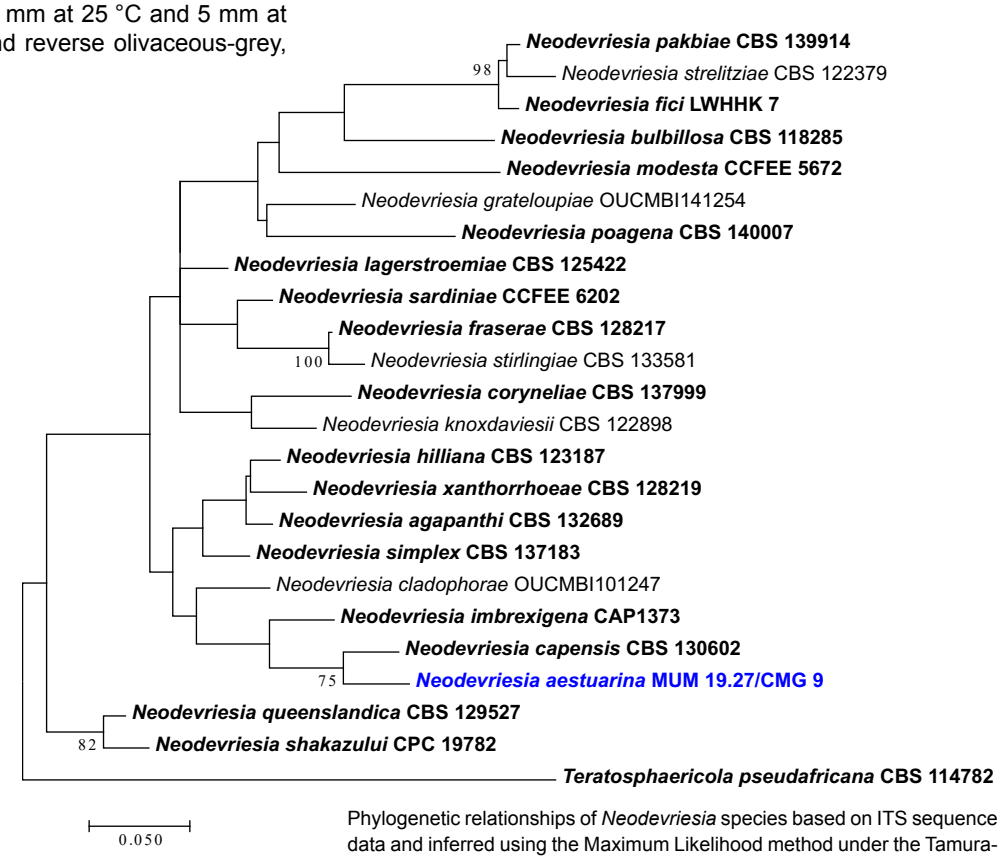
Classification — *Neodevriesiaceae*, *Mycosphaerellales*, *Dothideomycetes*.

Mycelium on synthetic nutrient-poor agar (SNA) consisting of branched, septate, olivaceous grey (Rayner 1970), moniliform hyphae with aerial hyphae absent. *Chlamydospores* not observed. *Conidiophores* arising from hyphae occasionally reduced to conidiogenous cells, thick-walled, cylindrical, straight to slightly curved, long, septate, brown with an apical conidiogenous apparatus. *Conidia* smooth, cylindrical, sometimes in acropetal chains, apex and base truncate with one and occasionally two septa, (13.2–)15.6(–18.9) × (2.2–)3.0(–3.7) µm (n = 100).

Culture characteristics — Optimum temperature for growth 25 °C. No growth at 35 °C on potato dextrose agar (PDA), cornmeal agar (CMA) and SNA. Colony radius after 30 d: on PDA, colonies have 2 mm at 10 °C, 5 mm at 15 °C, 10 mm at 20 °C, 12 mm at 25 °C and 5 mm at 30 °C; colony flat, circular, dense, obverse and reverse greenish black, aerial hyphae absent. On malt extract agar (MEA), colonies have 2 mm at 10 °C, 4 mm at 15 °C, 7 mm at 20 °C, 10 mm at 25 °C and 4 mm at 30 °C; colony circular, dense, obverse and reverse greenish black, aerial hyphae absent. On SNA, colonies have 2 mm at 10 °C, 4 mm at 15 °C, 6 mm at 20 °C, 7 mm at 25 °C and 5 mm at 30 °C; colony circular, obverse and reverse olivaceous-grey, aerial hyphae absent.

Typus. Portugal, Ria de Aveiro, from saline water, 2019, *M. Gonçalves* (holotype MUM H-19.27, a dried culture; ex-holotype living culture MUM 19.27 = CBS 146734 = CMG 9; ITS and LSU sequences GenBank MN046879 and MN653390, MycoBank MB831390).

Notes — The genus *Neodevriesia* was introduced by Quaedvlieg et al. (2014) to accommodate devriesia-like species. Although morphologically very similar to *Devriesia* it is phylogenetically distinguishable. *Neodevriesia aestuarina* is the first member of the genus isolated from saline water, but other species have been found in a marine environment associated with macroalgae. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence are *Neodevriesia capensis* (GenBank MK448259; Identities = 497/529 (94 %), 17 gaps (3 %)) and an uncultured marine ascomycete (GenBank AF423023; Identities = 495/531 (93 %), 19 gaps (3 %)). Closest hits using the **LSU** sequence had highest similarity to *Neodevriesia grateloupiae* (GenBank KU578120; Identities = 1 078/1 099 (98 %), 3 gaps (0 %)), *Neodevriesia cladophorae* (GenBank KU578114; Identities = 1 076/1 099 (98 %), 7 gaps (0 %)) and *Neodevriesia strelitziae* (GenBank GU301810; Identities = 1 061/1 091 (97 %), 7 gaps (0 %)).



Phylogenetic relationships of *Neodevriesia* species based on ITS sequence data and inferred using the Maximum Likelihood method under the Tamura-Nei model (MEGA v. 7.0) (Kumar et al. 2016). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site and rooted to *Teratosphaericola pseudoafricana* (CBS 114782). Bootstrap support values (> 70 %) are shown at the nodes. Ex-type strains are in **bold** and the isolate from the current study is in blue. The alignment and tree were deposited in TreeBASE (study S24538).

Colour illustrations. Estuary Ria de Aveiro (Portugal). Colony after 30 d at 25 °C on PDA, MEA and SNA; moniliform hyphae, conidiogenous cells and conidia on SNA. Scale bars = 2.5 µm.

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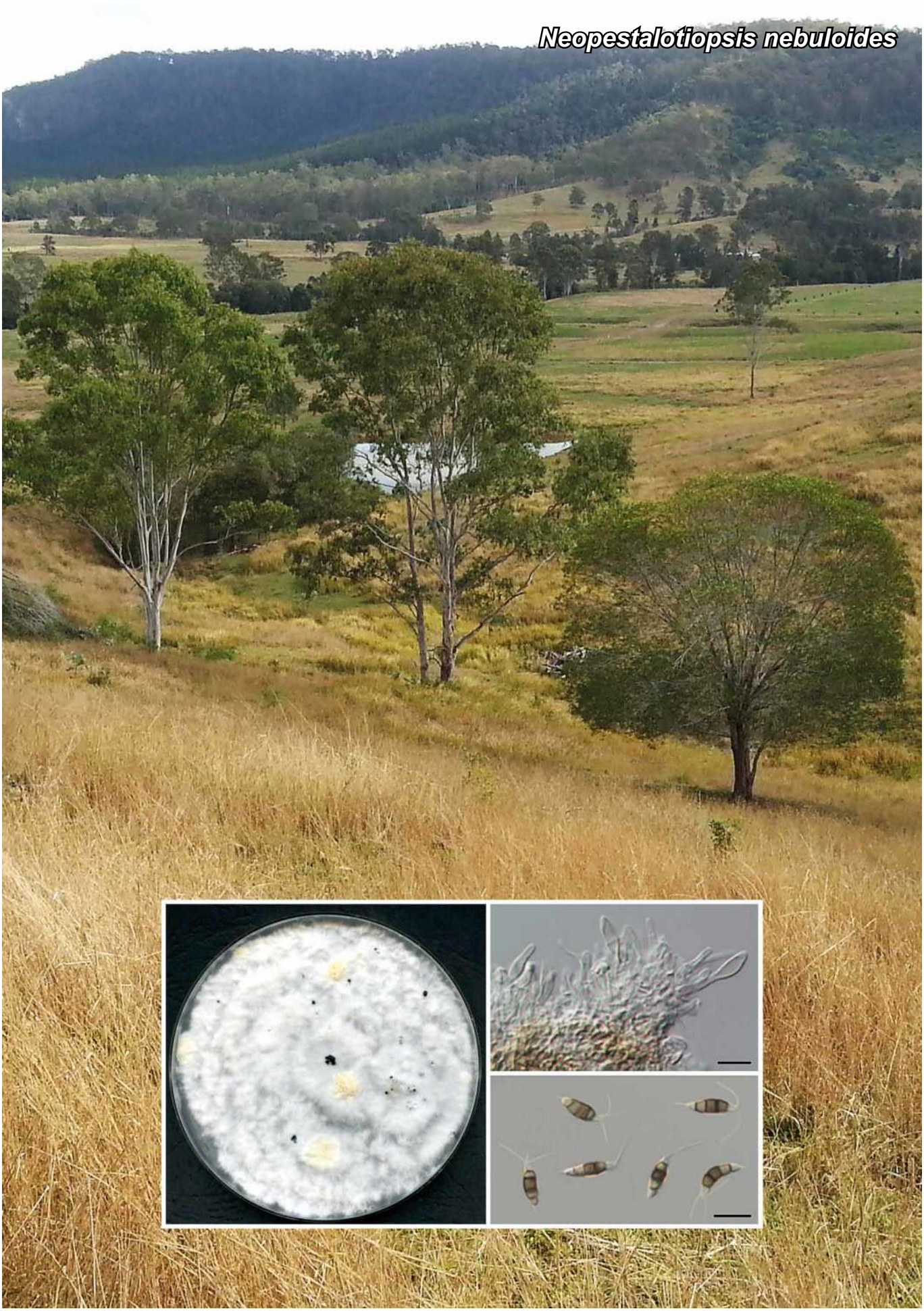

Neopestalotiopsis nebuloides

Fungal Planet 1097 – 29 June 2020

Neopestalotiopsis nebuloides C. Lock, Vitelli, Holdom, Y.P. Tan & R.G. Shivas, *sp. nov.*

Etymology. From the Latin *nebula*, meaning cloud, in reference to the fluffy, white, aerial mycelia.

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

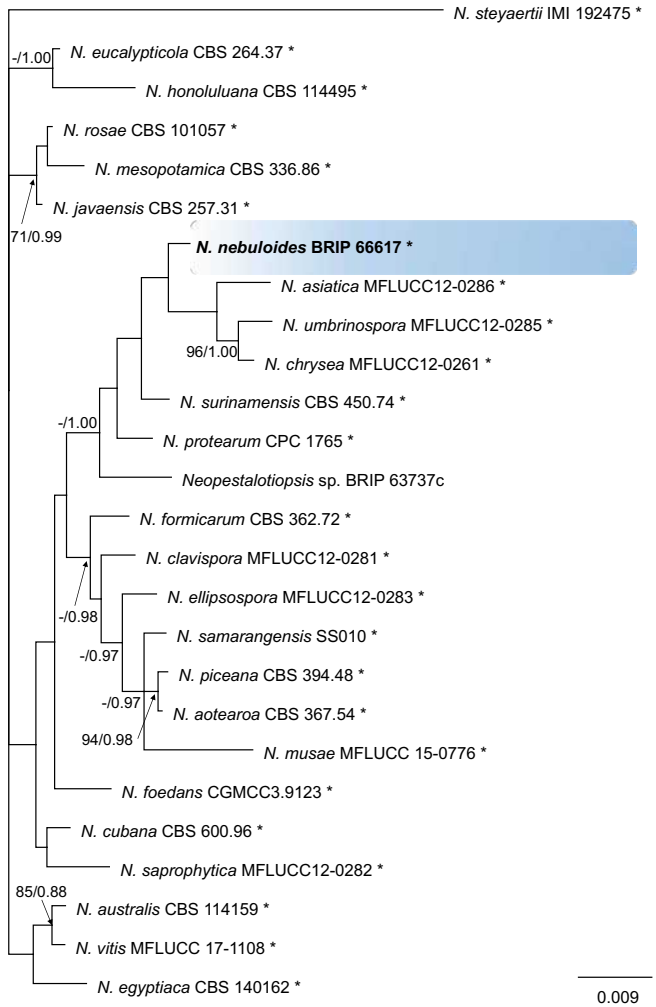
Conidiomata pycnidial on 1/2 potato dextrose agar (PDA), globose or clavate, scattered or aggregated, semi-immersed, black, up to 250 µm diam; exuding dark brown to black conidial masses. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* discrete, ampulliform, hyaline, smooth, 5–10 × 3–5 µm. *Conidia* fusoid, cylindrical, straight to slightly curved, 4-septate, 19–30 × 5–8 µm, basal cell conic, hyaline, smooth and thin-walled, 3–6 µm long; three median cells doliiform, 13–21 µm long, smooth, versicoloured, septa darker than the rest of the cell (second cell from base pale brown, 3.5–6.5 µm long; third cell medium to dark brown, 3.5–6.5 µm long; fourth cell medium to dark brown, 4–6 µm long); apical cell 3–5.5 µm long, hyaline, conic, thin-walled, smooth; with three tubular apical appendages, arising from the apical crest, unbranched, filiform, 3–19 µm; basal appendage tubular, centric, 3–6 µm long. *Sexual morph* not seen.

Culture characteristics — *Colonies* on PDA 8 cm diam after 7 d at 25 °C, margin irregular to undulating, whitish, zonate, with sparse to moderate aerial mycelia on the surface, with black conidiomata in the central part; reverse pale orange yellow.

Typus. Australia, Queensland, Logan, Greenbank, 527 Middle Road, S27°42'20.0" E153°00'10.6", from leaves of *Sporobolus elongatus* (*Poaceae*), 9 Nov. 2017, *G. Fichera* (holotype BRIP 66617, includes ex-type culture; ITS, *tub2* and *tef1a* sequences GenBank MK966339, MK977632 and MK977633, MycoBank MB831167).

Notes — The multilocus phylogenetic analysis placed *N. nebuloides* in a clade with *N. asiatica*, *N. chrysea* and *N. umbrinospora*. BLASTn searches in GenBank, restricted to ex-type strains, showed that *N. nebuloides* differs from *N. umbrinospora* in **ITS** (GenBank NR_111783; Identities 481/484 (99 %), 2 gaps (0 %)); ***tub2*** sequence differs from *N. asiatica* (GenBank JX399018; Identities 444/448 (99 %), no gaps) and *N. chrysea* (GenBank JX399020; Identities 441/448 (98 %), no gaps); and the ***tef1a*** sequence differs from *N. asiatica* (GenBank JX399049; Identities 475/492 (97 %), 5 gaps (1 %)), *N. chrysea* (GenBank JX399051; Identities 480/492 (98 %), 6 gaps (1 %)), and *N. umbrinospora* (GenBank JX399050; Identities 482/492 (98 %), 6 gaps (1 %)). Morphologically, *N. nebuloides* has shorter apical appendages than *N. asiatica* (20–30 µm), *N. chrysea* (22–30 µm) and *N. umbrinospora* (22–35 µm) (Maharachchikumbura et al. 2012). *Neopestalotiopsis nebuloides* is known only from *Sporobolus elongatus* in Australia. Its close relatives are *N. asiatica* from an unidentified tree in China; *N. chrysea* and *N. umbrinospora* from unidentified plant material in China (Maharachchikumbura et al. 2012).

Colour illustrations. Sporobolus natalensis infestation near Conondale, Australia. Colony on PDA at 1 wk; sporulating conidiomata on PDA; conidiogenous cells; conidia. Scale bars = 100 µm (conidiomata) and 10 µm (conidiogenous cells and conidia).



Phylogenetic tree of selected *Neopestalotiopsis* species based on a maximum likelihood analysis of a combined multilocus alignment (ITS, *tef1a* and *tub2*). Analyses were performed on the Geneious v. 11.1.2 platform (Biomatters Ltd.) using RAxML v. 8.2.11 (Stamatakis & Alachiotis 2010) and MrBayes v. 3.2.6 (Ronquist & Huelsenbeck 2003), both based on the GTR substitution model with gamma-distribution rate variation. Branch lengths are proportional to distance. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). *Neopestalotiopsis steyaertii* was used as outgroup. Novel taxon is indicated in **bold**. Ex-type strains are marked with an asterisk (*).

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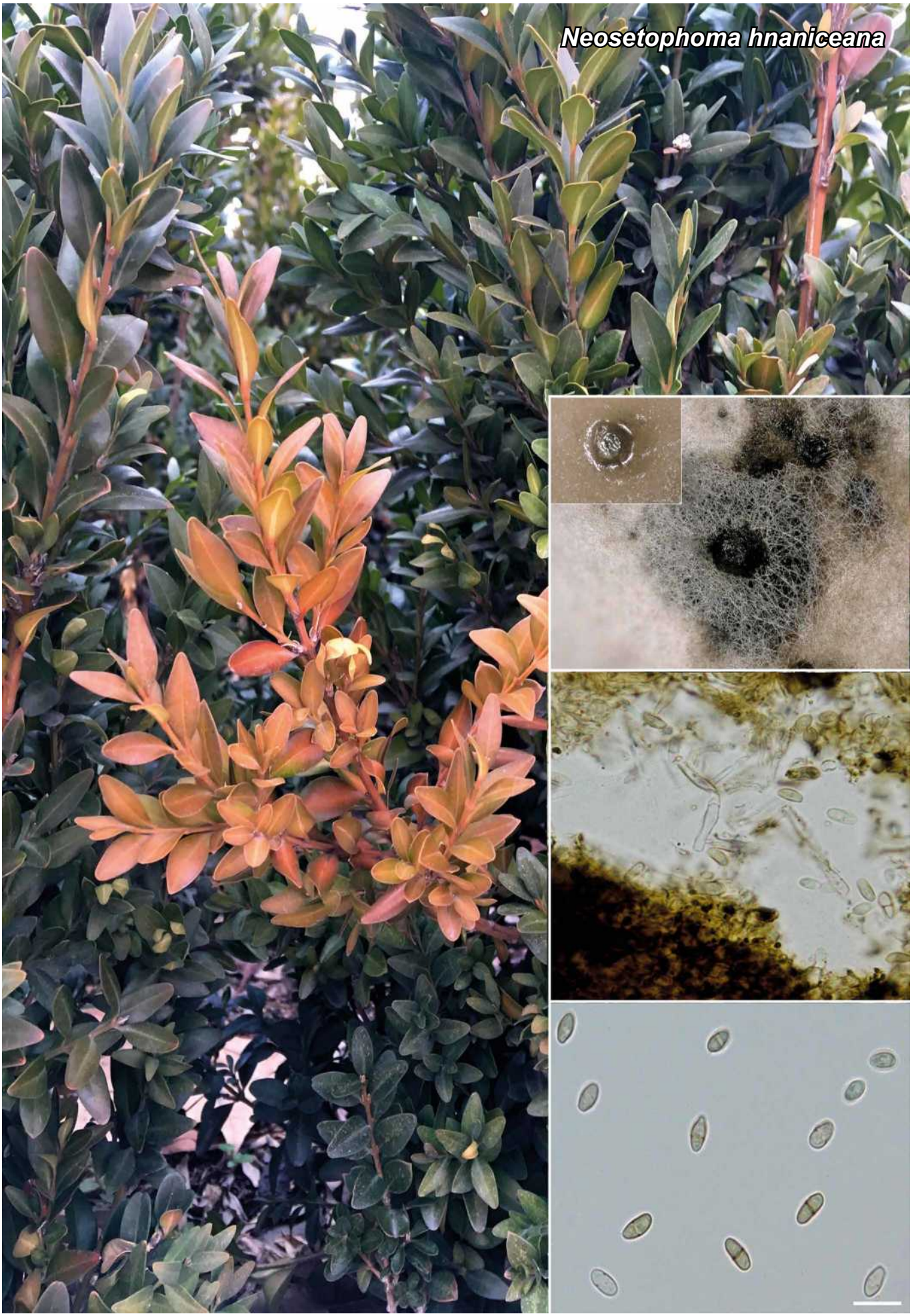

Neosetophoma hnaniceana

Fungal Planet 1098 – 29 June 2020

Neosetophoma hnaniceana Spetik, Eichmeier & Berraf-Tebbal, *sp. nov.*

Etymology. Named after Hnanice (Czech Republic) where the fungus was collected.

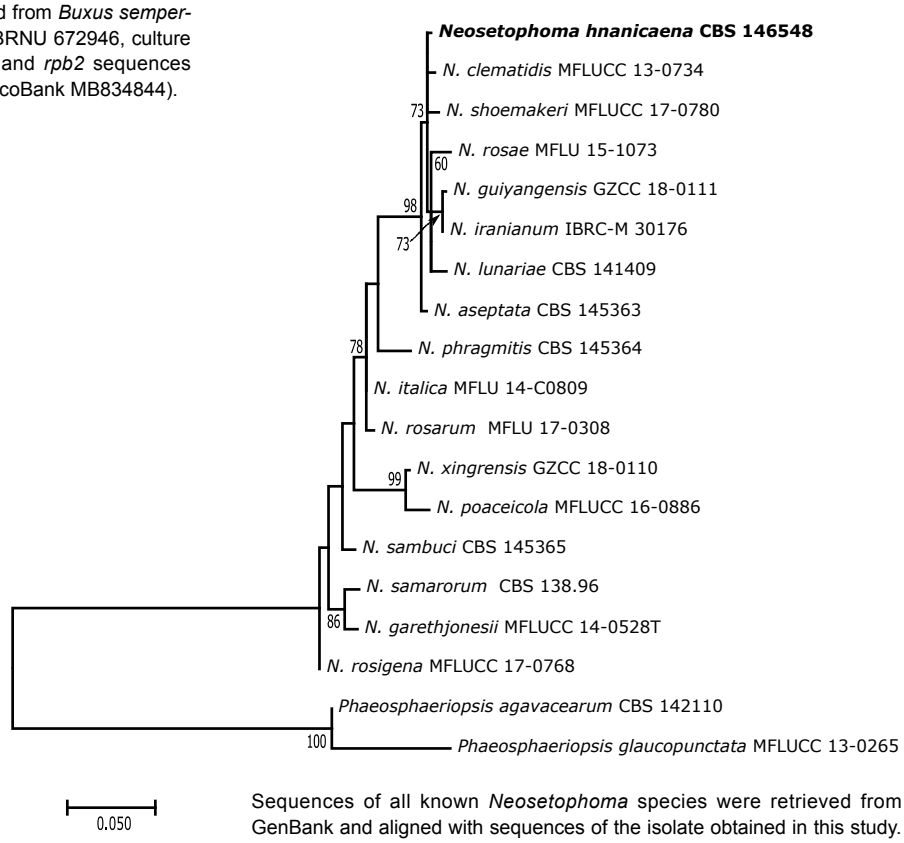
Classification — *Phaeosphaeriaceae*, *Pleosporales*, *Dothideomycetes*.

Saprobic on dead leaves and wood of *Buxus sempervirens*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* pycnidial, separate, dark to pale brown, globose, subepidermal, unilocular, thin-walled, papillate, 80–120 µm high, 85–130 µm diam. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* enteroblastic, phialidic, doliiform to ampulliform, determinate, hyaline, smooth-walled. *Conidia* subcylindrical, fusoid or ellipsoid to fusoid, individually hyaline, olivaceous green at maturity, with transverse septum, thin- and smooth-walled, (6.96–)8.14–8.79(–10.41) × (2.94–)3.3–3.64(–4.46) µm, mean ± S.D. 8.46 ± 0.9 × 3.47 ± 0.47 µm, L/W ratio = 2.5.

Culture characteristics — Colonies on malt extract agar (MEA) reaching 3–4 cm diam in the dark, at 25 °C, after 3 wk, slow growing, white to dirty white in the first week, becoming yellow-green with pale irregular margin after 3 wk, moderate aerial mycelium, reverse iron-grey to umber, with age.

Typus. Czech Republic, Znojmo, Hnanice, isolated from *Buxus sempervirens* (*Buxaceae*), Feb. 2019, *M. Spetik* (holotype BRNU 672946, culture ex-type CBS 146548 = MEND-F-0083; ITS, LSU and *rpb2* sequences GenBank MT119769, MT119767 and MT119768, MycoBank MB834844).

Notes — Based on a megablast search of NCBI nucleotide database, the closest hits using the **ITS** sequence had the highest similarity to *Neosetophoma aseptata* (GenBank NR_164449.1; Identities = 538/542 (99 %), no gaps), *Neosetophoma lunariace* (GenBank NR_154242.1; Identities = 535/543 (99 %), no gaps) and *Neosetophoma shoemakeri* (GenBank NR_161044.1; Identities = 524/530 (99 %), 1 gap (0 %)). The closest hits using the **LSU** sequence had the highest similarity to *Loratospora aestuarii* (GenBank GU301838.1; Identities = 1 117/1 124 (99 %), no gaps), *Ophiosphaerella herpotricha* (GenBank DQ767656.1; Identities = 1 114/1 125 (99 %), 1 gap (0 %)) and *Phoma cladoniicola* (GenBank JQ238625.1; Identities = 1 112/1 124 (99 %), no gaps); closest hits using the ***rpb2*** sequence are *Brunneomurispora lonicerae* (GenBank MK359079.1; Identities = 571/657 (87 %), no gaps), *Ophiosphaerella herpotricha* (GenBank DQ677958.1; Identities = 587/696 (94 %), 2 gaps (0 %)) and *Phaeopoacea festucae* (GenBank KY824768.1; Identities = 590/705 (84 %), no gaps).



Sequences of all known *Neosetophoma* species were retrieved from GenBank and aligned with sequences of the isolate obtained in this study. Alignments were done with ClustalX v. 1.83 (Thompson et al. 1997). Kimura's two parameter model with Gamma distribution (K2+G) was used as the best nucleotide substitution model. The Maximum Likelihood (ML) analysis was performed using MEGA v. 7 software (Kumar et al. 2016). The robustness of the ML tree was evaluated by 1 000 bootstrap replications. Maximum likelihood tree obtained from the ITS and LSU gene sequences of *Neosetophoma* species of our isolates and sequences retrieved from GenBank. The tree was built using MEGA v. 7.0. Bootstrap support values above 70 % are shown at the nodes. The species described here is highlighted in **bold**. The alignment and tree are available in TreeBASE (study S25862).

Colour illustrations. *Buxus sempervirens* growing in Hnanice. Conidiomata on MEA; conidiogenous cells and conidia. Scale bars = 10 µm.

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Paecilomyces penicilliformis
pharmacy
weight management
foot care

Fungal Planet 1099 – 29 June 2020

Paecilomyces penicilliformis Jurjević & Hubka, *sp. nov*.

Etymology. Refers to the production of penicillium-like conidiophores.

Classification — *Thermoascaceae*, *Eurotiales*, *Eurotiomycetes.*

Micromorphology (on malt extract agar; MEA): *Hyphae* hyaline to pale yellow-brown, 2.5–11 µm diam, *Conidiophores* borne on the surface or from aerial hyphae, commonly 5–75 × (2.5–)3–5 µm diam; with smooth walls, bearing terminal whorls of verticillately arranged branches. *Phialides* 2–7 per branch, cylindrical, occasionally flask shaped, 10–16(–21) × 2.5–3.5(–5) µm diam, tapering abruptly toward a long cylindrical collula, up to 7 µm long and 1–2 µm diam, solitary phialides rarely present. *Conidia* in long divergent chains, ellipsoidal or cylindrical with conspicuously truncated ends, rarely subglobose, 3–5(–8) × 2–4.5(–5) µm diam. *Chlamydospores* very rare, smooth. *Sexual morph* was not observed even after prolonged incubation at 25 °C.

Cultural characteristics — (in darkness, 25 °C after 7 d): Colonies on MEA > 90 mm diam, colony texture, floccose, mycelium white to yellow-brown (deep colonial buff to honey yellow, R30; Ridgway (1912)), sporulation very good, conidia *en masse* light-buff to warm-buff (R15), exudate absent, soluble pigments absent, reverse mustard yellow to primuline yellow (R16). Colonies on Czapek yeast autolysate agar (CYA) 37–40 mm diam, colony texture floccose, mycelium white yellow ochre (R15), sporulation good, conidia *en masse* light buff to warm buff (R15), exudate absent, soluble pigments absent, reverse light buff to warn buff (R15). Colonies on potato dextrose agar (PDA) > 90 mm diam, colony texture floccose, mycelium deep colonial buff to honey yellow (R30), sporulation very good, conidia *en masse* light-buff to warm-buff (R15), exudate absent, soluble pigments absent, reverse amber yellow to primuline yellow (R16). Colonies on Czapek yeast agar with 20 % sucrose, (CY20S) 24–26 mm diam, colony texture floccose, mycelium white yellow ochre (R15), sporulation good, conidia *en masse* light buff to warm buff (R15), exudate absent, soluble pigments absent, reverse light buff to warm buff (R15). Colonies on Dichloran glycerol agar (DG18) 16–18 mm diam, colony texture light floccose, sporulation very good, mycelium white to cream colour (R16), reverse warm buff (R15). No growth on CYA supplemented with 5 % (w/v) NaCl (CYAS). Colonies on OA 65–67 mm diam, colony texture floccose, mycelium white to honey yellow (R30), sporulation very good, conidia *en masse* light-buff to warm-buff (R15), exudate absent, soluble pigments absent. Colonies on creatine sucrose agar (CREA) 2–3 mm diam, poor growth, no acid production, mycelium white, colony subsurface to submerged into the agar. Colony diam (in mm after 7 d) at 30 °C/37 °C; MEA > 90/7–12; CYA 38–41/4–5; PDA > 90/10–12; CY20S 42–45/3–4; DG18 30–31/3–4; OA > 90/9–11; CREA 9–11/ng; no growth at 41 °C.

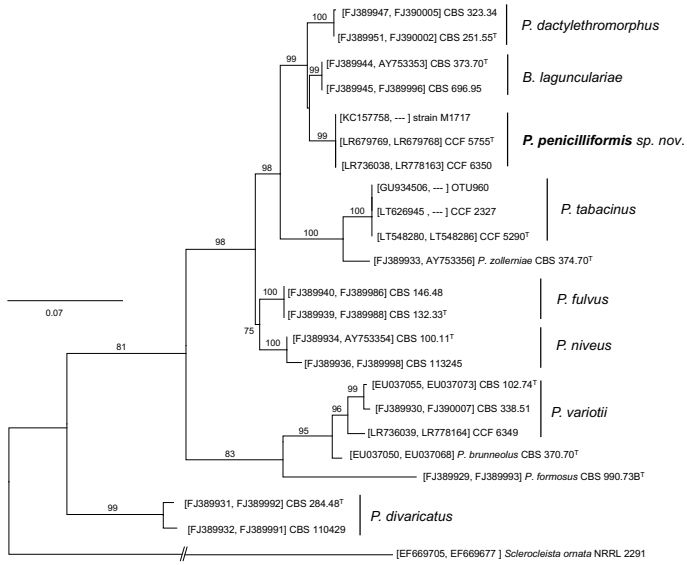
Typus. USA, Wisconsin, Menasha, pharmacy, air, 17 Mar. 2016, *Ž. Jurjević* (holotype BPI 911216, cultures ex-type CCF 5755 = CBS 146003 = EMSL 3392; ITS, LSU, β-tubulin and calmodulin sequences GenBank LR679769, LR679770, LR679768 and LR778299, MycoBank MB834874).

Colour illustrations. Inside of the pharmacy. Seven-day-old cultures of *Paecilomyces penicilliformis* on MEA (top to bottom 25 °C, 30 °C, 37 °C); conidia and conidiophores on MEA. Scale bars = 10 µm.

Additional material examined. USA, Massachusetts, Taunton, peach-mango juice, 25 Sept. 2018, *Ž. Jurjević*, CCF 6350 = EMSL 4943; ITS-LSU, β-tubulin and calmodulin sequences GenBank LR736038, LR778163 and LR778165.

Notes — BLAST analysis with the ITS, β-tubulin and calmodulin sequences of *P. penicilliformis* showed greatest similarity with *P. dactylethromorphus* (syn. *P. saturatus*) (98.8 %, 92.7 % and 93.1 %, respectively), *Byssochlamys lagunculariae* (98.8 %, 95.4 % and 96.3 %, respectively), *P. niveus* (98.4 %, 89.6 % and 91.4 %, respectively) and *P. fulvus* (98.2 %, 89.4 % and 90.3 %, respectively).

Paecilomyces penicilliformis produces predominantly long cylindrical conidia with conspicuously truncated ends, 3–5(–8) × 2–4.5(–5) µm compared to smaller and predominantly globose conidia with flattened base produced by the closely related *B. lagunculariae*, 2.7–4.5 × 2.2–3.3 µm (Samson et al. 2009). In addition, *B. lagunculariae* produces a sexual morph in culture (homothallic) and grows faster on MEA at 37 °C (25–55 mm after 7 d) (Samson et al. 2009). *Paecilomyces penicilliformis* is similar to *P. dactylethromorphus* by its cylindrical or ellipsoidal conidia and regularly branched conidiophores (penicillium-like). These species can be distinguished by wider conidia, 2–4.5(–5) µm produced by *P. penicilliformis* compared to *P. dactylethromorphus*, 1.7–3.4 µm wide (Samson et al. 2009).



A best scoring maximum likelihood tree based on the ITS region and the β-tubulin gene sequences shows the relationships of *P. penicilliformis* with other *Paecilomyces* and *Byssochlamys* species. The dataset contained 23 taxa and a total of 1056 characters of which 345 were variable and 234 parsimony-informative. Partitioning scheme and substitution models for analyses were selected using PartitionFinder v. 2 (Lanfear et al. 2017): the GTR+I+G model was proposed for the ITS1, ITS2 and β-tubulin gene exons; JC model for the 5.8S region; and K80+I model for the β-tubulin gene introns. The tree was constructed with IQ-TREE v. 1.4.4 (Nguyen et al. 2015). Support values at branches were obtained from 1000 bootstrap replicates. Only bootstrap support values ≥ 70 % are shown; ex-type strains are indicated by ^{T} and the novel species in **bold** text. The tree is rooted with *Sclerocleista ornata* NRRL 2291.

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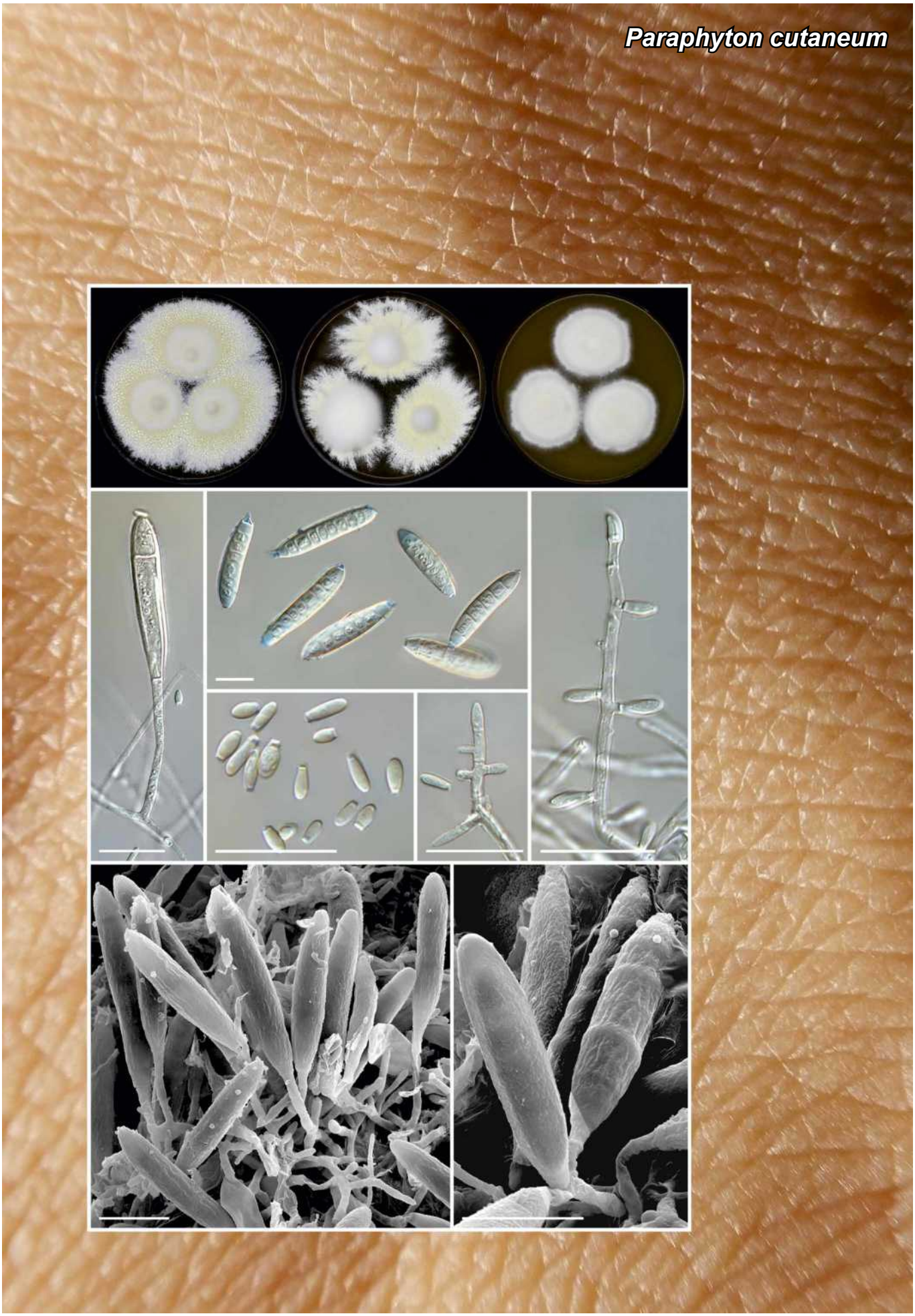
Paraphyton cutaneum

Fungal Planet 1100 – 29 June 2020

Paraphyton cutaneum Hubka, Kucerova, Gibas, Kubátová & Hamal, *sp. nov*.

Etymology. N.L. neut. adj. *cutaneum*, pertaining to the human skin (cutaneous), from which the fungus was isolated.

Classification — *Arthrodermataceae*, *Onygenales*, *Eurotiomycetes*.

Micromorphology (on malt extract agar (MEA), 25 °C, 2 wk): *Mycelium* consisting of branched, septate, hyaline, smooth, 1.5–3.5 mm diam hyphae; racquet hyphae, spiral hyphae and peridial hyphae not observed. *Conidiophores* simple, usually poorly differentiated from vegetative hyphae; conidiogenous hyphae unbranched or sparsely laterally branched. *Microconidia* sessile, borne laterally or terminally, clavate or pyriform, truncate, aseptate, smooth-walled, 3.5–7.5 × 1.5–2.5 µm (mean ± standard deviation: 5.1 ± 0.9 × 2.3 ± 0.3 µm), L/W 1.6–3.7. *Macroconidia* borne singly or on sparsely and irregularly branched conidiophores, fusiform or clavate with rounded apex (less frequently slightly acuminate) and truncate base, straight or slightly to strongly curved, multi-celled, thick-walled, usually with 4–7(–9) septa (median = 6), smooth-walled, hyaline to pale yellow *en masse*, 35–70(–80) × 9–14 µm (54 ± 9.6 × 12.2 ± 1.2 µm), L/W 2.8–6.2. *Chlamydospores* globose, subglobose to irregular, usually 5–10 µm diam. *Sexual morph* unknown.

Culture characteristics — Colonies on Sabouraud glucose agar (SGA) at 25 °C 33–40 mm diam after 1 wk, covering dish after 2 wk, flat, centrally raised to umbonate, granular, pale yellow (4A3; Kornerup & Wanscher 1978) to yellowish white (4A2), margins filamentous, reverse light brown (5D6) to orange yellow (4B7). Colonies on MEA at 25 °C 25–35 mm diam after 1 wk, covering dish after 2 wk, flat with elevated centre, granular (with or without cottony centre), pale yellow (4A3) to pinkish white (7A2), pink (13A4) sectors or concentric zone may be present in old cultures, margins filamentous, serrate to irregular, reverse greyish orange (5B4) to orange white (5A2), bright red pigment inconstantly exuded into the medium. Colonies on potato dextrose agar (PDA) at 25 °C 17–21 mm diam after 1 wk, 42–48 mm diam after 2 wk, centrally raised to raised, downy to delicately granular, pale yellow (4A3) to yellowish white (4A2), margins filamentous, reverse light brown (5D5) to greyish yellow (4B4). Colonies on MEA at 30 °C after 1 wk 24–29 mm diam, covering dish after 2 wk; no growth on MEA 37 °C.

Typus. South Africa, skin scrapings from human patient, before 1977, unknown collector (holotype PRM 951591, isotype PRM 951592, cultures ex-type UAMH 4027 = CCF 6192; ITS, LSU, β-tubulin and *tef1α* sequences GenBank MT192521, MT192523, MT210641 and MT210643, MycoBank MB835001).

Additional material examined. Czech Republic, skin scales, heel, 50-yr-old woman with suspected dermatophytosis, 16 Oct. 2017, *P. Hamal*, culture CCF 6334; ITS, LSU, β-tubulin and *tef1α* sequences GenBank MT192521, MT192524, MT210640 and MT210642.

Notes — BLAST analyses with the ITS and β-tubulin sequences of *Paraphyton cutaneum* showed the following similarities with currently accepted *Paraphyton* species (De Hoog et al. 2017): *P. cookei* (94.8 % and 95.6 %, respectively), *P. mirabile* (92.0 % and 90.8 %, respectively) and *P. cookiellum* (89.0 % and 92.9 %, respectively); LSU and *tef1α* sequences are not available for all accepted species.

Paraphyton cookei and *P. cookiellum* have echinulate to verrucose macroconidia and can be easily distinguished from *P. cutaneum* having smooth-walled macroconidia. Additionally, macroconidia of *P. cookiellum* are oval (18–34 × 16–18 µm) and predominantly 4-celled (Currah 1985). *Paraphyton mirabile* is a slow-growing species compared with *P. cutaneum*; its colonies attain approximately 24 mm diam after 2 wk on SGA (Choi et al. 2012).

Both isolates of *P. cutaneum* were isolated from patients with skin lesions suggestive of dermatophytosis but its pathogenicity is questionable because the detailed anamnestic data are not available. The strain from the Czech patient was isolated from a skin lesion on the heel (direct microscopic examination not performed due to insufficient amount of material). A complete clinical healing was observed after 1 mo treatment with topical oxiconazole. The species probably naturally occurs in soil, similarly to the remaining *Paraphyton* species which are also occasionally isolated from clinical material (Choi et al. 2012).

Colour illustrations. Human skin. Fourteen-day-old cultures of *Paraphyton cutaneum* grown at 25 °C on SGA, MEA and PDA (left to right); conidiophores bearing multi-celled macroconidia and one-celled microconidia, free macro- and microconidia, macroconidia in SEM. Scale bars = 20 µm.

Supplementary material

FP1100 A best scoring maximum likelihood (ML) tree based on the β-tubulin gene and the ITS region sequences.

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Penicillium taurinense

Fungal Planet 1101 – 29 June 2020

Penicillium taurinense S. Prencipe, Houbraken & D. Spadaro, *sp. nov.*

Etymology. Name refers to Turin, the city from which this type specimen was collected.

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

Conidiophores terverticillate; stipes coarsely roughened, 180–350 × 3–4.5 µm; *synnemata* up to 1 mm long; *branches* 15–30 µm; *metulae* 3–8, 10–13 × 2.5–3.5 µm; *phialides* ampulliform, 4–8 per metula, 8–9.8 × 2–3 µm. *Conidia* smooth, broadly ellipsoidal, 3–3.5 × 2.5–3 µm.

Culture characteristics — (25 °C, 7 d) Czapek yeast autolysate agar (CYA): Colonies slightly radially sulcate in centre, low; mycelium white; margins irregular; texture fasciculate; soluble pigments brown, moderately produced; exudate droplets small, copious, brown; sporulation moderate; conidia *en masse* pale grey-green; reverse brown, dark brown in centre. Malt extract agar (MEA): Colonies plane, elevated in the centre; mycelium white; margins slightly irregular; texture fasciculate; soluble pigments absent; exudate droplets large, pale brown; sporulation strong; conidia *en masse* dull to grey-green; reverse brown in centre, pale brown at edge. Yeast extract sucrose agar (YES): Colonies slightly radially sulcate, raised; mycelium white; margins entire; texture floccose; soluble pigment present, brown, weakly produced; exudates absent; sporulation moderate to strong; conidia *en masse* dull to grey-green; reverse reddish brown (copper). Dichloran 18 % glycerol agar (DG18): Colonies plane, raised at the centre; margins entire or slightly irregular; mycelium white; texture fasciculate; soluble pigments present, light brown, weak; exudates absent; sporulation strong; conidia *en masse* dull green; reverse reddish brown (copper) or reddish brown in centre, yellowish brown at edge. Oatmeal agar (OA): Colonies plane, low; margins regular, thin; mycelium white; texture fasciculate; soluble pigments light brown present, moderately produced; exudates brown present, small; sporulation strong; conidia *en masse* dark green. Colony diam after 7 d, in mm – CYA 22–24; CYA 15 °C 17–19; CYA 30 °C 22–25; CYA 37 °C no growth; MEA 27–31; DG18 19–22; YES 38–42; OA 37–42; CREA 13–16. Ehrlich reaction: None. Creatine sucrose agar (CREA): good growth, acid production absent, base production present.

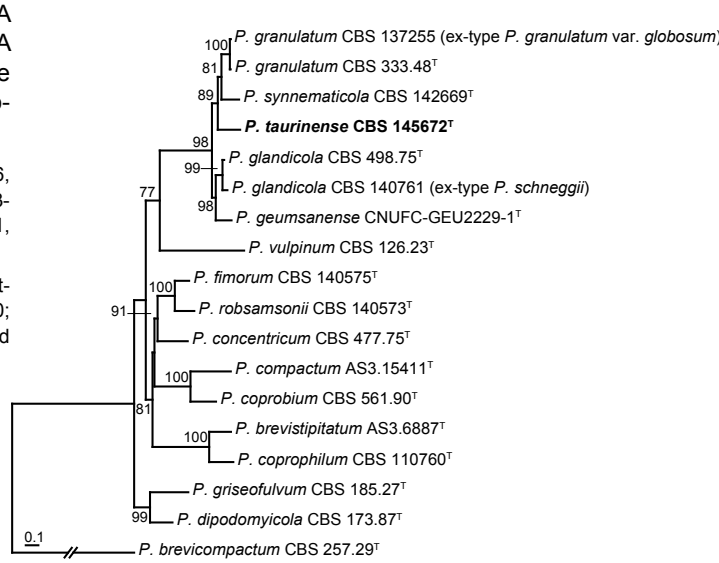
Typus. Italy, Piedmont Region, from indoor chestnut mill, Nov. 2016, *S. Prencipe* (holotype CBS H-24332, culture ex-type CBS 145672 = DTO 333-B8 = CAS16; ITS, *BenA*, *CaM* and *RPB2* sequences GenBank MF595981, MF595977, MF595979 and MT253108; MycoBank MB834715).

Additional material examined. Italy, Piedmont Region, from indoor chestnut mill, Nov. 2016, coll. *S. Prencipe*, CBS 145673 = DTO 333-B9 = CAS50; ITS, *BenA* and *CaM* sequences GenBank MF595982, MF595978 and MF595980.

Colour illustrations. Chestnut harvested in Piedmont region. Colonies (7 d, 25 °C) on MEA; conidiophores and conidia. Scale bars = 10 µm.

Notes — A BLAST search of *BenA*, *CaM* and ITS sequences of *P. taurinense* against an in-house reference sequence database containing data of all accepted *Penicillium* species, retrieved the highest similarities with *Penicillium glandicola*, *P. geumsanense* and *P. synnematicola*, clearly indicating that the species belongs to *Penicillium* sect. *Robsamsonia* ser. *Glandicolarum* (Houbraken et al. unpubl. data). Phylogenetic analyses showed that *P. taurinense* is sister to a clade containing CBS 142669 (ex-type strain of *P. synnematicola*), CBS 333.48 (ex-type of *P. granulatum*) and CBS 137255 (ex-type of *P. granulatum* var. *globosum*). The latter two strains were identified as *P. glandicola*; however, the ex-type of *P. glandicola* is more distantly related. Frisvad & Samson (2004) treated *P. granulatum* as a synonym of *P. glandicola* based on morphology and extrolite patterns. However, our phylogenetic analysis shows that *P. granulatum* is an accepted species, with *P. granulatum* var. *globosum* being a synonym of that species. Furthermore, *P. schneggii* is confirmed to be a synonym of *P. glandicola*.

Penicillium taurinense is phylogenetically distinct from *P. synnematicola* and *P. glandicola* (Houbraken et al. 2016, Guevara-Suarez et al. 2019). *Penicillium taurinense* grows faster than *P. synnematicola* on CYA (22–24 vs 33–37 mm), YES (38–42 vs 30–34 mm) and MEA (27–31 vs 11 13 mm) at 25 °C. Both grows at 30 °C while *P. glandicola* is not able to grow at this temperature (Frisvad & Samson 2004, Guevara-Suarez et al. 2019). Furthermore, *P. taurinense* produces brown exudates on CYA compared to hyaline exudate droplets of *P. synnematicola* and clear to pale yellow ones of *P. glandicola*. In addition, *P. taurinense* has a different colony reverse colour on CYA, MEA, DG18 and YES, no acid production on CREA and shorter phialides compared to *P. synnematicola*. A taxonomic study dealing with all accepted species in *Penicillium* ser. *Glandicolarum* is lacking, and could reveal more phenotypic differences.



Maximum likelihood tree of *Penicillium* strains belonging to sect. *Robsamsonia* based on 1 559 aligned nucleotides (combined *BenA*, *CaM* and *RPB2* sequences). Analysis performed using RAxML v. 8.2.12. Bootstrap support is based on 1 000 re-samplings; only bootstrap support values above 70 % are presented at the nodes. *Penicillium brevicompactum* was used as outgroup. The scale indicates the number of substitutions per site.

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Pestalotiopsis etonensis

Fungal Planet 1102 – 29 June 2020

Pestalotiopsis etonensis C. Lock, Vitelli, Holdom, Y.P. Tan & R.G. Shivas, *sp. nov.*

Etymology. Named after the town of Eton in Queensland, where the fungus was first collected.

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

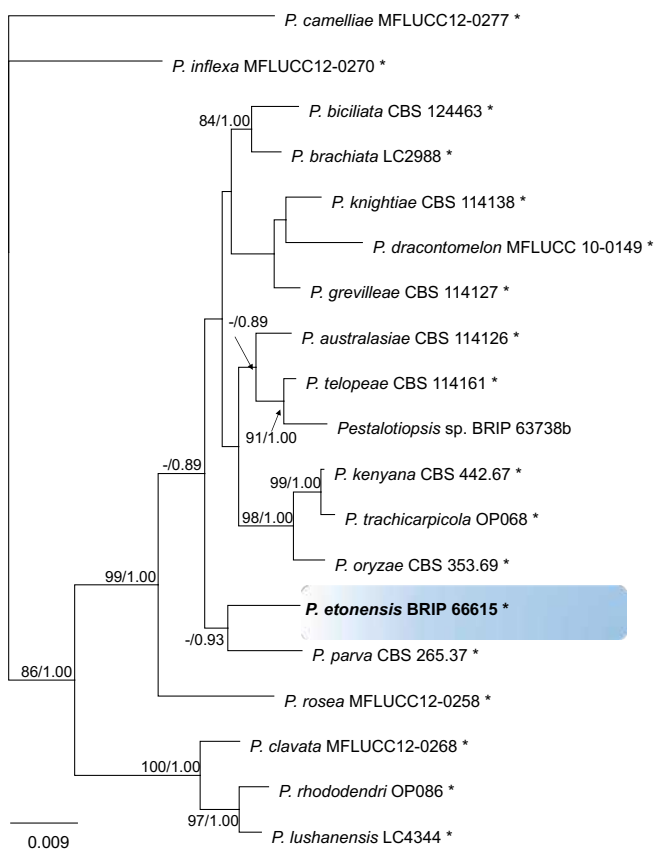
Conidiomata pycnidial on 1/2 potato dextrose agar (PDA), globose or clavate, scattered or aggregated, immersed or semi-immersed, dark brown to black, up to 470 µm diam; exuding dark brown to black conidial masses. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* discrete, cylindrical, hyaline, smooth, 5–10 × 1–2 µm. *Conidia* fusoid, cylindrical, straight to slightly curved, 4-septate, 15–21 × 4–7 µm, basal cell conic, hyaline, smooth and thin-walled, 2–5 µm long; three median cells doliiform, 10–15 µm long, smooth, concolourous, septa darker than the rest of the cell (second cell from base 3–5.5 µm long; third cell 3–4.5 µm long; fourth cell 3.5–6 µm long); apical cell 1.5–4.5 µm long, hyaline, conic, thin-walled, smooth; with three tubular apical appendages, unbranched, filiform, 6–16 µm; basal appendage tubular, centric, 2–4.5 µm long. *Sexual morph* not seen.

Culture characteristics — Colonies on PDA after 7 d 8 cm diam, adpressed with no aerial mycelium, margin entire, dark tan in the centre becoming lighter towards the margin, with dark radial striations in the middle part.

Typus. Australia, Queensland, Eton, Homebush Road, 1.2 km SE of Eton 4741, S21°16'24" E148°58'45", from leaves of *Sporobolus jacquemontii* (*Poaceae*), 07 Feb. 2017, *J. Vitelli* (holotype BRIP 66615, includes ex-type culture; ITS, *tub2* and *tef1a* sequences GenBank MK966339, MK977634 and MK977635, MycoBank MB831166).

Colour illustrations. Dense infestation of *Sporobolus natalensis* near collection site. Conidiomata sporulating on PDA; conidiogenous cells; conidia. Scale bars = 200 µm (conidiomata) and 10 µm (conidiogenous cells and conidia).

Notes — The multilocus phylogenetic analysis placed *P. etonensis* in a well-supported clade with *P. parva*. Based on a BLASTn search, *P. etonensis* differs from *P. parva* in ITS (GenBank NR_145237; Identities = 590/594 (99 %), 1 gap (0 %)), *tub2* (GenBank KM199405; Identities = 742/760 (98 %), 3 gaps (0 %)) and *tef1a* (GenBank KM199509; Identities = 468/478 (98 %), 1 gap (0 %)). Morphologically, *P. etonensis* conidia size and shape is indistinguishable from *P. parva* (fusoid, straight to slightly curved, 4-septate, 16–21 × 5–7 µm; Maharachchikumbura et al. 2014). Geographically, *P. etonensis* is only known from one location in Australia, while the origin and distribution of *P. parva* is unknown (Maharachchikumbura et al. 2014). *Pestalotiopsis etonensis* has only been isolated from *Sporobolus jacquemontii* in Australia, while *P. parva* is known from *Delonix regia* (*Caesalpiniaceae*) and *Leucothoe fontanesiana* (*Ericaceae*) (Maharachchikumbura et al. 2014).



Phylogenetic tree based on the Maximum Likelihood analysis from the combined ITS, *tef1a* and *tub2* sequence alignment. Analyses were done on the Geneious v. 11.1.2 platform (Biomatters Ltd.) using RAxML v. 8.2.11 (Stamatakis & Alachiotis 2010) and MrBayes v. 3.2.6 (Ronquist & Huelsenbeck 2003), both based on the GTR substitution model with gamma-distribution rate variation. Branch lengths are proportional to distance. RAxML bootstrap (bs) values > 70 % and Bayesian posterior probabilities (pp) > 0.8 are given at the nodes (bs/pp). *Pestalotiopsis camelliae* was used as outgroup. Novel taxon is indicated in **bold**. Ex-type strains are marked with an asterisk (*).

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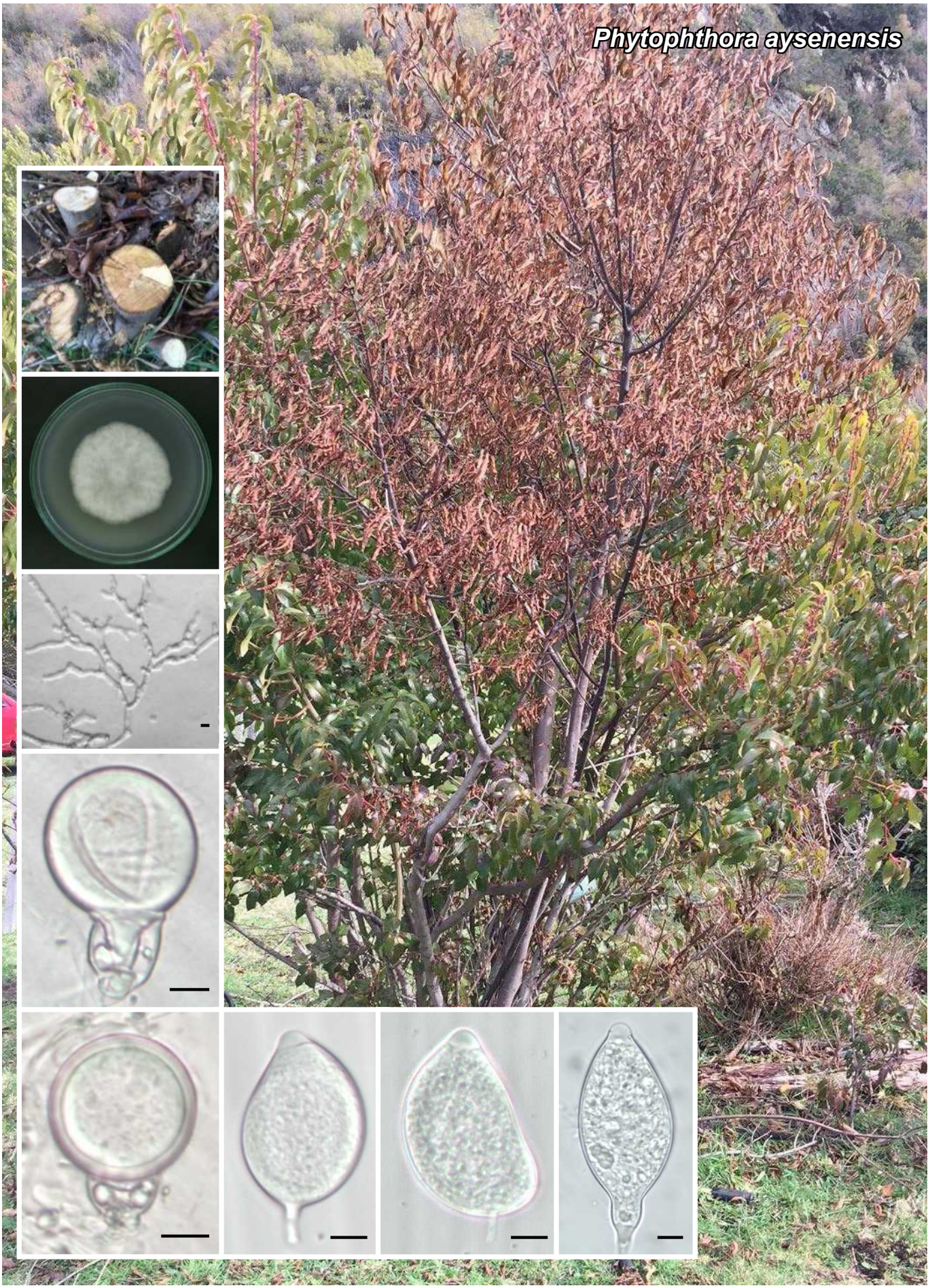

Phytophthora aysenensis

Fungal Planet 1103 – 29 June 2020

Phytophthora aysenensis M. Zapata, M.C. Asenjo & M. Gut., *sp. nov.*

Etymology. Name refers to the Aysén Region of Chile where this species was collected.

Classification — *Peronosporaceae*, *Peronosporidae*, *Oomycota*.

Hyphae hyaline, aseptate, tortuous, 2.5–11 µm diam. *Hyphal swellings* absent. *Sporangia* produced abundantly in non-sterile soil extract, noncaducous, papillate, mainly ovoid (53 %), globose (13 %), limoniform (10 %), distorted shapes (21 %), other shapes (3 %), (26–)35.5–58(–74) × (20–)24–38(–46.5) µm (av. 46.8 ± 9 × 31.2 ± 5), length/breadth ratio 1.5 ± 0.2. *Sporangiophores* sympodial. *Chlamydospores* not observed. *Homothallic*, abundant gametangia on 5 % carrot agar with β-sitosterol (CAS) after 7 d. *Oogonia* globose, smooth-walled, (26–)29–36(–39.5) µm diam (av. 32.2 ± 2.7), borne laterally and terminally. *Antheridia* amphigynous, 1-celled, (13.5–)14.5–18(–22.5) × 12.5–16(–17.5) µm (av. 16.1 ± 1.7 × 14.5 ± 1.1). *Oospores* observed after 2 wk on CAS, globose, plerotic, (25–)28–34.5(–39) µm diam (av. 31.1 ± 2.7), wall thickness (1.5–)2–4(–5) µm (av. 3.2 ± 0.7).

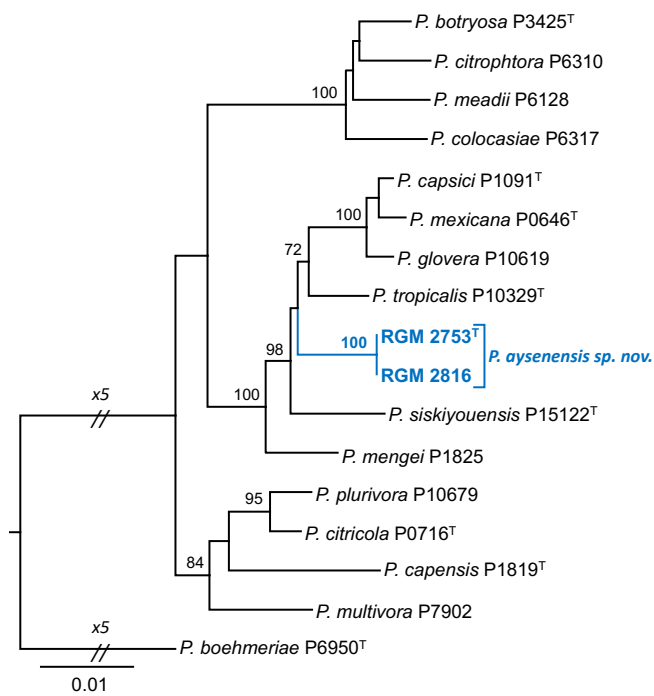
Culture characteristics — Colonies on CAS showed appressed to submerged mycelium, without distinct growth pattern, reaching 63.4 ± 1.3 mm diam after 7 d at 20 °C in darkness. Colonies on corn meal agar (CMA) white, with moderate to profuse aerial mycelium, cottoned, reaching 56.9 ± 2.5 mm diam.

Typus. Chile, Aysén, on collar rot and stem of *Aristotelia chilensis* (*Elaeocarpaceae*), 26 Sept. 2016, *M. González* (holotype RGM 2753, culture ex-type CCCT 19.159; ITS, LSU, *TUB*, *COX2*, *NAD9* and *RPS10* sequences GenBank MN557838, MN557839, MN557840, MN557841, MN557842 and MN557843, MycoBank MB833553).

Additional material examined. Chile, Aysén, on soil associated with rot of *A. chilensis*, 26 Sept. 2016, *M. González*, RGM 2816 = CCCT 19.162; ITS, LSU, *TUB*, *COX2*, *NAD9* and *RPS10* sequences GenBank MN557844, MN557845, MN557846, MN557847, MN557848 and MN557849.

Colour illustrations. *Aristorelia chilensis* exhibiting dieback and mortality by *Phytophthora aysenensis* in the collection site (Photo credit Milixsa González, 2016). Collar rot of *Aristorelia* tree; colony on CMA at 7 d; hyphae; oogonia with amphigynous antheridia; plerotic oospore; papillate sporangia. Scale bars = 10 µm (others) and 1 µm (hyphae).

Notes — *Phytophthora aysenensis* was isolated for the first time from root and collar rot of *Aristotelia chilensis*, a native Chilean plant known as Maqui or Chilean wineberry. *Phytophthora aysenensis* is a homothallic species, belonging to the Waterhouse's group II, which is characterised by amphigynous antheridia and papillate sporangia (Waterhouse 1963). Phylogenetically, *P. aysenensis* resides in clade 2 of the study of Martin et al. (2014), with species that were once part of the *P. citricola* complex. *Phytophthora aysenensis* is separated from other species by all the loci studied, with the mitochondrial genes *NAD9* and *RSP10* providing the best differential test. Based on a megablast search of NCBIs GenBank nucleotide database restricted to type material or authentic strains, the closest hit using the ***NAD9*** sequence were *P. capsici* (GenBank JF771674, Identities = 768/784 (98 %), 1 gap), *P. glovera* (GenBank JF771848; Identities = 767/784 (98 %), 1 gap) and *P. tropicalis* (GenBank JF771677; Identities = 765/784 (97.6 %), 1 gap). Closest hits using the ***RSP10*** sequence were *P. citrophthora* (GenBank JQ439181, Identities = 566/580 (97.9 %), 4 gaps), *P. mengei* (GenBank JQ439258; Identities = 565/580 (97.4 %), no gaps) and *P. botryosa* (GenBank JQ439165; Identities = 560/576 (97.2 %), 4 gaps).



Maximum Likelihood tree inferred from the combined ITS, LSU, *TUB*, *COX2*, *NAD9* and *RSP10* regions for selected *Phytophthora* species. DNA sequences were aligned using MAFFT v. 7.0 (Katoh & Standley 2013) with automatic strategy. The ML analysis was performed in RAxML-HPC BlackBox v. 8.2.12 (Stamatakis 2014) via the CIPRES Science Gateway v. 3.3 (Miller et al. 2015), using a GTR+G+I model of evolution. Bootstrap support values above 70 % are indicated on the nodes. The tree was rooted with *Phytophthora boehmeriae*. T = ex-type.

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Phytophthora personensis

Fungal Planet 1104 – 29 June 2020

Phytophthora personensis Z.G. Abad, W. Gut. & T.I. Burgess, *sp. nov.*

Etymology. Named after Person County, North Carolina, the location where the first specimen of the species was isolated.

Classification — *Peronosporaceae*, *Peronosporidae*, *Oomycota*.

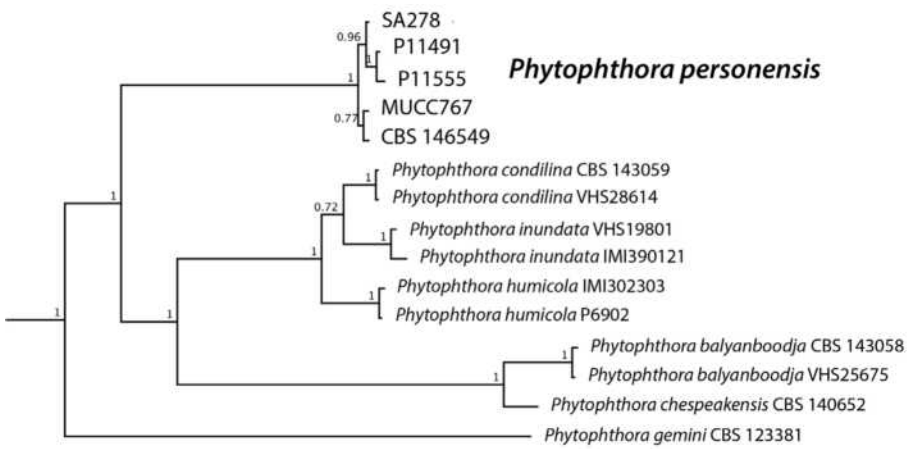
Sporangia produced abundantly in non-sterile soil extract; persistent and produced usually on unbranched sporangiophores, non-papillate, most commonly ovoid (73 %), often ellipsoid (18 %) and rarely limoniform or obpyriform; 62.8 ± 12.7 × 44.2 ± 9.9 µm (overall range 28.5–85.6 × 15.1–60.5 µm), length/breadth ratio 1.4 ± 0.2. *Sporangial proliferation* in chains of internally proliferating sporangia, both nested and extended. *Hyphal swellings* common, catenulate to globose 21–(31.6 ± 5.6)–49.4 µm. *Chlamydospores* common, globose 29.9–(54.8 ± 11.5)–78.1 µm. *Gametangia* not produced in single culture or when paired with A1 and A2 tester strains of *P. cinnamomi*, *P. tropicalis*, *P. cryptogea* and *P. cambivora*. Radial growth rates on V8 agar at optimum temperature (25–30 °C) and near the maximum temperature (37.5 °C), 12.6 ± 0.33 mm/d and 1.7 ± 0.23 mm/d, respectively.

Culture characteristics — Submerged colonies with no pattern were produced on malt extract, carrot and V8 agar. Cottony colonies with regular margins were produced on potato dextrose agar.

Typus. Australia, Western Australia, Busselton, baited from soil associated with dying *Grevillea mccutcheonii* (*Myrtaceae*), 2005, collected by Department of Parks and Wildlife (holotype MURU481, culture ex-type CBS 146549 = VHS14081; ITS, ß-tubulin, HSP90, *cox*I, *NADH* and LSU sequences GenBank EU301169, MF326805, MF326890, MF326887, MF326928 and MT159417, MycoBank MB834875).

Additional materials examined. Australia, Western Australia, Pemberton, baited from soil associated with dying *Rubus fruticosus* (*Rosaceae*) aggregate, 2012, *S. Aghighi*, culture SA278; Victoria, Ti-Tree Creek, baited from water, 2008, *W. Dunstan*, culture MUCC 767. – USA, Northern Carolina, Person County, from necrotic roots of *Nicotiana tabacum* (*Solanaceae*), 2002, *W. Gutierrez*, cultures by G. Abad at former NCSU-PPIL P11555 = CBS 121980 and P11491.

Notes — Phylogenetically, *P. personensis* resides in a strongly supported terminal clade and shares a common ancestor with *P. inundata* (Brasier et al. 2003), *P. condilina* (Burgess et al. 2018), *P. humicola* (Ko & Ann 1985), *P. balyanboodja* (Burgess et al. 2018) and *P. chesapeakensis* (Man in 't Veld et al. 2019). Together with *P. gemini* (Man in 't Veld et al. 2011) these species form a species cluster within clade 6 of the *Phytophthora* phylogeny (Burgess et al. 2018). In a multigene phylogeny of the ITS, *HSP90*, *BT*, *NADH* and *cox*I gene regions, *P. personensis* differs from both *P. condilina* and *P. humicola* by 4.4 %, *P. inundata* by 5.2 %, *P. balyanboodja* and *P. chesapeakensis* by 9.1 % and *P. gemini* by 8.3 %. All these species are morphologically similar; they all produce ovoid persistent, non-papillate sporangia that are borne terminally and they all have high temperature optima and maxima for growth. *Phytophthora personensis* appears to be sterile in culture and thus differs from *P. inundata*, *P. humicola* and *P. condilina* as these three species readily produce homothallic oogonia. *Phytophthora personensis* produces chlamydospores and thus differs from the three other sterile species in the clade, *P. balyanboodja*, *P. chesapeakensis* and *P. gemini*. *Phytophthora personensis* has been recovered from a variety of hosts on two continents, North America and Australia, and at this point in time its origin cannot be determined.



Bayesian inference tree based on a concatenated ITS, ß-tubulin, *HSP90*, *cox*I and *NADH* sequence alignment showing the placement of *P. personensis* in *Phytophthora* clade 6a generated in MrBayes v. 3.2.6 (Ronquist & Huelsenbeck 2003) as a plugin in Geneious Prime® 2019.2.3 (Biomatters Ltd.) using the GTR substitution model. The posterior probability values are shown at the nodes. The tree was rooted to *P. rosacearum* (not shown) and the novel species is shown in **bold** font.

Colour illustrations. *Grevillia* sp., host of the type isolate. Typical ovoid and ellipsoid sporangia; proliferation is internal and extended and chlamydospores were common; cottony colony on potato dextrose agar. Scale bar = 20 µm.

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Roridomyces pseudoirritans

Fungal Planet 1105 – 29 June 2020

Roridomyces pseudoirritans Kiyashko, *sp. nov.*

Etymology. Name refers to *Roridomyces irritans*, a species which is morphologically similar.

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

Pileus at first convex, then plano-convex with depressed or subumbilicate centre, up to 7.8 mm diam (dried specimens), radially pellucid-sulcate-striate almost up to centre, margin reflexed, crenulate, membranaceous, surface dry, velvety at centre, pallid, greyish orange (5B3–4, Kornerup & Wanscher 1978), turning yellowish white (4A2) to white towards margin, sometimes with blurred reddish brown (7D5–6, 7C5–6) spots. *Lamellae* arcuate decurrent, moderately distant (11–17 reach to the stipe), with 1–2 series of lamellulae, thin, whitish to pale greyish orange (like cap centre), sometimes also with spots, edge concolourous, slightly eroded. *Stipe* cylindrical, slightly attenuated towards apex, up to 28 × 1.5 mm, shiny, polished, faintly pellucid, whitish at apex, darkening to brownish orange or brownish yellow (5C6–7) towards base, covered with thick, glassy glutinous sheath, without strigose hairs at base. *Context* thin, concolourous with cap and stipe surfaces, *odour* not recorded. *Basidiospores* ellipsoid to oblong, rarely subcylindrical, 5.7–7.4(–8.1) × 3–3.9(–4.2) mm (x_{av} = 6.6 ± 0.5 × 3.5 ± 0.2 mm, Q = (1.6–)1.7–2.1(–2.3), Q_{av} = 1.9 ± 0.1, n = 59, s = 3), with small apiculus, smooth, hyaline, amyloid. *Basidia* 4-spored, clamped, subclavate, 12.9–17.6(–19.8) × 4.5–6 mm, thin-walled, inamyloid. *Basidiolae* subclavate or subfusoid, more rarely subutriform, 14–18.5 × 4.6–6 mm, thin-walled, inamyloid. *Lamellar edge* sterile. *Cheilocystidia* short and not much exceeding basidia, 14–31.4 × 4.2–11.7 mm (n = 37, s = 3), mostly clavate to subcapitate, rarely clear capitate, sometimes bifid or septate, thin-walled, occasionally with slightly thickened walls or yellowish content, colourless, smooth, inamyloid. *Pleurocystidia* absent. *Hyphae of subhymenium* cylindrical, smooth, hyaline 1.9–2.7(–3.5) mm diam. *Pileipellis* hymeniform, composed of spheropedunculate (sometimes on very long pedicel) or broadly clavate cells with or without constrictions, 23.2–49.8 × 14.7–29.2 mm, sometimes connected in short chains, smooth, with slightly thickened colourless or brownish walls, sometimes with yellowish content. *Stipitipellis* hyphae 2–3(–3.5) mm diam, cylindrical, smooth, uncoloured, thin-walled, parallel, with not abundant caulocystidia. *Caulocystidia* 16.8–30.2(–54.5) × 4.8–9.2(–11.8) mm, narrowly clavate to subcylindrical, rarely more or less capitate, thin-walled, sometimes with slightly thickened walls, smooth, uncoloured, inamyloid. *Clamp connections* on all hyphae.

Habitat & Distribution — Gregarious to caespitose on rotten wood in montane mixed forest of broad-leaved trees and *Pinus kesiya*.

Typus. Vietnam, Đắk Lắk Province, Lắk District, Chư Yang Sin National Park, ≈ 10 km to the south from Krông Kmar town, N12°23'49.207" E108°20'59.356", h ≈ 1071 m asl, on rotten wood, 24 May 2019, *A.A. Kiyasko*, 73-AK-19 (holotype LE 323311; ITS and LSU sequences GenBank MT300185 and MT276322, MycoBank MB834969).

Notes — *Roridomyces* includes 13 species, the most of which are described from the Southern Hemisphere. Morphologically, *R. irritans* from New Caledonia and Papua New Guinea is the closest to *R. pseudoirritans*. Although they have overlapping spore dimensions, *R. pseudoirritans* clearly differs from *R. irritans* by having short cheilocystidia: 14–31.4 mm vs 35–60 mm according to Horak (1978). Furthermore, cheilocystidia of *R. pseudoirritans* are not clearly capitate and may even be bifid or septate. Its caulocystidia are also short and narrowly clavate to subcylindrical. Among other small-spored species *R. lamprosporus* and *R. pruinosoviscidus* both have cheilo- and caulocystidia which are irregularly clavate to bifid with diverticulate projections (Horak 1978, Chew et al. 2015), *Mycena yirukensis* possesses cylindrical-ventricose, broadly ventricose-rostrate or strangulate cheilocystidia and cylindrical caulocystidia with one or few large branches (Grgurinovic 1995). *Roridomyces mauritianus* differs in having a dark brown cap and abundant pigmented caulocystidia with flexuous, contorted excrescences (Robich & Hausknecht 2001). *Roridomyces praeclarus* has an orange-red pileus, lageniform cheilocystidia and coralloid caulocystia; *R. palmensis* and *R. subglobosus* both are characterised by subglobose spores (Rexer 1994, Miersch & Dähncke 2007). The other species (*R. albororidus*, *R. appendiculatus*, *R. austrororidus*, *R. fuscororidus*, *R. ornatororidus* and *R. roridus*) possess larger spores with no overlapping dimensions (Rexer 1994, Maas Geesteranus & Meijer 1997). The majority of *Roridomyces* species from the Southern Hemisphere still lack DNA sequence data, and thus their phylogenetic relationships remain unknown.

Colour illustrations. Vietnam, southern Annamite Range, Chư Yang Sin National Park, montane mixed forest from broad-leaved trees and *Pinus kesiya* at the type locality. *In situ* basidiomata; spores; basidiae and basidiolae; cheilocystidia; cells of pileipellis; caulocystidia. Scale bars = 1 cm (basidiomata), 10 µm (all others).

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Trichophoma cylindrospora

Fungal Planet 1106 – 29 June 2020

Trichophoma Magaña-Dueñas, Cano & Stchigel, *gen. nov.*

Etymology. From Greek τρίχες-, hairs, due to the abundant setae on the sporocarps.

Classification — *Sporormiaceae*, *Pleosporales*, *Dothideomycetes*.

Conidiomata pycnidial, solitary, subglobose to pyriform, ostiolate, covered by brown to dark brown, septate, nodose setae. *Conidioma wall* of *textura angularis*, composed of brown to dark brown, flattened polygonal cells. *Conidiogenous cells* phialidic, hyaline, smooth walled, ampulliform. *Conidia* 0–1-septate, hyaline, guttulate, long cylindrical, with a narrowly flattened base and rounded at the end.

Type species. Trichophoma cylindrospora Magaña-Dueñas, Cano & Stchigel.

MycoBank MB833525.

Trichophoma cylindrospora Magaña-Dueñas, Cano & Stchigel, *sp. nov.*

Etymology. From Greek κυλινδρικό-, cylindrical, due to the shape of the conidia.

Hyphae hyaline to brown, septate, branched, thin-walled, smooth to tuberculate, 1.5–2 µm wide. *Conidiomata* pycnidial, brown to blackish brown, immersed to semi-immersed, solitary, scattered, subglobose to pyriform, 300–390 × 300–410 µm, ostiolate, setose. *Conidioma wall* 4–6-layered, 15–30 µm thick, covered by a mass of interwoven, brown to dark brown hyphae, followed by an outer layer of *textura angularis*, composed of brown to dark brown, flattened polygonal cells of 5–8 µm diam, incrusted with a dark brown to carbonaceous material around the neck; neck dark brown to carbonaceous, cylindrical, 130–145 × 100–145 µm, covered by brown to dark brown, septate, erect, nodose, thick-walled setae 100–180 × 2–4.5 µm, tapering towards the apex, mainly disposed around the ostiole. *Conidiophores* absent. *Conidiogenous cells* phialidic, determinate, hyaline, smooth-walled, ampulliform, 3–5 × 8–14 µm. *Conidia* 0–1-septate, hyaline, smooth- and thin-walled, long cylindrical, 18–20 × 2–3 µm, guttulate, with a narrowly flattened base and rounded at the end.

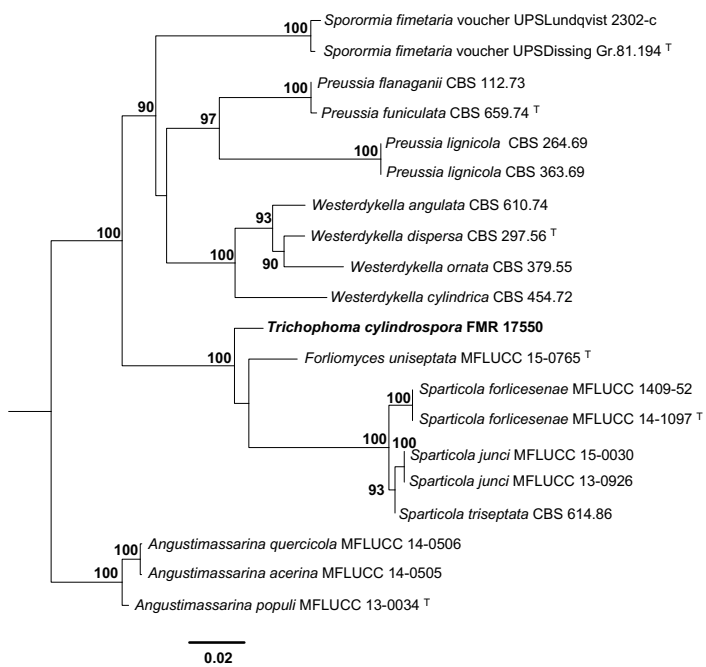
Culture characteristics — (7 d at 25 °C). Colonies on potato dextrose agar (PDA) reaching 24 mm diam, flattened, velvety, margins regular, yellowish white to reddish brown (M. 4A2 / 8D8; Kornerup & Wanscher 1978); reverse reddish brown to dark brown (M. 8E8 / 8F8), exopigment reddish brown to golden yellow (M. 8D8 / 5B7). Colonies on oatmeal agar (OA) reaching 40 mm diam, flattened, slightly floccose, margin regular, grey (M. 8F1); reverse grey (M. 8F1). Colonies on malt extract agar (MEA) 2 % reaching 25–29 mm diam, flattened, velvety to slightly floccose, margins lobate, dark brown to greyish yellow (M. 8F8 / 4C5); reverse greyish brown to greyish orange, with yellowish brown patches (M. 8F3 / 5B5 / 5F7).

Cardinal temperatures for growing — Optimum 30 °C, maximum 37 °C, minimum 15 °C.

Typus. Spain, Castilla y León community, Riaza, from plant debris, 4 May 2018, *I.A. Iturrieta-González* (holotype CBS H-24327; cultures ex-type CBS 146340 = FMR 17550; ITS, LSU and *tef-1α* sequences European Nucleotide Archive LR732023, LR732024 and LR732025, MycoBank MB833526).

Colour illustrations. Riaza, Spain. Colonies on PDA and OA after 14 d at 25 ± 1 °C; conidiomata; mycelial network on the pycnidial wall; conidiogenous cells and conidia. Scale bars = 50 µm (conidioma) and 10 µm (all others).

Notes — Based on the phylogenetic analysis of the ITS, LSU and *tef-1α* combined dataset, the closest relative of *T. cylindrospora* is *Forliomyces uniseptata*. *Forliomyces uniseptata* differs from *T. cylindrospora* in producing shorter and broader conidia (10–15 × 5–8 µm vs 18–20 × 2–3 µm), which are brown-coloured when mature (hyaline in *T. cylindrospora*) (Phukhamsakda et al. 2016). Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the LSU sequence was *Forliomyces uniseptata* MFLUCC 15-0765 (GenBank NG_059659, Identities = 814/827 (98 %), no gaps); the closest hits using ITS was *Forliomyces uniseptata* MFLUCC 15-0765 (GenBank NR_154006, Identities = 440/458 (96 %), 3 gaps (0 %)); and the closest hits using the *tef-1α* sequence was *Forliomyces uniseptata* MFLUCC 15-0765 (GenBank KU727897, Identities = 420/438 (96 %), no gaps).



Maximum likelihood tree obtained from the combined DNA sequences dataset from three loci (ITS, LSU and *tef-1α*) of our isolate and sequences retrieved from the GenBank. Alignment and tree building were performed by MEGA v. 6.06 (Tamura et al. 2013). Type strains of the different species are indicated with T. The new taxon proposed in this study is indicated in **bold**. The RAxML bootstrap support values (> 70 %) are provided at the nodes. *Angustimassarina quercicola*, *Angustimassarina acerina* and *Angustimassarina populi* were use as outgroup.

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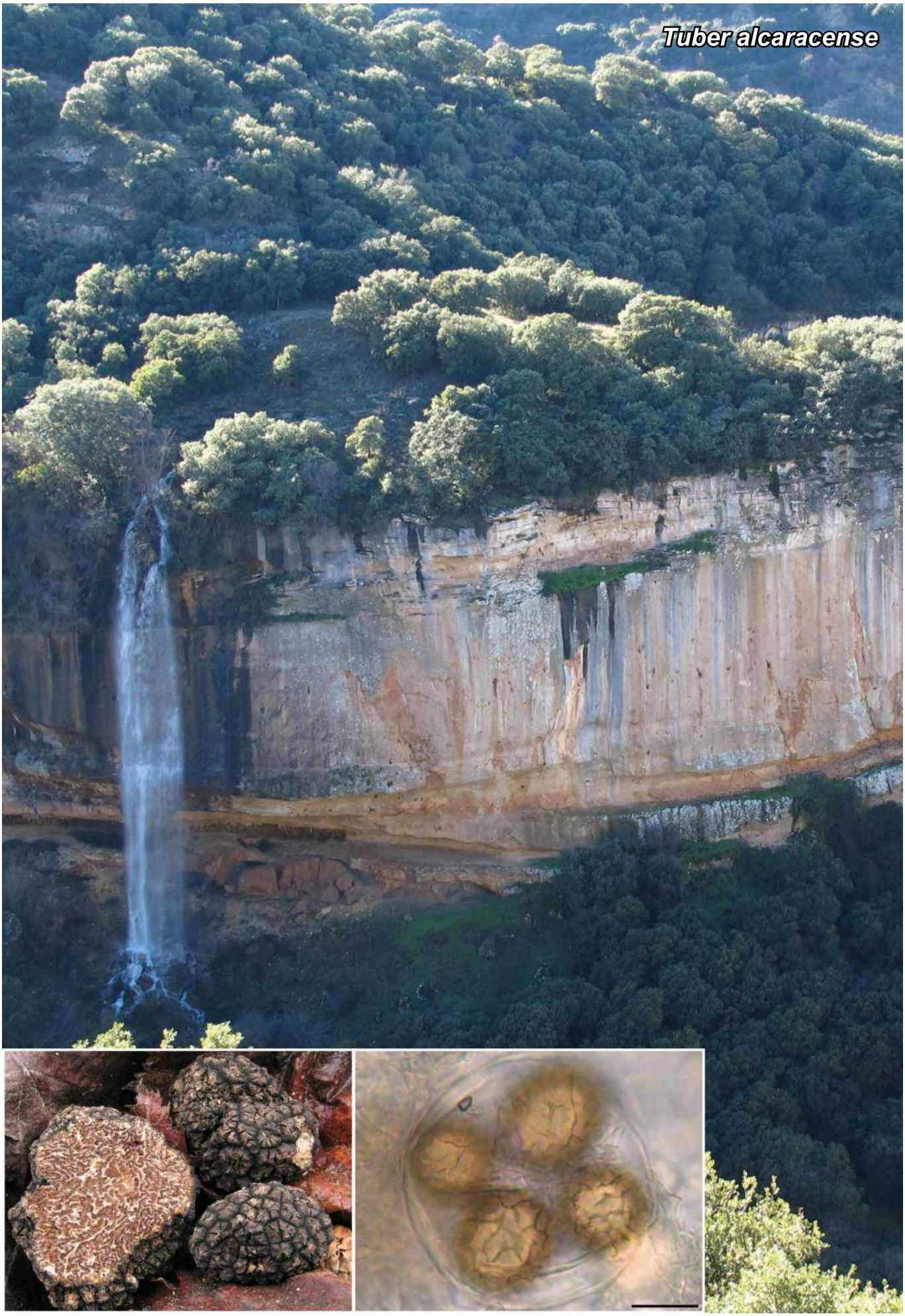

Tuber alcaracense

Fungal Planet 1107 – 29 June 2020

Tuber alcaracense Ant. Rodr. & Morte, *sp. nov.*

Etymology. Referring to Alcaraz mountain range, where the type specimen was collected.

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

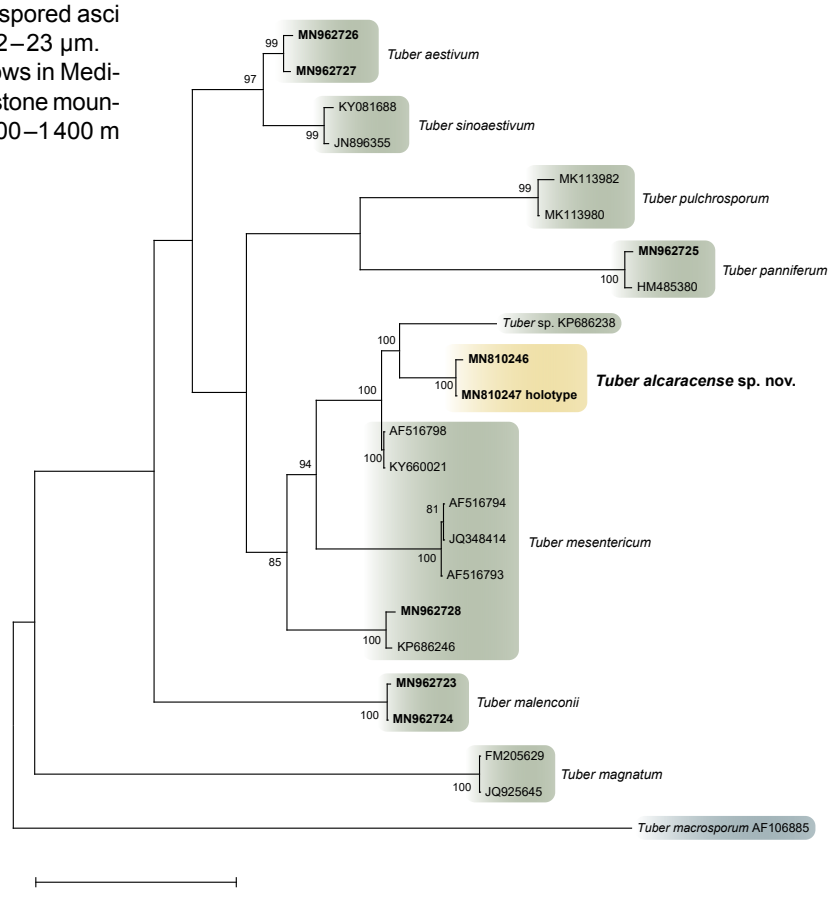
Ascomata hypogeous, 1–4 cm, subglobose, covered with brown-black pyramidal warts, 4–6-sided, 2–3(–4) mm across, 1–4 mm high, often depressed at the apex. *Peridium* 150–250 µm thick, pseudoparenchymatous, composed of subglobose, angular cells, 10–20 µm diam, pale yellow and thin-walled in the innermost layers, dark red-brown and with thicker walls in the outermost layers. *Gleba* firm, solid, white when immature, becoming dark brown at maturity, marbled with numerous, thin, white, meandering veins that do not change colour when exposed to the air. Pleasant *odour*. *Asci* inamyloid, 60–90 × 50–75 µm, walls thickened, 1–2 µm, ellipsoid to subglobose, with a short stalk, 10–35 × 5–7 µm, (1–)3–4(–5)-spored. *Ascospores* 26–47 × 22–37 µm, Q = 1.1–1.4, excluding ornamentation, yellowish, ellipsoid to subglobose, ornamented with a coarse irregular reticulum, 3–5 µm high, sometimes bending at the top. Meshes variable, usually 3–5 across width of spore and often with incomplete secondary crests inside. Ascospores from 1-spored asci 45–47 × 35–37 µm, 2-spored asci 38–41 × 30–35 µm, 3-spored asci 32–35 × 25–30 µm, 4-spored asci 28–33 × 23–27 µm and 5-spored asci 26–30 × 22–23 µm.

Ecology & Distribution — *Tuber alcaracense* grows in Mediterranean *Quercus ilex* subsp. *ballota* forest, in limestone mountains of the southeast of the Iberian Peninsula, 1 000–1 400 m alt., from December to February.

Typus. Spain, Albacete, Peñascosa, in calcareus soil, in *Quercus ilex* subsp. *ballota* (*Fagaceae*) forest, 15 Feb. 2017, *A. Rodríguez* (holotype MUB Fung-971; ITS and LSU sequences GenBank MN810047 and MN953777, MycoBank MB833685).

Additional material examined. Spain, Albacete, Vianos, in *Quercus ilex* subsp. *ballota* forest, 11 Jan. 2015, *A. Rodríguez*, MUB Fung-928; ITS sequence GenBank MN810046.

Notes — *Tuber alcaracense* is a black truffle of the aestivum clade characterised by its brown-black warty peridium, brown gleba marbled with thin white veins and reticulate-alveolate spores. It resembles *Tuber mesentericum*, but in addition to genetic differences it differs from *T. mesentericum* (Vittadini 1831) by having a pleasant odour and lacking a basal cavity.



Maximum likelihood (ML) phylogenetic tree inferred from ITS sequences, using RAxML-HPC v. 8 (Stamatakis 2014) on XSEDE in the CIPRES science gateway (Miller et al. 2010). GTR + G selected as model of evolution for analysis. The sequences obtained in the present study are highlighted in **bold**. Bootstrap support values (≥ 70 %) are indicated at the nodes. *Tuber macrosporum* AF106885 was used as outgroup. The scale bar indicates the expected changes per site.

Colour illustrations. Spain, Alcaraz mountain range (Albacete), Mediterranean *Quercus ilex* subsp. *ballota* forest. Ascocarps; mature ascospores. Scale bar = 20 µm.

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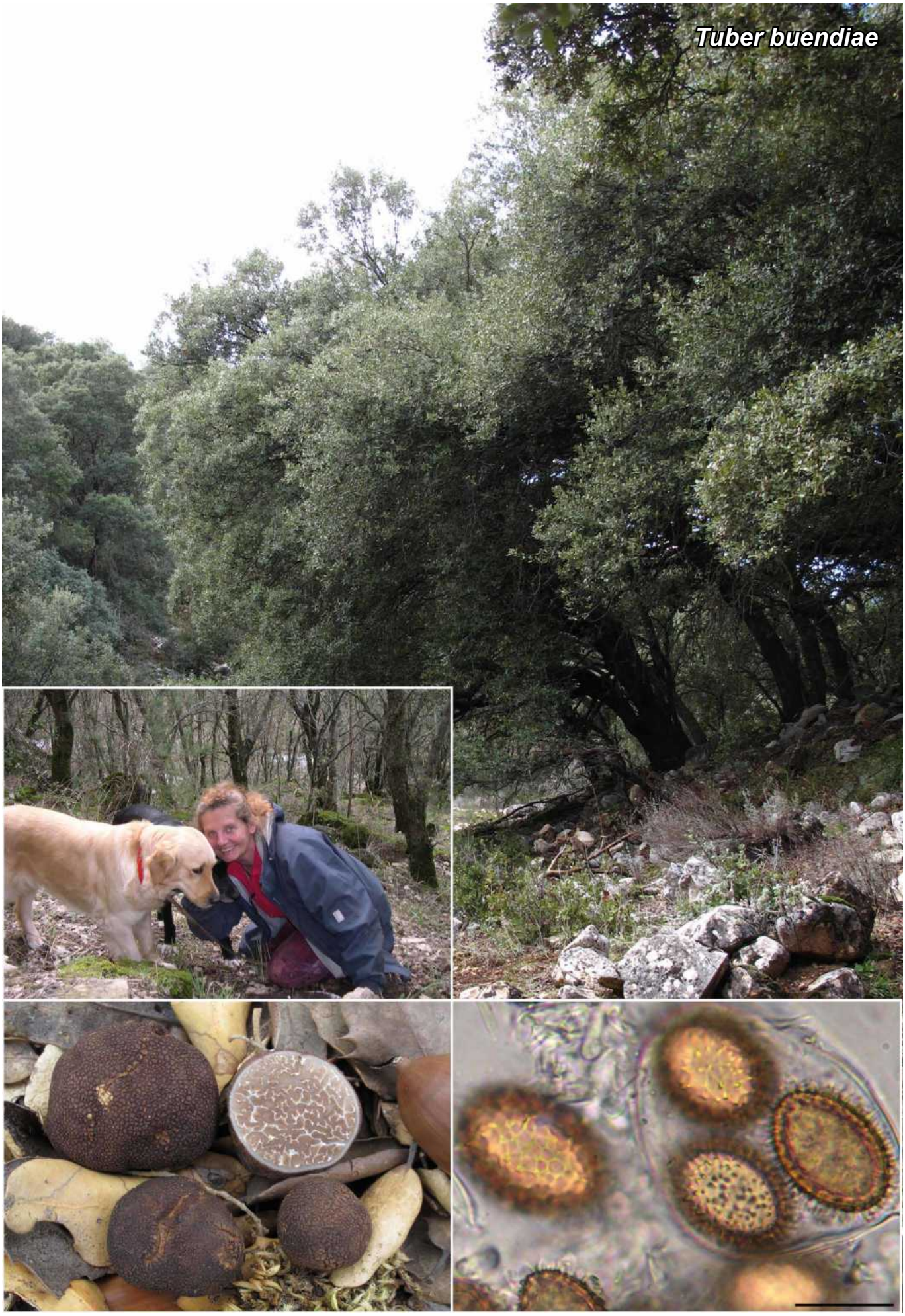

Tuber buendiae

Fungal Planet 1108 – 29 June 2020

Tuber buendiae Ant. Rodr. & Morte, *sp. nov.*

Etymology. Named after Encarnación Buendía, wife of the first author, who has been assisting in the collection of *Tuber* specimens, and is the collector of the type specimen.

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

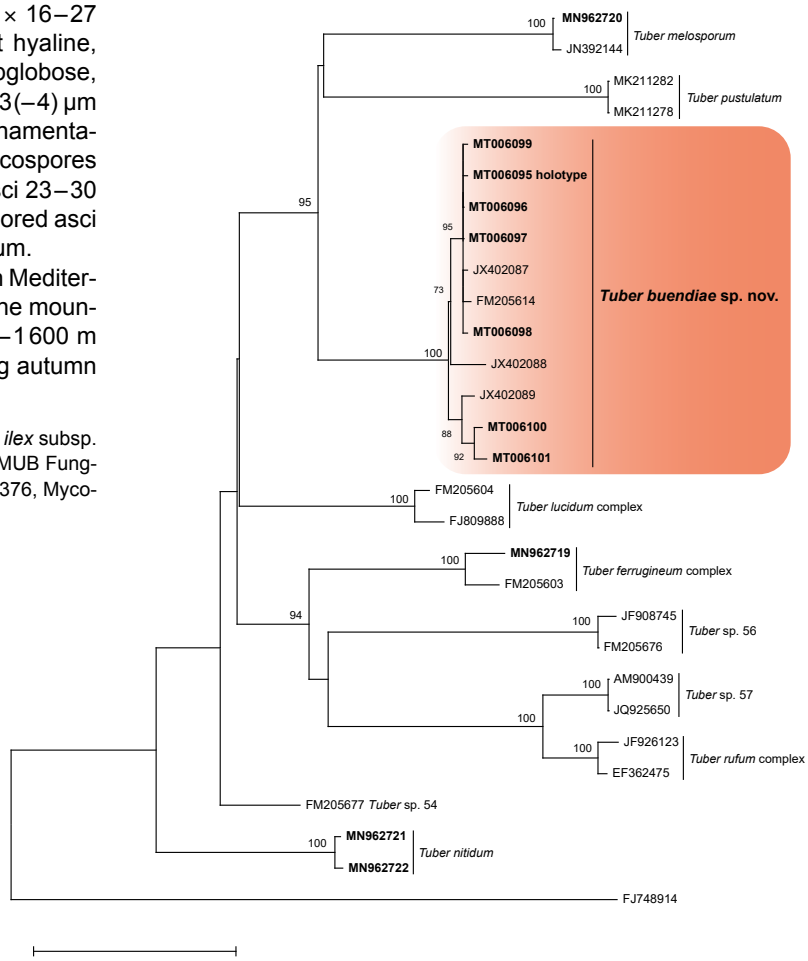
Ascomata hypogeous, 1–3 cm, subglobose or irregular in form, sometimes lobed, sometimes with a basal depression, fissured in age, yellow brown to reddish brown, minutely warted with pyramidal, flattened warts. *Peridium* 400–500 µm thick, composed of hyaline, agglutinated, interwoven hyphae (intricate texture), becoming pseudoparenchymatous towards the surface and forming pigmented, subangular, thick-walled cells, in a superficial layer 40–70 µm thick. *Gleba* firm, solid, whitish at first, becoming light-brown, dark-brown or red-brown at maturity, marbled with numerous, branching, white and dark veins. *Odour* pleasant. *Asci* inamyloid, 60–90 × 40–60 µm excluding stalk, pyriform to clavate or subglobose, with a long or short stalk arising from a crozier, 20–50 µm long, walls 1–2 µm thick, 1–4(–5)-spored. *Ascospores* 18–38 × 16–27 µm, Q = 1.1–1.5, excluding ornamentation, at first hyaline, yellowish brown at maturity, ellipsoid to ovoid or subglobose, ornamented with short spines, sometimes curved, 2–3(–4) µm long, often connected by lower ridges, making the ornamentation an irregular and incomplete spiny reticulum. Ascospores from 1-spored asci 33–38 × 23–27 µm, 2-spored asci 23–30 × 18–25 µm, 3-spored asci 21–28 × 16–22 µm, 4-spored asci 20–28 × 17–21 µm, 5-spored asci 18–22 × 16–17 µm.

Ecology & Distribution — *Tuber buendiae* grows in Mediterranean *Quercus ilex* subsp. *ballota* forest, in limestone mountains of the southeast of the Iberian Peninsula, 900–1600 m altitude. The species occurs all year; maturing during autumn and winter.

Typus. Spain, Albacete, Alcaraz, in calcareus soil, in *Quercus ilex* subsp. *ballota* forest (*Fagaceae*), 31 Dec. 2016, *E. Buendía* (holotype MUB Fung-974; ITS and LSU sequences GenBank MT006095 and MT102376, MycoBank MB834191).

Additional materials examined. Spain, Albacete, Masegoso, in *Quercus ilex* subsp. *ballota* forest, 9 Oct. 2012, *A. Rodríguez*, MUB Fung-978; ITS sequence GenBank MT006099; Riópar, 18 Oct. 2012, *A. Rodríguez*, MUB Fung-975; ITS sequence GenBank MT006096; Villaverde de Guadalimar, 21 Nov. 2016, *A. Rodríguez*, MUB Fung-976; ITS sequence GenBank MT006097; Vianos, 3 Dec. 2016, *A. Rodríguez*, MUB Fung-980; ITS sequence GenBank MT006101; Alcaraz, 18 Nov. 2016, *E. Buendía*, MUB Fung-977; ITS sequence GenBank MT006098; ibid., 20 Nov. 2017, *E. Buendía*, MUB Fung-979; ITS sequence GenBank MT006100.

Notes — *Tuber buendiae* is a reddish brown truffle that clusters in the rufum clade, and is characterised by its minutely warted peridium, brown gleba marbled with white and dark veins and spiny-reticulate spores. Healy et al. (2016) previously identified it as a hypothetical undescribed species *Tuber* sp. 83. *Tuber buendiae* resembles *Tuber pustulatum*, but in addition to genetic differences, it differs from *T. pustulatum* (Leonardi et al. 2019), by having a pleasant odour, a gleba with numerous veins and spores with shorter spines.



Maximum likelihood (ML) phylogenetic tree of *T. rufum* clade inferred from ITS sequences, using RAxML-HPC v. 8 (Stamatakis 2014) on XSEDE in the CIPRES science gateway (Miller et al. 2010). GTR + G selected as model of evolution for analysis. The sequences obtained in the present study are highlighted in **bold**. Bootstrap support values (≥ 70 %) are indicated at the nodes. *Tuber spinoreticulatum* (GenBank FJ748914) was used as outgroup. The scale bar indicates the expected changes per site. Species hypotheses for undescribed species (*Tuber* sp. followed by numbers) follow the conventions of Bonito et al. (2010).

Colour illustrations. Spain, Alcaraz mountain range (Albacete), Mediterranean *Quercus ilex* subsp. *ballota* forest. The collector and her truffle-hunting dog at the collection site; ascocarps; mature ascospores. Scale bar = 20 µm.

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Venturia paralias

Fungal Planet 1109 – 29 June 2020

Venturia paralias G.C. Hunter, I. Zeil-Rolfe, M. Jourdan & L. Morin, *sp. nov.*

Etymology. Named after *Euphorbia paralias*, the *Euphorbia* species from which the fungus was isolated.

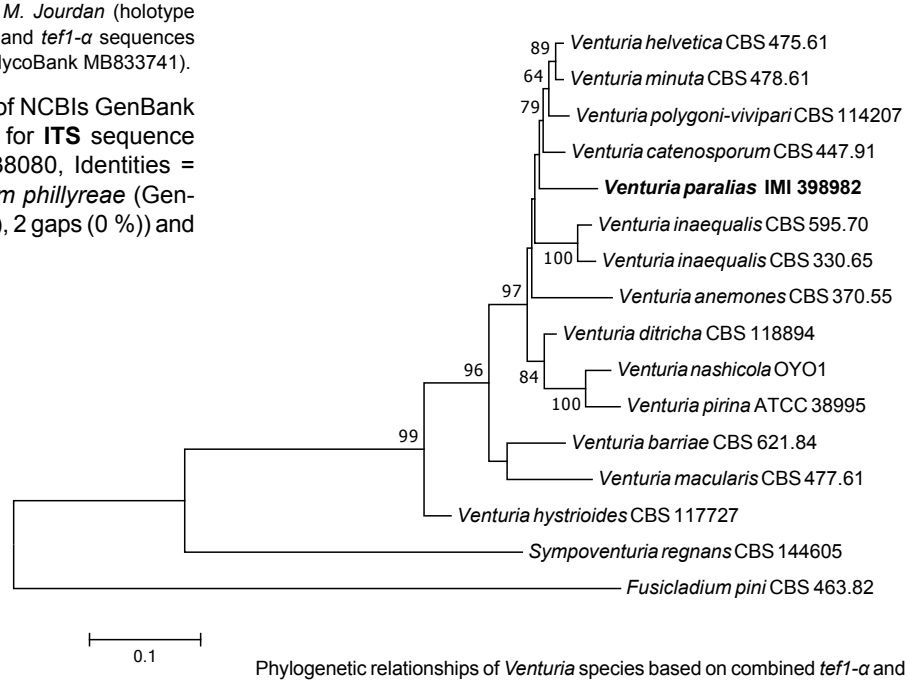
Classification — *Venturiaceae*, *Venturiales*, *Dothideomycetes*.

Lesions on leaves and stems, amphigenous, predominantly adaxial, circular to irregular, pale to dark brown, 2–8 mm diam, stem lesions pale to dark brown. *Mycelium* internal, 1.5–6 mm, subcuticular. *Stromata* oblong to subcircular, (49–)59–90(–110) × (29–)39–74(–103) µm, formed by swollen thick-walled cells. *Conidiophores* in loose to dense fascicles on stroma, unbranched, thin-walled, straight to slightly curved, pale brown and lighter towards the apex, occasionally thickened at the base, smooth, (16–)31–59(–81) × (2–)4–5(–6) µm, 0–3-septate. *Conidiogenous cells* integrated, terminal, one to several conidiogenous loci, slightly guttulate, proliferating sympodially, loci flat, hila convex and slightly thickened and darkened-refractive. *Conidia* solitary or catenate, fusiform, subcylindrical, obclavate, clavate, straight or slightly curved, (11–)17–29(–39) × (3–)4–6(–8) µm, 0–3-septate, slightly or not constricted at the septa, brown to pale brown, smooth to verruculose, thickened, apex obtuse, truncate or papillate.

Culture characteristics — Colonies on potato dextrose agar (PDA) flat to slightly raised, aerial mycelium feathery, circular to irregular with entire to undulate margin, 18 mm diam after 30 d at 20 °C under 12 h photoperiod. Outer edge of colony grey olivaceous, inner part olivaceous; reverse olivaceous to olivaceous black.

Typus. France, Gironde, Pyla-sur-Mer, Plage La Salie, on leaves of *Euphorbia paralias* (*Euphorbiaceae*), 1 July 2009, *M. Jourdan* (holotype IMI 398982, culture ex-type IMI 398982; ITS, LSU and *tef1-α* sequences GenBank MN864561, MN864538 and MT185924, MycoBank MB833741).

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest matches for **ITS** sequence were *Venturia oleaginea* (GenBank MN038080, Identities = 451/469 (96 %), 2 gaps (0 %)), *Fusicladium phillyreae* (GenBank EU035435, Identities = 451/469 (96 %), 2 gaps (0 %)) and *Venturia inaequalis* (GenBank MN958659, Identities = 447/468 (96 %), 1 gap (0 %)). Closest similarities using the ***tef1-α*** partial gene sequence were to *Venturia polygoni-vivipari* (GenBank KF853984, Identities 330/358 (92 %), 4 gaps (1 %)), *Venturia ditricha* (GenBank KF853970, Identities = 327/357 (92 %), 2 gaps (0 %)) and *Venturia chlorospora* (GenBank KF 853969, Identities 327/357 (92 %), 2 gaps (0 %)). *Venturia paralias* was shown in pathogenicity tests to cause disease on *E. paralias* and *Euphorbia segetalis* (unpubl. data). *Venturia paralias* is morphologically similar to *Fusicladium euphorbiae* (Schubert et al. 2003), which has been recorded from *E. amygdaloides*, *E. cyparissias*, *E. esula*, *E. exigua*, *E. lamprocarpa*, *E. villosa* and *E. virgata* (Schubert et al. 2003). We were not able to obtain lectotype material of *F. euphorbiae* from LE for comparison. For taxonomic stability we have therefore described the fungus isolated from *E. paralias* as *V. paralias*. *Fusicladium fasciculatum* var. *fasciculatum*, *F. fasciculatum* var. *didymium* and *F. fautreyi* are also morphologically similar to *V. paralias*. *Venturia paralias* produces distinctive pale to dark brown elongated stem lesions, dense fasciculate conidiophores with conidiogenous loci that are less conspicuous or prominent than those of *F. fasciculatum* var. *fasciculatum* and *F. fasciculatum* var. *didymium* (Deighton 1967, Schubert et al. 2003). *Venturia paralias* is distinguished from *F. fautreyi* by its pale brown conidiophores, less conspicuous conidiogenous loci and 3-septate conidia (Deighton 1967).



Phylogenetic relationships of *Venturia* species based on combined *tef1-α* and ITS DNA sequences inferred using the Maximum Likelihood method based on the Tamura-Nei model (Tamura & Nei 1993) as implemented in MEGA v. 7 (Kumar et al. 2016). The phylogram is drawn to scale with branch lengths measured in the number of substitutions per site. Bootstrap support values (> 50 %) after 1 000 replicates are presented at nodes and the phylogeny is rooted with *Fusicladium pini* CBS 463.82.

Colour illustrations. *Euphorbia paralias* on a beach at La Salie, France. Colony on PDA after 1 mo at 20 °C; conidiophores, catenate and single conidia. Scale bars = 10 µm.

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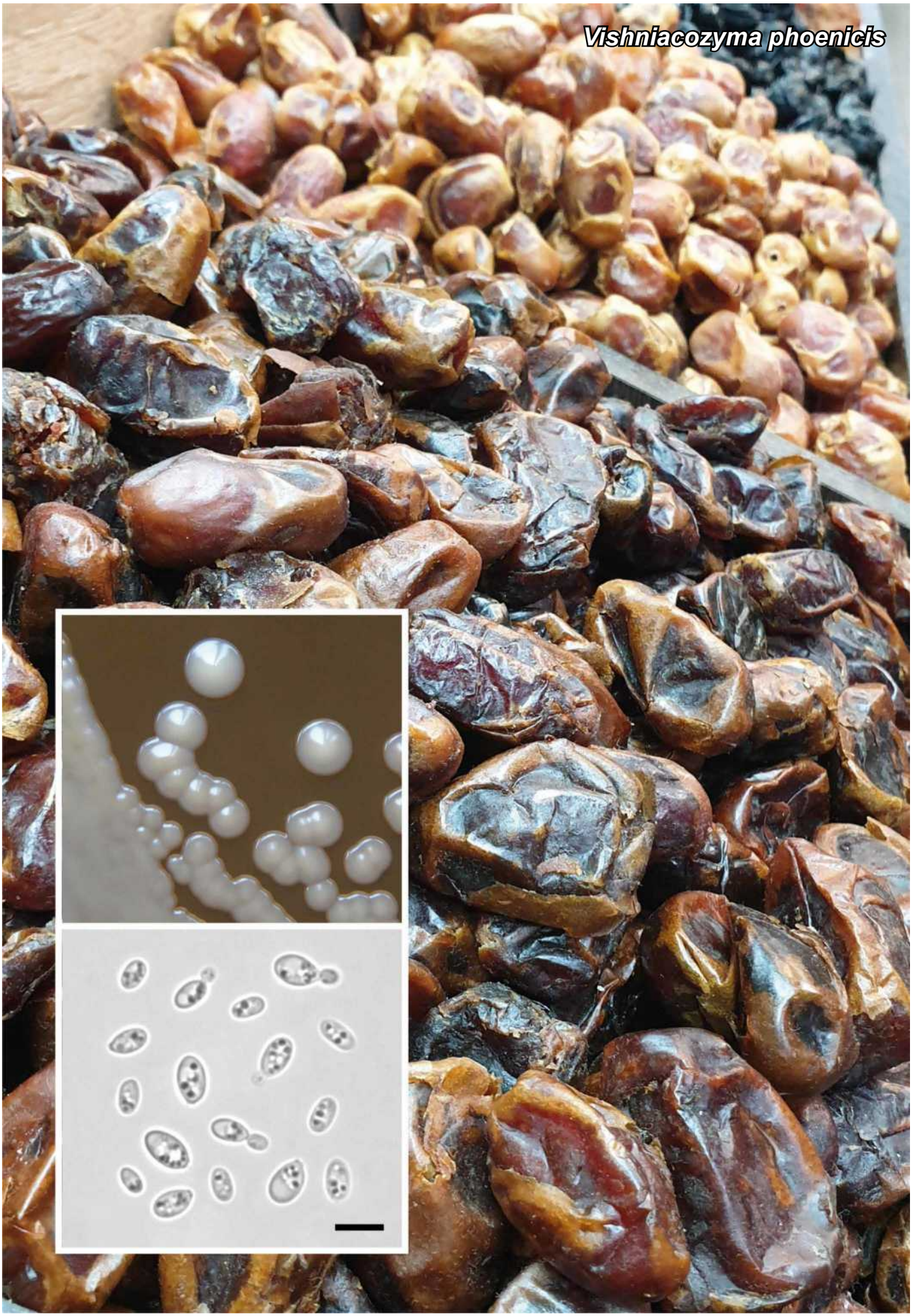

Vishniacozyma phoenicis

Fungal Planet 1110 – 29 June 2020

Vishniacozyma phoenicis Kachalkin, A.S. Venzhik & M.A. Tomashevskaya, *sp. nov.*

Etymology. Name *phoenicis* refers to the date palm, from which fruits the strains were isolated.

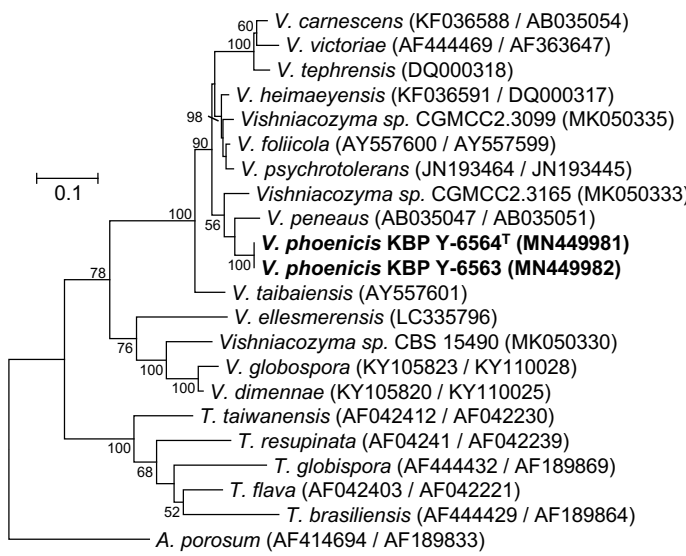
Classification — *Bulleribasidiaceae*, *Tremellales*, *Tremellomycetes*.

On glucose peptone yeast extract agar (GPYA) and 5 % malt extract agar (MEA), after 7 d at 22 °C, *streak* is pale yellow-brown to cream, shiny and mucoid, with an entire, somewhat undulating margin. *Cells* are ellipsoidal, 3–5 × 1.5–2 µm, occur singly or in pairs, divide by polar budding. *Sexual structures*, *pseudohyphae*, *true hyphae* and *ballistoconidia* not observed during 4 wk at 22 °C in culture (pure cultures and in mating test) grown on GPYA, MEA, potato dextrose agar (PDA), yeast nitrogen base with 0.5 % glucose (YNB) agar, cornmeal agar and Gorodkowa agar. Glucose is not fermented. Glucose, galactose, L-sorbose (weak), sucrose, maltose, lactose, melibiose, cellobiose, trehalose, raffinose, melezitose, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, soluble starch (weak), ethanol (weak), glycerol, erythritol, ribitol, galactitol, D-mannitol, D-glucitol, *myo*-inositol, methyl alpha-D-glucoside (weak), salicin, DL-lactic acid (weak), citric acid, succinic acid, D-gluconate, D-glucoronate, D-glucosamine (weak), N-Acetyl-D-glucosamine, 2-keto-D-gluconate, 5-keto-D-gluconate and arbutin are assimilated; no growth occurs on inulin, methanol, hexadecane. Nitrogen compounds: ammonium sulfate, potassium nitrate, L-lysine, D-glucosamine, creatinine and creatine are assimilated. Growth on vitamin-free medium, on MEA with 10 % NaCl and on 50 % w/w glucose / yeast extract (0.5 %) agar is positive. Growth with 0.01 % cycloheximide is weak. Starch-like compounds are produced. Diazonium blue B colour and urease reactions are positive. Maximum growth temperature is 31 °C.

Typus. Russia, Moscow, from dates fruit bought on local market, July 2017, *A.S. Venzhik*, 77m-1 (holotype KBP Y-6564 preserved in a metabolically inactive state, ex-type cultures VKM Y-3040 = DSM 110121 = CBS 16172; SSU, ITS-D1/D2 domains of LSU nrDNA, *TEF1* and *RPB1* sequences GenBank MN449979, MN449981, LR701186 and LR701187, MycoBank MB833068).

Additional material examined. Russia, Moscow, from dates fruit bought on local market, July 2017, *A.S. Venzhik*, KBP Y-6563; ITS-D1/D2 domains of LSU nrDNA sequence GenBank MN449982.

Notes — Analysis of the ITS-D1/D2 regions of the surveyed yeasts suggested that they were conspecific and represented a hitherto undescribed species of *Vishniacozyma*. Based on the NCBI GenBank database, the best hits using the **ITS** sequence are *V. heimaeyensis* CBS 8933^T (GenBank NR_077070; 95.20 % similar, 12 subst. and 7 gaps) and *V. pseudopenaeus* CGMCC2.3165^T (GenBank MK050333; 95.17 % similar, 12 subst. and 7 gaps); using **LSU** these are *V. peneaus* CBS 2409^T (GenBank NG_058433; 98.91 % similar, 6 subst.) and some strains (with 3–5 subst.) from coffee (GenBank KM246137, KM246008, KM246009, KM246021, KM246105, KM246144), soybean (Leite et al. 2013; GenBank KM246053) in Brazil and from *Atta texana* nest from USA (Rodrigues et al. 2009; GenBank FJ743602); using **SSU** these are strain *V. pseudopenaeus* CGMCC2.3165^T (GenBank MK050333; 99.58 % similar, 7 subst.) and *V. peneaus* CBS 2409^T (GenBank NG_062136; 99.46 % similar, 9 subst.); using ***TEF1*** it is *V. heimaeyensis* CBS 8933^T (GenBank KF037060; 89.36 % similar, 41 subst. and 12 gaps); and using ***RPB1*** it is *V. peneaus* CBS 2409^T (GenBank KF036392; 81.31 % similar, 120 subst. and 17 gaps). In compliance with a recent phylogenetic analysis of the genus (Tsuji et al. 2019), the placement of the new species is demonstrated using the combined ITS and LSU rDNA phylogeny. *Vishniacozyma phoenicis* differs from other species of the genus by good growth (*V. taibaiensis* with weak growth) on 50 % w/w glucose media. The new species can be also differentiated from *V. peneaus* based on its ability to assimilate ethanol, creatinine, potassium nitrate, growth on vitamin-free medium and on MEA with 10 % NaCl, and differ from *V. pseudopenaeus* by its ability to assimilate DL-lactic acid and soluble starch, production of starch-like compounds and its inability to growth at 32 °C



Maximum likelihood (ML) tree obtained from the combined analysis of ITS and LSU sequence data. Bootstrap support values above 55 % are shown at the nodes. The alignment included 1082 bp and was performed with MAFFT v. 7 (Katoh et al. 2019). The General Time Reversible model (GTR) with Gamma distribution and invariant sites (G+I) was used as the best nucleotide substitution model. Phylogenetic analysis was conducted in MEGA v. 6 (Tamura et al. 2013).

Colour illustrations. Russia, Moscow, dates fruit on local market. *Vishniacozyma phoenicis* KBP Y-6564: growth of yeast colonies on MEA, yeast cells on MEA (after 7 d at 22 °C). Scale bar = 5 µm.

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Volvariella paludosa

Fungal Planet 1111 – 29 June 2020

Volvariella paludosa Kapitonov & E.F. Malysheva, *sp. nov*.

Etymology. The epithet *paludosa* (boggy) refers to the preferred habitat of the species.

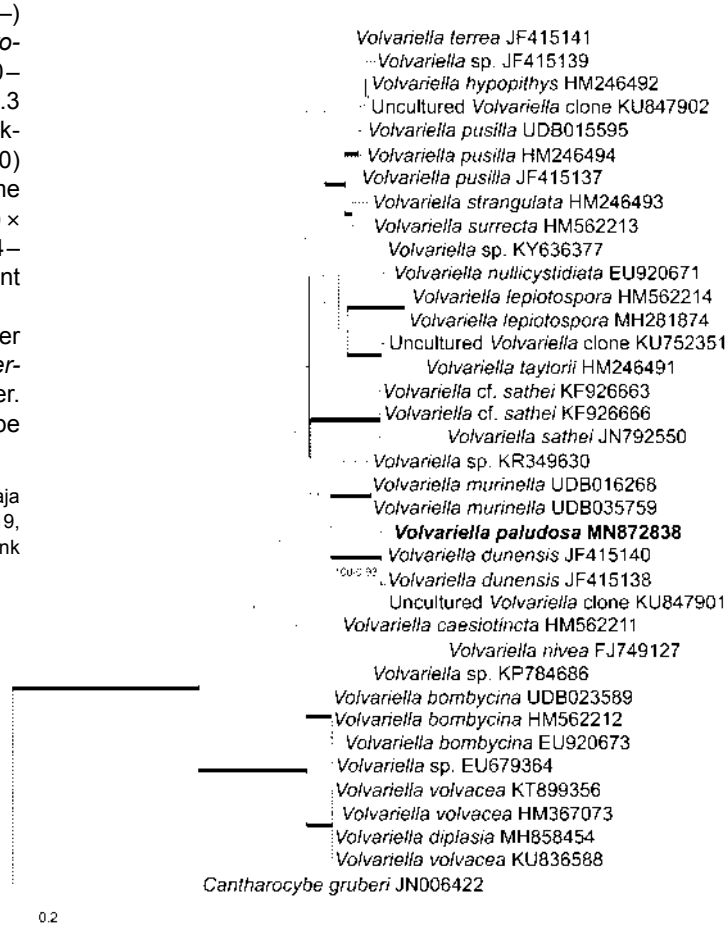
Classification — *Pluteaceae*, *Agaricales*, *Agaricomycetes*.

Basidiocarps medium-sized. *Pileus* 40–70 mm diam, at first convex to broadly campanulate, becoming plano-convex or plano-umbonate with low broad umbo, non-hygrophanous, surface not viscid, pale grey to whitish, covered with thin and short appressed hairs. *Lamellae* up to 7 mm broad, subcrowded, free, with lamellulae, slightly ventricose, initially whitish then pink, edge even or somewhat serrulate, entire concolourous. *Stipe* 50–80 × 7–12 mm, cylindrical, somewhat broadening towards base, smooth, white. *Context* in pileus and stipe white. *Volva* moderate, not voluminous (up to 20 mm high), friable, saccate, entire or lobate, felt-membranous, white, often with adhered moss fragments. *Smell* and *taste* indistinct. *Pileipellis* cutis, consisting of septate and elongate, non-gelatinous, slightly thick-walled hyphae, 4–12 µm wide. *Cheilocystidia* numerous, variable in size and shape: predominantly ventricose-lageniform, broadly fusiform, more rarely narrowly to broadly clavate or utriform, thick-walled, (30.8–)35.0–60.5(–67.7) × (8.8–)11.6–18.6(–23.0) µm, av. = 49.2 × 14.8 µm (n = 50). *Pleurocystidia* scarce, utriform or broadly clavate, (50.3–)54.0–79.5(–90.2) × (17.6–)19.1–32.3(–34.2) µm, av. = 64.0 × 24.3 µm (n = 30). *Basidia* (2–)4-spored, broadly clavate, thick-walled, (20.4–)22.5–27.4(–28.9) × (8.8–)9.0–10.0(–12.0) µm, av. = 25.0 × 9.7 µm (n = 35). *Basidiospores* ellipsoid, some slightly flattened, smooth, thick-walled, (7.6–)8.2–9.2(–9.7) × (4.9–)5.2–6.0(–6.7) µm, av. = 8.7 × 5.6 µm, Q = (1.24–)1.44–1.67(–1.90), av. Q = 1.56 (n = 180). *Clamp connections* absent in all tissues examined.

Habitat & Distribution — Growing solitary on a moss cover in the sedge (*Carex rostrata*)-brown moss (*Hamatocaulis versicosus*) rich fen with sparse birch (*Betula nana*) shrub layer. Uncommon in the studied area. So far only known from type locality.

Typus. Russia, Tyumen Region, Vagayskiy District, near Kobjakskaja village, low (minerotrophic) swamp, N58°04'08" E68°56'24", 25 June 2019, *V. Kapitonov* (holotype LE313556; ITS and LSU sequences GenBank MN872838 and MN877373, isotype TCCS1839, MycoBank MB834185).

Notes — *Volvariella paludosa* is characterised by its rather large basidiospores compared to other known species of *Volvariella*, medium-sized basidiocarps with light grey and hairy pilei, whitish volva and variable hymenial cystidia, and rich fen habitat. The preferred habitat, hairy pileus and spore size are the key characters for separating *V. paludosa* from other species with grey, fibrillose pilei, such as *V. volvacea*, *V. murinella*, *V. taylorii*. The phylogenetically closest species, *V. dunensis*, differs by its arenicolous habitat (in coastal dunes of Mediterranean basin and the Atlantic coast of Spain), smaller basidiospores (7–8.5 × 4.5–6 µm) and larger cheilocystidia of a different shape (Justo & Castro 2010, Vizzini et al. 2011).



Best tree from the ML analysis of the nrITS dataset for *Volvariella* species with *Cantharocybe gruberi* as outgroup, generated on RAxML server v. 0.9.0 (http://raxml-ng.vital-it.ch/#/) with 100 rapid bootstrap replicates. Thickened branches indicate bootstrap support values ≥ 70 % and Posterior probabilities ≥ 0.95 calculated in MrBayes v. 3.2.5 software (Ronquist et al. 2012). All tips are labelled with taxon name and GenBank accession number. The newly generated sequence is in **bold**.

Colour illustrations. Russia, Tyumen Region, Vagayskiy District, near Kobjakskaja village, rich fen, where the holotype was collected. Top: mature basidiocarp; median: pileus (view from above); bottom: lamellae and volva; bottom: basidiospores and basidia; on the right: four various cheilocystidia and two various pleurocystidia (all from holotype). Scale bars = 1 cm (basidiocarp, pileus, lamellae, volva) and 10 µm (microstructures).

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