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Key words

ITS nrDNA barcodes
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Abstract Novel species of fungi described in this study include those from various countries as follows: **Antarctica**, *Cladosporium arenosum* from marine sediment sand. **Argentina**, *Kosmimatamyces alatophylus* (incl. *Kosmimatamyces* gen. nov.) from soil. **Australia**, *Aspergillus banksianus*, *Aspergillus kumbius*, *Aspergillus luteorubrus*, *Aspergillus malvicolor* and *Aspergillus nanangensis* from soil, *Erysiphe medicaginis* from leaves of *Medicago polymorpha*, *Hymenotorrendiella communis* on leaf litter of *Eucalyptus bicostata*, *Lactifluus albopicri* and *Lactifluus austropiperatus* on soil, *Macalpinomyces collinsiae* on *Eriachne benthamii*, *Marasmius vagus* on soil, *Microdochium dawsoniorum* from leaves of *Sporobolus natalensis*, *Neopestalotiopsis nebuloides* from leaves of *Sporobolus elongatus*, *Pestalotiopsis etonensis* from leaves of *Sporobolus jacquemontii*, *Phytophthora personensis* from soil associated with dying *Grevillea mccutcheonii.* **Brazil**, *Aspergillus oxumiae* from soil, *Calvatia baixaverdensis* on soil, *Geastrum calycicoriaceum* on leaf litter, *Greeneria kielmeyerae* on leaf spots of *Kielmeyera coriacea*. **Chile**, *Phytophthora aysenensis* on collar rot and stem of *Aristotelia chilensis.* **Croatia**, *Mollisia gibbospora* on fallen branch of *Fagus sylvatica.* **Czech Republic**, *Neosetophoma hnaniceana* from *Buxus sempervirens.* **Ecuador**, *Exophiala frigidotolerans* from soil. **Estonia**, *Elaphomyces bucholtzii* in soil. **France**, *Venturia paralias* from leaves of *Euphorbia paralias.* **India**, *Cortinarius balteatoindicus* and *Cortinarius ulkhagarhiensis* on leaf litter. **Indonesia**, *Hymenotorrendiella indonesiana* on *Eucalyptus urophylla* leaf litter. **Italy**, *Penicillium taurinense* from indoor chestnut mill. **Malaysia**, *Hemileucoglossum kelabitense* on soil, *Satchmopsis pini* on dead needles of *Pinus tecunumanii.* **Poland**, *Lecanicillium praecognitum* on insects' frass. **Portugal**, *Neodevriesia aestuarina* from saline water. **Republic of Korea**, *Gongronella namwonensis* from freshwater. **Russia**, *Candida pellucida* from *Exomias pellucidus*, *Heterocephalacria septentrionalis* as endophyte from *Cladonia rangiferina*, *Vishniacozyma phoenicis* from dates fruit, *Volvariella paludosa* from swamp. **Slovenia**, *Mallocybe crassivelata* on soil. **South Africa**, *Beltraniella podocarpi*, *Hamatocanthoscypha podocarpi*, *Coleophoma podocarpi* and *Nothoseiridium podocarpi* (incl. *Nothoseiridium*

Abstract (cont.)

gen. nov.) from leaves of *Podocarpus latifolius*, *Gyrothrix encephalarti* from leaves of *Encephalartos* sp., *Paraphyton cutaneum* from skin of human patient, *Phacidiella alsophilae* from leaves of *Alsophila capensis*, and *Satchmopsis metrosideri* on leaf litter of *Metrosideros excelsa*. **Spain**, *Cladophialophora cabanerensis* from soil, *Cortinarius paezii* on soil, *Cylindrium magnoliae* from leaves of *Magnolia grandiflora*, *Trichophoma cylindrospora* (incl. *Trichophoma* gen. nov.) from plant debris, *Tuber alcaracense* in calcareus soil, *Tuber buendiae* in calcareus soil. **Thailand**, *Annulohypoxylon spougei* on corticated wood, *Poaceascoma filiforme* from leaves of unknown *Poaceae*. **UK**, *Dendrostoma luteum* on branch lesions of *Castanea sativa*, *Ypsilina buttingtonensis* from heartwood of *Quercus* sp. **Ukraine**, *Myrmecridium phragmiticola* from leaves of *Phragmites australis*. **USA**, *Absidia pararepens* from air, *Juncomyces californiensis* (incl. *Juncomyces* gen. nov.) from leaves of *Juncus effusus*, *Montagnula cylindrospora* from a human skin sample, *Muriphila oklahomaensis* (incl. *Muriphila* gen. nov.) on outside wall of alcohol distillery, *Neofabraea eucalyptorum* from leaves of *Eucalyptus macrandra*, *Diabolocovidia claustri* (incl. *Diabolocovidia* gen. nov.) from leaves of *Serenoa repens*, *Paecilomyces penicilliformis* from air, *Pseudopezicula betulae* from leaves of leaf spots of *Populus tremuloides*. **Vietnam**, *Diaporthe durionigena* on branches of *Durio zibethinus* and *Roridomyces pseudoirritans* on rotten wood. Morphological and culture characteristics are supported by DNA barcodes.

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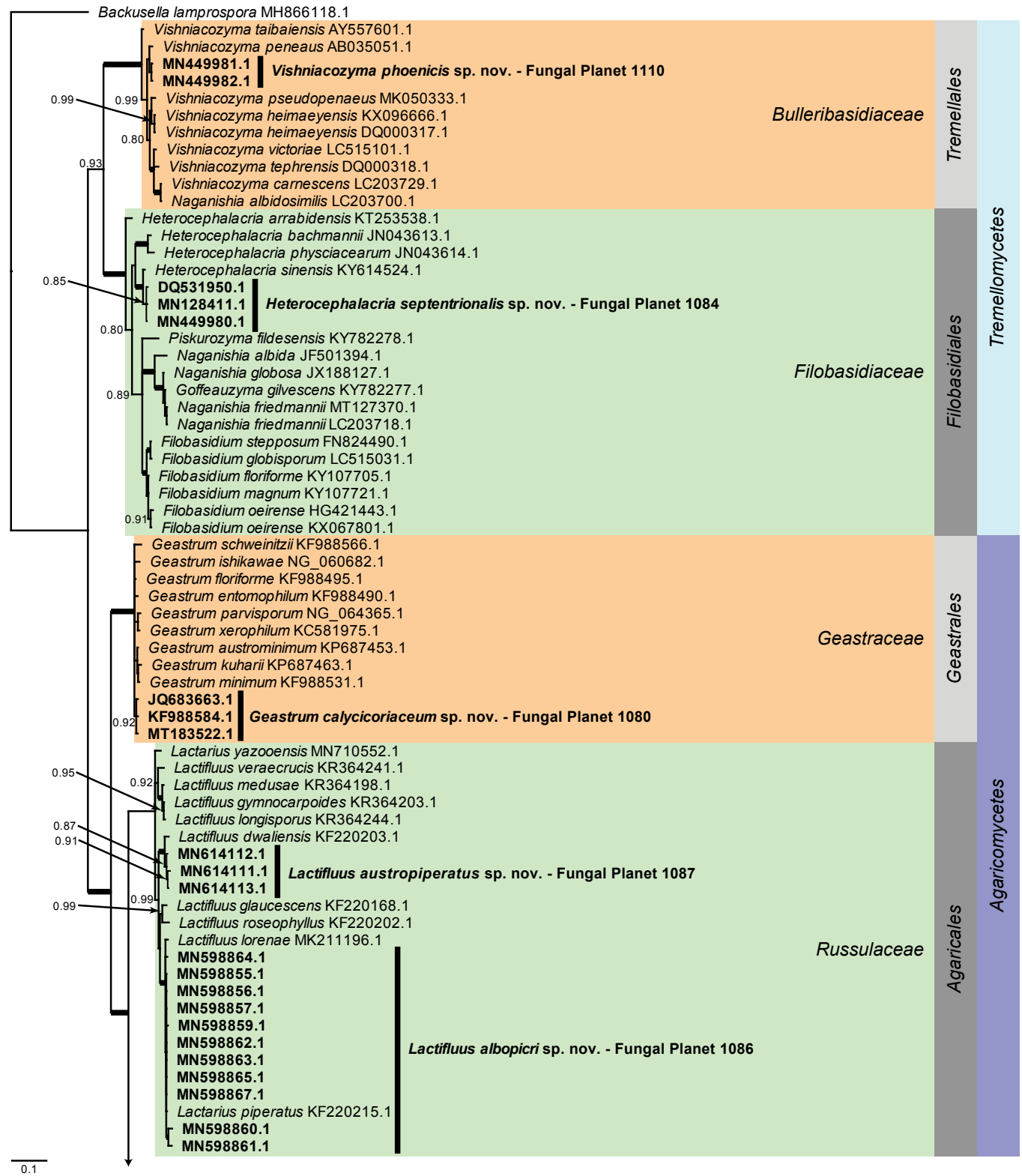
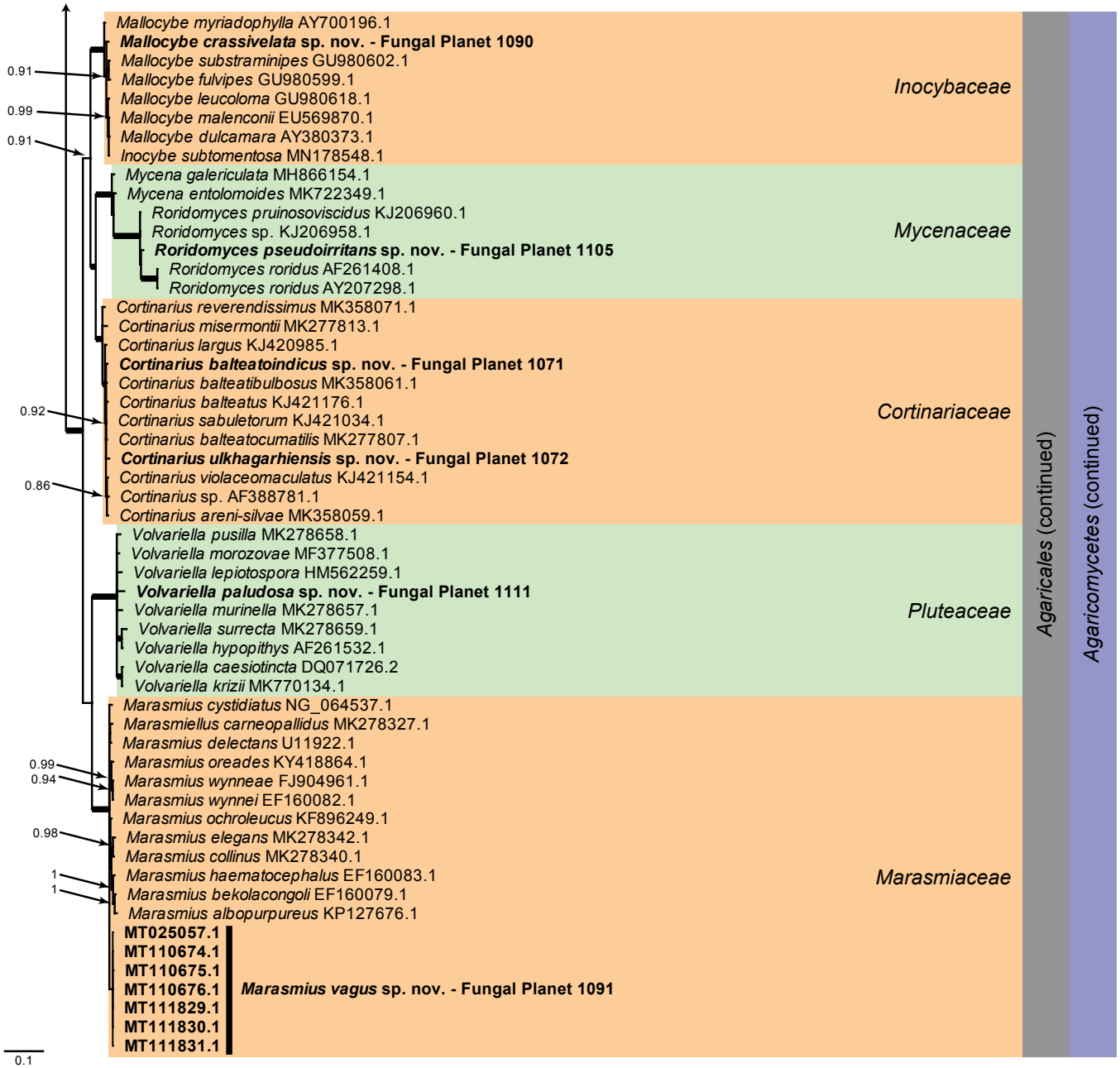
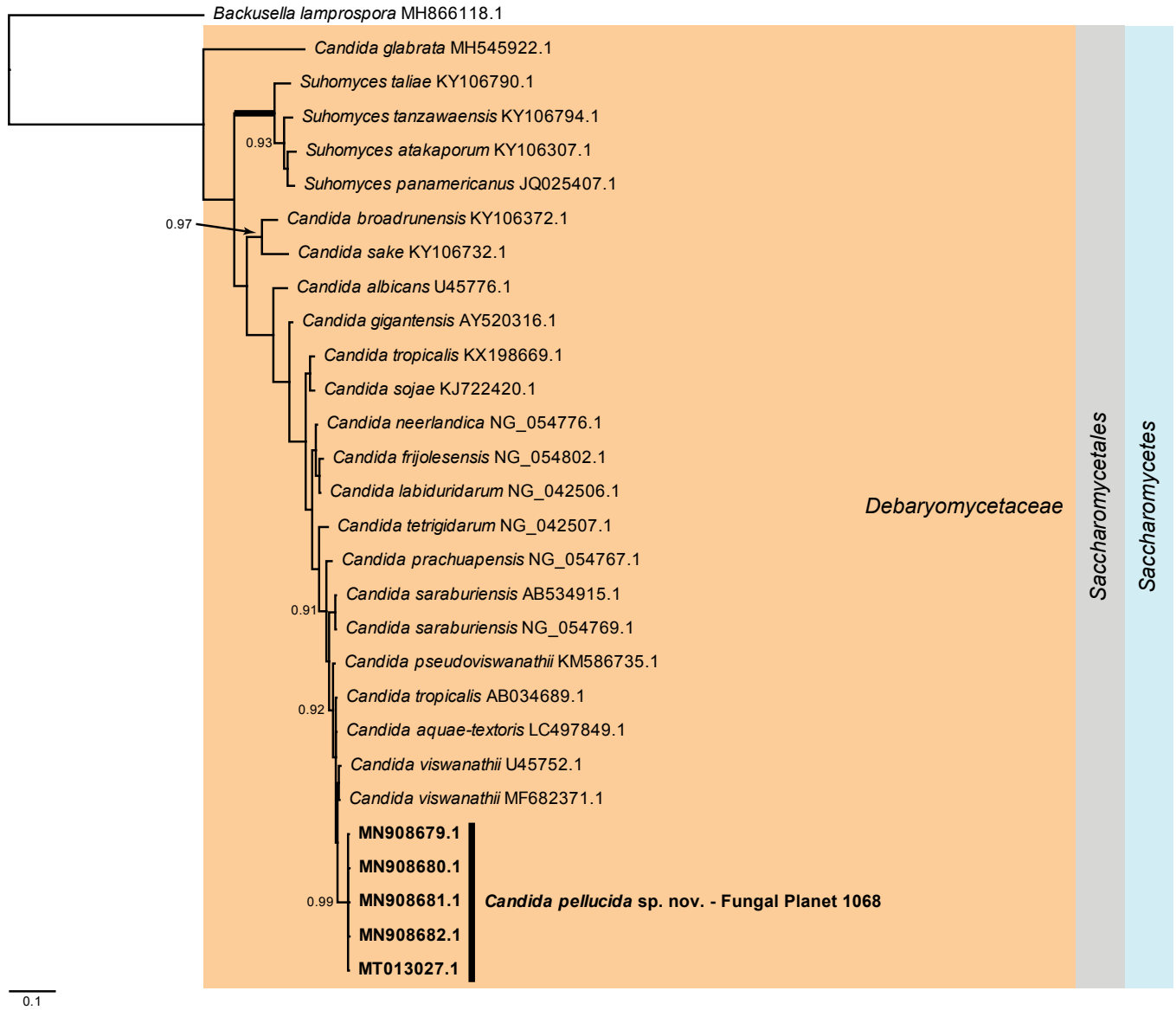


Overview *Tremellomycetes* and *Agaricomycetes* phylogeny – part 1

Consensus phylogram (50 % majority rule) of 416252 trees resulting from a Bayesian analysis of the LSU sequence alignment (122 sequences including outgroup; 745 aligned positions; 487 unique site patterns) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families, orders and classes are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Backusella lamprospora* (GenBank MH866118.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID S26166).

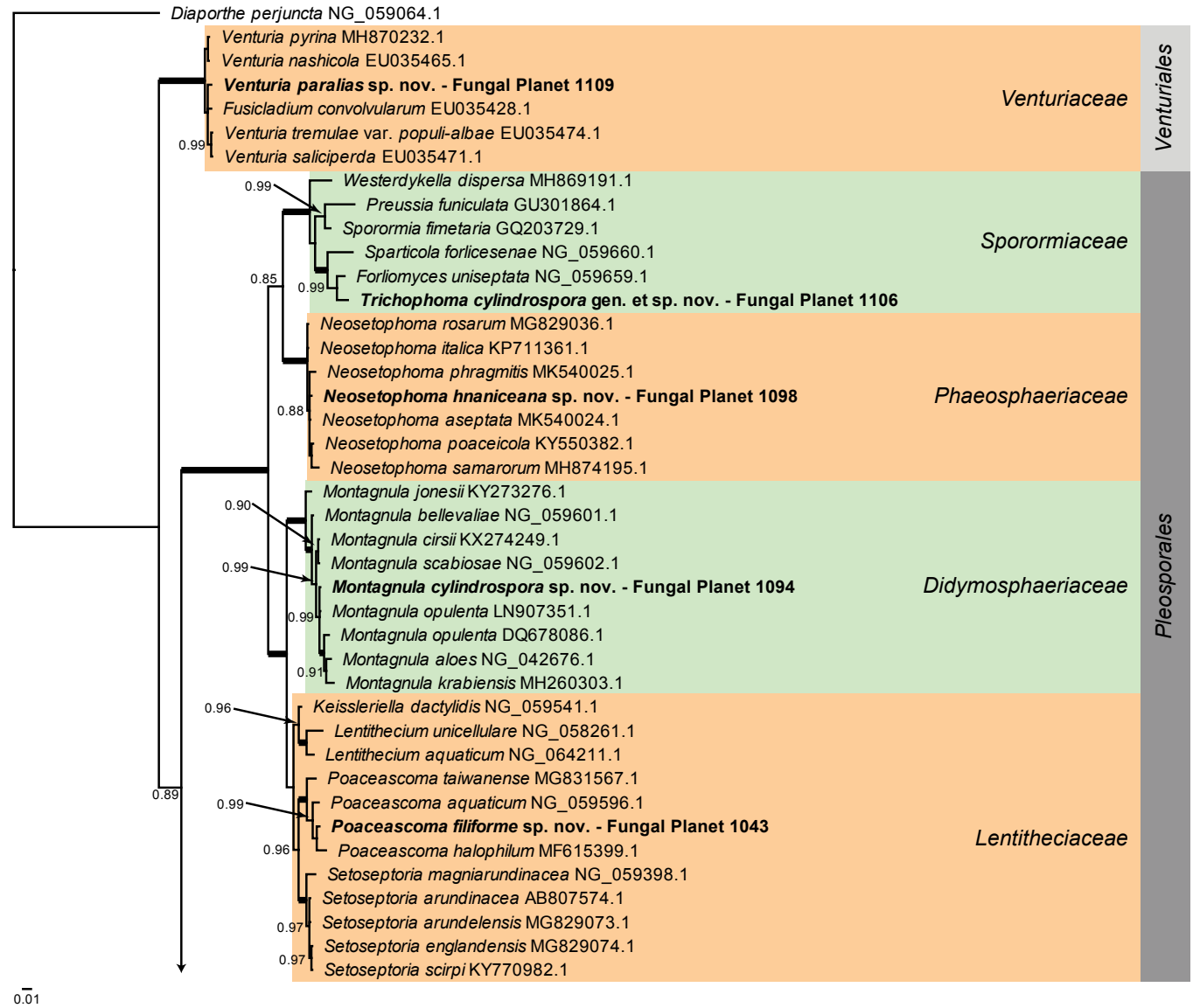


Overview *Tremellomycetes* and *Agaricomycetes* phylogeny (cont.) – part 2



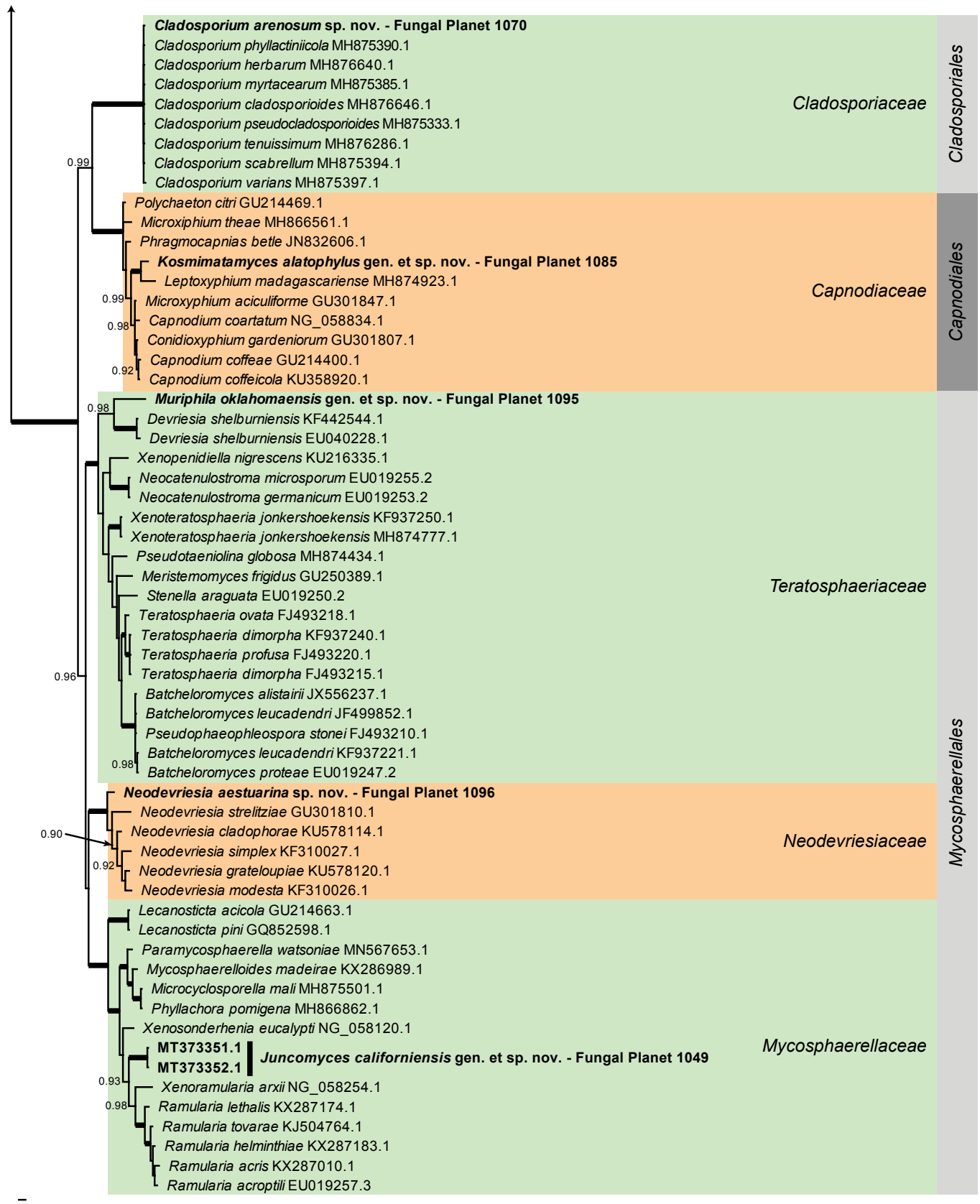
Overview *Saccharomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 198751 trees resulting from a Bayesian analysis of the LSU sequence alignment (29 sequences including outgroup; 520 aligned positions; 197 unique site patterns) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. The family, order and class are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Backusella lamprospora* (GenBank MH866118.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID S26166).

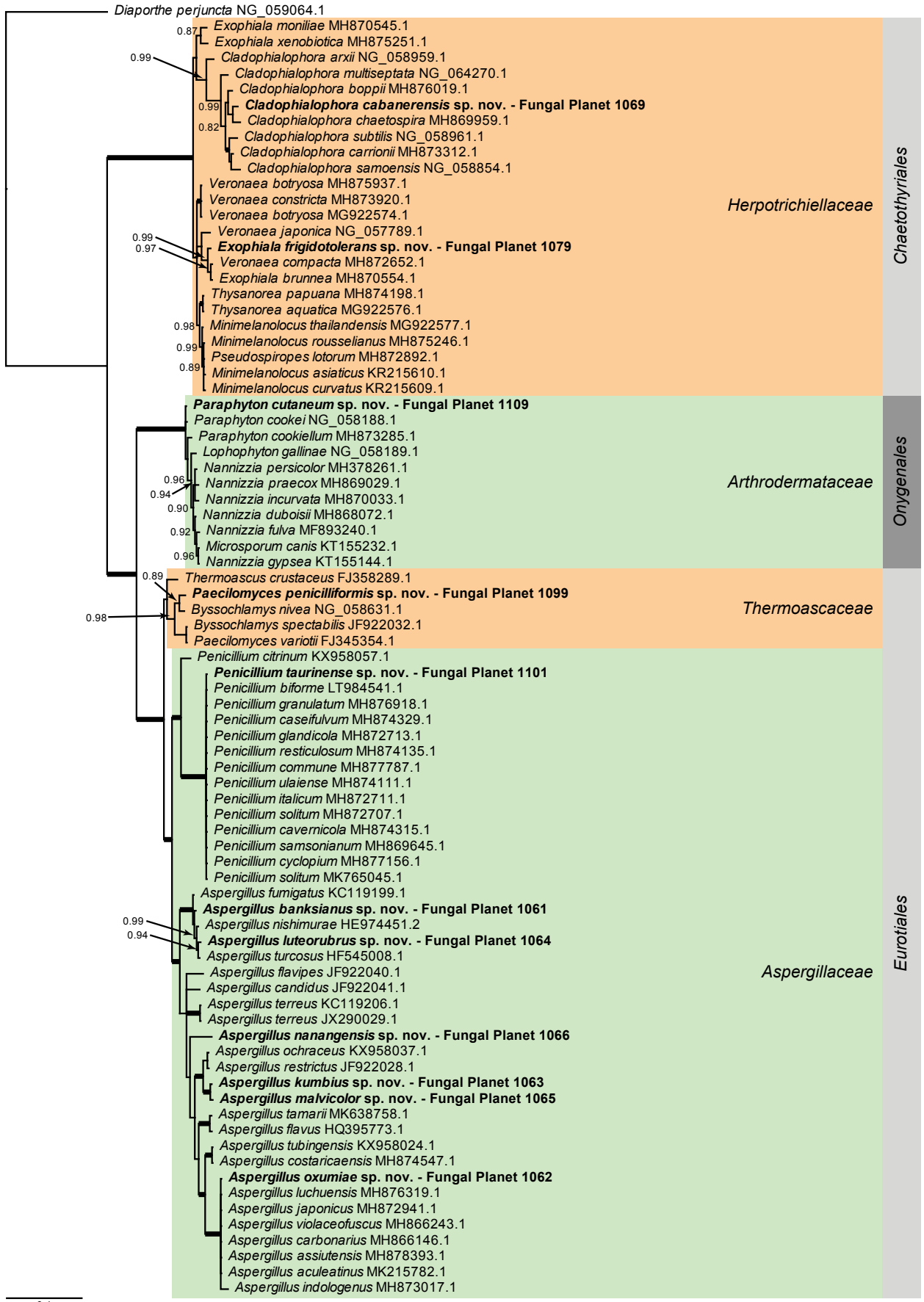


Overview *Dothideomycetes* phylogeny – part 1

Consensus phylogram (50 % majority rule) of 138002 trees resulting from a Bayesian analysis of the LSU sequence alignment (101 sequences including outgroup; 816 aligned positions; 351 unique site patterns) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Diaporthe perjuncta* (GenBank NG_059064.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID S26166).

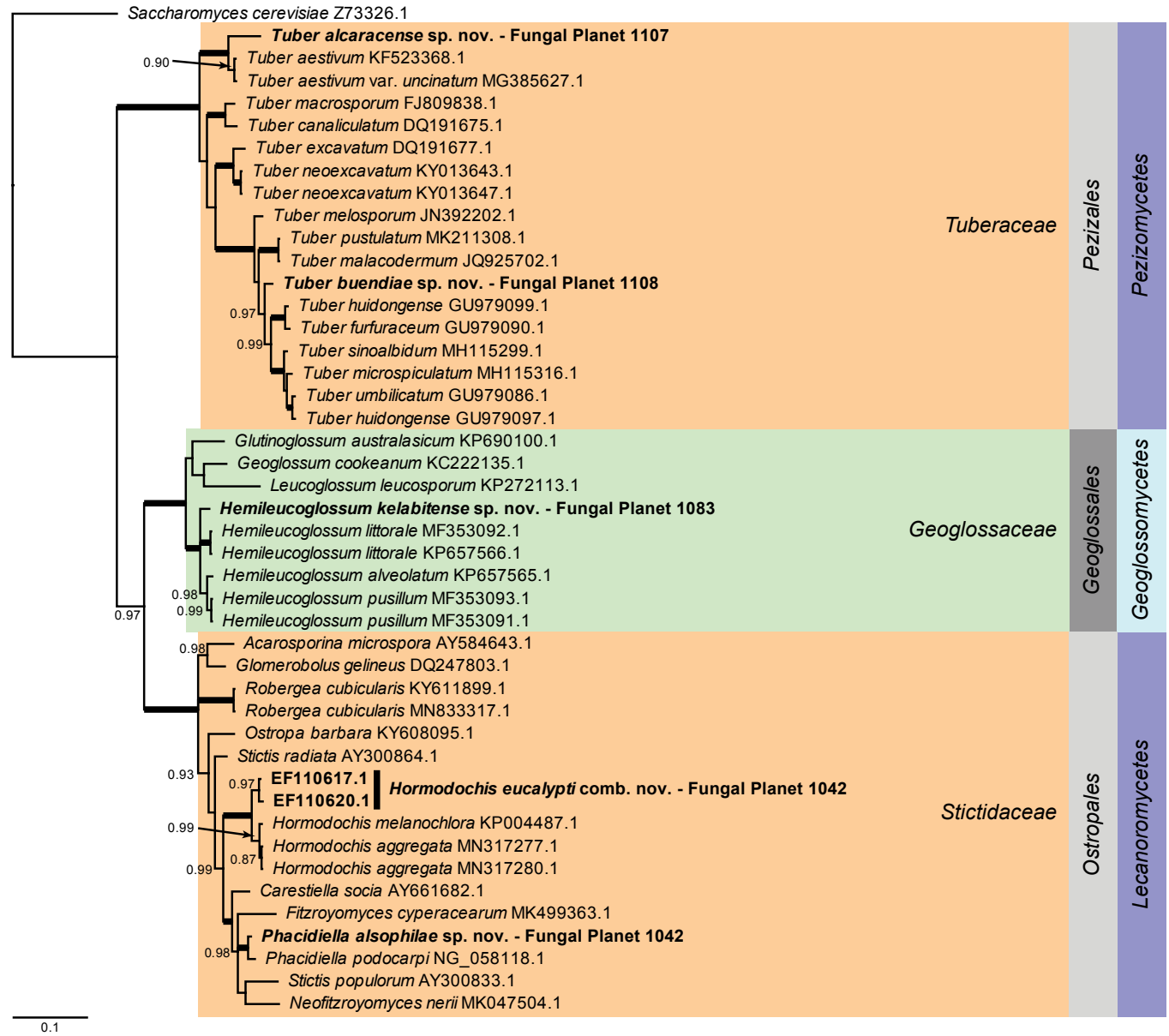


Overview *Dothideomycetes* phylogeny (cont.) – part 2



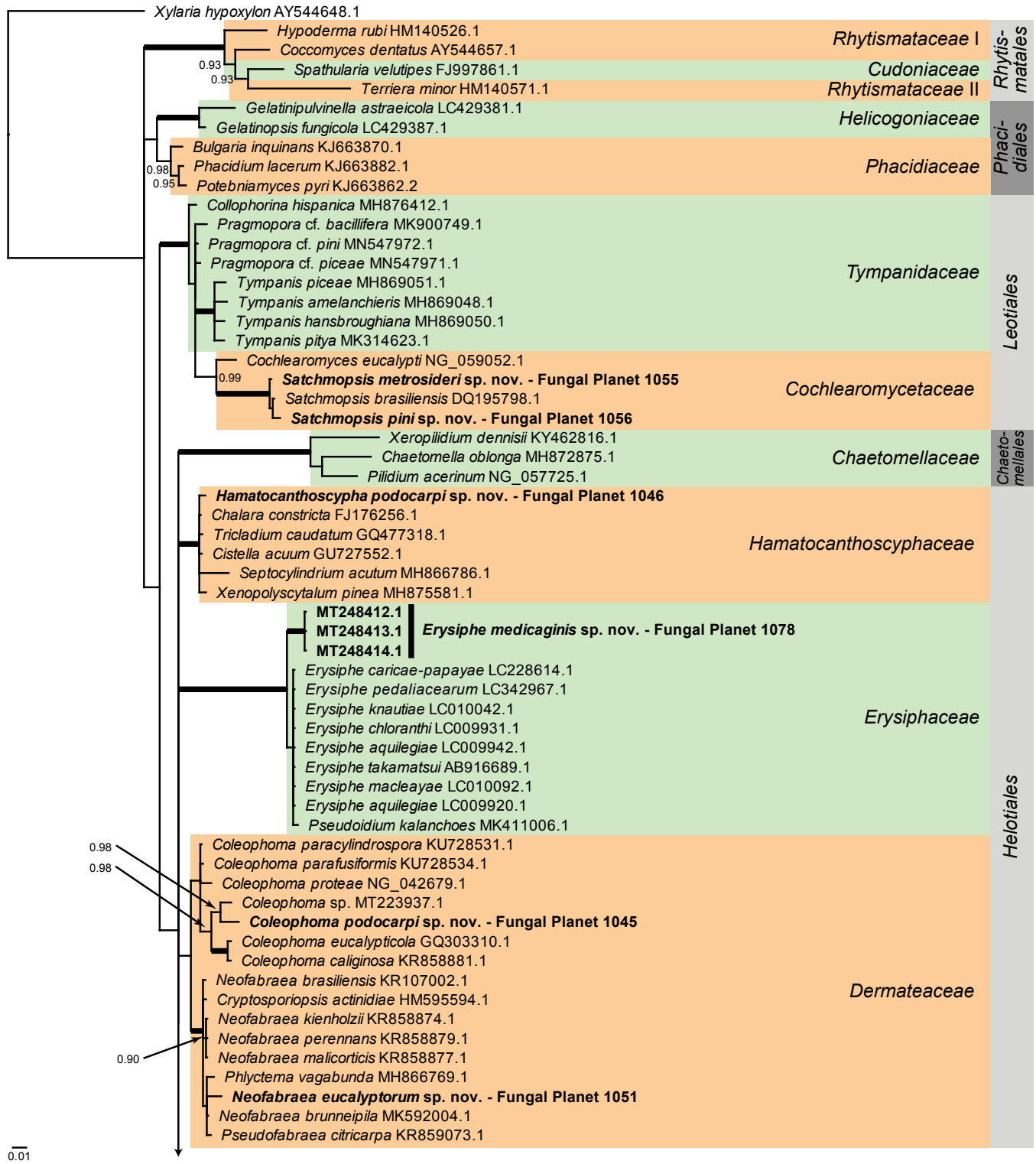
Overview *Eurotiomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 109 502 trees resulting from a Bayesian analysis of the LSU sequence alignment (82 sequences including outgroup; 826 aligned positions; 273 unique site patterns) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Diaporthe perjuncta* (GenBank NG_059064.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID S26166).



Overview *Geoglossomycetes*, *Lecanoromycetes* and *Pezizomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 21 002 trees resulting from a Bayesian analysis of the LSU sequence alignment (45 sequences including outgroup; 784 aligned positions; 310 unique site patterns) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families, orders and classes are indicated with coloured blocks to the right of the tree. GenBank accession or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Saccharomyces cerevisiae* (GenBank Z73326.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID S26166).



Overview *Leotiomycetes* phylogeny – part 1

Consensus phylogram (50 % majority rule) of 634 502 trees resulting from a Bayesian analysis of the LSU sequence alignment (116 sequences including outgroup; 839 aligned positions; 328 unique site patterns) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Xylaria hypoxylon* (GenBank AY544648.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID S26166).

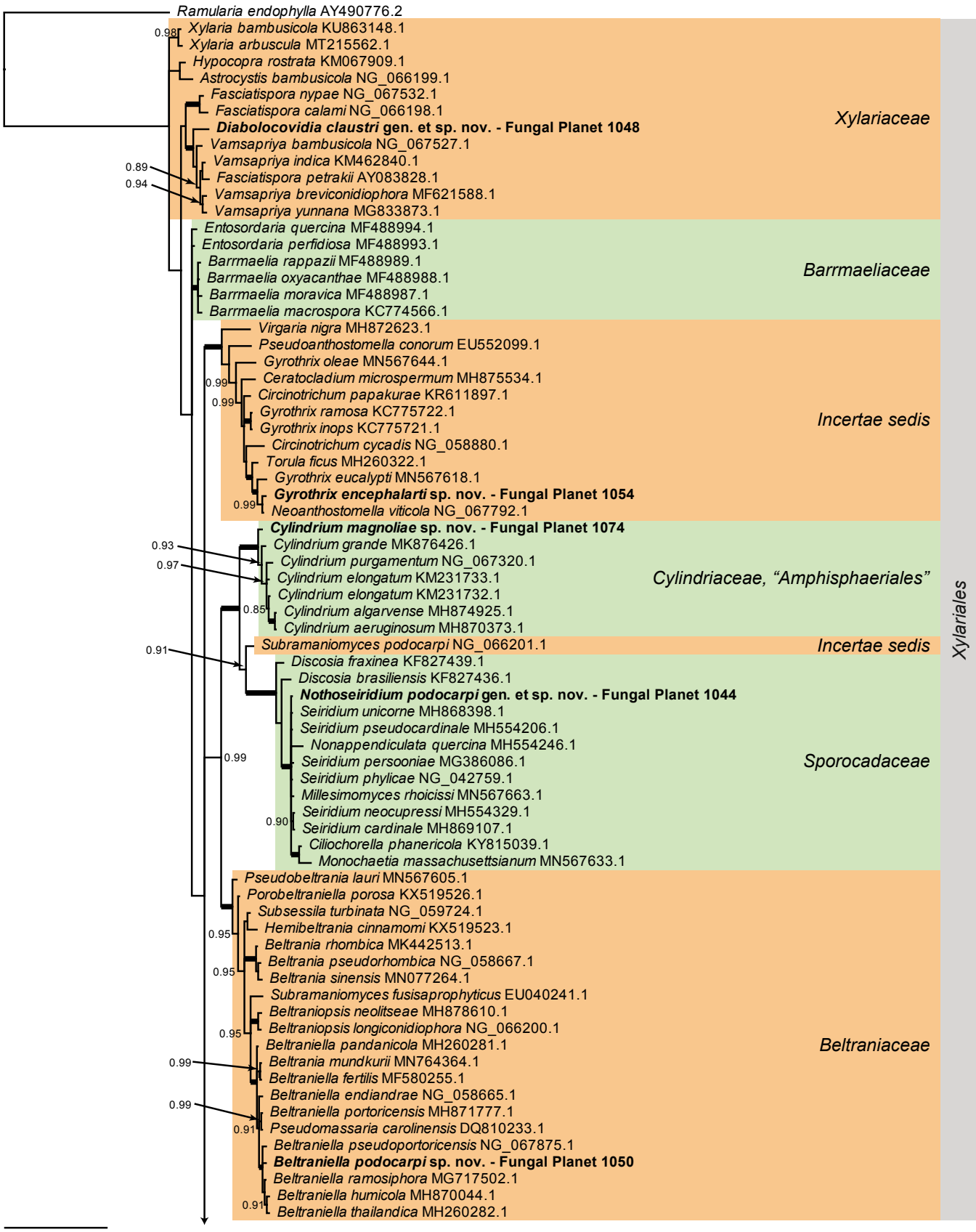
Overview *Leotiomycetes* phylogeny – part 2

Overview *Cunninghamellaceae* phylogeny

Consensus phylogram (50 % majority rule) of 97 502 trees resulting from a Bayesian analysis of the LSU sequence alignment (18 sequences including outgroup; 616 aligned positions; 278 unique site patterns) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. The higher order taxonomic classification is indicated with coloured blocks to the right of the tree. GenBank accession or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Chytridium lagenaria* (GenBank FJ804156.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID S26166).

Overview *Phytophthora* phylogeny

Consensus phylogram (50 % majority rule) of 337 502 trees resulting from a Bayesian analysis of the LSU sequence alignment (19 sequences including outgroup; 1 284 aligned positions; 63 unique site patterns) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. The higher order taxonomic classification is indicated with coloured blocks to the right of the tree. GenBank accession or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Absidia panacisoli* (GenBank NG_063948.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID S26166).



Overview *Sordariomycetes* phylogeny – part 1

Consensus phylogram (50 % majority rule) of 684 002 trees resulting from a Bayesian analysis of the LSU sequence alignment (132 sequences including outgroup; 786 aligned positions; 296 unique site patterns) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Ramularia endophylla* (GenBank AY490776.2) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID S26166).

Overview *Sordariomycetes* phylogeny (cont.) – part 2


Phacidiella alsophilae

Fungal Planet 1042 – 29 June 2020

Phacidiella alsophilae Crous, *sp. nov.*

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

Classification — *Stictidaceae*, *Ostropales*, *Lecanoromycetes.*

Conidiomata pycnidial, erumpent, hyaline on SNA and OA, solitary or aggregated, globose, up to 300 µm diam; wall of 3–6 layers of hyaline *textura angularis*; exuding a creamy conidial mass. *Conidiophores* lining the inner cavity, subcylindrical, smooth, hyaline, 0–1-septate, giving rise to 1–2 conidiogenous cells, 4–10 × 2–3 µm. *Conidiogenous cells* terminal, smooth, subcylindrical to doliiform, proliferating sympodially at apex, 5–10 × 2–3 µm. *Conidia* solitary, hyaline, smooth, subcylindrical, flexuous, apex obtuse, base truncate, (60–)90–135(–150) × (2–)2.5(–3) µm, 15–25-septate, disarticulating into phragmospores, cylindrical with truncate ends, 4–7 µm long; flexuous conidia enclosed in mucoid sheath, 1–1.5 µm diam.

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

Typus. South Africa, Western Cape Province, Knysna, on leaves of *Alsophila capensis* (= *Cyathea capensis*) (*Cyatheaceae*), Nov. 2018, *M.J. Wingfield*, HPC 2701 (holotype CBS H-24233, culture ex-type CPC 37041 = CBS 146134; ITS and LSU sequences GenBank MT373361.1 and MT373344.1, MycoBank MB835393).

Notes — *Phacidiella alsophilae* is related to *P. podocarpi* (conidia 1-septate, (7–)8–10(–12) × (2–)2.5(–3) µm; Crous et al. 2014), although they are morphologically distinct. Because the type species of *Phacidiella*, *P. salicina* (conidia aseptate, on twigs of *Salix viminalis*, Finland), is presently not known from culture, the phylogenetic relationships between species in the genus remains unresolved. *Phacidiella alsophilae* and *P. podocarpi* are thus tentatively retained in *Phacidiella*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phacidiella podocarpi* (strain CBS 138904, GenBank NR_137934.1; Identities = 558/614 (91 %), 10 gaps (1 %)), *Fitzroyomyces cyperi* (strain CBS 143170, GenBank MG386047.1; Identities = 626/729 (86 %), 18 gaps (2 %)), and *Fitzroyomyces cyperacearum* (voucher MFLU 18-0695b, GenBank MK499349.1; Identities = 626/731 (86 %), 22 gaps (3 %)). Closest hits using the **LSU** sequence were *Phacidiella podocarpi* (strain CBS 138904, GenBank NG_058118.1; Identities = 904/930 (97 %), 10 gaps (1 %)), *Stictis radiata* (voucher Palice (ESS 21520), GenBank AY300864.1; Identities = 754/783 (96 %), no gaps), and *Carestiella socia* (strain GG2437a, GenBank AY661682.1; Identities = 793/826 (96 %), 3 gaps (0 %)).

Colour illustrations. Unfolding leaf of *Alsophila capensis*. Conidiomata on OA; conidiogenous cells giving rise to conidia. Scale bars = 10 µm.

Hormodochis eucalypti (Crous) Crous, *comb. nov*.

MycoBank MB835394.

Basionym. *Phacidiella eucalypti* Crous, Fungal Diversity 25: 30. 2007.

Description & Illustration — Crous et al. (2019b).

Typus. South Africa, Western Cape Province, Stellenbosch Mountain, on *Eucalyptus* sp., 10 Jan. 2006, *P.W. Crous* (holotype CBS H-19768, cultures ex-type CBS 120255 = CPC 12745, CPC 12746, 12747; ITS-LSU sequence GenBank EF110617.1).

Notes — The genus *Hormodochis* was resurrected by Crous et al. (2020a) to accommodate taxa with erumpent, globose pycnidial conidiomata with aseptate conidia, arranged in cylindrical chains, olivaceous brown, smooth, subcylindrical to somewhat doliiform, with truncate ends. Morphologically and phylogenetically, *Phacidiella eucalypti* is better accommodated in *Hormodochis* than *Phacidiella*, as the latter has hyaline conidia (Sutton 1980). Another genus to consider with subhyaline conidia is *Trullula*, which differs in mode of conidiogenesis and conidium morphology (see Crous et al. 2020a).

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Poaceascoma filiforme

Fungal Planet 1043 – 29 June 2020

Poaceascoma filiforme Crous, *sp. nov.*

Etymology. Name refers to its characteristic filiform ascospores.

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

Ascomata developing on OA, immersed in agar, globose, brown, 80–140 µm diam, with smooth wall and central ostiole; wall of 2–4 layers of brown *textura angularis*. *Pseudoparaphyses* intermingled among asci, hyphae-like, hyaline, smooth, septate, anastomosing, 2–3 µm diam. *Asci* bitunicate, subcylindrical, apex obtuse with small apical chamber, base truncate, stipitate, 80–140 × 8–10 µm. *Ascospores* multiseriate in asci, spirally twisted, hyaline, smooth, filiform, subcylindrical with obtuse ends, guttulate, 70–120 × 2–2.5 µm.

Culture characteristics — Colonies spreading, with moderate aerial mycelium and even, lobate margin, covering dish after 2 wk at 25 °C. On MEA and PDA surface and reverse olivaceous grey. On PDA surface isabelline.

Typus. Thailand, Chiang Mai, Unknown *Poaceae*, 2008, *P.W. Crous* (holotype CBS H-24361, culture ex-type CPC 33467 = CBS 146689; ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MT373362.1, MT373345.1, MT375098.1, MT375108.1 and MT375118.1, MycoBank MB835395).

Notes — *Poaceascoma* was introduced by Phookamsak et al. (2015) to accommodate a genus of saprobic ascomycetes on *Poaceae* with setose ascomata and filiform ascospores. Although *P. filiforme* lacks setae, its spirally twisted, filiform ascospores are a good fit for the genus.

Based on a megablast search of NCBIs GenBank nucleotide database, the **ITS** sequence had distant, partial hits to *Poaceascoma taiwanense* (strain MFLUCC 18-0083, GenBank MG831569.1; Identities = 269/299 (90 %), 6 gaps (2 %)), *Setoseptoria phragmitis* (strain CBS 114966, GenBank KF251250.1; Identities = 346/388 (89 %), 8 gaps (2 %)), and *Setoseptoria englandensis* (strain MFLUCC 17-0778, GenBank MG828963.1; Identities = 342/383 (89 %), 9 gaps (2 %)). Closest hits using the **LSU** sequence are *Poaceascoma aquaticum* (strain MFLUCC 14-0048, GenBank NG_059596.1; Identities = 864/872 (99 %), 1 gap (0 %)), *Poaceascoma halophilum* (strain MFLUCC 15-0949, GenBank MF615399.1; Identities = 854/864 (99 %), 3 gaps (0 %)), and *Poaceascoma taiwanense* (strain MFLUCC 18-0083, GenBank MG831567.1; Identities = 837/849 (99 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Poaceascoma aquaticum* (strain MFLUCC 14-0048, GenBank KT373846.1; Identities = 798/875 (91 %), no gaps), *Poaceascoma helicoides* (strain MFLUCC 11-0136, GenBank KP998460.1; Identities = 728/833 (87 %), no gaps), and *Wettsteinina lacustris* (strain AFTOL-ID 1592 = CBS 618.86, GenBank DQ677972.1; Identities = 741/889 (83 %), 5 gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Darksidea zeta* (strain CBS 135640, GenBank KP184191.1; Identities = 324/407 (80 %), 24 gaps (5 %)), *Darksidea beta* (strain CBS 135637, GenBank KP184189.1; Identities = 323/406 (80 %), 25 gaps (6 %)), and *Darksidea gamma* (strain CBS 135633, GenBank KP184187.1; Identities = 315/396 (80 %), 25 gaps (6 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Pleurophoma acaciae* (strain CPC 29188, GenBank KY173612.1; Identities = 520/649 (80 %), 35 gaps (5 %)), *Crassiclypeus aquaticus* (strain KH 185, GenBank LC312616.1; Identities = 425/539 (79 %), 32 gaps (5 %)), and *Flabellascoma minimum* (strain KT 2040, GenBank LC312620.1; Identities = 424/540 (79 %), 36 gaps (6 %)).

Colour illustrations. Rainforest in Chiang Mai. Asci with spirally twisted ascospores. Scale bars = 10 µm.

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Nothoseiridium podocarpi

Fungal Planet 1044 – 29 June 2020

Nothoseiridium Crous, *gen. nov.*

Etymology. Name refers to the fact that it is related to *Seiridium*, but morphologically distinct from that genus.

Classification — *Sporocadaceae*, *Xylariales*, *Sordariomycetes.*

Plant pathogenic. *Conidiomata* black, round, flattened, acervular; wall of several layers of brown *textura epidermoidea*. *Conidiophores* reduced to conidiogenous cells, arising from basal layers of stroma, hyaline, smooth, subcylindrical to ampulliform, annellidic. *Conidia* fusoid, slightly curved, smooth-walled, guttulate, pale brown, unequally 4-euseptate; basal cell obconic with truncate hilum, hyaline; median cells pale brown; apical cell obtuse, hyaline; apical and basal appendage filiform, flexuous, unbranched, excentric.

Type species. Nothoseiridium podocarpi Crous.
MycoBank MB835396.

Nothoseiridium podocarpi Crous, *sp. nov.*

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

Associated with brown leaf spots. *Conidiomata* (on *Podocarpus* leaves and on SNA), black, round, flattened, acervular, 300–400 µm diam; wall of several layers of brown *textura epidermoidea*, splitting open all along outer margin, appearing saucer-shaped on leaf. *Conidiophores* reduced to conidiogenous cells, arising from basal layers of stroma, hyaline, smooth, subcylindrical to ampulliform, annellidic, 5–10 × 2.5–3 µm. *Conidia* fusoid, slightly curved, smooth-walled, guttulate, pale brown, unequally 4-euseptate; basal cell obconic with truncate hilum, hyaline; median cells pale brown; apical cell obtuse, hyaline. Apical cell 2.5–4 µm long; second cell 2.5–4 µm long; third cell 4–5 µm long; fourth cell 12–14 µm long; basal cell 3–4 µm long; conidia (22–)24–25(–27) × (2.5–)3 µm; apical appendage filiform, flexuous, unbranched, excentric, 7–10 µm long; basal appendage filiform, flexuous, unbranched, excentric, 6–7 µm long.

Culture characteristics — Colonies spreading, with moderate aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA surface smoke grey, reverse olivaceous grey. On PDA surface and reverse olivaceous grey. On OA surface pale olivaceous grey.

Typus. South Africa, Western Cape Province, Knysna, on leaf spots of *Podocarpus latifolius* (*Podocarpaceae*), Nov. 2018, *M.J. Wingfield*, HPC 2710 (holotype CBS H-24362, culture ex-type CPC 36967 = CBS 146690; ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MT373363.1, MT373346.1, MT375099.1, MT375109.1 and MT375119.1, MycoBank MB835397).

Notes — *Seimatosporium* and allied genera have recently been revised (Bonthond et al. 2018, Liu et al. 2019), with 23 genera being accepted in *Sporocadaceae*. *Nothoseiridium podocarpi* is allied to *Seiridium* (5-septate, appendaged conidia) and *Nonappendiculata* (3-septate, non-appendaged conidia), but is distinct in having 4-septate, fusoid conidia with unbranched, excentric apical and basal appendages. *Nothoseiridium* is further characterised by forming submerged acervuli that break through the epidermis with a saucer-like appearance, being associated with prominent leaf spots. It is not possible to distinguish *Nothoseiridium* from *Seiridium* based on LSU sequence data.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Seimatosporium lichenicola* (as *Discostroma fuscellum*; strain GSAA-0182, GenBank JF320818.1; Identities = 542/571 (95 %), 7 gaps (1 %)), *Sporocadus rosarum* (as *Seimatosporium pseudorosarum*; strain MFLUCC 14-0466, GenBank KT284775.1; Identities = 561/592 (95 %), 4 gaps (0 %)), *Seimatosporium lichenicola* (strain CBS 160.25, GenBank MH854829.1; Identities = 561/592 (95 %), 6 gaps (1 %)) and *Millesimomyces rhoicissi* (strain CPC 35297, GenBank NR_166350.1; Identities = 566/598 (95 %), 12 gaps (2 %)). Closest hits using the **LSU** sequence are *Seiridium unicorne* (strain CBS 320.51, GenBank MH868398.1; Identities = 870/870 (100 %), no gaps), *Seiridium pseudocardinale* (strain CBS 122613, GenBank MH554206.1; Identities = 834/834 (100 %), no gaps), and *Seiridium phylicae* (strain CPC 19962, GenBank NG_042759.1; Identities = 870/871 (99 %), 1 gap (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Seiridium cardinale* (strain CPC 23791, GenBank LT853119.1; Identities = 721/838 (86 %), no gaps), *Seiridium unicorne* (strain CBS 143873, GenBank MK058478.1; Identities = 636/741 (86 %), no gaps), and *Seiridium aquaticum* (voucher MFLU 18-1627, GenBank MN156531.1; Identities = 642/748 (86 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Seiridium marginatum* (strain CBS 140403, GenBank LT853199.1; Identities = 344/417 (82 %), 30 gaps (7 %)), *Seiridium papillatum* (strain CBS 340.97, GenBank LT853200.1; Identities = 332/404 (82 %), 22 gaps (5 %)), and *Seiridium podocarpi* (strain CBS 137995, GenBank LT853198.1; Identities = 331/403 (82 %), 31 gaps (7 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Seiridium cupressi* (strain CBS 224.55, GenBank LT853230.1; Identities = 652/791 (82 %), 46 gaps (5 %)), *Seiridium papillatum* (strain CBS 340.97, GenBank LT853250.1; Identities = 636/771 (82 %), 31 gaps (4 %)), and *Seiridium podocarpi* (strain CBS 137995, GenBank LT853248.1; Identities = 638/777 (82 %), 39 gaps (5 %)).

Colour illustrations. Leaf spot on *Podocarpus latifolius* with *Nothoseiridium podocarpi* and *Coleophoma podocarpi*. Conidioma on PNA; conidioma on OA; conidiogenous cells; conidia. Scale bars: conidiomata = 400 µm, all others = 10 µm.

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Coleophoma podocarpi

Fungal Planet 1045 – 29 June 2020

Coleophoma podocarpi Crous, *sp. nov.*

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

Classification — *Dermateaceae*, *Helotiales*, *Leotiomycetes.*

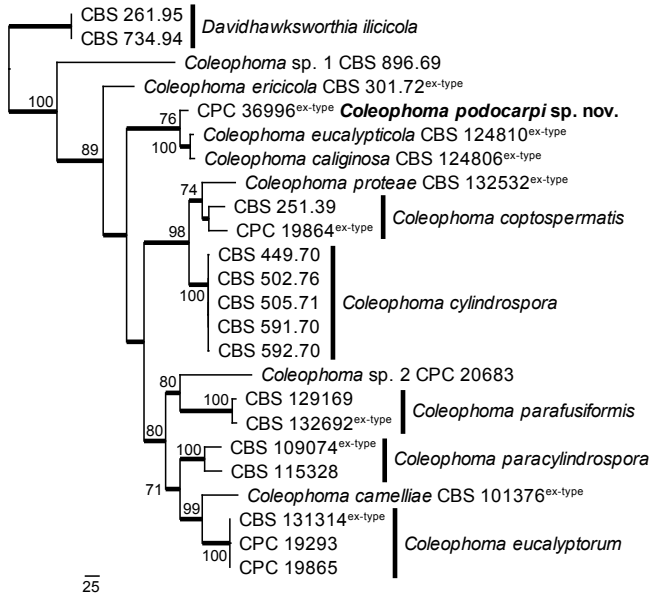
Associated with prominent brown leaf spots. *Conidiomata* pycnidial, grey-brown, 200–300 µm diam, with central ostiole. *Conidiophores* lining the inner cavity, intermingled among paraphyses, 0–2-septate, 20–35 × 5–7 µm, or reduced to conidiogenous cells, hyaline, smooth, guttulate, doliiform to ampulliform, 7–10 × 3–4 µm. *Paraphyses* intermingled among conidiophores, hyaline, smooth, cylindrical, aseptate, 3–4(–6) µm diam, up to 30 µm long, with age becoming multiseptate and with intercalary conidiogenous cells. *Conidiogenous cells* hyaline, smooth, guttulate, doliiform to ampulliform, 7–10 × 3–4 µm, phialidic, with minute periclinal thickening. *Conidia* aseptate, hyaline, smooth, guttulate, subcylindrical to fusoid to irregular, straight to somewhat curved, apex subobtuse, base truncate, (9–)14–22(–25) × (3.5–)4–5(–7) µm.

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

Typus. South Africa, Western Cape Province, Knysna, on leaf spots of *Podocarpus latifolius* (*Podocarpaceae*), Nov. 2018, *F. Roets*, HPC 2697 (holotype CBS H-24347, culture ex-type CPC 36996 = CBS 146625; ITS, LSU, *tef1* and *tub2* sequences GenBank MT373364.1, MT373347.1, MT375110.1 and MT375120.1, MycoBank MB835398).

Notes — *Coleophoma* includes species that are plant pathogenic or saprobic, occurring on a wide range of plant hosts (Crous et al. 2019b, 2020b). The genus was revised by Crous & Groenewald (2016), and shown to reside in the *Dermateaceae* (*Leotiomycetes*), with morphologically similar taxa also clustering in *Dothideomycetes*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Coleophoma parafusiformis* (strain CBS 132692, GenBank NR_154807.1; Identities = 525/550 (95 %), 3 gaps (0 %)), *Coleophoma ericicola* (strain CBS 301.72, GenBank NR_154805.1; Identities = 523/549 (95 %), no gaps), and *Coleophoma xanthosiae* (strain CPC 29214, GenBank NR_154838.1; Identities = 512/543 (94 %), 2 gaps (0 %)). Closest hits using the **LSU** sequence are *Coleophoma paracylindrospora* (strain CBS 109074, GenBank KU728531.1; Identities = 847/864 (98 %), no gaps), *Coleophoma parafusiformis* (strain CBS 132692, GenBank KU728534.1; Identities = 846/864 (98 %), no gaps), and *Coleophoma proteae* (strain CBS 132532, GenBank NG_042679.1; Identities = 845/864 (98 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Coleophoma ericicola* (strain CBS 301.72, GenBank KU728566.1; Identities = 428/500 (86 %), 22 gaps (4 %)), *Coleophoma parafusiformis* (strain CBS 132692, GenBank KU728573.1; Identities = 411/489 (84 %), 30 gaps (6 %)), and *Coleophoma eucalyptorum* (strain CPC 19865, GenBank KU728569.1; Identities = 402/483 (83 %), 31 gaps (6 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Coleophoma xanthosiae* (strain CPC 29214, GenBank KY173598.1; Identities = 399/449 (89 %), 2 gaps (0 %)), *Coleophoma ericicola* (strain KU728605.1, GenBank KU728605.1; Identities = 383/439 (87 %), 5 gaps (1 %)), and *Coleophoma proteae* (strain CBS 132532, GenBank KU728613.1; Identities = 384/442 (87 %), 9 gaps (2 %)).



The first of two equally most parsimonious trees obtained from a phylogenetic analysis of the *Coleophoma* ITS/*actA*/*tef1*/*tub2* alignment (24 strains including the outgroup; 1 324 characters including alignment gaps analysed: 766 constant, 126 variable and parsimony-uninformative and 432 parsimony-informative). PAUP v. 4.0b10 (Swofford 2003) was used to analyse the data. The novel species was added to the alignment of Crous & Groenewald (2016), where also the GenBank accession numbers of the reference sequences can be found. The tree was rooted to two strains of *Davidhawksworthia ilicicola* and the scale bar indicates the number of changes. Parsimony bootstrap support values higher than 70 % are shown at the nodes (PBS/NJBS) and the novel species is highlighted in **bold**. Type status is indicated in superscript. Branches present in the strict consensus tree are thickened. Tree statistics: TL = 1501, CI = 0.640, RI = 0.745, RC = 0.477. The alignment and tree were deposited in TreeBASE (Submission ID S26166).

Colour illustrations. Knysna forest with waterfall. Conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

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Hamatocanthoscypha podocarpi

Fungal Planet 1046 – 29 June 2020

Hamatocanthoscypha podocarpi Crous, *sp. nov.*

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

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

Mycelium consisting of hyaline, branched, 1.5–2 µm diam hyphae. *Conidiophores* smooth, pale to medium brown, erect, solitary or in clusters, subcylindrical, branched below, 0–4-septate, 12–60 × 3–5 µm. *Conidiogenous cells* 13–40 × 3–4 µm, integrated, terminal and intercalary, subcylindrical, pale brown, smooth, base tapering to long cylindrical, apical venter, 3–9 µm long, slightly flared or not, 2–3 µm diam. *Conidia* in long unbranched chains, aseptate, hyaline, smooth, guttulate, subcylindrical with truncate ends, (6–)7–8(–9) × (1.5–)2 µm.

Culture characteristics — Colonies flat, spreading, with folded surface, moderate aerial mycelium and smooth, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA surface honey, reverse cinnamon. On PDA surface honey with isabelline in outer region, reverse isabelline. On OA surface honey.

Typus. South Africa, Western Cape Province, Knysna, on leaf spots of *Podocarpus latifolius* (*Podocarpaceae*), Nov. 2018, *M.J. Wingfield*, HPC 2710 (holotype CBS H-24349, culture ex-type CPC 37055 = CBS 146626; ITS, LSU, *actA* and *rpb2* sequences GenBank MT373365.1, MT373348.1, MT375095.1 and MT375100.1, MycoBank MB835399).

Notes — The genus *Chalara* as circumscribed by Nag Raj & Kendrick (1976) is polyphyletic and awaits revision. *Hamatocanthoscypha podocarpi* is phylogenetically allied to the type species of *Hamatocanthoscypha*, *H. laricionis* (Svrček 1977), and placed in this genus based on DNA similarity. Several species of '*Chalara*' have been described from *Podocarpus*, namely *C. brevipes* (conidia (6–)8.9(–12) × 1.5–2 µm), *C. novaezelandiae* (conidia (5–)6.4(–8) × 1–1.5 µm), *C. cylindrosperma* (conidia (5.5–)11(–17) × (1.5–)1.9(–2.5) µm), *C. fusidioides* (conidia (4.5–)7.7(–12) × (1.5–)2.1(–3.5) µm), *C. acuaria* (conidia (12–)16(–20) × (2–)2.7(–3.5) µm) and *C. bicolor* (conidia 7-septate, (45–)50–60(–71) × 5.5–6 µm) (Nag Raj & Kendrick 1975). Of these, *H. podocarpi* is most similar to *C. brevipes*, but can be distinguished in having smaller conidiogenous cells, and conidiophores that are aggregated in clusters.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to numerous sequences wrongly labelled as '*Infundichalara microchona*' (e.g., strain KRP75-5, GenBank HM036588.1; Identities = 531/537 (99 %), 2 gaps (0 %)), *Chalara holubovae* (strain CCF 3978, GenBank NR_154760.1; Identities = 483/501 (96 %), 3 gaps (0 %)), and *Hamatocanthoscypha laricionis* (voucher TNS-F13530, GenBank JN033441.1; Identities = 540/567 (95 %), 4 gaps (0 %)). Closest hits using the **LSU** sequence are *Leptodontidium beauverioides* (strain CBS 672.76, GenBank MH872794.1; Identities = 836/840 (99 %), no gaps), *Tricladium caudatum* (strain CCM F-13498, GenBank GQ477318.1; Identities = 833/837 (99 %), no gaps), and *Chalara constricta* (strain CBS 248.76, GenBank FJ176256.1; Identities = 825/829 (99 %), no gaps). No significant hits were obtained when the ***actA*** and ***rpb2*** sequences were used in blastn and megablast searches.

Colour illustrations. Walkway in the Knysna forest. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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Myrmecridium phragmiticola

Fungal Planet 1047 – 29 June 2020

Myrmecridium phragmiticola Crous & Akulov, *sp. nov.*

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

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

On SNA: *Mycelium* consisting of hyaline, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* unbranched, erect, straight, medium brown, thick-walled, 2–4-septate, up to 70 µm tall, 3–3.5 µm diam; basal cell 4–6 µm diam. *Conidiogenous cells* terminal, integrated, subcylindrical, 25–35 µm long, pale brown, forming a rachis with pimple-shaped denticles less than 1 µm long and 0.5 µm diam; slightly thickened. *Conidia* solitary, aseptate, pale brown, thin-walled, smooth, guttulate, with or without a wing-like gelatinous sheath, ellipsoid to fusoid, (7–)8–9 × (2.5–)3 µm; hilum unthickened nor darkened, 0.5 µm diam.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface isabelline, reverse hazel. On PDA surface and reverse greyish sepia. On OA surface isabelline.

Typus. Ukraine, Sumy region, bank of Vorskla river, NNP Hetmanskyi, Klymentove village, on leaves of *Phragmites australis* (*Poaceae*), 5 Aug. 2018, *A. Akulov*, HPC 2554, AS 6809 (holotype CBS H-24351, culture ex-type CPC 36367 = CBS 146628; ITS and LSU sequences GenBank MT373366.1 and MT373349.1, MycoBank MB835400).

Notes — Arzanlou et al. (2007) established the genus *Myrmecridium* to accommodate taxa with hyaline mycelium, pigmented, solitary conidiophores with pimple-like denticles, and 0–1-septate, ellipsoid conidia with a mucoid sheath. *Myrmecridium phragmiticola* should be compared to *M. phragmites* (*Phragmites australis*, Netherlands), which has 0–1-septate conidia, (6.5–)7–8(–9) × (2.5–)3(–3.5) µm (Crous et al. 2011). Although the conidia are similar in size, those of *M. phragmiticola* are aseptate.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Myrmecridium phragmitis* (strain CBS 131311, GenBank NR_137782.1; Identities = 531/552 (96 %), 6 gaps (1 %)), *Myrmecridium spartii* (strain CBS 140006, GenBank NR_155376.1; Identities = 523/543 (96 %), 4 gaps (0 %)), and *Myrmecridium banksiae* (strain CBS 132536, GenBank NR_111762.1; Identities = 522/546 (96 %), 4 gaps (0 %)). Closest hits using the **LSU** sequence are *Myrmecridium schulzeri* (strain CBS 188.96, GenBank EU041829.1; Identities = 855/860 (99 %), no gaps), *Myrmecridium banksiae* (strain CBS 132536, GenBank NG_042684.1; Identities = 862/870 (99 %), no gaps), and *Myrmecridium flexuosum* (strain CBS 398.76, GenBank EU041825.1; Identities = 852/860 (99 %), no gaps).

Colour illustrations. *Phragmites australis* along the bank of the Vorskla river. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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Diabolocovidia claustri

Fungal Planet 1048 – 29 June 2020

Diabolocovidia Crous, *gen. nov.*

Etymology. This fungus was described during the coronavirus pandemic, April 2020. Name composed of *diabolicus* = devilish and covid, referring to COVID-19.

Classification — *Xylariaceae*, *Xylariales*, *Sordariomycetes.*

Mycelium consisting of branched, septate, hyaline to pale brown, smooth to finely roughened, hyphae. *Conidiophores* solitary, erect, flexuous, mostly reduced to a terminal conidiogenous cell. *Conidiogenous cells* pale brown, smooth, subcylindrical to slightly clavate, proliferating via single apical blastic locus, and remaining attached to acropetal chain of conidia that remain attached to one another via narrow isthmus. *Conidia* brown, thin-walled, smooth, guttulate, granular, ellipsoid to obovoid; conidia remaining attached in chains of propagules, disarticulating at maturity into single propagules or shorter chains.

Type species. Diabolocovidia claustri Crous.
MycoBank MB835401.

Diabolocovidia claustri Crous, *sp. nov.*

Etymology. Name refers to the closure or lockdown experienced in many countries during the COVID-19 pandemic.

Mycelium consisting of branched, septate, hyaline to pale brown, smooth to finely roughened, 2–3 µm diam hyphae. *Conidiophores* solitary, erect, flexuous, mostly reduced to a terminal conidiogenous cell. *Conidiogenous cells* pale brown, smooth, subcylindrical to slightly clavate, 8–10 × 3–4 µm, proliferating via single apical blastic locus, and remaining attached to acropetal chain of conidia that remain attached to one another via narrow isthmus. *Conidia* brown, thin-walled, smooth, guttulate, granular, ellipsoid to obovoid, (7–)8–9(–11) × (4–)5–6(–7) µm; conidia remaining attached in chains of 8–12 propagules, disarticulating at maturity into single propagules or shorter chains.

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

Typus. USA, Florida, Gainesville, on leaves of *Serenoa repens* (*Arecaceae*), 28 Feb. 2018, *M.J. Wingfield*, HPC 2792 (holotype CBS H-24353, culture ex-type CPC 37593 = CBS 146630; ITS and LSU sequences GenBank MT373367.1 and MT373350.1, MycoBank MB835402).

Notes — *Diabolocovidia* is reminiscent of genera such as *Ampullifera* (but conidiophores different and hyphopodia present) and *Junctospora* (but conidiophores sparingly branched, subhyaline; Seifert et al. 2011). Phylogenetically, it is allied to *Vamsapriya*, which is characterised by having brown, synnematous conidiophores, mono- to polytretic conidiogenous cells, and dark brown, septate conidia arranged in acropetal chains (Dai et al. 2014). Based on these differences, *Diabolocovidia* is herewith introduced as a new genus.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Vamsapriya khunkonensis* (voucher MFLU 13-0367, GenBank NR_154499.1; Identities = 427/464 (92 %), 5 gaps (1 %)), *Didymobotryum rigidum* (strain JCM 8837, GenBank LC228650.1; Identities = 517/561 (92 %), 7 gaps (1 %)), and *Vamsapriya bambusicola* (voucher MFLU 13-0368, GenBank NR_154500.1; Identities = 533/605 (88 %), 37 gaps (6 %)). Closest hits using the **LSU** sequence are *Vamsapriya bambusicola* (strain MFLUCC 11-0477, GenBank NG_067527.1; Identities = 849/864 (98 %), no gaps), *Fasciatispora petrakii* (strain HKUCC 207, GenBank AY083828.1; Identities = 832/848 (98 %), 1 gap (0 %)), and *Vamsapriya indica* (strain MFLUCC 12-0544, GenBank KM462840.1; Identities = 815/831 (98 %), no gaps).

Colour illustrations. Leaves of *Serenoa repens*. Conidiophores with conidiogenous cells giving rise to chains of conidia. Scale bars = 10 µm.

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Juncomyces californiensis

Fungal Planet 1049 – 29 June 2020

Juncomyces Crous, *gen. nov.*

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

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

Mycelium consisting of brown, smooth to warty, septate, branched. *Conidiophores* solitary, subcylindrical, mostly unbranched, erect, thick-walled, brown, verruculose, warty, multiseptate, rarely forming from a brown stroma, with a few fasciculate conidiophores. *Conidiogenous cells* integrated, terminal, straight to geniculate-sinuous, proliferating sympodially with several apical loci, flattened, thickened, darkened, and refractive. *Conidia* solitary, acicular to slightly obclavate, mostly thick-walled, verruculose, guttulate, apex subobtuse, base truncate, thickened, darkened and refractive, septate.

Type species. Juncomyces californiensis Crous.
MycoBank MB835403.

Juncomyces californiensis Crous, *sp. nov.*

Etymology. Name refers to the state of California, where it was collected.

Mycelium consisting of brown, smooth to warty, septate, branched, 2–3 µm diam hyphae. *Conidiophores* solitary, subcylindrical, mostly unbranched, erect, 80–180 × 5–7 µm, thick-walled, brown, verruculose, warty, multiseptate, rarely forming from a brown stroma, up to 120 µm diam, with 1–3 fasciculate conidiophores, up to 60 µm tall. *Conidiogenous cells* integrated, terminal, straight to geniculate-sinuous, 35–60 × 5–7 µm; proliferating sympodially with several apical loci, flattened, thickened, darkened, and refractive, 4.5–5.5 µm diam. *Conidia* solitary, acicular to slightly obclavate, mostly thick-walled, verruculose, guttulate, apex subobtuse, base truncate, 4.5–5 µm diam, thickened, darkened and refractive, 3(–6)-septate, (65–)70–85(–90) × (7–)8(–9) µm.

In vivo: *Conidiophores* on culms erect, solitary, rarely in fascicles of 2–3, straight, 2–6-septate, subcylindrical, rejuvenating percurrently, 50–110 × 5–7 µm, arising from immersed, brown, weakly developed stroma, 20–40 µm diam. *Conidiogenous cells* integrated, terminal and intercalary, medium brown, smooth, 10–45 × 5–6 µm with one to several loci, round, thickened, refractive, 3–4 µm diam. *Conidia* solitary, arranged in clusters on conidiophores, obclavate, slightly curved to straight, apex subobtuse, base truncate, 3–7-septate, at times constricted at some of the septa, thick-walled, medium brown, verruculose, hilum thickened, darkened, refractive, 4–5 µm diam, (45–)55–70(–75) × (6–)7(–8) µm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and smooth, feathery, even margin, reaching 12 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, reverse iron-grey.

Typus. USA, California, UC Davis, on leaves of *Juncus effusus* (*Juncaceae*), 3 Apr. 2019, *P.W. Crous*, HPC 2894 (holotype CBS H-24363, culture ex-type CPC 37989 = CBS 146682; ITS and LSU sequences GenBank MT373368.1 and MT373351.1, MycoBank MB835405).

Additional material examined. USA, California, UC Davis, on leaves of *J. effusus*, 3 Apr. 2019, *P.W. Crous*, HPC 2895, culture CPC 37993 = CBS 146631; ITS, LSU and *rpb2* sequences GenBank MT373369.1, MT373352.1 and MT375101.1.

Notes — *Juncomyces* is closely related to *Graminopassalora*, which was introduced to accommodate *Passalora graminis*, a widespread pathogen occurring on a broad range of grass (*Poaceae*) hosts (Videira et al. 2017). *Juncomyces* differs from *Graminopassalora* by chiefly having solitary conidiophores (rarely fascicles of 2–3), and multiseptate, obclavate conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 37989 had highest similarity to *Graminopassalora graminis* (strain CBS 113303, GenBank GU214666.1; Identities = 474/538 (88 %), 18 gaps (3 %)), *Mycosphaerella fimbriata* (strain CBS 120736, GenBank NR_137553.1; Identities = 465/526 (88 %), 16 gaps (3 %)), and *Zasmidium corymbiae* (strain CBS 145049, GenBank MK047423.1; Identities = 476/542 (88 %), 21 gaps (3 %)). The ITS sequences of CPC 37989 and 37993 are 100 % (528/528 bp) identical. Closest hits using the **LSU** sequence of CPC 37989 are *Xenosonderhenia eucalypti* (strain CBS 138858, GenBank NG_058120.1; Identities = 773/799 (97 %), 2 gaps (0 %)), *Ramularia lethalis* (strain CPC 25910, GenBank KX287174.1; Identities = 780/808 (97 %), no gaps), and *Ramularia acris* (strain CBS 109794, GenBank KX287010.1; Identities = 780/808 (97 %), no gaps). The LSU sequences of CPC 37989 and 37993 are 100 % (808/808 bp) identical. Closest hits using the ***rpb2*** sequence of CPC 37993 had highest similarity to *Ramularia gei* (strain CBS 344.49, GenBank KX288570.1; Identities = 637/840 (76 %), 14 gaps (1 %)), *Ramularia unterseheri* (strain CBS 124884, GenBank KP894709.1; Identities = 636/849 (75 %), 8 gaps (0 %)), and *Ramularia heraclei* (strain CPC 11507, GenBank KX288584.1; Identities = 634/848 (75 %), 6 gaps (0 %)).

Colour illustrations. *Juncus effusus* growing in California. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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Beltraniella podocarpi

Fungal Planet 1050 – 29 June 2020

Beltraniella podocarpi Crous, *sp. nov.*

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

Classification — *Beltraniaceae*, *Xylariales*, *Sordariomycetes*.

Setae solitary to aggregated, erect, flexuous, arising from a lobate basal cell, 15–25 µm diam, dark brown, warty, chiefly unbranched, up to 20-septate, thick-walled with large central guttules, tapering in upper part to acute apex, 120–300 × 5–8 µm. *Conidiophores* arranged in dense clusters around the base of setae, brown, smooth, subcylindrical, frequently branched at basal cell, 1–2-septate, 10–30 × 6–8 µm. *Conidiogenous cells* integrated, terminal and intercalary, 7–12 × 6–7 µm, pale brown, smooth, obclavate, tapering toward 1–3 denticulate loci, 1–1.5 µm long, 1 µm diam. *Separating cells* clavate to fusoid-ellipsoid, pale brown, smooth, finely guttulate, tapering toward long basal stalk and short apical locus, 17–21 × 4–5 µm. *Conidia* obovoid to narrowly turbinate, tapering toward base, apex rounded to subtruncate, aseptate, finely verruculose, guttulate, pale brown, (25–)27–28(–33) × (7–)8 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and feathery, lobate margin, covering dish after 2 wk at 25 °C. On MEA surface olivaceous grey, reverse honey with olivaceous grey margin. On PDA surface olivaceous grey, reverse iron-grey. On OA surface iron-grey with dirty white margin.

Typus. South Africa, Western Cape Province, Knysna, on leaves of *Podocarpus latifolius* (*Podocarpaceae*), 30 Nov. 2018, *M.J. Wingfield*, HPC 2710 (holotype CBS H-24354, culture ex-type CPC 36783 = CBS 146633; ITS and LSU sequences GenBank MT373370.1 and MT373353.1, MycoBank MB835406).

Notes — *Beltraniella* is characterised by brown, unbranched setae, setiform conidiophores, polyblastic, denticulate conidiogenous cells, and turbinate conidia with a distinct hyaline transverse band (Rajeshkumar et al. 2016). *Beltraniella podocarpi* is closely related to several species that tend to have some overlap in conidial length, but have narrower conidia (Rajeshkumar et al. 2016, Crous et al. 2019a).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Beltraniella portoricensis* (strain BCRC 34590, GenBank GU905993.1; Identities = 479/487 (98 %), 6 gaps (1 %)), *Beltraniella ramosiphora* (strain LCG 10-2, GenBank MG717500.1; Identities = 527/536 (98 %), 4 gaps (0 %)), and *Beltraniella pseudoportoricensis* (strain CBS 145547, GenBank NR_165552.1; Identities = 578/591 (98 %), 5 gaps (0 %)). Closest hits using the **LSU** sequence are *Beltraniella pseudoportoricensis* (strain CBS 145547, GenBank NG_067875.1; Identities = 821/825 (99 %), no gaps), *Beltraniella acaciae* (strain CPC 29498, GenBank NG_066374.1; Identities = 786/790 (99 %), no gaps), and *Beltraniella portoricensis* (strain CBS 856.70, GenBank MH871777.1; Identities = 842/848 (99 %), 1 gap).

Colour illustrations. Rainforest in Knysna, South Africa. Setae and conidiophores on PNA; dichotomously branched seta; conidiophores with conidiogenous cells; conidia with separating cell. Scale bars = 10 µm.

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Neofabraea eucalyptorum

Fungal Planet 1051 – 29 June 2020

Neofabraea eucalyptorum Crous, *sp. nov.*

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

Classification — *Dermateaceae*, *Helotiales*, *Leotiomycetes*.

Associated with brown, amphigenous leaf spots, 3–5 mm diam. *Conidiomata* 200–300 µm diam, acervular, erumpent, associated with dark brown, amphigenous leaf spots. *Conidiophores* hyaline, smooth, branched, septate, subcylindrical, phialidic, up to 80 µm long, 3–5 µm diam. *Conidiogenous cells* hyaline, smooth, subcylindrical, terminal and intercalary with visible periclinal thickening, 10–18 × 3–4 µm. *Conidia* subcylindrical to fusoid-ellipsoid, variously curved, hyaline, smooth, guttulate, apex subobtuse, base with flattened hilum, aseptate, but becoming up to 3-septate in older cultures, (25–)30–35(–40) × (6.5–)7–8(–9) µm.

Culture characteristics — Colonies spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 22 mm diam after 2 wk at 25 °C. On MEA surface buff, reverse cinnamon. On PDA surface honey, reverse hazel. On OA surface honey.

Typus. USA, California, UC Davis, on leaves of *Eucalyptus macrandra* (*Myrtaceae*), 30 Apr. 2019, *P.W. Crous*, HPC 2889 (holotype CBS H-24355, culture ex-type CPC 37985 = CBS 146634; ITS, LSU and *tub2* sequences GenBank MT373371.1, MT373354.1 and MT375121.1, MycoBank MB835407).

Notes — The *Neofabraea* generic complex was revised by Chen et al. (2016), and *Neofabraea eucalypti* was subsequently placed in *Coleophoma* (Crous & Groenewald 2016). *Neofabraea eucalyptorum* is thus the first confirmed species of the genus associated with leaf spots on *Eucalyptus* (Crous et al. 2019b).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neofabraea alba* (strain UASWS0614, GenBank HQ166388.1; Identities = 485/499 (97 %), 3 gaps (0 %)), *Neofabraea brunneipila* (voucher MFLU 15-0231, GenBank MK584984.1; Identities = 490/505 (97 %), 1 gap (0 %)), and *Neofabraea inaequalis* (strain CBS 326.75, GenBank NR_155470.1; Identities = 490/505 (97 %), 1 gap (0 %)).Closest hits using the **LSU** sequence are *Neofabraea brasiliensis* (voucher CNPUV499, GenBank KR107002.1; Identities = 857/865 (99 %), no gaps), *Pseudofabraea citricarpa* (strain CBS 130297, GenBank KR859073.1; Identities = 844/852 (99 %), no gaps), and *Neofabraea kienholzii* (strain CBS 318.77, GenBank KR858874.1; Identities = 854/863 (99 %), no gaps). No significant hits were obtained when the ***tub2*** sequence was used in blastn and megablast searches.

Colour illustrations. Leaf spots on *Eucalyptus macrandra*. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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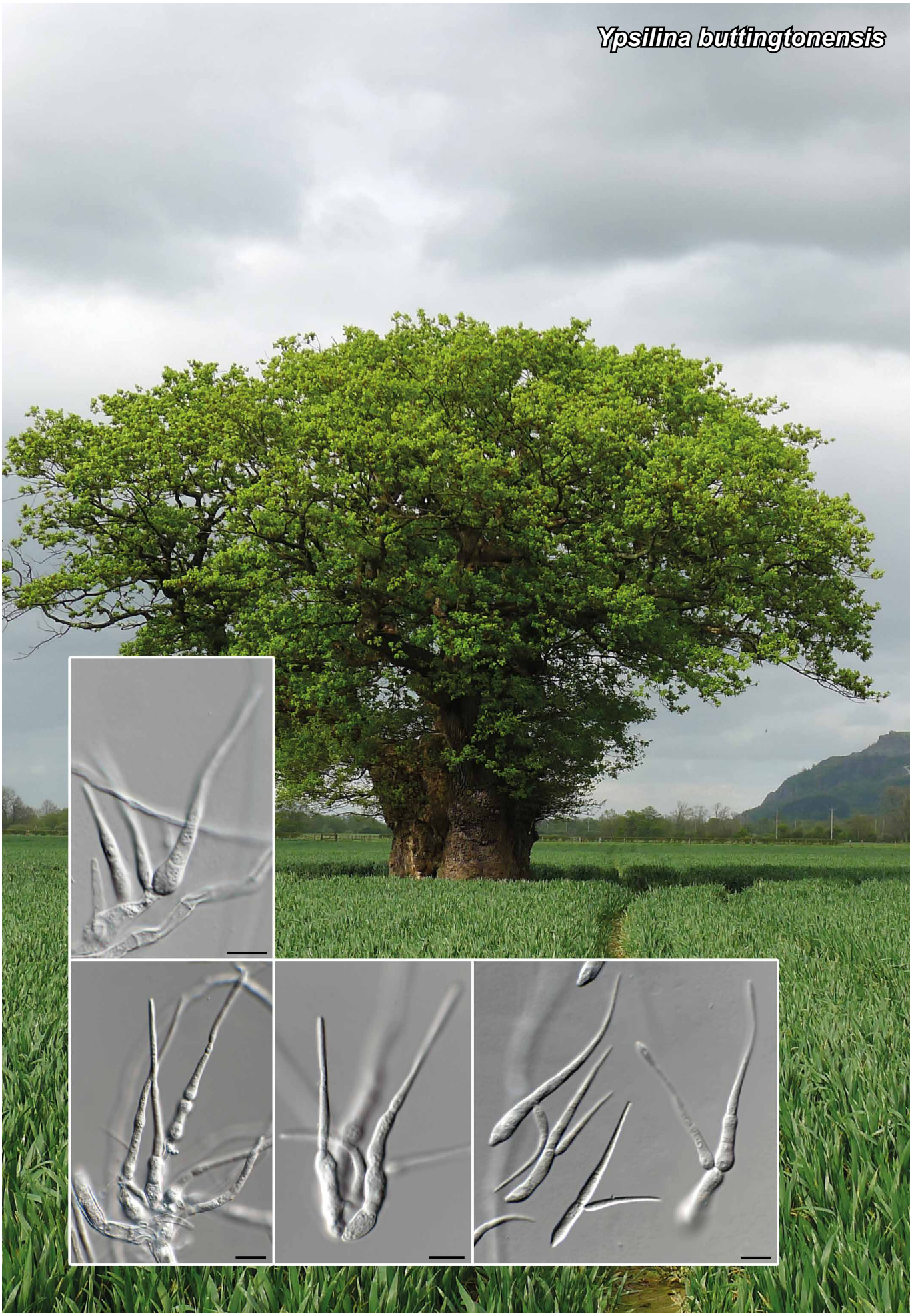
Ypsilina buttingtonensis

Fungal Planet 1052 – 29 June 2020

Ypsilina buttingtonensis Crous, Wainhouse & Brian Douglas, *sp. nov.*

Etymology. Name refers to the collection site, Buttington, Wales, UK, where it was collected.

Classification — *Ploettnerulaceae*, *Helotiales*, *Leotiomycetes.*

Mycelium consisting of hyaline, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* integrated, subcylindrical, hyaline, smooth, septate, sparingly branched, mostly terminal on hyphal ends, 30–100 × 4–6 µm. *Conidiogenous cells* integrated, terminal and intercalary, subcylindrical, smooth, 12–25 × 4–6 µm; proliferating sympodially. *Conidia* solitary but aggregating in mucoid mass, Y-shaped, smooth, hyaline; central cell obclavate, base with truncate hilum, 2 µm diam, apex subobtuse, 2–4-septate, (35–)40–50(–60) × (3–)4–5(–6) µm, with 1–2 lateral branches inserted below the median, pointing upwards, aseptate, obclavate, apex subobtuse, (8–)15–20(–25) × 2(–2.5) µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and folded surface (on MEA), with smooth, lobate margin, reaching 12 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white, reverse ochreous.

Typus. UK, Wales, Buttington, from heartwood of 1 000-yr-old *Quercus* sp. (*Fabaceae*), 14 Mar. 2018, *M. Wainhouse* (holotype CBS H-24356, culture ex-type B0.01.30 = CPC 39109 = CBS 146635; ITS and LSU sequences GenBank MT373372.1 and MT373355.1, MB835408).

Notes — Although the ecology of *Ypsilina* remains unknown, *Y. graminea* has been isolated from freshwater foam, roots and leaves of various plants (Descals et al. 1998). *Ypsilina buttingtonensis* was isolated from an ancient pedunculate oak *Quercus robur* in Buttington, Wales (longitude and latitude: 52.678236, -3.1108743). The tree, known as the Buttington Oak, was an open-grown lapsed pollard. At the time when the tree fell in February 2018, it had a trunk girth of 11.03 m at breast height and was believed to be the second oldest oak tree in Wales. The tree had a 1.5 m diam hollow through centre where brown cubical rot could be seen, attributed to *Fistulina hepatica*. The significance of the tree was realised in 2009 when it was 'discovered'.

Cores of wood were extracted from the tree with a 5.5 mm increment bore. Wood chips were taken from the 30 cm cores at 1 cm intervals and placed on low pH 2 % malt agar Petri dishes and incubated at 20 °C in the dark. *Ypsilina buttingtonensis* was cultured from a chip 30 cm into the heartwood.

In addition to *Ypsilina buttingtonensis*, *Fistulina hepatica*, and eight species of ascomycete were also cultured from the wood chips including *Cryphonectria radicalis*, a close relative of the aggressive canker pathogen *Cryphonectria parasitica*, responsible for chestnut blight.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Helgardia anguioides* (strain CBS 496.80, GenBank NR_158522.1; Identities = 522/533 (98 %), no gaps), *Oculimacula acuformis* (strain CBS 495.80, GenBank MH861289.1; Identities = 516/535 (96 %), 2 gaps (0 %)), and *Oculimacula aestiva* (strain CBS 114730, GenBank MG934454.1; Identities = 516/535 (96 %), 2 gaps (0 %)). Closest hits using the **LSU** sequence are *Ypsilina graminea* (strain CBS 114630, GenBank MH874529.1; Identities = 877/880 (99 %), 1 gap (0 %)), *Helgardia anguioides* (strain CBS 496.80, GenBank MH873055.1; Identities = 876/880 (99 %), no gaps), and *Rhynchosporium orthosporum* (strain 04CH-Bar-A.1.1.3, GenBank KU844335.1; Identities = 870/874 (99 %), no gaps).

Colour illustrations. The Buttington Oak (background photo credit: @thetreehunter Rob McBride). Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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Pseudopezicula betulae

Fungal Planet 1053 – 29 June 2020

Pseudopezicula betulae Crous, *sp. nov.*

Etymology. Name refers to *Betula*.

Classification — *Discinellaceae*, *Helotiales*, *Leotiomycetes.*

Conidiomata sporodochial, superficial, round, 200–300 µm diam, white, composed of tightly aggregated conidiophores. *Conidiophores* hyaline, smooth, subcylindrical, extensively branched, septate, 3–4 µm diam, up to 90 µm long. *Conidiogenous cells* hyaline, smooth, phialidic, subcylindrical to fusoid, apex with periclinal thickening, at times with percurrent proliferation and indistinct flared collarette (2–3 µm long), 4–13 × 2–5 µm. *Conidia* solitary, aseptate, guttulate, hyaline, smooth, aggregating in mucoid mass, subcylindrical, straight to curved, apex obtuse, base truncate, with minute marginal frill, (5–)7–10(–17) × 2–2.5 µm.

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

Typus. USA, California, Yosemite, on brown, amphigenous leaf spots of *Populus tremuloides* (*Salicaceae*), 2019, *S. Denman* (holotype CBS H-24357, culture ex-type CPC 36499 = CBS 146683; ITS, LSU, *rpb2*, and *tef1* sequences GenBank MT373373.1, MT373356.1, MT375102.1 and MT375116.1, MycoBank MB835409).

Pseudopezicula tracheiphila (Müll.-Thurg.) Korf & W.Y. Zhuang, Mycotaxon 26: 464. 1986

Basionym. *Pseudopeziza tracheiphila* Müll.-Thurg., Centralbl. Bakteriol. Parasitenk., 1. Abt. 10: 57. 1903.

Synonyms. *Botrytis tracheiphila* Sacc. & D. Sacc., Syll. Fung. (Abellini) 18: 157. 1906.

Phialophora tracheiphila (Sacc. & D. Sacc.) Korf, Mycotaxon 26: 464. 1986.

Typus. Neotype: Switzerland, Seemühle, Walenstadt, on leaves of *Vitis vinifera* cv. 'Blauburgunder', *H. Schüepp & M. Bodmer*, CUP-061784 (designated in Korf et al. 1986). Epitype: Luxembourg, on leaf of *Vitis vinifera*, coll. Sept. 1985, *R. Pearson*, isol. *W.-Y. Zhuang* (epitype designated here CUP 61766, MBT392064, culture ex-epitype CBS 308.86; ITS and LSU sequences GenBank MT373374.1 and MT373357.1).

Notes — *Pseudopezicula* accommodates two species of apothecial ascomycetes that cause angular leaf scorch on *Vitis vinifera*. An epitype is here designated for one of these, namely *P. tracheiphila.* In culture they produce phialophora-like asexual morphs (Korf et al. 1986), that resemble the phialidic asexual morph isolated in the present study. Although *Pseudopezicula betulae* was associated with prominent leaf spots, its occurrence was inconsistent, and therefore it is unknown whether it is a primary pathogen.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Gyoerffyella entomobryoides* (strain CBS 268.63, GenBank NR_145302.1; Identities = 512/529 (97 %), 1 gap (0 %)), *Gyoerffyella rotula* (strain 272Jb14, GenBank KU516477.1; Identities = 514/533 (96 %), 1 gap (0 %)), and *Fontanospora eccentrica* (strain UMB-881.11, GenBank KF730812.1; Identities = 495/514 (96 %), 2 gaps (0 %)). Closest hits using the **LSU** sequence are *Lemonniera aquatica* (strain CBS 167.46, GenBank MH867676.1; Identities = 831/837 (99 %), no gaps), *Margaritispora aquatica* (strain CBS 603.66, GenBank MH870561.1; Identities = 836/843 (99 %), 1 gap (0 %)), and *Gyoerffyella entomobryoides* (strain CBS 268.63, GenBank MH869886.1; Identities = 833/842 (99 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Gyoerffyella rotula* (strain CCM F-400, GenBank MK241434.1; Identities = 704/863 (82 %), 2 gaps (0 %)), *Lachnum virgineum* (strain AFTOL-ID 49 = voucher OSC 100002, GenBank DQ470877.1; Identities = 705/880 (80 %), 13 gaps (1 %)), and *Lachnellula hyalina* (strain CBS 185.66, GenBank XM_031145866.1; Identities = 699/877 (80 %), 11 gaps (1 %)). No significant hits were obtained when the ***tef1*** sequence was used in blastn and megablast searches.

Colour illustrations. Amphigenous leaf spots on *Populus tremuloides*. Conidiomata on PDA; conidiophores with conidiogenous cells; conidia. Scale bars = 300 µm (conidiomata), 10 µm (all others).

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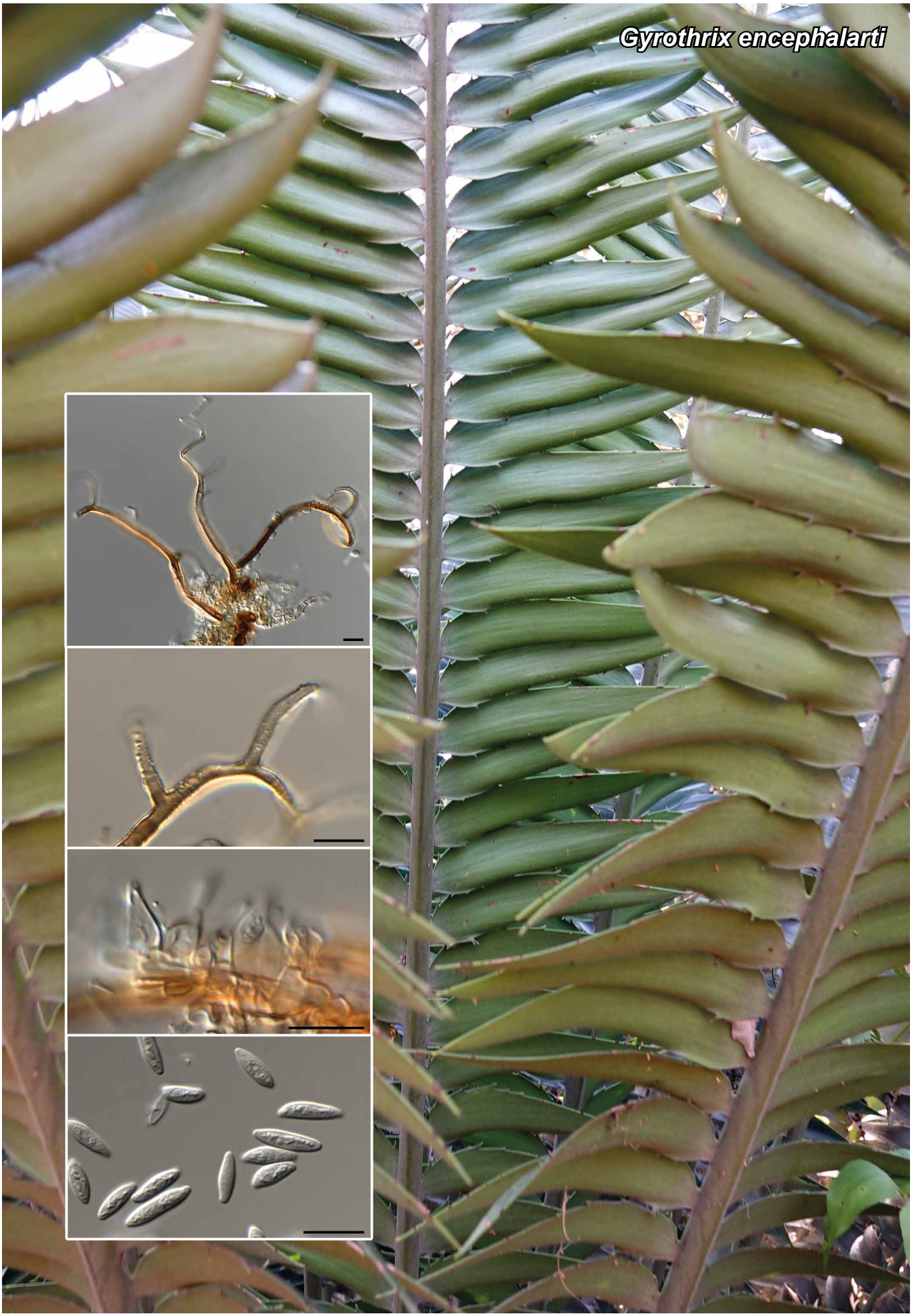
Gyrothrix encephalarti

Fungal Planet 1054 – 29 June 2020

Gyrothrix encephalarti Crous, *sp. nov.*

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

Classification — *Incertae sedis*, *Xylariales*, *Sordariomycetes.*

Culture sterile, morphology based on sporulation on dead leaf spots. *Mycelium* consisting of brown, smooth, septate, branched, 1.5–2 µm diam hyphae. *Setae* erect, 80–130 µm long, 3–4 µm diam, brown, multiseptate, thick-walled, verrucose, subcylindrical with apical taper, base bulbous, 5–6 µm diam, apex spirally twisted with twisted lateral branches in apical region. *Conidiophores* reduced to conidiogenous cells around base of setae, ampulliform to subcylindrical, pale brown, smooth, 6–10 × 3–4 µm, proliferating percurrently at apex. *Conidia* hyaline, smooth, aseptate, fusoid, inaequilateral, inner plane flat, outer plane convex, apex subobtuse, base truncate, (7–)10–12(–14) × 3(–3.5) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 55 mm diam after 2 wk at 25 °C. On MEA surface buff, reverse cinnamon. On PDA surface buff, reverse rosy buff. On OA surface rosy buff.

Typus. South Africa, Northern Province, Tzaneen, on leaves of *Encephalartos* sp. (*Zamiaceae*), 2015, *P.W. Crous*, HPC 2486 (holotype CBS H-24364, culture ex-type CPC 35966 = CBS 146684; ITS, LSU and *tef1* sequences GenBank MT373376.1, MT373358.1 and MT375117.1, MycoBank MB835410).

Notes — *Gyrothrix encephalarti* is closely related to *G. eucalypti* (*Eucalyptus* sp., South Africa; conidia (8–)10–13(–15) × (2–)2.5 µm, setae 100–180 µm tall, 4–5 µm diam at base; Crous et al. 2019c), but has wider conidia and shorter setae. DNA sequences of *G. eucalypti* and *G. encephalarti* are related to the type sequence deposited for *Neoanthostomella viticola* (NG_067792.1), which has a completely different asexual morph.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neoanthostomella viticola* (strain MFLUCC 16-0243, GenBank NR_165511.1; Identities = 503/537 (94 %), 22 gaps (4 %)), *Gyrothrix eucalypti* (strain CPC 36066, GenBank NR_166315.1; Identities = 540/581 (93 %), 8 gaps (1 %)), and *Calceomyces lacunosus* (strain CBS 633.88, GenBank KY610397.1; Identities = 524/588 (89 %), 22 gaps (3 %)). Closest hits using the **LSU** sequence are *Gyrothrix eucalypti* (strain CPC 35992, GenBank MN567618.1; Identities = 869/880 (99 %), no gaps), and *Torula ficus* (strain MFLUCC 18-0112, GenBank MH260322.1; Identities = 792/803 (99 %), no gaps). Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Gyrothrix ramosa* (strain MUCL54061, GenBank KJ476975.1; Identities = 447/472 (95 %), no gaps), *Gyrothrix inops* (strain BE108, GenBank KJ476974.1; Identities = 447/472 (95 %), no gaps), and *Metarhizium globosum* (strain ARSEF 2596, GenBank EU248846.1; Identities = 438/470 (93 %), no gaps).

Colour illustrations. Leaves of *Encephalartos* sp. Setae and conidiogenous cells; conidia. Scale bars = 10 µm.

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Satchmopsis metrosideri

Fungal Planet 1055 – 29 June 2020

Satchmopsis metrosideri Crous, *sp. nov.*

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

Classification — *Cochlearomycetaceae*, *Leotiales*, *Leotiomycetes*.

Conidiomata cupulate, superficial, 100–140 µm diam at apex, 130–180 µm deep, dark brown, attached to a basal stroma of dark brown cells that occupy the stomatal chamber; wall consisting of two regions, the lower region having thick-walled dark brown cells up to 5 layers thick; upper region on thin-walled paler cells, cylindrical, 10–17 × 3–4 µm, with even, smooth flat edge. In culture conidiomata are paler in colour and much larger, flattened, cupulate, and margins have cells that are lobate due to expanding growth (not flat as *in vivo*). *Conidiogenous cells* restricted to lower part of basal wall, 3–7 × 2–3 µm, doliiform to lageniform, phialidic with periclinal thickening, hyaline with indistinct collarette. *Conidia* hyaline, smooth, aseptate, guttulate, subcylindrical, predominantly straight with obtuse ends, (15–)16–17(–19) × 1–1.5 µm.

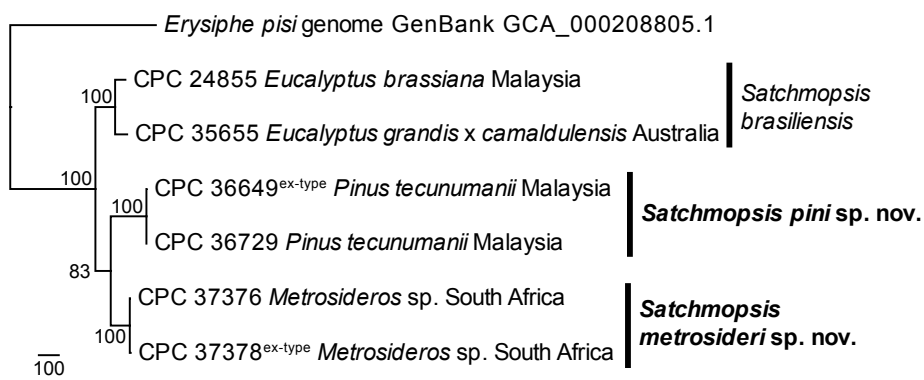
Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and feathery, lobate margin, reaching 60 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface umber with patches of sepia, reverse umber.

Typus. South Africa, Eastern Cape Province, Haga Haga, Amathole, on leaf litter of *Metrosideros excelsa* (*Myrtaceae*), 2015, *M.J. Wingfield*, HPC 2754 (holotype CBS H-24359, culture ex-type CPC 37378 = CBS 146686; ITS, LSU, *actA*, *rpb2*, *tef1* and *tub2* sequences GenBank MT373377.1, MT373359.1, MT432194.1, MT375103.1, MT375111.1 and MT375122.1, MycoBank MB835411).

Additional material examined. South Africa, Eastern Cape Province, Haga Haga, Amathole, on leaf litter of *M. excelsa*, 2015, *M.J. Wingfield*, HPC 2754, culture CPC 37376; ITS, *actA*, *rpb2*, *tef1* and *tub2* sequences GenBank MT432187.1, MT432188.1, MT432189.1, MT432190.1 and MT432190.1.

Notes — The genus *Satchmopsis*, based on *S. brasiliensis* (*Eucalyptus paniculata*, Brazil; conidia 11.5–15.5 × 1–1.5 µm) (Sutton 1975) was introduced for a genus of cupulate coelomycetes with aseptate conidia. *Satchmopsis* is commonly isolated from eucalypt leaf litter in South America (Crous et al. 2006). The present collection, from *Metrosideros excelsa* leaf litter collected in South Africa, differs from *S. brasiliensis* in being phylogenetically distinct, and also having longer conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Satchmopsis brasiliensis* (strain CPC 11017, GenBank DQ195786.1; Identities = 506/507 (99 %), no gaps), *Capturomyces luteus* (strain CBS 144839, GenBank NR_165905.1; Identities = 474/511 (93 %), 12 gaps (2 %)), and *Capturomyces funiculosus* (strain CBS 144840, GenBank NR_165904.1; Identities = 471/512 (92 %), 13 gaps (2 %)). Closest hits using the **LSU** sequence are *Satchmopsis brasiliensis* (strain CPC 11017, GenBank DQ195798.1; Identities = 857/858 (99 %), no gaps), *Cochlearomyces eucalypti* (strain CBS 142622, GenBank NG_059052.1; Identities = 828/862 (96 %), 4 gaps (0 %)), and *Pallidophorina paarla* (strain GLMC 791, GenBank MK314612.1; Identities = 824/863 (95 %), 10 gaps (1 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Chlorociboria spathulata* (strain D1822, GenBank JN985530.1; Identities = 695/887 (78 %), 8 gaps (0 %)), *Moellerodiscus lentus* (strain 10544, GenBank MH729344.1; Identities = 693/887 (78 %), 18 gaps (2 %)), and *Microscypha ellisii* (voucher KUS-F52489, GenBank JN086863.1; Identities = 687/890 (77 %), 16 gaps (1 %)). No significant hits were obtained when the ***actA***, ***tef1*** and ***tub2*** sequences were used in blastn and megablast searches. The ITS, *actA*, *rpb2* and *tef1* sequences of CPC 37378 and 37376 were identical; ITS: 508/508, *actA*: 644/644, *rpb2*: 911/911, and *tef1*: 552/552; and *tub2* almost identical: 695/701.



The single most parsimonious tree obtained from a phylogenetic analysis of the *Satchmopsis* ITS/*actA*/*rpb2*/*tef1*/*tub2* alignment (7 strains including the outgroup; 3220 characters including alignment gaps analysed: 1911 constant, 935 variable and parsimony-uninformative and 374 parsimony-informative). PAUP v. 4.0b10 (Swofford 2003) was used to analyse the data. The tree was rooted to *Erysiphe pisi* (genome GenBank GCA_000208805.1) and the scale bar indicates the number of changes. Parsimony bootstrap support values higher than 49 % are shown at the nodes and the novel species are highlighted in **bold**. Type status is indicated in superscript. Tree statistics: TL = 1572, CI = 0.964, RI = 0.880, RC = 0.849. The alignment and tree were deposited in TreeBASE (Submission ID S26166).

Colour illustrations. Beach area in Haga Haga, with *Metrosideros* in background. Conidioma on OA; conidioma on SNA; conidiomatal wall; conidia. Scale bars = 140 µm (conidiomata), 10 µm (all others).

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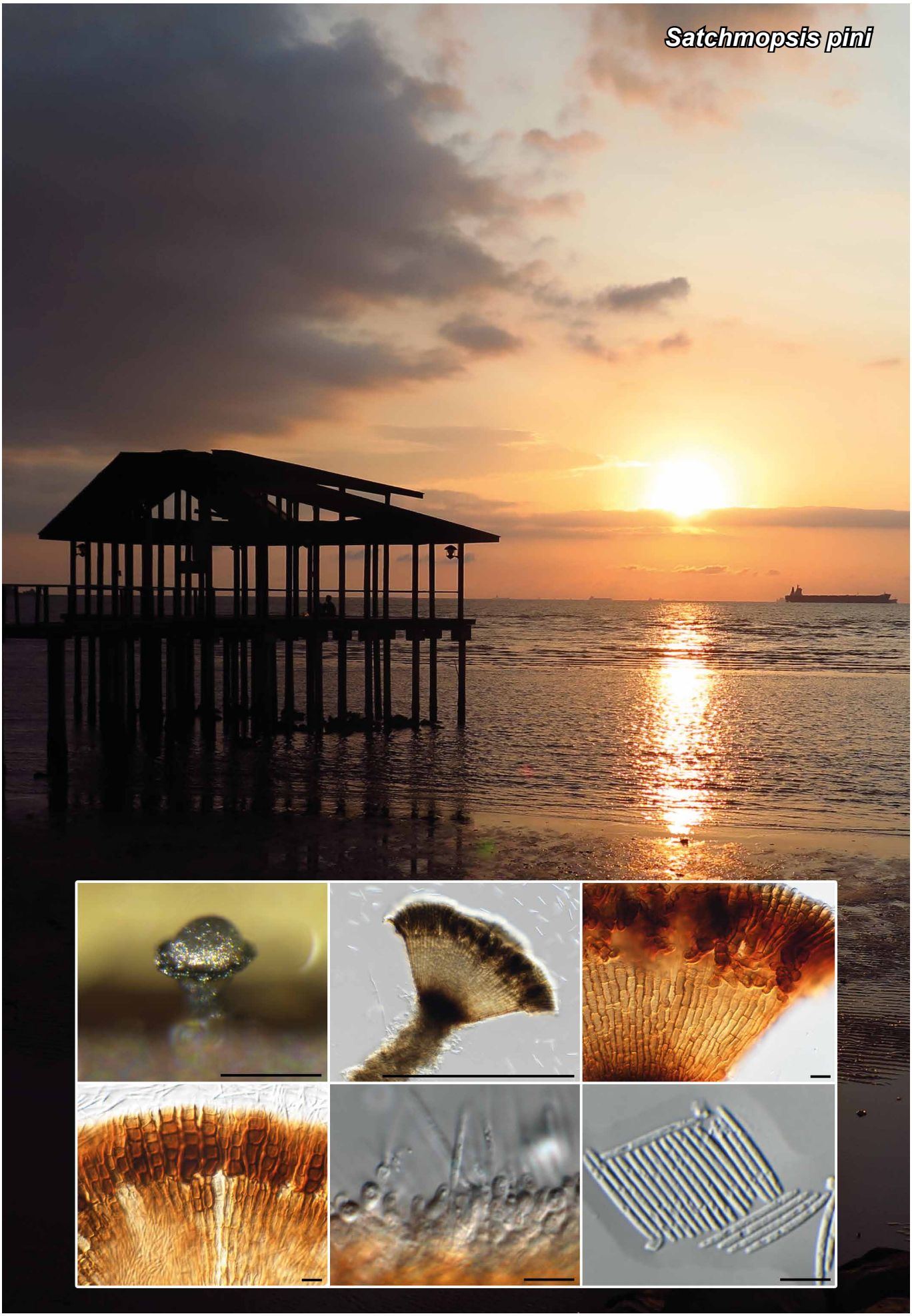
Satchmopsis pini

Fungal Planet 1056 – 29 June 2020

Satchmopsis pini Crous, *sp. nov.*

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

Classification — *Cochlearomycetaceae*, *Leotiales*, *Leotiomycetes*.

Conidiomata cupulate, superficial, 140–200 µm diam, and 120–160 µm deep, dark brown, attached centrally to a brown stroma via a dark brown stalk, up to 150 µm tall, 50 µm wide; conidiomatal wall of two regions, the lower region of brown cells, the upper region of cylindrical cells with flat to obtuse edge, 3–7 × 4–7 µm; terminal 5–13 cell layers are prominently thick-walled, darker brown, and can give rise to hyphal outgrowths on outside of conidiomatal margin. *Conidiogenous cells* restricted to lower part of basal wall, 4–10 × 2–3 µm, doliiform to lageniform, phialidic with periclinal thickening, hyaline with indistinct collarette. *Conidia* hyaline, smooth, aseptate, guttulate, subcylindrical, straight with obtuse ends, (11–)12–14(–15) × 1–1.5 µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and feathery, lobate margin, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface umber with patches of sepia, reverse umber.

Typus. Malaysia, on dead needles of *Pinus tecunumanii* (*Pinaceae*), 31 Oct. 2010, *M.J. Wingfield*, HPC 2657 (holotype CBS H-24360, culture ex-type CPC 36649 = CBS 146687; ITS, LSU, *actA*, *rpb2*, *tef1* and *tub2* sequences GenBank MT373378.1, MT373360.1, MT375096.1, MT375104.1, MT375112.1 and MT375123.1, MycoBank MB835412).

Additional material examined. Malaysia, on dead needles of *P. tecunumanii*, 31 Oct. 2010, *M.J. Wingfield*, HPC 2657, culture CPC 36729; ITS, *actA*, *rpb2* and *tef1* sequences GenBank MT373379.1, MT375097.1, MT375105.1 and MT375113.1.

Notes — *Satchmopsis pini* is morphologically distinct from *S. brasiliensis* and *S. metrosideri* in having cupulate conidiomata with a prominently thick-walled, darker brown upper region, giving rise to hyphal outgrowths on outside of conidiomatal margin. Furthermore, conidiomata are centrally attached to a brown stroma via a long, dark brown stalk, which is absent in *S. brasiliensis* and *S. metrosideri*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Satchmopsis brasiliensis* (strain CBS 420.93, GenBank DQ195784.1; Identities = 507/507 (100 %), no gaps), *Massarina corticola* (strain 4607, GenBank FR668004.1; Identities = 420/451 (93 %), 9 gaps (1 %)), and *Capturomyces luteus* (strain CBS 144839, GenBank NR_165905.1; Identities = 473/510 (93 %), 11 gaps (2 %)). Closest hits using the **LSU** sequence are *Satchmopsis brasiliensis* (strain CBS 420.93, GenBank DQ195796.1; Identities = 873/873 (100 %), no gaps), *Cochlearomyces eucalypti* (strain CBS 142622, GenBank NG_059052.1; Identities = 840/877 (96 %), 4 gaps (0 %)), and *Pragmopora* cf. *bacillifera* (voucher G.M. 2019-04-30.1, GenBank MK900749.1; Identities = 843/883 (95 %), 10 gaps (1 %)). No significant hits were obtained when the ***actA***, ***rpb2***, ***tef1*** and ***tub2*** sequences were used in blastn and megablast searches. The ITS, *actA*, *rpb2* and *tef1* sequences of CPC 36649 and 36729 were identical; ITS: 507/507, *actA*: 596/596, *rpb2*: 879/879 and *tef1*: 405/405.

Colour illustrations. Beach area in Malaysia. Conidioma on OA; conidioma on SNA; conidiomatal wall; conidiogenous cells; conidia. Scale bars = 200 µm (conidiomata), 10 µm (all others).

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Hymenotorrendiella communis

Fungal Planet 1057 & 1058 – 29 June 2020

Hymenotorrendiella communis Crous & P.R. Johnst., *sp. nov.*

Etymology. Name refers to the common occurrence of this species.

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

Apothecia scattered on leaves, at times aggregated in clusters of 2–3, erumpent, stipitate, arising from a subepidermal brown stroma. *Disc* plane to convex, greyish brown to olivaceous, smooth, 0.4–1.0 mm diam. *Receptacle* cupulate, usually darker than the hymenium, bearing dark brown setae. *Stipe* central, smooth, brown, 0.2–0.6 mm high, 180–200 µm diam. *Setae* 40–100 per apothecium, 150–300 µm long, smooth, dark brown, thick-walled, multiseptate, tip subobtusely rounded (2.5–3 µm diam), swollen at base, 9–15 µm diam. *Asci* cylindrical-clavate, apex conical-rounded, apical mechanism bluing slightly in Melzer's reagent, croziers present, 8-spored, 90–115 × 7–9 µm. *Ascospores* fusoid, aseptate, tapering towards ends, guttulate, hyaline with mucoid caps at each end, (16–)20–21(–22) × (3.5–)4 µm. *Paraphyses* simple or branched near base, obtuse, hyaline, somewhat inflated, 2.5–3 µm diam at apex.

Culture characteristics — Colonies flat, spreading, with even smooth margin and sparse to moderate aerial mycelium, covering dish after 2 wk at 25 °C. On MEA surface cinnamon with patches of hazel, reverse sienna to umber. On PDA surface amber to ochreous, reverse amber. On OA surface ochreous with patches of cinnamon.

Typus. Australia, New South Wales, La Trobe State Forest, on leaf litter of *Eucalyptus bicostata* (*Myrtaceae*), 30 Nov. 2015, *P.W. Crous*, HPC 1871 (holotype CBS H-24367, culture ex-type CPC 32835 = CBS 146703; ITS sequence GenBank MT373382.1, MycoBank MB835413).

Notes — The phylogeny and morphology of *Torrendiella* and *Hymenotorrendiella* was discussed in detail by Johnston et al. (2014). Although the name *Torrendiella eucalypti* has commonly been used for the species occurring on *Eucalyptus* leaf litter (Crous et al. 2006), Johnston et al. (2014) showed that the type of *T. eucalypti* occurred on fallen phyllodes of an *Acacia* sp. (Tasmania, Australia), which then became the type species of the new genus *Hymenotorrendiella.* However, this resulted in the common endophyte and saprobe occurring on eucalypt leaf litter not having a name. Several collections from *Eucalyptus* leaf litter were investigated in the present study, and two taxa were found to be present. The first, described here as *H. communis*, occurred in a clade with isolates from Australia, Colombia, Spain, and South Africa. Morphologically, however, the South African isolates differ from others in this clade based on macromorphology. Apothecia have shorter stalks, 100–200 µm high; setae vary from 60–80 per apothecium, but are much shorter, and wider that those from other collections in this clade, being 70–150 µm long, with obtuse apices, 4(–5) µm diam, and slightly inflated bases, 4–7 µm diam. Asci are similar however, being 85–110 × 6–8 µm, as well as ascospores, (15–)19–21(–23) × (3.5–)4 µm. *Hymenotorrendiella communis* can be distinguished from the second species, *H. indonesiana* (ascospores 17–25 × 3–4 µm), which occurs in Indonesia, by its shorter and wider ascospores.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Hymenotorrendiella indonesiana* (as *Torrendiella eucalypti*; strain 4876, GenBank FR668015.1; Identities = 522/527 (99 %), 5 gaps (0 %)), *Hymenotorrendiella andina* (as *Torrendiella andina*; strain PRJ SA193, GenBank KJ606682.1; Identities = 447/459 (97 %), no gaps), and *Hymenotorrendiella madsenii* (as *Torrendiella madsenii*; voucher PDD 58572, GenBank AY755336.1; Identities = 420/433 (97 %), 1 gap (0 %)).

Colour illustrations. *Eucalyptus* along roadside in La Trobe State Forest, where *H. communis* was collected. Apothecia with setae; cupulate receptacle with setae; asci; seta; ascus; ascospores. Scale bars: cupulate receptacle = 200 µm, all others = 10 µm.

Hymenotorrendiella indonesiana Crous & P.R. Johnst., *sp. nov.*

Etymology. Name refers to Indonesia, the country from which it was collected.

Description, Illustration & Discussion — See Crous et al. (2006), Stud. Mycol. 55: 61. 2006.

Typus. Indonesia, on *Eucalyptus urophylla* leaf litter, Mar. 2004, *M.J. Wing-field* (holotype CBS H-18041, single-ascospore cultures ex-type, CPC 11049 = CBS 115326, CPC 11050–11051; ITS, LSU and SSU sequences GenBank DQ195787.1–DQ195789.1, DQ195799.1–DQ195800.1 and DQ195810.1–DQ195811.1, MycoBank MB835414).

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 11049 had highest similarity to *Hymenotorrendiella andina* (as *Torrendiella andina*; strain PRJ SA193, GenBank KJ606682.1; Identities = 480/501 (96 %), 7 gaps (1 %)), *Hymenotorrendiella eucalypti* (voucher PDD 70105, GenBank MH578483.1; Identities = 470/495 (95 %), 7 gaps (1 %)), and *Hymenotorrendiella cannibalensis* (as *Torrendiella cannibalensis*; strain ICMP 18818, GenBank JN225947.1; Identities = 475/502 (95 %), 9 gaps (1 %)). The ITS sequences of CPC 11049, 11050 and 11051 are identical (498/498 bp). Closest hits using the **LSU** sequence of CPC 11049 are *Endoscypha perforans* (voucher PDD 102231, GenBank MK039717.1; Identities = 851/860 (99 %), no gaps), *Hymenotorrendiella madsenii* (as *Torrendiella madsenii*; strain PRJ D672, GenBank KJ606676.1; Identities = 817/829 (99 %), no gaps), and *Roesleria subterranea* (strain CBS 201.25, GenBank MH866343.1; Identities = 839/853 (98 %), no gaps).

Supplementary material

FP1057 & 1058-1 Additional materials examined - ***Hymenotorrendiella communis***

FP1057 & 1058-2 Additional materials examined - ***Hymenotorrendiella indonesiana***

FP1057 & 1058-3 The first of 28 equally most parsimonious trees obtained from a phylogenetic analysis of the *Hymenotorrendiella*

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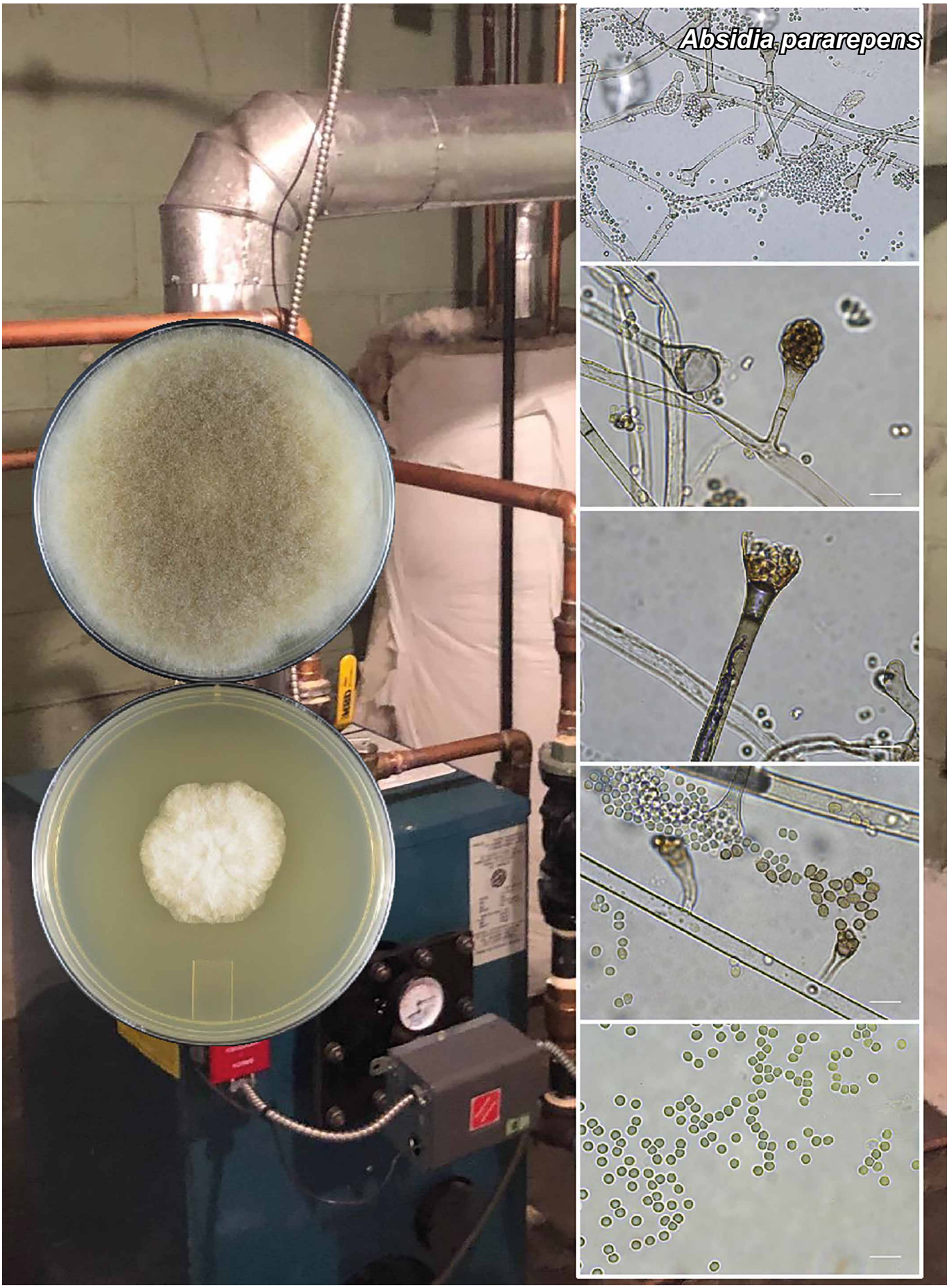
Absidia pararepens

Fungal Planet 1059 – 29 June 2020

Absidia pararepens Jurjević, M. Kolařík & Hubka, *sp. nov*.

Etymology. Refers to the phylogenetic proximity and phenotypic similarity to *A. repens*.

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

Micromorphology (on malt extract agar; MEA): *Hyphae* hyaline to brownish, coenocytic, smooth, finely roughened to definitely roughened near crustaceous, 3–13 µm diam. *Sporangiophores* hyaline to brown near dark brown, simple or branched, arising solitarily, occasionally in pairs, never grouped in whorls, arising from aerial hyphae or substrate, most commonly 10–150 × 3–6 µm; smooth, finely roughened to definitely roughened near crustaceous walls, with a single septum below the sporangium and rarely with additional septum at the base. *Sporangia* hyaline to brown to dark greyish brown, most commonly pyriform, (10–)14–24(–26) µm diam, smooth-walled. *Apophyses* funnel-shaped, smooth-walled. *Columellae* globose, hemispherical, with a short collarette, occasionally with one projection, smooth-walled, (6–)12–17(–22) µm diam. *Sporangiospores* of two types: sub-globose to globose, hyaline, smooth-walled, and oval, occasionally slightly irregular, brown, rough-walled (formed in the different sporangia), (3.3–)3.5–5(–9) × (3.3–)3.5–6 µm. *Chlamydospores* (terminal and intercalary) occasionally present in the aerial mycelia. *Zygospores* not observed.

Culture characteristics — (in darkness, 25 °C after 3 d / 7 d): Colonies on MEA 39–45/>90 mm diam, cottony, mycelium at first white, then becoming grey to grey-brown (light mouse grey to mouse grey, R51; Ridgway (1912)), abundant sporulation, reverse colonial buff to deep colonial buff (R30), smooth and wavy zonate. Colonies on potato dextrose agar (PDA 39–44/>90 mm diam, cottony, mycelium at first white, then becoming grey to grey-brown [R51), very good sporulation, reverse grey to grey with buckthorn brown shades (R15), radially sulcate. Colonies on OA 35–40/>90 mm diam, cottony, mycelium at first white, then becoming light mouse grey to mouse grey (R51), good sporulation. Colony diam at 30 °C (in mm after 7 d): MEA 4–37; PDA 4–48; OA 5–48. No growth on MEA, PDA and OA at 32 °°C.

Typus. USA, New York, Jericho, bathroom, air, 12 Dec. 2015, *Ž. Jurjević* (holotype BPI 911217, cultures ex-type CCF 6352 = CBS 146002 = EMSL 3235; ITS and LSU sequences GenBank MT193669 and MT192308, MycoBank MB834983).

Additional materials examined. USA, Maryland, Parkton, bedroom, air, 16 Nov. 2015, *Ž. Jurjević*, culture CCF 6351 = EMSL 3145 (ITS and LSU sequences GenBank MT193670 and MT192307); New Jersey, Tinton Falls, basement, air, 08 Mar. 2016, *Ž. Jurjević*, culture CCF 6353 = EMSL 3556 (ITS sequence GenBank MT193671); New York, Massapequa Park, basement, swab, 09 Aug. 2016, *Ž. Jurjević*, culture CCF 6354 = EMSL 3570 (ITS sequence GenBank MT193672); Ohio, hospital, air, 26 Sept. 2016, *Ž. Jurjević*, culture CCF 6355 = EMSL 3656 (ITS sequence GenBank MT193673); New Jersey, Marlton, basement, concrete floor, swab, 04 Apr. 2017, *Ž. Jurjević*, culture CCF 6356 = EMSL 4142 (ITS sequence GenBank MT193674).

Colour illustrations. House basement. Seven-day-old cultures of *Absidia pararepens* on MEA (top to bottom 25 °C, 30 °C); sporangiophores, sporangiospores, and chlamydospores on MEA. Scale bars = 10 µm.

Notes — BLAST analyses with the ITS and LSU sequences of *A. pararepens* showed greatest similarity with *A. repens* ex-type CBS 115583 (~87 % and ~95 % similarity, respectively). The American isolates KAS 3611 (GenBank FJ849793), FSU 939 (GenBank AY944891), CBS 101.32 = FSU 5891 (GenBank EF030527), CBS 102.32 = FSU 5892 (GenBank EF030528), NRRL 1336 (GenBank AF113448) and 14849A (GenBank AY234881) also represent *A. pararepens*, while European isolates CBS 115583 (GenBank EU484281, HM849706) and FSU 4726 (GenBank EU484288) represent *A. repens* s.str. However, this geographic pattern should be confirmed by analysis of additional strains.

Hesseltine & Ellis (1966) invalidly designated a neotype for *A. repens*. In conflict with Art. 8.4 (Turland et al. 2018), the authors selected a living culture, NRRL 1336. This culture originated from a collection of A.F. Blakeslee, and was probably isolated in America. However, as pointed out by Hoffmann et al. (2009) and Hoffmann (2010), there are large genetic differences between European and American isolates of '*A. repens*'. Consequently, the neotype of *A. repens* should be selected from among European strains in accordance with the original description of Van Tieghem (1878), who collected *A. repens* on fruit of *Bertholletia excelsa* lying on a layer of moist *Sphagnum* in France. The specimen CBS 115583 originating from England, UK, was mentioned as isotype of *A. repens* by Hoffmann et al. (2009) and Hoffmann (2010), but formal typification has never been published.

To formalize the typification, we designate here a lectotype of *A. repens* (illustration from the original material): pl. 12, f. 55–63 (not paginated) in P. van Tieghem, *Annales des Sciences Naturelles Botanique* Ser. 6, Vol. 4. 1878 [1876]. MycoBank typification no. is MBT392665. Epitype designated here: specimen CBS 115583 (preserved in metabolically inactive state), ex-epitype culture CBS 115583. MycoBank typification no. is MBT392666).

Absidia pararepens has on average shorter sporangiophores (10–150 × 3–6 µm), and larger sporangiospores ((3.3–)3.5–5(–9) × (3.3–)3.5–6 µm) than the closely related *A. repens* ((50–)140–250(–450) × 2.5–6 µm), and (2.8–5.5(–6.5) × 2–3 µm), respectively.

Supplementary material

FP1059 A best scoring maximum likelihood tree based on the ITS region sequences shows the relationships of *Absidia pararepens* sp. nov. with other species.

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Annulohypoxylon spougei

Fungal Planet 1060 – 29 June 2020

Annulohypoxylon spougei Suwannasai, M.P. Martín, Phosri & Whalley, *sp. nov.*

Etymology. Named after the American bioinformatician John L. Spouge who contributed to the discovery of this species, and for his efforts to implement tools for DNA barcoding analyses within the genus *Annulohypoxylon*.

Classification — *Hypoxylaceae*, *Xylariales*, *Sordariomycetes*.

Stromata glomerate to hemispherical, effused-pulvinate, with perithecial mounds 1/4 to 2/3 exposed and not covered by the outermost stromatal layer, 0.3–6 cm long × 0.3–3 cm broad and 1–1.6 mm thick; surface dark brown vinaceous, becoming black with reddish brown hues, finally black and shiny; black granules immediately below the surface, KOH pigments green olivaceous. *Perithecia* spherical, 0.5–0.7 mm diam. *Ostioles* conical papillate, surrounded by a flattened *bovei*-type disc, 0.2–0.5 mm diam. *Asci* 62–114 × 4–4.5 µm, the spore bearing parts 64–73 µm long with stipes 20–32(–46) µm long, with apical ring bluing in Melzer's iodine reagent, discoid 0.7 µm high × 1.5–2 µm broad. *Ascospores* pale brown, unicellular, ellipsoid-inequilateral with narrowly rounded ends, 6–10.5 × 3–4.5(–5.5) µm with straight germ slit along the full length of the spore; perispore dehiscent in 10 % KOH, epispore smooth.

Culture characteristics — Colonies on potato dextrose agar (PDA) covering Petri dish in 2 wk, at first white, becoming hazel to dull green, azonate, with diffuse margins, with scattered black patches; reverse dull green to dark brown. *Conidiogenous structure* nodulisporium-like, brown. *Conidia* hyaline, smooth, ellipsoid, 3.5–4.5 × 2–3 µm.

Typus. Thailand, Phitsanoluk, Khao KraYang Forest Planation, on corticated wood, Sept. 2006, *C. Phosri & N. Suwannasai* H099 (holotype SWUF-H099; ITS, α-actin and β-tubulin sequences GenBank FN252419, FR875158 and KP134519, MycoBank MB811164).

Additional materials examined. Herbarium number is indicated, as well as the ITS, α-actin, β-tubulin and *EF1-α* GenBank sequences between brackets, absent sequences are indicated with '–'. ***Annulohypoxylon spougei***: Thailand, Phitsanulok Province, *Dipterocarpaceae* forest, Sept. 2006, *C. Phosri & N. Suwannasai* SWUF-H087 (FN252418, KP134506, FR875164, –); SWUF-H181 (FN252420, KP134507, KP134520, –); SWUF-H203 (FN252421, FR875159, FR875165, –); SWUF-H215 (FN252422, KP134508, KP134521, –); SWUF-H254 (FN252423, FR875160, FR875166, –); Nakhon Ratchasima Province, *Dipterocarpaceae* forest, July 2003, *N. Suwannasai* SUT081 (DQ322105, –, –, –); Trad Ratchasima Province, *Dipterocarpaceae* forest, Aug. 2003, *C. Phosri & N. Suwannasai* SUT236 (DQ322106, –, –, –); SUT242 (DQ322107, –, –, –); SUT244 (DQ322108, –, –, –); SUT251 (DQ322109, –, –, –); Kanchanaburi Province, *Dipterocarpaceae* forest, Aug. 2003, *N. Suwannasai* SUT285 (DQ322110, –, –, –); Chaiyaphum Province, *Dipterocarpaceae* forest, June 2009, *C. Phosri & N. Suwannasai* PK09007 (KP134526, KP134509, KP134522, KP134499); PK09026 (KP134527, KP134510, –, KP134500); PK09027 (KP134528, KP134511, –, KP134500); PK09029 (KP134529, KP134512, –, –). ***Annulohypoxylon nitens***: Thailand, Chiang Rai Province, *Dipterocarpaceae* forest, Sept. 2006, *C. Phosri & N. Suwannasai* SWUF-H154 (FM209453, FR875161, KP134513, –); SWUF-H157 (FM209455, FR875162, KP134514, –); Phitsanulok Province, *Dipterocarpaceae* forest, Sept. 2006, *C. Phosri & N. Suwannasai* SWUF-H189 (FM209459, KP134502, FR875167, –); SWUF-H197 (FM209461, FR875163, KP134515, –); Chaiyaphum Province, *Dipterocarpaceae* forest, June 2009, *C. Phosri & N. Suwannasai* PK121044 (KP134523, KP134503, KP134516, KP134496); PK121063 (KP134524, KP134504, KP134517, KP134498); PK121086 (KP134525, KP134505, KP134518, KP134497).

Notes — During extensive studies of the *Hypoxylaceae* in Thailand over a period of almost 20 yr, problems were encountered in the identification of several taxa, especially *A. nitens.* A previous study on species of *Hypoxylon* and *Annulohypoxylon* using morphology and ITS nrDNA sequences (Suwannasai et al. 2013) indicated that this taxon was not monophyletic but could be separated into *A. nitens* and another species. Twenty-eight fungal specimens of *A. nitens* and a cryptic species collected from Thailand, previously named '*A. nitens*' in our study (Suwannasai et al. 2013), were carefully re-analysed based on morphological and asexual morph characters. The comparison of morphological characters between *A. nitens* and a cryptic species showed unclear distinction of these species. The cryptic species, here named as *A. spougei* possesses spherical perithecia (0.5–0.7 mm diam), which are slightly narrower than those of *A. nitens* described by Ju & Rogers (1996) ((0.4–)0.5–1(–1.2) mm). The ostiolar discs of both species groups are *bovei*-type and have the same dimensions of 0.2–0.5 mm. Ascospore sizes of *A. nitens* and the cryptic species are 7.5–9 × 2.8–4.2 µm and 6–10.5 × 3–4.5(–5.5) µm, respectively. These are similar to the species description for *A. nitens* (as *H. nitens*) (6.5–10(–11) × 3–4.5 µm) from Ju & Rogers (1996). The cultural and asexual morph characters were observed from both PDA and oatmeal agar. Colonies of *A. spougei* are white at first becoming hazel and dull green with scattered black patches. The asexual morph is nodulisporium-like and conidial size (3.5–4.5 × 2–3 µm) is similar to *A. nitens* (4–5 × 2.5–3 µm). With those similar features, it is very difficult to separate the *A. spougei* from *A. nitens* by using only morphological and asexual morph characters. However, although morphological data for all of the collections initially identified as *A. nitens* failed to provide clear separation of the two entities, there are clear supporting DNA data for their separation. In the present study based on α-actin, β-tubulin and elongation factor 1-α sequences, we confirm the separation of two taxa mentioned in Suwannasai et al. (2013).

Colour illustrations. Thailand, Chaiyaphum Province, Phu Khiao Wildlife Sanctuary, where the specimens were collected. From top to bottom: stromata with ostiolar discs (SWUF-H099); ascospores under SEM (SWUF-H099); fungal culture on PDA (SWUF-H099); nodulisporium-like anamorph (SWUF-H099); ascospores with apical apparatus (SWUF-H099). Scale bars = 0.5 mm (stromata), 5 µm (ascospores SEM), 1 cm (fungal culture), 15 µm (asexual morph), 5 µm (ascospores)

Supplementary material

FP1060 UPGMA reconstruction based on K2P distances of α-actin, β-tubulin and *EF1-α* sequences of *Annulohypoxylon nitens* and *A. spougei* specimens using PAUP* v. 4.0b10 (Swofford 2003).

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Aspergillus banksianus

Fungal Planet 1061 – 29 June 2020

Aspergillus banksianus Pitt, *sp. nov*.

Etymology. Named for the Australian endemic tree *Banksia integrifolia*, from the rhizosphere of which this species was isolated.

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

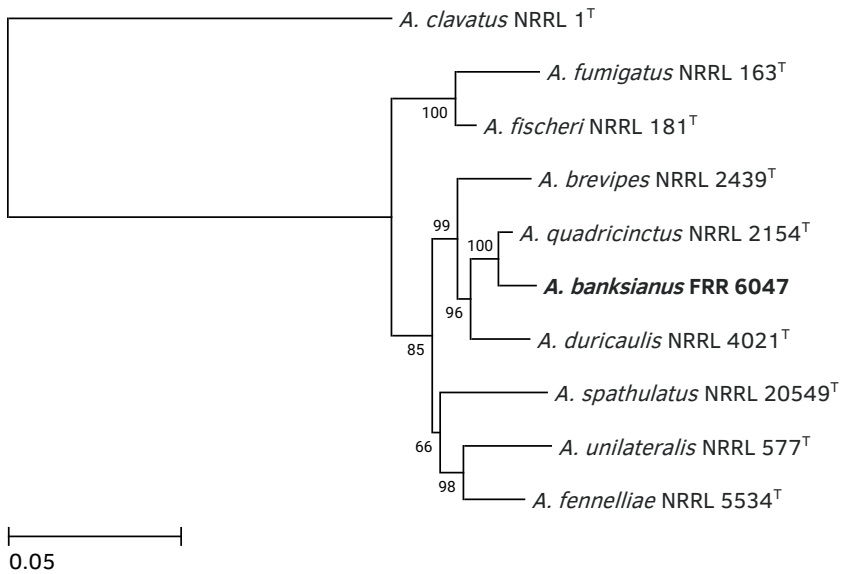
Culture characteristics — Czapek yeast extract agar (CYA), 25 °C, 7 d: Colonies 25–30 mm diam, low and dense, plane or irregularly wrinkled, with narrow margins of white mycelium; conidiogenesis moderate to heavy, dark grey to dark grey blue (M. 24–25D–E2–3); exudate absent, soluble pigment brown; reverse Deep Green (M. 29F3–4). MEA, 25 °C, 7 d: Colonies 40–45 mm diam, low and plane, with wide uncoloured margins, light to heavily sporing, coloured as on CYA or slightly greener (M. 26D3); exudate and soluble pigment absent; reverse centrally Dark Green (M. 27F5), paler towards the margins. 25 % Glycerol nitrate agar (G25N), 25 °C, 7 d: Colonies up to 5 mm diam, of white mycelium. 37 °C, CYA, 7 d: Colonies 40–45 mm diam, heavily sporing, dull green to grey green; reverse dark green, greyish green or black.

Conidiophores borne from aerial hyphae, sometimes unbranched, and then (5–)50–120 × 2.5–3 µm, sometimes bearing a short lateral stipe 10–40 µm long as well; broadening slowly to spathulate vesicles, 5–15 µm diam, fertile area characteristically hemispherical but sometimes asymmetrical to give a 'nodding' appearance. *Phialides* short and stout, 3.5–6 × 2.5–3 µm, with narrow bases and very short narrow necks, sometimes almost ellipsoidal. *Conidia* 2.5–3 µm diam, smooth to finely roughened, borne in short disordered chains, separating in wet mounts.

Media formulations are from Pitt & Hocking (2009); (M.) colours are from Kornerup & Wanscher (1978).

Typus. Australia, New South Wales, Collaroy, from rhizosphere soil beneath a specimen tree of the endemic species *Banksia integrifolia* (*Proteaceae*), 2004, *A.-L. Markovina* (holotype DAR 85042, cultures ex-type FRR 6047 = MST FP2248; ITS, *BenA*, *CaM* and *RPB2* sequences GenBank MH280013, MT184780, MT184786, MT184792, MycoBank MB835223).

Notes — *Aspergillus banksianus* clusters in *Aspergillus* subgenus *Fumigati*, in a small clade that includes *A. brevipes* and *A. duricaulis*, with which it shares slow growth at 25 °C, green conidial colouration and intermittent production of asymmetrical fruiting structures. Colonies of *A. banksianus* on CYA have a deep green reverse colour, in contrast with *A. duricaulis*, 'colorless to pinkish drab' or *A. brevipes* 'becoming purple-red' (Raper & Fennell 1965). Molecularly, *A. banksianus* is particularly close to *A. quadricinctus*, from which the most obvious difference is lack of the *Neosartorya* sexual morph. *Aspergillus banksianus* when grown on agar, liquid media or grain, displays a unique chemotaxonomic profile comprising banksialactones A-I, and banksiamarins A and B, which are not present in the closely related species *A. quadricinctus* and *A. duricaulis* (Chaudhary et al. 2018). *Aspergillus banksianus* also produces known metabolites clearanol and dothideomynone A, together with the pigments endocrocin and questin previously reported from other *Aspergillus* species.



A maximum likelihood tree inferred from the combined ITS, *BenA*, *CaM* and *RPB2* sequences of taxa within *Aspergillus* sect. *Fumigati*. The combined sequence alignment was partitioned by marker; substitution models for each partition were chosen according to the Bayesian Information Criteria using ModelTest-NG v. 0.1.6 (Darriba et al. 2020). The TrN+I model was used for ITS sequences, K80+G4 for *BenA*, TrNef+G4 for *CaM* and TIM2ef+I+G4 for *RPB2*. The tree was constructed using RAxML-NG v. 0.9.0 (Kozlov et al. 2019). Bootstrap support values are derived from 1 000 bootstrap replicates. Alignment available in TreeBASE (study S25912).

Colour illustrations. A specimen tree of the endemic species *Banksia integrifolia*, planted on a street in Collaroy, NSW, from under which a soil sample included *A. banksianus*. Colonies grown on CYA (upper) and malt extract agar (MEA) (lower) for 7 d at 25 °C; fruiting structures and conidia. Scale bars = 10 µm (fruiting structures) and 5 µm (conidia).

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Aspergillus oxumiae

Fungal Planet 1062 – 29 June 2020

Aspergillus oxumiae C.N. Figueiredo, L.S. Sales, Y.F. Figueiredo, J.P. Andrade & J.T. De Souza, *sp. nov*.

Etymology. *oxumiae*, in honour of Oxum, a female African deity from the Yoruba religion.

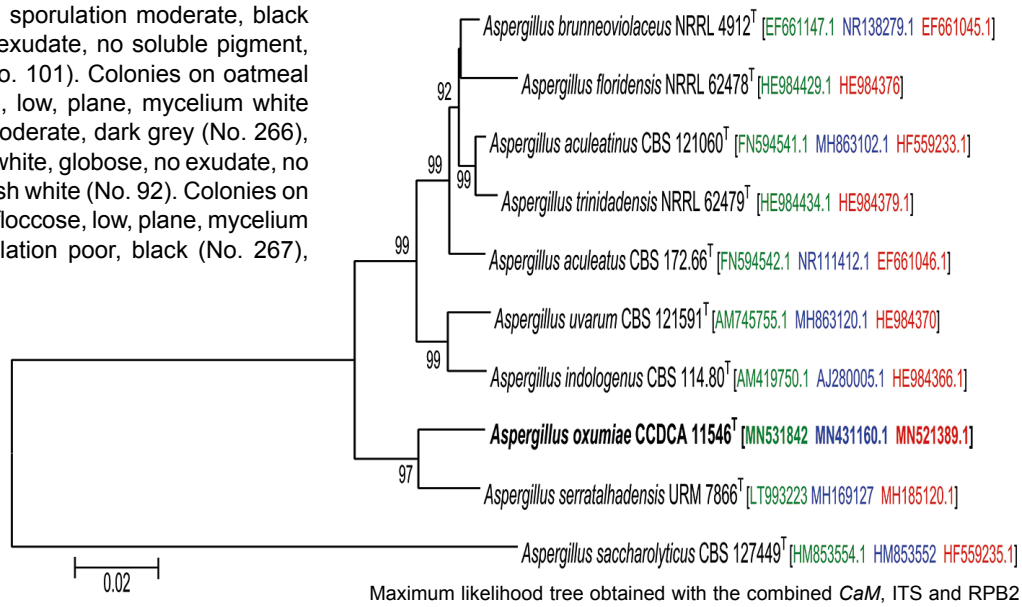
Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetes*.

Conidial heads radiate. *Conidiophores* uniseriate. *Stipes* smooth, frequently septate 48–890(–931) × 2–5(–7) µm, sometimes with subterminal branches and mycelial coils occasionally present. *Vesicles* pyriform to subglobose, pigmented, 8–20(–30) × 6.5–21(–30) µm (av. 12 ± 3.6 × 11 ± 3.2), phialides 4–13(–20) × 2–8 µm (av. 8 ± 2.7 × 4 ± 1.0) covering half to upper half of vesicle. *Conidia* globose to subglobose, 3–7 × 3.5–7 µm (av. 5 ± 0.77 × 5 ± 0.81), brown to greyish brown, with coarsely roughened to echinulate surface, average width/length = 1 ± 0.03, n = 74. *Sclerotia* observed.

Culture characteristics — Colonies on Czapek yeast autolysate agar (CYA 46–47 mm diam at 25 °C in 7-d-old, lanose to floccose, radially and concentrically wrinkled, mycelium white (ISCC-NBS No. 263), sporulation poor to abundant, dark greyish yellowish brown (No. 81) to black (No. 267), sclerotia abundant, white, globose, no exudate, no soluble pigment, reverse brownish pink (No. 33), yellowish white (No. 92), dark greyish olive (No. 111). Colonies on Blakeslee's malt extract agar (MEAbl) 53–54 mm, floccose, radially and concentrically wrinkled, mycelium white (No. 263), sporulation moderate to abundant, dark olive brown (No. 96), olive black (No. 114), sclerotia moderate, white, globose, no exudate, no soluble pigment, reverse pale yellow (No. 89), greyish yellow (No. 90). Colonies on yeast extract sucrose agar (YES) 27–28 mm, lanose, irregularly wrinkled, mycelium white (No. 263), sporulation moderate, black (No. 267), sclerotia absent, no exudate, no soluble pigment, reverse light greenish yellow (No. 101). Colonies on oatmeal agar (OA) 46–48 mm, floccose, low, plane, mycelium white (No. 263), sporulation poor to moderate, dark grey (No. 266), black (267), sclerotia abundant, white, globose, no exudate, no soluble pigment, reverse yellowish white (No. 92). Colonies on Czapek's agar (CZ) 50–52 mm, floccose, low, plane, mycelium yellowish white (No. 92), sporulation poor, black (No. 267), sclerotia absent, no exudate, no soluble pigment, reverse yellowish white (No. 92). Colonies on CYA with 5 % NaCl (CYAS) 23–25 mm, floccose, irregularly wrinkled, mycelium white (No. 263), sporulation poor to abundant, dark yellowish brown (No. 78), sclerotia absent, no exudate, no soluble pigment, reverse pale yellow (No. 89), dark greyish yellow (No. 91). Colonies on creatine sucrose agar (CREA) 19–22 mm, moderate mycelial growth, sclerotia absent, no acid production. The isolate did not grow in CYA at 10, 37 and 42 °C, but grows at 15 °C 20–22 mm, 20 °C 33–34 mm, 30 °C 32–33 mm and 33 °C 29–31.

Typus. Brazil, Bahia, municipality of Campo Formoso, S10°30' W40°19', in soil cultivated with *Agave sisalana*, 20 Oct. 2007, *J.R.Q. Silva* (holotype HURB 22369 - dried culture on MEAbl; culture ex-type CCDCA 11546 = UFLA115; ITS, LSU, *CaM*, *ben*A and *RPB2* sequences GenBank MN431160.1, MN508996, MN531842, MN521388 and MN521389, MycoBank MB832766).

Notes — *Aspergillus oxumiae* is phylogenetically related to the species *A. serratalhadensis* included in sect. *Nigri*, but it is clearly a different species. The morphological characteristics distinguishing *A. oxumiae* from *A. serratalhadensis* are: *A. oxumiae* grows slower on CYA and YES 25 °C and grows faster on OA 25 °C. *Aspergillus oxumiae* does not produce acid on CREA, the stipes and phialides are bigger and the vesicles are smaller. All macroscopic and microscopic measurements were done twice, independently, for isolate CCDCA 11546.



Maximum likelihood tree obtained with the combined *CaM*, ITS and RPB2 sequences from *A. oxumiae* and phylogenetically related species in section *Nigri* performed in MEGA v. 6.06 software (Tamura et al. 2013) employing the TN93+G model with 1000 bootstrap re-samplings. Bootstrap support values (BS > 80 %) are presented at the nodes. *Aspergillus saccharolyticus* CBS 127449^{T} was used as outgroup. The new species is presented in **bold** font (^{T} = ex-type). GenBank accession numbers are given after each strain (*CaM* = green, ITS = blue and *RPB2* = red).

Colour illustrations. *Agave sisalana*. Seven-day-old colonies growing at 25 °C, top row left to right, obverse CYA, MEAbl and CREA; bottom row left to right, reverse CYA, MEAbl and obverse OA; conidiophores, conidia and coiling of mycelia. Scale bars = 10 µm.

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Aspergillus kumbius

Fungal Planet 1063 – 29 June 2020

Aspergillus kumbius Pitt, *sp. nov*.

Etymology. Named for the small town of Kumbia, South Burnett District, Queensland, Australia, near where this species was collected.

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

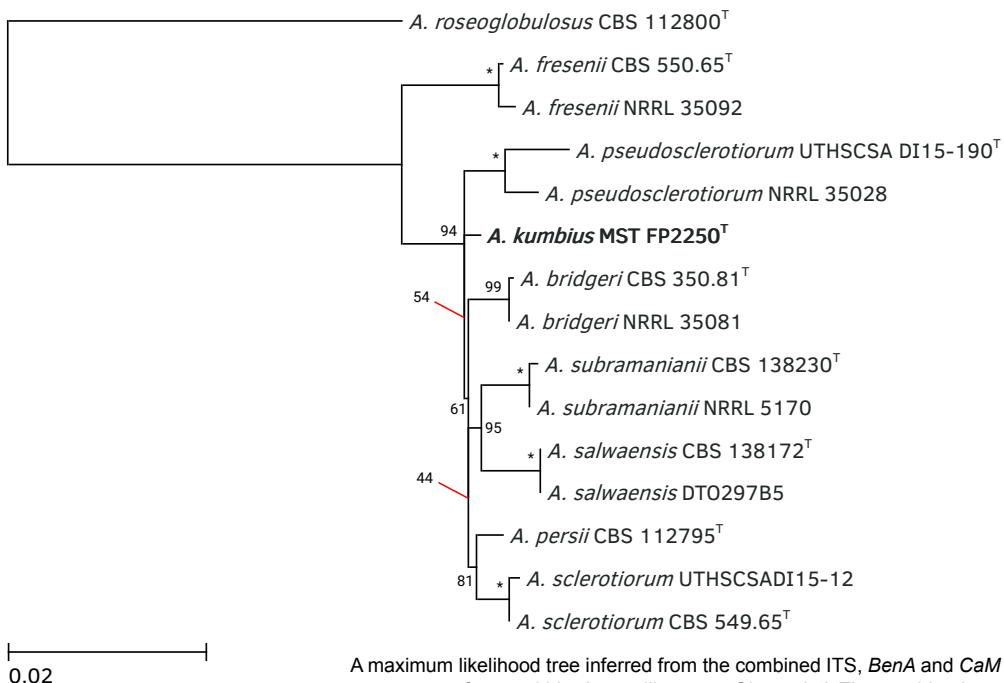
Conidiophores borne from aerial hyphae, stipes 300–400(–600) × 5–6 µm, uncoloured to pale brown, smooth walled. *Vesicles* spherical, 15–25 µm diam, fertile over the upper hemisphere or two thirds; metulae 6–8 × 2.5–3.0 µm; phialides acerose, 7–8 × 2.0–2.2 µm. *Conidia* spherical, 2.2–2.5 µm diam, walls smooth to finally roughened, borne in disordered chains.

Culture characteristics — Czapek yeast extract agar (CYA), 25 °C, 7 d: Colonies 45–50 mm diam, plane, low and relatively sparse, lightly sulcate, velutinous; margins entire, wide; mycelium white to pale yellow; abundant sclerotia borne on the agar surface, white at first, at maturity pale orange to orange grey (M. 5A–B3), spherical or near, 400–800 µm diam; conidial production sparse, pale yellow brown (M. 4–5A3); clear to pale brown exudate produced; soluble pigment absent; reverse pale yellow. Malt extract agar (MEA), 25 °C, 7 d: Colonies 50–55 mm diam, low, plane, sparse and velutinous; margins subsurface, entire; mycelium inconspicuous, white to pale yellow brown; sclerotia moderately abundant, as on CYA except sometimes enveloped in fine white hyphae; conidial production light, yellow brown (M. 4A–B3), exudate and soluble pigment not produced; reverse uncoloured to pale orange. 25 % Glycerol nitrate agar (G25N), 25 °C, 7 d: Colonies 26–30 mm diam, of white mycelium; reverse uncoloured. 37 °C, CYA, 7 d: Colonies 6–12 mm diam, of white mycelium, reverse pale.

Media formulations are from Pitt & Hocking (2009); (M.) capitalised colours and notations are from Kornerup & Wanscher (1978).

Typus. Australia, Queensland, Kumbia, from rhizosphere soil beneath pasture, 2004, *J.I. Pitt* (holotype DAR 85044, cultures ex-type FRR 6049 = MST FP2250 = CBS 146722; ITS, *BenA*, *CaM* and *RPB2* sequences GenBank MT179307, MT184782, MT184788 and MT184794, MycoBank MB835225).

Notes — *Aspergillus kumbius* belongs in *Aspergillus* subgenus *Circumdati* sect. *Circumdati*. Molecularly, it is very close to *Aspergillus bridgeri* and *A*, *subramanianii*. It is distinguished by rapid growth at 25 °C with abundant buff coloured spherical sclerotia. When grown on agar, liquid media or grain, *A. kumbius* displays a unique chemotaxonomic profile including kumbicins A–D, which are not present in the closely related species *A. bridgeri*, *A. subramanianii*, *A. salwaensis*, *A. persii* or *A. sclerotiorum*. *Aspergillus kumbius* also produces known metabolites asterriquinol D dimethyl ether, petromurins C and D, aspochracin, JBIR-15, and neohydroxyaspergillic acid, compounds previously reported from other *Aspergillus* species.



A maximum likelihood tree inferred from the combined ITS, *BenA* and *CaM* sequences of taxa within *Aspergillus* sect. *Circumdati*. The combined sequence alignment was partitioned by marker; substitution models for each partition were chosen according to the Bayesian Information Criteria using ModelTest-NG v. 0.1.6 (Darriba et al. 2020). The HKY model was used for ITS sequences, K80+G4 for *BenA* and K80 for *CaM*. The tree was constructed using RAxML-NG v. 0.9.0 (Kozlov et al. 2019). Bootstrap support values are derived from 1 000 bootstrap replicates. Alignment available in TreeBASE (study S25913).

Colour illustrations. A scene of pasture near Kumbia, Queensland, similar to the one from which this species was described. Colonies grown on CYA (left) and MEA (right) for 7 d at 25 °C; fruiting structures and conidia. Scale bars = 20 µm (fruiting structures) and 5 µm (conidia).

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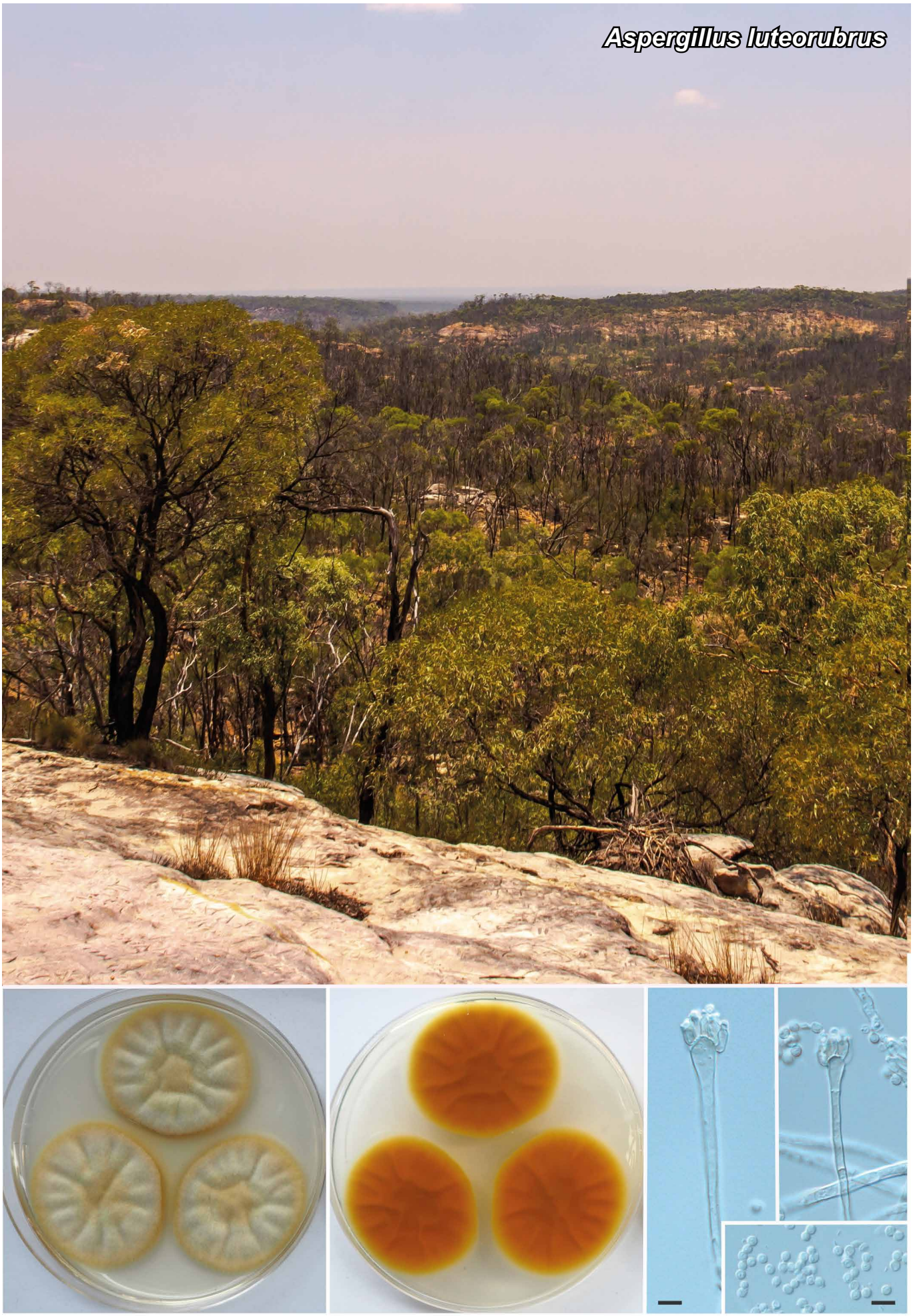

Aspergillus luteorubrus

Fungal Planet 1064 – 29 June 2020

Aspergillus luteorubrus Pitt, *sp. nov*.

Etymology. Named for the colony colours on CYA plates: Latin *luteus*, yellow and *ruber*, red.

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

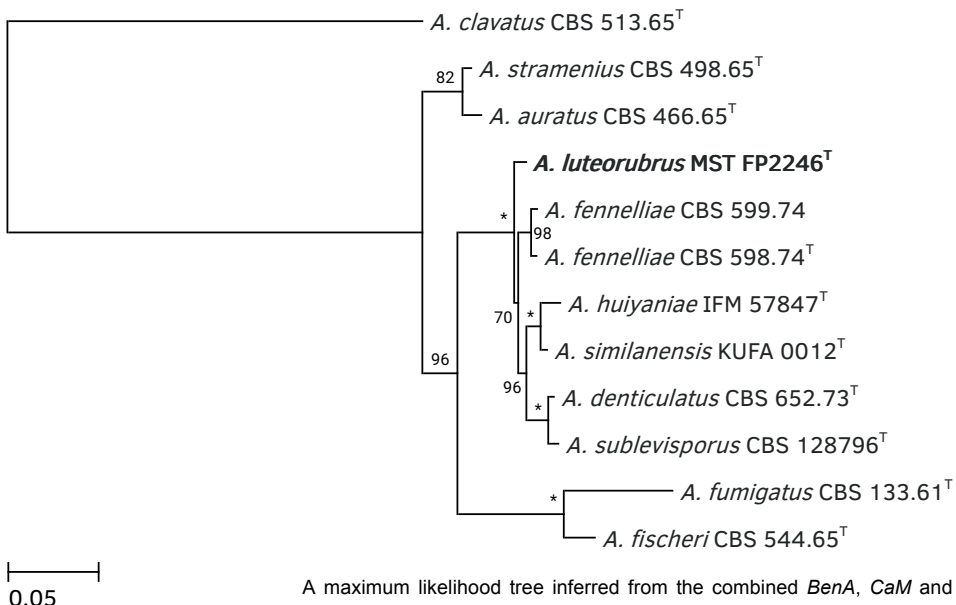
Conidiophores borne from aerial hyphae, slender, (40–)100–200(–300) × 2–2.5 µm, with thin smooth walls, enlarging slowly to very small spathulate vesicles, 4–6(–7) µm diam; bearing few short phialides, 5–7 × 2.5–3 µm. *Conidia* spherical, 2–2.5 µm diam, smooth-walled, borne in short disordered chains.

Culture characteristics — Czapek yeast extract agar (CYA), 25 °C, 7 d: Colonies 38–42 mm diam, dense and velutinous, plane or lightly wrinkled; margins low to moderately deep, entire; mycelium pale yellow (M. 3–4A2–3); sporulation very light, inconspicuous or pale brown (M. near 4B3); exudate absent, soluble pigment sometimes produced, pale yellow; reverse bright yellow at the margins, otherwise intensely coloured, Cadmium Orange to Brownish Red (M. 5–8A–C8). Malt extract agar (MEA), 25 °C, 7 d: Colonies 50–60 mm diam, plane, dense and velutinous to floccose; mycelium white to very pale yellow, in age becoming bright yellow (M. 4A3) centrally; sporulation inconspicuous; exudate and soluble pigment absent; reverse centrally Cadmium Orange (M. 5–6A–B7–8), paler yellow (M. 4A4–4A8) towards the margins. 25 % Glycerol nitrate agar (G25N), 25 °C, 7 d: Colonies 10–12 mm diam; pale yellow. 37 °C, CYA, 7 d: Colonies 55–60 mm diam, of white or pale yellow mycelium; reverse Amber to Yolk Yellow (M. between 3 and 4B7–8).

Media formulations are from Pitt & Hocking (2009); (M.) capitalised colours and notation are from Kornerup & Wanscher (1978).

Typus. Australia, Queensland, White Mountains National Park, from soil in a dry creek bed, 2004, *J.I. Pitt* (holotype DAR 85045, cultures ex-type FRR 5427 = MST FP2246 = CBS 146723; ITS, *BenA*, *CaM* and *RPB2* sequences MT179305, MT184781, MT184787 and MT184793, MycoBank MB835226).

Notes — *Aspergillus luteorubrus* clusters in *Aspergillus* subg. *Fumigati*, near *A. fennelliae*. This heterothallic species produces cleistothecia and ascospores characteristic of the sexual genus *Neosartorya*. As only a single strain of *A. luteobrunneus* is known, it is not clear whether this is an asexual species or, perhaps more likely, heterothallic. *Aspergillus luteorubrus* differs from this and other closely related species in colony colours, conidial size, shape and ornamentation. Differences also exist in molecular phylogeny and chemistry (unpubl. data).



A maximum likelihood tree inferred from the combined *BenA*, *CaM* and actin sequences of taxa within *Aspergillus* sect. *Fumigati*. The combined sequence alignment was partitioned by marker; substitution models for each partition were chosen according to the corrected Information Criteria using ModelTest-NG v. 0.1.6 (Darriba et al. 2020). The K80+G4 was used for *BenA* sequences, K80+G4 for *CaM* and TPM+I for actin. The tree was constructed using RAxML-NG v. 0.9.0 (Kozlov et al. 2019). Bootstrap support values are derived from 1 000 bootstrap replicates. Alignment in TreeBASE (study S25915).

Colour illustrations. View out over White Mountains National Park. Colonies of *Aspergillus luteorubrus* grown on CYA, left obverse, right reverse, for 7 d at 25 °C; fruiting structures and conidia. Scale bar = 5 µm.

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Aspergillus malvicolor

Fungal Planet 1065 – 29 June 2020

Aspergillus malvicolor A.D. Hocking, *sp. nov*.

Etymology. Named for the distinctive colour of the conidia. Latin *malvicolor*, mauve.

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

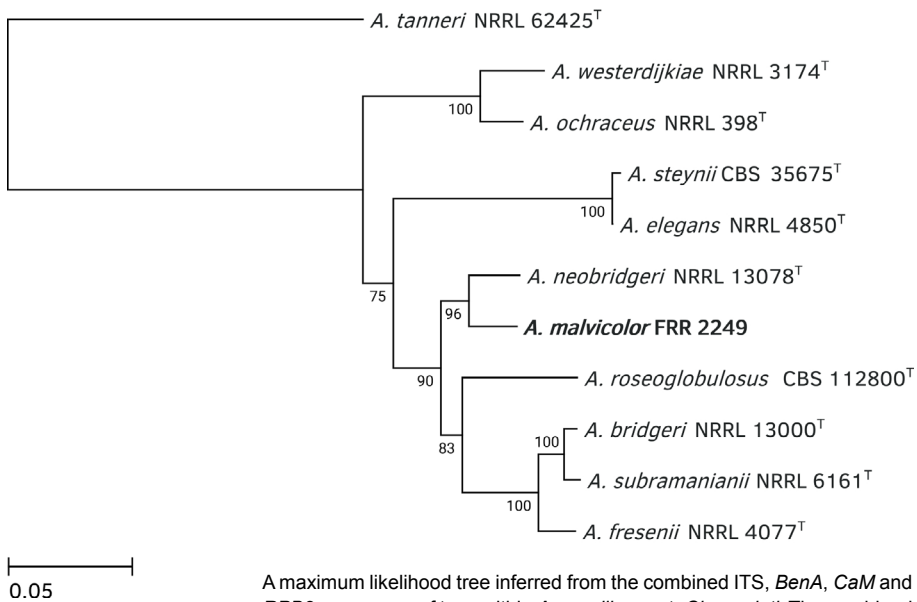
Conidiophores borne from subsurface or surface hyphae, stipes non-septate, 700–1000 × 8–10 µm, with thick, pale brown walls, often finely roughened, with small and undistinguished footcells. *Vesicles* 35–50 µm diam, sometimes with pinkish walls, bearing metulae and phialides over the entire surface area. *Metulae* mostly 8–10(–20) × 3–3.5(–5) µm; phialides closely packed, acerose, 8–10 × 2–2.5 µm. *Conidia* spherical, small, 2–2.2(–2.5) µm diam, with smooth to finely roughened walls, borne in radiate heads.

Culture characteristics — Czapek yeast extract agar (CYA), 25 °C, 7 d: Colonies 35–40 mm diam, plane or lightly radially sulcate, low to moderately deep; margins low, entire; mycelium inconspicuous; conidiogenesis heavy, coloured pink at the margins, grading to Greyish Magenta (M. 13C3) at the centres; colourless exudate sometimes produced; soluble pigment absent; reverse brown or pinkish brown. Malt extract agar (MEA), 25 °C, 7 d: Colonies 50–55 mm diam, low, plane and relatively sparse; margins subsurface to entire, low; mycelium pink or brown; sporulation heavy, coloured as on CYA; exudate and soluble pigment absent; reverse yellow brown. 25 % Glycerol nitrate agar (G25N), 25 °C, 7 d: Colonies 20–25 mm diam, low and dense, mycelium inconspicuous, moderately sporing in pink shades, reverse pinkish brown. 37 °C, CYA, 7 d: Colonies 15–20 mm diam, of pinkish brown mycelium, reverse pale to brown.

Media formulations are from Pitt & Hocking (2009); (M.) colour is from Kornerup & Wanscher (1978).

Typus. Australia, Queensland, Kingaroy, from rhizosphere soil beneath a commercial crop of peanuts (*Arachis hypogaea*), 1979, *A.D. Hocking* (holotype DAR 85046, cultures ex-type FRR 2383 = MST FP2244 = CBS 146724; ITS, *BenA*, *CaM*, *RPB2* sequences GenBank MT179308, MT184784, MT184790, MT184796, MycoBank MB835227).

Notes — *Aspergillus malvicolor* clusters in *Aspergillus* subg. *Circumdati*, sect. *Circumdati*, where it is related to *A. ochraceus*. It differs from all described species of *Aspergillus* by the mauve colour of its conidia. Phylogenetically, the nearest related species is *A. neobridgeri*, from which it is distinguished by conidial colour, by growth rate at 37 °C, and in metabolite production (unpubl. data).



A maximum likelihood tree inferred from the combined ITS, *BenA*, *CaM* and *RPB2* sequences of taxa within *Aspergillus* sect. *Circumdati*. The combined sequence alignment was partitioned by marker; substitution models for each partition were chosen according to the Bayesian Information Criteria using ModelTest-NG v. 0.1.6 (Darriba et al. 2020). The TrNef+I model was used for ITS sequences, K80+G4 for *BenA*, TrNef+G4 for *CaM* and *RPB2*. The tree was constructed using RAxML-NG v. 0.9.0 (Kozlov et al. 2019). Bootstrap support values are derived from 1 000 bootstrap replicates. Alignment available in TreeBASE (study S25914).

Colour illustrations. A commercial peanut crop, near Kingaroy, Queensland, similar to the one from under which this species was described. Colonies grown on CYA (left) and MEA (right) for 7 d at 25 °C; fruiting structures and conidia. Scale bars = 50 µm (fruiting structures) and 5 µm (conidia).

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Aspergillus nanangensis

Fungal Planet 1066 – 29 June 2020

Aspergillus nanangensis Pitt, *sp. nov*.

Etymology. Named for the town of Nanango, South Burnett District, Queensland, Australia, near which this species was collected.

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

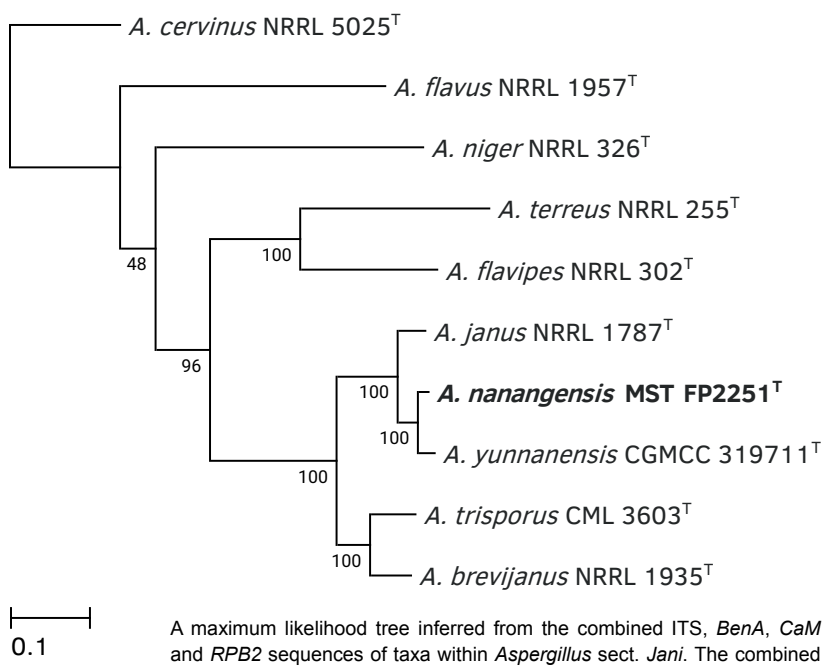
Conidiophores borne from surface hyphae, 200–400 × 7–9 µm, with thick, smooth, pale yellow walls, bearing very small vesicles. *Vesicles* 9–12 µm diam, ellipsoidal to somewhat irregular, bearing metulae and phialides over almost all of the vesicle surface, but sometimes bent to form only a hemispherical head; metulae 7–8 × 2.2–2.5 µm; phialides ampulliform 7–8 × 2.2–2.5 µm. *Conidia* spherical, 2.8–3.5 µm diam, with walls varying from almost smooth to conspicuously spiny, borne in compact spherical heads, even at age.

Culture characteristics — Czapek yeast extract agar (CYA), 25 °C, 7 d: Colonies growing slowly, 13–17 mm diam, rather sparse, lightly floccose; margins narrow and entire; mycelium white to off white; conidial production light, pale greenish grey (M. 25–26C3); exudate and soluble pigment absent; reverse greyish orange (M. 5B3–4). Malt extract agar (MEA), 25 °C, 7 d: Colonies growing slowly, 10–14 mm diam, low, dense and velutinous; margins narrow, entire; mycelium white; conidial production heavy, dark green near Bottle Green (M. 26F3–4); exudate and soluble pigment absent; reverse brownish orange (M. 5C3). 25 % Glycerol nitrate agar (G25N), 25 °C, 7 d: Colonies 3–5 mm diam, of white mycelium only. 37 °C, CYA, 7 d: No growth.

Media formulations are from Pitt & Hocking (2009); (M.) colours are from Kornerup & Wanscher (1978).

Typus. Australia, Queensland, Nanango, from undisturbed forest soil, 2004, *J.I. Pitt* (holotype DAR 84903, cultures ex-type CBS 146238 = FRR 6048 = MST FP2251; ITS, *BenA*, *CaM* and *RPB2* sequences GenBank MK979278, MT184783, MT184789 and MT184795, MycoBank MB836001).

Notes — *Aspergillus nanangensis* clusters in *Aspergillus* clade *Jani*, a small clade within *Aspergillus* subg. *Circumdati*, but is molecularly distinct. It is close to *Aspergillus janus* and *Aspergillus brevijanus*, but differs from both by lack of the larger white conidial heads that characterise these species. Culturally, growth rates of *A. nanangensis* on standard media are much slower. Microscopically, *A. nanangensis* produces smaller vesicles, fertile over a reduced area. When grown on agar, liquid media or grain, *A. nanangensis* displays a unique chemotaxonomic profile comprising isonanangenine B and D, nanangelenin, nanangenic acid, nanangenines A–H and nanoxepin not present in the closely related species *A. janus* and *A. brevijanus* (Lacey et al. 2019). *Aspergillus nanangensis* also produces known metabolites asperphenamate, benzomalvin B and C, cytochalasin E and WIN 66306, compounds previously reported from other *Aspergillus* species.



A maximum likelihood tree inferred from the combined ITS, *BenA*, *CaM* and *RPB2* sequences of taxa within *Aspergillus* sect. *Jani*. The combined sequence alignment was partitioned by marker; substitution models for each partition were chosen according to the Bayesian Information Criteria using ModelTest-NG v. 0.1.6 (Darriba et al. 2020). The TPM2uf+G4 model was used for ITS sequences, K80+I+G4 for *BenA*, TrNef+G4 for *CaM* and *RPB2*. The tree was constructed using RAxML-NG v. 0.9.0 (Kozlov et al. 2019). Bootstrap support values are derived from 1 000 bootstrap replicates. Alignment available in TreeBASE (study S25916).

Colour illustrations. Woodland near Nanango, Queensland, dominated by *Eucalyptus* species showing undisturbed soil from which *A. nanangensis* was collected. Colonies grown on CYA (left) and MEA (right) for 7 d at 25 °C; fruiting structures and conidia. Scale bars = 10 µm (fruiting structures) and 5 µm (conidia).

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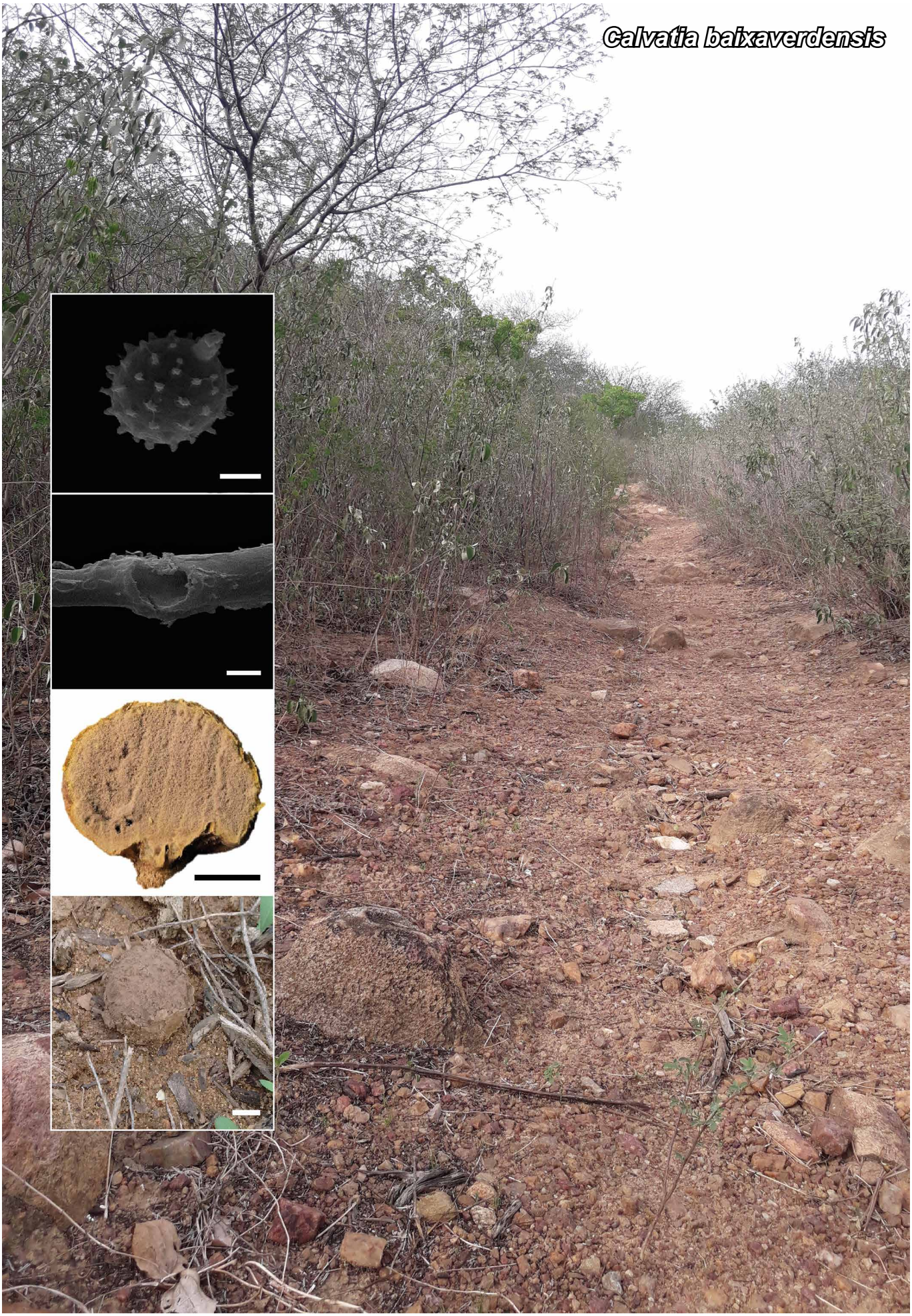
Calvatia baixaverdensis

Fungal Planet 1067 – 29 June 2020

Calvatia baixaverdensis R.L. Oliveira, R.J. Ferreira, P. Marinho, M.P. Martín & Baseia, *sp. nov.*

Etymology. In reference to the region where this species was collected, Baixa Verde, João Câmara, RN, Brazil.

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

Basidiomata growing solitary, epigeous, incrustations in the rooting base, subglobose and 31–36 mm wide × 16–28 mm high. *Exoperidium* < 0.1 mm thin, fragile, slightly tomentose, evanescent, white to yellowish white (3A1, 3A2; Kornerup & Wanscher 1978). *Mesoperidium* < 0.1 mm thin, fragile, membranaceous, persistent at the base, smooth with senescence, greyish brown to brown (4C4, 6D3, 6E4, 7F4). *Endoperidium* < 0.3 mm thin, fragile and brittle at the apex, resistant and persistent at the base, papyraceous, olive brown to brown (4D6, 6E4). *Rhizomorphs* not seen. *Subgleba* reduced, woolly, compact, brownish beige (6E3). *Gleba* powdery, not persistent, brownish beige, brown to dark brown (6E3, 6E4, 6F4), at maturity. *Exoperidium* hyphalic, 2.0–5.3 µm diam, intertwined, frequent and non-regular septa, double V branching, walls ≤ 1.1 µm thin, straight for curves, hyaline, dextrinoid, low reaction and cyanophilic. *Mesoperidium* compacted, collapsed, hyaline, not dextrinoid and cyanophilic. *Endoperidium* apical composed of two layers of hyphae continuous, all brown, not dextrinoid and cyanophilic, hyphae 2.4–6.6 µm diam, frequent and non-regular true septa, double V branching, and mycosclereids globose, subglobose, pyriform, ovoid, ellipsoid, or rectangular, 15.4–60.3 µm high × 4.6–57.6 µm diam, weakly interconnected, branched, breaking in the septa, regular and thick walls ≤ 1.4 µm thin and straight for curves. *Endoperidium* basal hyphalic, 1.9–3.9 µm diam, rare and non-regular true septa, V-shaped branches, single and double, and in T, walls < 1.0 µm thin, tortuous and regular, brown, dextrinoid, and cyanophilic. *Subgleba* hyphalic, 1.5–3.8 µm diam, rare true septa, branching V, single and double, and T, cyanophilic nodes frequent, regular walls ≤ 1.0 µm thin, straight for curves, reddish brown, not dextrinoid and cyanophilic. *Paracapillitium* absent. *Capillitium Calvatia*-type, 1.9–3.5 µm diam, hyaline to light brown, dextrinoid and cyanophilic; septa frequent and non-regular, V-branching, single and double, and in T, fragmenting in any part of the capillitium or frequent in the septa; walls ≤ 0.8 µm thin and regular, straight, with large and numerous conspicuous pits (1–3 µm wide). *Basidiospores* globose to subglobose, 3.4–5.3 µm wide × 3.3–5.0 µm high (χ = 4.1 ± 0.3 × 3.9 ± 0.3; Q_m (medium coefficient) = 1.05; n (measurement numbers) = 30), verrucose, ornamentation < 1 µm length; pedicels present in some basidiospores ≤ 0.7 µm in length.

Habit & Habitat — Basidiomata growing solitary on moist soil.

Typus. Brazil, Rio Grande do Norte, João Câmara, Serra do Torreão, 17 Feb. 2017, *R.L. Oliveira* (holotype UFRN-Fungos 3027; ITS sequence GenBank MT152990, MycoBank MB827690).

Additional materials examined. Brazil, Rio Grande do Norte, João Câmara, Serra do Torreão, 17 Feb. 2017, *R.L. Oliveira* (UFRN-Fungos 3027); ibid., 17 Feb. 2017, *R.L. Oliveira* (UFRN-Fungos 3028); ibid., 5 Mar. 2019, *R.L. Oliveira* (UFRN-Fungos 3117); ibid., 5 Mar. 2019, *R.L. Oliveira* (UFRN-Fungos 3118).

Notes — *Calvatia baixaverdensis* is morphologically related to species of sect. *Calvatia*: *C. craniiformis*, *C. subtomentosa*, *C. rugosa*, *C. nodulata*, and *C. holothurioides*. *Calvatia craniiformis*, *C. rugosa* and *C. subtomentosa* have a capillitium with large conspicuous pits (1–3 µm wide) similar to *C. baixaverdensis*. However, *C. craniiformis* presents subglobose to globose basidiospores with punctate ornamentation, and well-developed cellular subgleba. *Calvatia rugosa* has exoperidium granulose, furfuraceous to subvelutinous, endoperidium smooth, membranous, very thin (< 0.5 mm), subgleba well-developed and lanose to cellular (Reid 1977). *Calvatia subtomentosa* has basidiospores 3.6–4.4 µm diam, and capillitium 3.6–5.8 µm, branched, septate, rather short fragments (Dissing & Lange 1962), but is easily distinguished from *C. baixaverdensis* in the ornamentation of the basidiospores, equinulate, and in the absence of pedicels, besides the absence of large pits in the capillitium and nodules in the hyphae of subgleba in *C. subtomentosa*. *Calvatia nodulata* and *C. holothurioides* are other morphologically close species to *C. baixaverdensis* mainly by the basidiospores 3–5 µm diam and capillitium 2–4 µm diam; however, *C. nodulata* has exoperidium granulose to pilose, subgleba occupying half of the basidiomata, and capillitium with spaced nodules (Alfredo et al. 2014), and *C. holothurioides* has subgleba prominent, cellular, capillitium with pores up to 2 µm diam (Rebriev 2013).

Colour illustrations. Brazil, Rio Grande do Norte, João Câmara, Serra do Torreão, where the specimens were collected. From bottom to top: mature basidiome *in situ*; longitudinal section through mature basidiome; capillitium under SEM; basidiospores under SEM. Scale bars = 10 mm (basidiomes), 1 mm (SEM photos).

Supplementary material

FP1067 The ITS nrDNA consensus phylogenetic tree was obtained with a Bayesian analysis using MrBayes v. 3.2.7a (Ronquist & Huelsenbeck 2003) under T92+G+I evolutionary for 5 M generations.

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Candida pellucida

Fungal Planet 1068 – 29 June 2020

Candida pellucida A.M. Glushakova, M.A. Tomashevskaya & Kachalkin, *sp. nov.*

Etymology. The name refers to *Exomias pellucidus* from which the ex-type strain was isolated.

Classification — *Debaryomycetaceae*, *Saccharomycetales*, *Saccharomycetes*.

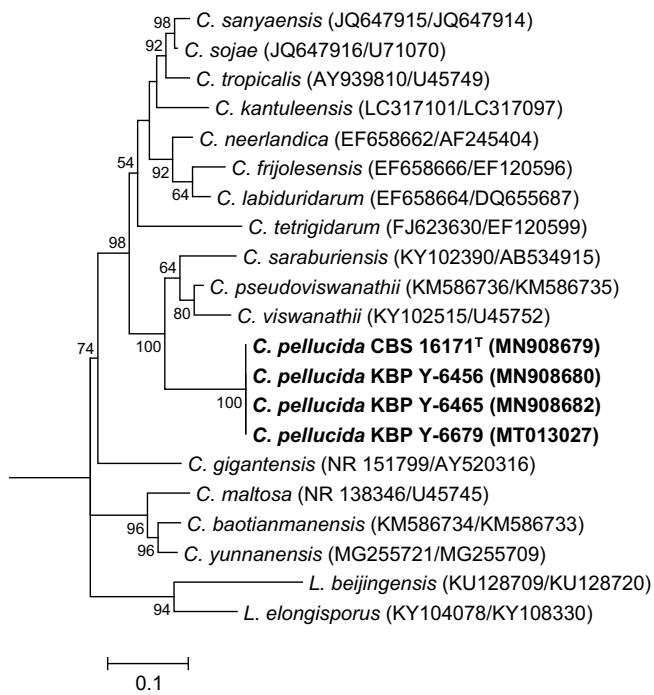
On glucose peptone yeast extract agar (GPYA) and 5 % malt extract agar (MEA), after 7 d at 25 °C, streak is white-cream, semi-glistening, with a smooth surface and entire margin. Cells are ovoid to elongate (2–6 × 5–8 µm) and occur singly or in pairs, dividing by polar and multilateral budding. Rare pseudohyphae are produced on potato dextrose agar (PDA) and cornmeal agar (CMA). *Ascospores* and *true hyphae* have not been observed during 4 wk at 10 and 25 °C in culture (pure cultures and in mating test) grown on GPYA, MEA, PDA, CMA and yeast nitrogen base with 0.5 % glucose (YNB) agar. Fermentation of glucose, galactose (delayed weak), trehalose and maltose (delayed) are positive, but negative for sucrose, lactose and raffinose. Glucose, sucrose, galactose, maltose, cellobiose, trehalose, melezitose, methyl alpha-D-glucoside, D-xylose, L-arabinose, D-glucosamine, ethanol, glycerol (weak), ribitol, D-mannitol, D-glucitol, salicin (weak), DL-lactic acid (weak), succinic acid (weak), citric acid, 2-keto-D-gluconate, arbutin are assimilated; no growth occurs on lactose, melibiose, raffinose, soluble starch, inulin, D-arabinose, D-ribose, L-sorbose, L-rhamnose, galactitol, erythritol, *myo*-inositol, 5-keto-D-gluconate, D-glucuronate and methanol. Nitrogen compounds: ammonium sulfate, potassium nitrate (weak), creatinine, creatine, L-lysine, D-glucosamine (weak) 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 % and 0.1 % cycloheximide is weak. Starch-like compounds are not produced. Gelatin liquefaction and casein hydrolysis tests are positive. Diazonium blue B colour and urease reactions are negative. Maximum growth temperature is 42–44 °C.

Typus. Russia, Moscow, Park Tsaritsyno, from *Exomias pellucidus* (*Curculionidae*), Oct. 2018, *A.M. Glushakova*, Ins19-23 (holotype KBP Y-6457 preserved in a metabolically inactive state, ex-type culture VKM Y-3050 = DSM 110120 = CBS 16171; SSU, ITS-D1/D2 domains of LSU nrDNA, *TEF1* and *RPB1* sequences GenBank MN908677, MN908679, LR745525 and LR745526, MycoBank MB834513).

Additional materials examined. Russia, Moscow, Park Tsaritsyno, from *E. pellucidus*, Oct. 2018, *A.M. Glushakova*, KBP Y-6456, KBP Y-6465 and KBP Y-6466; ITS-D1/D2 domains of LSU nrDNA sequences GenBank MN908680, MN908681 and MN908682; Moscow, as endophyte from almond seeds bought on local market, Oct. 2019, *A.M. Glushakova*, KBP Y-6679; ITS-D1/D2 domains of LSU nrDNA sequence GenBank MT013027.

Colour illustrations. Russia, Moscow, Park Tsaritsyno, meadows with herbaceous flowering plants (the habitat of *Exomias pellucidus*). *Candida pellucida* KBP Y-6457: growth of yeast colonies on MEA, yeast cells on MEA (after 7 d at 25 °C). Scale bar = 10 µm.

Notes — Analysis of the ITS-D1/D2 regions of the surveyed yeasts suggested that they were conspecific and represented a hitherto undescribed species of the *Candida/Lodderomyces* clade. Based on the NCBI GenBank nucleotide database, the best hits using the **ITS** sequence are *Candida viswanathii* CBS 7889 (GenBank KY102513; 90.24 % similar, 18 subst. and 23 gaps) and *Candida viswanathii* ATCC 22981T (GenBank NR_138345; 88.07 % similar, 24 subst. and 36 gaps), using **LSU** it is *Candida viswanathii* CBS 4024T (GenBank KY106885; 98.20 % similar, 9 subst.), using **SSU** it is *Candida labiduridarum* NRRL Y-27940T (GenBank NG_063271; 99.88 % similar, 2 subst.), using ***TEF1*** it is *Candida dubliniensis* CD36T (GenBank XM_002417390; 95.67 % similar, 19 subst.) and using ***RPB1*** it is *Candida viswanathii* CBS 4024T (GenBank AY497714; 88.83 % similar, 66 subst.). In compliance with a recent phylogenetic analysis of the genus (Zhai et al. 2019), the placement of the new species is demonstrated using the combined ITS and LSU rDNA phylogeny. *Candida pellucida* can be differentiated from the phylogenetically most close species *C. viswanathii* based on its ability to grow on vitamin-free medium, good growth at the temperature 42 °C, and negative growth on soluble starch.



Maximum likelihood (ML) tree obtained from the combined analysis of ITS and LSU sequence data. Bootstrap support values above 50 % are shown at the nodes. The alignment included 965 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. The phylogenetic analysis was conducted in MEGA v. 6 (Tamura et al. 2013). *Saccharomyces cerevisiae* (AB018043/JQ689017) was used as outgroup (hidden).

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Cladophialophora cabanerensis

Fungal Planet 1069 – 29 June 2020

Cladophialophora cabanerensis Maciá-Vicente, *sp. nov.*

Etymology. Named after the Cabañeros National Park in central Spain, where the soil sample was collected.

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

Mycelium consisting of hyaline, branched, septate hyphae, (0.5–) 0.7–1.3(–1.6) µm diam, forming hyphal strands. *Conidiophores* mostly single, sympodial, erect, subcylindrical, hyaline, smooth, bearing one phialide, often reduced to a conidiogenous cell. *Conidiogenous cells* phialidic, hyaline, smooth, fusiform with one locus at the apex that leaves a scar, (2.8–)3.6–6.2(–7.6) × (1.3–)1.7–2.6(–2.9) µm. *Conidia* aseptate, produced in mass, hyaline, smooth, globose with a scar, (1.7–)1.9–2.3(–2.4) µm diam (n = 40). *Chlamydospores* absent. *Sexual morph* unknown.

Culture characteristics — *Colonies* slow-growing, reaching 11–14 mm diam on malt extract agar (MEA), 13–17 mm diam on potato-dextrose agar (PDA), and 9–12 mm diam on cornmeal agar (CMA) after 7 d at 25 °C. Colonies velvety, white, becoming light earthy after 3–4 wk, with a compact and suede-like surface; reverse white-cream.

Typus. Spain, Ciudad Real, Cabañeros National Park, from rhizospheric soil from a wet heathland ('trampal'), N39.35 W4.36, 725 m asl, isolated from surface-sterilised, asymptomatic roots of an *Arabidopsis thaliana* plant inoculated with soil and grown under controlled conditions, 19 Apr. 2018, coll. *J.G. Maciá-Vicente*, isol. 20 June 2018, *J.G. Maciá-Vicente* (holotype FR 0214084, ex-type culture CBS 146718 = P6481; ITS and LSU sequences GenBank MN310213 and MN308512, MycoBank MB834845).

Additional materials examined. Spain, Ciudad Real, Cabañeros National Park, from rhizospheric soil from a wet heathland ('trampal'), N39.35 W4.36, 725 m asl, isolated from surface-sterilised, asymptomatic roots of an *A. thaliana* plant inoculated with soil and grown under controlled conditions, 19 Apr. 2018, coll. *J.G. Maciá-Vicente*, isol. 20 June 2018, *J.G. Maciá-Vicente*, culture P6476; ITS and LSU sequences GenBank MT179621 and MN308507; Ciudad Real, Cabañeros National Park, from rhizospheric soil from a wet heathland ('trampal'), N39.35 W4.36, 725 m asl, isolated from surface-sterilised, asymptomatic roots of an *A. thaliana* plant inoculated with soil and grown under controlled conditions, coll. 19 Apr. 2018, *J.G. Maciá-Vicente*, isol. 20 June 2018, *J.G. Maciá-Vicente*, culture P6479; ITS and LSU sequences GenBank MN310212 and MN308510.

Notes — The three isolates examined have identical morphologies and partial ITS and LSU sequences. Since they originate from the same soil sample, they likely represent clonal isolates. Based on a megablast search of NCBIs GenBank nucleotide database, the **ITS** sequence has low similarity with several unidentified *Chaetothyriales* strains (e.g., GenBank KX822488.1, identities 566/690 (82 %), 43 gaps (6 %); GenBank KF614863.1, identities 566/690 (82 %), 43 gaps (6 %); GenBank KF614863.1, identities 566/690 (82 %), 43 gaps (6 %)) and with *Cladophialophora immunda* (GenBank MH864254.1, identities 580/715 (81 %), 57 gaps (7 %)). However, the low identity values result from a long insert at the 3' end of the 18S rDNA gene, similarly to what has been found in other fungi (e.g., Tedersoo et al. 2015, Cross et al. 2017), but that is not present in most GenBank records. When analysing only the partial ITS1 region (nt 551–679) that is homologous to other sequences in GenBank, the megablast search yields highest similarity with 15 environmental sequences originating from a single study (e.g., GenBank MF793689.1, identities 129/129 (100 %), no gaps), and to two unidentified fungi (GenBank MG592689.1, identities 129/129 (100 %), no gaps; GenBank GQ996076.1, identities 127/129 (98 %), 1 gap (0 %)) and two *Cladophialophora* sp. isolates (GenBank LC189029.1, identities 129/129 (100 %), no gaps; and GenBank LC229675.1, identities 127/129 (98 %), 1 gap (0 %)). The closest hits using the **LSU** sequence are an unidentified fungus (GenBank GU552546.1, identities 675/676 (99 %), 1 gap (0 %)), *Cladophialophora* sp. (GenBank MF588895.1, identities 669/676 (99 %), 1 gap (0 %)), unidentified *Chaetothyriales* (GenBank KF614869.1, identities 666/676 (99 %), 1 gap (0 %)), and *Cladophialophora carrionii* (GenBank AF050262.1, identities 665/676 (98 %), 1 gap (0 %)).

The genus *Cladophialophora* is polyphyletic, including species that are commonly isolated from soil and living plants, but also found as causal agents of human infections. *Cladophialophora cabanerensis* is phylogenetically placed outside the *Carrionii* and *Bantiana* clades defined by Badali et al. (2008) that contain most species pathogenic to humans. All the closest hits in the megablast search using the insert-free ITS1 sequence originate from fungi associated with plant roots, like the type specimen of *C. cabanerensis*, suggesting a preference of the species toward this habitat

Colour illustrations. Wet heathland ('trampal') located in the Cabañeros National Park, Ciudad Real, Spain. Seven-day-old colonies growing at 25 °C on PDA; from top to bottom, overview of mycelium bearing conidiophores under phase-contrast microscopy; conidiophores under light microscopy; loose conidia under light microscopy. Scale bars = 10 µm (mycelium) and 5 µm (conidiophores and conidia).

Supplementary material

FP1069 Maximum likelihood phylogenetic tree inferred from concatenated ITS and LSU rDNA sequences using RAxML v. 8.2.12 (Stamatakis 2014) with the GTR+I+G model.

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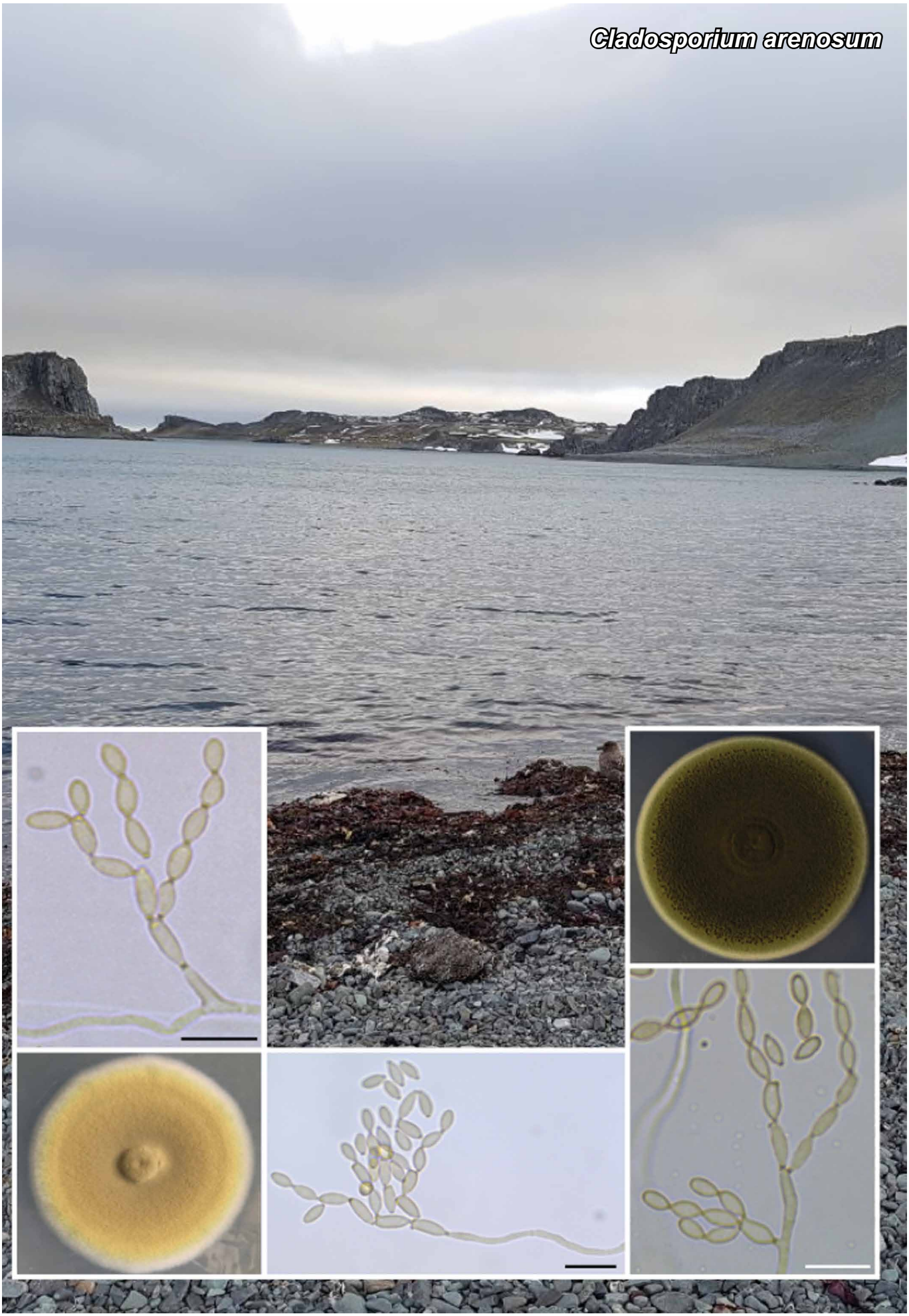

Cladosporium arenosum

Fungal Planet 1070 – 29 June 2020

Cladosporium arenosum C. Gil-Durán & L. Sanhueza, *sp. nov.*

Etymology. *arenosum* means sandy, referring to substrate (sea sand) from which the fungus was isolated.

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

Mycelium scarcely submerged and superficial; hyphae sinuous, unbranched, smooth, 1.8–3 µm wide, septate, not constricted at septa, subhyaline to olive brown. *Conidiophores* smooth, occasionally geniculate, multiseptate, erect to slightly flexuous, oblong, proliferating sympodially; macronematous conidiophores arising terminally or laterally from hyphae, up to 80 µm long, 3.1–4 µm wide; semimacronematous conidiophores arising terminally or laterally from hyphae, 1.3–1.6 µm wide, pale olive brown, with a single apical scar; micronematous conidiophore arising laterally from hyphae, 3.1–3.5 µm wide. *Ramoconidia* straight, smooth, concolourous, subcylindrical, 7.0–13.2 × 2.9–4.3 µm, 1-septate. *Secondary ramoconidia* ellipsoid to subcylindrical, smooth, 7.2–12 × 3.1–4.2 µm, 0–1-septate in the middle, with 2–3 distal hila, proliferating sympodially. *Conidia* numerous, catenated, dichotomously branched in all directions, straight, smooth, with up to 7 conidia; small terminal conidia obovoid, 2.5–5.8 × 1.4–2.8 µm; intercalary conidia ovoid or limoniform, 6–8.2 × 2.3–4.1 µm; microcyclic conidiogenesis not observed.

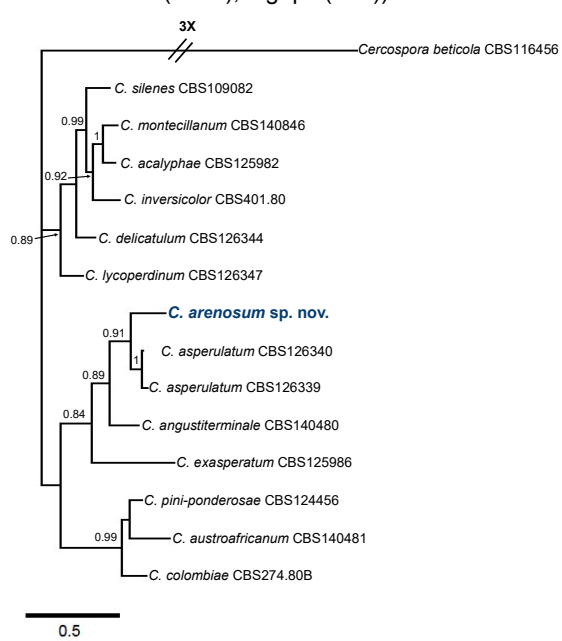
Culture characteristics — (after 2 wk at 20 °C in the dark): On potato dextrose agar (PDA), colonies reach 44–47 mm diam, round shape, flat, dark olive green, dusty, aerial mycelium absent, profuse sporulation, margin white and glabrous, exudates (blackish droplets) produced mainly on the outermost colony surface; reverse olive green to olive black. On malt extract agar (MEA), colonies reach 40–43 mm diam, irregular flat growth, elevated centre, dusty, olive green to yellowish green, aerial mycelium absent, exudates absent, white filiform margin; reverse, irregular olive-black. On synthetic nutrient-poor agar (SNA), colonies reach a 28–30 mm diam, irregular flat growth, dusty, olive-green, profuse sporulation mainly in the centre of the colony, exudates absent; reverse olive grey with white filiform margin. On oatmeal agar (OA), colonies reach 40–45 mm diam, round shape, flat, olive-green, abundant velvety aerial mycelium, absent on the outermost colony surface, profuse sporulation, exudates absent, margin grey-green, narrow and glabrous.

Cardinal temperature for growth — Optimum 20 °C, maximum 25 °C, minimum 5 °C.

Typus. Antarctica, South Shetland archipelago, King George Island, Fildes Bay, from marine sediment sand, 24 Feb. 2018, *L. Sanhueza* LS-2 (holotype CHFC-EA 566 stored in a metabolically inactive state in Chilean Fungal Collection; ITS, LSU, *actA* and *tef1* sequences GenBank MN879328, MT015967, MN890008 and MN890011, MycoBank MB834383).

Notes — Based on the combined analysis of ITS, *actA* and *tef1* markers, *Cladosporium arenosum* belongs to the *C. cladosporioides* complex (Bensch et al. 2015) and is phylogenetically related to *Cladosporium asperulatum*. However, *C. asperulatum* exhibits asperulate surface ornamentation of its conidia, conidiophores and mycelium (Bensch et al. 2010), characters not found in *C. arenosum*. In addition, *C. asperulatum* has longer conidiophores ((15–)45–210(–360) × (2–)3–4(–5) µm) and ramoconidia (15–50 × 3–4 µm)) (Bensch et al. 2010). Finally, *C. arenosum* produces exudates on PDA, limoniform conidia, and its colonies have a characteristic yellowish green colour after 2 wk at 20 °C on MEA, characters not found in *C. asperulatum* (Bensch et al. 2010).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence are *Cladosporium perangustum* ID58 (GenBank MN511354.1; Identities 551/551 (100 %), no gaps), *Cladosporium globisporum* DTO 220-D4 (GenBank KP701967.1; Identities 551/551 (100 %), no gaps), and *Cladosporium asperulatum* UTHSC DI-13-216 (GenBank LN834357.1; Identities 551/551 (100 %, no gaps). The closest hits using the **LSU** sequence are *Cladosporium cladosporioides* CBS 129108 (GenBank MH876646.1; Identities 608/608 (100 %), no gaps), *Cladosporium herbarum* CBS 129088 (GenBank MH876640.1; Identities 608/608 (100 %), no gaps), and *Cladosporium tenuissimum* CBS 125995 (GenBank MH876286.1; Identities 608/608 (100 %), no gaps). The closest hits using the *actA* sequence are *Cladosporium asperulatum* UTHSC DI-13-216 (GenBank LN834541.1; Identities 218/227 (96 %), 1 gap (0 %)), *Cladosporium myrtacearum* CBS 126350 (GenBank HM148606.1; Identities 204/227 (90 %), 4 gaps (1 %)), and *Cladosporium longicatenatum* CPC 17189 (GenBank KT600598.1; Identities 202/224 (90 %), 5 gaps (2 %)). The closest hits with *tef1* sequence are *Cladosporium asperulatum* BP3I2 (GenBank KU605784.1; Identities 242/242 (100 %), no gaps), *Cladosporium angustiterminale* CPC 15564 (GenBank KT600476.1; Identities 222/243 (91 %), 5 gaps (2 %)), and *Cladosporium lycoperdinum* CBS 126347 (GenBank HM148356.1; Identities 213/245 (87 %), 3 gaps (1 %)).



Phylogram obtained by combined analysis of ITS, *actA* and *tef1* sequences of *C. arenosum* and related species from the *C. cladosporoides* complex (Bensch et al. 2018). Analyses were done in MrBayes v. 3.2.6 (Huelsenbeck & Ronquist 2001) under GTR + G model for 5 M generations. Posterior probabilities values > 0.84 are shown at the nodes. *Cercospora beticola* CBS 116456 was used as outgroup.

Colour illustrations. Sea shore of Fildes Bay, Antarctica, where the sample was taken. *Cladosporium arenosum* growing on PDA and MEA; conidiophores and conidium on SNA after 14 d at 20 °C. Scale bars = 10 µm.

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Cortinarius balteatoindicus

Fungal Planet 1071 – 29 June 2020

Cortinarius balteatoindicus Dima, Semwal, V. Papp, Brandrud & V.K. Bhatt, *sp. nov*.

Etymology. The first part of the epithet ('*balteato*') refers to the relationship with *C. balteatocumatilis*, the second part ('*indicus*') refers to India where the species occurs.

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

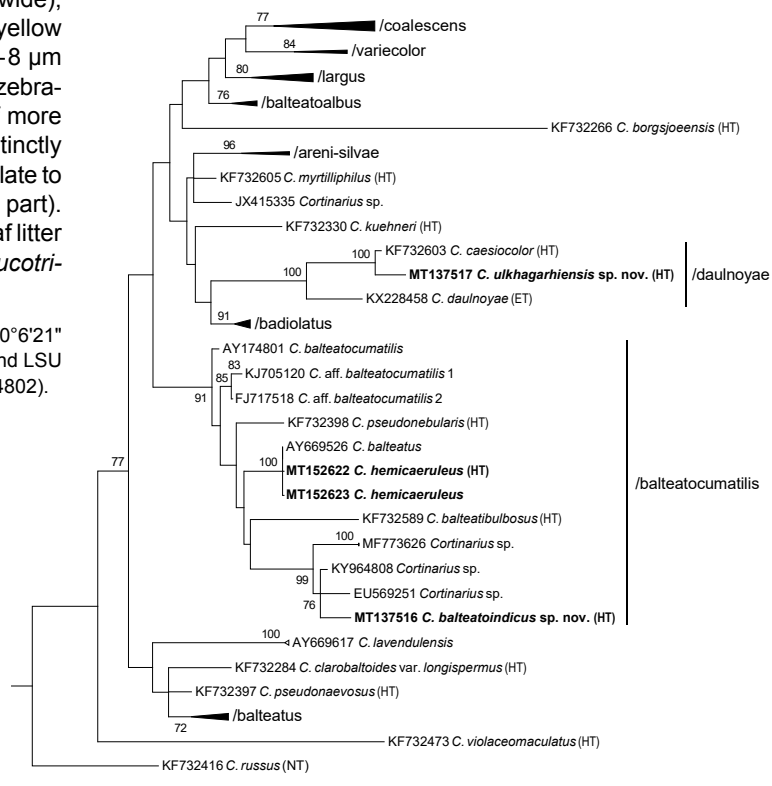
Pileus up to 75 mm diam, plano-convex to applanate, slightly glutinous when young, reddish golden to greyish orange (6B7–6B5); margin smooth or slightly innately fibrillose, incurved. *Lamellae* emarginate, moderately crowded, up to 6 mm broad, greyish when young, later greyish orange (6B4–6B6), lamellulae present, of various lengths. *Stipe* 65 × 17 mm, cylindrical, with slightly clavate base, up to 25 mm broad, greyish orange to brownish orange (6B5–6B6). *Context* dull lilac (15C3) to purplish in pileus and in stipe base. *Odour* distinct, earth-like. *Taste* indistinct. *Spore print* light brown (6D8). *Basidiospores* (9.4–)9.7–10.3(–10.7) × (5.4–)5.6–5.9(–6.1) µm, av. = 10.07 × 5.7 µm, Q = (1.65–)1.73–1.80(–1.85), Qav = 1.77, n = 50, amygdaloid, verrucose. *Basidia* 4-spored, 26–32 × 6–8 µm, clavate. *Pileipellis* more or less simplex (1-layered); strongly coloured in KOH. *Epicutis* at surface of narrow (2–4 µm wide), loosely erect-entangled, gelatinous, distinctly brownish yellow hyphae (many more or less collapsed); below wider (4–8 µm wide), parallel hyphae, with yellow thick walls or distinctly zebra-striped, encrusted pigment; the basal part of epicutis of more or less cemented hyphae up to ± 15 µm wide, with distinctly thickened, yellow walls, some filled with dark brown granulate to oleiferous pigment (most pigment in the basal, cemented part).

Habitat & Distribution — Solitary, occurring among leaf litter in temperate forests dominated mainly by *Quercus leucotrichophora* and *Pinus roxburghii*.

Typus. India, Uttarakhand, Pauri Garhwal, Teka, 1 965 m asl, N30°6'21" E78°45'12", 4 Sept. 2015, *K.C. Semwal* (holotype KCS 2509; ITS and LSU sequences GenBank MT137516 and MT241837, MycoBank MB834802).

Colour illustrations. India, Uttarakhand, Pauri Garhwal, Teka, type locality. Spores and basidiomata (from KCS 2509, holotype). Scale bar = 10 µm (spores).

Notes — *Cortinarius balteatoindicus* is a member of sect. *Phlegmacioides* based on morphological and molecular (nrDNA ITS and LSU regions) data, belonging to the /balteatocumatilis clade. It forms a well-supported (BS = 99 %) lineage with three sequences known from the Americas: USA, Tennessee (GenBank MF773626), USA, Minnesota (GenBank KY964808) and Mexico (GenBank EU569251). The closest sequence is the one from Minnesota; they differ by 5 nucleotide and indel positions, but only in the ITS1 region. Further studies are needed to unveil whether this sequence belongs to *C. balteatoindicus* with such a disjunct distribution. The other North American sequence from Tennessee differs by 8 nucleotide and indel positions, so it might well represent a separate species. The phylogenetically more distant European species of this clade have more robust basidiomata too, e.g., *C. balteatocumatilis*, *C. balteatobulbosus*, *C. pseudonebularis*, and the recently described *C. hemicaeruleus* (Brotzu et al. 2019; ITS sequence GenBank MT152622) and have slightly larger spores. The special ecology and the unique ITS sequence are, however, the best delimiting characters for the time being.



Phylogenetic tree derived from Maximum Likelihood analysis based on nrITS1-5.8S-ITS2 and binary data from indel coding with FastGap v. 1.2 (Borchsenius 2009). Analysis was performed in raxmlGUI v. 1.5.2 (Silvestro & Michalak 2012) using the GTRGAMMA substitution model for the partitioned (ITS1-5.8S-ITS2) nucleotide data and the default setting for binary (indel) data. ML bootstrap support (BS) values shown at the nodes (BS > 70 %). Sequences generated for this study are highlighted in **bold** face. HT and NT abbreviations refer to holotype and neotype sequences, respectively.

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Cortinarius ulkhagarhiensis
KCS2490

Fungal Planet 1072 – 29 June 2020

Cortinarius ulkhagarhiensis Dima, Semwal, V. Papp, Brandrud & V.K. Bhatt, *sp. nov*.

Etymology. The epithet refers to the type locality at Ulkhagarhi which is named after the temple of the goddess Ulkheshwari in Uttarakhand, India.

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

Pileus up to 110 mm diam, plano-convex to applanate, slightly inflated at centre, surface glabrous, slimy when young, slightly bluish greyish when young, but soon becoming reddish golden to light brown (6C8–6D8); margin smooth, fairly undulate. *Lamellae* emarginate, crowded, greyish when young, later greyish orange (6B4), brownish orange (6C5) when mature, lamellulae present, of various lengths. *Stipe* 60–90 × 10–22 mm, prominently clavate at the base, bulb up to 30 mm wide, pale brown, becoming brownish orange to reddish orange (6D5, 6B7–7B7) with greyish lilac (15B4-3) tinge throughout the stipe, especially at apex. *Context* greyish to bluish lilac. *Odour* and *taste* not recorded. *Spore print* brown (8E8). *Basidiospores* (10.2–)10.6–11.3(–11.7) × (5.7–)5.9–6.6(–6.8) µm, av. = 10.97 × 6.2 µm, Q = (1.63–)1.71–1.83(–1.94), Qav = 1.77, n = 50, amygdaloid, verrucose. *Basidia* 4-spored, 25–30 × 5–7 µm, clavate. *Pileipellis* more or less simplex (1-layered); rather weakly coloured in KOH. *Epicutis* at surface of narrow, 2–5 µm diam, loosely erect-entangled, gelatinous, pale yellow hyphae; below a few layers of slightly wider, 3–8 µm diam hyphae with slightly thickened yellow walls, a few with pale, weakly encrusted wall pigment; the basal part of epicutis of hyphae up to approx. 10 µm diam, with distinctly thickened, yellow walls, forming tightly cemented bundles which in surface view forms a zig-pattern.

Habitat & Distribution — Caespitose, occurring among leaf litter of *Quercus leucotrichophora*, on humicolous soil, in temperate broadleaved forests dominated by mainly *Q. leucotrichophora*, *Rhododendron arboreum*, and *Myrica esculenta*.

Typus. India, Uttarakhand, Pauri Garhwal, Ulkhagarhi, 2025 m asl, N30°09'36" E78°50'53", 31 Aug. 2015, *K.C. Semwal* (holotype, KCS 2490; ITS and LSU sequences GenBank MT137517 and MT241838, MycoBank MB834804).

Notes — *Cortinarius ulkhagarhiensis* belongs to sect. *Phlegmacioides* based on both morphological and molecular (nrDNA ITS and LSU regions) data. Within the section it belongs to the /daulnoyae clade, where it forms a close sister species of the European *C. caesiocolor*. They differ by 5 nucleotide and indel positions, and in morphological characters. The spores of *C. ulkhagarhiensis* are significantly larger than those of *C. caesiocolor* (av. 10.97 × 6.2 µm vs 9.85 × 5.8 µm, respectively), and they are also longer (Qav = 1.77 vs 1.70). Macromorphologically they are rather similar, with e.g., bluish context. Another closely related species is the European *C. daulnoyae* (syn.: *C. chromataphilus* and *C. sabuletorum*) which has a strong earth-like smell, yellowing, never bluish context, and phylogenetically is more distant. Morphologically, other species in sect. *Phlegmacioides* might also resemble *C. ulkhagarhiensis*, but the ecology and ITS sequence data will be helpful in identification.

Colour illustrations. India, Uttarakhand, Pauri Garhwal, Ulkhagarhi, type locality. Spores and basidiomata (from KCS 2490, holotype). Scale bar = 10 µm (spores).

For phylogenetic tree see FP1071.

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Cortinarius paezii

Fungal Planet 1073 – 29 June 2020

Cortinarius paezii Garrido-Benavent, Ballarà, Liimat. & Mahiques, *sp. nov.*

Etymology. The species is named after the Spanish Jesuit missionary Pedro Páez (1564–1622), who was the first European that visited the Blue Nile source in Ethiopia and described the natural history of this country.

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

Basidiomata rather small. *Pileus* 10–25(–35) mm diam, at first hemispheric, later convex with a persistent, obtuse, rounded and low umbo; margin first very incurved and highly lobulated and later extended and slightly serrate, retaining whitish veil remnants; surface hygrophanous, smooth to fibrous, dark grey, dark grey-brown (Caill. T31, T30; Cailleux 1981) to ochraceous, pale ochraceous or reddish brown (Caill. M49, M35, M25) when dry; mature pilei with necropigments. *Lamellae* moderately dense, uncinated, pale ochraceous to beige ochraceous (Caill. M29, N30); lamellae edges slightly paler, and slightly mustard brown with age; lamellulae present. *Stipe* (15–)20–35(–45) mm long and 3–6(–8) mm wide, cylindrical to clavate or subglobose at the base; surface white, later pale beige, with universal veil copious towards the base, partial veil fugacious, not forming an annular area. *Context* generally fibrous, pale ochraceous, and brownish in the stipe cortex. *Taste* mild and *smell* indistinguishable. *Macrochemical reactions*: negative to KOH, guaiac tincture, Ph.A. and methol. *Basidiospores* broadly ellipsoid in front and side view, (10–)11–*11.8*–12.5(–13) × (6.25–)7–*7.3*–7.5(–8) µm in size, with a Q (length/width ratio) = (1.5–)1.55–*1.61*–1.73(–1.8), and with a marked apical depression; spore surface densely ornamented with projecting warts of moderate size. *Basidia* 36–45 × 9–12 µm, 4-spored; lamellar edge with basidia and some claviform cells, 26–34 × 9–11 µm. *Pileipellis* a cutis formed by a layer of 4–8 µm wide, clamped, more or less cylindrical hyphae, with scattered pale ochraceous incrusted wall pigments; *subcutis* composed of short and irregularly-arranged, septate hyphae, 30–75 × 20–32 µm; hyphae of the veil remnants 2–3 µm diam.

Habitat & Distribution — Restricted to the alpine belt (> 2000 m asl) in association with *Dryas octopetala*. So far found in the Pre-Pyrenees (north-eastern Iberian Peninsula). The existence of an ITS sequence in GenBank (FR852009) identical to the ones obtained in the present study indicates the presence of *C. paezii* in the Hyrcanian forests of Iran.

Typus. Spain, Catalonia, Barcelona province, Berguedà, Saldes, Serra d'Encija, Creu de Ferro, N42°18'28" E1°76'69", 2250 m asl, associated with *Dryas octopetala* on calcareous soil, 26 Aug. 2018, *J. Ballarà* JB-9511-18 (holotype MA-90461; ITS sequence GenBank MT184898, MycoBank MB833243).

Colour illustrations. Spain, Catalonia, Serra d'Encija, prairie with *Dryas octopetala* in the alpine belt, > 2000 m asl, where the holotype of *Cortinarius paezii* was collected (MA-90461). Basidiomata in upper photos correspond with the holotype; bottom left photo corresponds with MA-90460; holotype basidiospores. Scale bar = 10 µm.

Notes — *Cortinarius paezii* is a rather small telamonioid species with relatively large spores that we initially considered to conform to the morphological variability of *C. casimiri* due to the general size, habitat and pigmentation. However, basidiomata of the latter species are in general slenderer than those of *C. paezii*, and show reddish and somewhat lilaceous tinges, their smell is more or less raphanoid, and the spores are smaller, 10–11.5 × 6–7 µm (Brandrud et al. 1998). *Cortinarius paezii* produces hygrophanous pilei that are very dark when hydrated, without lilaceous traces, and instead shows pale ochraceous to reddish brown tinges with time. Furthermore, *C. casimiri* distributes preferentially in altimontane-subalpine habitats, and more rarely forms mycorrhizal associations with *Salix* spp. in the alpine belt. Considering other species growing in the alpine belt, *C. cavipes* would share two additional characters with *C. paezii*: the evident change in colour of pilei after drying and the clavate stipe (Favre 1955). As indicated by its epithet, however, *C. cavipes* has a hollow stipe; additionally, it shows lilaceous traces in the stipe apex and context (as in *C. casimiri*), and produces smaller, less ornamented spores.

Two additional alpine species described by Favre (1955) were *C. levipileus* and *C. rusticellus*. The former differs from *C. paezii* in producing smaller basidiomata, with a finely granulose pileus cuticle, with the surface dark to reddish brown, and by the less abundant veil remnants and the slightly smaller, more ovoid spores (lower Q value). Lamoure (1978) obtained similar values for spore size in *C. levipileus* and provided further evidence of its habitat on calcareous soils in the alpine belt. *Cortinarius rusticellus* produces spores more similar in size to those of the new species but has smaller basidiomata, pilei are more umbonate and fibrous to felty, lamellae are darker, and there is an abundant and persistent veil forming an evident annulus on the stipe.

The two ITS sequences obtained for the new species were 19 bp (plus four indels), 16 bp (plus eight indels), and 19 bp (plus six indels) different from those of *C. casimiri*/*subsertipes*, *C. levipileus* and *C. rusticellus*, respectively. The phylogenetic tree revealed *C. tatrensis* as a close relative of *C. paezii*. This species was described from *Salix* and *Dryas* communities in the alpine belt of the Belaer Tatras, in northern Slovakia (Fellner & Landa 1993). Apart from the similar habitat, *C. paezii* and *C. tatrensis* share the general habitat of basidiomata, the hygrophaneity of pilei and their pigmentation, and the spores, which the authors described as broadly ovoid, (10–)10.5–12.5 × (6.5–)7–8.5 µm. However, lilaceous to vinaceous tinges were originally noticed in the surface of the stipe base and in the stipe context of *C. tatrensis* while these characters are absent in *C. paezii*. Additionally, the stipe in *C. tatrensis* is described as 'cylindrical, slightly narrowing towards the base', whereas in the new species it is markedly clavate. The ITS sequence of *C. tatrensis* is provided for the first time in the present work, and shows five different nucleotides from *C. paezii* at the ITS1 region.

Supplementary material

FP1073-1 Additional materials examined.

FP1073-2 Phylogram depicting the evolutionary relationships of *Cortinarius paezii* and their relatives based on ITS sequence data.

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Cylindrium magnoliae

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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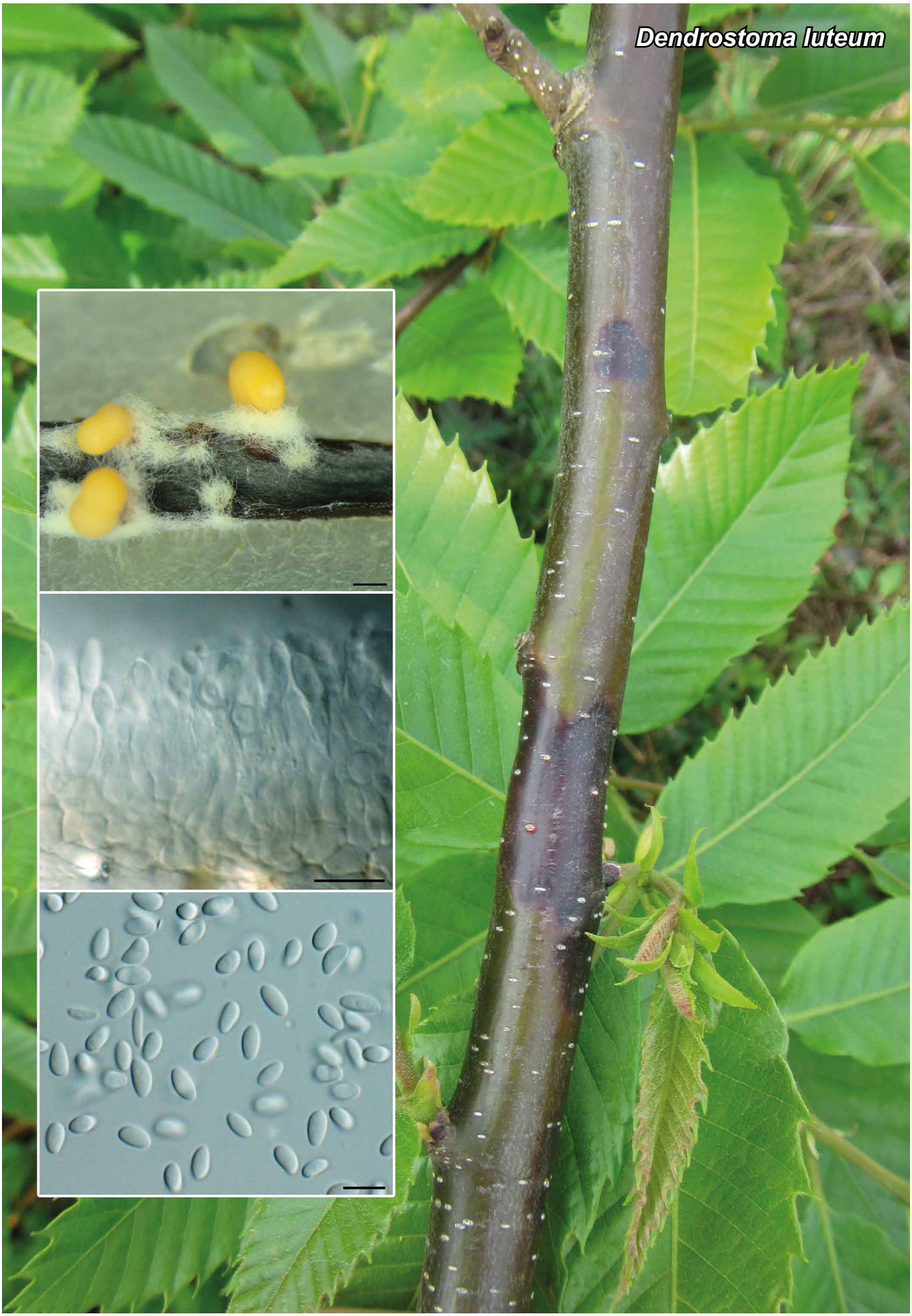

Dendrostoma luteum

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.

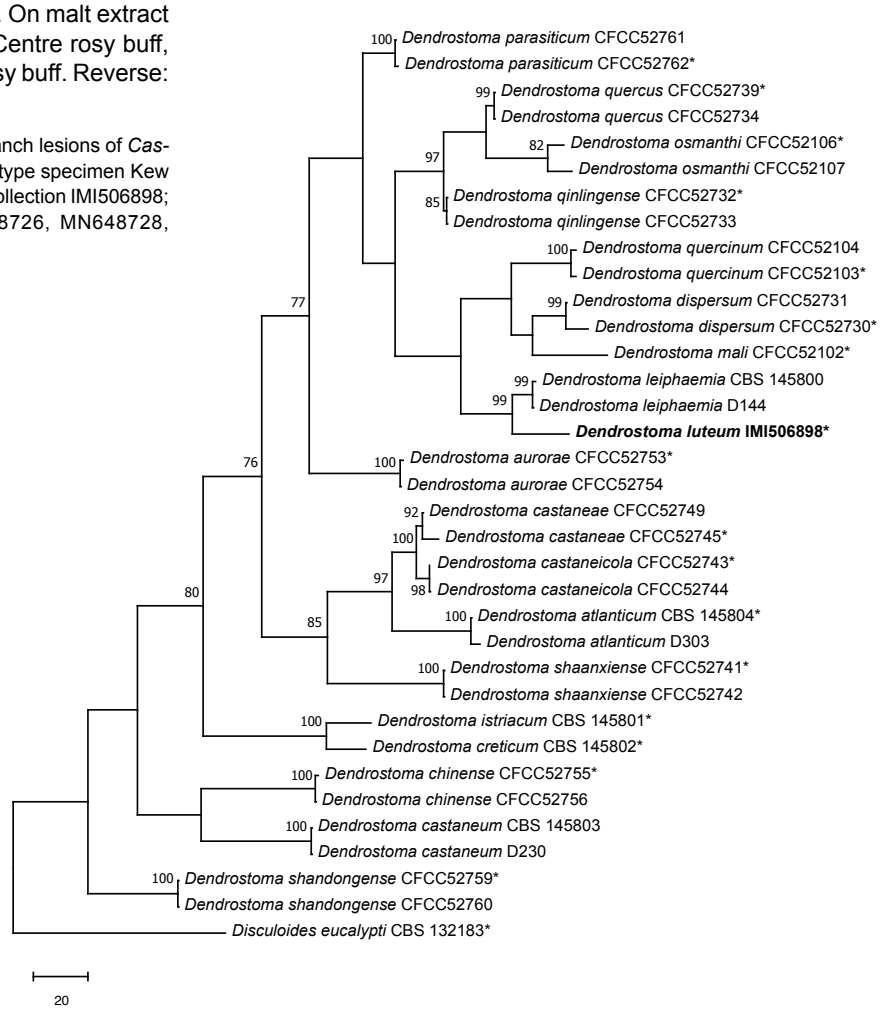
Classification — *Erythrogloeaceae*, *Diaporthales*, *Sordariomycetidae*, *Sordariomycetes*.

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.

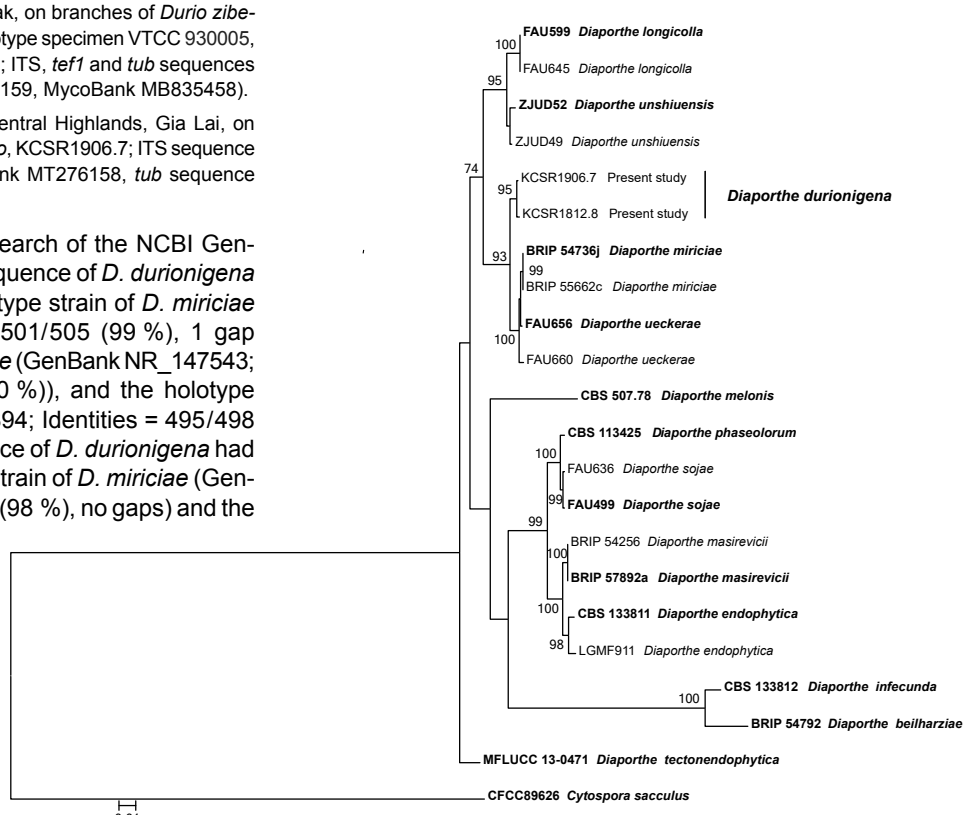
Culture characteristics — On potato dextrose agar (PDA), colonies white, fast-growing, covering dish after 10 d at 25 °C, surface buff with patches of purplish grey (Rayner 1970), reverse purplish grey, with patches of dirty white. On malt extract agar (MEA) with moderate aerial mycelium, and even, smooth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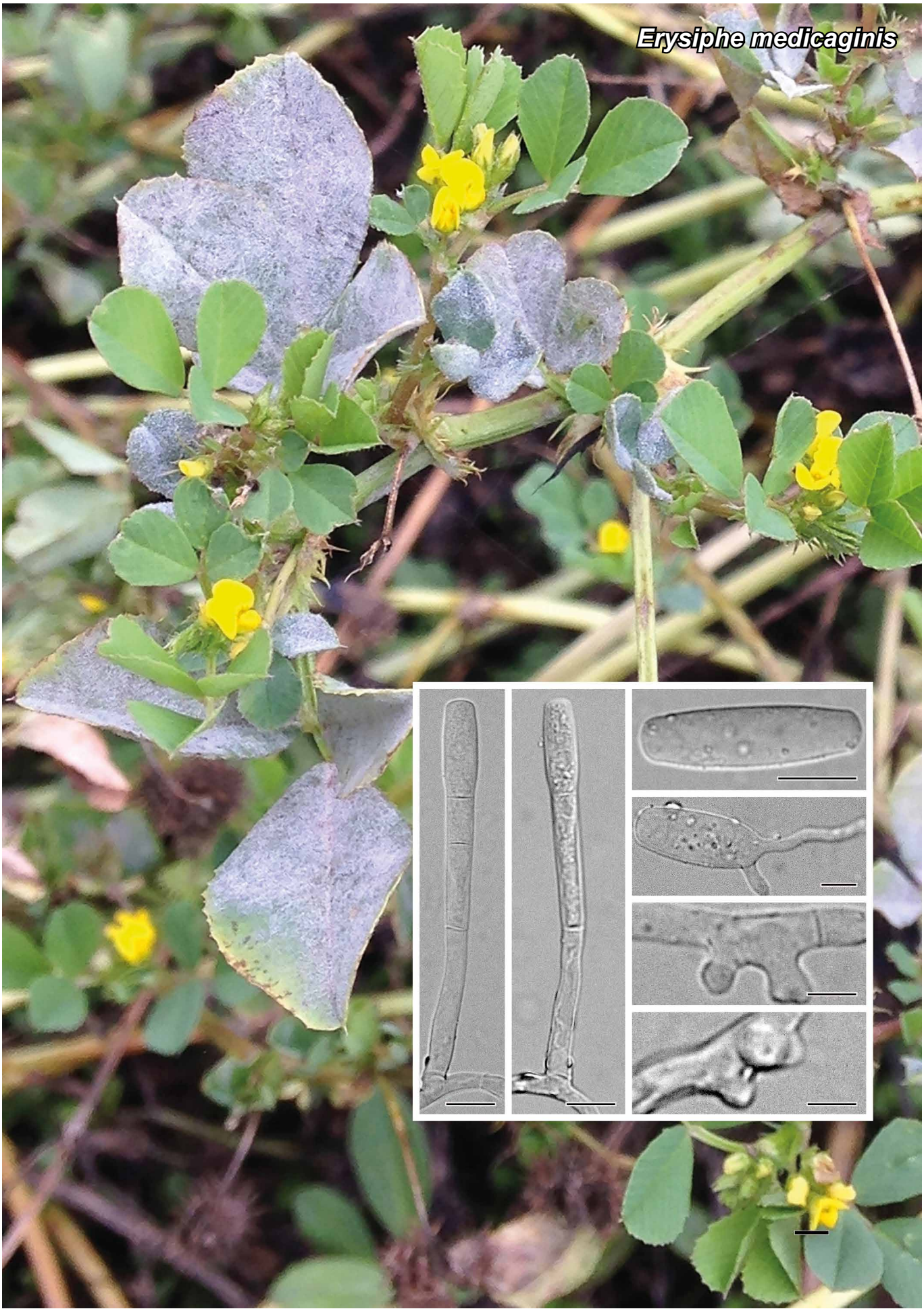

Erysiphe medicaginis

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).

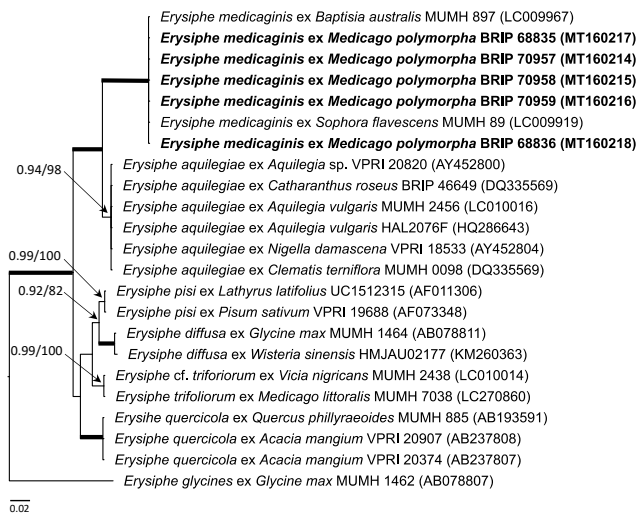
Additional material examined. Australia, Queensland, Tipton, -27.4403, 151.2465, on leaves of *M. polymorpha*, 19 Oct. 2017, *J.D.W. Dearnaley*, BRIP 68835; ITS sequence GenBank MT160217; Toowoomba, -27.5813, 151.9730, on leaves of *M. polymorpha*, 21 June 2018, *S. Takamatsu*, BRIP 68836; ITS sequence 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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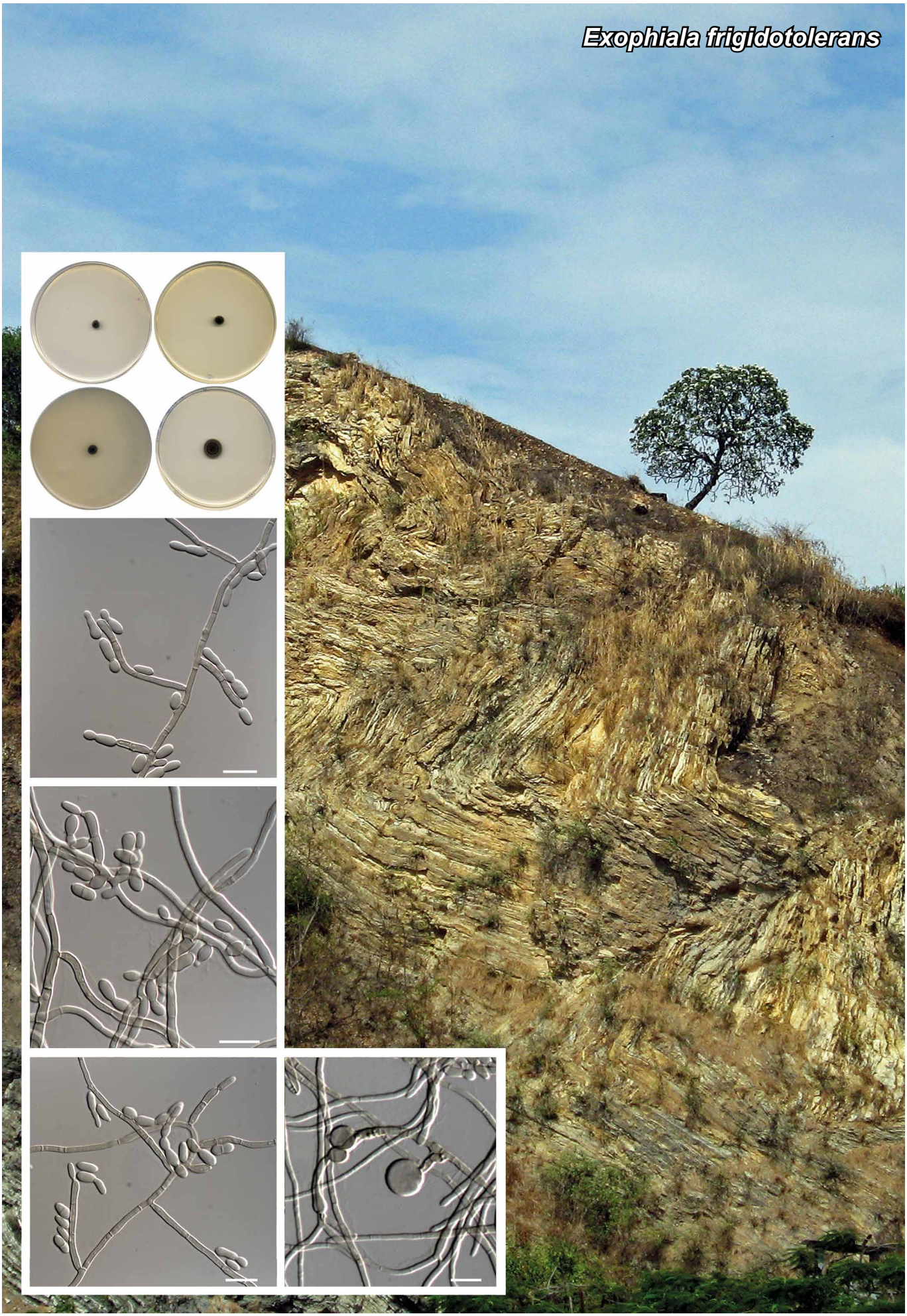

Exophiala frigidotolerans

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*.

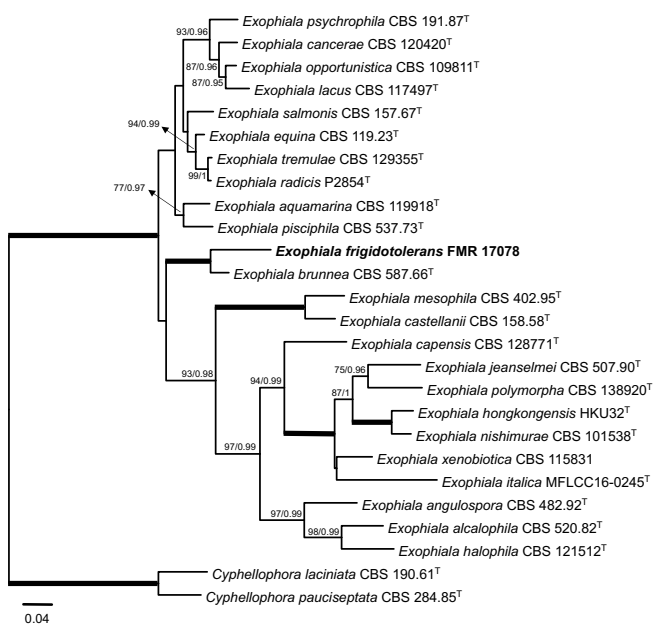
Mycelium composed of pale olivaceous brown, septate, branched, smooth- and thin-walled hyphae, 1–3 µm wide; older hyphae being more strongly pigmented. *Spirally twisted hyphae* present. *Moniliform cells* scarce, globose to ellipsoidal, in short chains (–5 cells). *Conidiophores* semi-micronematous, 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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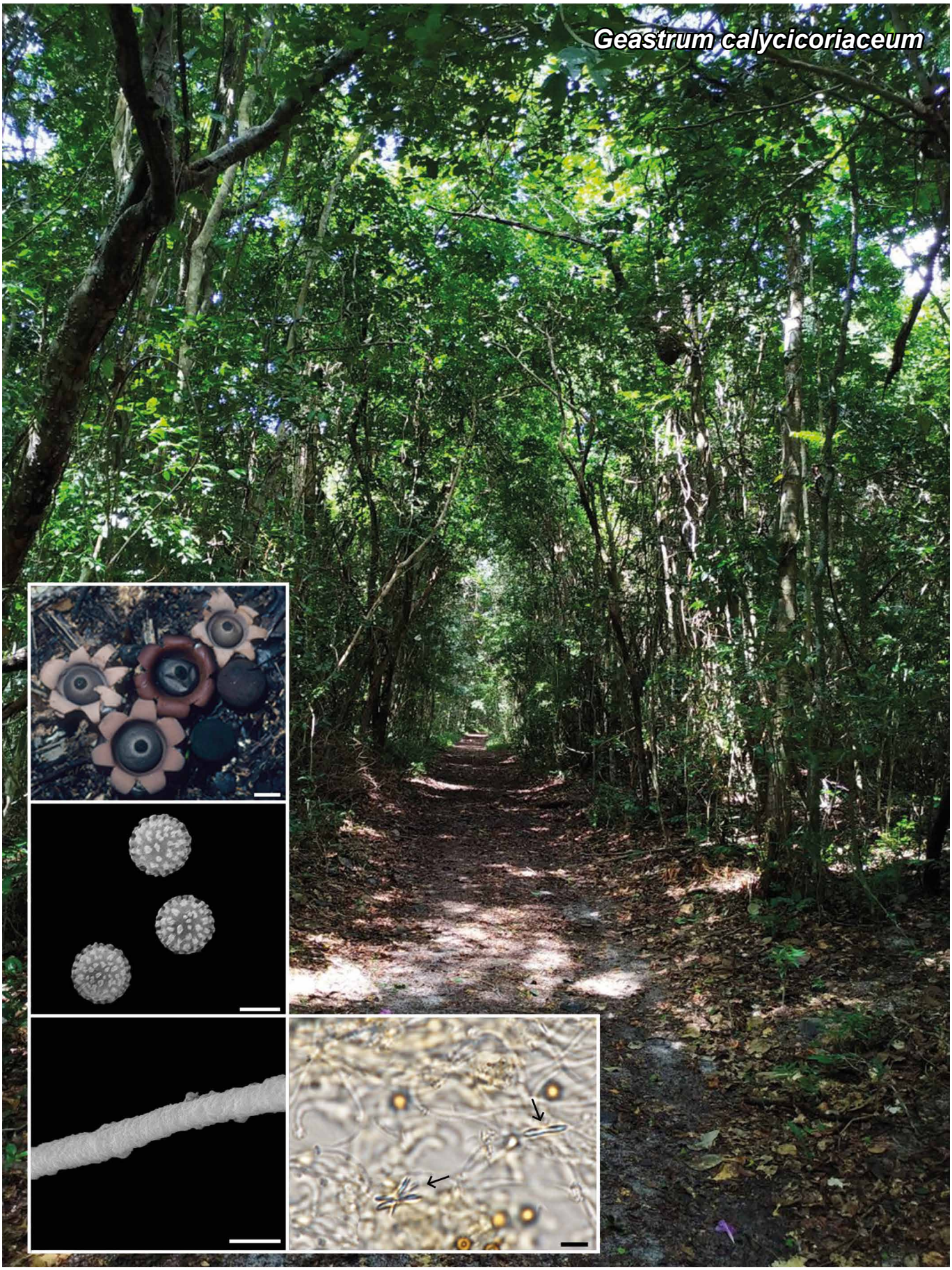
Geastrum calycicoriaceum

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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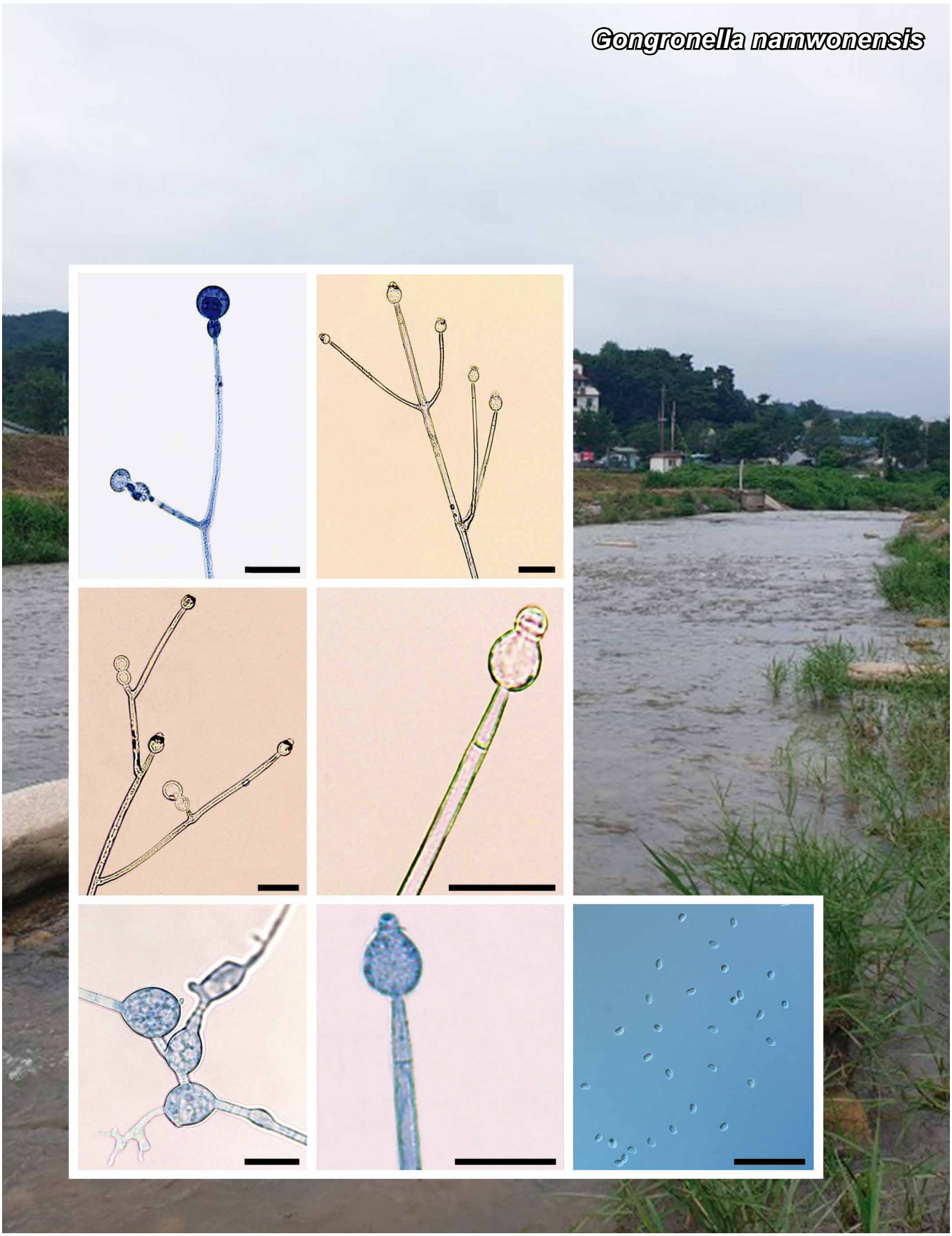

Gongronella namwonensis

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.

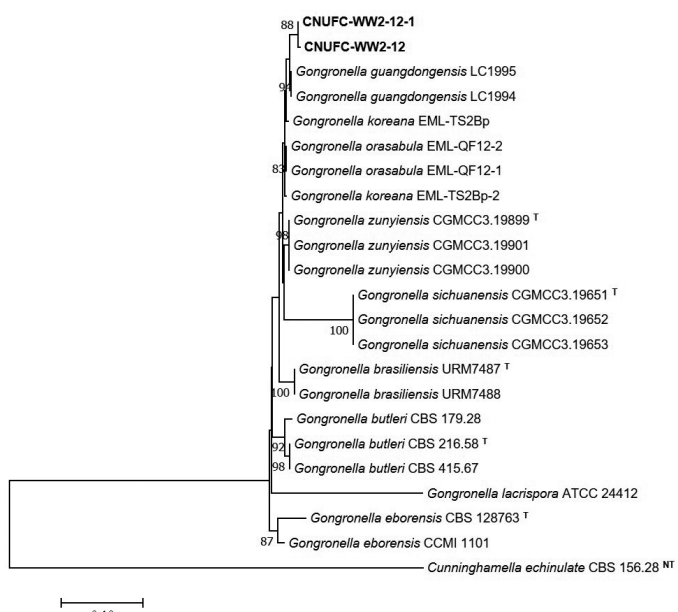
Classification — *Cunninghamellaceae*, *Mucorales*, *Mucoromycotina*, *Mucoromycota*, *Mucoromyceta.*

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*.

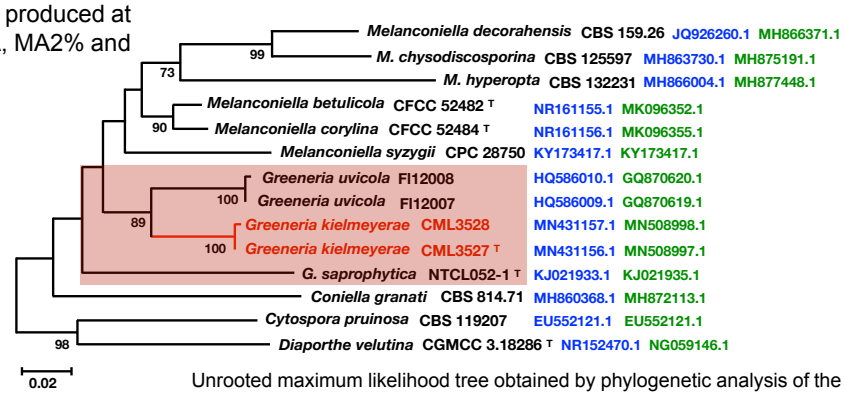
Pathogenic on leaves of *Kielmeyera coriacea*. *Leaf spots* up to 3 cm diam, rather irregular, sometimes confluent and covering almost the whole blade, often at the margins, amphigenous, showing small dark points of conidiomata at the upper side of the leaves. *Conidiomata* acervular at maturity, 175–300 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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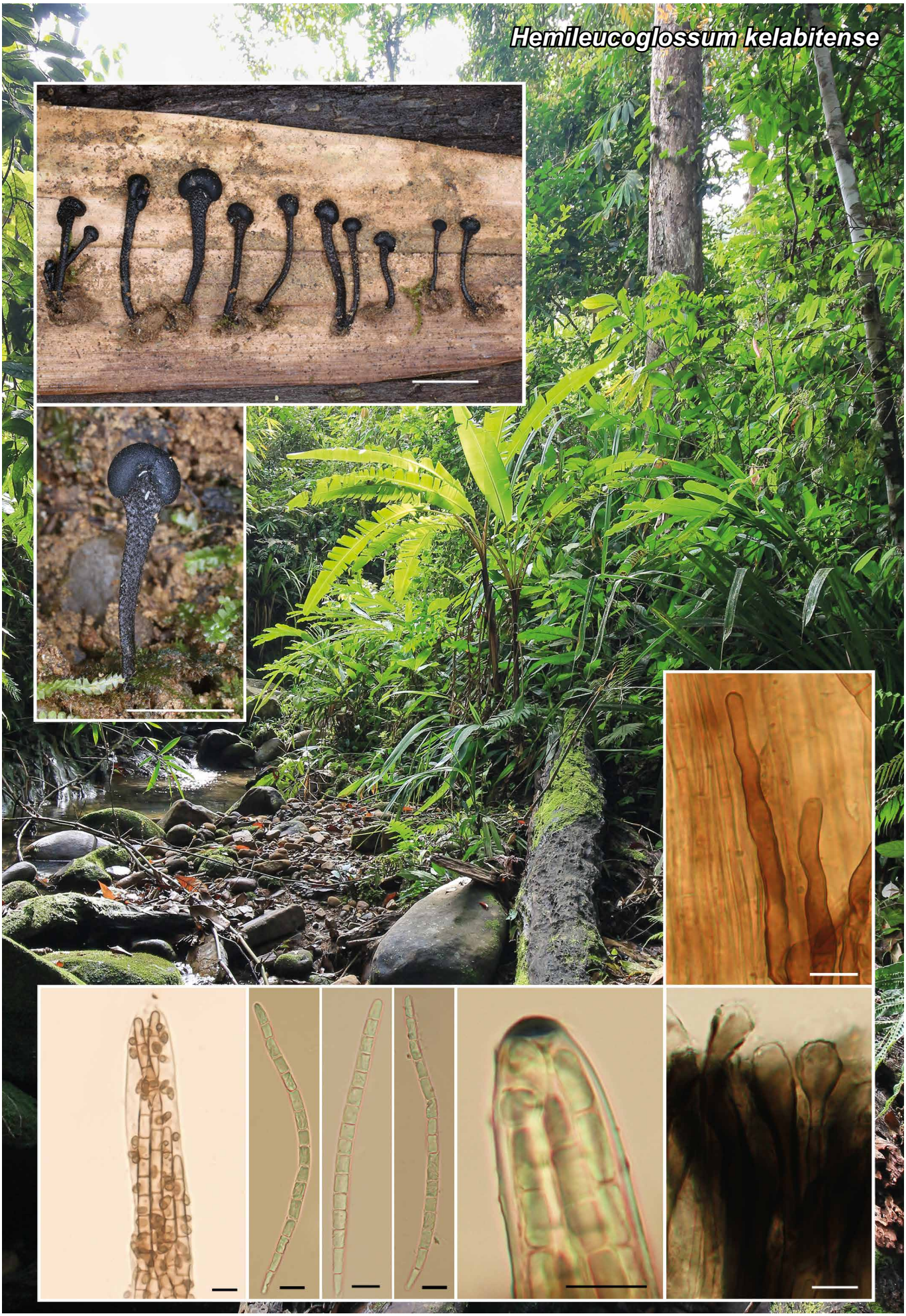

Hemileucoglossum kelabitense

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.

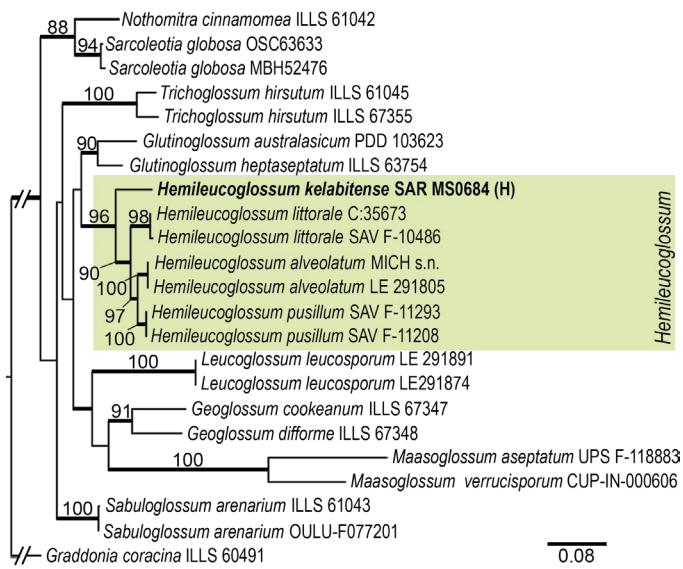
Classification — *Geoglossaceae*, *Geoglossales*, *Geoglossomycetes*.

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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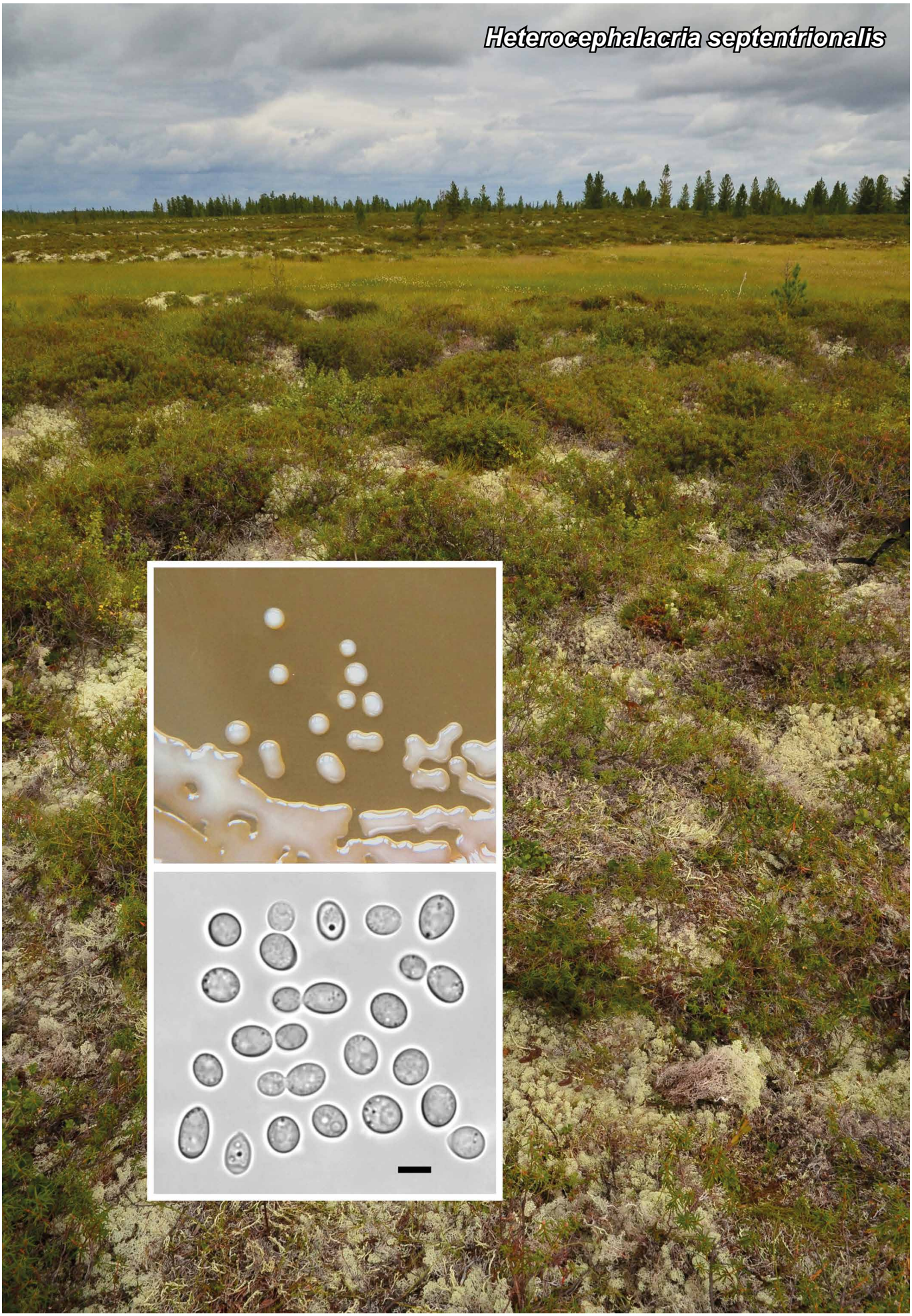

Heterocephalacria septentrionalis

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*.

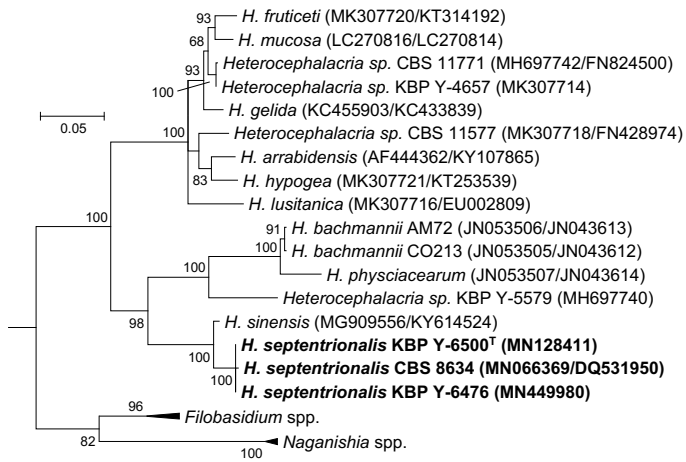
On glucose peptone yeast extract agar (GPYA) and 5 % malt extract agar (MEA), after 7 d at 20 °C, *streak* is cream-coloured, shiny and mucoid, with an entire margin, and flat profile. After a month, the colour of the streak is pinkish cinnamon. *Cells* are globose, ovoid to ellipsoid, 4–7 × 2.5–4 µm, 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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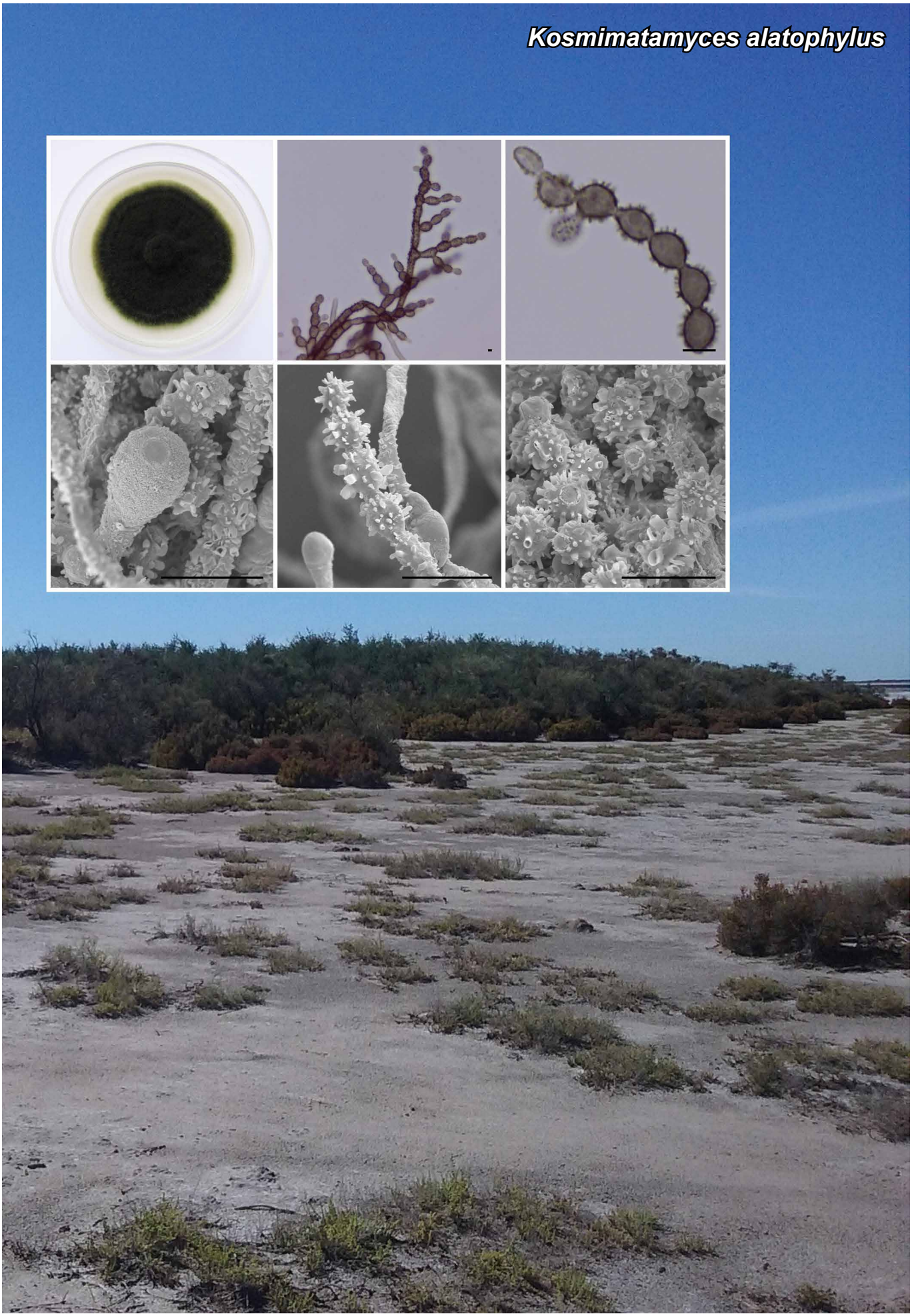
Kosmimatamyces alatophylus

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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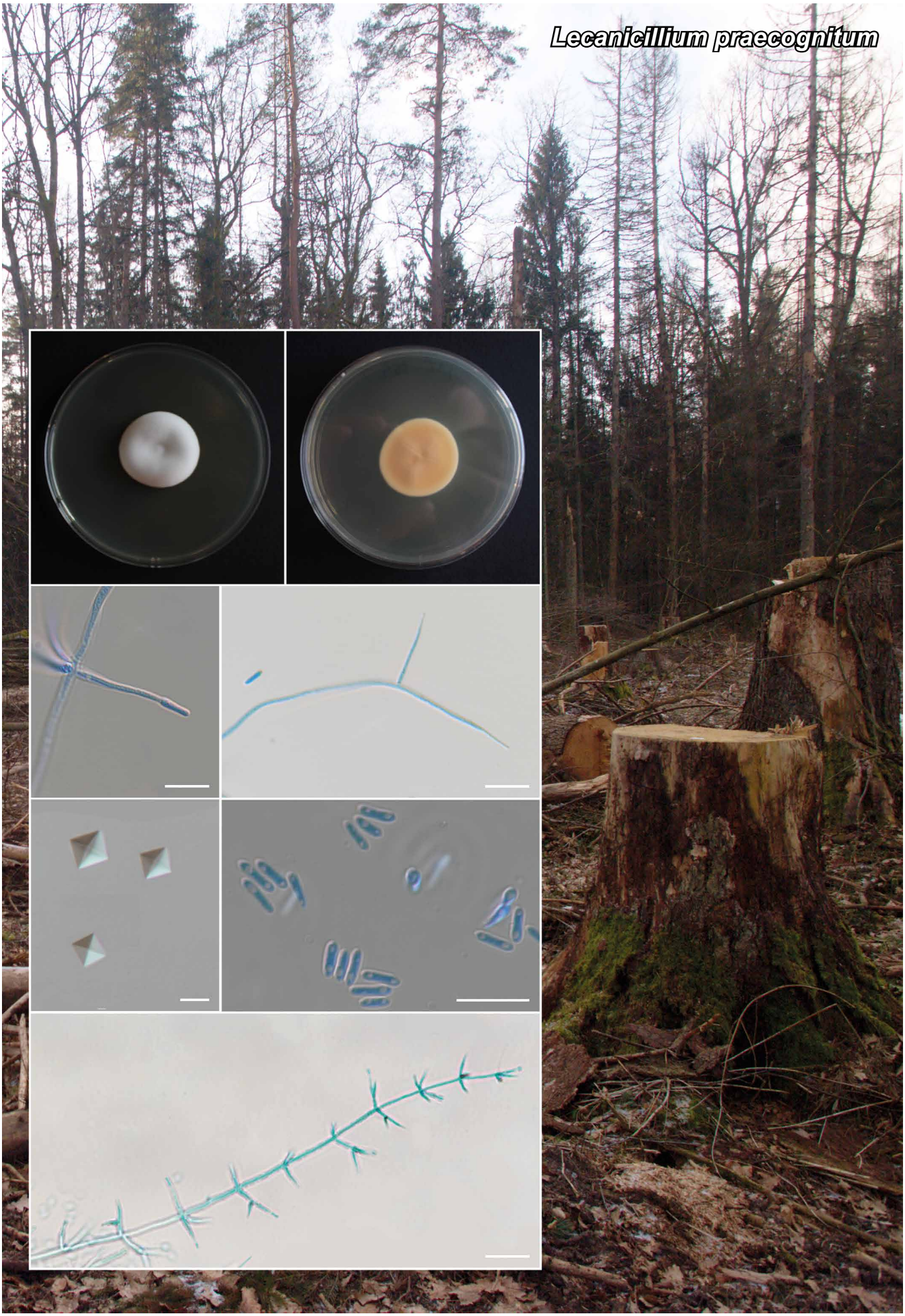

Lecanicillium praecognitum

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.

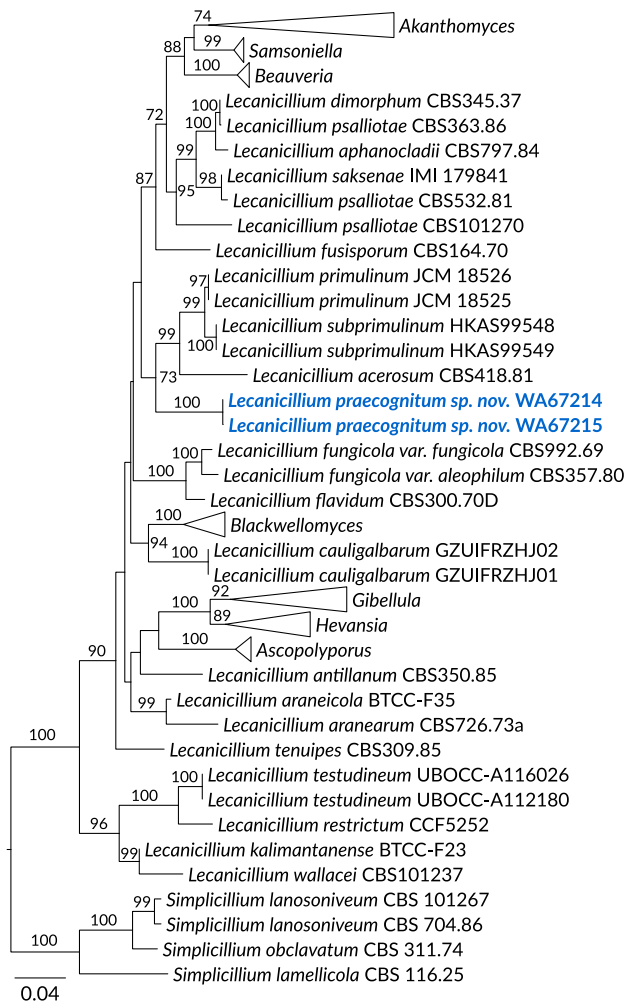
Culture characteristics — (in darkness, 20 ± 2 °C). Colonies cottony, margin even to slightly irregular, with dense and abundant aerial mycelium. On SDA and potato dextrose agar (PDA) averse white, reverse creamy to yellow, reaching 3 cm in 14 d, 5.5 cm in 21 d. Octahedral crystals produced in the medium 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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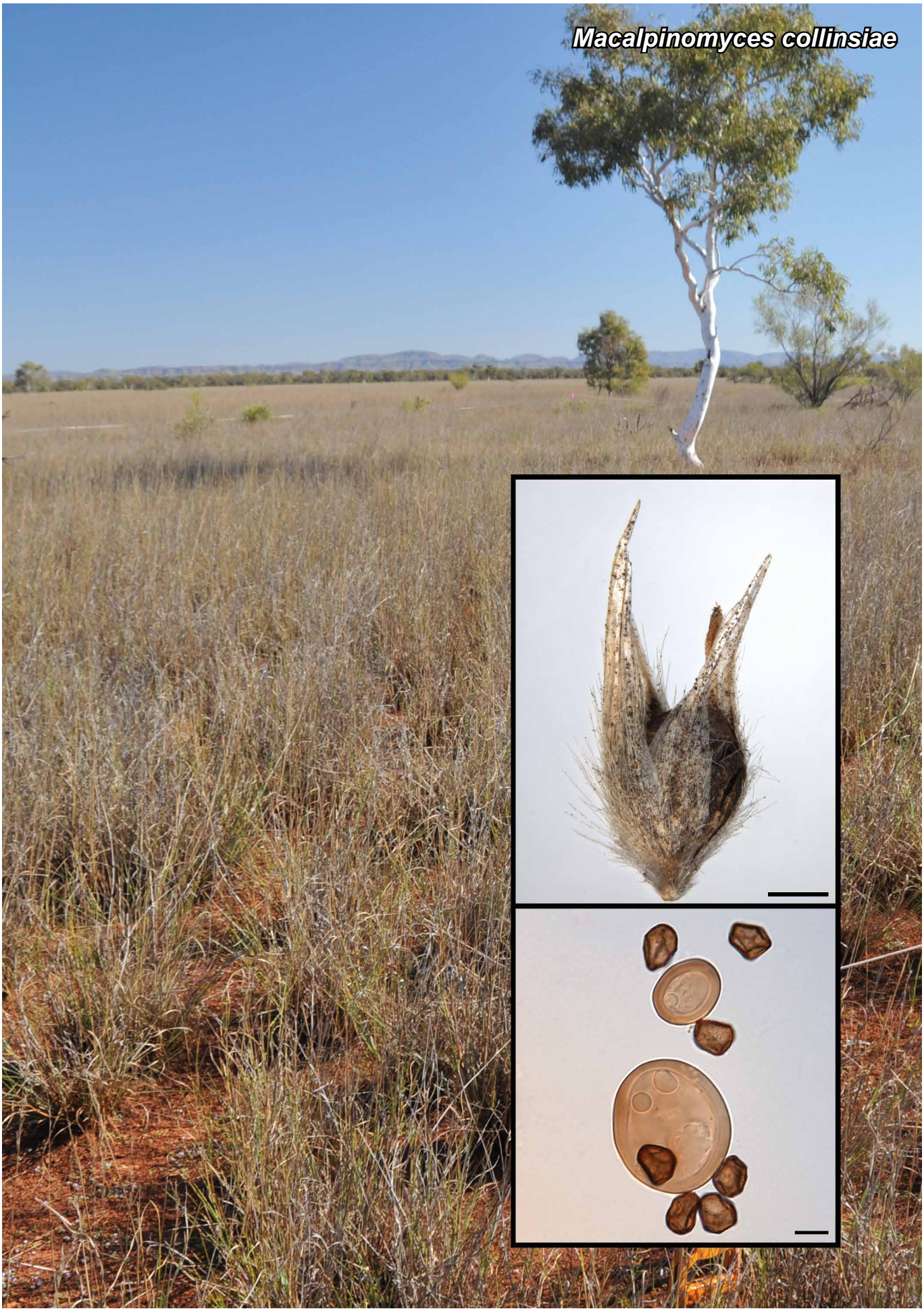

Macalpinomyces collinsiae

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.

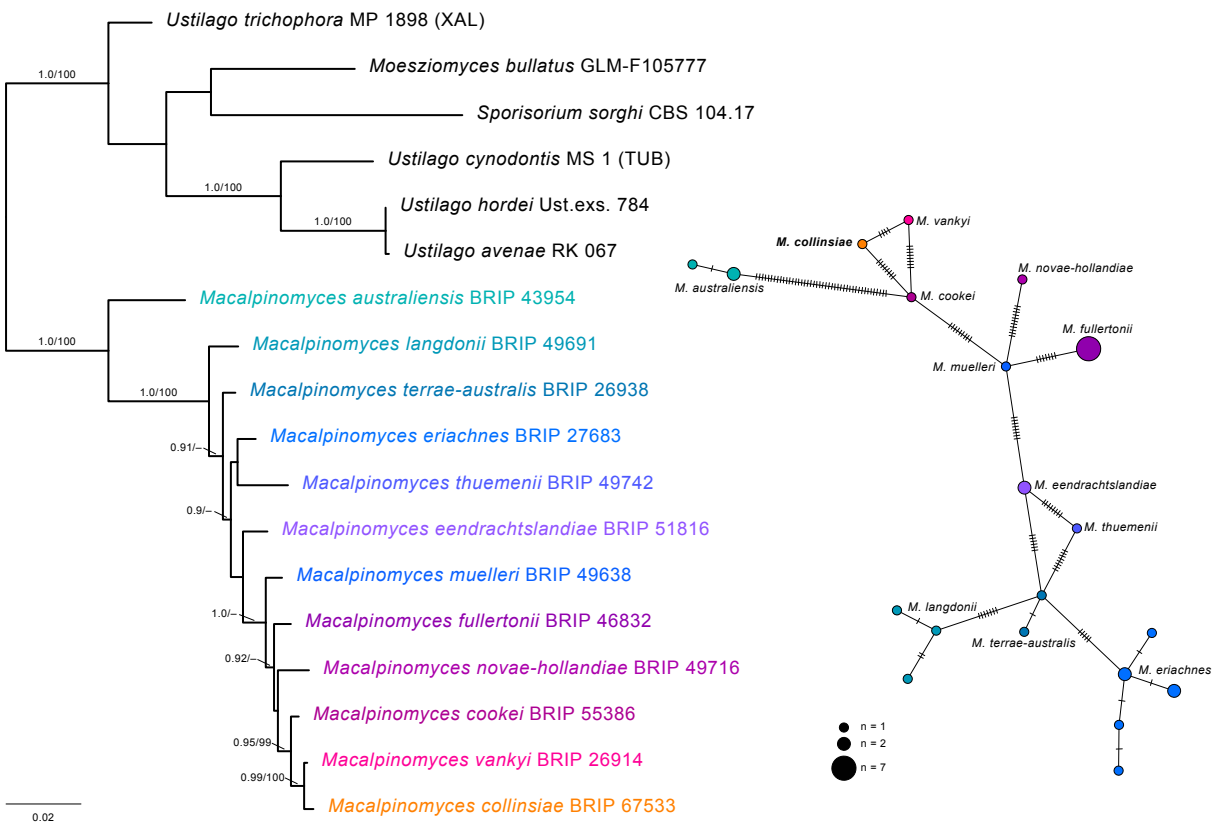
Classification — *Ustilaginaceae*, *Ustilaginales*, *Ustilaginomycetes*.

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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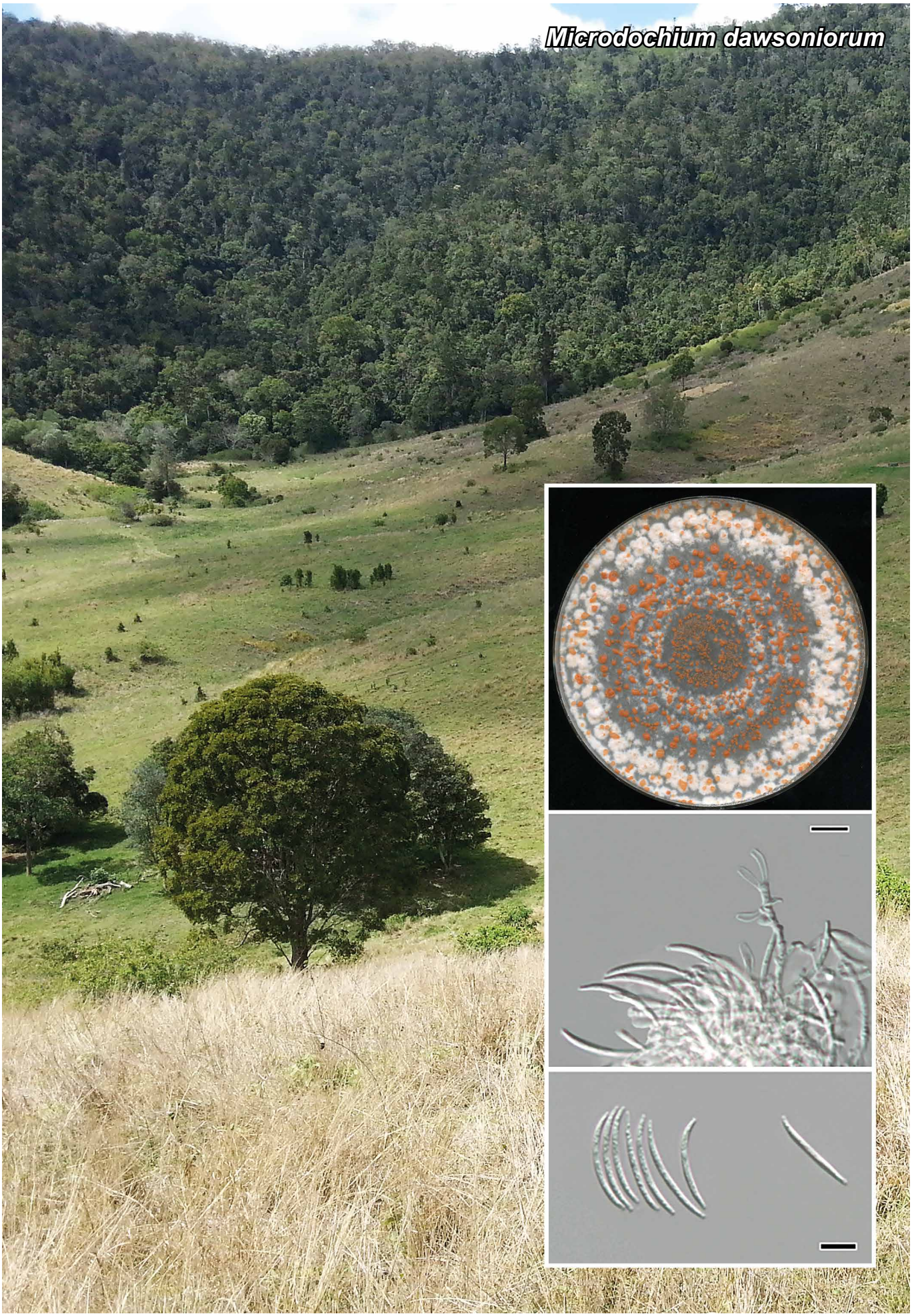

Microdochium dawsoniorum

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.

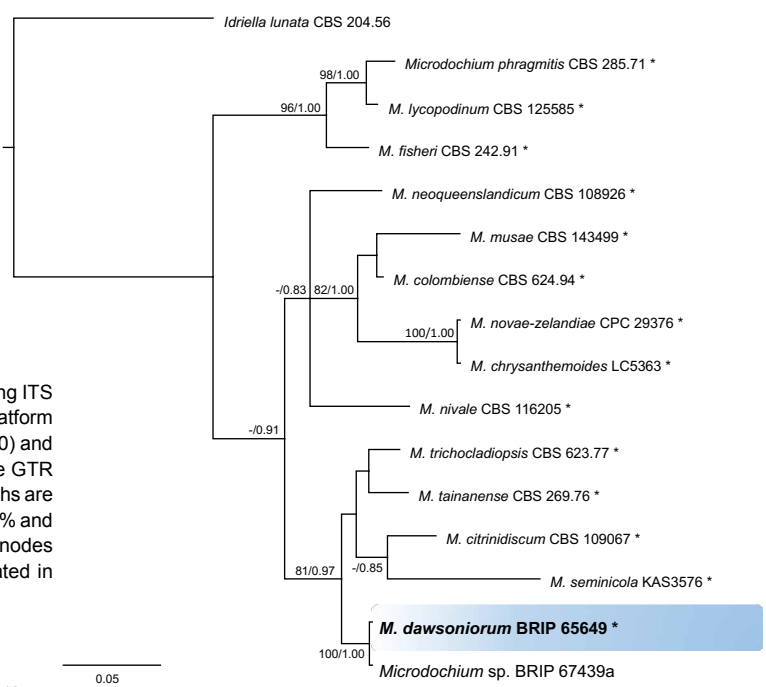
Culture characteristics — *Colonies* on oatmeal agar (OA) after 2 wk covering 9 cm diam plates, flat, mycelium in compact irregular to concentric scattered salmon tufts, with abundant slimy apricot sporodochia up to 3 mm arranged in irregular to concentric rings. Reverse pale saffron with sporodochia 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.

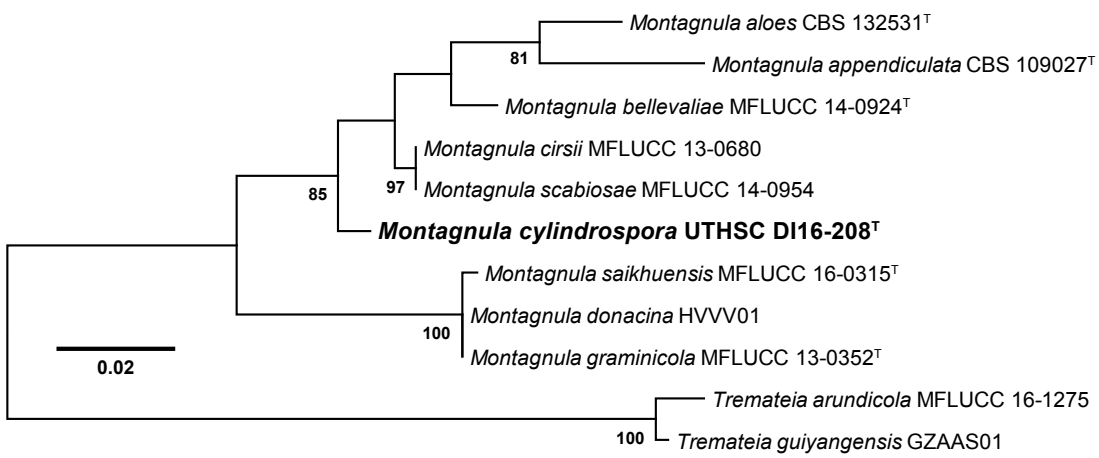
Classification — *Didymosphaeriaceae*, *Pleosporales*, *Dothideomycetes*.

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.

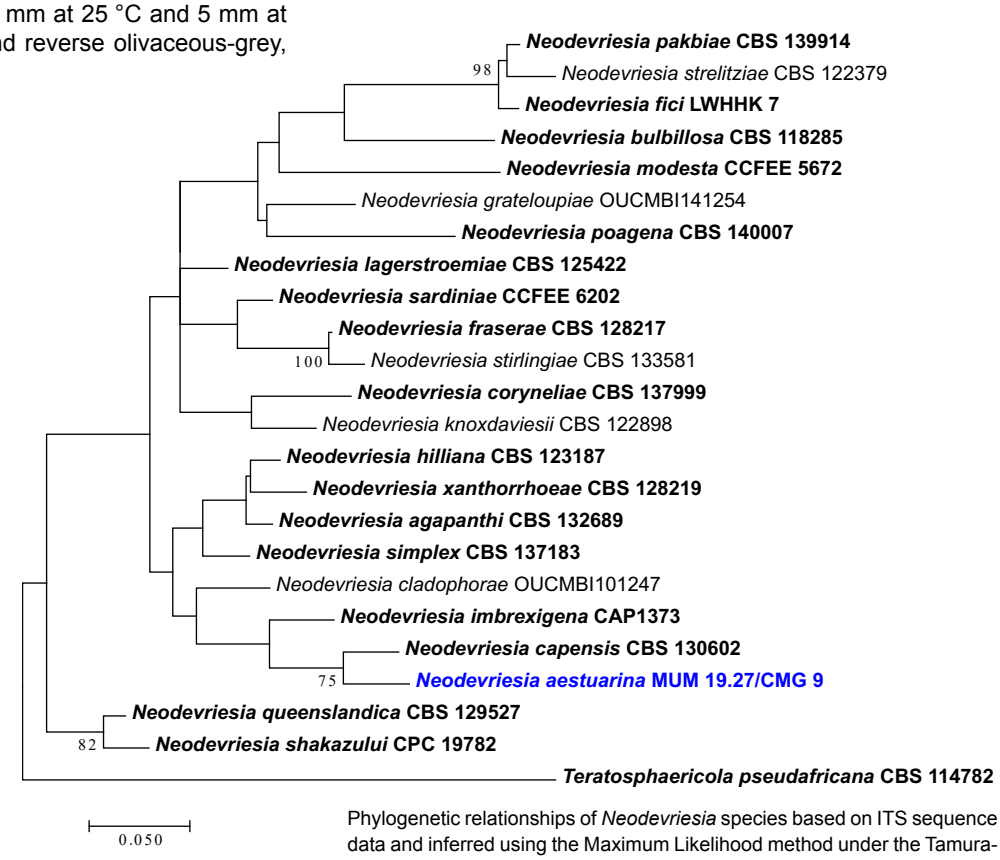
Classification — *Neodevriesiaceae*, *Mycosphaerellales*, *Dothideomycetes*.

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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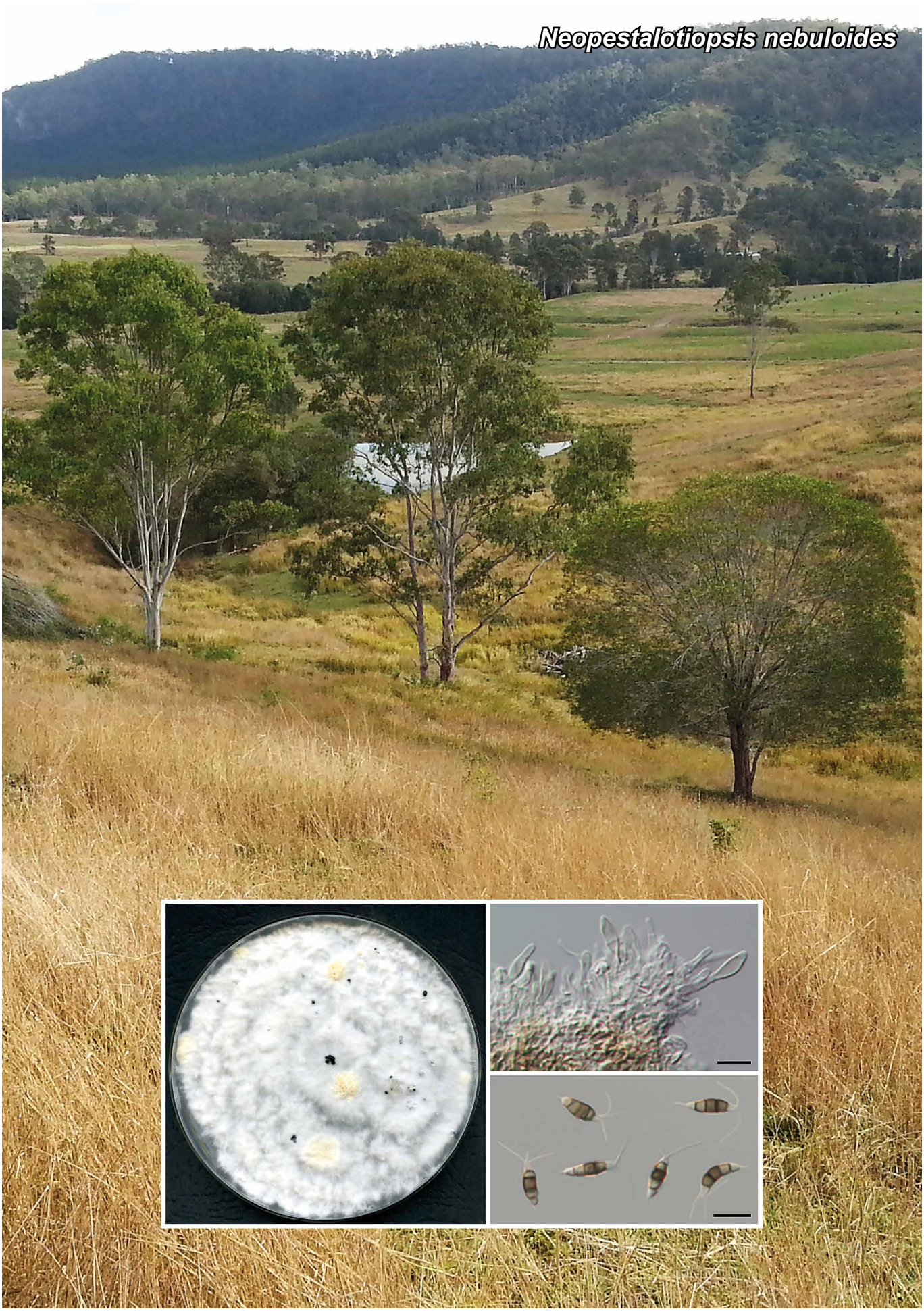

Neopestalotiopsis nebuloides

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.*

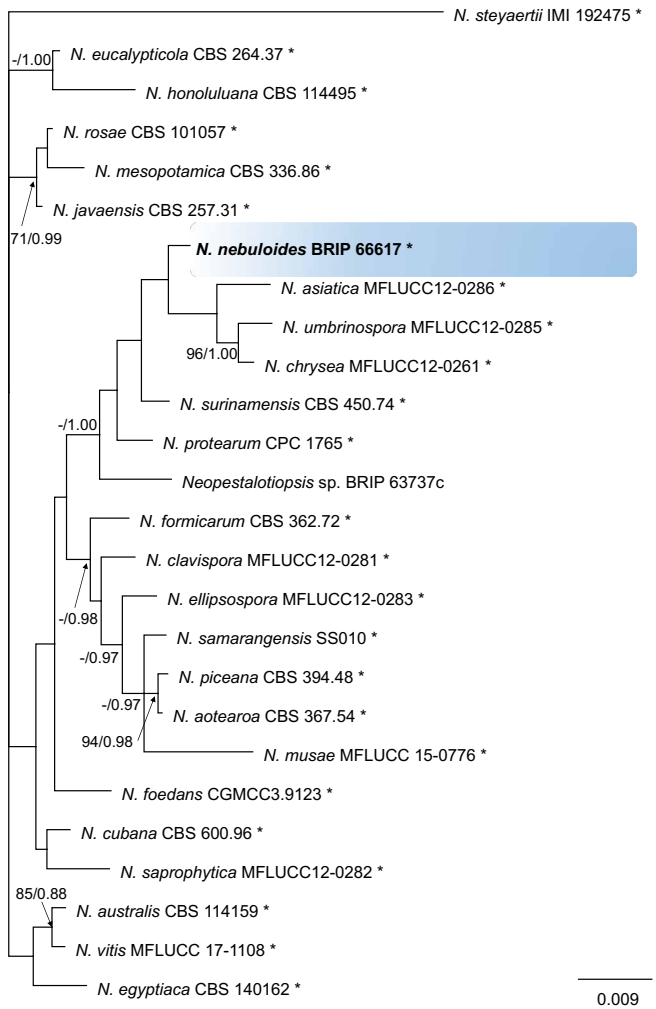
Conidiomata pycnidial on 1/2 potato dextrose agar (PDA), globose or clavate, scattered or aggregated, semi-immersed, black, up to 250 µm diam; exuding dark brown to black conidial masses. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* discrete, ampulliform, hyaline, smooth, 5–10 × 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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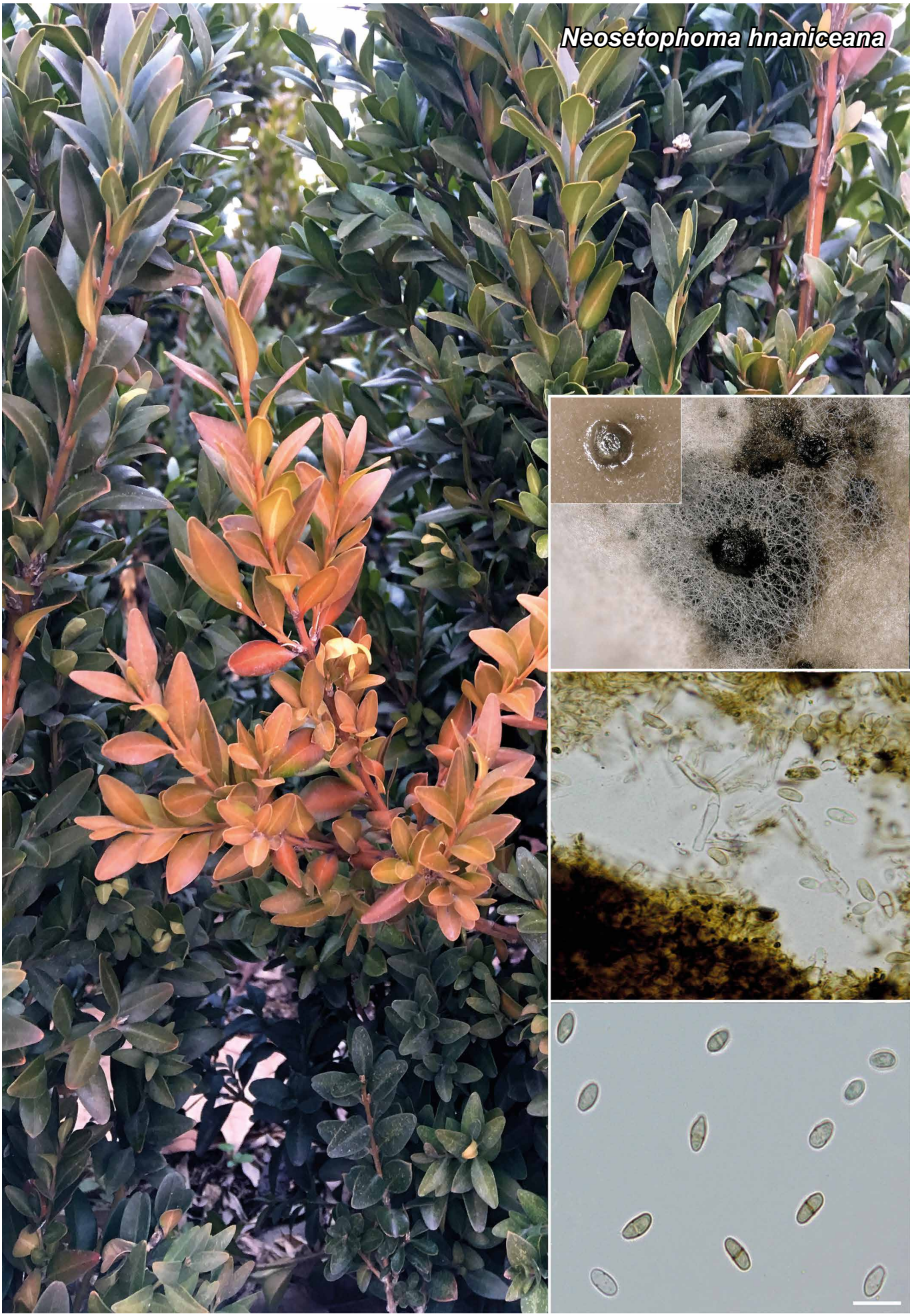

Neosetophoma hnaniceana

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.

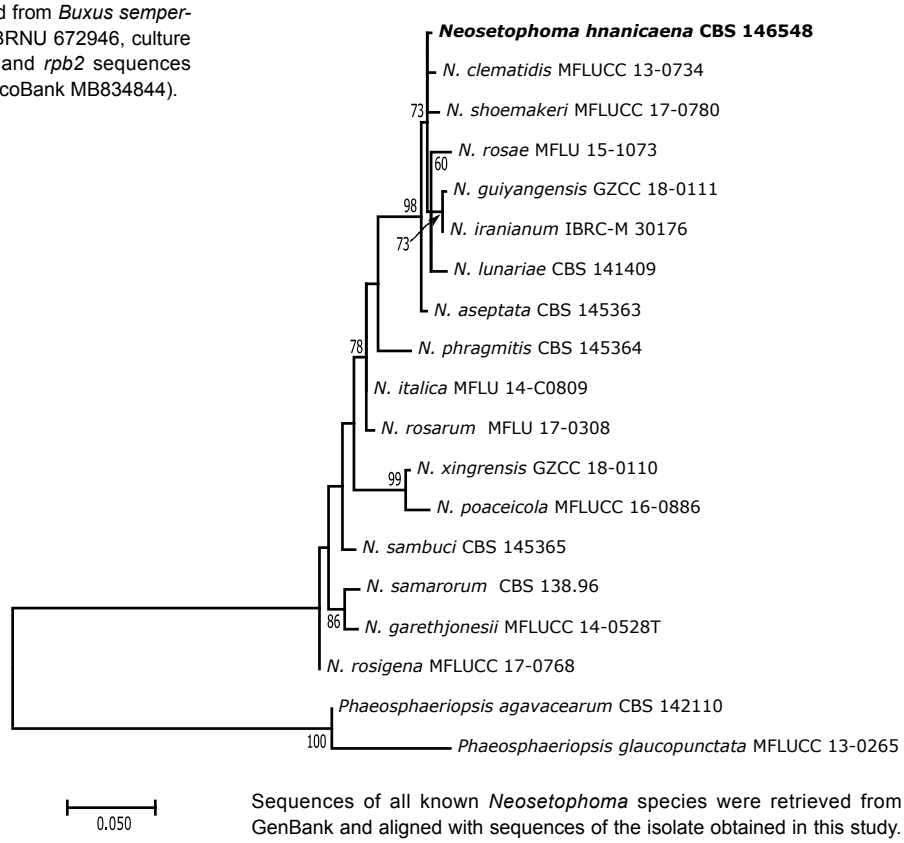
Classification — *Phaeosphaeriaceae*, *Pleosporales*, *Dothideomycetes*.

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.

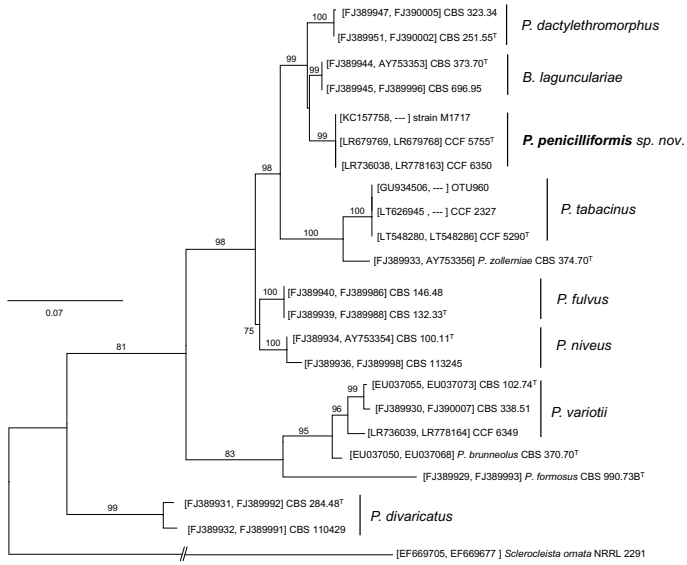
Typus. USA, Wisconsin, Menasha, pharmacy, air, 17 Mar. 2016, *Ž. Jurjević* (holotype BPI 911216, cultures ex-type CCF 5755 = CBS 146003 = EMSL 3392; ITS, LSU, β-tubulin and calmodulin sequences GenBank LR679769, LR679770, LR679768 and LR778299, MycoBank MB834874).

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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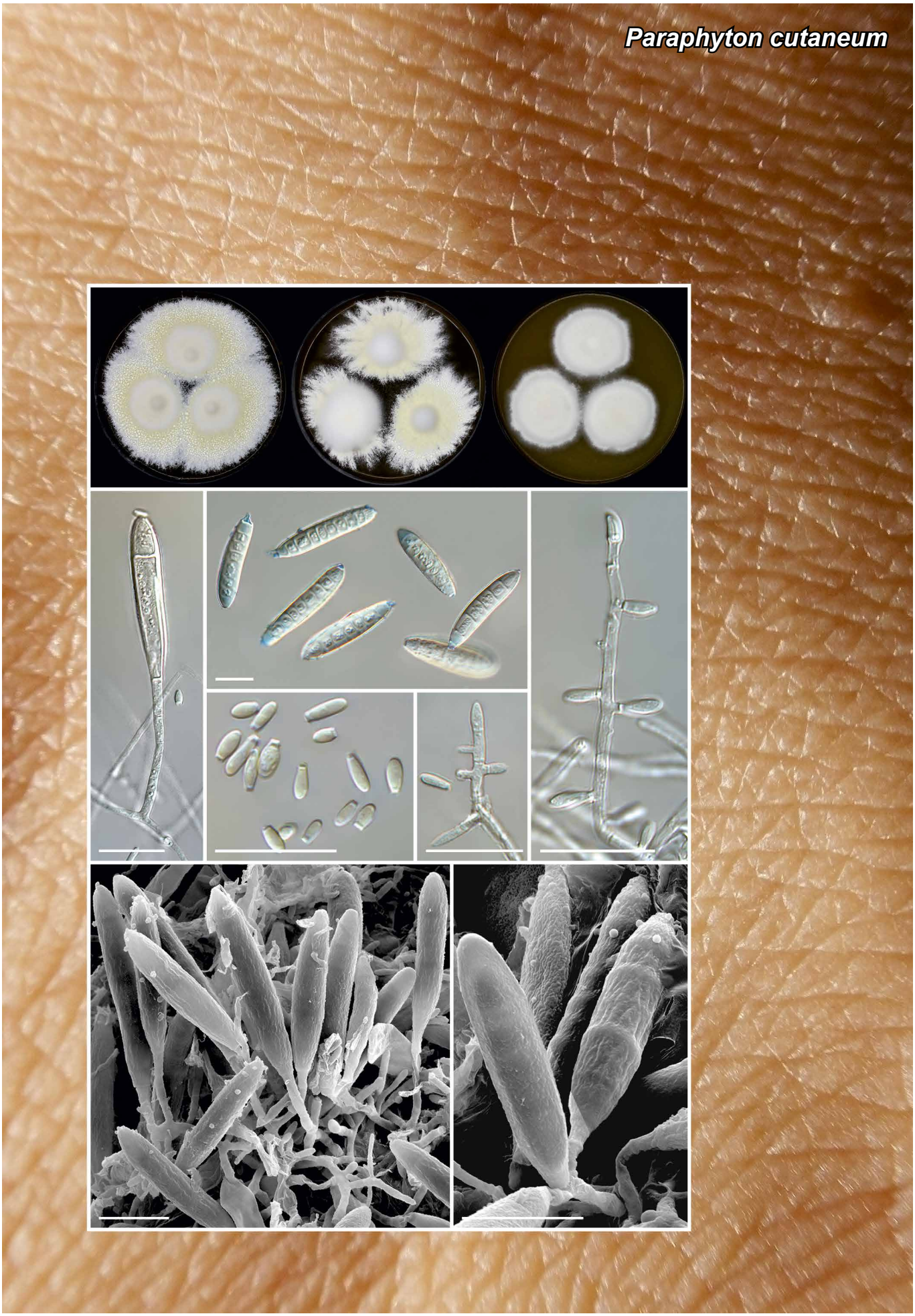
Paraphyton cutaneum

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.

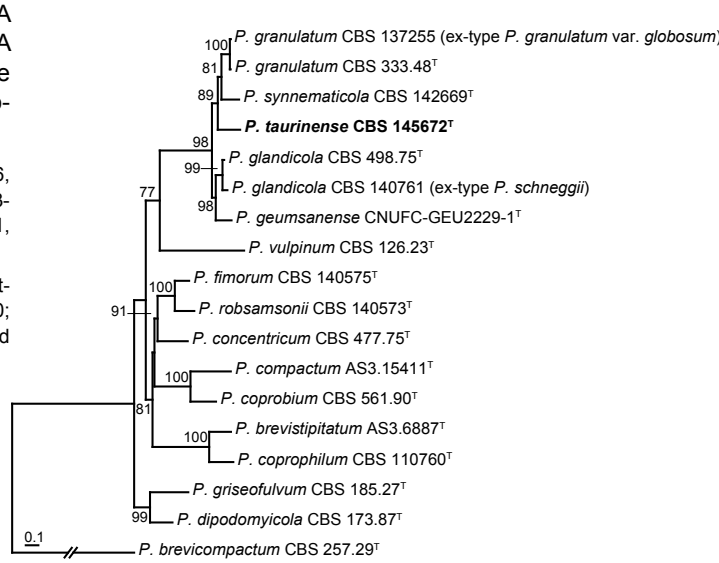
Typus. Italy, Piedmont Region, from indoor chestnut mill, Nov. 2016, *S. Prencipe* (holotype CBS H-24332, culture ex-type CBS 145672 = DTO 333-B8 = CAS16; ITS, *BenA*, *CaM* and *RPB2* sequences GenBank MF595981, MF595977, MF595979 and MT253108; MycoBank MB834715).

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*.

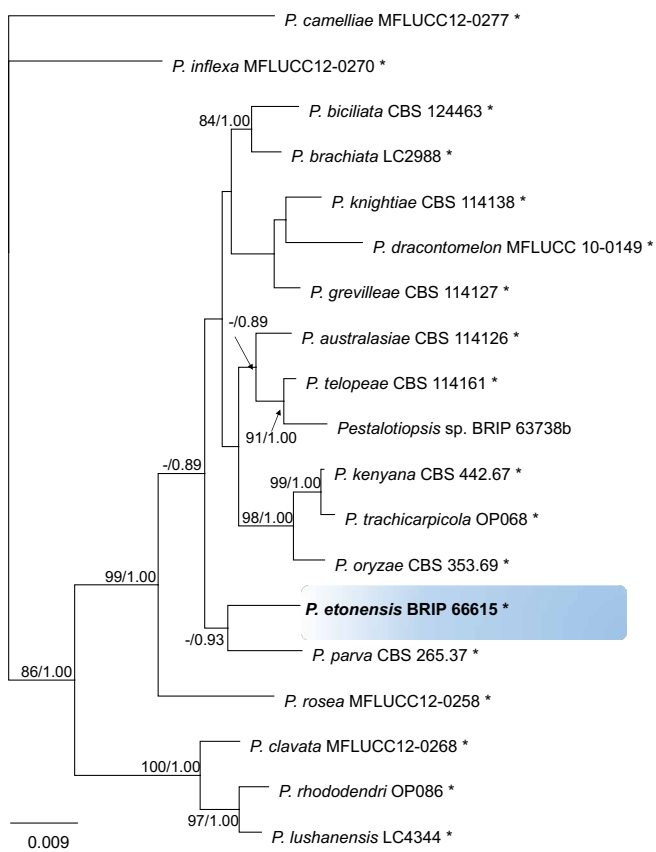
Conidiomata pycnidial on 1/2 potato dextrose agar (PDA), globose or clavate, scattered or aggregated, immersed or semi-immersed, dark brown to black, up to 470 µm diam; exuding dark brown to black conidial masses. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* discrete, cylindrical, 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).

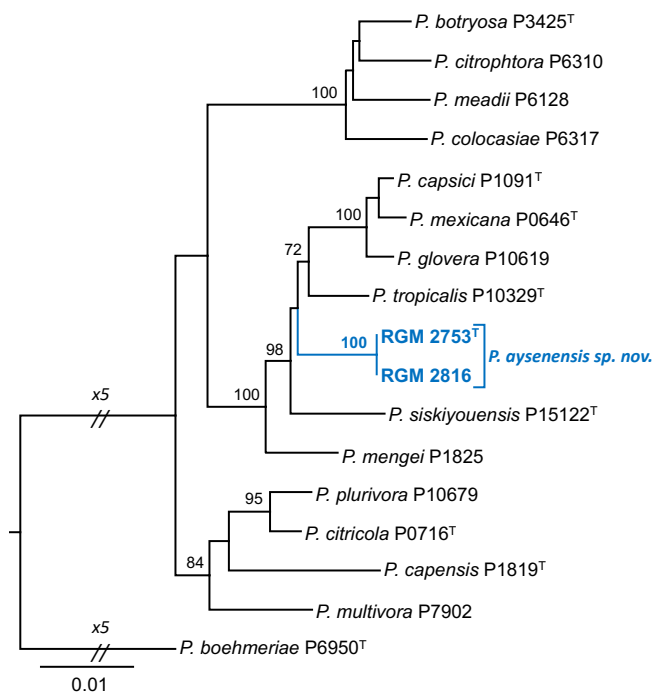
Culture characteristics — Colonies on CAS showed appressed to submerged mycelium, without distinct growth pattern, reaching 63.4 ± 1.3 mm diam after 7 d at 20 °C in darkness. Colonies on corn meal agar (CMA) white, with moderate to profuse aerial mycelium, cottoned, reaching 56.9 ± 2.5 mm diam.

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*.

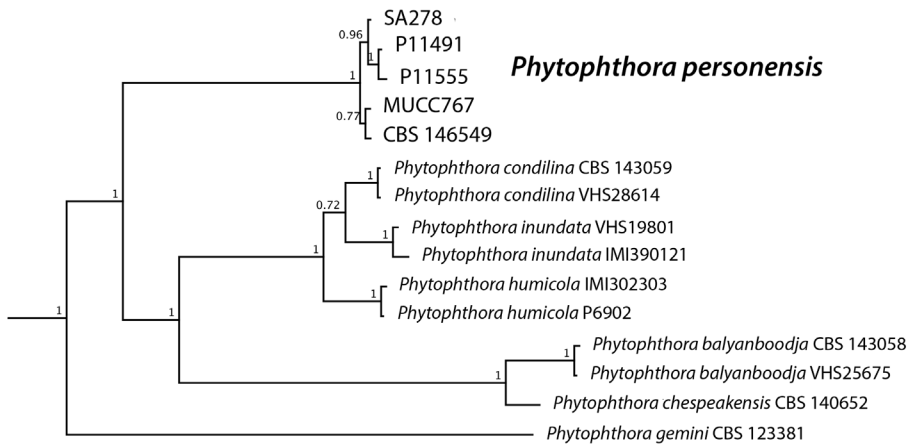
Sporangia produced abundantly in non-sterile soil extract; persistent and produced usually on unbranched sporangiophores, non-papillate, most commonly ovoid (73 %), often ellipsoid (18 %) and rarely limoniform or obpyriform; 62.8 ± 12.7 × 44.2 ± 9.9 µm (overall range 28.5–85.6 × 15.1–60.5 µm), length/breadth 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.

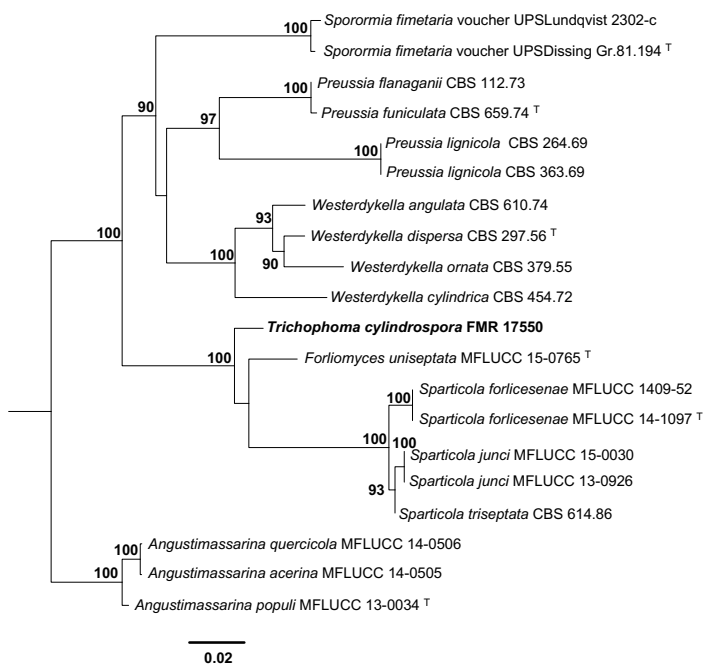
Culture characteristics — (7 d at 25 °C). Colonies on potato dextrose agar (PDA) reaching 24 mm diam, flattened, velvety, margins regular, yellowish white to reddish brown (M. 4A2 / 8D8; Kornerup & Wanscher 1978); reverse reddish brown to dark brown (M. 8E8 / 8F8), exopigment reddish brown to golden 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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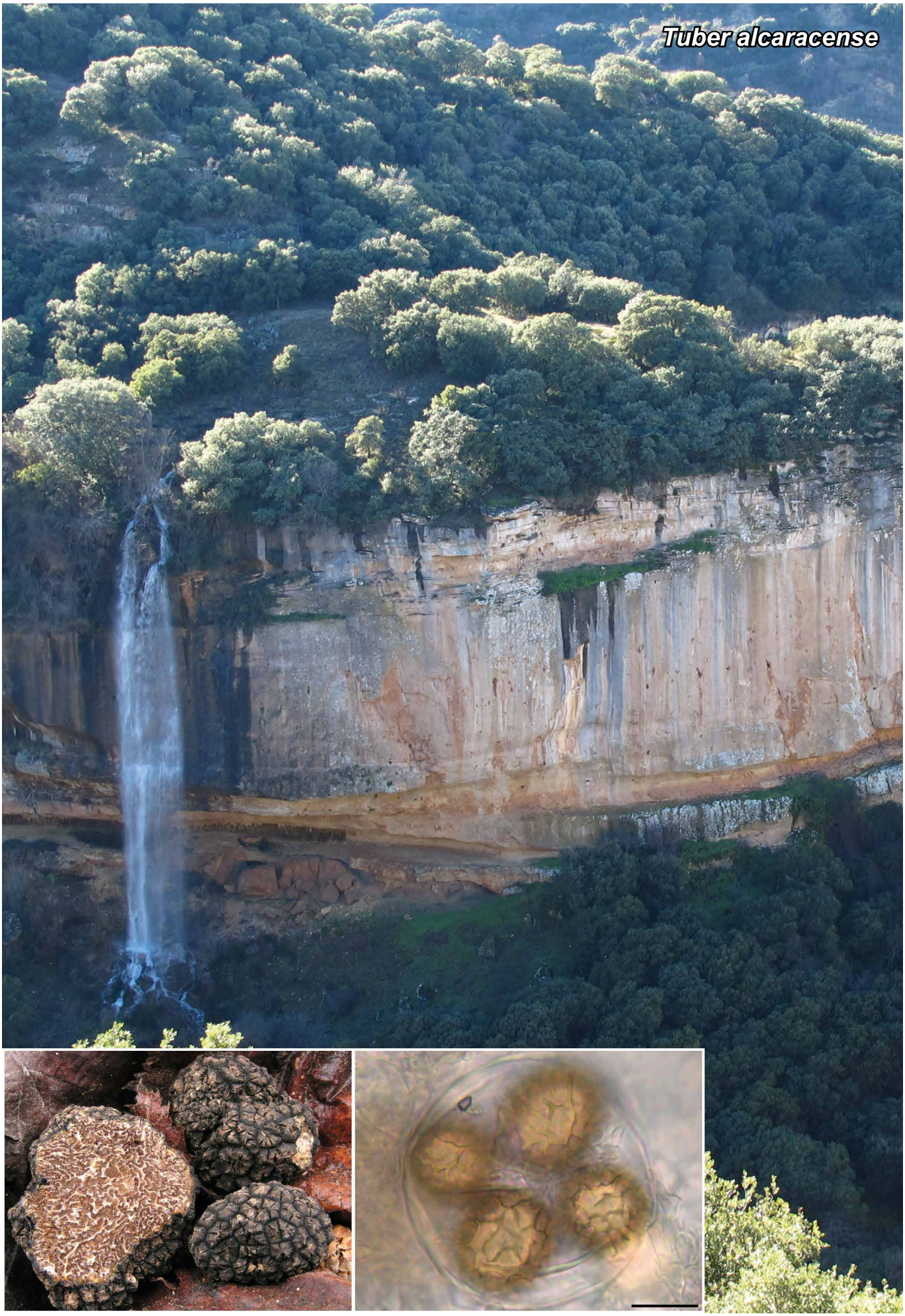

Tuber alcaracense

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.*

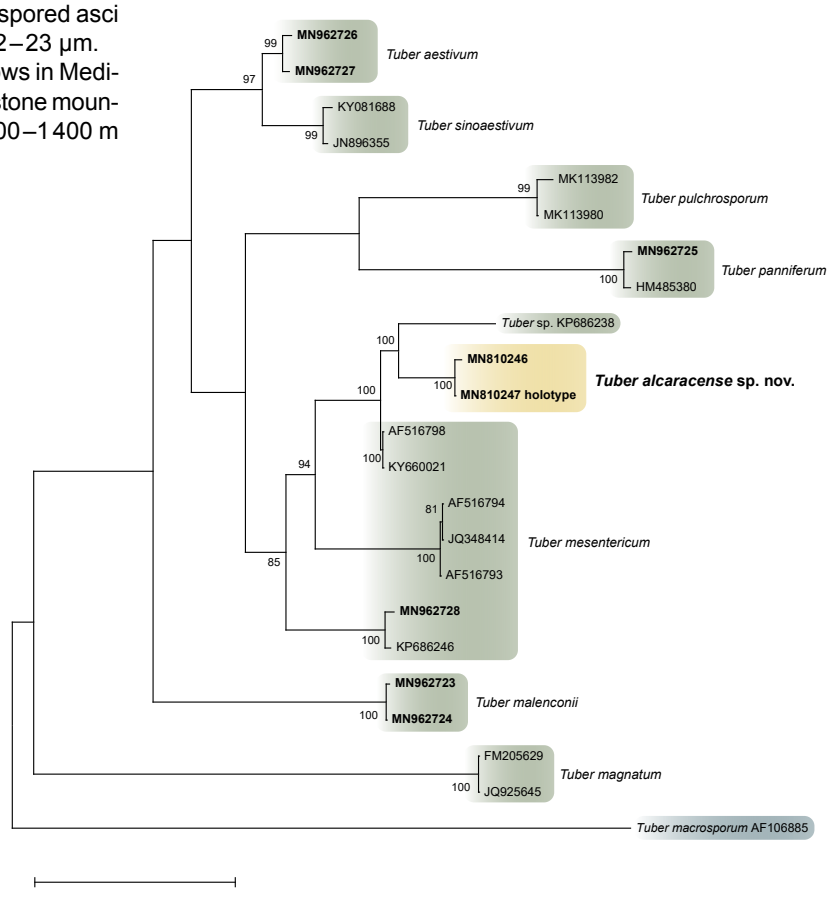
Ascomata hypogeous, 1–4 cm, subglobose, covered with brown-black pyramidal warts, 4–6-sided, 2–3(–4) mm across, 1–4 mm high, often depressed at the apex. *Peridium* 150–250 µm thick, pseudoparenchymatous, composed of subglobose, angular cells, 10–20 µm diam, pale yellow and thin-walled in the innermost 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*.

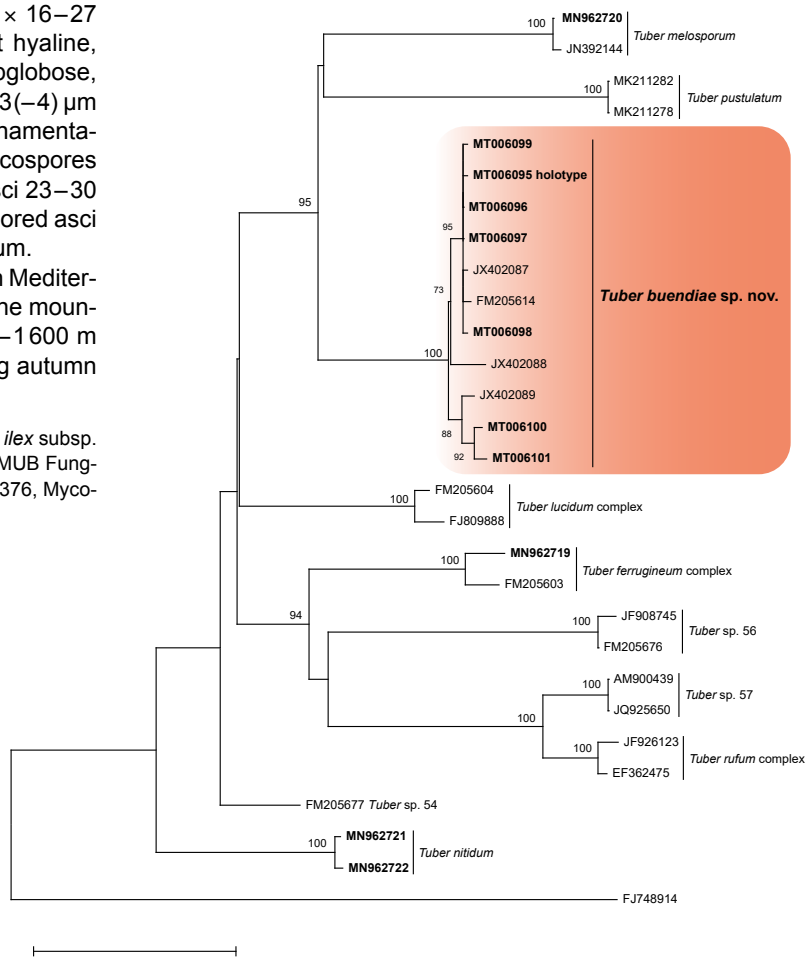
Ascomata hypogeous, 1–3 cm, subglobose or irregular in form, sometimes lobed, sometimes with a basal depression, fissured in age, yellow brown to reddish brown, minutely warted with pyramidal, flattened warts. *Peridium* 400–500 µm thick, composed of hyaline, agglutinated, interwoven hyphae (intricate 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.

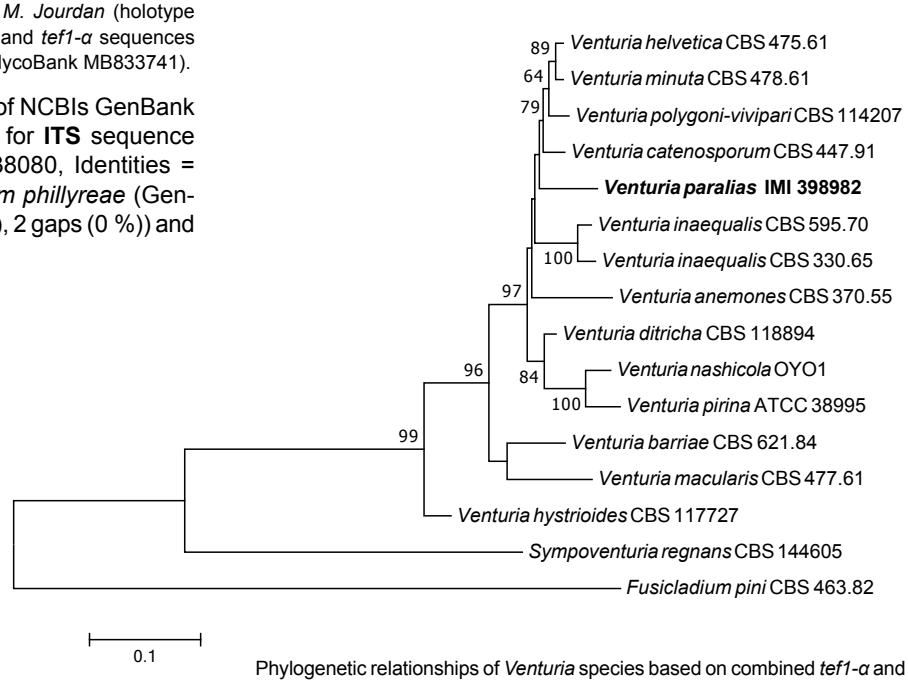
Classification — *Venturiaceae*, *Venturiales*, *Dothideomycetes*.

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.

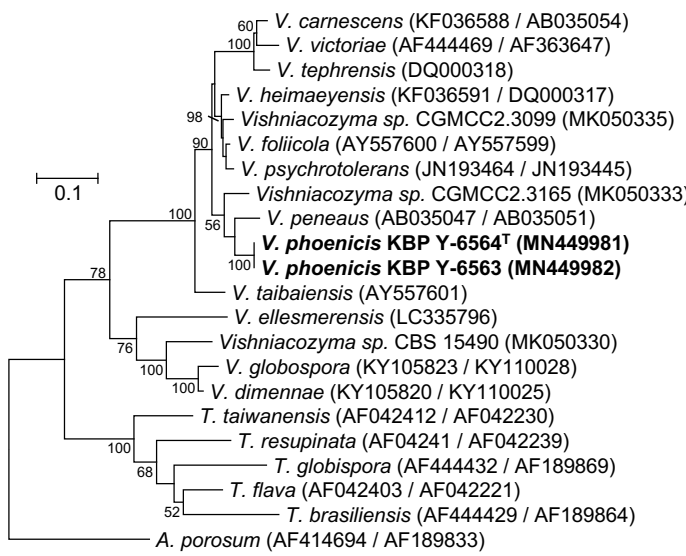
Classification — *Bulleribasidiaceae*, *Tremellales*, *Tremellomycetes*.

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.

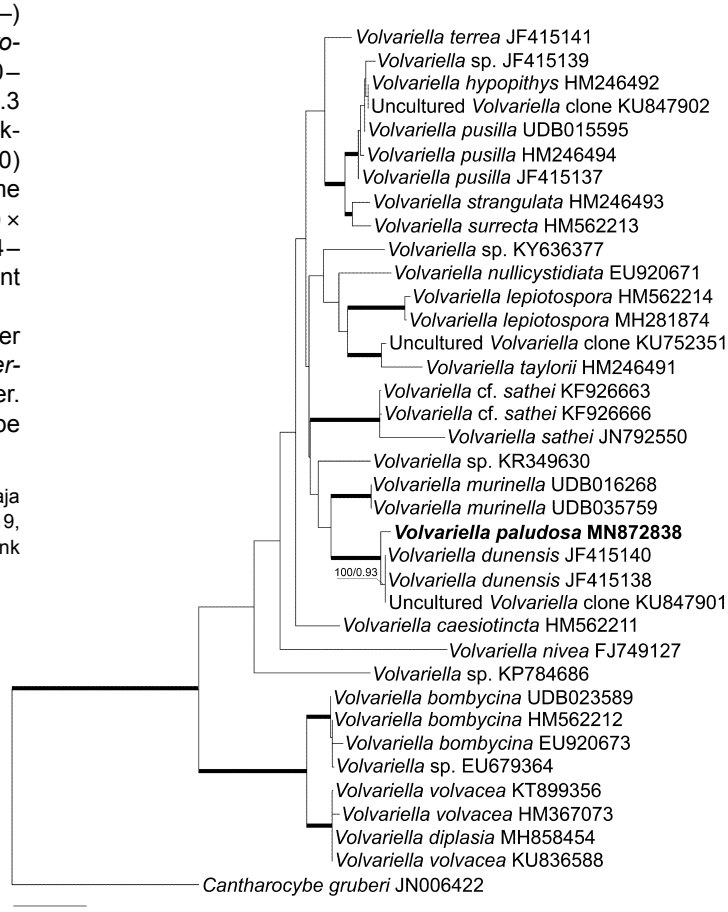
Classification — *Pluteaceae*, *Agaricales*, *Agaricomycetes*.

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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