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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: **Australia**, *Chaetomella pseudocircinoseta* and *Coniella pseudodiospyri* on *Eucalyptus microcorys* leaves, *Cladophialophora eucalypti*, *Teratosphaeria dunnii* and *Vermiculariopsiella dunnii* on *Eucalyptus dunnii* leaves, *Cylindrium grande* and *Hypsotheca eucalyptorum* on *Eucalyptus grandis* leaves, *Elsinoe salignae* on *Eucalyptus saligna* leaves, *Marasmius lebeliae* on litter of regenerating subtropical rainforest, *Phialoseptomonium eucalypti* (incl. *Phialoseptomonium* gen. nov.) on *Eucalyptus grandis* × *camaldulensis* leaves, *Phlogicylindrium pawpawense* on *Eucalyptus tereticornis* leaves, *Phyllosticta longicauda* as an endophyte from healthy *Eustrephus latifolius* leaves, *Pseudosydowia eucalyptorum* on *Eucalyptus* sp. leaves, *Saitozyma wallum* on *Banksia aemula* leaves, *Teratosphaeria henryi* on *Corymbia henryi* leaves. **Brazil**, *Aspergillus bezerrae*, *Backusella azygospora*, *Mariannaea terricola* and *Talaromyces pernambucoensis* from soil, *Calonectria matogrossensis* on *Eucalyptus urophylla* leaves, *Calvatia brasiliensis* on soil, *Carcinomyces nordestinensis* on *Bromelia antiacantha* leaves, *Dendryphiella stromaticola* on small branches of an unidentified plant, *Nigrospora brasiliensis* on *Nopalea cochenillifera* leaves, *Penicillium alagoense* as a leaf endophyte on a *Miconia* sp., *Podosordaria nigrobrunnea* on dung, *Spegazzinia bromeliacearum* as a leaf endophyte on *Tilandsia catimbauensis*, *Xylobolus brasiliensis* on decaying wood. **Bulgaria**, *Kazachstania molopis* from the gut of the beetle *Molops piceus*. **Croatia**, *Mollisia endocrystallina* from a fallen decorticated *Picea abies* tree trunk. **Ecuador**, *Hygrocybe rodomaculata* on soil. **Hungary**, *Alfoldia vorosii* (incl. *Alfoldia* gen. nov.) from *Juniperus communis* roots, *Kiskunsagia ubrizsyi* (incl. *Kiskunsagia* gen. nov.) from *Fumana procumbens* roots. **India**, *Aureobasidium tremulum* as laboratory contaminant, *Leucosporidium himalayensis* and *Naganishia indica* from windblown dust on glaciers. **Italy**, *Neodevriesia cycadicola* on *Cycas* sp. leaves, *Pseudocercospora pseudomyrticola* on *Myrtus communis*

Abstract (cont.)

leaves, *Ramularia pistaciae* on *Pistacia lentiscus* leaves, *Neognomoniopsis quercina* (incl. *Neognomoniopsis* gen. nov.) on *Quercus ilex* leaves. **Japan**, *Diaporthe fructicola* on *Passiflora edulis* × *P. edulis* f. *flavicarpa* fruit, *Entoloma nipponicum* on leaf litter in a mixed *Cryptomeria japonica* and *Acer* spp. forest. **Macedonia**, *Astraeus macedonicus* on soil. **Malaysia**, *Fusicladium eucalyptigenum* on *Eucalyptus* sp. twigs, *Neoacrodontiella eucalypti* (incl. *Neoacrodontiella* gen. nov.) on *Eucalyptus urophylla* leaves. **Mozambique**, *Meliola gorongosensis* on dead *Philenoptera violacea* leaflets. **Nepal**, *Coniochaeta dendrobiicola* from *Dendriobium lognicornu* roots. **New Zealand**, *Neodevriesia sexualis* and *Thozetella neonivea* on *Archontophoenix cunninghamiana* leaves. **Norway**, *Calophoma sandfjordenica* from a piece of board on a rocky shoreline, *Clavaria parvispora* on soil, *Didymella finnmarkica* from a piece of *Pinus sylvestris* driftwood. **Poland**, *Sugiyamaella trypani* from soil. **Portugal**, *Colletotrichum feijoicola* from *Acca sellowiana*. **Russia**, *Crepidotus tobolensis* on *Populus tremula* debris, *Entoloma ekaterinae*, *Entoloma erhardii* and *Suillus gastroflavus* on soil, *Nakazawaea ambrosiae* from the galleries of *Ips typographus* under the bark of *Picea abies*. **Slovenia**, *Pluteus ludwigii* on twigs of broadleaved trees. **South Africa**, *Anungitiomyces stellenboschiensis* (incl. *Anungitiomyces* gen. nov.) and *Niesslia stellenboschiana* on *Eucalyptus* sp. leaves, *Beltraniella pseudoportoricensis* on *Podocarpus falcatus* leaf litter, *Corynespora encephalarti* on *Encephalartos* sp. leaves, *Cytospora pavettae* on *Pavetta revoluta* leaves, *Helminthosporium erythrinicola* on *Erythrina humeana* leaves, *Helminthosporium syzygii* on a *Syzygium* sp. bark canker, *Libertasomyces aloeticus* on *Aloe* sp. leaves, *Penicillium lunae* from *Musa* sp. fruit, *Phyllosticta lauridiae* on *Lauridia tetragona* leaves, *Pseudotruncatella bolusanthi* (incl. *Pseudotruncatellaceae* fam. nov.) and *Dactylella bolusanthi* on *Bolusanthus speciosus* leaves. **Spain**, *Apenidiella foetida* on submerged plant debris, *Inocybe grammatoides* on *Quercus ilex* subsp. *ilex* forest humus, *Ossicaulis salomii* on soil, *Phialemonium guarroi* from soil. **Thailand**, *Pantospora chromolaenae* on *Chromolaena odorata* leaves. **Ukraine**, *Cadophora helianthi* from *Helianthus annuus* stems. **USA**, *Boletus pseudopinophilus* on soil under slash pine, *Botryotrichum foricae*, *Penicillium americanum* and *Penicillium minnesotense* from air. **Vietnam**, *Lycoperdon vietnamense* on soil. Morphological and culture characteristics are supported by DNA barcodes.

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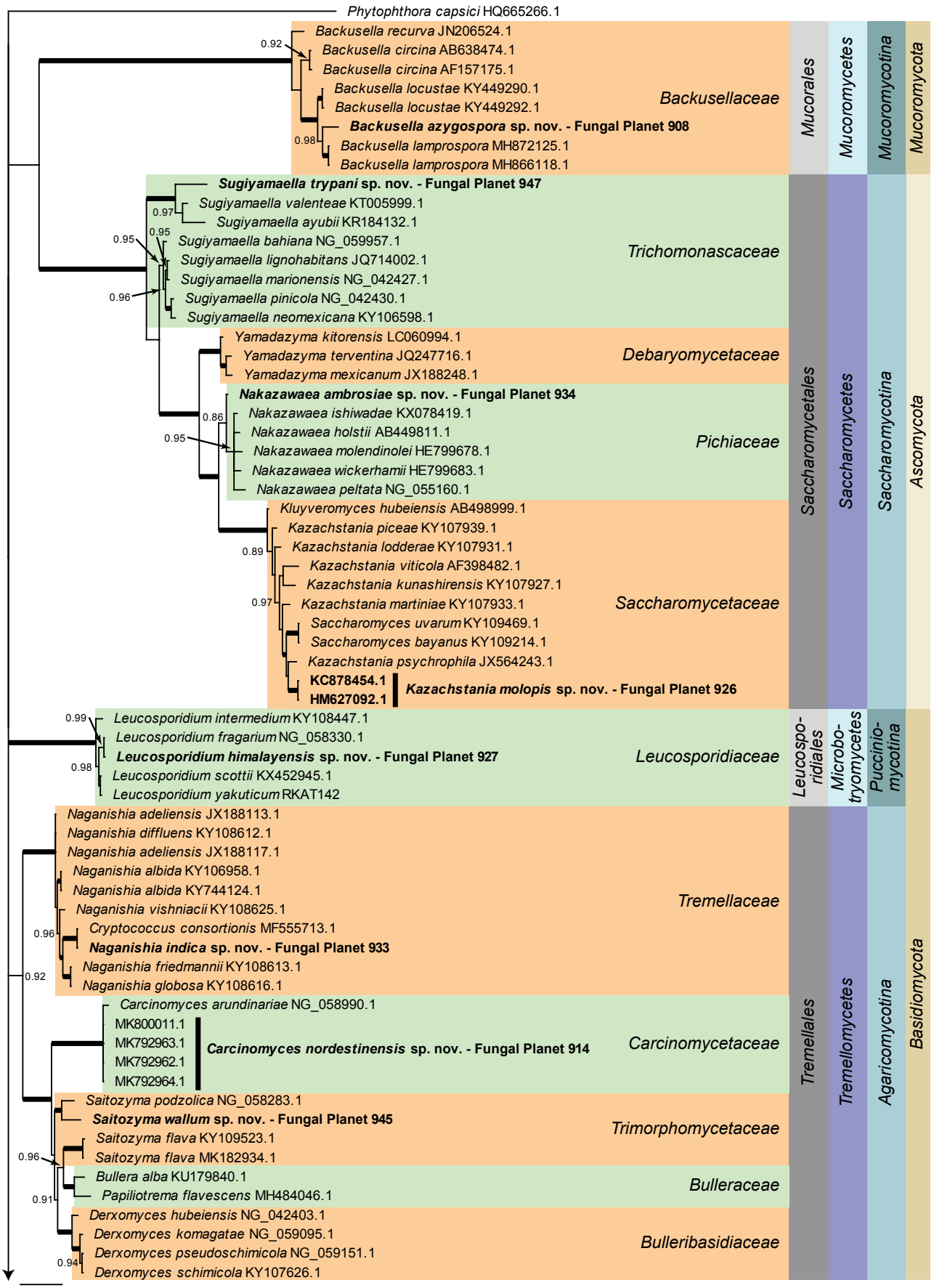
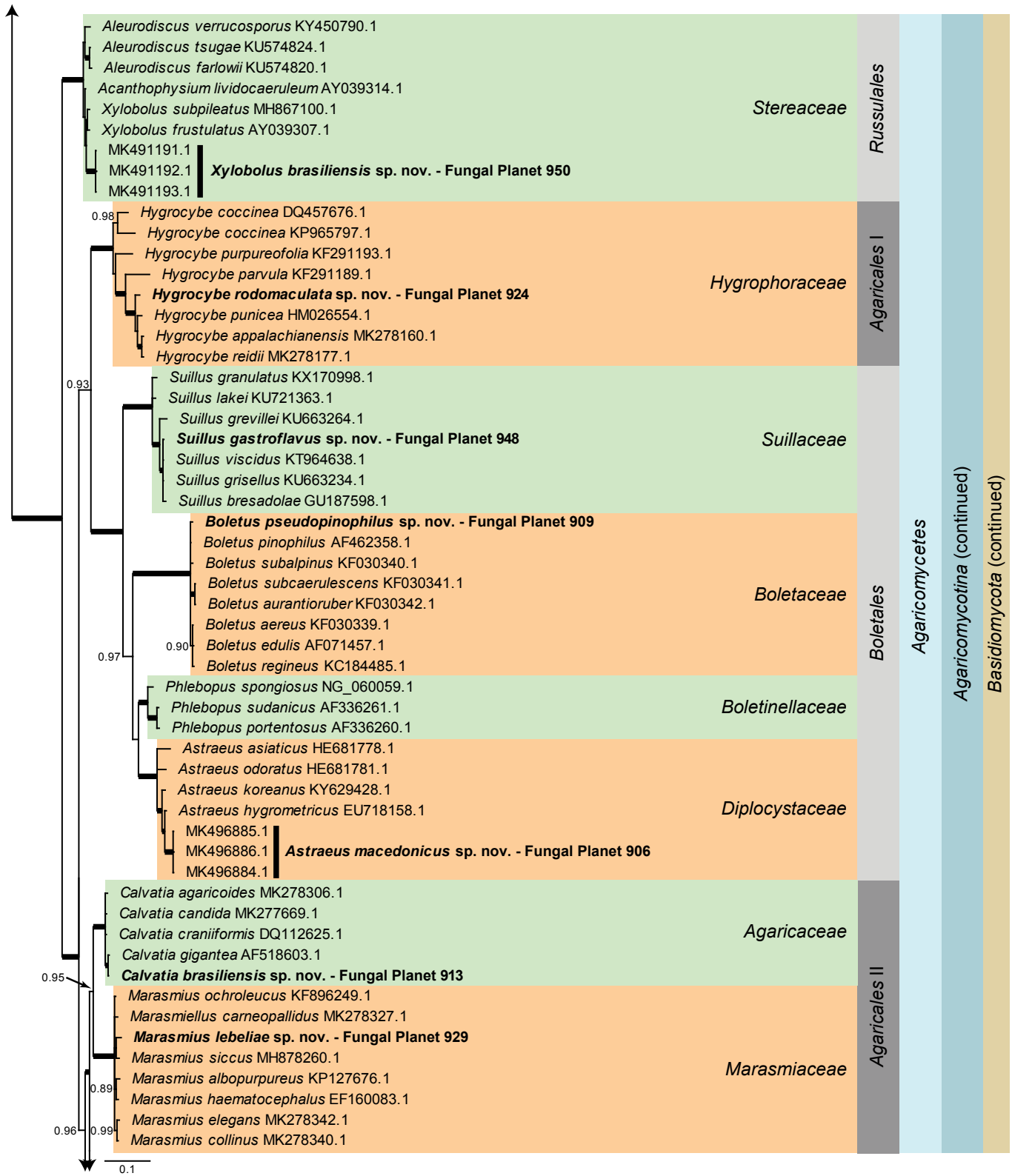
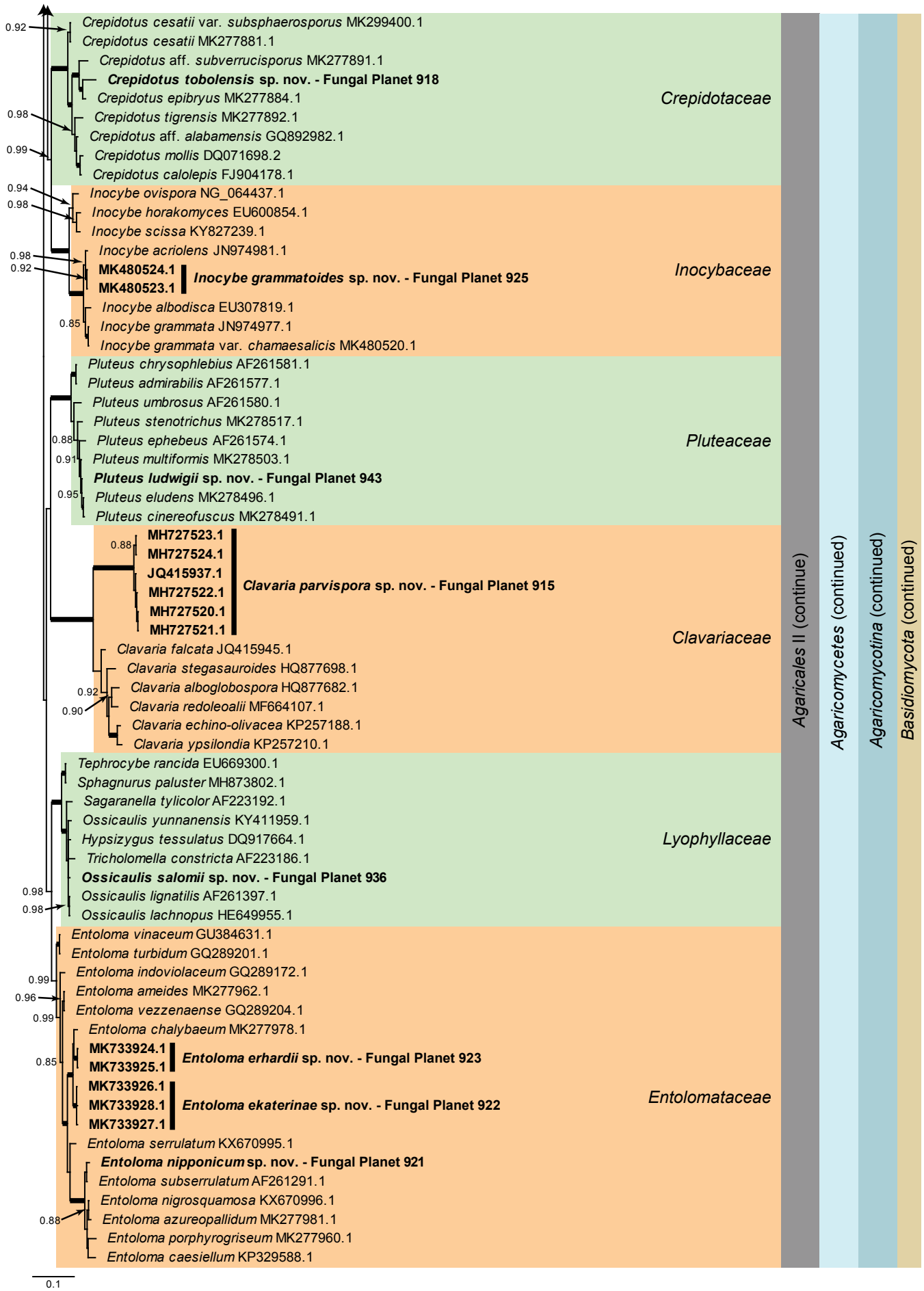


Overview *Mucoromycota*, *Ascomycota* and *Basidiomycota* phylogeny – part 1

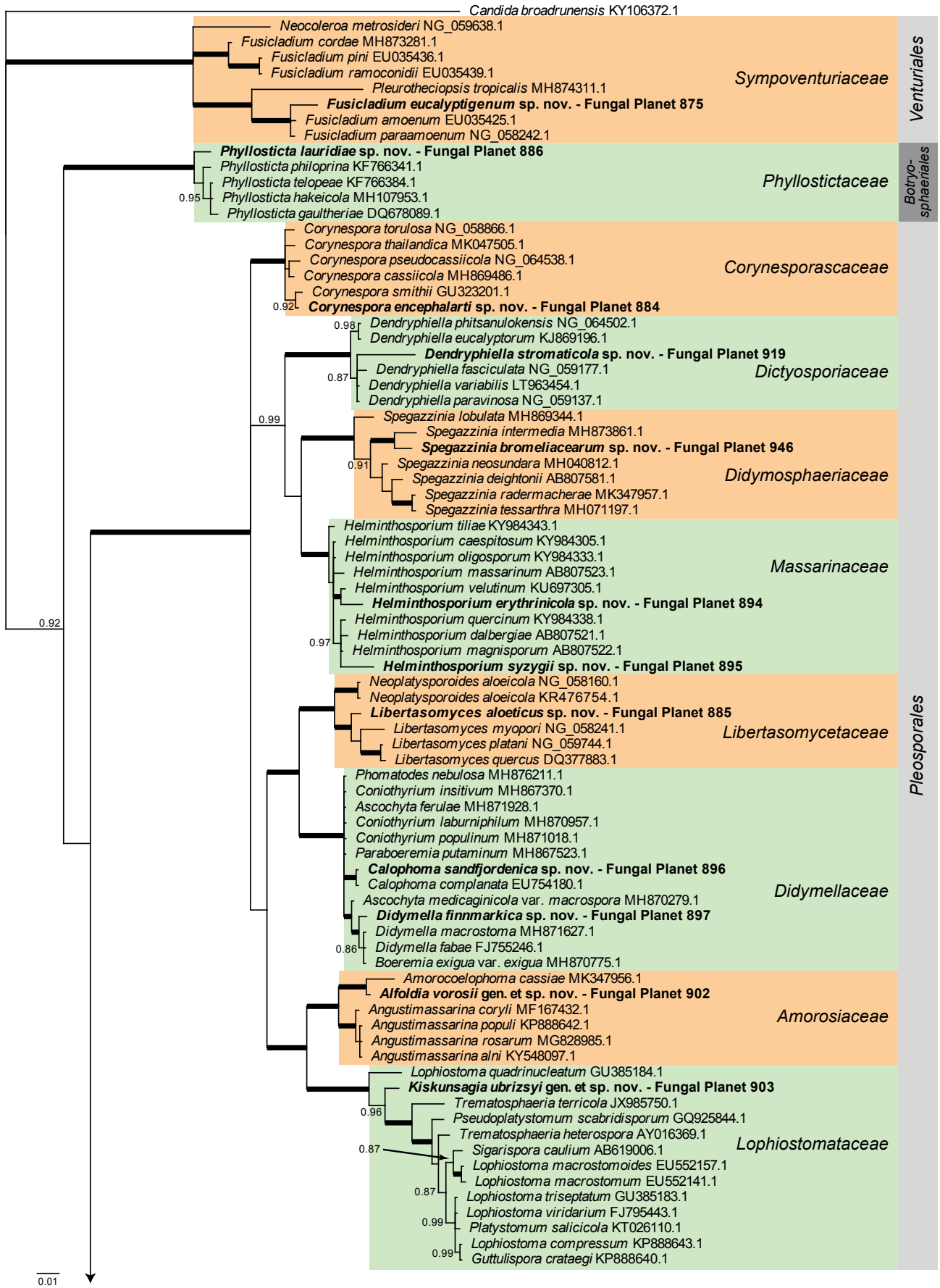
Consensus phylogram (50 % majority rule) of 40 878 trees resulting from a Bayesian analysis of the LSU sequence alignment (188 taxa including outgroup; 947 aligned positions; 656 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) >0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families, orders, classes, subdivisions and phyla 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 *Phytophthora capsici* (GenBank HQ665266.1) 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 S24386).



Overview *Mucoromycota*, *Ascomycota* and *Basidiomycota* phylogeny (cont.) – part 2

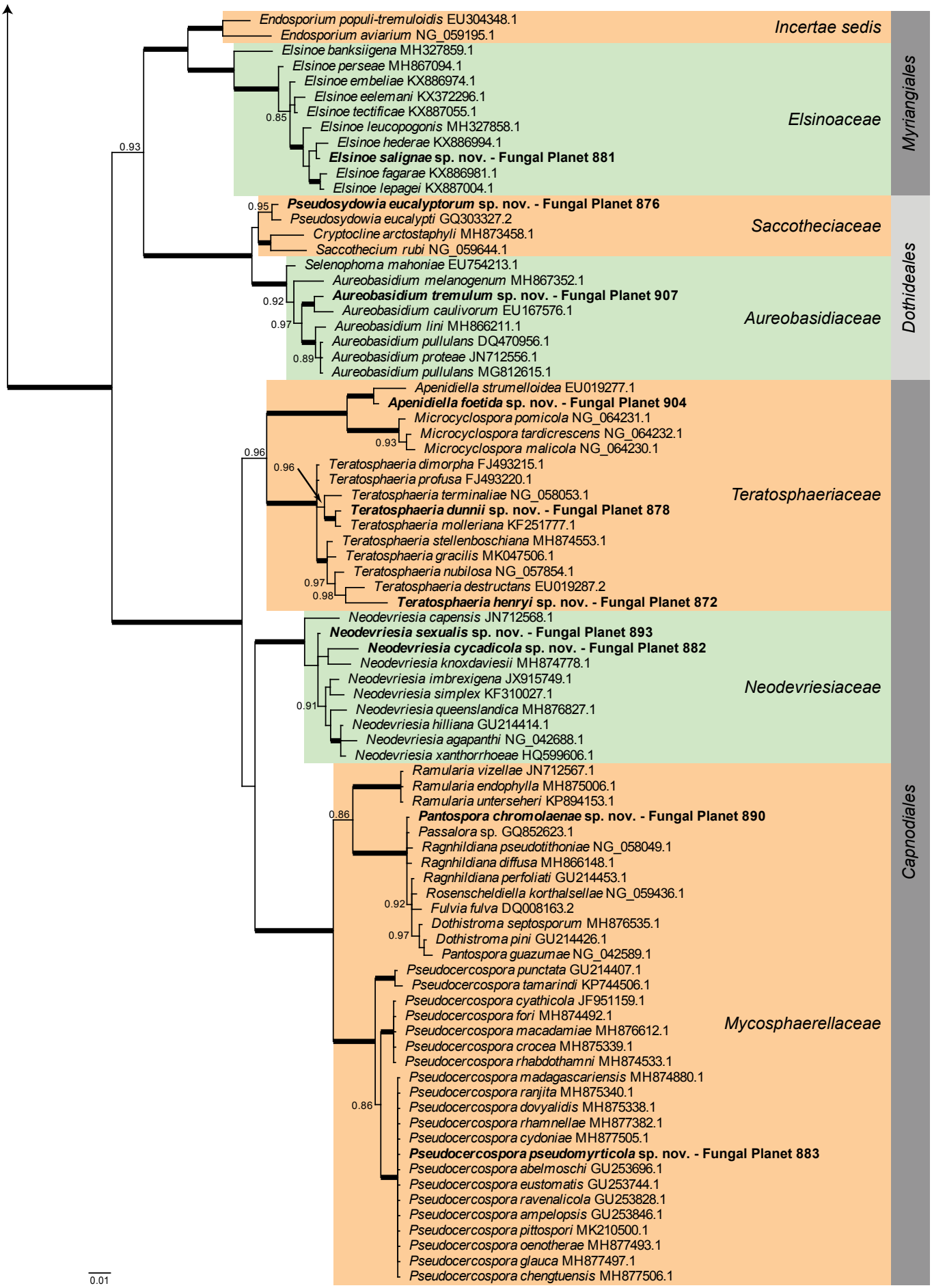


Overview *Mucoromycota*, *Ascomycota* and *Basidiomycota* phylogeny (cont.) – part 3



Overview *Dothideomycetes* phylogeny – part 1

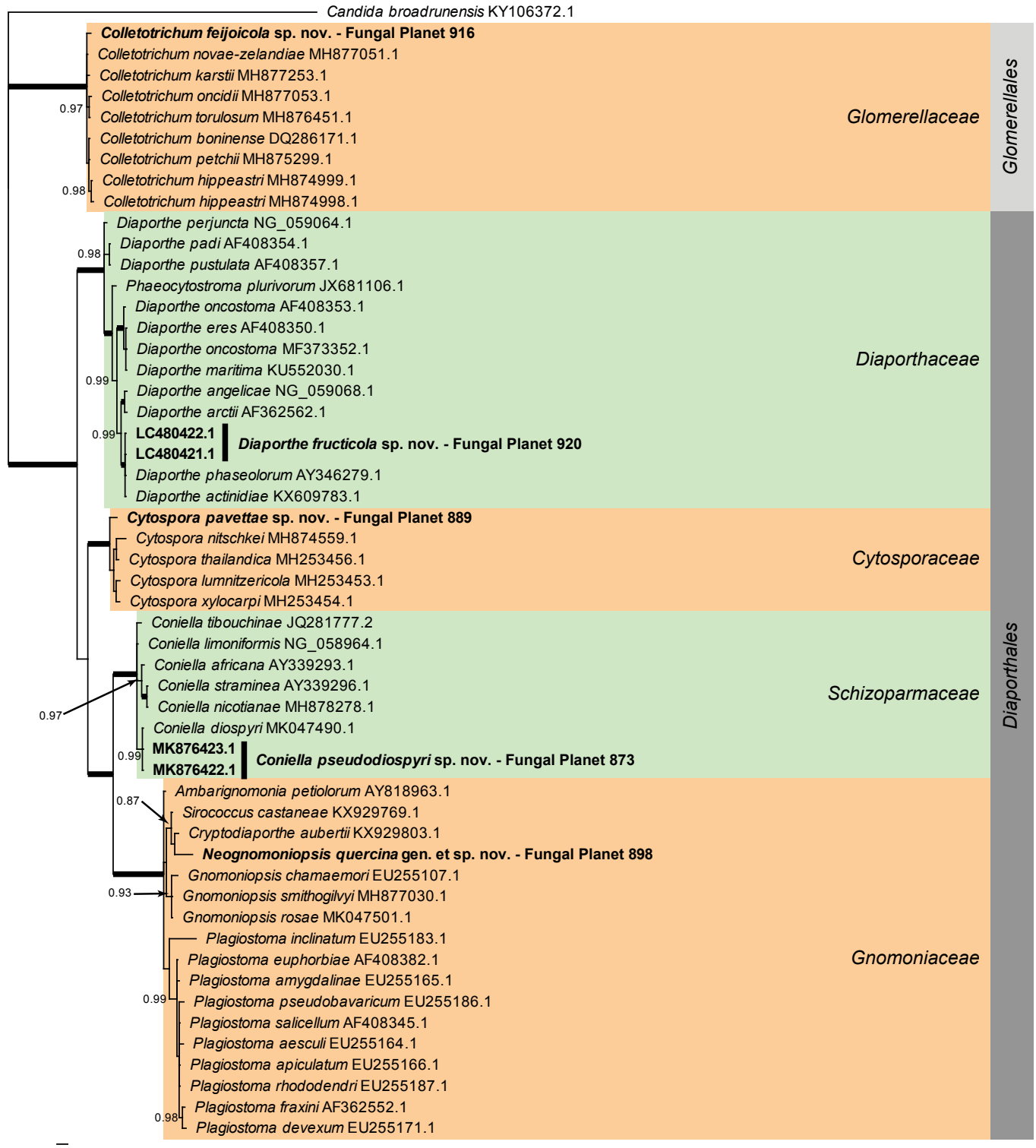
Consensus phylogram (50 % majority rule) of 22 278 trees resulting from a Bayesian analysis of the LSU sequence alignment (164 taxa including outgroup; 809 aligned positions; 394 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) >0.84 are shown 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 *Candida broadrunensis* (GenBank KY106372.1) 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 S24386).



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

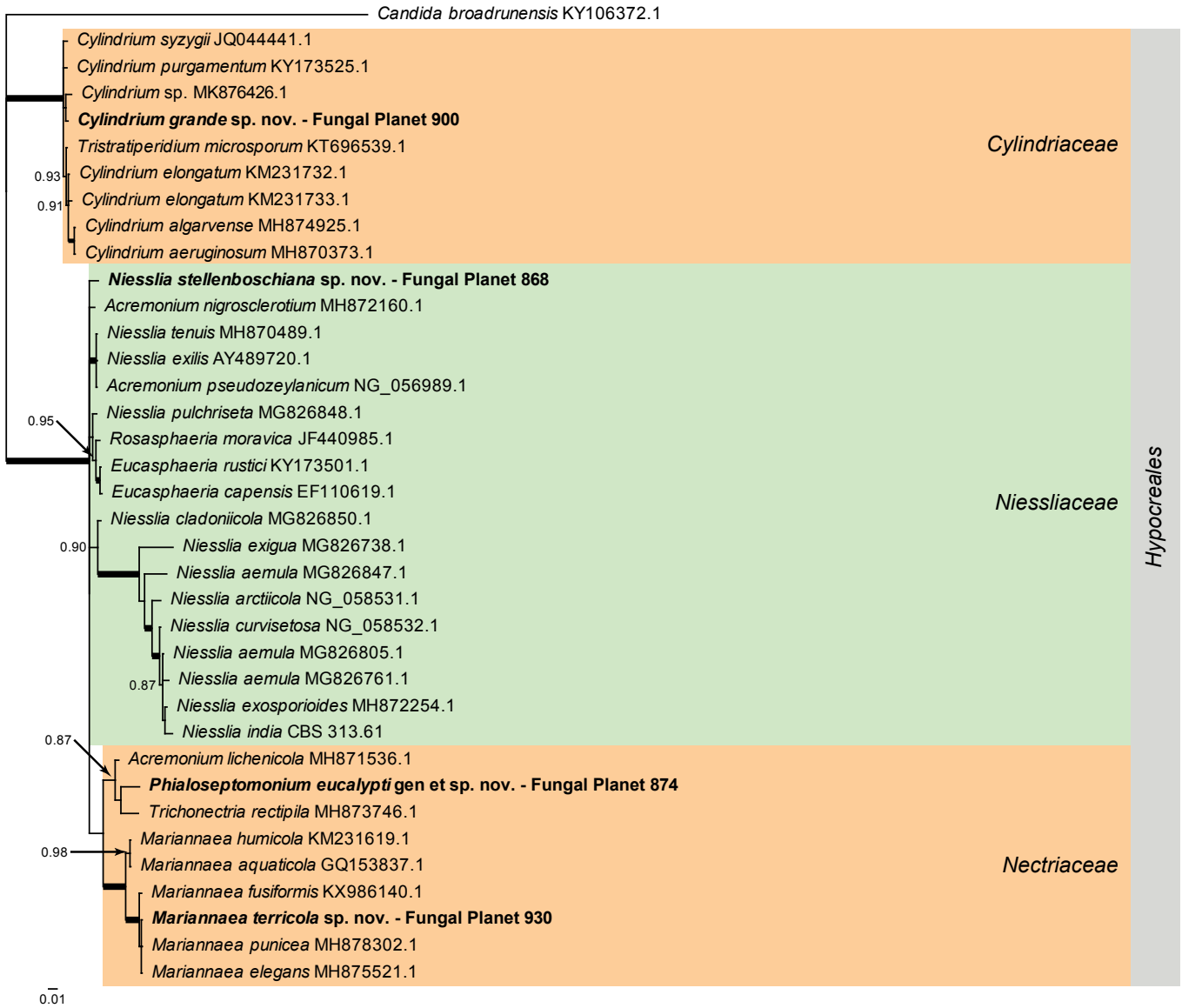
Overview *Eurotiomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 7 802 trees resulting from a Bayesian analysis of the LSU sequence alignment (46 taxa including outgroup; 816 aligned positions; 282 unique site patterns) using MrBayes v. 3.2.6 (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 *Candida broadrunensis* (GenBank KY106372.1) 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 S24386).



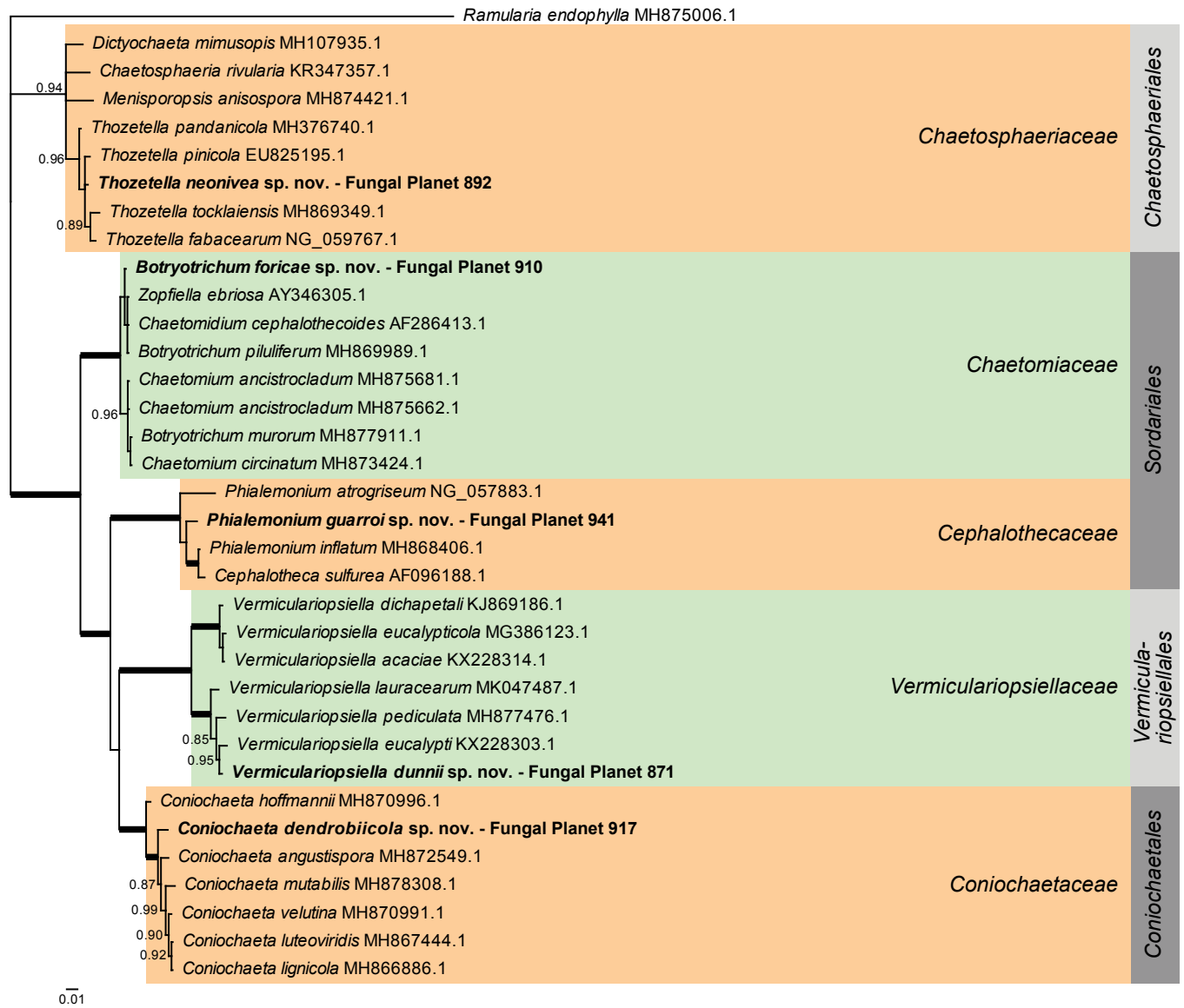
Overview *Diaporthales* and *Glomerellales* (*Sordariomycetes*) phylogeny

Consensus phylogram (50 % majority rule) of 21 752 trees resulting from a Bayesian analysis of the LSU sequence alignment (54 taxa including outgroup; 781 aligned positions; 185 unique site patterns) using MrBayes v. 3.2.6 (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 *Candida broadrunensis* (GenBank KY106372.1) 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 S24386).



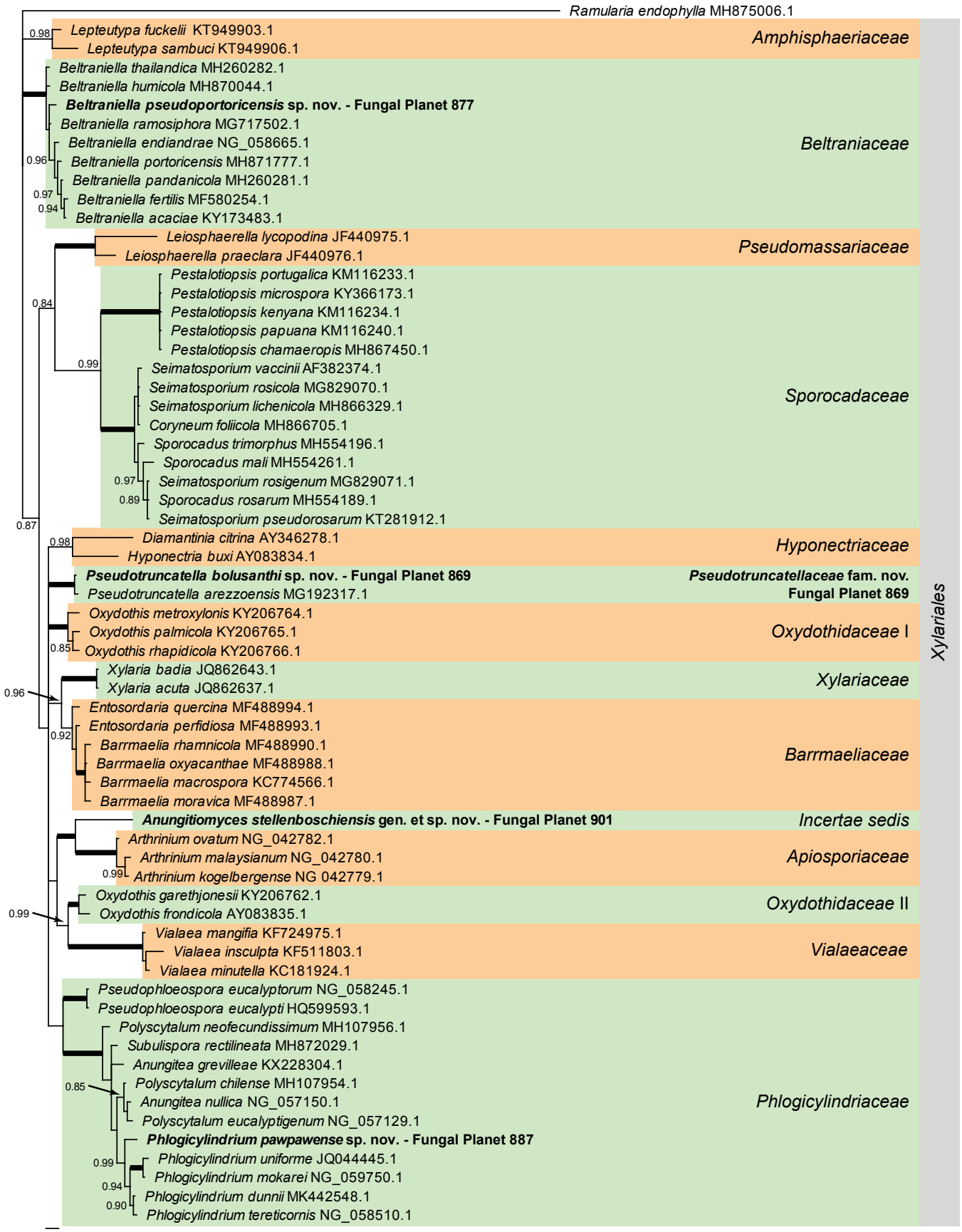
Overview *Hypocreales* (*Sordariomycetes*) phylogeny

Consensus phylogram (50 % majority rule) of 13 052 trees resulting from a Bayesian analysis of the LSU sequence alignment (37 taxa including outgroup; 761 aligned positions; 181 unique site patterns) using MrBayes v. 3.2.6 (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 *Candida broadrunensis* (GenBank KY106372.1) 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 S24386).



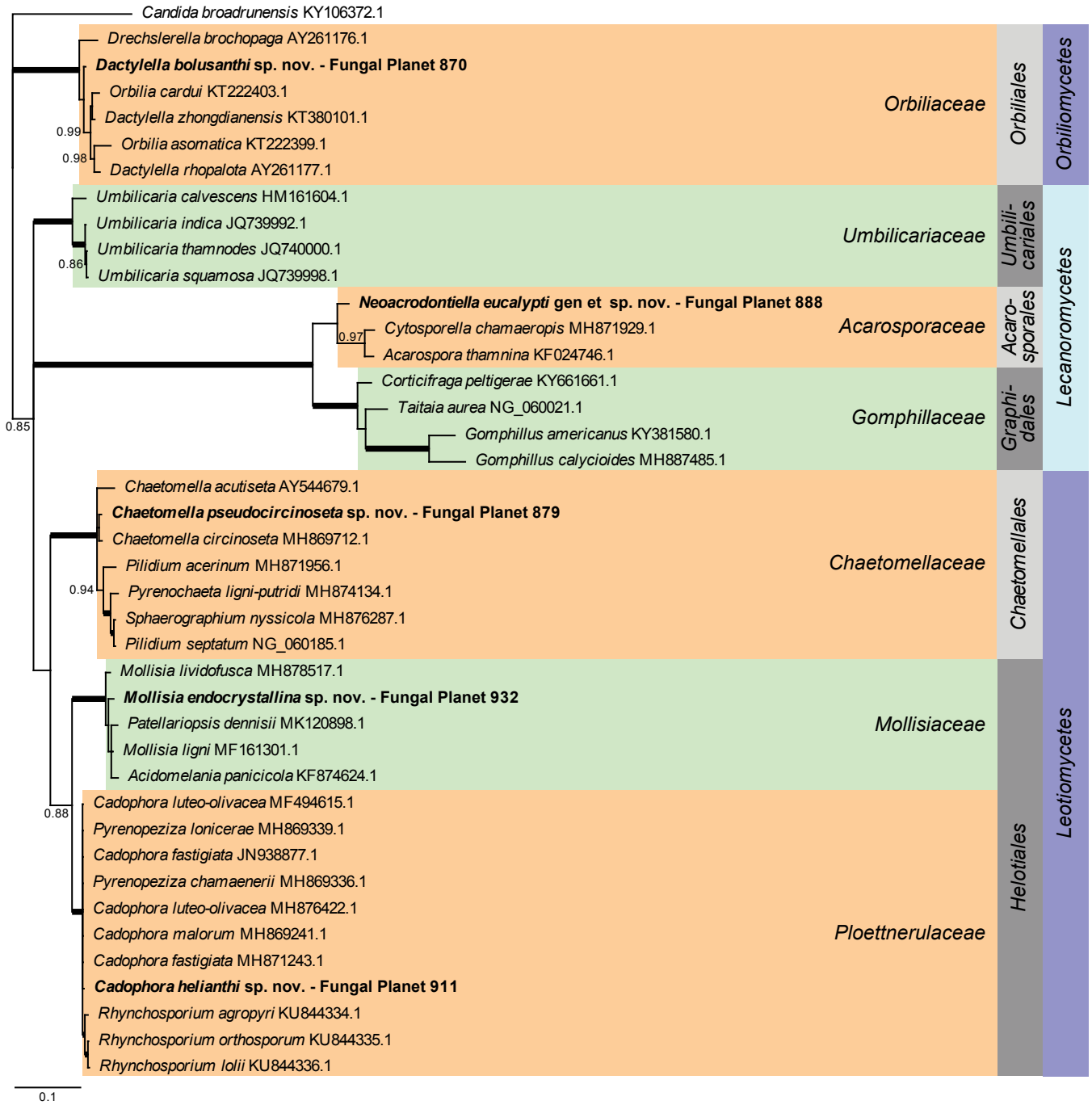
Overview other orders (*Sordariomycetes*) phylogeny

Consensus phylogram (50 % majority rule) of 14 252 trees resulting from a Bayesian analysis of the LSU sequence alignment (35 taxa including outgroup; 724 aligned positions; 192 unique site patterns) using MrBayes v. 3.2.6 (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 MH875006.1) 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 S24386).



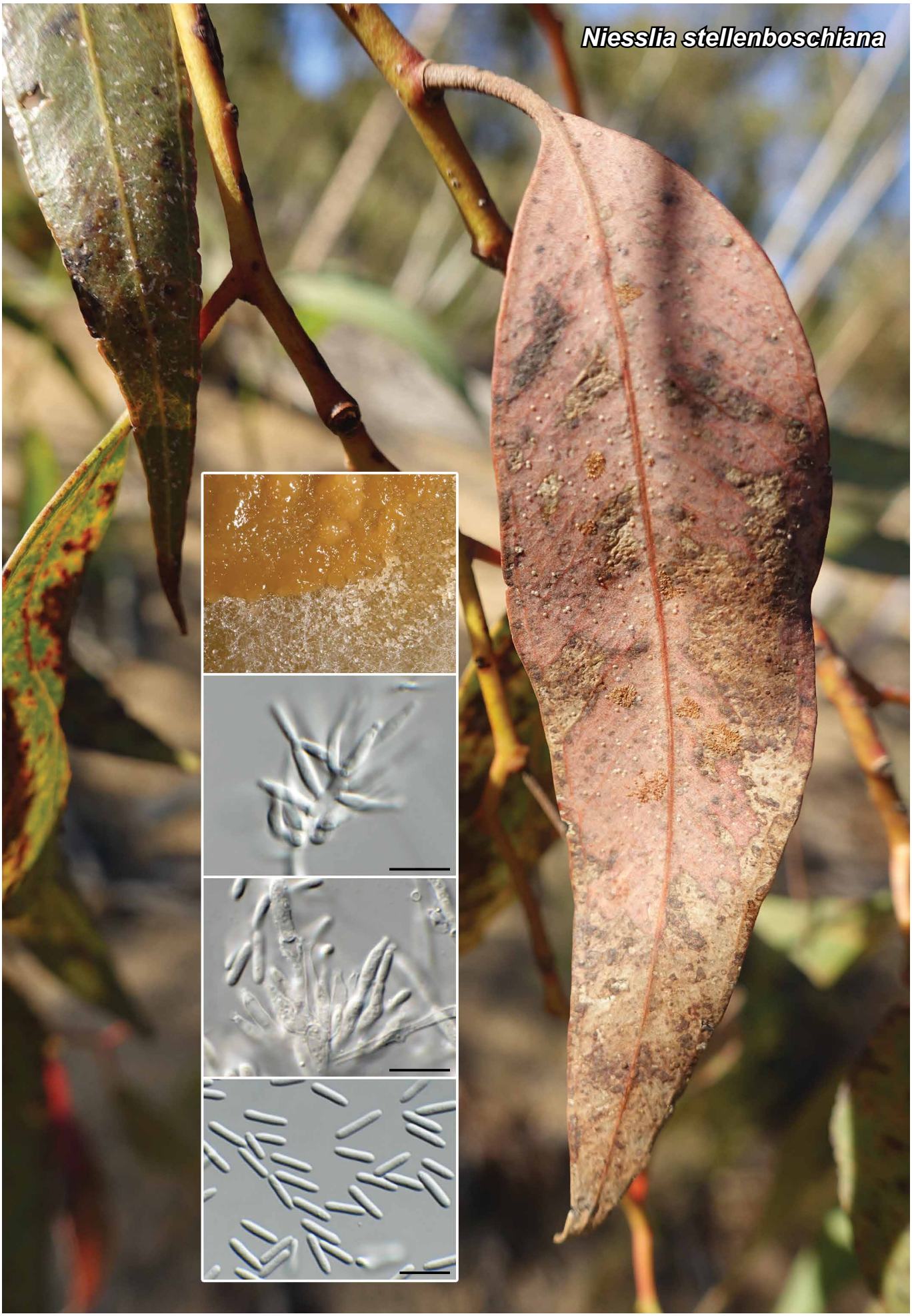
Overview *Xylariales* (*Sordariomycetes*) phylogeny

Consensus phylogram (50 % majority rule) of 35 702 trees resulting from a Bayesian analysis of the LSU sequence alignment (65 taxa including outgroup; 736 aligned positions; 194 unique site patterns) using MrBayes v. 3.2.6 (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 MH875006.1) 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 S24386).



Overview *Orbiliomycetes*, *Lecanoromycetes* and *Leotiomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 58 402 trees resulting from a Bayesian analysis of the LSU sequence alignment (41 taxa including outgroup; 812 aligned positions; 350 unique site patterns) using MrBayes v. 3.2.6 (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 *Candida broadrunensis* (GenBank KY106372.1) 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 S24386).


Niesslia stellenboschiana

Fungal Planet 868 – 19 July 2019

Niesslia stellenboschiana Crous, *sp. nov.*

Etymology. Name refers to Stellenbosch, South Africa, where this fungus was collected.

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

Colonies flat, spreading, forming mucoid orange conidial masses on densely aggregated sporodochia. *Mycelium* of hyaline, smooth, branched, septate, 1.5–2.5 mm diam hyphae. *Conidiophores* aggregated in clusters, subcylindrical, hyaline, smooth, 1–3-septate, 7–35 × 2.5–3.5 mm, branched, with secondary and tertiary branches 6–10 × 2.5–3.5 mm, giving rise to 1–4 cymbiform phialides, 8–10 × 2–3 mm, with visible periclinal thickening, and short, non-flared collarettes, 0.5–1.5 mm long. *Conidia* aseptate, solitary, aggregating in mucoid mass, hyaline, smooth, guttulate, cylindrical, straight, apex obtuse, base tapered, truncate, 0.5 mm diam, (6–)6.5–7(–8) × (1.5–)2 mm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface and reverse saffron. On PDA and OA surface and reverse amber with diffuse amber pigment.

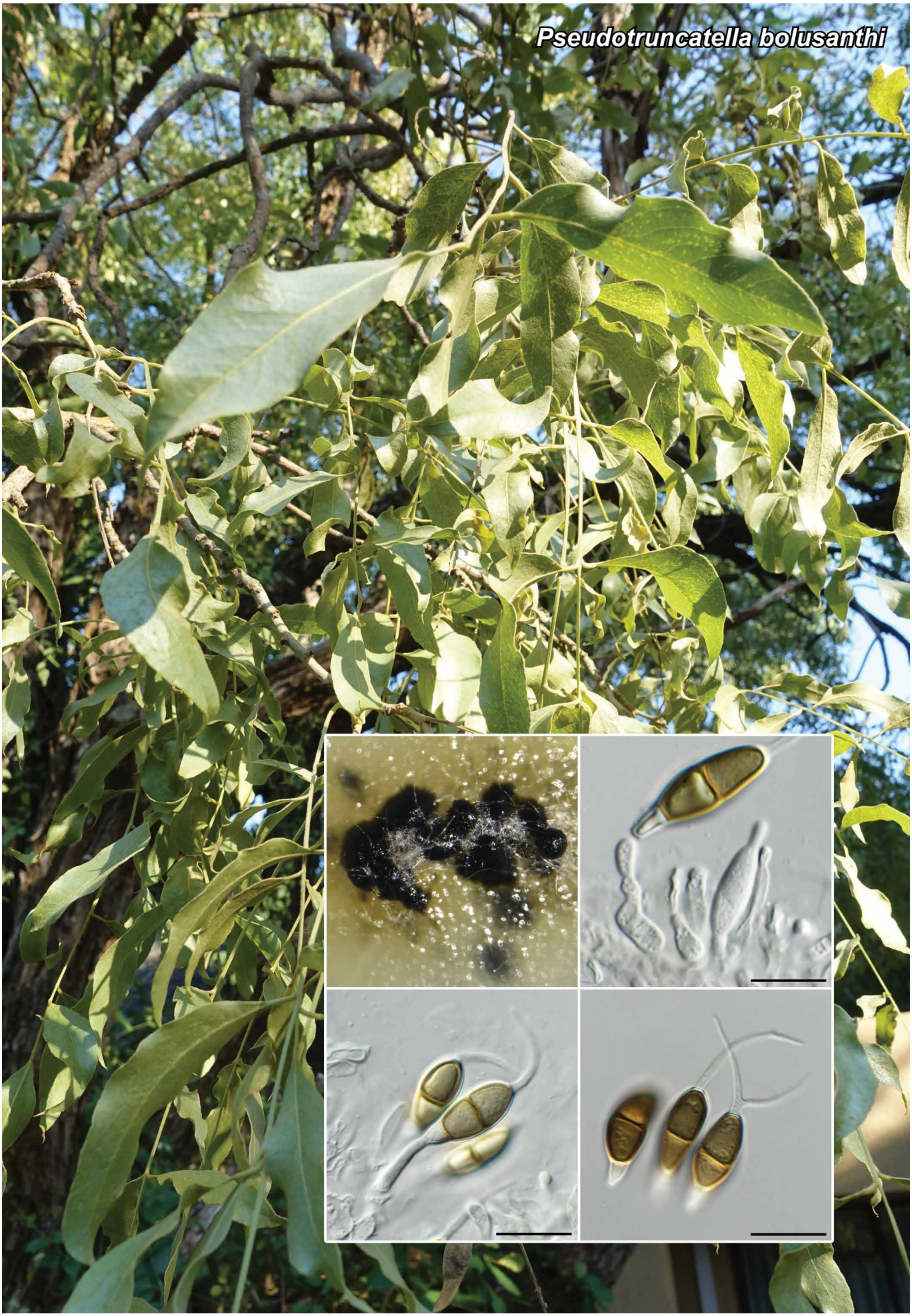
Typus. South Africa, Western Cape Province, Stellenbosch Mountain, on leaves of *Eucalyptus* sp. (*Myrtaceae*), 2016, *P.W. Crous* (holotype CBS H-23933, culture ex-type CPC 34689 = CBS 145531, ITS and LSU sequences GenBank MK876400.1 and MK876441.1, MycoBank MB830822).

Notes — Species of *Niesslia* are commonly isolated from plant litter. As presently defined, *Niesslia* includes asexual morphs formerly known as *Monocillium* (Gams et al. 2019). *Niesslia stellenboschiana* clustered between *N. tenuis* and '*Acremonium*' *nigrosclerotium*, and further phylogenetic studies will be required to resolve the taxonomy of this complex.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Monocillium ligusticum* (GenBank MF681489.1; Identities = 530/568 (93 %), 10 gaps (1 %)), *Monocillium tenue* (GenBank MG826947.1; Identities = 538/577 (93 %), 16 gaps (2 %)) and *Niesslia subiculosa* (GenBank MG826970.1; Identities = 523/562 (93 %), 12 gaps (2 %)). Closest hits using the **LSU** sequence are *Acremonium nigrosclerotium* (GenBank MH872160.1; Identities = 824/836 (99 %), 1 gap (0 %)), *Monocillium tenue* (GenBank MH870489.1; Identities = 822/836 (98 %), 1 gap (0 %)), *Niesslia exilis* (GenBank AY489720.1; Identities = 822/836 (98 %), 1 gap (0 %)) and *Acremonium pseudozeylanicum* (GenBank HQ232101.1; Identities = 811/826 (98 %), 2 gaps (0 %)).

Colour illustrations. *Eucalyptus* leaf *N. stellenboschiana* was isolated from. Colony on oatmeal agar; conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl


Pseudotruncatella bolusanthi

Fungal Planet 869 – 19 July 2019

Pseudotruncatellaceae Crous, *fam. nov.*

Etymology. Name refers to the genus *Pseudotruncatella*.

Classification — *Pseudotruncatellaceae*, *Amphisphaeriales*, *Sordariomycetes*.

Conidiomata acervular to pycnidioid, gregarious, oval. *Conidiophores* arising from basal and lateral cells in cavity, cylindrical, septate, branched, at times reduced to conidiogenous cells, smooth, hyaline. *Conidiogenous cells* subcylindrical, hyaline, smooth, proliferating percurrently at apex. *Conidia* fusoid, straight, septate, with central tubular apical appendage, unbranched or bifurcate; basal cell, narrowly obconic with a truncate base, hyaline, smooth; two median cells dark brown, smooth, guttulate, thick-walled, fusoid. *Sexual morph* unknown.

Type genus: *Pseudotruncatella* R.H. Perera et al.
MycoBank MB830823.

Pseudotruncatella bolusanthi Crous, *sp. nov.*

Etymology. Name refers to *Bolusanthus*, the host genus from which this fungus was isolated.

Conidiomata acervular to pycnidioid, gregarious, oval, 150–200 mm diam. *Conidiophores* arising from basal and lateral cells in cavity, cylindrical, 0–3-septate, branched, at times reduced to conidiogenous cells, smooth, hyaline, 10–30 × 3–4 mm. *Conidiogenous cells* subcylindrical, hyaline, smooth, proliferating percurrently at apex, 8–12 × 2–3 mm. *Conidia* (15–)17–20(–22) × (5–)6.5–7 mm, fusoid, straight, 2-septate, constricted at medium septum, with central tubular apical appendage, unbranched or bifurcate, 15–30 × 1.5–2 mm; basal cell 3–5 × 4–5 mm, narrowly obconic with a truncate base, hyaline, smooth; two median cells (13–)14–15(–17) × (5–)6.5–7 mm, dark brown, smooth, guttulate, thick-walled, fusoid.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface hazel, reverse isabelline. On PDA surface honey, reverse isabelline in centre, honey in outer region. On OA surface honey.

Typus. South Africa, Mpumalanga Province, Kruger National Park, on leaves of *Bolusanthus speciosus* (*Fabaceae*), 19 Nov. 2010, *P.W. Crous*, HPC 2263 (holotype CBS H-23934, culture ex-type CPC 34700 = CBS 145532, ITS and LSU sequences GenBank MK876407.1 and MK876448.1, MycoBank MB830824).

Notes — The genera of appendaged coelomycetes in *Sporocadaceae* have recently been treated by Liu et al. (2019). The monotypic genus *Pseudotruncatella* was introduced by Perera et al. (2018) for a truncatella-like coelomycete occurring on dead branches of *Cytisus* and *Helichrysum* in Italy. *Pseudotruncatella bolusanthi* can be distinguished from *P. arezzoensis* (conidia 20–25 × 5.4–6.5 µm, 3-septate), based on its smaller, 2-septate conidia. *Pseudotruncatellaceae* is allied to a sequence of *Hyponectria buxi* (*Hyponectriaceae*), although there are no cultures to confirm the placement of the latter family.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pseudotruncatella arezzoensis* (GenBank MG192321.1; Identities = 477/508 (94 %), 9 gaps (1 %)), *Castanediella eucalypti* (GenBank KR476723.1; Identities = 468/518 (90 %), 14 gaps (2 %)) and *Castanediella communis* (GenBank KY173393.1; Identities = 475/527 (90 %), 14 gaps (3 %)). Closest hits using the **LSU** sequence are *Pseudotruncatella arezzoensis* (GenBank MG192317.1; Identities = 784/786 (99 %), 1 gap (0 %)), *Pseudophloeospora eucalyptorum* (GenBank MH878224.1; Identities = 760/786 (97 %), 1 gap (0 %)) and *Oxydothis garethjonesii* (GenBank KY206762.1; Identities = 760/787 (97 %), 3 gaps (0 %)).

Colour illustrations. Leaves of *Bolusanthus speciosus*. Conidiomata on oatmeal agar; conidiogenous cells and conidia; conidia. Scale bars = 10 µm.

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Dactylella bolusanthi

Fungal Planet 870 – 19 July 2019

Dactylella bolusanthi Crous, *sp. nov.*

Etymology. Name refers to *Bolusanthus*, the host genus from which this fungus was isolated.

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

Mycelium consisting of branched, septate, hyaline, smooth, 2.5–3 mm diam hyphae, frequently forming hyphal coils. *Conidiophores* 0–1-septate, mostly reduced to conidiogenous cells, erect, straight, hyaline, smooth, with apical taper to truncate apex, 10–50 × 3–4 mm. *Conidiogenous cells* hyaline, smooth, subcylindrical with apical taper, phialidic, apex 2 mm diam, collarette mostly not visible, 10–30 × 3–4 mm. *Conidia* solitary, fusoid, straight to flexuous, widest in middle, apex subobtuse, base truncate, 2 mm diam, hyaline smooth, guttulate, 5–11-septate, (42–)50–65(–75) × 5(–6) mm.

Culture characteristics — Colonies flat, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface salmon, reverse saffron. On PDA surface and reverse dirty white. On OA surface pale luteous to saffron.

Typus. South Africa, Mpumalanga Province, Kruger National Park, on leaves of *Bolusanthus speciosus* (*Fabaceae*), 19 Nov. 2010, *P.W. Crous*, HPC 2263 (holotype CBS H-23935, culture ex-type CPC 34702 = CBS 145533, ITS and LSU sequences GenBank MK876387.1 and MK876428.1, MycoBank MB830825).

Notes — *Dactylella bolusanthi* is similar to other species of *Dactylella* (Seifert et al. 2011), as conidiophores are mostly reduced to solitary, erect, monophialides on superficial mycelium (periclinal thickening inconspicuous), and all structures remain hyaline with age.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Dactylella zhongdianensis* (GenBank KT222436.1; Identities = 702/836 (84 %), 44 gaps (5 %)), *Dactylella rhopalota* (GenBank DQ494369.1; Identities = 493/559 (88 %), 25 gaps (4 %)) and *Orbilia cardui* (GenBank KT222403.1; Identities = 503/575 (87 %), 22 gaps (3 %)). Closest hits using the **LSU** sequence are *Dactylella zhongdianensis* (GenBank KT380101.1; Identities = 822/836 (98 %), 2 gaps (0 %)), *Orbilia cardui* (GenBank KT222403.1; Identities = 817/833 (98 %), no gaps) and *Dactylella rhopalota* (GenBank AY261177.1; Identities = 820/840 (98 %), 2 gaps (0 %)).

Colour illustrations. Leaves of *Bolusanthus speciosus*. Conidiogenous cells and conidia. Scale bars = 10 µm.

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Vermiculariopsiella dunnii

Fungal Planet 871 – 19 July 2019

Vermiculariopsiella dunnii Crous & Carnegie, *sp. nov.*

Etymology. Name refers to *Eucalyptus dunnii*, the host species from which this fungus was isolated.

Classification — *Helminthosphaeriaceae*, *Sordariales*, *Sordariomycetes.*

Colonies sporulating profusely throughout on SNA. *Setae* erect, brown, cylindrical, straight to flexuous, 150–200 × 3–4 µm, thick-walled, smooth, 8–10-septate, tapering towards apex, developing a head of lateral coiled to whip-like branches (constricted at base where attached to setae), that are brown, septate, tapering, containing coiled, septate lateral branches that could again contain coiled, lateral, branched, mostly aseptate branches. *Conidiophores* arranged in a whorl around base of setae, pale brown, smooth, subcylindrical, branched or not, 0–6-septate, containing conidiogenous cells that are arranged laterally along its length or at times reduced to conidiogenous cells. *Conidiogenous cells* solitary, monophialidic, discrete, ampulliform to subulate, pale brown, 15–20 × 4–5 µm, apex 1–1.5 µm diam, with minute collarette (1–2 µm long), at times with percurrent proliferation at apex. *Conidia* asymmetrical, fusoid to subfusoid or oblong, attenuated, base bluntly rounded to somewhat inflated, aseptate, smooth, hyaline, finely granular, (6–)7.5–9(–10) × (2–)2.5(–3) µm.

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

Typus. Australia, New South Wales, Yabbra State Forest, Boomi Creek plantation, on leaves of *Eucalyptus dunnii* (*Myrtaceae*), 19 Apr. 2016, *A.J. Carnegie*, HPC 2430 (holotype CBS H-23938, culture ex-type CPC 35649 = CBS 145538, ITS and LSU sequences GenBank MK876412.1 and MK876452.1, MycoBank MB 830826).

Notes — *Vermiculariopsiella dunnii* is closely related to *V. eucalypti* (conidia (5–)7–9(–10) × (2–)2.5 µm; on leaves of *Eucalyptus regnans*, Australia, Victoria, Toolangi State Forest; Crous et al. 2016). In our overview phylogeny of *Vermiculariopsiella* it clusters apart with isolate KAS819, suggesting it to be a distinct species. A revision of the genus is presently in preparation, and will be published elsewhere.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Vermiculariopsiella eucalypti* (GenBank NR_154637.1; Identities = 525/538 (98 %), 6 gaps (1 %)), *Vermiculariopsiella pediculata* (as *Gyrothrix pediculata*, GenBank HF678527.1; Identities = 494/519 (95 %), 12 gaps (2 %)) and *Vermiculariopsiella lauracearum* (GenBank MK047436.1; Identities = 516/548 (94 %), 9 gaps (1 %)). Closest hits using the **LSU** sequence are *Vermiculariopsiella eucalypti* (GenBank KX228303.1; Identities = 806/812 (99 %), no gaps), *Vermiculariopsiella pediculata* (GenBank MH877476.1; Identities = 831/839 (99 %), 1 gap (0 %)) and *Vermiculariopsiella lauracearum* (GenBank MK047487.1; Identities = 804/812 (99 %), no gaps).

Colour illustrations. *Eucalyptus dunnii* plantation. Colony on oatmeal agar; setae and conidiogenous cells; conidia. Scale bars = 10 µm.

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Teratosphaeria henryi

Fungal Planet 872 – 19 July 2019

Teratosphaeria henryi Crous & Carnegie, *sp. nov.*

Etymology. Name refers to *Corymbia henryi*, the host species from which this fungus was isolated.

Classification — *Teratosphaeriaceae*, *Capnodiales*, *Dothideomycetes.*

Conidiomata pycnidial, solitary, brown, 90–120 mm diam; wall of 6–8 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining cavity. *Conidiogenous cells* brown, verruculose, subcylindrical with slight apical taper, proliferating percurrently at apex, 6–12 × 3–4 mm. *Conidia* solitary, brown, verruculose, aseptate, granular, fusoid, apex subobtuse, base truncate, 2 mm diam, with minute marginal frill, (7–)8–10(–11) × (2.5–)3(–4) mm.

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

Typus. Australia, New South Wales, Tallawandi plantation, South Grafton, on leaves of *Corymbia henryi* (*Myrtaceae*), 17 Apr. 2016, *A.J. Carnegie*, HPC 2417 (holotype CBS H-23939, culture ex-type CPC 35715 = CBS 145539, ITS, LSU, *actA*, *cmdA*, *rpb2*, *tef1* and *tub2* sequences GenBank MK876410.1, MK876450.1, MK876464.1, MK876470.1, MK876492.1, MK876501.1 and MK876505.1, MycoBank MB830827).

Notes — *Teratosphaeria henryi* is phylogenetically closely related to *T. pseudocryptica* (conidia 0–3-septate, 26–)31–40(–58) × (1.7–)2–2.5(–3.5) µm (Andjic et al. 2010), *P. rubida* (conidia aseptate, 11–)12.5–13.5(–16) × (4.5–)5.5–6(–6.5) µm (Taylor et al. 2012) and *T. sieberi* (conidia aseptate, 4–)6–7 × (2.5–)3 µm) (Crous et al. 2018c), but is distinct based on its conidial dimensions.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Teratosphaeria pseudocryptica* (GenBank KF442508.1; Identities = 465/490 (95 %), 10 gaps (2 %)), *Teratosphaeria rubida* (GenBank MH863388.1; Identities = 482/508 (95 %), 9 gaps (1 %)) and *Teratosphaeria sieberi* (GenBank MH327816.1; Identities = 474/501 (95 %), 5 gaps (0 %)). Closest hits using the **LSU** sequence are *Teratosphaeria stellenboschiana* (GenBank MH874553.1; Identities = 790/806 (98 %), no gaps), *Teratosphaeria nubilosa* (GenBank NG_057854.1; Identities = 790/806 (98 %), no gaps) and *Teratosphaeria destructans* (GenBank GU214702.1; Identities = 790/806 (98 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Teratosphaeria corymbiae* (GenBank KF903560.1; Identities = 505/541 (93 %), 3 gaps (0 %)), *Teratosphaeria viscida* (GenBank KF903563.1; Identities = 505/541 (93 %), 6 gaps (1 %)) and *Teratosphaeria destructans* (GenBank KF903447.1; Identities = 504/541 (93 %), 6 gaps (1 %)). Closest hits using the ***cmdA*** sequence had highest similarity to *Teratosphaeria gauchensis* (GenBank KF902727.1; Identities = 412/464 (89 %), 15 gaps (3 %)), *Teratosphaeria molleriana* (GenBank KF902737.1; Identities = 413/467 (88 %), 15 gaps (3 %)) and *Teratosphaeria majorizuluensis* (GenBank KF902733.1; Identities = 410/465 (88 %), 16 gaps (3 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Teratosphaeria sieberi* (GenBank MH327872.1; Identities = 824/929 (89 %), no gaps), *Teratosphaeria molleriana* (GenBank KX348104.1; Identities = 764/882 (87 %), 4 gaps (0 %)) and *Teratosphaeria gracilis* (GenBank MK047548.1; Identities = 766/886 (86 %), 2 gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Teratosphaeria gracilis* (GenBank MK047568.1; Identities = 357/427 (84 %), 24 gaps (5 %)), *Teratosphaeria zuluensis* (GenBank KF903369.1; Identities = 316/371 (85 %), 20 gaps (5 %)) and *Teratosphaeria corymbiae* (GenBank KF903293.1; Identities = 308/362 (85 %), 10 gaps (2 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Teratosphaeria gracilis* (GenBank MK047583.1; Identities = 543/613 (89 %), 17 gaps (2 %)), *Teratosphaeria nubilosa* (GenBank AY725599.1; Identities = 515/606 (85 %), 21 gaps (3 %)) and *Teratosphaeria destructans* (GenBank KT343568.1; Identities = 508/603 (84 %), 22 gaps (3 %)).

Colour illustrations. Corymbia plantation. Colony on malt extract agar; conidiogenous cells; conidia. Scale bars = 10 µm.

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Coniella pseudodiospyri

Fungal Planet 873 – 19 July 2019

Coniella pseudodiospyri Crous & Carnegie, *sp. nov.*

Etymology. Name refers to a morphological similarity with *Coniella diospyri*.

Classification — *Schizoparmaceae*, *Diaporthales*, *Sordariomycetes.*

Conidiomata separate, immersed to superficial, hyaline, becoming black, 200–300 mm diam, with central dark brown ostiole; wall of 3–6 layers of brown *textura angularis. Conidiophores* densely aggregated, subulate, frequently branched below, 1–2-septate, 15–25 × 3–4 mm. *Conidiogenous cells* hyaline, smooth, subcylindrical with apical taper, 8–12 × 2.5–3.5 mm, covered in mucoid sheath, apex with periclinal thickening and long collarette. *Conidia* solitary, aseptate, subhyaline, cylindrical, straight, smooth-walled, apex subobtuse, base truncate, guttulate, germ slit absent, (21–)23–26(–27) × 3(–3.5) mm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium, covering dish in 2 wk at 25 °C, with concentric circles of pycnidia on surface. On MEA and PDA surface and reverse umber. On OA surface pale luteous with patches of umber.

Typus. Australia, New South Wales, Bulladelah State Forest, on leaves of *Eucalyptus microcorys* (*Myrtaceae*), 16 Apr. 2016, *A.J. Carnegie*, HPC 2420 (holotype CBS H-23940, culture ex-type CPC 35725 = CBS 145540, ITS, LSU, *rpb2* and *tef1* sequences GenBank MK876381.1, MK876422.1, MK876479.1 and MK876493.1, MycoBank MB830828).

Notes — The genus *Coniella* was recently revised by Alvarez et al. (2016). *Coniella pseudodiospyri* (on *Myrtaceae*) is closely related to *C. diospyri* ((19–)21–23(–25) × 3(–3.5) mm, on *Diospyros* and *Trichilia* in South Africa; Crous et al. 2018a), but can be distinguished from that species based on its conidial dimensions, which are generally larger than those of *C. diospyri*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 35725 had highest similarity to *Coniella diospyri* (GenBank NR_161131.1; Identities = 609/609 (100 %), no gaps), *Coniella duckerae* (GenBank NR_154851.1; Identities = 602/613 (98 %), 2 gaps (0 %)) and *Coniella quercicola* (GenBank AY339345.1; Identities = 564/579 (97 %), 6 gaps (1 %)). The ITS sequences of CPC 35725 and CPC 35609 are identical over 609 nucleotides. Closest hits using the **LSU** sequence of CPC 35725 are *Coniella diospyri* (GenBank MK047490.1; Identities = 830/830 (100 %), no gaps), *Coniella limoniformis* (GenBank NG_058964.1; Identities = 813/817 (99 %), no gaps) and *Coniella tibouchinae* (GenBank JQ281777.2; Identities = 823/830 (99 %), no gaps). The LSU sequences of CPC 35725 and CPC 35609 are identical over 818 nucleotides. Closest hits using the ***rpb2*** sequence of CPC 35725 had highest similarity to *Coniella diospyri* (GenBank MK047543.1; Identities = 789/813 (97 %), no gaps), *Coniella limoniformis* (GenBank KX833492.1; Identities = 702/767 (92 %), no gaps) and *Coniella tibouchinae* (GenBank KX833507.1; Identities = 701/767 (91 %), no gaps). The *rpb2* sequences of CPC 35725 and CPC 35609 are identical over 831 nucleotides. Closest hits using the ***tef1*** sequence of CPC 35725 had highest similarity to *Coniella diospyri* (GenBank MK047563.1; Identities = 444/472 (94 %), 3 gaps (0 %)), *Coniella tibouchinae* (GenBank JQ281779.1; Identities = 301/346 (87 %), 11 gaps (3 %)) and *Coniella africana* (GenBank KX833600.1; Identities = 300/357 (84 %), 21 gaps (5 %)). The *tef1* sequences of CPC 35725 and CPC 35609 are identical over 473 nucleotides.

Colour illustrations. *Eucalyptus microcorys* forest. Conidiomata on oatmeal agar; conidiogenous cells; conidia. Scale bars = 300 µm (conidiomata), 10 µm (all others).

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Phialoseptomonium eucalypti

Fungal Planet 874 – 19 July 2019

Phialoseptomonium Crous & Carnegie, *gen. nov.*

Etymology. Phialo = phialides, *septo* = conidial septa, and *-monium* – from *Acremonium*.

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

Mycelium consisting of hyaline, smooth, branched, septate hyphae. *Conidiophores* erect, straight to flexuous, arising directly from hyphae or from a basal stalk, subcylindrical, septate, giving rise to a rosette of conidiophores. *Conidiophores* erect, flexuous, subcylindrical with apical taper, hyaline but base at times appearing greenish olivaceous, septate. *Conidiogenous cells* apical, integrated, subcylindrical, phialidic with minute non-flared collarette. *Conidia* solitary, aggregating in mucoid mass, hyaline, smooth, granular, fusoid, straight, medianly 1-septate, apex obtuse, base truncate.

Type species. *Phialoseptomonium eucalypti* Crous & Carnegie. MycoBank MB830829.

Phialoseptomonium eucalypti Crous & Carnegie, *sp. nov.*

Etymology. Name refers to *Eucalyptus*, the host genus from which this fungus was isolated.

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 mm diam hyphae. *Conidiophores* erect, straight to flexuous, arising directly from hyphae or from a basal stalk, subcylindrical, 0–2-septate, 10–30 × 3–4.5 mm, giving rise to a rosette (2–6) of conidiophores. *Conidiophores* erect, flexuous, subcylindrical with apical taper, hyaline but base at times appearing greenish olivaceous, 5–7-septate, 190–220 × 2.5–3 mm. *Conidiogenous cells* apical, integrated, subcylindrical, phialidic with minute non-flared collarette (1 mm long), apex 1.5–2 mm diam, 90–120 × 2.5–3 mm. *Conidia* solitary, aggregating in mucoid mass, hyaline, smooth, granular, fusoid, straight, medianly 1-septate, apex obtuse, base truncate, 1.5 mm diam, (16–)19–21(–23) × 3(–3.5) mm.

Culture characteristics — Colonies flat, spreading, with folded surface, moderate aerial mycelium and smooth, lobate margin, reaching 60 mm diam after 2 wk at 25 °C. On MEA surface and reverse luteous. On PDA surface and reverse pale luteous. On OA surface saffron.

Typus. Australia, New South Wales, Boorabee State Forest, McCorquodale plantation, on leaves of *Eucalyptus grandis* × *camaldulensis* clone (*Myrtaceae*), 20 Apr. 2016, *A.J. Carnegie*, HPC 2431 (holotype CBS H-23941, culture ex-type CPC 35732 = CBS 145542, ITS and LSU sequences GenBank MK876402.1 and MK876443.1, MycoBank MB830830).

Notes — *Phialoseptomonium eucalypti* clusters with two acremonium-like isolates (Giraldo & Crous 2019), namely '*A. lichenicola*' CBS 303.70 and '*A. rhabdosporum*' CBS 438.66, which may be congeneric. Both the latter species have cylindrical, septate conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Acremonium lichenicola* (GenBank MH859549.1; Identities = 542/596 (91 %), 14 gaps (2 %)), *Acremonium rhabdosporum* (GenBank MH858850.1; Identities = 535/593 (90 %), 10 gaps (1 %)) and *Trichonectria rectipila* (GenBank NR_160175.1; Identities = 465/523 (89 %), 13 gaps (2 %)). The ITS sequence is also 2–6 nucleotides similar to unidentified sequences from an unpublished study on dark pigmented epifoliar fungi forming sooty patches on trees in a tropical rainwood forest (GenBank HE584928.1–HE584933.1). Closest hits using the **LSU** sequence are *Acremonium lichenicola* (GenBank MH871536.1; Identities = 798/816 (98 %), no gaps), *Sarcopodium flavolanatum* (GenBank MH876362.1; Identities = 794/816 (97 %), no gaps) and *Sarcopodium macalpinei* (GenBank MH876364.1; Identities = 791/816 (97 %), no gaps).

Colour illustrations. Eucalyptus grandis × *camaldulensis* plantation. Conidiophores on pine needle agar; conidia; flexuous conidiophores. Scale bars = 10 µm.

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Fusicladium eucalyptigenum

Fungal Planet 875 – 19 July 2019

Fusicladium eucalyptigenum Crous & M.J. Wingf., *sp. nov.*

Etymology. Name refers to *Eucalyptus*, the host genus from which this fungus was isolated.

Classification — *Sympoventuriaceae*, *Venturiales*, *Dothideomycetes.*

Mycelium consisting of medium brown, smooth, branched, septate, 2–2.5 mm diam hyphae. *Conidiophores* erect, 0–1-septate, mostly reduced to conidiogenous cells, straight to geniculous-sinuous, subcylindrical, 5–20 × 2.5–3 mm, medium brown, smooth, proliferating sympodially, scars thickened, darkened, not refractive, 1–1.5 mm diam. *Conidia* occurring in branched chains; ramoconidia medium brown, subcylindrical, 0–1-septate, 12–20 × 2–3 mm; conidia subcylindrical, straight, hyaline to pale brown, guttulate, medianly 1-septate; hila thickened and darkened, 1–1.5 mm diam, (13–)16–18(–20) × (1.5–)2–2.5 mm.

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

Typus. Malaysia, on twigs of *Eucalyptus* sp. (*Myrtaceae*), 22 Mar. 2018, *M.J. Wingfield*, HPC 2394 (holotype CBS H-23942, culture ex-type CPC 35746 = CBS 145543, ITS and LSU sequences GenBank MK876390.1 and MK876431.1, MycoBank MB830831).

Notes — '*Fusicladium*' *eucalyptigenum* is closely related to '*Fusicladium*' *amoenum* (conidia (6–)10.5–12.8(–17.3) × (1.5–)2.4–3(–3.8) µm) and '*F.' paraamoenum* (conidia (13–)15–20(–28) × (3–)3.5(–4) µm; Crous et al. 2016), but is distinct based on its conidial dimensions. The *Fusicladium* generic complex is presently being revised and will be published elsewhere.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to '*Fusicladium*' *amoenum* (GenBank MH862514.1; Identities = 529/554 (95 %), 1 gap (0 %)), '*Fusicladium*' *paraamoenum* (GenBank NR_155093.1; Identities = 527/557 (95 %), 4 gaps (0 %)) and '*Fusicladium*' *intermedium* (GenBank EU035432.1; Identities = 489/530 (92 %), 3 gaps (0 %)). Closest hits using the **LSU** sequence are '*Fusicladium*' *paraamoenum* (GenBank NG_058242.1; Identities = 721/728 (99 %), no gaps), '*Fusicladium*' *amoenum* (GenBank EU035425.1; Identities = 720/728 (99 %), no gaps) and '*Fusicladium*' *intermedium* (GenBank EU035432.1; Identities = 712/729 (98 %), 1 gap (0 %)).

Colour illustrations. *Eucalyptus* forest. Colony on oatmeal agar; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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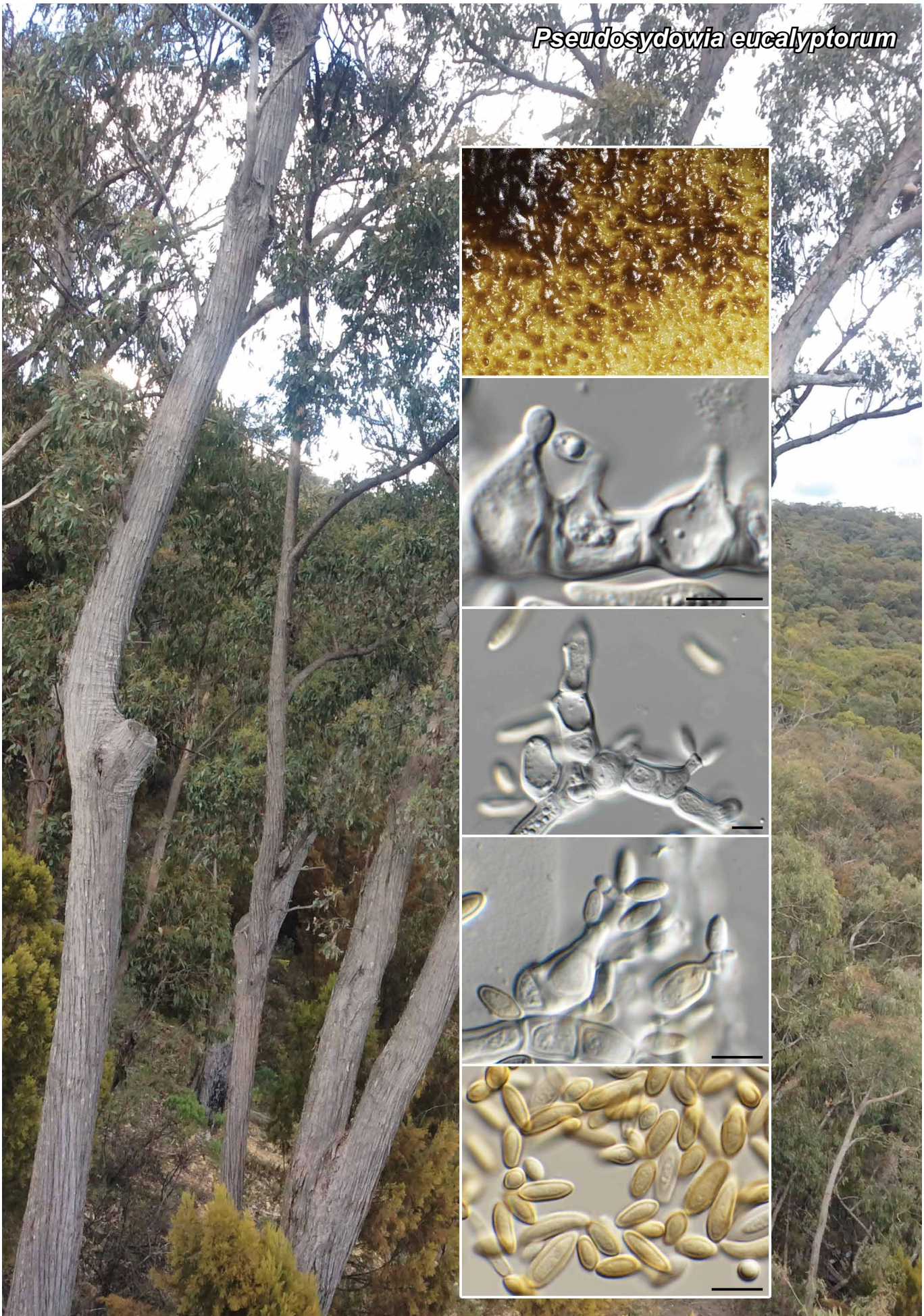
Pseudosydowia eucalyptorum

Fungal Planet 876 – 19 July 2019

Pseudosydowia eucalyptorum Crous & Carnegie, *sp. nov.*

Etymology. Name refers to *Eucalyptus*, the host genus from which this fungus was isolated.

Classification — *Saccotheciaceae*, *Dothideales*, *Dothidiomycetes.*

Mycelium consisting of branched, septate, smooth, hyaline, 5–6 mm diam hyphae. *Conidiomata* appearing as sporodochia on agar surface, consisting of aggregated clusters of conidiogenous cells arising directly from hyphae, reduced to loci on hyphae or ampulliform, hyaline, proliferating percurrently at apex, (2–)10–20 × (2–)5–6 mm. *Conidia* solitary, fusoid-ellipsoid, aseptate, apex obtuse, base truncate, hyaline, smooth-walled, becoming thick-walled and medium brown with age, straight to curved; hyaline conidia 5–10(–13) × (2.5–)3(–3.5) mm; pigmented conidia (11–)15–17(–21) × (3.5–)4–5 mm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface and reverse saffron. On PDA surface umber, reverse greenish olivaceous. On OA surface umber.

Typus. Australia, New South Wales, Nundle State Forest, Boundary Road, on leaves of *Eucalyptus* sp. (*Myrtaceae*), 23 May 2016, *A.J. Carnegie*, HPC 2455 (holotype CBS H-23943, culture ex-type CPC 35811 = CBS 145546, ITS and LSU sequences GenBank MK876406.1 and MK876447.1, MycoBank MB830832).

Notes — *Pseudosydowia eucalyptorum* is closely related to *P. eucalypti* (hyaline conidia, 8–13(–15) × 2–4(–5) µm; pigmented conidia 6–8(–10) × (2.3–)3–5.5 mm; Cheewangkoon et al. 2009), but has larger conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Sydowia* sp. (GenBank MF683457.1; Identities = 583/594 (98 %), 2 gaps (0 %)), *Pseudosydowia eucalypti* (as *Selenophoma eucalypti*, GenBank AY293059.1; Identities = 551/568 (97 %), 4 gaps (0 %)) and *Saccothecium rubi* (GenBank NR_148096.1; Identities = 525/561 (94 %), 11 gaps (1 %)). Closest hits using the **LSU** sequence are *Pseudosydowia eucalypti* (GenBank GQ303327.2; Identities = 824/828 (99 %), no gaps), *Selenophoma mahoniae* (GenBank EU754213.1; Identities = 833/853 (98 %), no gaps) and *Saccothecium rubi* (GenBank NG_059644.1; Identities = 811/833 (97 %), 2 gaps (0 %)).

Colour illustrations. Eucalyptus forest. Colony on oatmeal agar; conidiogenous cells and conidia. Scale bars = 10 µm.

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Beltraniella pseudoportoricensis

Fungal Planet 877 – 19 July 2019

Beltraniella pseudoportoricensis Crous, *sp. nov.*

Etymology. Name refers to a morphology similar to that of *Beltraniella portoricensis*.

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

Setae simple, erect, straight, thick-walled, coarsely verruculose toward apex, brown, 1–3-septate, arising from globose to lobate basal cell, tapering to acute apex, 75–230 × 3–6 mm. *Conidiophores* simple or branched, pale olivaceous, 10–20 × 4–6 mm, 1-septate, denticulate. *Conidiogenous cells* subcylindrical, smooth, pale brown, 8–12 × 4–6 mm, with several denticles, 1 mm diam. *Supporting cells* hyaline, oval to fusoid or obclavate with a single denticle, 10–12 × 3.5–4.5 mm. *Conidia* aseptate, smooth, lageniform to navicular, distal end truncate, proximal end rostrate, subhyaline with hyaline transverse band, (23–)25–27(–30) × 6–6.5(–7) mm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and even, smooth margins, covering dish after 2 wk at 25 °C. On MEA and PDA surface and reverse olivaceous grey. On OA surface smoke grey with patches of olivaceous grey.

Typus. South Africa, Western Cape Province, Cape Town, Kirstenbosch Botanical Garden, on leaf litter of *Podocarpus falcatus* (*Podocarpaceae*), 1 Mar. 2016, *P.W. Crous* (holotype CBS H-23944, culture ex-type CPC 34929 = CBS 145547, ITS and LSU sequences GenBank MK876377.1 and MK876416.1, MycoBank MB830833).

Notes — *Beltraniella pseudoportoricensis* forms part of the *B. portoricensis* species complex. The type (on *Odina wodier* from India) is not known from culture, but a recent reference isolate (on *Mangifera indica*, culture NFCCI 3993; conidia 20–25(–31) × 5.5–7 mm; Rajeshkumar et al. 2016) is phylogenetically distinct. We consequently describe the South African collection as new.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Beltraniella* sp. CGL-2017a (as *Beltraniella ramosiphora*, GenBank MG717500.1; Identities = 531/536 (99 %), no gaps), *Beltraniella portoricensis* (GenBank KU212349.1; Identities = 584/591 (99 %), 1 gap (0 %)) and *Beltraniella fertilis* (GenBank MF580247.1; Identities = 543/552 (98 %), 2 gaps (0 %)). Closest hits using the **LSU** sequence are *Beltraniella pandanicola* (GenBank MH260281.1; Identities = 828/834 (99 %), 1 gap (0 %)), *Beltraniella portoricensis* (GenBank MH871777.1; Identities = 828/834 (99 %), 1 gap (0 %)) and *Beltraniella humicola* (GenBank MH870044.1; Identities = 828/834 (99 %), 1 gap (0 %)).

Colour illustrations. Leaves and fruit of *Podocarpus falcatus*. Setae, conidiogenous cells, supporting cells and conidia. Scale bars = 10 µm.

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Teratosphaeria dunnii

Fungal Planet 878 – 19 July 2019

Teratosphaeria dunnii Crous & Carnegie, *sp. nov.*

Etymology. Name refers to *Eucalyptus dunnii*, the host species from which this fungus was isolated.

Classification — *Teratosphaeriaceae*, *Capnodiales*, *Dothideomycetes.*

Conidiomata pycnidial, solitary, brown, globose, 90–200 mm diam, with central ostiole; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* lining the inner cavity, subcylindrical, pale brown, 1–2-septate, branched or not, 7–20 × 2.5–4 mm, or reduced to conidiogenous cells. *Conidiogenous cells* subcylindrical to doliiform, medium brown, verruculose, proliferating percurrently at apex, 5–8 × 3.5–4 mm. Conidia solitary, aseptate, thick-walled, guttulate, golden brown, verruculose, subcylindrical to fusoid-ellipsoid, apex subobtuse, base truncate, 1.5–2 mm diam with minute marginal frill, (6–)8–9(–11) × (2.5–)3(–3.5) mm.

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

Typus. Australia, New South Wales, Yabbra State Forest, Boomi Creek plantation, on leaves of *Eucalyptus dunnii* (*Myrtaceae*), 19 Apr. 2016, *A.J. Carnegie*, HPC 2430 (holotype CBS H-23945, culture ex-type CPC 35653 = CBS 145548, ITS, LSU, *actA*, *cmdA*, *rpb2*, *tef1* and *tub2* sequences GenBank MK876409.1, MK876449.1, MK876463.1, MK876469.1, MK876491.1, MK876500.1 and MK876504.1, MycoBank MB830834).

Notes — *Teratosphaeria dunnii* is phylogenetically closely related (98 %, 8 bp difference in ITS) to *T. molleriana* (conidia (7–)9–12(–13) × (2.5–)3–3.5(–4) µm; Crous & Wingfield 1997), but can be distinguished based on its smaller conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Teratosphaeria molleriana* (GenBank MH862864.1; Identities = 515/523 (98 %), 1 gap (0 %)), *Teratosphaeria xenocryptica* (GenBank MH863258.1; Identities = 490/499 (98 %), 1 gap (0 %)) and *Teratosphaeria sieberi* (GenBank MH327816.1; Identities = 510/520 (98 %), 3 gaps (0 %)). Closest hits using the **LSU** sequence are *Teratosphaeria molleriana* (GenBank KF251777.1; Identities = 777/779 (99 %), no gaps), *Teratosphaeria profusa* (GenBank FJ493220.1; Identities = 773/779 (99 %), no gaps) and *Teratosphaeria dimorpha* (GenBank FJ493215.1; Identities = 773/779 (99 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Teratosphaeria molleriana* (GenBank KF903394.1; Identities = 525/540 (97 %), 2 gaps (0 %)), *Teratosphaeria viscida* (GenBank KF903563.1; Identities = 504/542 (93 %), 7 gaps (1 %)) and *Teratosphaeria eucalypti* (GenBank KF903452.1; Identities = 504/543 (93 %), 8 gaps (1 %)). Closest hits using the ***cmdA*** sequence had highest similarity to *Teratosphaeria molleriana* (GenBank KF902737.1; Identities = 432/457 (95 %), no gaps), *Teratosphaeria blakelyi* (GenBank KF902704.1; Identities = 420/460 (91 %), 6 gaps (1 %)) and *Teratosphaeria toledana* (GenBank KF902774.1; Identities = 416/457 (91 %), 6 gaps (1 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Teratosphaeria molleriana* (GenBank KX348104.1; Identities = 855/881 (97 %), no gaps), *Teratosphaeria eucalypti* (GenBank KX348102.1; Identities = 812/913 (89 %), 2 gaps (0 %)) and *Teratosphaeria gracilis* (GenBank MK047548.1; Identities = 790/886 (89 %), 2 gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Teratosphaeria molleriana* (GenBank KF903326.1; Identities = 318/361 (88 %), 27 gaps (7 %)), *Teratosphaeria blakelyi* (GenBank KF903288.1; Identities = 316/365 (87 %), 10 gaps (2 %)) and *Teratosphaeria toledana* (GenBank KF903361.1; Identities = 314/367 (86 %), 17 gaps (4 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Teratosphaeria gracilis* (GenBank MK047583.1; Identities = 529/597 (89 %), 14 gaps (2 %)), *Teratosphaeria* aff. *nubilosa* (GenBank AY725611.1; Identities = 514/595 (86 %), 19 gaps (3 %)) and *Teratosphaeria destructans* (GenBank KT343568.1; Identities = 514/597 (86 %), 13 gaps (2 %)).

Colour illustrations. *Eucalyptus dunnii* forest. Conidiomata on malt extract agar; conidiogenous cells; conidia. Scale bars = 10 µm.

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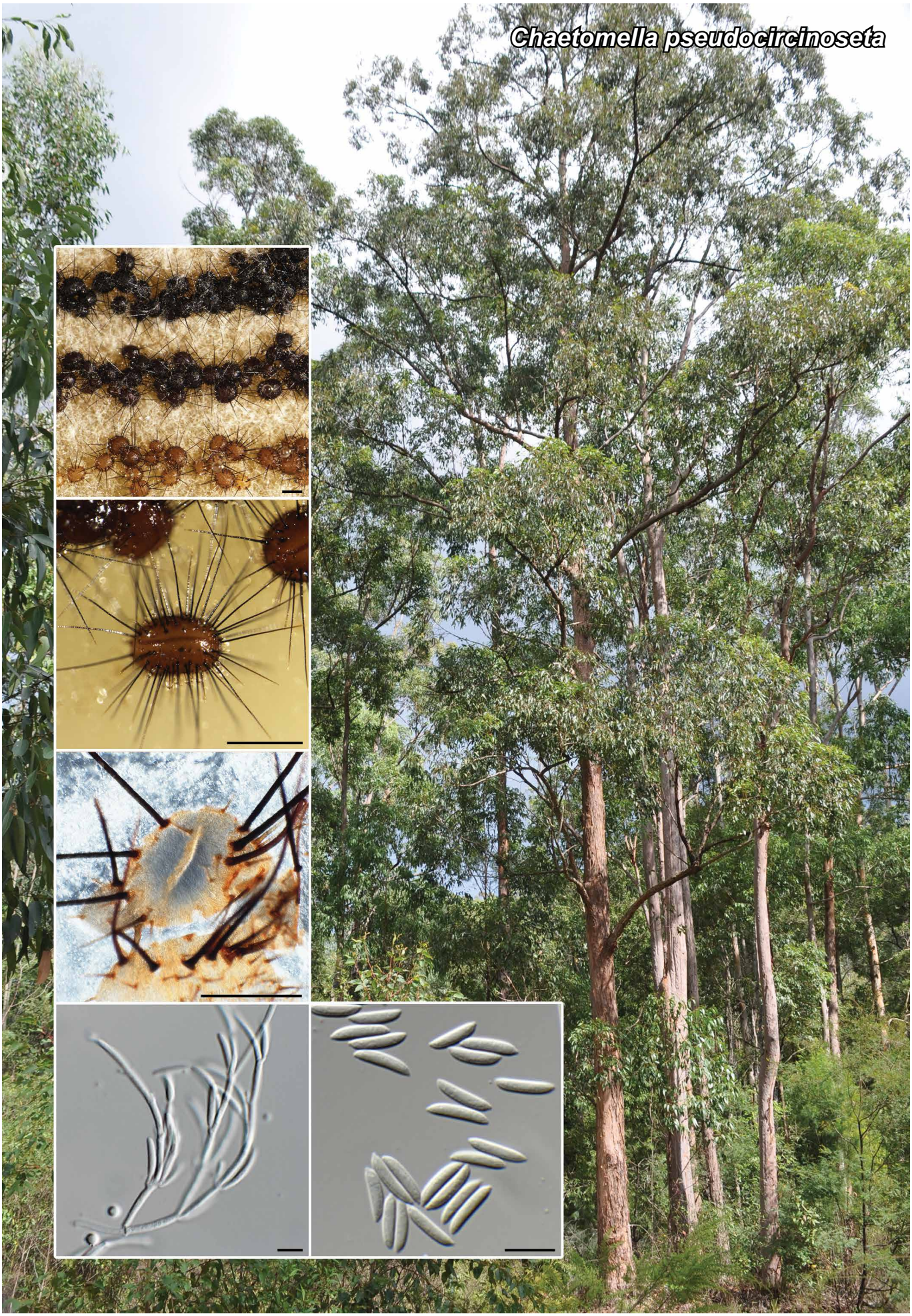
Chaetomella pseudocircinoseta

Fungal Planet 879 – 19 July 2019

Chaetomella pseudocircinoseta Crous & Carnegie, *sp. nov.*

Etymology. Name refers to a morphology similar to that of *Chaetomella circinoseta*.

Classification — *Chaetomellaceae*, *Chaetomellales*, *Leotiomycetes.*

Conidiomata pycnidial, solitary, becoming aggregated, superficial, dark brown, globose, 300–400 mm diam with elongate raphe of paler pigment visible across top of conidiomata. *Setae* brown, smooth, unbranched, thick-walled, multi-septate, tapering towards obtuse to clavate apex, 150–750 × 10–20 mm. *Conidiophores* hyaline, smooth, filiform, subcylindrical, branched, 2–6-septate, 50–120 × 1.5–2 mm. *Conidiogenous cells* phialidic, subcylindrical, terminal and intercalary, smooth, hyaline, 10–50 × 1.5–2 mm. *Conidia* aseptate, hyaline, fusoid to falcate with pointed ends, slightly curved, (9–)11–12 × (2–)2.5 mm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and prominent circadian rings on surface, margin smooth, lobate, reaching 60 mm diam after 2 wk at 25 °C. On MEA surface chestnut, reverse umber. On PDA surface chestnut, reverse pale luteous with patches of umber. On OA surface chestnut.

Typus. Australia, New South Wales, Bulladelah State Forest, on leaves of *Eucalyptus microcorys* (*Myrtaceae*), 16 Apr. 2016, *A.J. Carnegie*, HPC 2420 (holotype CBS H-23946, culture ex-type CPC 35721 = CBS 145549, ITS and LSU sequences GenBank MK876379.1 and MK876418.1, MycoBank MB830835).

Notes — *Chaetomella pseudocircinoseta* is phylogenetically closely related to *C. circinoseta* (CBS 159.62, type), which is characterised by the fact that it has spiral setae (Rossman et al. 2004), which are, however, lacking in *C. pseudocircinoseta.*

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Chaetomella circinoseta* (GenBank MH858129.1; Identities = 460/467 (99 %), no gaps), *Chaetomella raphigera* (GenBank MH864530.1; Identities = 435/473 (92 %), 14 gaps (2 %)) and *Chaetomella cinnamomea* (GenBank MH858845.1; Identities = 434/473 (92 %), 14 gaps (2 %)). Closest hits using the **LSU** sequence are *Chaetomella circinoseta* (GenBank MH869712.1; Identities = 813/818 (99 %), no gaps), *Sphaerographium nyssicola* (GenBank MH876287.1; Identities = 807/827 (98 %), no gaps) and *Pilidium septatum* (GenBank NG_060185.1; Identities = 763/783 (97 %), no gaps).

Colour illustrations. *Eucalyptus microcorys* forest. Conidiomata on malt extract agar; conidiomata with setae; conidiophore with conidiogenous cells; conidia. Scale bars = 400 µm (conidiomata), 10 µm (conidiophores and conidia).

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Cladophialophora eucalypti

Fungal Planet 880 – 19 July 2019

Cladophialophora eucalypti Crous & Carnegie, *sp. nov.*

Etymology. Name refers to *Eucalyptus*, the host genus from which this fungus was isolated.

Classification — *Trichomeriaceae*, *Chaetothyriales*, *Eurotiomycetes.*

Mycelium consisting of hyaline to olivaceous, smooth-walled, branched, septate, 1.5–2 mm diam hyphae. *Conidiophores* solitary, erect, subcylindrical, unbranched, straight to geniculous-sinuous, medium brown, smooth, 10–65 × 3–4 mm, 1–5-septate. *Conidiogenous cells* terminal, integrated, subcylindrical, medium brown, smooth, 10–15 × 3–4 mm; proliferating sympodially, scars terminal, thickened and darkened, 0.5–1 mm diam. *Conidia* in branched chains, olivaceous smooth-walled, granular, obclavate to subcylindrical, straight to flexuous; ramoconidia obclavate, 3–8-septate, 40–100 × 2–3 mm; conidia subcylindrical, 0(–1)-septate, (8–)13–15(–20) × 2.5(–3) mm.

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

Typus. Australia, New South Wales, Keybarbin State Forest, Tabulum, on leaves of *Eucalyptus dunnii* (*Myrtaceae*), 17 Apr. 2016, *A.J. Carnegie*, HPC 2433 (holotype CBS H-23947, culture ex-type CPC 35667 = CBS 145551, ITS, LSU and *actA* sequences GenBank MK876380.1, MK876419.1 and MK876454.1, MycoBank MB830836).

Notes — *Cladophialophora eucalypti* is related to a *Cladophialophora* isolate (CBS 376.54) deposited under the name '*Pyricularia parasitica*' and clusters in a clade typified by *Cladophialophora* and *Exophiala* spp.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Exophiala encephalarti* (GenBank HQ599588.1; Identities = 446/534 (84 %), 32 gaps (5 %)), *Brycekendrickomyces acaciae* (GenBank KM246230.1; Identities = 505/620 (81 %), 57 gaps (9 %)) and *Knufia cryptophialidica* (GenBank NR_121501.1; Identities = 443/537 (82 %), 38 gaps (7 %)). Closest hits using the **LSU** sequence are *Brycekendrickomyces acaciae* (GenBank MH874874.1; Identities = 795/826 (96 %), 4 gaps (0 %)), *Exophiala encephalarti* (GenBank HQ599589.1; Identities = 784/822 (95 %), 8 gaps (0 %)) and *Cladophialophora proteae* (GenBank EU035411.1; Identities = 785/829 (95 %), 6 gaps (0 %)). No significant hits were obtained when the ***actA*** sequence was used in blastn and megablast searches.

Colour illustrations. *Eucalyptus* forest. Hyphae; conidiophores with conidiogenous cells; conidial chains. Scale bars = 10 µm.

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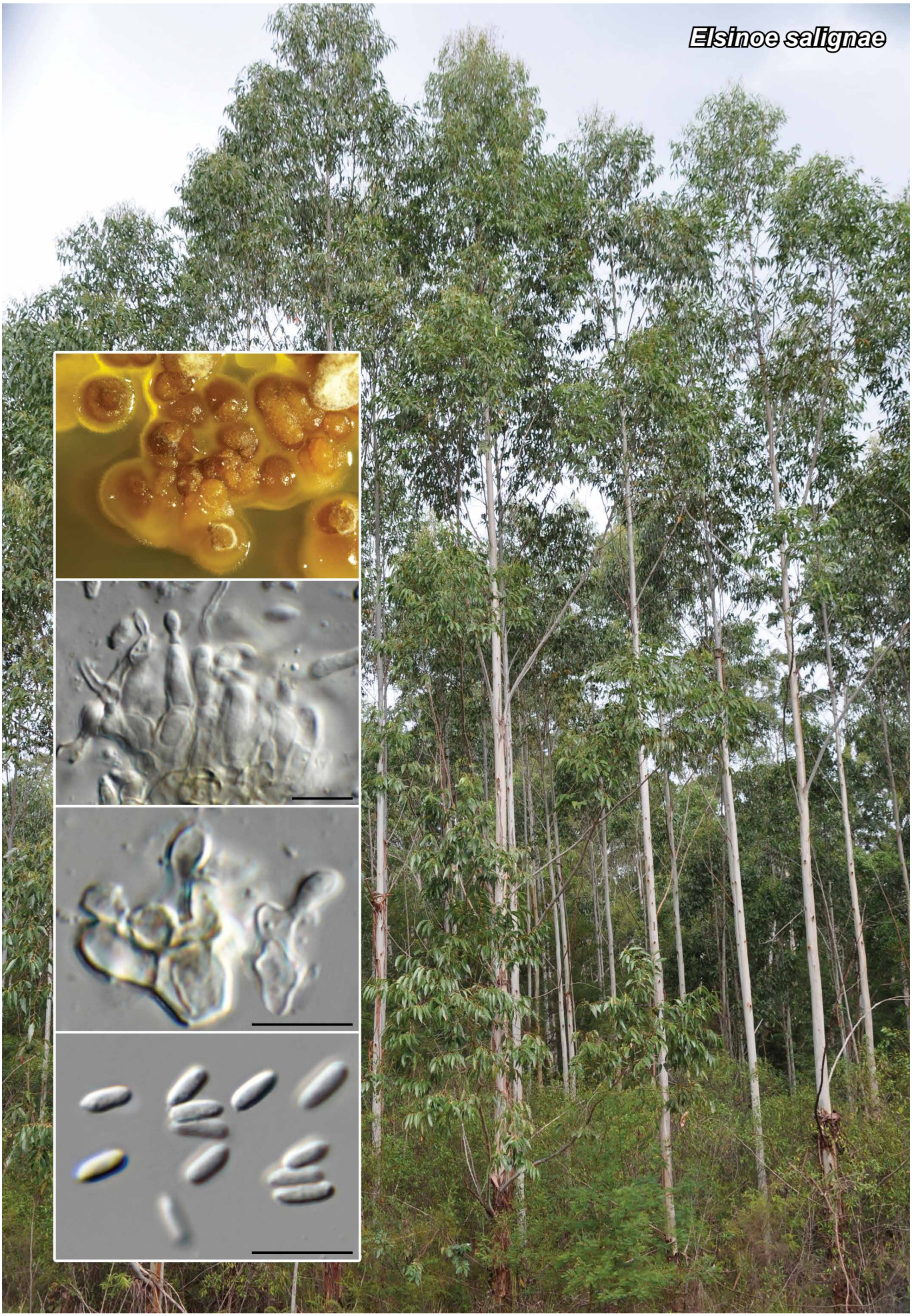
Elsinoe salignae

Fungal Planet 881 – 19 July 2019

Elsinoe salignae Crous & Carnegie, *sp. nov.*

Etymology. Name refers to *Eucalyptus saligna*, the host species from which this fungus was isolated.

Classification — *Elsinoaceae*, *Myriangiales*, *Dothideomycetes.*

Conidiomata erumpent, sporodochial, 50–150 mm diam, based on a pale brown stroma giving rise to densely aggregated conidiophores. *Conidiophores* unbranched, hyaline to pale brown, smooth-walled, subcylindrical, 1–2-septate, 15–25 × 3–5 mm. *Conidiogenous cells* integrated, subcylindrical, hyaline, smooth-walled, mono- to polyphialidic, 8–12 × 3–4 mm. *Conidia* solitary, aggregating in mucoid mass, aseptate, hyaline, smooth-walled, guttulate, subcylindrical to ellipsoid, apex obtuse, base truncate, (4.5–)5–6(–6.5) × (2–)2.5 mm.

Culture characteristics — Colonies erumpent, surface folded, with sparse aerial mycelium and smooth, lobate margin, reaching 7 mm diam after 2 wk at 25 °C. On MEA surface sienna, reverse ochreous. On PDA surface ochreous to umber, reverse luteous with diffuse luteous pigment. On OA surface ochreous.

Typus. Australia, New South Wales, Bulladelah State Forest, on leaves of *Eucalyptus saligna* (*Myrtaceae*), 16 Apr. 2016, *A.J. Carnegie*, HPC 2415 (holotype CBS H-23948, culture ex-type CPC 35713 = CBS 145552, ITS, LSU and *rpb2* sequences GenBank MK876389.1, MK876430.1 and MK876485.1, MycoBank MB830837).

Notes — The genus *Elsinoe* was recently revised by Fan et al. (2017), who also provided a key to the species occurring on *Eucalyptus*. *Elsinoe salignae* is phylogenetically related to, but distinct from *E. leucopogonis* (on *Leucopogon* sp., Australia) (Crous et al. 2018c).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Elsinoe leucopogonis* (GenBank NR_159836.1; Identities = 567/580 (98 %), 3 gaps (0 %)), *Elsinoe hederae* (GenBank NR_148146.1; Identities = 502/521 (96 %), 12 gaps (2 %)) and *Elsinoe lepagei* (GenBank MH856598.1; Identities = 519/549 (95 %), 14 gaps (2 %)). Closest hits using the **LSU** sequence are *Elsinoe hederae* (GenBank KX886994.1; Identities = 733/736 (99 %), no gaps), *Elsinoe lepagei* (GenBank KX887004.1; Identities = 732/736 (99 %), no gaps) and *Elsinoe fagarae* (GenBank KX886981.1; Identities = 732/736 (99 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Elsinoe leucopogonis* (GenBank MH327874.1; Identities = 848/872 (97 %), no gaps), *Elsinoe hederae* (GenBank KX887113.1; Identities = 634/744 (85 %), no gaps) and *Elsinoe lepagei* (GenBank KX887122.1; Identities = 617/741 (83 %), 2 gaps (0 %)).

Colour illustrations. *Eucalyptus saligna* plantation. Colony on malt extract agar; conidiogenous cells; conidia. Scale bars = 10 µm.

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Neodevriesia cycadicola

Fungal Planet 882 – 19 July 2019

Neodevriesia cycadicola Crous, *sp. nov.*

Etymology. Name refers to *Cycas*, the host genus from which this fungus was isolated.

Classification — *Neodevriesiaceae*, *Capnodiales*, *Dothideomycetes*.

Mycelium consisting of pale olivaceous, smooth, branched, septate, 2–3 mm diam hyphae. *Conidiophores* solitary, erect, pale olivaceous, smooth, subcylindrical, 1–2-septate, straight, 5–15 × 2–3 mm. *Conidiogenous cells* terminal, subcylindrical, pale olivaceous, smooth, 5–9 × 2–3 mm; scars thickened and darkened, 1.5 mm diam. *Conidia* occurring in branched chains, subcylindrical, pale olivaceous, smooth-walled, guttulate; ramoconidia 0–1-septate, 8–12 × 2.5–3 mm; conidia 0–1-septate, (7–)8–9 × 2–2.5 mm.

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

Typus. Italy, Sicily, on leaves of *Cycas* sp. (*Cycadaceae*), 10 Apr. 2018, *P.W. Crous*, HPC 2365 (holotype CBS H-23949, culture ex-type CPC 35833 = CBS 145553, ITS and LSU sequences GenBank MK876397.1 and MK876438.1, MycoBank MB830838).

Notes — *Neodevriesia* was established by Quaedvlieg et al. (2014) for a genus of hyphomycetes with medium brown, unbranched conidiophores, thick-walled, medium brown, rarely septate conidia, occurring in short and mostly unbranched conidial chains, and lacking chlamydospores. *Neodevriesia cycadicola* is closely related to *N. lagerstroemiae* (ramoconidia 9–15 × 3–5 µm, (0–)1(–2)-septate; conidia narrowly ellipsoid, 0–1-septate, (5–)8–12(–15) × 2–3(–4) µm (Crous et al. 2009, 2015a), but can be distinguished based on its conidial morphology.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neodevriesia metrosideri* (GenBank NR_161141.1; Identities = 513/551 (93 %), 19 gaps (3 %)), *Neodevriesia lagerstroemiae* (GenBank GU214634.1; Identities = 515/554 (93 %), 23 gaps (4 %)) and *Neodevriesia hilliana* (GenBank NR_145098.1; Identities = 515/559 (92 %), 20 gaps (3 %)). Closest hits using the **LSU** sequence are *Neodevriesia agapanthi* (GenBank NG_042688.1; Identities = 806/820 (98 %), no gaps), *Neodevriesia imbrexigena* (as *Devriesia imbrexigena*, GenBank JX915749.1; Identities = 813/828 (98 %), no gaps) and *Neodevriesia knoxdaviesii* (GenBank MH874778.1; Identities = 802/817 (98 %), 2 gaps (0 %)).

Colour illustrations. *Cycas* sp. Symptomatic leaves; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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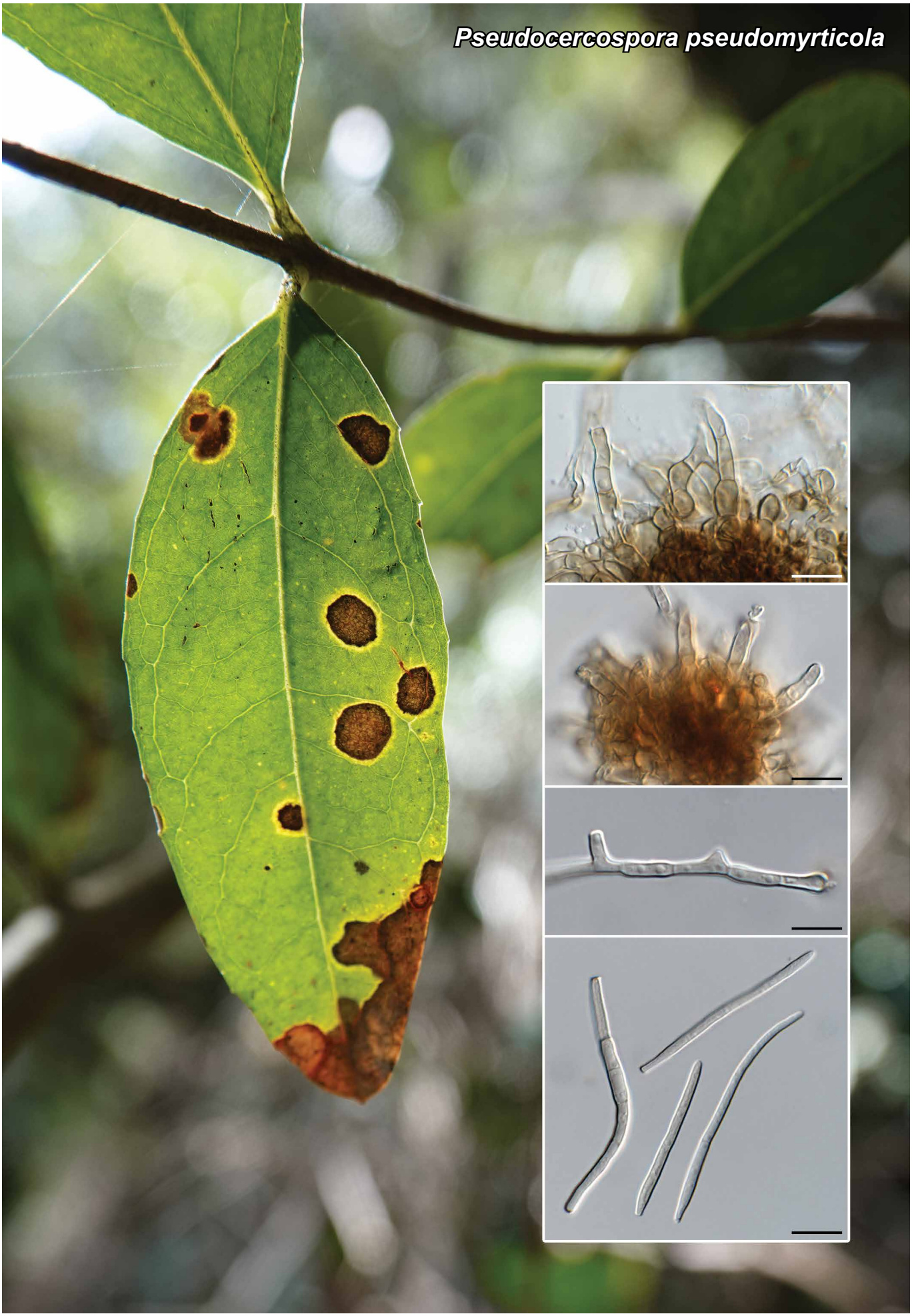
Pseudocercospora pseudomyrticola

Fungal Planet 883 – 19 July 2019

Pseudocercospora pseudomyrticola Crous, *sp. nov.*

Etymology. Name refers to a morphology similar to that of *Pseudocercospora myrticola*.

Classification — *Mycosphaerellaceae*, *Capnodiales*, *Dothideomycetes.*

Caespituli hypophyllous, brown, erumpent, arising from a weakly developed brown stroma, 30–50 mm diam. *Conidiophores* tightly aggregated in fascicles, subcylindrical, medium brown, roughened, straight, mostly unbranched, 0–1-septate, 10–15 × 3–4 mm, proliferating percurrently at apex; conidiophores also reduced to loci on aerial mycelium, truncate, 2–7 × 2 mm. *Conidia* pale olivaceous brown, smooth-walled, guttulate, subcylindrical with apical taper, apex subobtuse, base truncate, 3–9-septate, straight to slightly flexuous, (30–)45–75(–90) × (2–)2.5 mm; hila not thickened nor darkened.

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

Typus. Italy, Rome, on leaves of *Myrtus communis* (*Myrtaceae*), 12 Apr. 2018, *P.W. Crous*, HPC 2357 (holotype CBS H-23950, culture ex-type CPC 35448 = CBS 145554, ITS, LSU, *actA*, *rpb2* and *tef1* sequences GenBank MK876405.1, MK876446.1, MK876461.1, MK876490.1 and MK876499.1, MycoBank MB830839).

Notes — *Pseudocercospora pseudomyrticola* differs from *P. myrticola* in that it sporulates primarily on superficial mycelium (mostly absent in *P. myrticola*), lacks well-developed fascicles (prominent in *P. myrticola*), and has shorter, narrower conidia (Crous 1999).

Based on a megablast search of NCBIs GenBank nucleotide database, the **ITS** sequence is identical to sequences of several species, e.g., to *Pseudocercospora jahnii* (GenBank KM393283.1; Identities = 537/537 (100 %), no gaps), *Pseudocercospora elaeodendri* (GenBank GU980950.1; Identities = 537/537 (100 %), no gaps) and *Pseudocercospora indonesiana* (GenBank MH863211.1; Identities = 535/535 (100 %), no gaps). The **LSU** sequence is identical to sequences of several species, e.g., to *Pseudocercospora pittospori* (GenBank MK210500.1; Identities = 836/836 (100 %), no gaps), *Pseudocercospora ampelopsis* (GenBank GU253846.1; Identities = 836/836 (100 %), no gaps) and *Pseudocercospora ravenalicola* (GenBank GU253828.1; Identities = 836/836 (100 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Pseudocercospora flavomarginata* (GenBank JX902134.1; Identities = 528/537 (98 %), no gaps), *Pseudocercospora schizolobii* (GenBank JX902151.1; Identities = 527/537 (98 %), no gaps) and *Pseudocercospora paraguayensis* (GenBank KF903444.1; Identities = 510/521 (98 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Pseudocercospora punicae* (GenBank KX462655.1; Identities = 609/616 (99 %), no gaps), *Pseudocercospora cercidicola* (GenBank KX462618.1; Identities = 608/616 (99 %), no gaps) and *Pseudocercospora breonadiae* (GenBank MH108006.1; Identities = 636/671 (95 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Pseudocercospora* sp. (GenBank GU384369.1; Identities = 310/310 (100 %), no gaps), *Pseudocercospora oenotherae* (GenBank GU384466.1; Identities = 309/310 (99 %), no gaps) and *Pseudocercospora struthanthi* (GenBank KT290195.1; Identities = 496/498 (99 %), no gaps).

Colour illustrations. Leaf spots on *Myrtus* sp. Conidiogenous cells, conidiogenous loci and conidia. Scale bars = 10 µm.

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Corynespora encephalarti

Fungal Planet 884 – 19 July 2019

Corynespora encephalarti Crous & M.J. Wingf., *sp. nov.*

Etymology. Name refers to *Encephalartos*, the host genus from which this fungus was isolated.

Classification — *Corynesporascaceae*, *Pleosporales*, *Dothideomycetes.*

Conidiophores erect, straight, unbranched, olivaceous brown, smooth-walled, subcylindrical, 150–400 × 6–8 mm, 5–11-septate. *Conidiogenous cells* monotretic, integrated, terminal, cylindrical to slightly swollen, 25–50 × 6–7 mm; scar terminal, darkened, truncate, 2–3 mm diam. *Conidia* solitary, obclavate, medium olivaceous brown, 1–12-distoseptate, apex subobtuse, base truncate, 4–5 mm diam, dark brown, (65–)100–150 (–200) × (10–)11–15(–18) mm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse sienna. On PDA surface dirty white, reverse chestnut. On OA surface dirty white.

Typus. South Africa, Limpopo Province, Tzaneen, on leaves of *Encephalartos* sp. (*Zamiaceae*), 22 June 2016, *P.W. Crous*, HPC 2487 (holotype CBS H-23951, culture ex-type CPC 35867 = CBS 145555, ITS and LSU sequences GenBank MK876383.1 and MK876424.1, MycoBank MB830840).

Notes — *Corynespora* was recently treated by Voglmayr & Jaklitsch (2017). As far as we could establish, no species have ever been described from *Encephalartos*, and *C. encephalarti* is phylogenetically distinct from all species presently known from culture or DNA sequence.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Corynespora citricola* (GenBank FJ852593.1; Identities = 534/550 (97 %), 5 gaps (0 %)), *Corynespora smithii* (GenBank KY984300.1; Identities = 530/554 (96 %), 11 gaps (1 %)) and *Corynespora thailandica* (GenBank NR_161145.1; Identities = 522/553 (94 %), 12 gaps (2 %)). Closest hits using the **LSU** sequence are *Corynespora smithii* (GenBank GU323201.1; Identities = 894/896 (99 %), no gaps), *Corynespora cassiicola* (GenBank MH869486.1; Identities = 889/894 (99 %), no gaps) and *Corynespora torulosa* (GenBank NG_058866.1; Identities = 863/871 (99 %), no gaps).

Colour illustrations. *Encephalartos* sp. Symptomatic leaves; conidiogenous cells and conidia. Scale bars = 10 µm.

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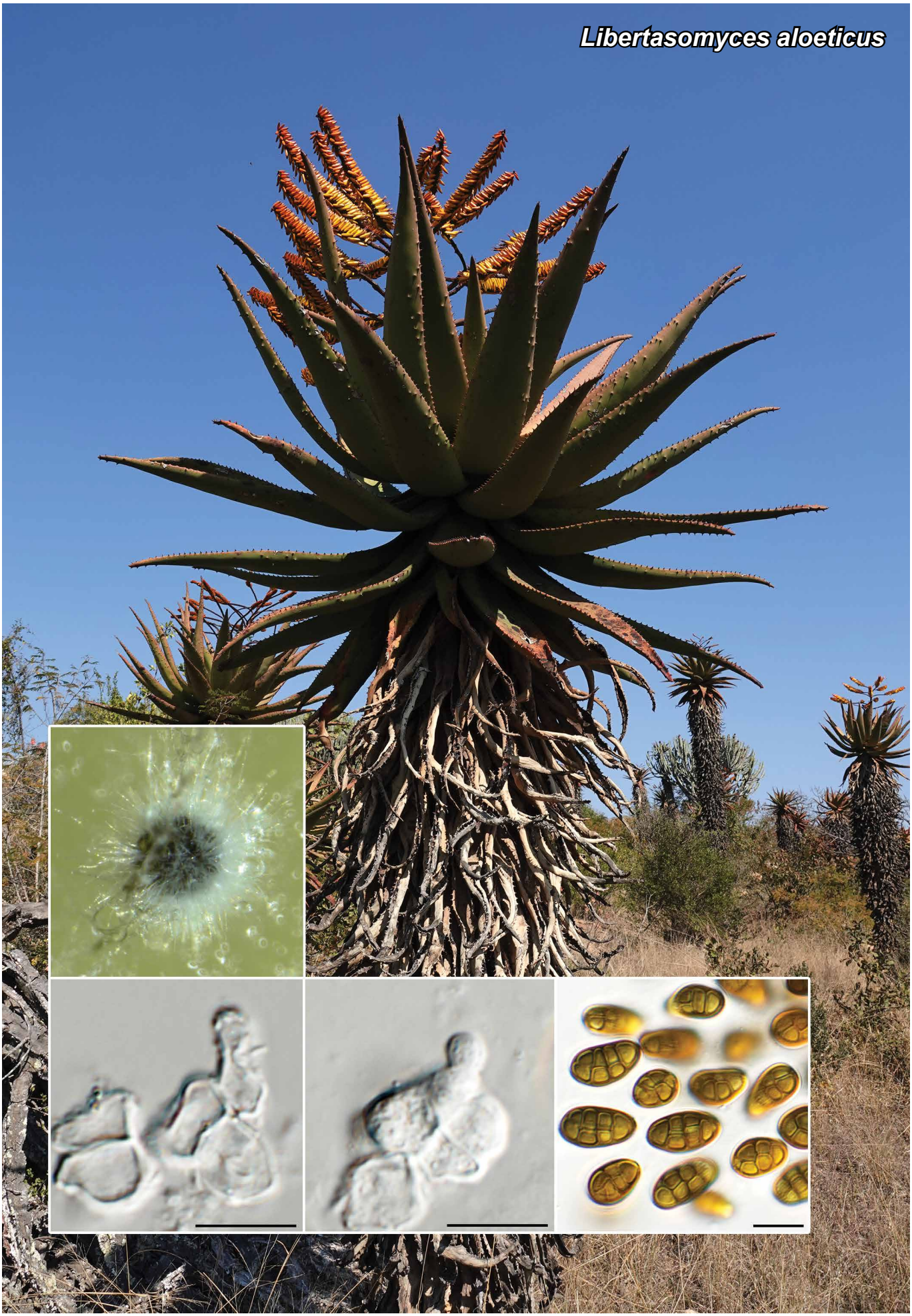
Libertasomyces aloeticus

Fungal Planet 885 – 19 July 2019

Libertasomyces aloeticus Crous & M.J. Wingf., *sp. nov.*

Etymology. Name refers to *Aloe*, the host genus from which this fungus was isolated.

Classification — *Libertasomycetaceae*, *Pleosporales*, *Dothideomycetes*.

Conidiomata pycnidial, unilocular, separate, globose, immersed to erumpent, brown, globose, 150–250 mm diam, with central ostiole; wall of 3–6 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, ampulliform to doliiform with prominent periclinal thickening, 5–7 × 5–6 mm. *Conidia* solitary, golden-brown, becoming dark brown, ellipsoid to subglobose, muriformly septate, with (1–)3(–4) transverse septa and 1–4 oblique septa, thick-walled, roughened and with striations covering length of conidium body, apex obtuse, base bluntly rounded, (9–)11–13(–15) × (7–)8(–9) mm.

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

Typus. South Africa, Limpopo Province, Tzaneen, on leaves of *Aloe* sp. (*Asphodelaceae*), 22 June 2016, *P.W. Crous*, HPC 2479 (holotype CBS H-23952, culture ex-type CPC 35863 = CBS 145558, ITS and LSU sequences GenBank MK876395.1 and MK876436.1, MycoBank MB830841).

Notes — *Libertasomyces aloeticus* is intermediate between *Neoplatysporoides* (based on *N. aloeicola*; conidia 0–1-septate, (8–)9–10(–12) × (4–)5(–6) µm, on leaves of *Aloe* sp. in Tanzania; Crous et al. 2015b) and *Libertasomyces*. *Neoplatysporoides aloeticus* has conidia that are similar in morphology to those of *L. quercus* (conidia (15–)17–19(–21) × (6–)7–8(–10) µm; Crous & Groenewald 2017), though larger in size.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neoplatysporoides aloeicola* (GenBank MK398281.1; Identities = 535/583 (92 %), 13 gaps (2 %)), *Libertasomyces quercus* (GenBank NR_155337.1; Identities = 519/572 (91 %), 14 gaps (2 %)) and *Libertasomyces platani* (GenBank NR_155336.1; Identities = 515/572 (90 %), 13 gaps (2 %)). Closest hits using the **LSU** sequence are *Neoplatysporoides aloeicola* (GenBank NG_058160.1; Identities = 794/807 (98 %), 4 gaps (0 %)), *Libertasomyces myopori* (GenBank MH878216.1; Identities = 793/808 (98 %), 4 gaps (0 %)) and *Libertasomyces platani* (GenBank NG_059744.1; Identities = 791/806 (98 %), 4 gaps (0 %)).

Colour illustrations. *Aloe* sp. Conidioma on oatmeal agar; conidiogenous cells and conidia. Scale bars = 200 mm (conidioma), 10 µm (all others).

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Phyllosticta lauridiae

Fungal Planet 886 – 19 July 2019

Phyllosticta lauridiae Crous & M.J. Wingf., *sp. nov.*

Etymology. Name refers to *Lauridia*, the host genus from which this fungus was isolated..

Classification — *Phyllostictaceae*, *Botryosphaeriales*, *Dothideomycetes.*

Leaf spots amphigenous, 3–7 mm diam, round, medium brown, with a dark red-brown margin. *Conidiomata* pycnidial, aggregated, black, erumpent, globose, 200–250 mm diam, exuding a hyaline conidial mass; wall of several layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* terminal, subcylindrical, hyaline, smooth, encased in mucoid layer, 7–12 × 3–4 mm, proliferating percurrently near apex. *Conidia* (9–)12–13(–14) × 6(–7) mm, solitary, hyaline, smooth-walled, guttulate, ellipsoid to obovoid, tapering towards truncate base, 3–4 mm diam, encased in mucoid sheath, 1–1.5 mm diam, bearing a single hyaline mucoid appendage, 15–20(–30) mm long, tapering to acutely rounded tip.

Culture characteristics — Colonies erumpent, spreading, with folded surface, sparse to moderate aerial mycelium and feathery margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface olivaceous grey, reverse iron-grey. On PDA and OA surface and reverse iron-grey.

Typus. South Africa, Eastern Cape Province, Haga Haga, Amathole, on leaves of *Lauridia tetragona* (*Celastraceae*), 15 Dec. 2016, *M.J. Wingfield*, HPC 2290 (holotype CBS H-23953, culture ex-type CPC 35305 = CBS 145559, ITS, LSU, *actA*, *gapdh*, *rpb2* and *tef1* sequences GenBank MK876404.1, MK876445.1, MK876460.1, MK876472.1, MK876489.1 and MK876498.1, MycoBank MB830842).

Notes — *Phyllosticta* was revised by Wikee et al. (2013). *Phyllosticta lauridiae* is closely related to *P. podocarpicola* (conidia 12–13(–16) × 8–9(–9.5) µm. On *Podocarpus maki*, Florida, USA), but morphologically distinct based on its shorter and narrower conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phyllosticta podocarpicola* (GenBank NR_145233.1; Identities = 538/569 (95 %), 11 gaps (1 %)), *Phyllosticta foliorum* (GenBank NR_145231.1; Identities = 536/570 (94 %), 12 gaps (2 %)) and *Phyllosticta concentrica* (as *Guignardia philoprina*, GenBank AF312014.1; Identities = 567/603 (94 %), 14 gaps (2 %)). Closest hits using the **LSU** sequence are *Phyllosticta gaultheriae* (as *Guignardia gaultheriae*, GenBank DQ678089.1; Identities = 804/813 (99 %), no gaps), *Phyllosticta hakeicola* (GenBank MH107953.1; Identities = 820/830 (99 %), 1 gap (0 %)) and *Phyllosticta philoprina* (GenBank KF766341.1; Identities = 812/822 (99 %), 1 gap (0 %)). Closest hits using the ***actA*** sequence had highest similarity to *Phyllosticta hakeicola* (GenBank MH107984.1; Identities = 225/233 (97 %), 3 gaps (1 %)), *Phyllosticta abieticola* (GenBank KF289238.1; Identities = 220/228 (96 %), 3 gaps (1 %)) and *Phyllosticta ligustricola* (GenBank AB704212.1; Identities = 220/231 (95 %), 4 gaps (1 %)). Closest hits using the ***gapdh*** sequence had highest similarity to *Phyllosticta hakeicola* (GenBank MH107999.1; Identities = 478/520 (92 %), 7 gaps (1 %)), *Phyllosticta musarum* (GenBank KM816632.1; Identities = 485/534 (91 %), 11 gaps (2 %)) and *Phyllosticta capitalensis* (GenBank KM816629.1; Identities = 485/534 (91 %), 11 gaps (2 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Phyllosticta gaultheriae* (as *Guignardia gaultheriae*, GenBank DQ677987.1; Identities = 528/579 (91 %), no gaps), *Phyllosticta aloeicola* (GenBank KY855816.1; Identities = 657/742 (89 %), 13 gaps (1 %)) and *Phyllosticta eugeniae* (GenBank KY855891.1; Identities = 632/728 (87 %), 7 gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Phyllosticta hakeicola* (GenBank MH108025.1; Identities = 359/384 (93 %), 9 gaps (2 %)), *Phyllosticta illicii* (GenBank MF198236.1; Identities = 368/403 (91 %), 15 gaps (3 %)) and *Phyllosticta yuccae* (GenBank JX227948.1; Identities = 378/418 (90 %), 16 gaps (3 %)).

Colour illustrations. Ocean view at Haga Haga. Leaf spot on *Lauridia tetragona*; colony on potato dextrose agar; conidiogenous cells; conidia. Scale bars = 10 µm.

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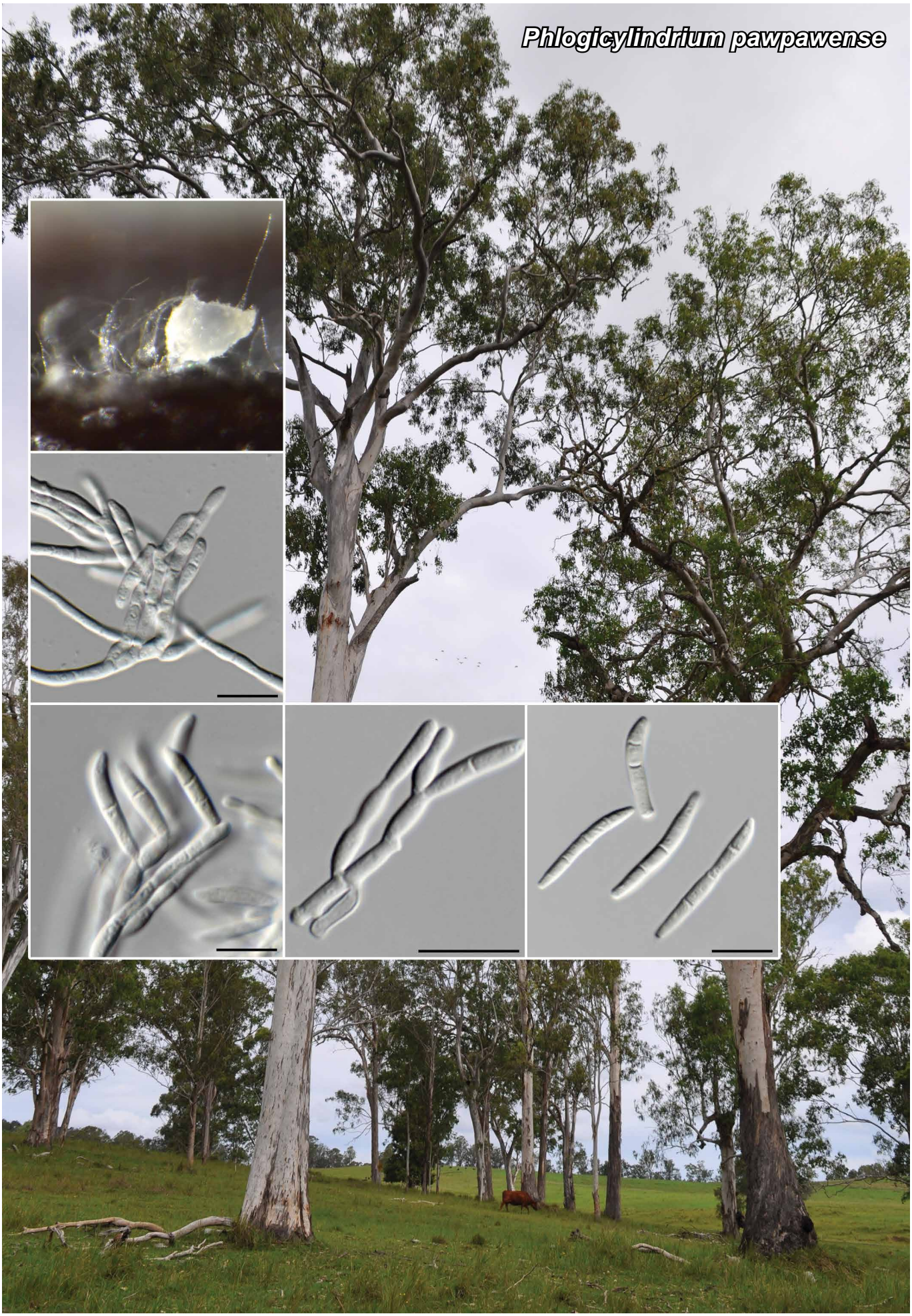
Phlogicylindrium pawpawense

Fungal Planet 887 – 19 July 2019

Phlogicylindrium pawpawense Crous & Carnegie, *sp. nov.*

Etymology. Name refers to the location where this fungus was isolated, Paw Paw Skids Road, Australia.

Classification — *Phlogicylindriaceae*, *Xylariales*, *Sordariomycetes.*

Mycelium consisting of hyaline, branched, septate, 1.5–2 mm diam hyphae. *Conidiomata* sporodochial, 150–300 mm diam, erumpent, round, hyaline, consisting of tightly aggregated *conidiophores* or conidiophores erect, penicillate with tightly aggregated conidiogenous apparatus; conidiophores 80–150 mm tall, stipe 40–50 × 2.5–3 mm. *Conidiophores* with penicillate conidiogenous apparatus: branches (3–5) subcylindrical, hyaline, smooth, straight to curved, 5–7 × 2.5–3 mm. *Conidiogenous cells* terminal and intercalary, hyaline, smooth, subcylindrical, straight to slightly curved, 5–14 × 2–2.5 mm, proliferating sympodially. *Conidia* solitary, hyaline, smooth, guttulate to granular, subcylindrical, 1–3-septate, curved, rarely straight, tapering to subacutely rounded apex, base truncate, 1–1.5 mm diam, (12–)17–22(–25) × 2–2.5 mm.

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

Typus. Australia, New South Wales, Richmond Range SF, Paw Paw Skids Road, on juvenile leaves of *Eucalyptus tereticornis* (*Myrtaceae*), 19 Apr. 2016, *A.J. Carnegie*, HPC 2424 (holotype CBS H-23954, culture ex-type CPC 35536 = CBS 145560, ITS and LSU sequences GenBank MK876403.1 and MK876444.1, MycoBank MB830843).

Notes — ITS sequence data of *Phlogicylindrium pawpawense* is related to species of *Cylindrium* and *Polyscytalum*, which were treated by Crous et al. (2014, 2018b). Morphologically however, it is a better fit for *Phlogicylindrium*, being related to *P. dunnii* (conidia (32–)35–42(–47) × (2–)2.5(–3) µm; Crous et al. 2019), though distinct in having smaller conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Polyscytalum chilense* (GenBank NR_158958.1; Identities = 523/565 (93 %), 11 gaps (1 %)), *Polyscytalum eucalyptigenum* (GenBank MH107909.1; Identities = 527/571 (92 %), 14 gaps (2 %)) and *Polyscytalum grevilleae* (GenBank NR_154719.1; Identities = 520/564 (92 %), 7 gaps (1 %)). Closest hits using the **LSU** sequence are *Phlogicylindrium dunnii* (GenBank MK442548.1; Identities = 727/736 (99 %), 1 gap (0 %)), *Phlogicylindrium tereticornis* (GenBank NG_058510.1; Identities = 726/736 (99 %), 1 gap (0 %)) and *Polyscytalum chilense* (GenBank MH107954.1; Identities = 724/735 (99 %), no gaps).

Colour illustrations. *Eucalyptus tereticornis* trees. Sporodochial conidioma; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Neoacrodontiella eucalypti

Fungal Planet 888 – 19 July 2019

Neoacrodontiella Crous & M.J. Wingf., *gen. nov.*

Etymology. Name refers to a morphological similarity with the genus *Acrodontiella*.

Classification — *Acarosporaceae*, *Acarosporales*, *Lecanoromycetes.*

Mycelium consisting of branched, septate, hyaline, smooth hyphae. *Conidiophores* aggregated in sporodochia, arising from a hyaline stroma, subcylindrical, smooth, branched, multiseptate. *Conidiogenous cells* terminal and intercalary, subcylindrical, irregularly curved, rarely straight, with apical taper and pimple-like loci, not to slightly thickened. *Conidia* solitary, hyaline, smooth-walled, guttulate, fusoid, straight, aseptate, apex subacute, base truncate, not to slightly thickened.

Type species. *Neoacrodontiella eucalypti* Crous & M.J. Wingf. MycoBank MB830844.

Neoacrodontiella eucalypti Crous & M.J. Wingf., *sp. nov.*

Etymology. Name refers to *Eucalyptus*, the host genus from which this fungus was isolated.

Mycelium consisting of branched, septate, hyaline, smooth, 2–3 mm diam hyphae. *Conidiophores* aggregated in sporodochia, arising from a hyaline stroma, subcylindrical, smooth, branched, multiseptate, 30–50 × 3–4 mm. *Conidiogenous cells* terminal and intercalary, subcylindrical, irregularly curved, rarely straight, with apical taper, 20–30 × 2.5–3 mm, with pimple-like loci, not to slightly thickened. *Conidia* solitary, hyaline, smooth-walled, guttulate, fusoid, straight, aseptate, apex subacute, base truncate, not to slightly thickened, (11–)12–15(–17) × (2.5–)3(–3.5) mm.

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

Typus. Malaysia, on leaves of *Eucalyptus urophylla* (*Myrtaceae*), 31 Mar. 2018, *M.J. Wingfield*, HPC 2392 (holotype CBS H-23955, culture ex-type CPC 35693 = CBS 145561, ITS and LSU sequences GenBank MK876396.1 and MK876437.1, MycoBank MB830845).

Notes — *Neoacrodontiella* is somewhat reminiscent of *Acrodontiella* (Seifert et al. 2011), though distinct in that it forms sporodochia, and the conidiogenous loci are flattened and more prominent than in *Acrodontiella*, with conidia also having prominently truncate hila.

No significant hits were obtained when the **ITS** sequence was used in a megablast search of NCBIs GenBank nucleotide database; the closest hits were with *Corticifraga peltigerae* (GenBank KY462801.1; Identities = 377/451 (84 %), 42 gaps (9 %)), *Taitaia aurea* (GenBank NR_160480.1; Identities = 367/444 (83 %), 36 gaps (8 %)) and *Gomphillus americanus* (GenBank KY381580.1; Identities = 177/181 (98 %), no gaps). Closest hits using the **LSU** sequence are '*Spermospora avenae*' (GenBank MH878416.1; Identities = 790/825 (96 %), 2 gaps (0 %)), *Cytosporella chamaeropis* (GenBank MH871929.1; Identities = 759/810 (94 %), 4 gaps (0 %)) and *Acarospora thamnina* (GenBank KF024746.1; Identities = 475/508 (94 %), 4 gaps (0 %)). The LSU sequence of *Spermospora avenae* is most likely incorrect as it is not congeneric with other sequences of the genus in the database.

Colour illustrations. Eucalyptus leaf litter. Colony on oatmeal agar; conidiogenous cells and conidia. Scale bars = 10 µm.

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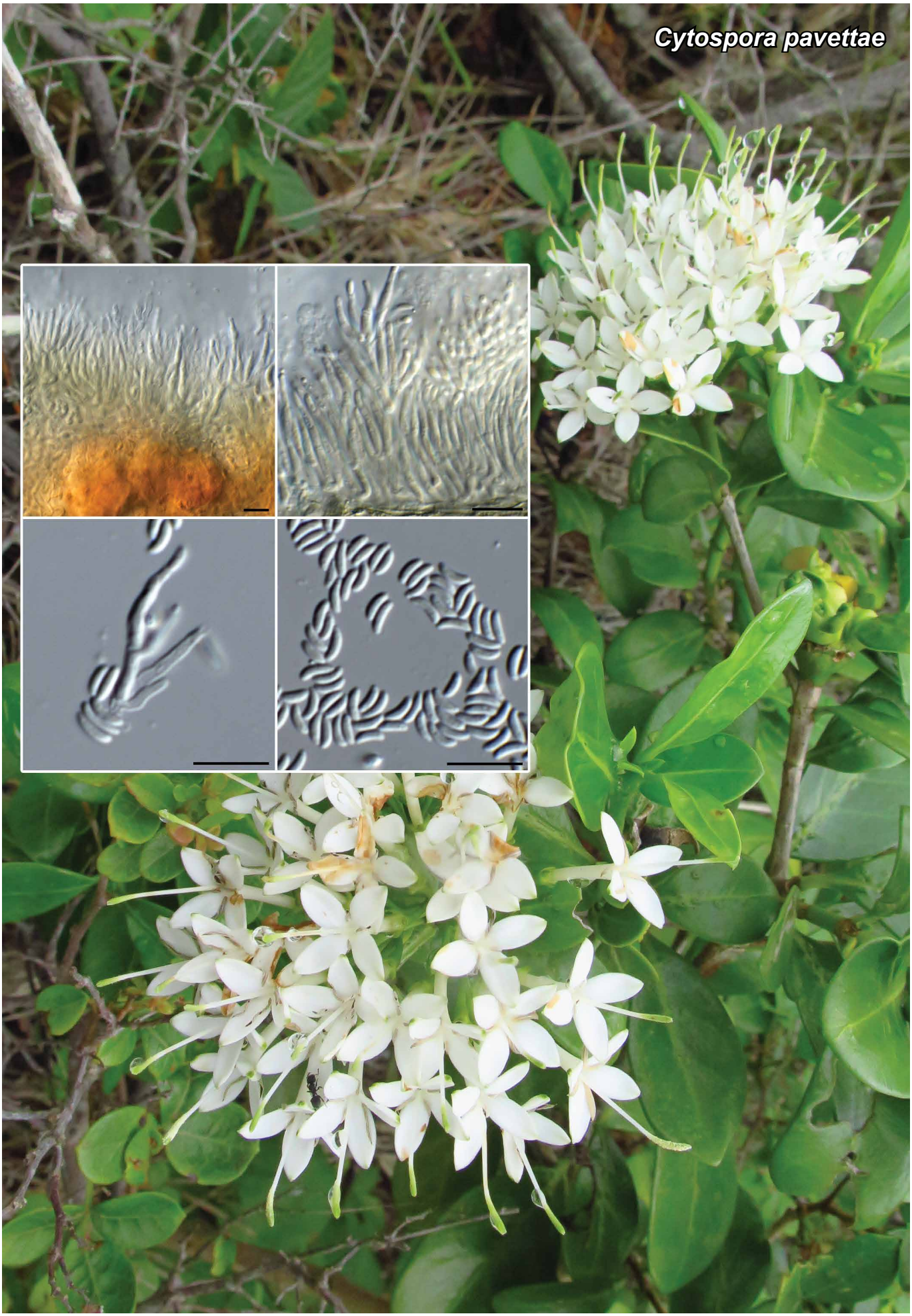
Cytospora pavettae

Fungal Planet 889 – 19 July 2019

Cytospora pavettae Crous & M.J. Wingf., *sp. nov.*

Etymology. Name refers to *Pavetta*, the host genus from which this fungus was isolated.

Classification — *Cytosporaceae*, *Diaporthales*, *Sordariomycetes.*

Colonies nearly sterile, sporulating on PNA. *Conidiomata* pycnidial, erumpent, dark brown, globose, 200–300 mm diam. *Conidiophores* lining the inner cavity, hyaline, smooth-walled, branched, 1–3-septate, 10–25 × 2.5–3 mm. *Conidiogenous cells* terminal and intercalary, frequently in rosette, subcylindrical with apical taper, hyaline, smooth-walled, phialidic, with minute non-flared collarette, 1 mm long, 4–10 × 1.5–2 mm. *Conidia* aseptate, solitary, hyaline, smooth-walled, ellipsoid, curved, ends subobtuse, (3.5–)4(–5) × 1.5 mm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA surface ochreous to sienna, reverse umber. On PDA surface and reverse pale luteous. On OA surface umber.

Typus. South Africa, Eastern Cape Province, Haga Haga, Amathole, on leaf spots of *Pavetta revoluta* (*Rubiaceae*), 24 Dec. 2016, *M.J. Wingfield*, HPC 2299 (holotype CBS H-23956, culture ex-type CPC 35293 = CBS 145562, ITS, LSU, *actA*, *rpb2*, *tef1* and *tub2* sequences GenBank MK876386.1, MK876427.1, MK876457.1, MK876483.1, MK876497.1 and MK876503.1, MycoBank MB830846).

Notes — Several phylogenetic studies have recently been published on *Cytospora* (Jami et al. 2018, Lawrence et al. 2018). Based on available data, *C. pavettae* is most similar to *C. lumnitzericola*, which occurs on *Lumnitzera racemosa* in Thailand (conidia (3.7–)4–4.5 × 1–1.3(–1.5) µm; Norphanphoun et al. 2017). There are few morphological differences between the two species, which are best distinguished based on their DNA phylogeny.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cytospora nitschkei* (GenBank KY051843.1; Identities = 519/532 (98 %), 1 gap (0 %)), *Cytospora sacculus* (GenBank KY051824.1; Identities = 517/534 (97 %), 3 gaps (0 %)) and *Cytospora brevispora* (GenBank KY051803.1; Identities = 517/534 (97 %), 3 gaps (0 %)). Closest hits using the **LSU** sequence are *Cytospora xylocarpi* (GenBank NG_064535.1; Identities = 790/797 (99 %), 2 gaps (0 %)), *Cytospora lumnitzericola* (GenBank NG_064534.1; Identities = 790/797 (99 %), 2 gaps (0 %)) and *Cytospora thailandica* (GenBank NG_064536.1; Identities = 789/797 (99 %), 2 gaps (0 %)). Closest hits using the ***actA*** sequence had highest similarity to *Cytospora lumnitzericola* (GenBank MH253457.1; Identities = 180/197 (91 %), 7 gaps (3 %)), *Cytospora xylocarpi* (GenBank MH253458.1; Identities = 166/183 (91 %), 2 gaps (1 %)) and *Cytospora parakantschavelii* (GenBank MG972053.1; Identities = 163/181 (90 %), 8 gaps (4 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Cytospora lumnitzericola* (GenBank MH253461.1; Identities = 686/741 (93 %), no gaps), *Cytospora xylocarpi* (GenBank MH253462.1; Identities = 684/741 (92 %), no gaps) and *Cytospora thailandica* (GenBank MH253464.1; Identities = 681/741 (92 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Cytospora sacculus* (GenBank KP310860.1; Identities = 295/329 (90 %), 4 gaps (1 %)), *Cytospora punicae* (GenBank MG971654.1; Identities = 279/317 (88 %), 13 gaps (4 %)) and *Cytospora californica* (GenBank MG971662.1; Identities = 403/464 (87 %), 12 gaps (2 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Cytospora ceratosperma* (as *Valsa ceratosperma*, GenBank EU219136.1; Identities = 501/600 (84 %), 30 gaps (5 %)), *Cytospora sacculus* (GenBank KR045688.1; Identities = 501/601 (83 %), 33 gaps (5 %)) and *Cytospora cincta* (GenBank KR045665.1; Identities = 443/524 (85 %), 20 gaps (4 %)).

Colour illustrations. *Pavetta revoluta*. Conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Pantospora chromolaenae

Fungal Planet 890 – 19 July 2019

Pantospora chromolaenae Crous & Cheew., *sp. nov.*

Etymology. Name refers to *Chromolaena*, the host genus from which this fungus was isolated.

Classification — *Mycosphaerellaceae*, *Capnodiales*, *Dothideomycetes.*

Mycelium consisting of pale brown, smooth-walled, septate, branched, 2.5–3 mm diam hyphae. *Conidiophores* solitary, erect, straight to flexuous, subcylindrical, 1–6-septate, 20–70 × 3–6 mm, medium brown, smooth to verruculose, mostly unbranched. *Conidiogenous cells* medium brown, subcylindrical, smooth to verruculose, 10–15 × 3–6 mm, terminal and intercalary, scars thickened, darkened, refractive, 2–3 mm diam. *Conidia* solitary, unbranched, obclavate, straight to flexuous, medium brown, verruculose, granular, apex obtuse, base truncate, 2–2.5 mm diam, thickened, darkened, refractive, (3–)6–8(–12) transversely septate, conidia becoming muriformly septate, starting with basal cells, (24–)50–65(–80) × (4–)5–6(–7) mm.

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

Typus. Thailand, Songkhla, Hat Yai, on leaves of *Chromolaena odorata* (*Asteraceae*), 2008, *R. Cheewangkoon* (holotype CBS H-23957, culture ex-type MC14 = CPC 34870 = CBS 145563, ITS, LSU, *actA*, *his3* and *rpb2* sequences GenBank MK876401.1, MK876442.1, MK876459.1, MK876476.1 and MK876488.1, MycoBank MB830848).

Notes — *Pantospora* is characterised by conidiogenous cells with sympodial and percurrent proliferation, and pseudocercospora-like conidia that have transverse, and often also oblique to longitudinal septa (Minnis et al. 2011, Videira et al. 2017). *Pantospora chromolaenae* represents a new species on *Chromolaena odorata* in Thailand.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Rhachisphaerella mozambica* (GenBank MH863208.1; Identities = 506/514 (98 %), 3 gaps (0 %)), *Pantospora guazumae* (GenBank NR_119971.1; Identities = 506/514 (98 %), 3 gaps (0 %)) and *Amycosphaerella africana* (as *Mycosphaerella aurantia*, GenBank EU853468.1; Identities = 506/514 (98 %), 3 gaps (0 %)). Closest hits using the **LSU** sequence are *Ragnhildiana diffusa* (GenBank MH866148.1; Identities = 831/833 (99 %), 1 gap (0 %)), *Ragnhildiana pseudotithoniae* (GenBank NG_058049.1; Identities = 831/833 (99 %), 1 gap (0 %)) and *Ragnhildiana perfoliati* (GenBank GU214453.1; Identities = 815/817 (99 %), 1 gap (0 %)). Closest hits using the ***actA*** sequence had highest similarity to *Amycosphaerella africana* (GenBank KF903407.1; Identities = 496/520 (95 %), 5 gaps (0 %)), *Rhachisphaerella mozambica* (as *Mycosphaerella mozambica*, GenBank EU514319.1; Identities = 504/531 (95 %), 4 gaps (0 %)) and *Camptomeriphila leucaenae* (GenBank KY173563.1; Identities = 446/474 (94 %), 5 gaps (1 %)). No *actA* sequence of *Pantospora* was available for comparison. Closest hits using the ***his3*** sequence had highest similarity to *Rhachisphaerella mozambica* (as *Mycosphaerella mozambica*, GenBank EU514371.1; Identities = 371/382 (97 %), 2 gaps (0 %)), *Pseudocercosporella bakeri* (GenBank KX288752.1; Identities = 353/371 (95 %), 3 gaps (0 %)) and *Pseudocercospora indonesiana* (GenBank EU514393.1; Identities = 356/390 (91 %), 7 gaps (1 %)). No *his3* sequence of *Pantospora* was available for comparison. Closest hits using the ***rpb2*** sequence had highest similarity to *Amycosphaerella africana* (GenBank MF951432.1; Identities = 765/871 (88 %), no gaps), *Asperisporium caricicola* (GenBank MF951439.1; Identities = 794/908 (87 %), no gaps) and *Asperisporium caricae* (GenBank MF951438.1; Identities = 813/930 (87 %), no gaps). The *rpb2* sequence is 804/923 (87 %, including 4 gaps) similar to the *rpb2* sequence of *Pantospora guazumae* voucher BPI 880778 (JN190952.1).

Colour illustrations. Temple at Songkhla, Hat Yai. Leaf spots; conidiophores, conidiogenous cells, and muriformly septate conidia. Scale bars = 10 µm.

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Ramularia pistaciae

Fungal Planet 891 – 19 July 2019

Ramularia pistaciae Crous, *sp. nov.*

Etymology. Name refers to *Pistacia*, the host genus from which this fungus was isolated.

Classification — *Mycosphaerellaceae*, *Capnodiales*, *Dothideomycetes.*

Mycelium consisting of branched, septate, hyaline, smooth-walled, 2–2.5 mm diam hyphae. *Conidiophores* reduced to conidiogenous cells on hyphae, or 1-septate, erect, straight to flexuous, hyaline, smooth-walled, 5–25 × 2.5–3 mm. *Conidiogenous cells* terminal, subcylindrical, hyaline, smooth, 5–12 × 2.5–3 mm, proliferating sympodially; scars thickened, darkened and refractive, 1 mm diam. *Conidia* subcylindrical to fusoid-ellipsoid, hyaline, smooth-walled; ramoconidia 0–1-septate, 10–18 × 2.5–3 mm; intermediary and terminal conidia in branched chains, aseptate, (5–)6–7(–8) × 2.5–3 mm; hila thickened, darkened, and refractive, 0.5–1 mm diam.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface and reverse saffron. On PDA surface dirty white, reverse olivaceous grey in middle, plate luteous in outer region. On OA surface saffron.

Typus. Italy, Rome, on leaves of *Pistacia lentiscus* (*Anacardiaceae*), 13 Apr. 2018, *P.W. Crous*, HPC 2340 (holotype CBS H-23958, culture ex-type CPC 35443 = CBS 145564, ITS, *actA* and *gapdh* sequences GenBank MK876408.1, MK876462.1 and MK876473.1, MycoBank MB830849).

Notes — *Ramularia* was recently revised by Videira et al. (2015, 2016). *Ramularia pistaciae* is the first species known to occur on *Pistacia*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Ramularia pratensis* var. *pratensis* (GenBank EU019284.2; Identities = 520/532 (98 %), 1 gap (0 %)), *Ramularia eucalypti* (GenBank EF394861.1; Identities = 520/532 (98 %), 1 gap (0 %)) and *Ramularia gei* (GenBank KX287412.1; Identities = 519/531 (98 %), 1 gap (0 %)). Closest hits using the ***actA*** sequence had highest similarity to *Ramularia gaultheriae* (GenBank KX287693.1; Identities = 540/585 (92 %), no gaps), *Ramularia unterseheri* (GenBank KP894376.1; Identities = 545/592 (92 %), 3 gaps (0 %)) and *Ramularia diervillae* (GenBank KX287689.1; Identities = 536/586 (91 %), 3 gaps (0 %)). Closest hits using the ***gapdh*** sequence had highest similarity to *Ramularia vizellae* (GenBank KP894637.1; Identities = 414/455 (91 %), 8 gaps (1 %)), *Ramularia actinidia* (GenBank KX288152.1; Identities = 407/452 (90 %), 12 gaps (2 %)) and *Ramularia inaequalis* (GenBank KP894555.1; Identities = 405/451 (90 %), 12 gaps (2 %)).

Colour illustrations. Forest with diverse trees near Rome. Conidiophores sporulating on synthetic nutrient-poor agar; conidiophores and conidia. Scale bars = 10 µm.

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Thozetella neonivea
& Neodevriesia sexualis

Fungal Planet 892 & 893 – 19 July 2019

Thozetella neonivea Crous & Thangavel, *sp. nov.*

Etymology. Name refers to a morphology similar to that of *Thozetella nivea.*

Classification — *Chaetosphaeriaceae*, *Chaetosphaeriales*, *Sordariomycetes.*

Conidiomata solitary, dispersed, sporodochial, erect, oval, 70–300 mm diam, superficial, cream to pale brown, arising from a hyaline hyphal network; supporting cells subcylindrical, pale brown to brown, giving rise to an apical layer of conidiogenous cells. *Conidiogenous cells* discrete, pale brown, smooth, doliiform to subcylindrical, 12–26 × 2.5–3.5 mm, apex 1.5–2 mm diam, phialidic, with periclinal thickening and minute collarette. *Conidia* hyaline, smooth, aseptate, eguttulate, fusoid, straight or slightly curved, (12–)13–14(–15) × (2.5–)3 mm with an unbranched appendage at each end, central at apex and excentric at base, 5–8 mm long. *Microawns* also produced enteroblastically from phialides, hyaline, tapering towards base, verruculose and curved towards obtuse apex, 40–55 × 3–4 mm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium and feathery margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface olivaceous grey, reverse isabelline. On PDA surface and reverse olivaceous grey. On OA surface umber.

Typus. New Zealand, Northland, on leaves of *Archontophoenix cunninghamiana* (*Arecaceae*), 2017, *R. Thangavel*, T17_03360H (holotype CBS H-23959, culture ex-type CPC 34886 = CBS 145534, ITS and LSU sequences GenBank MK876411.1 and MK876451.1, MycoBank MB830850).

Note — *Thozetella neonivea* is characterised by sporodochia with aseptate, setulate conidia, (12–)13–14(–15) × (2.5–)3 mm, and having microawns (verruculose, curved, 40–55 × 3–4 mm). Based on ITS sequence data, it is phylogenetically closest to *Thozetella nivea* (conidia 17.5–24 × 3–3.8 µm, microawns curved, 50–70 × 1.3–3 µm; Pirozynski & Hodges 1973), but is distinct from that species based on its conidial dimensions and the morphology of its microawns. A key to species in the genus has been provided by Barbosa et al. (2011), with several species linked to *Chaetosphaeria* sexual morphs, although it is relevant to recognise that the latter genus is polyphyletic.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Thozetella nivea* (GenBank EU825201.1; Identities = 492/509 (97 %), 5 gaps (0 %)), *Thozetella tocklaiensis* (GenBank MH857817.1; Identities = 457/474 (96 %), 6 gaps (1 %)) and *Thozetella pinicola* (as *Thozetella* sp. RJ-2008, GenBank EU825197.1; Identities = 490/510 (96 %), 5 gaps (0 %)). The ITS sequence was also highly similar to several sequences deposited in GenBank under '*Thozetella* sp.' and representing endophytes of *Rhododendron* hair roots in China (GenBank HM208719.1), *Populus deltoides* roots in USA (e.g., GenBank JX243958.1), *Erica demissa* and *Erica dominans* roots in South Africa (e.g., GenBank KF270075.1 and KY228489.1), *Nicotiana benthamiana* and *Nicotiana simulans* roots and leaves in Australia (e.g., GenBank KU059808.1 and KY582136.1) and from the roots of *Festuca rubra* subsp. *pruinosa* in Spain (GenBank MH633956.1). Closest hits using the **LSU** sequence are *Thozetella nivea* (GenBank EU825200.1; Identities = 815/817 (99 %), 1 gap (0 %)), *Thozetella pinicola* (as *Thozetella* sp. RJ-2008, Gen-Bank EU825195.1; Identities = 814/819 (99 %), 1 gap (0 %)) and *Thozetella pandanicola* (GenBank MH376740.1; Identities = 813/820 (99 %), 2 gaps (0 %)).

Neodevriesia sexualis Crous & Thangavel, *sp. nov.*

Etymology. Name refers to the sexual morph that forms in culture.

Classification — *Neodevriesiaceae*, *Capnodiales*, *Dothideomycetidae.*

Colonies nearly sterile, sporulating sparsely on PNA. *Ascomata* pseudothecial, solitary on aerial hyphae, globose, brown, 40–70 mm diam with central ostiole; wall of 2–3 layers of brown *textura angularis. Asci* bitunicate, obovoid, 8-spored, 20–30 × 7–11 mm, with apical chamber 2 mm diam. *Ascospores* multiseriate, hyaline, smooth-walled, guttulate, straight, thick-walled, widest in middle of apical cell, 12–13 × 3–4 mm; with non-persistent mucoid sheath.

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

Typus. New Zealand, Northland, on leaves of *Archontophoenix cunninghamiana* (*Arecaceae*), 9 Oct. 2017, *R. Thangavel* (holotype CBS H-23960, culture ex-type T17_03360I = CPC 34887 = CBS 145568, ITS and LSU sequences GenBank MK876398.1 and MK876439.1, MycoBank MB830851).

Notes — *Neodevriesia* was established by Quaedvlieg et al. (2014) for a genus of hyphomycetes with teratosphaeria-like sexual morphs. *Neodevriesia sexualis* differs from the majority of species known in the genus, in that it produces only a sexual morph in culture.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neodevriesia capensis* (as *Teratosphaeria capensis*, GenBank JN712501.1; Identities = 511/541 (94 %), 18 gaps (3 %)), *Neodevriesia agapanthi* (GenBank NR_111766.1; Identities = 451/482 (94 %), 11 gaps (2 %)) and *Neodevriesia imbrexigena* (as *Devriesia imbrexigena*, GenBank JX915748.1; Identities = 446/480 (93 %), 16 gaps (3 %)). Closest hits using the **LSU** sequence are *Neodevriesia imbrexigena* (as *Devriesia imbrexigena*, GenBank JX915749.1; Identities = 822/828 (99 %), 1 gap (0 %)), *Neodevriesia simplex* (GenBank KF310027.1; Identities = 758/764 (99 %), no gaps) and *Neodevriesia hilliana* (GenBank GU214414.1; Identities = 821/828 (99 %), 1 gap (0 %)).

Colour illustrations. Leaves of *Archontophoenix cunninghamiana*. Left column, *Thozetella neonivea*; colony on oatmeal agar; conidiogenous cells; microawns; conidia. Right column, *Neodevriesia sexualis*; asci; ascospores. Scale bars = 10 µm.

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Helminthosporium erythrinicola

Fungal Planet 894 – 19 July 2019

Helminthosporium erythrinicola Crous & M.J. Wingf., *sp. nov.*

Etymology. Name refers to *Erythrina*, the host genus from which this fungus was isolated.

Classification — *Massarinaceae*, *Pleosporales*, *Dothideomycetes.*

Colony on natural substrate black, hairy, effuse, 1–2 cm long. *Mycelium* mostly immersed, forming a brown stroma on the surface, 150–200 mm diam, giving rise to erect, flexuous conidiophores. *Conidiophores* 500–1200 × 6–10 mm, multiseptate, finely roughened, subcylindrical with slight apical taper, arising in fascicles, unbranched, brown, becoming pale brown at apex, rejuvenating percurrently. *Conidiogenous cells* terminal and intercalary with well-defined pores (4–5 × 2–3 mm), thickened and darkened, 25–40 × 6–8 mm. *Conidia* (70–)80–90(–110) × (9–)10–11(–12) mm, obclavate, straight to curved, apex subobtuse, smooth, medium brown, (6–)7–8(–12)-distoseptate, with angular lumina; wall 3–4 mm thick, hila thickened, darkened, 3–4 mm diam.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and feathery margin on PDA, smooth on OA and MEA, reaching 60 mm diam after 2 wk at 25 °C. On MEA surface olivaceous grey, reverse iron-grey with patches of olivaceous grey. On PDA surface and reverse iron-grey. On OA surface iron-grey.

Typus. South Africa, Eastern Cape Province, Haga Haga, Amathole, on leaves of *Erythrina humeana* (*Fabaceae*), 26 Dec. 2016, *M.J. Wingfield*, HPC 2301 (holotype CBS H-23961, culture ex-type CPC 35291 = CBS 145569, ITS, LSU and *rpb2* sequences GenBank MK876391.1, MK876432.1 and MK876486.1, MycoBank MB830852).

Notes — *Helminthosporium* was recently revised by Voglmayr & Jaklitsch (2017) and Hernández-Restrepo et al. (2018). *Helminthosporium erythrinicola* is related to *H. genistae* (CBS 142597), and represents the first species described from *Erythrina humeana*. *Helminthosporium erythrinae* (on *Erythrina suberosa*, India; conidia 4–8-septate, 39–62 × 8 mm; Thirumalachar 1950) differs in having smaller conidia with fewer septa.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Helminthosporium submersum* (as *Helminthosporium* sp. ZLL-2017a, GenBank MG098780.1; Identities = 462/483 (96 %), 4 gaps (0 %)), *Helminthosporium velutinum* (GenBank JN198435.1; Identities = 473/499 (95 %), 4 gaps (0 %)) and *Helminthosporium magnisporum* (GenBank AB811452.1; Identities = 436/461 (95 %), 3 gaps (0 %)). Closest hits using the **LSU** sequence are *Helminthosporium velutinum* (GenBank KY984355.1; Identities = 814/823 (99 %), 1 gap (0 %)), *Helminthosporium oligosporum* (GenBank KY984333.1; Identities = 813/823 (99 %), 1 gap (0 %)) and *Helminthosporium caespitosum* (GenBank KY984305.1; Identities = 813/823 (99 %), 1 gap (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Helminthosporium genistae* (GenBank KY984377.1; Identities = 832/884 (94 %), no gaps), *Helminthosporium quercinum* (GenBank KY984401.1; Identities = 828/884 (94 %), no gaps) and *Helminthosporium velutinum* (GenBank KY984416.1; Identities = 826/884 (93 %), no gaps).

Colour illustrations. *Erythrina humeana* at Haga Haga. Sporulation on host tissue; conidiogenous loci and conidia. Scale bars = 10 µm.

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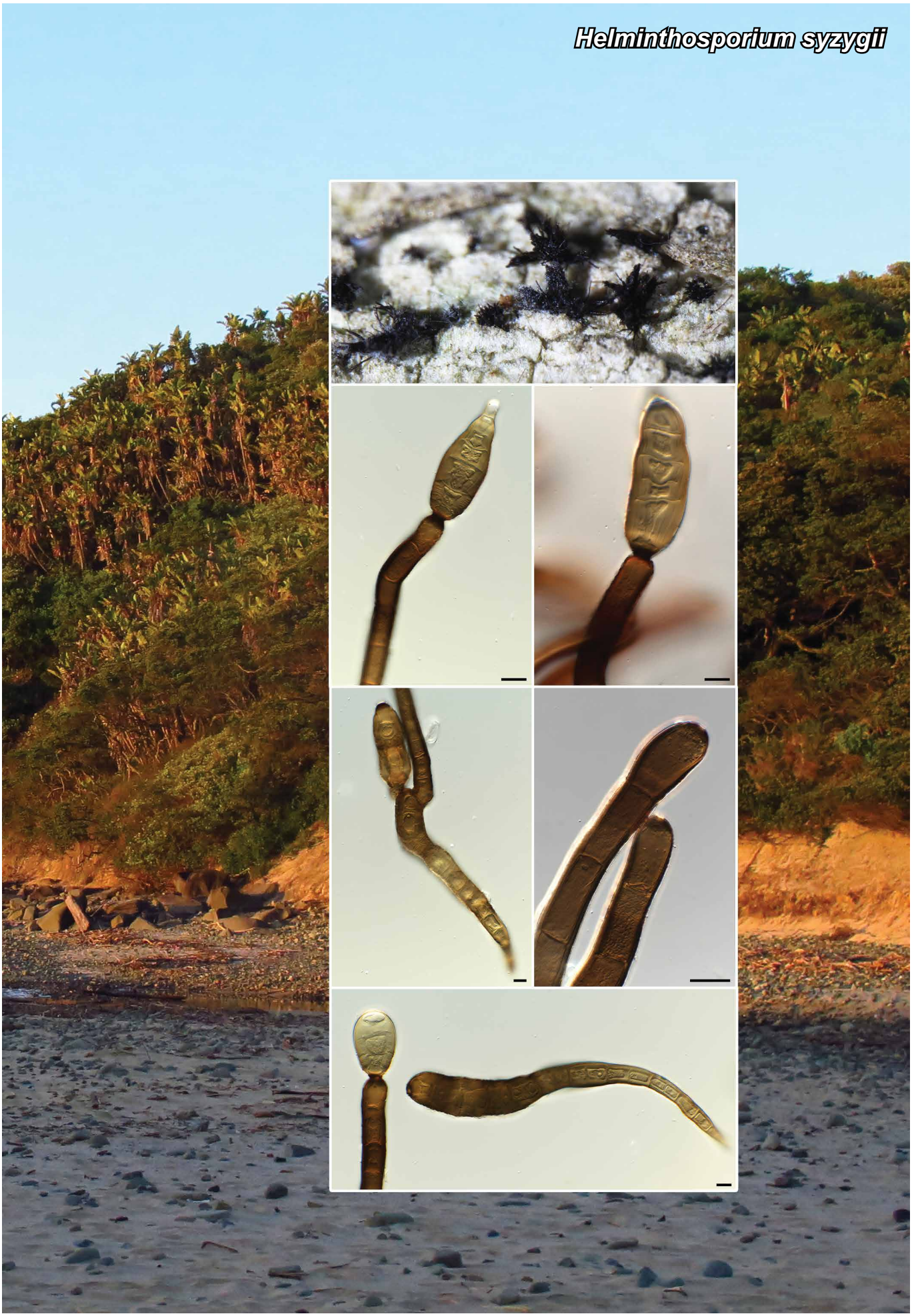
Helminthosporium syzygii

Fungal Planet 895 – 19 July 2019

Helminthosporium syzygii Crous & M.J. Wingf., *sp. nov.*

Etymology. Name refers to *Syzygium*, the host genus from which this fungus was isolated.

Classification — *Massarinaceae*, *Pleosporales*, *Dothideomycetes*.

Colony on natural substrate black, hairy, effuse, 1–2 mm long. *Mycelium* immersed, forming a brown stroma on the surface, 40–150 mm diam, giving rise to erect conidiophores. *Conidiophores* 150–400 × 10–15 mm, multiseptate, arising in fascicles, unbranched, dark brown, somewhat clavate at apex, rejuvenating percurrently. *Conidiogenous cells* terminal with well-defined pore, 3–4 mm diam, thickened and darkened, 20–40 × 13–15 mm. *Conidia* (70–)80–100(–150) × (19–)22–23(–25) mm, obclavate, curved, apex subobtuse, warty, inner surface striate, medium brown, (7–)9–12-distoseptate, with angular lumina; wall 5–7 mm thick; hila thickened and darkened, 4–5 mm diam.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 60 mm diam after 2 wk at 25 °C. On MEA surface mouse grey, reverse greyish sepia. On PDA surface mouse grey, reverse olivaceous grey. On OA surface pale luteous in centre, mouse grey in outer region.

Typus. South Africa, Eastern Cape Province, Haga Haga, Amathole, on bark canker of *Syzygium* sp. (*Myrtaceae*), 20 Dec. 2016, *M.J. Wingfield*, HPC 2295 (holotype CBS H-23962, culture ex-type CPC 35312 = CBS 145570, ITS, LSU and *rpb2* sequences GenBank MK876392.1, MK876433.1 and MK876487.1, MycoBank MB830853).

Notes — *Helminthosporium syzygii* is phylogenetically related to but morphologically distinct from *H. hispanicum* (Voglmayr & Jaklitsch 2017), and characterised by an association with bark cankers on *Syzygium* sp. in the Eastern Cape Province of South Africa.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Helminthosporium hispanicum* (GenBank NR_155196.1; Identities = 551/588 (94 %), 7 gaps (1 %)), *Helminthosporium quercinum* (GenBank KY984337.1; Identities = 433/495 (87 %), 18 gaps (3 %)) and *Helminthosporium microsorum* (GenBank KY984329.1; Identities = 496/589 (84 %), 25 gaps (4 %)). Closest hits using the **LSU** sequence are *Helminthosporium magnisporum* (GenBank AB807522.1; Identities = 845/857 (99 %), 2 gaps (0 %)), *Helminthosporium quercinum* (GenBank KY984338.1; Identities = 844/857 (98 %), 2 gaps (0 %)) and *Helminthosporium microsorum* (GenBank KY984326.1; Identities = 844/857 (98 %), 2 gaps (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Helminthosporium hispanicum* (GenBank KY984381.1; Identities = 912/949 (96 %), no gaps), *Helminthosporium quercinum* (GenBank KY984401.1; Identities = 892/949 (94 %), no gaps) and *Helminthosporium microsorum* (GenBank KY984386.1; Identities = 885/949 (93 %), no gaps).

Colour illustrations. Beach at Haga Haga. Conidiophores on host tissue; conidiogenous cells and conidia. Scale bars = 10 µm.

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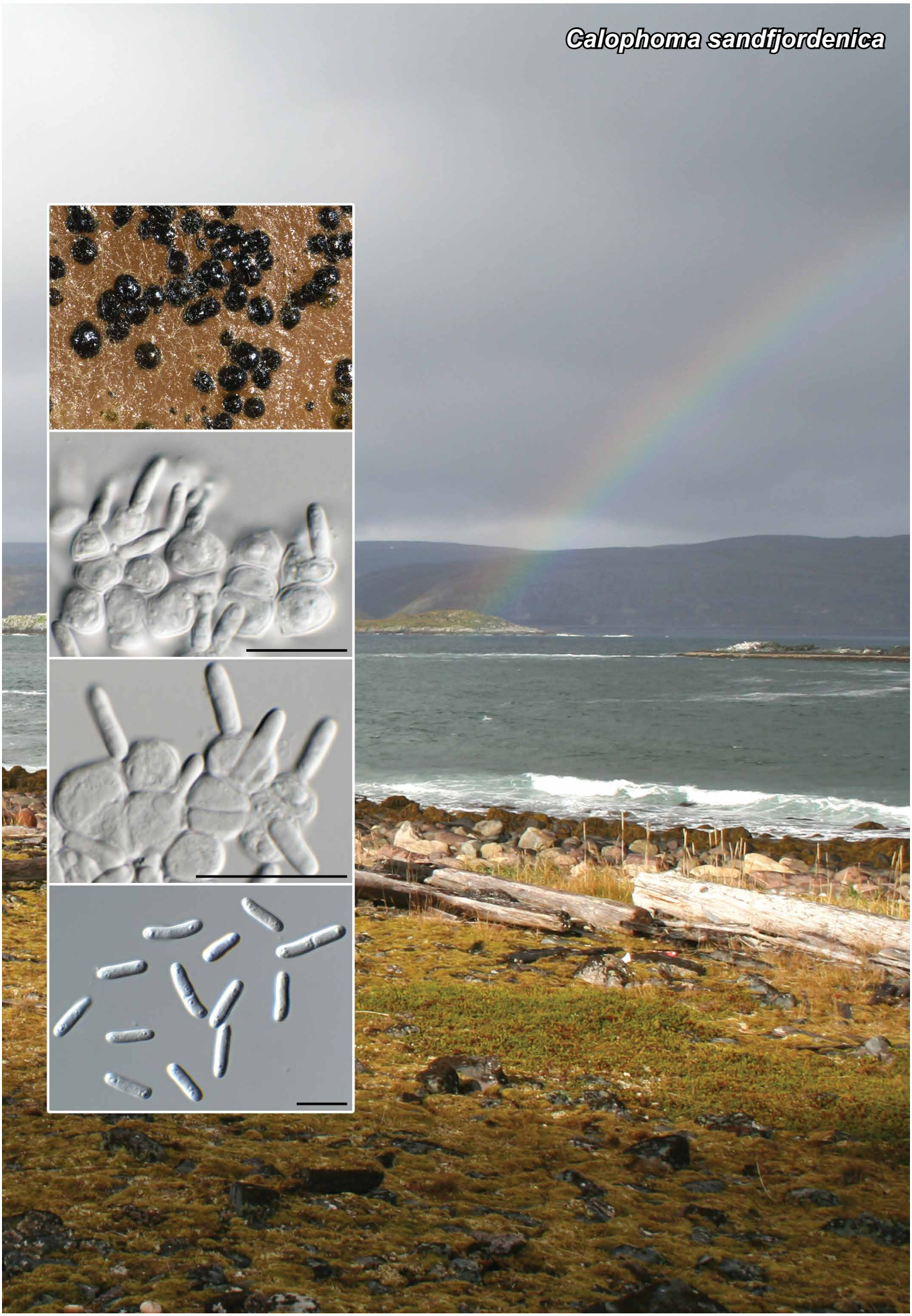
Calophoma sandfjordenica

Fungal Planet 896 – 19 July 2019

Calophoma sandfjordenica Crous & Rämä, *sp. nov.*

Etymology. Name refers to Sandfjorden, Berlevåg, Norway, a landscape preservation area with a long sandy beach and dunes, where this fungus was collected.

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

Conidiomata pycnidial, solitary, black, globose, immersed to erumpent, ostiolate, 200–300 mm diam; wall of 3–6 layers of brown *textura angularis. Micropycnidia* present. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, ampulliform to doliiform, hyaline, smooth, phialidic with periclinal thickening, 5–10 × 5–7 mm. *Conidia* subcylindrical, straight to curved, ends obtuse, hyaline, smooth, 0(–1)-septate, guttulate, (8–)10–14(–18) × (2–)3 mm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA surface dirty white, reverse umber with patches of sienna. On PDA surface and reverse hazel. On OA surface isabelline.

Typus. Norway, Finnmark, Berlevåg, Sandfjorden, isolated from a piece of board found in the breaker zone on a rocky shore, N70°47'36" E29°16'43", 7 Sept. 2010, *T. Rämä*, 077bU1.2 (holotype CBS H-23963, culture ex-type 050aE2.1 = CPC 36272 = CBS 145571, ITS, LSU, *actA* and *rpb2* sequences GenBank MK876378.1, MK876417.1, MK876453.1 and MK876478.1, MycoBank MB830854).

Notes — Species of *Phoma* and related coelomycetous genera have long been known to be frequent in the marine environment, but little effort has been made to identify these fungi to species level. Due to their very indistinct morphological features, the only means to separate species is by phylogenetic inference based on DNA sequence data supplemented with culture characteristics (Kohlmeyer & Volkmann-Kohlmeyer 1991, Jones et al. 2015). *Calophoma sandfjordenica* described here is the first marine member of this recently established genus (Chen et al. 2015). The species was isolated from driftwood at three locations along the Northern Norwegian coast. Two of the substrates were of *Pinus* and one on the wood of an unidentified tree. All locations are at the open ocean (Barents Sea). The ITS sequence showed greatest similarity with *C. complanata*. Some closely related species, such as *Phoma herbarum* and *Phomatodes nebulosa* are also known to thrive in the marine environment (Jones et al. 2015).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Microsphaeropsis olivacea* (GenBank MG020349.1; Identities = 521/536 (97 %), 7 gaps (1 %)), *Calophoma aquilegiicola* (GenBank MH855149.1; Identities = 518/534 (97 %), 4 gaps (0 %)) and *Epicoccum huancayense* (GenBank MH861244.1; Identities = 520/537 (97 %), 7 gaps (1 %)). Closest hits using the **LSU** sequence are *Calophoma complanata* (GenBank EU754180.1; Identities = 875/875 (100 %), no gaps), *Phomatodes nebulosa* (GenBank MH876211.1; Identities = 889/893 (99 %), no gaps) and *Ascochyta ferulae* (GenBank MH871928.1; Identities = 889/893 (99 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Didymella rabiei* (GenBank KM244530.1; Identities = 587/632 (93 %), 8 gaps (1 %)), *Stagonosporopsis cucurbitacearum* (GenBank KX246908.1; Identities = 578/635 (91 %), 11 gaps (1 %)) and *Stagonosporopsis citrulli* (GenBank KX246907.1; Identities = 577/635 (91 %), 11 gaps (1 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Calophoma complanata* (GenBank GU371778.1; Identities = 829/890 (93 %), no gaps, *Ascochyta herbicola* (GenBank KP330421.1; Identities = 739/823 (90 %), 2 gaps (0 %)) and *Nothophoma gossypiicola* (GenBank LT593082.1; Identities = 817/912 (90 %), 4 gaps (0 %)).

Colour illustrations. Sørsandfjorden (Hasvik, Sørøya) is one of the locations where *Calophoma sandfjordenica* was collected from driftwood. Conidiomata on potato dextrose agar; conidiogenous cells and conidia. Scale bars = 10 µm.

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Didymella finnmarkica

Fungal Planet 897 – 19 July 2019

Didymella finnmarkica Crous & Rämä, *sp. nov.*

Etymology. Name reflects the most north-eastern county of Norway, Finnmark, where the species was collected.

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

Conidiomata pycnidial, solitary to aggregated, globose, 200–300 mm diam, with 1–2 ostioles; conidiomata (on SNA) subhyaline with prominent dark ostiole, 20–30 mm diam, peripysate, with a dark brown rosette of cells and short setae, thick-walled, septate, cylindrical with obtuse apices, 15–50 × 3–4 mm. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, ampulliform, phialidic with periclinal thickening, 5–8 × 4–5 mm. *Conidia* dimorphic, subcylindrical, straight to slightly curved, ends obtuse, hyaline, smooth, granular, guttulate, consisting of smaller aseptate, and larger 1-septate conidia: aseptate conidia (6–)7–9(–11) × (2–)2.5(–3) mm; 1-septate conidia (12–)13–16(–18) × (3–)3.5 (–4) mm. *Chlamydospores* not observed.

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

Typus. Norway, Finnmark, Båtsfjord, Hamningberg, Skjåvika, isolated from a piece of *Pinus sylvestris* driftwood that was found among algal debris on a sandy shore, N70°32'32" E30°35'22", 9 Sept. 2010, *T. Rämä*, 086aN2.2 (holotype CBS H-23964, culture ex-type 086aN2.2 = CPC 36275 = CBS 145572, ITS, LSU, *actA* and *rpb2* sequences GenBank MK876388.1, MK876429.1, MK876458.1 and MK876484.1, MycoBank MB830855).

Notes — No new marine *Didymella* species has been described since 1985 (Jones et al. 2015). The four known species are *D. avicenniae* (found on *Avicennia* in mangroves), *D. fucicola* (on marine brown algae *Fucus* and *Pelvetia*), *D. gloiopeltidis* (on red alga *Gloiopeltis furcata*) and *D. magnei* (on red alga *Palmaria palmata*). These species are rarely collected and sequence data are available only for *D. fucicola*. *Didymella finnmarkica* described here is recognised as a new species based on ITS sequence data and ecology. None of the previously described *Didymella* species have been observed or isolated from driftwood (excluding mangroves). *Didymella finnmarkica* was isolated from a single piece of *Pinus sylvestris* driftwood in north-eastern Norway that was heavily colonised with marine dwelling invertebrates.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Didymella pinodella* (as *Phoma pinodella*, GenBank AY831556.1; Identities = 521/532 (98 %), 2 gaps (0 %)), *Didymella glomerata* (GenBank MH864401.1; Identities = 528/540 (98 %), 2 gaps (0 %)) and *Didymella macrostoma* (GenBank MH855806.1; Identities = 528/540 (98 %), 2 gaps (0 %)). Closest hits using the **LSU** sequence are *Didymella macrostoma* (GenBank MH871627.1; Identities = 835/838 (99 %), no gaps), *Didymella fabae* (GenBank FJ755246.1; Identities = 835/838 (99 %), no gaps) and *Ascochyta medicaginicola* var. *macrospora* (GenBank MH870279.1; Identities = 834/838 (99 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Peyronellaea combreti* (GenBank KJ869228.1; Identities = 586/634 (92 %), no gaps), *Stagonosporopsis caricae* (GenBank KX246909.1; Identities = 592/648 (91 %), 10 gaps (1 %)) and *Stagonosporopsis citrulli* (GenBank KX246907.1; Identities = 591/648 (91 %), 10 gaps (1 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Didymella microchlamydospora* (GenBank MH133221.1; Identities = 635/695 (91 %), no gaps), *Macroventuria anomochaeta* (GenBank GU456346.1; Identities = 624/695 (90 %), no gaps) and *Didymella aliena* (GenBank MG571231.1; Identities = 621/697 (89 %), no gaps).

Colour illustrations. Type locality on seashore in Hamningberg, Norway. Conidiomata on oatmeal agar; ostiole; conidiogenous cells and conidia. Scale bars = 10 µm.

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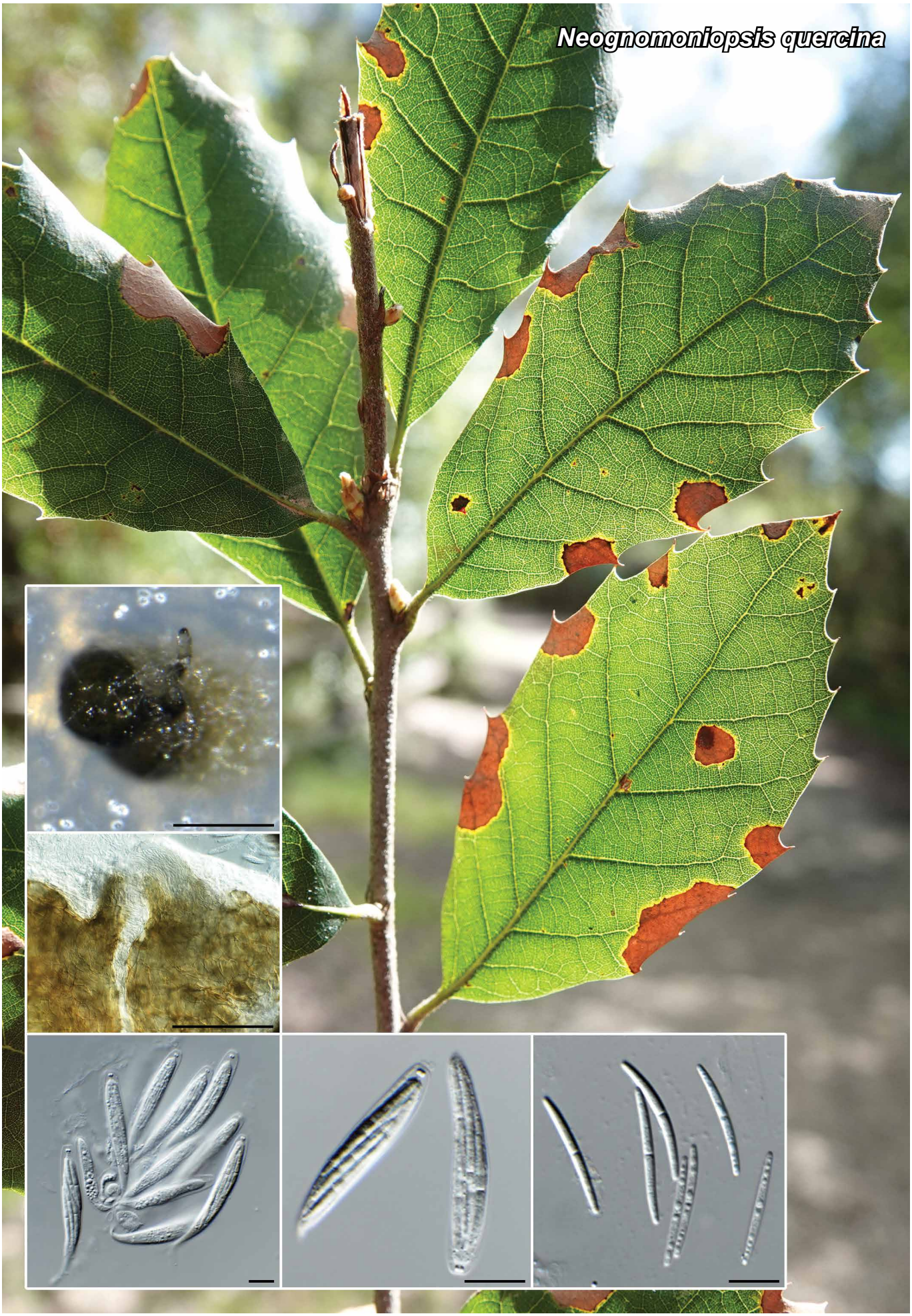
Neognomoniopsis quercina

Fungal Planet 898 – 19 July 2019

Neognomoniopsis Crous, *gen. nov.*

Etymology. Name refers to the genus *Gnomoniopsis*.

Classification — *Gnomoniaceae*, *Diaporthales*, *Sordariomycetes*.

Ascomata perithecial, solitary or in groups of up to three, dark brown, globose, with solitary, central neck, straight to curved, apex pale brown, obtuse. *Asci* hyaline, uniseriate, inoperculate, subcylindrical with a long, tapered stalk, with visible apical ring, containing eight multiseriate ascospores. *Ascospores* hyaline, smooth, guttulate, fusoid, widest at median septum, straight or slightly curved, ends subobtuse, lacking mucoid appendages.

Type species. *Neognomoniopsis quercina* Crous.
MycoBank MB830856.

Neognomoniopsis quercina Crous, *sp. nov.*

Etymology. Name refers to *Quercus*, the host genus from which this fungus was isolated.

Ascomata perithecial, sparsely formed on SNA, immersed to superficial, solitary or in groups of up to three, dark brown, globose, 200–250 µm diam, with solitary, central neck, straight to curved, apex pale brown, obtuse, 50–200 × 25–30 µm. *Asci* hyaline, uniseriate, inoperculate, subcylindrical with a long, tapered stalk, 40–55 × 6–7 µm, with visible apical ring, containing eight multiseriate ascospores. *Ascospores* hyaline, smooth, guttulate, fusoid, widest at median septum, straight or slightly curved, ends subobtuse, lacking mucoid appendages, (17–)18–19(–24) × 2 µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface sienna, reverse ochreous. On PDA surface sienna with patches of dirty white, reverse umber. On OA surface ochreous.

Typus. Italy, Rome, on leaves of *Quercus ilex* (*Fagaceae*), 13 Apr. 2018, *P.W. Crous*, HPC 2333 (holotype CBS H-23965, culture ex-type CPC 35562 = CBS 145575, ITS and LSU sequences GenBank MK876399.1 and MK876440.1, MycoBank MB830857).

Colour illustrations. Leaf spots on *Quercus ilex*. Ascomata with necks on synthetic nutrient-poor agar; asci; ascospores. Scale bars = 200 mm (ascomata with necks), 10 µm (all others).

Notes — Members of *Gnomoniaceae* are characterised by ascomata that are generally immersed, solitary, without a stroma, or aggregated in leaves or woody tissues of predominantly hardwood trees from temperate zones in the Northern Hemisphere. Monod (1983) included 22 genera in the family, some of which were excluded by Castlebury et al. (2002). Species of *Gnomonia* typically have solitary, thin-walled, immersed perithecia with long necks and lack any stroma, and generally have ascospores that are medianly septate. However, *Gnomonia* was shown to not be monophyletic (Sogonov et al. 2005, 2008). *Gnomoniopsis*, which is mostly associated with either *Fagaceae* or *Rosaceae*, was originally described for species having ascospores that develop additional septa (Sogonov et al. 2008). One species to consider is *Gnomonia quercus-ilicis*, which was described from *Quercus ilex* in Italy, was listed as 'doubtful' by Monod (1983), having not found any material in PAD. However, based on the original description provided by Saccardo (1895), perithecia are 100–110 mm diam, asci 45–50 × 12–16 mm, and ascospores 1-septate, 20–24 × 7–8 mm, thus quite different from the present collection, which we describe here as new.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Plagiostoma conradii* (GenBank KX929768.1; Identities = 437/491 (89 %), 11 gaps (2 %)), *Gnomoniopsis paraclavulata* (GenBank MH863162.1; Identities = 456/524 (87 %), 17 gaps (3 %)) and *Discula quercina* (GenBank GQ452263.1; Identities = 456/524 (87 %), 17 gaps (3 %)). Closest hits using the **LSU** sequence are *Cryptodiaporthe aubertii* (GenBank KX929803.1; Identities = 831/845 (98 %), 2 gaps (0 %)), *Sirococcus castaneae* (GenBank KX929769.1; Identities = 831/845 (98 %), 2 gaps (0 %)) and *Ambarignomonia petiolorum* (as *Gnomonia petiolorum*, GenBank AY818963.1; Identities = 831/845 (98 %), 2 gaps (0 %)).

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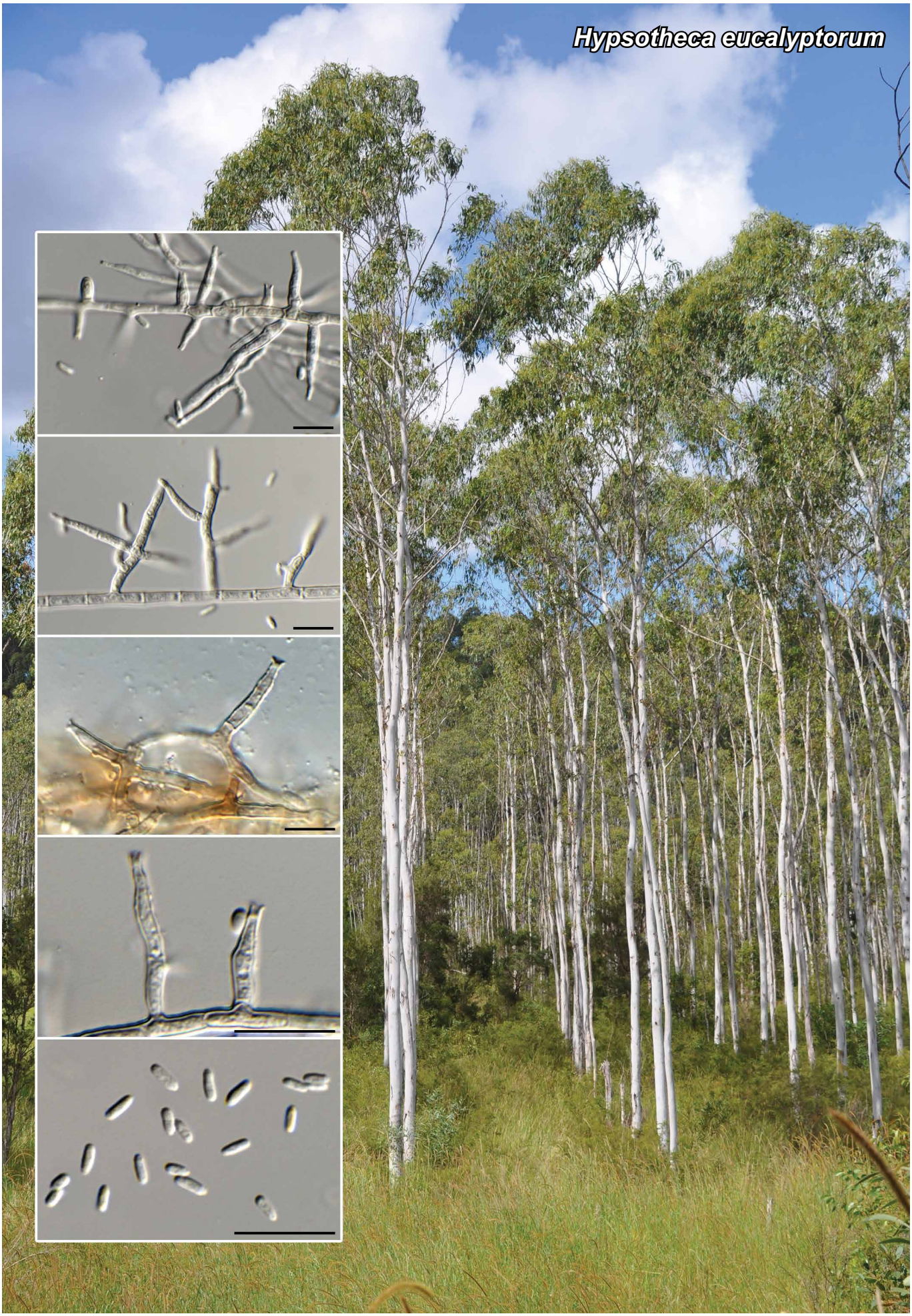
Hypsotheca eucalyptorum

Fungal Planet 899 – 19 July 2019

Hypsotheca eucalyptorum Crous & Carnegie, *sp. nov.*

Etymology. Name refers to *Eucalyptus*, the host genus from which this fungus was isolated.

Classification — *Coryneliaceae*, *Coryneliales*, *Eurotiomycetes.*

Conidiomata sparsely formed in culture, pycnidial, brown, globose, 180–200 µm diam, developing in aerial mycelium. Dominant morph hyphomycetous. *Mycelium* initially hyaline, smooth, becoming brown, verruculose to warty, septate, branched, 2–3 µm diam. *Conidiophores* erect on superficial hyphae, 0–1-septate, unbranched, subcylindrical, straight to flexuous, brown, verruculose, 5–20 × 1.5–2.5 µm. *Conidiogenous cells* terminal, pale brown, verruculose, subcylindrical, phialidic with flared collarette, 2–3 µm diam, 5–15 × 1.5–2.5 µm. *Conidia* aseptate, solitary, hyaline, smooth, guttulate, subcylindrical with obtuse ends, (3–)3.5–4(–4.5) × 1.5(–2) µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 60 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface brown vinaceous, reverse leaden black.

Typus. Australia, New South Wales, Boorabee State Forest, McCorquodale plantation, on leaves of *Eucalyptus grandis* × *camaldulensis* clone (*Myrtaceae*), 20 Apr. 2016, *A.J. Carnegie*, HPC 2431 (holotype CBS H-23966, culture ex-type CPC 35734 = CBS 145576, ITS and LSU sequences GenBank MK876393.1 and MK876434.1, MycoBank MB830858).

Additional material examined. Australia, New South Wales, Orara State Forest, on leaves of *Eucalyptus grandis*, 7 Mar. 2016, *D. Sargeant*, HPC 2304, CPC 35391 = CBS 145577, ITS and LSU sequences GenBank MK876394.1 and MK876435.1.

Notes — The genus *Hypsotheca* was recently resurrected as sister genus to *Caliciopsis*. Species of *Hypsotheca* are distinguished from *Caliciopsis* in having a phaeoacremonium-like synasexual morph in culture (Pascoe et al. 2018, Crous et al. 2019). *Hypsotheca eucalyptorum* is related to *H. pleomorpha* (conidia (3–)4–5(–6) × 1.5(–2) µm), but distinct in that the hyphomycetous morph is dominant in culture.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 35734 had highest similarity to *Hypsotheca pleomorpha* (as *Caliciopsis pleomorpha*, GenBank MG641785.1; Identities = 500/552 (91 %), 23 gaps (4 %)), *Caliciopsis eucalypti* (GenBank NR_154836.1; Identities = 396/429 (92 %), 10 gaps (0 %)) and *Corynelia uberata* (GenBank KU204606.1; Identities = 497/551 (90 %), 26 gaps (4 %)). The ITS sequences of CPC 35734 and CPC 35391 are 541/549 (99 %, including two gaps) similar. Closest hits using the **LSU** sequence are *Hypsotheca pleomorpha* (GenBank MK442528.1; Identities = 800/829 (97 %), 3 gaps (0 %)), *Caliciopsis valentina* (GenBank NG_060419.1; Identities = 776/824 (94 %), no gaps) and *Caliciopsis pinea* (GenBank DQ678097.1; Identities = 776/824 (94 %), no gaps). The LSU sequences of CPC 35734 and CPC 35391 are 831/835 (99 %, including one gap) similar.

Colour illustrations. *Eucalyptus grandis* × *camaldulensis* plantation. Hyphae with solitary conidiophores and conidiogenous cells; conidia. Scale bars = 10 µm.

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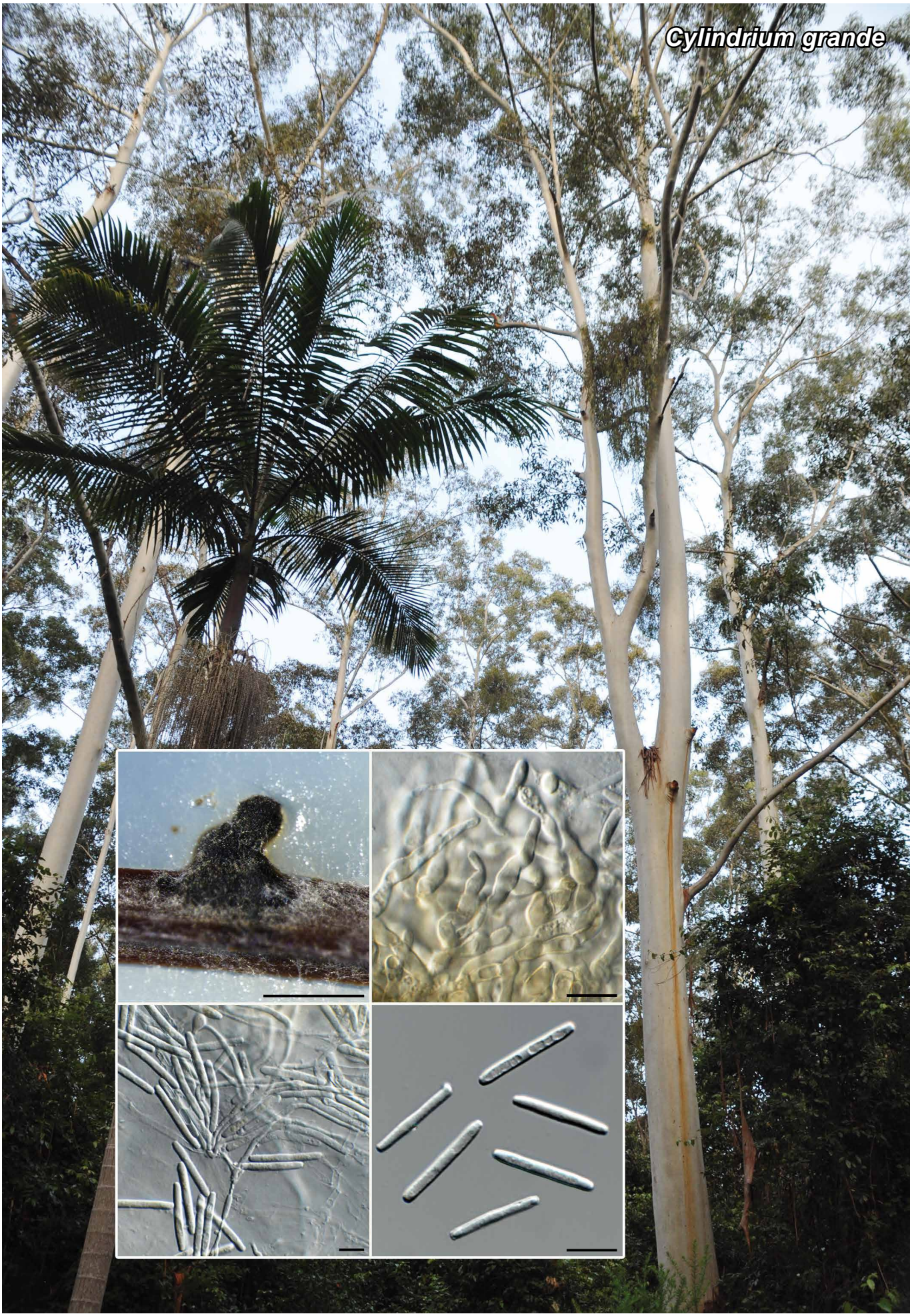
Cylindrium grande

Fungal Planet 900 – 19 July 2019

Cylindrium grande Crous & Carnegie, *sp. nov.*

Etymology. Name refers to *Eucalyptus grandis*, the host species from which this fungus was first isolated.

Classification — *Cylindriaceae*, *Hypocreales*, *Sordariomycetes*.

Mycelium consisting of branched, septate, hyaline, 1.5–2.5 µm diam hyphae that form large, black, globose to lobed fertile structures up to 500 µm diam on SNA, MEA, PDA and OA. *Conidiomata* sporodochial, sporulating on SNA, brown, 80–200 µm diam. *Conidiophores* arising from a pale brown stroma, smooth, pale brown, subcylindrical, branched below, 1–3-septate, 20–30 × 4–6 µm. *Conidiogenous cells* integrated, pale brown, smooth, subcylindrical to somewhat ampulliform, proliferating sympodially, terminal and intercalary, 15–20 × 2–4 µm; scars inconspicuous. *Conidia* solitary, subcylindrical, straight, aseptate, hyaline, smooth, apex obtuse, base bluntly rounded to truncate, (13–)18–20(–22) × (2–)2.5–3 µm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA surface ochreous with patches of dirty white, reverse umber to sienna. On PDA surface and reverse pale luteous with patches of chestnut. On OA surface pale luteous.

Typus. Australia, New South Wales, Orara State Forest, on leaves of *Eucalyptus grandis* (*Myrtaceae*), 7 Mar. 2016, *D. Sargeant*, HPC 2304 (holotype CBS H-23967, culture ex-type CPC 35403 = CBS 145655, ITS, LSU, *actA*, *cmdA*, *rpb2*, *tef1* and *tub2* sequences GenBank MK876384.1, MK876425.1, MK876455.1, MK876467.1, MK876481.1, MK876495.1 and MK876502.1, MycoBank MB830859).

Additional material examined. *Cylindrium* sp. Australia, New South Wales, Wedding Bells State Forest, Crabtree plantation, on leaves of *Eucalyptus dunnii*, 17 Apr. 2016, *A.J. Carnegie*, HPC 2414, CPC 35622 = CBS 145578, ITS, LSU, *actA*, *cmdA*, *rpb2* and *tef1* sequences GenBank MK876385.1, MK876426.1, MK876456.1, MK876468.1, MK876482.1 and MK876496.1.

Colour illustrations. *Eucalyptus dunnii* forest. Sporodochium on pine needle agar; conidiogenous cells and conidia. Scale bars = 500 µm (sporodochium), 10 µm (all others).

Notes — *Cylindrium* was treated by Crous et al. (2018b). *Cylindrium grande* is phylogenetically related to *C. elongatum* (on *Quercus* leaf litter, conidia 15–18 × 2 mm; Ellis & Ellis 1997), but the latter has smaller conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** of CPC 35403 sequence had highest similarity to *Cylindrium elongatum* (GenBank KM231852.1; Identities = 528/544 (97 %), 3 gaps (0 %)), *Cylindrium syzygii* (GenBank NR_157430.1; Identities = 519/545 (95 %), 16 gaps (2 %)) and *Cylindrium algarvense* (GenBank NR_132837.1; Identities = 495/528 (94 %), 14 gaps (2 %)). The ITS sequences of CPC 35403 and CPC 35622 are 537/541 (99 %, including one gap) similar. Closest hits using the **LSU** sequence of CPC 35403 are *Tristratiperidium microsporum* (GenBank KT696539.1; Identities = 732/736 (99 %), no gaps), *Cylindrium syzygii* (as *Pseudoidriella syzygii*, GenBank JQ044441.1; Identities = 833/839 (99 %), 1 gap) and *Cylindrium purgamentum* (GenBank KY173525.1; Identities = 813/820 (99 %), 1 gap). The LSU sequences of CPC 35403 and CPC 35622 are 827/833 (99 %, including one gap) similar. Closest hits using the ***actA*** sequence of CPC 35403 had highest similarity to *Cylindrium elongatum* (GenBank KM231264.1; Identities = 616/672 (92 %), 16 gaps (2 %)) and *Cylindrium aeruginosum* (GenBank KM231265.1; Identities = 515/560 (92 %), 16 gaps (2 %)). The *actA* sequences of CPC 35403 and CPC 35622 are 631/667 (95 %, including three gaps) similar. Closest hits using the ***cmdA*** sequence of CPC 35403 had highest similarity to *Cylindrium elongatum* (GenBank KM231448.1; Identities = 557/692 (80 %), 42 gaps (6 %)) and *Cylindrium aeruginosum* (GenBank KM231450.1; Identities = 492/604 (81 %), 35 gaps (6 %)). The *cmdA* sequences of CPC 35403 and CPC 35622 are 645/727 (89 %, including 18 gaps) similar. Closest hits using the ***rpb2*** sequence of CPC 35403 had highest similarity to *Cylindrium elongatum* (GenBank KM232428.1; Identities = 707/801 (88 %), 6 gaps (0 %)) and *Cylindrium aeruginosum* (GenBank KM232430.1; Identities = 748/859 (87 %), 3 gaps (0 %)). The *rpb2* sequences of CPC 35403 and CPC 35622 are 798/864 (92 %, no gaps) similar. Closest hits using the ***tef1*** sequence of CPC 35403 had highest similarity to *Cylindrium elongatum* (GenBank KM231988.1; Identities = 358/408 (88 %), 20 gaps (4 %)). The *tef1* sequences of CPC 35403 and CPC 35622 are 414/469 (88 %, including 10 gaps) similar. Closest hits using the ***tub2*** sequence of CPC 35403 had highest similarity to *Cylindrium elongatum* (GenBank KM232123.1; Identities = 521/640 (81 %), 29 gaps (4 %)).

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Anungitiomyces stellenboschiensis

Fungal Planet 901 – 19 July 2019

Anungitiomyces Crous, *gen. nov.*

Etymology. Name relates to the host genus *Anungitea* on which this fungus was collected.

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

Mycelium consisting of hyaline, branched, septate hyphae. *Conidiophores* arising directly from hyphae, erect, flexuous to geniculate-flexuous, subcylindrical, brown, smooth, unbranched or branched below, septate. *Conidiogenous cells* integrated, terminal, medium brown, smooth, subcylindrical, with slight apical taper to truncate apex, proliferating sympodially; loci flattened, not thickened nor darkened. *Conidia* solitary, hyaline, guttulate, smooth, (0–)1-septate, obclavate, straight to slightly curved, base truncate, apex obtuse, thick-walled.

Type species. *Anungitiomyces stellenboschiensis* Crous.
MycoBank MB830860.

Anungitiomyces stellenboschiensis Crous, *sp. nov.*

Etymology. Name refers to Stellenbosch, South Africa, where this fungus was collected.

Mycelium consisting of hyaline, branched, septate, 2–2.5 mm diam hyphae. *Conidiophores* arising directly from hyphae, erect, flexuous to geniculate-flexuous, subcylindrical, brown, smooth, unbranched or branched below, 3–8-septate, 50–100(–150) × 3–5 mm. *Conidiogenous cells* integrated, terminal, medium brown, smooth, subcylindrical, with slight apical taper to truncate apex, proliferating sympodially, 20–50 × 3–4 mm; loci flattened, 1.5–2 mm diam, not thickened nor darkened. *Conidia* solitary, hyaline, guttulate, smooth, (0–)1-septate, obclavate, straight to slightly curved, base truncate, apex obtuse, thick-walled, (22–)29–35(–42) × (3–)3.5(–4) mm.

Culture characteristics — Colonies flat, spreading, hardly growing, lacking aerial mycelium on MEA, PDA and SNA. On OA umber, with sparse to no aerial mycelium, reaching 3–4 mm diam after 2 wk at 25 °C.

Typus. South Africa, Western Cape Province, Stellenbosch Mountain, on leaves of *Eucalyptus* sp. (*Myrtaceae*), 2010, *P.W. Crous* (holotype CBS H-23968, culture ex-type CPC 34726, ITS and LSU sequences GenBank MK876376.1 and MK876415.1, MycoBank MB830861).

Notes — The present collection is reminiscent of *Anungitea*/*Anungitopsis* (Seifert et al. 2011), except that the conidiogenous loci are terminal, and the conidia are solitary, not in chains, and obclavate, (0–)1-septate. A new genus is therefore introduced to accommodate it.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Robillarda sessilis* (GenBank FJ825373.1; Identities = 496/622 (80 %), 47 gaps (7 %)), *Robillarda terrae* (GenBank NR_132902.1; Identities = 493/620 (80 %), 45 gaps (7 %)) and *Seimatosporium pistaciae* (GenBank KP004464.1; Identities = 493/622 (79 %), 46 gaps (7 %)). Closest hits using the **LSU** sequence are *Oxydothis metroxylonis* (GenBank KY206764.1; Identities = 792/830 (95 %), 4 gaps (0 %)), *Entosordaria quercina* (GenBank MF488994.1; Identities = 793/832 (95 %), 5 gaps (0 %)) and *Oxydothis garethjonesii* (GenBank KY206762.1; Identities = 803/843 (95 %), 5 gaps (0 %)).

Colour illustrations. Leaf of *Eucalyptus* sp. Colony on oatmeal agar; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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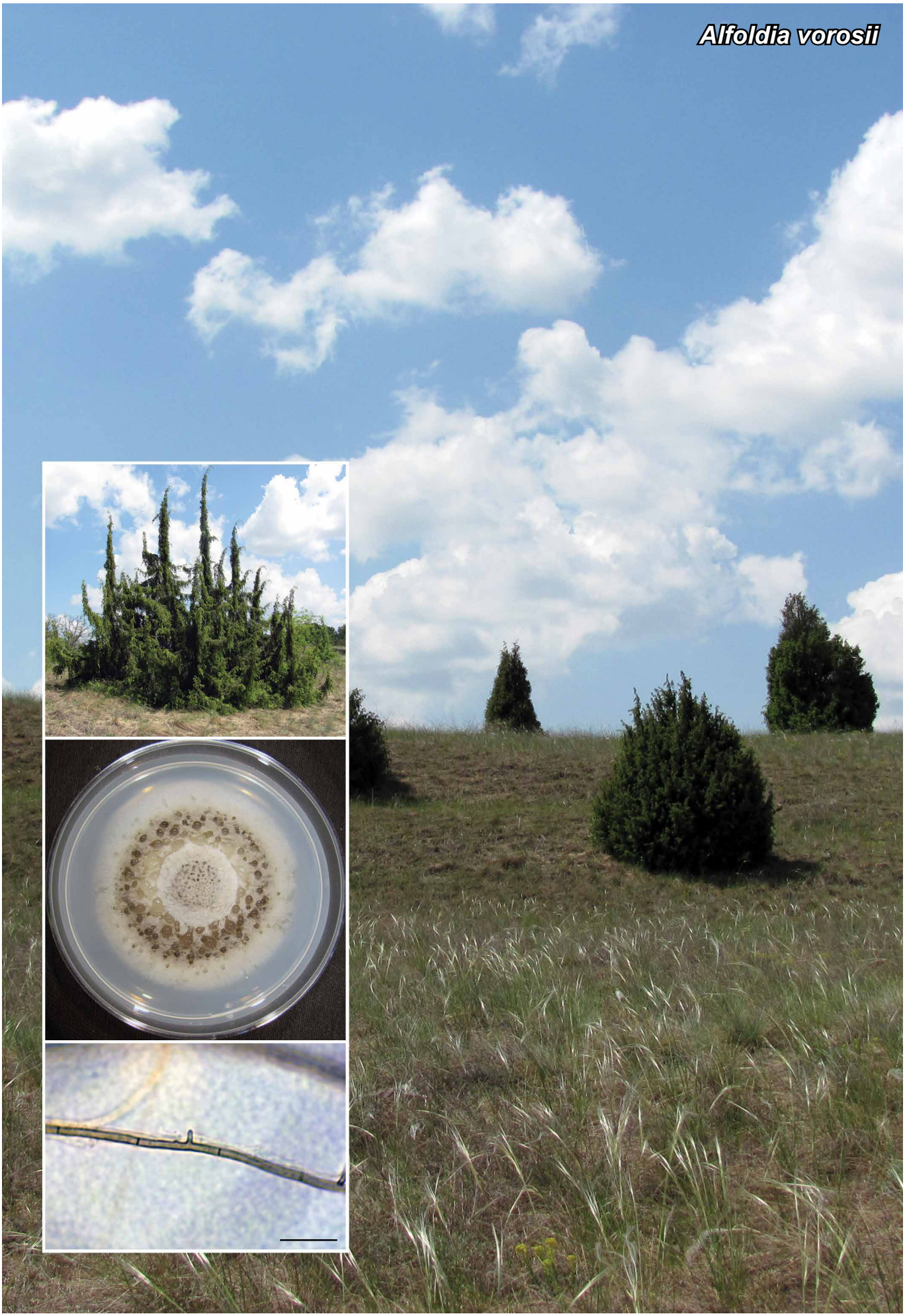
Alfoldia vorosii

Fungal Planet 902 – 19 July 2019

Alfoldia D.G. Knapp, Imrefi & Kovács, *gen. nov.*

Etymology. Referring to the sampling site, the Great Hungarian Plain, which is called 'Alföld' in Hungarian.

Classification — *Amorosiaceae*, *Pleosporales*, *Dothideomycetes*.

Alfoldia isolates can be collected from surface-sterilised roots and can be cultured and maintained on general media. Isolates of the genus *Alfoldia* are root endophytes associated with woody plant species of semiarid grasslands of the Great Hungarian Plain.

Type species. *Alfoldia vorosii* D.G. Knapp, Imrefi & Kovács. MycoBank MB830105.

Alfoldia vorosii D.G. Knapp, Imrefi & Kovács, *sp. nov.*

Etymology. We name the species in honour of the 90th anniversary of the birth of the outstanding Hungarian mycologist József Vörös (1929–1991), who contributed significantly to the discipline.

Alfoldia vorosii differs from its closest phylogenetic neighbour, *Angustimassarina populi* (MFLUCC 13-0034), by unique fixed alleles in the ITS, LSU, SSU and *tef1* loci based on alignments of the separate loci deposited in TreeBASE as study S24077: ITS positions: 96 (T), 102 (insertion), 122 (C), 202 (T), 206 (T), 227 (T), 235 (T), 236 (C), 237 (T), 250 (A), 254 (A), 423 (T), 428 (T), 436 (G), 462 (T), 466 (insertion), 474 (A), 492 (T), 544 (G), 546 (C), 553 (A), 554 (A), 555 (A), 572 (T), 573 (A), 575 (G), 576 (C), 577 (A), 578 (C), 581 (C), 585 (T), 592 (T); LSU positions: 92 (C), 93 (T), 416 (C), 418 (T), 423 (A), 429 (T), 435 (T), 439 (G), 451 (A), 452 (T), 505 (T), 507 (T), 532 (T), 534 (C), 550 (T); SSU positions: 32 (A), 38 (insertion), 117 (A), 246 (insertion), 341 (T), 349 (G); *tef1* positions: 224 (G), 245 (C), 248 (A), 275 (T), 311 (G), 319 (C), 329 (G), 360 (T), 366 (G), 368 (T), 369 (T), 443 (C), 467 (C), 510 (G), 512 (T), 533 (C), 554 (C), 599 (C), 607 (T), 609–611 (deletion), 629 (C).

Culture characteristics — Colonies covering the Petri dish in 3 wk. Colony on PDA fluffy, smoke, olivaceous grey to white, spreading with abundant aerial mycelium, exudates often observed in concentric rings. Colony on MEA smoke grey to white with an entire edge and sparse aerial mycelium, exudates generally observed. Cultures sterile.

Typus. Hungary, Fülöpháza, from roots of *Juniperus communis* (*Cupressaceae*), 2008, *D.G. Knapp & G.M. Kovács* (holotype BP110341, culture extype REF116 = CBS 145501, ITS, LSU, SSU and *tef1* sequences GenBank JN859336, MK589354, MK589346 and MK599320, MycoBank MB830106).

Additional materials examined. Hungary, Fülöpháza, from roots of *J. communis*, 2008, *D.G. Knapp & G.M. Kovács*, REF117, ITS, LSU, SSU and *tef1* sequences GenBank JN859337, MK589355, MK589347 and MK599321; ibid., from roots of *Ailanthus altissima* (*Simaroubaceae*), 2008, *D.G. Knapp & G.M. Kovács*, REF114, ITS sequence GenBank JN859334; Tatárszentgyörgy, from roots of *J. communis*, 2008, *D.G. Knapp & G.M. Kovács*, REF113, ITS, LSU, SSU and *tef1* sequences GenBank JN859333, MK589353, MK589345 and MK599319; ibid., REF115, ITS sequence GenBank JN859335.

Colour illustrations. Semiarid sandy grassland in the Great Hungarian Plain (= Alföld) with juniper trees. The host (*Juniperus communis*) of *Alfoldia vorosii*; colony on PDA media; dark septate hyphae of the strain REF116. Scale bar = 10 µm.

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits of *Alfoldia vorosii* (CBS 145501) using the **ITS** sequence are *Lophiostoma corticola* (GenBank KU712227.1; Identities = 507/538 (94 %), 15 gaps (2 %)), *Angustimassarina populi* (GenBank MF409170.1; Identities = 491/521 (94 %), 14 gaps (2 %)) and *Angustimassarina rosarum* (GenBank MG828869.1; Identities = 483/514 (94 %), 15 gaps (2 %)). The closest hits using the **LSU** sequence are *Angustimassarina populi* (GenBank MF409166.1; Identities = 892/907 (98 %), no gaps), *Angustimassarina coryli* (GenBank MF167432.1; Identities = 876/891 (98 %), 1 gap (0 %)) and *Exosporium stylobatum* (GenBank JQ044447.1; Identities = 875/890 (98 %), no gaps). The closest hits using the **SSU** sequence are *Ulospora bilgramii* (GenBank DQ384071.1; Identities = 522/526 (99 %), no gaps), *Phoma herbarum* (GenBank AY293777.1; Identities = 522/526 (99 %), no gaps) and *Lepidosphaeria nicotiae* (GenBank NG_061050.1; Identities = 521/526 (99 %), no gaps). The closest hits using the ***tef1*** sequence are *Angustimassarina coryli* (GenBank MF167433.1; Identities = 890/938 (95 %), 3 gaps (0 %)), *Cycasicola goaensis* (GenBank MG829198.1; Identities = 876/935 (94 %), no gaps), and *Pteridiospora javanica* (GenBank KJ739606.1; Identities = 885/951 (93 %), no gaps). *Alfoldia vorosii* represents 'Group 9' *sensu* Knapp et al. (2012). No sporulation was observed in any of the media PDA, MEA, MMN and WA supplemented with autoclaved plant tissues *sensu* Knapp et al. (2015).

Supplementary material

FP902 Maximum Likelihood (RAxML) tree of concatenated ITS, LSU, SSU and *tef1* sequences of isolates of *Alfoldia vorosii* and representative taxa of related lineages. RAxML analysis was performed by raxmlGUI 1.3 (Silvestro & Michalak 2012), bootstrap support values (≥ 70 %) are shown above branches and before slashes; Bayesian analysis was performed with MrBayes v. 3.1.2 (Ronquist & Huelsenbeck 2003) and Bayesian posterior probabilities (≥ 0.90) are shown below branches and after slashes. *Melanomma pulvis-pyrius* (CBS 124080) served as an outgroup. The scale bar indicates expected changes per site per branch.

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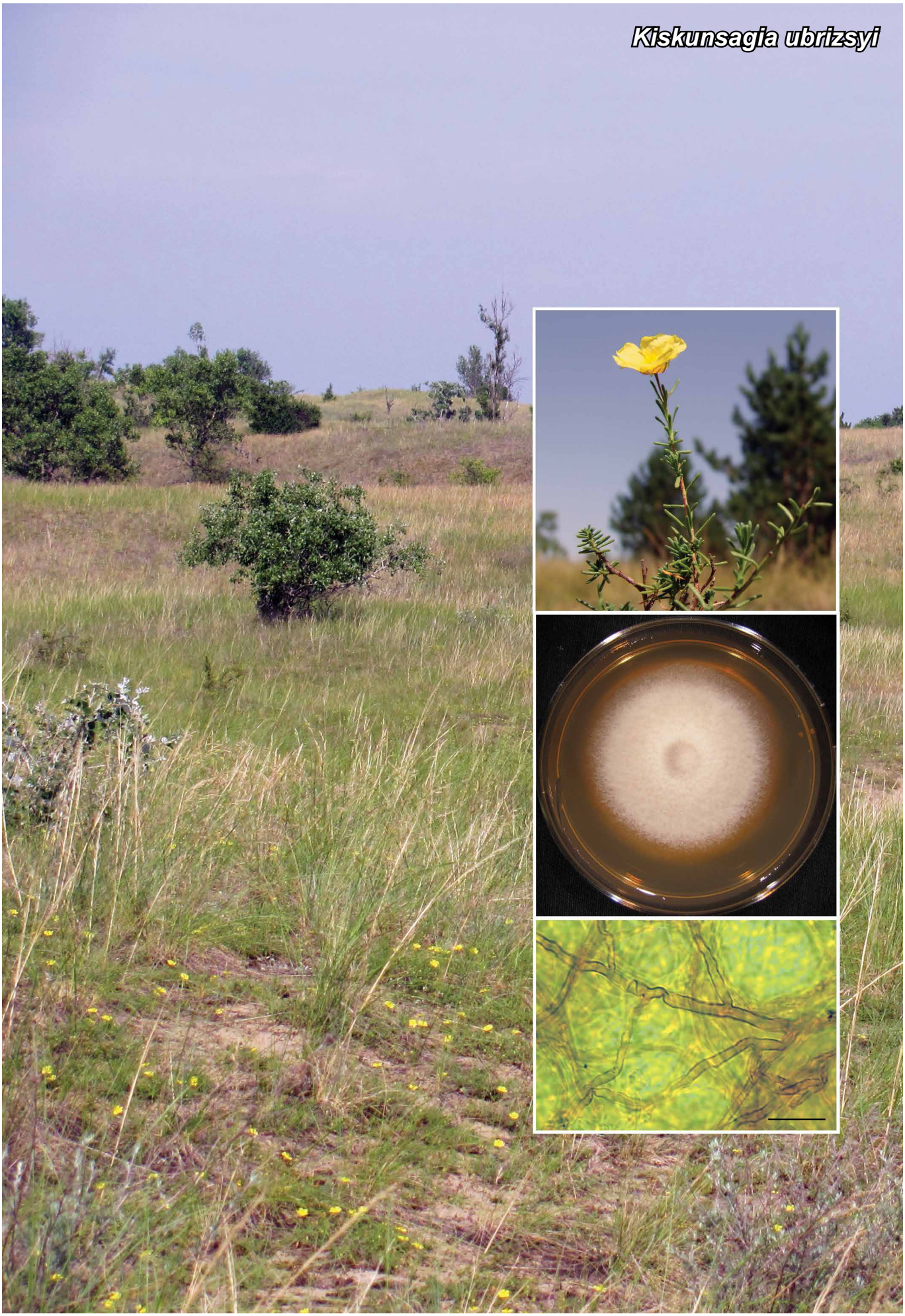
Kiskunsagia ubrizsyi

Fungal Planet 903 – 19 July 2019

Kiskunsagia D.G. Knapp, Imrefi & Kovács, *gen. nov.*

Etymology. Referring to the sandy collection site within the Kiskunság National Park.

Classification — *Lophiostomataceae*, *Pleosporales*, *Dothideomycetes*.

Kiskunsagia isolates can be collected from surface-sterilised roots and can be cultured and maintained on general media. Isolates of the genus *Kiskunsagia* are root endophytes associated with woody plant species of semiarid grasslands near Fülöpháza, Hungary.

Type species. *Kiskunsagia ubrizsyi* D.G. Knapp, Imrefi & Kovács. MycoBank MB830107.

Kiskunsagia ubrizsyi D.G. Knapp, Imrefi & Kovács, *sp. nov.*

Etymology. We name the species in honour of the 100th anniversary of the birth of the outstanding Hungarian mycologist Gábor Ubrizsy (1919–1973), who contributed significantly to our knowledge on fungi.

Kiskunsagia ubrizsyi differs from its closest phylogenetic neighbour, *Guttulispora crataegi* (MFLUCC 13_0442), by unique fixed alleles in the ITS, LSU, SSU and *tef1* loci based on alignments of the separate loci deposited in TreeBASE as study S24077: ITS positions: 14 (A), 16–21 (insertion), 23 (C), 25 (G), 26 (G), 27 (G), 28 (C), 30 (T), 31 (T), 32 (A), 33 (A), 38–40 (deletion), 41 (C), 42 (T), 46 (C), 47 (C), 50 (G), 52–56 (insertion), 59 (C), 65 (T), 74 (G), 75 (C), 77 (T), 78 (A), 80 (deletion), 82 (G), 83 (T), 86 (C), 102 (C), 170 (G), 191 (C), 192 (A), 205 (T), 217 (C), 230 (C), 231 (C), 233 (T), 234 (T), 398 (insertion), 441 (A), 444 (G), 504 (T), 506 (T), 529 (T), 532 (T), 536 (A), 537 (A), 539 (C), 541 (T), 547 (T), 550 (G), 552 (A), 575 (A), 576 (A), 580 (T), 581 (C), 585 (G); LSU positions: 113 (C), 134 (T), 165 (G), 186 (T), 198 (C), 201 (C), 202 (T), 223 (C), 286 (C), 404 (T), 405 (A), 419 (G), 424 (C), 444 (T), 445 (A), 446 (C), 487 (A), 505 (T), 524 (T), 527 (G), 665 (C), 692 (C), 697 (G); SSU position: 21 (deletion); *tef1* positions: 108 (T), 138 (C), 159 (G), 195 (G), 200 (A), 202 (A), 204 (C), 207 (A), 243 (T), 246 (A), 264 (C), 267 (C), 309 (A), 310 (C), 311 (C), 358 (A), 359 (C), 365 (T), 366 (T), 384 (A), 396 (C), 406 (C), 408 (C), 411 (G), 432 (T), 468 (C), 483 (C), 486 (T), 517 (G), 526 (G), 531 (T), 543 (C), 558 (T), 648 (T), 651 (G), 691 (C), 693 (G), 696 (T), 702 (C), 726 (C), 738 (C), 756 (G), 768 (A), 777 (T), 837 (T), 840 (C), 918 (T), 927 (A), 957 (T).

Culture characteristics — Colonies covering the Petri dish in 2 wk. Colony on PDA flat, spreading, with moderate aerial mycelium and smooth, lobate margin, no exudates observed. Colony on MEA creamy, yellow to white with an entire edge and sparse aerial mycelium, no exudates observed. Strains generally stain the media to pale orange. Cultures sterile.

Typus. Hungary, Fülöpháza, from roots of *Fumana procumbens* (*Cistaceae*), 2008, *D.G. Knapp & G.M. Kovács* (holotype BP110342, culture extype REF121 = CBS 145502, ITS, LSU, SSU and *tef1* sequences GenBank JN859341, MK589359, MK589351 and MK599325, MycoBank MB830108).

Colour illustrations. Semiarid sandy grassland in the Kiskunság National Park with flowering needle sunroses. The host (*Fumana procumbens*) of *Kiskunsagia ubrizsyi*; colony on PDA; pigmented hyphae of the strain REF121. Scale bar = 10 µm.

Additional materials examined. Hungary, Fülöpháza, from roots of *F. procumbens*, 2008, *D.G. Knapp & G.M. Kovács*, REF120, ITS, LSU, SSU and *tef1* sequences GenBank JN859340, MK589358, MK589350 and MK599324; ibid., REF 122, ITS, LSU, SSU and *tef1* sequences GenBank JN859342, MK589360, MK589352 and MK599326; from roots of *Helianthemum ovatum* (*Cistaceae*), 2008, *D.G. Knapp & G.M. Kovács*, REF118, ITS, LSU, SSU and *tef1* sequences GenBank JN859338, MK589356, MK589348 and MK599322; ibid., REF119, ITS, LSU, SSU and *tef1* sequences GenBank JN859339, MK589357, MK589349 and MK599323.

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits of *Kiskunsagia ubrizsyi* (CBS 145502) using the **ITS** sequence are *Guttulispora crataegi* (GenBank NR_154070.1; Identities = 437/469 (93 %), 6 gaps (1 %)), *Platystomum rosae* (GenBank KY264742.1; Identities = 443/480 (92 %), 11 gaps (2 %)) and *Neopaucispora rosaecae* (GenBank MG828924.1; Identities = 438/474 (92 %), 7 gaps (1 %)). The closest hits using the **LSU** sequence are *Trematosphaeria terricola* (GenBank JX985750.1; Identities = 884/905 (98 %), no gaps), *Lophiostoma compressum* (GenBank KP888643.1; Identities = 885/907 (98 %), no gaps) and *Lophiostoma quadrinucleatum* (GenBank GU385184.1; Identities = 877/896 (98 %), no gaps). The closest hits using the **SSU** sequence are *Massariosphaeria grandispora* (GenBank EF165038.1; Identities = 512/514 (99 %), 2 gaps (0 %)), *Trematosphaeria biappendiculata* (GenBank GU205254.1; Identities = 511/513 (99 %), 1 gap (0 %)) and *Ulospora bilgramii* (GenBank DQ384071.1; Identities = 520/527 (99 %), 1 gap (0 %)). The closest hits using the ***tef1*** sequence are *Platystomum scabridisporum* (GenBank GU479856.1; Identities = 886/921 (96 %), no gaps), *Coelodictyosporium rosarum* (GenBank MG829195.1; Identities = 885/937 (94 %), no gaps) and *Lophiostoma compressum* (GenBank KR075165.1; Identities = 874/921 (95 %), no gaps).

Kiskunsagia ubrizsyi represents 'Group 10' *sensu* Knapp et al. (2012). No sporulation of the strains was observed in any of the media PDA, MEA, MMN and WA supplemented with autoclaved plant tissues *sensu* (Knapp et al. 2015).

Supplementary material

FP903 Maximum Likelihood (RAxML) tree of concatenated ITS, LSU, SSU and *tef1* sequences of isolates of *Kiskunsagia ubrizsyi* and representative taxa of related lineages. RAxML analysis was performed by raxmlGUI 1.3 (Silvestro & Michalak 2012), bootstrap support values (≥ 70 %) are shown above branches and before slashes; Bayesian analysis was performed with MrBayes v. 3.1.2 (Ronquist & Huelsenbeck 2003) and Bayesian posterior probabilities (≥ 0.90) are shown below branches and after slashes. *Melanomma pulvis-pyrius* (CBS 124080) served as an outgroup. The scale bar indicates expected changes per site per branch.

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Apenidiella foetida

Fungal Planet 904 – 19 July 2019

Apenidiella foetida Iturrieta-González, Gené, Dania García, *sp. nov.*

Etymology. Name refers to the unpleasant odour produced in older cultures.

Classification — *Teratosphaeriaceae*, *Capnodiales*, *Dothideomycetes*.

Mycelium consisting of branched, septate, subhyaline to pale olivaceous, smooth-walled, 1–2 µm diam hyphae. *Conidiophores* mononematous, macronematous, unbranched, erect, subcylindrical, up to 6-septate, pale olivaceous, smooth-walled, up to 130 µm long, 3–5 µm wide. *Conidiogenous cells* terminal, integrated, mono- or polyblastic, with up to 5 conidiogenous loci thickened and darkened, commonly giving rise to a set of ramoconidia at the same level, ramoconidia at different levels also present, pale olivaceous, smooth-walled, 18–27 × 3–4 µm. *Ramoconidia* aseptate, with up to 2–3(–4) terminal conidiogenous loci thickened and darkened, pale olivaceous, smooth-walled, some slightly verruculose, 12–21 × 4–5 µm, forming conidia in acropetal chains. *Conidia* aseptate, fusiform, limoniform or lanceolate, pale olivaceous, smooth-walled, some slightly verruculose, 7–21 × 3–5 µm. *Sexual morph* not observed.

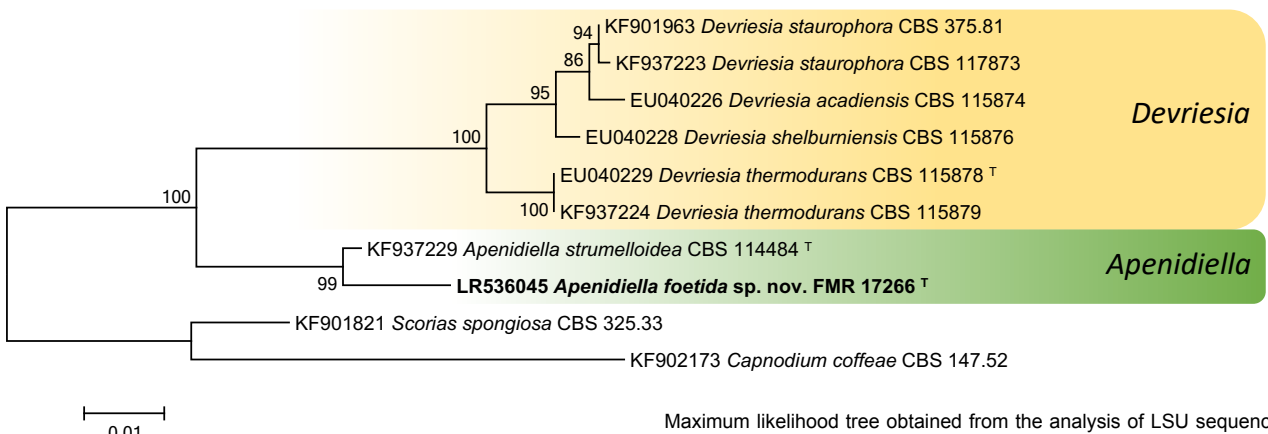
Culture characteristics — Colonies on PDA reaching 28–33 mm diam after 30 d at 25 °C, olive brown (4F3) (Kornerup & Wanscher 1978), velvety, radially folded, aerial mycelium scarce, regular margin; reverse dark green (30F8) to black. On PCA reaching 27 mm after 30 d at 25 °C, olive (3F3/3E3), slightly granular, flat, aerial mycelium scarce, regular margin; reverse yellowish brown to greyish brown (5F8/5E3). On OA reaching 20–23 mm diam after 30 d at 25 °C, olive (3F3), slightly granular, flat, aerial mycelium scarce; reverse yellowish brown (5F8/5F4). An unpleasant smell was appreciated in old cultures of PCA and OA.

Cardinal temperature for growth — Optimum 25 °C, maximum 28 °C, minimum 5 °C.

Typus. Spain, Catalonia, Baix Camp, Arbolí River, on submerged plant debris, Feb. 2018, *I. Iturrieta-González*, *E. Carvalho & J. Gené* (holotype CBS H-23919, culture ex-type CBS 145590 = FMR 17266; ITS and LSU sequences GenBank LR536044 and LR536045, MycoBank MB830227).

Notes — *Apenidiella* is a monotypic genus recently introduced in the family *Teratosphaeriaceae* to accommodate *A. strumelloidea* (previously *Cladosporium strumelloideum*), a fungus isolated from a leaf of *Carex* sp. collected in stagnant water from the Sutka River in Russia (Crous et al. 2007, Quaedvlieg et al. 2014). Interestingly, the novel species was recovered from a similar habitat than the type species of the genus. *Apenidiella strumelloidea* differs from *A. foetida* in having shorter conidiophores (up to 80 µm long) and conidiogenous cells (8–12 µm) and its conidia frequently show one side flat and the other convex, even slightly curved conidia are also present (Crous et al. 2007). In addition, in *A. strumelloidea* macro- and microconidiophores were described, while in our species only macroconidiophores were observed.

Based on a megablast search of NCBIs GenBank nucleotide database, the **LSU** sequence of *A. foetida* showed a similarity of 98.82 % (839/849) with that of *A. strumelloidea* (CBS 114484, GenBank KF937229), while the similarity between **ITS** sequences (GenBank LR536044 vs GenBank EU019277) was 93.67 % (459/490).



Maximum likelihood tree obtained from the analysis of LSU sequences of *Apenidiella* and related genera of the family *Teratosphaeriaceae*. Bootstrap support values above 70 % are indicated on the nodes. The alignment included 751 bp and was performed with ClustalW. Kimura 2 parameters with Gamma distribution (K2+G) was used as the best nucleotide substitution model. Both the alignment and tree were constructed with MEGA v. 6 software (Tamura et al. 2013). The new species proposed in this study is indicated in **bold**. A superscript T denotes ex-type cultures.

Colour illustrations. Arbolí, Catalonia, Spain. Colony sporulating on PCA after 30 d at 25 °C, and conidiophores and conidia after 14 d at 25 °C. Scale bars = 10 µm.

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Aspergillus bezerrae

Fungal Planet 905 – 19 July 2019

Aspergillus bezerrae J.P. Andrade, C.N. Figueiredo, H.G. de Souza, J.T. De Souza & P.A.S Marbach, *sp. nov.*

Etymology. *bezerrae*, in honour of Dr José Luiz Bezerra, a Brazilian mycologist who has significantly contributed to our knowledge of Brazilian fungal biodiversity and the training of young mycologists in general.

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

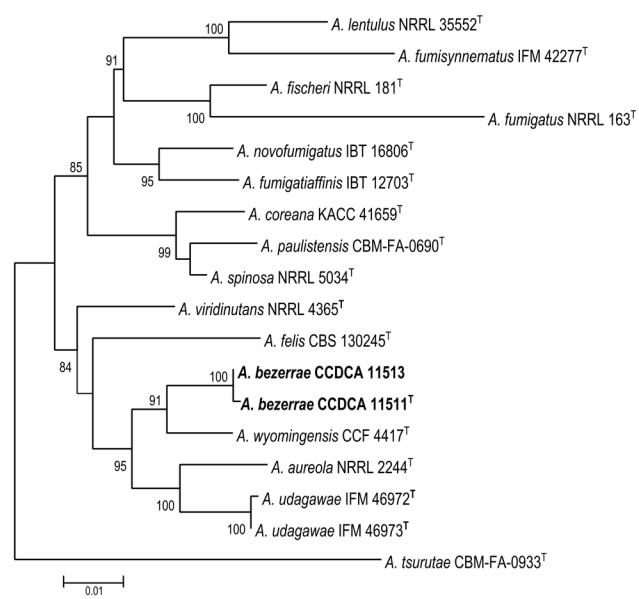
Conidial heads columnar. *Stipes* frequently sinuous or curved, smooth, frequently septate, (4–)13–718(–963) × 2–3(–4) µm, sometimes with subterminal branches, mycelial coils occur frequently and nodding heads occasionally present. Conidial heads uniseriate, *vesicles* pyriform to subglobose, pigmented, 6–16 × 4–16 µm (av. 12 ± 2 × 9 ± 3), *phialides* ampulliform, covering half to upper half of vesicle. *Conidia* globose to subglobose, delicately rough, 2–3 × 2–3 µm (av. 2 ± 0.12 × 2 ± 0.17), light green in mass, average width/length = 1 ± 0.01, n = 81. Sexual morph was observed in compatible combinations of isolates. Heterothallic; ascomata visible after 4 wk of incubation on OA at 25 and 30 and absent at 37 °C, mature ascospores present in 5 wk. *Cleistothecia* white to pale, globose or subglobose (80–)150–890 µm diam, covered by a dense felt of white hyphae; asci 8-spored, globose to subglobose, 9–12.5 × 7.5–12.5 µm; *ascospores* lenticular, with equatorial crests, spore bodies 2–5 × 3–5 µm.

Culture characteristics — Colonies on Czapek Yeast Autolysate agar (CYA) 40–43 mm diam at 25 °C after 7 d, floccose, radially and concentrically wrinkled, mycelium white (ISCC-NBS No. 263; Kelly 1964), sporulation light yellow (No. 86), pale yellow (No. 89), no exudate, soluble pigment brilliant yellow (No. 83), reverse pale greenish yellow (No. 104), pale yellow (No. 89). After 14 d, sporulation pale yellow green (No. 121), brilliant greenish yellow (No. 98), yellow exudate, soluble pigment light yellow (No. 86), reverse light yellow (No. 86) and moderate yellow (No. 87). Colonies at 37 °C 29–34 mm, lanose to floccose, radially and concentrically wrinkled, sporulation pale yellow (No. 89), reverse pale yellow (No. 89). Colonies on Blakeslee's Malt extract agar (MEAbl) 35–41 mm, floccose, slightly radially and concentrically wrinkled; mycelium white (No. 263); sporulation pale greenish yellow (No. 104), pale yellow (No. 89), light yellow (No. 86), no exudate, soluble pigment brilliant yellow (No. 83) sometimes present; reverse yellowish white (No. 92), pale yellow (No. 89), moderate yellow (No. 87), light yellow (No. 86). After 14 d, slightly radially wrinkled, sporulation moderate yellow green (No. 120); reverse pale yellow (No. 89), moderate yellow (No. 87). Colonies on Yeast extract sucrose agar (YES) 36–44 mm, floccose, concentrically and irregularly wrinkled, mycelium white (No. 263), sporulation light greenish yellow (No. 101), yellowish white (No. 92), no exudate, no soluble pigment, reverse light greenish yellow (No. 101), brilliant yellow (No. 83). Colonies on Czapek's agar (CZ) 36–41 mm, floccose, sometime with areas submerged, plane, white mycelium (No. 263), very pale green (No. 148), sporulation absent, no exudate, no soluble pigment, reverse white (No. 263), very pale green (No. 148). Colonies on Creatine sucrose agar (CREA) 35–41 mm, moderate mycelial growth, no acid production. Isolates did not grow in MEAbl at 47 °C, only some isolates were able to grow restrictedly (up to 7) at 45 °C and all grew at 42 °C 7–24 mm.

Typus. Brazil, Bahia, in soil from the Guaibim sandbank, S13°18' W38°57', 20 Nov. 2011, *P.A.S. Marbach* (holotype HURB 22323 - dried culture on MEAbl, culture ex-type CCDCA 11511 = 9EM2, *BenA* and *CaM* sequences GenBank MK597913 and MK597915, MycoBank MB830186).

Additional materials examined. Brazil, Bahia, in soil from the Guaibim sandbank, CCDCA 11513 = 4M5, 5 Oct. 2011, *P.A.S. Marbach*, LSU, *BenA* and *CaM* sequences GenBank MK595451, MK597912 and MK597914; ibid., 10 Dec. 2011, *P.A.S. Marbach*, cultures 63EM7, 9EM7, 22EM3 and 33EM6. A dried paired culture of isolates CCDCA 11511^{T} (= 9EM2) × 63EM7 containing the sexual fruiting bodies was deposited as HURB 22371.

Notes — Phylogenetically and morphologically *A. bezerrae* resembles *A. wyomingensis* (Nováková et al. 2014, Samson et al. 2014) included in the section *Fumigati*. The characteristics distinguishing *A. bezerrae* from *A. wyomingensis* are: 1) *A. bezerrae* grows slower than *A. wyomingensis* on all media and temperatures tested; 2) *A. bezerrae* may produce a brilliant yellow soluble pigment in CYA and no acid in CREA; 3) *A. bezerrae* has longer stipes, produces mycelial coils, ascomata are absent at 37 °C, the cleistothecia are larger and the ascospores have equatorial crests. All macroscopic and microscopic measurements were done twice, independently, for isolates CCDCA 11511 and CCDCA 11513.



Maximum likelihood tree obtained by phylogenetic analysis of the combined *BenA* and *CaM* sequences from *Aspergillus bezerrae* and phylogenetically related species in section *Fumigati* performed in MEGA v. 6.06 software employing K2+G model with 1 000 bootstrap re-samplings. Bootstrap support values (BS > 80 %) are presented at the nodes. *Aspergillus tsurutae* CBMFA 0933^{T} was used as outgroup. The new species is presented in **bold** (^{T} = ex-type).

Colour illustrations. Guaibim environmental protection area located in Bahia, Brazil. 7-d-old colonies growing at 25 °C (top row left to right, obverse CYA, MEAbl, YES and CREA; bottom row left to right, reverse CYA, MEAbl, YES and obverse fertile cleistothecia (crossing between the isolates 9EM2^{T} and 63EM7)); cleistothecia; asci; ascospores; conidiophores; conidiophores; conidia; coiling of mycelia. Scale bars = 10 µm.

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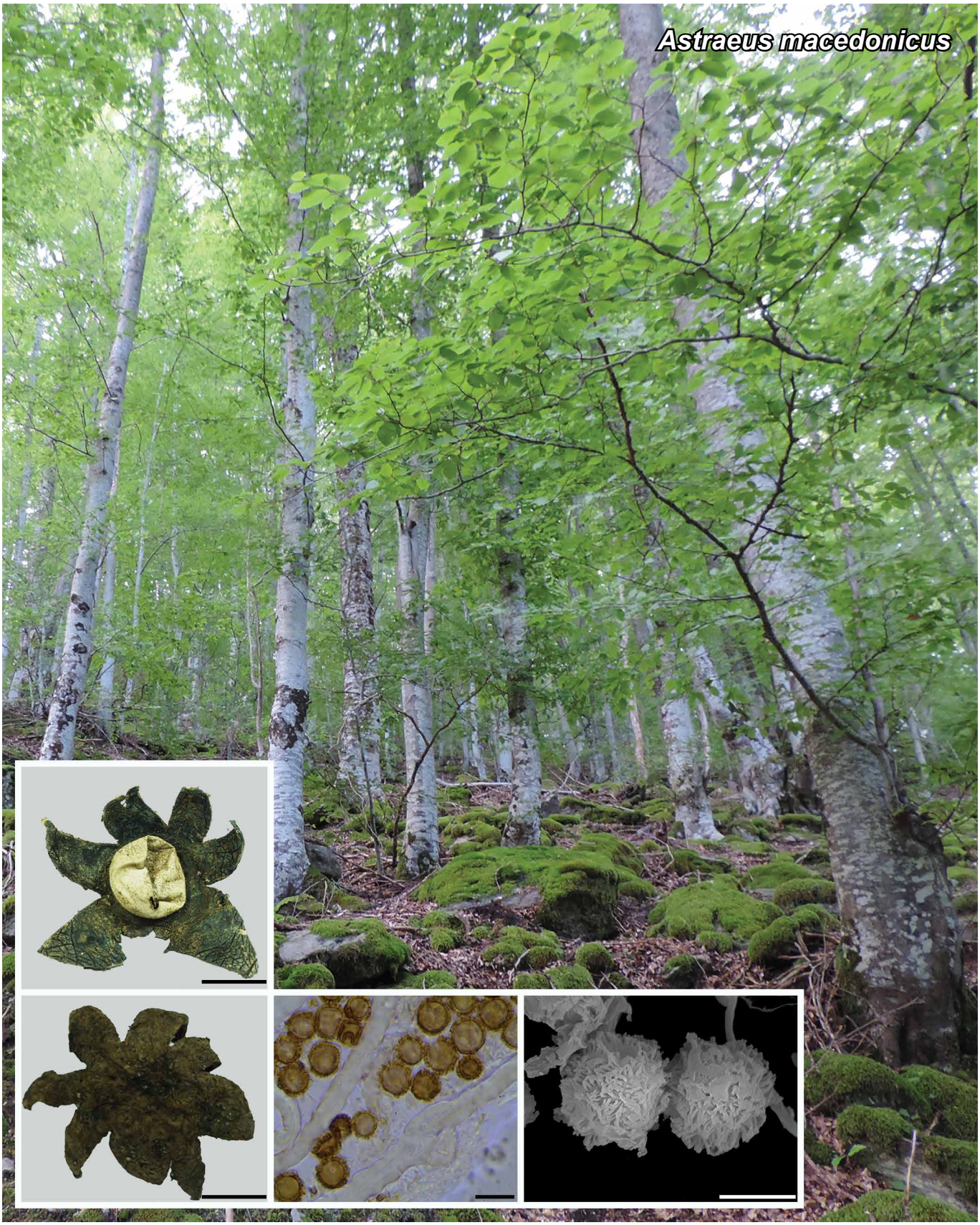

Astraeus macedonicus

Fungal Planet 906 – 19 July 2019

Astraeus macedonicus Rusevska, Karadelev, Telleria & M.P. Martín, *sp. nov.*

Etymology. Named after the country where this species was collected, the Republic of Macedonia.

Classification — *Diplocystaceae*, *Boletales*, *Agaricomycetes*.

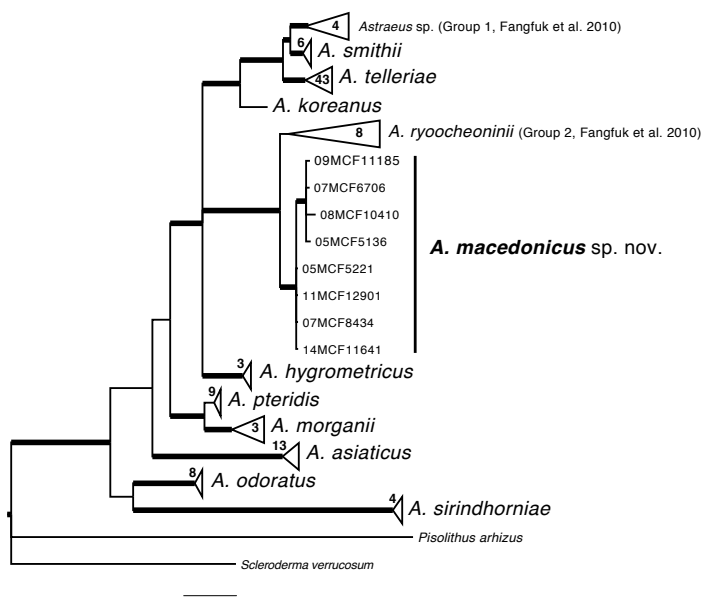
Basidiomata from closed specimens 17 × 22 mm, not fully opened 25 × 30 mm, and almost opened 27 × 37 mm; regularly globose to slightly subglobose, epigeous, sessile. *Outer peridium* splitting to star shaped when mature into (6–)8–10 rough rays, expanding to 14–33 mm in length, 10–11 mm in width (at the middle, at the longest part), hygroscopic. *Endoperidium* sessile, subglobose to globose, papery-thin sack, 18–23 mm diam, pale cream to very light grey coloured, the surface papery-fibrillose; opening as an irregular slit. *Gleba* pale brownish to dark brownish, without columella. *Capillitium* hyaline, thick-walled, branched and interwoven, 4.2–10 µm diam, with capitates ends up to 12 µm diam, with rare septa, some of them with a clamp connection-like structure. *Basidiospores* globose, 7.3–10.1 µm diam, with dense, rounded, narrow, tapered, separate tubercles (up to 1 µm) which coalesce in groups.

Typus. Macedonia, Bistra, Lazaropole village, footpath to St. Gjorgija church, 1300 m asl, 8 Aug. 2005, *K. Rusevska* (holotype 05MCF5221, ITS and LSU sequences GenBank MK491320 and MK496886, MycoBank MB829660).

Additional materials examined. Macedonia, Bilina Planina, Zhidilovo vill., deciduous forest (*Quercus* sp., *Fagus*, *Betula pendula*), 19 May 2011, *K. Rusevska*, 11MCF12901, ITS sequence GenBank MK491321; Kozhuf, r. Stara Reka (vicinity), riparian vegetation, 18 July 2005, *K. Rusevska*, 05MCF5136, ITS sequence GenBank MK491319; Osogovski Planini, Stanci vill., deciduous forest (*Carpinus*, *Betula*, *Fagus*), 900–970 m asl, 13 May 2007, *K. Rusevska*, 07MCF6706, ITS and LSU sequences GenBank MK491317 and MK496884; ibid., Ponikva, *Fagus* forest, 1500–1600 m asl, 11 July 2007, *K. Rusevska*, 07MCF8434, ITS sequence GenBank MK491322; ibid., Sasa, *Quercus frainetto* forest, 685 m asl, 9 Apr. 2008, *K. Rusevska*, 08MCF10410, ITS and LSU sequences GenBank MK49318 and MK496885; Plachkovica, above Laki vill., Selska Reka, *Fagus* forest with *Pinus nigra*, 21 Oct. 2014, *K. Rusevska*, 14MCF11641, ITS sequence GenBank MK491323. – Serbia, Vuchje (vicinity), edge of deciduous forest, 12 Sept. 2009, *K. Rusevska*, 09MCF11183, ITS and LSU sequences GenBank MK491316 and MK496886.

Additional materials examined of other Astraeus species from Macedonia. Herbarium number is indicated, as well as the ITS sequence GenBank between brackets: *Astraeus hygrometricus*. 05MCF5511 [MK491324]. — *Astraeus pteridis*. 06MCF5817 [MK491326]; 07MCF8009 [MK491327]; 09MCF10671 [MK491325]. — *Astraeus telleriae*. 83MCF7728 [MK491314]; 83MCF7729 [MK491297]; 83MCF7730 [MK491294]; 83MCF7731 [MK491307]; 87MCF9566 [MK491300 and MK491304]; 88MCF9574 [MK491295]; 98MCF6531 [MK491280]; 01MCF3439 [MK491303]; 03MCF2896 [MK491296]; 04MCF4362 [MK491292]; 04MCF6532 [MK491288]; 05MCF911 [MK491310]; 05MCF4908 [MK491293]; 05MCF5329 [MK491284]; 05MCF5422 [MK491283]; 05MCF7977 [MK491275]; 06MCF1244 [MK491305]; 06MCF8811 [MK491309]; 07MCF6640 [MK491287]; 07MCF6887 [MK491281]; 07MCF6896 [MK491306]; 07MCF8028 [MK491282]; 07MCF8228 [MK491279]; 07MCF8549 [MK491290]; 08MCF9078, [MK491277]; 08MCF10109 [MK491285]; 08MCF10272 [MK491286]; 08MCF10282 [MK491299]; 09MCF9816 [MK491298]; 09MCF11502 [MK491313]; 09MCF11527 [MK491315]; 09MCF13788 [MK491302]; 10MCF12021 [MK491289]; 10MCF12678 [MK491308]; 11MCF9817 [MK491291]; 11MCF12654 [MK491276 and MK491278]; 12MCF14080 [MK491311]; 12MCF13532 [MK491312]; 13MCF14623 [MK491301].

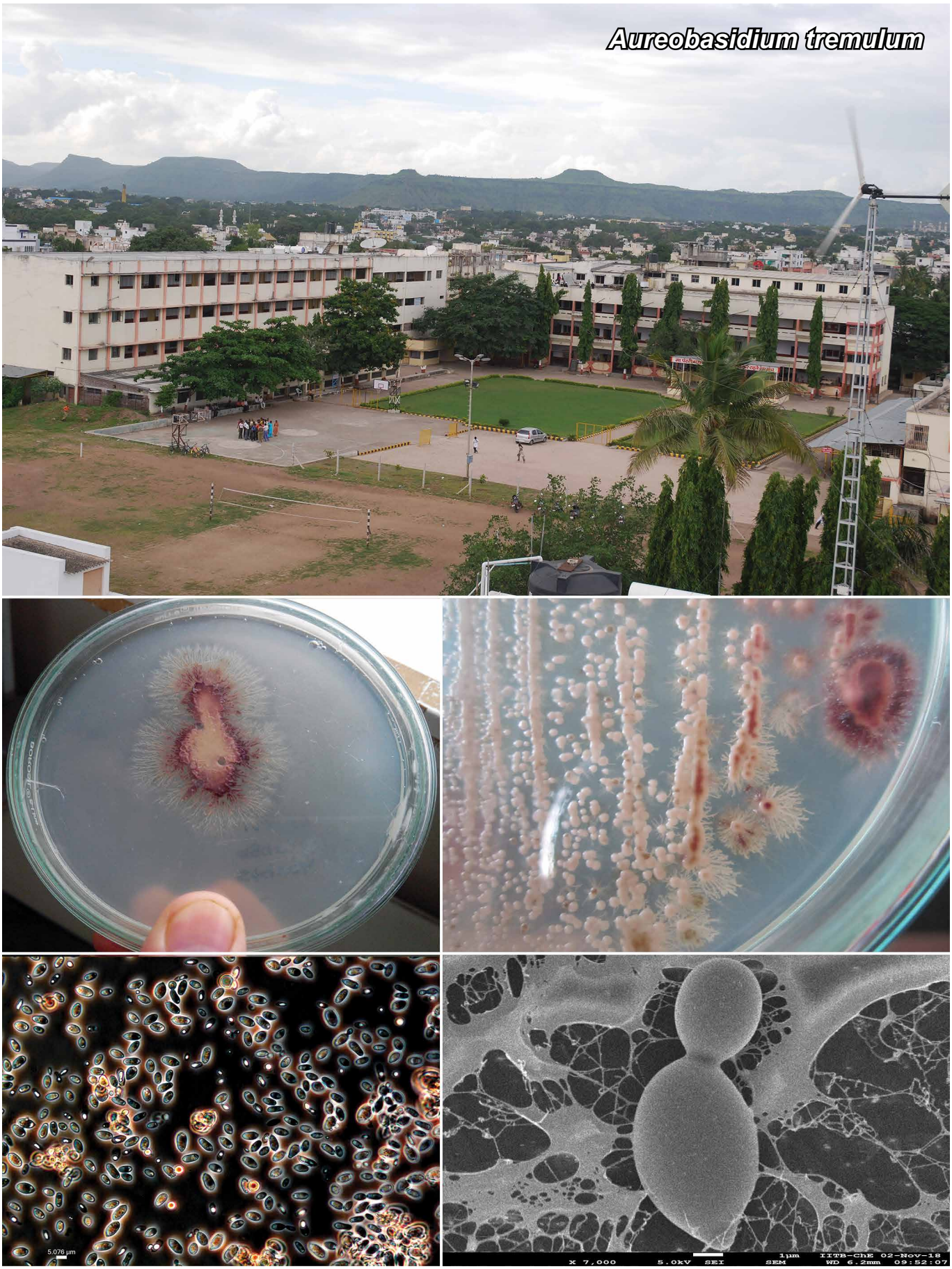
Notes — *Astraeus macedonicus* is known from deciduous forests in four Macedonian localities (the mountains located in the west, north, south and east part of the country). Morphologically, this species is very similar to *A. hygrometricus*, *A. pteridis* and *A. telleriae*, not only in its habitat but also in its microscopic characters, such as capillitium and spores; therefore all records (collected up to 2007) were previously published as *A. hygrometricus* (Karadelev et al. 2008). However, the Bayesian analyses, based on 53 collections from Macedonia, and a number of published sequences mainly from Phosri et al. (2007, 2013, 2014), Fangfuk et al. (2010) and Ryoo et al. (2017), clearly grouped eight Macedonian collections as a sister clade of *Astraeus ryoocheoninii*, a species described from Japan and Korea, and separated *A. hygrometricus*, *A. pteridis* and *A. telleriae*.



The 50 % majority rule Bayesian tree inferred from ITS nrDNA sequences with the GTR+I+G model and using MrBayes v. 3.1.2 (Ronquist & Huelsenbeck 2003) for 2 M generations. Posterior probabilities values > 0.90 are marked as thick branches. In every collapsed clade, the number of sequences is indicated in or close to the triangle. *Astraeus macedonicus* holotype in **bold**. *Pisolithus arhizus* (GenBank AJ629887) and *Scleroderma verrucosum* (GenBank AJ629886) were included as outgroup.

Colour illustrations. Macedonia, Bistra mountain, beech forest, 1300 m asl, where the holotype species was collected (05MCF5221). Basidiomata; basidiospores and capillitium under LM; basidiospores under SEM. Scale bars = 1 cm (basidiomata), 10 µm (basidiospores and capillitium) and 5 µm (basidiospores).

Katerina Rusevska & Miko Karadelev, Institute of Biology, Faculty of Natural Sciences and Mathematics, Ss. Cyril and Methodius University, Skopje, Republic of Macedonia; e-mail: krusevska@pmf.ukim.mk & mitkok@pmf.ukim.mk
M. Teresa Telleria & María P. Martín, Departamento de Micología, Real Jardín Botánico, RJB-CSIC, Plaza de Murillo 2, 28014 Madrid, Spain; e-mail: telleria@rjb.csic.es & maripaz@rjb.csic.es


Aureobasidium tremulum
5.076 µm
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Fungal Planet 907 – 19 July 2019

Aureobasidium tremulum Inamdar, Roh. Sharma & Adhapure, *sp. nov*.

Etymology. Named after the shaking and trembling behaviour of the yeast when observed under a light microscope (Latin *tremulum*= shaking, trembling).

Classification — *Aureobasidiaceae*, *Dothideales*, *Dothideomycetes.*

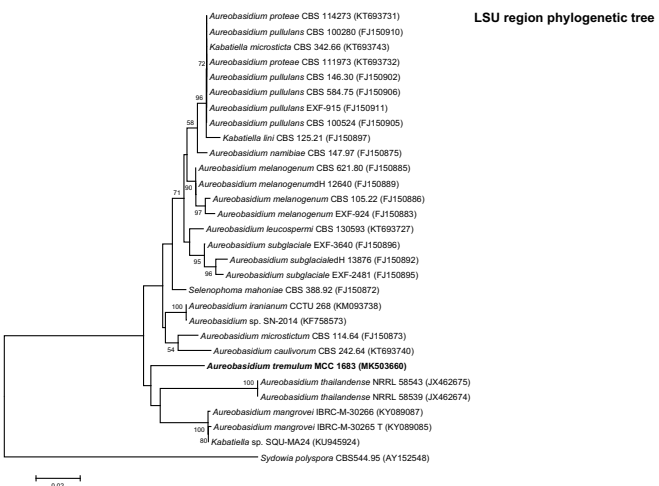
Initial growth as creamy white colonies on potato dextrose agar, later turning brown to dark brown. Colonies appear to be rough and dry. Each colony is round with a convex elevation from a cross-sectional viewpoint and the edges appear to be undulated. Growth is optimal on Saboraud dextrose agar (SDA). Colonies on nutrient agar did not become dark brown. *Cells* are generally oblong-shaped with very few cells assuming an irregular shape. *Budding* occurs frequently. The average size of mature, non-budding cells is 2.8 × 6.4 µm. *Sexual reproduction* was not observed. *Pseudohyphal* formation not observed. Optimal growth occurred at 20–25 °C, with some growth at 5–15 °C. The following carbon compounds are assimilated: D-glucose, L-arabinose, D-xylose, D-maltose, D-saccharose, D-Trehalose, D-melezitose, D-raffinose. No growth observed with glycerol, calcium-2-keto-gluconate, L- lactose while weak assimilation was observed for adonitol, xylitol, D-galactose, methyl-alpha- D-glucopyranoside and D-cellobiose.

Habitat — *Aureobasidium tremulum* was isolated as a culture contaminant in the laboratory of Department of Biotechnology and Microbiology of Vivekanand Arts, Sardar Dalipsingh Commerce and Science College, Aurangabad.

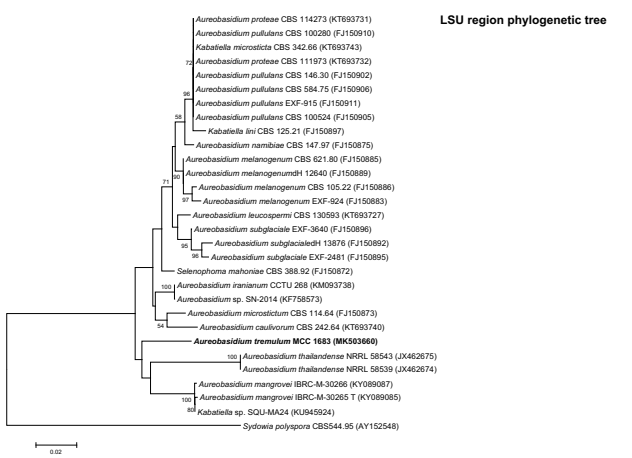
Distribution — India (Aurangabad, Maharashtra).

Typus. India, Aurangabad, Maharashtra, laboratory contaminant, July 2016, *A. Inamdar* (holotype MCC 1683 preserved as metabolically inactive strain, ITS and LSU sequences GenBank MK503657 and MK503660, MycoBank MB829941).

Notes — An initial BLASTn similarity search using the **LSU** region sequence in the NCBI type sequences nucleotide database showed the highest similarity to *A. lini* CBS 125.21 (GenBank MH866211; 98 % identity, 99 % query cover) followed by *A. melanogenum* strain CBS 105.22 (GenBank MH866219; 98 % identity; query coverage 97 %). The BLASTn similarity search in the NCBI type sequences database using the **ITS** sequence showed the highest similarity to *Kabatiella bupleuri* CBS 131304 (GenBank NR_121524; 95 % identity, 100 % query coverage) followed by *Aureobasidium iranianum* CCTU 268 (GenBank KM093738; 95 % identity, 99 % query coverage) and *A. melanogenum* CBS 105.22 (GenBank NR_159598, 95 % identity, 99 % query coverage). The neighbour-joining (NJ) phylogenetic analyses of ITS and LSU rRNA gene regions were done using sequences of other species of *Aureobasidium*. The phylogenetic tree topology clearly shows that the present strain UN-1 is novel and does not cluster with any known species of the genus. The phylogenetic analysis based on the ITS alignment shows that it forms a sister branch to *A. thailandense* NRRL 58543 (GenBank JX462675) and *A. mangrovei* IBRC-M-30266 (GenBank KY089087). In the phylogenetic analysis based on the LSU alignment, it does not group with known species but was placed at equal evolutionary distance with *A. caulivorum* CBS 242.64 (GenBank FJ150944).



Neighbour-joining tree based on the D1/D2 LSU rDNA region showing the position of *Aureobasidium tremulum* sp. nov. among related species within genus *Aureobasidium*. Bootstrap values of above 50 % are given at nodes based on 1 000 replications. The scale bar represents 2 % sequence difference.



Neighbour-joining tree based on the ITS region showing the position of *Aureobasidium tremulum* sp. nov. among related species within genus *Aureobasidium*. Bootstrap values of above 50 % are given at nodes based on 1 000 replications. The scale bar represents 1 % sequence difference.

Colour illustrations. India, Maharashtra, Aurangabad, Vivekanand Arts, Sardar Dalipsingh Commerce and Science College, Aurangabad. Growth of *A. tremulum* on potato dextrose agar; light microscopic (LM) view of *A. tremulum*; Cryo Scanning Electron Microscopic (CSEM) image of *A. tremulum.* Scale bars = 5 µm (LM image), 1 µm (CSEM image).

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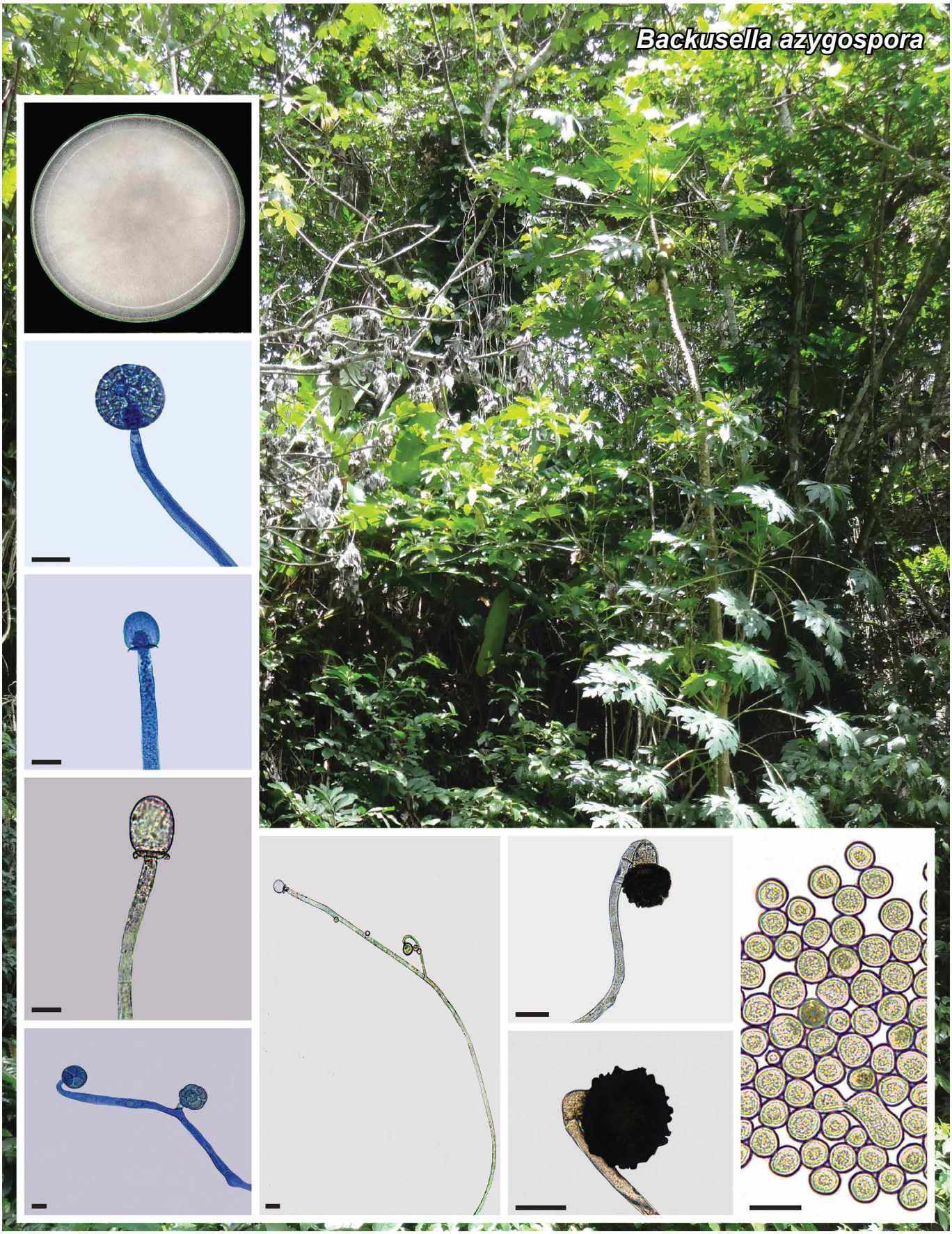

Backusella azygospora

Fungal Planet 908 – 19 July 2019

Backusella azygospora T.R.L. Cordeiro, Hyang B. Lee & A.L. Santiago, *sp. nov.*

Etymology. Name refers to the production of azygospores.

Classification — *Backusellaceae*, *Mucorales*, *Mucoromycotina*, *Mucoromycota*.

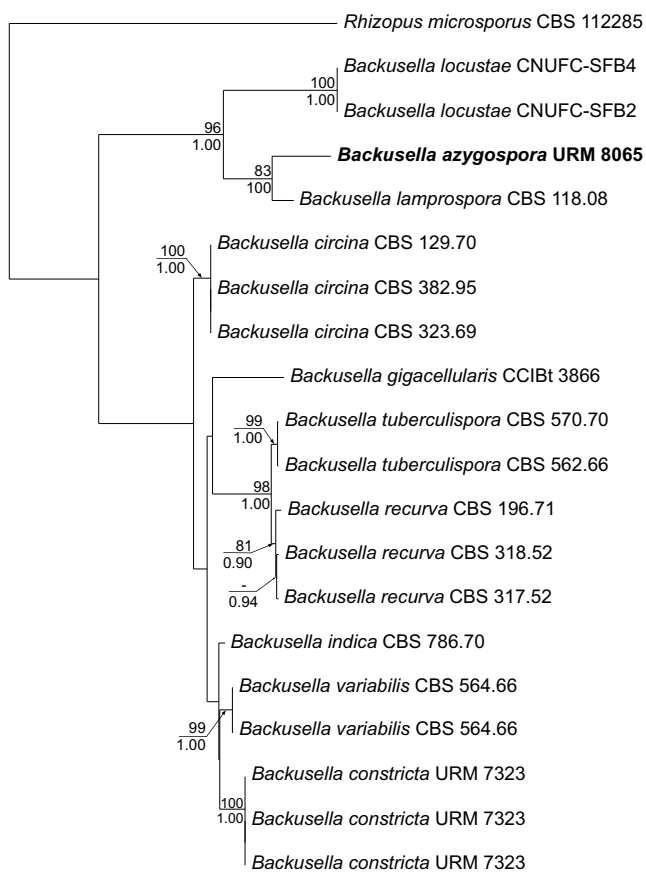
Mycelium hyaline. *Rhizoids* present, well branched, balled and matted. *Sporangiophores* arising directly from the substrate, curved when young and becoming erect in maturity, with smooth or slightly encrusted walls, up to 12 µm diam, constrictions below the sporangia; majority with simple or sympodial branches with long and short asymmetrical ramifications. Shorter branches may be circinate, usually supporting pedicels from which sporangiola originate. A septum observed near the point of azygosporangial formation or below the sporangia, and not always present. *Sporangia* yellowish, becoming light brown, globular or slightly flattened with short, hyaline and vitreous spines, and a deliquescent wall up to 70 µm diam. *Columellae of sporangiophores* hyaline, smooth or slightly encrusted, majority ellipsoid, cylindrical, ellipsoid to slightly piriform (18–)22–35(–42) × (19–)22–30(–35) µm, globose and subglobose, (14–)20–40(–50) µm diam. Collar evident with no needle-like spines. *Sporangiola* present, easily found after fifth day of inoculation, abundant when multispored and rarely unispored, both with persistent, spinulose and vitreous walls, up to 40 µm diam. *Columellae of sporangiola* hyaline, smooth-walled, globose, subglobose up to 15 µm diam and subglobose to conical (7–)12 × 14(–20) µm. *Sporangiospores* globose and subglobose (4.5–)9–22(–30) µm diam, some irregular (14.5–)33 × 12(–18) µm, smooth-walled, hyaline. *Azygosporangia* up to 110 µm diam, initially hyaline or yellow, becoming dark brown to black, globose, some flattened, wall with conical projections. *Azygospores* up to 50 µm diam, globose, smooth-walled. *Suspensor cells* up to 55 × 48 µm, heavily encrusted walls. *Zygosporangia* not observed.

Culture characteristics and temperature tests — Colony light grey, powdery in aspect (MP5 A7), exhibiting rapid growth (9 cm diam and 0.5 cm height) after 5 d in MEA, at 25 °C. Reverse yellow to cloudy amber (MP12 K3) on MEA (Maerz & Paul 1950). Azygosporangia visible to the naked eye. At 10 °C – lack of growth and sporulation. At 15 °C – slow growth (9 cm diam in 360 h); poor sporulation. At 20 °C – good growth (9 cm diam in 240 h); good sporulation. At 25 °C – better growth (9 cm diam in 96 h); excellent sporulation. At 30 °C – slow growth (9 cm diam in 360 h); poor sporulation. At 35 °C – lack of growth and sporulation. *Backusella azygospora* exhibited better growth and sporulation in MEA than in PDA at all tested temperatures.

Typus. Brazil, Saloá municipality, Pernambuco State, S09°00.418' W036°46.898', isolated from soil samples, 22 Nov. 2018, *T.R.L. Cordeiro* (holotype URM 92986, culture ex-type URM 8065, ITS and LSU sequences GenBank MK625216 and MK625222, MycoBank MB830270).

Colour illustrations. Fragment of an Upland Atlantic Forest within the semi-arid region in the municipal region of Saloá, in the state of Pernambuco, in north-eastern Brazil. Colony surface on MEA; simple sporangiophore with sporangium; simple sporangiophore with columellae; simple sporangiophore with sporangiola; branched sporangiophore with columella and sporangiolum; azygosporangia; sporangiospores. Scale bars = 25 µm.

Notes — *Backusella azygospora* differs from other species of the genus based on its morphological characters and the phylogenetic relationships established based on the ITS and LSU rDNA regions. Morphologically, *B. azygospora* is the only species of *Backusella* that produces azygosporangia and azygospores. In the ITS rDNA phylogenetic tree *B. azygospora* was nested near the *B. lamprospora* clade, and data provided by BLASTn revealed 84 % and 95 % (ITS and LSU rDNA, respectively) of similarity between both species. However, *B. lamprospora* is characterised by producing globular or ovoid hemispherical columellae, differing from those found in *B. azygospora*, which may be cylindrical, ellipsoid, ellipsoid to slightly pyriform, globose and subglobose to conical. Additionally, sporangiospores of *B. azygospora* are globose and subglobose, some irregular in size and shape, and larger than the subglobose sporangiospores of *B. lamprospora* (6.8–)8–13(–14.5) × (6.4–)7.6–13(–14) µm (Benny & Benjamin 1975).



Phylogenetic tree of *Backusella* conducted using the ITS rDNA sequences. *Rhizopus microsporus* CBS 112285 was used as outgroup. Sequences are labelled with their database accession numbers. Support values are from maximum likelihood analyses and Bayesian inference (values above and below the branches, respectively). Bayesian inference and maximum likelihood analyses were performed with MrBayes (Ronquist & Huelsenbeck 2003) and PhyML (Guindon & Gascuel 2003), respectively, launched from TOPALi (Milne et al. 2004). The new species is in **bold**. Bootstrap support values above 80 % are indicated.

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Boletus pseudopinophilus

Fungal Planet 909 – 19 July 2019

Boletus pseudopinophilus A.R. Bessette, Bessette, J. Craine & J.L. Frank, *sp. nov.*

Etymology. A combination of the Latin *pseudo* = 'not true, but similar to' and *pinophilus* = 'pine-loving' referring to the close affinity to the pine-loving European species, *Boletus pinophilus*.

Classification — *Boletaceae*, *Boletales*, *Agaricomycetes*.

Medium-sized to large *basidiocarps* with pinkish brown to red-brown caps, white tubes stuffed with hyphae when young becoming yellow to olive-yellow in age, whitish reticulated stipe darkening to light brown as it ages, and white unchanging flesh. *Pileus* 5–16 cm wide, rounded to convex at first, becoming broadly convex to nearly plane in age, margin incurved at first, with a narrow band of sterile tissue, becoming even or undulating at maturity; surface slightly viscid when fresh, becoming dry, subtomentose, smooth, pinkish brown to greyish brown when young, becoming reddish brown and finally dull reddish brown to yellowish brown in age. *Context* thick, firm white, pinkish brown under the pileipellis, unchanging when exposed; *odour* and *taste* not distinctive. *Hymenophore* whitish at first, becoming yellow to olive-yellow, finally brownish yellow, unchanging when bruised. *Pores* stuffed with white hyphae when young, angular, 2–3 per mm; tubes 8–20 mm long, depressed around the stalk in age. *Stipe* 6–12 cm long, 1.5–4 cm thick, club-shaped, enlarged downward, typically with a pinched base, and white basal mycelium. Surface whitish to pale brown at first, darkening in age, dry, conspicuously reticulate overall, reticulum delicate, whitish at the apex and over the upper one third or more, darkening downward toward the base in age or when bruised; negative with the application of NH_4OH. Context firm, solid, white, unchanging when exposed. *Spores* olive-brown in mass, 15.8 × 4.8 (14–18 × 4–6) µm, Q = 3.28, elliptic-fusiform to subfusiform, smooth, yellowish in KOH. Basidia clavate, (2–)4-spored; cheilocystidia not observed; pleurocystidia sparse, 42–60 × 7–9 µm, narrowly fusoid-ventricose, smooth, thin-walled, hyaline in KOH. Pileipellis a trichodermium of interwoven, thin-walled, non-encrusted hyphae, 4–12 µm wide, lacking clamp connections.

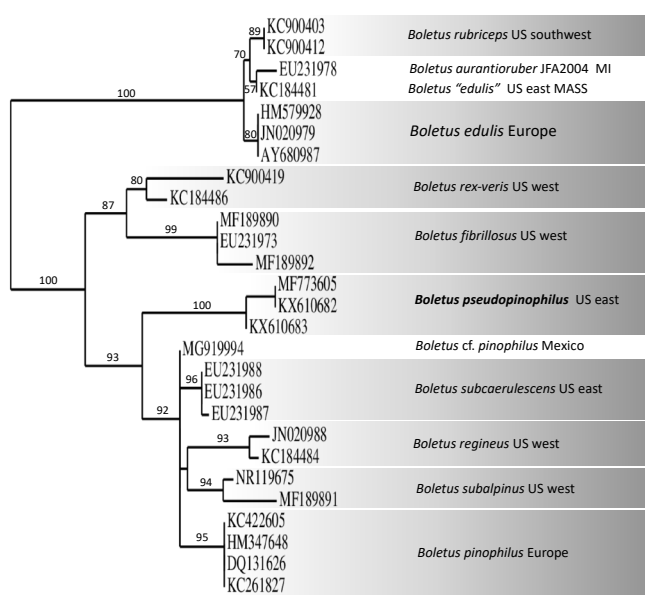
Habit, Habitat & Distribution — Solitary or scattered on the ground under Slash Pine (*Pinus elliottii*) and Longleaf Pine (*Pinus palustris*) along the coastal plains across the south-eastern United States from southern Virginia at lower elevations south and west into Texas. It seems to prefer younger forests and can be common in pine plantations. Fruiting in summer and fall.

Typus. USA, Georgia, Elbert County, near Ruckersville Road, 15 Sept. 2014, *A.R. Besette* (holotype ARB1267, FLAS, ITS and LSU sequences GenBank KX610682 and KX610680, MycoBank MB829952).

Additional material examined. USA, Georgia, Gwinnett County, 11 June 2014, *J. Craine* MO167169 (FLAS), ITS sequence GenBank KX610683; Mississippi, Harrison County, Harrison Experimental Forest, 5 Dec. 1982, *D. Lewis* 3382 (F1132005); Texas, Tyler County, 19 Sept. 1980, *D. Lewis* 2318 (F1101782).

Colour illustrations. Top and bottom right: MO167169 under *Pinus elliottii*, Gwinnett County, GA; bottom left: holotype ARB1267 under *Pinus elliottii* and *Pinus palustris*, Elbert County, GA, USA.

Notes — *Boletus pseudopinophilus* is included in Weber & Smith (1985) and in Bessette et al. (2000, 2007, 2016) as *Boletus pinophilus*, the European name that, prior to molecular studies, was misapplied in North America not only to this south-eastern porcini, but also to the Spring King (*B. rex-veris*) and to the Rocky Mountain Ruby-capped King (*B. rubriceps*) in the western United States. Molecular analysis of ITS rDNA data shows *Boletus pseudopinophilus* to be closely related to, but separate from, *B. pinophilus*, in a strongly supported clade that includes *B. subcaerulescens*, *B. regineus*, *B. subalpinus* and a taxon reported as '*Boletus* cf. *pinophilus*' from Oaxaca Mexico, GenBank MG919994. *Boletus subcaerulescens* is very similar, but typically has more vinaceous tones on the pileus and stipe, a pore surface that stains bluish grey when bruised, a northerly distribution and typically grows with spruce and short-needle pines including Scots Pine (*Pinus sylvestris*), Pitch Pine (*Pinus rigida*) and Jack Pine (*Pinus banksiana*). *Boletus aurantioruber* has a darker, rusty orange pileus, and a pinkish cinnamon to rusty red or red-brown reticulum. It usually grows associated with two and three needle pines such as Jack Pine and Pitch Pine and is more northerly in its distribution, typically found in north-eastern North America. *Boletus separans* grows with oak, has a variable coloured cap that tends to be more vinaceous to pink when young, and a white, finely reticulated stipe. Lilac areas of the pileipellis and stipitipellis of *B. separans* stain aquamarine to deep blue with the addition of NH_4OH. The European *Boletus pinophilus* differs in having a darker reddish brown pileus and grows in coniferous or mixed forests in Europe, mycorrhizal with pines (*Pinus*) or spruce (*Picea*), but has not been verified to occur in North America.



Maximum likelihood tree inferred from ITS nrDNA, using RAxML v. 8 (Stamatakis 2014), showing placement of *Boletus pseudopinophilus* in *Boletus* s.str. Bootstrap support values (> 50 % with 1000 replicates) are shown above branches.

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Botryotrichum foricae

Fungal Planet 910 – 19 July 2019

Botryotrichum foricae Jurjević & Hubka, *sp. nov.*

Etymology. Refers to the restroom (forica) from where the sample was isolated.

Classification — *Chaetomiaceae*, *Sordariales*, *Sordariomycetes*.

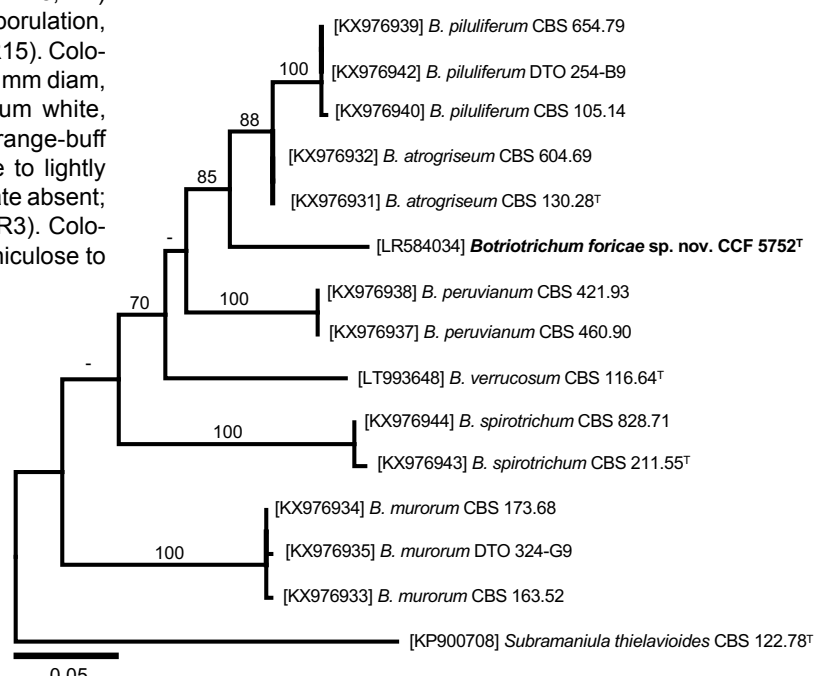
Micromorphology (on malt extract agar; MEA): *Hyphae* hyaline to lightly pigmented, 1.5–4.5 µm diam. *Conidiophores* hyaline to pale yellowish brown, produced laterally from hyphae, commonly sympodially branched, up to 35 µm long, 2–5 µm diam near the base. *Conidiogenous cells* terminal or intercalary, monoblastic or sympodially polyblastic, commonly cylindrical, occasionally with a broad denticle, 0–13 × 2–4 µm, occasionally swollen beneath the conidium. Sterile setae present only on potato carrot agar (PCA) after prolonged cultivation, absent on other media. *Conidia* single, rarely in chains of a few spores, globose to subglobose, occasionally pyriform, hyaline, with age becoming pale brown, smooth, rarely slightly roughened, (7–)8–13(–14.5) µm diam. *Sexual morph* unknown.

Culture characteristics — (in darkness, 25 °C after 7 d): Colonies on MEA (Oxoid) 22–23 mm diam, floccose, moderate deep sulcate, mycelium white to pinkish buff, good sporulation, (R29; Ridgway 1912), exudate absent; reverse warm buff to light ochraceous-buff (R15). Colonies on MEA supplemented with 0.01 % chloramphenicol (Healthlink®, Jacksonville, FL) 44–47 mm diam, floccose, mycelium white, good sporulation, exudate absent; warm buff to ochraceous-orange (R15). Colonies on Czapek yeast autolysate agar (CYA) 58–61 mm diam, floccose, moderate deep to deep sulcate, mycelium white, exudate absent; reverse light orange-yellow to orange-buff (R3). Colonies on PCA 42–50 mm diam, floccose to lightly funiculose, mycelium white, good sporulation, exudate absent; reverse pale yellow-orange to light orange-yellow (R3). Colonies on corn meal agar (CMA) 30–32 mm diam, funiculose to floccose, mycelium white, exudate absent; reverse uncoloured to cream colour (R16). Colonies on modified cellulose agar (MCA) 47–49 mm diam, subsurface or submerged, sporulation not observed. Colonies on oatmeal agar (OA) 45–47 mm diam, floccose to funiculose, mycelium white, exudate absent, reverse faint brown. Colony diam (in mm after 7 d) at 30 °C: MEA 18–20, MEA with chloramphenicol 30–32, CYA 51–54, PCA 29–31, CMA 29–31, MCA 48–50. No growth on MEA, CYA, PCA, CMA and MCA at 37 °C.

Typus. USA, New Jersey, Glenwood, restroom air, Feb. 2015, isol. *Ž. Jurjević* (holotype BPI 910933, culture ex-type CCF 5752 = EMSL 2683; ITS, LSU, SSU and β-tubulin sequences GenBank LR584032, LR584033, LR584031 and LR584034, MycoBank MB830668).

Notes — BLAST analysis with the ITS and β-tubulin sequences of *Botryotrichum foricae* with the reference sequences published by Wang et al. (2016, 2019) showed greatest similarity with *B. atrogriseum* (99.2 % and 95.4 %), *B. piluliferum* (99.2 % and 92.9 %) and *B. peruvianum* (99.4 % and 92.3 %).

Botryotrichum foricae produces on average smaller conidia, (7–)8–13(–14.5) µm diam, compared to *B. piluliferum*, (9–)11–17.5(–18.5) µm diam, *B. peruvianum*, (10–)12–16(–17.5) µm diam and *B. atrogriseum* 10–25 µm diam.



A best scoring maximum likelihood tree based on β-tubulin gene sequences shows the relationships of taxa within the genus *Botryotrichum*. The dataset contained 15 taxa and a total of 416 characters of which 131 were variable and 83 parsimony-informative. Partitioning scheme and substitution models for analyses were selected using PartitionFinder 2 (Lanfear et al. 2017): the TrNef+I model was proposed for 1st codon positions, JC model for the 2nd codon positions, TrN for the 3rd codon positions and K80+G for 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 superscript ^{T} and the novel species in **bold**. The tree is rooted with *Subramaniula thielavioides* CBS 122.78^{T}.

Colour illustrations. Air, restroom. 7-d-old cultures at 25 °C of *Botryotrichum foricae* (from left to right on MEA, CYA, PCA and OA); conidia and conidiophores on MEA. Scale bars = 10 µm.

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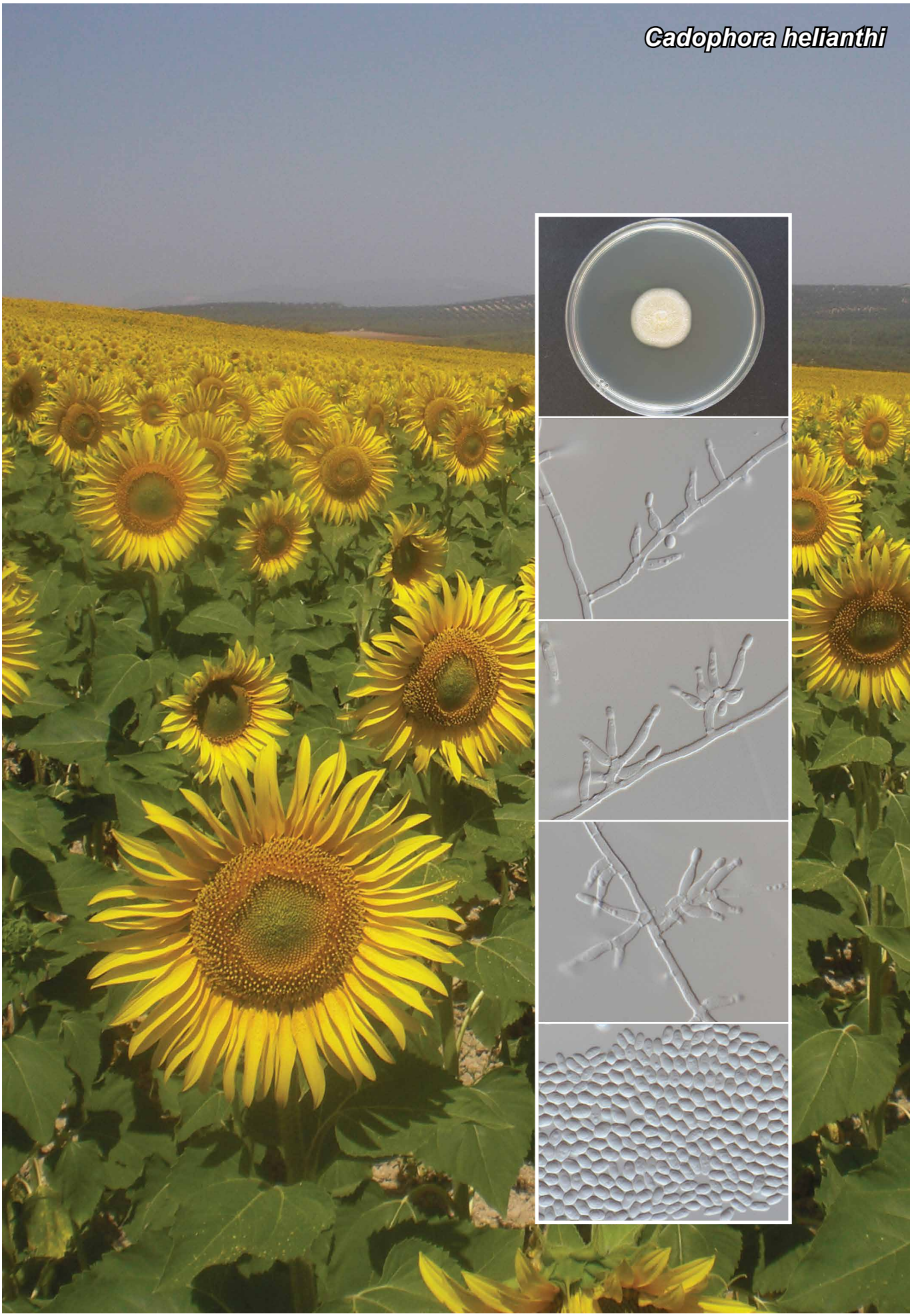

Cadophora helianthi

Fungal Planet 911 – 19 July 2019

Cadophora helianthi L. Molinero-Ruiz, A. Martín-Sanz, C. Berlanas & Gramaje, *sp. nov.*

Etymology. Named after the host genus (*Helianthus annuus*), from which it was isolated.

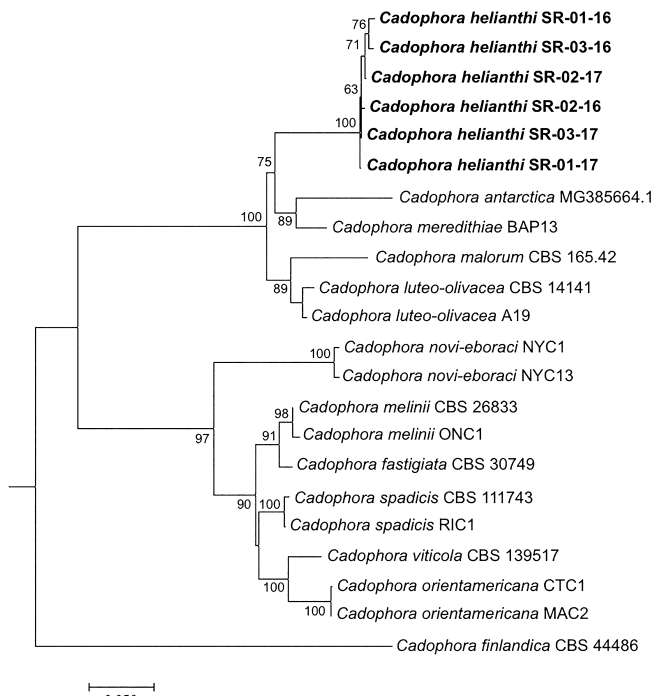
Classification — *Ploettnerulaceae*, *Helotiales*, *Leotiomycetes*.

Mycelium composed of branched, septate hyphae occurring singly or in bundles of up to 10; hyphae tuberculate with warts up to 2.5 µm diam, verruculose to smooth, olivaceous brown, 2.5–3.5 µm diam. *Conidiophores* mostly short, usually branched, arising from aerial or submerged hyphae, erect to flexuous, up to 6-septate, pale brown to brown, (9–)10.5–46(–59) (av. = 23) µm long and 2–3.5 (av. = 2.5) µm wide. *Phialides* terminal or lateral, mostly monophialidic, smooth to verruculose, hyaline, with 1.5–3 µm long, 2–3 µm wide, mostly cylindrical collarettes, some elongate-ampulliform, attenuated at the base or navicular, (4–)6.5–12.5(–14) × 1.5–3(–4) (av. = 7.5 × 2.5) µm. *Conidia* hyaline, with up to 3 guttules, ovoid or oblong ellipsoidal, (3–)3.5–5.5 × 1.5–2.5 (av. = 4.5 × 2) µm, L/W = 2.0.

Culture characteristics — Colonies reached a radius of 14.5–17 mm after 8 d at 25 °C. The minimum temperature for growth was 5 °C, the optimum 20–25 °C and the maximum 30 °C. Colonies on MEA were flat, felty, with an even edge; after 16 d, white to grey olivaceous close to the centre above an in reverse. Colonies on PDA were flat, felty, with an even edge; after 16 d, white to olivaceous buff close to the centre above and in reverse. Colonies on OA were raised with striating furrows, woolly when close to the centre, with an even edge; after 16 d, they were olivaceous to olivaceous buff above. Colours rated according to Rayner (1970).

Typus. Ukraine, Uman, Cherkasi, isolated from necrotic tissues in stems of *Helianthus annuus* showing wilting, 2017, *A. Martín-Sanz* (holotype CBS H-23647, culture ex-type SR-03-16 = CBS 144752, ITS, LSU, beta-tubulin (*Btub*) and translation elongation factor 1-alpha (*tef1*) gene sequences GenBank MF962601, MK813837, MH733391 and MH719029, MycoBank MB827327).

Notes — The genus *Cadophora* is characterised by having pale to hyaline phialidic collarettes with the vegetative hyphae more or less pigmented. The known *Cadophora* species and their relatives occur in many habitats such as decaying wood (Nilsson 1973, Blanchette et al. 2004), soil (Kerry 1990, Hujslová et al. 2010, Agustí-Brisach et al. 2013, Crous et al. 2017) or plants (Halleen et al. 2003, Di Marco et al. 2004, Gramaje et al. 2014, Travadon et al. 2015). *Cadophora helianthi* was previously identified as *C. malorum* based on *Btub* phylogenies, albeit with low statistical support (Martín-Sanz et al. 2018).



Maximum likelihood tree obtained from the ITS, *tef1* and *Btub* gene sequences of *Cadophora* species of our isolates and sequences retrieved from GenBank. The tree was built using MEGA v. 6.0. Bootstrap support values above 70 % are shown at the nodes. The species described here is printed in **bold**. The alignment and tree are available in TreeBASE (Submission ID 23150).

Colour illustrations. *Helianthus annuus* plants growing in a field in Montoro (Andalucía, Spain). 16-d-old colony on PDA; conidiophores and phialides; conidia. Scale bars = 10 µm.

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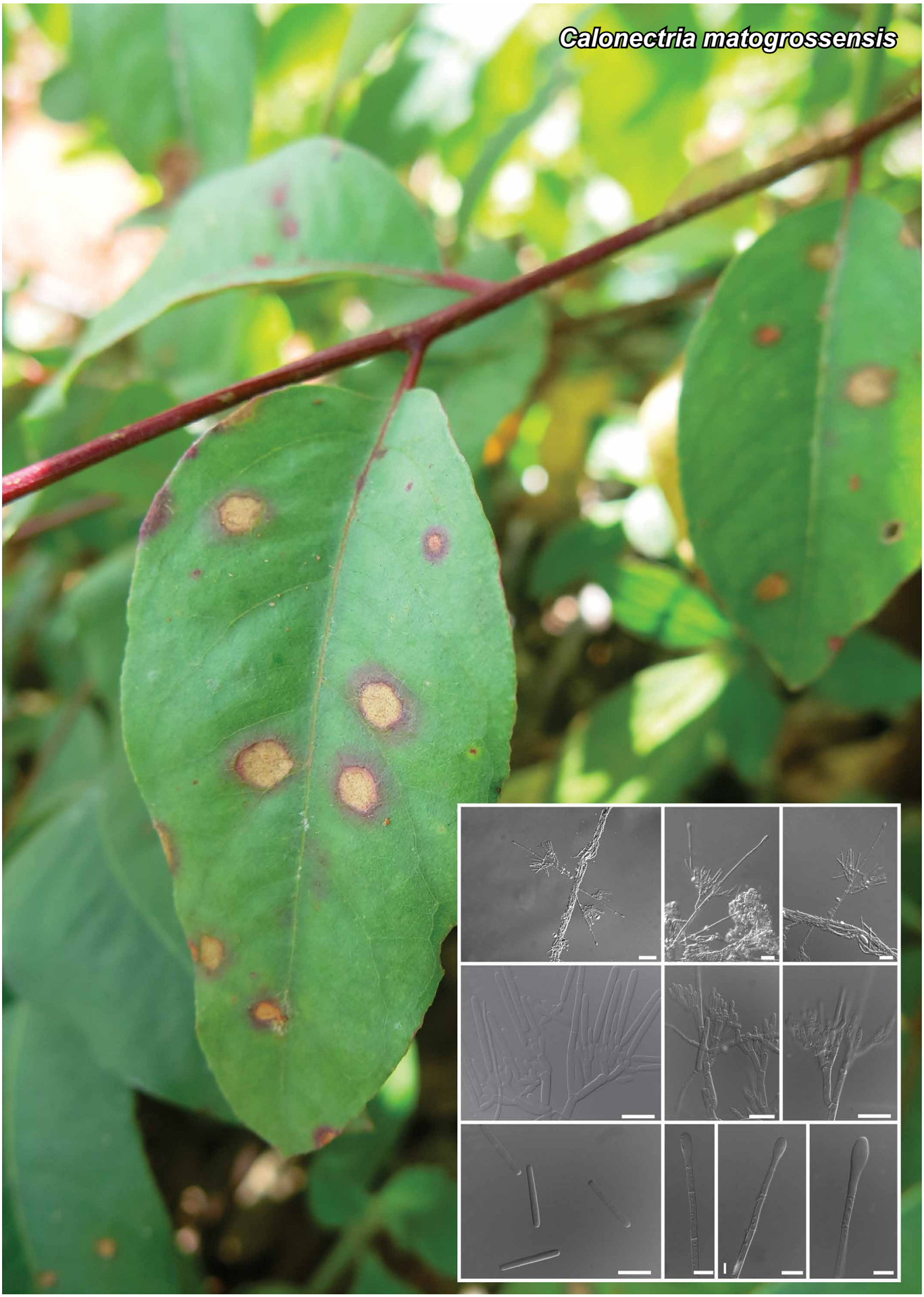

Calonectria matogrossensis

Fungal Planet 912 – 19 July 2019

Calonectria matogrossensis R.A. Fernandes, Alfenas & R.F. Alfenas, *sp. nov*.

Etymology. Name refers to the collection site of the fungus, Mato Grosso, a state in Brazil.

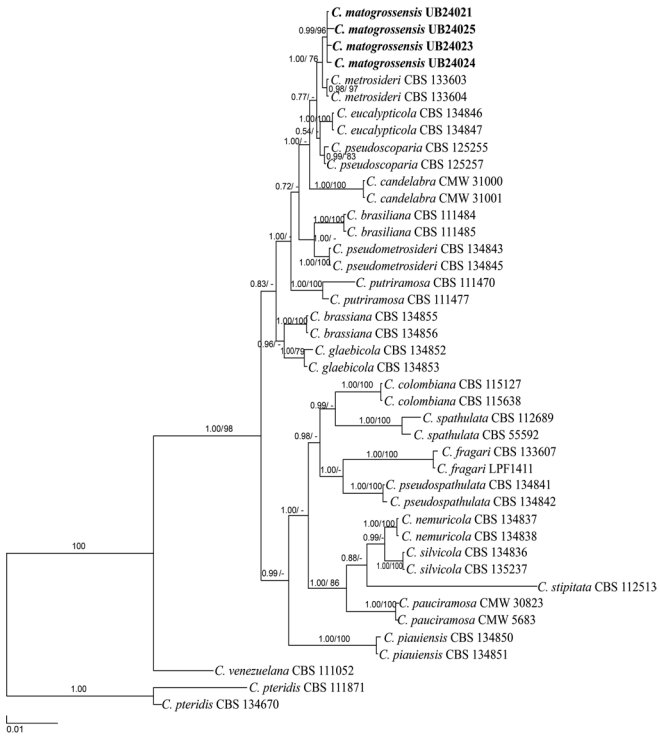
Classification — *Nectriaceae*, *Hypocreales*, *Sordariomycetes*.

Sexual morph not observed. *Macroconidiophores* consisting of a stipe bearing a penicillate arrangement of fertile branches, and stipe extension terminating in a vesicle; stipe septate hyaline, smooth, 113–214 × 2–5 µm; stipe extension septate, hyaline, straight to flexuous, 92–181 µm long, 2–4 µm wide at the apical septum, terminating in a vesicle ellipsoid to obpyriform, 6–9 µm diam, lateral stipe extensions (90° to main axis), septate, straight to flexuous, 77–180 µm long, 2–3 µm wide at the apical septum, terminating in a vesicle ellipsoid to obpyriform, 4–6 µm diam. *Conidiogenous apparatus* 33–100 µm long and 45–100 µm wide; primary branches aseptate, 17–30 × 3–6 µm; secondary branches, aseptate, 12–26 × 3–5 µm; tertiary branches, aseptate, 6–16 × 3–5 µm; additional branches 7–10 × 3–4 µm, each terminal branch producing 2–4 phialides, doliiform to reniform, hyaline, aseptate, 10–17 × 3–5 µm, apex with minute periclinal thickening and inconspicuous collarette. *Macroconidia* cylindrical, rounded at both ends, straight, (42–)47–50 × (3.5–)4–5 µm (av. 47 × 4 µm), 1-septate, lacking a visible abscission scar, held in parallel cylindrical clusters by colourless slime. *Mega-* and *microconidia* not observed.

Culture characteristics — Colonies fast growing at 26 °C on MEA (50–55 mm after 7 d), producing abundant white mycelium and sporulating on the medium surface; culture with colour blight brown to dark brown after 7 d; chlamydospores abundant throughout the medium, forming microsclerotia.

Typus. Brazil, Mato Grosso, Primavera do Leste, on leaves of *Eucalyptus urophylla* clone I144 (*Myrtaceae*), 2015, *R.A. Alfenas* (holotype UB24025, *tef-1α*, *cmdA*, *his3* and *tub2* sequences GenBank MH837659–MH837663, MH837653–MH837658, MH837648–MH837652 and MH837664–MH837669, MycoBank MB829570).

Notes — *Calonectria matogrossensis* is a new member of the *Ca. candelabra* complex (Alfenas et al. 2015). Morphologically and phylogenetically it can be distinguished from other species of the *Ca. candelabra* complex. Phylogenetically, *Ca. matogrossensis* forms a well-support clade (0.99 for Bayesian probability posterior and 96 % for maximum likelihood bootstrap support), closely related but separate from *Ca. metrosideri*, *Ca. eucalypticola* and *Ca. pseudoscoparia*. Morphologically, it differs from its nearest neighbours in having lateral stipe extensions. *Calonectria piauienses* is morphologically similar to *Ca. matogrossensis*, but it has smaller conidia, and the species are phylogenetically distant.



Maximum likelihood tree obtained from the combined DNA sequences of *tef-1α*, *tub2*, *cmdA* and *his3* of the *Calonectria candelabra* complex. Bootstrap support values from Maximum Likelihood (RAxML-HPC v. 8.2.10) and Bayesian (MrBayes v. 3.2.4) posterior probabilities, respectively, are indicated at the nodes. The new species is indicated in **bold**. The tree was rooted to *Ca. pteridis* (CBS 111871 and CBS 134670).

Table Distinctive morphological characters of *Calonectria* species closely related to *C. matogrossensis*.

Species	Conidiogenous apparatus		Stipe extension	Vesicle		Lateral vesicle	Macroconidia size (µm)	References
	Size	Branches (µm)		Diam (µm)	Shape			
C. eucalypticola	45–75 × 35–62	3	145–170 × 2–4	5–7	ellipsoidal to obpyriform	absent	(43–)49–52(–55) × 3–5	Alfenas et al. (2015)
C. metrosideri	60–75 × 40–65	4	90–170 × 2–4	5–9	spathulate to obpyriform	absent	(40–)44–46(–51) × 3–5	Alfenas et al. (2013)
C. pseudoscoparia	52–74 × 34–87	4	124–201 × 4–6	6–10	obpyriform to ellipsoidal	absent	(41–)45–51(–52) × 3–3	Lombard et al. (2010)
C. matogrossensis	33–99 × 45–100	3(–4)	113–214 × 2–5	6–9	ellipsoidal to obpyriform	present	(42–)47–50 × (3.5–)4–5	This study

Colour illustrations. Leaves of *Eucalyptus urophylla*. *Calonectria matogrossensis* (ex-type UB24025): macroconidiophores (scale bars = 50, 20, 20 µm); conidiogenous apparatus with conidiophore branches and phialides; macroconidia (scale bars = 20 µm); ellipsoidal to obpyriform vesicles (scale bars = 10 µm).

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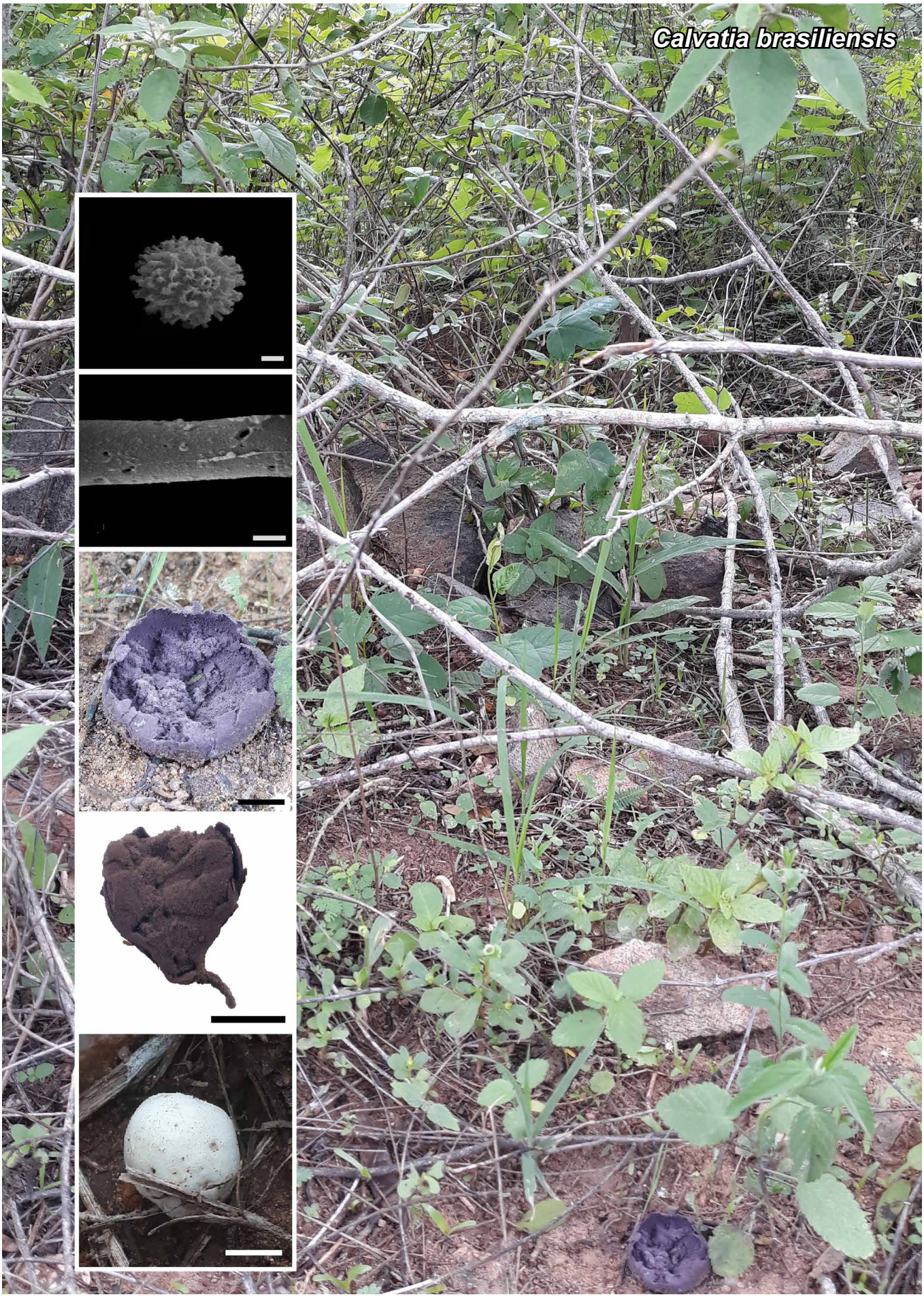
Calvatia brasiliensis

Fungal Planet 913 – 19 July 2019

Calvatia brasiliensis R.J. Ferreira, R.L. Oliveira, B.D.B. Silva, M.P. Martín & Baseia, *sp. nov.*

Etymology. In reference to the country where this species was collected.

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

Basidiomata growing solitary or in small groups, pyriform to subglobose, 19–37 mm wide × 27–29 mm high. *Exoperidium* subtomentose, evanescent, greyish yellow (1B3 and 1B4, Kornerup & Wanscher 1978), at the base with sand encrusted at maturity. *Mesoperidium* papery, dark brown, greyish brown to violet brown (9F4, 9F6, 10E3, 10E4) at maturity. *Endoperidium* papyraceous in the outer surface and tomentose in the surface inner, fragile and dark brown to violet brown (6F4, 10F4, 10F5). *Rhizomorphs* brown (7E4) densely encrusted with sand. *Subgleba* reduced, compact, occupying a third of the basidioma, when mature greyish yellow (4B3). *Gleba* lanose, greyish brown to violet brown (10E3, 10E4, 10F5), at maturity. *Exoperidium* composed of hyphae measuring 3.2–6.4 µm diam, with regular walls ≤ 1.0 µm thin, straight, septate and rarely branched, hyaline in 5 % KOH, and dextrinoid (low reaction). *Mesoperidium* pseudoparenchymatous composed of cells measuring 13–18.6 × 10.7–14.1 µm diam, with regular walls ≤ 0.56 thin, hyaline in 5 % KOH, and non-dextrinoid. *Endoperidium* with hyphae measuring 2.7–4.6 µm diam, with regular walls ≤ 0.8 µm thin, straight, branched, non-septate, brown in 5 % KOH, and non-dextrinoid; in the apical portion, mycosclereids globose, subglobose, pyriform, ovoid, ellipsoid or rectangular in shape, 13.5–42 µm × 7.4–15.7 µm diam, with regular walls ≤ 0.9 µm thick, and straight. *Hyphae of the rhizomorphs* 2.1–3.5 µm diam, regular walls, ≤ 0.7 µm thin, curved, branched, non-septate, hyaline in 5 % KOH, and dextrinoid. Subgleba with hyphae measuring 2.5–3.8 µm diam, with regular walls ≤ 1.0 µm thin, curved, branched, septate, hyaline in 5 % KOH, and dextrinoid. *Paracapillitium* absent. *Capillitium Lycoperdon*-type, elastic, hyphae 2.3–4.1 µm diam with regular walls ≤ 1.02 µm thin, straight, frequently branched, septate, with small and numerous circular pits, hyaline in 5 % KOH, dextrinoid (low reaction). *Basidiospores* globose to subglobose, equinulated, 5.8–6.6 × 5.2–6.5 µm (av. = 6.1 ± 0.3 × 5.9 ± 0.3; Qm (medium coefficient) = 1.04; n (measurement numbers) = 20), pedicels present in some spores, ≤ 0.89 µm, brown in 5 % KOH, non-dextrinoid and acyanophilic.

Habit & Habitat — Basidiomata growing solitary or in pairs on moist soil.

Typus. Brazil, Rio Grande do Norte, João Câmara, Serra do Torreão, near trail, soil, 17 Feb. 2017, *R.L. Oliveira* (holotype UFRN-Fungos 3039, ITS and LSU sequences GenBank MK660463 and MK660493, MycoBank MB830236).

Additional materials examined. Brazil, Rio Grande do Norte, João Câmara, Serra do Torreão, near trail, soil, 20 Feb. 2019, *R.L. Oliveira* (UFRN-Fungos 3115); ibid., 20 Feb. 2019, *R.L. Oliveira* (UFRN-Fungos 3116).

Notes — *Calvatia brasiliensis* is a typical species of sect. *Hippoperdon* (Kreisel 1992). Based on morphological and molecular characters, it is close to some other *Calvatia* species, such as *Calvatia cyathiformis*, *C. lilacina*, *C. fragilis* and *C. caatinguensis*. *Calvatia cyathiformis* has a cellular and well-developed subgleba, gleba powdery, verrucose to echinate basidiospores, and capillitium with short and branched hyphae with numerous circular pits (Dissing & Lange 1962, Zeller & Smith 1964), characteristics not found in *Calvatia brasiliensis. Calvatia fragilis* has an extremely powdery and dark brown gleba; reduced subgleba; *Calvatia*-type capillitium, with hyphae with numerous small circular pits and numerous septa; basidiospores smaller (4.0–5.5 µm) with finely equinulated to columnar ornamentation (Morgan 1890, Silveira 1943). *Calvatia lilacina* has morphological characters close to *C. brasiliensis*; but *C. lilacina* shows a distinct colour band at the apex of the well-developed cellular subgleba, and smaller spores (3–5 µm) (Bottomley 1948). *Calvatia caatinguensis*, a species recently described in Crous et al. (2018a) has similar morphological characteristics to *C. brasiliensis*, such as a violaceous gleba, tomentose endoperidium, and when mature, marked incrustations in basal exoperidium; however, *C. caatinguensis* has a well-developed subgleba occupying two-thirds of the basidioma, and with a distinct colour band at the apex. Morphological and molecular data (ITS nrDNA) provide strong support for considering *C. brasiliensis* as a good and new species.

Colour illustrations. Brazil, Rio Grande do Norte, João Câmara, Serra do Torreão, where the specimens were collected. From bottom to top: immature basidiome *in situ* (UFRN-Fungos 3116); longitudinal section through mature basidiome (UFRN-Fungos 3039); mature basidiome *in situ* (UFRN-Fungos 3115); basidiospores under SEM (UFRN-Fungos 3039); capillitium under SEM (UFRN-Fungos 3039). Scale bars = 10 mm (others), 1 µm (SEM images).

Supplementary material

FP913 ITS nrDNA phylogenetic tree obtained with MrBayes v. 3.1.2 (Huelsenbeck & Ronquist 2001) under T92+G model for 5 M generations. The new species is marked with a rectangle. The posterior probabilities greater than 0.9 are indicated on the branches. *Bovista paludosa* was included as outgroup. Figtree v. 1.42 and Adobe Illustrator CS5 software were used to edit the final tree.

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Carcinomyces nordestinensis

Fungal Planet 914 – 19 July 2019

Carcinomyces nordestinensis D.A. Andrade, C.R. Félix, F.S. Bomfim, R.P. Neves & Landell, *sp. nov*.

Etymology. Name refers to the Brazilian region, Nordeste (in Portuguese), where all yeast isolates were obtained.

Classification — *Carcinomycetaceae*, *Tremellales*, *Tremellomycetes*.

On YEPD agar after 3 d at 22–25 °C, cells are globose to subglobose (3–5 × 1.5–3.5 µm), and colonies are cream to pale pink, mucoid and glistening. *Vegetative reproduction* is by multipolar budding. After 3 wk in Dalmau plate culture on cornmeal agar, pseudohyphae are formed. *Sexual reproduction* is not observed. *Ballistoconidia* production is absent. *Fermentation ability* is negative. The following *carbon compounds* are assimilated: N-Acetyl-D-glucosamine, L-arabitol, cellobiose, erythritol, galactose, melezitose, raffinose, soluble starch, sucrose, D-arabinose (slow), L-arabinose (slow), inulin (slow), galactorunote (slow), D-glucose (slow), glycerol (slow), lactose (slow), maltose (slow), D-mannitol (slow), melibiose (slow), myo-Inositol (slow), D-ribose (slow), trehalose (slow), xylitol (slow), D-xylose (slow), galactitol (variable), D-glucitol, (variable), succinate (variable), L-rhamnose (weak). No assimilation of citrate, gluconate, DL-lactate, salicin, tween 20, tween 80. Assimilation of nitrogen compound are L-lysine (slow) and potassium nitrate (weak). No assimilation of sources nitrogen of creatine, creatinine, sodium nitrite, ethylamine and cadaverine. Growth at 22, 25 and 30 °C and no growth at 35 °C. Growth was not observed on YEPD with 50 % glucose, in the 10 % sodium chloride and 1 % in the acetic acid. After 21 d, growth was observed in the presence of 0.01 % cycloheximide and in 0.1 % no growth was observed. Urease activity and diazonium blue B reaction are positive. No starch formation.

Typus. Brazil, Santana do Ipanema municipality, Alagoas state, Private Reserve of Natural Heritage (S9°21'49" W37°14'54") as epiphytic yeast on leaves of *Bromelia antiacantha* (*Bromeliaceae*), 11 Sept. 2017, *C.R. Félix & M.F. Landell* (holotype as metabolically inactive culture, UFMG-CM-Y6457, LSU and ITS sequences GenBank MH909022 and MK659873, MycoBank MB830322); isotype as metabolically inactive culture URM 8088 = CBS 15981 = BRT 317.

Additional materials examined. Brazil, Recife municipality, Pernambuco state, Federal University of Pernambuco campus (S8°03'02.30" W34°56'54.41") as endophytic yeast from the medicinal plant *Handroanthus impetiginosus* (*Bignoniaceae*), 20 Jan. 2013, *F.S. Bomfim* (cultures URM 7675, URM 7676, URM 7677 and isolate 20F, ITS sequences GenBank MK792995, MK792959, MK792960, MK792965, and LSU sequences GenBank MK792962, MK792963, MK800011, MK792964, respectively).

Colour illustrations. *Bromelia antiacantha* in the Private Reserve of Natural Heritage, Santana do Ipanema, Alagoas, Brazil. Microscopy showing the colony macromorphology and yeast microstructures. Scale bar =10 µm.

Notes — *Carcinomyces nordestinensis* is proposed as new species based on phylogenetic analysis, physiological and biochemical features. The strains had 100 % identity in the LSU and between 98–100 % in the ITS region (0–4 substitutions). Phylogenetic inferences of LSU (D1/D2 domain) and ITS rDNA sequences indicated *Carcinomyces arundinariae* (CBS 9931) as the closest species. According to BLASTn searches (9 Apr. 2019) the **LSU** rDNA sequences have 98.6 % identity to *C. arundinariae* (CBS 9931, GenBank NG_058990; 7 nucleotide substitutions), 97 % to sequences deposited as *Carcinomyces* sp. (BPT 70, GenBank KY305115; 19 nucleotide substitutions) 96.8 % to *Bullera* sp. (TO 115, GenBank KJ156986; 18 nucleotide substitutions), and 96.07 % to *Bullera* sp. (BI 335, GenBank EU678937; 17 nucleotide substitutions). The closest hits using **ITS** sequences are 95.1 % identity to *C. arundinariae* (CBS 9931, GenBank NR_077092; 22 nucleotide substitutions), 86.1 % to *Bullera* sp. (TO 115, GenBank KJ156987; > 50 nucleotide substitutions) and 85.8 % to *Carcinomyces* sp. (BPT 70, GenBank KY305146; 64 nucleotide substitutions). *Carcinomyces nordestinensis* differs physiologically and biochemically from *C. arundinariae* by inulin and glycerol assimilation and no assimilation of salicin and citrate (Kurtzman et al. 2011, Liu et al. 2015a).

Supplementary material

FP914-1 Phylogenetic placement of *Carcinomyces nordestinensis* was obtained by neighbour-joining (Kimura two-parameter distance method) analysis of the LSU (D1/D2 domains) rRNA gene using MEGA v. 7 (Kumar et al. 2016). Bootstrap support values higher than 50 % are shown (1000 replicates). The novel species is indicated in **bold** and type cultures with a superscript ^{T}. The tree was rooted to *Rhodotorula glutinis*. Bar = 0.02 substitutions per nucleotide position.

FP914-2 Phylogenetic placement of *Carcinomyces nordestinensis* was obtained by neighbour-joining (Kimura two-parameter distance method) analysis of the ITS region using MEGA v. 7 (Kumar et al. 2016). Bootstrap support values higher than 50 % are shown (1000 replicates). The novel species is indicated in **bold** and type cultures with a superscript ^{T}. The tree was rooted to *Rhodotorula glutinis*. Bar = 0.02 substitutions per nucleotide position.

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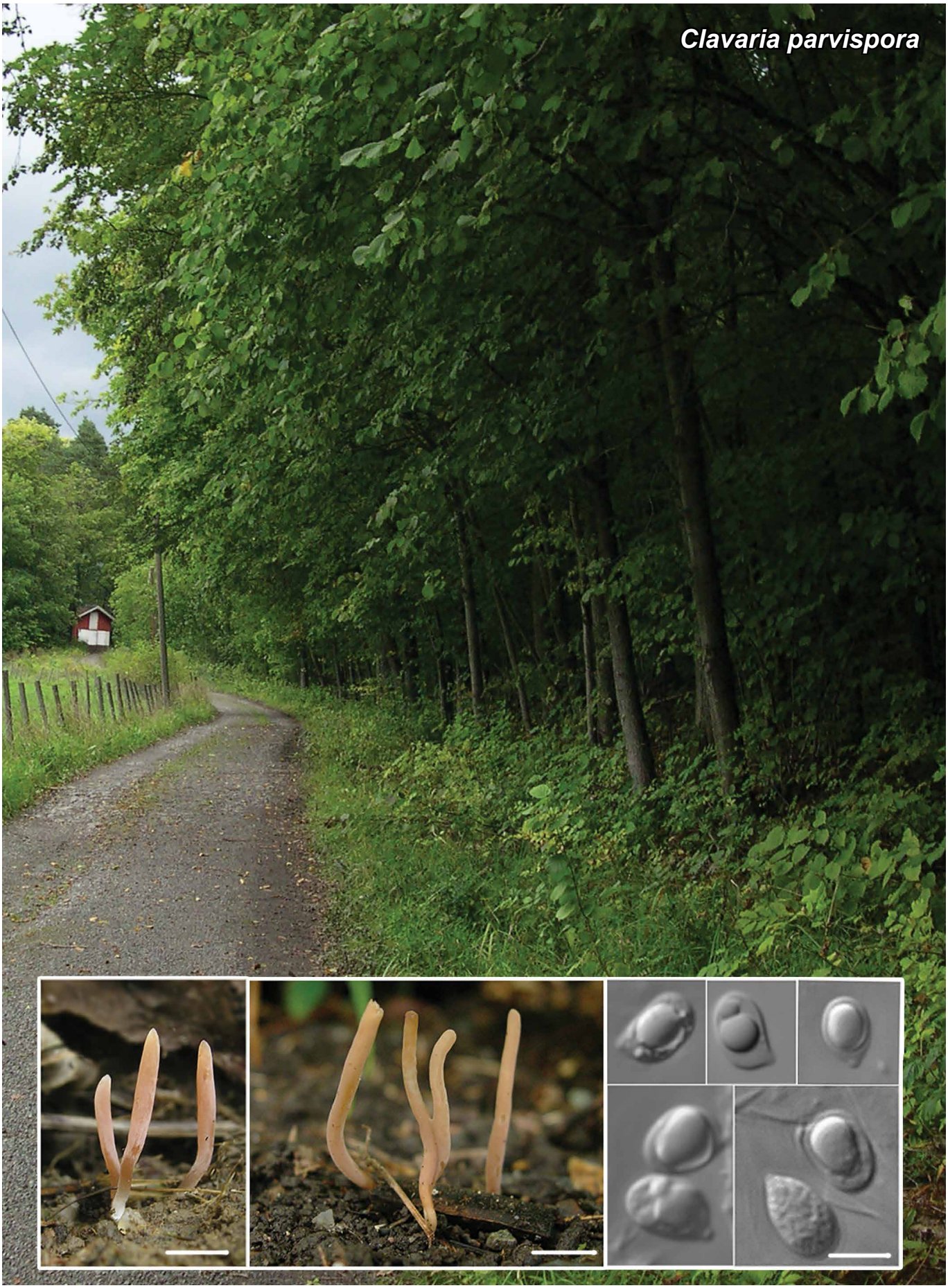

Clavaria parvispora

Fungal Planet 915 – 19 July 2019

Clavaria parvispora Kautman., Majerová & Olariaga, *sp. nov*.

Etymology. Name refers to the spore size, which is the smallest among pink-coloured *Clavaria* species.

Classification — *Clavariaceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata gregarious or in small clumps of 2–5 basidiomata, rarely solitary, 5–20(–30) mm long, simple, with well-delimited, but quite short stipe (up to 3 mm). *Clavula* 5–25 × 0.5–1.5 mm, cylindrical, smooth, tomentose, pale pink (Pantone 162UP), darkening upon drying (Pantone 190UP). Apex obtuse and paler, almost white in young basidiomata. *Stipe* 2–3 × 1–1.5 mm, cylindrical, smooth, silky, yellowish (Pantone 7508C) with white, tomentose basal mycelium. *Context* watery, yellowish, *taste* mild, *smell* indistinctive. Reaction with $FeCl_3$ positive, blackening, slow after 3–5 min. *Basidiospores* ellipsoid to broadly ellipsoid, thin-walled, smooth, hyaline, non-amyloid, usually with one big vacuole, 5.2–6.1(–6.4) × 3.8–4.3 µm (Lm = 5.8; Wm = 4.0; Qm = 1.41). *Apiculus* short, up to 0.5 µm. *Ornamentation* of spores not observed. *Basidia* claviform, 4-spored, with a loop-like basal clamp, 28–35 × 2.5–4 µm. *Cystidia* absent. *Subhymenium* 25–35 µm thick, formed by densely interwoven hyphae, cylindrical to inflated, thin-walled, clampless, 2.0–3.5 µm broad. *Context* hyphae parallel, inflated, thin-walled, secondarily septate, hyaline, smooth, clampless, 10–20 µm wide, mostly (20–)70–100 µm long. Basal mycelium white, composed of interwoven hyphae, cylindrical, thick-walled, scarcely septate, hyaline, clampless, 1–2 µm wide.

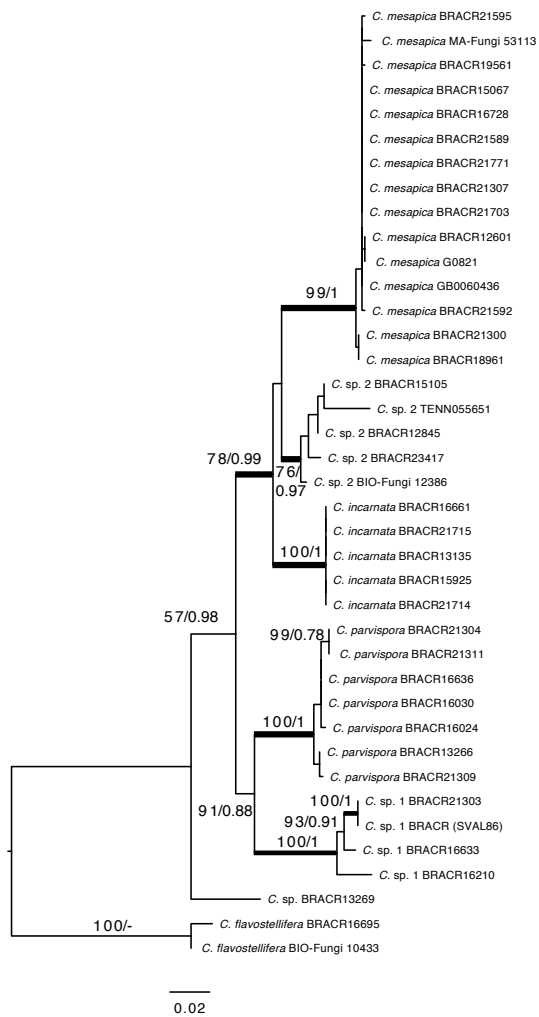
Distribution — Known from Slovakia, Czech Republic and Norway, probably more widespread but overlooked. Preferred habitat is probably represented by bare soil and mosses under shrubs in outgrown pastures and semi-natural grasslands.

Typus. Norway, Oslo, Bygdøy, Dronningberget Nature Reserve, in deciduous trees and shrubs along the old outgrown forest road, in bare soil and mosses, N59.914164 E10.683094, alt. 10 m, 7 Sept. 2009, *I. Kautmanová* (holotype BRA CR13266, LSU sequence GenBank MH727523, MycoBank MB828902).

Additional materials examined. Slovakia, Považský Inovec Mts, Banka village, in shrubs (*Prunus spinosa*, *Crataegus* sp., *Corylus avellana*) in outgrown pasture, among mosses on bare soil, alt. 230 m, 26 Sept. 2014, *V. Kučera*, BRA CR 21309, LSU sequence GenBank MH727524; Žilinská kotlina Basin, Žilina, in city park in meadow, alt. 450 m, 18 Oct. 2008, *L. Jánošík*, BRA CR16030, LSU sequence GenBank JQ415937; Podtatranská kotlina Basin, Hybe village, under shrubs (*Prunus spinosa*, *Rosa* sp.,*Corylus avellana*) in old orchard, on bare soil, alt. 810 m, 15 Aug. 2008, *I. Kautmanová*, BRA CR16024, LSU sequence GenBank JQ15936; ibid., 12 Aug. 2011, *I. Kautmanová*, BRA CR16636, LSU sequence GenBank MH727522; Javorníky Mts, Trenčín, Zlatovce, in bare soil in shrubs (*Crataegus* sp., *Corylus avellana*, *Prunus spinosa*) in outgrown pasture, alt. 230 m, 17 Sept. 2014, *V. Kautman*, BRA CR 21304, LSU sequence GenBank MH727520; ibid., 17 Sept. 2014, *V. Kautman*, BRACR 21311, LSU sequence GenBank. MH727521.

Notes — *Clavaria parvispora* differs from other pink-coloured species of the *Clavaria* subg. *Holocoryne* by small broadly ellipsoid spores. *Clavaria mesapica* is characterised by much larger basidiomata (up to 7 cm tall), which are pale pink, drying to pale cream colour without pink tones, hymenial cystidia and ellipsoid to almost rhomboid spores 7.2 × 5.2 µm. Spore ornamentation frequently observed in *C. mesapica* and other pink *Clavaria* subg. *Holocoryne* species, was not found in any of the *C. parvispora* specimens.

In the ML tree based on the LSU alignment *C. parvispora* sequences are grouped in a well-supported clade, although showing a certain degree of sequence divergence. Other clades represent three species of the *Clavaria incarnata* complex, where *Clavaria* sp. 1 is probably an undescribed species characterised by big spores (up to 9.5 × 6.5 µm), *Clavaria* sp. 2 possesses typically a high proportion of ornamented spores and is probably conspecific with *Clavaria stellifera*, and the third species can be attributed to *C. incarnata* s.str.



Bayesian inference 50 % majority rule consensus phylogram of *Clavaria incarnata* group from LSU sequence data constructed by MrBayes 3.2.6 (Ronquist et. al. 2012). Bayesian posterior probabilities (PP) ≥ 95 % and Maximum Likelihood bootstrap values (ML-BP) ≥ 70 % are shown at the nodes (ML-BP / PP). Thickened branches received support by both analyses. The tree was rooted to *C. flavostellifera*.

Colour illustrations. Type locality of *Clavaria parvispora* in Oslo, Norway. Type specimen *in situ* (Photo credit: I. Kautmanová); collection from Slovakia, Žilina (Photo credit: L. Jánošík); basidiospores. Scale bars = 1 cm (macromorphology), 5 µm (spores).

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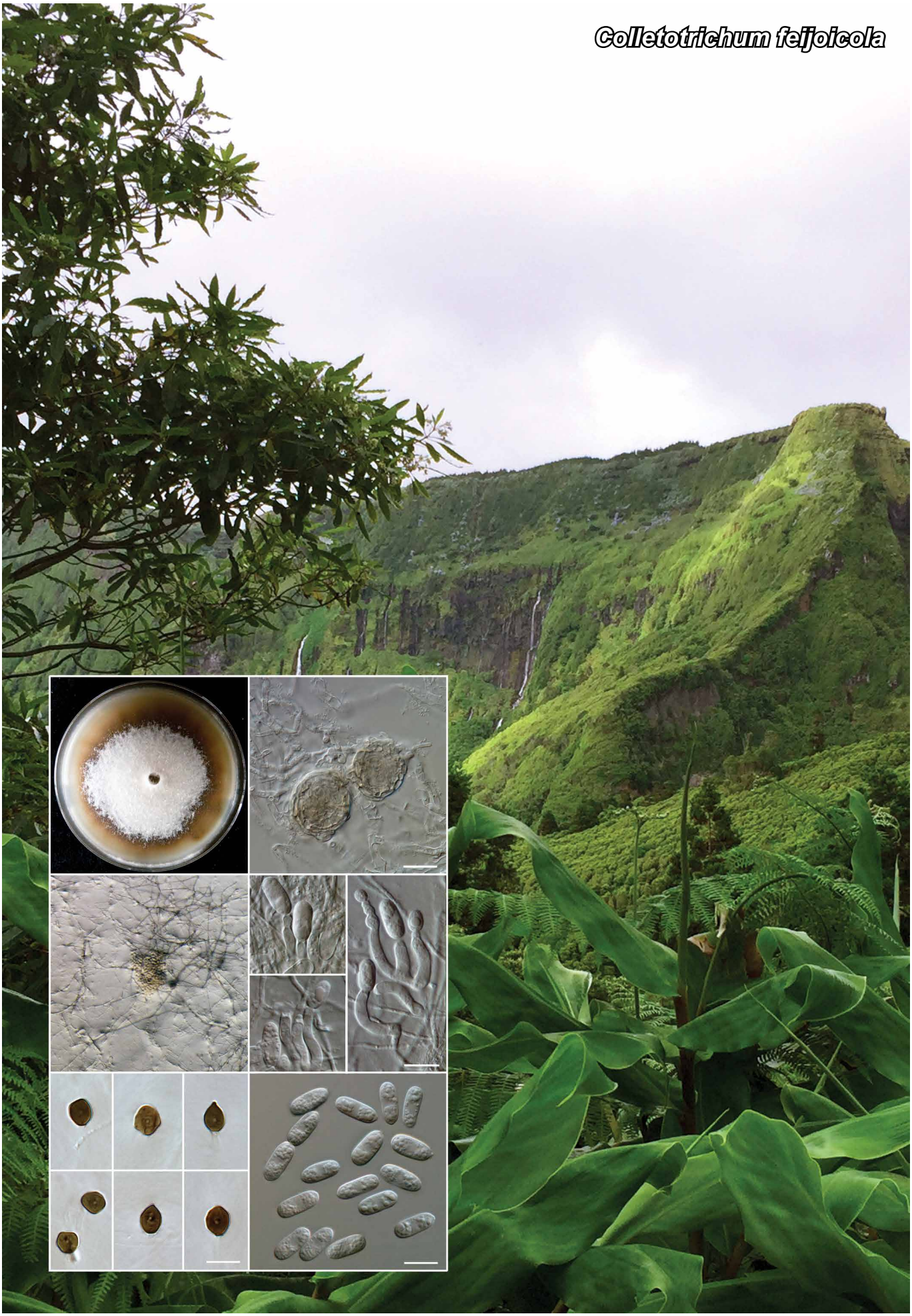
Colletotrichum feijoicola

Fungal Planet 916 – 19 July 2019

Colletotrichum feijoicola Guarnaccia & Damm, *sp. nov.*

Etymology. Name refers to feijoa, the host plant from which this fungus was collected.

Classification — *Glomerellaceae*, *Glomerellales*, *Sordariomycetes*.

Sexual morph not observed, but pale brown, subglobose, glabrous immature ascomata formed after > 3 wk on SNA, 20–65 µm diam. *Asexual morph on SNA. Vegetative hyphae* 1–8.5 µm diam, hyaline, smooth-walled, septate, branched. *Chlamydospores* not observed. *Conidiomata* absent, conidiophores and setae formed directly on hyphae. *Setae* not observed. *Conidiophores* hyaline, smooth-walled, septate, branched, to 30 µm long. *Conidiogenous cells* hyaline, smooth-walled, cylindrical to clavate, sometimes flexuous, sometimes extending to form new conidiogenous loci, 5.5–21 × 3–4 µm, opening 1.5–2.5 µm diam, collarette 1–1.5 µm long, periclinal thickening distinct. *Conidia* hyaline, smooth-walled, aseptate, straight, cylindrical, with round ends, already germinating and becoming septate after 10 d, (11.5–)12–14(–15) × (4.5–)5–5.5 µm, mean ± SD = 12.9 ± 0.9 × 5.1 ± 0.3 µm, L/W ratio = 2.5. *Appressoria* single or in loose groups, pale to medium brown, smooth-walled, bullet-shaped, navicular, subsphaerical, ovoidal to irregular in outline, with an entire, undulate to lobate margin, (6.5–)8.5–13(–17) × (4.5–)6–9.5(–12.5) µm, mean ± SD = 10.6 ± 2.3 × 7.7 ± 1.7 µm, L/W ratio = 1.4. No sporulation on *Anthriscus* stem or OA. Strain GMLC 1898 remained sterile.

Culture characteristics — (near UV light with 12 h photoperiod, 20 °C after 10 d): Colonies on SNA flat with entire margin, hyaline to saffron, filter paper partly pure yellow, filter paper and *Anthriscus* stem covered with white felt-like aerial mycelium, reverse same colours; growth 23.5–28 mm in 7 d (34.5–39 mm in 10 d). Colonies on OA flat with entire to undulate margin; buff, pale luteous, saffron, apricot to dark brick, partly covered with white felt-like aerial mycelium, reverse buff, pale luteous, saffron, cinnamon to dark brick, growth 27.5–32.5 mm in 7 d (37.5– ≥ 40 mm in 10 d). *Conidia in mass* not observed.

Typus. Portugal, Azores Islands, Sao Miguel, from a leaf spot of *Acca sellowiana* (feijoa, *Myrtaceae*), 17 July 2017, *V. Guarnaccia* (GML-F116096 holotype, culture ex-type CBS 144633 = GMLC 1899 = CPC 34246; *act*, *gapdh*, ITS, LSU and *tub2* sequences GenBank MK876466.1, MK876475.1, MK876413.1, MK876420.1 and MK876507.1, MycoBank MB830862).

Additional material examined. Portugal, Azores Islands, Sao Miguel, from a leaf spot of *A. sellowiana*, 17 July 2017, *V. Guarnaccia*, GML-F116095, culture GMLC 1898 = CPC 34245; *act*, *chs-1*, *gapdh*, *his3*, ITS, LSU and *tub2* sequences GenBank MK876465.1, MK876471.1, MK876474.1, MK876477.1, MK876414.1, MK876421.1 and MK876506.1.

Colour illustrations. Forest in Azores Islands, Sao Miguel, where the species was collected. Left: colony on PDA; conidiomata; appressoria; right: immature ascomata; conidiophores; conidia. Scale bars = 10 µm.

Notes — *Acca sellowiana* is native to South America and is grown as an ornamental plant or for its tropical fruit production in Europe, where cultivation is affected by fungal pathogens such as *Calonectria* spp. (Guarnaccia et al. 2014). *Colletotrichum feijoicola* was found associated with reddish leaf spots of *A. sellowiana* cultivated in a small orchard in Sao Miguel, the main island of the Azores archipelago.

No *Colletotrichum* species has previously been described from *Acca* spp. and none was reported on *Acca* spp. in Europe (Farr & Rossman 2018). However, there are three previous reports of *Colletotrichum* spp. on *A. sellowiana* from other regions: *C. gloeosporioides* in Uruguay (Bettucci et al. 2004), *C. siamense* in Brazil (Fantinel et al. 2017) and *C. theobromicola* in New Zealand (Weir et al. 2012); all of these species belong to the *C. gloeosporioides* species complex. However, the report of *C. gloeosporioides* in Uruguay is unreliable as the study was conducted prior to the revision of the *C. gloeosporioides* species complex (Weir et al. 2012), and could refer to probably any *Colletotrichum* species with cylindrical conidia and rounded ends including species e.g. in the *C. boninense*, *C. gloeosporioides* and *C. orchidearum* species complexes (Damm et al. 2012, 2019, Weir et al. 2012).

In contrast to these reports, BLASTn searches with ITS, LSU, *act*, *tub2* and *gapdh* sequences of *C. feijoicola* in NCBIs GenBank nucleotide database restricted to ex-type strains resulted in different species of the *C. boninense* species complex: 98 % similarity with *C. oncidii* and *C. colombiense* (CBS 129828 and CBS 129818; Damm et al. 2012) using ITS, 99 % with *C. hippeastri* (CBS 125376; Vu et al. 2019) using LSU, 96 % with *C. camelliae-japonicae* and *C. annellatum* (LC6416 and CBS 129826; Hou et al. 2016, Damm et al. 2012) using *act*, 97 % with *C. annellatum* (CBS 129826; Damm et al. 2012) using *tub2* and 90 % with *C. petchii* (CBS 378.94; Damm et al. 2012) using *gapdh*.

Based on these results we regard the strains from *A. sellowiana* as a new species belonging to the *C. boninense* species complex. Several *Colletotrichum* species are known as pathogens of various plants mainly in tropical and subtropical regions of the world; some of them have recently been reported as pathogens of other tropical fruit trees in Europe (Guarnaccia et al. 2016). Thus, *C. feijoicola* should be considered as a potential threat for fruit production.

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Coniochaeta dendrobiicola

Fungal Planet 917 – 19 July 2019

Coniochaeta dendrobiicola Sujit Shah, *sp. nov*.

Etymology. Name reflects the host genus it was isolated from, *Dendrobium longicornu*.

Classification — *Coniochaetaceae*, *Coniochaetales*, *Sordariomycetes*.

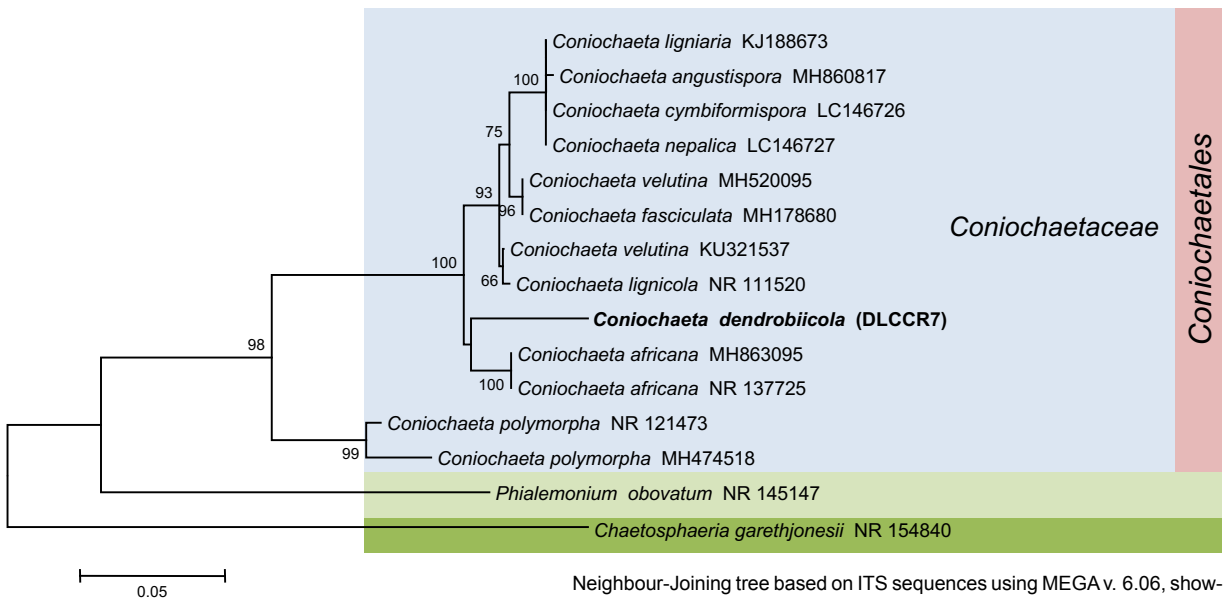
Vegetative hyphae thin, septate, smooth 1.2–2.4 µm wide. *Conidiogenous cells* arising laterally from vegetative hyphae, broader at base tapering towards apex (1.4 µm at base and 0.67 µm at apex). *Conidia* hyaline, smooth, cylindrical to allantoid, variable in size, 4.35–11.28 × 1.2–2.3 µm. *Sexual morph* absent which is reported in *Coniochaeta velutina*, *C. prunicola*, *C. africana* isolated from *Prunus* (Damm et al. 2010, Weber 2002, Abdalla & Al-Rokibah 2003, Asgari & Zare 2006).

Cultural characteristics — *Coniochaeta dendrobiicola* was first isolated on Czapek-Dox agar (CDA). The shape of the colony was circular, with lemon yellow colour and pale regular margin with pale white band as growing zone. The surface was smooth with flat topography and submerged mycelium. Colony 4 cm diam after 15 d of incubation, with 2–3 concentric rings. On potato dextrose agar (PDA) the colony was circular with regular margin, pale brown with yellowish margin having radiating furrows. The surface was glistening, smooth with flat topography and the presence of submerged mycelium. Colonies reach 4 cm diam after 15 d of incubation, with 1–2 concentric rings present. On oatmeal agar (OA) the colony shape was circular with regular margin, lemon yellow with 1 cm thick white growing margin. The colony surface was smooth, shiny with flat topography and submerged mycelium. Colonies reach 4.5 cm diam after 15 d of incubation, with a single concentric brown ring present.

Habitat — Roots of *Dendrobium longicornu*, District Makwanpur, Nepal.

Typus. Nepal, District Makwanpur, roots of *Dendriobium lognicornu* (*Orchidaceae*), 25 May 2017, *S. Shah* (holotype culture and specimen, MCC1811, preserved as metabolically inactive, ITS and LSU sequences GenBank MK225602 and MK225603, MycoBank MB830652).

Notes — Phylogenetic trees of the ITS region was prepared using sequences of *C. dendrobiicola* and other *Coniochaeta* species obtained from GenBank. An NCBI BLASTn search of **ITS** sequences showed closest similarity to be 93 % with *C. africana* (CBS 120868, GenBank MH863095), 92 % with *C. velutina* (STE-U 8315, GenBank KY312638), 92 % with *Coniochaeta angustispora* (CBS 871.73, GenBank MH860816) and 92 % with *Coniochaeta nepalica* (NBRC 30584, GenBank LC146727).



Neighbour-Joining tree based on ITS sequences using MEGA v. 6.06, showing the phylogenetic position of the new species among closely related 11 *Coniochaeta* species whose sequences were retrieved from the NCBI database. *Coniochaeta dendrobiicola* (DLCCR7) clustered in a clade containing the majority of the *Coniochaeta* species with a bootstrap support value of 100 %. The analysis involved 15 nucleotide sequences with *Chaetosphaeria garethjonesii* and *Phialemonium obovantum* as outgroups.

Colour illustrations. *Dendrobium longicornu* orchid species from Chitlang village, Makwanpur district, Nepal. Colony after 15 d on PDA, OA and CDA; conidia, conidiogenous cells and hyphae. Scale bars = 10, 10 and 100 µm.

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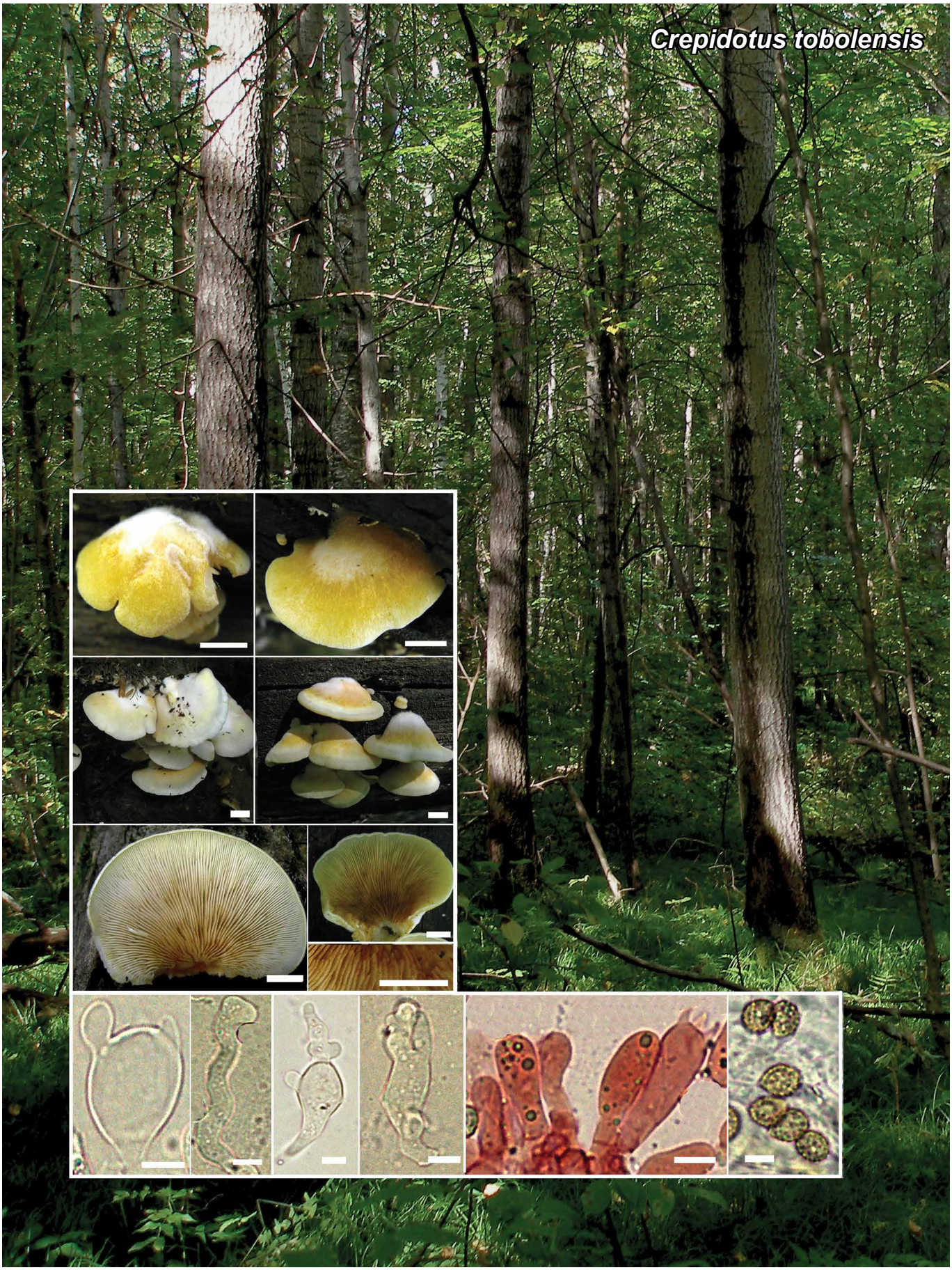
Crepidotus tobolensis

Fungal Planet 918 – 19 July 2019

Crepidotus tobolensis Kapitonov, Biketova & Zmitr., *sp. nov*.

Etymology. The name refers to a geographic area of the type locality, namely Tobol river and Tobolsk city (Russia, Tyumen Region).

Classification — *Crepidotaceae*, *Agaricales*, *Agaricomycetes*.

Pileus hygrophanous, soft and brittle, 7–43 mm wide, sessile to subpendent, reniform to ungulate or flabelliform, at first more or less hemispherical, then becoming convex-plane, the upperside initially subtomentose then, starting from the attachment point, velutinous to glabrous with internal hygrophanous radially-fibrillose texture and snow-white tomentum around the attachment point, luteous to honey-yellow and creamy-white at the margin, at maturity less bright, with orange-ochraceous tinges in median zone; *context* as a thin hygrophanous layer 1–2.8 mm thick, creamy-white. *Margin* straight, entire, crenate to crisped. *Gills* frequent, 1–3 mm wide, thin, not serrate, but serrulate in marginal zone, gradually narrowing downward on stipe, convergent under basidiome vault, soft-ceraceous, easily cracked, lamellulae in 3–4 ranks, ivory-white, staining yellowish ochraceous starting from attachment point (many gills are covered with rufous spots). *Stipe* absent. *Odour* and *taste* not distinctive. *Spore-print* brownish orange to yellowish brown. *Spores* (5.4–)5.9–7(–7.6) × (4.4–)4.6–5.6(–6.3) µm, av. = 6.5 × 5.1 µm, Q = (1.11–)1.21–1.35(–1.44), Qav. = 1.28 (n = 100/1), ovoid to widely lacrymoid, slightly ventrally flattened, with a germpore, hyaline to yellowish; exosporium warted, golden-brown, perisporium hyaline, strictly follows the exosporium ornamentation. *Basidia* (19.8–)21–24.4(–25.1) × (6.1–)6.13–8.1(–8.5) µm, av. = 22.3 × 7 µm (n = 13), sterigmata (2.3–)2.4–3.2(–3.6) µm long, av. = 2.9 µm (n = 17), 4-spored, clavate to subpedunculate, hyaline. *Cheilocystidia* numerous, (28–)33.2–45.2(–73) × (6.5–)6.9–11.2(–12.8) µm, av. = 41.1 × 8.8 µm (n = 15), variable in shape: fusiform, hyphoid, flexuose, clavate (often swollen to sphaeropedunculate), mostly branched, branches strangulate or capitate. *Pleurocystidia* especially not differentiated. *Pileipellis* a trichoderm, transforming into the cutis when mature; cutis 45–100 µm, thin, repent hyphae 3–11.7 µm diam, hyaline; terminal cells resemble the pleurocystidia in shape and size. *Subpellis* lacking. *Pigment deposits* lacking. *Clamp connections* present in all tissues.

Habitat & Distribution — Growing gregarious on wood debris of *Populus tremula.* Uncommon in the studied area. So far known only from Russia.

Typus. Russia, Tyumen Region, Tobolsk city, Betuleto-Tremuletum variiherbosum, on debris of *Populus tremula*, 28 Aug. 2018, *V.I. Kapitonov* (holotype LE 287655, isotype TCSS UB RAS 2732, ITS and LSU sequences GenBank MK522393 and MK560762, MycoBank MB829922).

Additional materials examined. *Crepidotus tobolensis*: Russia, Tyumen Region, Tobolsk district, Priirtyshskyi vicinity, Betuleto-Tremuletum variiherbosum, on debris of *Populus tremula*, 1 July 2018, *V.I. Kapitonov* (TCSS UB RAS 9477, ITS sequence GenBank MK522392).

Notes — As it is shown on the molecular phylogram, *C. tobolensis* represents a distinct species, sister to the South European *C. macedonicus*. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequences were *C. macedonicus* (GenBank MH780922.1 and MH780921.1; Identities = 671/683 (98 %), 4 gaps (0 %)) and *C. praecipuus* (GenBank KY827311.1; Identities = 716/763 (94 %), 20 gaps (2 %)). The closest hits using the **LSU** sequence were *Crepidotus* sp. PBM3237 (GenBank KT382279.1; Identities = 1367/1378 (99 %), no gaps) and *C. macedonicus* (GenBank MK277889.1; Identities = 1286/1290 (99 %), no gaps).

Two other closely related species are *C. lutescens* from China and *C. praecipuus* from New Zealand. The similarities and differences of the listed taxa are summarised in the supplementary table FP918-1.

Crepidotus tobolensis can be well distinguished only by a complex set of characters. As can be seen (supplementary table FP918-1), it is similar to the closely related *C. lutescens* and *C. praecipuus* by basidiomata size and rather intense yellow pigmentation, whereas in its spore quotient to *C. macedonicus*. The new species can be differentiated from these Chinese and New Zealand species by elongated spores resembling those of *C. macedonicus*. The new species differs from *C. macedonicus* by smaller basidiomata with more intensely-coloured pileus surface, paler gills when young and its ecological preferences. The convergent morpho-anatomical similarities of *C. tobolensis* should also be noted to the more phylogenetically distant European *C. cesatii* and North American *C. croceitinctus* (supplementary table FP918-1).

Colour illustrations. Russia, Tyumen Region, Tobolsk city, Betuleto-Tremuletum variiherbosum, where the holotype was collected. Young basidiomata (top range: isotype); mature basidiomata upperside (median range: holotype LE 287655 left, isotype right); mature basidiomata hymenophore in field; bottom range: four various cheilocystidia; basidia in hymenium; basidiospores. Scale bars = 5 mm (basidiomata) and 5 µm (microstructures).

Supplementary material

FP918-1 Table: Differentiating characters of closely related *Crepidotus* species.

FP918-2 Maximum likelihood tree of *Crepidotus tobolensis* sp. nov. and closely related species. Analysis of the nrDNA ITS region was conducted using RAxML v. 8.1.2 (Stamatakis 2014) implemented in raxmlGUI v. 1.5b2 (Silvestro & Michalak 2012). *Crepidotus parietalis* was chosen as outgroup. Bootstrap support values ≥ 50 % are given at the nodes. The new species is indicated in **bold**, holotypes indicated with asterisk (*).

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Dendryphiella stromaticola

Fungal Planet 919 – 19 July 2019

Dendryphiella stromaticola Cantillo, Gusmão & Madrid, *sp. nov.*

Etymology. Name refers to the presence of stroma.

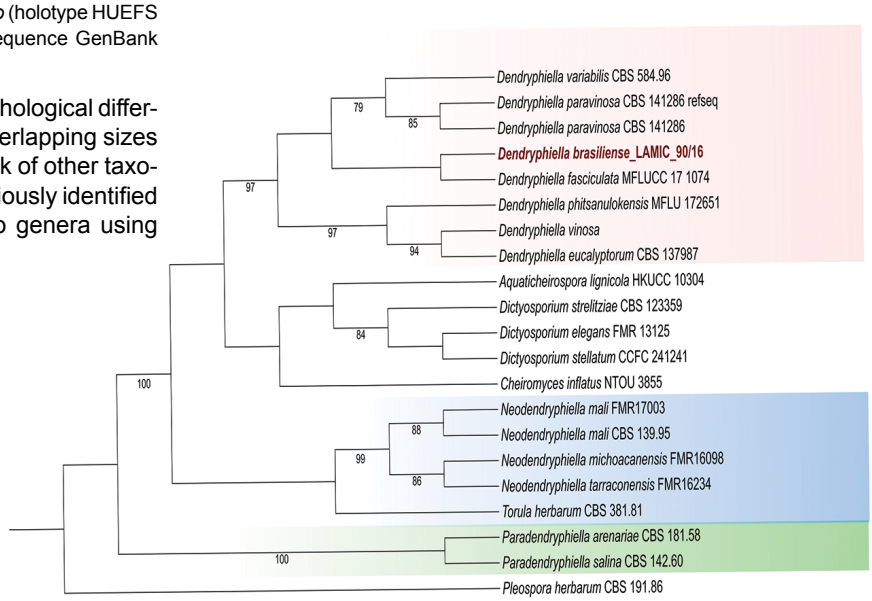
Classification — *Dictyosporiaceae*, *Pleosporales*, *Dothideomycetes.*

On natural substrate: *Colonies* superficial, effuse, dark brown, releasing a yellow pigment in the substrate. *Mycelium* immersed, composed of smooth, subhyaline, septate, branched, 3–4.5 µm diam hyphae. *Stromata* pseudoparenchymatous, intraepidermal to erumpent, convex, black, composed of cells with *textura globosa. Conidiophores* macronematous, mononematous, emerging through stroma in loose groups of 3–5(–7) conidiophores, brown, wider at the base, slightly paler at the apex, thick, smooth or verrucose, erect, straight or slightly flexuous, septate, sometimes branched, up to 250(–290) µm high, 3–7 µm wide. *Conidiogenous cells* polytretic, integrated, terminal and intercalary, verrucose near the geniculate conidiogenous zones, with 1–3 pores, 26–37 × 3–6(–7) µm. *Ramoconidia* rare, cylindrical with rounded ends, yellowish brown, verruculose, 1-septate, 22.5–35 × 4–6.5 µm. *Conidia* cylindrical with rounded apex, truncate or blunt at the base, (1–)3-septate, yellowish brown, verruculose to verrucose, forming short chains, 20–35 × 4–6.5 µm, constricted at septa when older; loci thickened, darkened and refractive.

Culture characteristics — *Conidia* germinated on Water Agar (WA) within 24 h, germ tubes produced from apical and/or basal ends, mycelium hyaline, sparse. *Colonies* on PDA reaching 60 mm diam after 7 d (25 °C/ daylight cycle), cottony, dark grey, with regular margins, reverse black; diffusible pigments absent in culture media.

Typus. Brazil, Rio Grande do Norte, Portalegre, on small branches of unidentified plant, S6°01' W37°59', 30 Apr. 2016, *T. Cantillo* (holotype HUEFS 239363, culture ex-type LAMIC 90/16, ITS and LSU sequence GenBank MK829079 and MK156678, MycoBank MB828657).

Notes — In *Dendryphiella*, an accurate morphological differentiation of certain species is difficult due to overlapping sizes of reproductive structures and the apparent lack of other taxonomically informative traits. Some species previously identified as *Dendryphiella* has been segregated in two genera using ecological, molecular and morphological characters: *Paradendryphiella*, with marine species (Woudenberg et al. 2013) and *Neodendryphiella* (Iturrieta-González et al. 2018). The blast analysis of the **ITS** sequence indicates a relatively close affinity of *Dendryphiella stromaticola* with *D. fasciculata* (GenBank MF399213, Identities = 89 %, no gaps), *D. paravinosa* (GenBank NR_154012, Identities = 89 %, no gaps) and of the **LSU** sequence with *D. variabilis* (GenBank LT963454, Identities = 97 %, no gaps); morphological differences with these species are mainly in the size of conidia and conidiophores, conidiophore aggrupation and the presence of stromata. *Dendryphiella stromaticola* is also morphologically similar to *D. eucalyptorum* and *D. vinosa*, which also produces mostly 3-septate conidia. *Dendryphiella eucalyptorum* can be differenced from *D. stromaticola* based on its smooth and smaller conidia (20–23 × 5–7 µm) and larger conidiogenous cells (20–40 × 6–10 µm). Phylogenetically, *D. stromaticola* appears distinct from the ex-epitype sequence of *D. vinosa* (NBRC 32669), but based on morphological characters, both species share many features such as size, colour and conidial morphology, distinguished only by the longer conidiophores in the latter species and the absence of stromata. It has been suggested by Crous et al. (2014) that the type species, *D. vinosa*, probably represents a species complex, and Iturrieta-González et al. (2018) segregated a new species, *D. variabilis*, previously identified as *D. vinosa* based mostly on molecular characters and the number of septa. However, molecular data in *Dendryphiella* are still scarce and available only for a few species, and so this genus requires further phylogenetic and taxonomic revision.



Phylogenetic tree inferred from Maximum likelihood and Bayesian analysis based on LSU nrDNA sequence data. ML Bootstrap support ≥ 75 % and BI values ≥ 0.90 are shown at the nodes. The alignment was performed with MAFFT v. 7 and the General Time Reversible model with Gamma distribution and invariant sites (GTR+G+I) was used as the best nucleotide substitution model. *Dendryphiella stromaticola* is marked in red.

Colour illustrations. Portalegre, Rio Grande do Norte. Colonies on natural substrate, conidiogenous cells and conidia. Scale bars = 0.5 mm (colonies in natural substrate), 30 µm (conidia and conidiogenous cell).

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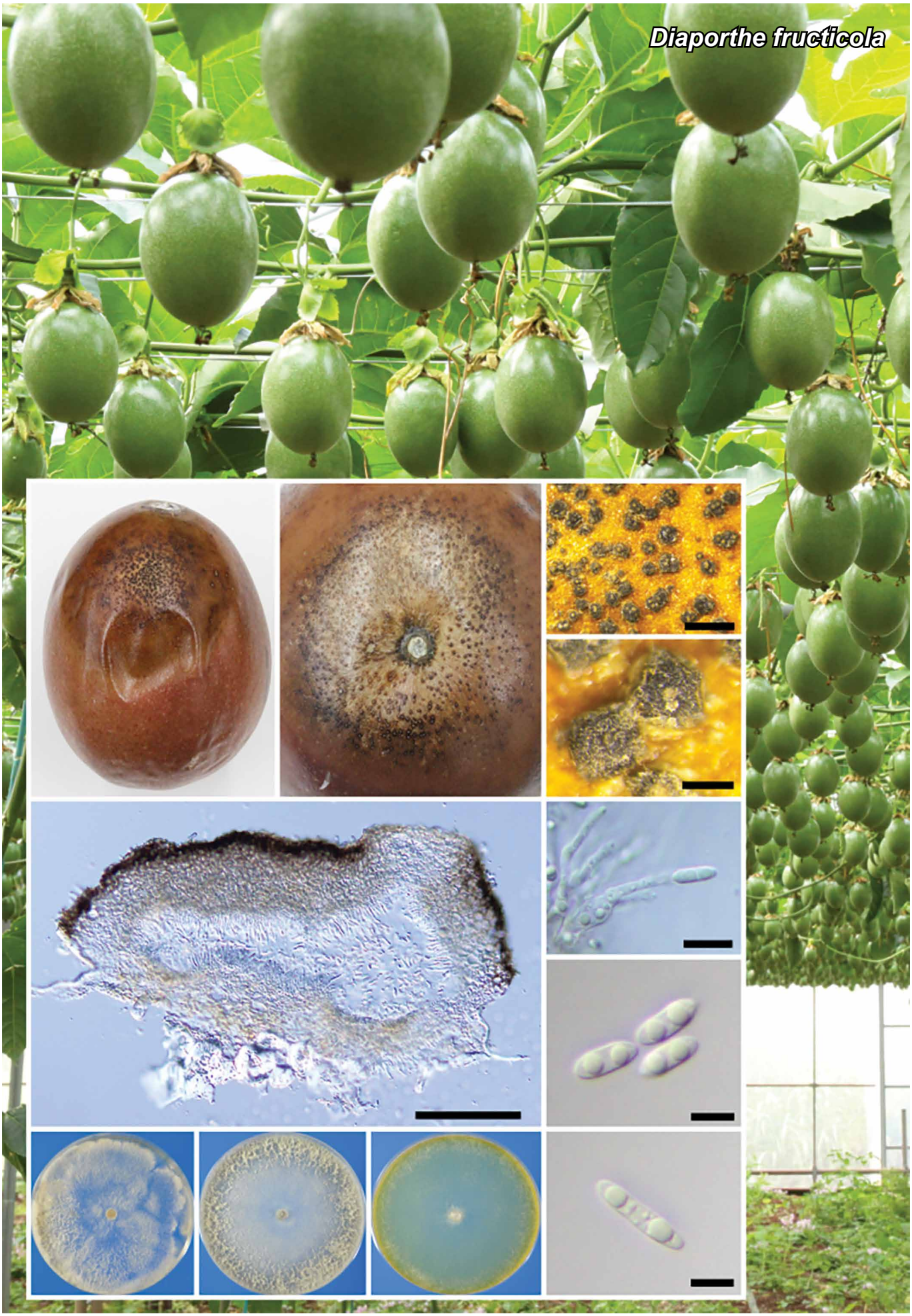

Diaporthe fructicola

Fungal Planet 920 – 19 July 2019

Diaporthe fructicola Minosh., T. Ono & Hirooka, *sp. nov.*

Etymology. Name refers to fruit, the substrate from which the ex-type strain was isolated.

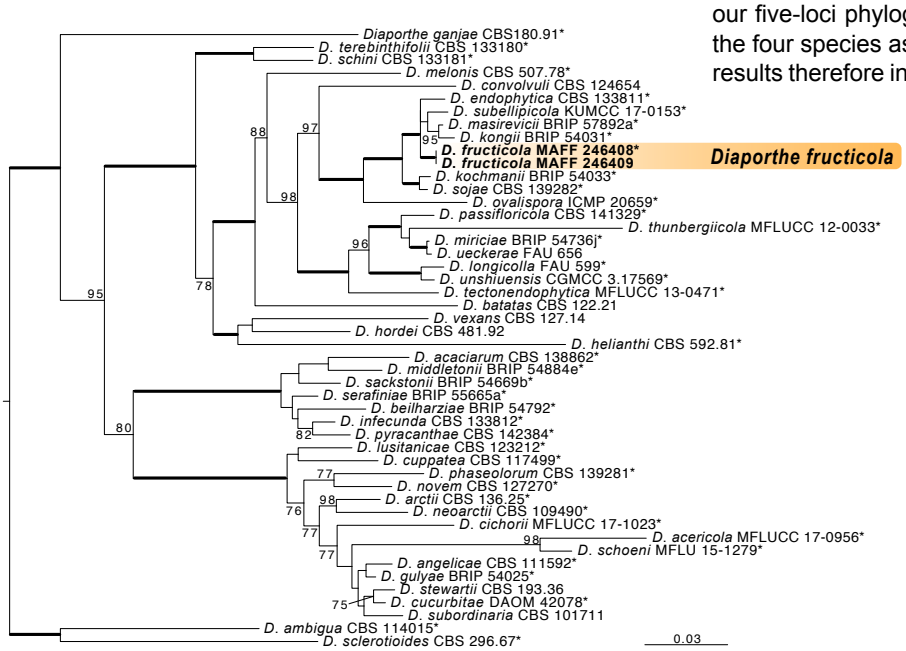
Classification — *Diaporthaceae*, *Diaporthales*, *Sordariomycetes*.

Only the asexual morph formed on the surface of post-harvest passion fruit (*Passiflora edulis* × *P. edulis* f. *flavicarpa*). *Conidiomata* pycnidial, scattered to aggregated in small groups including two or three conidiomata, ampulliform to ellipsoidal, up to 490 µm wide, black, lacking necks, exuding creamy droplets from central ostioles. *Conidial walls* c. 57–104 µm thick, consisting of two layers; outer layer dark brown, medium brown, c. 8–16 µm thick, cells forming *textura angularis*; inner layer ochraceous c. 38–68 µm thick, cells forming *textura angularis* or *textura globosa*. *Conidiophores* hyaline, smooth, straight to slightly sinuous, unbranched, (8–)13.5–21(–26.5) × 1–2(–3) µm. *Conidiogenous cells* phialidic, ampulliform to subcylindrical, filiform, tapering towards the apex, collarette not observed, (6–)9–14.5(–16.5) × 1–1.5 µm. *Paraphyses* lacking. *Alpha conidia* aseptate, hyaline, smooth, biguttulate, fusiform to ellipsoid, base truncate, (6–)6.5–8.5(–10) × (2–)2.5–3(–3.5) µm. *Gamma conidia* aseptate, hyaline, smooth, multiguttulate, ellipsoid, base truncate, (9.5–)10–12(–15.5) × 2–2.5(–3) µm. *Beta conidia* not observed.

Culture characteristics — After 3 d at 25 °C, colonies 58.5–60.3 mm (av. 57.6 mm). Colony surface on PDA covering with floccose mycelium, white to buff, formed in rosaceous. On MEA covering aerial mycelium thin, buff to yellow. On OA surface olivaceous grey to buff, central velvet.

Typus. Japan, Tokyo, Hahajima, on fruit of *Passiflora edulis* × *P. edulis* f. *flavicarpa* (*Passifloraceae*), June 2015, *T. Ono* HM15-390 (holotype TNS-F-54762, culture ex-type OGC15-11 = HM15-390C = MAFF 246408, ITS, *TUB*, *HIS*, *TEF* and *CAL* sequences GenBank LC342734, LC342736, LC342737, LC342735 and LC342738, MycoBank MB823768)..

Notes — Four species of *Diaporthe* and *Phomopsis*, i.e., *D. eres*, *D. passiflorae*, *D. passifloricola* and *Phomopsis tersa*, have been reported on *Passiflora* spp. (Farr & Rossman 2018). *Diaporthe fructicola* has alpha and gamma conidia, whereas *D. eres*, *D. passifloricola* and *P. tersa* produce only alpha conidia (Lutchmeah 1992, Udayanga et al. 2014, Crous et al. 2016). Of the four species, *Diaporthe fructicola* is morphologically quite similar to *D. passiflorae* (Crous et al. 2012). However, the alpha and gamma conidia of *D. fructicola* are much longer than those of *D. passiflorae*. Based on a MegaBLAST search of NCBIs, GenBank nucleotide database, the ITS sequence of *D. fructicola* is 99 % similar to *D. aspalathi* (GenBank KX769842), *D. endophytica* (GenBank NR_111847), *D. phaseolorum* (GenBank KP182390, etc.), *D. masirevicii* (GenBank KY011888, etc.), *D. terebinthifolii* (GenBank NR_111862, etc.), *D. novem* (GenBank NR_111855, etc.), *D. schini* (GenBank MF185331, etc.) and *P. asparagi* (GenBank JQ613999). In our five-loci phylogeny, *D. fructicola* was clearly distinct from the four species as a fully supported monophyletic clade. The results therefore indicate that *D. fructicola* is a distinct species.



Phylogenetic tree of the combined ITS, *TEF*, *TUB*, *HIS* and *CAL* MAFFT-aligned datasets obtained using maximum likelihood. A heuristic search was performed in RAxML v. 0.6.0 with support at the nodes calculated using bootstrap analyses with 100 replicates. The new species is indicated by **bold** text and highlight, * = ex-type strain. The ML bootstrap values ≥ 75 % are indicated at the nodes. Fully supported branches are indicated with thickened lines. *Diaporthe ambigua* (CBS 114015) and *D. sclerotioides* (CBS 296.67) were used as outgroup.

Colour illustrations. Passion fruit (*Passiflora edulis* × *P. edulis* f. *flavicarpa*) growing in Hahajima. Fruit rot of passion fruit; conidiomata on fruit; conidiophore and conidiogenous cells; alpha conidia; gamma conidia; colonies on PDA, OA and MEA. Scale bars = 1 mm, 200 µm and 100 µm (conidiomata), 10 µm (conidiophore), 5 µm (conidia).

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Entoloma nipponicum
1cm

Fungal Planet 921 – 19 July 2019

Entoloma nipponicum T. Kasuya, Nabe, Noordel. & Dima, *sp. nov*.

Etymology. The epithet refers to Nippon (Japan), the origin of the new species.

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

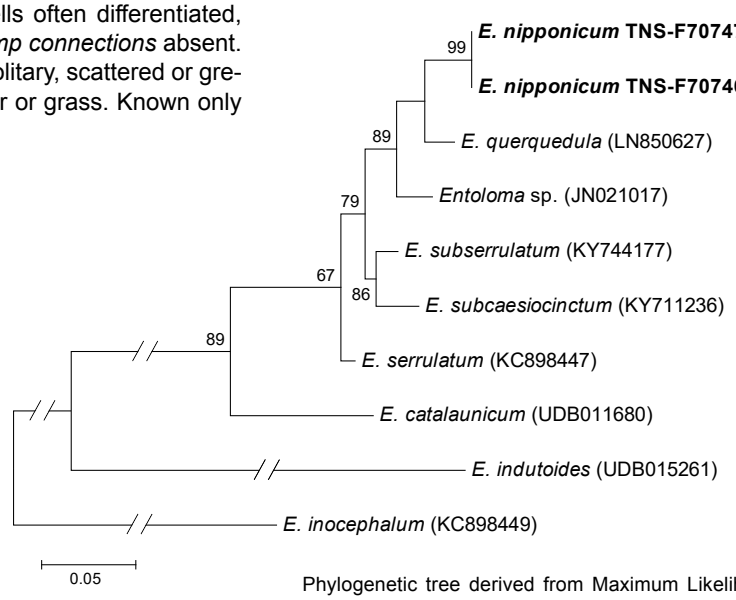
Basidiomata small, collybioid. *Pileus* 10–50 mm diam, initially hemispherical to hemispheric-convex expanding to convex to planoconvex with a depressed to umbilicate centre, not hygrophanous, not translucently striate, light orange to greyish red with a darker centre, often with lilac to dark blue tinge near margin, entirely fibrillose or minutely squamulose, sometimes radially splitting with age. *Lamellae* subdistant, white or cream-colour at first, then flesh coloured, edges serrulate and flocculose, concolorous or sometimes with dark blue tinge. *Stipe* 25–60 × 3–5 mm, almost cylindrical, sometimes slightly thickened at base, rarely somewhat twisted, pale orange or whitish to grey towards base, sometimes with slight blue-green tinge, smooth, almost polished, white tomentose at base. *Context* thin, concolorous with surface, odour and taste indistinct. *Basidiospores* 8–11(–12) × 6.5–8 µm (n = 50, mounted in water), Q = 1.07–1.42, 6–9-angled in side view. *Basidia* 25–39 × 7–10 µm (excluding sterigmata), clavate, 4-spored, without clamp connections. *Lamella edge* of serrulatum-type. *Cheilocystidia* 32–63 × 7–18 µm, clustered densely, cylindrical to subfusiform or sublageniform, sometimes septate, often with violaceus blue, granular intracellular pigment. *Pleurocystidia* absent. *Pileipellis* a trichoderm composed of hyphae 4–10 µm across with inflated terminal elements, 15–30 µm; intracellular pigments pink to brown with violet tinges. *Stipitipellis* a cutis of 4–8 µm wide hyphae, made up of cylindrical hyphae with granular dark blue intracellular pigment, terminal cells often differentiated, clavate, particularly in apical part. *Clamp connections* absent.

Habitat & Distribution — Growing solitary, scattered or gregarious on the ground among leaf litter or grass. Known only from Japan.

Typus. Japan, Hyogo Pref., Kobe-shi, Kita-ku, Yamada-cho, Shimotanigami, N34°46'2.88" E135°9'53.11", among leaf litter in mixed forest of *Cryptomeria japonica* and *Acer* spp., 29 June 2016, *M. Nabe* (holotype TNS-F-70747, ITS and LSU sequences GenBank MK693223 and MK696392, MycoBank MB830303).

Additional materials examined. Japan, Chiba Pref., Tonosho-machi, Awano, among leaf litter in bamboo grove (*Phyllostachys* spp.), 7 July 2015, *T. Kasuya*, TNS-F-70746, ITS and LSU sequences GenBank MK693222 and MK696391; Kyoto Pref., Kyoto-shi, Kita-ku, Kyoto University Kamigamo Experimental Station, among leaf litter of *Sequoia sempervirens*, 13 June 2018, *M. Nabe*, TNS-F-70748; Nara Pref., Kashihara-shi, Kashihara-jingu, among leaf litter in bamboo grove (*Phyllostachys* spp.), 17 June 2018, *M. Nabe*, TNS-F-70749; Okayama Pref., Shouo-cho, Oka, among grass, 8 July 2017, *M. Nabe*, TNS-F-70751.

Notes — *Entoloma nipponicum* forms a distinct clade in our phylogram where it clusters in the serrulatum clade of subg. *Cyanula*, together with species from Europe, China and North America. It is characterised by a serrulatum-type, blue pigmented lamella edge. Distinctive characters of *E. nipponicum* are the rather light coloured fruiting bodies with predominantly yellow-orange to greyish red pileus. As such it reminds of *Entoloma catalaunicum* from Europe, described with a pinkish red pileus and blue stipe, which, however, comes in a distant phylogenetic position outside the serrulatum clade. Blue tinges, so eminent in the European *E. serrulatum* and *E. querquedula*, are almost lacking in *E. nipponicum. Entoloma subcaesiocinctum* from China has a browner coloured pileus and a fibrous stipe (He et al. 2017). *Entoloma subserrulatum* from North America has a more yellowish grey pileus, and a pallid, almost white stipe (Noordeloos 2008).



Phylogenetic tree derived from Maximum Likelihood analysis based on nrITS1-5.8S-ITS2 data. Analysis was performed in PhyML v. 3.0 (Guindon et al. 2010) using the non-parametric Shimodaira-Hasegawa version of the approximate likelihood-ratio test (SH-aLRT) and the GTR+I+Γ model of evolution. ML bootstrap support values > 60 % are shown at the nodes. Sequences of the new species generated for this study are highlighted in **bold**.

Colour illustrations. Japan, Hyogo Pref., Kobe-shi, Kita-ku, Yamada-cho, Shimo-tanigami, type locality. Holotype TNS-F-70747: pileipellis; cheilocystidia; spores; basidiomata. Scale bars = 1 cm (basidiomata), 10 µm (pileipellis, spores and cheilocystidia).

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Entoloma ekaterinae

Fungal Planet 922 – 19 July 2019

Entoloma ekaterinae O.V. Morozova, Noordel., K. Nara, Dima & Brandrud, *sp. nov*.

Etymology. Named in honour of Ekaterina Malysheva, Russian agaricologist, known particularly as an investigator of the mycobiota of Far East and collector of the type specimen of this species.

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

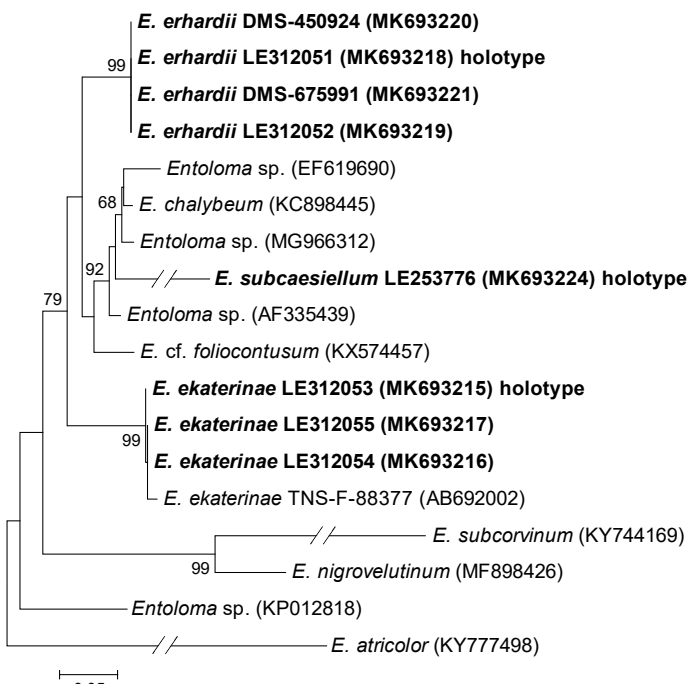
Basidiomata small to medium-sized, collybioid. *Pileus* 10–25 mm diam, conico-convex soon expanding to plano-convex with flat to slightly depressed centre, with deflexed then straight margin, hygrophanous, translucently striate almost up to the centre, at first densely covered with dark blue squamules (20D5–7, 20E5–7, 21D5–7, 21E6–8; Kornerup & Wanscher 1978), moving apart with age, showing light greyish blue background between them and stripes (21B3–4, 21C3–5). *Lamellae* moderately distant, adnate-emarginate, ventricose, whitish, becoming pink, with entire concolorous edge. *Stipe* 30–70 × 1.5–2 mm, cylindrical, smooth, polished, dark blue, concolorous with the pileus (20D5–7, 20E5–7, 21D5–7), white tomentose at base. *Context* white, greyish under the surface. *Smell* indistinct, *taste* not reported. *Basidiospores* 8–10(–11) × (5.5–)6.5–7(–8) µm, Q = (1.2–)1.4–1.5(–1.6), heterodiametrical, with 5–6 angles in side-view, relatively simple. *Basidia* 25–31 × 7.5–12.5 µm, 4-spored, narrowly clavate to clavate, clampless. *Cheilocystidia* 19–39 × 5–18 µm, broadly clavate, subglobose or sphaeropedunculate, sometimes septate, with several cylindrical or lageniform cells, not pigmented, forming sterile lamellae edge. *Pileipellis* cutis of cylindrical hyphae 2–7 µm broad with bundles of rising hyphae with globose to broadly clavate terminal elements (26–39 × 18–25 µm), forming squamules and central disk of pileus. *Clamp connections* absent.

Habitat & Distribution — In small groups on soil in *Quercus mongolica* forest and along the road in mixed forest of *Quercus mongolica*, *Acer mono*, *Tilia amurensis*, *Pinus koreana*, or in perennial herbaceous shrubs dominated by *Fallopia japonica*, some other *Poaceae* and *Asteraceae* plants. Known from Russia (Far East) and Japan.

Typus. Russia, Primorsky Krai, Sikhote-Alin Nature Reserve, vicinities of Blagodatnoye, N44.956033° E136.535133°, 15 Aug. 2013, *E. Malysheva* (holotype LE312053, ITS and LSU sequences GenBank MK693215 and MK733926, MycoBank MB830279).

Additional materials examined. Japan, Fuji Mt, Gotenba, Shizuoka prefecture, N35.339128° E138.791317°, 15 Sept. 2000, *K. Nara* (TNS-F-88377, as *Entoloma* sp. No242 (Kinoshita et al. 2012), ITS and LSU sequences GenBank AB692002 and AB692011). – Russia, Primorsky Krai, Sikhote-Alin Nature Reserve, vicinities of Maisa, N45.238833° E136.511117°, 22 Aug. 2013, *O. Morozova* (LE312054, LE312055, ITS and LSU sequences GenBank MK693216, MK693217 and MK733927, MK733928).

Notes — *Entoloma ekaterinae* is characterised by the entirely delicate-blue basidiomata, by the initially uniformly coloured pileus, which becomes distinctly translucently striate with dark squamules on a paler greyish blue background with age, and the trichodermal nature of the squamules, composed of globose elements. Microscopically, the sterile lamella edge composed of dense layer of clavate to subglobose and sphaeropedunculate cystidia is distinctive but, especially, in young specimens they can be mixed with cylindrical and lageniform cystidia. *Entoloma subcaesiellum*, described from the same region, is very similar morphologically, differing mainly in pileipellis structure (Noordeloos & Morozova 2010), but phylogenetically it is distinct. According to the molecular data, *Entoloma ekaterinae* belongs to the /chalybeum subclade of the /Cyanula clade.



Phylogenetic tree derived from a Maximum Likelihood analysis based on nrITS1-5.8S-ITS2 data. Analysis performed in PhyML v. 3.0 (Guindon et al. 2010) using the non-parametric Shimodaira-Hasegawa version of the approximate likelihood-ratio test (SH-aLRT) and the GTR+I+Γ model of evolution. ML bootstrap support values > 60 % shown at the nodes. Sequences of the new species generated for this study are highlighted in **bold**.

Colour illustrations. Russia, Primorski Territory, Sikhote-Alin Nature Reserve, Maisa River. Spores, cheilocystidia, basidiomata (from holotype); basidioma (LE312054). Scale bars = 1 cm (basidiomata), 10 µm (spores and cheilocystidia).

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Entoloma erhardii

Fungal Planet 923 – 19 July 2019

Entoloma erhardii Noordel., Dima, Svetash., Læssøe & Kehlet, *sp. nov*.

Etymology. Named in honour of Erhard Ludwig (1938–2019), mycologist and master painter, remembered for his monumental Pilzkompendium.

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

Basidiomata medium-sized, collybioid. *Pileus* 10–35 mm diam, conico-convex soon expanding to plano-convex with convex or slightly umbilicate centre, with deflexed then straight or reflexed margin, not hygrophanous, not translucently striate or in the cap margin only, initially uniformly coloured blackish blue, blackish indigo (19F6–7, 19F5–8; Kornerup & Wanscher 1978), discolouring to bluish grey (18E3–5, 19E3–5) or with a violet tinge, minutely radially fibrillose-tomentose all over, metallic-shining when drying. *Lamellae* moderately distant, adnate-emarginate, segmentiform to narrowly ventricose, white, contrasting with the pileus surface, becoming pink, with irregular, concolorous or brown edge. *Stipe* 30–70 × 1.5–3 mm, cylindrical, sometimes compressed with longitudinal groove, smooth, polished or minutely longitudinally striate, concolorous with pileus or paler (up to 19D3–5, 19E5–7) or tinged in green, white tomentose at base. *Context* white, greyish under the surface. *Smell* distinct, like flowers, pleasant, *taste* not reported. *Basidiospores* (9–)9.5–10(–12) × (5.5–)6–6.5(–7) µm, Q = (1.4–)1.5(–1.7), heterodiametrical, with 5–6 angles in side-view, relatively simple. *Basidia* 36–49.5 × 9.5–10.5 µm, 4-spored, narrowly clavate to clavate, clampless. *Lamella edge* either heterogeneous or sterile, and then of the *serrulatum*-type, with or without brown intracellular pigment. *Cheilocystidia* 33–85 × 5–14.5 µm, cylindrical, lageniform, fusiform or irregularly clavate, sometimes septate with or without brown intracellular pigment. *Pileipellis* cutis with transition to a trichoderm of cylindrical to slightly inflated hyphae 10–20 µm wide with inflated terminal elements and dark intracellular pigment, brownish in KOH. *Caulocystidia* absent. *Clamp connections* absent.

Habitat & Distribution — In small groups on soil in alpine and subalpine grasslands and also in damp woodland on rich black soil. Known from Russia (Caucasus) and Denmark.

Typus. Russia, Karachaevo-Cherkesia Republic, Teberda Nature Reserve, Klukhor pass, N43.252741° E41.857758°, asl ± 2700 m, 23 Aug. 2012, *T. Svetasheva* (holotype LE312051, ITS and LSU sequences GenBank MK693218 and MK733924, MycoBank MB830278).

Additional materials examined. Denmark, Sjælland, Eskebjerg Vesterlyng, Mareskov, 22 July 2012, *T. Kehlet*, DMS-450924, C, ITS sequence GenBank MK693220; Sjælland, Helvigstrup Skov, 1 Sept. 2014, *T. Kehlet* & *T. Læssøe*, DMS-675991, C, ITS sequence GenBank MK693221. – Russia, Karachaevo-Cherkesia Republic, Teberda Nature Reserve, Malaya Khatipara Mt, N43.445828° E41.712153°, asl ± 2500 m, 16 Aug. 2009, *O. Morozova*, LE312052, ITS and LSU sequences GenBank MK693219 and MK733925.

Colour illustrations. Russia, Karachaevo-Cherkesia Republic, Teberda Nature Reserve, Klukhor pass, type locality. Spores, cheilocystidia, basidiomata (from holotype); basidiomata (DMS-675991). Scale bars = 1 cm (basidiomata), 10 µm (spores and cheilocystidia).

Notes — *Entoloma erhardii* is nested within the /chalybeum subclade of the /Cyanula clade (data not shown). Members of the /chalybeum subclade are characterised by the entirely blue basidiocarps with not or hardly striate pileus, lamellae with sterile edge, and polished or at most finely striate stipe. *Entoloma erhardii* is distinguished by rather uniformly coloured bluish black not translucently striate pileus with contrasting white lamellae, concolorous or greenish stipe and mostly sterile lamella edge with differentiated cheilocystidia. It can be distinguished from *E. chalybeum* by the darker basidiomata, white lamellae (lamellae of *E. chalybeum* are bluish), and smaller spores (Noordeloos 1992). The macro- and microscopical features of *E. erhardii* resemble those of *E. corvinum*, except for the smaller spores. Current research on the phylogeny of *Cyanula* species reveals that *E. corvinum* based on a morphological species concept covers several distantly related more or less cryptic taxa. *Entoloma porphyrogriseum*, which is almost pure black in youth, can be differentiated by the strong brownish or purplish brown discoloration when maturing, initially distinctly fibrillose stem (Noordeloos 1987), and is phylogenetically distant (data not shown).

See tree in Fungal Planet 922.

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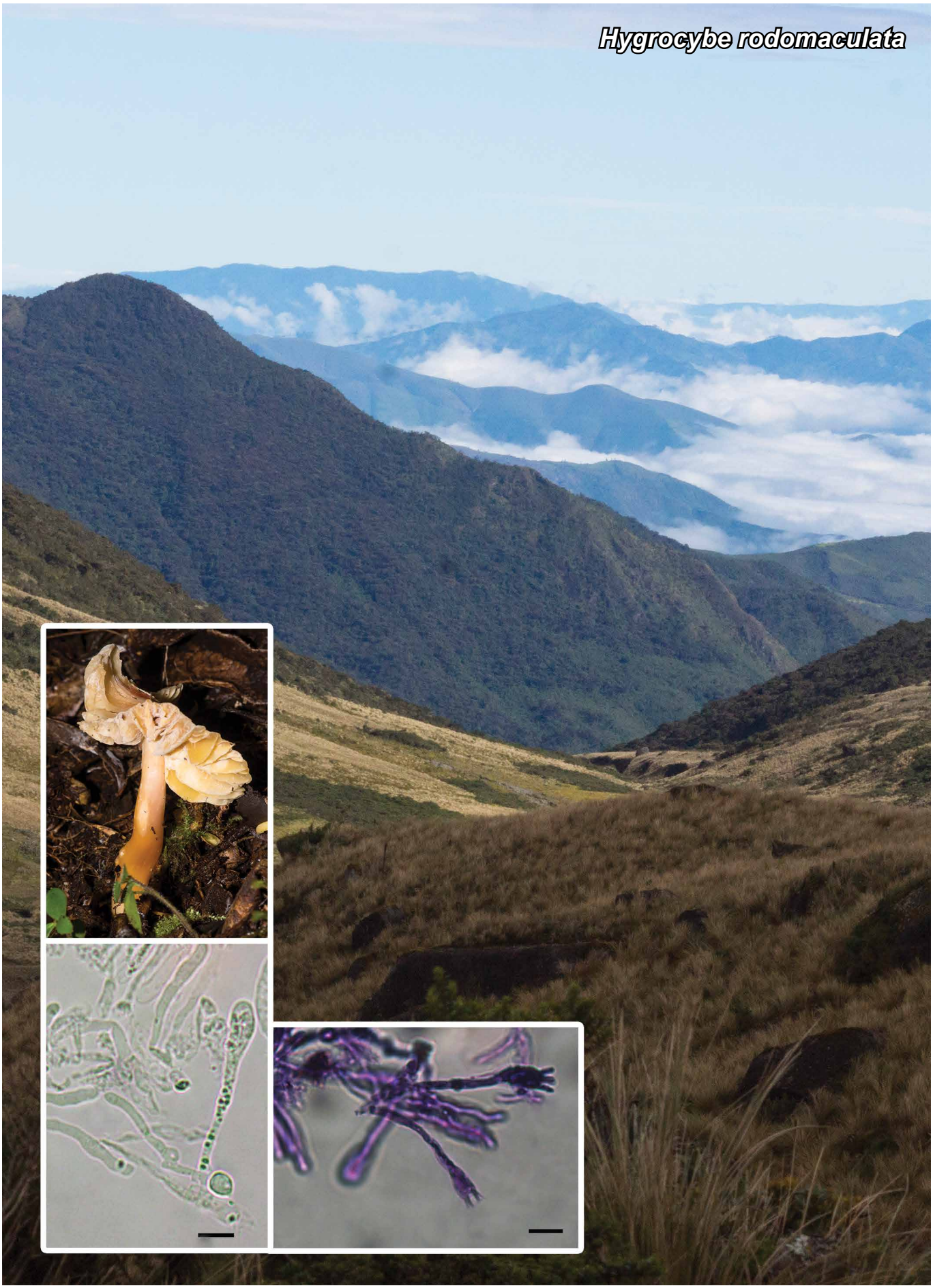

Hygrocybe rodomaculata

Fungal Planet 924 – 19 July 2019

Hygrocybe rodomaculata A. Barili, C.W. Barnes & Ordoñez, *sp. nov.*

Etymology. Name reflects the colour of the pileus.

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

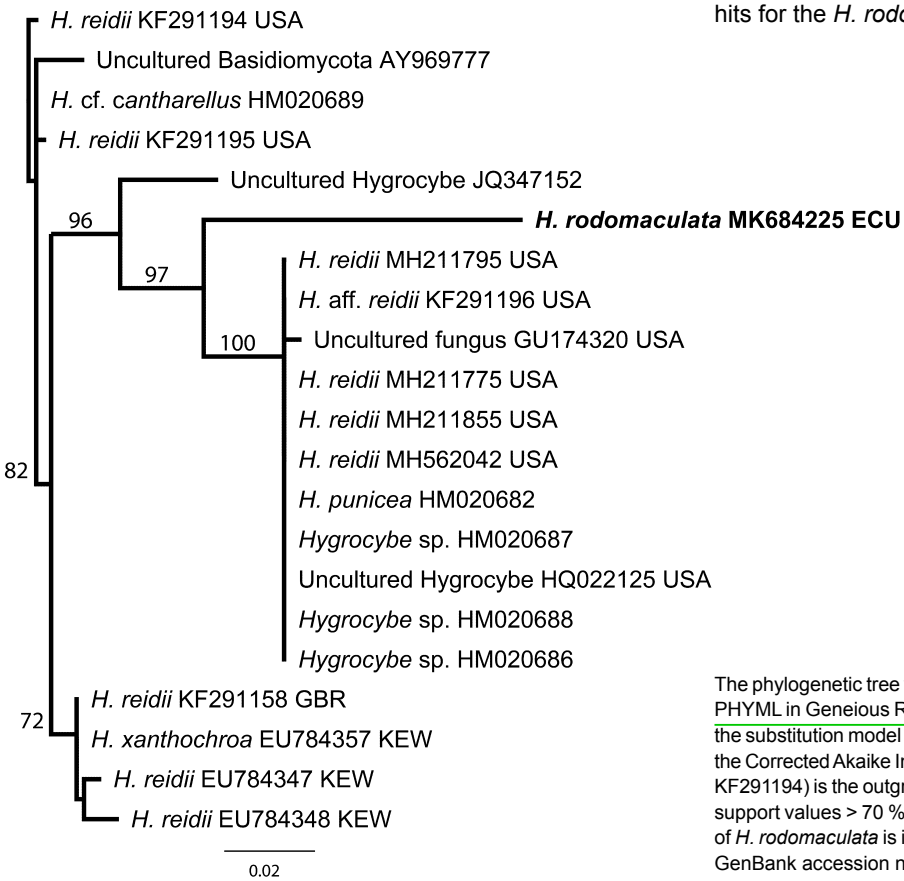
Basidiomata stipitate, pileus 45 mm diam, conical to flattened, with umbo, surface glabrous, dry, sericeous, margin entire, sinuose, undulate, rimose, fragile texture, whitish with orange and pink tones towards the centre. *Lamellae* broadly adnate, thick, ventricose, distant, with decurrent teeth or emarginate, anastomosed, sometimes forked, ochre yellow with whitish parts, edge entire. *Stipe* central, 120 × 10 mm, whitish with pink spots towards the apex, ochre at the centre and whitish at the base, cylindrical sinuose, hollow, fragile, glabrous. *Pileipellis* as a cutis, short cylindrical hyphae 52 × 8 µm with simple septa, *clamp connections* present. *Gill trama* irregular. *Basidia* 41–70 × 4–9 µm, clavate, very elongate, 4-spored, sometime with basal clamp, sterigmata elongate 5.5–9.5 µm. *Basidiospores* 7.5–10 × 5–7 µm, mainly ellipsoid, some oblong, smooth, hyaline, cyanophilic, non-amyloid, weakly metachromatic. Q = 1.3–1.7.

Habitat — Gregarious on the ground in humid montane forest.

Typus. Ecuador, Zamora Chinchipe province, Yacuri National Park, alt. 3234 m, May 2015, *A. Barili* (holotype QCAM5904, ITS and LSU sequences GenBank MK684225 and MK684352, MycoBank MB830309).

Notes — *Hygrocybe rodomaculata* belongs to the section *Coccinae*, considering pink as a discoloration of the characteristic red pileic surface of the group, with a dry or somewhat viscous stipe (Boccardo et al. 2008). The closest species based on morphological characters, according to Boertmann (2008) and Boccardo et al. (2008), is *H. calyptriformis*. However, it differs from *H. rodomaculata* by the pointed umbo, absence of yellow colour of the stipe and is non-radicate. In addition, *H. calyptriformis* belongs to the section *Microspore* whose distinctive feature is spore dimensions below 9 µm, while *H. rodomaculata* exceeds this size. The closest species determined by DNA sequence analysis was *H. reidii*, which is distinguished mainly by not having an umbo, by the slightly felted, scaly and uniform colouration, gills more or less decurrent, a proportionally shorter stipe, slightly smaller basidiospores, and characteristic honey odour.

A megablast search of NCBIs GenBank nucleotide database using the full **ITS** sequence showed that the holotype of *H. rodomaculata* was distinct from other species presently available for the genus. The first five hits were *Hygrocybe* aff. *reidii* (GenBank KF291196), *Hygrocybe* sp. (GenBank HM020688), *Hygrocybe* sp. (GenBank HM020687), *Hygrocybe* sp. (GenBank HM020686) and *H. pucicia* (GenBank HM020682); all with Identities = 564/627 (90 %) and 26 gaps (4 %). The top five sequences from the blast search aligned perfectly within the ITS region. The ITS phylogenetic tree includes the top 20 megablast hits for the *H. rodomaculata* sequence.



The phylogenetic tree was constructed using the Maximum Likelihood plugin PHYML in Geneious R9 (http://www.geneious.com; Kearse et al. 2012), and the substitution model determined by jModelTest (Posada 2008) according to the Corrected Akaike Information Criterion (AICc). *Hygrocybe reidii* (GenBank KF291194) is the outgroup based on the megablast search results. Bootstrap support values > 70 % are given above branches. The phylogenetic position of *H. rodomaculata* is indicated in **bold**. The species name is followed by the GenBank accession number, and when the country of origin was indicated, the three letter United Nations country code was used, in order of appearance USA: United States of America; ECU: Ecuador; GBR: United Kingdom. Samples ending with KEW are from Kew Royal Botanic Gardens, England. TreeBASE Submission ID 24152.

Colour illustrations. Yacuri National Park, Ecuador. Basidiocarp; non-mature basidia with basal clamp; basidia. Scale bars = 10 µm.

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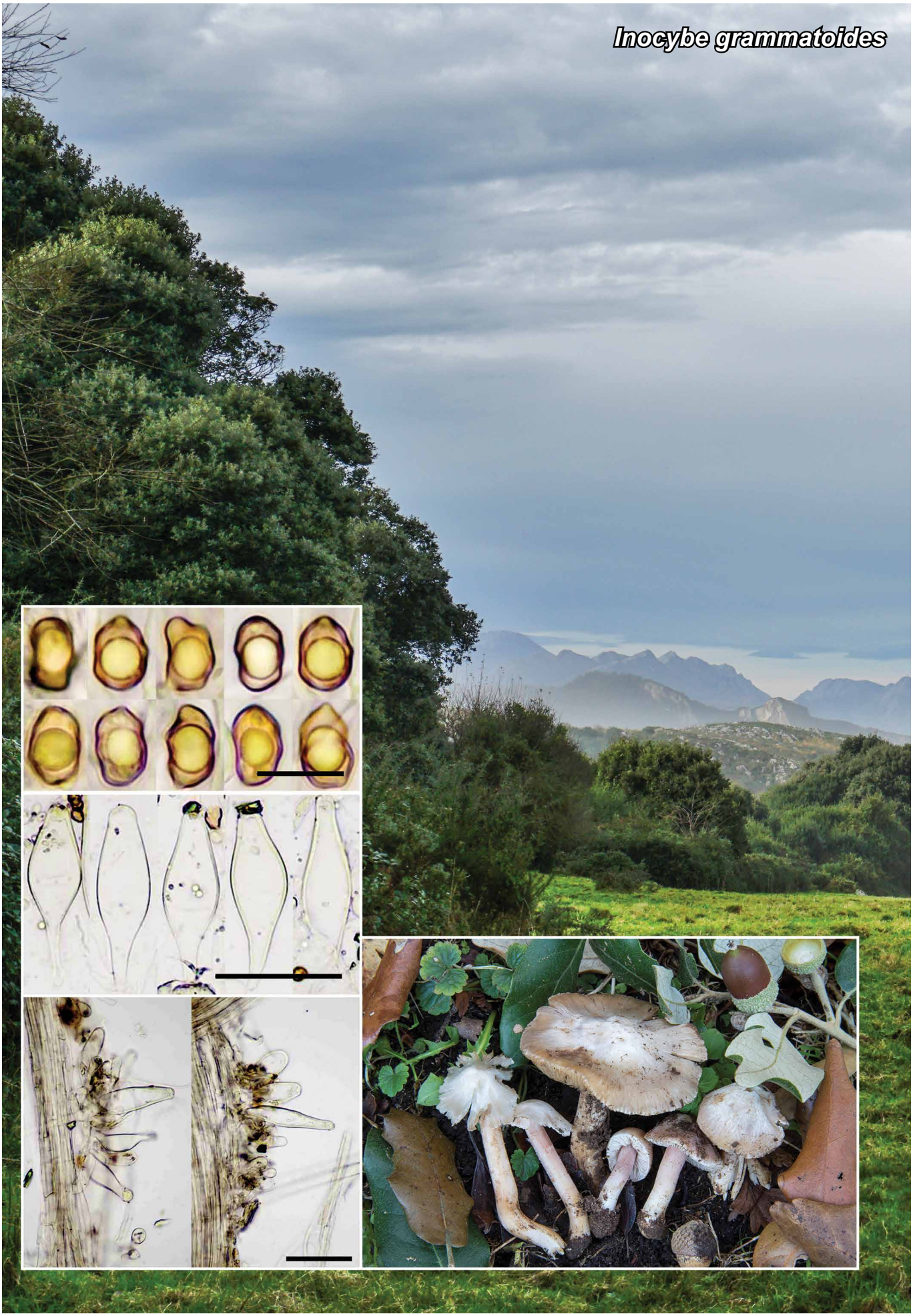
Inocybe grammatoides

Fungal Planet 925 – 19 July 2019

Inocybe grammatoides Esteve-Rav., Pancorbo & E. Rubio, *sp. nov.*

Etymology. Name refers to its resemblance to *Inocybe grammata*.

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

Basidiomata agaricoid and stipitate. *Pileus* 15–55 mm, at first conical-campanulate, then convex to plano-convex, broadly umbonate to subumbonate, slightly hygrophanous; margin straight, regular to hardly wavy with age, fissurate at times, surface usually covered by a dense whitish velipellis; colour pinkish grey (Mu 5YR 5/2, 6/2) when young or moistened, to light grey or very pale brown (Mu 10YR 7/1-3) when drying, uniform; surface radially fibrillose, smooth, not rimose towards the margin, sticky when humid, often agglutinating soil remains. *Lamellae* moderately crowded (L = 34–40; l = 1–2), adnexed to emarginate, ventricose, initially whitish, becoming pale grey to beige, then light brown, edge paler to concolorous with age, finely crenulate. *Stipe* 30–65 × 5–10 mm, straight to curved towards base, cylindrical, clavate to subbulbous, but never distinctly bulbous to marginately bulbous; colour often distinctly pinkish (Mu 5YR 6/3–4) at the apex or upper half, whitish becoming beige to ochraceous (Mu 10YR 8/2; 7/3) towards the lower half with age or when handled; surface densely pruinose at the upper half, becoming sparsely pruinose towards the base. *Cortina* not seen. *Context* fibrose, whitish, pinkish at the upper part of the stipe. *Smell* intense and penetrating, aromatic, reminiscent of elder flowers (*Sambucus nigra*), sometimes with a subspermatic component, *taste* not recorded. *Spores* (7.3–)7.4–*8.7*–10.1(–10.8) × (4.5–)5.1–*5.8*–6.6(–7.1) µm, Qm = (1.2–)1.3–*1.5*–1.7(–1.9) (n = 236 / N = 4), heterodiametric, polygonal-subrectangular under the optical microscope ('entolomatoid'), at times provided with 1–5 low knobs (–0.5 µm high), yellowish, apicula distinct. *Basidia* 27–37 × 7.5–10 µm, 4-spored, rarely 2-spored, clavate, sterigmata 3.5–6 µm long. *Lamella edge* heterogeneous, composed by dispersed protruding cheilocystidia mixed with abundant hyaline, clavate paracystidia. *Pleurocystidia* abundant, (49.1–)55.9–*66.7*–78(–88) × (10.4–)12.1–*16.3*–22.3(–25) µm, Qm = (2.67–)2.87–*4.2*–5.38(–6.05) (n = 118 / N = 3), narrowly utriform to fusiform, rarely sublageniform, hyaline, base often pedicellate, crystalliferous at the apex, walls (1–)1.11–*1.6*–2.23(–3.01) µm thick, pale to moderately yellowish in 10 % NH_4OH. *Cheilocystidia* similar in size and shape to pleurocystidia. *Stipitipellis* a cutis bearing numerous caulocystidia, more scattered towards the base, similar in shape and size to hymenial cystidia, mixed with clavate to broadly clavate hyaline paracystidia. *Pileipellis* a cutis formed by parallel cylindrical cells, 3–8 µm wide, broader (–18 µm) towards a hardly differentiated subcutis, showing minute pale intracellular pigment, slightly gelified. *Clamp connections* abundant in all tissues.

Habitat & Distribution — Gregarious in both basic and acidic soils; found in natural environments, such as deciduous humid forests.

Colour illustrations. Spain, Asturias, Ribadedeva, Pimiango, in *Quercus ilex* subsp. *ilex* forest, same locality as the holotype was collected. From top to bottom: basidiospores; pleurocystidia; caulocystidia; basidiomata (bottom right). Scale bars = 10 µm (spores), 50 µm (cystidia).

Typus. Spain, Asturias, Ribadedeva, Pimiango, N43°23'48" W4°31'39", 39 m alt., in humus of very humid *Quercus ilex* subsp. *ilex* forest, with *Crataegus monogyna* shrub in calcareous soil, 26 Nov. 2016, *P. Zapico* (holotype AH 46618, isotype ERD-6897, ITS and LSU sequences GenBank MK480531 and MK480524, MycoBank MB829589).

Additional materials examined. Italy, Piamonte, Novara, city of Novara, in a garden area under *Pinus strobus*, 9 Sept. 2000, *E. Ferrari*, EF 46/2000, ITS and LSU sequences GenBank MK480530 and MK480523. – Spain, Valencia, Pinet, Pla de El Surar, in humus of *Quercus suber* forest in decarbonated soil, 6 Dec. 1993, *R. Mahiques & F.D. Calonge*, H 15714, ITS sequence GenBank MK480529; Esteve-Raventós & Calonge (1996: 293, as *Inocybe olida*).

Notes — Colour codes are taken from Munsell (1994), terminology follows Kuyper (1986) and Vellinga (1988). *Inocybe grammatoides* differs from *I. grammata* in the absence of a marginate bulb in the stipe, which may be cylindrical, claviform or sometimes subbulbous; most collections of *I. grammatoides* show more slender cystidia (Qm = 4.2; Qm = 3.7 in *I. grammata*) with a thinner wall (e_m = 1.6; e_m = 2.5 in *I. grammata*); the sporal characteristics of both species appear overlapping. According to the data, *I. grammatoides* behaves as a mesophilic species, usually associated with *Quercus* (*Fagaceae*) and other broad-leaved trees in humid and warm environments; part of the records of *I. albodisca* in Moënne-Loccoz et al. (1990), seem to correspond to *I. grammatoides* (record n° 87114, Tab.151 bottom left). *Inocybe grammata* is a common species in boreal and circumboreal areas, associated with coniferous and birch forests in Europe and Eastern North America; it extends to the hyperhumid mountain enclaves of southern Europe, often associated with birch, but also with conifers. *Inocybe albodisca*, originally collected from coniferous forests in North Elba (Essex County, Eastern USA), appears to correspond morphologically to *I. grammata* (Moënne-Loccoz et al. 1990, Vauras 1997, Matheny pers. comm.).

Genetically, *I. grammatoides* is closely related (99 % ITS rDNA similarity) with the type specimen of *I. acriolens* (WTU:AU10493, GenBank NR_153186), although it probably represents an independent taxon because of the lack of significant phylogenetic support for a monophyletic origin and, morphologically, by the different spores, the latter containing distinct knobs. In addition, *I. grammatoides* has a 98 % BLAST identity with European sequences of *I. grammata* (Osmundson et al. 2013, Vauras & Larsson 2016 unpubl. data, as well as those produced for the present work from specimens AH 22127, AH 15662 and AH 47717). The isotype of *I. permucida* and a paratype of *I. grammata* var. *chamaesalicis* are not significantly different from other sequences of *I. grammata*. Besides, several sequences of *I. grammata* coming from North America probably represent different species (see phylogram).

Supplementary material

FP925-1 Table: Collections used in the molecular phylogenetic analyses, with voucher information and GenBank accession numbers for ITS and LSU regions. The GenBank accessions of sequences generated in this study are in **bold**.

FP925-2 Collections studied by the authors are indicated in **bold** in the phylogenetic tree for ITS and LSU sequences; type collections are annotated. Country of origin for each collection is given using ISO 3166/2 country codes.

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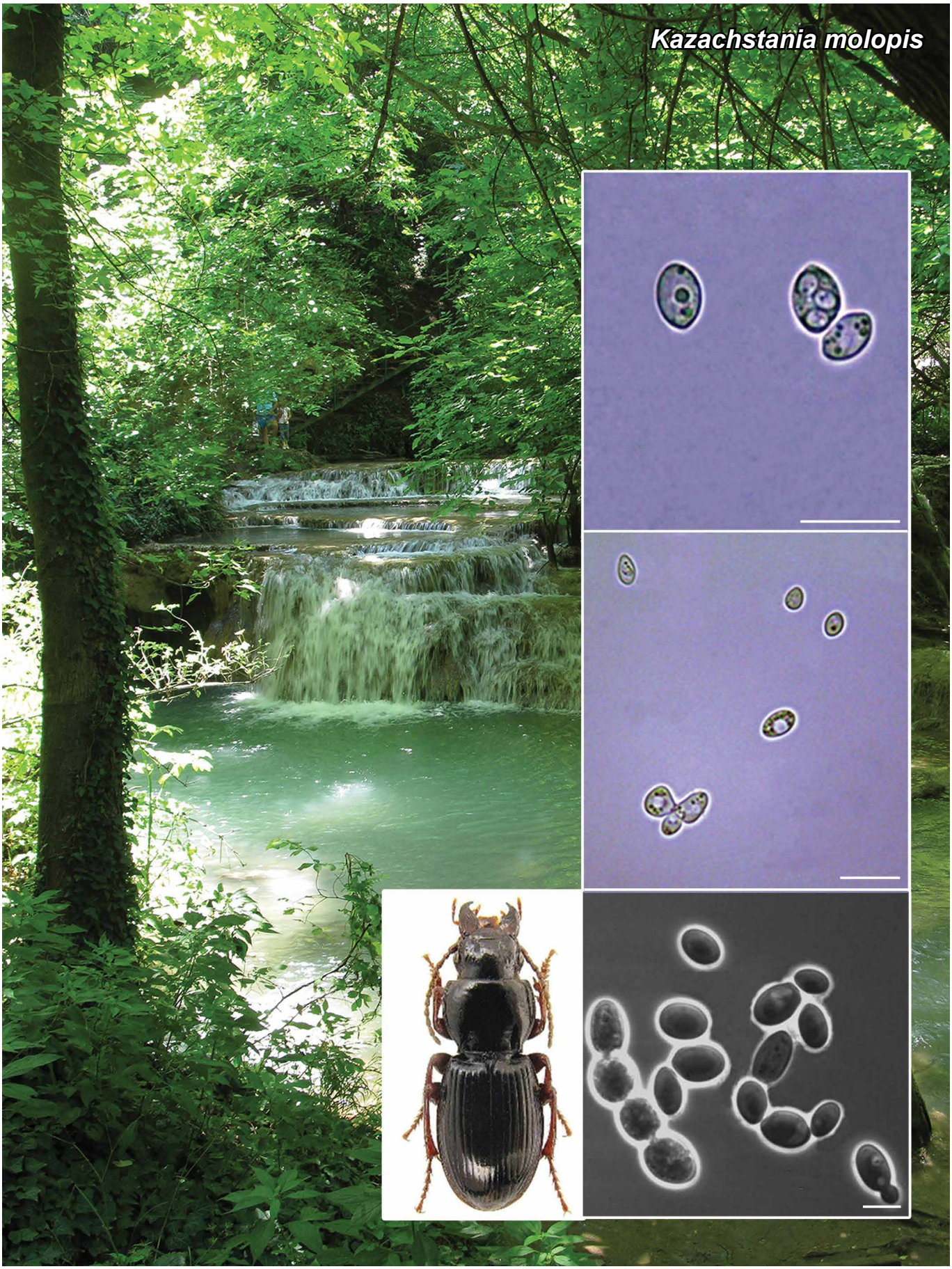

Kazachstania molopis

Fungal Planet 926 – 19 July 2019

Kazachstania molopis Gouliamova, R.A. Dimitrov, *sp. nov.*

Etymology. *mo-lo-pis*, referring to the host beetle *Molops piceus* (*Carabidae*) from which two new strains were isolated.

Classification — *Saccharomycetaceae*, *Saccharomycetales*, *Saccharomycetes.*

After 7 d at 25 °C in 5 % glucose broth, the cells are ovoid to ellipsoidal, 2–4 × 4–7 µm, occurring singly or in clusters. Asexual reproduction occurs by multilateral budding. Poorly developed pseudohyphae can be present. After 7 d at 25 °C on YPGA (yeast extract, pepton, glucose agar) the colony is cream, butyrous, glistening, convex and with an entire margin. Dalmau plate culture after 10 d on morphology agar did not show pseudohyphae or true hyphae. Sexual reproduction was detected on yeast extract, malt extract, peptone, glucose (YM) and McClary acetate agar. Conjugation between independent cells was observed. Asci contained one to four globose ascospores.

Fermentation — Glucose and galactose are fermented. Sucrose, maltose, lactose and raffinose are not fermented.

Carbon assimilation — D-glucose, D-galactose, L-sorbose, D-ribose, sucrose, maltose, α,α-trehalose, α-methyl-D-glucoside, cellobiose (delayed), salicin, arbutin (delayed), melezitose, soluble starch, glycerol, ribitol, D-glucitol, D-mannitol, D-glucono 1,5-lactone, 2-keto-D-gluconate (delayed), ethanol, quinic acid are assimilated. D-xylose, D-arabinose, D-glucosamine, L-arabinose, L-rhamnose, melibiose, raffinose, lactose, inulin, meso-erythritol, *myo*-inositol, xylitol, D-gluconate, D-glucuronate, D-galacturonate, succinate, citrate, DL-lactate, methanol, propane 1,2 diol, butane 2,3 diol, galactonic acid, galactitol, galactonic acid and saccharate are not assimilated.

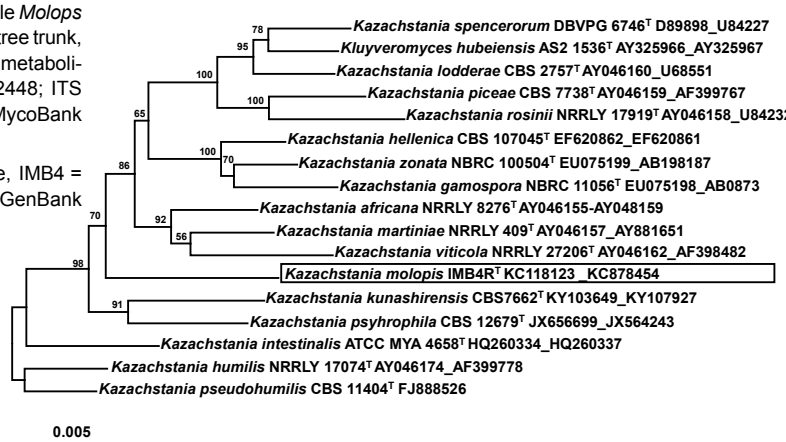
Nitrogen assimilation — Nitrate, nitrite, ethylamine, creatine, creatinine, L-lysine, cadaverine and imidazole are not assimilated.

Other tests — Starch formation test is negative. Growth in 10 % is negative. Growth in 0.01 % is negative. Growth in 50 % glucose is negative. Urea hydrolysis and DBB reaction tests are negative. Growth without all vitamins test is negative. Growth at 25 °C is positive. Growth at 30 °C is negative.

Typus. Bulgaria, Nature park Zlatni Pyasatsi from the gut of beetle *Molops piceus* (Carabidae, Coleoptera) collected in oak forest under fallen tree trunk, 23–24 Apr. 2009, *D. Gouliamova* (holotype IMB 4R preserved in metabolically inactive state, ex-type cultures NBIMCC 9029 and CBS 12448; ITS and D1/D2 LSU sequences GenBank KC118123 and KC878454, MycoBank MB802456)

Additional material examined. Bulgaria, same details as type, IMB4 = NBIMCC 9028 = CBS 12566, ITS and D1/D2 LSU sequences GenBank HM627145 and HM627092.

Notes — In our previous article we determined the lower and upper bounds for the range of species discrimination in the *Kazachstania* clade based on sequence identity value (SI) and distance between physiological profiles (DPP): SI (98.5–83.7 %) and DPP (8–18) (Dimitrov & Gouliamova 2019). A phylogenetic analysis of combined ITS and LSU sequences placed the new strain IMB 4R on a separate branch between *K. viticola* and *K. kunashiriensis*. Pairwise analysis of sequences in a multiple alignment showed that the new strains show 87.95 % identity (847 identical nt., 90 nt subst., 123 gaps) with *K. kunashiriensis* and 85.49 % identity (884 identical nt., 137 subst., 138 gaps) with *K. viticola.* The new strains can be differentiated from both *K. kunashiriensis* and *K. viticola* based on 14 common physiological characteristics. The new species can assimilate L-sorbose, D-ribose, sucrose, maltose, α-methyl-D-glucoside, cellobiose, salicin, arbutin, melezitose, soluble starch, ribitol, D-glucitol, 2-keto-D-gluconate and quinic acid. It cannot grow in the presence of 10 % NaCl. In addition the new species can be differentiated from *K. viticola* based on its ability to assimilate α,α-trehalose and its inability to assimilate D-gluconate and growth in the presence of 15 % NaCl. The new species differ from *K. kunashiriensis* based on its inability to assimilate L-lysine. The obtained SI and DPP data for the new strain IMB 4R fall within the limits for species discrimination of the *Kazachstania* clade. Thus, based on our results we propose a new yeast species, *Kazachstania molopis*, to accommodate Bulgarian yeast strains IMB 4R and IMB 4 (100 % SI in both ITS and LSU sequences). So far, only three species of *Kazachstania* were isolated from insects. A strain of *K. spencerorum* was isolated from larva of a *Psychidae* moth (*Lepidoptera*) collected from an acacia tree (South Africa) (CBS database). Three strains of *K. intestinalis* were isolated from the gut of the passalid beetle, *O. disjunctus*, collected from rotten oak tree (Virginia, USA) (Suh & Zhou 2011). Recently two strains of *K. chrysolinae* were isolated from the guts of *Chrysolinae polita* in Bulgaria (Gouliamova & Dimitrov unpubl. data).



Phylogenetic tree obtained by the analysis of combined ITS and LSU rDNA sequences of *Kazachstania molopis* IMB 4R^T and related species using a neighbour-joining method (Kimura two-parameter model; MEGA v. 7; 100 bootstrap replicates). *Kazachstania humilis* and *K. pseudohumilis* represent an outgroup species. GenBank accession numbers of ITS and LSU rDNA sequences are presented on the tree.

Colour illustrations. Krushuna Waterfalls, Bulgaria. *Molops piceus* (Photo credit: Ruslan Panin, http://carabidae.org); bottom to top: morphology of cells of *Kazachstania molopis* IMB4R^T in 5 % glucose broth after 1 wk; asci with ascospores in YM agar. Scale bars = 5 µm (cell morphology), 10 µm (ascospores).

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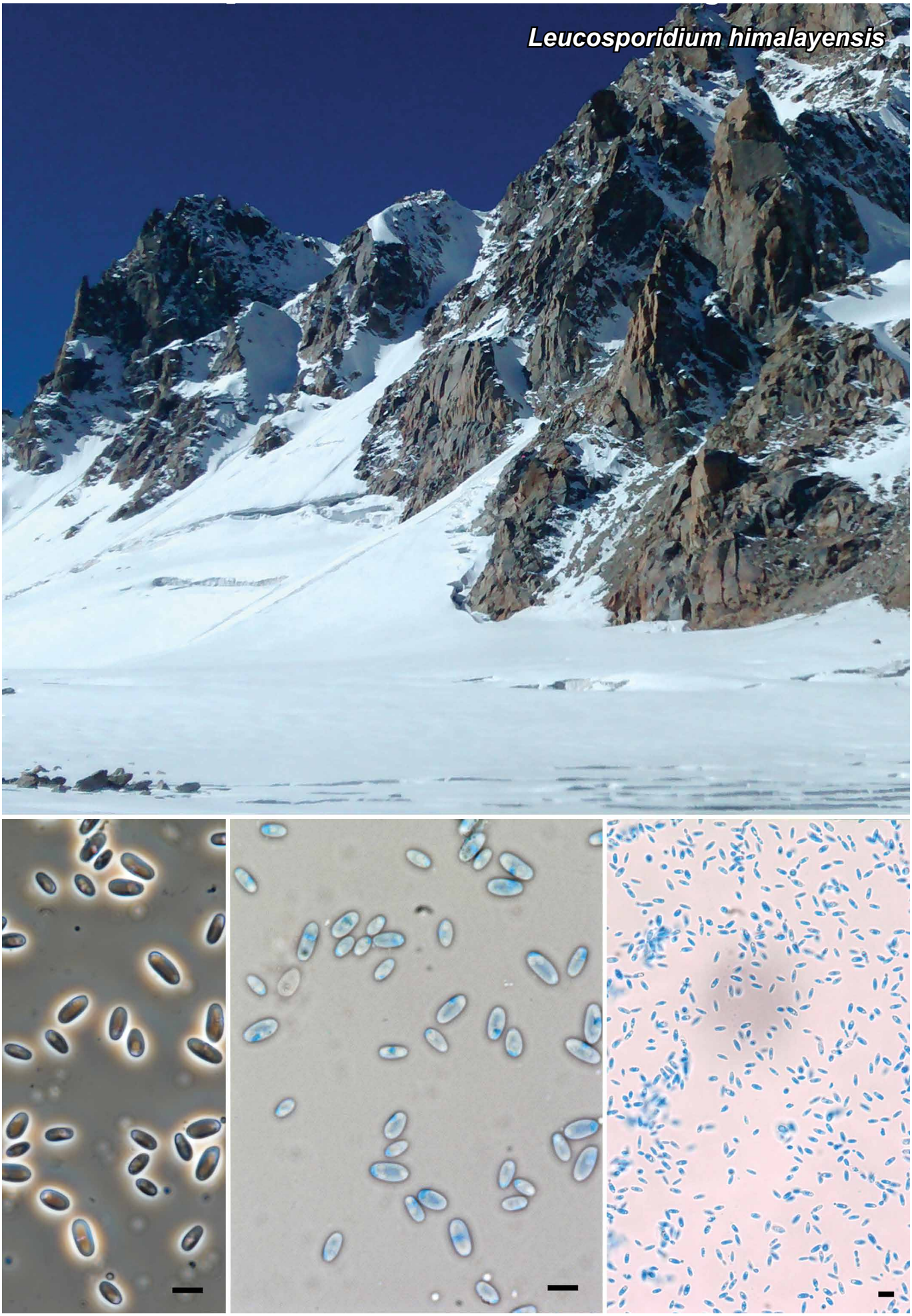

Leucosporidium himalayensis

Fungal Planet 927 – 19 July 2019

Leucosporidium himalayensis S.M. Singh, Roh. Sharma & Shouche, *sp. nov.*

Etymology. Name reflects the Himalaya, the place where this fungus was collected.

Classification — *Leucosporidiaceae*, *Leucosporidiales*, *Incertae sedis*, *Microbotryomycetes.*

Yeast colonies on SD agar Petri dishes are creamy-white, raised, margin entire. In external appearance, the colonies have a glabrous texture. Cells are subglobose to ovoid, 2–5 µm, occurring singly and budding is mostly polar, occurring frequently and repeatedly from the site of the primary budding scar. Sexual reproduction was not observed. Pseudohyphae formation absent. Growth occurred at 15 °C which is very similar to the primary habitat of this strain. Optimum growth was observed after 15 d. The following compounds are assimilated: D-xylose, D-saccharose, L-arabinose, Calcium-2-keto-gluconate. The following compounds are not assimilated: D-lactose, D-maltose, D-galactose, D-raffinose, D-trehalose, Glycerol, Inositol, Sorbitol, Adonitol, Methyl-Alpha-D-Glucopyranoside, D-cellobiose, D-melezitose, Xylitol.

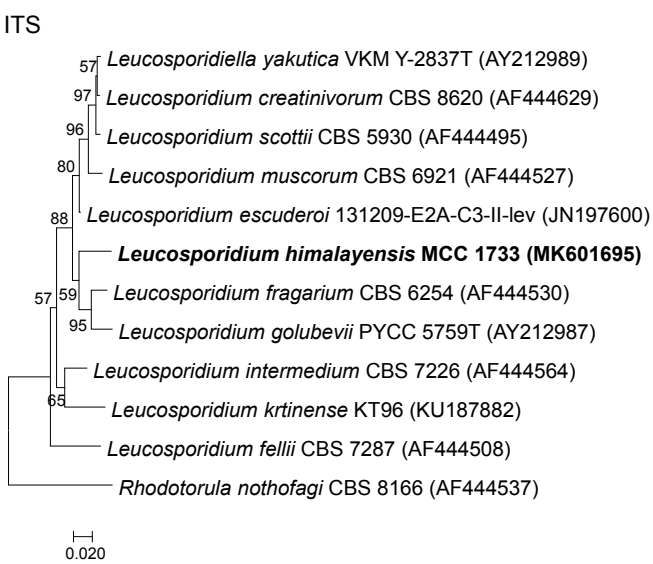
Culture characteristics — On CMA the colonies are white-cream, round, margin entire, ± 0.5 mm after 10 d.

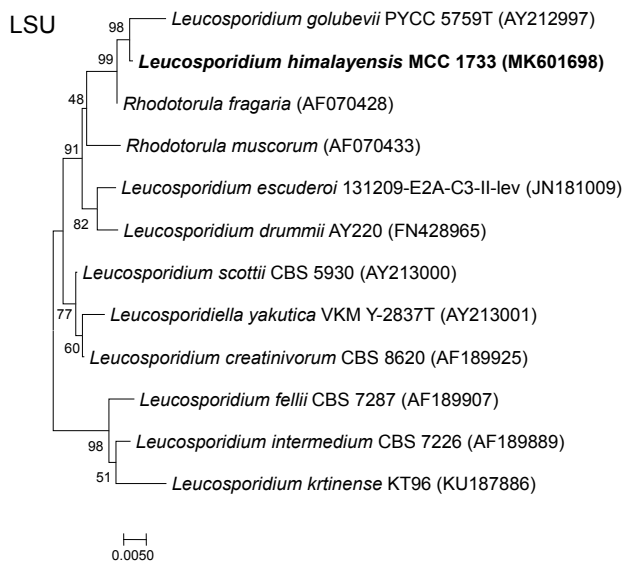
Habitat — Powdery windblown dust on glaciers (Cryoconites).

Distribution — India (Chhota Shigri glacier, Gramphu-Batal-Kaza Rd, Himachal Pradesh).

Typus. India, Gramphu-Batal-Kaza Road, Chandra river basin, Pir Pinjal range, Lahul valley, Himachal Pradesh, cryoconites, 4 Aug. 2015, *P. Sharma* & *S.M. Singh* MCC 1733 (holotype RNF079 as metabolically inactive culture, ITS and LSU sequences GenBank MK601695 and MK601698, MycoBank MB823364).

Notes — An initial BLASTn similarity search using the **LSU** sequence of the ex-type culture with the NCBI nucleotide database showed the highest similarity to *Leucosporidium fragarium* CBS 6254 (GenBank NG_058330; 99.5 % identity, 97 % query cover) followed by *Sampaiozyma ingeniosa* CBS 4240 (GenBank NG_058398; 96.60 % identity; query coverage 96 %). The BLASTn similarity search of the ex-type **ITS** sequence with NCBIs database showed the highest similarity to *Leucosporidium fragarium* CBS 6254 (GenBank NR_073287; 94.45 % identity, 99 % query coverage) followed by *Leucosporidium drummii* CBS 11562 (GenBank NR_137036; 95.02 % identity, 99 % query coverage). The neighbour-joining (NJ) phylogenetic analyses of ITS and LSU rRNA regions was done using sequences of other species of *Leucosporidium*. The combine phylogenetic tree topology of both regions clearly showed that strain RNF079 is novel.





Phylogenetic relationship of *Leucosporidium himalayensis* with other members of the genus based on a neighbour-joining tree of ITS and LSU sequences using MEGA v. 7.0.21. The bootstrap values of above 50 % are given at the nodes using 1 000 replications.

Colour illustrations. India, Himachal Pradesh, Chhota Shigri glacier, Chandra river basin, Lahul valley. Yeast cells at 100× under phase contrast and light (CMA after 10 d); yeast cells at 40× (SDA after 15 d). Scale bars = 5 µm.

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Lycoperdon vietnamense
2 000 µm
1 000 µm
10 µm
2 µm
3 µm

Fungal Planet 928 – 19 July 2019

Lycoperdon vietnamense Rebriev, A.V. Alexandrova, *sp. nov.*

Etymology. Name refers to the country where the type specimen was collected.

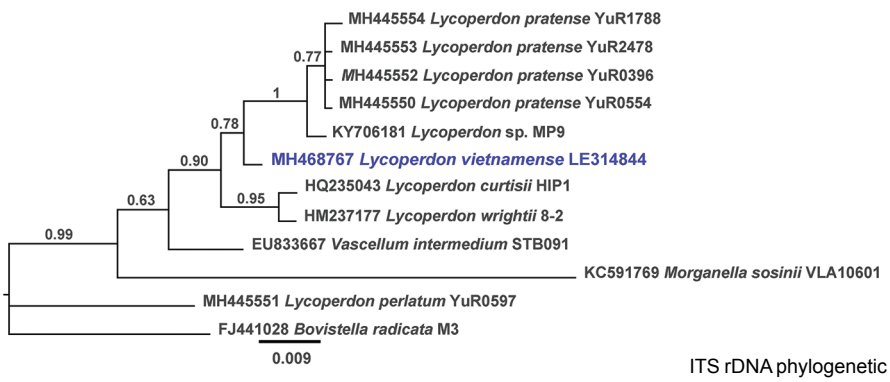
Classification — *Agaricaceae*, *Agaricales*, *Agaricomycetes.*

Basidiomes turbinate, 0.5–1.5 cm high and 1.5–2.3 cm broad, with upper surface ± flattened, dehiscing by a ragged roundish or sometimes slit-like opening. *Exoperidium* of white crowded spines up to 0.5 mm in upper part united by their tips into persistent stellate groups, fine felty material present between the spines; spines falling away at maturity leaving an inconspicuous reticulate pattern on endoperidium. *Endoperidium* light-brown. *Gleba* brown or concolorous with subgleba. *Subgleba* prominent, cellular, olive-brown, occupying up to 1/2 of the basidiome, in age separated from the gleba by a line (an apparent diaphragm). *Diaphragm* well developed. *Basidiospores* globose, pale brown, 2.8–3.3 µm, verrucose in LM and with robust conic spines 0.3–0.5 µm in SEM, with stump of a pedicel up to 1 µm. *Capillitium* abundant, 2.5–3.5(–4) µm diam, poorly branched, sometimes slightly swollen at rare septa, light brown, with pores up to 0.5 µm. *Paracapillitium* scanty developed.

Ecology & Distribution — The specimen was found on soil in tropical open deciduous forest, in group of three basidiomes. Until now the known distribution is restricted to Vietnam.

Typus. Vietnam, Đắk Lắk Province, Buôn Đôn District, Krông Na commune, Bản Đôn, Yok Đôn National Park, alt. 196 m, N12°56'24" E107°43'31", margin of tropical open deciduous forest, on soil, 10 May 2014, *A.V. Alexandrova* (holotype LE 314844, ITS sequence GenBank MH468767, MycoBank MB826727).

Notes — *Lycoperdon vietnamense* belongs to *Lycoperdon* subg. *Vascellum* by having a diaphragm. It is characterised by the verrucose spores, abundantly septate eucapillitium and stellate-echinulate exoperidium. Morphologically, it is close to *L. curtisii* (= *L. wrightii*) which has a stellate-echinulate exoperidium and spinulate spores, but the latter differs in having a poor capillitium. *Lycoperdon qudenii* differs in having larger spores with long pedicels as well as a furfuraceous exoperidium. The more common *L. pratense* has larger, finely ornamented spores, a poorly developed capillitium and a non-stellate exoperidium. Based on the ITS rDNA phylogenetic analyses, *L. vietnamense* clusters in the *Vascellum* clade, close to *L. pratense* and *L. curtisii*.



ITS rDNA phylogenetic tree obtained with MrBayes v. 3.2.6 under GTR+I+G model for 2 M generations. The GenBank accession numbers are indicated before species names. Support values are indicated on the branches (posterior probabilities). The novel species is shown in blue text and *Bovistella radicata* was used as outgroup.

Colour illustrations. Vietnam, Yok Đôn National Park, tropical open deciduous forest. Matured basidiome; peridium with areolate pattern; basidiospores and capillitium with pores in LM; basidiospores and paracapillitium in SEM; basidiospores, capillitium and paracapillitium under SEM. Scale bars (from top to bottom) = 2 mm, 1 mm, 10 µm, 2 µm, 3 µm.

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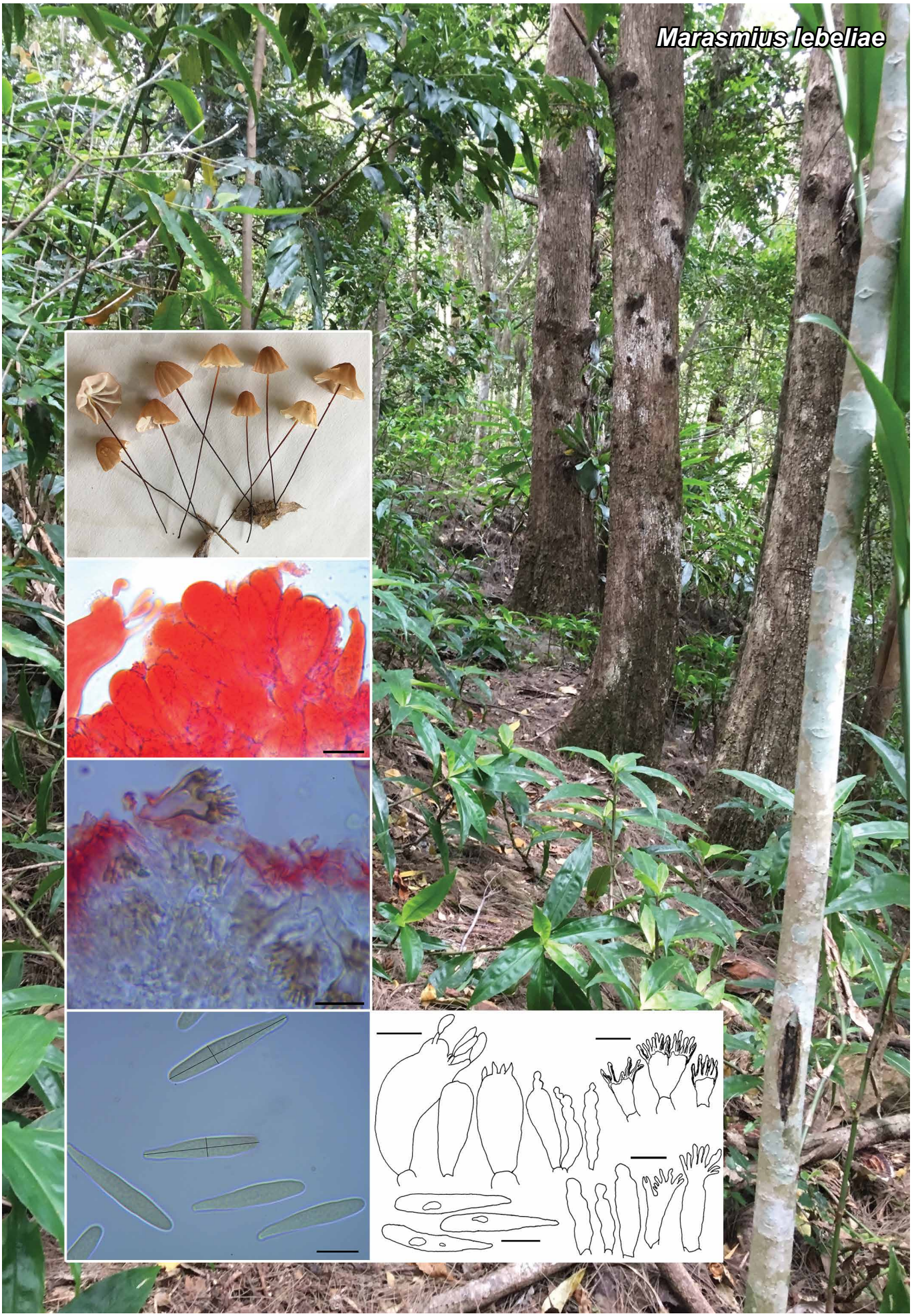
Marasmius lebeliae

Fungal Planet 929 – 19 July 2019

Marasmius lebeliae Guard, *sp. nov.*

Etymology. Named for its delicate beauty and in acknowledgement of mycologist Teresa Lebel, for elevating the study of Australian *Marasmius* into the DNA Era of the 21st Century.

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

Basidiomata small, marasmioid. *Pileus* 5–12 mm, conico-convex when young to campanulate at maturity, cinnamon (10; Royal Botanic Garden Edinburgh 1969) to rusty tawny (14), centre darker and occasionally wrinkled, margins paler buff (52), dry, deeply sulcate, flesh thin, white. *Lamellae* free to adnexed, sparse, 7–11, with occasional lamellulae, narrow, off-white, margins non-coloured. *Stipe* central, wiry, 35–60 × < 0.5–0.5 mm, glossy, black to purplish chestnut (21) in lower half, dark brick (20) in mid stem, buff (52) in upper end, tiny basal pad present (hand lens required). *Spore print* white. *Basidiospores* (27.5–)28.5–34.5(–35.5) × 4.5–5.5 µm (av. 32 × 5 µm, Q = 5.1–6.9, Q_m = 6.1 ± 0.4, n = 50), long, narrowly clavate, with widest diameter approximately 2/3 along length of spore, hyaline, inamyloid. *Basidia* 25–30 × 11–13 µm, sterigmata average 5.4 µm long; occasional basidia up to 40 × 15.5 µm. *Cheilocystidia* present in two forms – constricted cylindrical cells, 29–33 × 5–9 µm, and occasional *Siccus*-type broom cells with cylindrical bodies 16–27 × 3.5–5.5 µm with apical digitate projections 3.3–5.5 × 0.7–0.9 µm. *Pleurocystidia* narrow, cylindrical with constrictions (moniliform), or narrow to broadly clavate with swollen mucronate apices 11–25(–29) × 3.5–6(–8) µm. *Pileipellis* is a hymeniderm composed of *Siccus*-type broom cells: 7–12(–20) × 7–12 µm, main body cylindrical to broadly clavate, occasionally branched, thin-walled at base and often thick-walled in upper third, projections digitate, nodulose, or obtuse to subacute, thick-walled, 2.7–5.5 × 0.5–0.9 µm. Thick walled portion of broom cells is yellow-brown in KOH. *Caulocystidia* absent. *Stipitipellis* of parallel hyphae, dextrinoid in Melzers'.

Habit, Habitat & Distribution — Fruits in troops in mid-summer after significant periods of rain, usually in deep leaf litter, with an apparent preference for *Casuarina* needles in forest that has been regenerating for 10–30 years. To date this species has only been found from four sites in privately conserved land on Dilkusha Nature Refuge, Maleny, Queensland. It is expected that the distribution is in fact much wider, but *Marasmius* species are frequently overlooked in fungal surveys.

Typus. Australia, Queensland, Dilkusha Nature Refuge, Maleny, Site 1, in leaf litter and *Casuarina* needles under *Elaeocarpus grandis* and *Allocasuarina cunninghamiana*, in regenerating subtropical rainforest, 3 Feb. 2018, *F. Guard* F2018011 (holotype AQ799986; ITS sequence GenBank MK211200, MycoBank MB828485).

Additional materials examined. Australia, Queensland, Dilkusha Nature Refuge, Maleny, Site 2, in leaf litter and twigs, in regenerating riparian subtropical rainforest, 2 Jan. 2018, *F. Guard* F2018002 (AQ876930; ITS sequence GenBank MK211197, LSU sequence GenBank MK801676); Dilkusha Nature Refuge, Maleny, Site 3, roadside in *Allocasuarina cunninghamiana* needles, in regenerating subtropical rainforest, 3 Feb. 2018, *F. Guard* F2018012 (AQ799987; ITS sequence GenBank MK211198, LSU sequence GenBank MK801678); Dilkusha Nature Refuge, Maleny, Site 4, in leaf litter and dead *Cordyline rubra* leaves, in revegetated subtropical rainforest, 5 Feb. 2018, *F. Guard* F2018018 (AQ 799989; ITS and LSU sequences GenBank MK211199 and MK801677).

Notes — *Marasmius lebeliae* is characterised by a small pale brown pileus, distant lamellae, very large basidiospores, strangulate pleurocystidia, and two types of cheilocystidia – common strangulate and common to uncommon *Siccus* type broom cells. These features in the absence of caulocystidia and with a well-developed, non-collariate, non-insititious stipe place this species in sect. *Globulares* (group *Sicci*), subsect. *Siccini*, ser. *Haematocephali*.

Marasmius lebeliae is part of a small but well-supported clade that includes a strongly supported sister species, *Marasmius crinipes* described from Korea (Antonin et al. 2012). However, it differs significantly in having shorter spores (av. 22.8 × 4.3 µm), different coloured pileus (brownish orange), longer stipe and different type of cystidia. Another species similar in shape, size and habitat is *Marasmius bambusiniformis*. It differs in being brighter orange, having more lamellae (10–16), which have a concolorous margin, significantly smaller spores (av. 16 × 4.3 µm) and lacking pleurocystidia (Singer 1976).

Colour illustrations. Regenerating subtropical rainforest, in Dilkusha Nature Reserve, Maleny, Queensland, Australia, holotype site; basidiomata, large basidium with immature spores, basidioles and pleurocystidium, golden-brown colour of thick-walled sections of broom cells in KOH, mature spores; basidia and pleurocystidia; *Siccus* type broom cells in pileipellis; basidiospores; cheilocystidia of two types – thin walled, strangulate and *Siccus* type broom cells. Scale bars = 10 µm.

Supplementary material

FP929 Bayesian (Mr Bayes v. 3.2.6) 50 % majority-rule consensus tree of the ITS-nrDNA for a selection of *Marasmius* species. Bold lines indicate PP support > 0.95. G - sect. *Globulares*; N - sect. *Neosessiles*; L - sect. *Leveilleani*; MM - sect. *Marasmius* subsect. *Marasmius*; MS - sect. *Marasmius* subsect. *Sicciformes*; S - sect. *Sicci*; SA - sect. *Sicci* ser. *Atrorubentes*; SL - sect. *Sicci* ser. *Leonini*; SS - sect. *Sicci* ser. *Spinulosi*; SH - sect. *Sicci* ser. *Haematocephali.*

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Mariannaea terricola

Fungal Planet 930 – 19 July 2019

Mariannaea terricola A.L. Alves, A.C.S. Santos, R.N. Barbosa, Souza-Motta, P.V. Tiago, *sp. nov.*

Etymology. *terricola*, terri means soil, referring to substrate from which the fungus was isolated.

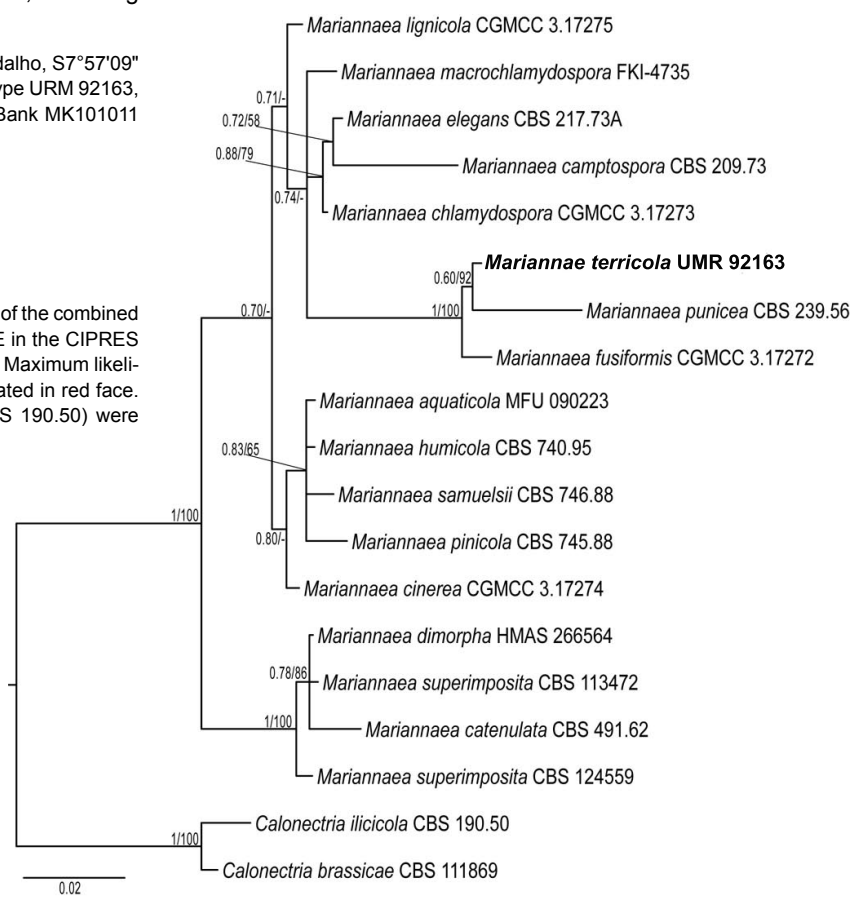
Classification — *Nectriaceae*, *Hypocreales*, *Sordariomycetes*.

On PDA: *Hyphae* 2–12 µm wide, septate, hyaline, smooth, thin-walled, branched. *Conidiophores* up to 575 × 5–12 µm length/width at the base cell, macronematous, mononematous, erect, straight, smooth or verrucose, thin-walled, septate, hyaline, cylindrical, tapering with base cell wall slightly verrucose, bearing short branches in the upper part, with three phialides at each branch. *Phialides* 14–22 × 2–5 µm length/width, flask-like, hyaline, smooth-walled. *Conidia* 3–9 × 2–4 µm length/width, globose to fusoid, hyaline, thin-walled, smooth, aseptate, produced in imbricate chains. *Chlamydospores* single, globose when in a terminal position, 7.5–8 µm diam, and doliiform when in an intercalary position, 7.5–20 × 4–10 µm length/width, hyaline, thick-walled. Ascomatal morph not observed.

Culture characteristics — (in the dark, 25 °C after 7 d): Colonies on PDA reaching 4–6 cm diam, at first white, rosy buff close to margins and honey to cinnamon at centre; zonate; reverse white close to margins to cinnamon at centre, becoming wine coloured after 14 d.

Typus. Brazil, Pernambuco state, Mata São João, Paudalho, S7°57'09" W35°06'19", isolated from soil, July 2017, *A.L. Alves* (holotype URM 92163, ex-type culture URM 8023, ITS and LSU sequences GenBank MK101011 and MK101012, MycoBank MB828377).

Notes — ITS and LSU sequences are important identification markers for *Mariannaea*. Based on the current phylogenetic analysis, the new species *Mariannaea terricola* represents a distinct lineage, clustering close to *M. fusiformis* and *M. punicea*. However, *M. fusiformis* is characterised by its hyphae, 2–8 µm wide, conidiophores up to 800 µm long, phialides 14–22 × 2–5 µm, smooth-walled or occasionally verrucose, conidia 5–10 × 3–4 µm, fusiform to subglobose, chlamydospores 8–10 × 5–7 µm, globose to subglobose. *Mariannaea punicea* is characterised by its conidiophores c. 160–300 µm long, 6–9 µm wide at the basal cell, conidia 4–7 × 2–3.5 µm, ellipsoidal to fusoid, chlamydospores yellow-brown, 6–10 µm diam (Hu et al. 2016). These two species also have red-purple colonies, but *M. punicea* differs from *M. fusiformis* in its conidial shape that is broadest at the 1/4 part from the apex (Samson 1974, Cai et al. 2010). The new species described here also differs in colony colour and zonation. *Mariannaea terricola* initially has white colonies, rosy buff close to margins and honey to cinnamon at centre, zonate. *Mariannaea terricola* was isolated from soil collected in the Brazilian Tropical Atlantic Forest, in the city of Paudalho, Pernambuco state.



Bayesian inference tree obtained by phylogenetic analyses of the combined ITS and LSU sequences conducted in MrBayes on XSEDE in the CIPRES science gateway. Bayesian posterior probability values and Maximum likelihood are indicated at the nodes. The new species is indicated in red face. *Calonectria brassicae* (CBS 111869) and *C. ilicicola* (CBS 190.50) were used as outgroup.

Colour illustrations. Atlantic forest's soil, isolation source of *Mariannaea terricola*. 7-d-old (left) and 14-d-old (right) colonies; conidiophores, conidia and chlamydospores from 7-d-old colonies on PDA. Scale bars = 10 µm.

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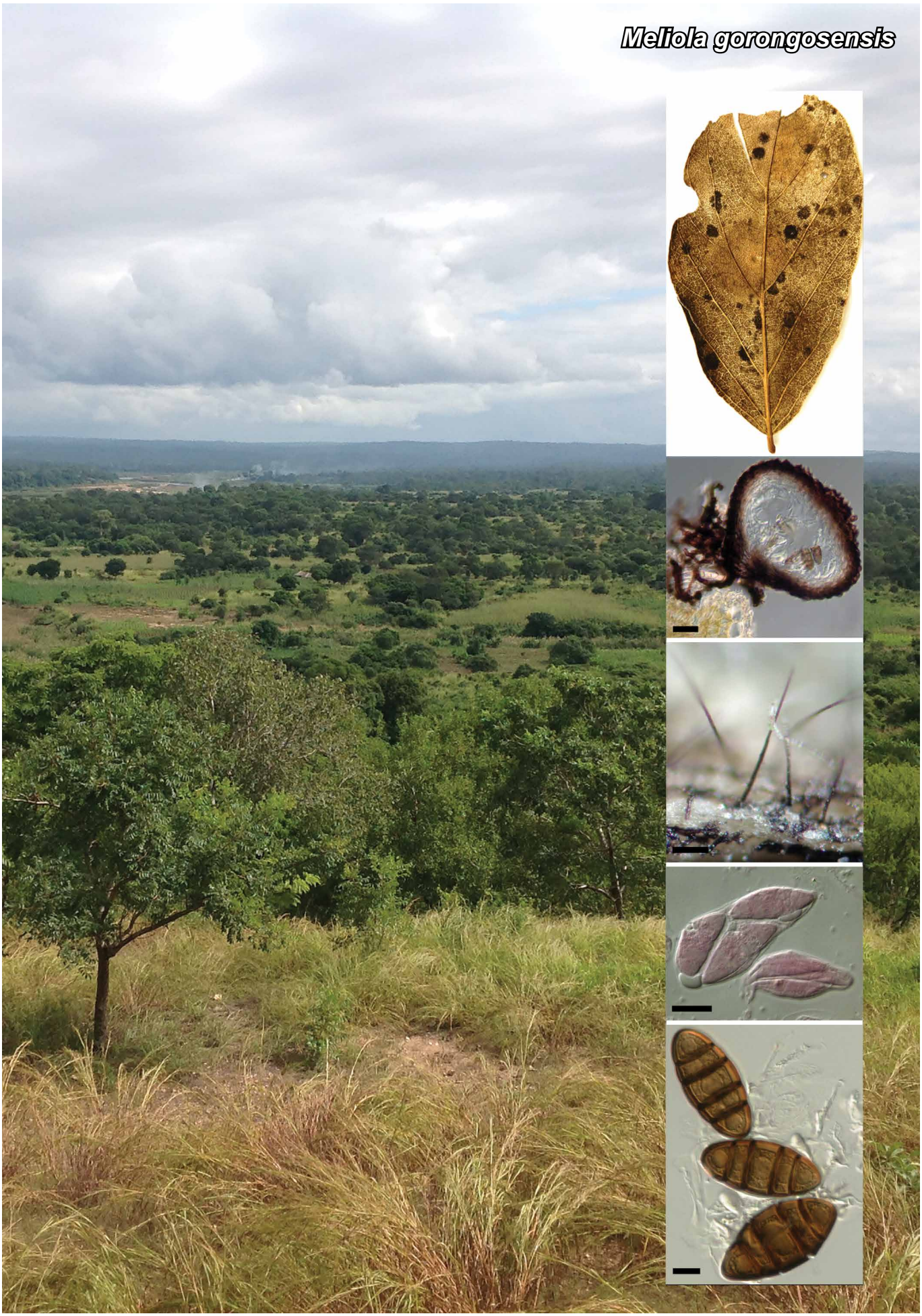
Meliola gorongosensis

Fungal Planet 931 – 19 July 2019

Meliola gorongosensis Iturr., Raudabaugh & A.N. Mill., *sp. nov.*

Etymology. Name refers to the locality in which it was collected, Gorongosa National Park.

Classification — *Meliolaceae*, *Meliolales*, *Sordariomycetes.*

Mycelium forming ovate to irregular black patches on both surfaces of leaflets, up to 10 mm diam, hyphae dark brown, 5–7 µm diam, thick-walled, wall 1 µm wide, septate, closely branched forming a dense network on the surfaces of the leaflet, bearing numerous short hyphopodia. *Hyphopodia* arranged in a variety of manners: on opposites sides of the hyphae or alternately or unilaterally on one side of the hyphae, arising from a short basal cell, 12–17 µm long, terminating in a swollen, rounded to slightly curved head, 7.6–10.3 × 8.8–11.6 µm. *Setae* arising from the hyphae, multiple, stiff, erect, dark-brown, septate, more than 1 mm high, tapering towards the apex, smooth-walled with walls equally thickened the entire length. *Ascomata* on both surfaces of leaves, numerous, black, lenticular-to-spherical, 220 × 165 µm, arising from the hyphae. *Ascomatal wall* of *textura globulosa-angularis* in surface view, with a distinguishable pattern composed of groups of 4–5 dark brown cells with each group circumscribed by a dark perimeter, cells 10–11 µm, 3–4 layers thick, brown, outer cells dark-brown, isodiametric. *Asci* arranged in a basal layer, oblong when young, 53.5–80.4 × 31–36.3 µm, widening as they mature to become subspherical, with a short point of attachment, 71–75 × 34–51 µm, 3-spored with one aborted spore, evanescent when mature. *Ascospores* dark-brown when mature, thick-walled, wall 3–3.5 µm wide, broadly ellipsoidal, slightly curved, inequilateral, with one rounded end and the other end tapering or both ends tapering, 40–50(–55) × 14–22(–24) µm, with four very dark and thick-walled septa, sometimes constricted at the septa; with one large guttule per cell.

Habitat — On living and fallen, dead leaflets of *Philenoptera violacea*.

Distribution — Known only from Gorongosa National Park, Mozambique.

Typus. Mozambique, Sofala Province, Gorongosa National Park, Great Rift Valley of central Mozambique, road south of Chitengo base camp toward Pungue River and Vinho community on opposite bank, mixed palm forest, on fallen, dead leaflets of *Philenoptera violacea* (*Fabaceae*), -18.9889S, 34.3525E, 40 m elev., 21 May 2016, *T. Iturriaga* MOZ 9 (holotype CUP 70689, isotype ILLS 82564, ITS sequence GenBank MK802897, MycoBank MB830654).

Additional material examined. Meliola carvalhoi: in foliis *Lonchocarpi cyanescentis* (*Papilionaceae*). Africa orientalis (Portuguese East Africa): Larde, 30 Aug. 1946, *T. Carvalho*, IMI 16646 (typus). *Meliola carvalhoi*: Sydowia 5: 4. 1951.

Colour illustrations. Typical African savannah mixed with patches of forest in Gorongosa National Park, Mozambique. Fallen leaflet of *Philenoptera violacea* with blackened areas of *M. gorongosensis*; longitudinal section through ascoma; erect and pointed setae on superficial hyphae; two young asci with three ascospores each (in Congo Red); three dark brown 4-septate ascospores. Scale bars = 40 µm (ascomal section), 40 µm (setae), 20 µm (immature asci), 10 µm (ascospores). Photo credits: T. Iturriaga, D. Raudabaugh.

Notes — The phylogenetic placement of *Meliola* has been the subject of debate for many years. Saenz & Taylor (1999) showed that *Meliola* belongs to the 'unitunicate pyrenomycetes', today treated in the *Meliolaceae* (*Sordariomycetes*). The new species described here, *Meliola gorongosensis*, possesses the typical characters known for the genus: dark mycelium as a superficial mat of thick, dark-septate hyphae; hyphopodia, setae and ascomata superficial on the mycelium; ascomatal wall with thick-walled dark-cells, with or without a pattern, and ascospores usually 4-septate with a thick dark-brown wall. Most species occur in tropical areas as highly specialised biotrophs on leaves of specific genera or species of higher plants. A 'Beeli formula' (Beeli 1920) is a numerical code traditionally used to characterise each species, in this case Beeli number 3113.4344. The type of *Meliola carvalhoi* (Deighton 1951) was compared to our material since it was described from the same plant genus *Philenoptera* (as *Lonchocarpus cyanescens*, a nomenclatural synonym of *Philenoptera cyanescens*), both in the family *Leguminosae* (Schrire 2000) and also both from Mozambique. Both species were collected in the same general area (-18.25S, 35.00E). *Meliola gorongosensis* differs from *M. carvalhoi* in that the former has an ascomatal wall with a defined cell pattern, whereas *M. carvalhoi* shows no specific pattern. *Meliola gorongosensis* has only one type of appressorium, while *M. carvalhoi* has two kinds of appressoria. In *M. gorongosensis* the appressorium terminal cell is rounded with a rugose cell wall. In *M. carvalhoi*, one type of appressoria terminal cell is also rounded, but with a smooth cell wall, while the second type of appressoria has mucronate apical cells. Ascospores of *M. gorongosensis* are ellipsoid and inequilateral, while those in *M. carvalhoi* are cylindrical to slightly ellipsoid and equilateral. Setae in *M. gorongosensis* are smooth-walled with walls equally thickened the entire length unlike those in *M. carvalhoi* with walls irregularly thickened. Deighton (1951) describes the setae in *M. carvalhoi* as being spiny, although we were not able to observe the spines in the material that we examined. The host of *M. gorongosensis* is *Philenoptera violacea*, while the host of *M. carvalhoi* is *Philenoptera cyanescens*.

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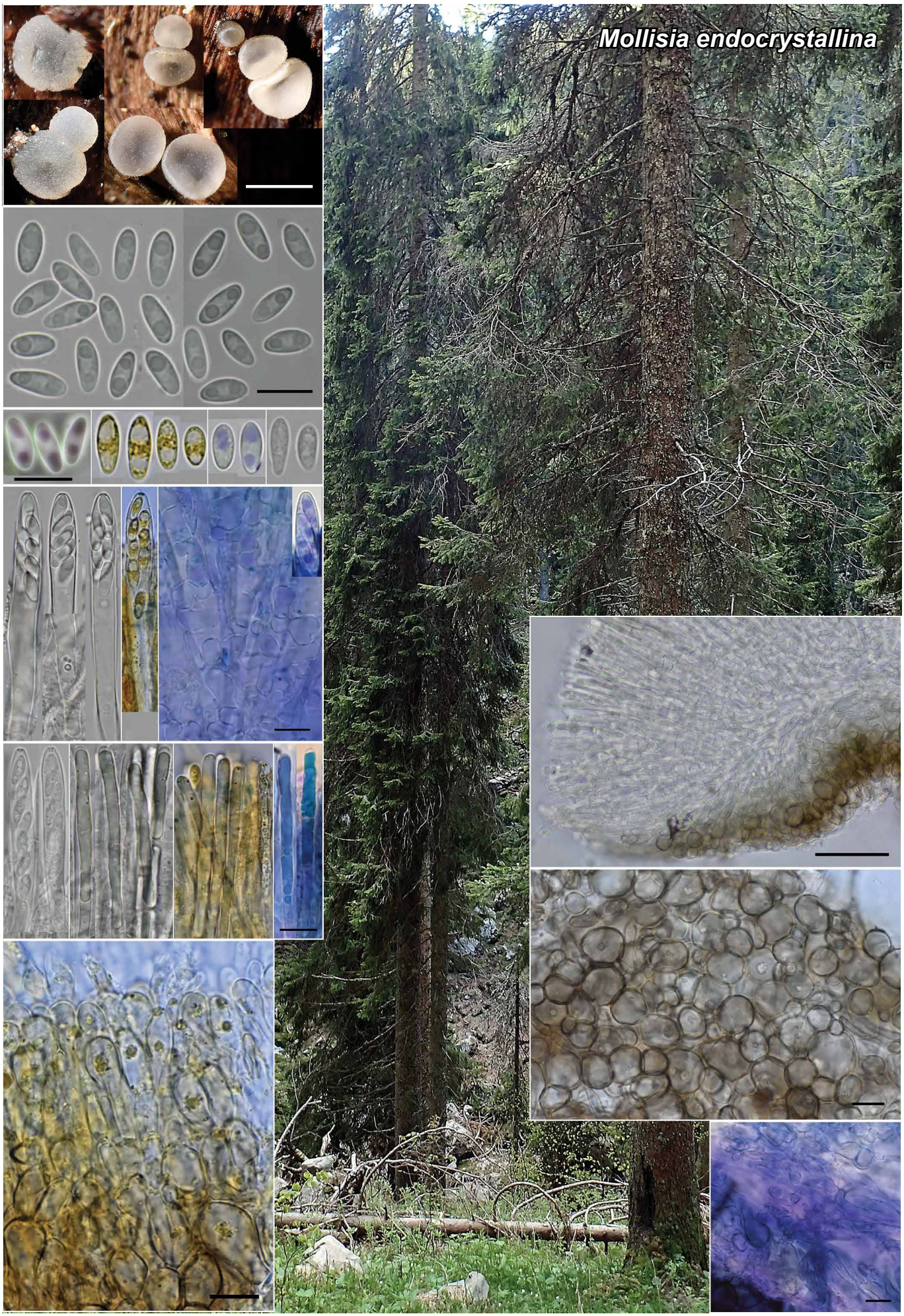
Mollisia endocrystallina

Fungal Planet 932 – 19 July 2019

Mollisia endocrystallina Matočec, I. Kušan, Jadan, Mešić & Tkalčec, *sp. nov.*

Etymology. Named after the crystalloid matter found in the ectal excipular and marginal cells.

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

Ascomata apothecial, shallowly cupulate when young, then expanding to discoid or plate-shaped, becoming subpulvinate when fully mature, superficial, sessile, ± circular from the top view, *0.6–1.3 mm diam, solitary or gregarious (up to few apothecia). Hymenium pale grey in young stage to pale lead-grey in maturity, not wrinkled; margin ± sharp and whitish but lowered down at full maturity, smooth, entire, not lobed, ex-rolled in maturity; excipular surface pale brownish grey from base almost to the margin, smooth. Basal hyphae macroscopically indistinguishable. Asexual morph not seen. *Hymenium* *95–125 µm thick. *Asci* cylindrical with conical-subtruncate apex, *88.7–117 × (6.6–)7–8.1(–8.6) µm, †64–73.5 × 5.7–6.5 µm, *pars sporifera* *24–34.6 µm, 8-spored, in living state protruding above paraphyses up to 20 µm, base cylindrical-truncate, containing cytoplasmic refractive hyaline globule, arising from repetitive croziers, apical apparatus strongly refractive and visible already in water and especially in †KOH, in Lugol's solution (IKI) apical ring medium to strongly amyloid (2-3bb) of *Calycina*-type. *Ascospores* ciborioid to piscioid, with notably rounded poles, bilaterally symmetrical, 1-celled, *(6.8–)7–*8.4*–11(–11.3) × (3.1–)3.3–*3.7*–4.3(–4.5) µm, *Q = (1.8–)1.9–*2.5*–2.9(–3), hyaline, smooth, uninucleate, freshly ejected without sheath, biseriate inside *asci, lipid bodies absent, *cytoplasm containing two, rarely one, bipolar refractive vacuoles, 1.9–3.3 µm diam; in IKI cytoplasm yellow, nucleus contrasted, bipolar vacuoles hyaline and non-refractive; in brilliant cresyl blue (CRB) vacuoles greyish rose to pale purplish, disappearing after adding KOH. *Paraphyses* cylindric-obtuse to subclavate, apical cell *32.6–64 × 2.8–4.2(–5) µm, straight, simple, sometimes branched below apical cell, *containing single cylindrical strongly refractive vacuolar body (VB), in some cells few VBs compacted next to each other, wall thin and hyaline; in KOH without yellow reaction; in IKI VBs not stained, soon collapse, some yellow-orange particles remain peritunically; in CRB turquoise-blue to deep blue, immediately collapse after adding KOH. *Subhymenium* *25–32 µm thick at the middle flank, hyaline, richly beset with highly repetitive croziers, composed of hyaline densely packed epidermoid and ± cylindric cells *4.2–8.4 µm wide. *Medullary excipulum* *37–45 µm at the middle flank, composed of hyaline markedly gelatinised *textura porrecta-intricata*, cells *2.9–5.6 µm wide, outer cells somewhat swollen and perpendicularly oriented towards ectal excipulum, *11.6–18.8 × 5.7–9.9 µm, thin-walled, occasionally with few lipid bodies, devoid of crystals and KOH-soluble cytoplasmic bodies; in CRB intercellular spaces purplish. *Ectal excipulum* *33–44 µm thick at the middle flank, composed of *textura globulosa-angularis*, cells *6–19.5 µm, †4.6–15.3 µm wide, walls ochre-brown, *0.7–0.9 µm thick, most cells in the cortical layer contain ± central, freely floating, hyaline and moderately refractive, rosettiform, CRB stainable and KOH soluble crystalloid body, 1.8–4.5 µm diam, devoid of true intercellular crystals; in IKI crystalloid bodies golden yellow, while in CRB violet blue or greyish blue. *Marginal tissue* thin, *13–26 µm thick, composed of few non-protruding, terminal, clavate, thin-walled, ± elongated cells, *16–22 × 5.7–7.7 µm, containing crystalloid bodies as in ectal excipulum. *Subicular hyphae* arising from basal flank, confined to an apothecial base only, 2–7 individual hyphae firmly cemented together forming flexuous fascicles, hyphae only occasionally branched, smooth, sparingly septate, without lateral protuberations, greyish brown, *2–2.7 µm wide, walls *0.5–0.7 µm thick.

Distribution & Habitat — This species is known so far only from the type locality on Mt Velebit, Croatia. It is found on coarse woody debris of *Picea abies*, lying near the almost continuous snow deposit, under permanently humid conditions at the sinkhole bottom in the boreal type of forest.

Typus. Croatia, Lika-Senj County, Sjeverni Velebit National Park, northern part of the Mt Velebit, Škrbina draga area, 1600 m SW from Mali Rajinac peak (1699 m), 1220 m asl, N44°47'07" E14°59'51"; on fallen decorticated trunk of *Picea abies* in a forest of *P. abies* with *Vaccinium myrtillus*, *Rubus* sp. and *Oxalis acetosella*, 26 May 2017, *N. Matočec* (holotype CNF 2/10055, ITS and LSU sequences GenBank MK088059 and MK088060, MycoBank MB828351).

Notes — According to our analysis (see Supplementary Fig. FP932) and recent molecular phylogenetic studies certain members of the asexual genera *Acephala*, *Acidomelania*, *Barrenia*, *Cystodendron*, *Phialocephala* and *Trimmatostroma* (Crous et al. 2007, Grünig et al. 2009, Walsh et al. 2014, 2015, Tanney et al. 2016, Hamim et al. 2017) cluster with *Mollisia* spp. in a *Loramyces*-*Vibrissea*-*Mollisia* clade (cf. Wang et al. 2006).

Mollisia endocrystallina displays certain similarity to *M. rivularis* and *M. uda* ss. auct. Certain critical microscopic characters found in *M. endocrystallina* are unique: 1) ectal excipular and marginal cells contain freely floating, hyaline and moderately refractive, rosettiform crystalloid bodies which are differentially stained in CRB and IKI, and soluble in KOH; 2) sporoplasm regularly contains refractive vacuoles while true oil drops are missing; and 3) lack of VBs in the outermost cells of margin and ectal excipulum. *Mollisia rivularis* is KOH negative like *M. endocrystallina* but its spores contain oil drops while *M. uda* is KOH positive (unlike *M. endocrystallina*) and has eguttulate ascospores (unpubl. data). Furthermore, *M. rivularis* has narrower spores: 1.8–2.4 µm in Krieglsteiner (2004) and 1.7–2 µm in Svrček (1987) vs 3.3–4.3 µm in *M. endocrystallina* and shorter asci, while *M. uda* has considerably more elongated spores Q = 2.9–3.6 vs 1.9–2.9 in *M. endocrystallina*. *Mollisia rivularis* and *M. uda* are found exclusively on hardwood (mostly *Fagus*) submersed in a creek (Svrček 1987, Krieglsteiner 2004, unpubl. data) while *M. endocrystallina* was found on *Picea* remnants in an air-humid environment in a hyperkarst waterless area. Fisher & Webster (1983) described *Mollisia gigantea* from a submerged *Picea* branch but contrary to the new species it is creamy to buff-coloured and has longer spores (10–12 vs 7–11 µm) without sporoplasmic inclusions. Phylogenetically, close *M. caesia* is imperfectly known species found on smaller wood remnants of *Fagus*, *Salix* and *Alnus* with much longer spores (e.g., 12–14 µm, see Rehm 1896).

Colour illustrations. Croatia, Mt Velebit, Škrbina draga area, type locality. *Apothecia; *ascospores in H_2O, IKI, CRB, †ascospores (KOH); *asci (H_2O, IKI, CRB), subhymenium (CRB); †asci (KOH), *paraphyses (H_2O, IKI, CRB); marginal cells with crystalloids (IKI); vertical median section of the apoth.; ectal exc. cells with crystalloids (H_2O); medulla (CRB). Scale bars = 1 mm (apoth.), 10 µm (microscopic elements), 50 µm (apoth. anatomy).

* = living material, † = chemically fixed material. Amyloidity after Baral (1987).

Supplementary material

FP932 ML phylogenetic tree inferred from the dataset of ITS1-5.8S-ITS2 gene sequences from *Mollisia endocrystallina* and related species.

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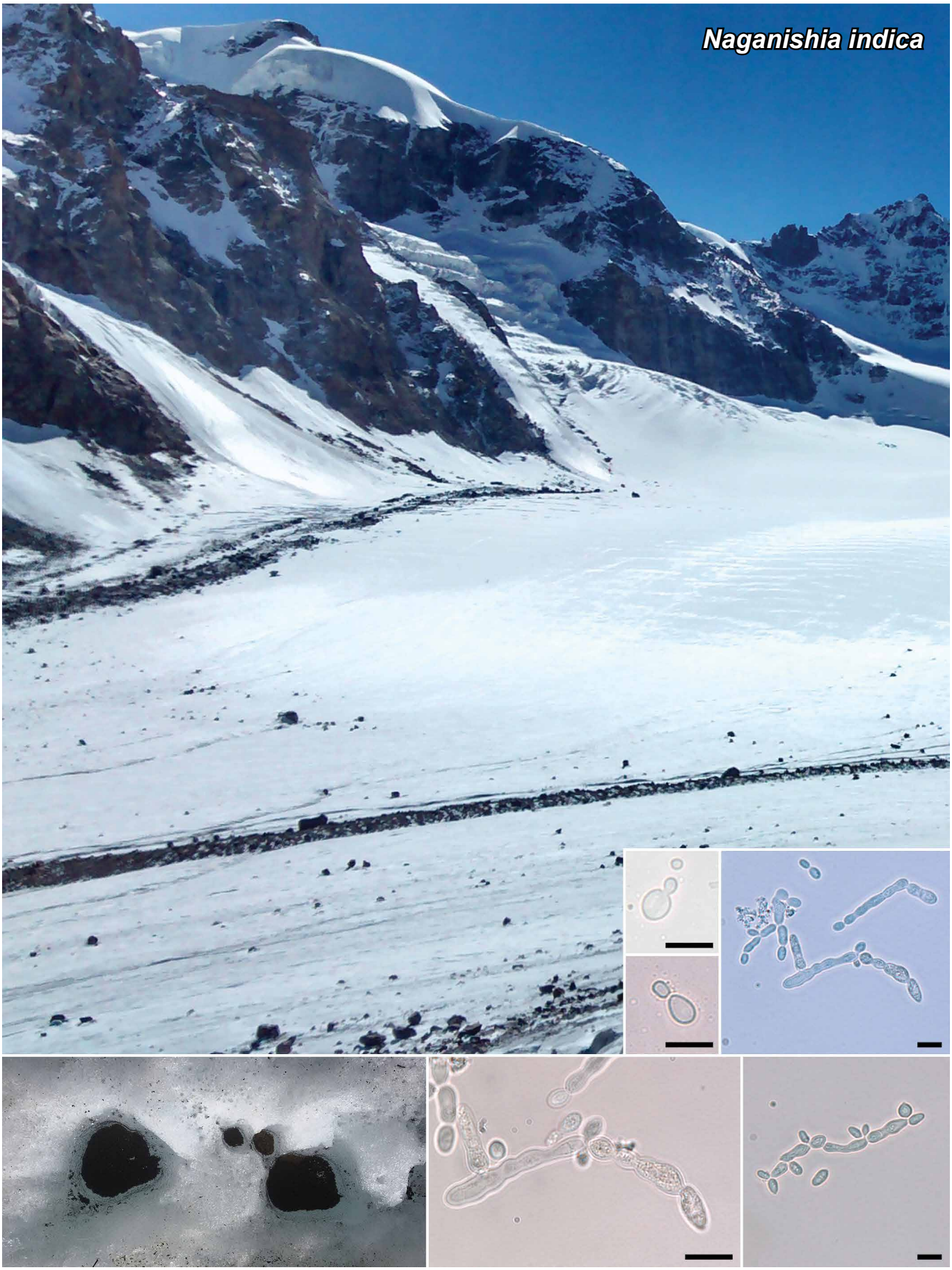

Naganishia indica

Fungal Planet 933 – 19 July 2019

Naganishia indica Roh. Sharma, S.M. Singh & Shouche, *sp. nov*.

Etymology. Name reflects the country from where it was isolated.

Classification — *Tremellaceae*, *Tremellales*, *Tremellomycetes.*

After 7–10 d at 15 °C on Sabouraud dextrose agar (SDA), the cells are ovoid to ellipsoidal, 3 × 5 µm (2.2–4.5 × 3.5–6.9 µm) occurring singly, single budding, sedimentation occurs. After 15 d at 15 °C on SDA medium only pseudohyphae are produced and no true hyphae are observed. On SDA, the colony of RNF072 is yellowish cream on the surface, and yellow in reverse, raised, smooth entire margin, > 1 mm after 10 d. No asci and ascospores were observed after 20 d of incubation on SDA medium as well as Corn Meal Agar (CMA). Assimilation of carbon compounds: D-xylose, D-maltose, D-saccharose, L-Arabinose, Calcium-2-keto-Gluconate, Methyl-Alpha-D-Glucopyranoside, D-melezitose were assimilated. D-galactose, D-raffinose, D-trehalose, Glycerol, Inositol, Sorbitol, Adonitol, D-cellobiose, Xylitol were not assimilated.

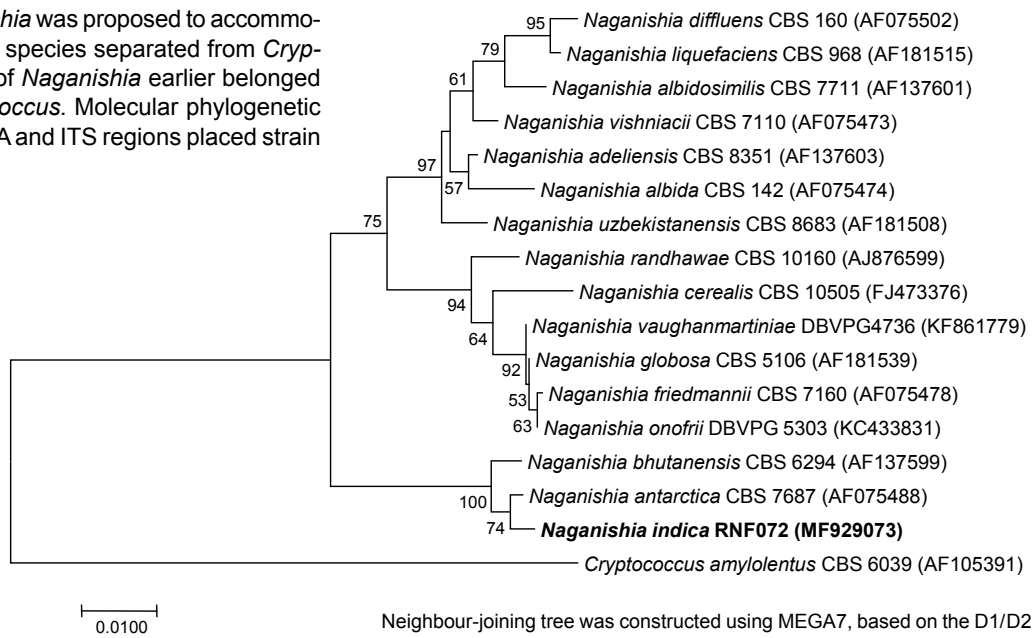
Cultural characteristics — On CMA the colonies are white, round, smooth margin, small, pointed > 0.1 mm after 10 d. The strain was grown at different temperatures from 5–25 °C and it showed optimal growth at 15 °C.

Habitat — Powdery windblown dust on snow/glaciers (Cryoconites).

Distribution — India (Chhota Shigri glacier, Gramphu-Batal-Kaza Rd, Himachal Pradesh).

Typus. India, Gramphu-Batal-Kaza Road, Kiato (Lahaul and Spiti), Himachal Pradesh, cryoconites, 4 Aug. 2015, *S.M. Singh* (holotype RNF072, preserved as metabolically inactive culture in NCMR, LSU sequence GenBank MF929073, MycoBank MB822675).

Notes — The genus *Naganishia* was proposed to accommodate *Naganishia albida* with 15 species separated from *Cryptococcus*. Most of the species of *Naganishia* earlier belonged to the albidus clade of *Cryptococcus.* Molecular phylogenetic analysis of the D1/D2 LSU rDNA and ITS regions placed strain RNF072^T in the *Naganishia* clade. In terms of pairwise sequence divergence, strain RNF072^T differed from other existing *Naganishia* species and showed highest similarity with the ex-type strains of *Naganishia friedmannii* CBS 7160^T (GenBank KY108613) and *Naganishia globosa* CBS 5106^T (GenBank KY108616). It differed from ex-type strains of *N. friedmannii* CBS 7160^T and *N. globosa* CBS 5106^T by 39 (4 %) and 43 (5 %) nucleotide substitution, respectively in the D1/D2 LSU rDNA region. A phylogenetic tree based on D1/D2 LSU rDNA gene was constructed by Neighbour-Joining. The tree discriminates the strain RNF072^T from *N. bhutanensis* CBS 6294^T and *N. antarctica* CBS 7687^T indicating its novel stature. A phylogenetic tree was also constructed by Maximum Parsimony and Maximum Likelihood method using all the species of the genus *Naganishia*, but no difference was obtained in the topology of trees and position of the proposed novel species within the genus *Naganishia*. We propose this yeast isolate as a novel species which is supported by phylogenetic, morphological and physiological data. The morphological characteristics of *N. indica* RNF072^T is in accordance with the genus *Naganishia.* Cell morphology is ovoid to ellipsoidal with well-developed pseudohyphae. The strain RNF072^T proliferated by single budding. The novel yeast *N. indica* RNF072^T is isolated from the cryoconites of Chhota Shigri glacier, Indian Himalayas. The present novel species shares similarity with its closest phylogenetic relatives *N. antarcticus* and *N. bhutanensis* as all three are isolated from soils in extremely cold environments, but from different geographical regions, i.e., from India, Antarctica and Bhutan.



Neighbour-joining tree was constructed using MEGA7, based on the D1/D2 LSU rDNA region showing the position of *Naganishia indica* sp. nov. among related species within *Naganishia*. Bootstrap support values > 50 % are given at nodes based on 1 000 replications. The scale bar represents 2 % sequence difference.

Colour illustrations. Chhota Shigri Glacier, India. Cryoconites from which the yeast was isolated; pseudohyphae (SDA, 15 d); budding yeast cells (CMA, 7 d). Scale bars = 10 µm.

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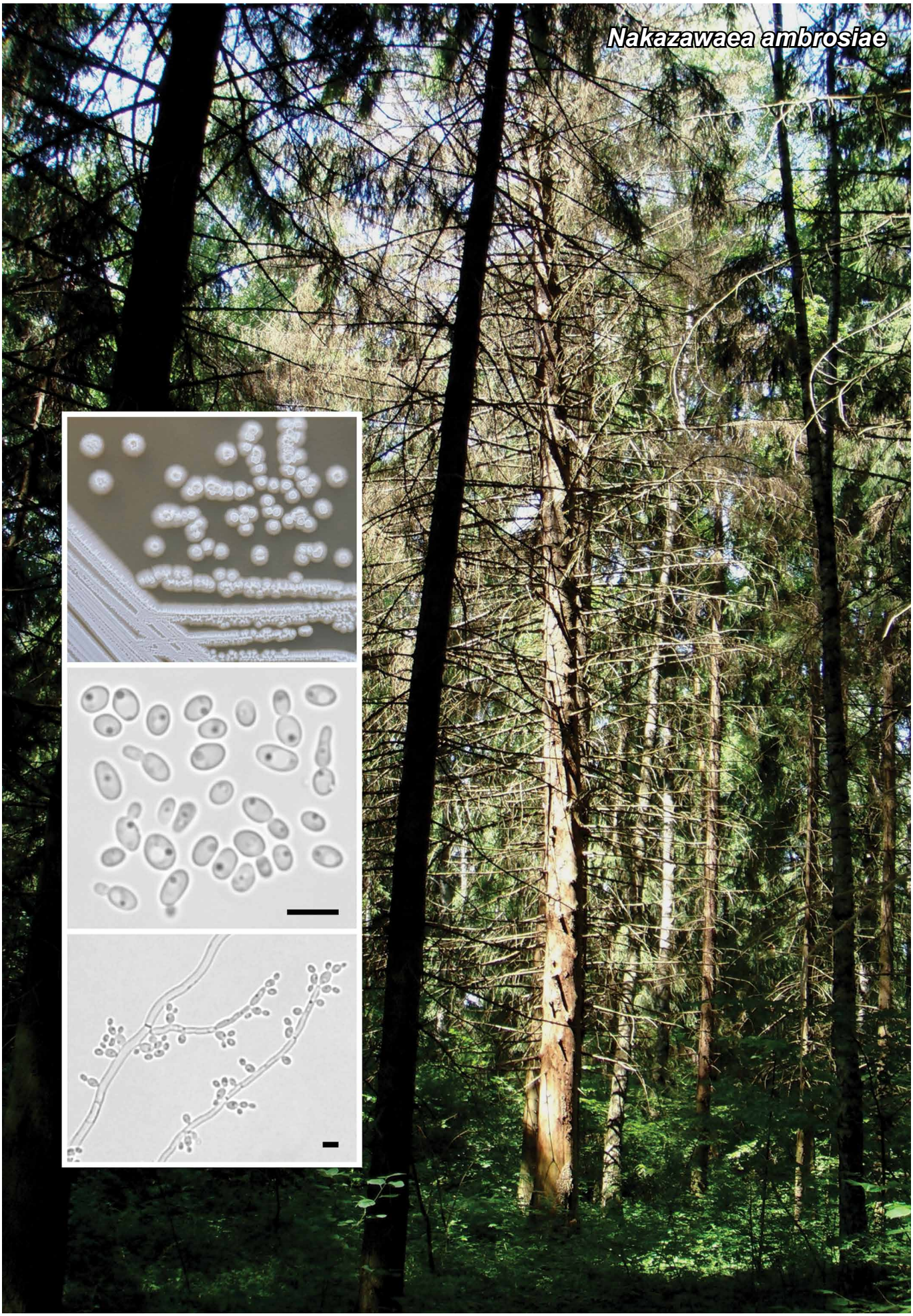

Nakazawaea ambrosiae

Fungal Planet 934 – 19 July 2019

Nakazawaea ambrosiae Kachalkin, M.A. Tomashevskaya, T.A. Kuznetsova & M.V. Vecherskii, *sp. nov.*

Etymology. Name refers to ambrosia beetles, the *galleries* and the larvae of which served as the source of the strains.

Classification — *Pichiaceae*, *Saccharomycetales*, *Saccharomycetes*.

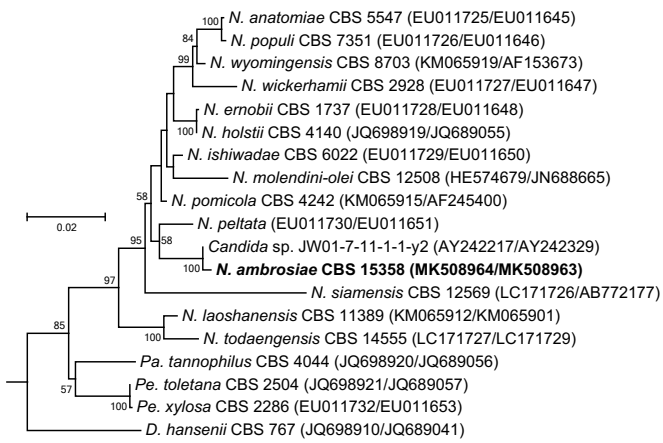
On glucose peptone yeast extract agar (GPYA) and 5 % malt extract agar (MEA), after 7 d at 22 °C, streak is white, glistening, smooth and butyrous, raised, with hyphal production at the lobed margin; the surface of the colony is rugose or smooth. Cells are globose, subglobose and ovoid, 3.0–4.5 × 1.5–2.5 µm, occur singly or in pairs, divide by multilateral budding, cells with one or two buds. Pseudohyphae and true hyphae with subglobose and ovoid blastoconidia are formed. Ascospores have not been 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, trehalose, maltose (variable) and cellobiose (slowly and variable) are fermented, but galactose is not fermented. Glucose, galactose, L-sorbose, sucrose, maltose, cellobiose, trehalose, raffinose (weak and variable), melezitose, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, ethanol, glycerol, erythritol (weak), ribitol, galactitol, D-mannitol, D-glucitol, methyl alpha-D-glucoside, salicin, DL-lactic acid, citric acid (weak), D-gluconate (weak), D-glucosamine, and arbutin are assimilated; no growth occurs on lactose, melibiose, inulin, soluble starch, *myo*-inositol, methanol, D-glucoronate, succinic acid, 2-keto-D-gluconate and 5-keto-D-gluconate. Nitrogen compounds: ammonium sulfate, potassium nitrate (variable), L-lysine, D-glucosamine, creatinine (weak) and creatine (weak) are assimilated. Growth on vitamin-free medium and on MEA with 10 % NaCl is not present. Growth on 50 % w/w glucose / yeast extract (0.5 %) agar is positive. Growth with 0.01 % cycloheximide and 0.1 % cycloheximide is present. Starch-like compounds are not produced. Diazonium blue B colour and urease reactions are negative. Maximum growth temperature is 41 °C.

Typus. Russia, Moscow region, in the vicinity of Zvenigorod town, from the galleries of *Ips typographus* under the bark of the *Picea abies (Pinaceae)*, Mar. 2017, *A.V. Kachalkin* UL1 (holotype KBP Y-6137 preserved in a metabolically inactive state, ex-type cultures VKM Y-3024 = DSM 106748 = CBS 15358, SSU, ITS-D1/D2 domains of LSU nrDNA, *TEF1* and *RPB1* sequences GenBank MK508964, MK508963, LR215815 and LR216143, MycoBank MB830277).

Additional materials examined. Russia, Moscow region, in the vicinity of Dmitrov town, from the galleries of *Ips typographus* under the bark of the *Pinus sylvestris*, Dec. 2017, *A.V. Kachalkin*, KBP Y-6306; Moscow region, in the vicinity of Ruza town, from *Ips typographus* larvae in the wood of the *Picea abies*, from the galleries of *Ips typographus* under the bark of the *Picea abies*, from the wood of the *Picea abies*, May 2018, *A.V. Kachalkin*, KBP Y-6362 and Y-6397, KBP Y-6378, KBP Y-6380. ITS sequences GenBank MK562506–MK562510.

Colour illustrations. Russia, Moscow region, spruce forest infected by bark beetles. Growth of yeast colonies on MEA; yeast cells and hyphal structures on MEA (after 7 d at 22 °C). Scale bars = 5 µm.

Notes — Analysis of the ITS region of the surveyed yeasts suggested that they were conspecific and represented a hitherto undescribed species of *Nakazawaea*. Based on the NCBI GenBank database, the best hits using the **ITS** sequence are *N. holstii* CBS 4140 (GenBank KY104365; 90 % similar, 36 subst. and 15 gaps) and uncultured clone S57 from pine shoot beetle (*Tomicus piniperda*) in Finland, GenBank KJ512850 (99.8 %, 1 subst.), using **LSU** these are *N. laoshanensis* NRRL Y-63634 (GenBank NG_055165; 98 % similar, 9 subst.) and some strains (with 1–2 subst.) from plum in China (GenBank KU240039), from bark beetles in Canada (GenBank AY761152), from gut of scolytid beetle in USA (Suh et al. 2005; GenBank AY242329), from *Dendroctonus brevicomis* in USA (Davis et al. 2011; GenBank HQ413286), from associations with *Dendroctonus* spp. in USA and Mexico (Rivera et al. 2009; GenBank EF016026, EF016034, EF016040, EF016061), using **SSU** these are *N. peltata* strain NRRL Y-6888 (GenBank EU011730; 99 % similar, 16 subst. and 2 gaps) and strain *Candida* sp. from gut of scolytid beetle in USA (Suh et al. 2005; GenBank AY242217; 99.8 % similar, 3 subst.), using ***TEF1*** it is *N. anatomiae* NRRL Y-17641 (GenBank EU014756; 92 % similar, 32 subst. and 2 gaps) and using ***RPB1*** it is *N. ernobii* MUCL 30037 (GenBank EU344100; 81 % similar, 122 subst. and 4 gaps). In compliance with a recent phylogenetic analysis of the genus (Polburee et al. 2017), the placement of the new species is demonstrated using the combined SSU and LSU rDNA phylogeny. *Nakazawaea ambrosiae* differ from the phylogenetically (by rDNA) closely related species by no galactose fermentation, no growth on soluble starch, growth at 41 °C (differ from *N. holstii*, *N. laoshanensis*, *N. peltata*) and pseudohyphae and hyphae formation (differ from *N. laoshanensis*, *N. peltata*).



Maximum likelihood (ML) tree obtained from the combined analysis of SSU and LSU sequence data. Bootstrap support values above 55 % are shown at the nodes. *Trigonopsis variabilis* CBS 1040 (JQ698933/U45827) was used as outgroup (hidden). The alignment included 2111 bp and was performed with MAFFT v. 7. 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.

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Nigrospora brasiliensis

Fungal Planet 935 – 19 July 2019

Nigrospora brasiliensis A.C.Q. Brito, C. Conforto, A.R. Machado, *sp. nov.*

Etymology. Name refers to the country where the species was collected, Brazil.

Classification — *Apiosporaceae*, *Xylariales*, *Sordariomycetes*.

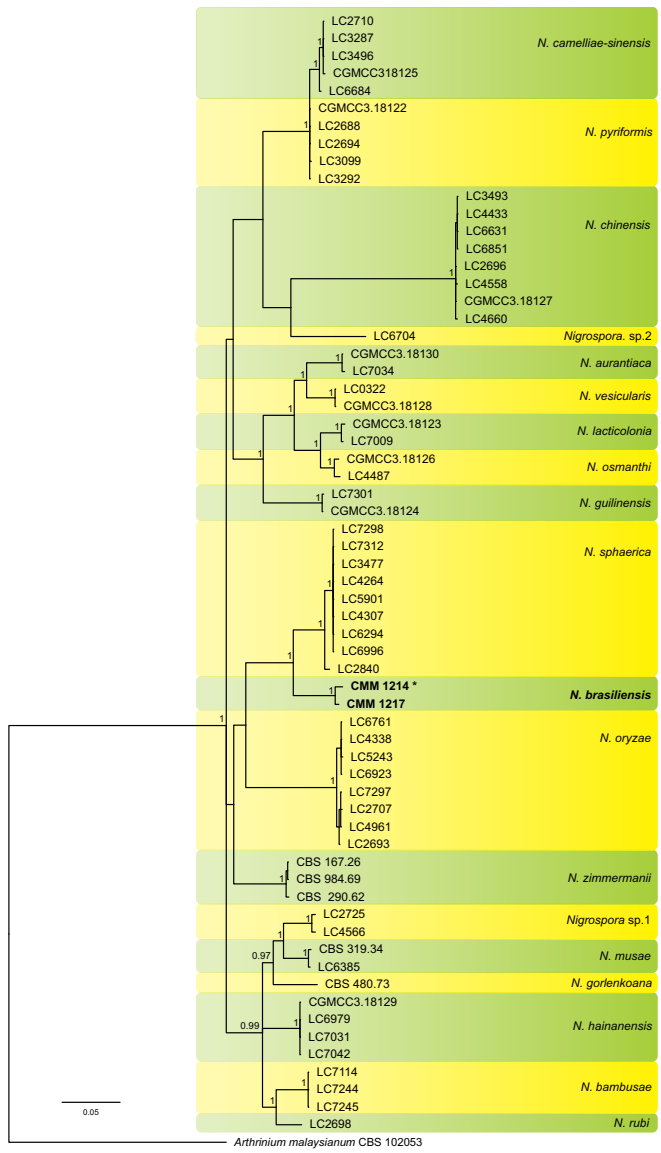
Hyphae septate, hyaline to pale brown, branched, smooth, 2.6–5.2 µm diam. *Conidiophores* reduced to conidiogenous cells. *Hyaline vesicles* around the septum delimiting the conidia and their conidiogenous cells. *Conidiogenous cells* solitary, monoblastic, discrete, determinate, pale brown to dark brown, doliiform, ampulliform, subglobose or globose, 7.8–13 × 5.2–13 µm. *Conidia* solitary, acrogenous, smooth, aseptate, black, shiny, ovoid, subglobose or globose, 15.6–28.6 µm diam.

Culture characteristics — On PDA, the colonies are woolly, floccose, margin circular, white, reaching 9 cm diam at 25 °C in 12 d in the dark.

Typus. Brazil, Pernambuco state, São João (S08°51'14.5" W36°22'43.7"), isolated from cladode brown spot of *Nopalea cochenillifera* (*Cactaceae*), 15 Aug. 2013, *C. Conforto* (holotype URM 93057, culture ex-type CMM 1214, ITS, *TEF1-α* and *TUB2* sequences GenBank KY569629, MK753271 and MK720816, MycoBank MB830434).

Additional material examined. Brazil, Pernambuco state, São João (S08°48'50" W36°26'42"), isolated from cladode brown spot of *N. cochenillifera*, 3 Sept. 2013, *C. Conforto*, CMM 1217, ITS, *TEF1-α* and *TUB2* sequences GenBank KY569630, MK753272 and MK720817.

Notes — The specimens obtained were identified causing initially brown and then black spots, circular or elliptical in shape, 1–3 cm diam on the cladodes of *Nopalea cochenillifera*. The lesions may extend from one side to the other of the cladodes, causing perforations due to the fall of the affected tissue. Such lesions can coalesce to form large necrotic areas which cause cladode drop. Based on megablast searches in GenBank, the *N. brasiliensis* **ITS** sequences have 98.46 % identity to *N. sphaerica* (LC6996; GenBank KX986085), while on ***TEF1-α*** sequences and ***TUB2*** the percentage identity was 89.19 % to *N. sphaerica* (LC2840; GenBank KY019318) and 91.55 % to *N. sphaerica* (LC7312; GenBank KY019618), respectively. According to the phylogenetic analyses, *N. brasiliensis* is most closely related to *N. sphaerica*. Conidiophores in *N. brasiliensis* are reduced to conidiogenous cells, whereas in *N. sphaerica* conidiophores are micronematous or semi-macronematous, flexuous or straight, extensively branched, multiseptate (Wang et al. 2017). The conidiogenous cells are also different, since in *N. sphaerica* they have a subspherical shape (Wang et al. 2017), but in *N. brasiliensis* they are doliiform, ampulliform, subglobose to globose. In *N. sphaerica* conidia are globose or subglobose (Wang et al. 2017), in *N. brasiliensis* they are subglobose to globose (in general) and ovoid. In addition, *N. brasiliensis* has slightly larger conidia. The additional material examined (CMM 1217) under the same conditions as the ex-type culture CMM 1214 (PDA, 12 d, 25 °C in the dark) shows a different colony appearance, white mycelium in the centre to greyish near the edge of the Petri plates, becoming black with time.



Bayesian inference tree was obtained by analysis of concatenated matrix of ITS, *TEF1-α* and *TUB2* sequences in MrBayes v. 3.2.6 at CIPRES science gateway. The nucleotide substitution model used was SYM+I+G for ITS, HKY+I+G for *TEF1-α* and GTR+G for *TUB2*, selected separately by MrMODELTEST v. 2.3 according Akaike Information Criterion (AIC). Bayesian posterior probability values above 0.95 are indicated at the nodes. The new species is indicated in **bold**. (*) indicates the ex-type culture. *Arthrinium malaysianum* (CBS 102053) was used as outgroup. The alignment was deposited in TreeBASE (Submission ID 24256).

Colour illustrations. Cladode of *Nopalea cochenillifera* with brown spot in Pernambuco. Colony on PDA after 12 d at 25 ºC in the dark; conidia; conidium and conidiogenous cell; hyaline vesicle delimiting the conidium and their conidiogenous cell (indicated by arrow). Scale bars = 10 µm.

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Ossicaulis salomii

Fungal Planet 936 – 19 July 2019

Ossicaulis salomii Siquier & Bellanger, *sp. nov.*

Etymology. Named in honour of the mycologist Joan Carles Salom, for his significant contribution to our knowledge of the Balearic Funga.

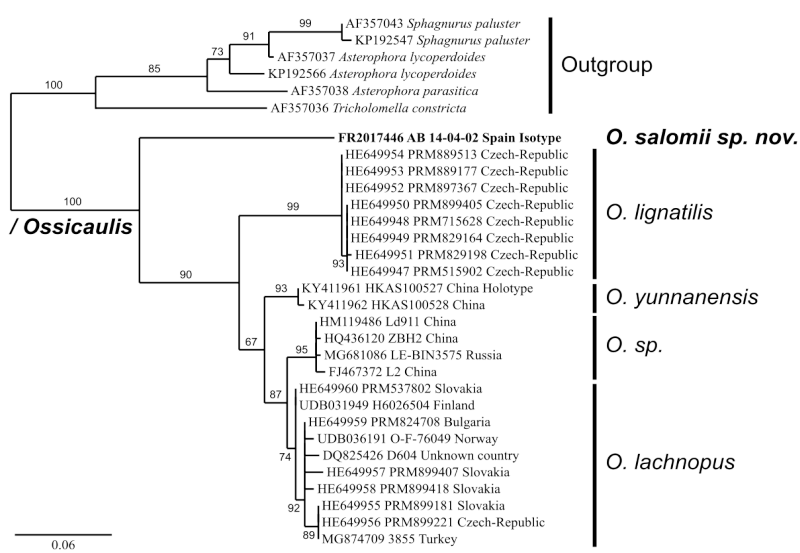
Classification — *Lyophyllaceae*, *Agaricales*, *Agaricomycetes*.

Pileus up to 11 mm diam, soon flat-convex and somewhat depressed in the centre with involute margin for a long time; surface dry, with white rimulose coating, cracked with time, exposing more or less clear caramel colour. *Lamellae* emarginate to slightly decurrent, somewhat ventricose, white at first, white cream when ageing or dehydrating. *Stipe* up to 19 × 1.5 mm, central, cylindrical, slightly thickened towards base, subpruinose o pruinose, especially in the upper zone and towards base, whitish to light grey or slightly brownish with age. *Context* thin, whitish, with a strongly farinaceous *odour* and *taste*. *Spore print* white. *Basidiospores* 4–5(–6) × 3–4 µm, Q: (1.33–)1.42–1.66, Q_{av}: 1.4–1.6, ovoid to ellipsoidal, pruniform or, very often, larmiform, with rounded to slightly conical base and rounded apex, not flattened, smooth, non-amyloid, non-dextrinoid and non-cyanophil, thin-walled and with the apicule somewhat marked. *Basidia* 20–25 × 4.5–5.5 µm, 4-spored, cylindrical and narrowly clavate, with sterigmata up to 4 µm, accompanied by some cylindrical hyphae, up to 3 µm, that are interspersed between the basidia and that undoubtedly correspond to terminations of the trama, which appears regular. *Cheilocystidia* and *pleurocystidia* not observed. *Pileipellis* a cutis composed by cylindrical hyphae up to 5 µm wide, from parallel to more or less interwoven, with obtuse extremities, not so apparent, with few emerging elements, of greater calibre in the area of the subcutis; brownish parietal pigment slightly encrusting and intracellular pigment of ochraceous colour. *Stipitipellis* a cutis of parallel hyphae with rare cylindrical and very thin hairs. *Clamp connections* abundant and present in all tissues.

Distribution & Habitat — Spain, Balearic Islands, on dead and very wet remains of *Juncus* sp. or of *Posidonia oceanica*, in the dune zone next to the sea.

Typus. Spain, Balearic Islands, Minorca, Alaior, Arenal de Son Bou, 2 m asl, 16 Nov. 2011, *J.L. Siquier*, JLS 3421 (holotype MA-FUNGI 91823 in Herbarium Real Jardín Botánico de Madrid, isotype AB 14-04-02 in personal herbarium of A. Bidaud, ITS, LSU and *TEF1* sequences GenBank MK650044, MK650043 and MK644259, MycoBank MB830239).

Notes — Initially these samples were determined as *Clitocybe augeana sensu* Kuyper (Siquier et al. 2015), but recent molecular investigations revealed that the species actually belongs to *Lyophyllaceae*, in the vicinity of the genus *Ossicaulis*, and that it is so far not represented in the fungal sequence databases (GenBank & UNITE). This small genus introduced in 1985 currently includes the two European species *O. lignatilis* (Redhead & Ginns 1985) and *O. lachnopus* (Contu 2007), as well as *O. yunnanensis* recently described from China (Yang et al. 2018). Based on LSU, *O. salomii* is closest to *O. yunnanensis* (seven substitutions + three indels, 98.8 % identity) but using *TEF1* sequences, the species is closer to *O. lignatilis* than *O. yunnanensis*, with quite an important phylogenetic distance to these two species though (87.2 % vs 84.7 % identity, respectively). The ITS rDNA analysis confirms the extent of molecular divergence of *O. salomii* within the genus, as it differs from sequences in the clade by 9.6 % to 11.4 %. The new species occupies a basal position in the ITS phylogeny, which may support a dedicated genus. However, in addition to the LSU data, the gross morphology, anatomy, organoleptic features and ecology of the Balearic collections, fit well with the classic delineation of *Ossicaulis* (Holec & Kolařík 2013). With *O. lachnopus*, *O. salomii* shares the shape, but not the size, of the spores; with *O. lignatilis*, spore calibre but not the shape. The new species differs from all *Ossicaulis* species known to date, by its unique ecology and the absence of cystidia.



ITS phylogeny of *Ossicaulis*. Maximum likelihood phylogenetic analysis of 25 ITS rDNA sequences belonging to the genus *Ossicaulis*, including the newly generated sequence from *O. salomii* sp. nov., performed on www.phylogeny.fr. Branch support is assessed by the SH-aLRT, significant when > 81 %.

Colour illustrations. Dune area where the samples were found, in the Arenal de Son Bou (Minorca island, Spain). Basidiomata *in situ*; basidiospores in congo red; basidia; clamp connections; elements of stipitipellis; elements of pileipellis. Scale bar = 10 mm (basidiomata), 10 µm (microstructures).

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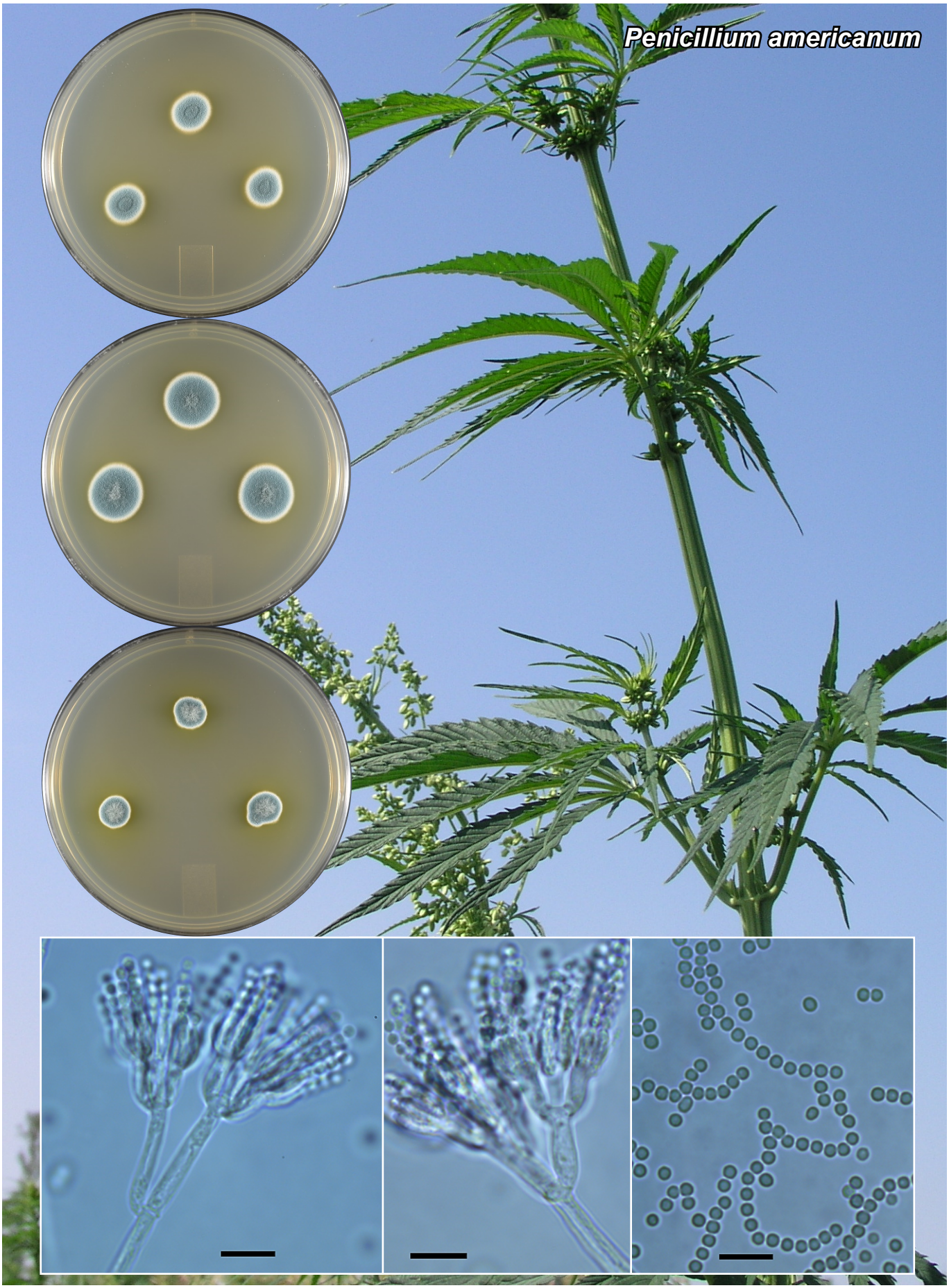
Penicillium americanum

Fungal Planet 937 – 19 July 2019

Penicillium americanum Jurjević, G. Perrone, S.W. Peterson, D. Magistà, *sp. nov.*

Etymology. Named for USA, where the culture was isolated.

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

Micromorphology (on malt extract agar; MEA): *Conidiophores* borne on surface, occasionally on aerial hyphae, (100–)150–350(–375) × (3–)4–5(–6) µm, with smooth, occasionally finely roughened walls, bearing terminal biverticillate or terverticillate penicillin; rami commonly with divergent asymmetric branching 2–3(–4), (8–)10–25 × 4–5 µm; (3–)5–9(–11) metulae in verticils, (6–)7–12(–14) × 3–4(–4.5) µm; phialides (3–)5–9(–11) per metula, ampulliform, 7–9(–9.5) × (2–)2.5–3.5 µm, with short collarettes. *Conidia* spherical to subspherical, occasionally broadly ellipsoidal, 2.5–3.5(–5) × 2.5–4.5 µm, with smooth to finely roughened walls. Borne in long, loose to disordered chains.

Culture characteristics — (in darkness, 25 °C after 7 d): Colonies on **MEA** 11–12 mm diam, colony texture velutinous to floccose centrally, rising c. 3 mm, mycelium white, visible at margins, sporulation heavy, conidia *en masse*, Medici blue to deep green-blue grey (R48; Ridgway 1912), exudate absent, soluble pigments yellow ochre (R15) to primuline yellow (R16), reverse wax yellow to strontium yellow (R16). Colonies on Czapek yeast autolysate agar (**CYA**) 12–13 mm diam, colony texture velutinous to rudimentally floccose centrally, rising c. 4 mm, mycelium white, mainly visible at margins, sporulation heavy, conidia *en masse*, greyish greenish blue (Medici blue to dark Medici blue, R48), exudate abundant, mustard yellow to wax yellow (R16), at the centre of the colony c. 5 mm diam, soluble pigments mustard yellow to primuline yellow (R16), reverse wax yellow to strontium yellow (R16), near straw yellow marginally. Colonies on potato dextrose agar (**PDA**) 11–12 mm diam, colony texture velutinous to rudimentally floccose centrally, rising c. 3 mm, mycelium white, sporulation heavy, conidia *en masse*, Medici blue to deep green-blue grey (R48), exudate barium yellow to wax yellow, abundant (R16), soluble pigments mustard yellow (R16) to honey yellow (R30), reverse wax yellow to strontium yellow (R16). Colonies on Czapek yeast agar with 20 % sucrose (**CY20S**) 10–11 mm diam, colony texture velutinous, mycelium white, sporulation very good, conidia *en masse* pale light dull glaucous-blue to greenish glaucous-blue (R42), exudate absent, soluble pigments absent, reverse uncoloured to cartridge buff (R30). Colonies on dichloran-glycerol agar (**DG18**) 14–15 mm diam, colony texture velutinous, centrally rising c. 3 mm, and c. 4 mm diam, button-like, mycelium white, mainly visible at margins c. 2 mm diam, very heavy sporulation, conidia *en masse*, greyish greenish blue (Medici blue to dark Medici blue, R48), exudate absent, soluble pigments absent, reverse cartridge buff (R30) to pale glass green (R31). Colonies on CYA with 5 % NaCl (**CYAS**) 17–18 mm diam, colony texture velutinous to rudimentally floccose, centrally rising c. 4 mm, radially moderate to deep sulcate, mycelium white, sporulation heavy, conidia *en masse*, greyish greenish blue (light Medici blue to deep Medici blue, R48), exudate absent, soluble pigments absent, reverse cartridge buff to colonial buff, near reed yellow (R30). Colonies on oatmeal agar (**OA**) 9–10 mm diam, colony texture velutinous, centrally rising c. 2 mm, button like, mycelium white, visible at margins c. 2 mm diam, sporulation heavy, conidia *en masse*, greyish greenish blue (Medici blue to dark Medici blue, R48), exudate clear to brown, soluble pigments absent, reverse in pale brown shades. Colonies on creatine sucrose agar (**CREA**), 4–5 mm diam, no acid production, poor growth. On CYA/MEA (colony diam in mm) at 15 °C 11–13/13–24; 20 °C 18–19/19–20; no growth at 5 °C, 30 °C or 37 °C.

Typus. USA, Colorado, Medicinal Marijuana greenhouse, air, 22 July 2011, *Ž. Jurjević* (holotype BPI 910642, culture ex-type NRRL 66819 = ITEM 17520 = EMSL1473, ITS, β-tubulin (*BenA*) and calmodulin (*CaM*) sequences GenBank MK791278, MK803427 and MK803428, MycoBank MB830667).

Notes — BLAST searches of the sequences of *Penicillium americanum* sp. nov. showed a ß-tubulin similarity to *P. soppi* GenBank MF351761 (90.65 %) and a calmodulin similarity to *P. lenticrescens* GenBank KJ775404 (91.06 %). The ITS barcode was 98.72 % similar to *P. soppi* GenBank MF303707 and *P. lenticrescens* GenBank KJ775675 (98.53 %).

Penicillium americanum produces conidiophores (100–)150–350(–375) µm long, while sclerotial production is not observed, compared to *P. soppii* which produces abundant sclerotia and conidiophores up to 500 µm long (Raper & Thom 1949); *Penicillium lenticrescens* produces conidiophores 150–415 µm long (Visagie et al. 2014a).

Colour illustrations. Air, medicinal marijuana greenhouse. 7-d-old cultures of *Penicillium americanum* on MEA (top to bottom 15 °C, 20 °C, 25 °C); conidia and conidiophores on MEA. Scale bars = 10 µm.

Supplementary material

FP937 Maximum likelihood tree of *Penicillium americanum* sp. nov. and closely related species (30 strains in total) of the Sections *Ramosa* and *Brevicompacta* based on concatenated *BenA*, *CaM*, ITS DNA sequences give evidence of net separation of this new species from the other well-resolved branch. All positions with less than 90 % site coverage were eliminated, i.e., fewer than 10 % alignment gaps, missing data, and ambiguous bases were allowed at any position (partial deletion option); 1 141 positions were used in the final dataset. The evolutionary history was inferred by using the Maximum Likelihood method and Kimura 2-parameter model as implemented in MEGA X (Kumar et al. 2018). The tree with the highest log likelihood (-7673.46) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Support values at branches were obtained from 1 000 bootstrap replicates. Bootstrap support values greater than 70 % are shown.

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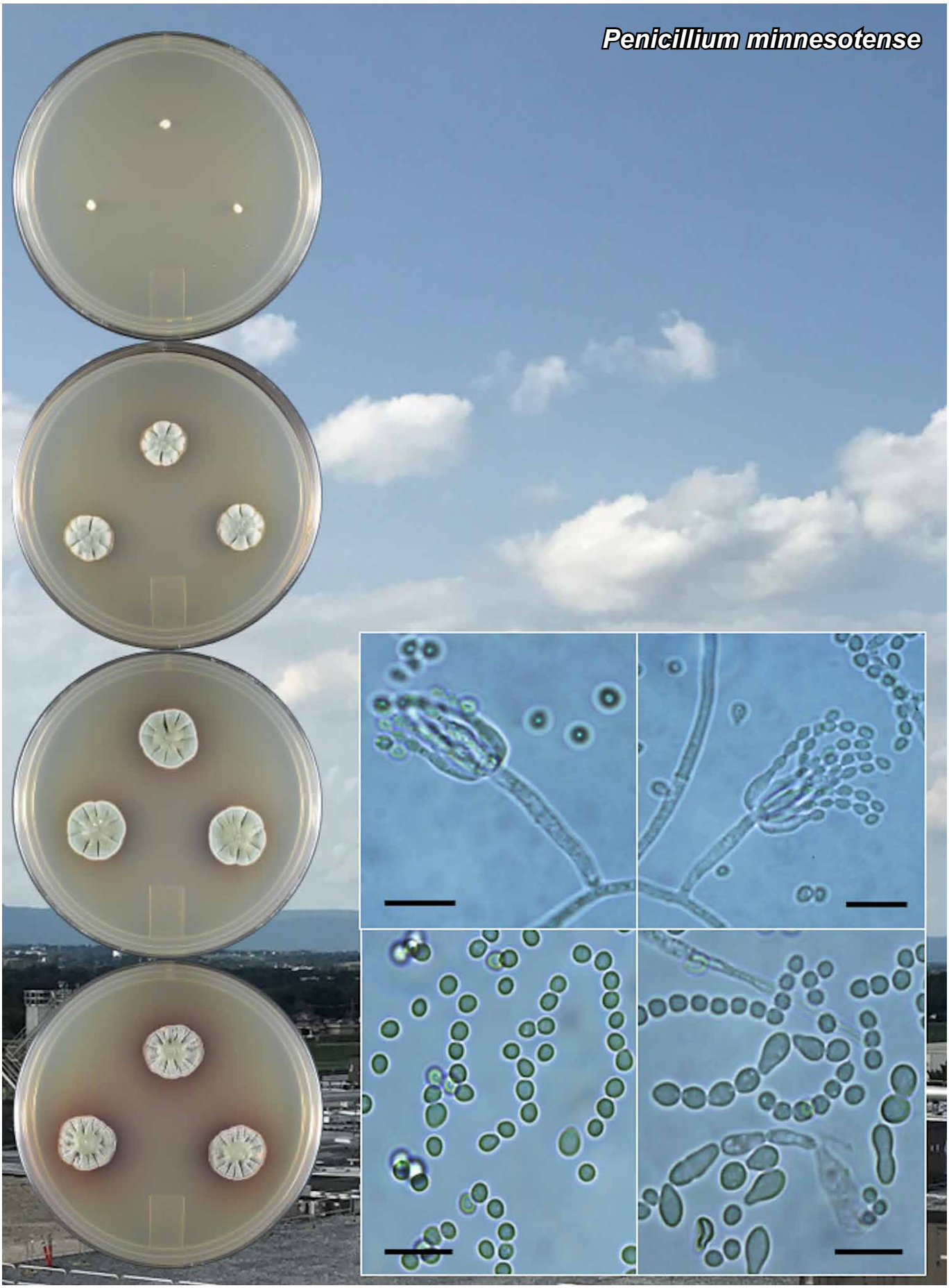
Penicillium minnesotense

Fungal Planet 938 – 19 July 2019

Penicillium minnesotense Jurjević, G. Perrone, S.W. Peterson, D. Magistà, *sp. nov.*

Etymology. Named for state Minnesota, where the culture was isolated..

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

Micromorphology (on malt extract agar; MEA): *Conidiophores* borne on the surface or from aerial hyphae, (8–)25–80(–130) × 2.5–3.5 µm, with smooth to finely roughened walls, apically swollen up to 7 µm diam, bearing a terminal whorl of (2–)5–11(–13) ampulliform *phialides*, (7–)8–12(–17) × 2.5–3(–3.5) µm, occasionally finally roughened. *Conidia* subspherical to spherical to broadly ellipsoidal, occasionally nearly pyriform, (2.8–)3–4.5(–9) × (2.2–)3–4.5(–5) µm, with smooth to finely roughened walls. Borne in short disordered chains.

Culture characteristics — (in darkness, 25 °C after 14 d): Colonies on **MEA** 17–20 mm diam, colony texture velutinous, rising c. 4 mm, radially moderate deep to deep sulcate, mycelium white to cartridge buff (R30), sporulation heavy, conidia *en masse*, pale glaucous-green to glaucous-green (R33; Ridgway 1912), exudate absent, soluble pigments neutral red to vinaceous-purple (R38) strong, soluble pigments on MEA with chloramphenicol not observed, reverse brick red (R13) to vinaceous-rufous (R14). Colonies on Czapek yeast autolysate agar (**CYA**) 18–20 mm diam, colony texture velutinous, abruptly rising c. 5–6 mm, centrally concave 5–9 mm diam, radially deep sulcate near wrinkled, mycelium white occasionally with laelia pink near eupatorium purple (R38) spots, sporulation heavy, conidia *en masse*, pale glaucous-green to glaucous-green (R33), exudate when present vinaceous, soluble pigments absent to feint purplish red; reverse dark vinaceous-brown to deep brownish vinaceous (R39). Colonies on potato dextrose agar (**PDA**) 15–16 mm diam, colony texture velutinous, abruptly rising c. 5–6 mm, centrally concave 5–8 mm diam, radially deep sulcate near wrinkled, mycelium white to light laelia pink, near vinaceous-purple (R38), sporulation very good, conidia *en masse*, pale glaucous-green to glaucous-green (R33), exudate when present vinaceous, soluble pigments daphne red to vinaceous-purple (R38); reverse brownish vinaceous to vinaceous-brown (R39). Colonies on Czapek yeast agar with 20 % sucrose (**CY20S**) 14–15 mm diam, colony texture velutinous, mycelium white to cartridge buff (R30), good sporulation, conidia *en masse*, pale glaucous-green to glaucous-green (R33), exudate absent, soluble pigments absent; reverse uncoloured to pale ochraceous-salmon (R15). Colonies on dichloran-glycerol agar (**DG18**) 20–21 mm diam, colony texture velutinous, centrally rising c. 4–5 mm, radially and concentrically moderate deep to deep sulcate, mycelium white nearly inconspicuous, sporulation heavy, conidia *en masse*, glaucous green to Niagara green (R33), exudate absent, soluble pigments Pompeian red to Vandyke red (R13), reverse English red to mahogany red (R2). Colonies on CYA with 5 % NaCl (**CYAS**) 30–31 mm diam, colony texture velutinous, rising c. 5 mm, centrally concave, radially and concentrically deep sulcate near wrinkled, mycelium white, inconspicuous, sporulation heavy, conidia *en masse*, gnaphalium green to celandine green (R47), exudate absent, soluble pigments faint red; reverse walnut brown to vinaceous-russet (R28). Colonies on oatmeal agar (**OA**) 20–21 mm diam, colony texture velutinous, rising c. 3–4 mm, radially light to moderate sulcate, mycelium white to vinaceous lilac (R44), sporulation very good, conidia *en masse*, court grey to gnaphalium green (R47), exudate clear to light vinaceous lilac (R44), soluble pigments vinaceous lavender to vinaceous purple (R44), reverse dull violet-black to vinaceous-purple (R44). Colonies on creatine sucrose agar (**CREA**), 14–15 mm diam, no acid production, good growth. On CYA/MEA (colony diam in mm after 14 d) at 5 °C 3–4/3–4; 15 °C 18–20/13–18; 20 °C 25–27/20–25; no growth at 30 °C or 37 °C.

Typus. USA, Minnesota, Air, outside, 10 Aug. 2012, *Ž. Jurjević* (holotype BPI 910934, culture ex-type NRRL 66823 = ITEM 17524 = EMSL 1719, ITS, β-tubulin (*BenA*), calmodulin (*CaM*) and RNA polymerase II second largest subunit (*RPB2*) sequences GenBank MK791277, MK803429, MK803430 and MK796158, MycoBank MB830666).

Notes — BLAST searches of the sequences of *Penicillium minnesotense* sp. nov. showed ß-tubulin similarity to *P. salmoniflumine* GenBank KF932928 (98.81 %), calmodulin similarity to *P. salmoniflumine* GenBank KF932945 (98.12 %), RNA polymerase II second largest subunit similarities to *P. salmoniflumine* GenBank KF932999 (98.43 %). The ITS barcode was 100 % similar to *P. salmoniflumine* GenBank NR_137849.

Penicillium minnesotense produces shorter conidiophores, on average (8–)25–80(–130) µm, than *P. salmoniflumine*, 15–250 µm long; also *P. minnesotense* produces larger conidia on average; subspherical to spherical to broadly ellipsoidal, occasionally nearly pyriform (2.8–)3–4.5(–9) µm, in short disordered chains, with smooth to finely roughened walls, in contrast to *P. salmoniflumine* with conidia ellipsoidal to spherical (2–)2.5–3.5(–6) µm, in loose to well-defined columns, with smooth to finely roughened walls (Peterson et al. 2015).

Colour illustrations. Air, office. 14-d-old cultures of *Penicillium minnesotense* on MEA (from top to bottom 5 °C, 15 °C, 20 °C, 25 °C); conidia and conidiophores on MEA. Scale bars = 10 µm.

Supplementary material

FP938 Maximum likelihood tree of *Penicillium minnesotense* sp. nov. and closely related species (19 strains in total) based on concatenated *BenA*, *CaM*, ITS and *RPB2* DNA sequences give evidence of net separation of this new species from the other well-resolved branch. All positions with less than 90 % site coverage were eliminated, i.e., fewer than 10 % alignment gaps, missing data, and ambiguous bases were allowed at any position (partial deletion option); 2 144 positions were used in the final dataset. The evolutionary history was inferred by using the Maximum Likelihood method and Tamura 3-parameter model as implemented in MEGA X (Kumar et al. 2018). The tree with the highest log likelihood (-11093.69) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Support values at branches were obtained from 1 000 bootstrap replicates. Bootstrap support values greater than 70 % are shown.

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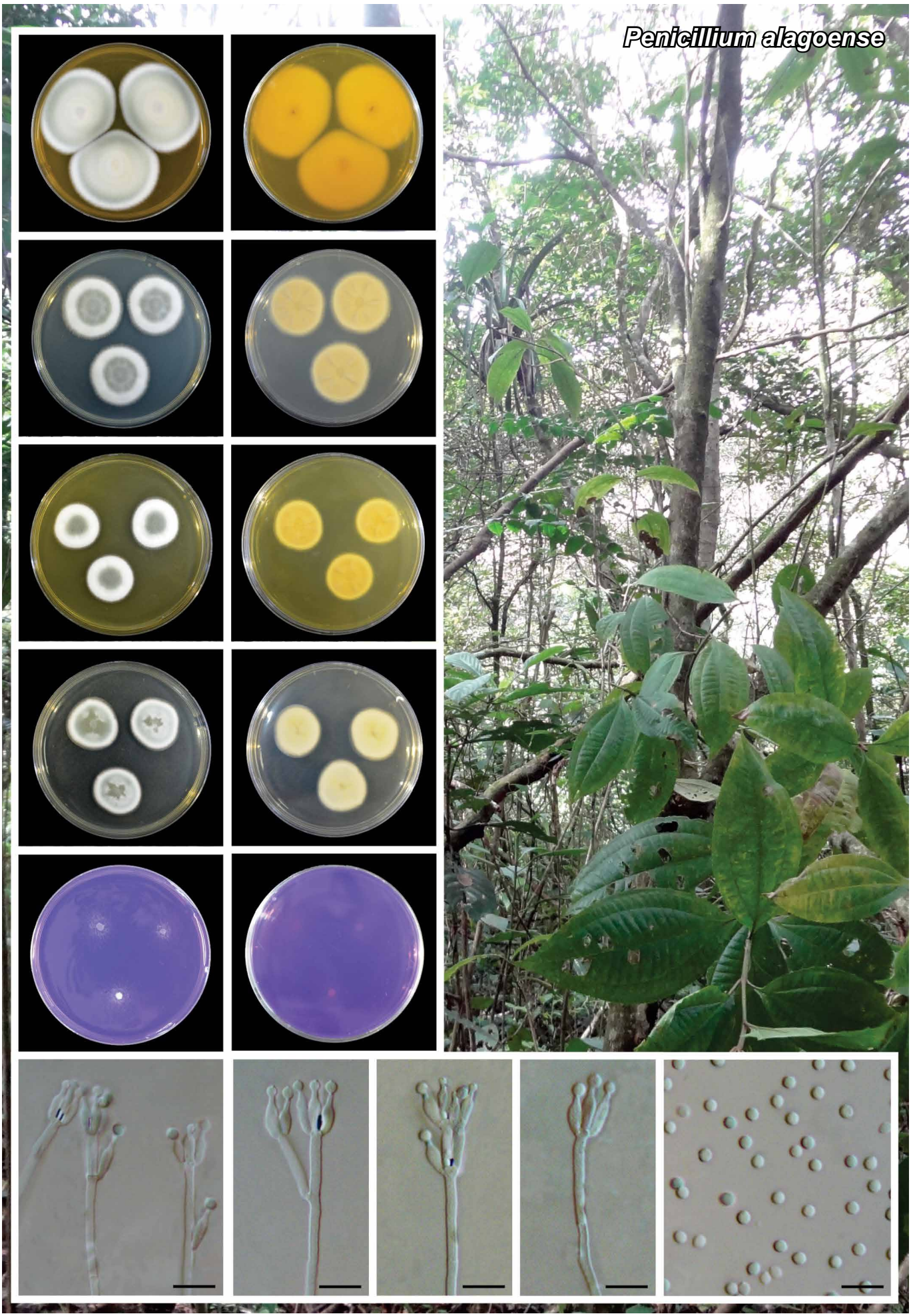

Penicillium alagoense

Fungal Planet 939 – 19 July 2019

Penicillium alagoense L.O. Ferro, A.D. Cavalcanti, O.M.C. Magalhães, Souza-Motta & J.D.P. Bezerra, *sp. nov.*

Etymology. The name refers to the Brazilian state, Alagoas, where this fungus was found.

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

On malt extract agar (MEA), *conidiophores* varying in length, erect not ramified, 70–300 × 2–2.5 µm; *stipes* septate with wall echinulate and apice enlarged (4 µm); asymmetric *penicilli*, monoverticillate, occasionally with *branch*, biverticillate, lightly echinulate, spathulate, 10.5–15.5 × 2–2.5 µm; *phialides* ampulliform, 3–4(–5) phialides per metulae, 7.5–10 × 2–2.5 µm; *conidia* smooth to echinulate, globose, greenish, 2–3.5 µm.

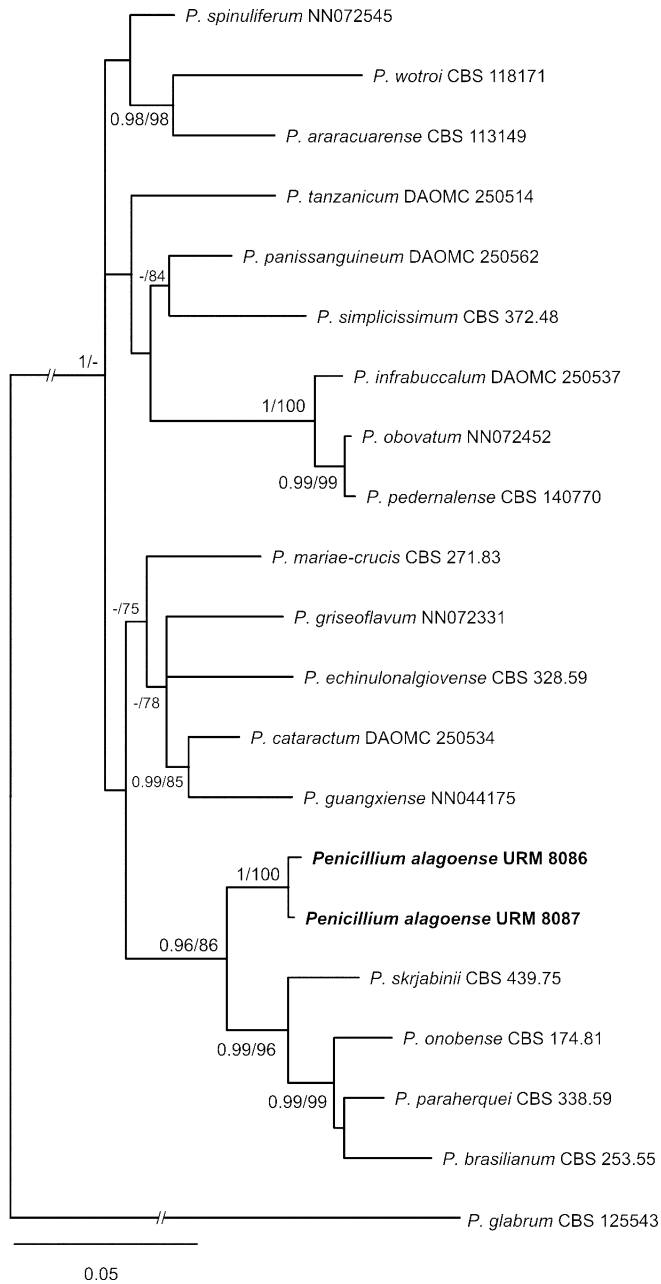
Culture characteristics (25 °C, 7 d, darkness) — On *Czapek Yeast* extract Agar (CYA): colonies slightly raised, texture velvety, radially sulcate, slow sporulation, centrally purplish grey, hyaline mycelium with whitish margin, exudate and pigment absent; reverse cream. On MEA: colonies low, plane, texture velvety, light sporulation, greyish green to greenish glaucous, hyaline mycelium with whitish margin, exudate and pigment absent; reverse brownish to umber. On Yeast Extract Sucrose agar (YES): colonies slightly raised, texture velvety radially sulcate, slow sporulation, centrally purplish grey, hyaline mycelium with whitish margin, exudate and pigment absent; reverse cream to brownish. On oatmeal agar (OA): colonies low, plane, texture velvety, greenish olivaceous, hyaline mycelium with whitish margin, aerial mycelium centrally observed, exudate and pigment absent; reverse whitish. On Dichloran 18 % Glycerol agar (DG18): colonies low, plane, texture velvety, greyish to centrally greenish olivaceous, hyaline mycelium with whitish margin, exudate and pigment absent; reverse cream to yellowish. On *Creatine sucrose agar* (CREA): weak growth and very weak or no acid production. Colony diam, in mm, after 7 d, darkness – CYA: 15 °C 13–15, 25 °C 26–28, 30 °C 19, 37 °C no growth; MEA: 15 °C 18, 25 °C 35–43, 30 °C 31, 37 °C no growth; YES: 15 °C 13–14, 25 °C 19–21, 30 °C 18–19, 37 °C no growth; AO: 15 °C 13–14, 25 °C 32–37, 30 °C 35–38, 37 °C no growth; DG18: 15 °C 5, 25 °C 23–24, 30 °C 19–29, 37 °C no growth; CREA: 15 °C 8, 25 °C 5–7, 30 °C 3, 37 °C no growth.

Typus. Brazil, Alagoas state, Quebrangulo, Pedra Talhada Biological Reserve, S09°15'26.8" W36°25'53.7", as endophyte from leaves of *Miconia* sp. (*Melastomataceae*), July 2018, *L.O. Ferro* (holotype URM 93058, culture ex-type URM 8086, ITS, *BenA*, *CaM* and *RPB2* sequences GenBank MK804503, MK802333, MK802336 and MK802338, MycoBank MB830760).

Additional materials examined. Brazil, Alagoas state, Quebrangulo, Pedra Talhada Biological Reserve, S09°14'47.0" W36°25'15.0", as endophyte from leaves of *Miconia* sp., July 2018, *L.O. Ferro*, URM 8087, ITS, *BenA*, *CaM* and *RPB2* sequences GenBank MK804502, MK802332, MK802335 and MK802337; Alagoas state, Quebrangulo, Pedra Talhada Biological Reserve, S09°14'47.0" W36°25'15.0", as endophyte from leaves of *Handroathus albus* (*Bignoniaceae*), July 2018, *A.D. Cavalcanti*, B17B, *BenA* sequence GenBank MK802334.

Notes — *Penicillium alagoense* exhibits phylogenetic and morphological similarities to *P. skrjabinii*. *Penicillium alagoense* differs from *P. skrjabinii* by the numbers and size of phialides (6–8 per metulae, 7.7–10.5 × 2.3–3 µm), metulae (26.4–32 × 2.4–3 µm) and by the production of conidia that are ellipsoidal, globose or subglobose (3.5–5 × 1.8–2.4 µm) (Ramírez 1982). In addition, *P. alagoense* differs from *P. skrjabinii* by macroscopic characteristics presenting lower growth in the colonies and no growth at 37 °C.

Colour illustrations. Atlantic Forest area in Pedra Talhada Biological Reserve. Cultures on MEA, CYA, YES, DG18 and CREA after 7 d at 25 °C; conidiophores, phialides, metulae and conidia. Scale bars = 10 µm.



Bayesian inference (BI) tree obtained by a phylogenetic analysis of the combined ITS rDNA, *BenA* and *CaM* sequences conducted in MrBayes on XSEDE and Maximum Likelihood (ML) analysis in RAxML in the CIPRES science gateway (Miller et al. 2010). The substitution model GTR+I+G was used for ITS, SYM+G for *CaM*, and GTR+G for *BenA* alignments in the BI and GTR+G+I in the ML. Bayesian posterior probability and Maximum Likehood bootstrap support values are indicated at the nodes. The new species is indicated in **bold**. *Penicillium glabrum* (CBS 125543) was used as outgroup.

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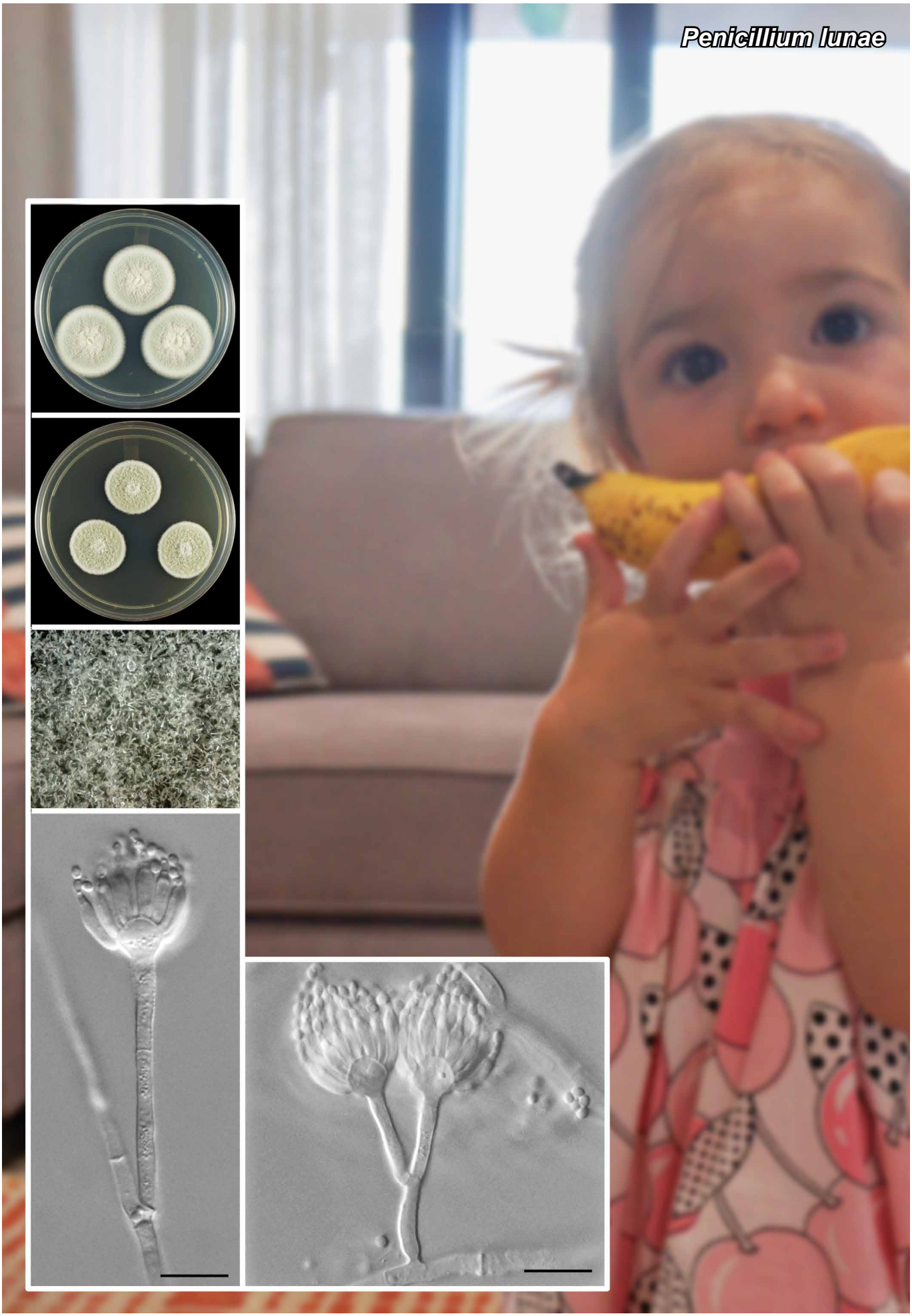

Penicillium lunae

Fungal Planet 940 – 19 July 2019

Penicillium lunae Visagie & Yilmaz, *sp. nov*.

Etymology. Latin, *lunae*, named after Luna Visagie. This species was isolated from a banana she was about to eat.

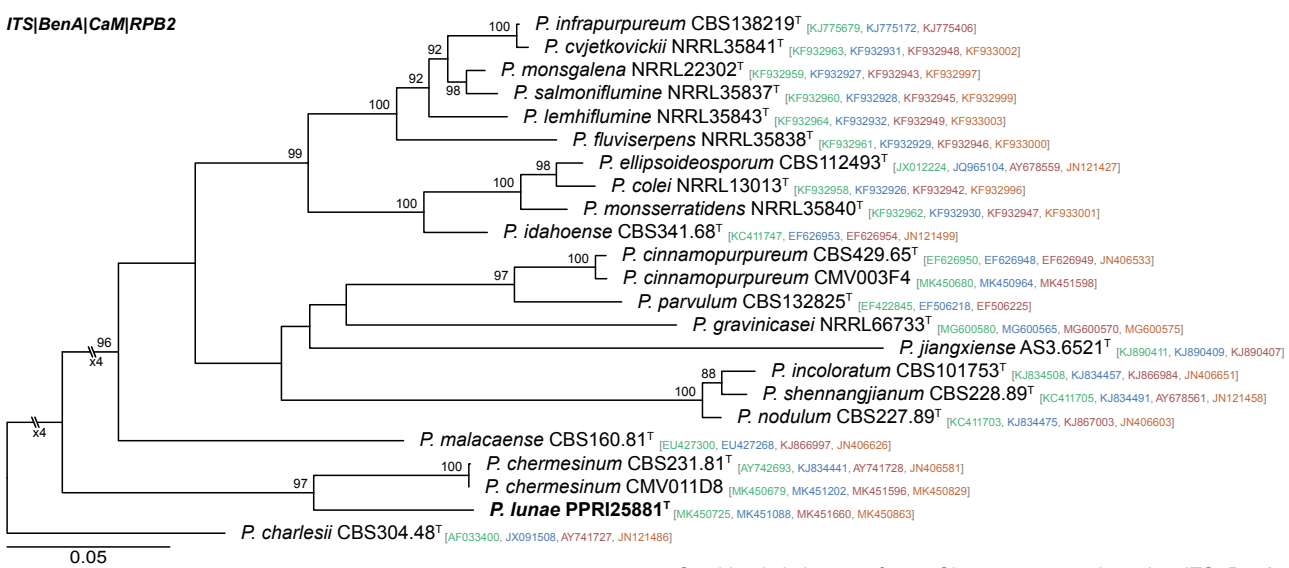
Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetes*.

Conidiophores monoverticillate, miner proportion biverticillate; *stipes* smooth-walled, 13–60 × 2–3(–3.5) µm; *vesicle* 5–7 µm; *metulae* two when present, 18–30 × 2–3(–3.5) µm; *phialides* ampulliform, 10–20 per vesicle, (7.5–)8–10 × 2–3 µm (8.8 ± 0.8 × 2.5 ± 0.4); average length metula/phialide 2.5; *conidia* smooth-walled, subglobose to broadly ellipsoid, 2–3(–3.5) × 1.5–2(–2.5) µm (2.2 ± 0.4 × 1.8 ± 0.2), average width/length = 1.2, n = 70.

Culture characteristics (25 °C, 7 d) — On Czapek yeast autolysate agar (CYA): Colonies low, slightly radially sulcate, sunken in centrally; margins low, wide (3 mm), entire; mycelia white; texture floccose; sporulation moderately dense, conidia *en masse* greyish to dull green (26B3–C3–D4); soluble pigments absent; exudates clear, minute droplets; reverse greenish white (30A2), yellowish white to pale yellow (2A2–3). On malt extract agar (MEA): Colonies low, plain, raised centrally; margins low, narrow (1 mm), entire; mycelia white; texture floccose; sporulation moderately dense, conidia *en masse* greyish to dull green (26B3–C3–D4); soluble pigments absent; exudates clear, minute droplets; reverse yellowish white to pale yellow (2A2–3). On yeast extract sucrose agar (YES): Colonies low, slightly radially sulcate; margins low, wide (3 mm), entire; mycelia white; texture floccose; sporulation moderately dense, conidia *en masse* greyish to dull green (26B3–C3–D4); soluble pigments absent; exudates clear, minute droplets; reverse pale to light yellow (3A3–4). On dichloran 18 % glycerol agar (DG18): Colonies low, plain, sunken in centrally; margins low, wide (3 mm), entire; mycelia white; texture floccose, loosely funiculose; sporulation moderately dense, conidia *en masse* greyish to dull green (26B3–C3–D4); soluble pigments absent; exudates clear, minute droplets; reverse greenish white (30A2), yellowish white to pale yellow (2A2–3). *Colony diam (in mm):* CYA 34–36; CYA 30 °C 28–29; CYA 37 °C no growth; CYAS 33–35; MEAbl 25–26; DG18 24–25; YES 34–35; OA 28; PDA 29–30.

Typus. South Africa, Gauteng Province, Pretoria, from *Musa* sp. (*Musaceae*), 2018, coll. *N. Yilmaz*, isol. *C.M. Visagie* (holotype PREM 62233, cultures ex-type PPRI 25881 = CMV006E6, LSU, ITS, *BenA*, *CaM* and *RPB2* sequences GenBank MK598746, MK450725, MK451088, MK451660 and MK450863; MycoBank MB830682).

Notes — A BLAST search against an ex-type reference sequence dataset placed the new species in *Penicillium* sect. *Cinnamopurpurea* (Visagie et al. 2014b). A multigene phylogeny based on ITS, *BenA*, *CaM* and *RPB2* resolves *Penicillium lunae* as sister to *P. chermesinum*. All four genes can be used to make an identification. Morphologically, the new species is easily distinguished from *P. chermesinum* based on the absence of sclerotia and no growth on CYA at 37 °C. Microscopically, they are very similar except for *P. lunae* producing longer phialides ((7.5–)8–10 vs 7–8 µm) (Pitt 1980).



Combined phylogeny of sect. *Cinnamopurpurea* based on ITS, *BenA*, *CaM* and *RPB2*. Aligned datasets were analysed in IQ-tree v. 1.6.8. Bootstrap support values (≥ 80 %) are given above branches. The new species is indicated by **bold** text, T = ex-type strain. GenBank accession numbers are given between square brackets (ITS = green, *BenA* = blue, *CaM* = red, *RPB2* = orange). The tree is rooted to *P. charlesii*.

Colour illustrations. Luna Visagie with her banana. Colonies on CYA; colonies on MEA; colony texture on MEA; conidiophores. Scale bars = 10 µm.

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Phialemonium guarroi

Fungal Planet 941 – 19 July 2019

Phialemonium guarroi Rodr.-Andr., Cano & Stchigel, *sp. nov.*

Etymology. In honour of the mycologist Josep Guarro Artigas.

Classification — *Cephalothecaceae*, *Sordariales*, *Sordariomycetes.*

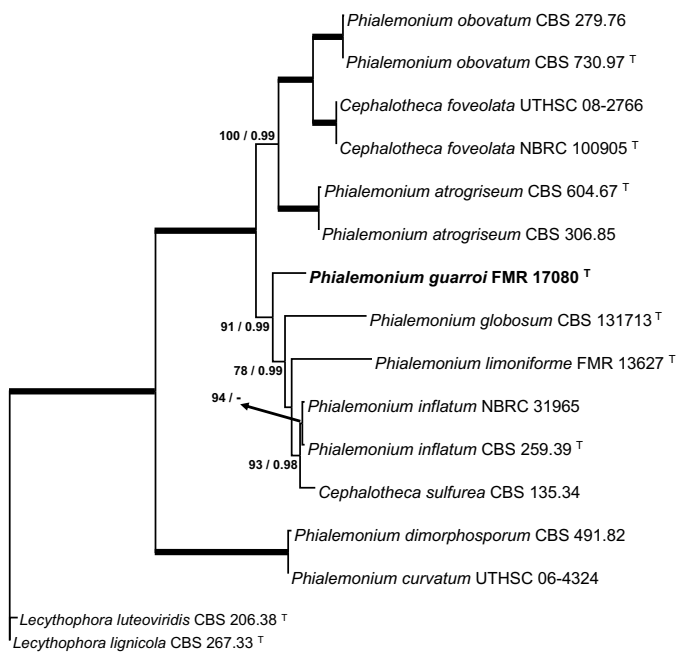
Mycelium composed of septate, hyaline, smooth- and thin-walled hyphae, 1.5–2 µm wide, becoming cinnamon and moniliform in old cultures, whose cells reach up to 10 µm diam. *Conidiophores* absent or poorly differentiated, often consisting in single lateral phialides and adelophialides borne directly from aerial hyphae, occasionally composed of a short stipe of up to 15 µm long and bearing 1–3 phialides in an irregular arrangement. *Phialides* abundant, hyaline, smooth-walled, flask-shaped, with more or less inflated at the base and tapering towards the top, 12–15 × 1.5–2 µm, percurrently proliferating to form long chains in old cultures. *Adelophialides* hyaline, smooth-walled, cylindrical but slightly tapering towards the top, 12–15 × 1.5–2 µm. *Conidia* hyaline, aseptate, lemon-shaped, 3–3.5 × 1.5–2 µm, smooth-walled, produced in chains of up to 25 conidia, with a cylindrical-truncate scar at both ends. *Chlamydospores* and *sexual morph* not observed.

Culture characteristics — *Colonies* on OA reaching 9–10 mm diam after 2 wk at 25 °C, flattened, velvety, grey (6B1; Kornerup & Wanscher 1978), margins regular, sporulation sparse, exudate absent; reverse pale yellow (3A3), diffusible pigment absent. *Colonies* on PCA attaining 10–11 mm diam after 2 wk at 25 °C, flattened, velvety, white (4A2), margins regular, sporulation abundant, exudate absent; reverse yellowish grey (3B2), diffusible pigment absent. *Colonies* on PDA of 12–13 mm diam after 2 wk at 25 °C, elevated, velvety to floccose, margin irregular, yellowish brown (5E4) at centre and yellowish grey (3B2) at edge, exudate absent, sporulation abundant; reverse olive brown (4E6) at centre and white (4A1) at edge, diffusible pigments absent. Minimum, optimal and maximum temperature of growth (on PDA): 15 °C, 25 °C and 30 °C, respectively.

Typus. Spain, Canarias, Santa Cruz de Tenerife province, La Palma, Punta Gorda, isolated from soil, Aug. 2009, *A.M. Stchigel & M. Calduch* (holotype CBS H-23924, cultures ex-type FMR 17080 = CBS 145626; ITS and LSU sequences GenBank LR535737 and LR535738, MycoBank MB830182).

Colour illustrations. Typical vegetation of La Palma island, Canary Islands archipelago, Spain (Photo credit: A. DeCort). Moniliform cells, adelophialides, phialides and conidia. Scale bars = 10 µm.

Notes — *Phialemonium guarroi* was recovered from a soil sample collected in Punta Gorda, La Palma, Canary Islands, Spain. The genus *Phialemonium* was established by Gams & McGinnis (1983). *Phialemonium* contains seven accepted species, mostly isolated from environmental sources and human specimens (Rivero et al. 2009, Perdomo et al. 2011, Guarro 2012, Crous et al. 2015b). *Phialemonium guarroi* is morphologically similar to *Phialemonium inflatum*. However, the new species can be distinguished from the latter due to the production of phialides which proliferate percurrently to form long chains (feature not reported in *P. inflatum*) and the production of smaller conidia than those of *P. inflatum*. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the **ITS** sequence is the ex-type strain of *P. inflatum* CBS 259.39 (GenBank LT633912; Identities = 490/535 (92 %), 10 gaps (1 %)); using the **LSU** sequence was the same ex-type strain of *P. inflatum* (GenBank LT633912; Identities = 845/857 (99 %), no gaps). The ITS-LSU phylogenetic tree corroborated the placement of our isolate as a new species of *Phialemonium*, being located phylogenetically close to *P. inflatum.*



Maximum likelihood tree obtained from the ITS-LSU 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. 3.2.6 (Ronquist et al. 2012). Bootstrap support (BS) values ≥ 70 % and Bayesian posterior probability (PP) values ≥ 0.95 are presented at the nodes. Fully supported branches (100 % BS / 1 PP) are indicated in **bold**. *Lecythophora luteoviridis* CBS 206.38 and *Lecythophora lignicola* CBS 267.33 were used as outgroup. The new species proposed in this study is indicated in **bold**. TRepresents the ex-type strains of the taxa employed in this analysis.

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Phyllosticta longicauda

Fungal Planet 942 – 19 July 2019

Phyllosticta longicauda Mapperson, Bransgr., R.G. Shivas & Dearnaley, *sp. nov.*

Etymology. Name refers to the long apical appendages on the conidia.

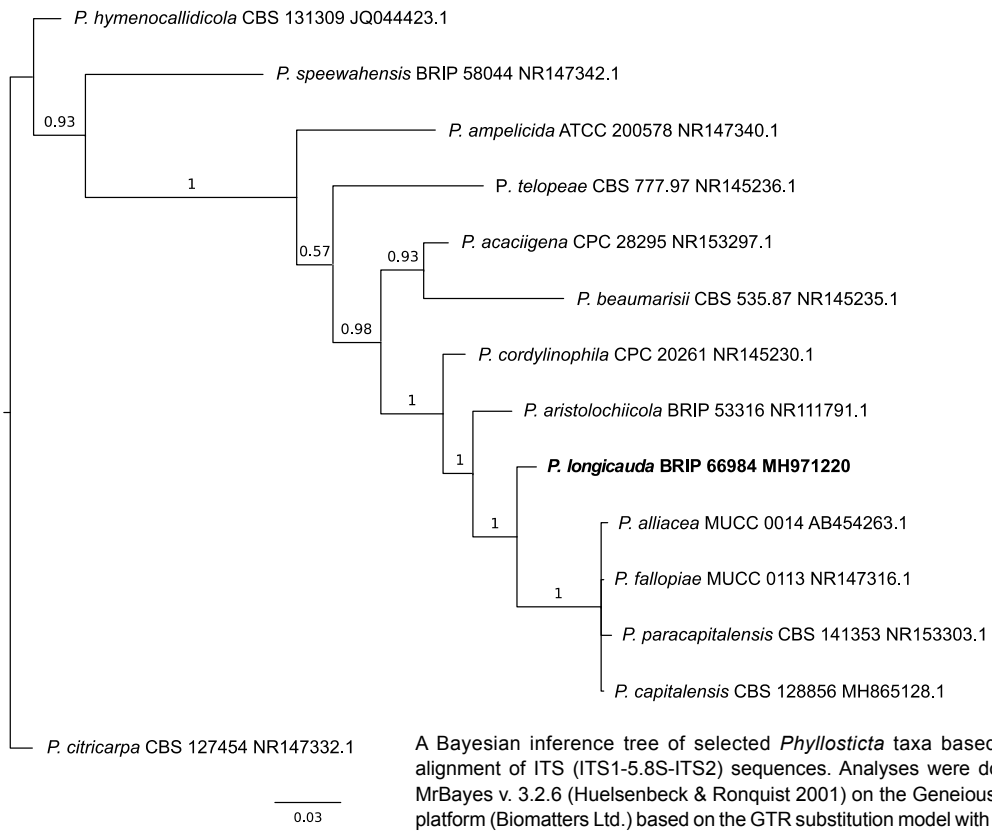
Classification — *Phyllostictaceae*, *Botryosphaeriales*, *Dothideomycetes*.

Conidiomata produced on PDA after 4 wk at 23 °C. *Pycnidia* black, abundant and aggregated on surface of agar, unilocular, subglobose, up to 500 µm diam; wall dark reddish brown. *Conidiophores* subcylindrical, up to 3-septate, 10–40 × 2–6 µm, subhyaline to hyaline, sometimes branched, often with a swollen basal cell up to 12 µm diam. *Conidiogenous cells* terminal, hyaline, smooth, subcylindrical, 10–20 × 2–4 µm. *Conidia* subglobose, broadly ellipsoidal or obovoid, with a truncate base and rounded apex, hyaline, 6–12 × 6–8 µm, aseptate, smooth, with a large subglobose vacuole, enclosed in an inconspicuous mucilaginous sheath, with an inconspicuous apical tapered hyaline appendage up to 30 µm long. *Sexual morph* not seen.

Culture characteristics — Colonies on PDA up to 3 cm diam after 1 mo at 23 °C, flattened, without aerial mycelium, margins irregular, surface grey in the central part, pale yellow in the outer part, reverse buff becoming lighter towards the margin; up to 5 cm diam after 6 mo, surface and reverse dark grey to black, margins coralloid to irregular, subhyaline conidial ooze on parts of surface.

Typus. Australia, Queensland, Mt Kingsthorpe, Kingsthorpe, next to walking track at top of mountain, S27°28'48" E151°49'55", alt. 620 m, isolated as an endophyte from healthy leaves of *Eustrephus latifolius* (*Asparagaceae*), 8 June 2010, *R.R. Mapperson* RMELV3.21 (holotype BRIP 66984, ITS sequence GenBank MH971220, MycoBank MB828031).

Notes — *Phyllosticta* is a large genus of foliar *Dothideomycetes* with more than 3 000 epithets currently listed in MycoBank. *Phyllosticta* contains many significant plant pathogenic species as well as saprobic and endophytic species (Van der Aa & Vanev 2002, Glienke et al. 2011, Wikee et al. 2013). Recent studies of rainforest plants in southern and northern Queensland (Mapperson 2014, Bransgrove unpubl.) indicated that there were many undescribed species of *Phyllosticta* that occurred as endophytes. Based on ITS sequence BLAST searches against the GenBank database, *P. longicauda* has 96 % identity to a number of fungal taxa including *P. cordylinophila* (582/604; GenBank AB454357) and *P. aristolochiicola* (580/604; GenBank NR111791). Morphologically, *P. longicauda* has larger pycnidia than *P. cordylinophila* (80–160 µm diam in *P. cordylinophila*) and longer conidial appendages than *P. aristolochiicola* (3–7 µm long in *P. aristolochiicola*). Phylogenetically, *P. longicauda* was sister to a clade containing *P. alliacea*, *P. fallopiae*, *P. paracapitalensis* and *P. capitalensis*.



A Bayesian inference tree of selected *Phyllosticta* taxa based on the alignment of ITS (ITS1-5.8S-ITS2) sequences. Analyses were done with MrBayes v. 3.2.6 (Huelsenbeck & Ronquist 2001) on the Geneious v. 9.1.8 platform (Biomatters Ltd.) based on the GTR substitution model with gamma-distribution rate variation. The scale bar represents expected substitutions per site. Posterior probability values are indicated on the nodes. *Phyllosticta citricarpa* was used as the outgroup. The new species proposed in this study is indicated in **bold**.

Colour illustrations. Eustrephus latifolius at Mt Kingsthorpe (Photo credit: John Dearnaley). Colony of *Phyllosticta longicauda* on PDA; conidiomata; conidia. Scale bars = 1 cm, 1 mm, 10 µm.

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Pluteus ludwigii

Fungal Planet 943 – 19 July 2019

Pluteus ludwigii Ferisin, Justo & Dovana, *sp. nov*.

Etymology. Named in honour of the famous German mycologist Erhard Ludwig.

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

Basidiomata medium-sized, agaricoid. *Pileus* 20–30 mm, hemispherical at first, then plano-concave to concave, with straight margin sometimes reflexed, not hygrophanous, dark brown at centre, pallescent towards margin to light brown, surface glabrous, weakly to strongly venous at centre, surface occasionally cracked demonstrating whitish context underneath. *Lamellae* moderately crowded, free, slightly ventricose, up to 4 mm broad, first whitish later pink with flocculose edge. *Stipe* 30–45 × 2–4 mm, cylindrical, bulbous, pubescent, white all over, sometimes grey at the base. *Context* white. *Smell* and *taste* not distinctive. *Basidia* 21–26 × 8–10 µm, clavate, 4-spored. *Basidiospores* (5.3–)5.8–6.6(–6.9) × (4.9–)5.2–5.7(–6) µm, Q = (1.02–)1.09–1.21(–1.29), subglobose to broadly ellipsoid, thick-walled, non-amyloid, cyanophilous. *Cheilocystidia* 50–77 × 19–25 µm, abundant, thin-walled, hyaline, variable in shape, fusiform, narrowly utriform, subcapitate to clavate, so numerous as to make the lamellar edge sterile. *Pleurocystidia* 70–90 × 22–32 µm, thin-walled, hyaline; shape variable from fusiform to clavate. *Pileipellis* a hymeniderm made up of broadly clavate or sphaeropedunculate elements, some mucronate, 33–51 × 20–30 µm, pigment intracellular (vacuolar), light brown or brown. *Stipitipellis* a cutis of light brown, 4–10 µm wide hyphae. *Caulocystidia* present only in apical part of the stipe, clavate. *Clamp connections* absent in all tissues.

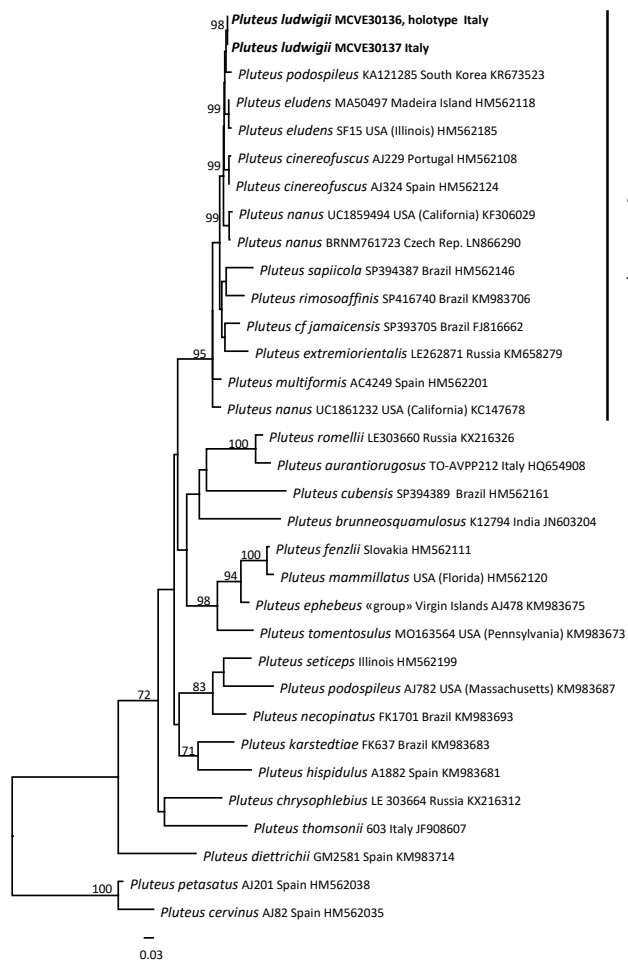
Habitat & Distribution — Solitary, on twigs of broadleaved trees. So far only known from the type locality.

Typus. Slovenia, Nova Goricâ, Panoveč Park, on twigs of broadleaved trees, in wet shady places, 9 Sept. 2018, *G. Ferisin* (holotype MCVE30136, ITS and LSU sequences GenBank MK834525 and MK834527, MycoBank MB830750).

Additional material examined. Slovenia, Nova Goricâ, Panoveč Park, on twigs of broadleaved trees, in wet shady places, 12 May 2018, *G. Ferisin*, MCVE30137, ITS sequence GenBank MK834526.

Notes — Terminology for descriptive terms is according to Vellinga (1988). Maximum-likelihood analysis of the ITS region was performed with RAxML v. 8.2.1 (Stamatakis 2014) using the GTR+G model as implemented in Geneious v. 11.1.4. *Pluteus ludwigii* is characterised by its small-sized basidiomata with a brown and venous centre pileus, small ((5.3–)5.8–6.6(–6.9) × (4.9–)5.2–5.7(–6) µm), subglobose to broadly ellipsoid basidiospores, hymeniderm with clavate or sphaeropedunculate elements and cheilocystidia variable in shape. Morphologically, *P. ludwigii* is close to *P. cinereofuscus*, *P. eludens*, *P. phlebophorus* and *P. nanus*. *Pluteus cinereofuscus* can be distinguished from *P. ludwigii* by a hygrophanous pileus with olivaceous tinges and larger spore size ((6.5–)7–9(–10.5) × (5–)5.5–7(–7.5) µm; Vellinga (1990)). *Pluteus eludens* recently reported from Portugal, Russia and USA, is distinguished by a pileus margin rugose-venose or translucently striate, longer spores (6–8.2 × 5.2–7.3 µm), different pileipellis with variable terminal elements in shape, darkly pigmented cheilocystidia and cylindrical or lageniform caulocystidia (Justo et al. 2011). *Pluteus phlebophorus* differs in larger spore size ((5.5–)7–8(–9.5) × (4.5–)5–7 µm) and larger terminal elements of the pileipellis (Vellinga 1990). *Pluteus nanus* differs mainly in a non-venous pileus centre and larger spores (6.5–)7–9.5(–10) × 5.5–7 µm (Vellinga 1990).

The two collections of *P. ludwigii* clustered in a strongly supported clade (maximum likelihood bootstrap support value (MLB) = 98 %) which is sister (with no support) to a collection from Korea incorrectly determined as *P. podospileus* (GenBank KR673523) and are placed within the /cinereofuscus clade (MLB = 95 %). Compared to *P. ludwigii*, *P. podospileus* has a subtomentose to squamulose at centre pileus, larger spores 5.5–7.5(–8) × (4–)4.5–6 µm and presence of narrowly conical to fusiform elements in the pileipellis, (20–)36–120(–200) × (11–)15–35(–40) µm (Vellinga 1990).



The ITS phylogenetic tree was inferred using the Maximum likelihood (ML) method based on the GTR+G model in RAxML v. 8.2.1. Only bootstrap values ≥ 70 % are indicated on the nodes (1 000 bootstraps).

Colour illustrations. Panoveč Park, Nova Goricâ, Slovenia. *Pluteus ludwigii* basidiomata in habitat; basidiospores; pileipellis elements; pleurocystidia and cheilocystidia. Scale bars = 10 µm.

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Podosordaria nigrobrunnea

Fungal Planet 944 – 19 July 2019

Podosordaria nigrobrunnea R.F.R. Melo & A.C.S. Silva, *sp. nov.*

Etymology. *nigrobrunnea* refers to the colour of the stroma, dark brown to black.

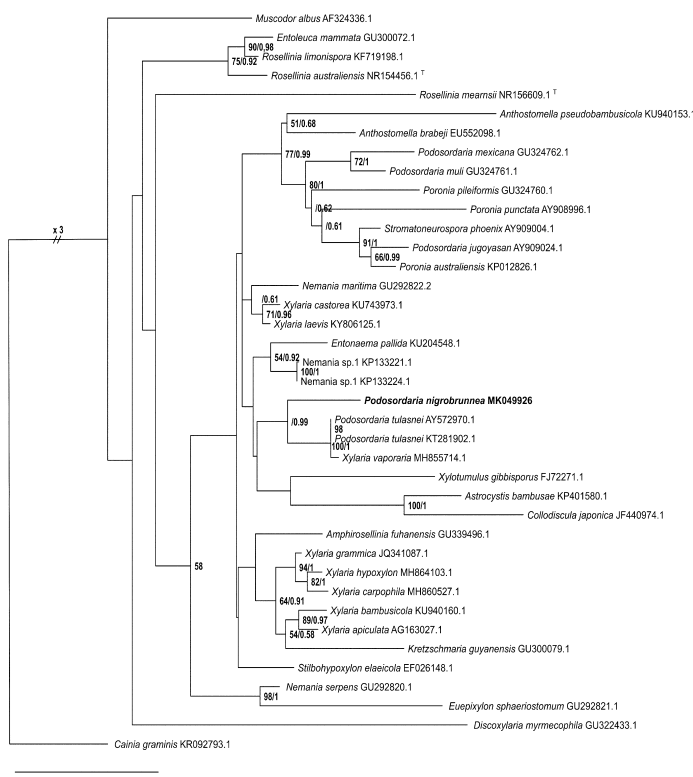
Classification — *Xylariaceae*, *Xylariales*, *Sordariomycetes.*

On dung of unknown origin: *Stromata* erect, monopodial, dichotomously branched to finally antler-like, straight to tortuous, with one to three branching points, 46–59 mm long, 3.5–4 mm diam; stipe cylindrical near the base, eventually flattened near the first branching point, glabrous to slightly pilose at the base, dark brown to black, with surface composed of parallel to anastomosing ridges, with *ectostromal* surface cracking in a somewhat reticulated pattern towards its tip, 39–42 mm; conidiogenous part usually with thin to flabelliform branches, occasionally interlaced at the tip, greyish to yellowish white, finally pale yellow, with surface composed by a powdery to fibrillose mass of mature conidia, 15–17.5 mm. *Conidiophores* formed at the stromatal branches, from the first branching point up to most tips, with a supporting hyphae branching near base to form a subhyaline to pale brown nodulisporium-like palisade, smooth, up to 90 µm long. *Conidiogenous cells* solitary, hyaline, smooth, terminal, tightly clustered, cylindrical or obconical due the occasional swelling at its tip, weakly to non-cyanophilous, 17.5–25 × 2.5–5 µm, with discoid to denticulate secession denticles. *Conidia* solitary, hyaline, smooth, varying in shape: subglobose, ellipsoid, oblong, turbinate, napiform or hexagonal, tapering towards to a subacute to acute apex, with truncate or obconically truncate base, usually straight, occasionally slightly flexuous, aseptate, (10–)11–12.5 × 4.5–7.5 µm, 6.5–7.5 µm diam when subglobose. *Sexual morph* not observed.

Typus. Brazil, Paraíba, Cabedelo, S7°3'58.3" W34°51'16.39", on dung, 2015, *A. de Meiras-Ottoni* (holotype URM 92162, ITS sequence GenBank MK049926, MycoBank MB828271).

Colour illustrations. Floresta Nacional da Restinga de Cabedelo, Paraíba State. Fresh stromata *in situ*; dry stromata; conidiogenous part of the stromata; conidiogenous nodulisporium-like cells, with visible denticles; conidia. Scale bars = 10 mm (stromata), 10 µm (conidiogenous part of the stromata and conidia), 5 µm (conidiogenous nodulisporium-like cells).

Notes — Based on a megablast search of NCBIs GenBank nucleotide database using the ITS sequence, the closest species (91 %) was *Podosordaria tulasnei* (GenBank AY572970.1 and KT281902.1). The MAFFT alignment consisted of 39 sequences, mainly species of *Xylarioideae*, which includes *Podosordaria*. *Cainia graminis* (GenBank KR092793.1) was elected as outgroup. Maximum Likelihood (ML) and Bayesian Inference (BI) analyses were constructed on the CIPRES Science Gateway portal using the RAxML-HPC BlackBox v. 8.2.10 and MrBayes v. 3.2.6, respectively. The ML phylogenetic tree is shown with both Bayesian posterior probability and maximum likelihood bootstrap support values. The sequence clustered with the *Podosordaria tulasnei* and *Xylaria vaporaria* sequences. This grouping was well supported by the BI analysis (0.99), but had low bootstrap support in the ML analysis (47 %), which may be due the limited number of *Xylariaceae* sequences in the database. Species of *Poronia* and *Podosordaria* are usually coprophilous representatives of *Xylariaceae*. The material presented here shows that both a geniculosporium-like as a nodulisporium-like asexual morph can be observed in *Podosordaria*. Stromata of *P. nigrobrunnea* were collected directly on herbivore dung at field. Although phylogenetically closely related to *P. tulasnei*, the conidial morph of *P. nigrobrunnea* presents larger (11–12.5 × 4.5–7.5 µm), variously shaped conidia, in contrast with the minute, ovate-globose conidia of *P. tulasnei*.



Maximum Likelihood tree inferred with RAxML-HPC BlackBox v. 8.2.10 from the ITS region. Bootstrap support (BS) values ≥ 50 % and Bayesian posterior probabilities (PP) ≥ 0.5 are displayed at the nodes as BS/PP. GenBank accession numbers are indicated behind the species names. Bar represents the expected substitutions per site. Type strains are indicated with superscript T. The novel species is indicated in **bold**. Alignment and tree in TreeBASE under 23082.

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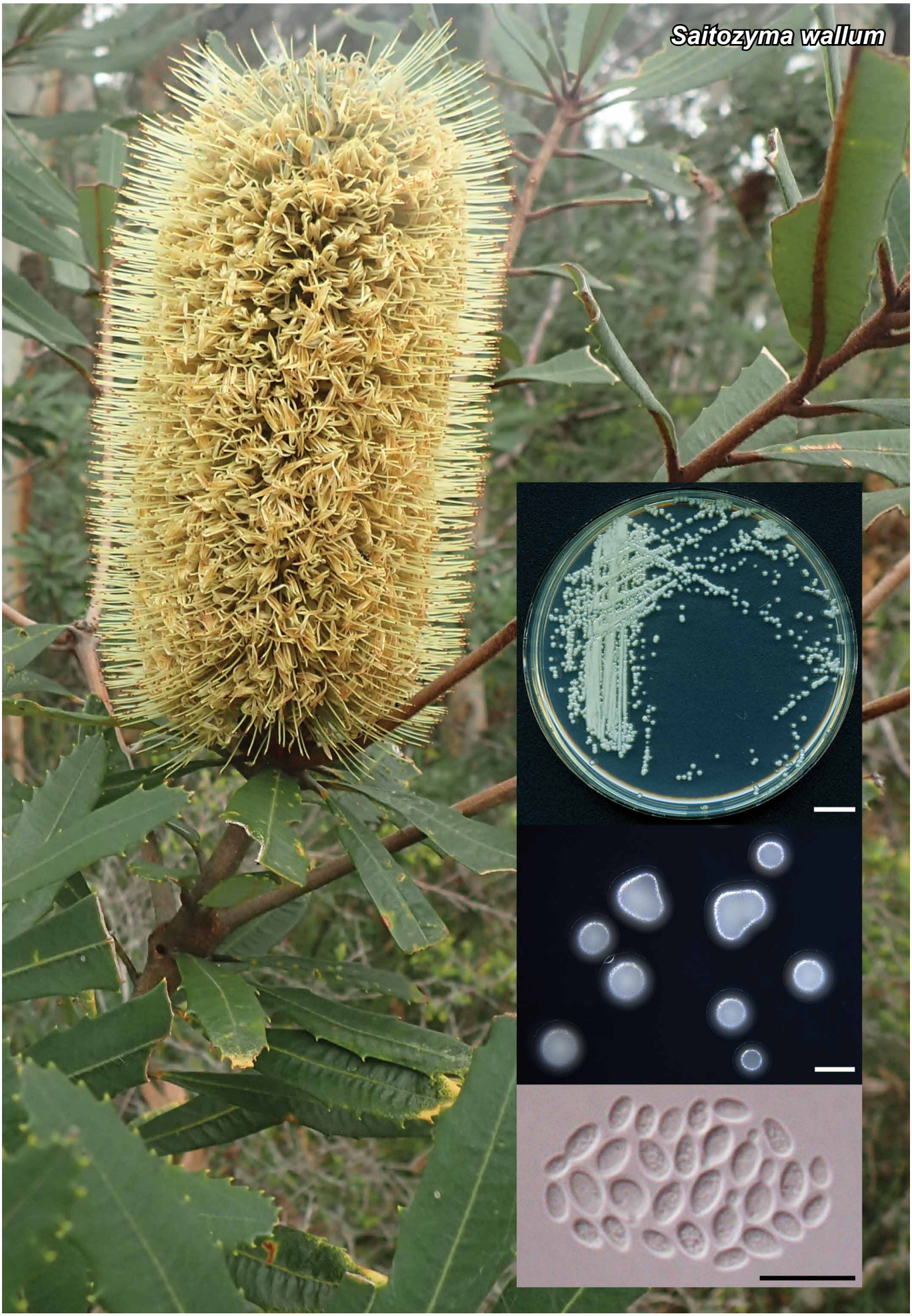

Saitozyma wallum

Fungal Planet 945 – 19 July 2019

Saitozyma wallum Gogorza Gondra, J. Kruse, McTaggart, Boekhout & R.G. Shivas, *sp. nov*.

Etymology. Derived from the word 'wallum', which in the Kabi Kabi language is the name for *Banksia aemula*, the plant species from which this fungus was isolated in the Sunshine Coast, Australia.

Classification — *Trimorphomycetaceae*, *Tremellales*, *Tremellomycetes*.

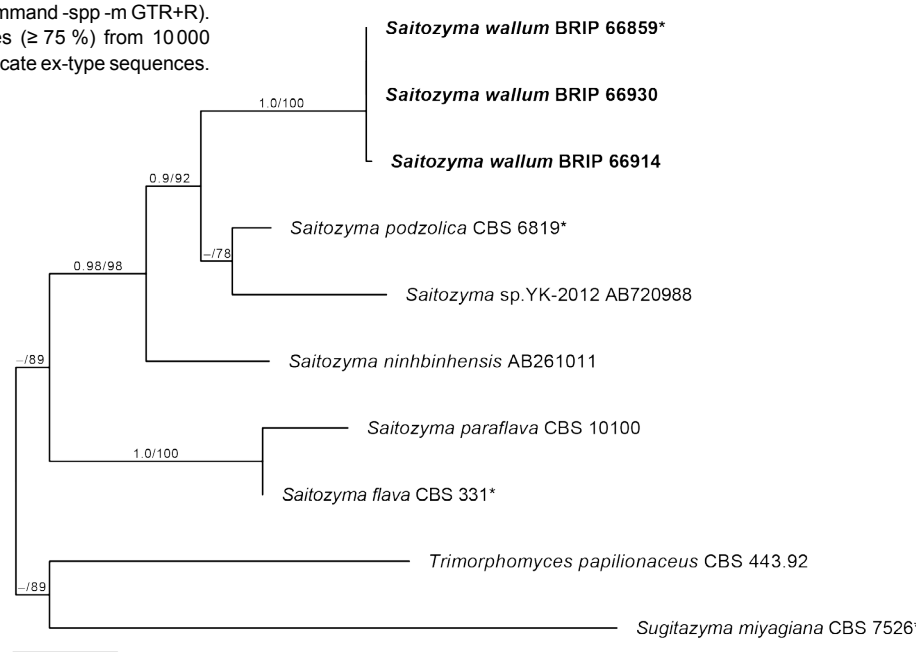
On MYPGA (Malt 0.3 %, Yeast 0.3 %, Peptone 0.5 %, Glucose 1 %, Agar 1.5 %), after 5 d at 25 °C, colony is raised, smooth, glossy, cream to white, 1–1.5 mm with an entire margin; cells are subglobose to ellipsoidal, 2–5 × 1.5–3.5 µm, occurring singly or in small clusters and proliferating by polar budding on a narrow base. Sexual spores, pseudohyphae or hyphae were not observed. Fermentation and assimilation of carbon compounds – see MycoBank MB827331.

Typus. Australia, Queensland, Bribie Island, S27°00'11.3" E153°07'14.1", on leaves of *Banksia aemula* (*Proteaceae*), 21 Feb. 2018, *R.A. Gogorza Gondra*, *N.V. Wolter*, *M.D.E. Shivas & R.G. Shivas* (holotype preserved as metabolically inactive culture BRIP 66859; culture ex-type BRIP 66859, ITS and LSU sequences GenBank MH793357and MH793355, MycoBank MB827331).

Notes — *Saitozyma wallum* is the fifth species described in this genus of basidiomycetous yeasts and filamentous fungi (Liu et al. 2015a). *Saitozyma* was proposed for yeasts in the *flavus* clade *sensu* Liu et al. (2015b), which is equivalent to the *podzolicus* clade *sensu* Boekhout et al. (2011). *Saitozyma* contains species formerly assigned to *Cryptococcus* and *Bullera*, namely *C. flavus*, *C. paraflavus*, *C. podzolicus* and *B. ninhbinhensis*. *Saitozyma wallum* was isolated using a spore fall technique (Pennycook & Newhook 1978) from the abaxial surface of a leaf of *Banksia aemula*, collected in wallum heathland on Bribie Island. The wallum heathland is floristically diverse and endemically rich, restricted to coastal parts of southern Queensland and northern New South Wales (Keith et al. 2014).

Saitozyma wallum had high sequence identity to *S. podzolica* (GenBank NR_073213, 451/483 base pairs, 93 % in the ITS region; GenBank NG_058283.1, 847/894 base pairs, 95 % in the LSU region) and *S. ninhbinhensis* (GenBank AB261011, 541/583 base pairs, 93 % in the LSU region) in a BLAST search against sequences from ex-types. *Saitozyma wallum* was sister to *S. podzolica* (CBS 6819) and an as yet unpublished *Saitozyma* species (GenBank AB720988) isolated from the bark of a cinnamon tree in India. There was intraspecific diversity within *S. wallum* as evidenced by two SNPs in the ITS region of three specimens.

Phylogram obtained from a maximum likelihood search in IQ-TREE v. 1.7 beta, with a GTR gamma FreeRate heterogeneity model of evolution and different rates for ITS and LSU ribosomal DNA loci (command -spp -m GTR+R). aRLT values (≥ 0.9) and bootstrap support values (≥ 75 %) from 10 000 replicates are shown above nodes. Asterisks (*) indicate ex-type sequences.



Colour illustrations. *Banksia aemula* in wallum heathland on Bribie Island, Australia. Colonies on MYPG agar; budding cells. Scale bars = 1 cm, 1 mm, 10 µm.

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Spegazzinia bromeliacearum

Fungal Planet 946 – 19 July 2019

Spegazzinia bromeliacearum S.S. Nascimento & J.D.P. Bezerra, *sp. nov.*

Etymology. The name refers to the host plant family, *Bromeliaceae*.

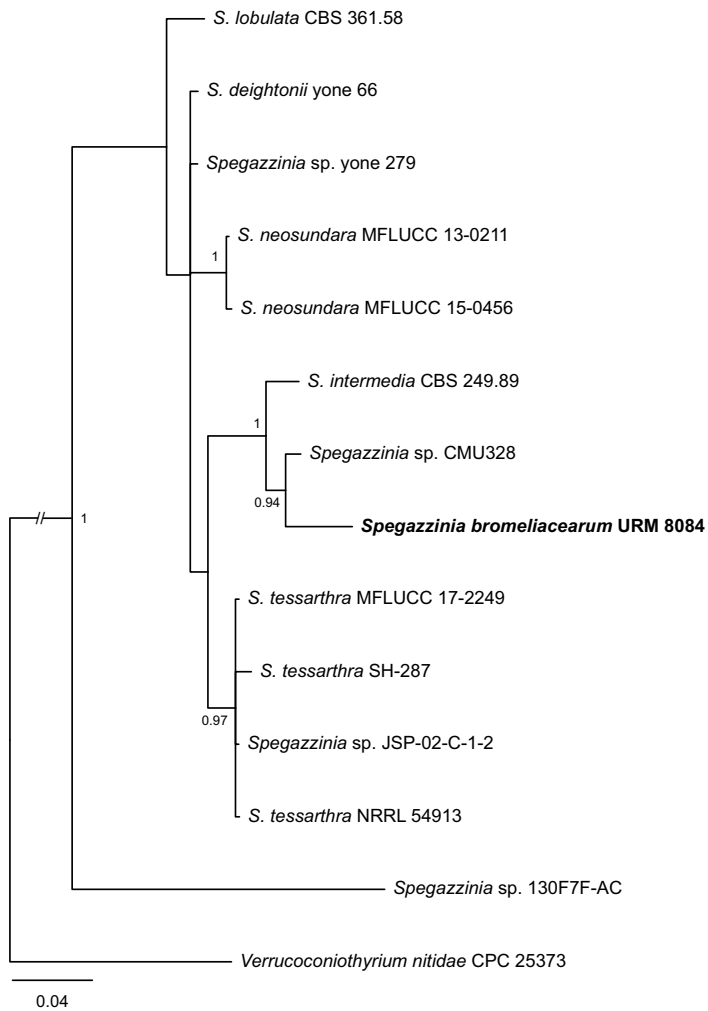
Classification — *Didymosphaeriaceae*, *Pleosporales*, *Dothideomycetes*.

Hyphae hyaline when young and becoming brown to dark brown with age, smooth to slightly verruculose, 2–3 µm wide. *Conidiophores* straight or flexuous, smooth to slightly verruculose, pale brown, 0(–2)-septate, 17–32 × 2–3 µm. *Conidiogenous cells* monoblastic, ampulliform, smooth to slightly verruculose, (6.5–)7–8.5(–14) × (3–)4–5 µm. *Conidia* globose, initially hyaline to pale brown, becoming brown to dark brown with age, 4-celled, crossed-septate, (7.5–)11.5–19(–26.5) µm diam excluding the spines; old conidia conspicuously spinulate, with spines measuring up to 5 µm long, globose, (21–)26.5–28(–30.5) µm diam. *Fertile coils* observed.

Culture characteristics — Colonies at 25 °C for 7 d in darkness. On PDA, colonies reaching 5 cm diam, flat, lightly velvety, surface smooth, olivaceous and reverse olivaceous to black, with whitish margins. On MEA, colonies growing up to 6 cm diam, greenish olivaceous, with whitish margins, flat, velvety, moderately dense, reverse brownish olivaceous to black. Conidia forming before 7 d.

Typus. Brazil, Pernambuco state, Buíque, Catimbau National Park (S8°36'35" W37°14'40"), as endophyte from leaves of *Tilandsia catimbauensis* (*Bromeliaceae*), June 2015, *K.T.L.S. Freire* (holotype URM 93059, culture ex-type URM 8084, ITS and LSU sequences GenBank MK804501 and MK809513, MycoBank MB830761).

Notes — The genus *Spegazzinia* was introduced by Saccardo (1880) and currently 27 records are listed in Index Fungorum and MycoBank (Feb. 2019). BLASTn searches using the **ITS** rDNA sequence from *S. bromeliacearum* demonstrated 92.41 % identity to *S. intermedia* (CBS 249.89, GenBank MH862171.1) and 88.52 % to *S. tessarthra* (MFLUCC 17-2249, GenBank MH071193.1), amongst others. The **LSU** rDNA sequence is 99.23 % identical to *Spegazzinia* sp. isolated as endophyte from *Camellia sinensis* var. *assamica* in Thailand (CMU328, GenBank MH734521.1) and 98.07 % to *S. intermedia* (CBS 249.89, GenBank MH873861.1). Morphologically, *S. bromeliacearum* resembles *S. intermedia*, but differs from it by the size of its conidiophores (up to 30 µm long and 1–4 µm wide) and conidia (18–28 µm diam) (Ellis 1976). The production of fertile coils in *S. bromeliacearum* has never been reported in any species of *Spegazzinia*.



Bayesian inference tree obtained by a phylogenetic analysis of the combined ITS and LSU rDNA sequences conducted in MrBayes on XSEDE in the CIPRES science gateway (Miller et al. 2010). The substitution model GTR+I+G was used for ITS and LSU alignments. Bayesian posterior probability values are indicated at the nodes. The new species is indicated in **bold**. *Verrucoconiothyrium nitidae* (CPC 25373) was used as outgroup.

Colour illustrations. Brazilian tropical dry forest. Developing conidia, conidiophores, conidiogenous cells, conidia and fertile coils. Scale bars = 10 µm.

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Sugiyamaella trypani

Fungal Planet 947 – 19 July 2019

Sugiyamaella trypani A. Gęsiorska & J. Pawłowska, *sp. nov.*

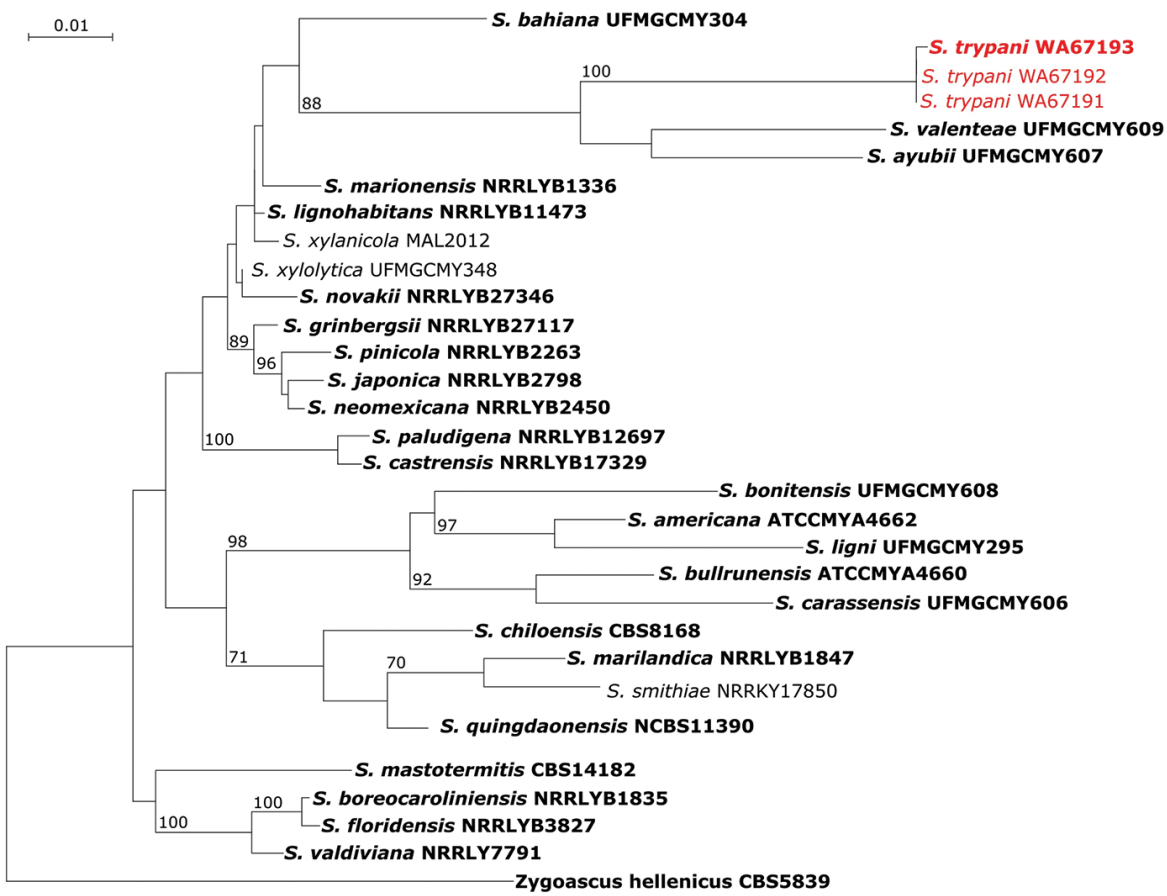
Etymology. The specific epithet 'trypani' was derived from the name of azo dye – trypan blue – from which the novel yeast strain was isolated.

Classification — *Trichomonascaceae*, *Saccharomycetales*, *Saccharomycetes.*

On maltose extract agar (MEA) after 14 d at 17 °C, colony is raised, cream, cerebriform, with undulate margin. After 3 d of growth at 17 °C on 10 % ME broth, cells are sphaerical, ovoid, oblong, 1–3 × 2–8 µm, occurring singly, in pairs, in chains or in small clusters, and proliferating by multilateral budding. Pseudohyphae and hyphae formation confirmed on MEA, potato glucose agar (PGA), glucose yeast peptone agar (GYPA) and in ME broth. Blastospores on hyphae are formed on short denticles. No sexual reproduction was detected.

Typus. Poland, Warsaw, Pole Mokotowskie Park, from soil submerged in trypan blue solution, 16 Nov. 2017, *J. Pawłowska* (holotype WA67193, culture ex-type CBS 15876, ITS and LSU sequences GenBank MK388412 and MK387312, MycoBank MB829450).

Notes — The genus *Sugiyamaella* was delimited by Kurtzman & Robnett (2007) to accommodate ascosporic yeasts which are characterised by the production of globose to ellipsoidal asci with an apical cell or with a short protuberance and common formation of pseudohyphae. The genus belongs to the family *Trichomonascaceae* (Sena et al. 2017). The genus presently accommodates 27 species. The majority of described species was isolated from rotting plant materials or soil (Urbina et al. 2013). Representatives of this genus are known to assimilate D-xylose (Morais et al. 2013). The strain WA67193 was isolated from trypan blue solution remains after grass roots dyeing. Phylogenetic analyses using an alignment of concatenated sequences of the LSU and ITS regions showed that it represents a novel yeast species, closely related to *S. valenteae* and *S. ayubii* (85 % sequence similarity on ITS region in both cases). Physiological profiles (see MycoBank MB829450) further supported the delimitation of a new species distinct from *S. valenteae* and *S. ayubii.* The new species can be distinguished from *S. valenteae* and *S. ayubii* by its ability to grow on Sucrose, Melezitose and Glycerol as a sole carbon source; in contrast to these species it is unable to grow on Xylitol. Similar to *S. ayubii*, the isolate is unable to grow at 37 °C.



Colour illustrations. Pole Mokotowskie Park, Warsaw, Poland where the sample was collected. Budding cells, pseudohyphae and blastospores formation; hyphae; colony on SDA after 14 d at 20 °C; colony on water agar with 1 % trypan blue solution after 30 d at 20 °C. Scale bar = 20 µm (others), 10 µm (hyphae).

PhyML v. 3.5 tree obtained from ITS and LSU (D1/D2 domains) rRNA gene sequences data (GTR model, 3156 sites, ln(L) = -10020.4, bootstrap replicates = 100) of selected representatives of the genus *Sugiyamaella*. Bootstrap support values > 70 % are given above branches. Type strains are shown in **bold**, with the new species shown in red.

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Suillus gastroflavus

Fungal Planet 948 – 19 July 2019

Suillus gastroflavus Zvyagina, Rebriev, Sazanova & E.F. Malysheva, *sp. nov.*

Etymology. '*gastro*' refers to the artificial genus *Gastrosuillus*; '*flavus*' refers to similarity with *Suillus flavus*.

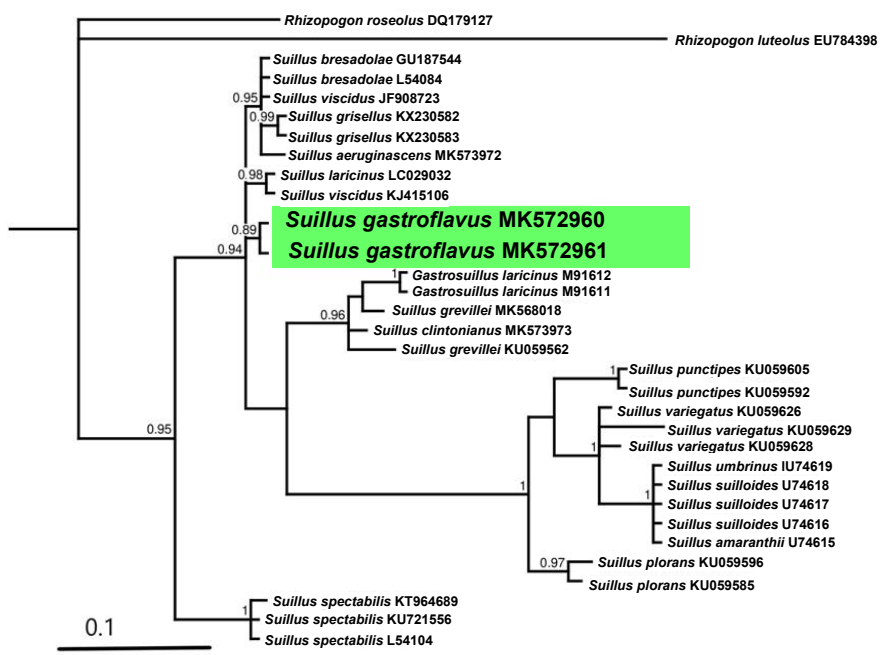
Classification — *Suillaceae*, *Boletales*, *Agaricomycetes.*

Mature basidiomata epigeous or subhypogeous, secotioid, 1.5–3.3 cm broad, 1.5–2.7 cm high in dry specimens and 3–5 cm broad, 5–7 cm high when fresh. *Pileus* completely enclosing the gleba, adpressed, subspherical to slightly irregular with margin fused with stipe and partial veil. Surface mucous and pale yellow in wet weather, yellow-brown in herbarium, covered by scales of yellowish brown stuck hairs. *Context* partly hygrophanous, fleshy, white in central part, yellowish and thin under peridium. *Tubes* disorganised, angular, big and different in size, fused with stipe and partial veil, lilaceous-grey. *Stipe* rudimental, conical, more or less centrally attached, in central part 0.5–0.8 cm long and 0.2–0.5 cm broad in herbarium specimen, 1–3 cm long and 1–1.5 cm broad when fresh, concolorous or lighter than pileus, covered by yellowish brown hairs. *Context* hygrophanous, white in young specimens and yellowish to brownish in old. *Basidiospores* 10.3–13(–13.8) × 5.7–6.8(–7.2) µm, Q = 1.6–2.1(–2.3), ellipsoid, ovoid, inequilateral in profile, often with narrowed and elongated apiculus, moderately thick-walled, brown, smooth. *Basidia* 22–32 × 6.5–9 µm, clavate to subclavate, hyaline or with yellowish brown context in KOH. *Cystidia* 39–95 × 5.7–8.1 µm, cylindric and slightly widened in upper part, hyaline or with brown context in KOH, arranged in fascicles. *Pileipellis* ixocutis, covered by septate and swollen interwoven hyphae, 7–21 µm broad.

Typus. Russia, Magadan Region, Srednekansky district, vicinity of Seimchan village, meadow of Seimchanka river, N62.96157° E152.3382°, on soil in flooded mixed forests with *Larix cajanderi* and *Salix schwerinii*, *S. bebiana*, 15 Aug. 2010, *N. Sazanova* (holotype MAG 3480, ITS and LSU sequences GenBank MK572960 and MK607461, MycoBank MB830213).

Additional materials examined. Russia, Magadan Region, Ten'kinsky district, Orotuk station, N62.03089° E148.65059°, on soil in mixed forests with *Larix cajanderi* and *Betula middendorffii*, 25 Aug. 1995, *N. Sinelnikova*, MAG 1339; Magadan Region, Srednekansky district, vicinity of Seimchan village, meadow of Kolyma river, N62.83388° E152.43129°, on soil in wet mixed forests with *Larix cajanderi*, *Betula platyphylla*, *Salix* spp., 28 Sept. 2018, *N. Sazanova*, MAG 5122, ITS sequence GenBank MK572961.

Notes — The greyish hymenophore and scales on the pileus indicate that our taxon belongs to a group of closely related species in *Suillus viscidus* s.lat. The main microscopic difference of the new species from another species of this group is in spore size and form. *Suillus gastroflavus* has broader spores, the majority having a narrowed and elongated apiculus. *Suillus gastroflavus* clearly differs from another known secotioid *Suillus* spp. by a greyish hymenophore. According to phylogenetic analysis, the nearest species for the new taxon is *Suillus viscidus* s.lat. Differences from other secotioid *Suillus* spp. ranged 8–12 %. *Suillus gastroflavus* is a third known secotioid *Suillus* species and first secotioid *Suillus* taxon in Eurasia.



ITS rDNA phylogenetic tree obtained with MrBayes v. 3.2.5 under GTR+I+G model for 10 M generations. The GenBank accession numbers are indicated after species names. Support values are indicated on the branches (posterior probabilities). Scale bar = 0.1 expected substitution per site.

Colour illustrations. Mixed forest with *Larix cajanderi*, Magadan Region, Russia. Holotype basidiomata, spores and cystidia. Scale bars = 10 µm.

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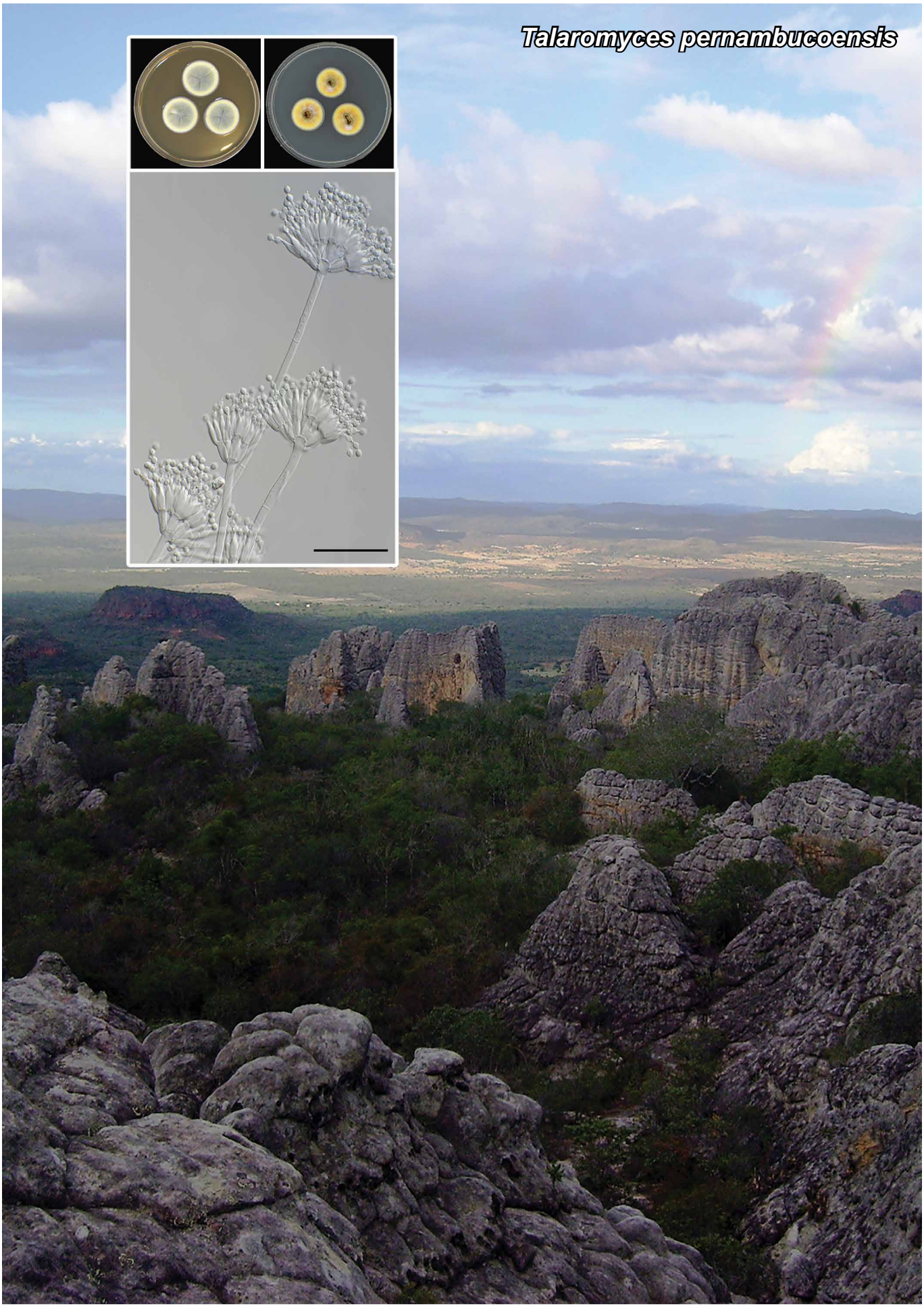

Talaromyces pernambucoensis

Fungal Planet 949 – 19 July 2019

Talaromyces pernambucoensis R. Cruz, C. Santos, Houbraken, R.N. Barbosa, Souza-Motta, *sp. nov.*

Etymology. *pernambucoensis*, refers to the Brazilian State of Pernambuco (Brazil), which is the geographical location of the ex-type strain of this species.

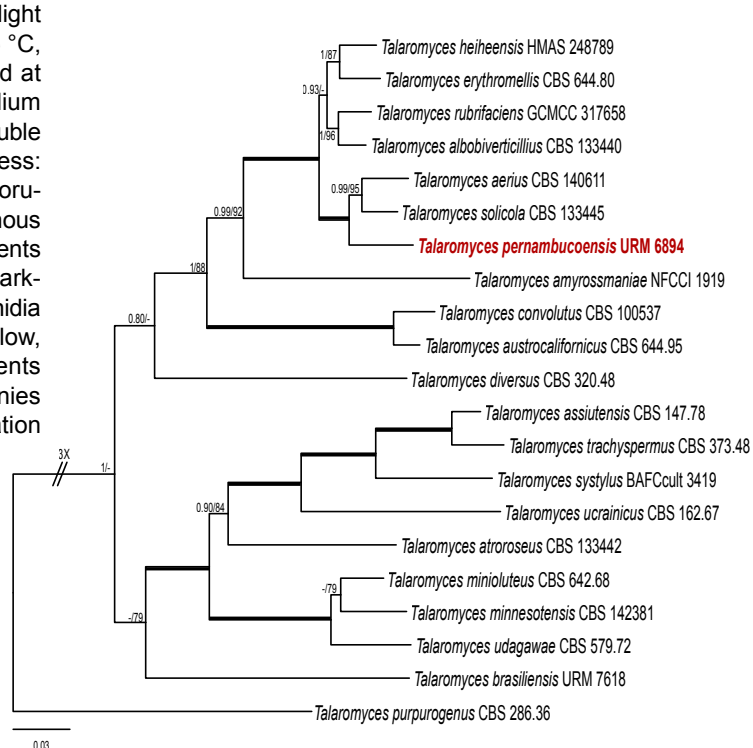
Classification — *Trichocomaceae*, *Eurotiales*, *Eurotiomycetes*.

On MEA: *Stipes* hyaline, smooth, (30–)50–130(–140) × 2.5–3(–3.5) µm; *conidiophores* symmetrical biverticillate; *metulae* generally in numbers of five, measuring (8–)10–15 × (2–)2.5–3(–3.5) µm; *phialides* acerose, (8–)10–21 × (2–)2.5–3(–3.5) µm; *conidia* globose occasionally subglobose, rough-walled to spinose, *en masse* green, 2.5–3 µm diam including ornamentation. *Ascomata* not observed.

Culture characteristics — MEA 25 °C, 7 d, in darkness: Colonies 32–35 mm diam, plane, raised at centre, conidia *en masse* blue to dark green, sporulation strong, mycelium white to yellow, colony texture floccose, exudate absent, soluble pigments absent, reverse orange. CYA 25 °C, 7 d, in darkness: Colonies 17–25 mm diam, flat, conidia *en masse* in shades of green to blue, sporulation strong, mycelium greyish green, colony texture velutinous to slightly floccose, exudate reddish to brown, soluble pigments absent, reverse brown to dark brown. OA 25 °C, 7 d, in darkness: Colonies 30–32 mm diam low, plane, colony texture velutinous; margins low, entire; mycelium yellowish white and white; sporulation moderate at centre; exudates absent, soluble pigments absent, reverse light yellow to white. No growth on CYAS and CREA. MEA 15 °C, 7 d, in darkness: Colonies 20–25 mm diam, plane, raised at centre, conidia *en masse* green, sporulation strong, mycelium white to yellow, colony texture floccose, exudate absent, soluble pigments absent, reverse orange. CYA 15 °C, 7 d, in darkness: Colonies 12–18 mm diam, flat, conidia *en masse* green, sporulation strong, mycelium greyish green, colony texture velutinous to slightly floccose, exudate reddish to brown, soluble pigments absent, reverse brown to dark brown. MEA 37 °C, 7 d, in darkness: Colonies 25–30 mm diam, plane, raised at centre, conidia *en masse* green, sporulation strong, mycelium white to yellow, colony texture floccose, exudate absent, soluble pigments absent, reverse orange. CYA 37 °C, 7 d, in darkness: Colonies 15–20 mm diam, flat, conidia *en masse* green, sporulation strong, mycelium greyish green, colony texture velutinous to slightly floccose, exudate reddish to brown, soluble pigments absent, reverse brown to dark brown.

Typus. Brazil, Pernambuco, Parque Nacional do Catimbau - Buíque, S08°04'25" W37°15'52", isolated from soil, Aug. 2009. *R. Cruz* (holotype URM 93054, culture ex-type = URM 6894, ITS, β-tubulin (*BenA*), calmodulin (*CaM*) and RNA polymerase second largest subunit (*RPB2*) sequences GenBank LR535947, LR535945, LR535946 and LR535948, MycoBank MB830189).

Notes — *Talaromyces pernambucoensis* was isolated from soil in a Brazilian dry forest (Caatinga). Various other species are reported from this soil that seems to contain a high *Talaromyces*, *Penicillium* and *Aspergillus* diversity (Cruz et al. 2013, Barbosa et al. 2016). ITS, *BenA*, *RPB2* and *CaM* are commonly used to study the phylogenetic relationships within *Talaromyces* (Yilmaz et al. 2014, Chen et al. 2016, Barbosa et al. 2018). The phylogenetic relationship of *T. pernambucoensis* with other members of section *Trachyspermi* is difficult to determine using single-gene phylogenies. Based on the combined dataset, consisting of ITS, *BenA*, *CaM* and *RPB2* sequences, *T. pernambucoensis* belongs to the same clade as *T. aerius* and *T. solicola*. *Talaromyces pernambucoensis* can be distinguished from *T. aerius* and *T. solicola* by its ability to grow on CYA incubated at 37 °C (15–20 mm vs no growth).



Phylogeny based on the combined ITS, *BenA*, *CaM* and *RPB2* sequence dataset for species classified in *Talaromyces* sect. *Trachyspermi* conducted in MrBayes on XSEDE and RAxML-HPC BlackBox in the CIPRES science gateway. Bayesian posterior probability and RAxML bootstrap support values are indicated at the nodes. The new species is indicated in **bold**. *Talaromyces purpurogenus* CBS 286.36 was chosen as outgroup.

Colour illustrations. Catimbau National Park. Colony on MEA and CYA after 7 d at 25 °C; conidiophores and conidia. Scale bar = 10 µm.

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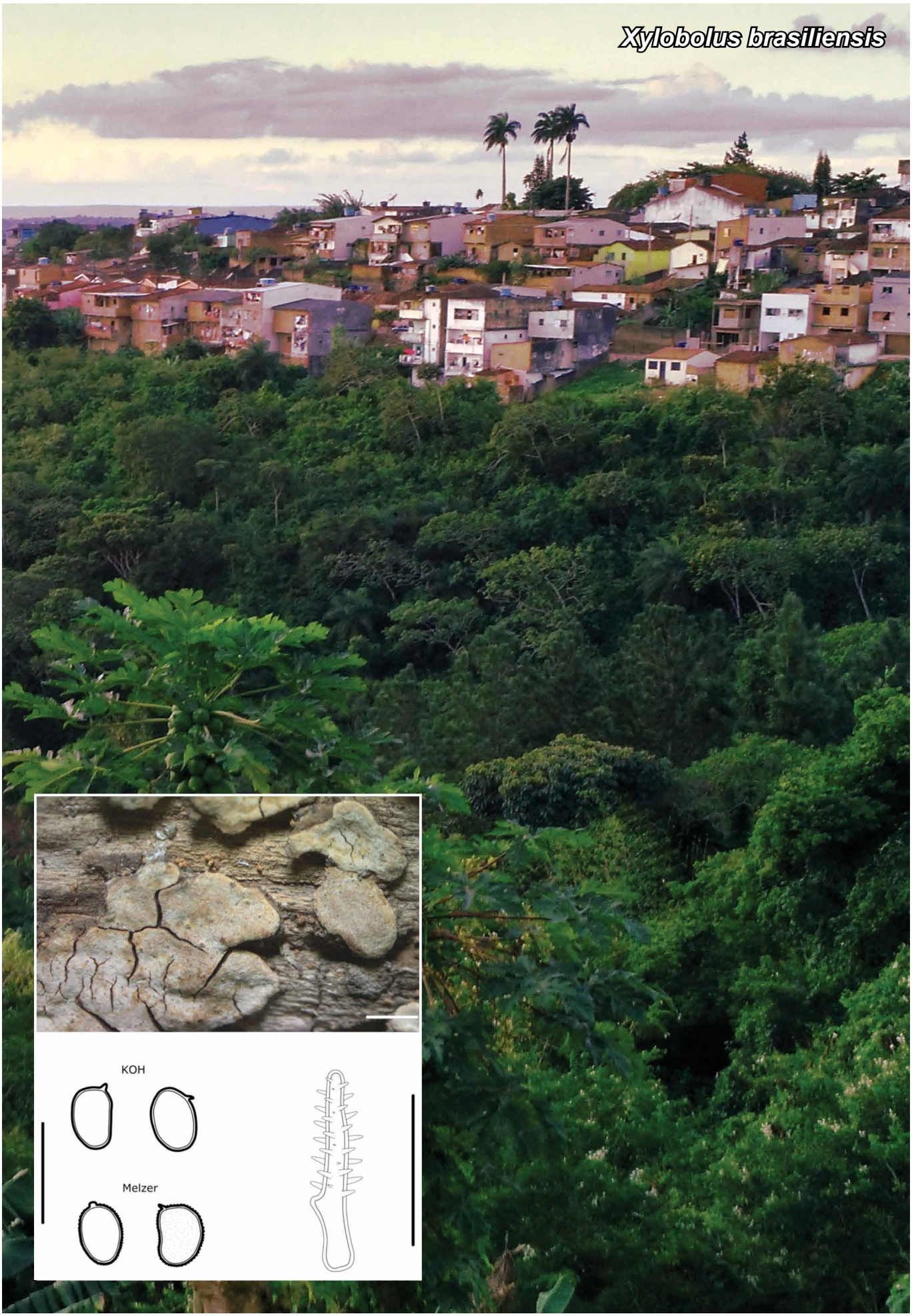

Xylobolus brasiliensis
KOH
Melzer

Fungal Planet 950 – 19 July 2019

Xylobolus brasiliensis Chikowski, C.R.S. de Lira, Gibertoni & K.H. Larss., *sp. nov.*

Etymology. Name refers to the country where the fungus was collected.

Classification — *Stereaceae*, *Russulales*, *Agaricomycetes*.

Basidiomata perennial, stratified in several layers, resupinate to effused reflexed, 1–2 mm thick, corky to woody, separated in small irregular patches (0.6–3 × 2.5–10 mm), slightly rimose. *Abhymenial surface* glabrous, dark brown (cigar brown 16). *Context* and *margin* concolorous with the abhymenial surface. *Hymenial surface* greyish brown (Clay buff 32) (Watling 1969), glabrous, smooth to slightly pilose. *Hyphal system* monomitic to pseudodimitic due to the acanthohyphidia, vertically arranged, hyphae clamped. *Acanthohyphidia* numerous in trama and hymenium, cylindrical with obtuse apex, 20–74 × 4–8 µm (L = 40.40 µm, W = 6.17 µm, Q = 6.54 µm). *Basidia* not seen. *Basidiospores* yellowish to brownish, subglobose to ellipsoid, 5–6(–6.5) × (3–)3.5–5 µm (L = 5.8 µm, W = 3.75 µm, Q = 1.52 µm), slightly thick-walled, smooth in KOH 3 %, minutely ornamented in Melzer, with a lateral prominent apiculus, distinctly amyloid.

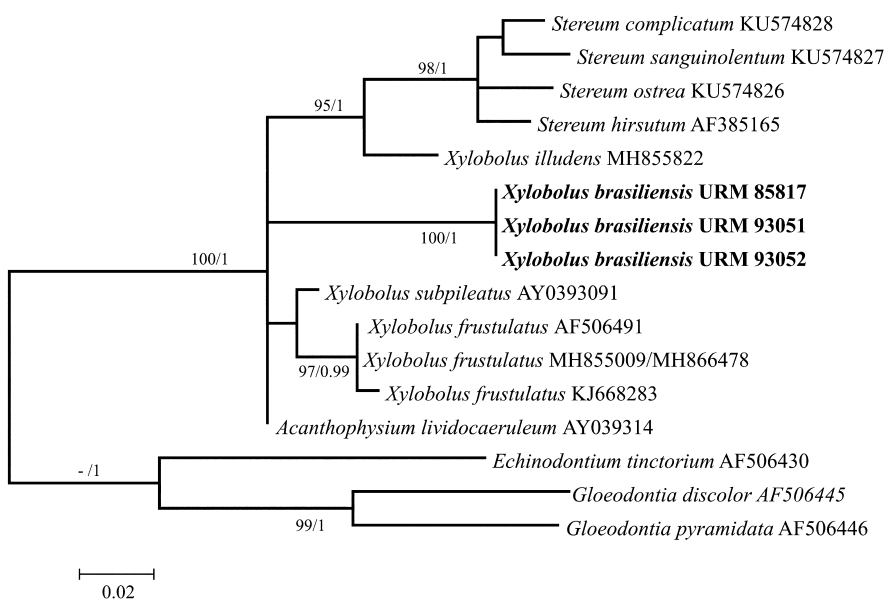
Typus. Brazil, Paraíba, Areia, Reserva Estadual Mata do Pau-Ferro, S6°59' W35°45', on decaying wood, Apr. 2013, *C.R.S. Lira* CL 632 (holotype URM 93051, isotype in O, ITS and LSU sequences GenBank MK491193 and MK491189, MycoBank MB830132).

Additional materials examined. Brazil, Alagoas, Pilar, RPPN Fazenda de São Pedro, on decaying wood, Nov. 2001, *T.B. Gibertoni* TBG 106, URM 77155; Paraíba, Areia, Reserva Estadual Mata do Pau-Ferro, on decaying wood, Apr. 2013, *C.R.S. Lira* CL 619, URM 93052; Pernambuco, Jaqueira, Reserva Particular do Patrimônio Natural Frei Caneca, S08°42'41" W35°50'30", on decaying wood, June 2012, *R.S. Chikowski* RC 71, URM 85814; ibid., Mar. 2013, *R.S. Chikowski* RC 552, URM 85815; ibid., Mar. 2013, *R.S. Chikowski*, RC 553, URM 85818; ibid, Apr. 2013, *R.S. Chikowski* RC 659, URM85817.

Notes — Morphologically, *X. brasiliensis* is quite similar to *X. frustulatus*, but the latter has shorter acanthohyphidia (25–30 × 4–5 µm) and basidiospores (4.5–5(–5.5) × 3–3.2(–3.5) µm), rare pseudocystidia and elongated basidia (25–30 × 4–5 µm) (Hjortstam et al. 1988).

Based on a BLASTn search of NCBIs GenBank database, the closest hits using the **ITS** sequence are *X. subpileatus* (GenBank KX578084; Identities = 559/634 (88 %), 27 gaps (4 %)), *X. subpileatus* (GenBank KX578082; Identities = 558/633 (88 %), 27 gaps (4 %)) and *X. subpileatus* (GenBank KX578080; Identities = 558/634 (88 %), 27 gaps (4 %)). Using the **LSU** sequence, the closest hits are *Acanthophysium lividocaeruleum* (GenBank AY039314; Identities = 929/947 (98 %), 3 gaps (0 %)), *X. subpileatus* (GenBank AY039309; Identities = 927/947 (98 %), 4 gaps (0 %)) and *X. subpileatus* (GenBank AY039307; Identities = 927/947 (98 %), 3 gaps (0 %)).

Although genetically close to *X. subpileatus*, this species differs by effused-reflexed basidiomata, tuberculated hymenium when young, smaller, acute to subcylindrical acanthohyphidia (20–30 × 4–5 µm) and longer basidia (20–30 × 4–5 µm) (Bernicchia & Gorjón 2010).



Phylogenetic reconstruction of *Stereaceae* based on alignment of 1593 nucleotides of combined ITS and LSU rDNA sequences. Bootstrap values (%) were generated from Maximum Likelihood (ML) analysis, and posterior probabilities (PP) from Bayesian algorithm (BA), respectively. Species in **bold** were sequenced in this study. *Gloeodontia discolor* (GenBank AF506445) and *G. pyramidata* (GenBank AF506446) were selected as outgroup.

Colour illustrations. Environment where the type specimen was collected, Reserva Estadual Mata do Pau-Ferro, Areia, Paraíba, Brazil. Dried basidioma (type specimen); basidiospores; acanthohyphidia. Scale bars = 1 mm (basidioma), 5 µm (basidiospores), 30 µm (acanthohyphidia).

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