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Abstract Novel species of fungi described in this study include those from various countries as follows: **Antarctica**, *Apenidiella antarctica* from permafrost, *Cladosporium fildesense* from an unidentified marine sponge. **Argentina**, *Geastrum wrightii* on humus in mixed forest. **Australia**, *Golovinomyces glandulariae* on *Glandularia aristigera, Neoanungitea eucalyptorum* on leaves of *Eucalyptus grandis, Teratosphaeria corymbiicola* on leaves of *Corymbia ficifolia, Xylaria eucalypti* on leaves of *Eucalyptus radiata.* **Brazil**, *Bovista psammophila* on soil, *Fusarium awaxy* on rotten stalks of *Zea mays, Geastrum lanuginosum* on leaf litter covered soil, *Hermetothecium mikaniae-micranthae* (incl. *Hermetothecium* gen. nov.) on *Mikania micrantha, Penicillium reconvexovelosoi* in soil, *Stagonosporopsis vannaccii* from pod of *Glycine max.* **British Virgin Isles**, *Lactifluus guanensis* on soil. **Canada**, *Sorocybe oblongispora* on resin of *Picea rubens.* **Chile**, *Colletotrichum roseum* on leaves of *Lapageria rosea.* **China**, *Setophoma caverna* from carbonatite in Karst cave. **Colombia**, *Lareunionomyces eucalypticola* on leaves of *Eucalyptus grandis.* **Costa Rica**, *Psathyrella pivae* on wood. **Cyprus**, *Clavulina iris* on calcareous substrate. **France**, *Chromosera ambigua* and *Clavulina iris* var. *occidentalis* on soil. **French West Indies**, *Helminthosphaeria hispidissima* on dead wood. **Guatemala**, *Talaromyces guatemalensis* in soil. **Malaysia**, *Neotracylla pini* (incl. *Tracyllales* ord. nov. and *Neotracylla* gen. nov.) and *Vermiculariopsiella pini* on needles of *Pinus tecunumanii.* **New Zealand**, *Neoconiothyrium viticola* on stems of *Vitis vinifera, Parafenestella pittospori* on *Pittosporum tenuifolium, Pilidium novae-zelandiae* on *Phoenix* sp. **Pakistan**, *Russula quercus-floribundae* on forest floor. **Portugal**, *Trichoderma aestuarinum* from saline water. **Russia**, *Pluteus liliputianus* on fallen branch of deciduous tree, *Pluteus spurius* on decaying deciduous wood or soil. **South Africa**, *Alloconiothyrium encephalarti, Phyllosticta encephalarticola* and *Neothyrostroma encephalarti* (incl. *Neothyrostroma* gen. nov.) on leaves of *Encephalartos* sp., *Chalara eucalypticola* on leaf spots of *Eucalyptus grandis* × *urophylla, Clypeosphaeria oleae* on leaves of *Olea capensis, Cylindrocladiella postalofficium* on leaf litter of *Sideroxylon inerme*, *Cylindromonium eugeniicola* (incl. *Cylindromonium* gen. nov.) on leaf litter of *Eugenia capensis*, *Cyphellophora goniomatis* on leaves of *Gonioma kamassi*, *Nothodactylaria nephrolepidis* (incl. *Nothodactylaria* gen. nov. and *Nothodactylariaceae* fam. nov.) on leaves of *Nephrolepis exaltata*, *Falcocladium eucalypti* and *Gyrothrix eucalypti* on leaves of *Eucalyptus* sp., *Gyrothrix oleae* on leaves of *Olea capensis* subsp. *macrocarpa*, *Harzia metrosideri* on leaf litter of *Metrosideros* sp., *Hippopotamyces phragmitis* (incl. *Hippopotamyces* gen. nov.) on leaves of *Phragmites australis*, *Lectera philenopterae* on *Philenoptera violacea*, *Leptosillia mayteni* on leaves of *Maytenus heterophylla*, *Lithohypha aloicola* and *Neoplatysporoides aloes* on leaves of *Aloe* sp., *Millesimomyces rhoicissi* (incl. *Millesimomyces* gen. nov.) on leaves of *Rhoicissus digitata*, *Neodevriesia strelitziicola* on leaf litter of *Strelitzia nicolai*, *Neokirramyces syzygii* (incl. *Neokirramyces* gen. nov.) on leaf spots of

Abstract (cont.)

Syzygium sp., *Nothoramichloridium perseae* (incl. *Nothoramichloridium* gen. nov. and *Anungitiomycetaceae* fam. nov.) on leaves of *Persea americana*, *Paramycosphaerella watsoniae* on leaf spots of *Watsonia* sp., *Penicillium cuddlyae* from dog food, *Podocarpomyces knysnanus* (incl. *Podocarpomyces* gen. nov.) on leaves of *Podocarpus falcatus*, *Pseudocercospora heteropyxidicola* on leaf spots of *Heteropyxis natalensis*, *Pseudopenidiella podocarpi, Scolecobasidium podocarpi* and *Ceramothyrium podocarpicola* on leaves of *Podocarpus latifolius*, *Scolecobasidium blechni* on leaves of *Blechnum capense*, *Stomiopeltis syzygii* on leaves of *Syzygium chordatum*, *Strelitziomyces knysnanus* (incl. *Strelitziomyces* gen. nov.) on leaves of *Strelitzia alba*, *Talaromyces clemensii* from rotting wood in goldmine, *Verrucocladosporium visseri* on *Carpobrotus edulis.* **Spain**, *Boletopsis mediterraneensis* on soil, *Calycina cortegadensisi* on a living twig of *Castanea sativa*, *Emmonsiellopsis tuberculata* in fluvial sediments, *Mollisia cortegadensis* on dead attached twig of *Quercus robur*, *Psathyrella ovispora* on soil, *Pseudobeltrania lauri* on leaf litter of *Laurus azorica*, *Terfezia dunensis* in soil, *Tuber lucentum* in soil, *Venturia submersa* on submerged plant debris. **Thailand**, *Cordyceps jakajanicola* on cicada nymph, *Cordyceps kuiburiensis* on spider, *Distoseptispora caricis* on leaves of *Carex* sp., *Ophiocordyceps khonkaenensis* on cicada nymph. **USA**, *Cytosporella juncicola* and *Davidiellomyces juncicola* on culms of *Juncus effusus*, *Monochaetia massachusettsianum* from air sample, *Neohelicomyces melaleucae* and *Periconia neobrittanica* on leaves of *Melaleuca styphelioides* × *lanceolata*, *Pseudocamarosporium eucalypti* on leaves of *Eucalyptus* sp., *Pseudogymnoascus lindneri* from sediment in a mine, *Pseudogymnoascus turneri* from sediment in a railroad tunnel, *Pulchroboletus sclerotiorum* on soil, *Zygosporium pseudomasonii* on leaf of *Serenoa repens.* **Vietnam**, *Boletus candidissimus* and *Veloporphyrellus vulpinus* on soil. Morphological and culture characteristics are supported by DNA barcodes.

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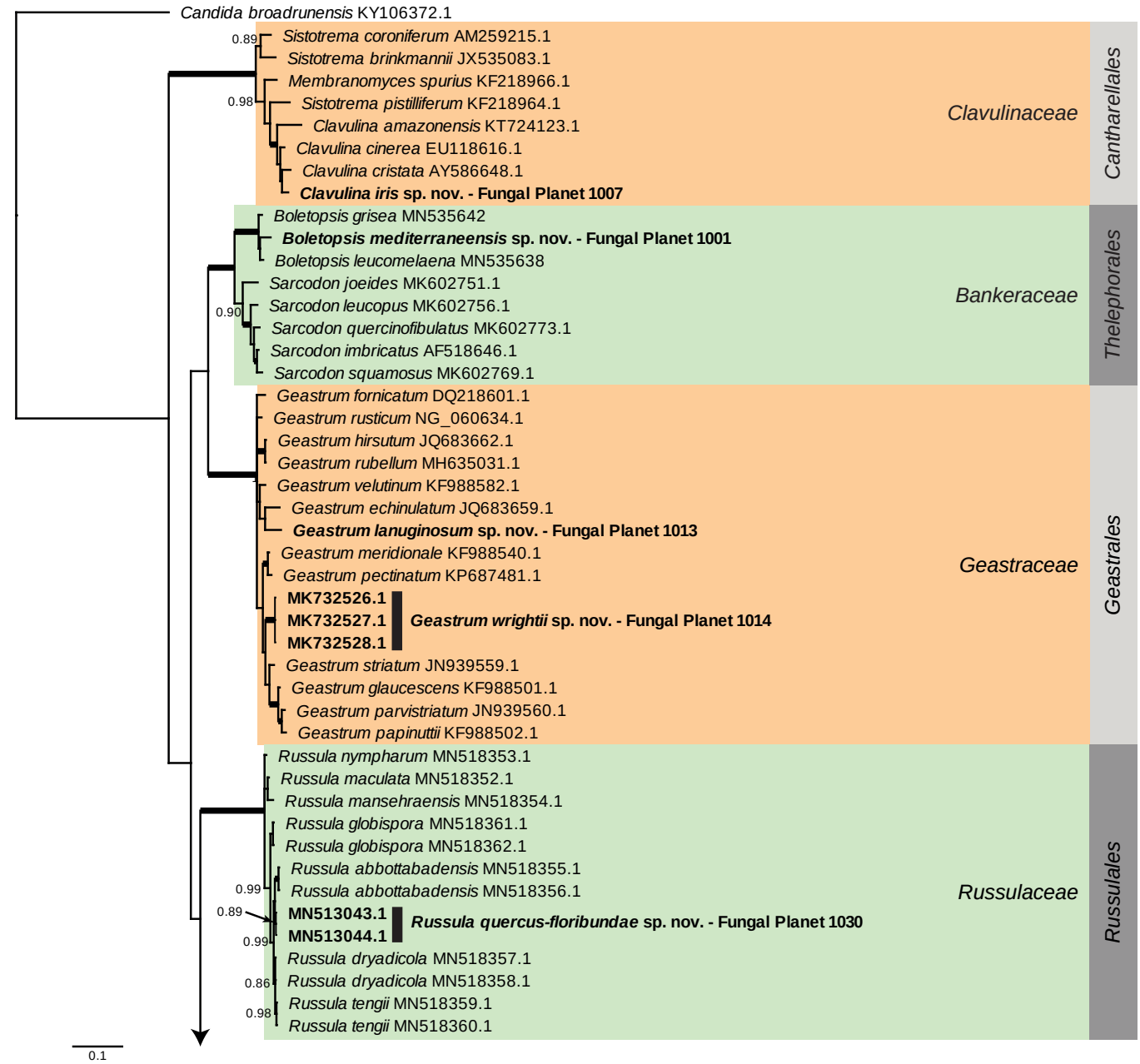
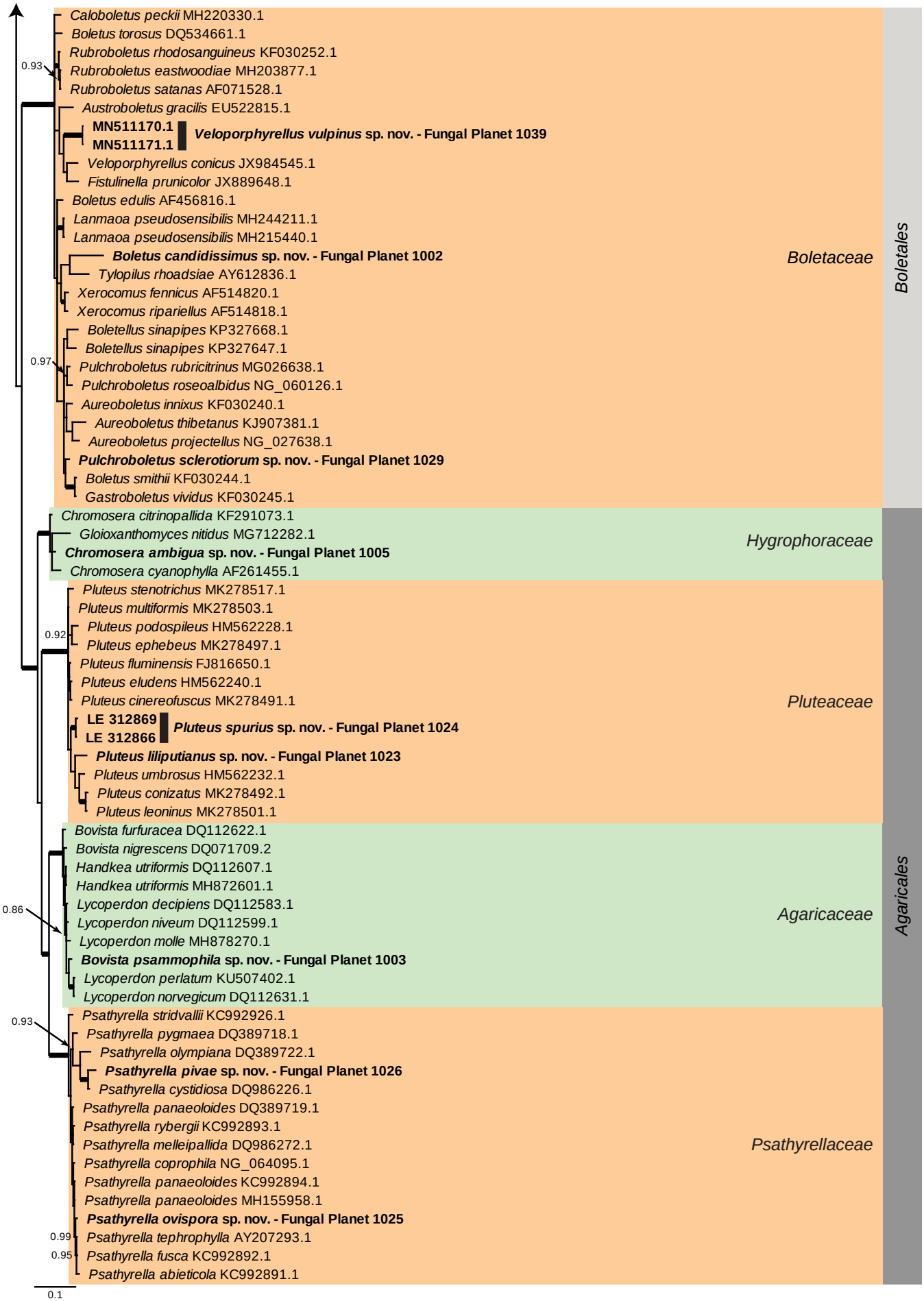


Overview *Agaricomycetes* (*Basidiomycota*) phylogeny – part 1

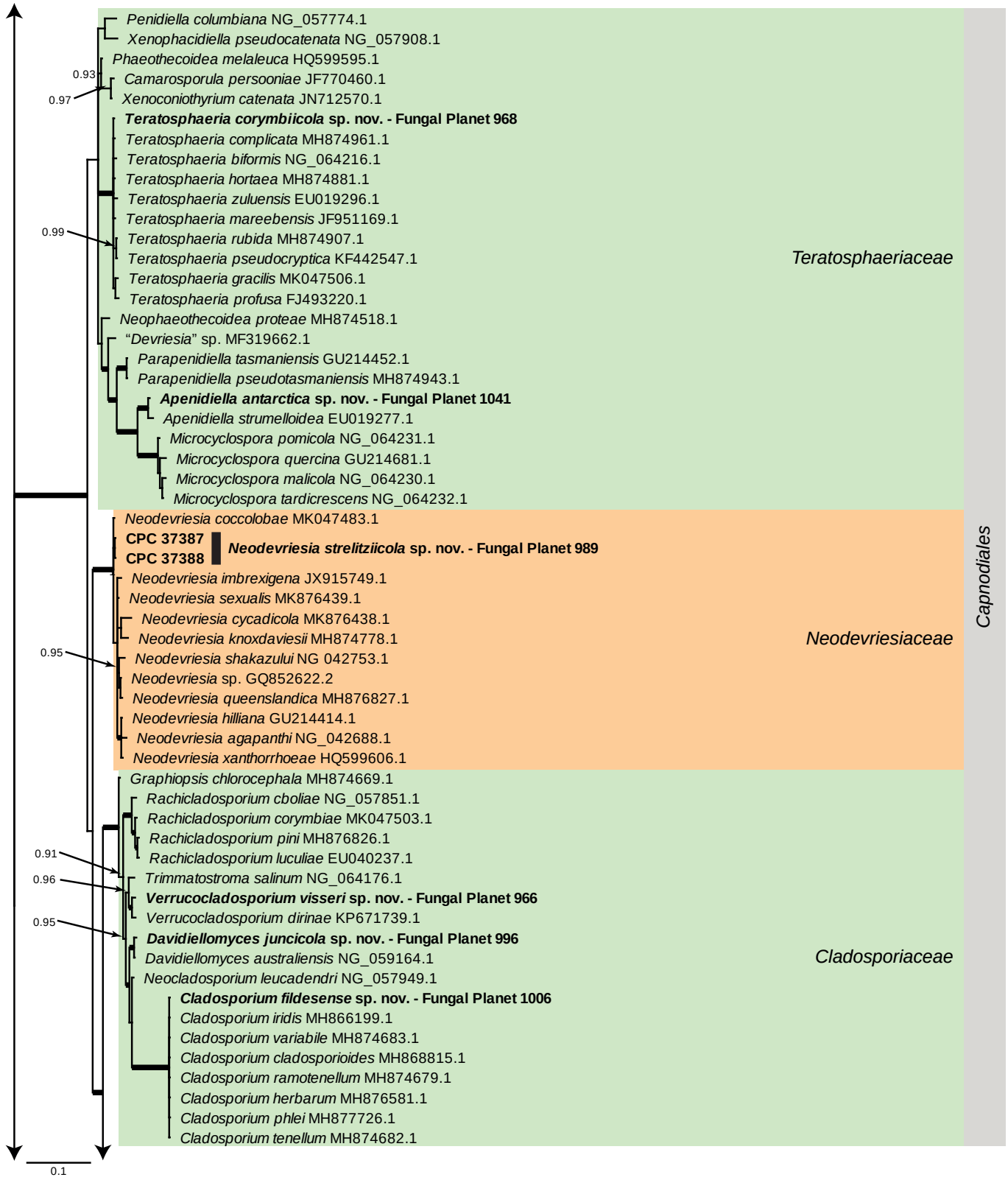
Consensus phylogram (50 % majority rule) of 3602 trees resulting from a Bayesian analysis of the LSU sequence alignment (115 sequences including outgroup; 764 aligned positions; 427 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown 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 S25229).



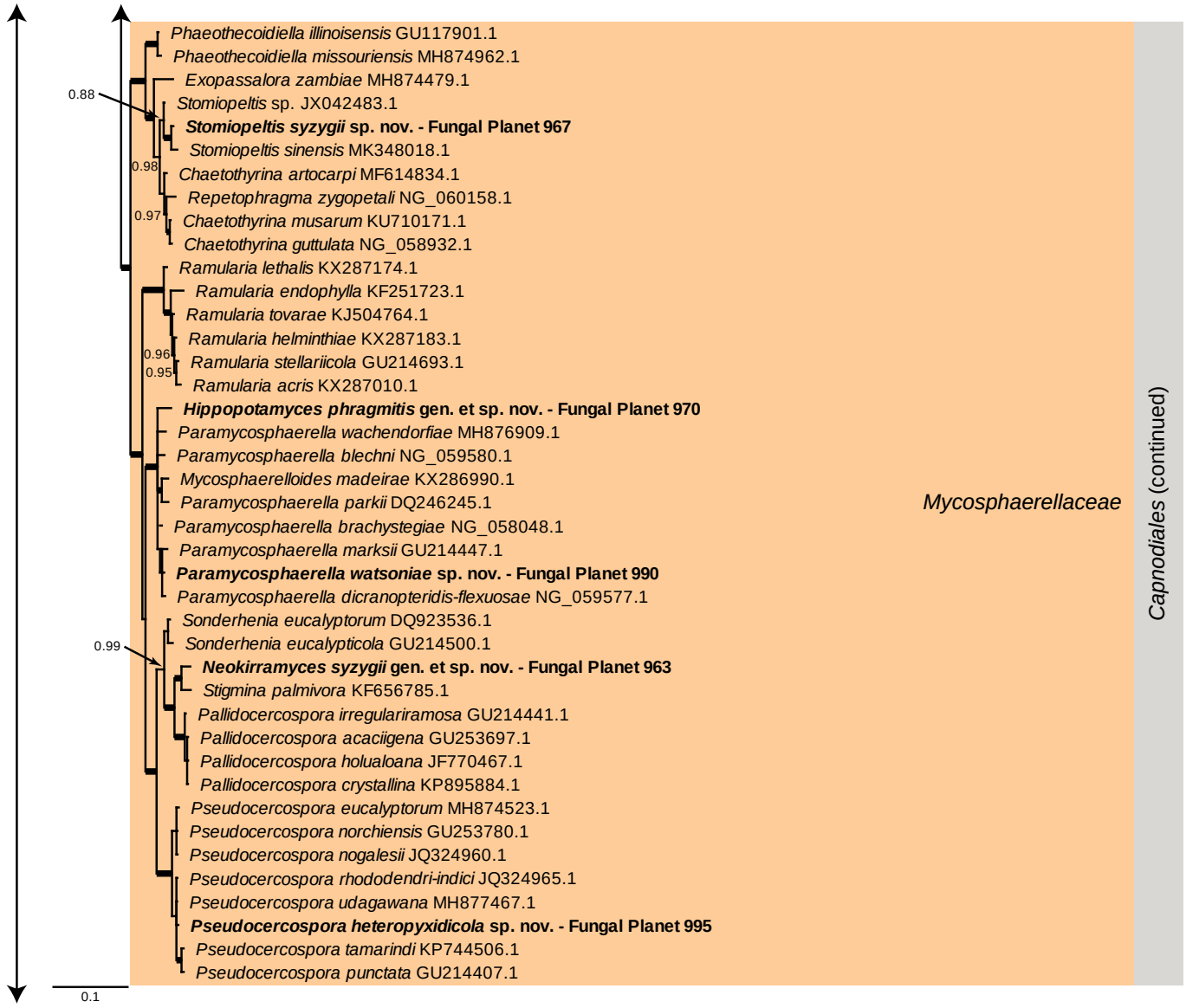
Overview *Agaricomycetes* (*Basidiomycota*) phylogeny (cont.) – part 2

Overview *Dothideomycetes* phylogeny – part 1

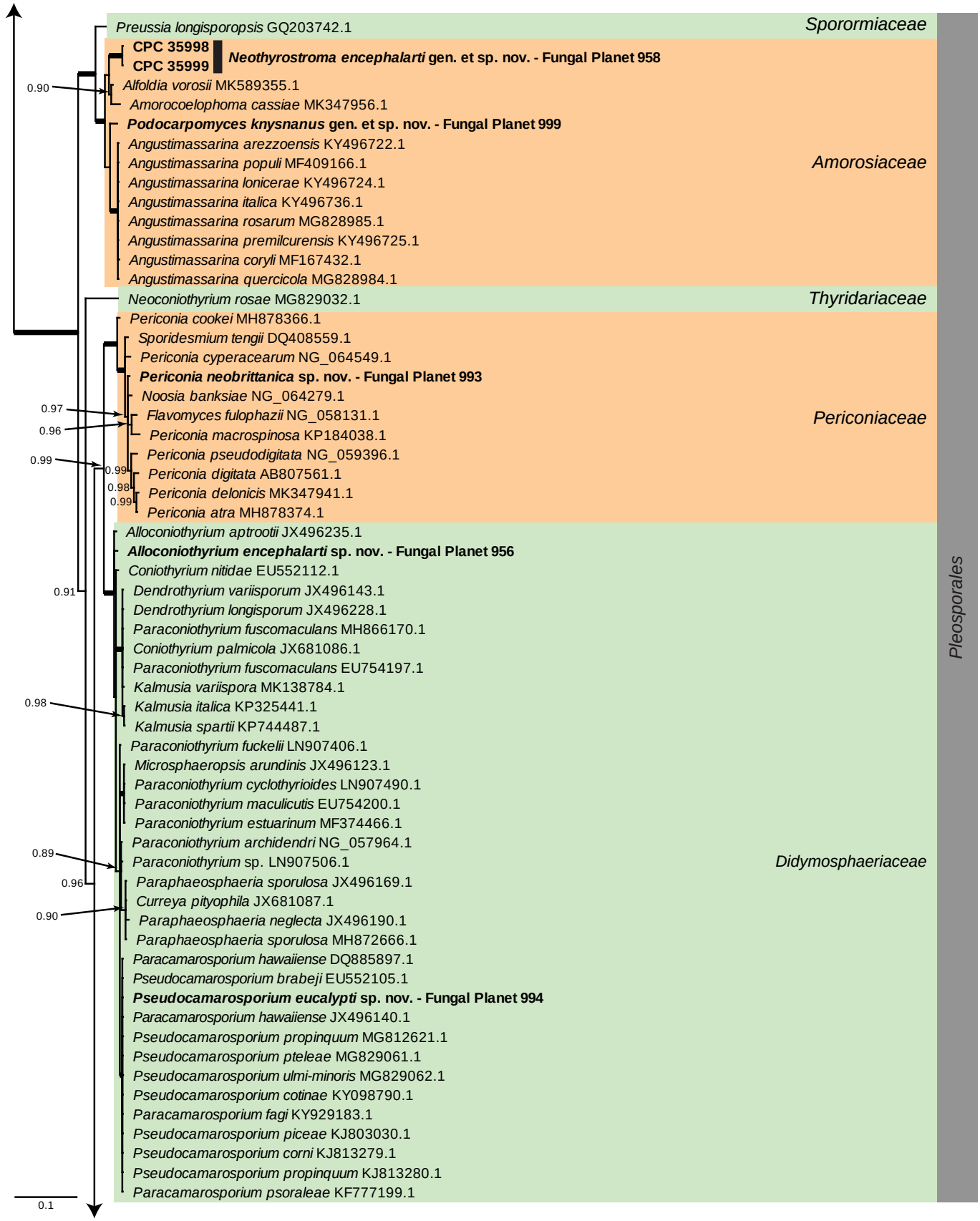
Consensus phylogram (50 % majority rule) of 80 252 trees resulting from a Bayesian analysis of the LSU sequence alignment (284 sequences including outgroup; 797 aligned positions; 431 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are 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 S25229).



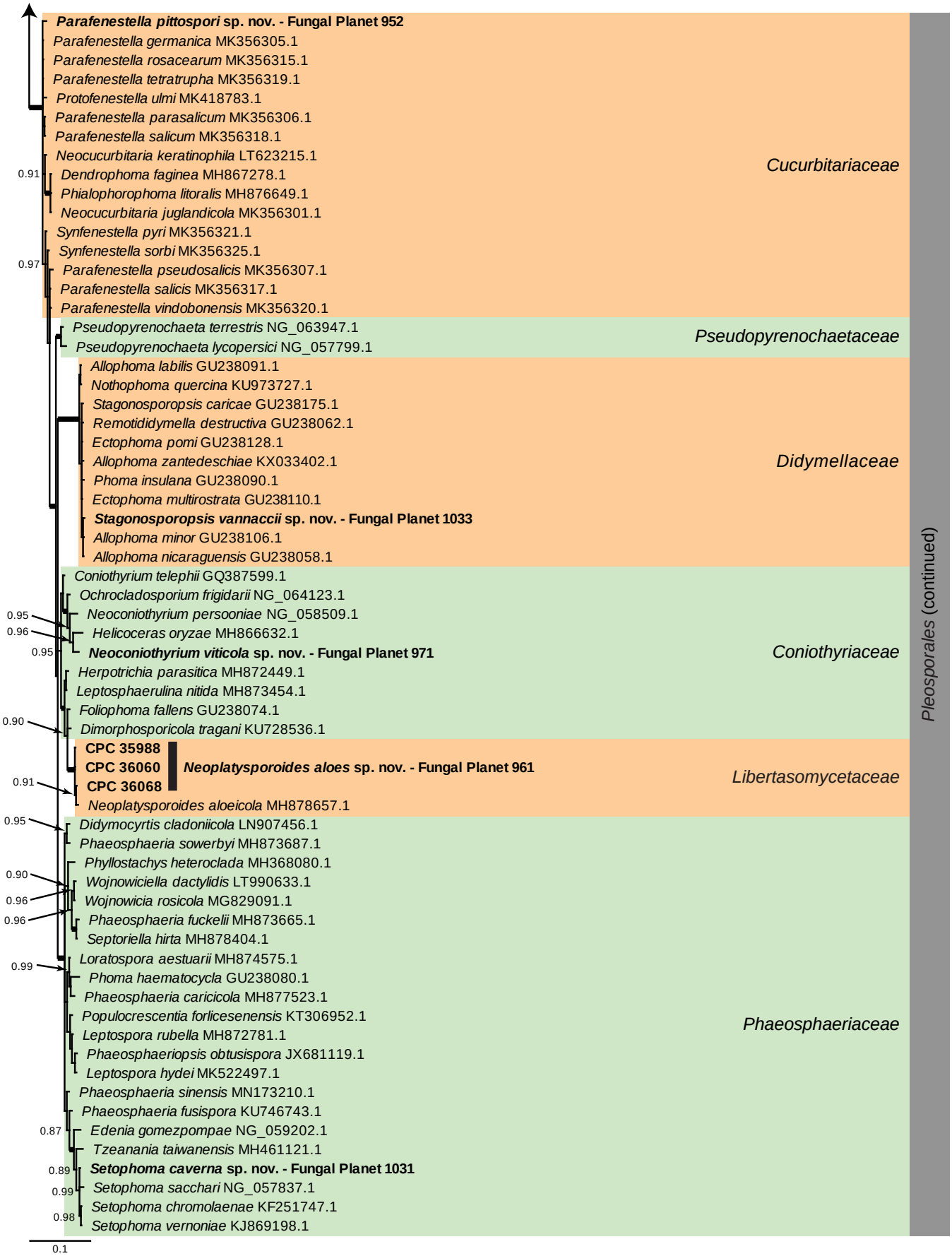
Overview *Dothideomycetes* phylogeny (cont.) – part 2



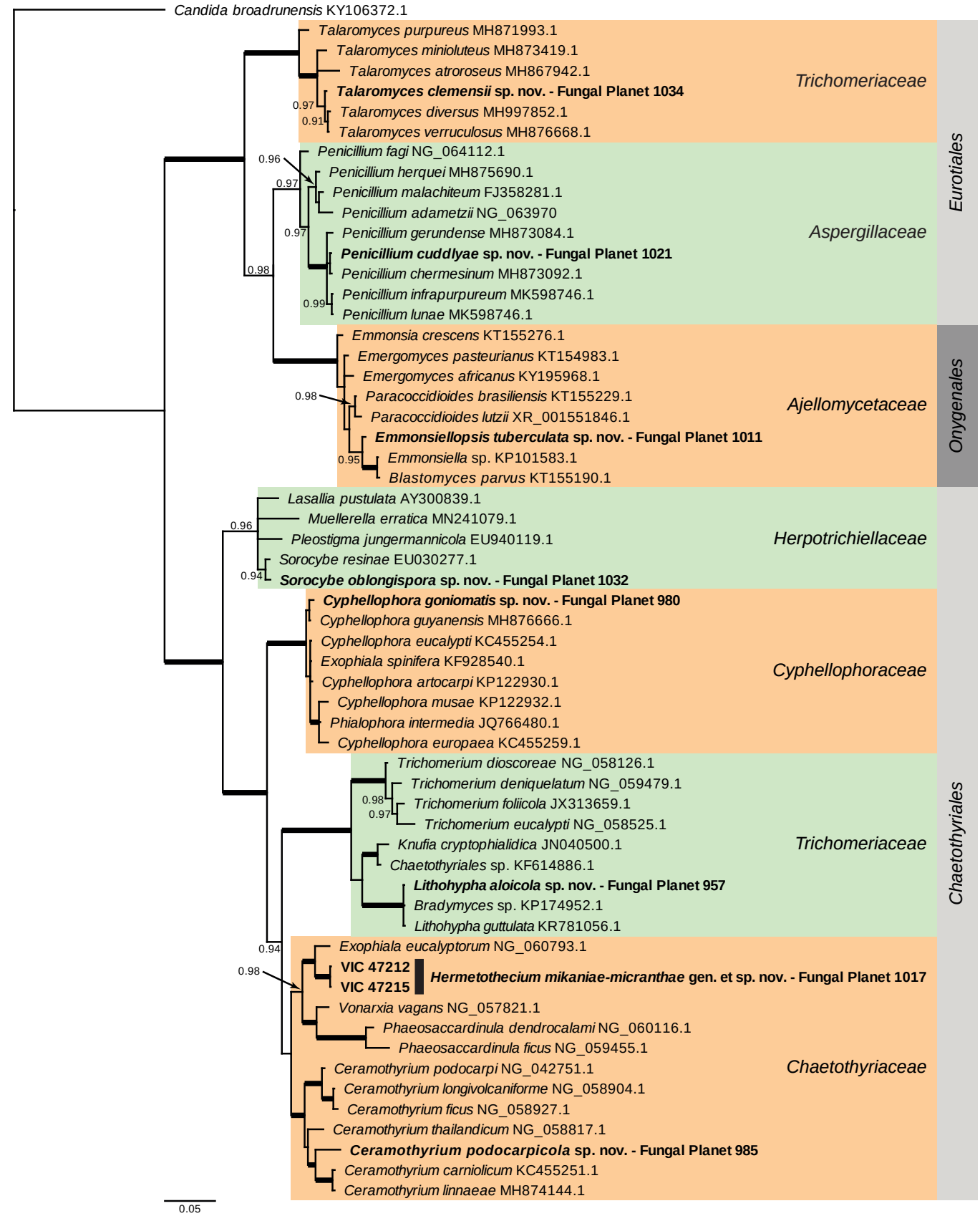
Overview *Dothideomycetes* phylogeny (cont.) – part 3



Overview *Dothideomycetes* phylogeny (cont.) – part 4

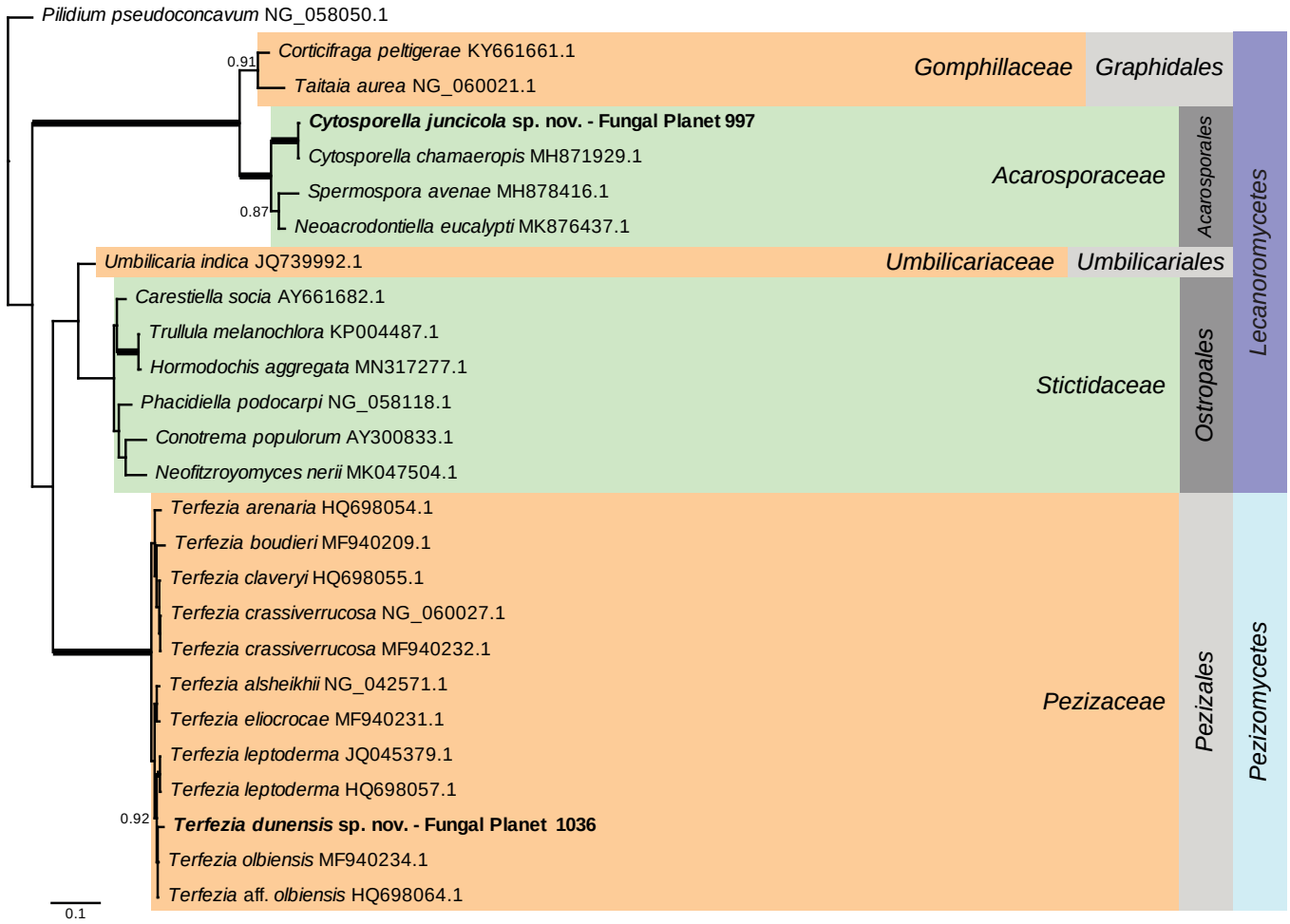


Overview *Dothideomycetes* phylogeny (cont.) – part 5



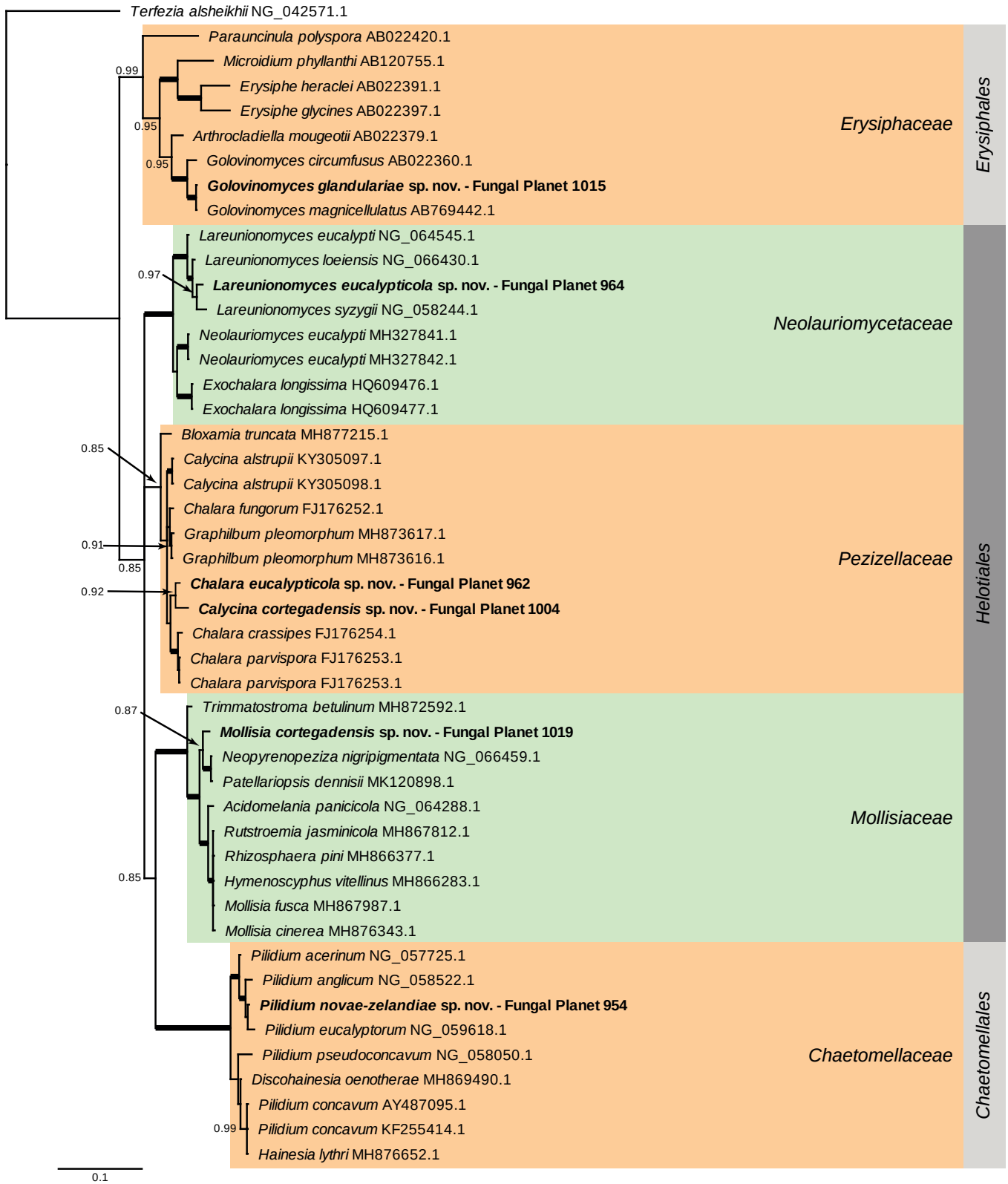
Overview *Eurotiomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 9 002 trees resulting from a Bayesian analysis of the LSU sequence alignment (59 sequences including outgroup; 796 aligned positions; 308 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 S25229).



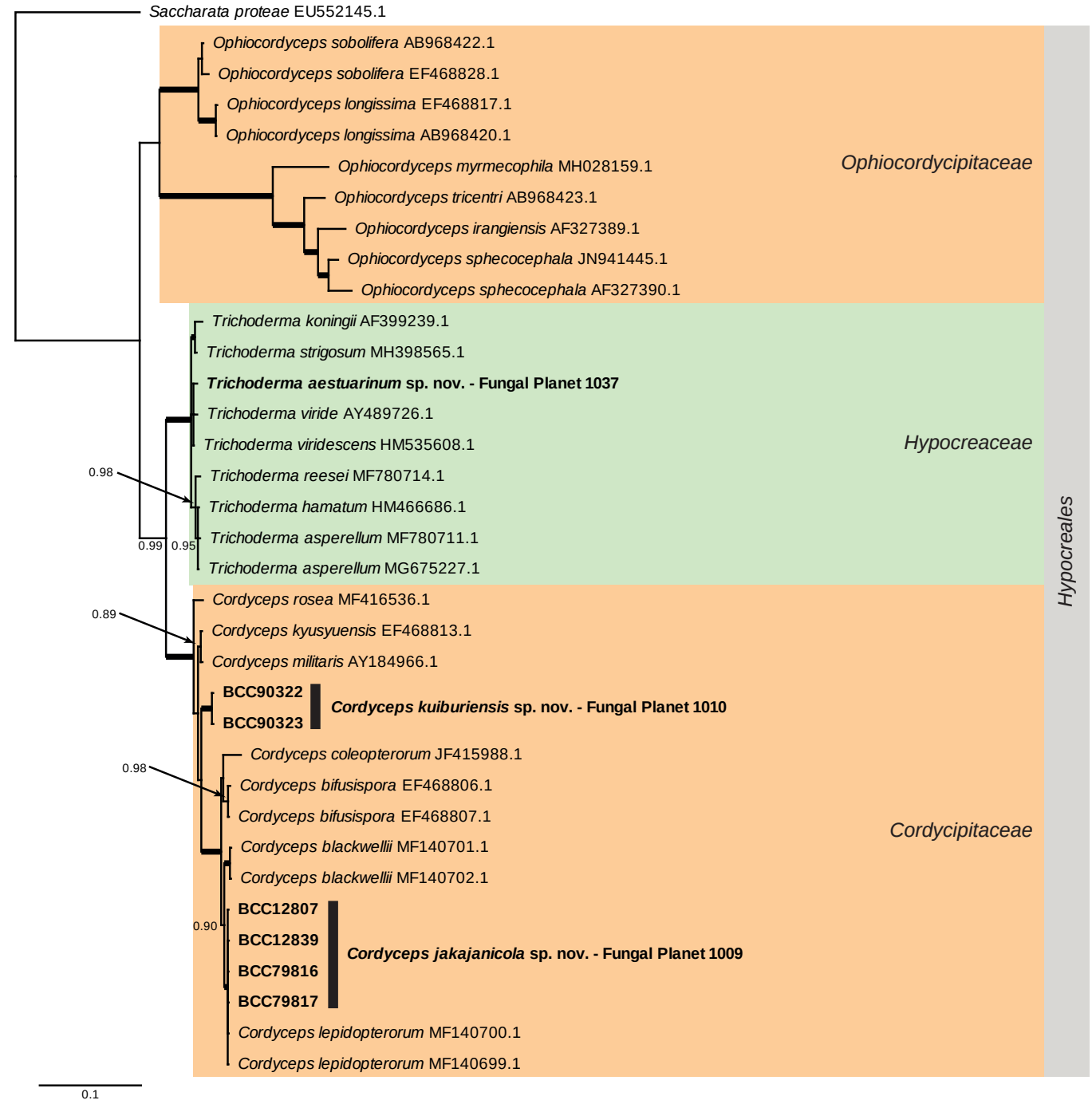
Overview *Lecanoromycetes* and *Pezizomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 3 002 trees resulting from a Bayesian analysis of the LSU sequence alignment (26 sequences including outgroup; 760 aligned positions; 264 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 *Pilidium pseudoconcavum* (GenBank NG_058050.1) 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 S25229).



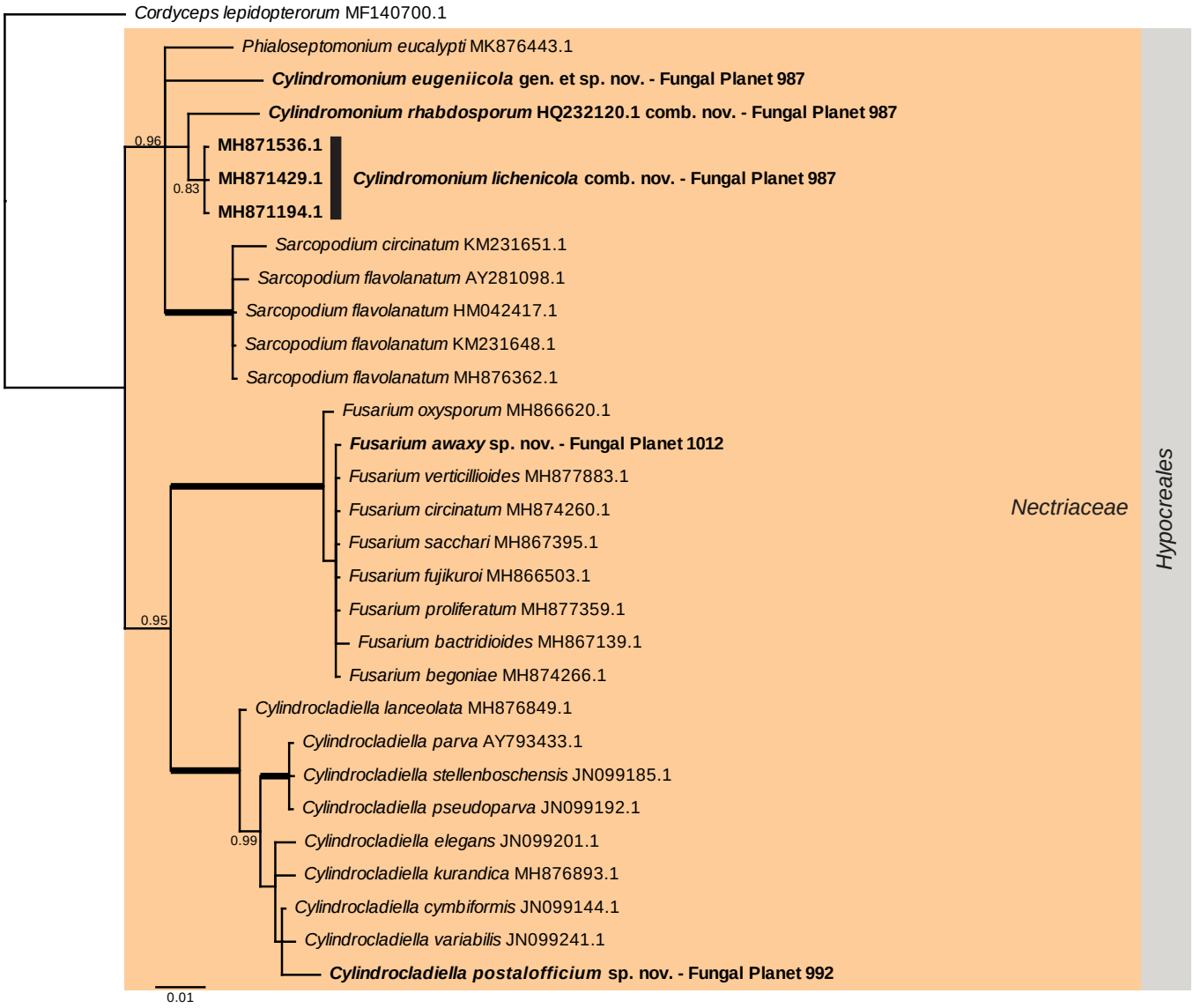
Overview *Leotiomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 3 752 trees resulting from a Bayesian analysis of the LSU sequence alignment (47 sequences including outgroup; 752 aligned positions; 199 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 or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Terfezia alsheikhii* (GenBank NG_042571.1) 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 S25229).



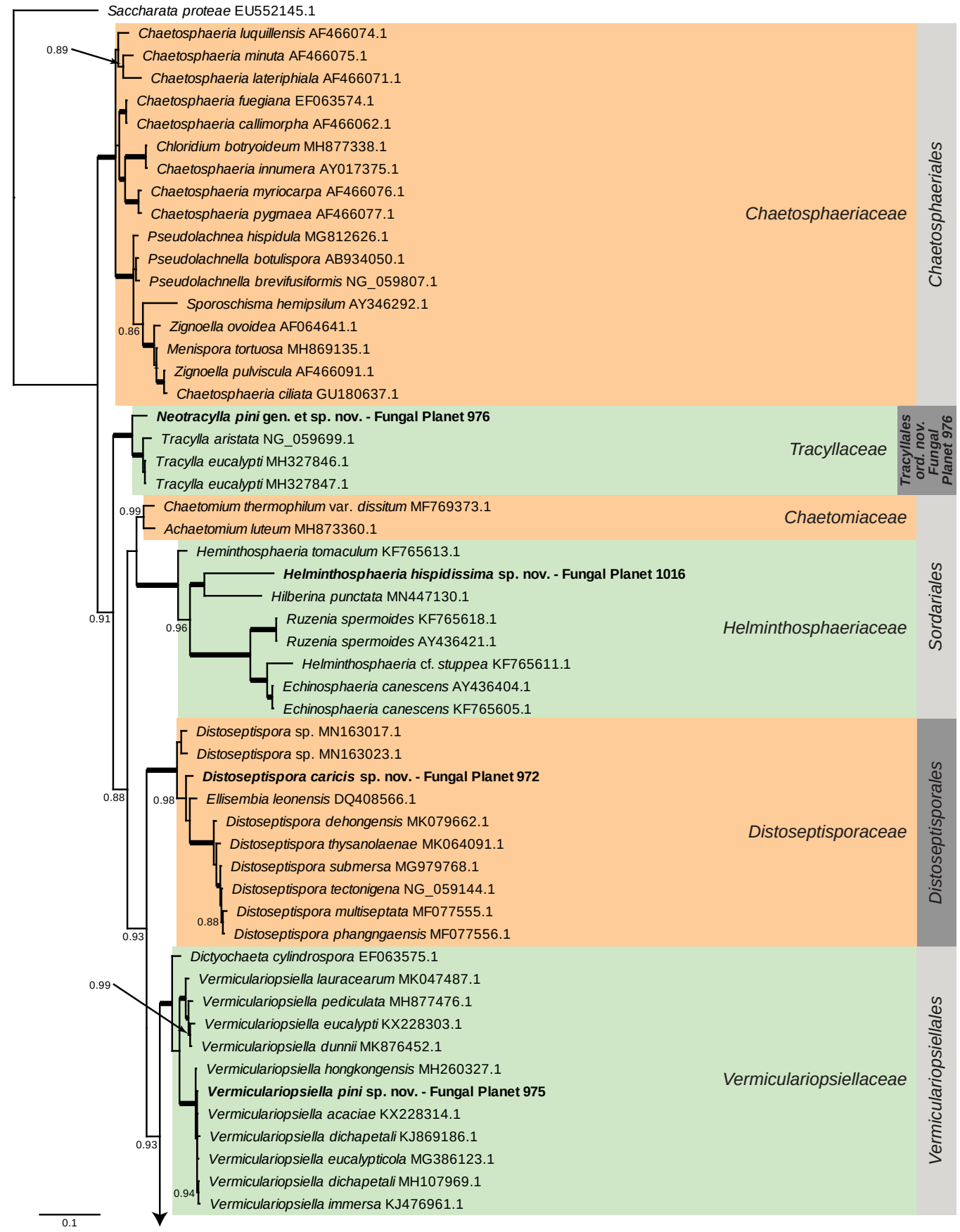
Overview *Cordycipitaceae* and *Ophiocordycipitaceae* (*Hypocreales*, *Sordariomycetes*) phylogeny

Consensus phylogram (50 % majority rule) of 1 502 trees resulting from a Bayesian analysis of the LSU sequence alignment (35 sequences including outgroup; 798 aligned positions; 242 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 *Saccharata proteae* (GenBank EU552145.1) 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 S25229).



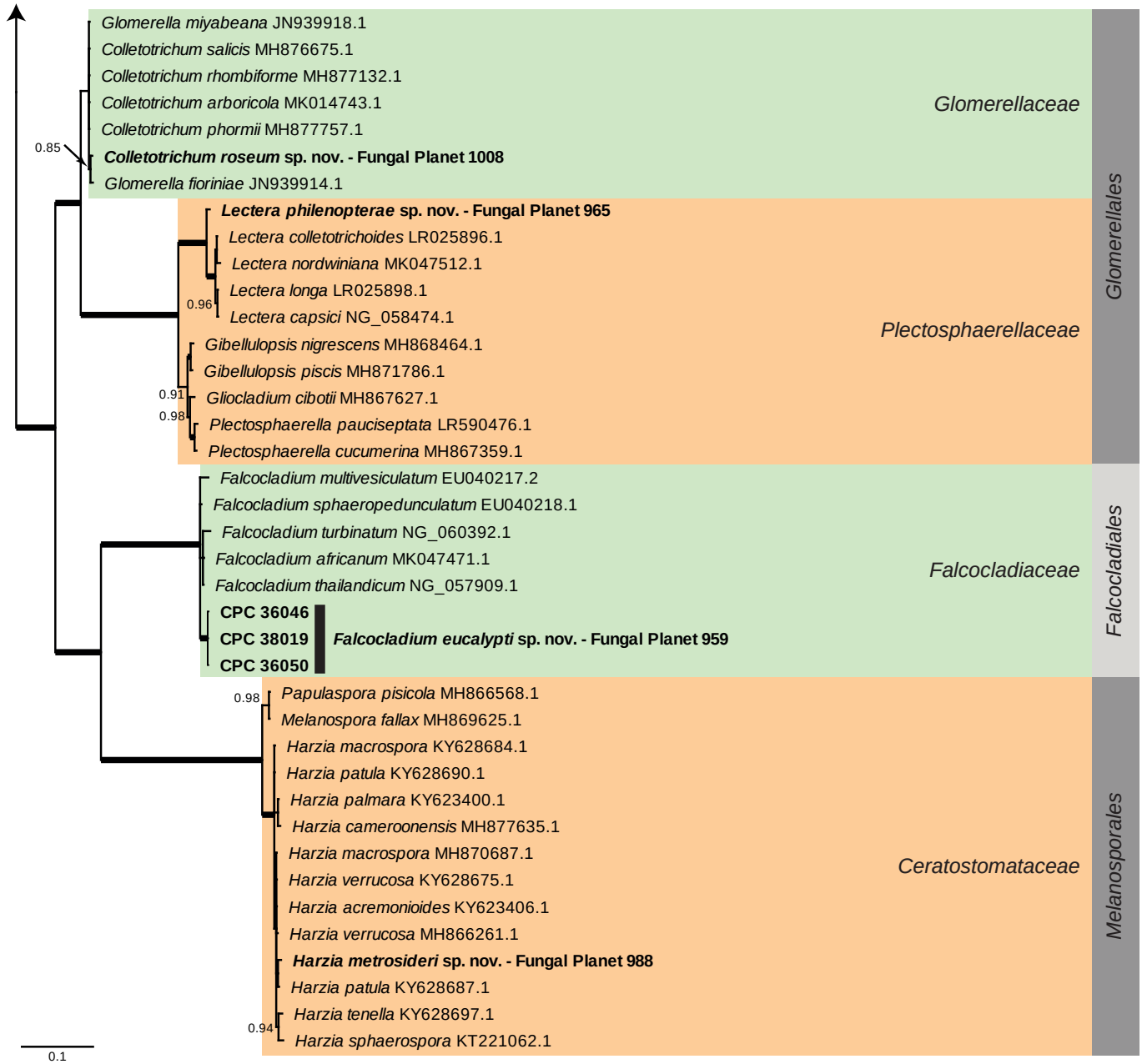
Overview *Nectriaceae* (*Hypocreales*, *Sordariomycetes*) phylogeny

Consensus phylogram (50 % majority rule) of 2 252 trees resulting from a Bayesian analysis of the LSU sequence alignment (30 sequences including outgroup; 778 aligned positions; 95 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. The family and order 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 *Cordyceps lepidopterorum* (GenBank MF140700.1) 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 S25229).



Overview other orders (*Sordariomycetes*) phylogeny – part 1

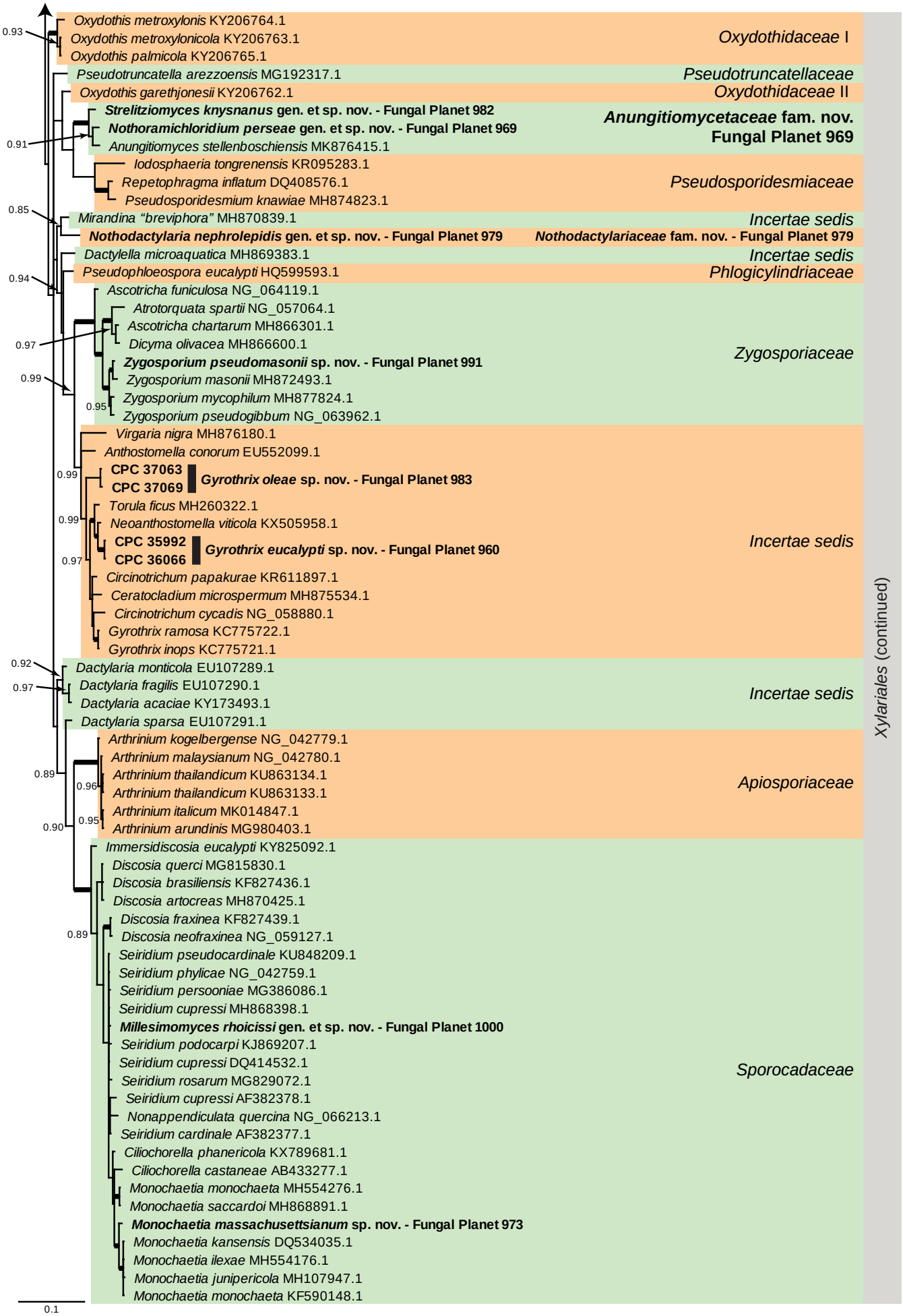
Consensus phylogram (50 % majority rule) of 6 002 trees resulting from a Bayesian analysis of the LSU sequence alignment (93 sequences including outgroup; 825 aligned positions; 405 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown 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 *Saccharata proteae* (GenBank EU552145.1) 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 S25229).



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

Overview *Xylariales* (*Sordariomycetes*) phylogeny – part 1

Consensus phylogram (50 % majority rule) of 25278 trees resulting from a Bayesian analysis of the LSU sequence alignment (117 sequences including outgroup; 899 aligned positions; 248 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 *Saccharata proteae* (GenBank EU552145.1) 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 S25229).



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


Pseudobeltrania lauri

Fungal Planet 951 – 18 December 2019

Pseudobeltrania lauri Crous, *sp. nov.*

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

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

Setae erect, dark brown, thick-walled, 1–4-septate, straight to flexuous, tapering to and acute apex, 90–300 × 2–3 µm; basal cell not lobed. *Conidiophores* erect, branched or not, medium brown, smooth, 1–2-septate, 25–40 × 4–6 µm. *Conidiogenous cells* terminal, medium brown, smooth, 7–17 × 4–6 µm, polyblastic, with several flat-tipped denticles, 1.5–2 µm; supporting cells not seen. *Conidia* solitary, turbinate, pale brown, aseptate, with indistinct median band of paler pigment, (20–)21–23(–27) × (6–)7 µm.

Culture characteristics — Colonies spreading, with moderate aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA surface dirty white, reverse cinnamon. On PDA surface honey, reverse isabelline. On OA surface buff.

Typus. Spain, La Gomera, on leaf litter of *Laurus azorica* (*Lauraceae*), 1300 m alt., 30 Mar. 2017, *A.L. van Iperen*, HPC 2058 (holotype CBS H-24151, culture ex-type CPC 33589 = CBS 146025, ITS, LSU and *tef1* sequences GenBank MN562097.1, MN567605.1 and MN556828.1, MycoBank MB832856).

Notes — *Pseudobeltrania* was recently treated by Rajeshkumar et al. (2016). *Pseudobeltrania lauri* is closely related to *P. ocoteae* (conidia (21–)23–27(–29) × (9–)10(–11) µm), but is distinct in having larger conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Subsessila turbinata* (strain MFLUCC 15-0831, GenBank NR_148122.1; Identities = 495/521 (95 %), 1 gap (0 %)), *Porobeltraniella porosa* (strain NFCCI 3995, GenBank KX519519.1; Identities = 531/559 (95 %), 5 gaps (0 %)), and *Pseudobeltrania ocoteae* (strain CPC 26219, GenBank NR_138416.1; Identities = 552/584 (95 %), 6 gaps (1 %)). Closest hits using the **LSU** sequence are *Porobeltraniella porosa* (strain NFCCI 3996, GenBank KX519526.1; Identities = 857/864 (99 %), 1 gap (0 %)), *Pseudobeltrania ocoteae* (strain CPC 26219, GenBank KT950870.1; Identities = 863/871 (99 %), no gaps), and *Subsessila turbinata* (strain MFLUCC 15-0831, GenBank NG_059724.1; Identities = 815/828 (98 %), 2 gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Subsessila turbinata* (strain MFLUCC 15-0831, GenBank KX762291.1; Identities = 422/435 (97 %), no gaps), *Neopestalotiopsis samarangensis* (as *Pestalotiopsis* sp. SSNM-2012c, strain SS010, GenBank JQ968611.1; Identities = 413/428 (96 %), no gaps), and *Pestalotiopsis portugalica* (strain LC4370, GenBank KX895226.1; Identities = 408/423 (96 %), no gaps).

Colour illustrations. *Laurus azorica* trees in La Gomera. Setae, conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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Parafenestella pittospori

Fungal Planet 952 – 18 December 2019

Parafenestella pittospori Crous, *sp. nov.*

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

Classification — *Cucurbitariaceae*, *Pleosporales*, *Dothideomycetes.*

Conidiomata pycnidial, aggregated in clusters via a pale brown stroma, globose, pale brown, 60–120 µm diam, with papillate neck and central ostiole, up to 20 µm diam; wall of 2–3 layers of brown *textura angularis. Conidiophores* subcylindrical, 1–3-septate, branched or not, hyaline, smooth, up to 20 µm tall. *Conidiogenous cells* phialidic, subcylindrical, hyaline, smooth, 4–6 × 2 µm. *Conidia* solitary, hyaline, smooth, subcylindrical, straight or slightly curved, apex obtuse, base truncate, (2.5–)3–4(–4.5) × 1.5 µm.

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

Typus. New Zealand, Auckland, Rotorua, leaf spots on *Pittosporum tenuifolium* (*Pittosporaceae*), 25 Aug. 2017, *R. Thangavel* (holotype CBS H-24152, culture ex-type T17_03008A = CPC 34462 = CBS 146026, ITS and LSU sequences GenBank MN562098.1 and MN567606.1, MycoBank MB832857).

Notes — *Parafenestella* was recently treated (Jaklitsch et al. 2018, Valenzuela-Lopez et al. 2018, Crous et al. 2019b), and shown to have phoma-like asexual morphs. Within the genus *Parafenestella*, *P. pittospori* is phylogenetically distinct from other species known from DNA sequence data.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Ochrocladosporium elatum* (strain 17C006, GenBank MH734786.1; Identities = 421/437 (96 %), 3 gaps (0 %)), *Neocucurbitaria vachelliae* (strain CBS 142397, GenBank NR_156363.1; Identities = 412/428 (96 %), 3 gaps (0 %)), and *Ochrocladosporium frigidarii* (strain CZ549, GenBank FJ755255.1; Identities = 406/423 (96 %), 3 gaps (0 %)). Closest hits using the **LSU** sequence are *Parafenestella tetratrupha* (strain C304, GenBank MK356319.1; Identities = 900/906 (99 %), no gaps), *Parafenestella salicum* (strain C311, GenBank MK356318.1; Identities = 900/906 (99 %), no gaps), and *Parafenestella rosacearum* (strain C320, GenBank MK356315.1; Identities = 900/906 (99 %), no gaps), as well as species of *Neocucurbitaria*, such as *Neocucurbitaria unguis-hominis* (strain CNM-CM 8717, GenBank LT966028.1; Identities = 881/887 (99 %), no gaps) and *Neocucurbitaria keratinophila* (strain CBS 121759, GenBank LT623215.1; Identities = 884/891 (99 %), no gaps).

Colour illustrations. *Pittosporum* hedge *Parafenestella pittospori* was isolated from. Conidiomata on synthetic nutrient poor agar; conidiomatal ostiole and wall; conidiogenous cells; conidia. Scale bars = 120 µm (conidiomata), 20 µm (ostiole), 10 µm (all others).

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Neoanungitea eucalyptorum

Fungal Planet 953 – 18 December 2019

Neoanungitea eucalyptorum Crous, *sp. nov.*

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

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

Mycelium consisting of brown, smooth to warty, 2.5–3 µm diam hyphae. *Conidiophores* dimorphic. *Microconidiophores* reduced to conidiogenous loci on hyphae, subcylindrical to doliiform with truncate apex, 5–10 × 5–6 µm. *Macroconidiophores* erect, subcylindrical, flexuous, dark brown, thick-walled, multiseptate, up to 200 µm tall, 4–7 µm wide, arising from superficial to immersed hyphae. *Conidiogenous cells* terminal, subcylindrical, dark brown, 15–25 × 5–7 µm; proliferating sympodially with subdenticulate scars, 2 µm diam, not thickened nor darkened. *Conidia* occurring in unbranched chains, fusoid-ellipsoid, apex subobtuse, base truncate, 1.5–2 µm diam, brown, smooth, guttulate, 3-septate, (17–)20–23(–25) × (3–)4–5(–6) µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and feathery, lobate margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface sepia, reverse brown vinaceous.

Typus. Australia, New South Wales, Yabbra State Forest, Boomi Creek plantation, on leaves of *Eucalyptus grandis* (*Myrtaceae*), 19 Apr. 2018, *A.J. Carnegie*, HPC 2432 (holotype CBS H-24156, culture ex-type CPC 35763 = CBS 146028, ITS and LSU sequences GenBank MN562099.1 and MN567607.1, MycoBank MB832858).

Notes — *Neoanungitea eucalyptorum* is closely related to *N. eucalypti* (conidia (0–)3-septate, (13–)15–17(–22) × (3.5–)4–5 µm) described from leaves of *Eucalyptus obliqua* collected in Australia (Crous et al. 2017a). The two species can be distinguished in that *N. eucalyptorum* has longer conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neoanungitea eucalypti* (strain CBS 143173, GenBank NR_156383.1; Identities = 477/526 (91 %), 18 gaps (3 %)), *Anungitopsis speciosa* (strain CBS 181.95, GenBank EU035401.1; Identities = 387/467 (83 %), 26 gaps (5 %)), and *Anungitopsis lauri* (strain CBS 145067, GenBank NR_161129.1; Identities = 414/507 (82 %), 30 gaps (5 %)). Closest hits using the **LSU** sequence are *Anungitopsis speciosa* (strain CBS 181.95, GenBank EU035401.1; Identities = 763/790 (97 %), no gaps), *Spirosphaera beverwijkiana* (strain CBS 470.66, GenBank MH870500.1; Identities = 727/796 (91 %), 8 gaps (1 %)), and *Microthyrium quercus* (strain HKAS 92487, GenBank KY911453.1; Identities = 726/795 (91 %), 6 gaps (0 %)).

Colour illustrations. *Eucalyptus grandis* trees where *N. eucalyptorum* was collected. Colony on synthetic nutrient poor agar; conidiophores with conidiogenous cells. Scale bars = 10 µm.

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Pilidium novae-zelandiae

Fungal Planet 954 – 18 December 2019

Pilidium novae-zelandiae Crous, *sp. nov.*

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

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

Conidiomata sporodochial, superficial, separate, 180–300 µm diam, red-brown, becoming cupulate; wall of red-brown *textura angularis. Conidiophores* hyaline, smooth, branched, septate, filiform, giving rise to terminal and intercalary conidiogenous cells and paraphyses, up to 100 µm long, 2–2.5 µm wide. *Conidiogenous cells* monophialidic, subcylindrical, straight to curved, smooth, hyaline, with periclinal thickening and minute collarette, 4–15 × 1–1.5 µm. *Conidia* hyaline, smooth, aseptate, cymbiform, guttulate, ends acute, (9–)10–12(–14) × (1.5–)2 µm.

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 cinnamon, reverse sepia. On PDA surface buff, reverse isabelline. On OA surface buff.

Typus. New Zealand, Auckland, 21 Mullagh place, *Phoenix* sp., 4 Feb. 2018, *R. Thangavel* (holotype CBS H-24157, culture ex-type T18_00344D = CPC 35872 = CBS 146029, ITS and LSU sequences GenBank MN562100.1 and MN567608.1, MycoBank MB832859).

Notes — *Pilidium* was treated by Rossman et al. (2004) and Marin-Felix et al. (2017). *Pilidium novae-zelandiae* (conidia (9–)10–12(–14) × (1.5–)2 µm) is phylogenetically closely related to *P. anglicum* (*Eucalyptus* sp., UK; conidia (12–)13–14(–15) × 1.5(–2) µm; Crous et al. 2017a), but on average has smaller conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pilidium anglicum* (strain CBS 143402, GenBank NR_156670.1; Identities = 459/471 (97 %), 5 gaps (1 %)), *Pilidium acerinum* (strain CBS 736.68, GenBank NR_119500.1; Identities = 455/472 (96 %), 5 gaps (1 %)), and *Pilidium eucalyptorum* (strain CPC 26594, GenBank NR_145311.1; Identities = 449/466 (96 %), 2 gaps (0 %)). Closest hits using the **LSU** sequence are *Pilidium eucalyptorum* (strain CPC 26594, GenBank NG_059618.1; Identities = 794/798 (99 %), no gaps), *Pilidium acerinum* (strain CBS 403.71C, GenBank MH871958.1; Identities = 881/886 (99 %), no gaps), and *Pilidium anglicum* (strain CBS 143402, GenBank NG_058522.1; Identities = 842/847 (99 %), no gaps).

Colour illustrations. *Phoenix* sp. in New Zealand. Colony on oatmeal agar; conidiophores with conidiogenous cells; conidia. Scale bars = 300 µm (conidiomata), 10 µm (all others).

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Phyllosticta encephalarticola

Fungal Planet 955 – 18 December 2019

Phyllosticta encephalarticola Crous, *sp. nov.*

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

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

Conidiomata pycnidial, solitary, black, erumpent, globose, exuding colourless to opaque conidial masses; pycnidia up to 200 µm diam; pycnidial wall of several layers of *textura angularis*, up to 20 µm thick. *Ostiole* central, 20 µm diam. *Conidiophores* subcylindrical to ampulliform, reduced to conidiogenous cells, hyaline, smooth, coated in mucoid layer, 5–20 × 3–6 µm, proliferating percurrently at apex. *Conidia* 12–13(–17) × (7–)8(–9) µm, solitary, hyaline, aseptate, thin- and smooth-walled, coarsely guttulate, ellipsoid to obovoid, tapering towards base, 3–4 µm diam, enclosed in mucoid sheath, 1.5–2.5 µm diam, bearing a hyaline apical mucoid appendage that can be up to 100 µm long.

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

Typus. South Africa, Limpopo Province, Tzaneen, on leaves of *Encephalartos* sp. (*Zamiaceae*), 2010, *P.W. Crous*, HPC 2487 (holotype CBS H-24160, culture ex-type CPC 35970 = CBS 146014, ITS, LSU, *actA* and *tef1* sequences GenBank MN562101.1, MN567609.1, MN556783.1 and MN556818.1, MycoBank MB832860).

Notes — Although phylogenetically distinct from species of *Phyllosticta* known from DNA sequence data (Marin-Felix et al. 2017, Crous et al. 2018b), *P. encephalarticola* should be compared to *P. encephalarti* (on leaves of *Encephalartos laurentiana*, Indonesia, conidia 10–15 × 3.5–6 µm, apical appendage 6–10 µm long; Van der Aa 1973), from which it is morphologically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phyllosticta owaniana* (GenBank AF312011.1; Identities = 534/569 (94 %), 8 gaps (1 %)), *Phyllosticta pseudotsugae* (strain CBS 111649, GenBank KF154277.1; Identities = 543/580 (94 %), 14 gaps (2 %)), and *Phyllosticta podocarpi* (strain CBS 111647, GenBank KF766217.1; Identities = 567/609 (93 %), 14 gaps (2 %)). Closest hits using the **LSU** sequence are *Phyllosticta hagahagaensis* (strain CBS 144592, GenBank MK442550.1; Identities = 876/884 (99 %), no gaps), *Phyllosticta austroafricana* (strain CBS 144593, GenBank MK442549.1; Identities = 872/882 (99 %), no gaps), and *Phyllosticta carissicola* (strain CPC 25665, GenBank KT950863.1; Identities = 848/858 (99 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Phyllosticta hagahagaensis* (strain CBS 144592, GenBank MK442641.1; Identities = 606/619 (98 %), 1 gap (0 %)), *Phyllosticta austroafricana* (strain CBS 144593, GenBank MK442640.1; Identities = 605/621 (97 %), 1 gap (0 %)), and *Phyllosticta lauridiae* (strain CBS 145559, GenBank MK876460.1; Identities = 583/623 (94 %), 4 gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Phyllosticta hagahagaensis* (strain CBS 144592, GenBank MK442705.1; Identities = 381/387 (98 %), no gaps), *Phyllosticta podocarpi* (strain CBS 111647, GenBank KF766434.1; Identities = 255/260 (98 %), no gaps), and *Phyllosticta carissicola* (strain CPC 25665, GenBank KT950879.1; Identities = 389/399 (97 %), 2 gaps (0 %)).

Colour illustrations. *Encephalartos* sp. Colony on oatmeal agar; conidiogenous cells; conidia. Scale bars = 10 µm.

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Alloconiothyrium encephalarti

Fungal Planet 956 – 18 December 2019

Alloconiothyrium encephalarti Crous, *sp. nov.*

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

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

Conidiomata separate, pycnidial, globose, 180–200 µm diam, medium brown, opening via central ostiole; wall of 3–6 layers of pale brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining inner cavity, hyaline, smooth, ampulliform to subcylindrical, 4–6 × 2–3.5 µm, phialidic with periclinal thickening. *Conidia* solitary, aseptate, subcylindrical, straight, hyaline, smooth with obtuse ends, (3.5–)4(–6) × 1.5(–2) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and feathery margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA and PDA surface and reverse olivaceous grey. On OA surface iron-grey.

Typus. South Africa, Limpopo Province, Tzaneen, on leaves of *Encephalartos* sp. (*Zamiaceae*), 2010, *P.W. Crous*, HPC 2491 (holotype CBS H-24161, culture ex-type CPC 35980 = CBS 146012, ITS and LSU sequences GenBank MN562102.1 and MN567610.1, MycoBank MB832861).

Notes — *Alloconiothyrium encephalarti* represents a new species related to species in the coniothyrium-complex, including *Alloconiothyrium* and *Verrucoconiothyrium* (Crous et al. 2015a), and is tentatively named in *Alloconiothyrium*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Microsphaeropsis arundinis* (strain SCAU194, GenBank MK281564.1; Identities = 452/474 (95 %), 11 gaps (2 %)), *Huperzia serrata* (strain HS8-2-3, GenBank MK424445.1; Identities = 452/474 (95 %), 11 gaps (2 %)), and *Paraconiothyrium cyclothyrioides* (strain UTHSC DI16-346, GenBank LT796893.1; Identities = 452/474 (95 %), 11 gaps (2 %)). Closest hits using the **LSU** sequence are *Alloconiothyrium aptrootii* (strain CBS 981.95, GenBank JX496235.1; Identities = 869/875 (99 %), 1 gap (0 %)), *Verrucoconiothyrium nitidae* (as *Coniothyrium nitidae*, strain CBS 119209, GenBank EU552112.1; Identities = 881/888 (99 %), 1 gap (0 %)), and *Paraconiothyrium archidendri* (strain CBS 168.77, GenBank NG_057964.1; Identities = 880/888 (99 %), 1 gap (0 %)).

Colour illustrations. *Encephalartos* sp. Symptomatic leaf; conidiomata on pine needle agar; conidiogenous cells; conidia. Scale bars = 200 µm (conidiomata), 10 µm (all others).

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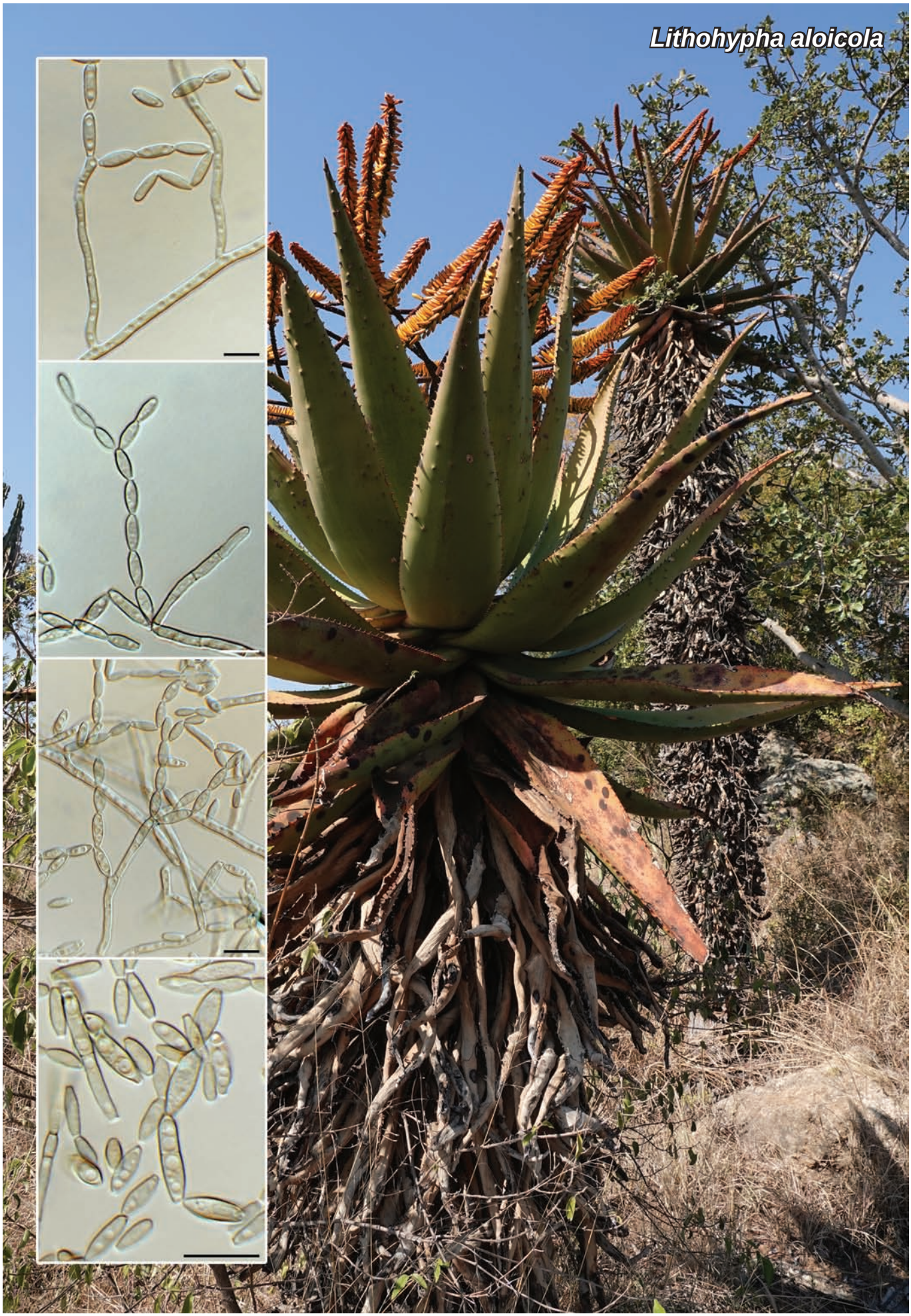
Lithohypha aloicola

Fungal Planet 957 – 18 December 2019

Lithohypha aloicola Crous, *sp. nov.*

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

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

Mycelium consisting of smooth, pale brown, branched, septate, 2–2.5 µm diam hyphae. *Conidiophores* reduced to conidiogenous loci on hyphae. *Conidiogenous cells* pale brown, smooth, 6–10 µm long, with truncate locus, 1 µm diam, not thickened nor darkened. *Conidia* ramoconidia 10–13 × 2.5–3 µm; terminal conidia occurring in branched chains, (6–)7–9(–10) × 2.5–3 µm; hila not thickened nor darkened.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface mouse grey, reverse dark mouse grey.

Typus. South Africa, Limpopo Province, Tzaneen, on leaves of *Aloe* sp. (*Asphodelaceae*), 2010, *P.W. Crous*, HPC 2481 (holotype CBS H-24159, culture ex-type CPC 35996 = CBS 146070, ITS, LSU, *rpb1*, *tef1* and *tub2* sequences GenBank MN562103.1, MN567611.1, MN556797.1, MN556829.1 and MN556837.1, MycoBank MB832862).

Notes — *Lithohypha* (as *Lithophila*) was introduced by Isola et al. (2016) for a fungus growing on marble stone in Italy. Other than the dark brown hyphae with enteroblastic conidiation, it lacked any visible morphology. *Lithohypha aloicola* is closely related to *L. guttulata*, but quite distinct morphologically, producing conidia arranged in chains, and occurring on leaves of *Aloe* in South Africa. Of interest is the fact that both substrates could be regarded as extreme environments.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Lithophila guttulata* (as *Trichomeriaceae* sp. LS-2015c, strain CCFEE 5908, GenBank KP791770.1; Identities = 566/572 (99 %), 2 gaps (0 %)), *Bradymyces* sp. LS-2015b (strain CGMCC 3.16362, GenBank KP174849.1; Identities = 545/552 (99 %), 1 gap (0 %)), and *Knufia aspidiotus* (as *Knufia* sp. FH-2012, strain BJ01A17, GenBank JX843780.1; Identities = 406/461 (88 %), 18 gaps (3 %)). Closest hits using the **LSU** sequence are *Lithophila guttulata* (as *Trichomeriaceae* sp. LS-2015c, strain CCFEE 5884, GenBank KR781056.1; Identities = 855/855 (100 %), no gaps), *Bradymyces* sp. LS-2015b (strain CGMCC 3.17221, GenBank KP174952.1; Identities = 823/823 (100 %), no gaps), and *Neophaeococcomyces catenatus* (strain CBS 650.76, GenBank MH872793.1; Identities = 822/865 (95 %), 6 gaps (0 %)). Closest hits using the ***rpb1*** sequence had highest similarity to *Bradymyces* sp. LS-2015a (strain CGMCC 3.14008, GenBank KP226519.1; Identities = 447/632 (71 %), 14 gaps (2 %)), *Bradymyces graniticola* (strain CCF 5193, GenBank LT558716.1; Identities = 507/745 (68 %), 22 gaps (2 %)), and *Knufia peltigerae* (strain CGMCC 3.17283, GenBank KP226513.1; Identities = 312/436 (72 %), 7 gaps (1 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Furfurella luteostiolata* (strain CE3, GenBank MK523302.1; Identities = 417/462 (90 %), 2 gaps (0 %)), *Gyrothrix inops* (strain BE108, GenBank KJ476974.1; Identities = 415/461 (90 %), no gaps), and *Gyrothrix ramosa* (strain MUCL 54061, GenBank KJ476975.1; Identities = 414/461 (90 %), no gaps). Closest hits using the ***tub2*** sequence had highest similarity to *Bradymyces* sp. LS-2015b (strain CGMCC 3.17221, GenBank KP226553.1; Identities = 216/222 (97 %), no gaps), *Arthrocladium caudatum* (strain CBS 457.67, GenBank LT558710.1; Identities = 347/451 (77 %), 32 gaps (7 %)), and *Aphanophora eugeniae* (strain CBS 124105, GenBank KC455221.1; Identities = 329/430 (77 %), 25 gaps (5 %)).

Colour illustrations. *Aloe* sp. *Lithophila aloicola* was isolated from. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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Neothyrostroma encephalarti

Fungal Planet 958 – 18 December 2019

Neothyrostroma Crous, *gen. nov.*

Etymology. Name refers to its morphological similarity with *Thyrostroma*.

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

Conidiomata sporodochial, black, superficial on leaves, solitary. *Conidiophores* arising from brown stroma, subcylindrical, hyaline, smooth, branched, septate. *Conidiogenous cells* subcylindrical, hyaline, smooth, terminal and intercalary, proliferating percurrently at apex. *Conidia* solitary, brown, smooth, fusoid-ellipsoid, apex acutely rounded, base truncate, distoseptate, with 3–5 horizontal septa, and 3–5 oblique or vertical septa.

Type species. Neothyrostroma encephalarti Crous.
MycoBank MB832863.

Neothyrostroma encephalarti Crous, *sp. nov.*

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

Conidiomata sporodochial, black, erumpent in agar and superficial on leaves in nature, solitary, 200–500 µm diam (in culture). *Conidiophores* arising from brown stroma, subcylindrical, hyaline, smooth, branched, septate, up to 50 µm tall, 4–5 µm wide. *Conidiogenous cells* subcylindrical, hyaline, smooth, terminal and intercalary, 10–30 × 4–5 µm, proliferating percurrently at apex. *Conidia* solitary, brown, smooth, fusoid-ellipsoid, apex acutely rounded, base truncate, 2–3 µm diam, distoseptate, with 3–5 horizontal septa, and 3–5 oblique or vertical septa, (20–)21–24(–27) × (8–)9–10(–11) µm.

Culture characteristics — Colonies flat, 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, reverse olivaceous grey. On PDA surface and reverse olivaceous grey. On OA surface dirty white to smoke grey.

Typus. South Africa, Limpopo Province, Tzaneen, on leaves of *Encephalartos* sp. (*Zamiaceae*), 2010, *P.W. Crous*, HPC 2486 (holotype CBS H-24162, cultures ex-type CPC 35999, CPC 35998 = CBS 146037, ITS, LSU and *tef1* sequences GenBank MN562104.1–MN562105.1, MN567612.1–MN567613.1 and MN556830.1–MN556831.1, MycoBank MB832864).

Notes — *Neothyrostroma* is reminiscent of the genus *Thyrostroma*, which was recently treated by Marin-Felix et al. (2017). The two genera are distinct phylogenetically, and *Neothyrostroma* can also be distinguished morphologically in having distoseptate conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 35998 had highest similarity to *Angustimassarina* sp. DP-2019a (voucher MFLU 18-0057, GenBank MN244197.1; Identities = 427/461 (93 %), 8 gaps (1 %)), *Exosporium stylobatum* (strain AN122R, GenBank MH397653.1; Identities = 416/450 (92 %), 8 gaps (1 %)), and *Lophiostoma corticola* (strain Z26, GenBank MK907710.1; Identities = 438/474 (92 %), 11 gaps (2 %)). The ITS sequences of CPC 35998 and 35999 are identical (545/545 bases). Closest hits using the **LSU** sequence of CPC 35998 are *Alfoldia vorosii* (as *Dothideomycetes* sp. DGK-2019a, strain REF117, GenBank MK589355.1; Identities = 863/883 (98 %), 4 gaps (0 %)), *Amorocoelophoma cassiae* (voucher C259, GenBank MK347956.1; Identities = 857/883 (97 %), 5 gaps (0 %)), and *Angustimassarina coryli* (strain MFLUCC 14-0981, GenBank MF167432.1; Identities = 854/881 (97 %), 6 gaps (0 %)). The LSU sequences of CPC 35998 and 35999 are identical (883/883 bases). Closest hits using the ***tef1*** sequence had highest similarity to *Alfoldia vorosii* (as *Dothideomycetes* sp. DGK-2019a, strain REF117, GenBank MK599321.1; Identities = 438/466 (94 %), no gaps), *Parathyridaria percutanea* (strain UTHSC DI16-292, GenBank LT797111.1; Identities = 433/462 (94 %), no gaps), and *Splanchnonema platani* (strain CBS 221.37, GenBank DQ677908.2; Identities = 435/466 (93 %), no gaps).

Colour illustrations. *Encephalartos* sp. *Neothyrostroma encephalarti* was isolated from. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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Falcocladium eucalypti

Fungal Planet 959 – 18 December 2019

Falcocladium eucalypti Crous, *sp. nov.*

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

Classification — *Falcocladiaceae*, *Falcocladiales*, *Sordariomycetes.*

Conidiophores penicillate on host, but rarely penicillate in culture, mostly aggregated in sporodochia, arising from superficial mycelium or from chlamydospores that are intercalary, in chains, brown, globose, 10–12 µm diam. *Conidiophores* with hyaline stipe extensions, aseptate, thick-walled, 40–70 × 1.5–2 µm, terminating in ellipsoid to globose vesicles, 4–6(–7) µm diam. *Conidiophores* with compact conidiogenous apparatus, consisting of primary and secondary branches, smooth, hyaline, giving rise to phialidic conidiogenous cells, ampulliform, 5–10(–20) × 2.5(–3) µm. *Conidia* hyaline, smooth, aseptate, falcate with a short acute apical beak (1.5–2 µm long), and a basal appendage, 2–3 µm long, (22–)32–37(–41) × (2–)2.5(–3) µm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 5 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse cinnamon to buff.

Typus. South Africa, Limpopo Province, Tzaneen, near turnoff coach road, on leaves of *Eucalyptus* sp. (*Myrtaceae*), 2010, *P.W. Crous*, HPC 2472 (holotype CBS H-24248, culture ex-type CPC 36050 = CBS 146052, ITS, LSU, *actA* and *rpb2* sequences GenBank MN562106.1, MN567614.1, MN556784.1 and MN556798.1, MycoBank MB832865).

Additional material examined. Australia, New South Wales, Dundurrabin, Neaves Plantation, on leaf of *Eucalyptus dunnii*, 21 Feb. 2017, *A.J. Carnegie*, HPC 2836, culture CPC 38019 = CBS 146061, ITS, LSU and *actA*, MN562107.1, MN567615.1 and MN556785.1. – South Africa, Limpopo Province, Tzaneen, on leaf litter of *Eucalyptus* sp., 2010, *P.W. Crous*, HPC 2465, culture CPC 36046 = CBS 146051, ITS, LSU, *actA* and *rpb2* sequences GenBank MN562108.1, MN567616.1, MN556786.1 and MN556799.1.

Notes — Species of *Falcocladium* are commonly isolated from leaf litter, and considered to be weak foliar pathogens of *Eucalyptus* (Crous et al. 1994, 1997, 2018a). Five species are presently known, having been collected on eucalypt leaves in Africa, Asia, Australia and South America. *Falcocladium eucalypti* represents the second species known from Africa, being closely related to *F. sphaeropedunculatum*, which is distinct in having sphaeropedunculate vesicles (Crous et al. 1997). Of interest is the fact that one collection originates from Australia, suggesting this fungus could have been introduced to South Africa along with its host.

Based on a blastn search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 36050 had highest similarity to *Falcocladium sphaeropedunculatum* (strain CBS 111294, GenBank EU040220.1; Identities = 625/659 (95 %), 15 gaps (2 %)), *Falcocladium turbinatum* (strain BCC 22055, GenBank NR_138378.1; Identities = 620/688 (90 %), 41 gaps (5 %)), and *Falcocladium multivesiculatum* (strain CBS 120386, GenBank EU040217.2; Identities = 597/667 (90 %), 46 gaps (6 %)). The ITS sequences of CPC 36046, 36050 and 38019 are identical (650/650 bases). Closest hits using the **LSU** sequence of CPC 36050 are *Falcocladium sphaeropedunculatum* (strain CBS 111292, GenBank EU040218.1; Identities = 842/853 (99 %), no gaps), *Falcocladium africanum* (strain CPC 34007, GenBank MK047471.1; Identities = 851/863 (99 %), no gaps), and *Falcocladium thailandicum* (strain CPC 13489, GenBank EU040216.2; Identities = 848/861 (98 %), no gaps). The LSU sequences of CPC 36046, 36050 and 38019 are identical (824/824 bases). Closest hits using the ***actA*** sequence of CPC 36050 had highest similarity to *Falcocladium africanum* (strain CBS 145046, GenBank MK047519.1; Identities = 392/407 (96 %), no gaps), *Falcocladium thailandicum* (strain CBS 121717, GenBank KM231261.1; Identities = 391/407 (96 %), no gaps), and *Falcocladium sphaeropedunculatum* (strain CBS 111292, GenBank KM231260.1; Identities = 403/428 (94 %), no gaps). The *actA* sequences of CPC 36050 and 36046 are identical (651/651 bases), and CPC 36050 and 38019 are almost identical (649/652 bases, of which two bases are represented by an extra repetitive nucleotide). Closest hits using the ***rpb2*** sequence had highest similarity to *Falcocladium africanum* (strain CBS 145046, GenBank MK047533.1; Identities = 720/836 (86 %), no gaps), *Trichoderma austriacum* (strain CBS 122494, GenBank FJ860525.1; Identities = 688/904 (76 %), 24 gaps (2 %)), and *Trichoderma sulawesense* (strain G.J.S. 85-228, GenBank AY391954.1; Identities = 681/893 (76 %), 31 gaps (3 %)). The *rpb2* sequences of CPC 36050 and 36046 are identical (912/912 bases).

Colour illustrations. *Eucalyptus* trees *Falcocladium eucalypti* was isolated from. Conidiophores with conidiogenous cells; stipe extensions with vesicles; chlamydospores; conidia. Scale bars = 10 µm.

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Gyrothrix eucalypti

Fungal Planet 960 – 18 December 2019

Gyrothrix eucalypti Crous, *sp. nov.*

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

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

Mycelium internal and external, consisting of branched, septate, hyaline to pale brown, 2–3 µm diam hyphae. *Setae* erect, straight to geniculate-sinuous, dark brown, thick-walled, verruculose to warty, 100–180 µm tall, 4–5 µm wide at base, 4–10-septate, branched, forming 2–6 lateral branches. *Conidiophores* reduced to conidiogenous cells (rarely with a supporting cell), arranged on hyphae around bases of setae, smooth, olivaceous, ampulliform, 5–10 × 3–4 µm, giving rise to conidia via conspicuous annellations. *Conidia* forming in a slimy mass, hyaline, smooth, falcate, aseptate, with excentric hilum, 0.5–1 µm diam, (8–)10–13(–15) × (2–)2.5 µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium folded surface, and smooth, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface buff, reverse cinnamon to honey.

Typus. South Africa, Limpopo Province, Tzaneen, near turnoff coach road, on leaves of *Eucalyptus* sp. (*Myrtaceae*), 2010, *P.W. Crous*, HPC 2472 (holotype CBS H-24163, culture ex-type CPC 36066 = CBS 146023, ITS, LSU and *tef1* sequences GenBank MN562109.1, MN567617.1 and MN556832.1, MycoBank MB832866).

Additional material examined. South Africa, Limpopo Province, Tzaneen, on *Eucalyptus dunnii*, 2010, *P.W. Crous*, HPC 2469, culture CPC 35992 = CBS 146022, ITS and LSU sequences GenBank MN562110.1 and MN567618.1.

Notes — *Gyrothrix* is characterised by producing brown, branched, sterile setae that arise from superficial hyphae, and lageniform conidiogenous cells that form hyaline, aseptate, cylindrical to falcate, straight to slightly curved conidia. *Gyrothrix* is close to *Circinotrichum*, but distinguished based on its branched setae (Ellis 1971). *Gyrothrix eucalypti* is distinguished from *G. circinata* (setae 80–180 µm, conidia 12–15 × 1.5–1.8 µm) and *G. podosperma* (setae 120–260 µm, conidia 8–16 × 1.5–2 µm) by the dimensions of its setae and conidia (Ellis 1971).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 36066 had highest similarity to *Lopadostoma lechatii* (strain CBS 133694, GenBank NR_132032.1; Identities = 373/412 (91 %), 16 gaps (3 %)), *Calceomyces lacunosus* (strain CBS 633.88, GenBank KY610397.1; Identities = 516/583 (89 %), 18 gaps (3 %)), *Anthostomella* sp. DAD-2016a (strain MFLUCC 16-0243, GenBank KX505957.1; Identities = 487/540 (90 %), 19 gaps (3 %)), and *Ceratocladium microspermum* (strain CBS 126092, GenBank MH864077.1; Identities = 529/600 (88 %), 35 gaps (5 %)). The ITS sequences of CPC 35992 and 36066 differ at a single position (576/577 bases similar). Closest hits using the **LSU** sequence of CPC 36066 are *Torula ficus* (strain MFLUCC 18-0112, GenBank MH260322.1; Identities = 791/803 (99 %), no gaps), *Circinotrichum papakurae* (strain CBS 101373, GenBank KR611897.1; Identities = 874/891 (98 %), 3 gaps (0 %)), and *Gyrothrix ramosa* (strain MUCL 54061, GenBank KC775722.1; Identities = 797/816 (98 %), 4 gaps (0 %)). The LSU sequences of CPC 35992 and 36066 are identical (894/894 bases). Closest hits using the ***tef1*** sequence of CPC 36066 had highest similarity to *Furfurella luteostiolata* (strain CE3, GenBank MK523302.1; Identities = 431/476 (91 %), 2 gaps (0 %)), *Gyrothrix inops* (strain BE108, GenBank KJ476974.1; Identities = 429/475 (90 %), no gaps), and *Gyrothrix ramosa* (strain MUCL 54061, GenBank KJ476975.1; Identities = 428/475 (90 %), no gaps).

Colour illustrations. *Eucalyptus* leaves *Gyrothrix eucalypti* was isolated from. Conidiogenous cells; conidia; setae. Scale bars = 10 µm.

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Neoplatysporoides aloes

Fungal Planet 961 – 18 December 2019

Neoplatysporoides aloes Crous, *sp. nov.*

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

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

Conidiomata unilocular, separate, globose, immersed to erumpent, brown, 200–250 µm diam, opening via central ostiole, exuding a brown conidial mass; wall of 3–6 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining inner cavity, hyaline, smooth, ampulliform to doliiform, 5–9 × 4–5 µm, with percurrent proliferation at apex. *Conidia* solitary, golden brown, subcylindrical to ellipsoid, straight to curved, 0–1-septate, apex obtuse, base truncate with longitudinal striations along the length of the conidium, (7–)8–9(–10) × (4–)4.5(–5) µm.

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

Typus. South Africa, Limpopo Province, Tzaneen, on leaves of *Aloe* sp. (*Asphodelaceae*), 2010, *P.W. Crous*, HPC 2476 (holotype CBS H-24249, culture ex-type CPC 36068 = CBS 146054, ITS and LSU sequences GenBank MN562111.1 and MN567619.1, MycoBank MB832867).

Additional material examined. South Africa, Gauteng Province, Pretoria, University of Pretoria campus, on leaf of *Aloe* sp., 2010, *P.W. Crous*, HPC 2457, cultures CPC 35988 = CBS 146090, CPC 36060 = CBS 146053, ITS and LSU sequences GenBank MN562112.1–MN562113.1 and MN567620.1–MN567621.1.

Notes — *Neoplatysporoides aloes* is similar to *N. aloeicola* (on leaves of *Aloe* sp., Tanzania; conidia (8–)9–10(–12) × (4–)5(–6) µm; Crous et al. 2015b), but distinguished based on its slightly smaller conidia. *Neoplatysporoides* is presently only known from leaves of *Aloe* spp. occurring in Africa.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 36068 had highest similarity to *Neoplatysporoides aloeicola* (strain CBS 139901, GenBank NR_154230.1; Identities = 544/564 (96 %), 2 gaps (0 %)), *Libertasomyces myopori* (strain CBS 141302, GenBank NR_145200.1; Identities = 522/568 (92 %), 14 gaps (2 %)), and *Libertasomyces quercus* (strain CBS 134.97, GenBank NR_155337.1; Identities = 513/559 (92 %), 11 gaps (1 %)). The ITS sequence of CPC 36068 is 99 % (558/564 bases, including 1 gap) similar to those of CPC 36060 and CPC 35988. Closest hits using the **LSU** sequence of CPC 36068 are *Neoplatysporoides aloeicola* (strain CBS 139901, GenBank MH878657.1; Identities = 853/858 (99 %), 3 gaps (0 %)), *Foliophoma fallens* (strain CBS 284.70, GenBank GU238078.1; Identities = 860/871 (99 %), 1 gap (0 %)), and *Camarosporium quaternatum* (strain CBS 483.95, GenBank DQ377884.1; Identities = 851/863 (99 %), no gaps). The LSU sequence of CPC 36068 differs with a single nucleotide from CPC 35988 and CPC 36060 (884/885 bases similar).

Colour illustrations. *Aloe* sp. *Neoplatysporoides aloes* was isolated from. Conidioma on pine needle agar; conidiogenous cells; conidia. Scale bars = 250 µm (conidioma), 10 µm (all others).

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Chalara eucalypticola

Fungal Planet 962 – 18 December 2019

Chalara eucalypticola Crous, *sp. nov.*

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

Classification — *Pezizellaceae*, *Helotiales*, *Leotiomycetes.*

Mycelium consisting of hyaline, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* solitary, erect, flexuous, straight, subcylindrical, brown, smooth, 1–10-septate, 50–130 × 4–5 µm. *Conidiogenous cells* terminal, integrated, brown, smooth, 40–55 × 5–6 µm, consisting of a basal cylindrical venter, 22–30 µm long, that tapers abruptly to a cylindrical collarette, 15–30 × 3 µm. *Conidia* in long unbranched chains, hyaline, smooth, guttulate, subcylindrical, ends bluntly rounded, 0–1-septate, (9–)11–15(–21) × (2.5–)3 µm.

Culture characteristics — Colonies erumpent, spreading, with sparse to moderate aerial mycelium and even, lobate margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA surface isabelline, reverse hazel. On PDA surface and reverse isabelline. On OA surface dirty white.

Typus. South Africa, KwaZulu-Natal Province, Terra Nera, on leaf spots of *Eucalyptus grandis* × *urophylla* (*Myrtaceae*), 1 June 2018, *M.J. Wingfield*, HPC 2508 (holotype CBS H-24239, culture ex-type CPC 36078 = CBS 146042, ITS, LSU, *tef1* and *tub2* sequences GenBank MN562114.1, MN567622.1, MN556819.1 and MN556838.1, MycoBank MB832868).

Notes — *Chalara* is paraphyletic within *Helotiales* (Cai et al. 2009). *Chalara eucalypticola* is distinct from *C. cylindrica* (on *Eucalyptus*, conidia 3–9.5 × 1–1.5 µm; Nag Raj & Kendrick 1976) and represents a new species on *Eucalyptus*, that is phylogenetically distinct from all chalara-like taxa presently known from their DNA sequence data.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Calycina alstrupii* (voucher BILAS Motiejunaite 10761, GenBank NR_154846.1; Identities = 522/562 (93 %), 18 gaps (3 %)), *Calycina herbarum* (strain 1370, GenBank AM262399.1; Identities = 421/454 (93 %), 16 gaps (3 %)), and *Graphilbum pleomorphum* (strain CBS 110.86, GenBank MH861928.1; Identities = 521/562 (93 %), 16 gaps (2 %)). Closest hits using the **LSU** sequence are *Chalara parvispora* (strain CBS 385.94, GenBank FJ176253.1; Identities = 818/829 (99 %), no gaps), *Chalara crassipes* (strain CBS 829.71, GenBank FJ176254.1; Identities = 818/830 (99 %), no gaps), and *Chalara fungorum* (strain CBS 942.72, GenBank FJ176252.1; Identities = 813/825 (99 %), no gaps). No ITS sequences are available in GenBank for comparison of these three *Chalara* species with our novel species. No significant hits were obtained when the ***tef1*** and ***tub2*** sequences were used in blastn and megablast searches.

Colour illustrations. *Eucalyptus grandis* × *urophylla* trees. Colony on synthetic nutrient poor agar; conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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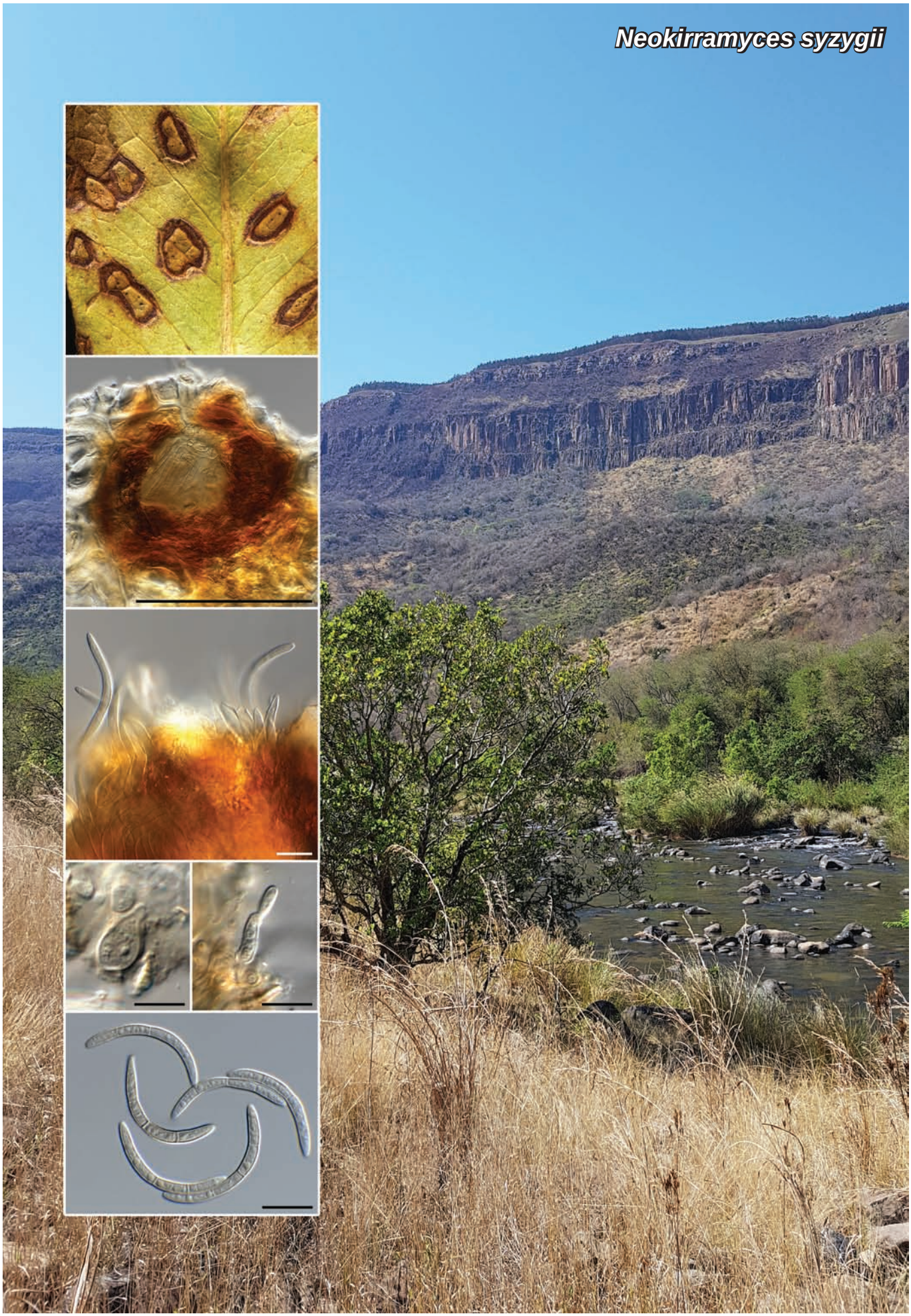
Neokirramyces syzygii

Fungal Planet 963 – 18 December 2019

Neokirramyces Crous, *gen. nov.*

Etymology. Name reflects its morphological similarity to *Kirramyces*.

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

Conidiomata amphigenous, pycnidial, immersed, globose, brown; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, brown, smooth to finely verruculose, ampulliform to subcylindrical, proliferating percurrently near apex. *Conidia* solitary, subcylindrical, prominently curved, guttulate, medium brown, smooth, euseptate, apex subobtuse, tapering in basal cell to a truncate hilum.

Type species. Neokirramyces syzygii Crous.
MycoBank MB832869.

Neokirramyces syzygii Crous, *sp. nov.*

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

Leaf spots amphigenous, angular to subcircular, 2–4 mm diam, pale brown with raised dark brown border surrounded by red-purple zone. *Conidiomata* amphigenous, pycnidial, immersed, globose, brown, 80–120 µm diam; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, brown, smooth to finely verruculose, ampulliform to subcylindrical, 6–8 × 3.5–4 µm, proliferating percurrently near apex. *Conidia* solitary, subcylindrical, prominently curved, guttulate, medium brown, smooth, 3(–4)-euseptate, apex subobtuse, tapering in basal cell to a truncate hilum, 1.5–2 µm diam, (30–)35–45(–50) × (2.5–)3 µm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 4 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus. South Africa, KwaZulu-Natal Province, Richmond, Hela Hela, on leaf spots of *Syzygium* sp. (*Myrtaceae*), 2 June 2010, *J. Roux*, HPC 2521 (holotype CBS H-24247, culture ex-type CPC 36122 = CBS 146050, ITS and LSU sequences GenBank MN562115.1 and MN567623.1, MycoBank MB832870).

Notes — *Neokirramyces* resembles the *Kirramyces* asexual morph of *Teratosphaeria* (*Teratosphaeriaceae*) (Quaedvlieg et al. 2014, Andjic et al. 2019), but is phylogenetically related to *Sonderhenia* (*Mycosphaerellaceae*) (Videira et al. 2017, Crous et al. 2019c). Morphologically *Neokirramyces* is distinct from *Sonderhenia* in that it has euseptate conidia that are kirramyces-like in morphology.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pallidocercospora ventilago* (strain CPC 21817, GenBank KF777177.1; Identities = 488/528 (92 %), 3 gaps (0 %)), *Pallidocercospora crystallina* (strain 148B3, GenBank JQ732910.1; Identities = 446/483 (92 %), 2 gaps (0 %)), and *Trochophora fasciculata* (strain CPC 10282, GenBank FJ839632.1; Identities = 490/531 (92 %), 2 gaps (0 %)). Closest hits using the **LSU** sequence are *Stigmina palmivora* (strain VIC 39741, GenBank KF656785.1; Identities = 769/782 (98 %), no gaps), *Sonderhenia eucalypticola* (as *Mycosphaerella walkeri*, strain CMW 20333, GenBank DQ267574.1; Identities = 764/782 (98 %), no gaps), and *Pallidocercospora irregulariramosa* (strain CPC 1362, GenBank GU214441.1; Identities = 762/782 (97 %), no gaps).

Colour illustrations. Leaf spots on *Syzygium* sp. Section through conidioma; conidiogenous cells; conidia. Scale bars = 10 µm.

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Lareunionomyces eucalypticola

Fungal Planet 964 – 18 December 2019

Lareunionomyces eucalypticola Crous, *sp. nov.*

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

Classification — *Neolauriomycetaceae*, *Helotiales*, *Leotiomycetes.*

Conidiophores solitary, erect, dark brown, smooth, thick-walled, straight to slightly flexuous, subcylindrical, arising from superficial hyphae, base swollen with brown rhizoids, 150–250 × 5–9 µm, sparsely 2–3-septate. *Conidiogenous region* consisting of a penicillate series of branches. Primary branches brown, smooth, aseptate, subcylindrical to clavate, 9–15 × 5–7 µm. Secondary branches pale brown, subcylindrical, smooth, 7–10 × 4–6 µm. Tertiary branches 7–9 × 3–4 µm, and quaternary branches 6–9 × 3–4 µm, giving rise to 1–4 conidiogenous cells. *Conidiogenous cells* subcylindrical, pale brown, smooth, 12–15 × 1.5–2 µm, apex proliferating inconspicuously percurrently. *Conidia* forming in cylindrical, unbranched chains, eventually forming a mucoid mass, hyaline, smooth, cylindrical, apex obtuse, base truncate, 4–4.5(–6) × 2–2.5 µm.

Culture characteristics — Colonies erumpent, with folded surface, sparse aerial mycelium and smooth, lobate margin, reaching 8 mm diam after 2 wk at 25 °C. On MEA surface umber in middle, buff at margin, reverse umber. On PDA surface and reverse sepia. On OA surface umber.

Typus. Colombia, San Bernardo, on leaves of *Eucalyptus grandis* (*Myrtaceae*), 3 June 2010, *M.J. Wingfield*, HPC 2497 (holotype CBS H-24240, culture ex-type CPC 36155 = CBS 146043, ITS, LSU, *rpb2* and *tef1* sequences GenBank MN562116.1, MN567624.1, MN556800.1 and MN556820.1, MycoBank MB832871).

Notes — *Lareunionomyces* was established for a genus of hyphomycetes that resembles *Sporendocladia*, except that it has a more intricate conidiogenous apparatus (Crous et al. 2016b). *Lareunionomyces eucalypticola* is phylogenetically related to *L. loeiensis* (on leaf litter, Thailand). The two species are easily distinguished based on their conidiophores, those of the latter being smaller, 90–150(–165) × 5–6.5 µm, and lacking rhizoids (Crous et al. 2018a).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Lareunionomyces loeiensis* (strain BCC 84472, GenBank NR_161149.1; Identities = 511/522 (98 %), 1 gap (0 %)), *Lareunionomyces eucalypti* (strain CPC 32621, GenBank NR_160352.1; Identities = 526/543 (97 %), 3 gaps (0 %)), and *Lareunionomyces syzygii* (strain CBS 141326, GenBank NR_145315.1; Identities = 532/553 (96 %), 3 gaps (0 %)). Closest hits using the **LSU** sequence are *Lareunionomyces loeiensis* (strain BCC 84472, GenBank MK047510.1; Identities = 863/871 (99 %), no gaps), *Lareunionomyces syzygii* (strain CBS 141326, GenBank NG_058244.1; Identities = 878/891 (99 %), no gaps), and *Lareunionomyces eucalypti* (strain CPC 32621, GenBank NG_064545.1; Identities = 854/867 (99 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Lareunionomyces eucalypti* (strain CPC 32621, GenBank MH327867.1; Identities = 713/790 (90 %), no gaps), *Neolauriomyces eucalypti* (strain CPC 32623, GenBank MH327868.1; Identities = 753/901 (84 %), no gaps), and *Diplococcium spicatum* (strain CBS 852.73, GenBank EF204483.1; Identities = 695/895 (78 %), 26 gaps (2 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Lareunionomyces eucalypti* (strain CPC 32621, GenBank MH327878.1; Identities = 431/519 (83 %), 28 gaps (5 %)), *Porodiplodia vitis* (strain CBS 144634, GenBank MK442707.1; Identities = 218/248 (88 %), 12 gaps (4 %)), and *Cadophora luteo-olivacea* (strain Clo-15, GenBank HQ661073.1; Identities = 218/251 (87 %), 10 gaps (3 %)).

Colour illustrations. *Eucalyptus grandis* trees. Sporulation on oatmeal agar; conidiophores with swollen bases; conidiogenous cells; conidia. Scale bars = 10 µm.

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Lectera philenopterae

Fungal Planet 965 – 18 December 2019

Lectera philenopterae Crous, *sp. nov.*

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

Classification — *Plectosphaerellaceae*, *Glomerellales*, *Sordariomycetes.*

Conidiomata sporodochial, cushion-shaped, 100–200 µm diam, pale olivaceous with intermixed setae, brown, verruculose to warty, thick-walled, flexuous, 3–6-septate, tapering to acutely rounded apices, 60–150 × 5–8 µm. *Conidiogenous cells* cylindrical, proliferating percurrently at apex, 7–10 × 2.5–3.5 µm. *Conidia* (on SNA) straight, hyaline (olivaceous in mass), smooth, aseptate, cylindrical with obtuse ends, base with truncate scar, 0.5–1 µm diam, (10–)11(–12) × 2(–2.5) µm.

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

Typus. South Africa, Mpumalanga Province, Kruger National Park, Letaba lodge, on *Philenoptera violacea* (*Fabaceae*), 6 Aug. 2014, *P.W. Crous*, HPC 2578 (holotype CBS H-24242, culture ex-type CPC 36266 = CBS 146045, ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MN562117.1, MN567625.1, MN556801.1, MN556821.1 and MN556839.1, MycoBank MB832872).

Notes — *Lectera* was recently revised (Giraldo & Crous 2019, Giraldo et al. 2019). *Lectera philenopterae* is phylogenetically related to *L*. *nordwiniana* (from soil, the Netherlands, conidia 6–8 × 2–3 µm; Crous et al. 2018a), but 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 *Lectera nordwiniana* (strain CBS 144922, GenBank MK047463.1; Identities = 538/561 (96 %), 5 gaps (0 %)), *Lectera colletotrichoides* (strain CBS 109728, GenBank KM231851.1; Identities = 539/563 (96 %), 6 gaps (1 %)), and *Lectera capsici* (strain CBS:142534, GenBank NR_155338.1; Identities = 533/559 (95 %), 6 gaps (1 %)). Closest hits using the **LSU** sequence are *Lectera capsici* (strain CBS 142534, GenBank NG_058474.1; Identities = 816/829 (98 %), no gaps), *Lectera longa* (strain IMI 366179, GenBank LR025898.1; Identities = 778/791 (98 %), no gaps), and *Lectera colletotrichoides* (strain IMI 265740, GenBank LR025896.1; Identities = 778/791 (98 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Lectera colletotrichoides* (strain CBS 109728, GenBank KM232427.1; Identities = 312/353 (88 %), 1 gap (0 %)), *Lectera longa* (strain IMI 181698, GenBank LR026170.1; Identities = 638/743 (86 %), no gaps), and *Lectera colletotrichoides* (strain IMI 332702, GenBank LR026168.1; Identities = 638/743 (86 %), no gaps). No significant hits were obtained when the ***tef1*** and ***tub2*** sequences were used in blastn and megablast searches.

Colour illustrations. *Phenoptera violacea* tree at Letaba lodge. Colony on synthetic nutrient poor agar; conidiophores with conidiogenous cells; setae; conidia. Scale bars = 10 µm.

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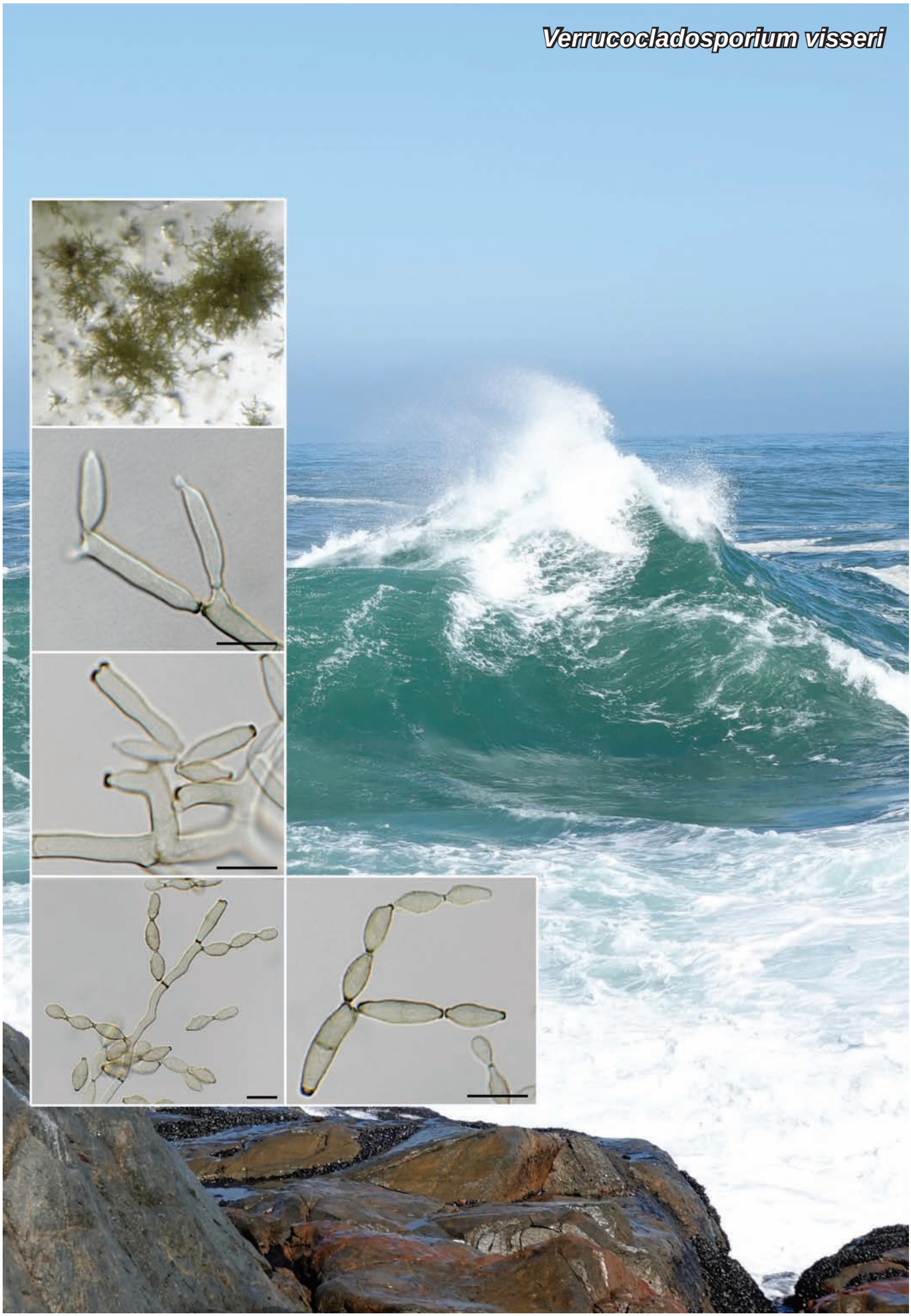
Verrucocladosporium visseri

Fungal Planet 966 – 18 December 2019

Verrucocladosporium visseri Crous, *sp. nov.*

Etymology. In honour of Johan Visser, former Springbok and Captain of the Stellenbosch University Waveski Surfing Team, who regularly practiced with his team members at Skaapeiland, IJzerfontein, during the 1980s.

Classification — *Cladosporiaceae*, *Capnodiales*, *Dothideomycetes.*

Mycelium consisting of branched, septate, brown, smooth, 3–4 µm diam hyphae. *Conidiophores* solitary, dimorphic, macro- and micronematous, reduced to conidiogenous cells. *Micronidiophores* 0–1-septate, brown, verruculose, straight to geniculate-sinuous, 20–40 × 4–5 µm. *Macroconidiophores* erect, flexuous to geniculate-flexuous, subcylindrical, up to 150 µm tall, 4–5 µm diam, brown, verruculose, 2–7-septate. *Conidiogenous cells* terminal and intercalary, subcylindrical, brown, verruculose, 10–30 × 4–5 µm; scars thickened, darkened and refractive, 1.5–2 µm diam. *Conidia* occurring in branched chains, brown, verruculose to warty. Primary ramoconidia subcylindrical, 15–35 × 3.5–4(–5) µm, 0–2-septate. Secondary ramoconidia subcylindrical, 0–1-septate, 13–20 × 3.5–4(–5) µm. Intercalary conidia subcylindrical to ellipsoid, aseptate, verruculose to warty, (8–)9–10(–11) × (3.5–)4(–4.5) µm. Small terminal conidia aseptate, verruculose to warty, 6–7 × 3–4 µm; hila thickened, darkened, refractive, 1–1.5 µm diam.

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

Typus. South Africa, Western Cape Province, IJzerfontein, on *Carpobrotus edulis* (*Aizoaceae*), 2016, *P.W. Crous*, HPC 2556 (holotype CBS H-24243, culture ex-type CPC 36317 = CBS 146046, ITS and LSU sequences GenBank MN562118.1 and MN567626.1, MycoBank MB832873).

Notes — *Verrucocladosporium visseri* is phylogenetically closely related to *V. dirinae* (isolated from the lichen *Dirina massiliensis*, UK, conidiophores macronematous, ramoconidia 16–21 × (2–)2.5–3 µm, conidia 4–18(–23) × (2–)2.5–3.5 µm, 0–1-septate; Crous et al. 2007b), but distinct in having dimorphic conidiophores, larger ramoconidia and smaller conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Verrucocladosporium dirinae* (strain HF16, GenBank KR081411.1; Identities = 612/637 (96 %), 9 gaps (1 %)), *Graphiopsis chlorocephala* (strain SDAU Forestry402-4, GenBank KJ682320.1; Identities = 439/465 (94 %), 7 gaps (1 %)), and *Trimmatostroma salinum* (strain MZKI B-962, GenBank AJ238676.1; Identities = 421/450 (94 %), 8 gaps (1 %)). Closest hits using the **LSU** sequence are *Verrucocladosporium dirinae* (strain MUT 4857, GenBank KP671739.1; Identities = 864/870 (99 %), no gaps), *Graphiopsis chlorocephala* (strain CBS 121523, GenBank MH874669.1; Identities = 862/870 (99 %), no gaps), and *Trimmatostroma salinum* (strain CBS 100461, GenBank MH874308.1; Identities = 860/870 (99 %), no gaps).

Colour illustrations. Surf spot at 'Skaapeiland', IJzerfontein. Colony on synthetic nutrient poor agar; conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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Stomiopeltis syzygii

Fungal Planet 967 – 18 December 2019

Stomiopeltis syzygii Crous, *sp. nov.*

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

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

Conidiomata globose, brown, 80–120 µm diam, pycnidial, opening via irregular rupture. *Conidiophores* lining the inner cavity, hyaline to pale brown, subcylindrical, septate, branched or not, 5–20 × 3–4 µm. *Conidiogenous cells* terminal and intercalary, phialidic, subcylindrical, hyaline to pale brown, 6–8 × 3–5 µm. *Conidia* solitary, hyaline, smooth, subcylindrical with obtuse ends, aseptate, mostly straight, (5–)8–10(–12) × 1.5 µm.

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

Typus. South Africa, Mpumalanga Province, Nelspruit, on leaves of *Syzygium cordatum* (*Myrtaceae*), 9 Aug. 2014, *P.W. Crous*, HPC 2564 (holotype CBS H-24254, culture ex-type CPC 36323 = CBS 146129, ITS, LSU, *actA*, *cmdA* and *tef1* sequences GenBank MN562119.1, MN567627.1, MN556787.1, MN556793.1 and MN556822.1, MycoBank MB832874).

Notes — Colonies were established from single ascospores shot out onto agar. Germinating ascospores were 1-septate, with germ tubes parallel to the long axis of the spore, germinating from both ends, becoming brown, verruculose, 5 µm diam, not to very slightly constricted at the septum. The sexual morph could not be located on the leaf material, but poor sporulation was induced in culture, and two asci were observed. The asexual morph that formed in culture is relatively nondescript, and the taxon is tentatively named in *Stomiopeltis* based on DNA sequence similarity to other deposited sequences. However, *Stomiopeltis* has thyrothecia, and thus cannot belong to the *Mycosphaerellaceae*, further suggesting that the sexual morph of this fungus will have pseudothecial ascomata. Future collections of the sexual morph will hopefully clarify its taxonomy, and its relationship with *Stomiopeltis* s.str.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Stomiopeltis phyllanthi* (voucher MFLU 18-2115, GenBank NR_163328.1; Identities = 389/426 (91 %), 10 gaps (2 %)), *Exopassalora zambiae* (strain CBS 112971, GenBank NR_156200.1; Identities = 361/400 (90 %), 8 gaps (2 %)), and *Clypeosphaerella quasiparkii* (strain IHBF 2280, GenBank MF326624.1; Identities = 419/481 (87 %), 16 gaps (3 %)). Closest hits using the **LSU** sequence are *Stomiopeltis sinensis* (voucher C450, GenBank MK348018.1; Identities = 751/756 (99 %), no gaps), *Chaetothyrina artocarpi* (strain MFLUCC 15-1082, GenBank MF614834.1; Identities = 802/816 (98 %), no gaps), and *Chaetothyrina musarum* (strain MFLUCC 15-0383, GenBank KU710171.1; Identities = 791/806 (98 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Davidiellomyces australiensis* (strain CBS 142165, GenBank KY979853.1; Identities = 385/408 (94 %), no gaps), *Exopassalora zambiae* (strain CBS 112970, GenBank KF903458.1; Identities = 424/461 (92 %), 5 gaps (1 %)), and *Ramularia inaequalis* (strain CPC 25742, GenBank KP894336.1; Identities = 469/519 (90 %), 11 gaps (2 %)). Closest hits using the ***cmdA*** sequence had highest similarity to *Septoria carvi* (strain KML93, GenBank KX822095.1; Identities = 289/304 (95 %), no gaps), *Septoria astericola* (strain CBS 128587, GenBank KF253998.1; Identities = 284/298 (95 %), no gaps), and *Septoria chrysanthemella* (strain CBS 128622, GenBank KF254028.1; Identities = 284/298 (95 %), no gaps). No significant hits were obtained when the ***tef1*** sequence was used in blastn and megablast searches.

Colour illustrations. *Syzygium cordatum* tree *Stomiopeltis syzygii* was isolated from. Conidiogenous cells; conidia; germinating ascospores; asci and ascospores. Scale bars = 10 µm.

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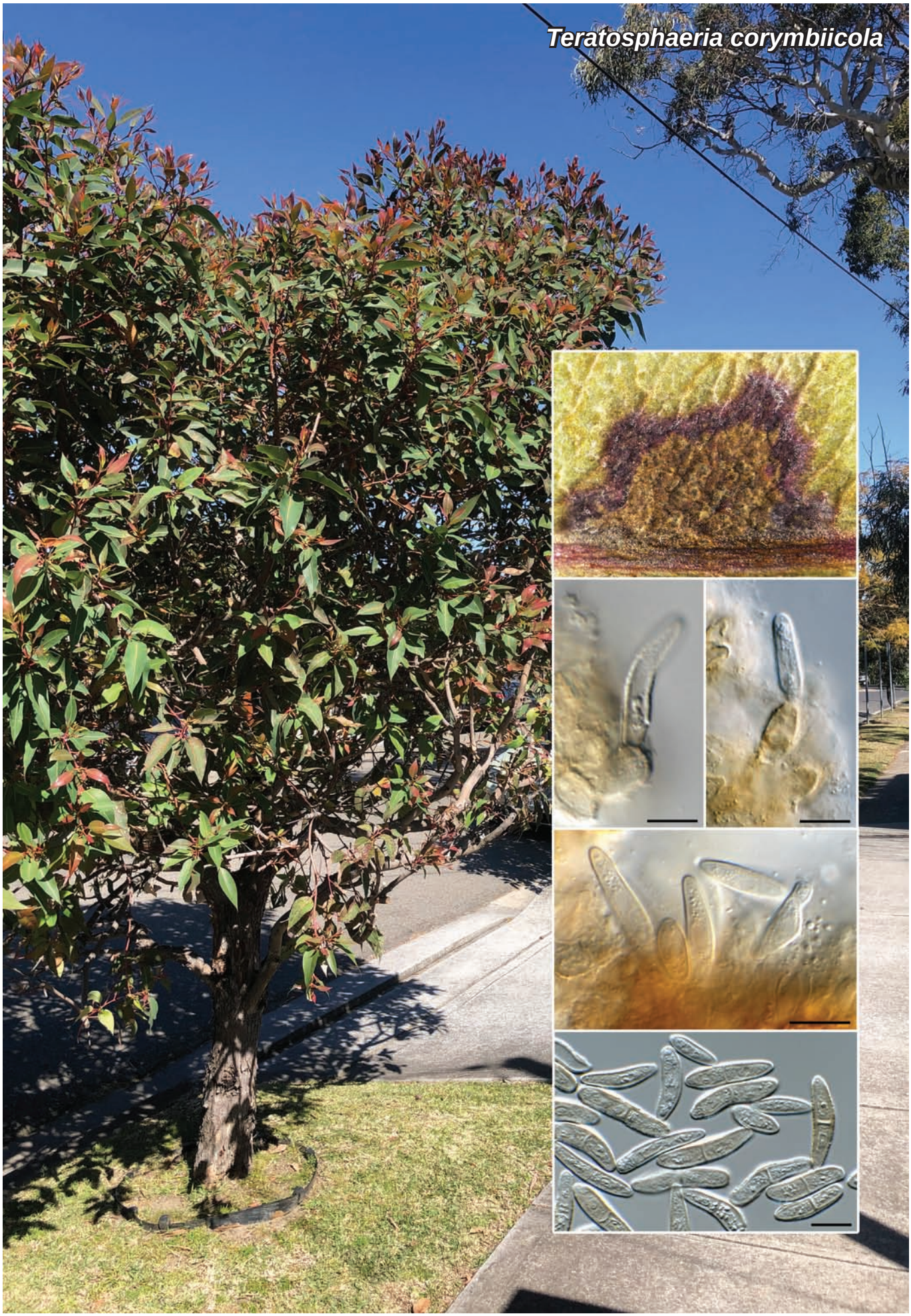
Teratosphaeria corymbiicola

Fungal Planet 968 – 18 December 2019

Teratosphaeria corymbiicola Crous, *sp. nov.*

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

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

Leaf spots amphigenous, 3–6 mm diam, subcircular, brown with a broad red-purple margin. *Conidiomata* amphigenous, exuding a mucoid conidial mass; pycnidia brown, globose, 180–250 µm diam with central ostiole, or opening via irregular split. *Conidiophores* reduced to conidiogenous cells lining inner cavity, brown, verruculose, doliiform to ampulliform, proliferating percurrently at apex, 5–10 × 5–6 µm. *Conidia* solitary, brown, verruculose, guttulate, 0–1-septate, subcylindrical, straight to irregularly curved, apex subobtuse, base truncate, 2.5–3 µm diam, with marginal frill, (17–)25–27(–33) × (4–)5(–6) µm, in culture 1(–3)-septate, and up to 40 µm long.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 5 mm diam after 2 wk at 25 °C. On MEA surface isabelline to dirty white, reverse brown vinaceous. On PDA surface isabelline to dirty white, reverse sepia with diffuse brick pigment. On OA surface isabelline with diffuse brick pigment.

Typus. Australia, New South Wales, Sydney, Longueville, on leaves of *Corymbia ficifolia* (*Myrtaceae*), 4 Sept. 2016, *A.J. Carnegie*, HPC 2539 (holotype CBS H-24244, culture ex-type CPC 36371 = CBS 146047, ITS, LSU, *actA*, *cmdA*, *rpb2*, *tef1* and *tub2* sequences GenBank MN562120.1, MN567628.1, MN556788.1, MN556794.1, MN556802.1, MN556823.1 and MN556840.1, MycoBank MB832875).

Notes — *Teratosphaeria corymbiicola* is a typical species of *Teratosphaeria* that belongs to the species complex that causes leaf spots and shoot blight of eucalypts (Andjic et al. 2019, Crous et al. 2019c). Phylogenetically it is close to *T. pseudocryptica* (conidia aseptate, (10–)12–14(–17) × (3.5–)4(–6) µm), although it is morphologically quite distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Kirramyces* sp. (strain A16, GenBank EU300986.1; Identities = 505/506 (99 %), 1 gap (0 %)), *Teratosphaeria pseudocryptica* (strain CBS 118504, GenBank KF901687.1; Identities = 466/475 (98 %), 1 gap (0 %)), and *Teratosphaeria rubida* (strain CBS 124579, GenBank MH863388.1; Identities = 531/542 (98 %), 4 gaps (0 %)). Closest hits using the **LSU** sequence are *Teratosphaeria complicata* (strain CBS 125216, GenBank MH874961.1; Identities = 788/790 (99 %), no gaps), *Teratosphaeria hortaea* (strain CBS 124156, GenBank MH874881.1; Identities = 788/790 (99 %), no gaps), and *Teratosphaeria mareebensis* (strain CBS 129529, GenBank MH876828.1; Identities = 787/790 (99 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Teratosphaeria pseudocryptica* (strain CBS 118504, GenBank KF903598.1; Identities = 521/528 (99 %), no gaps), *Teratosphaeria rubida* (strain CBS 124579, GenBank KF903552.1; Identities = 521/528 (99 %), no gaps), and *Teratosphaeria hortaea* (strain CBS 124156, GenBank KF903550.1; Identities = 490/533 (92 %), 9 gaps (1 %)). Closest hits using the ***cmdA*** sequence had highest similarity to *Teratosphaeria pseudocryptica* (strain CBS 118504, GenBank KF902760.1; Identities = 443/455 (97 %), no gaps), *Teratosphaeria rubida* (strain CBS 124579, GenBank KF902764.1; Identities = 442/455 (97 %), no gaps), and *Austroafricana associata* (strain CBS 120732, GenBank KF902532.1; Identities = 275/292 (94 %), 1 gap (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Teratosphaeria molleriana* (strain CBS 118359, GenBank KX348104.1; Identities = 754/879 (86 %), no gaps), *Teratosphaeria fimbriata* (strain CPC 13324, GenBank LT799766.1; Identities = 574/671 (86 %), no gaps), and *Teratosphaeria dunnii* (strain CBS 145548, GenBank MK876491.1; Identities = 777/916 (85 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Teratosphaeria pseudocryptica* (strain CBS 118504, GenBank KF903348.1; Identities = 347/365 (95 %), 5 gaps (1 %)), *Teratosphaeria rubida* (strain CBS 124579, GenBank KF903352.1; Identities = 346/365 (95 %), 6 gaps (1 %)), and *Teratosphaeria dunnii* (strain CBS 145548, GenBank MK876500.1; Identities = 269/322 (84 %), 11 gaps (3 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Teratosphaeria pseudocryptica* (strain CPC 11264, GenBank FJ952512.1; Identities = 318/334 (95 %), 2 gaps (0 %)), *Teratosphaeria rubida* (strain MUCC 659, GenBank FJ532013.1; Identities = 319/337 (95 %), 2 gaps (0 %)), and *Teratosphaeria australiensis* (strain MUCC 695, GenBank FJ532010.1; Identities = 295/342 (86 %), 13 gaps (3 %)).

Colour illustrations. *Corymbia ficifolia* tree *Teratosphaeria corymbiicola* was isolated from. Leaf spot; conidiogenous cells; conidia. Scale bars = 10 µm.

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Nothoramichloridium perseae

Fungal Planet 969 – 18 December 2019

Anungitiomycetaceae Crous, *fam. nov.*

Etymology. Based on the genus *Anungitiomyces*.

Classification — *Anungitiomycetaceae*, *Xylariales*, *Sordariomycetes*.

Mycelium consisting of hyaline, smooth, septate, branched hyphae. *Conidiophores* solitary, erect, flexuous to geniculous-flexuous, subcylindrical, brown, smooth to finely verruculose, septate. *Conidiogenous cells* terminal, integrated, subcylindrical, upper part forming a rachis with tightly aggregated sympodial loci, truncate, flattened to subdenticulate, not thickened nor darkened. *Conidia* solitary, obclavate to clavate, hyaline to pale brown, guttulate, thick-walled, smooth to verruculose, apex obtuse, base truncate, not thickened nor darkened, septate.

Type genus. *Anungitiomyces* Crous.
MycoBank MB832876.

Genera included — *Anungitiomyces*, *Nothoramichloridium*, *Strelitziomyces.*

Nothoramichloridium Crous, *gen. nov.*

Etymology. Name reflects its morphological similarity to *Ramichloridium*.

Mycelium consisting of hyaline, smooth, septate, branched hyphae. *Conidiophores* solitary, erect, flexuous, subcylindrical, brown, finely verruculose, septate. *Conidiogenous cells* terminal, integrated, subcylindrical, straight to geniculous-sinuous; upper part forming a rachis with tightly aggregated sympodial loci, truncate, subdenticulate, 1 µm diam, not thickened nor darkened. *Conidia* solitary, clavate, pale brown, guttulate, thick-walled, verruculose, straight, apex obtuse, base truncate, not thickened nor darkened, septate.

Type species. *Nothoramichloridium perseae* Crous.
MycoBank MB832877.

Nothoramichloridium perseae Crous, *sp. nov*.

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

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

Mycelium consisting of hyaline, smooth, septate, branched, 1.5–2.5 µm diam hyphae. *Conidiophores* solitary, erect, flexuous, subcylindrical, brown, finely verruculose, 2–3-septate, 80–150 × 4–5 µm. *Conidiogenous cells* terminal, integrated, subcylindrical, straight to geniculous-sinuous, 40–70 × 4–5 µm; upper part forming a rachis with tightly aggregated sympodial loci, truncate, subdenticulate, 1 µm diam, not thickened nor darkened. *Conidia* solitary, clavate, pale brown, guttulate, thick-walled, verruculose, straight, apex obtuse, base truncate, 1 µm diam, not thickened nor darkened, 1(–2)-septate, with septa forming a protruding rift visible in conidial outline, (19–)21–23(–26) × 5(–6) µm.

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

Typus. South Africa, Mpumalanga Province, Nelspruit, on leaves of *Persea americana* (*Lauraceae*), 9 Aug. 2014, *P.W. Crous*, HPC 2565 (holotype CBS H-24245, culture ex-type CPC 36383 = CBS 146048, ITS and LSU sequences GenBank MN562121.1 and MN567629.1, MycoBank MB832878).

Colour illustrations. Nelspruit Botanical Garden. Colony on synthetic nutrient poor agar; conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

Notes — *Nothoramichloridium* is phylogenetically allied to *Anungitiomyces* and *Strelitziomyces*, and these genera represent an undescribed family in the *Xylariales* (Crous et al. 2019a).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Hypoxylon lenormandii* (voucher EBS228, GenBank KM610287.1; Identities = 330/377 (88 %), 18 gaps (4 %)), *Rhinocladiella pyriformis* (strain CBS 469.94, GenBank MH862476.1; Identities = 393/449 (88 %), 14 gaps (3 %)), and *Anungitiomyces stellenboschiensis* (strain CPC 34726, GenBank MK876376.1; Identities = 374/428 (87 %), 15 gaps (3 %)). Closest hits using the **LSU** sequence are *Anungitiomyces stellenboschiensis* (strain CPC 34726, GenBank MK876415.1; Identities = 828/841 (98 %), 1 gap (0 %)), *Oxydothis garethjonesii* (strain MFLUCC 15-0287, GenBank KY206762.1; Identities = 827/863 (96 %), 4 gaps (0 %)), and *Arthrinium malaysianum* (strain CBS 102053, GenBank NG_042780.1; Identities = 826/864 (96 %), 4 gaps (0 %)).

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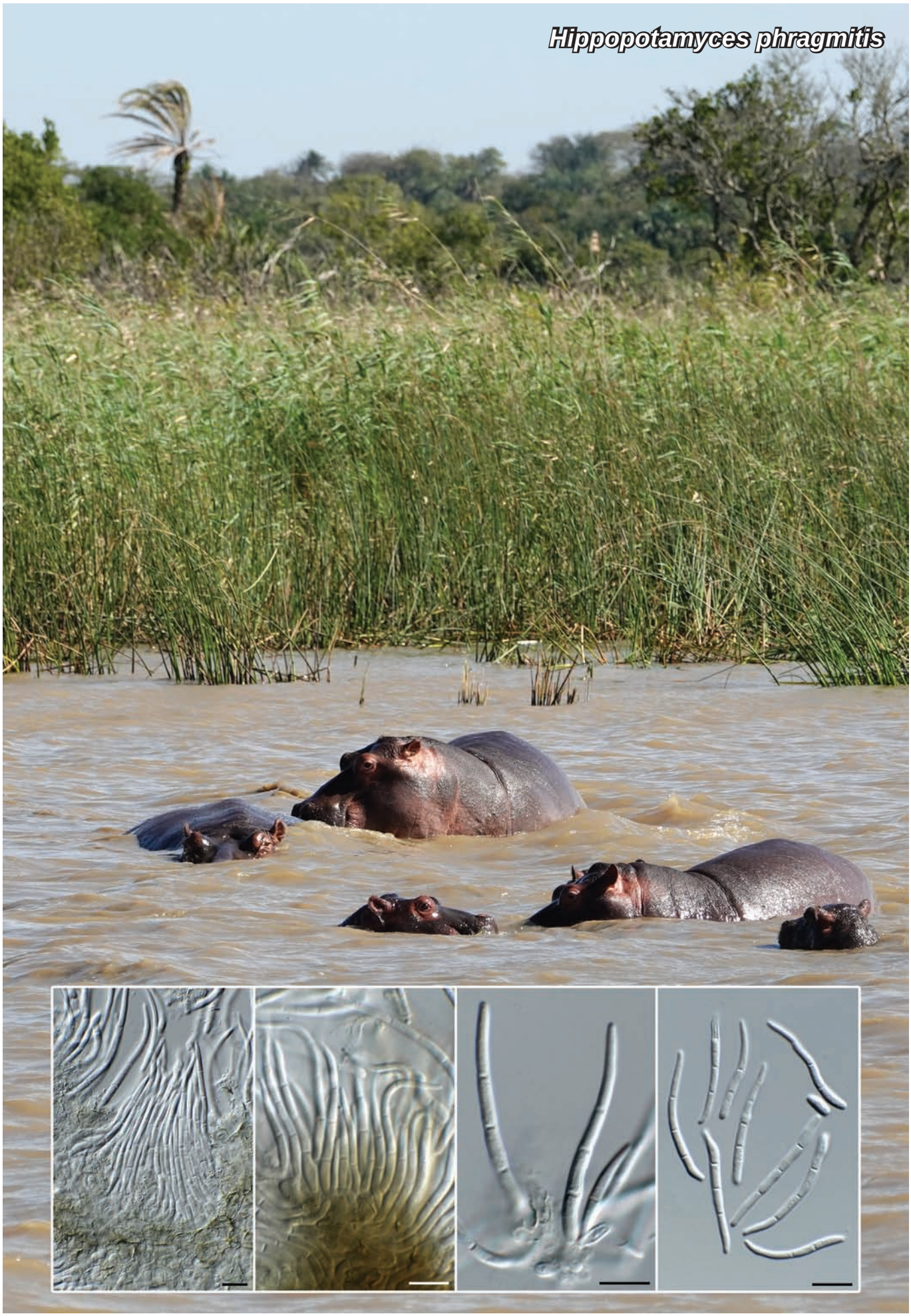
Hippopotamyces phragmitis

Fungal Planet 970 – 18 December 2019

Hippopotamyces Crous, *gen. nov.*

Etymology. *Hippopota-* (from *Hippopotamus*) grazing at the collection site.

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

Conidiomata pycnidial, globose, brown, opening via irregular rupture; wall of 6–8 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, but green olivaceous in mass, ampulliform to doliiform, phialidic. *Conidia* solitary, hyaline, smooth, guttulate, thick-walled, acicular to subcylindrical with taper in upper region to subobtuse apex, base truncate, irregularly curved, septate.

Type species. *Hippopotamyces phragmitis* Crous.
MycoBank MB832879.

Hippopotamyces phragmitis Crous, *sp. nov.*

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

Conidiomata pycnidial, globose, 180–200 µm diam, brown, opening via irregular rupture; wall of 6–8 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, but green olivaceous in mass, ampulliform to doliiform, phialidic, 3–4 × 3–4 µm. *Conidia* solitary, hyaline, smooth, guttulate, thick-walled, acicular to subcylindrical with taper in upper region to subobtuse apex, base truncate, irregularly curved, 3(–5)-septate, (25–)32–37(–45) × 2.5(–3) µm.

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

Typus. South Africa, KwaZulu-Natal Province, St Lucia, on leaves of *Phragmites australis* (*Poaceae*), 2010, *P.W. Crous*, HPC 2570 (holotype CBS H-24165, culture ex-type CPC 36385 = CBS 146086, ITS, LSU and *rpb2* sequences GenBank MN562122.1, MN567630.1 and MN556803.1, MycoBank MB832880).

Notes — *Hippopotamyces* is septoria-like in morphology (Quaedvlieg et al. 2013, Verkley et al. 2013), but is phylogenetically distinct, and represents a new genus in the *Mycosphaerellaceae* (Videira et al. 2017).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Xenosonderhenia eucalypti* (strain CBS 138858, GenBank NR_137937.1; Identities = 494/550 (90 %), 19 gaps (3 %)), *Uwemyces elaeidis* (strain CPUwZC-01, GenBank KX228299.1; Identities = 494/551 (90 %), 19 gaps (3 %)), and *Paramycosphaerella wachendorfiae* (strain CBS 129579, GenBank MH865448.1; Identities = 493/551 (89 %), 17 gaps (3 %)). Closest hits using the **LSU** sequence are *Paramycosphaerella marksii* (strain CBS 110693, GenBank DQ204758.1; Identities = 792/807 (98 %), 1 gap (0 %)), *Paramycosphaerella brachystegiae* (strain CBS 136436, GenBank NG_058048.1; Identities = 791/807 (98 %), 1 gap (0 %)), and *Pseudozasmidium vietnamense* (as *Mycosphaerella vietnamensis*, strain AGI099A, GenBank EU882134.1; Identities = 783/799 (98 %), 1 gap (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Zasmidium syzygii* (strain CBS 133580, GenBank MF951730.1; Identities = 690/888 (78 %), 22 gaps (2 %)), *Zasmidium cellare* (strain CBS 892.85, GenBank KT356875.1; Identities = 719/930 (77 %), 28 gaps (3 %)), and *Zasmidium musigenum* (strain CBS 190.63, GenBank MF951718.1; Identities = 699/911 (77 %), 14 gaps (1 %)).

Colour illustrations. *Phragmites australis* plants in St Lucia. Section through conidioma on synthetic nutrient poor agar; conidiogenous cells; conidia. Scale bars = 10 µm.

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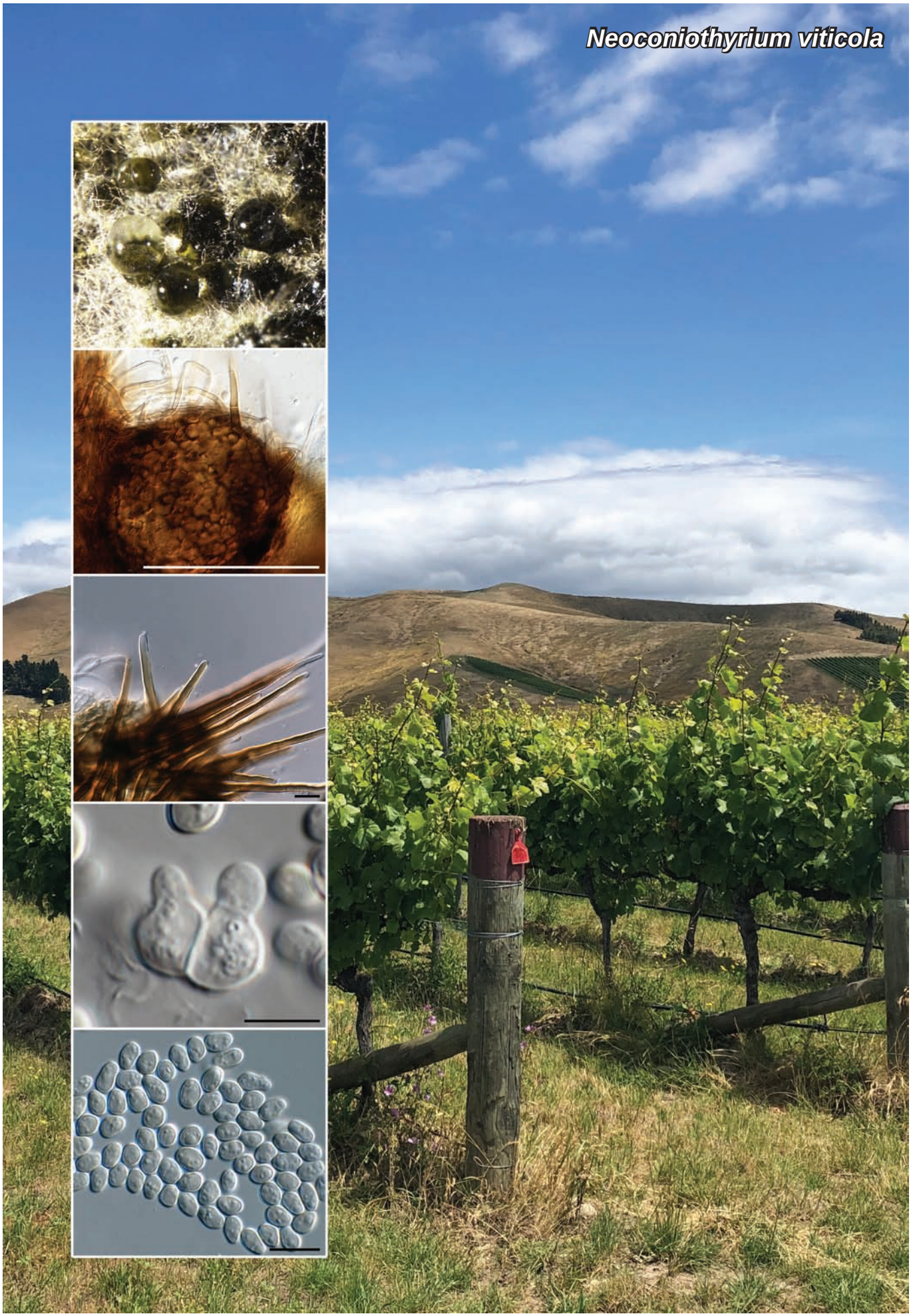
Neoconiothyrium viticola

Fungal Planet 971 – 18 December 2019

Neoconiothyrium viticola Crous, *sp. nov.*

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

Classification — *Coniothyriaceae*, *Pleosporales*, *Dothideomycetes.*

Conidiomata immersed to erumpent, solitary, brown, globose, 100–200 µm diam, with central ostiole; wall of 3–6 layers of brown *textura angularis*; wall covered in brown setae, flexuous, thick-walled, unbranched, smooth, apex obtuse, septate, up to 100 µm long, 4–5 µm wide. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining inner cavity, hyaline, smooth, ampulliform to doliiform, 4–6 × 5–6 µm; phialidic with periclinal thickening or percurrent proliferation at apex. *Conidia* solitary, aseptate, globose or broadly ellipsoid, becoming golden brown, smooth to finely roughened, (4–)5–6(–6.5) × (3–)4 µm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, lobate margin, reaching 45 mm diam after 2 wk at 25 °C. On MEA surface pale olivaceous grey, reverse olivaceous grey. On PDA surface fawn to diffuse vinaceous pigment, reverse sepia. On OA surface iron-grey.

Typus. New Zealand, North Island, Hastings, 2091 Maraekakaho Road, on stems of *Vitis vinifera* (*Vitaceae*), 4 Nov. 2010, *M. Romney* (holotype CBS H-24246, culture ex-type T10_04730 = CPC 36397 = CBS 146049, ITS, LSU and *rpb2* sequences GenBank MN562123.1, MN567631.1 and MN556804.1, MycoBank MB832881).

Notes — *Neoconiothyrium* is characterised by species that can have conidiomata covered in setae, phialidic conidiogenous cells, and hyaline to medium brown, smooth to finely verruculose, ellipsoid to subclavate or subcylindrical, 0–1-septate conidia (Crous et al. 2017a). Although the taxonomy of the coniothyrium-like genera is still far from settled, the present collection is tentatively named in *Neoconiothyrium*, being closely related to *N. hakeae*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Querciphoma carteri* (strain CBS 101633, GenBank JF740180.1; Identities = 452/472 (96 %), 2 gaps (0 %)), *Coniothyrium hakeae* (strain CPC 27620, GenBank NR_154839.1; Identities = 553/581 (95 %), 14 gaps (2 %)), and *Coniothyrium multiporum* (strain SRMC-MYCO6, GenBank KY806410.1; Identities = 460/484 (95 %), 2 gaps (0 %)). Closest hits using the **LSU** sequence are *Ochrocladosporium frigidarii* (strain CBS 103.81, GenBank NG_064123.1; Identities = 879/891 (99 %), no gaps), *Coniothyrium telephii* (strain UTHSC DI16-189, GenBank LN907332.1; Identities = 880/893 (99 %), no gaps), and *Wojnowicia rosicola* (strain MFLUCC 15-0128, GenBank MG829091.1; Identities = 865/878 (99 %), 4 gaps (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Coniothyrium hakeae* (strain CPC 29612, GenBank KY173584.1; Identities = 877/909 (96 %), no gaps), *Pyrenophora dictyoides* (strain DAOM 75616, GenBank JN993617.1; Identities = 624/756 (83 %), 9 gaps (1 %)), and *Drechslera phlei* (strain DAOM 226243, GenBank JN993628.1; Identities = 616/756 (81 %), 8 gaps (1 %)).

Colour illustrations. *Vitis vinifera* in New Zealand. Colony on potato dextrose agar; conidioma; conidiomatal setae; conidiogenous cells; conidia. Scale bars = 150 µm (conidioma), 10 µm (all others).

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Distoseptispora caricis

Fungal Planet 972 – 18 December 2019

Distoseptispora caricis Crous, *sp. nov.*

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

Classification — *Distoseptisporaceae*, *Distoseptisporales*, *Sordariomycetes.*

Mycelium consisting of pale brown, smooth, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* erect, subcylindrical, dark brown, smooth, 2–4-septate, 35–90 × 6–7 µm. *Conidiogenous cells* integrated, terminal, cylindrical, brown, smooth, monoblastic, 13–16 × 5–6 µm. *Conidia* solitary, obclavate, brown, smooth, 5–10-distoseptate, septa with central pore, wall thick, tapering abruptly at base; basal cell pale brown, with truncate hilum, 3.5–4 µm diam; apex obtuse, but in culture developing further, becoming elongated, flexuous, 3–4-euseptate, frequently with visible mucoid appendage surrounding conidial apex, conidia (55–)65–85(–100) × 15–16(–17) µm.

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

Typus. Thailand, Chiang Mai, on leaves of *Carex* sp. (*Cyperaceae*), 2008, *P.W. Crous*, HPC 2251 (holotype CBS H-24238, cultures ex-type CPC 36498 = CBS 146041, CPC 36442 = CBS 146040, ITS, LSU and *rpb2* sequences GenBank MN562124.1–MN562125.1, MN567632.1 (CPC 36498) and MN556805.1–MN556806.1, MycoBank MB832882).

Notes — *Distoseptispora* has macronematous, septate, unbranched, brown conidiophores, terminal, blastic conidiogenous cells and olivaceous to brown, septate conidia (Su et al. 2016). The genus presently includes 18 species, of which *D. caricis* is phylogenetically most closely related to *D. tectonigena* (148–225(–360) × 11–12 µm, cylindrical-obclavate, 20–46-distoseptate) and *D. multiseptata* (95–290 × 11–20 µm, obclavate, rostrate, dark-olivaceous green, multi-distoseptate). Morphologically it is quite distinct, having smaller conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 36442 had highest similarity to *Distoseptispora tectonigena* (strain MFLUCC 12-0292, GenBank NR_154018.1; Identities = 355/411 (86 %), 16 gaps (3 %)), *Distoseptispora multiseptata* (voucher MFLU 15-1144, GenBank NR_154017.1; Identities = 345/402 (86 %), 16 gaps (3 %)), and *Arthropsis truncata* (strain CBS 584.82, GenBank NR_159641.1; Identities = 323/378 (85 %), 18 gaps (4 %)). The ITS sequences of CPC 36442 and 36498 are identical (607/607 bases). Closest hits using the **LSU** sequence of CPC 36498 are *Ellisembia leonensis* (voucher HKUCC 10822, GenBank DQ408566.1; Identities = 828/847 (98 %), 1 gap (0 %)), *Distoseptispora* sp. DB-2019c (strain MFLUCC 18-0376, GenBank MN163017.1; Identities = 824/850 (97 %), no gaps), and *Distoseptispora dehongensis* (as *Distoseptispora* sp. SNZ-2018a, strain KUMCC 18-0090, GenBank MK079662.1; Identities = 774/809 (96 %), 6 gaps (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Ellisembia leonensis* (voucher HKUCC 10822, GenBank DQ435089.1; Identities = 732/830 (88 %), no gaps), *Penicillium vanluykii* (strain DTO 148I2, GenBank JX996615.1; Identities = 256/318 (81 %), 6 gaps (1 %)), and *Trichoderma longibrachiatum* (strain GJS 01-121, GenBank JN175507.1; Identities = 251/312 (80 %), no gaps). The *rpb2* sequences of CPC 36442 and 36498 differ with a single nucleotide (843/844 bases similar).

Colour illustrations. Garden in Thailand where *D. caricis* was collected. Conidiogenous cells and conidia. Scale bars = 10 µm.

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Monochaetia massachusettsianum

Fungal Planet 973 – 18 December 2019

Monochaetia massachusettsianum Crous & Jurjević, *sp. nov.*

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

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

Conidiomata acervular, superficial on agar, unilocular, 200–300 µm diam; wall of several layers of brown *textura angularis. Conidiophores* arising from upper layer of basal stroma, septate, branched, or reduced to conidiogenous cells, hyaline, smooth, subcylindrical to lageniform, dissolving at maturity, 6–20 × 2.5–3.5 µm; proliferating percurrently at apex. *Conidia* fusoid, brown, smooth, mostly straight, 3(–5)-euseptate with appendages; basal cell obconic, hyaline with truncate hilum; median cells brown; apical cell conical, hyaline, (23–)25–28(–30) × (7–)8–9(–10) µm. Appendages cellular, unbranched, attenuated; apical appendage single central, 7–12 µm long; basal appendage single, unbranched, centric, 2–7 µm long (when present).

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 60 mm diam after 2 wk at 25 °C. On MEA surface cinnamon, reverse brick. On PDA surface cinnamon, reverse isabelline. On OA surface isabelline. On Czapek Yeast Extract *Agar* 23 mm / 25 °C / 7 d, no growth / 37 °C / 7 d.

Typus. USA, Massachusetts, Cohasset, air in basement, 30 Oct. 2018, *Ž. Jurjević* (holotype CBS H-24170, culture ex-type EMSL 5009 = CPC 36626 = CBS 146013, ITS, LSU, *rpb2* and *tef1* sequences GenBank MN562126.1, MN567633.1, MN556807.1 and MN556824.1, MycoBank MB832883).

Notes — *Monochaetia* is characterised by acervular conidiomata, fusoid and transversely septate conidia, with brown median cells and a single cellular apical and basal (when present) appendage (Liu et al. 2019a). *Monochaetia massachusettsianum* is phylogenetically related to *M. monochaeta* (conidia 4(–5)-septate, 17–23 × 4.5–7 µm), and *M. kansensis* (conidia 4-septate, 17.5–19 × 5.5–7(–8) µm; Nag Raj 1993), but distinct in having larger conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Monochaetia monochaeta* (strain CBS 118.66, GenBank MH858742.1; Identities = 565/592 (95 %), 5 gaps (0 %)), *Monochaetia kansensis* (strain PSHI2004Endo1031, GenBank DQ534045.1; Identities = 503/528 (95 %), 4 gaps (0 %)), and *Magnohelicospora iberica* (strain FMR 12414, GenBank KY853450.1; Identities = 523/549 (95 %), 4 gaps (0 %)). Closest hits using the **LSU** sequence are *Monochaetia kansensis* (strain PSHI2004Endo1030, GenBank DQ534035.1; Identities = 832/839 (99 %), no gaps), *Monochaetia ilexae* (strain CBS 101009, GenBank MH554176.1; Identities = 827/834 (99 %), no gaps), and *Monochaetia junipericola* (strain CBS 143391, GenBank MH107947.1; Identities = 839/847 (99 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Monochaetia junipericola* (strain CBS 143391, GenBank MH108004.1; Identities = 704/805 (87 %), no gaps), *Monochaetia quercus* (strain CBS 144034, GenBank MH555068.1; Identities = 723/830 (87 %), no gaps), and *Monochaetia monochaeta* (strain CBS 658.95, GenBank MH554977.1; Identities = 719/830 (87 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Monochaetia ilexae* (strain CBS 101009, GenBank MH554371.1; Identities = 327/382 (86 %), 15 gaps (3 %)), *Monochaetia quercus* (strain CBS 144034, GenBank MH554606.1; Identities = 289/335 (86 %), 11 gaps (3 %)), and *Monochaetia monochaeta* (strain CBS 658.95, GenBank MH554499.1; Identities = 271/314 (86 %), 8 gaps (2 %)).

Colour illustrations. Basement where *Monochaetia massachusettsianum* was isolated from. Colony on oatmeal agar; conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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Xylaria eucalypti

Fungal Planet 974 – 18 December 2019

Xylaria eucalypti Crous, *sp. nov.*

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

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

Colonies established from ascospores shot out onto agar that were aseptate, hyaline, smooth, ellipsoid, resembling those of *Neophysalospora* and *Clypeophysalospora*. *Conidiomata* sporodochial, 180–200 µm diam, buff to pale brown, consisting of densely aggregated conidiophores in mucoid droplet. *Conidiophores* subcylindrical, smooth, pale brown at base, branched, septate, 20–40 × 2–3 µm. *Conidiogenous cells* hyaline to pale brown, smooth, terminal and intercalary, subcylindrical with apical taper, 7–15 × 1.5–2 µm, proliferating inconspicuously sympodially at apex. *Conidia* solitary, aseptate, hyaline, smooth, subcylindrical, apex subobtuse, base truncate, curved, (13–)15–17(–18) × 1.5 µm. In older cultures on oatmeal agar acervular conidiomata develop, 200–300 µm diam, brown, opening via irregular flaps, containing a similar asexual morph as observed on sporodochia in young colonies.

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, PDA and OA surface and reverse rosy buff.

Typus. Australia, New South Wales, Bombala, Coolanguba State Forest, on leaves of *Eucalyptus radiata* (*Myrtaceae*), 2016, *A.J. Carnegie*, HPC 2652 (holotype CBS H-24173, culture ex-type CPC 36723 = CBS 146092, ITS, LSU and *tub2* sequences GenBank MN562127.1, MN567634.1 and MN556841.1, MycoBank MB832884).

Notes — *Xylaria eucalypti* is tentatively placed in *Xylaria*, as it is phylogenetically closely related to the genus. However, the fact that it was cultured from neophysalospora-like ascospores, suggests that it probably represents an undescribed genus in *Xylariaceae.*

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Anthostomella brabeji* (strain CBS 110128, GenBank NR_153509.1; Identities = 526/605 (87 %), 26 gaps (4 %)), *Xylaria ianthinovelutina* (strain C24, GenBank JQ936302.1; Identities = 518/596 (87 %), 27 gaps (4 %)), and *Xylaria grammica* (strain KCTC 13121BP, GenBank KY490692.1; Identities = 514/592 (87 %), 22 gaps (3 %)). Closest hits using the **LSU** sequence are *Xylaria enteroleuca* (strain CBS 128357, GenBank MH876349.1; Identities = 809/829 (98 %), 1 gap (0 %)), *Xylaria vaporaria* (strain CBS 386.35, GenBank MH867226.1; Identities = 797/818 (97 %), 1 gap (0 %)), and *Xylaria longipes* (strain CBS 148.73, GenBank MH872351.1; Identities = 807/829 (97 %), 1 gap (0 %)). No significant hits were obtained when the ***tub2*** sequence was used in blastn and megablast searches.

Colour illustrations. *Eucalyptus radiata* trees at Coolanguba State Forest. Symptomatic leaves with purple leaf spots; conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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Vermiculariopsiella pini
& Neotracylla pini

Fungal Planet 975 & 976 – 18 December 2019

Vermiculariopsiella pini Crous, *sp. nov.*

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

Classification — *Vermiculariopsiellaceae*, *Vermiculariopsiellales*, *Sordariomycetes.*

Conidiomata sporodochial, 200–600 µm diam, with slimy, creamy conidial mass; base of brown pseudoparenchymatal cells giving rise to densely aggregated conidiophores. *Setae* dispersed throughout sporodochium, thick-walled, brown, smooth, unbranched, flexuous, subcylindrical, with taper to subacute apex, multiseptate, 140–300(–550) µm long, base bulbous, (4–)8–10 µm. *Conidiophores* subcylindrical, pale brown, smooth, 0–2-septate, 20–40 × 3–4 µm, branched, giving rise to 1–4 conidiogenous cells. *Conidiogenous cells* terminal, cymbiform to ampulliform, pale brown, smooth, phialidic, apex twisted to the side, periclinal thickening and collarette present, 10–20 × 2.5–3.5 µm. *Conidia* solitary, septate, hyaline, smooth, guttulate, fusoid, integrated, inner plane straight, outer plane convex, base truncate, hilum excentric, 0.5–1 µm, (17–)19–21(–22) × 2.5(–3) µm; ends with mucoid caps, which appears to be unique for the genus.

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

Typus. Malaysia, on needles of *Pinus tecunumanii* (*Pinaceae*), 1 Oct. 2018, *M.J. Wingfield*, HPC 2657 (holotype CBS H-24174, culture ex-type CPC 36727 = CBS 146009, ITS and LSU sequences GenBank MN562128.1 and MN567635.1, MycoBank MB832885).

Note — *Vermiculariopsiella* is characterised by sporodochia with brown, erect setae (branched or not), subhyaline conidiophores, phialidic conidiogenous cells, and hyaline, aseptate conidia (Crous et al. 2014, Hernández-Restrepo et al. 2017). *Vermiculariopsiella pini* is phylogenetically closely related to *V. dichapetali* (on *Dichapetalum rhodesicum*, Botswana; setae 100–300 × 6–10 µm, conidia (10–)17–22(–24) × 2.5(–3) µm). The two species are best separated based on their DNA data.

Tracyllales Crous, *ord. nov.*

Etymology. Name based on the genus *Tracylla*.

Classification — *Tracyllaceae*, *Tracyllales*, *Sordariomycetes.*

Pycnothyria superficial on leaves, round, brown, with central column of cells; ostiole lacking, margin of catenate, darker brown cells. *Conidiophores* reduced to conidiogenous cells arising from a central columella, doliiform to ellipsoid, hyaline, smooth, with a single conidiogenous locus, phialidic. *Conidia* solitary, hyaline, aseptate, smooth, guttulate, falcate to naviculate or ellipsoid to subcylindrical, apex subobtusely rounded, base truncate; with or without unbranched polar appendages, not delimited by septa.

Type family. *Tracyllaceae* Crous.
MycoBank MB832986.

Neotracylla Crous, *gen. nov.*

Etymology. Name reflects its morphological similarity to *Tracylla*.

Conidiomata pycnothyrial, brown, round, scutellum consisting of a radiating mass of brown cells, verruculose, bifurcating into two additional radial rows; margin smooth, lobate or with pointed terminal cells; surface of pycnothyrium cells with dark brown circular striations, at times conidiomata consisting of smaller circular scutella that overlap like roof tiles. *Conidiophores* reduced to conidiogenous cells, subcylindrical to doliiform, pale brown, smooth, phialidic. *Conidia* aseptate, formed singly, hyaline, smooth, subcylindrical, apex obtuse, slightly curved, inner plane flat, outer plane convex, base pointed, curved towards inner plane.

Type species. *Neotracylla pini* Crous.
MycoBank MB832886.

Neotracylla pini Crous, *sp. nov.*

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

Conidiomata pycnothyrial, brown, round, scutellum 80–150 µm diam, consisting of a radiating mass of brown cells, verruculose, bifurcating into two additional radial rows; margin smooth, lobate or with pointed terminal cells, 2–4 µm long; surface of pycnothyrium cells with dark brown circular striations, at times conidiomata consisting of smaller circular scutella that overlap like roof tiles. *Conidiophores* reduced to conidiogenous cells, subcylindrical to doliiform, pale brown, smooth, 7–10 × 3–4 µm, phialidic, occurring under scutellum (although hard to discern). *Conidia* aseptate, formed singly, hyaline, smooth, subcylindrical, apex obtuse, slightly curved, inner plane flat, outer plane convex, base pointed, curved towards inner plane, (8–)9–10(–11) × 3(–3.5) µm.

Typus. Malaysia, on needles of *Pinus tecunumanii* (*Pinaceae*), 1 Oct. 2018, *M.J. Wingfield*, HPC 2657 (holotype CBS H-24175, culture ex-type CPC 36731 = CBS 146010, ITS and LSU sequences GenBank MN562129.1 and MN567636.1, MycoBank MB832887).

Notes — *Tracylla* is characterised by having brown, superficial pycnothyria, with hyaline, aseptate conidia with or without polar appendages (Crous et al. 2018c). Three species are presently recognised in the genus, which can all be distinguished from *T. pini* based on their conidium morphology.

Colour illustrations. Canopy of *Pinus tecunumanii* trees seen from below. Left column *Vermiculariopsiella pini*: Setae; conidiogenous cells; conidia. Right column *Tracylla pini*: Conidiomata on oatmeal agar; overlapping pycnothyrial conidiomata; conidiogenous cells and conidia. Scale bars = 10 µm.

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Clypeosphaeria oleae

Fungal Planet 977 – 18 December 2019

Clypeosphaeria oleae Crous, *sp. nov.*

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

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

Associated with pale brown, subcircular, amphigenous leaf spots, 1–3 cm diam, with red brown border. Cultures were derived from 1–3-septate fusoid, brown ascospores, but ascomata could not be located on host material. *Mycelium* consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* solitary, erect, medium brown, smooth, 1–2-septate, subcylindrical with apical taper, 30–50 × 3 µm. *Conidiogenous cells* integrated, terminal, medium brown, smooth, 20–30 × 2–3 µm, forming a rachis with sympodial loci, pimple-like, 0.5 µm diam, not thickened nor darkened. *Conidia* solitary, aggregated in mucoid mass, hyaline, smooth, aseptate, spindle-shaped, curved, apex subobtuse, base truncate, (17–)19–22(–25) × 1.5(–2) µm.

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, PDA and OA surface buff, reverse cinnamon.

Typus. South Africa, Western Cape Province, Knysna, Knysna area, on leaves of *Olea capensis* (*Oleaceae*), 21 Nov. 2018, *M.J. Wingfield*, HPC 2706 (holotype CBS H-24177, culture ex-type CPC 36779 = CBS 146080, ITS and LSU sequences GenBank MN562130.1 and MN567637.1, MycoBank MB832888).

Notes — The genus *Clypeosphaeria* (based on *C. mamillana*) is a member of the *Xylariaceae*, and has brown, septate ascospores (Jaklitsch et al. 2016). Although the sexual morph of the present collection could not be traced (other than the geminating ascospores shot out onto agar plates), the xylariaceous asexual morph, ascospores, and DNA phylogeny suggest that it is presently best to accommodate it as a new species of *Clypeosphaeria.*

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Anthostomella eucalyptorum* (strain 2741, GenBank AM922205.1; Identities = 432/478 (90 %), 9 gaps (1 %)), and *Digitodochium rhodoleucum* (strain NBRC 32296, GenBank LC146732.1; Identities = 434/491 (88 %), 23 gaps (4 %)). Closest hits using the **LSU** sequence are *Clypeosphaeria mamillana* (strain CBS 140735, GenBank MH554225.1; Identities = 783/801 (98 %), 1 gap (0 %)), *Anthostomella eucalyptorum* (strain CBS 120036, GenBank DQ890026.1; Identities = 806/825 (98 %), 1 gap (0 %)), and *Xylaria arbuscula* (strain CBS 126416, GenBank MH875561.1; Identities = 806/826 (98 %), 3 gaps (0 %)).

Colour illustrations. Knysna forest in South Africa. Sporulation on synthetic nutrient poor agar; conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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Leptosillia mayteni

Fungal Planet 978 – 18 December 2019

Leptosillia mayteni Crous, *sp. nov.*

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

Classification — *Leptosilliaceae*, *Xylariales*, *Sordariomycetes.*

Conidiomata solitary to aggregated, pycnidial, globose, brown, 180–200 µm diam, with central ostiole; wall of 6–8 layers of pale brown *textura angularis. Conidiophores* lining the inner cavity, hyaline, smooth, subcylindrical, 0–3-septate, branched at base or not, 7–30 × 1.5–2 µm. *Conidiogenous cells* hyaline, smooth, subcylindrical, 5–8 × 1.5 µm, proliferating percurrently at apex, at times with three conidia still attached to apex. *Conidia* hyaline, smooth, aseptate, bean-shaped, slightly curved, inequilateral, inner plane flat, outer plan convex, apex and base rounded toward inner plane, (4–)5(–6) × 1.5 µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse cinnamon. On PDA surface and reverse cinnamon. On OA surface dirty white with diffuse cinnamon pigment.

Typus. South Africa, Western Cape Province, Knysna, Knysna area, on leaves of *Maytenus heterophylla* (*Celastraceae*), 23 Nov. 2018, *F. Roets*, HPC 2721 (holotype CBS H-24178, culture ex-type CPC 37000 = CBS 146079, ITS, LSU and *rpb2* sequences GenBank MN562131.1, MN567638.1 and MN556808.1, MycoBank MB832889).

Notes — The genus *Leptosillia* was recently treated by Voglmayr et al. (2019). Although *L. mayteni* was isolated from leaves, most species of *Leptosillia* are isolated from bark and twigs. Morphologically, the asexual morph of *L. mayteni* is most similar to that of *L. wienkampii*, conidia (5–)5.5–6.2(–7) × (1.4–)1.6–1.9(–2.1) µm, although the two species are phylogenetically quite distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Leptosillia wienkampii* (as *Leptosillia* sp. HV-2019e, strain CRW, GenBank MK527865.1; Identities = 398/427 (93 %), 4 gaps (0 %)), *Liberomyces saliciphilus* (as *Sordariomycetes* sp. SP-2010b, strain H041, GenBank FR715510.1; Identities = 397/427 (93 %), 3 gaps (0 %)), and *Leptosillia slaptonensis* (as *Leptosillia* sp. HV-2019d, strain CRU1, GenBank MK527859.1; Identities = 389/428 (91 %), 5 gaps (1 %)). Closest hits using the **LSU** sequence are *Leptosillia slaptonensis* (as *Leptosillia* sp. HV-2019d, strain CRU2, GenBank MK527860.1; Identities = 822/842 (98 %), 3 gaps (0 %)), *Leptosillia wienkampii* (as *Leptosillia* sp. HV-2019e, strain CRW, GenBank MK527865.1; Identities = 808/828 (98 %), 2 gaps (0 %)), and *Leptosillia acerina* (as *Leptosillia* sp. HV-2019a, strain CRA2, GenBank MK527850.1; Identities = 818/839 (97 %), no gaps). No significant hits were obtained when the ***rpb2*** sequence was used in blastn and megablast searches.

Colour illustrations. Knysna forest with *Maytenus heterophylla* trees. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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Nothodactylaria nephrolepidis

Fungal Planet 979 – 18 December 2019

Nothodactylariaceae Crous, *fam. nov.*

Etymology. Name refers to the genus *Nothodactylaria*.

Classification — *Nothodactylariaceae*, *Xylariales*, *Sordariomycetes.*

Mycelium consisting of hyaline, smooth, branched, septate, hyphae. *Conidiophores* solitary or aggregated in clusters, subcylindrical, unbranched, erect, hyaline to pale brown, smooth, with slight apical taper, septate. *Conidiogenous cells* terminal, integrated, hyaline to pale brown, smooth, subcylindrical with apical taper, forming a rachis with sympodially proliferating pimple-like denticles. *Conidia* solitary, aggregating in a mucoid mass, septate, hyaline, smooth, subcylindrical to fusoid-ellipsoid, straight, apex obtuse, tapering to truncate hilum.

Type genus. Nothodactylaria Crous.
MycoBank MB833022.

Nothodactylaria Crous, *gen. nov.*

Etymology. Name refers to its similarity with *Dactylaria*.

Mycelium consisting of hyaline, smooth, branched, septate, hyphae. *Conidiophores* solitary or aggregated in clusters, subcylindrical, unbranched, erect, hyaline to pale brown, smooth, with slight apical taper, septate. *Conidiogenous cells* terminal, integrated, hyaline to pale brown, smooth, subcylindrical with apical taper, forming a rachis with sympodially proliferating pimple-like denticles. *Conidia* solitary, aggregating in a mucoid mass, septate, hyaline, smooth, subcylindrical to fusoid-ellipsoid, straight, apex obtuse, tapering to truncate hilum.

Type species. Nothodactylaria nephrolepidis Crous.
MycoBank MB833023.

Nothodactylaria nephrolepidis Crous, *sp. nov.*

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

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* solitary or aggregated in clusters of 2–6, subcylindrical, unbranched, erect, hyaline to pale brown, smooth, with slight apical taper, 1–2-septate, 30–50 × 3–4.5 µm. *Conidiogenous cells* terminal, integrated, hyaline to pale brown, smooth, subcylindrical with apical taper, forming a rachis with sympodially proliferating pimple-like denticles, 0.5 µm diam, 25–45 × 3–4 µm. *Conidia* solitary, aggregating in a mucoid mass, 1(–3)-septate, hyaline, smooth, guttulate to granular, subcylindrical to fusoid-ellipsoid, straight, apex obtuse, tapering to truncate hilum, 1 µm diam, (7–)12–16(–18) × 2(–2.5) µm.

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

Typus. South Africa, Western Cape Province, Knysna, Knysna area, on leaves of *Nephrolepis exaltata* (*Lomariopsidaceae*), 23 Nov. 2018, *F. Roets*, HPC 2722 (holotype CBS H-24179, culture ex-type CPC 37028 = CBS 146078, ITS, LSU and *rpb2* sequences GenBank MN562132.1, MN567639.1 and MN556809.1, MycoBank MB832890).

Colour illustrations. Knysna forest where *Nothodactylaria nephrolepidis* was collected. Colony on synthetic nutrient poor agar; conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

Notes — *Dactylaria* is characterised by having hyaline conidiophores and septate, hyaline conidia formed on denticles (De Hoog 1985). The genus *Dactylaria* is polyphyletic, and the phylogeny of its type species (*D. purpurella*) remains unresolved. *Nothodactylaria nephrolepidis* resembles *Dactylaria*, but clusters apart from other species considered to belong to *Dactylaria* s.lat.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Inocybe ochroalba* (strain 254, GenBank EU326165.1; Identities = 504/554 (91 %), 21 gaps (3 %)), *Dactylaria fragilis* (strain MG12, GenBank KM246212.1; Identities = 366/409 (89 %), 15 gaps (3 %)), and *Cylindrium purgamentum* (strain CPC 29580, GenBank NR_155691.1; Identities = 474/553 (86 %), 17 gaps (3 %)). Closest hits using the **LSU** sequence are *Pseudotruncatella arezzoensis* (strain MFLUCC 14-0988, GenBank MG192317.1; Identities = 813/843 (96 %), 1 gap (0 %)), *Dactylaria sparsa* (strain P055, GenBank EU107291.1; Identities = 798/829 (96 %), 6 gaps (0 %)), and *Dactylaria fragilis* (strain P057, GenBank EU107290.1; Identities = 795/826 (96 %), 4 gaps (0 %)). No significant hits were obtained when the ***rpb2*** sequence was used in blastn and megablast searches.

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Cyphellophora goniomatis

Fungal Planet 980 – 18 December 2019

Cyphellophora goniomatis Crous, *sp. nov.*

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

Classification — *Cyphellophoraceae*, *Chaetothyriales*, *Eurotiomycetes.*

Mycelium consisting of pale brown, smooth, septate, branched, 2–3 µm diam hyphae. *Conidiophores* reduced to conidiogenous loci on hyphae, pale brown, smooth, phialidic, collarettes flared, 2–2.5 µm diam, loci 1–1.5 µm diam. *Conidia* aggregating in mucoid droplets, pale brown, smooth, guttulate, fusoid, inner plane flat, outer plane convex, apex subobtuse, tapering toward inner plane, base truncate, 1 µm diam, (0–)1(–3)-septate, (10–)15–18(–20) × (1.5–)2(–2.5) µm.

Culture characteristics — Colonies flat, 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. South Africa, Western Cape Province, Knysna, Knysna area, on leaves of *Gonioma kamassi* (*Apocynaceae*), 23 Nov. 2018, *F. Roets*, HPC 2698 (holotype CBS H-24180, culture ex-type CPC 37032 = CBS 146077, ITS, LSU, *actA*, *tef1* and *tub2* sequences GenBank MN562133.1, MN567640.1, MN556789.1, MN556825.1 and MN556842.1, MycoBank MB832891).

Notes — *Cyphellophora* is characterised by pigmented phialides occurring directly on hyphae or occasionally on flask-shaped conidiogenous cells, and producing small clusters of olivaceous, septate, mostly curved conidia (Cheewangkoon et al. 2009, Crous et al. 2019b). *Cyphellophora goniomatis* is phylogenetically related to *C. guyanensis* (from angiosperm, French Guyana, conidia (2–)3–6-septate, (18–)19.7–28(–29) × 1.5–2 µm; Decock et al. 2003), although it has smaller conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cyphellophora guyanensis* (strain MUCL 43737, GenBank GU225943.1; Identities = 564/578 (98 %), 3 gaps (0 %)), *Exophiala spinifera* (strain CBS 126014, GenBank KF928476.1; Identities = 532/549 (97 %), 4 gaps (0 %)), and *Cyphellophora eucalypti* (strain CBS 124764, GenBank GQ303274.1; Identities = 592/611 (97 %), 5 gaps (0 %)). Closest hits using the **LSU** sequence are *Cyphellophora guyanensis* (strain CBS 129342, GenBank MH876666.1; Identities = 837/841 (99 %), 1 gap (0 %)), *Cyphellophora eucalypti* (strain CBS 124764, GenBank KC455254.1; Identities = 835/841 (99 %), 1 gap (0 %)), and *Cyphellophora artocarpi* (strain CHCJHB-JBLM, GenBank KP122930.1; Identities = 756/762 (99 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Cyphellophora eucalypti* (strain CBS 124764, GenBank JQ325009.1; Identities = 511/528 (97 %), no gaps), *Scolecostigmina mangiferae* (strain CBS 125467, GenBank GU320566.1; Identities = 510/527 (97 %), no gaps), and *Ophionectria trichospora* (strain CBS 314.75, GenBank KM231181.1; Identities = 517/539 (96 %), 1 gap (0 %)). No significant hits were obtained when the ***tef1*** sequence was used in blastn and megablast searches. Closest hits using the ***tub2*** sequence had highest similarity to *Cyphellophora guyanensis* (strain CBS 125756, GenBank JQ766338.1; Identities = 358/377 (95 %), no gaps), *Cyphellophora artocarpi* (strain CHCJHBJBLM, GenBank KP122925.1; Identities = 362/390 (93 %), 1 gap (0 %)), and *Ophionectria trichospora* (strain CBS 314.75, GenBank KM232047.1; Identities = 228/252 (90 %), 6 gaps (2 %)).

Colour illustrations. Knysna forest with *Gonioma kamassi* trees. Conidiogenous cells; conidia. Scale bars = 10 µm.

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Scolecobasidium blechni

Fungal Planet 981 – 18 December 2019

Scolecobasidium blechni Crous, *sp. nov.*

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

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

Mycelium consisting of medium brown, smooth, branched, septate, 1.5–2 µm diam hyphae, giving rise to hyphal coils. *Conidiophores* erect, solitary or at times two arising from the same basal cell, 2–3-septate, unbranched, straight to irregularly curved, brown, smooth, subcylindrical, 18–40 × 2.5–3 µm. *Conidiogenous cells* terminal, medium brown, smooth, subcylindrical, 8–22 × 2.5–3 µm with 1–4 terminal denticles, 1–1.5 × 1 µm. *Conidia* solitary, medianly 1-septate (or up to 3-septate), fusoid-ellipsoid to subcylindrical, curved to straight, apex obtuse, base with basal marginal frill, 0.5 µm long, medium brown, verruculose, (9–)11–12(–14) × (3–)3.5–4 µm.

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 isabelline.

Typus. South Africa, Western Cape Province, Knysna, Knysna area, on leaves of *Blechnum capense* (*Blechnaceae*), 23 Nov. 2018, *F. Roets*, HPC 2704 (holotype CBS H-24181, culture ex-type CPC 37047 = CBS 146055, ITS, LSU, *tef1* and *tub2* sequences GenBank MN562134.1, MN567641.1, MN556826.1 and MN556843.1, MycoBank MB832892).

Notes — *Scolecobasidium* represents an older name for the genus commonly referred to as *Ochroconis* (Seifert et al. 2011). *Scolecobasidium blechni* is phylogenetically related to *Ochroconis cordanae* (conidia 1-septate, obovoidal to broadly fusiform, ((5–)7–9(–10) × (2.5–)3–3.5 µm; Samerpitak et al. 2014) and *O. macrozamiae* ((5–)8–10(–12) × (3–)3.5(–4) µm; Crous et al. 2014), but is distinct based on its slightly longer conidia and DNA phylogeny.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Ochroconis cordanae* (strain CBS 101179, GenBank KF156020.1; Identities = 548/622 (88 %), 42 gaps (6 %)), *Ochroconis macrozamiae* (strain CBS 102491, GenBank KF156021.1; Identities = 569/653 (87 %), 48 gaps (7 %)), and *Ochroconis musae* (strain CBS 145061, GenBank MK442605.1; Identities = 353/404 (87 %), 16 gaps (3 %)). Closest hits using the **LSU** sequence are *Ochroconis macrozamiae* (strain CBS 102491, GenBank KF156152.1; Identities = 773/789 (98 %), 10 gaps (1 %)), *Ochroconis constricta* (strain CBS 269.61, GenBank MH869616.1; Identities = 828/869 (95 %), 13 gaps (1 %)), and *Ochroconis robusta* (strain NH673, GenBank LC469382.1; Identities = 820/860 (95 %), 11 gaps (1 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Ochroconis macrozamiae* (strain CBS 102491, GenBank KF155983.1; Identities = 370/419 (88 %), 20 gaps (4 %)), *Scolecobasidium variabile* (strain NBRC 32268, GenBank DQ307356.1; Identities = 229/257 (89 %), 6 gaps (2 %)), and *Ochroconis humicola* (strain NBRC 32054, GenBank AB564640.1; Identities = 380/473 (80 %), 4 gaps (9 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Ochroconis macrozamiae* (strain CBS 102491, GenBank KF156191.1; Identities = 405/438 (92 %), 1 gap (0 %)), *Acremonium exuviarum* (strain UAMH 9995, GenBank AY882947.1; Identities = 228/264 (86 %), 5 gaps (1 %)), and *Setophoma pseudosacchari* (strain CBS 145373, GenBank MK540176.1; Identities = 226/265 (85 %), 5 gaps (1 %)).

Colour illustrations. Knysna forest with *Blechnum capense* trees. Conidiophores with conidiogenous cells and conidia. Scale bars = 10 µm.

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Strelitziomyces knysnanus

Fungal Planet 982 – 18 December 2019

Strelitziomyces Crous, *gen. nov.*

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

Classification — *Anungitiomycetaceae*, *Xylariales*, *Sordariomycetes.*

Mycelium consisting of hyaline, smooth, hyphae. *Conidiophores* arising from superficial hyphae, erect, solitary, subcylindrical, hyaline to pale brown at base, septate, mostly unbranched, with terminal conidiogenous cells that are subcylindrical, hyaline, smooth, rarely pale brown, with terminal rachis of subdenticulate loci; loci truncate, not thickened nor darkened. *Conidia* solitary, hyaline, smooth, medianly 1-septate, fusoid, apex subobtuse, base truncate. *Sclerotium-like bodies* formed prominently on and in agar, dark brown, muriformly septate, globose.

Type species. Strelitziomyces knysnanus Crous.
MycoBank MB 832893.

Strelitziomyces knysnanus Crous, *sp. nov.*

Etymology. Name refers to the location where it was collected, Knysna.

Mycelium consisting of hyaline, smooth, 1.5–2 µm diam hyphae. *Conidiophores* arising from superficial hyphae, erect, solitary, subcylindrical, 5–35 × 2–3 µm, hyaline to pale brown at base, 0–3-septate, mostly unbranched, with terminal conidiogenous cells that are subcylindrical, hyaline, smooth, rarely pale brown, 5–25 × 2–2.5 µm, with terminal rachis of subdenticulate loci, 1–2 × 0.5–1 µm; loci truncate, not thickened nor darkened. *Conidia* solitary, hyaline, smooth, medianly 1-septate, fusoid, apex subobtuse, base truncate, 1 µm diam, (24–)30–32 × 2 µm. *Sclerotium-like bodies* formed prominently on and in agar, dark brown, muriformly septate, 30–80 µm diam, globose, lacking an ostiole, and remaining sterile although they are reminiscent of a coelomycete synasexual morph.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA surface isabelline with diffuse isabelline pigment, reverse isabelline. On PDA surface smoke grey, reverse isabelline. On OA surface isabelline.

Typus. South Africa, Western Cape Province, Knysna, Knysna area, on leaves of *Strelitzia alba* (*Strelitziaceae*), 21 Nov. 2018, *F. Roets*, HPC 2727 (holotype CBS H-24183, culture ex-type CPC 37067 = CBS 146056, ITS, LSU and *rpb2* sequences GenBank MN562135.1, MN567642.1 and MN556810.1, MycoBank MB832894).

Notes — *Strelitziomyces* is closely related to *Anungitiomyces*, a monotypic genus occurring on *Eucalyptus* leaf litter in South Africa (Crous et al. 2019a). *Anungitiomyces* is characterised by brown, erect conidiophores, 0–1-septate, obclavate, hyaline conidia, arising via sympodial conidiogenesis. The main differences between the two genera lie in the lack of pigmentation in *Strelitziomyces*, and the prominently formed sclerotium-like bodies.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Anungitiomyces stellenboschiensis* (strain CPC 34726, GenBank MK876376.1; Identities = 537/616 (87 %), 31 gaps (5 %)), *Rhinocladiella pyriformis* (strain CBS 469.94, GenBank MH862476.1; Identities = 379/434 (87 %), 15 gaps (3 %)), and *Pseudotruncatella arezzoensis* (strain MFLUCC 14-0988, GenBank NR_157489.1; Identities = 352/399 (88 %), 19 gaps (4 %)). Closest hits using the **LSU** sequence are *Anungitiomyces stellenboschiensis* (strain CPC 34726, GenBank MK876415.1; Identities = 810/826 (98 %), 1 gap (0 %)), *Oxydothis garethjonesii* (strain MFLUCC 15-0287, GenBank KY206762.1; Identities = 804/837 (96 %), 4 gaps (0 %)), and *Entosordaria quercina* (strain RQ, GenBank MF488994.1; Identities = 800/837 (96 %), 4 gaps (0 %)). No significant hits were obtained when the ***rpb2*** sequence was used in blastn and megablast searches.

Colour illustrations. *Strelitzia alba* plants in Knysna forest. Colony on synthetic nutrient poor agar; conidiophores and conidiogenous cells; conidia; sclerotia. Scale bars = 80 µm (sclerotia), 10 µm (conidia and conidiogenous cells).

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Gyrothrix oleae

Fungal Planet 983 – 18 December 2019

Gyrothrix oleae Crous, *sp. nov.*

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

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

Mycelium consisting of hyaline, smooth, branched, septate, 2–3 µm diam hyphae. *Setae* erect, 100–150 µm long, 3–4 µm diam, brown, multiseptate, thick-walled, verruculose to warty, subcylindrical with apical taper, base bulbous, 4–6 µm diam, apex spirally curved, apical region frequently with curved lateral branches. *Conidiophores* reduced to conidiogenous cells arranged around the base of setae, subcylindrical to ampulliform, hyaline to subhyaline, smooth, 7–13 × 2–3 µm, proliferating percurrently at apex. *Conidia* hyaline, smooth, aseptate, fusoid, inequilateral, inner plane flat, outer plane convex, apex subobtuse, tapering toward inner plane, base with excentric, truncate hilum, tapering towards inner plane, (7–)9–10(–11) × (1.5–)2 µm.

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

Typus. South Africa, Western Cape Province, Knysna, Knysna area, on leaves of *Olea capensis* subsp. *macrocarpa* (*Oleaceae*), 22 Nov. 2018, *F. Roets*, HPC 2728 (holotype CBS H-24184, culture ex-type CPC 37069 = CBS 146069, ITS and LSU sequences GenBank MN562136.1 and MN567643.1, MycoBank MB832895).

Additional material examined. South Africa, Western Cape Province, Knysna, Knysna area, on *Diospyros whyteana* (*Ebenaceae*), 22 Nov. 2018, *F. Roets*, HPC 2720, culture CPC 37063 = CBS 146068, ITS and LSU sequences GenBank MN562137.1 and MN567644.1.

Notes — The hyphomycete genus *Gyrothrix* closely resembles *Circinotrichum* (see FP960). *Gyrothrix oleae* is closely related to *Circinotrichum papakurae* (setae unbranched, conidia 11–17 × 1.5–2 µm; Hughes & Pirozynski 1971) and *Gyrothrix ramosa* (setae branched, conidia 14–19 × 2–2.7 µm; Zucconi & Onofri 1989), 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 of CPC 37069 had highest similarity to *Ascotricha pusilla* (strain CBS 132.60, GenBank MH857921.1; Identities = 506/592 (85 %), 29 gaps (4 %)), *Xylaria liquidambaris* (voucher HMJAU 22124, GenBank JX256826.1; Identities = 506/597 (85 %), 33 gaps (5 %)), and *Virgaria boninensis* (strain JCM 18622, GenBank AB670709.1; Identities = 395/439 (90 %), 15 gaps (3 %)). The ITS sequences of CPC 37063 and 37069 differ with a single nucleotide (581/582 bases similar). Closest hits using the **LSU** sequence of CPC 37069 are *Circinotrichum papakurae* (strain CBS 101373, GenBank KR611897.1; Identities = 819/840 (98 %), 2 gaps (0 %)), *Gyrothrix ramosa* (strain MUCL 54061, GenBank KC775722.1; Identities = 781/802 (97 %), 3 gaps (0 %)), and *Gyrothrix inops* (strain BE108, GenBank KC775721.1; Identities = 790/814 (97 %), 6 gaps (0 %)). The LSU sequences of CPC 37063 and 37069 differ with a single nucleotide (837/838 bases similar).

Colour illustrations. *Olea capensis* subsp. *macrocarpa* trees in Knysna forest. Conidiogenous cells; conidia; setae. Scale bars = 10 µm.

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Scolecobasidium podocarpicola

Fungal Planet 984 – 18 December 2019

Scolecobasidium podocarpicola Crous, *sp. nov.*

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

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

Mycelium consisting of smooth, medium brown, septate, branched, 1.5–2 µm diam hyphae, forming hyphal coils. *Conidiophores* erect, 1-septate, unbranched, medium brown, smooth, subcylindrical, 9–17 × 2.5–3 µm. *Conidiogenous cells* terminal, medium brown, smooth, subcylindrical, 6–10 × 2.5–3 µm, with 1–4 terminal cylindrical denticles, 1–1.5 × 1 µm. *Conidia* solitary, 1(–3)-septate, subcylindrical, apex obtuse, base with marginal frill, 0.5 µm long, medium brown, verruculose, (19–)22–25(–26) × (2.5–)3 µm.

Culture characteristics — Colonies flat, spreading, 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 umber.

Typus. South Africa, Western Cape Province, Knysna, Knysna area, on leaves of *Podocarpus latifolius* (*Podocarpaceae*), 20 Nov. 2018, *F. Roets*, HPC 2739 (holotype CBS H-24185, culture ex-type CPC 37078 = CBS 146057, ITS, LSU and *rpb2* sequences GenBank MN562138.1, MN567645.1 and MN556811.1, MycoBank MB832896).

Notes — *Scolecobasidium podocarpicola* is related to but distinct from species of *Scolecobasidium* (incl. *Ochroconis*) based on its conidial morphology, being subcylindrical, 1(–3)-septate, (19–)22–25(–26) × (2.5–)3 µm. Of interest is the fact that *S. podocarpicola* was cultured from spermatia oozing from a spermatogonium, suggesting that it could have a sexual morph, and that it proved to be closely related to a sexual species, *Ochroconis sexualis* (Samerpitak et al. 2014).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Ochroconis sexualis* (strain PPRI 12991, GenBank NR_132049.1; Identities = 454/522 (87 %), 22 gaps (4 %)), *Ochroconis mirabilis* (strain UTHSC 04-2378, GenBank LM644513.1; Identities = 416/495 (84 %), 32 gaps (6 %)), and *Ochroconis icarus* (strain CBS 536.69, GenBank MH859368.1; Identities = 400/476 (84 %), 26 gaps (5 %)). Closest hits using the **LSU** sequence are *Ochroconis sexualis* (strain PPRI 12991, GenBank NG_060299.1; Identities = 747/778 (96 %), 3 gaps (0 %)), *Ochroconis robusta* (strain CBS 112.97, GenBank NG_058141.1; Identities = 803/837 (96 %), 6 gaps (0 %)), and *Ochroconis bacilliformis* (strain CBS 100442, GenBank NG_058140.1; Identities = 800/838 (95 %), 7 gaps (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Ochroconis musicola* (strain CPC 32927, GenBank MH327876.1; Identities = 686/838 (82 %), 12 gaps (1 %)), *Scolecobasidium terreum* (strain CBS 536.69, GenBank FR832487.1; Identities = 667/818 (82 %), 4 gaps (0 %)), and *Ochroconis humicola* (strain HGUP1204, GenBank JX546578.1; Identities = 662/843 (79 %), 21 gaps (2 %)).

Colour illustrations. Base of *Podocarpus latifolius* tree in Knysna. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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Ceramothyrium podocarpicola

Fungal Planet 985 – 18 December 2019

Ceramothyrium podocarpicola Crous, *sp. nov.*

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

Classification — *Chaetothyriaceae*, *Chaetothyriales*, *Eurotiomycetes.*

Mycelium consisting of pale brown, smooth, septate, branched, 2–3 µm diam hyphae. *Conidiophores* reduced to phialidic conidiogenous cells arising from superficial hyphae, separate, not aggregated in clusters, ampulliform to subcylindrical, medium brown, smooth, 3–7 µm long, apex with long cylindrical neck, 1–3 µm long, slightly flared, base frequently ellipsoid, 3–7 µm diam, attached to hyphae laterally via small hyphal peg. *Conidia* hyaline, smooth, aseptate, triangular, with apex obtuse, tapering towards truncate base, 2–3 µm long, 1.5–2 µm diam, base 1 µm diam; older conidia becoming swollen, ellipsoid.

Culture characteristics — Colonies erumpent, spreading, surface folded, with sparse aerial mycelium and feathery margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA surface greyish sepia, reverse dark mouse grey. On PDA and OA surface and reverse mouse grey.

Typus. South Africa, Western Cape Province, Knysna, Knysna area, on leaves of *Podocarpus latifolius* (*Podocarpaceae*), 20 Nov. 2018, *F. Roets*, HPC 2696 (holotype CBS H-24186, culture ex-type CPC 37080 = CBS 146093, ITS and LSU sequences GenBank MN562139.1 and MN567646.1, MycoBank MB832898).

Notes — *Ceramothyrium podocarpicola* is phylogenetically related to *Ceramothyrium,* an epiphyllous genus of ascomycetes with *Stanhughesia* asexual morphs (see *Ceramothyrium podocarpi*; Crous et al. 2012a). Morphologically, the present collection is quite distinct from *Stanhughesia*, but we suspect that what we observed in culture is actually a synasexual morph, as the species was originally isolated as a *Stanhughesia* morph from *Podocarpus* leaves.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Chaetothyrium agathis* (strain MFLUCC 12-0113, GenBank NR_132914.1; Identities = 451/509 (89 %), 22 gaps (4 %)), *Ceramothyrium exiguum* (strain VTCC F-1209, GenBank NR_159757.1; Identities = 438/499 (88 %), 18 gaps (3 %)), and *Ceramothyrium exiguum* (strain VTCC F-1209, GenBank LC360297.1; Identities = 438/499 (88 %), 18 gaps (3 %)). Closest hits using the **LSU** sequence are *Ceramothyrium thailandicum* (voucher MFLU 13-0632, GenBank KP324930.1; Identities = 794/824 (96 %), 1 gap (0 %)), *Ceramothyrium carniolicum* (strain CBS 175.95, GenBank KC455251.1; Identities = 835/867 (96 %), 2 gaps (0 %)), and *Ceramothyrium linnaeae* (strain CBS 742.94, GenBank MH874144.1; Identities = 834/866 (96 %), 2 gaps (0 %)).

Colour illustrations. Knysna forest with *Podocarpus latifolius* trees. Hyphae with conidiogenous cells and conidia. Scale bars = 10 µm.

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Pseudopenidiella podocarpi

Fungal Planet 986 – 18 December 2019

Pseudopenidiella podocarpi Crous, *sp. nov.*

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

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

Mycelium consisting of pale brown, verruculose, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* solitary, erect, medium brown, smooth but verruculose in upper cell, subcylindrical, unbranched, 1–6-septate, 10–110 × 3–4 µm; base swollen, 4–7 µm diam. *Conidiogenous cells* integrated, terminal, subcylindrical, pale to medium brown, verruculose, 10–15 × 3–3.5 µm, proliferating sympodially with one to several flat-tipped apical loci, 1 µm diam. *Conidia* pale brown, verruculose, aseptate, guttulate, ends obtuse, hila truncate, 0.5–1 µm diam, not thickened nor darkened. Secondary ramoconidia (9–)12–13 × (2.5–)3–3.5 µm; conidia in unbranched chains (–30), (9–)11–12(–15) × 2.5(–3) µm; hila not thickened nor darkened.

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

Typus. South Africa, Western Cape Province, Knysna, Knysna area, on leaves of *Podocarpus latifolius* (*Podocarpaceae*), 22 Nov. 2018, *F. Roets*, HPC 2710 (holotype CBS H-24187, culture ex-type CPC 37092 = CBS 146067, ITS and LSU sequences GenBank MN562140.1 and MN567647.1, MycoBank MB832899).

Additional material examined. South Africa, Western Cape Province, Knysna, Knysna area, on leaves of *Podocarpus latifolius* (*Podocarpaceae*), 22 Nov. 2018, *F. Roets*, HPC 2710, culture CPC 37094, ITS and LSU sequences GenBank MN562141.1 and MN567648.1.

Notes — *Pseudopenidiella* is characterised by having erect, brown conidiophores, sympodial conidiogenesis, and aseptate conidia with somewhat thickened scars and hila (Bensch et al. 2012, Crous et al. 2012b). *Pseudopenidiella podocarpi* is related to *P. piceae* (ramoconidia 8–12 × 2–3 µm, conidia (6–)7–9(–10) × (2.5–)3 µm; Crous et al. 2012b), but distinct in having larger conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 37092 had highest similarity to *Pseudopenidiella piceae* (strain CBS 131453, GenBank NR_111761.1; Identities = 443/484 (92 %), 9 gaps (1 %)), *Morenoina calamicola* (strain MFLUCC 14-1162, GenBank NR_154210.1; Identities = 327/394 (83 %), 20 gaps (5 %)), and *Leptomelanconium allescheri* (strain LA_kult_01, GenBank MF573935.1; Identities = 314/376 (84 %), 21 gaps (5 %)). The ITS sequence of CPC 37092 differs with a single nucleotide from that of CPC 37094 (554/555 bases similar). Closest hits using the **LSU** sequence of CPC 37092 are *Pseudopenidiella piceae* (strain CBS 131453, GenBank NG_042681.1; Identities = 802/824 (97 %), no gaps), *Heliocephala gracilis* (strain MUCL 41200, GenBank HQ333479.1; Identities = 741/829 (89 %), 10 gaps (1 %)), and *Heliocephala zimbabweensis* (strain MUCL 40019, GenBank HQ333481.1; Identities = 738/826 (89 %), 4 gaps (0 %)). The LSU sequences of CPC 37092 and CPC 37094 are identical (824/824 bases).

Colour illustrations. *Podocarpus latifolius* trees in Knysna forest. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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Cylindromonium eugeniicola

Fungal Planet 987 – 18 December 2019

Cylindromonium Crous, *gen. nov.*

Etymology. Name refers to its cylindrical conidia and acremonium-like morphology.

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

Mycelium consisting of hyaline, smooth, septate, branched, hyphae. *Conidiophores* hyaline, smooth, appearing as individual unbranched conidiophores, septate with a terminal phialide, or as complex structures with a basal cylindrical cell that gives rise to 2–4 phialides; basal cell subcylindrical, hyaline, smooth, septate. *Conidiogenous cells* hyaline, smooth, phialidic, subcylindrical with apical taper; apex with flared collarette. *Conidia* solitary, aggregated in mucoid packets, cylindrical with obtuse ends, medianly 1-septate, hyaline, smooth, granular.

Type species. Cylindromonium eugeniicola Crous.
MycoBank MB832900.

Cylindromonium eugeniicola Crous, *sp. nov.*

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

Mycelium consisting of hyaline, smooth, septate, branched, hyphae. *Conidiophores* hyaline, smooth, appearing as individual unbranched conidiophores, septate with a terminal phialide, or as complex structures with a basal cylindrical cell that gives rise to 2–4 phialides; basal cell subcylindrical, hyaline, smooth, septate. *Conidiogenous cells* hyaline, smooth, phialidic, subcylindrical with apical taper; apex with flared collarette. *Conidia* solitary, aggregated in mucoid packets, cylindrical with obtuse ends, medianly 1-septate, hyaline, smooth, granular.

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

Typus. South Africa, Eastern Cape Province, Amathole, Haga Haga, on leaf litter of *Eugenia capensis* (*Myrtaceae*), 2010, *M.J. Wingfield*, HPC 2750 (holotype CBS H-24189, culture ex-type CPC 37170 = CBS 146075, ITS and LSU sequences GenBank MN562142.1 and MN567649.1, MycoBank MB832901).

Notes — *Cylindromonium* is related to *Phialoseptomonium* (Crous et al. 2019a), but distinct in that it has cylindrical conidia, similar to '*A. lichenicola*' CBS 303.70 and '*A. rhabdosporum*' CBS 438.66, which appear to be congeneric, also having cylindrical conidia (Giraldo & Crous 2019).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Acremonium lichenicola* (strain CBS 188.70, GenBank MH859549.1; Identities = 544/600 (91 %), 15 gaps (2 %)), *Acremonium rhabdosporum* (strain CBS 438.66, GenBank MH858850.1; Identities = 543/600 (91 %), 17 gaps (2 %)), and *Phialoseptomonium eucalypti* (strain CBS 145542, GenBank MK876402.1; Identities = 541/599 (90 %), 17 gaps (2 %)). Closest hits using the **LSU** sequence are *Acremonium lichenicola* (strain CBS 415.70A, GenBank MH871536.1; Identities = 805/830 (97 %), no gaps), *Phialoseptomonium eucalypti* (strain CBS 145542, GenBank MK876443.1; Identities = 789/814 (97 %), no gaps), and *Sarcopodium flavolanatum* (strain CBS 128370, GenBank MH876362.1; Identities = 804/830 (97 %), no gaps).

Cylindromonium lichenicola (W. Gams) Crous, *comb. nov*.

MycoBank MB832902.

Basionym. *Acremonium lichenicola* W. Gams, Cephalosporium-artige Schimmelpilze (Stuttgart): 134. 1971.

Cylindromonium rhabdosporum (W. Gams) Crous, *comb. nov*.

MycoBank MB832903.

Basionym. *Acremonium rhabdosporum* W. Gams, Cephalosporium-artige Schimmelpilze (Stuttgart): 136. 1971.

Colour illustrations. Beach at Haga Haga with *Eugenia capensis*. Leaf spot on *Eugenia capensis* with various fungi; sporulation on synthetic nutrient poor agar; conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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Harzia metrosideri

Fungal Planet 988 – 18 December 2019

Harzia metrosideri Crous, *sp. nov.*

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

Classification — *Ceratostomataceae*, *Melanosporales*, *Sordariomycetes.*

Mycelium consisting of hyaline, smooth, branched, septate, 3.5–4 µm diam hyphae. *Conidiophores* macronematous, hyaline, smooth, subcylindrical, multiseptate, up to 1 mm long, with conidiogenous cells terminal and intercalary; terminal conidiogenous cells (1–2 cells) hyaline, smooth, subcylindrical with prominent apical taper, 10–20 × 4–5 µm; intercalary conidiogenous cells denticles-like, tapered, 3–5 × 2 µm. *Conidia* golden brown, smooth to finely roughened, granular, aseptate, dry, ovoid, (15–)16–18(–20) × (12–)15–16 µm, with minute marginal frill.

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

Typus. South Africa, Eastern Cape Province, Amathole, Haga Haga, on leaf litter of *Metrosideros* sp. (*Myrtaceae*), 2010, *M.J. Wingfield*, HPC 2753 (holotype CBS H-24191, culture ex-type CPC 37374 = CBS 146065, ITS and LSU sequences GenBank MN562143.1 and MN567650.1, MycoBank MB832904).

Notes — *Harzia* is characterised by sympodially branched, hyaline superficial mycelium, brown conidia and a *Proteophiala* synasexual morph (Domsch et al. 2007, Schultes et al. 2017). *Harzia metrosideri* is related to *Harzia patula* (conidia (16–)25–37.5(–50) × (12.5–)15–28(–37.5) µm; Holubová-Jechová 1974) and *H. acremonioides* (conidia 20–30 × 15–20 µm; Domsch et al. 2007), but 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 *Harzia patula* (strain CBS 379.88, GenBank NR_161009.1; Identities = 640/667 (96 %), 11 gaps (1 %)), *Harzia acremonioides* (strain CBS 598.71, GenBank MH860282.1; Identities = 638/666(96%), 11 gaps (1 %)), and *Harzia tenella* (as *Olpitrichum tenellum*, strain CBS 121.81, GenBank KY628696.1; Identities = 627/656 (96 %), 10 gaps (1 %)). Closest hits using the **LSU** sequence are *Harzia patula* (as *Olpitrichum patulum*, strain CBS 121524, GenBank KY628687.1; Identities = 840/843 (99 %), 1 gap (0 %)), *Harzia macrospora* (as *Olpitrichum macrosporum*, strain CBS 343.67, GenBank MH870687.1; Identities = 838/842 (99 %), no gaps), and *Harzia verrucosa* (strain CBS 113456, GenBank KY628675.1; Identities = 838/842 (99 %), no gaps).

Colour illustrations. Beach area at Haga Haga. Hyphae with integrated conidiogenous loci; conidia. Scale bars = 10 µm.

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Neodevriesia strelitziicola

Fungal Planet 989 – 18 December 2019

Neodevriesia strelitziicola Crous, *sp. nov.*

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

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

Mycelium consisting of pale brown, smooth, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* solitary, erect, straight to geniculous-sinuous, 1–4-septate, subcylindrical, brown, smooth, unbranched, 5–30 × 2.5–3 µm. *Conidiogenous cells* terminal, integrated, subcylindrical, pale brown, smooth, 5–12 × 2.5–3 µm; proliferating sympodially with loci thickened and darkened, 0.5 µm diam. *Conidia* and ramoconidia pale brown, smooth, 0(–1)-septate, occurring in branched chains, subcylindrical to fusoid-ellipsoid, (5–)7–9(–11) × 2 µm; loci thickened and darkened, 0.5 µm diam.

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

Typus. South Africa, Eastern Cape Province, Amathole, Haga Haga, on leaf litter of *Strelitzia nicolai* (*Strelitziaceae*), 2010, *M.J. Wingfield*, HPC 2748 (holotype CBS H-24192, cultures ex-type CPC 37387 = CBS 146019, CPC 37388 = CBS 146020, ITS, LSU, *rpb2* and *tub2* sequences GenBank MN562144.1–MN562145.1, MN567651.1–MN567652.1, MN556812.1–MN556813.1 and MN556844.1 (CPC 37387), MycoBank MB832905).

Notes — *Neodevriesia* is characterised by medium brown conidiophores and thick-walled, medium brown, sparsely septate conidia arranged in short, mostly unbranched chains (Quaedvlieg et al. 2014). *Neodevriesia strelitziicola* is related to *N. coccolobae* (on leaves of *Coccoloba uvifera*, Puerto Rico; conidia (6–)7–8(–10) × (2–)2.5(–3) µm; Crous et al. 2018a). and *N. tabebuiae* (on leaves of *Tabebuia chrysantha*, Puerto Rico, conidia (6–)7–8(–10) × (2–)2.5(–3) µm; Crous et al. 2018a), and is best distinguished based on its narrower conidia, and DNA phylogeny.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 37388 had highest similarity to *Neodevriesia coccolobae* (strain CBS 145064, GenBank NR_161126.1; Identities = 480/500 (96 %), 8 gaps (1 %)), *Neodevriesia tabebuiae* (strain CBS 145065, GenBank NR_161127.1; Identities = 498/533 (93 %), 15 gaps (2 %)), and *Neodevriesia lagerstroemiae* (strain CBS 125422, GenBank MH863701.1; Identities = 489/533 (92 %), 22 gaps (4 %)). The ITS sequence of CPC 37388 differs with 7 nucleotides from that of CPC 37387 (525/532 bases similar). Closest hits using the **LSU** sequence of CPC 37388 are *Neodevriesia coccolobae* (strain CBS 145064, GenBank MK047483.1; Identities = 816/817 (99 %), no gaps), *Neodevriesia cladophorae* (as *Devriesia* sp. MW-2016a, voucher OUCMBI11011, GenBank KU578114.1; Identities = 811/817 (99 %), no gaps), and *Neodevriesia knoxdaviesii* (strain CBS 122898, GenBank MH874778.1; Identities = 799/808 (99 %), 2 gaps (0 %)). The LSU sequences of CPC 37387 and CPC 37388 are identical (815/815 bases). No significant hits were obtained when the ***rpb2*** sequence was used in blastn and megablast searches. The *rpb2* sequences of CPC 37387 and CPC 37388 are identical (834/834 bases). No significant hits were obtained when the ***tub2*** sequence of CPC 37387 was used in blastn and megablast searches.

Colour illustrations. Forest area at Haga Haga. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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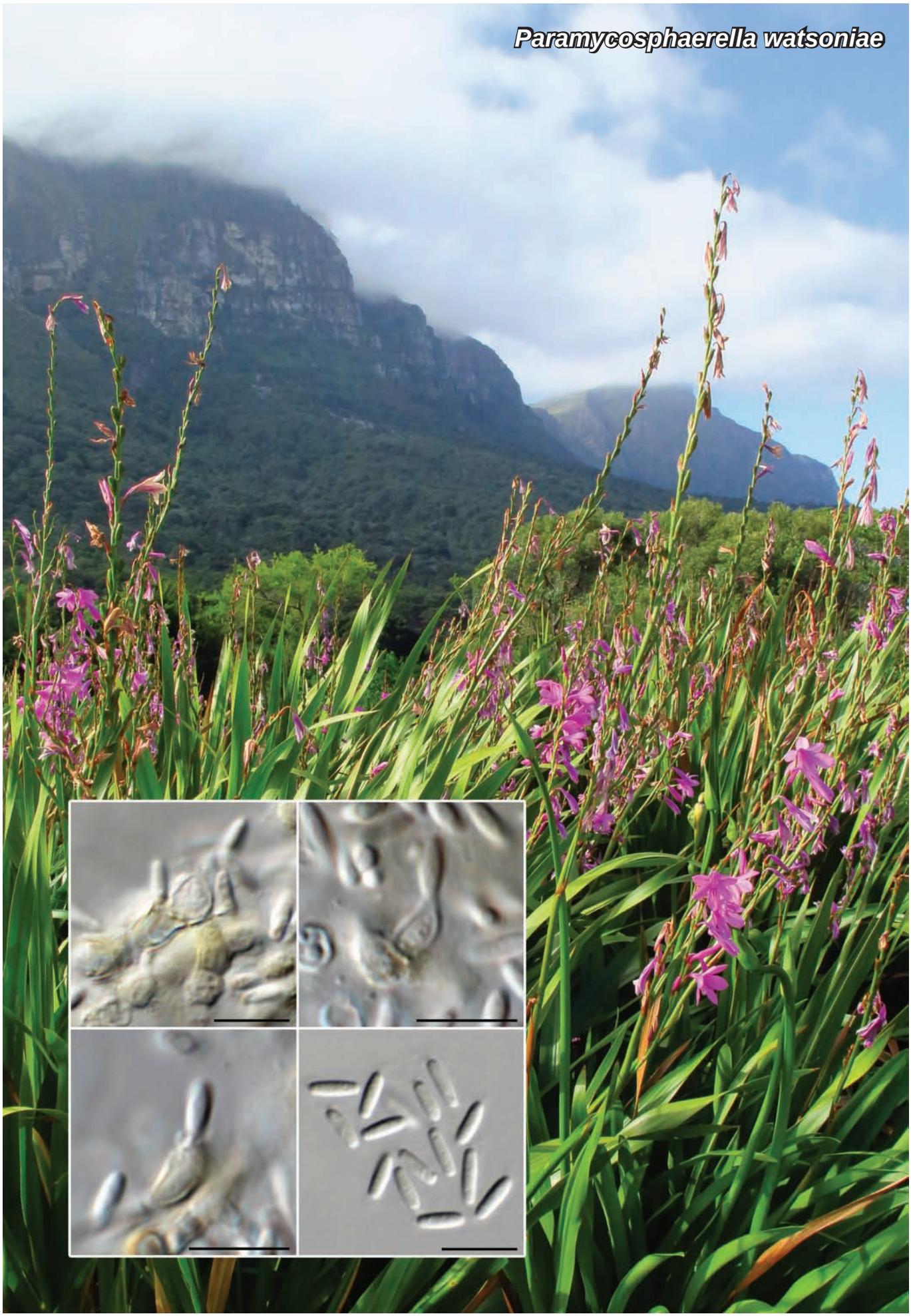
Paramycosphaerella watsoniae

Fungal Planet 990 – 18 December 2019

Paramycosphaerella watsoniae Crous, *sp. nov.*

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

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

Conidiomata pycnidial, globose, brown, 200–250 µm diam, with central ostiole; wall of 3–6 layers of brown *textura angularis. Conidiophores* lining the inner cavity, reduced to conidiogenous cells, or 0–2-septate, subhyaline, smooth, branched, 4–24 × 3–4 µm. *Conidiogenous cells* terminal and intercalary, subhyaline, smooth, 4–5 × 3–4 µm, subcylindrical with periclinal thickening. *Conidia* solitary, hyaline, smooth, guttulate, aseptate, fusoid-ellipsoid, apex obtuse, base truncate, 0.5 µm diam, (3.5–)4–5(–6) × 2 µm.

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

Typus. South Africa, Western Cape Province, Cape Town, Kirstenbosch, on leaf spots of *Watsonia* sp. (*Iridaceae*), 2016, *M.J. Wingfield*, HPC 2757 (holotype CBS H-24193, culture ex-type CPC 37392 = CBS 146064, ITS, LSU, *actA*, *cmdA* and *rpb2* sequences GenBank MN562146.1, MN567653.1, MN556790.1, MN556795.1 and MN556814.1, MycoBank MB832906).

Notes — *Paramycosphaerella* is a mycosphaerella-like genus that lacks a *Ramularia* asexual morph as in *Mycosphaerella* s.str. (Crous et al. 2013b, Videira et al. 2017). *Paramycosphaerella watsoniae* is closely related but phylogenetically distinct from *P. sticheri* (on fronds of *Sticherus penniger*, Brazil; only known from its sexual morph; Guatimosim et al. 2016).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Paramycosphaerella sticheri* (strain COAD 1422, GenBank NR_155660.1; Identities = 489/518 (94 %), 5 gaps (0 %)), *Paramycosphaerella wachendorfiae* (strain CBS 129579, GenBank MH865448.1; Identities = 508/542 (94 %), 7 gaps (1 %)), and *Pseudozasmidium vietnamense* (as *Mycosphaerella vietnamensis*, strain CMW37695, GenBank JQ732923.1; Identities = 461/501 (92 %), 13 gaps (2 %)). Closest hits using the **LSU** sequence are *Paramycosphaerella brachystegiae* (strain CBS 136436, GenBank NG_058048.1; Identities = 844/848 (99 %), no gaps), *Paramycosphaerella dicranopteridis-flexuosae* (strain CPC 24743, GenBank NG_059577.1; Identities = 803/808 (99 %), 1 gap (0 %)), and *Paramycosphaerella marksii* (strain CPC 11222, GenBank GU214447.1; Identities = 842/848 (99 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Paramycosphaerella intermedia* (strain CBS 114356, GenBank KF903466.1; Identities = 505/552 (91 %), 13 gaps (2 %)), *Paramycosphaerella marksii* (strain CBS 110750, GenBank KF903404.1; Identities = 503/552 (91 %), 14 gaps (2 %)), and *Hyalozasmidium aerohyalinosporum* (strain CBS 125011, GenBank KF903576.1; Identities = 501/553 (91 %), 20 gaps (3 %)). Closest hits using the ***cmdA*** sequence had highest similarity to *Hyalozasmidium aerohyalinosporum* (strain CBS 125011, GenBank KF902788.1; Identities = 270/294 (92 %), no gaps), *Paramycosphaerella intermedia* (strain CBS 114356, GenBank KF902579.1; Identities = 266/293 (91 %), no gaps), and *Virosphaerella irregularis* (strain CBS 123242, GenBank KF902543.1; Identities = 266/294 (90 %), no gaps). No significant hits were obtained when the ***rpb2*** sequence was used in blastn and megablast searches.

Colour illustrations. *Watsonia* sp. at the foot of Table Mountain. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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Zygosporium pseudomasonii

Fungal Planet 991 – 18 December 2019

Zygosporium pseudomasonii Crous, *sp. nov.*

Etymology. Name refers to its morphological similarity to *Zygosporium masonii*.

Classification — *Zygosporiaceae*, *Xylariales*, *Sordariomycetes.*

Mycelium consisting of hyaline to pale brown, smooth to verruculose, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* erect, unbranched, subcylindrical, medium brown, smooth, consisting of a stipe, lateral conidiogenous cells and a stipe extension, 20–26 µm long, terminating in a clavate to ovoid vesicle, 2.5–3 µm diam, at times with mucoid droplet, 2–4-septate, 10–30 × 2–3 µm; conidiogenous region consisting of 2–4 hook-like cells, brown, smooth, 5–7 × 2.5–3 µm, lateral hook 2–4 × 2.5–3 µm, the hook frequently alternating left to right, but not consistently. *Conidiogenous cells* (1–2) arising from hook-like cells, pale brown, smooth, ovoid-acuminate, phialidic, 4–6 × 2.5–3 µm. *Conidia* solitary, aseptate, hyaline to subhyaline, verruculose, ellipsoid, apex often tapering to truncate hilum, 0.5 µm diam, (6–)7(–8) × (2–)2.5(–3) µm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface buff, reverse cinnamon. On PDA surface buff with patches of hazel, reverse hazel. On OA surface hazel with patches of buff.

Typus. USA, Florida, Gainesville, on leaf of *Serenoa repens* (*Arecaeae*), 24 Feb. 2019, *M.J. Wingfield*, HPC 2792 (holotype CBS H-24198, culture ex-type CPC 37503 = CBS 146059, ITS, LSU and *rpb2* sequences GenBank MN562147.1, MN567654.1 and MN556815.1, MycoBank MB832907).

Notes — *Zygosporium* is characterised by dark brown conidiophores (with or without stipe extension and vesicle), and 2–4 ampulliform conidiogenous cells. Conidia are aseptate, ellipsoid to globose, hyaline to pale brown, smooth to verruculose. *Zygosporium pseudomasonii* resembles *Z. masonii* (on *Cocos nucifera*, Gold Coast, with up to six lateral hook-like cells, stipe extension 7–12 µm, vesicles 4–5 µm diam; Ellis 1971), but can be distinguished based on its conidiophore morphology, having less lateral hook-like cells, longer stipe extensions and narrower vesicles.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Zygosporium masonii* (strain CBS 557.73, GenBank MH860771.1; Identities = 547/567 (96 %), 4 gaps (0 %)), *Podosordaria muli* (strain DFFSCS030, GenBank JX156376.1; Identities = 507/532 (95 %), 8 gaps (1 %)), and *Zygosporium mycophilum* (strain CBS 894.69, GenBank MH859474.1; Identities = 534/576 (93 %), 12 gaps (2 %)). Closest hits using the **LSU** sequence are *Zygosporium masonii* (strain CBS 557.73, GenBank MH872493.1; Identities = 856/861 (99 %), no gaps), *Zygosporium pseudogibbum* (strain CBS 143503, GenBank NG_063962.1; Identities = 837/844 (99 %), no gaps), and *Zygosporium mycophilum* (strain CBS 533.76, GenBank MH877824.1; Identities = 851/859 (99 %), no gaps). No significant hits were obtained when the ***rpb2*** sequence was used in blastn and megablast searches.

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

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Cylindrocladiella postalofficium

Fungal Planet 992 – 18 December 2019

Cylindrocladiella postalofficium Crous, *sp. nov.*

Etymology. The famous milkwood tree in Mossel Bay is over 500 years old. It is commonly known as the Post Office Tree, as in 1500 a sailor left a letter in a shoe at the tree, found by Joao da Nova in 1501 en-route to India. Name derived from L. *postalis* = postal, and L. *officium* = service; isolated from leaf litter of the Post Office Tree.

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

Conidiophores penicillate, comprising a stipe, a penicillate arrangement of fertile branches, a stipe extension and a terminal vesicle; stipe septate, hyaline, smooth, 30–60 × 4–6 µm. *Stipe extension* aseptate, straight, thick-walled, 100–150 µm long, with a basal septum, terminating in a thin-walled, narrowly lanceolate to ellipsoid *vesicle*, 3.5–4 µm wide. Penicillate conidiogenous apparatus with primary branches aseptate, 12–25 × 3.5–5 µm, secondary branches aseptate, 18–22 × 3.5–4 µm, tertiary branches 12–15 × 3.5–4 µm, each terminal branch producing 2–4 phialides; *phialides* cymbiform to cylindrical, hyaline, 12–15 × 2.5–4 µm, with minute periclinal thickening and cylindrical collarette. *Conidia* cylindrical, rounded at both ends, straight, 1-septate, (10–)14–15(–17) × 2(–2.5) µm, straight, held in clusters by colourless slime.

Culture characteristics — Colonies flat, spreading, with moderate to abundant aerial mycelium, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white to buff, reverse buff with patches of cinnamon.

Typus. South Africa, Western Cape Province, Mossel Bay, 'Post Office tree', on leaf litter of *Sideroxylon inerme* (*Sapotaceae*), 19 Feb. 2016, *L. Lombard*, HPC 2801 (holotype CBS H-24199, culture ex-type CPC 37513 = CBS 146060, ITS, LSU, *his3* and *tub2* sequences GenBank MN562148.1, MN567655.1, MN556796.1 and MN556845.1, MycoBank MB832908).

Notes — *Cylindrocladiella* was recently treated (Lombard et al. 2012, Pham et al. 2018, Marin-Felix et al. 2019). *Cylindrocladiella postalofficium* is related to *C. lageniformis* (vesicles lageniform to ovoid, conidia (9–)11(–15) × (1.5–)1.8(–2) µm; Crous & Wingfield 1993) and *C. pseudocamelliae* (vesicles ellipsoidal to lageniform to lanceolate, conidia (9–)11–15(–16) × 2–4 µm; Lombard et al. 2012), but distinct based on its lanceolate to ellipsoid vesicles and longer conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cylindrocladiella lageniformis* (strain CPC 17600, GenBank JN100631.1; Identities = 498/508 (98 %), 4 gaps (0 %)), *Cylindrocladiella pseudocamelliae* (strain CBS 129555, GenBank NR_111644.1; Identities = 504/515 (98 %), 3 gaps (0 %)), and *Cylindrocladiella hawaiiensis* (strain CBS 129569, GenBank NR_111651.1; Identities = 501/512 (98 %), 3 gaps (0 %)). Closest hits using the **LSU** sequence are *Cylindrocladiella cymbiformis* (strain CBS 129554, GenBank JN099144.1; Identities = 840/847 (99 %), 1 gap (0 %)), *Cylindrocladiella variabilis* (strain CPC 17504, GenBank JN099241.1; Identities = 838/846 (99 %), no gaps), and *Cylindrocladiella stellenboschensis* (strain CBS 115611, GenBank JN099185.1; Identities = 837/846 (99 %), no gaps). Closest hits using the ***his3*** sequence had highest similarity to *Cylindrocladiella parva* (strain TRR-CL, GenBank JQ859985.1; Identities = 344/370 (93 %), 9 gaps (2 %)), *Cylindrocladiella peruviana* (strain CMW47333, GenBank MH017013.1; Identities = 425/474 (90 %), 22 gaps (4 %)), and *Cylindrocladiella queenslandica* (strain CBS 129574, GenBank JN098861.1; Identities = 420/469 (90 %), 20 gaps (4 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Cylindrocladiella camelliae* (strain CPC 237, GenBank JN098749.1; Identities = 321/336 (96 %), 4 gaps (1 %)), *Cylindrocladiella nederlandica* (strain CBS 152.91, GenBank JN098800.1; Identities = 320/336 (95 %), 4 gaps (1 %)), and *Cylindrocladiella pseudocamelliae* (as *Cylindrocladiella* sp. LL-2011j, strain CBS 129556, GenBank JN098815.1; Identities = 319/336 (95 %), 4 gaps (1 %)).

Colour illustrations. Post Office Tree in Mossel Bay. Conidiophores with stipe extensions; conidiogenous cells; conidia. Scale bars = 10 µm.

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Periconia neobrittanica

Fungal Planet 993 – 18 December 2019

Periconia neobrittanica Crous, *sp. nov.*

Etymology. Name refers to its morphological similarity with *Periconia brittanica*.

Classification — *Periconiaceae*, *Pleosporales*, *Dothideomycetes.*

Mycelium consisting of brown, verruculose, branched, septate, 2–3 µm diam hyphae. *Conidiophores* dimorphic. *Microconidiophores* reduced to conidiogenous cells occurring directly on hyphae, tretic, giving rise to a single conidium, but at times also clusters of conidial chains occur. *Macroconidiophores* 100–300 × 10–17 µm, solitary, or in clusters of 2–3, arising from a brown stroma, subcylindrical, straight to flexuous, unbranched, dark brown, smooth, thick-walled, base swollen, 15–25 µm diam; stipe mostly aseptate, with 2–5 septa in upper conidiogenous region; primary branches subcylindrical, brown, verruculose, 0–1-septate, 10–25 × 7–10 µm. *Conidiogenous cells* terminal and intercalary, occurring in an apical chain on primary, or directly on conidiophore, 10–15 µm long, tretic. *Conidia* aseptate, spherical, pale to medium brown, with delicate spines, occurring in branched chains, (6–)8–10(–12) µm diam; conidiogenous apparatus usually unilateral on conidiophore.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and even margin, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse iron-grey.

Typus. USA, California, Davis, UC Davis, on leaves of *Melaleuca styphelioides* × *lanceolata* (*Myrtaceae*), 2 Apr. 2019, *P.W. Crous*, HPC 2897 (holotype CBS H-24203, culture ex-type CPC 37903 = CBS 146062, ITS and LSU sequences GenBank MN562149.1 and MN567656.1, MycoBank MB832909).

Notes — *Periconia* was treated by Tanaka et al. (2015). *Periconia neobrittanica* is similar to *P. britannica* in having unilateral conidiophores and micro- plus macroconidiophores. It is distinct in that it has larger conidia with delicate spines, and shorter conidiophores (Ellis 1976).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Ascomycete* sp. (strain nasa64 from the Atcama desert in Chile, GenBank DQ683977.1; Identities = 528/528 (100 %), no gaps), *Periconia aquatica* (strain HKAS 92754, GenBank NR_158841.1; Identities = 438/475 (92 %), 5 gaps (1 %)), and *Periconia submersa* (strain HKAS 92738, GenBank NR_158842.1; Identities = 437/476 (92 %), 6 gaps (1 %)). The ITS sequence is 90 % (439/487, including 11 gaps) similar to *Noosia banksiae* (strain CPC 17282, GenBank JF951147.1), which represents the most similar species obtained when the LSU sequence was used in the megablast search. Closest hits using the **LSU** sequence are *Noosia banksiae* (strain CBS 129526, GenBank NG_064279.1; Identities = 889/896 (99 %), no gaps), *Sporidesmium tengii* (strain voucher HKUCC 10837, GenBank DQ408559.1; Identities = 849/856 (99 %), 1 gap (0 %)), and *Periconia cyperacearum* (strain CPC 32138, GenBank NG_064549.1; Identities = 888/896 (99 %), no gaps).

Colour illustrations. Branch of *Melaleuca styphelioides* × *lanceolata* in California. Conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Pseudocamarosporium eucalypti

Fungal Planet 994 – 18 December 2019

Pseudocamarosporium eucalypti Crous, *sp. nov.*

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

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

Conidiomata solitary, globose, brown, 180–250 µm diam, with central ostiole, exuding a brown conidial mass; wall of 6–8 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, phialidic with periclinal thickening, 5–8 × 5–6 µm. *Conidia* solitary, medium brown, smooth, medianly 1-septate, ellipsoid, straight, thick-walled, ends obtuse, (7–)8–9(–10) × (4–)5 µm. *Spermatogonia* (forming on MEA) separate, globose, brown, up to 200 µm diam, with central ostiole; wall of 3–4 layers of brown *textura angularis*. *Spermatophores* reduced to spermatogenous cells. *Spermatogenous cells* lining the inner cavity, ampulliform to doliiform, hyaline, smooth, 4–6 × 3–5 µm, apex with visible periclinal thickening and minute collarette. *Spermatia* solitary, smooth, hyaline, subcylindrical, straight to slightly curved, apex obtuse, base truncate, 3–6 × 1.5–2.5 µm.

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

Typus. USA, California, Davis, UC Davis, on leaves of *Eucalyptus* sp. (*Myrtaceae*), 2 Apr. 2019, *P.W. Crous*, HPC 2896 (holotype CBS H-24205, culture ex-type CPC 37995 = CBS 146084, ITS, LSU and *tef1* sequences GenBank MN562150.1, MN567657.1 and MN556833.1, MycoBank MB832910).

Notes — The *Camarosporium* complex was recently treated by Wanasinghe et al. (2017). *Pseudocamarosporium eucalypti* is closely related to *P. brabeji* (on branch of *Platanus* sp., Switzerland, conidia ellipsoid or subcylindrical, (9–)10–12(–13) × (4–)5(–6) µm, 1–3-transversely septate; Crous et al. 2018b), from which it is distinct by having smaller, 1-septate conidia, (7–)8–9(–10) × (4–)5 µm.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pseudocamarosporium brabeji* (strain NW-FVA2387, GenBank MG098280.1; Identities = 581/588 (99 %), no gaps), *Pseudocamarosporium tilicola* (strain MFLUCC 13-0550, GenBank KJ747050.1; Identities = 551/558 (99 %), no gaps), and *Pseudocamarosporium piceae* (strain cp48, GenBank MK796148.1; Identities = 518/525 (99 %), no gaps). Closest hits using the **LSU** sequence are *Pseudocamarosporium propinquum* (strain MFLUCC 17-1211, GenBank MG812621.1; Identities = 844/844 (100 %), no gaps), *Pseudocamarosporium ulmi-minoris* (strain MFLUCC 17-0671, GenBank MG829062.1; Identities = 844/844 (100 %), no gaps), and *Pseudocamarosporium pteleae* (strain MFLUCC 17-0724, GenBank MG829061.1; Identities = 844/844 (100 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Pseudocamarosporium pteleae* (strain MFLUCC 17-0724, GenBank MG829233.1; Identities = 434/442 (98 %), no gaps), *Paraconiothyrium cyclothyrioides* (strain UTHSC DI16-327, GenBank LT797124.1; Identities = 456/468 (97 %), no gaps), and *Paraconiothyrium brasiliense* (strain UTHSC DI16-311, GenBank LT797116.1; Identities = 428/440 (97 %), no gaps).

Colour illustrations. Leaves of *Eucalyptus* sp. in California *Pseudocamarosporium eucalypti* was isolated from. Conidiomata on pine needle agar; conidiogenous cells; conidia. Scale bars: conidiomata = 200 µm, all others = 10 µm.

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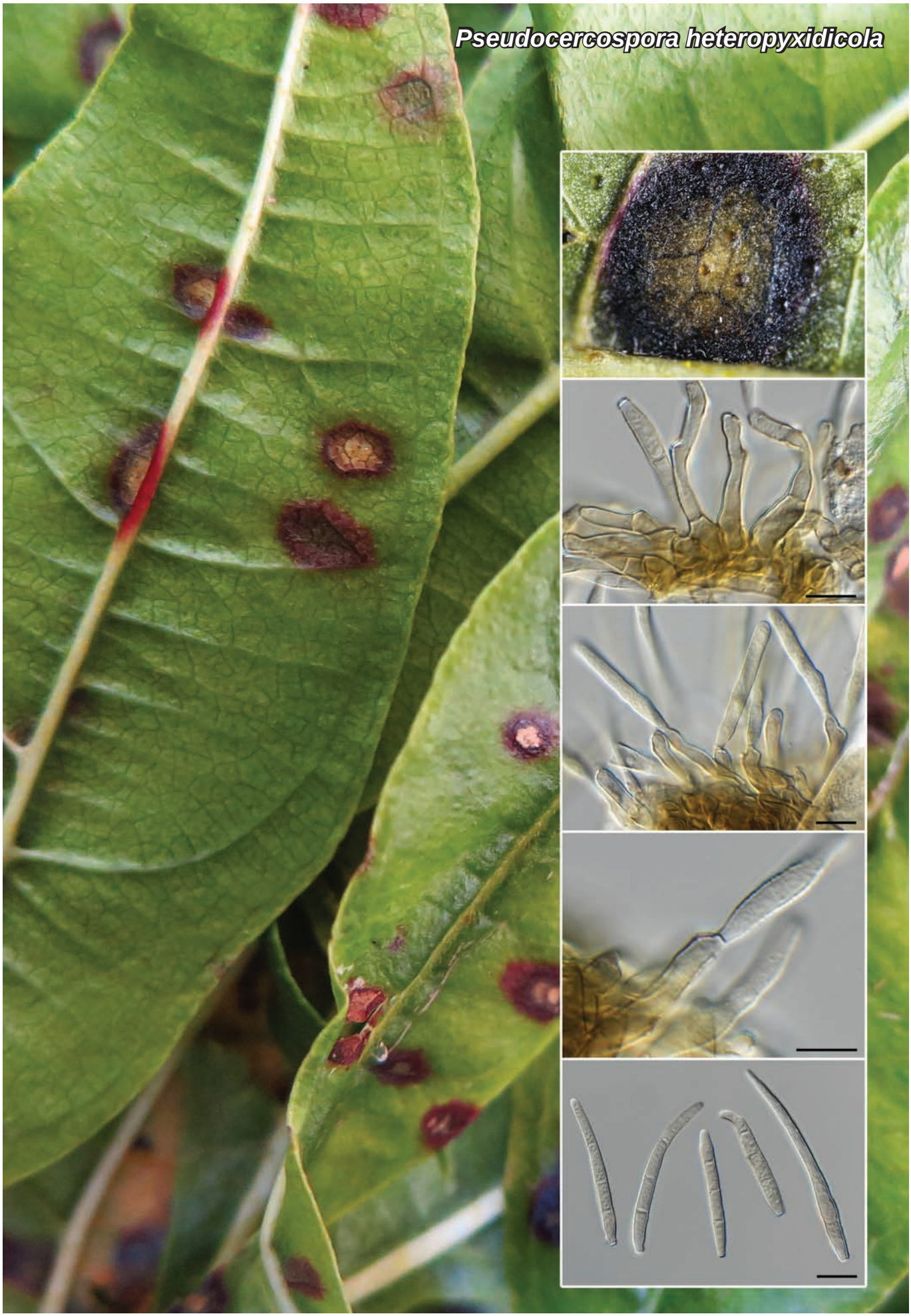
Pseudocercospora heteropyxidicola

Fungal Planet 995 – 18 December 2019

Pseudocercospora heteropyxidicola Crous, *sp. nov.*

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

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

Leaf spots amphigenous, circular, 2–3 mm diam, pale brown with broad red-purple margin. *Caespituli* forming on a weakly developed brown stroma of pseudoparenchymatal cells up to 40 µm diam, 20 µm high. *Conidiophores* arranged in fascicles of 20–30 conidiophores, subcylindrical, geniculate-sinuous, rarely branched above, medium brown, verruculose, 1(–2)-septate, 25–50 × 4–6 µm. *Conidiogenous cells* integrated, terminal, medium brown, verruculose, subcylindrical, 13–30 × 3–6 µm, with flat-tipped loci 2 µm diam, thickened, somewhat darkened and refractive. *Conidia* solitary, obclavate, curved, rarely straight, apex obtuse, base obconically truncate, olivaceous brown, verruculose, guttulate, (20–)40–55(–65) × (3–)4(–5) µm, (1–)3(–5)-septate, hila truncate, somewhat darkened, thickened and refractive. In culture conidia are pale brown, smooth to finely verruculose and hila are unthickened nor darkened.

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 dirty white with patches of olivaceous grey, reverse olivaceous grey.

Typus. South Africa, KwaZulu-Natal Province, Kwambonambi, on leaf spots of *Heteropyxis natalensis* (*Heteropyxidaceae*), 16 Apr. 2010, *M.J. Wingfield*, HPC 2863 (holotype CBS H-24207, culture ex-type CPC 38030 = CBS 146082, ITS, LSU and *actA* sequences GenBank MN562151.1, MN567658.1 and MN556791.1, MycoBank MB832911).

Notes — Based on the morphology on the host material, the present collection is a passalora-like fungus in the sense of Crous & Braun (2003), but based on its morphology in culture, it is a typical *Pseudocercospora* (Crous et al. 2013a, Videira et al. 2017). No species of *Pseudocercospora* is presently known from *Heteropyxis natalensis*, and thus it is herewith described as new.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pseudocercospora tamarindi* (strain MFLUCC 14-0805, GenBank KP744461.1; Identities = 496/509 (97 %), 1 gap (0 %)), *Pseudocercospora eriodendri* (GenBank AF222840.1; Identities = 494/508 (97 %), no gaps), and *Pseudocercospora punctata* (strain CBS 113315, GenBank EU167582.1; Identities = 524/542 (97 %), no gaps). Closest hits using the **LSU** sequence are *Pseudocercospora rhododendri-indici* (strain CBS 131591, GenBank JQ324965.1; Identities = 799/800 (99 %), 1 gap (0 %)), *Pseudocercospora udagawana* (strain CBS 131931, GenBank MH877467.1; Identities = 801/803 (99 %), 2 gaps (0 %)), and *Pseudocercospora punctata* (strain CBS 132116, GenBank GU253791.1; Identities = 796/802 (99 %), 1 gap (0 %)). Closest hits using the ***actA*** sequence had highest similarity to *Pseudocercospora cercidis-chinensis* (voucher BJFC LZC1609256, GenBank MG733154.1; Identities = 450/500 (90 %), 4 gaps (0 %)), *Pseudocercospora punctata* (strain CBS 132116, GenBank GU320468.1; Identities = 518/580 (89 %), 4 gaps (0 %)), and *Pseudocercospora udagawana* (strain CBS 131931, GenBank GU320527.1; Identities = 519/583 (89 %), 6 gaps (1 %)).

Colour illustrations. Symptomatic leaves of *Heteropyxis natalensis*. Close-up of leaf spot; conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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Davidiellomyces juncicola

Fungal Planet 996 – 18 December 2019

Davidiellomyces juncicola Crous, *sp. nov.*

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

Classification — *Cladosporiaceae*, *Capnodiales*, *Dothideomycetes.*

Ascomata pseudothecial, dark brown, erumpent, globose, 80–120 µm diam, with central ostiole 10 µm diam; ascomata aggregated in clusters and linked via a brown stroma (in agar, not observed on host); wall of 2–3 layers of brown *textura angularis. Asci* aparaphysata, fasiculate, bitunicate, subsessile, obovoid, straight to slightly curved, 8-spored, with apical chamber, 30–35 × 9–10 µm. *Ascospores* multiseriate, hyaline guttulate, constricted at median septum, thick-walled, surrounded by mucoid sheath, tapering towards both ends, but more prominently towards lower end, (9–)11–12(–13.5) × (3.5–)4 µm. Ascospores germinating initially via both ends, 5–6 µm diam, becoming brown, verruculose, with mucoid sheath, distorting, the two original ascospore cells dividing into two; outer two cells germinating via two germ tubes parallel to the long axis, inner two cells germinating later, with germ tubes perpendicular to the long axis of the ascospore.

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, PDA and OA surface and reverse olivaceous grey.

Typus. USA, California, Davis, UC Davis, on culms of *Juncus effusus* (*Juncaceae*), 2 Apr. 2019, *P.W. Crous*, HPC 2894 (holotype CBS H-24255, culture ex-type CPC 38038 = CBS 146130, ITS, LSU and *actA* sequences GenBank MN562152.1, MN567659.1 and MN556792.1, MycoBank MB832912).

Notes — *Davidiellomyces* (on leaves of *Cyperaceae*, Western Australia) is characterised by a mycosphaerella-like sexual morph in which ascospores are encased in a prominent mucoid sheath, and become brown and verruculose upon germination (Crous et al. 2017b). *Davidiellomyces juncicola* represents a new species in this hitherto monotypic genus.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Davidiellomyces australiensis* (strain CBS 142165, GenBank NR_154036.1; Identities = 655/683 (96 %), 4 gaps (0 %)), *Verrucocladosporium dirinae* (strain CR16, GenBank KY111909.1; Identities = 418/443 (94 %), 11 gaps (2 %)), and *Neocladosporium leucadendri* (strain CBS 131317, GenBank NR_152324.1; Identities = 489/528 (93 %), 15 gaps (2 %)). Closest hits using the **LSU** sequence are *Davidiellomyces australiensis* (strain CBS 142165, GenBank NG_059164.1; Identities = 810/812 (99 %), no gaps), *Neocladosporium leucadendri* (strain CBS 131317, GenBank NG_057949.1; Identities = 809/819 (99 %), no gaps), and *Verrucocladosporium dirinae* (strain CBS 112794, GenBank MH874471.1; Identities = 806/819 (98 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Davidiellomyces australiensis* (strain CBS 142165, GenBank KY979853.1; Identities = 495/528 (94 %), 2 gaps (0 %)), *Cladosporium sinuosum* (strain CPC 18365, GenBank KT600643.1; Identities = 451/499 (90 %), 4 gaps (0 %)), and *Cladosporium rugulovarians* (strain CPC 18444, GenBank KT600656.1; Identities = 467/523 (89 %), 18 gaps (3 %)).

Colour illustrations. *Juncus effusus* plants *Davidiellomyces juncicola* was isolated from. Colony on oatmeal agar; asci with ascospores; germinating ascospores. Scale bars = 120 µm (ascomata), 10 µm (all others).

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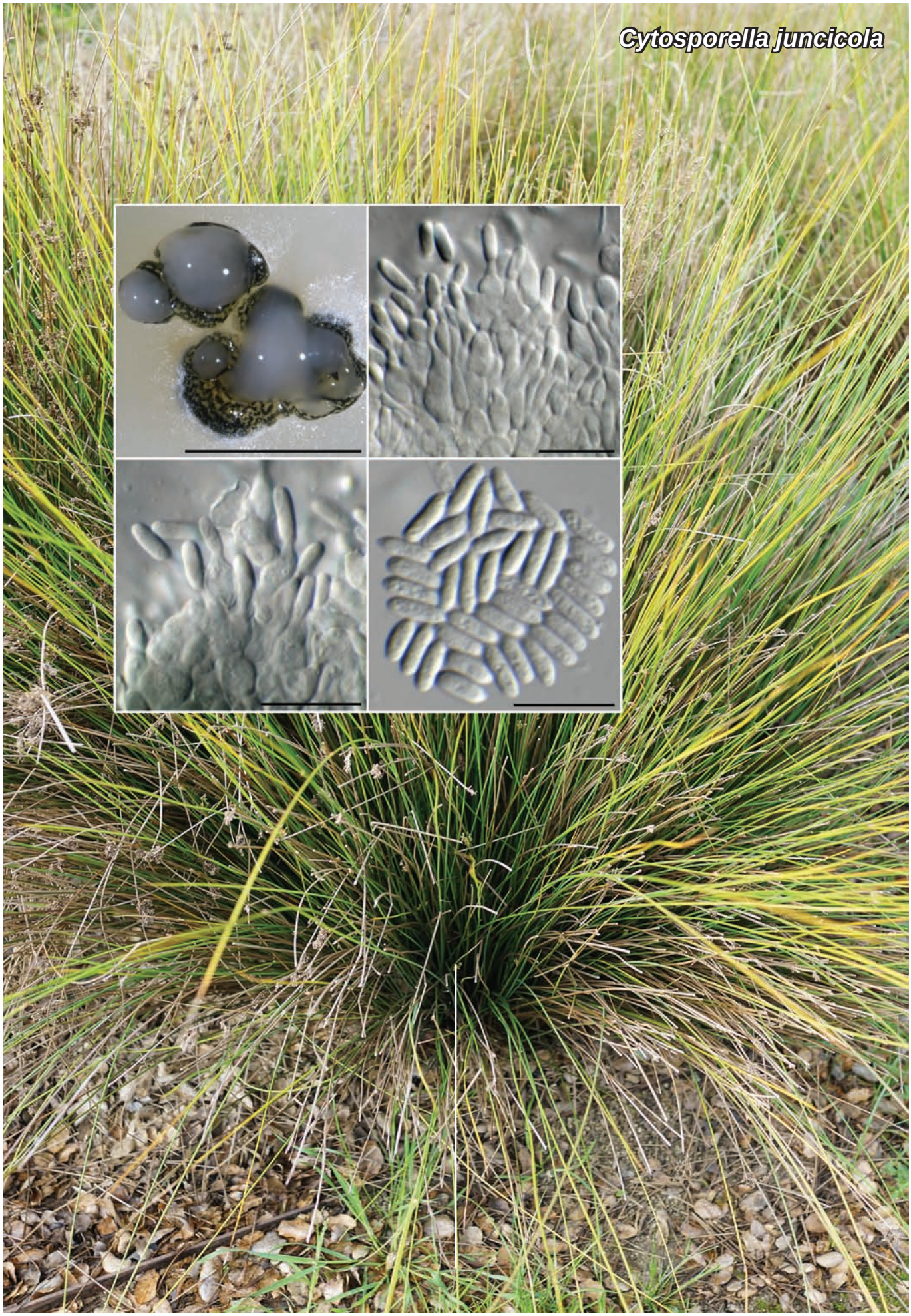
Cytosporella juncicola

Fungal Planet 997 – 18 December 2019

Cytosporella juncicola Crous, *sp. nov.*

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

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

Conidiomata flat, erumpent, separate, eustromatic, brown, upper layer disintegrating at maturity, becoming acervular, up to 2 mm diam, exuding a creamy conidial mass. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, but green olivaceous in mass, ampulliform, phialidic, 5–7 × 3–4 µm. *Conidia* solitary, aseptate, hyaline, guttulate, smooth, cylindrical, straight, apex obtuse, base bluntly rounded, (4–)5–6(–7) × 2 µm on SNA.

Culture characteristics — Colonies erumpent, spreading, surface folded, with sparse aerial mycelium and smooth, lobate margin, reaching 12 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface buff with patches of cinnamon, reverse buff to rosy buff.

Typus. USA, California, Davis, UC Davis, on culms of *Juncus effusus* (*Juncaceae*), 2 Apr. 2019, *P.W. Crous*, HPC 2894 (holotype CBS H-24208, culture ex-type CPC 38040 = CBS 146071, ITS, LSU and *tef1* sequences GenBank MN562153.1, MN567660.1 and MN556834.1, MycoBank MB832913).

Notes — *Cytosporella* has eustromatic conidiomata, opening by irregular dehiscence, branched phialidic conidiophores, and hyaline, aseptate, thin-walled, ellipsoid conidia (Sutton 1980). Although the taxonomy of *Cytosporella* is still in flux, the present collection is tentatively placed in this genus.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had distant hits with *Neoacrodontiella eucalypti* (strain CBS 145561, GenBank MK876396.1; Identities = 374/427 (88 %), 24 gaps (5 %)), *Corticifraga peltigerae* (strain RP282, GenBank KY661634.1; Identities = 268/289 (93 %), 9 gaps (3 %)), and *Taitaia aurea* (voucher TU 56326, GenBank NR_160480.1; Identities = 197/203 (97 %), 1 gap (0 %)). Closest hits using the **LSU** sequence are *Cytosporella chamaeropis* (strain CBS 355.71, GenBank MH871929.1; Identities = 806/808 (99 %), no gaps), *Acarospora thamnina* (voucher DS8352, GenBank KF024746.1; Identities = 522/535 (98 %), 2 gaps (0 %)), and *Neoacrodontiella eucalypti* (strain CBS 145561, GenBank MK876437.1; Identities = 775/826 (94 %), 4 gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Julella fallaciosa* (strain MPN141, GenBank JN887424.1; Identities = 376/429 (88 %), 10 gaps (2 %)), *Lophodermium resinosum* (strain DAOMC 251482, GenBank KY702582.1; Identities = 404/461 (88 %), 7 gaps (1 %)), and *Monilinia fructicola* (strain DH41, GenBank KT900540.1; Identities = 406/466 (87 %), 14 gaps (3 %)).

Colour illustrations. Culms of *Juncus effusus* in California. Conidiomata on oatmeal agar; conidiogenous cells and conidia. Scale bars = 2 mm (conidiomata), 10 µm (all others).

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Neohelicomyces melaleucae

Fungal Planet 998 – 18 December 2019

Neohelicomyces melaleucae Crous, *sp. nov.*

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

Classification — *Tubeufiaceae*, *Tubeufiales*, *Dothideomycetes.*

Mycelium consisting of pale to medium brown, smooth, septate, branched, 3–4 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells, integrated on hyphae, pale brown, smooth, 3–15(–35) × 3–4 µm, with one to several flat-tipped denticles, 2 µm diam; at times reduced to a single denticles directly on hyphae. *Conidia* single, pale brown, smooth, multiseptate, coiled in three rings (13–17 µm diam), base truncate, 2 µm diam.

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

Typus. USA, California, Davis, UC Davis, on leaves of *Melaleuca styphelioides* × *lanceolata* (*Myrtaceae*), 2 Apr. 2019, *P.W. Crous*, HPC 2897 (holotype CBS H-24209, culture ex-type CPC 38042 = CBS 146081, ITS, LSU and *tef1* sequences GenBank MN562154.1, MN567661.1 and MN556835.1, MycoBank MB832914).

Notes — *Neohelicomyces* differs from *Tubeufia* and *Helicomyces* in having elongate, erect, conspicuous conidiophores (Tsui et al. 2006, Crous et al. 2019b). *Neohelicomyces melaleucae* is closely related to '*Tubeufia*' *helicomyces* (CBS 272.52) and *N. pandanicola* but is distinct based on its DNA phylogeny.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Tubeufia helicomyces* (strain MUCL 15702, GenBank AY916459.1; Identities = 557/601 (93 %), 25 gaps (4 %)), *Neohelicomyces deschampsiae* (strain CBS 145029, GenBank NR_163367.1; Identities = 546/598 (91 %), 24 gaps (4 %)), and *Helicosporium lumbricoides* (strain CBS 284.51, GenBank MH856861.1; Identities = 551/605 (91 %), 26 gaps (4 %)). Closest hits using the **LSU** sequence are *Tubeufia helicomyces* (strain CBS 272.52, GenBank MH868562.1; Identities = 825/828 (99 %), no gaps), *Neohelicomyces pandanicola* (strain KUMCC 16-0143, GenBank MH260307.1; Identities = 790/793 (99 %), no gaps), and *Neohelicomyces submersus* (as *Tubeufiaceae* sp. ZL-2017c, strain KUMCC 15-0251, GenBank KY320547.1; Identities = 824/828 (99 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Neohelicomyces hyalosporus* (strain GZCC 16-0086, GenBank MH550936.1; Identities = 417/436 (96 %), no gaps), *Tubeufia helicomyces* (strain CBS 245.49, GenBank DQ767638.1; Identities = 403/423 (95 %), no gaps), and *Tubeufia guangxiensis* (strain MFLUCC 17-0046, GenBank MH550977.1; Identities = 414/437 (95 %), 2 gaps (0 %)).

Colour illustrations. Branch of *Melaleuca styphelioides* × *lanceolata* in California. Hyphae, conidiogenous cells and conidia. Scale bars = 10 µm.

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Podocarpomyces knysnanus

Fungal Planet 999 – 18 December 2019

Podocarpomyces Crous, *gen. nov.*

Etymology. Name refers to the host genus on which it occurs, *Podocarpus*.

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

Conidiomata solitary, globose, brown, with central ostiole; wall of 3–6 layers of *textura angularis. Conidiophores* lining inner cavity, hyaline, smooth, subcylindrical, branched at base, septate*. Conidiogenous cells* terminal and intercalary, hyaline, smooth, subcylindrical with apical taper, phialidic. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, apex subobtuse, base truncate.

Type species. Podocarpomyces knysnanus Crous.
MycoBank MB832915.

Podocarpomyces knysnanus Crous, *sp. nov.*

Etymology. Name refers to the location in South Africa where the fungus was collected, Knysna.

Conidiomata solitary, globose, brown, 200–250 µm diam, with central ostiole; wall of 3–6 layers of *textura angularis. Conidiophores* lining inner cavity, hyaline, smooth, subcylindrical, branched at base, 1–2-septate, 15–30 × 2.5–4 µm*. Conidiogenous cells* terminal and intercalary, hyaline, smooth, subcylindrical with apical taper, phialidic, 7–15 × 2.5–3 µm. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, apex subobtuse, base truncate, 1.5–2 µm diam, 5–6(–7.5) × 2(–2.5) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA and PDA surface pale olivaceous grey, reverse olivaceous grey. On OA surface buff to cinnamon.

Typus. South Africa, Western Cape Province, Knysna, Knysna area, on leaves of *Podocarpus falcatus* (*Podocarpaceae*), 23 Nov. 2018, *F. Roets*, HPC 2725 (holotype CBS H-24182, culture ex-type CPC 37065 = CBS 146076, ITS, LSU, *rpb2* and *tef1* sequences GenBank MN562155.1, MN567662.1, MN556816.1 and MN556836.1, MycoBank MB832916).

Notes — *Podocarpomyces* is a sister genus to *Alfodia* and *Amorocoelophoma* (*Amorosiaceae*) in the *Pleosporales* (Crous et al. 2019a). *Podocarpomyces knysnanus* (known as asexual morph) is related to *Neothyrostroma* (on leaves of *Encephalartos*, South Africa; see FP958), but the two genera are morphologically and phylogenetically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Angustimassarina alni* (strain MFLUCC 15-0184, GenBank KY548099.1; Identities = 345/363 (95 %), 2 gaps (0 %)), *Lophiostoma corticola* (strain Z26, GenBank MK907710.1; Identities = 387/410 (94 %), 2 gaps (0 %)), *Angustimassarina rosarum* (strain MFLUCC 15-0080, GenBank MG828869.1; Identities = 387/410 (94 %), 2 gaps (0 %)), *Atrocalyx asturiensis* (strain OF, GenBank MG912912.1; Identities = 675/792 (85 %), 34 gaps (4 %)), *Hermatomyces tucumanensis* (voucher PRM 946202, GenBank LS398290.1; Identities = 660/779 (85 %), 40 gaps (5 %)), and *Shrungabeeja longiappendiculata* (strain BCC 76464, GenBank KT376475.1; Identities = 666/810 (82 %), 62 gaps (7 %)). Closest hits using the **LSU** sequence are *Angustimassarina populi* (strain MFLUCC 17-1069, GenBank MF409166.1; Identities = 821/835 (98 %), 2 gaps (0 %)), *Angustimassarina premilcurensis* (strain MFLUCC 15-0074, GenBank KY496725.1; Identities = 821/835 (98 %), 2 gaps (0 %)), and *Angustimassarina lonicerae* (strain MFLUCC 15-0087, GenBank KY496724.1; Identities = 821/835 (98 %), 2 gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Alfoldia vorosii* (as *Dothideomycetes* sp. DGK-2019a, strain REF117, GenBank MK599321.1; Identities = 427/457 (93 %), no gaps), *Angustimassarina coryli* (strain MFLUCC 14-0981, GenBank MF167433.1; Identities = 421/451 (93 %), no gaps), and *Teichospora trabicola* (strain C134, GenBank KU601601.1; Identities = 425/457 (93 %), no gaps). No significant hits were obtained when the ***rpb2*** sequence was used in blastn and megablast searches.

Colour illustrations. *Podocarpus falcatus* tree in Knysna forest. Colony on oatmeal agar; conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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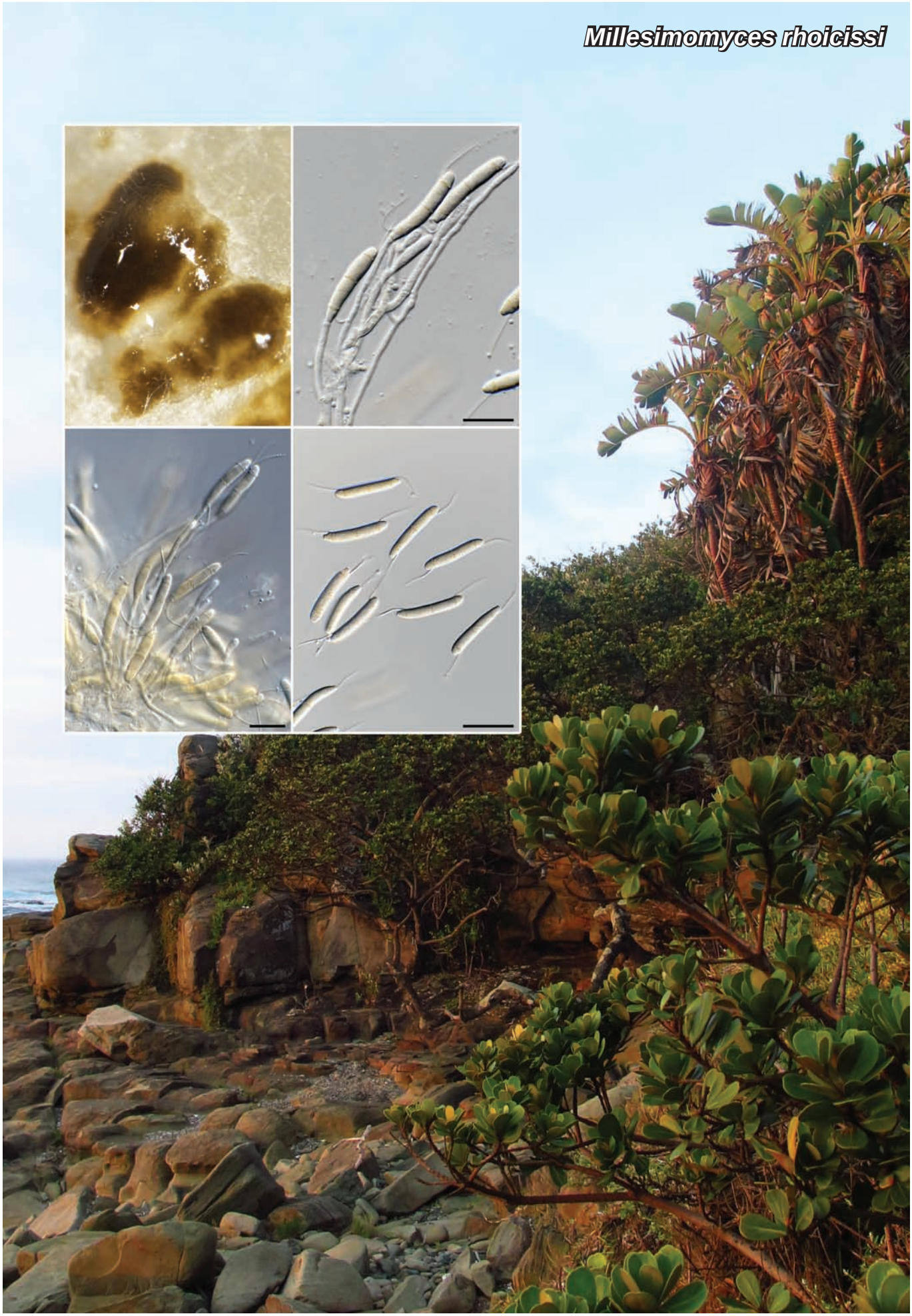
Millesimomyces rhoicissi

Fungal Planet 1000 – 18 December 2019

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

Etymology. Composed of *millesimus* (thousandth; for species No. 1000 described in Fungal Planet) and the suffix *-myces* (múkēs, Greek, fungus).

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

Conidiomata gregarious, black, stromatic, acervular, exuding a brown conidial mass. *Conidiophores* hyaline, smooth, septate, branched, flexuous or reduced to conidiogenous cells. *Conidiogenous cells* discrete, subcylindrical or lageniform, hyaline, smooth. *Conidia* subcylindrical, straight or slightly curved, pale brown, 3-septate, smooth, not constricted at septa, basal cell cylindrical, thin-walled, subhyaline; median two cells cylindrical, hyaline, thin-walled, unequal; apical cell subcylindrical with obtuse apex; appendages tubular, slender, flexuous; apical appendage single, unbranched, excentric; basal appendage single, unbranched, excentric.

Type species. *Millesimomyces rhoicissi* Crous & M.J. Wingf. MycoBank MB832917.

Millesimomyces rhoicissi Crous & M.J. Wingf., *sp. nov.*

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

Conidiomata gregarious, black, stromatic, acervular, exuding a brown conidial mass. *Conidiophores* hyaline, smooth, septate, branched, flexuous or reduced to conidiogenous cells. *Conidiogenous cells* discrete, subcylindrical or lageniform, hyaline, smooth, 5–30 × 2–2.5 µm. *Conidia* subcylindrical, straight or slightly curved, pale brown, 3-septate, smooth, not constricted at septa, (18–)22–25(–27) × (3.5–)4 µm, basal cell cylindrical, thin-walled, subhyaline, 3–4 µm long; median two cells cylindrical, hyaline, thin-walled, unequal, second cell from base 8–10 µm long, third cell from base 8–9 µm long, apical cell subcylindrical with obtuse apex, 2.5–4 µm long; appendages tubular, slender, flexuous; apical appendage single, unbranched, excentric, 10–16 µm long, inserted c. 1.5 µm from apex; basal appendage single, unbranched, excentric, 11–14 µm long, inserted 2–3 µm from basal septum.

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

Typus. South Africa, Eastern Cape Province, Haga Haga, on leaves *Rhoicissus digitata* (*Vitaceae*) with dieback, 12 Dec. 2016, *M.J. Wingfield*, HPC 2296 (holotype CBS H-23936, culture ex-type CPC 35297 = CBS 145536, ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MN562156.1, MN567663.1, MN556817.1, MN556827.1 and MN556846.1, MycoBank MB832918).

Notes — *Millesimomyces* resembles the genus *Discosia* in morphology, having stromatic acervuli, and long, hyaline, subcylindrical or lageniform phialides that give rise to subcylindrical, pale brown, 3-septate conidia with excentric apical and basal appendages (Liu et al. 2019a). However, based on phylogenetic inference, the fungus clusters apart from species of *Discosia*, and hence *Millesimomyces* is established to accommodate it.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Monochaetia monochaeta* (strain CBS 118.66, GenBank MH858742.1; Identities = 569/595 (96 %), 3 gaps (0 %)), *Seimatosporium pistaciae* (strain CBS 138865, GenBank NR_137942.1; Identities = 559/586 (95 %), 9 gaps (1 %)), and *Ciliochorella phanericola* (voucher MFLU 14-0776, GenBank NR_153928.1; Identities = 526/552 (95 %), 9 gaps (1 %)). Other more distant hits include *Discostroma fuscellum* (strain GSAA-0182, GenBank JF320818.1; Identities = 551/582 (95 %), 7 gaps (1 %)), *Discosia pseudoartocreas* (strain CBS 136438, GenBank NR_132068.1; Identities = 579/612 (95 %), 9 gaps (1 %)), and *Discosia artocreas* (strain CBS 241.66, GenBank MH858787.1; Identities = 559/592 (94 %), 8 gaps (1 %)). Closest hits using the **LSU** sequence are *Seiridium pseudocardinale* (as *Seiridium* sp. DW-2016a, strain MFLUCC 13-0525, GenBank KU848209.1; Identities = 843/847 (99 %), 2 gaps (0 %)), *Seiridium cardinale* (as *Seiridium unicorne*, strain CBS 908.85, GenBank DQ414532.1; Identities = 829/833 (99 %), 2 gaps (0 %)), and *Seiridium cupressi* (as *Seiridium unicorne*, strain CBS 320.51, GenBank MH868398.1; Identities = 853/858 (99 %), 3 gaps (0 %)). Other more distant hits include *Discosia querci* (strain MFLUCC 16-0642, GenBank MG815830.1; Identities = 841/858 (98 %), 3 gaps (0 %)), *Immersidiscosia eucalypti* (strain 17RA1, GenBank KY825092.1; Identities = 840/858 (98 %), 3 gaps (0 %)), and *Discosia fraxinea* (strain NTIT469, GenBank KF827439.1; Identities = 838/856 (98 %), 3 gaps (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Monochaetia monochaeta* (strain CBS 658.95, GenBank MH554977.1; Identities = 699/830 (84 %), no gaps), *Seiridium podocarpi* (strain CBS 137995, GenBank LT853148.1; Identities = 721/860 (84 %), no gaps), and *Monochaetia junipericola* (strain CBS 143391, GenBank MH108004.1; Identities = 674/805 (84 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Pestalotiopsis jinchanghensis* (strain LC8191, GenBank KY464155.1; Identities = 215/241 (89 %), 8 gaps (3 %)), *Pestalotiopsis colombiensis* (strain CBS 118553, GenBank KM199488.1; Identities = 215/241 (89 %), 8 gaps (3 %)), and *Pestalotiopsis terricola* (strain CBS 141.69, GenBank MH554438.1; Identities = 217/244 (89 %), 17 gaps (6 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Monochaetia ilexae* (strain CBS 101009, GenBank MH554612.1; Identities = 474/598 (79 %), 31 gaps (5 %)), *Nonappendiculata quercina* (strain CBS 270.82, GenBank MH554701.1; Identities = 331/405 (82 %), 27 gaps (7 %)), and *Monochaetia quercus* (strain CBS 144034, GenBank MH554844.1; Identities = 472/600 (79 %), 34 gaps (5 %)).

Colour illustrations. Collection site at Haga Haga. Conidiomata on oatmeal agar; conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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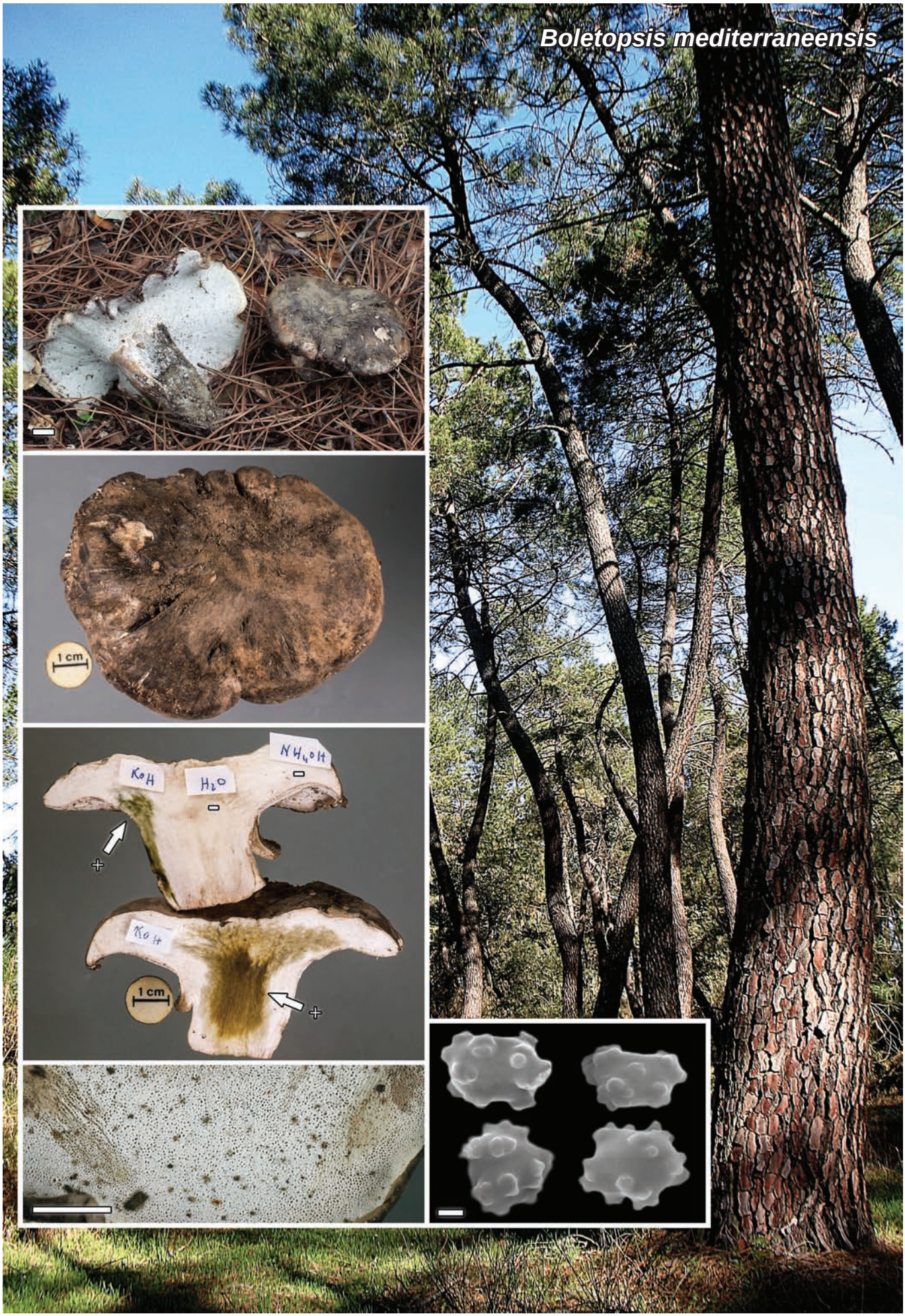
Boletopsis mediterraneensis
1 cm
KOH
H2O
NH4OH
KOH
1 cm

Fungal Planet 1001 – 18 December 2019

Boletopsis mediterraneensis G. Moreno, Carlavilla, Bellanger, Olariaga, P.-A. Moreau, Bidaud, Loizides & Manjón, *sp. nov.*

Etymology. Referring to its Mediterranean distribution.

Classification — *Bankeraceae, Thelephorales, Agaricomycetes*.

Basidiocarps annual, with a central or eccentric stipe. *Cap* 4–12 (–15) cm broad, convex to plane-convex, later depressed at centre, colour variable, pale grey, brownish grey to ochraceous brown or dark brown when mature, surface dry, smooth, innately fibrillose, breaking up into small scales or cracked, especially at centre; *context* in cap very pale grey to grey, very pale red when cut, with green tones when desiccated or with 5 % KOH (no reaction with H_2O and 5 % NaOH). Margin straight, irregular, concolorous or slightly paler, not hygrophanous, smooth, often incised due to its thinness. *Pores* small, 1–3 per mm, round to angular, whitish turning slightly very pale grey upon bruising, grey brown when desiccated. *Tubes* 2–5 mm thick, decurrent, tightly adhered to the context. *Stem* 2.5–7 × 1–3 cm, cylindrical, sometimes curved, central or eccentric, solid, tapering downwards, of the same colour as the cap or paler, greyish white at the apex, surface smooth to slightly squamulose; *context* in stem very pale greyish white. *Odour* not distinctive or sometimes farinaceous, *taste* bitter in young specimens. *Context* with green tones when desiccated. *Spores* 4.5–6.7 × 3.3–5.2 µm, av. 5.6–4.3 µm (holotype), Q_{av}: 1.3 (n = 20), globose to subglobose, nodulose, without iodine reactions, colourless to very pale yellow-brown; ornamentation formed by broad obtuse nodules appearing furcate. *Basidia* 4-spored, (14–)18–24 × 5–7 µm, sterigmata up to 4 µm long, clavate, hyaline. *Pleurocystidia* and *cheilocystidia* absent. Context formed by hyphae 1–2 µm broad. *Pileipellis* a cutis with cylindrical hyphae, septate, thin-walled to slightly thick-walled (2.5–4 µm diam), swollen at septa (8–10(–16) µm diam), clamped, hyaline or with a faint olivaceous hue in H_2O and 5 % KOH. Hyphal system monomitic, hyphae hyaline, thin-walled, clamped.

Habitat & Distribution — Growing solitary to gregarious on basic and acidic soils, mainly under *Pinus* spp.

Typus. Spain, Madrid, San Martín de Valdeiglesias, Las Cruces, 30TUK8365, 810 m, under *Pinus pinaster, P. pinea, Quercus ilex* subsp. *ballota* and *Cistus ladanifer,* on acid soil, 30 Nov. 2013, *J.C. Campos & M. Hinojosa* (holotype AH 44080, ITS and LSU sequences GenBank MN536723 and MN535629, MycoBank MB832765).

Notes — *Boletopsis mediterraneensis* is characterised by its medium to large size, a cap generally not black but with grey or brown tones, with context becoming very pale red when cut, turning green with KOH and acquiring conspicuous green tones when dry. So far, *B. mediterraneensis* is only known from the Mediterranean area, mostly under *Pinus*, but also under *Cedrus*. Our ITS-LSU analyses recovered specimens of *B. mediterraneensis* in a well-supported clade (see Supplementary Fig. FP1001-2), weakly supported as sister to *B. nothofagi*, and distinct from other well-supported clades corresponding to *B. grisea*, *B. leucomelaena* and *B. watlingii*. The latter three species form a major supported clade. Although the *B. mediterraneensis* clade shows phylogenetic structure, attempts to find correlated morphological, ecological or macrochemical characters defining the three major subclades were unsuccessful. Thus, we treat *B. mediterraneensis* as a single species, rather than a clade including several cryptic species.

Boletopsis mediterraneensis has so far been mistaken for *B. grisea*, and most Mediterranean records of the latter may correspond in fact to *B. mediterraneensis*. Both species constitute two distinct and well-supported clades (see Supplementary Fig. FP1001-2). *Boletopsis grisea* is very similar to *B. mediterraneensis*, but the former differs by its context turning only faintly greenish in KOH in fresh specimens, and black brown upon drying (Niemelä & Saarenoksa 1989). According to our observations, the two species have different distributions. Whereas *B. grisea* is broadly distributed in the Eurosiberian area and is extremely rare in the Mediterranean area, *B. mediterraneensis* has a mostly Mediterranean distribution. *Boletopsis leucomelaena* is characterised by its greyish sepia to black-brown cap surface, turning sepia black in KOH, and by its association with *Picea* (Niemelä & Saarenoksa 1989). *Boletopsis nothofagi* has a cap turning blackish upon bruising, becoming black with KOH and is associated with *Nothofagus* in the Southern Hemisphere (Cooper & Leonard 2012). *Boletopsis watlingii* (= *B. perplexa*), described using European material, differs from *B. mediterraneensis* by its dark cap and slightly smaller basidiospores (4.5–4.8(–5) × 3.5–4.5 µm) (Watling & Milne 2006).

Colour illustrations. Spain, Madrid, San Martín de Valdeiglesias, *Pinus pinaster* forest at the type locality. *In situ* basidiomata; detail of cap surface; basidioma section in NaOH, KOH and H_2O; detail of the hymenophore; nodulose basidiospores under SEM (holotype AH 44080). Scale bars = 1 cm, except for spores in SEM (bar = 1 µm).

Supplementary material

FP1001-1 Additional specimens examined.

FP1001-2 The single best tree resulting from the Maximum Likelihood analysis of the ITS-LSU regions of *Boletopsis*. Maximum Likelihood bootstrap values (ML-BP) and Bayesian posterior probabilities (PP) are shown by branches, ordered as ML-BP/PP. Thickened branches received support at least in one analysis (ML-BP ≥ 70 % and/or PP ≥ 95 %). The holotype of *B. mediterraneensis* is marked in **bold**.

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Boletus candidissimus

Fungal Planet 1002 – 18 December 2019

Boletus candidissimus T.H.G. Pham, A.V. Alexandrova & O.V. Morozova, *sp. nov*.

Etymology. The epithet refers to the pure white colour of the basidiomata.

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

Basidiomata medium sized, boletoid. *Pileus* 18–35 mm diam, initially hemispherical, becoming convex with slightly appendiculate margin, projecting 1–2 mm beyond the pores, white (4A1, Kornerup & Wanscher 1978), cream (4A2–3) on drying, surface dry, velutinous, tomentose or felted. *Hymenophore* adnate, up to 4 mm thick, white, becoming cream, except for the edge of the tubes that remain white; pores almost not seen due to long cheilocystidia, round or angular under the cheilocystidia layer, up to 0.3 mm diam. *Stipe* 60–80 × 6–8 mm, almost cylindrical, broadened slowly towards the base, solid; longitudinally irregularly striate to irregularly reticulate in an upper part; dry, with transparent drops of exudate in the lower part; white (4A1). *Context* white, with darker hygrophanous spots in the upper part of stipe, unchanging. *Smell* weak, *taste* mild. *Spores* (12.5–)13.5–14(–15.5) × (3.5–)4–5(–5.5) µm, Q = (2.5–)3–3.5(–4), fusoid, subfusoid and inequilateral in side view with weak suprahilar depression, yellowish brown in KOH, smooth. *Basidia* 32–41 × 9.5–11 µm, 4-spored, narrowly clavate to clavate, clampless. *Cheilocystidia* cylindrical to narrowly clavate, sometimes septate, with terminal cells 37–85 × 6–8 µm, often thick-walled in the upper part, hyaline, forming sterile tube edge. *Pleurocystidia* 41–70 × 8–11 µm, lageniform or fusiform. *Hymenophoral trama* divergent, boletoid. *Pileipellis* a trichoderm, made up of palisade of chains of swollen elliptic cells, 27–56 × 12–15 µm, larger in the base of hairs, smaller in their apex, end cells conical or lageniform or tapering into the long neck, 23–52 × 7–13 µm, hyaline. *Stipitipellis* a caulohymenium of basidiolae-like clavate cells, 19–30 × 7–10 µm, with scattered basidia. *Caulocystidia* 55–110 × 11–15 µm, cylindrical to narrowly clavate, usually septate. *Clamp connections* absent.

Habit, Habitat & Distribution — Solitary or in groups on soil in evergreen tropical forests. Known from Vietnam.

Typus. Vietnam, Dak Lak Province, Krong Bong District, Chu Yang Sin National Park, Krong Kmar, 8 km west of Chu Yang Sin, 12.37958°N, 108.3523°E, 1680 m alt., mountain polydominant rainforest with the participation of *Fagaceae, Magnoliaceae, Theaceae*, *Podocarpaceae*, 1 Apr. 2013, *A.V. Alexandrova & T.H.G. Pham* (holotype LE315542, ITS, *tef1α* and LSU sequences GenBank MN511175, MN597966 and MN392934, MycoBank MB832741).

Additional material examined. Vietnam, Dak Lak Province, Krong Bong District, Chu Yang Sin National Park, Krong Kmar, 7 km northwest of Chu Yang Sin mountain, 12.414833°N, 108.378222°E, 1240 m alt., mountain polydominant rainforest with the participation of *Fagaceae, Magnoliaceae, Theaceae, Podocarpaceae*, 27 May 2014, *A.V. Alexandrova & T.H.G. Pham* (LE315543, ITS sequence GenBank MN511176).

Notes — *Boletus candidissimus* is characterised by the pure white basidiomata and pileipellis structure consisting of a palisade of hairs composed of chains of swollen elliptic cells, ending by conical or lageniform cells, sometimes tapering into the long neck. White forms lacking pigment appear in the different groups of boletoid fungi. Due to the appendiculate pileus margin and fusoid spores it resembles *Leccinum* species, from which it differs by the special pileipellis structure, not squamulose stipe and lack of any colour changes of context. Superficially *B. candidissimus* is close to *B. purus* (Corner 1972), although that species possesses large clavate cheilocystidia, and a pileipellis consisting of a palisade of clavate cells. The North American species *Tylopilus rhoadsiae* (Bessette et al. 1999) differs by the adnexed hymenophore, pileipellis and stipitipellis structure, bitter taste and an association with pine. In the phylogenetic tree, sequences of the species are nested within the /Boletoideae clade (data not shown) in the sense of Wu et al. (2016). They do not cluster with any known boletoid genera. In spite of this, we avoid introducing a new genus until more data becomes available.

Colour illustrations. Vietnam, Dak Lak Province, Krong Bong District, Chu Yang Sin National Park, type locality. Spores (from holotype and LE315543 (SEM)); pileus (from LE315543); longitudinal section and basidiomata *in situ* (from holotype); elements of pileipellis; trama and hymenium with pleurocystidia; pleurocystidium; cheilocystidia; caulocystidia (all from holotype). Scale bars = 10 µm (spores), 1 cm (basidiomata), 20 µm (microstructures).

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Bovista psammophila

Fungal Planet 1003 – 18 December 2019

Bovista psammophila A.C.M. Rodrigues, Baseia & M.P. Martín, *sp. nov.*

Etymology. In reference to the sandy habit.

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

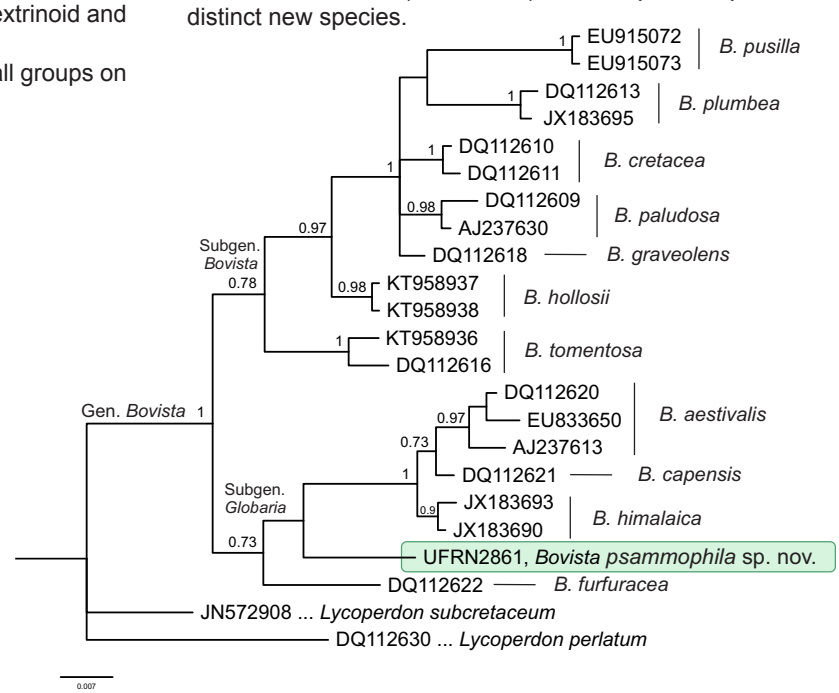
Basidiomata growing in small groups, subglobose, 13–19 mm wide × 10–18 mm high, white in young basidiomata. *Exoperidium* granulose to furfuraceous, evanescent, brown (5F8, Kornerup & Wanscher 1978) at maturity. *Endoperidium* papery, dark blond (5D4) at maturity, fragile, smooth, with irregular opening. *Gleba* cottony, brown (6E5) at maturity. *Subgleba* absent. *Rhizomorphs* thin, whitish (1A1), encrusted with sand. *Exoperidium* composed of two layers: the inner layer with pseudoparenchymatous cells, globose, subglobose, pyriform, and clavate, 17.1–30.2 × 13.2–9.8 µm, with regular walls ≤ 1 µm thin, hyaline in 5 % KOH, non-dextrinoid, mycosclereids with irregular shape, and the outer layer composed of spherocysts in chains, 14.1–24.7 × 11.7–15.2(–19.5) µm, with regular walls ≤ 1 µm thin, yellowish in 5 % KOH. *Endoperidium* with filamentous hyphae measuring 3.1–3.9 µm diam, with regular walls ≤ 1 µm, branched, aseptate, hyaline in 5 % KOH, and non-dextrinoid. *Capillitium* lycoperdon-type along the gleba, subelastic to elastic, hyphae 3–4.8 µm diam, with regular walls ≤ 1 µm, dichotomously branched, with numerous pits, yellowish in 5 % KOH, non-dextrinoid, septa lacking. *Paracapillitium* absent. *Basidiospores* globose, verrucose, 3.6–4.4 × 3.6–4.3 µm [Q_m = 1.03; *x* = 4.0 ± 0.2 × 4.1 ± 0.2; n = 30], with short pedicels, 0.7–1.2 µm, hyaline in 5 % KOH, non-dextrinoid and acyanophilic.

Habit & Habitat — Basidiomata growing in small groups on sandy soil.

Typus. Brazil, Rio Grande do Norte, Natal, Parque Estadual Dunas do Natal, Trilha da Peroba, soil, 7 Apr. 2016, *A.C.M. Rodrigues, N.M. Assis & I.G. Baseia* (holotype UFRN-Fungos 2861, ITS and LSU sequences GenBank MN243154 and MN243155, MycoBank MB832116).

Additional material examined. Brazil, Rio Grande do Norte, Parque Estadual Dunas do Natal, soil, 5 July 2008, *E.P. Fazolino* (UFRN-Fungos 776).

Notes — Based on morphological and molecular characters, *Bovista psammophila* belongs to the subgenus *Globaria,* in the genus *Bovista* (Kreisel 1967), and is recognised by its granulose exoperidium, capillitium lycoperdon-type along the gleba, with numerous pores, presence of mycosclereids in the inner layer of the exostratum, and verrucose basidiospores. *Bovista psammophila* is closely related to *B. aestivalis*, *B. furfuracea*, and *B. himalaica*. However, *B. aestivalis* exhibits a compact subgleba, an intermediary-type capillitium in the centre of the gleba with numerous pores, and globose to ovoid basidiospores (Calonge & Demoulin 1975, Demoulin 1979), characters not found in *B. psammophila. Bovista furfuracea* is morphologically similar to *B. psammophila*, but *B. furfuracea* has a lycoperdon-type capillitium, with fragile hyphae and numerous septa, smooth to verruculose basidiospores, and a robust rhizomorph (Moyersoen & Demoulin 1996). *Bovista himalaica* exhibits globose to pyriform basidiomata, rudimentary subgleba, and intermediary-type capillitium along the gleba with no pits (Yousaf et al. 2013), which differs from *B. psammophila.* Morphological and molecular data (ITS nrDNA) show *B. psammophila* as a distinct new species.



Colour illustrations. Brazil, Rio Grande do Norte, Natal, Parque Estadual Dunas do Natal, where the specimens were collected. From bottom to top: immature and expanded basidiomata *in situ* (UFRN-Fungos 2861); lycoperdon-type capillitium (UFRN-Fungos 2861); capillitium under SEM (UFRN-Fungos 2861); basidiospores under SEM (UFRN-Fungos 2861); Scale bars = 10 mm (basidiomata), 50 µm (capillitium), 1 µm (capillitium SEM), 2 µm (basidiospores SEM).

ITS nrDNA phylogenetic tree obtained with MrBayes v. 3.2.7a (Ronquist et al. 2012) under GTR+G+I model for 5 M generations. The new species is marked with a rectangle. The posterior probabilities greater than 0.70 are indicated on the branches. Two *Lycoperdon* species were included as outgroup. FigTree v. 1.42 and CorelDRAW v. 20.0.0.633 software were used to edit the final tree.

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Calycina cortegadensis

Fungal Planet 1004 – 18 December 2019

Calycina cortegadensis De la Peña-Lastra, P. Alvarado & Requejo, *sp. nov*.

Etymology. The epithet refers to the place where it was found (Illa de Cortegada, Parque Nacional Marítimo-Terrestre de las Islas Atlánticas, Galicia, Spain).

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

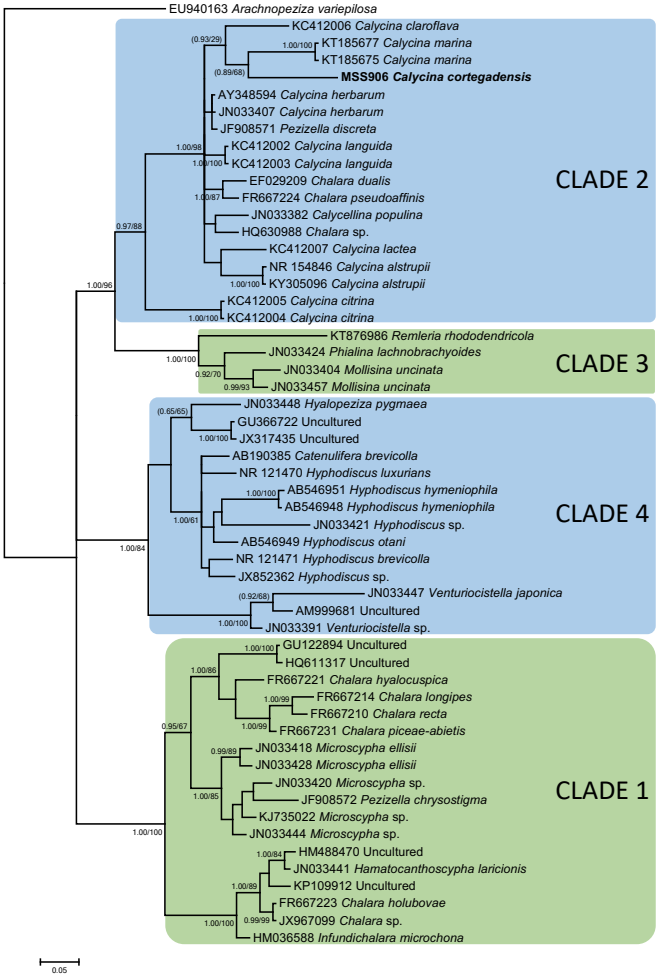
Apothecia solitary to gregarious (–5), with a short but stout stipe, disc flat to slightly concave, finely pruinose, 0.1–0.4 cm diam when dry, 0.2–0.5 cm upon rehydration; translucent brown to pale yellowish brown when fresh, beige brown to bluish brown when dry; margin elevated, occasionally slightly incurved due to hairs, pruinose, white when dry; receptacle concolorous with the disc or slightly paler, furfuraceous, pruinose when dry. Flesh concolorous with the disc too, or slightly paler. Not hygrophanous. *Asci* containing 8 uniseriate to biseriate spores, (40–)42–48(–53) × 3.5–4.5(–5) µm, cylindrical to subcylindrical, with a simple septum at the base and a conical or obtuse apex, with a small apical ring structure of the *Calycina*-type, slightly bluish to brownish red in Lugol´s solution (IKI: 1 % I_2; 3 % KI). *Ascospores* ellipsoid with obtuse apices, hyaline, smooth, with one drop at each end (about 0.5 µm diam), aseptate, about 4–6.5(–7.5) × 2–2.8; 5.2 ± 0.6 × 2.3 ± 0.3, Q_n = 2.5 (n = 36) µm after death. *Paraphyses* filiform, unbranched, 1.75–2(–3.7) µm diam, not exceeding the length of asci, with a rounded apex and abundant small vacuoles, sometimes presenting several septa at the base, *Ectal excipulum* composed of parallel, slightly interwoven hyphae of (4.5–)5.5–7(–10) µm diam, brown coloured with bluish tinges. The terminal cells of the calycle edge are hyphoid, with rounded apices of up to 9 µm wide. *Medullary excipulum* arranged as a *textura porrecta*, with disordered, interwoven gelatinized elements.

Distribution — Currently known only from the type location in north-western Spain.

Phylogeny — The analysis of ITS rDNA suggests that the specimen found in Cortegada represent a distinct lineage of *Calycina* (clade 2 in Han et al. 2014). No significant phylogenetic relationships with other species of this genus could be inferred, but sub-significant values (PP 0.89, BP 68) suggest a putative relation with *C. marina*.

Typus. Spain, Galicia, Pontevedra, Parque Nacional de las Islas Atlánticas de Galicia, Illa de Cortegada, N42°36'59.65" W8°46'59.22", 9.4 m asl, several apothecia found together on a living twig of *Castanea sativa*, 22 Dec. 2017, *S. De la Peña-Lastra* (holotype MSS906, ITS and LSU sequences GenBank MN017444 and MN017503, MycoBank MB831334).

Notes — *Calycina cortegadensis* is characterised by its apothecia with an apical disc furfuraceous-pruinose but lacking external hairs, its yellowish beige to bluish brown tones when dried, and its spores measuring 4–6.5(–7.5) × 2–2.8 µm. The recently proposed lichenicolous species *C. alstrupii* has similar spore dimensions, (5–)5.8(–7) × (1.5–)2.03(–2.5) µm, but those of *C. cortegadensis* can be as short as 4 µm. In addition, the apical ring of asci in *C. corticatensis* becomes slightly blue to reddish brown in Lugol, and young ascomata of *C. alstrupii* are yellowish cream to pale orange (Suija & Motiejūnaitė 2017). Other species similar to *C. alstrupii* such as *C. venceslai* and *C. langida* can be found in the same locality, but they have different spore dimensions and lack the beige-brown to bluish brown tones when dry (Suija & Motiejūnaitė 2017). The putative phylogenetic relationship with *C. marina* is not supported by any shared ecological or morphological trait, since *C. marina* fruits over seaweed, develops pulvinate ascocarps, has spores 8–13 × 3.3–4(–4.5), and claviform to capitate multiseptate paraphyses (Baral & Rämä 2015).



50 % majority rule ITS rDNA consensus phylogram of genus *Calycina* and related clades in the family *Hyaloscyphaceae* (Han et al. 2014) obtained in MrBayes from 4 725 sampled trees. Nodes were annotated if supported by ≥ 0.95 Bayesian PP (left) or ≥ 70 % ML BP (right). Non-significant support values are exceptionally represented inside parentheses.

Colour illustrations. Location where *C. cortegadensis* was collected on Cortegada Island. Ascomata in different developmental stages; asci and paraphyses, ascospores, terminal cells of the calycle edge, medullary excipulum; apothecia section. Scale bar = 10 µm.

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Chromosera ambigua

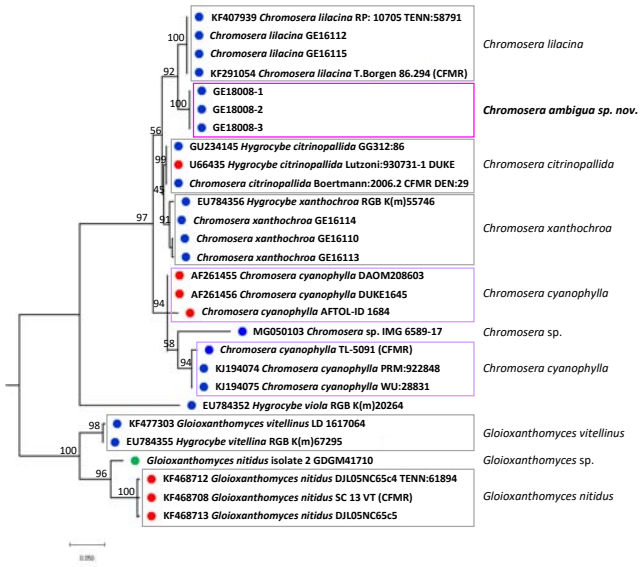
Fungal Planet 1005 – 18 December 2019

Chromosera ambigua Tanchaud, Jargeat & Eyssart., *sp. nov.*

Etymology. The epithet reflects the difficulties encountered in separating this species from morphologically close *Chromosera* – from Latin *ambigua* (doubtful, uncertain).

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

Basidiomata small-sized, omphalioid. *Pileus* 5–20(–30) mm diam, initially convex to plano-convex with a central depression or soon umbilicate, translucently striate up to the centre, hygrophanous, at first distinctly viscid, entirely whitish, yellow, lilac or with a combination of these colours. *Lamellae* moderately distant, decurrent, concolorous with the cap, sometimes yellowish with a whitish cap. *Stipe* 10–40 × 1–3 mm, cylindrical, viscid when young, concolorous with the cap or more or less lilac especially at the top. *Context* concolorous with the surface or paler, without distinctive *smell* or *taste*. *Spores* (7.2–)7.4–9.3(–11) × (4.3–)4.5–5.5(–5.8) µm, Q = (1.4–)1.5–1.9(–2.1), ellipsoid or amygdaliform, sometimes with concave side or constricted in apical part. *Basidia* 30–40 × 8–9 µm, predominantly 4-spored, narrowly clavate, clamped. *Cystidia* absent. *Gill trama* interwoven, with cylindrical elements measuring 35–50 × 8–13 µm, with yellow extracellular granules on fresh material. *Pileipellis* a thin ixocutis of cylindrical hyphae, 2–5(–8) µm wide. *Clamp connections* present.



PhyML analysis (Guindon & Gascuel 2003) of a combined SSU, ITS, LSU and *RPB2* sequence dataset (3413 positions, including gaps), conducted with the Geneious® platform placed this species in *Chromosera*, closely allied to *C. lilacina, C. citrinopallida* and *C. xanthochroa*. *Chromosera cyanophylla* is more divergent and appears to be separated into two groups, one American and one European. The scale bar indicates the number of substitutions per site and the bootstrap support values (based on 500 replicates) are indicated above branches. Blue dots are for European specimens, red dots for American specimens and green dots for Asiatic specimens. The alignment and the tree were deposited in TreeBASE (study 24563).

Colour illustrations. France, La Grande-Vergne, part of the heathland where the holotype was collected. Basidiomata *in situ* (holotype); spores from holotype. Scale bars = 1 cm (basidiomata), 10 µm (spores).

Habit, Habitat & Distribution — In small groups on poor sandy and clay soil not far from ponds, in a heathland with lichens (*Cladonia* sp.), and surrounded by *Erica arborea*, *E. cinerea*, *Calluna vulgaris*, *Ulex europaeus* and *Pinus pinaster*. Other rare and interesting species found at the same locality included *Arrhenia chlorocyanea*, *Hydropus moserianus*, *Galerina nana*, *Psathyrella flexispora*, *Plectania rhytidia* and *Rommelaarsia flavovirens*.

Typus. France, Charente-Maritime, Saint-Gemme, La Grande-Vergne, 45.764873°N, -0.931785°E, alt. 10–20 m, 31 Jan. 2016, *P. Tanchaud* (holotype GE18008, ITS, SSU, LSU, *RPB2* sequences GenBank MK645573 to MK645575, MK645581 to MK645583, MK645587 to MK645589 and MK645593 to MK645595, MycoBank MB830214).

Notes — Because of its viscid pileus and stipe, decurrent lamellae with non-gelatinised edge but with interwoven trama and sometimes constricted and white spores, this new species fits the genus *Chromosera* subgenus *Oreocybe* (Boertmann 1990, Lodge et al. 2013) that already includes *C. xanthochroa*, *C. citrinopallida* and *C. lilacina*. According to Boertmann (1990, 2010), Candusso (1997) and Borgen & Arnolds (2004), *C. citrinopallida* and *C. lilacina* have an arctic and alpine distribution while *C. xanthochroa* can also be found in oceanic temperate areas. Because of its habitat, *C. ambigua* could therefore be compared with *C. xanthochroa*, but the latter has the narrowest spores of the subgenus, measuring on average less than 4.5 µm diam, while the average width of the spores of our new species easily reaches 5 µm diam.

On the other hand, considering the three species with spores on average larger than 4.5 µm, *C. citrinopallida* is chrome-yellow and pales to white as it ages, and therefore never presents lilac tones, while *C. lilacina* has a brownish orange to lilac cap and a lilac stem (Consiglio 1997, Hausknecht et al. 2003, Consiglio & Contu 2007, Boertmann 2010). But as already pointed by Boertmann (1990) and Consiglio & Contu (2007), discoloured specimens of the last two species can only be distinguished by their ecological preferences, *C. lilacina* being more hygrophilous than *C. citrinopallida*. Without considering the different ecological preferences of the species, yellow and lilac specimens of *C. ambigua* can therefore be respectively confused with *C. citrinopallida* and *C. lilacina*, from which they differ essentially by their always clearly striate cap vs 'sometimes short translucently striate from margin' or '± translucently striate' (Boertmann 2010, see also Borgen & Arnolds 2004). *Chromosera viola*, which belongs to the subgenus *Subomphalia*, is readily distinguished by its completely dry pileus and stipe and broad, subglobose and non-constricted spores (Boertmann 2010, Lodge et al. 2013, Sánchez & Gibert 2015).

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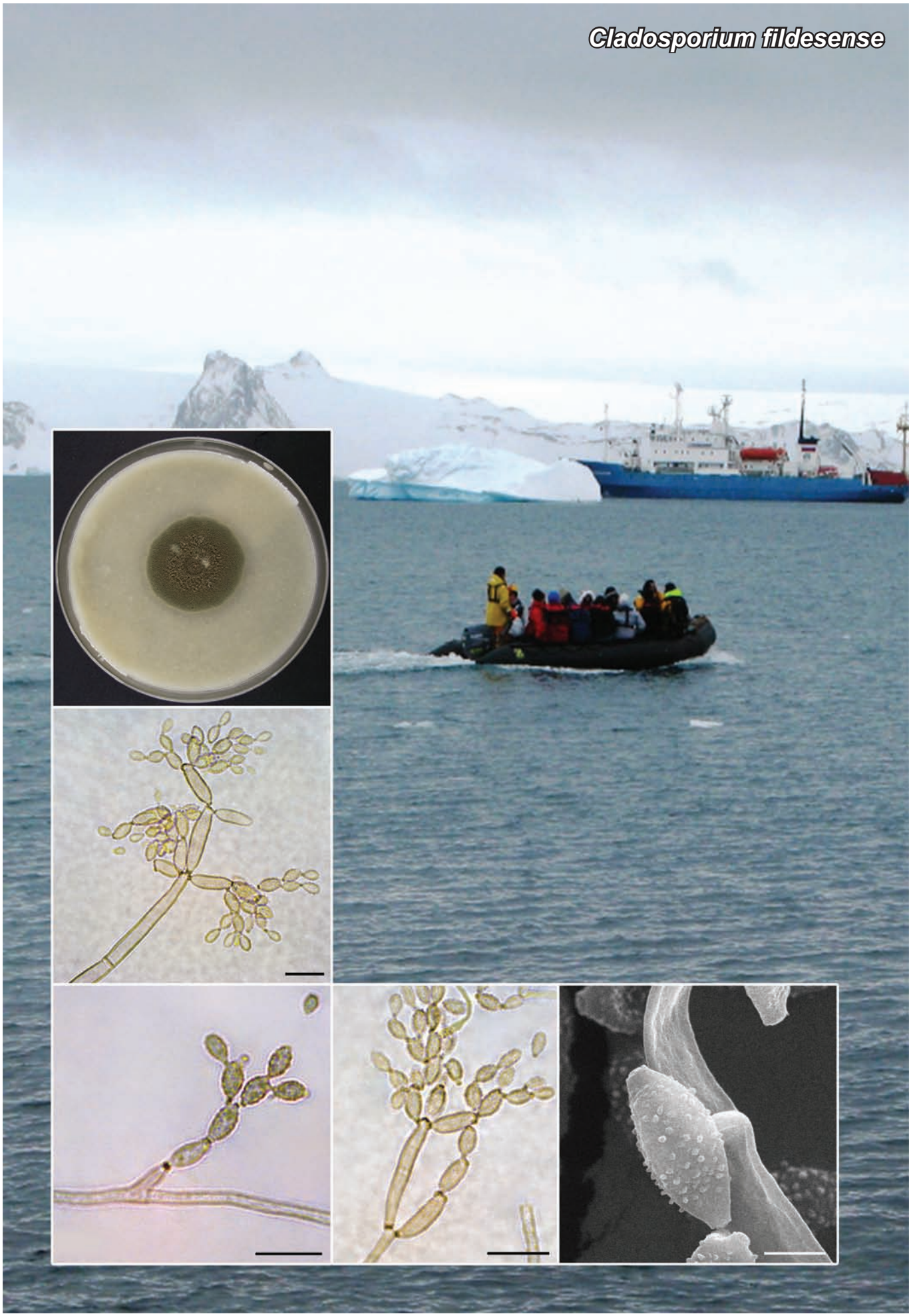
Cladosporium fildesense

Fungal Planet 1006 – 18 December 2019

Cladosporium fildesense C. Gil-Durán, Vaca & R. Chávez, *sp. nov.*

Etymology. Name refers to Fildes Bay Area, King George Island, Antarctica, where the fungus was isolated.

Classification — *Cladosporiaceae*, *Capnodiales*, *Dothideomycetes.*

Conidiophores dimorphic, cylindrical or subcylindrical, solitary or in small groups, septate, erect, flexuous or straight, arising from the terminal or generally lateral hyphae, pale brown or pale olivaceous brown. Micronematous conidiophores much shorter, small and lateral, occasionally geniculate, subcylindrical to cylindrical-oblong, 6.3–8.1 × 2.3–3 µm, proliferating sympodially, with 1–3 conidiogenous loci. Macronematous conidiophores 50–79.8 × 4.5–5.8 µm. *Ramoconidia* 26–39 × 3.2–4.8 µm; secondary ramoconidia ellipsoid, subcylindrical, 11.10–18.08 × 3.88–4.58 µm, 0–1-septate, surface ornamentation verruculose with one or three distal hilum. Numerous catenate conidia in branched chains, 4.7–6.2 × 2.9–4.1 µm, obovoid, limoniform or subglobose, surface with pustulate ornamentation.

Culture characteristics — (after 2 wk at 20 °C in the dark): On potato dextrose agar colonies reach 29–32 mm diam, without the presence of diffusible pigments and/or exudates. The morphology of the colony seen on the back is characterised by a velvety mycelium immersed in the agar, radially furrowed, olive-green, while on the obverse of the plate the colony has a flat growth, with a somewhat elevated colony centre, velvety olive-black colour, and dense sporulation. In the outer part of the colony, there is an edge with a white filiform margin. On oatmeal agar the colony reaches 32–35 mm diam without presence of diffusible pigments and/or exudates. The colony has round shape, with abundant velvety olive-green aerial mycelium immersed in the agar, profuse sporulation, and presents filiform edges. On malt extract agar, the colony reaches 25–27 mm diam, and does not produce diffusible pigments and/or exudates. The colony seen on the back has a rounded shape, dark green colour and opaque texture. On the obverse of the plate, the colony has a flat growth with abundant aerial velvety mycelium of olive-yellow colour immersed in the agar, and filiform edges. On synthetic nutrient-poor agar, colonies reach 23–25 mm diam without presence of diffusible pigments and/or exudates. On the reverse of the plate, a flat round colony of dark green colour is observed. On the obverse of the plate, the colony has olive-green aerial mycelium and profuse sporulation mainly in the centre of the colony.

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

Typus. Antarctica, South Shetland archipelago, King George Island, Fildes Bay, from an unidentified marine sponge, 13 Dec. 2009, *I. Vaca* (holotype F09-T12-1, culture ex-type ChFC-554, ITS, LSU, *actA* and *tef1* sequences GenBank JX845290, MN245038, MN233632 and MN233633, MycoBank MB832139).

Colour illustrations. Picture taken during sampling showing typical landscape of Fildes Bay, King George Island, Antarctica. *Cladosporium fildesense* growing on oatmeal agar; conidiophores and conidium on SNA after 14 d at 20 °C. Scale bars = 10 µm (conidiophores), 2 µm (conidium).

Notes — Based on the combined analysis of ITS, *actA* and *tef1* markers, *Cladosporium fildesense* belongs to the *C. herbarum* complex (Bensch et al. 2015) and is phylogenetically related to *C. soldanellae*, *C. ossifragi* and *C. spinulosum*. *Cladosporium spinulosum* differs from our new species by the digitate ornamentation of conidia and the absence of secondary ramoconidia (Zalar et al. 2007). Regarding *C. soldanellae,* this species has stromatic cells and occasionally forms ramoconidia (Bensch et al. 2012) while *C. fildesense* does not show stromatic cells and ramoconidia were always observed. Finally, *C. ossifragi* differs from *C. fildesense* by having shorter conidiogenous cells (5–31 µm long), the muricate conidial ornamentation, and by lacking primary ramoconidia (Schubert et al. 2007).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence are *Cladosporium ramotenellum* (GenBank MF473250.1; Identities 549/549 (100 %), no gaps), *Cladosporium cladosporioides* SLBB (GenBank JN565298.1; Identities 549/549 (100 %), no gaps), and *Cladosporium cucumerinum* (GenBank DQ681347.1; Identities 549/551 (99 %), 2 gaps (0 %)). The closest hits using the **LSU** sequence are *Cladosporium phlei* CBS 358.69 (GenBank MH877726.1; Identities 608/608 (100 %), no gaps), *Cladosporium herbarum* CBS 128892 69 (GenBank MH876581.1; Identities 608/608 (100 %), no gaps), and *Cladosporium cladosporioides* CBS 127051 (GenBank MH875838.1; Identities 608/608 (100 %), no gaps). The closest hits using the ***actA*** sequences were *Cladosporium spinulosum* CBS 102044 (GenBank EF679541.1; Identities 213/231 (92 %), 1 gap (0 %)), *Cladosporium ossifragi* CBS 842.91 (GenBank EF679535.1; Identities 212/233 (91 %), 4 gaps (1 %)), and *Cladosporium soldanellae* CPC 13153 (GenBank JN907001.1 Identities 207/231 (90 %), 4 gaps (1 %)). The closest hits with ***tef1*** sequences were *Cladosporium ramotenellum* (GenBank LN834482.1; Identities 214/245 (87 %), 6 gaps (2 %)), *Cladosporium soldanellae* CPC 13153 (GenBank JN906994.1; Identities 207/236 (88 %), 5 gaps (2 %)), and *Cladosporium ossifragi* CBS 843.91 (GenBank EF679460.1; Identities 204/236 (88 %), 5 gaps (2 %)).

Supplementary material

FP1006 Maximum likelihood (ML) phylogeny of *C. fildesense* and related species within *C. herbarum* complex was inferred from the combined analysis of ITS, *actA* and *tef1* sequences (Bensch et al. 2015). Alignments and ML analyses were performed with MegaX (Kumar et al. 2018). Model used was HKY + G + I. Bootstrap support values (> 50 %) are shown at the nodes (bootstrap iterations = 1000). The tree was rooted using combined ITS and *actA* sequences from *Toxicocladosporium banksiae* CBS 128215 (type strain).

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Clavulina iris

Fungal Planet 1007 – 18 December 2019

Clavulina iris Loizides, Bellanger & P.-A. Moreau, *sp. nov.*

Etymology. In honour of the mythical Greek goddess *Iris* (Ἶρις), associated with the rainbow.

Classification — *Clavulinaceae*, *Cantharellales*, *Agaricomycetes*, *Agaricomycotina*.

Basidiomata coralloid, 2–7 cm high × 1–5 cm wide, comprised of a sterile base and multiple fertile branches. Base 1–2.5 cm high × 1–1.5 cm wide, white-pruinose. Branches amphigenous, up to 1 cm thick, polychotomous-bifurcate (V-shaped), sometimes partially or extensively fused, smooth to strongly rugose with age; surface pruinose, ranging in colour from cream-white to ochraceous-yellow, pink, mouse grey or dull lilac; apices blunt to acute, mostly unbranched but frequently with multiple cristate ends, pale and often with a green hue when young, progressively browning and finally blackening with age. Trama pliant-cartilaginous, concolorous or paler than the branches. *Odour* unpleasant, somewhat of chlorine. Spore deposit cream-white. *Basidiospores* (8–)9.2–10.4(–11.3) × 6.5–8.5(–9.5) µm (Me = 9.2–7.3; Q = 1.07–1.45; Qm = 1.26), subspherical to ovoid or lacrymoid, sometimes broadly ellipsoid to cylindrical, smooth, thick-walled (0.5–1 µm), eguttulate, inamyloid, subhyaline to translucent ochraceous-grey in KOH, with a short hilar appendage. *Basidia* mostly bisporic, less frequently (~10 %) monosporic and rarely also trisporic, 45–80 × 6–9(–11) µm, slenderly clavate to subcylindrical, flexuous, thick-walled, with coarse vacuolar content, mostly filled with yellowish necropigment after spore discharge; postpartal septa infrequent on the upper third; sterigmata incurved, acute to somewhat rounded at the apices, 4–6 mm long; clusters of cylindrical to somewhat deformed basidioles frequent at bases of basidia. *Cystidia* absent, but long, 7–9 µm wide hyphal ends (pseudocystidia) often protruding 15–40 µm above the hymenium, thickened and incrusted at the apex by mucus. Hyphal system monomitic, comprised of smooth, 5–9(–11) µm wide, cylindrical to somewhat inflated and thick-walled hyphae frequently branching. *Clamp connections* common.

Habit, Habitat & Distribution — Terrestrial, fruiting solitary or in small groups of loosely coalescing basidiomata between January and April, on calcareous substrates under *Quercus coccifera* subsp. *calliprinos*, *Pinus brutia* and *Cistus*.

Typus. Cyprus, Dora, on calcareous substrate under *Quercus coccifera* subsp. *calliprinos*, *Pinus brutia* and *Cistus* shrubs, 5 Mar. 2015, *M. Loizides* (holotype in Herbarium of the Faculty of Pharmacy of Lille: LIP 0401586; isotype in herb. pers. *M. Loizides* n° ML5135C1, ITS and LSU sequences GenBank MN028412 and MN028396, MycoBank MB832755).

Additional materials examined. Cyprus (var. *iris*), Souni, 2 Mar. 2015, *M. Loizides*, ML5132C/LIP 0001618 (paratype, GenBank MN028411); Dora, 5 Mar. 2015, *M. Loizides*, ML5135C2 (GenBank MN028413); Anogyra, 17 Feb. 2015, *M. Loizides*, ML51271-CC (GenBank MN028414); Kelefos, 3 Jan. 2019, *M. Loizides*, ML9113CLI (GenBank MN028415). – France (var. *occidentalis*), Bonifacio, îlot Fazzio, 21 Nov. 2005, *P.-A. Moreau*, PAM05112103 (as '*C. cristata* var. *curta*', GenBank MN028407); Mérindol, 27 Nov. 2011, *J.-M. Bellanger, D. Borgarino, G. Corriol, P.-A. Moreau & F. Richard*, PAM11122702 (GenBank MN028408); Pézilla-de-Conflent, Chenil Sauvage, under *Quercus ilex* on calcareous soil, 27 Nov. 2012, *F. Richard & P.-A. Moreau*, PAM12112740 (GenBank MN028409).

Colour illustrations. Collection area of ML9131C at Kelefos. From top to bottom: holotype coll. *in situ* LIP 0401586; basidiospores; hymenium with projecting pseudocystidia; basidium; coll. ML71322V5 *in situ*. Scale bars 10 mm (specimens *in situ*), 30 µm (hymenium), 10 µm (basidiospores and basidium).

Notes — *Clavulina iris* is a species of exceptional morphochromatic variability, often displaying a blend of ochraceous, cream, pink, green and lilac colours all in the same specimen, as well as a mixture of smooth and rugose branches with both blunt and cristate tips. It is common on the island of Cyprus, where it is found from late winter to early spring in a variety of calcareous habitats (300–700 m asl). Lilac tinges are present in very few European species of *Clavulina*, most notably *C. amethystina* (Donk 1933), a species originally described in genus *Clavaria* by Bulliard (1791). European collections identified as this taxon, however, display vibrant violet-lilac colours (Corner 1970), lacking the ochraceous, cream or green tinges seen in *C. iris*, and cluster in a different phylogenetic lineage (Olariaga et al. 2009; Supplementary Fig. FP1007-1). *Clavulina reae*, proposed by Olariaga & Salcedo (2012) for collections previously identified as '*C. cinerea* var. *gracilis*' (Rea 1918), is also characterised by lilac-grey tinges, but produces smaller, slender and sparsely branched fruit bodies nesting in a distant lineage (Olariaga et al. 2009; Supplementary Fig. FP1007-1). Among the many forms and variants of *C. cinerea* formerly described, '*Clavaria cinerea* f. *sublilascens*' (Bourdot & Galzin 1928), later invalidly renamed '*Clavulina crassa*' by Corner (1950), is morphologically close to *C. iris*. We refrain from adopting Bourdot & Galzin's epithet, because the very short original description could also apply to *C. reae*, among others, but also because the Arvernian authors did not prospect Mediterranean localities in their description, with their collections likely originating from temperate deciduous forests, where *C. iris* has yet to be documented.

Clavulina iris var. ***occidentalis*** Bellanger, P.-A. Moreau & Loizides, *var. nov.*

Differs from the type by more slender, smooth basidiomata and abundant pseudocystidia.

Typus. France, Pézilla-de-Conflent, Pathy-Danglade, 26 Nov. 2012, *P.-A. Moreau & F. Richard* (holotype in Herbarium of the Faculty of Pharmacy of Lille: LIP 0401619; isotype in herb. pers. *P.-A. Moreau* n° PAM12112617, ITS sequence GenBank MN028410, MycoBank MB832819).

Notes — The variability of *C. iris* is also geographical and, to some extent, phylogenetic. In the type collections from Cyprus specimens are usually stout, early rugose and with few pseudocystidia. Collections from France, on the other hand, all found under *Quercus ilex* in late autumn, are more slender, smooth and with abundant pseudocystidia (Supplementary Fig. FP1007-2). No significant differences in spore size could be found, but the geographical and subtle morphological patterns correlated to few but significant differences in ITS sequences (1 indel and 2 SNPs), which led us to propose West-European collections at the rank of variety.

Supplementary material

FP1007-1 ITS phylogeny of *Clavulina*. Alignment with Muscle 3.7, Maximum likelihood phylogenetic analysis with PhyML 3.0, tree building with TreeDyn 198.3, all performed online at phylogeny.fr (Dereeper et al. 2008). Lineage supports indicated on each branch are SH-aLRT values, significant when > 0.8.

FP1007-2 *Clavulina iris* var. *occidentalis*. Collection area at Pézilla-de-Conflent (France). From left to right: holotype coll. *in situ* LIP 0401619, and coll. PAM11112702. Scale bars = 10 mm.

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Colletotrichum roseum

Fungal Planet 1008 – 18 December 2019

Colletotrichum roseum M. Zapata, M.A. Palma, M.J. Aninat & Piont., *sp. nov.*

Etymology. The epithet refers to the rose-coloured aerial mycelia in culture.

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

Sexual morph not observed. *Asexual morph on synthetic nutrient poor agar* (microscopic preparations in 60 % lactic acid, with at least 50 measurements per structure). *Vegetative hyphae* 1–9.5 µm diam, hyaline, sometimes pale brown, smooth-walled, septate, branched. *Chlamydospores* not observed. *Conidiomata* acervular, consisting of conidiophores and setae formed directly on hyphae. *Setae* abundant, medium brown, smooth-walled, slightly curved or zig-zag-shaped, 0–2-septate, 35–90 µm long, base cylindrical, sometimes inflated, 3.5–6.5 µm diam at the widest part, tip rounded to acute. *Conidiophores* hyaline, smooth-walled, simple or septate and branched, up to 65 µm long. *Conidiogenous cells* hyaline, thick-walled, smooth, cylindrical, thinner towards the apex, (10–)15–28(–30) × (2–)2.5–3.5(–4), apex 0.5–1 µm diam, with periclinal thickening visible. *Conidia* hyaline, smooth-walled, aseptate, straight, cylindrical to fusiform, with one end round and one end slightly acute, cytoplasm appearing granular, (16–)18–21.5(–25) × (4–)5–5.5(–6) µm, mean ± SD = 19.5 ± 1.5 × 5.3 ± 0.3 µm, L/W ratio = 3.7. *Appressoria* single or in small groups of 2–3, medium brown to olive, smooth-walled, clavate, ovate or irregular outline, the edge entire or undulate, sometimes lobate, (6.5–)8–12.5(–16.5) × (4.5–)6–8.5(–9) µm, mean ± SD = 10.5 ± 1.8 × 6.9 ± 0.9 µm, L/W ratio = 1.6.

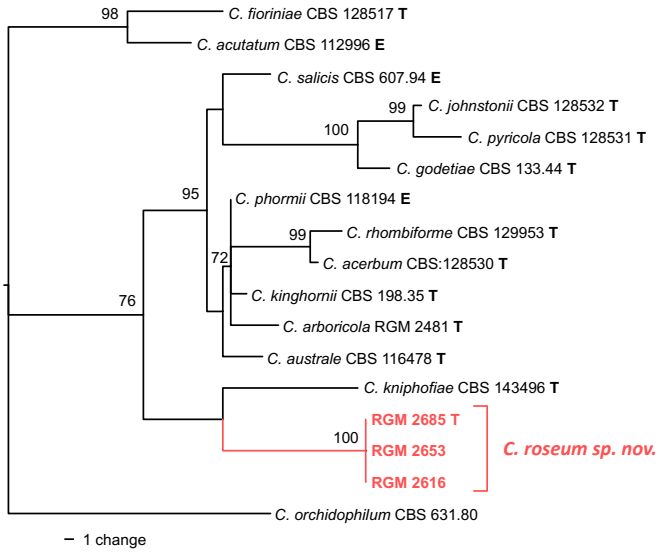
Cultural characteristics — (near UV light with a 12 h photoperiod, 20 °C after 10 d): Colonies on SNA flat with entire margin, surface hyaline to rose-violet coloured, reverse same colour, covered with appressed mycelium, reaching 30.1 ± 1.8 mm diam. Colonies on OA flat with entire margin, surface rose to grey with age, reverse reddish, covered with felty aerial mycelium, reaching 53.0 ± 1.7 mm. *Conidia in mass* salmon, more abundant in strain RGM 2616.

Typus. Chile, Concepción, Cerro Caracol, on leaves of *Lapageria rosea* (*Philesiaceae*), 4 Dec. 2018, *F. Franco* (holotype RGM 2685, culture ex-type CBS 145754 = SAG-99199-18; ITS, LSU, *GAPDH*, *ACT* and *TUB2* sequences GenBank MK903611, MK903608, MK903603, MK903604 and MK903607, MycoBank MB830891).

Additional materials examined. Chile, Alto BíoBío, on leaves of *L. rosea*, 26 Apr. 2018, *J. Silva,* RGM 2616 = CBS 144798 = SAG 47521-18, ITS, *GAPDH* and *TUB2* sequences GenBank MK903609, MK903601 and MK903605; Quillón, on leaves of *L. rosea*, 12 Sept. 2018, *G. Atanasovici*, RGM 2653 = CBS 145292 = SAG 71721-18, ITS, *GAPDH* and *TUB2* sequences GenBank MK903610, MK903602 and MK903306.

Notes — *Colletotrichum roseum* was isolated from conidiomata emerging from leaf spots on *Lapageria rosea* (Copihue). All strains examined produced infertile perithecia in culture that were immersed in the agar (after 3 mo), even though they were inoculated onto plates containing pieces of autoclaved leaves of Copihue. One strain of *C. roseum* was collected on the same host and locality to that of *Physalospora lapageriae*, an older fungus described by Spegazzini (1910) which was later reclassified as *Glomerella lapageriae* (Petrak & Sydow 1934). However, it proved impossible to compare our asexual fungus with *G. lapageriae*. Type material of *G. lapageriae* is deposited at the Museo La Plata (Argentina) and is not currently available for loan to attempt DNA isolation and comparison. Under these circumstances, and considering that *C. gloeosporioides, C. godetiae* and *C. pyricola* have also been diagnosed on Copihue by The National Plant Protection Organization in areas close to where *C. roseum* was found, there is no certainty that *G. lapageriae* is the same species, and therefore we propose to describe the new strains as a new species.

Colletotrichum roseum belongs to the *Colletotrichum acutatum* species complex (Damm et al. 2012), and is phylogenetically close but clearly distinct from *C. kniphofiae*. The new species differs from *C. kniphofiae* by its shorter conidia and characteristic rose-coloured culture. *Colletotrichum roseum* can be identified with all loci studied, except LSU, with *GAPDH* and *ACT* performing best as a diagnostic sequence. Based on a megablast search of NCBIs GenBank nucleotide database restricted to ex-type strains, the closest hit using the ***GAPDH*** sequences were *C. phormii* (GenBank JQ948777, Identities = 238/252 (94.4 %), 3 gaps), *C. acerbum* (GenBank JQ948790; Identities = 235/252 (93.3 %), 3 gaps) and *C. johnstonii* (GenBank JQ948775; Identities = 234/252 (92.9 %), 3 gaps). Closest hits using the ***ACT*** sequence were *C. phormii* (GenBank JQ949767, Identities = 239/247 (96.8 %), no gaps), *C. arboricola* (GenBank MH817956; Identities = 242/252 (96.0 %), no gaps) and *C. salicis* (GenBank JQ949781; Identities = 237/247 (96.0 %), no gaps).



One of the six equally most parsimonious trees (212 steps, CI = 0.670, HI = 0.330, RI = 0.741) obtained from the multi-locus phylogenetic analysis (ITS-*GAPDH*-*ACT*-*TUB2*) for selected *Colletotrichum* species. The analysis was conducted with PAUP v. 4.0b10 (Swofford 2003). DNA sequences were aligned using MAFFT v. 7.0 employing the E-INS-i strategy. Bootstrap support values ≥ 70 % are shown above nodes (1 000 replicates). The tree was rooted with *Colletotrichum orchidophilum*. T = ex-type, E = ex-epitype.

Colour illustrations. *Lapageria rosea* growing in its natural habitat in Chile (courtesy Mhylton Jiménez-Castillo, 2019). Symptomatic leaf; colony on oatmeal at 10 d; conidiophores with seta (in lactophenol cotton-blue); conidia; setae; appressoria. Scale bars = 10 µm.

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Cordyceps jakajanicola

Fungal Planet 1009 – 18 December 2019

Cordyceps jakajanicola Luangsa-ard, Tasan., Noisrip. & Hywel-Jones, *sp. nov.*

Etymology. Named after the host, *jakajan*, cicada in Thai and *cola* - Latin suffix meaning 'inhabitant of, residing on'.

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

Stromata pale yellow (blackish brown after drying), simple, fusiform, fleshy, erect, protruding from the ground with several stromata loosely connected emerging from between the head and the thorax of the cicada nymph, 32–45 mm long. Fertile part on the terminal end c. 1/3 of the stroma. Mycelia scarce, whitish, covering the host, slightly rhizoidal in the soil joining together to form a compact stipe upon emerging from the soil. *Perithecia* semi-immersed, ovoid, 400–650 × 300–400 µm. *Asci* cylindrical, 265–360 × 4–5 µm, ascus tip 2–3 µm. *Ascospores* whole, bola-shaped, 250–310 × 1 µm, terminal part fusiform 54–60 × 1 µm, central part filiform, < 1 µm diam. *Asexual morph Isaria. Synnemata* erect and simple with branching near the apex, often clavate, growing from a white to creamy mycelium which covers the host, powdery and floccose near the apex due to heavy conidiation. *Conidiophores* consisting of verticillate branches with whorls. *Phialides* 4–5.3(–6) × 2–3.5(–4) µm, consisting of a globose, oval or occasionally conical swollen basal portion tapering suddenly into a thin neck, 0.5 µm wide. *Conidia* ellipsoid or cylindrical, mostly symmetrical, rarely slightly curved, (4–)4.5–6(–7) × (1.5–)2–2.5(–3) µm.

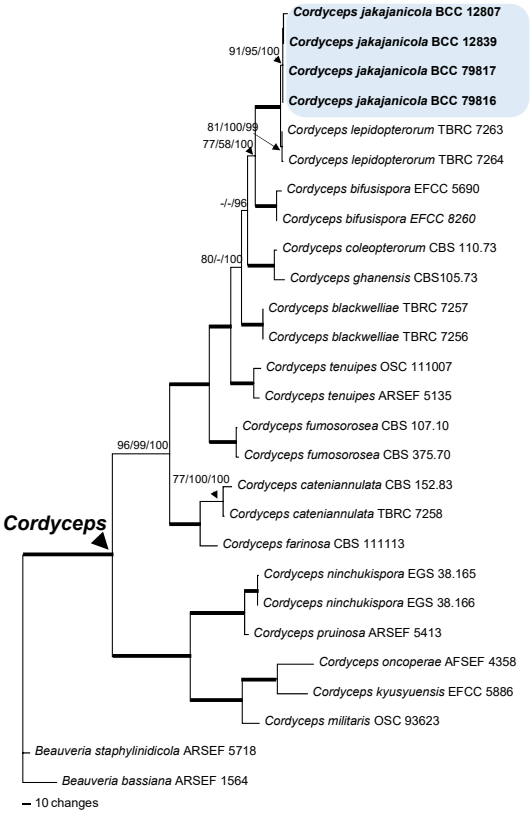
Culture characteristics — Discharged ascospores germinated within 24–36 h. Colonies had a white to cream funiculose appearance with a cream reverse. Cultures readily produced phialides and conidia after 2 wk on potato dextrose agar at room temperature showing a powdery appearance due to profuse conidiation. From the *sexual morph*: Colonies on PDA fast growing, attaining 15–20 mm diam within 14 d at 25 °C. Colonies floccose, at first white, turning into cream-brown and looking powdery with age. *Phialides* flask-shaped with long neck, (4–)5.5–8(–9) × (2–)2.5–3.5 µm. *Conidia* in long chains, cylindrical, (6–)7–9(–10) × 2–3 µm. *Chlamydospores* solitary, clavate, cylindrical, unicellular, (9–)10–15(–17) × (3–)4.5–6.5(–7) µm.

Typus. Thailand, Nakhon Ratchasima Prov., Khao Yai National Park, on cicada nymph, buried in soil, 9 July 2015, *K. Tasanathai, W. Noisripoom & D. Thanakitpipattana* (holotype BBH40246, culture ex-type BCC79816, SSU, LSU, *TEF, RPB1* and *RPB2* sequences GenBank MN296394, MN275696, MN338479, MN338484 and MN338489, MycoBank MB832492).

Additional materials examined. Thailand, Nakhon Ratchasima Prov., Khao Yai National Park, on cicada nymph, buried in soil, 9 July 2015, *K. Tasanathai, W. Noisripoom & D. Thanakitpipattana* (BBH 40247, BCC 79817, SSU, LSU, *TEF, RPB1* and *RPB2* sequences GenBank MN296395, MN275697, MN338480, MN338485 and MN338490); Kanchanaburi Prov., Thung Yai Naresuan Wildlife Sanctuary, on cicada nymph, buried in soil, 15 Sept. 2002, *R. Nasit, W. Thongsridam & B. Tongnuch* (BBH8628, BCC12807, SSU, LSU and *TEF* sequences GenBank MN296392, MN275694 and MN338477); ibid., (BBH8629, BCC12839, SSU, LSU and *TEF* sequences GenBank MN296393, MN275695 and MN338478).

Colour illustrations. Type locality – a trail in Khao Yai National Park. Fungus on cicada nymph (sexual morph); perithecia on stroma; ovoid perithecium; asci; bola ascospore; fungus on cicada nymph (asexual morph); phialides; conidia. Scale bars =15 mm (stromata), 300 µm (perithecia on stroma), 120 µm (asci), 20 µm (perithecium), 15 µm (ascospore), 5 µm (phialides, conidia).

Notes — *Cordyceps jakajanicola* is parasitic on cicadas that can be found buried in the soil. The macromorphologies of the natural samples of *C. jakajanicola* closely resemble *Cordyceps bifusispora* (Eriksson 1982) by producing fusiform, pale yellow ascomata on the terminal part of the stroma. It differs significantly in the host, sizes of the perithecia, asci and ascospores. In *C. jakajanicola*, perithecia and asci are longer and wider than those reported for *C. bifusispora* (300 × 150–170 µm; 200–220 × 3–4.5 µm; 145–220 × 4 µm). It shares similarities with *C. lepidopterorum* (Mongkolsamrit et al. 2018) in phialide and conidial dimensions. In *C. lepidopterorum* the phialides and conidia are larger (5–8 × 4–5 µm; 6–10 × 3–4 µm) compared to *C. jakajanicola* and differs in their respective hosts. The results of our molecular phylogenetic study strongly support and separate *C. jakajanicola* from other species. *Cordyceps jakajanicola* is therefore proposed as a new species belonging to *Cordyceps.*



Phylogenetic tree with *C. jakajanicola* was constructed from a combined dataset comprising SSU, LSU, *TEF*, *RPB1* and *RPB2* sequences. The phylogenetic tree was analysed using Maximum parsimony (MP), Maximum likelihood (ML) and Bayesian inference. The MP analysis was conducted on the combined dataset using PAUP v. 4.0b10 (Swofford 2003), adopting random addition sequences (100 replications), with gaps being treated as missing data. A bootstrap (BP) analysis was performed using the maximum parsimony criterion in 1 000 replications. The ML analysis was run with RAxML-VI-HPC2 v. 8.2.12 (Stamatakis 2014) under a GTR model, with 1 000 bootstrap replicates. Bayesian phylogenetic inference was calculated with MrBayes v. 3.2.6 (Ronquist & Huelsenbeck 2003), with 5 M generations and under the same model. Numbers at the significant nodes represent MP bootstrap support values/RAxML bootstrap support values/Bayesian posterior probabilities (BPP) times 100. Thickened lines in the tree represent 99–100 % BP values and 99–100 BPP.

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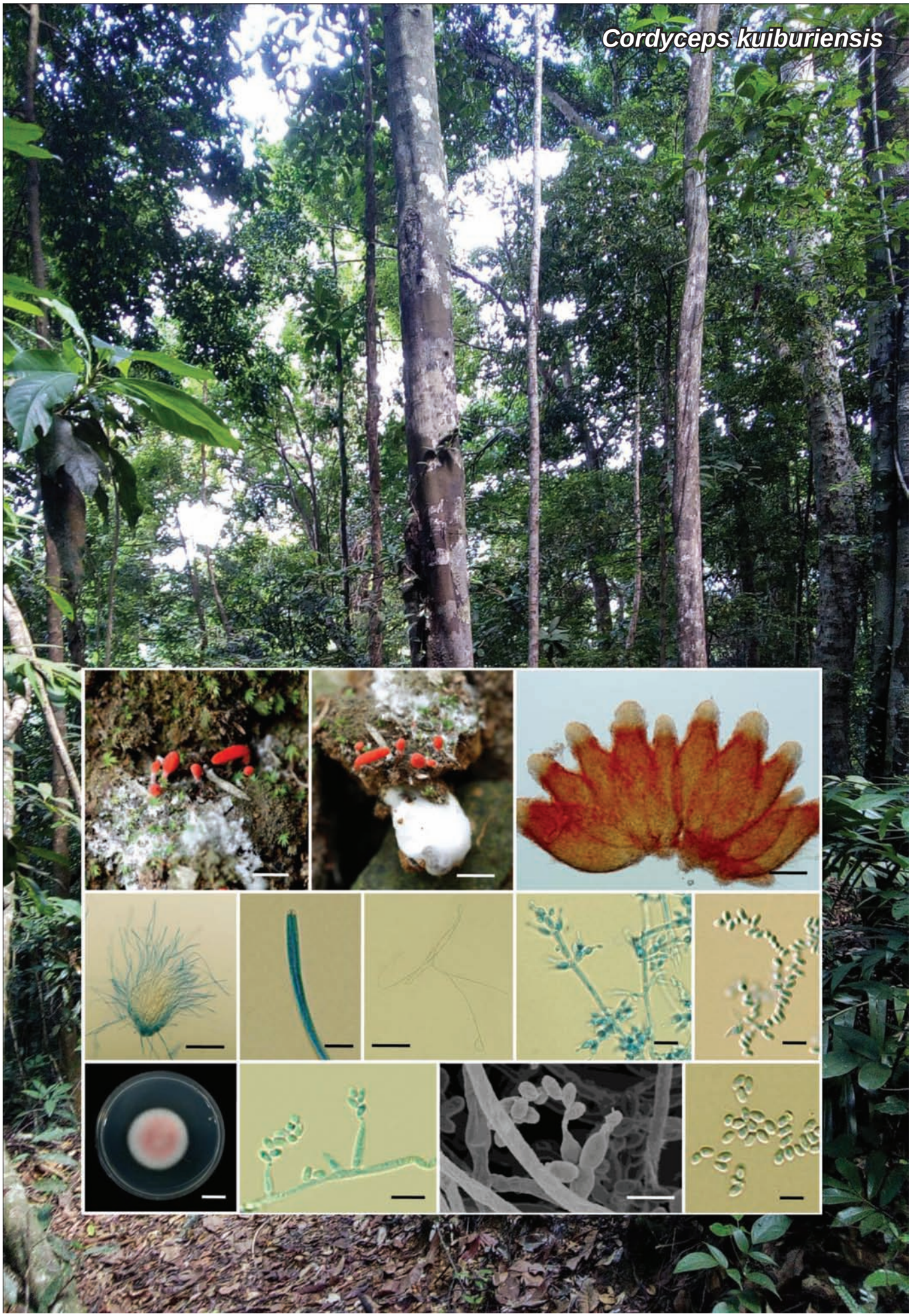

Cordyceps kuiburiensis

Fungal Planet 1010 – 18 December 2019

Cordyceps kuiburiensis Himaman, Mongkols., Noisrip. & Luangsa-ard, *sp. nov.*

Etymology. The name refers to the location where the species was collected – Kui Buri National Park, Thailand.

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

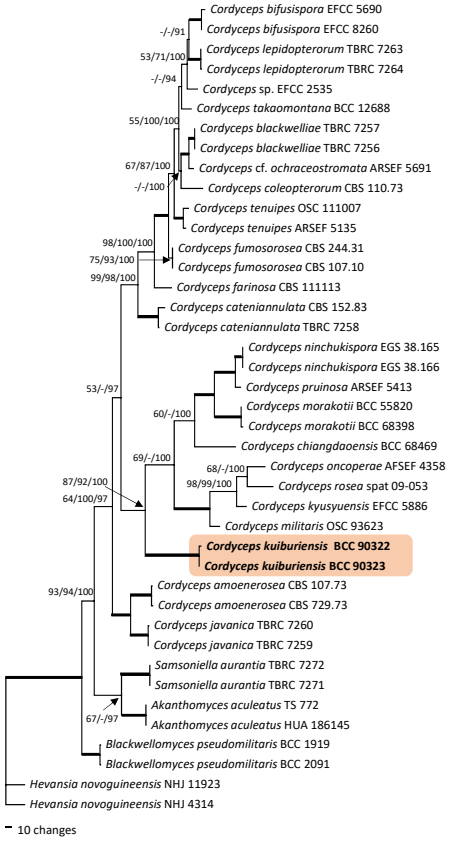
Stroma solitary, up to 8 mm long and 1–1.5 mm in width, cylindrical, pale red-orange. *Rhizoids* flexuous, arising from the body of spiders (*Araneidae*), c. 2–5 mm long, buried under the ground. Fertile part at apex. *Ascomata* clavate to subglobose, red-orange, 1.5–5 mm long, 1–2.5 mm in width. *Perithecia* pseudo-immersed, obpyriform, (350–)370–460(–550) × (120–)140–190(–240) µm. *Asci* cylindrical, up to 280 µm long, 3–5 µm in width. *Ascospores* hyaline, filiform with septations, up to 250 µm long, 1 µm in width. *Asexual morph*, evlachovaea-like, produced on base of the stroma and on the soil surface, powdery because of heavy sporulation, whitish, *synnemata* up to 1.5 mm long, *conidiophores* usually forming verticillate branches with phialides in whorls of 2–5. Entire phialides 5–10 × 2–3.5 µm, with swollen, ellipsoidal basal portion, tapering into a neck, 1–5 × 1 µm. *Conidia* hyaline, mostly ellipsoidal, fusiform, aseptate, 2–3.5 × 1–1.5 µm.

Culture characteristics — Colonies developed from germinating conidia. The conidia germinated within 24 h on PDA. Evlachovaea-like conidial morphs developing after c. 7 d. Colonies on PDA fast growing, c. 2.5 cm diam in 14 d at 25 °C. Colonies pale pink, becoming white when sporulating abundantly after 30 d, reverse deep pink. Conidial structures consisting of erect conidiophores borne or aerial hyphae, verticillate with phialides in whorls of two to four. Some phialides borne directly and singly on aerial hyphae. Phialides (3–)4–8(–10) × 1.5–2 µm, with swollen, ellipsoidal basal portion, necks present, 1–3 × 1 µm. Conidia hyaline, ellipsoidal, fusiform, aseptate, 3–4 × 1.5–2 µm.

Typus. Thailand, Prachuap Khiri Khan Prov., Kui Buri National Park, on spiders (*Araneidae*), buried in soil, 7 Jan. 2011, *W. Himaman* (holotype BBH45453, culture ex-type BCC90322, LSU, *TEF*, *RPB1* and ITS sequences GenBank MK968816, MK988030, MK988032 and MN099707, MycoBank MB831637).

Additional materials examined. Thailand, Prachuap Khiri Khan Prov., Kui Buri National Park, on spider (*Araneidae*), buried in soil, 7 Jan. 2011, *W. Himaman*, BBH45454 (BBC90323), LSU, *TEF*, *RPB1* and ITS sequences GenBank MK968817, MK988031, MK988033 and MN099708; ibid., BBH45452 (BCC90321).

Notes — Most of the species in *Cordyceps* have been reported as parasites of insects such as *Coleoptera*, *Hymenoptera*, *Lepidoptera*, and *Orthoptera*, producing brightly coloured, fleshy stromata. In this study, *Cordyceps kuiburiensis* is parasitic on spiders (*Araneidae*) that can be found buried in the soil. This species is only found in PraktaKhoo Waterfall, Kui Buri National Park, Prachuap Khiri Khan Province. The gross macromorphology of the natural samples of *C. kuiburiensis* closely resembles *C. ninchukispora* (Sung et al. 2007) that can also be found in soil or in leaf litter (Luangsa-ard et al. 2008) by producing clavate to subglobose, orange to orangish red ascomata on the terminal part of the stroma. It differs significantly in the sizes of the perithecia and asci. In *C. kuiburiensis*, perithecia and asci are longer and wider than those reported for *C. ninchukispora* (95–145 × 50–60 µm; 75–100 × 2.1–3.1 µm) by Su & Wang (1986). Additionally, the ascospores in *C. kuiburiensis* are filiform, while ascospores in *C. ninchukispora* are whole, bola-shaped, with expanded fusoid end parts, and its hosts are lepidopteran pupae, not spiders. The results of our molecular phylogenetic study strongly support and separate *C. kuiburiensis* from other species. *Cordyceps kuiburiensis* is therefore proposed as a new species belonging to *Cordyceps.*



Phylogenetic tree with *C. kuiburiensis* was constructed from the combined dataset comprising LSU, *TEF* and *RPB1* sequences. The phylogenetic tree was analysed using maximum parsimony (MP), maximum likelihood (ML) and bayesian inference. The MP analysis was conducted on the combined dataset using PAUP v. 4.0b10 (Swofford 2003), adopting random addition sequences (100 replications), with gaps being treated as missing data. A bootstrap (BP) analysis was performed using the maximum parsimony criterion in 1000 replications. ML analysis was run with RAxML-VI-HPC2 v. 8.2.10 (Stamatakis 2014) under a GTR model, with 1000 bootstrap replicates. Bayesian phylogenetic inference was calculated with MrBayes v. 3.2.6 (Ronquist & Huelsenbeck 2003), with 3 M generations and under the same model. Numbers at the significant nodes represent MP bootstrap support values/RAxML bootstrap support values/Bayesian posterior probabilities (BPP) times 100. Thickened lines in the tree represent 99–100 % bootstrap support values and 99–100 BPP.

Colour illustrations. Background photo of forest in Prachuap Khiri Khan Province. Fertile part with ascomata and asexual morph; perithecia; asci; ascus tip; ascospores; phialides; conidia; culture on PDA, evlachovaea-like asexual morph on PDA; conidia. Scale bars = 10 mm (plate culture), 5 mm (stromata), 120 µm (perithecia), 50 µm (asci), 10 µm (ascus), 50 µm (ascospores), 5 µm (phialides and conidia, evlachovaea-like morph on PDA with conidia), 3 µm (conidia).

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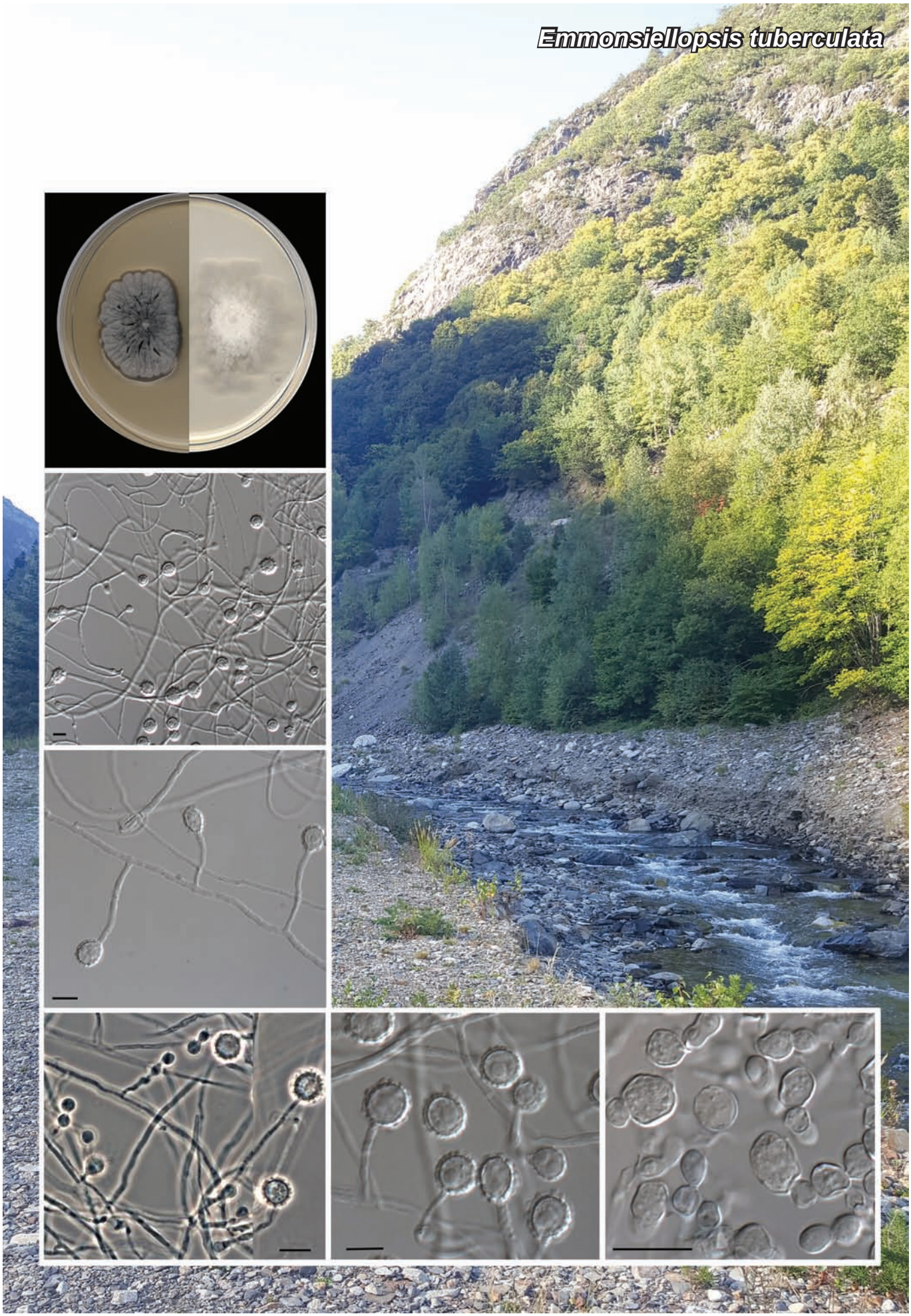

Emmonsiellopsis tuberculata

Fungal Planet 1011 – 18 December 2019

Emmonsiellopsis tuberculata Torres-Garcia, Guarro & Gené, *sp. nov.*

Etymology. Name refers to the conidial ornamentation of the species.

Classification — *Ajellomycetaceae*, *Onygenales*, *Eurotiomycetes.*

On potato carrot agar (PCA) at 25 °C. *Mycelium* consisting of branched, septate, hyaline, smooth- and thin-walled 1–3 µm diam hyphae. *Conidiophores* unbranched, erect, cylindrical, 12–60 × 1–2 µm, bearing terminal conidia. *Conidia* solitary, more rarely in chains of 2–3, globose to subglobose, hyaline, verrucose to tuberculate, thick-walled, 6–9 × 6–8 µm. On malt extract agar (MEA) at 37 °C giant cells of 9–22.5 × 9–14.5 µm, and yeast-like cells of 7.5–11.8 × 7.5–9 were observed after 3 wk. *Sexual morph* absent.

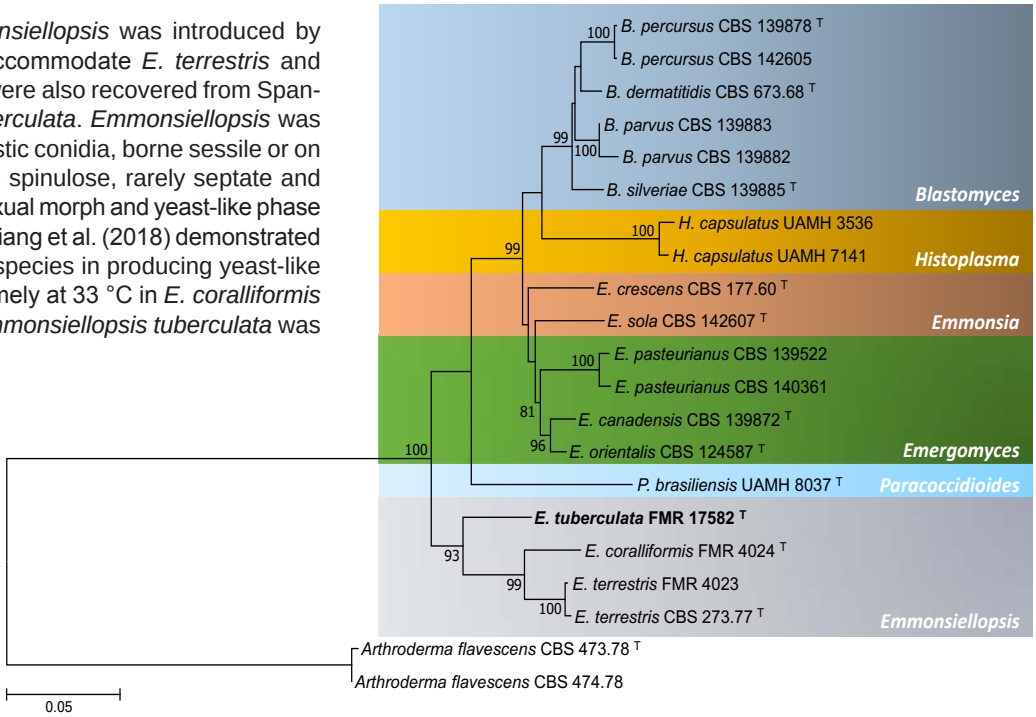
Culture characteristics at 25 °C in 3 wk — Colonies on MEA reaching 17.5–19 mm diam, flat, yellowish white (4A2) to yellowish orange (4B7) (Kornerup & Wanscher 1978), velvety, margin lobulated; reverse yellowish orange (4B7); sporulation sparse. On potato dextrose agar (PDA) reaching 35–38 mm, felted, greenish white (282A), irregularly sulcate, margin lobulated; reverse dark green (28F7); sporulation sparse. On PCA reaching 44–49 mm diam, cottony, white, margin irregular; reverse colourless; sporulation abundant.

Cardinal temperatures for growth — Minimum 15 °C, optimum 30 °C, maximum 37 °C.

Typus. Spain, Aragón, Huesca, Remáscaro stream, fluvial sediments, Sept. 2018, *D. Torres-Garcia* (holotype CBS H-24082, culture ex-type CBS 145944 = FMR 17582; LSU, ITS and *BenA* sequences GenBank LR598891, LR598892 and LR599029, MycoBank MB831790).

Notes — The genus *Emmonsiellopsis* was introduced by Marin-Felix et al. (2015) to accommodate *E. terrestris* and *E. coralliformis*, both of which were also recovered from Spanish fluvial sediments as *E. tuberculata*. *Emmonsiellopsis* was characterised by producing blastic conidia, borne sessile or on pedicels, smooth, verrucose to spinulose, rarely septate and intercalary, and by the lack of sexual morph and yeast-like phase (Marin-Felix et al. 2015). Later Jiang et al. (2018) demonstrated the ability of *Emmonsiellopsis* species in producing yeast-like cells after 4–5 wk on MEA, namely at 33 °C in *E. coralliformis* and at 37 °C in *E. terrestris*. *Emmonsiellopsis tuberculata* was able to produce the yeast morph at 37 °C as in *E. terrestris*, but with a faster conversion time (3 wk). Besides, our species differs from the other two by its verrucose to tuberculate conidia, the lack of sessile and intercalary conidia, and colonies with a dark green in reverse when growing on PDA at 25 °C. Colony reverse on PDA in *E. coralliformis* was pale yellow to olive brown and in *E. terrestris* yellowish white to pale yellow (Marin-Felix et al. 2015).

Our phylogenetic reconstruction with the barcodes LSU, ITS and *BenA* places *E. tuberculata* in a basal lineage distant from the clade formed by the other species of *Emmonsiellopsis.* A megablast search in the NCBIs GenBank nucleotide database using LSU sequences showed that *E. tuberculata* was 98.83 % (675/683) similar with *E. terrestris* (CBS 273.77; GenBank KT155190.1) and 97.85 % (684/699) with *E. coralliformis* (CBS 137500; GenBank NG_059238.1), whereas the similarity using ITS sequences was 90.80 % (533/587) with *E. terrestris* (CBS 273.77; GenBank NR_153965.1) and 92.98 % (503/541) with *E. coralliformis* (CBS 137500; GenBank NR_153996.1), respectively. *BenA* sequences showed a similarity of 80.17 % (380/474) between *E. tuberculata* and *E. terrestris* (CBS 273.77; GenBank KT155526.1) and of 79.33 % (330/416) between *E. tuberculata* and *E. coralliformis* (CBS 137500; GenBank KY710967.1).



Maximum likelihood tree obtained from the concatenated analysis of LSU, ITS and *BenA* sequences of *Emmonsiellopsis* and related genera of the family *Ajellomycetaceae*. Bootstrap support values above 70 % are indicated on the nodes. The alignment included 1443 bp and was performed using Tamura-Nei with Gamma distribution with Invariant sites (G+I) 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** face. A superscript T denotes ex-type cultures.

Colour illustrations. Cerler, Aragón, Spain. Colony on PDA and PCA after 3 wk at 25 °C; conidiophores and conidia after 14 d at 25 °C; yeast-like cells from MEA after 3 wk at 37 °C. Scale bars = 10 µm.

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Fusarium awaxy

Fungal Planet 1012 – 18 December 2019

Fusarium awaxy Petters-Vandresen, Galli-Terasawa, Terasawa & Glienke, *sp. nov.*

Etymology. Named after the Tupi-Guarani word for maize, '*awaxy*', referring to the substrate (maize ears and stalks) and geographical location (Arapoti and Guarapuava cities in Paraná, as these names come from the Tupi-Guarani language).

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

On synthetic nutrient agar (SNA) with carnation leaves: *Microconidia* forming abundantly in false heads in aerial mycelium, arising in monophialides and polyphialides, oval, 7.8–16 µm ($\bar{x}$ = 11.7 µm) long, 2.1–5.7 µm ($\bar{x}$ = 4.4 µm) wide, aseptate. *Chlamydospores* absent. *Sporodochia* tan to cream coloured, formed on the surface of carnation leaves and seldom covered with aerial mycelium, occasionally formed on the surface of carnation leaf agar (CLA) or potato dextrose agar (PDA). *Macroconidia* 3-septate, 24.1–43.5 µm ($\bar{x}$ = 30.4 µm) long, 3.2–5.1 µm ($\bar{x}$ = 4.2 µm) wide, less abundant than microconidia, and observed only in sporodochia.

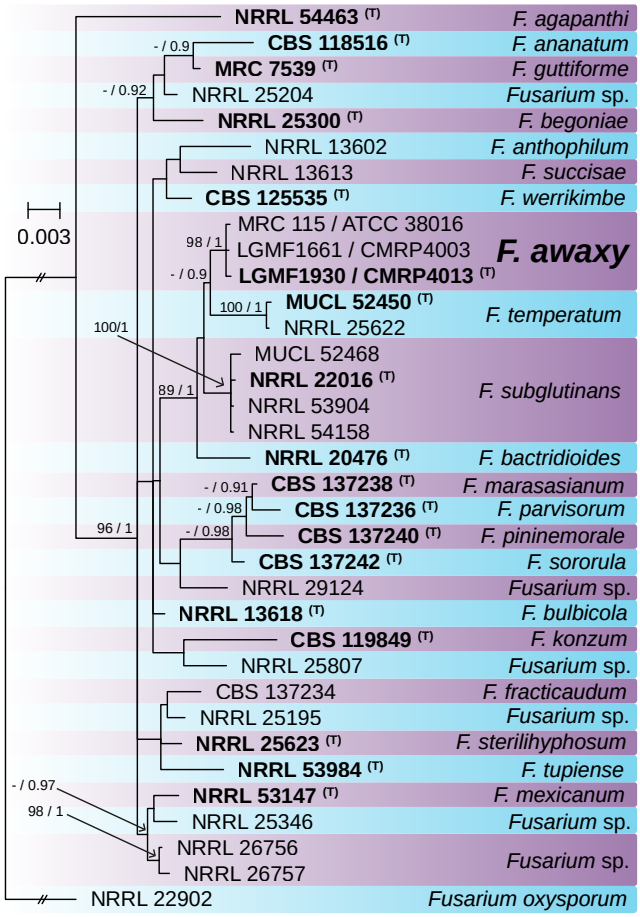
Culture characteristics — Colonies on PDA growing in the dark with average radial growth rate of 5.9 mm/d at 24 °C (reaching 74–80 mm diam in 7 d at 24 °C), with abundant aerial mycelium. Colony white, pale pink, pale violet or peach, occasionally becoming dark pink, vinaceous or violet in older cultures. Odour absent. Minimum observed temperature for growth at 16 °C, maximum at 32 °C, and optimal at 23–28 °C on potato dextrose agar, oatmeal agar and SNA.

Typus. Brazil, Paraná, Guarapuava, on rotten stalks of *Zea mays* (*Poaceae*), 2016, *F. Terasawa* (holotype UPCB93138-H, cultures ex-type LGMF1930 = CMRP 4013, ITS, LSU, *tef1*, *tub*, *cal* and *rpb2* sequences GenBank MH252922, MN566091, MG839004, MG839013, MK766940 and MK766941, MycoBank MB824048).

Notes — *Fusarium awaxy* was identified as a new member from the American clade of the *Fusarium fujikuroi* species complex in a phylogenetic analysis using *tef1, tub, ITS*, *cal* and *rpb2* sequences. *Fusarium temperatum* and *F. subglutinans*, both species already described causing maize stalk rot (Leslie & Summerell 2006, Scauflaire et al. 2011) are the closest phylogenetic relatives. *Fusarium temperatum* and *F. subglutinans* show some morphological similarities, both producing microconidia on mono- and polyphialides arranged in false heads in the aerial mycelium, only differing in the degree of septation of the macroconidia, as *F. temperatum* macroconidia are usually 4-septate and *F. subglutinans* are 3-septate (Scauflaire et al. 2011). Besides the difference in sporodochia colour, there is not a clear morphological delimitation between *F. awaxy* and *F. subglutinans*. Nevertheless, many other species morphologically similar to *F. subglutinans* have been described (e.g., *F. bulbicola*, *F. guttiforme*, *F. sacchari*) and can be properly differentiated only with the use of molecular information (Leslie & Summerell 2006). *Fusarium subglutinans* and *F. temperatum* have already been described causing human infections (Al-Hatmi et al. 2014), but *F. awaxy* did not grow above 32 °C, suggesting inability to cause infection in humans.

Colour illustrations. *Zea mays* growing in a field trial near Curitiba. *Fusarium awaxy* colony on potato dextrose agar plate; sporodochia on carnation leaves; aerial conidiophores: polyphialide, false head and monophialide; aerial oval conidia (microconidia); sporodochial conidia (macroconidia). Photos: D.A.L. Petters-Vandresen. Scale bars = 10 µm.

Additionally, based on a BLAST search and a phylogenetic analysis using *tef1* sequences, other strains, which were misidentified as *F. subglutinans*, are now identified as *F. awaxy*. Such strains include isolates from *Zea mays* from China (GenBank KT716223; Identities = 630/630 (100 %)) (Zhang et al. 2016), South Korea (GenBank JX867945; Identities = 641/641 (100 %)) (Kim et al. 2012), Argentina (GenBank MG857113; Identities = 641/641 (100 %)) (Martinez et al. unpubl. data) and Brazil (GenBank KP336408; Identities = 545/545 (100 %)) (Faria et al. 2012), as well as one strain isolated from *Sorghum bicolor* in the USA (GenBank KX681493; Identities = 634/634 (100 %)) (Funnell-Harris et al. 2017). Furthermore, another isolate from *Zea mays* from South Africa (MRC 115, GenBank MH582309; Identities = 649/649 (100 %)), which was previously identified both as *F. subglutinans* and also as a putatively novel species ('*Fusarium* sp. 8') (O'Donnell et al. 2018), can now be referred as *F. awaxy*.



Bayesian Inference tree produced with MrBayes v. 3.2.6 (Ronquist et al. 2012) at CIPRES Science Gateway (Miller et al. 2012) based on *tef1*, *tub2*, ITS, *cal* and *rpb2* sequences of *Fusarium awaxy* and other reference strains belonging to the American clade of *Fusarium fujikuroi* species complex. ML bootstrap values above 70 % (obtained using GARLI 2.01 (Zwickl 2006) at CIPRES Science Gateway) and Bayesian posterior probability values (PP) values above 0.9 indicated to the left of the nodes. Ex-type strains included in analysis are indicated in **bold** and with (T). The tree was rooted to *Fusarium oxysporum* NRRL 22902. Scale bar indicates the number of substitutions per nucleotide. TreeBASE: http://purl.org/phylo/treebase/phylows/study/TB2:S24292.

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Geastrum lanuginosum

Fungal Planet 1013 – 18 December 2019

Geastrum lanuginosum R.V.B. Araújo, J.O. Sousa, M.P. Martín, Baseia & B.D.B Silva, *sp. nov.*

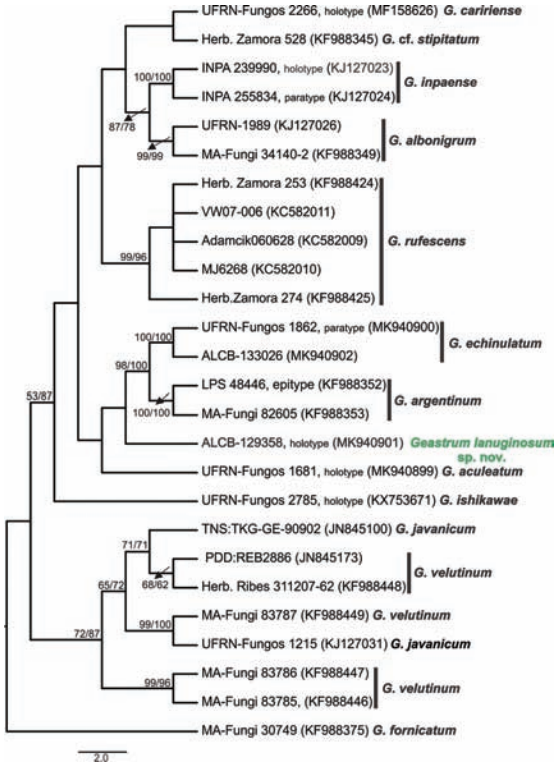
Etymology. Name reflects the woolly appearance of the exoperidium surface.

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

Unexpanded basidiomata epigeous, dark to pale brown (N70Y99M50 to N60Y99M40; Küppers 2002), globose to subglobose, 1.8–6.8 × 2.8–14 mm, surface cottony, spongy, with hyphal tufts forming an areolate pattern, lacking encrusting debris, presence of subiculum white (N00M00C00) little developed covering the substrate, with rhizomorphs adhered to the base. *Expanded basidiomata* saccate, 5.7–11.2 × 16.5–30.2 mm (including peristome). *Exoperidium* splitting into 5–6 rays, planar to revolute, recurved under the basidiomata, non-hygroscopic. *Mycelial layer* dark brown (N70Y99M50, N80Y99M50) when fresh, becoming paler (N60Y99M40, N70Y99M40) when dry, not encrusted with debris, persistent, there is no double layer, surface free of incrustations, cottony and persistent in all basidiomata, formed by hyaline hyphae, acuminate-strangled. *Fibrous layer* light beige (N00Y50M20), papery surface, formed by filamentous hyphae with thin walls, 0.5–1 µm diam. *Pseudoparenquimatous layer* white ice (N10M00C00), rimose when dried, persistent, consists of brown hyphae, 13–50 × 15–47 µm. Endoperidial body pale grey (N60Y20M20), globose, 4–10 × 8–21.3 mm, sessile, glabrous surface. *Apophysis* and *pedicel* absent. *Peristome* fibrillose, slightly delimited, up to 1 mm high, mammiform, same colour as endoperidium. *Columella* circular to columnar, central, yellowish white (N00C00Y10). *Mature gleba* dark brown (N90Y70M40). *Basidiospores* globose, brownish in 5 % KOH, 3–4 µm diam [av. = 3.4 ± 1.2 × 3.7 ± 0.5 µm, Qm = 1, n = 20], verrucose in SEM, columnar warts, up to 0.5 µm, rounded at apex. *Eucapillitium* brownish, thin-walled (< 1 µm diam), 2–5 µm diam.

Typus. Brazil, Bahia, Salvador, Federal University of Bahia, on leaf litter covered soil and wood, near to *Guareaguidonea* (*Meliaceae*) in an anthropised area, 29 May 2017, *B.D.B. Silva, M.L.V.D. Costa & R.R. Fermiano* (holotype ALCB-129358, isotype UFRN 3168, ITS and LSU sequences GenBank MK940901 and MK936167, MycoBank MB830896).

Notes — The phylogenetic analysis grouped *Geastrum lanuginosum* in the section *Exareolata* (Zamora et al. 2014) with *G. aculeatum*, *G. albonigrum*, *G. argentinum*, *G. carirense*, *G. echinulatum, G. inpaense*, *G. ishikawae* and *G. rufensens.* All these species have hyphal projections on their exoperidium, as does *G. lanuginosum.* Morphologically, *G. aculeatum* and *G. echinulatum* are similar to *G. lanuginosum*; however, *G. aculeatum* has larger basidiospores (5–7.5 µm diam) and an exoperidium with aculeate hyphal tufts, and *G. echinulatum* has a well-developed subiculum, non-delimited peristome, and pseudoparenquimatous layer that is reddish when fresh (Silva et al. 2013a). The other species of the section are morphologically distinguished by: hirsute mycelial layer and peristome not delimited in *G. albonigrum* (Calonge & Mata 2004); hirsute mycelial layer and larger basidiospores (up to 6.4 µm) in *G. inpaense* (Cabral et al. 2014); non-delimited peristome and larger basidiospores (up to 7 µm) in *G. ishikawae* (Crous et al. 2016a); lightly encrusted mycelial layer, orange to pale brown, and larger basidiospores in *G. carirense* (Crous et al. 2017a); non-delimited peristome, mycelial layer strongly encrusted with debris and sand, and larger basidiospores (5–6 µm) in *G. rufescens* (Sunhede 1989); and non-delimited peristome, developed subiculum and larger basidiospores (4.8–5.6 µm) in *G. argentinum* (Zamora et al. 2014). *Geastrum lanuginosum* could be morphologically compared to *G. javanicum* and *G. velutinum*, although these species cluster in a different phylogenetic section (sect. *Myceliostroma* subsect. *Velutinae*). Furthermore, these two species also have a well-developed subiculum, distinct delimited peristome and an ephemeral mycelial layer without strangulated-acuminate hyphae.



The first of three equally most parsimonious trees of the ITS nrDNA sequence alignment were obtained from a heuristic search. The analysis was conducted with PAUP v. 4.0b10 (Swofford 2003) with 10 000 bootstrap replicates. The new *Geastrum* species described here is indicated in green. The accession numbers from EMBL/GenBank databases are indicated on the tree. Bootstrap support values greater than 50 % for Parsimony and Maximum-Likelihood are indicated on the branches. Maximum-Likelihood analysis was run with RAxML-HPC2 v. 8.2.10 (Stamatakis 2014) under a GTRGAMMA model. *Geastrum fornicatum* was included as outgroup. CorelDRAW® X8 software was used to edit the final tree.

Colour illustrations. Brazil, Bahia, Salvador, Universidade Federal da Bahia, where the specimens were collected. Immature basidiomata; mature basidiomata; organization of exoperidium hyphae; hyphae acuminate-strangled from mycelial layer; basidiospores under SEM. All images from holotype ALCB-129358. Scale bars = 10 mm (mature basidiomata), 5 mm (immature basidiomata), 1.4 mm (organization of exoperidium hyphae), 30 µm (hyphae acuminate-strangled), 1 µm (basidiospores under SEM).

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Geastrum wrightii

Fungal Planet 1014 – 18 December 2019

Geastrum wrightii J.C. Zamora, Dios, G. Moreno, Hern. Caff. & L.S. Domínguez, *sp. nov.*

Etymology. Named after Jorge E. Wright, Argentinian mycologist who contributed to the study of numerous neotropical gasteroid fungi, including the genus *Geastrum*.

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

Immature basidiomata not seen. Mature *basidiomata* reaching 4 cm diam and 2.5 cm high (including the peristome). *Exoperidium* opened in 6–9 not truly hygrometric rays, but with tips that may be either involute or curved under the exoperidial disk. *Mycelial layer* densely encrusting debris, bistratificate, with the external part formed by hyaline to pale yellowish, skeletal hyphae with inconspicuous lumen, and the internal part with hyaline, thin-walled, clamped, generative hyphae, difficult to distinguish. *Fibrous layer* coriaceous, cream-coloured to brownish, formed by yellowish skeletal hyphae with a ± distinct lumen. *Pseudoparenchymatous layer* pale cream at first, soon becoming brownish, around 1 mm thick when fresh, less than 0.5 mm thick when dried, slightly thicker towards the stalk, not persistent in old basidiomata, formed by thin-walled inflated cells of variable size and shape, up to about 40 µm wide, smaller towards the fibrous layer. *Mesoperidium* as a pale cream farinaceous cover over the endoperium in young basidiomata, formed by small calcium oxalate dihydrate crystals (≤ 12 µm diam) and some generative hyphae. *Endoperidial body* prominently stalked, subglobose-applanate to almost disc-like, up to 1.5 cm diam; endoperidium brown to blackish, glabrous, sometimes with distinct concentric grooves in the upper half and radial grooves in the lower half showing the hyphal arrangement, farinaceous when young due to the mesoperidial cover, formed by brownish skeletal hyphae with distinct lumen. *Peristome* plicate, 2–4 mm high, with 14–20 folds, conical, not delimited to ± distinctly delimited, dark brown. *Apophysis* very well developed, ring-like, with a solid and an acute edge. *Stalk* 2–4 mm long, brownish. *Columella* damaged in the studied sporocarps, but intruding at least 1/2 into the glebal mass. *Gleba* dark brown to blackish. *Capillitium* formed by yellowish brown to brownish skeletal hyphae, the broadest about 4–5.5 µm diam, thick-walled (up to 2.5 µm thick), with visible lumen, unbranched; surface smooth or sometimes covered with irregular debris. *Basidiospores* globose to subglobose, 4–5(–5.5) µm diam, verrucose, brownish yellow under the compound microscope. Basidiospore ornamentation under the scanning electron microscope well-defined, up to 0.8 µm in height, irregularly baculate, generally isolated or forming short crests, tending to be radially arranged around the hilar appendix.

Colour illustrations. Argentina, Dpto. Paclin, La Merced, ecotone between the Yungas forest and the Chaco Serrano, where the holotype was collected. Detail of a basidioma and basidiospores under the SEM, AH 49090 (holotype); detail of basidiomata and basidiospores under the SEM, MLHC 526 (paratype). Scale bars = 1 cm (basiomata), 1 µm (basidiospores).

Habitat & Distribution — Growing solitary to gregarious among vegetal debris, in mixed broadleaf forests. Only known from the Humid Chaco (tropical and subtropical grasslands, savannas and shrublands biome) and the ecotone between the Southern Andean Yungas (tropical and subtropical moist broadleaf forests biome) and the Chaco Serrano (tropical and subtropical dry broadleaf forests biome) (Olson et al. 2001).

Typus. Argentina, Catamarca, Dpto. Paclin, La Merced, close to the tunnels entrance, on humus in mixed forest, in ecotone with the Chaco Serrano/Yungas, May 2009, *M.M. Dios 589* (holotype AH 49090, isotype BAFC 52280, ITS, 28S nrDNA, *RPB1* and *ATP6* sequences GenBank MK732525, MK732526, MK732533 and MK732530, MycoBank MB832754).

Additional materials examined. Argentina, Chaco, Dpto. Sargento Cabral y Presidencia de la Plaza, Parque Nacional Chaco, on humus in mixed forest with *Aspidosperma quebracho-blanco* as a dominant species, 5 May 2010, *L. Hernández Caffot* MLHC 526 (CORD, ITS/28S nrDNA, *RPB1* and *ATP6* sequences GenBank MK732527, MK732534 and MK732531); ibid., MLHC 1903 (CORD, ITS/28S nrDNA, *RPB1* and *ATP6* sequences GenBank MK732528, MK732535 and MK732532).

Notes — The morphological description is based on nine sporocarps from three specimens, and consequently, we expect a much larger intraspecific variation. Intense surveys were conducted during several years to collect additional samples, but without success, so the species appears to be rare. *Geastrum wrightii* belongs to *G.* subsect. *Sulcostomata* (Zamora et al. 2014), and is macromorphologically very close to *G. striatum*, sharing the very unusual solid, ring-like apophysis under the endoperidium. Both species can be morphologically distinguished by the basidiospore size and colour, 4–5(–5.5) µm and brownish yellow in *G. wrightii*, vs 5–6(–6.5) µm and distinctly brown in *G. striatum*. In addition, the ecology and distribution are different, since confirmed records of *G. striatum* s.str. are only known from temperate areas of the Northern Hemisphere. One specimen of *Geastrum* aff. *striatum* (AH 18521) from Mexico shares the small basidiospore size, but the stalk of the endoperidium is much stouter and shorter, and the apophysis less marked, with a blunt edge, as explained in detail by Zamora et al. (2015).

The three studied specimens of *G. wrightii* form a fully supported clade in our multilocus phylogeny, with both *G. striatum* s.str. and *G.* aff. *striatum* from Mexico being well-separated. The three known species in the *G. glaucescens* group (*G. glaucescens*, *G. papinuttii* and *G. parvistriatum*) are also clearly distinct based on molecular data of the analysed DNA regions, and are further characterised morphologically by the absence of a sharp ring-like apophysis.

Supplementary material

FP1014 Fifty percent majority-rule Bayesian phylogram for the *G. striatum* and *G. glaucescens* groups, obtained in MrBayes v. 3.2 (Ronquist et al. 2012), using the settings indicated in Zamora et al. (2017). Statistical support on the branches means posterior probabilities from the Bayesian analysis, and bootstrap values based on 1000 non-parametric replicates in IQ-Tree (Nguyen et al. 2015).

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Golovinomyces glandulariae

Fungal Planet 1015 – 18 December 2019

Golovinomyces glandulariae L. Kiss & Vaghefi, *sp. nov.*

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

Classification — *Erysiphaceae*, *Erysiphales*, *Leotiomycetes*.

Mycelium on stems, leaves, and sepals, amphigenous, producing dense, white patches that can cover the aerial host plant surfaces. *Hyphae* hyaline, thin-walled, 3–6 µm wide, with simple, nipple-shaped *hyphal appressoria*. *Conidiophores* erect, consisting of a *foot-cell*, 38–95 × 9–15 µm, basal septum at the branching point or up to 2–3 µm displaced, increasing in width from base to top, followed by 1–4 shorter cells, forming catenescent conidia. *Conidia* ellipsoid-cylindrical or doliiform, 20–36 × 11–17 µm. *Germ tubes* arising from an end, mostly shorter than the conidial length, and terminating in a simple, often swollen appressorium. *Sexual morph* not seen.

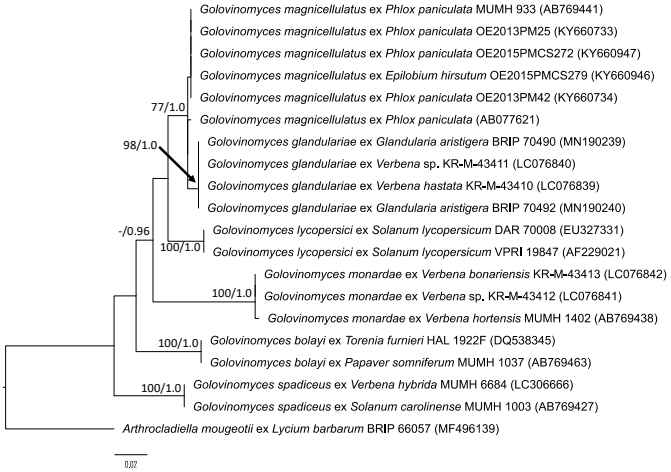
Typus. Australia, Queensland, Bunya Mountains, -26.8002, 151.5686, alt. 969 m, on leaves, stems and sepals of *Glandularia aristigera* (*Verbenaceae*), 4 July 2019, *L. Kiss* (holotype BRIP 70490, ITS and LSU sequences GenBank MN190239 and MN539541, MycoBank MB831976).

Additional materials examined. Australia, Queensland, Bunya Mountains - Maclagan Road, close to the intersection with Bunya Mountains Road, -26.9708, 151.6133, alt. 555 m, on leaves, stems and sepals of *Glandularia aristigera,* 10 June 2019, *L. Kiss*, BRIP 70491, ITS sequence GenBank MN190241; Bunya Mountains, -26.8799, 151.5975, alt. 967 m, on leaves, stems and sepals of *Glandularia aristigera,* 18 Feb. 2017, *L. Kiss*, BRIP 70492, ITS sequence GenBank MN190240; Bunya Mountains, -26.8811, 151.5975, alt. 963 m, on leaves, stems and sepals of *Glandularia aristigera,* 10 Mar. 2018, *L. Kiss*, BRIP 68801, ITS sequence GenBank MN190242; Bunya Mountains Road, -26.8002, 151.5686, alt. 686 m, 10 June 2019, on leaves, stems and sepals of *Glandularia aristigera, L. Kiss*, BRIP 70531, ITS sequence GenBank MN190243.

Notes — *Golovinomyces* contains approximately 60 species of powdery mildew (Braun & Cook 2012), including many common, widespread, plurivorous taxa (Braun et al. 2019). Amongst these, *G. orontii* s.lat., *G. verbenae* and *G. spadiceus* infect diverse host plant species in the *Verbenaceae* (Braun & Cook 2012, Braun et al. 2019). *Glandularia aristigera* is a verbenaceous species native to South America that has been naturalised in parts of Australia.

Golovinomyces glandulariae is the first powdery mildew reported on *Gl. aristigera* globally, causing severe local epidemics in 2017–2019 in Australia. One other species, *G. verbenae*, has been reported on *Gl. phlogiflora* (Braun & Cook 2012); other *Glandularia* spp. are not known as hosts of powdery mildews. *Golovinomyces glandulariae* differs from *G. verbenae* by having conidiophores with foot-cells followed by up to four shorter cells, basal septa sometimes 2–3 µm displaced from the point of branching, and smaller conidia. ITS sequences are not available in GenBank for *G. verbenae*, thus the phylogenetic relationship between these two species cannot be determined. Phylogenetically, *G. glandulariae* is sister to *G. magnicellulatus*, which is morphologically similar, although its conidia are larger. As of 26 July 2019, the ITS sequence of *G. glandulariae* is identical to only two *Golovinomyces* specimens, KR-M-43410 and KR-M-43411, available in GenBank (acc. nos. LC076839 and LC076840, respectively). These were collected from *Verbena* in Germany and were recognised as representing a distinct lineage, without being identified at the species level (Scholler et al. 2016). The next closest hits using the ITS sequence of *G. glandulariae* are 10 *G. magnicellulatus* specimens with four to six nucleotide position differences in the ITS2 sequences.

Most of the powdery mildew mycelium on *Gl. aristigera* consisted of hyphae, conidiophores and conidia of *G. glandulariae*, although small patches of *Podosphaera xanthii* were also found on the aerial plant surfaces. *Podosphaera xanthii* has conidia with fibrosin bodies, which distinguishes it from *G. glandulariae*. The ITS sequence of *P. xanthii* was determined in each specimen (acc. nos. MN190026–MN190029 and MN190244), and these were all identical to those available in GenBank for over 30 other specimens of *P. xanthii* collected from diverse host plant species in different parts of the world. This is the first report of *P. xanthii* on *Gl. aristigera* globally. It has long been known that the same plants, and even the same leaves may be infected by multiple powdery mildew species (Kiss et al. 2008, Desprez-Loustau et al. 2018) as detected in this study.



Maximum likelihood phylogram based on the internal transcribed spacer sequences of the nuclear ribosomal DNA and the intervening 5.8S region. The alignment was deposited in TreeBASE (acc. no. 24823). The analysis was performed using RAxML v. 8 (Stamatakis 2014) in Geneious Prime (Biomatters Ltd.) based on the GTR substitution model with gamma-distribution rate variation. A second measure of branch support was estimated through Bayesian Inference of the same alignment using MrBayes v. 3.2.4 (Ronquist et al. 2012). The tree is rooted to *Arthrocladiella mougeotii* BRIP 66057. Maximum Likelihood bootstrap values > 80 % and Bayesian Posterior Probability values > 0.80 are shown above or below the branches. The scale bar represents nucleotide substitutions per site.

Colour illustrations. A roadside population of *Glandularia aristigera* heavily infected with powdery mildew in Bunya Mountains, Queensland, Australia. A close-up of an infected plant; conidiophores, non-germinating and germinating conidia, and a hyphal appressorium of *Golovinomyces glandulariae*. Scale bars = 15 µm (conidiophores, conidia), 5 µm (hyphal appressorium).

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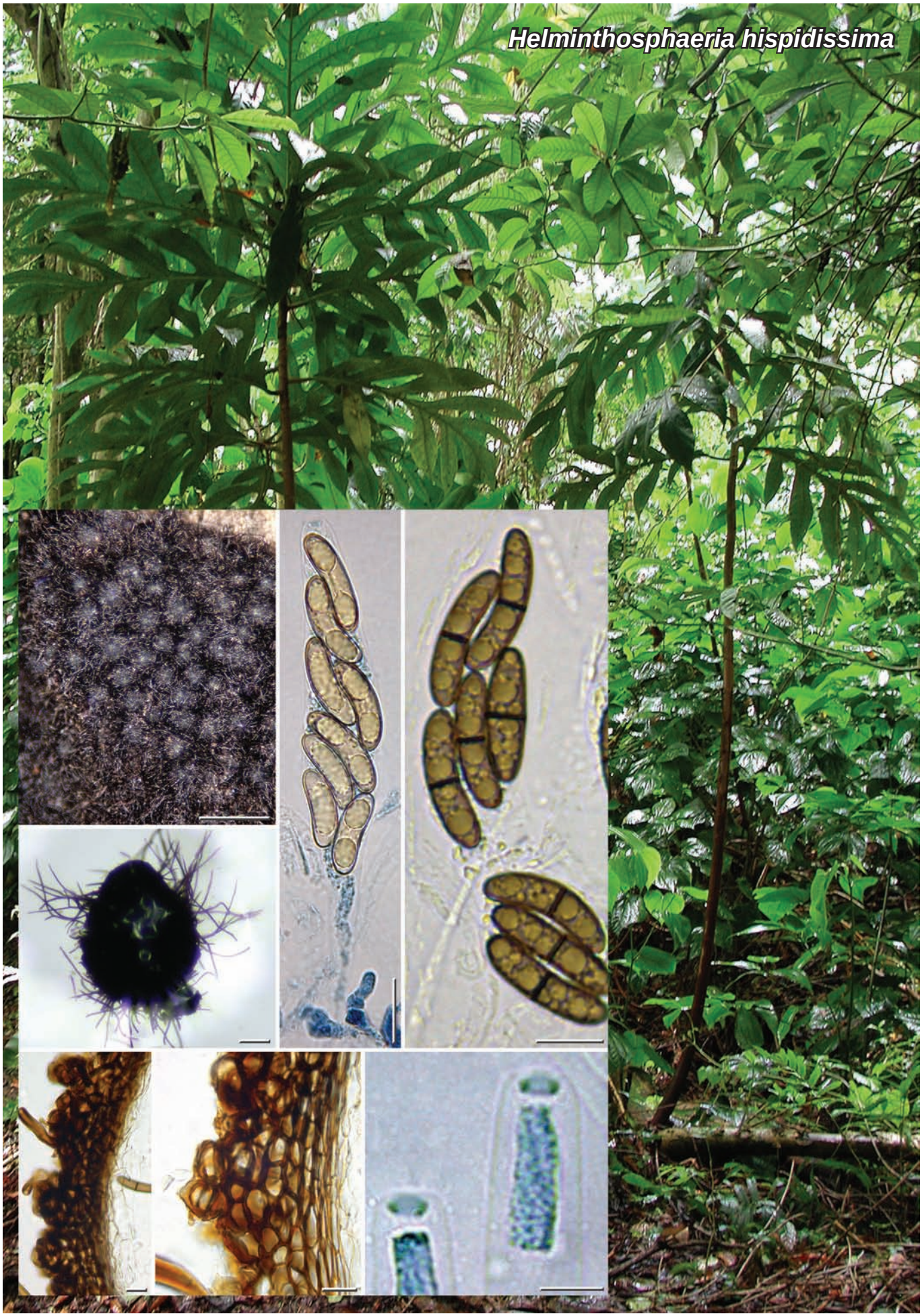

Helminthosphaeria hispidissima

Fungal Planet 1016 – 18 December 2019

Helminthosphaeria hispidissima J. Fourn. & A.N. Mill., *sp. nov.*

Etymology. Name refers to the very bristly hairs covering the ascomata.

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

Ascomata ovoid, papillate, with an obtusely rounded to slightly conical and cruciform apex, 340–380 µm diam, 420–550 µm high, numerous, densely clustered, superficial, black, barely emerging from a dense, shiny dark brown subiculum with tufts surrounding the ascomata and projecting above, occasionally covering the ascomata entirely; subiculum hyphae dark reddish brown, slightly sinuous, branched, remotely septate, 5–8 µm wide, thick-walled with a lumen, walls 1.5–2.5 µm thick, smooth-walled, with rounded tips. *Ascomatal wall* of *textura angularis* in surface view, in longitudinal section 2-layered, 40–55 µm thick, inner layer *textura prismatica*, 5–10 µm thick, composed of 2–5 layers of elongate, flattened, thin-walled, brown cells, outer layer *textura angularis*, 35–45 µm thick, composed of several layers of thick-walled, brown cells, cells 4.5–13.5 µm in their greatest dimension, walls 1.8–2 µm thick, with Munk's pores; tubercles composed of clusters of subglobose cells, 6–9 µm diam, walls up to 3.5 µm thick, bearing long hyphal hairs indistinguishable from the subiculum hyphae. *Ascomatal apex* composed of a palisade of thick-walled, rectangular cells converging around the ostiole and terminating as small, opaque cells on the surface, with periphyses arising from an inner hyaline basal layer. *Paraphyses* filiform, 1.5–2.5 µm wide, embedded in a dense mucilaginous matrix, hyaline, sparse, remotely septate, unbranched, persistent. *Asci* broadly fusiform, 78–90 × 13.5–18 µm, stipitate, stipe 34–56 µm, unitunicate, thin-walled, apex truncate; ring narrow, 0.6–0.8 × 3–3.5 µm, shallow, refractive, I-, faintly stained by blue and blue-black inks; with 8 bi- to triseriate ascospores. *Ascospores* cylindrical, allantoid, with obtuse ends, (17.5–)18.5–23(–24) × (4.5–)5–6(–6.5) µm (av. 21.2 × 5.7), yellowish and aseptate in the ascus before maturity, eventually light to yellow brown and 1-septate, septum medial, thick, blackish brown, not constricted; with large and small guttules, smooth-walled, without sheath or appendages.

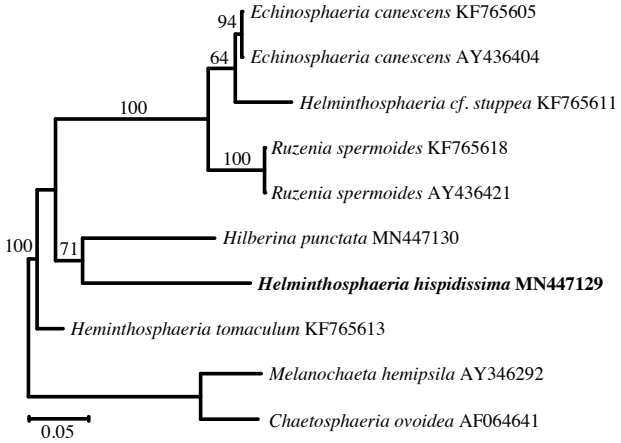
Habitat — Decayed wood in a tropical forest, possibly fungicolous on *Hypoxylon investiens*.

Distribution — Known only from Martinique, French West Indies.

Typus. French West Indies, Martinique, Prêcheur, Anse Couleuvre, coastal mesophilic forest, on dead blackened wood, associated with old stromata of *Hypoxylon investiens*, N14.84 W61.22, 9 June 2014, *J. Fournier & C. Lechat*, MJF 14113 (holotype ILLS00121145 (ILLS), ITS-LSU sequence GenBank MN447129, MycoBank MB832757).

Additional material examined. French West Indies, Martinique, Prêcheur, Anse Couleuvre, coastal mesophilic forest, on dead blackened wood, associated with old stromata of *Hypoxylon investiens*, N14.84 W61.22, 16 Aug. 2013, *J. Fournier & C. Lechat*, MJF 13262 = ILLS00121146.

Notes — *Helminthosphaeria hispidissima* at first appears to resemble *Lasiosphaeris hirsuta* since they share tuberculate, hairy ascomata (Miller & Huhndorf 2004). However, their ascospores differ greatly being allantoid and lacking appendages in *H. hispidissima* and vermiform with awl-like appendages in *L. hirsuta*. Six other species in the *Helminthosphaeriaceae* possess allantoid to cylindrical and curved ascospores ranging in shape and septation from short, fat and aseptate in *H. stuppea* and *H. tomaculum* to longer, narrower and up to 1-septate in *Echinosphaeria canescens* and *Ruzenia spermoides* to long, narrow and 1–5-septate in *E. heterostoma* and *Hilberina punctata* (Miller et al. 2014). *Helminthosphaeria hispidissima* is easily distinguished by its brown, 1-septate ascospores, whereas the other six species possess hyaline to pale brown (or brown, but much longer ascospores in *E. heterostoma*), aseptate or multiseptate (rarely 1-septate) ascospores.



Maximum likelihood tree generated using PhyML in SeaView v. 4.5.4 (Gouy et al. 2010). *Helminthosphaeria hispidissima* is in **bold**. Numbers above branches refer to bootstrap support values. GenBank accession numbers for the LSU region are given after taxon names.

Colour illustrations. Background photo of typical tropical undergrowth in Anse Couleuvre (Martinique). Ascomata; ascus; young and older ascospores; ascoma; longitudinal sections through ascomal wall; ascal apices. Scale bars = 1 mm (ascomata), 100 µm (ascoma), 10 µm (young ascus, older ascospores, ascomal walls), 5 µm (ascal apices). Photos: Jacques Fournier.

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Hermetothecium mikaniae-micranthae

Fungal Planet 1017 – 18 December 2019

Hermetothecium T.F. Nóbrega, B.W. Ferreira, H.C. Evans & R.W. Barreto, *gen. nov.*

Etymology. Having a sealed sporocarp.

Classification — *Chaetothyriaceae*, *Chaetothyriales*, *Eurotiomycetes.*

Ascomata chasmothecium (similar to sporocarps of the *Erysiphales*), without an ostiole, epiphytic, formed on a subiculum on living leaves, globose, brown. *Hymenium* containing asci but no sterile filaments. *Asci* bitunicate, subglobose, fasciculate. *Ascospores* ellipsoid, 0–2-septate, hyaline. *Asexual morph* unknown.

Type species. Hermetothecium mikaniae-micranthae T.F. Nóbrega, B.W. Ferreira, H.C. Evans & R.W. Barreto
MycoBank MB832759.

Hermetothecium mikaniae-micranthae T.F. Nóbrega, B.W. Ferreira, H.C. Evans & R.W. Barreto, *sp. nov.*

Etymology. Name reflects the host, *Mikania micrantha.*

Colonies hypophyllous, forming irregular white patches on the host surfaces, powdery mildew-like. *Mycelium* superficial, composed of very narrow (1–4 µm diam), branched, almost indistinguishably septate, thin-walled, hyaline, hyphae, forming a dense colourless subiculum. *Ascomata* chasmothecium (similar to fruit bodies of the *Erysiphales*), scattered to gregarious, globose, 51–74 × 55–76 µm diam, without an ostiole, walls thickened composed of 3–4 layers of brown *textura globulosa*, 7–17 µm, smooth. *Asci* fasciculate, subglobose, 19–27 × 7–12 µm, bitunicate, 8-spored. *Sterile filaments* absent. *Ascospores* ellipsoid, 7–13 × 2–5 µm, 0–2-septate, hyaline, smooth. *Asexual morph* absent.

Typus. Brazil, Minas Gerais, Viçosa, campus of the Universidade Federal de Viçosa, coffee experimental area (Viveiro de Café), on living leaves of *Mikania micrantha* (*Asteraceae*), 4 Dec. 2018, *R.W. Barreto* (holotype VIC 47212, ITS and LSU sequences GenBank MN537723 and MN537725, MycoBank MB832760).

Notes — Numerous attempts to isolate this fungus on a range of general-purpose culture media failed to produce any culture, leading to the conclusion that this is a biotrophic taxon. Furthermore, detailed observations under the compound microscope and via scanning electron microscopy failed to produce any evidence of appressoria, or other penetration structures of leaf tissue, or any internal growth of mycelium. It appears that *H. mikaniae-micranthae* is an epiphyte relying strictly on plant exudates for its growth and is a specialised colonist of this plant host. *Mikania micrantha* is a relatively uncommon but widespread ruderal climber in Brazil, frequently associated with marshy areas. However, in its exotic range in the Palaeotropics, especially in Asia, it is highly invasive and damaging (mile-a-minute weed) in both natural and agricultural ecosystems (Ellison & Sankaran 2017).

Phylogenetic trees constructed from the analysis of Maximum Parsimony and Bayesian Inference demonstrated that the fungus belongs to the *Chaetothyriaceae*. Many species included in this family are epiphytes, colonising the surface of living leaves with mycelium limited to the host cuticle (Chomnunti et al. 2012). Sequences of the fungus, obtained directly from colonies on living leaves of *M. micrantha*, formed a clade isolated from other genera of *Chaetothyriacae*, with high support (bootstrap = 100 / posterior probability = 1) justifying the recognition of a new monotypic genus for this species.

The closest genera to *Hermetothecium* in the phylogenetic study are *Phaeosaccardinula* and *Vonarxia*. Fungi in *Phaeosaccardinula* have ascomata, with a dark, non-setose pellicle, saccate, bitunicate asci and muriform, hyaline to brownish ascospores (Yang et al. 2014). *Vonarxia* is based on an asexual morph which is sporodochial, with septate setae (Batista et al. 1960).

Colour illustrations. *Hermetothecium mikaniae-micranthae* forming whitish, powdery-mildew-like colonies on the underside of *Mikania micrantha* leaves. Brown, thick-walled ascoma; colony formed abaxially (note brown sphaeroid ascomata associated with whitish subiculum); squash-mounted ascoma releasing asci-only hymenium; fascicle of immature asci; 8-spored mature asci. Scale bars = 10 µm.

Supplementary material

FP1017 Maximum Parsimony Tree inferred from the combined datasets of ITS and LSU sequences from species belonging to the families *Chaetothyriaceae* and *Cyphellophoraceae*, including two specimens of *Hermetothecium mikaniae-micranthae* obtained in this study (indicated in **bold**). Bootstrap support values (≥ 70 %) and later Bayesian probabilities (≥ 0.90) are given at each node. The tree is rooted to *Cladophialophora australiensis* CBS 112793 and *C. potulentorum* CBS 112222.

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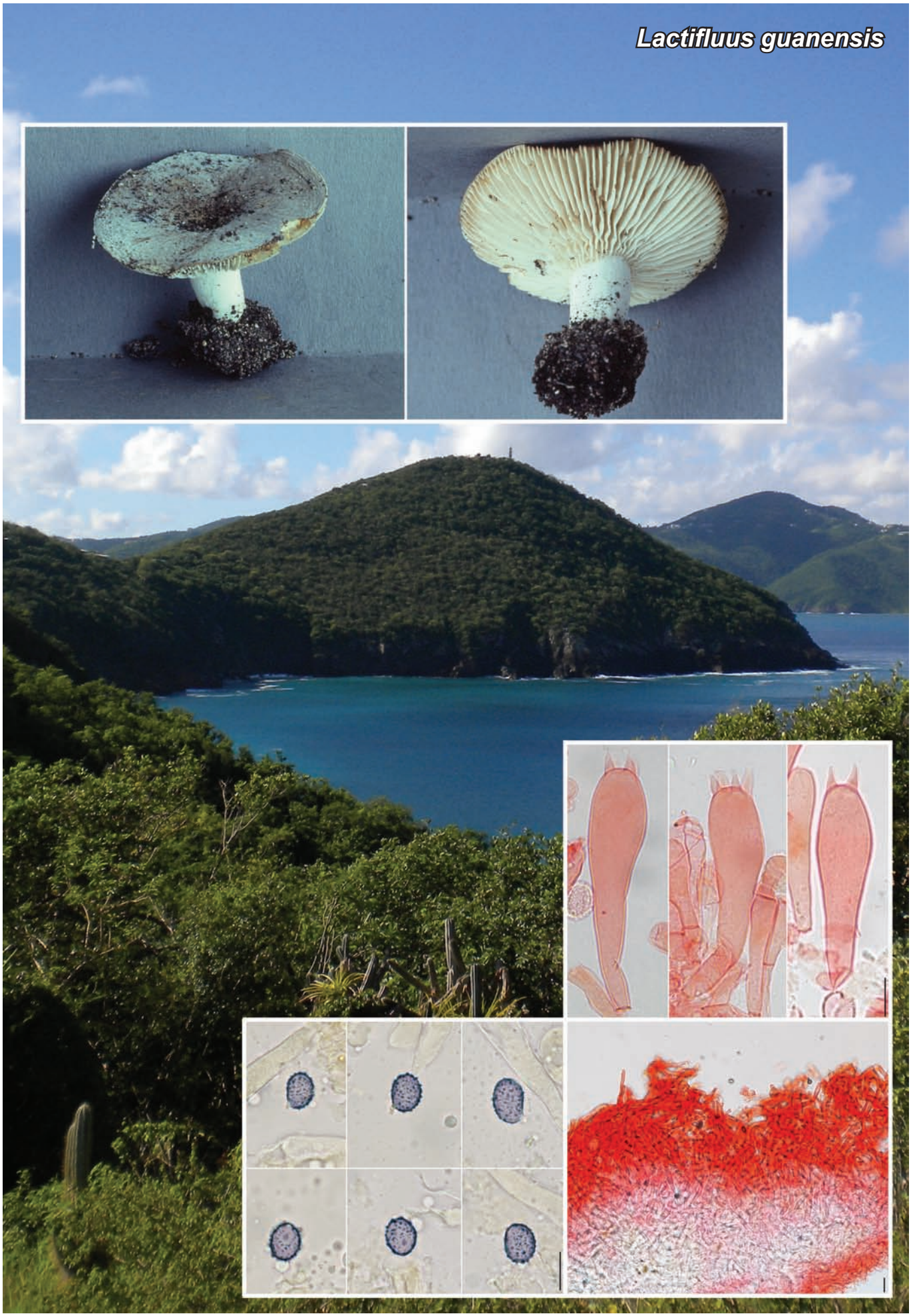

Lactifluus guanensis

Fungal Planet 1018 – 18 December 2019

Lactifluus guanensis Delgat & Lodge, *sp. nov.*

Etymology. Refers to the island where the species was found.

Classification — *Russulaceae*, *Russulales*, *Agaricomycetes*.

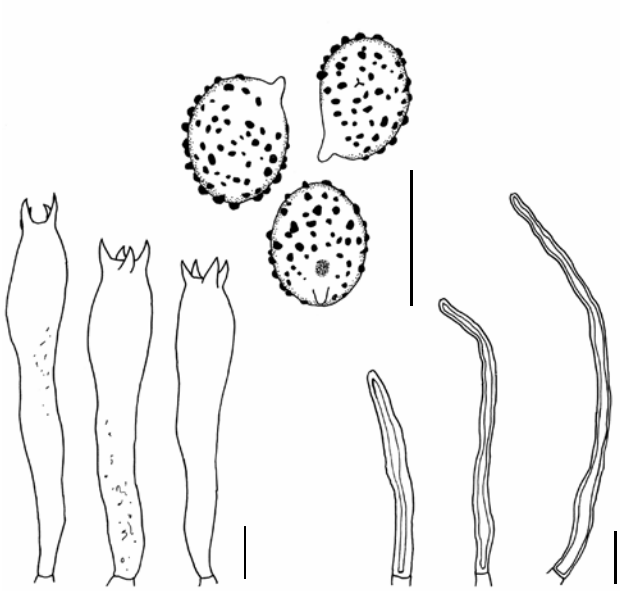
Pileus 56 mm diam, planoconvex with depressed centre; margin straight; surface minutely pubescent, wrinkled near the margin, dry, light drab fading to drab grey. *Stipe* 21 × 8–12 mm, regular and cylindrical, slightly tapering downwards, stuffed; surface smooth, dry, white. *Lamellae* adnate, some forked near stipe, some crisped, subdistant, more than 1 mm apart halfway the radius, with abundant lamellulae in a regular short-long-short pattern (3–7 between two lamellae), cream to pale horn, staining slowly raw sienna; edge concolorous and entire. *Context* white, brown at the base and in the centre, rapidly turning cinnamon when cut. *Smell* slightly foetid, like rotting meat. *Taste* sweet, very slowly faint acrid. *Latex* white, staining brown. *Basidiospores* broadly ellipsoid to ellipsoid, (7.3–) 7.5–*9.5*–11.4(–11.7) × 6–*7.2*–8.4 µm (Q = 1.15–*1.32*–1.49); ornamentation amyloid, composed of isolated warts, up to 1 µm high; plage distinct and often weakly centrally to distally amyloid. *Basidia* 52.5–*62.5*–72.5 × 9.5–*12*–14(–14.5) µm, subclavate, 4-spored. *Pleurocystidia* absent. *Pseudocystidia* inconspicuous, 6.5–8 µm wide, not emergent. *Lamellar edge* fertile. *Hymenophoral trama* mixed, with sphaerocytes, hyphae and abundant lactifers. *Pileipellis* a dense lamprotrichoderm; terminal elements 22.5–*70*–117 × 2–*3*–4 µm, cylindrical, rarely subcapitate, thick-walled, often refringent; subpellis composed of thick-walled interwoven hyphae. *Stipitipellis* as pileipellis.

Distribution — So far only known from the type locality, the North Bay woods on Guana Island. Occurring on sandy soil under *Coccoloba uvifera*.

Typus. British Virgin Isles, Guana Island, North Bay woods, N18°28'42" W64°34', 24 Oct. 1997, *D.J. Lodge* (holotype GUA-104 (CFMR), ITS sequence GenBank MK046851, MycoBank MB831225).

Notes — *Lactifluus guanensis* belongs to *L.* subg. *Gymnocarpi*, which is supported by molecular data (ITS phylogeny: see Supplementary Fig. FP1018), as well as by morphological characters, such as the absence of true pleurolamprocystidia and a brownish colour reaction of the latex and/or the context when exposed to air. *Lactifluus guanensis* is part of an unnamed section (Clade 1; Clade 9 in De Crop et al. 2017), a section which contains exclusively Neotropical species, mostly species from the Antilles. Morphologically this species has similar characters to the other species in this section (e.g., *L. murinipes*, *L. nebulosus, L. putidus*), such as dull basidiocarp colours, brown staining of the latex and context, unpleasant smell and spore ornamentation consisting of isolated warts.

There is only one other *Lactifluus* species known from the Greater Antilles or associated with *Coccolobo uvifera. Lactarius coccolobae** closely resembles *Lactifluus guanensis*. However, *L. coccolobae* has more narrow basidia (8–9.5 µm wide), slightly shorter spores (7.2–9(–10.8) µm long), lower spore ornamentation (up to 0.3 µm) and a gelatinised pileipellis (Miller et al. 2000). On the other hand, *Lactifluus guanensis* is easily distinguishable from *Lactifluus* species from the Lesser Antilles, notably due to the often amyloid plage, the absence of macrocystidia and the lamprotrichoderm structure of the pileipellis consisting of thick-walled elements. Only *L. caribaeus* also lacks macrocystidia and has a trichodermial pileipellis, but differs by the distinctly smaller and more globose spores (6.6–*7.6*–8.5 × 5.8–*6.3*–6.8 µm (Q = 1.06–*1.20*–1.35)) with inamyloid plage, and by the thin-walled terminal elements of the pileipellis.



Lactifluus guanensis: basidiospores; basidia; pileipellis terminal elements. Scale bars = 10 µm.

* this species is yet to be recombined in *Lactifluus*.

Colour illustrations. Guana Island, British Virgin Isles. Basidiocarp of *Lactifluus guanensis* (holotype GUA-104); pileipellis; basidia; basidiospores. Scale bars = 10 µm.

Supplementary material

FP1018 Maximum Likelihood phylogeny based on ITS sequence data of *Lactifluus* subg. *Gymnocarpi*.

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Mollisia cortegadensis

Fungal Planet 1019 – 18 December 2019

Mollisia cortegadensis De la Peña-Lastra & P. Alvarado, *sp. nov*.

Etymology. The epithet refers to the place where it was found (Illa de Cortegada, Parque Nacional Marítimo-Terrestre de las Islas Atlánticas, Galicia, Spain).

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

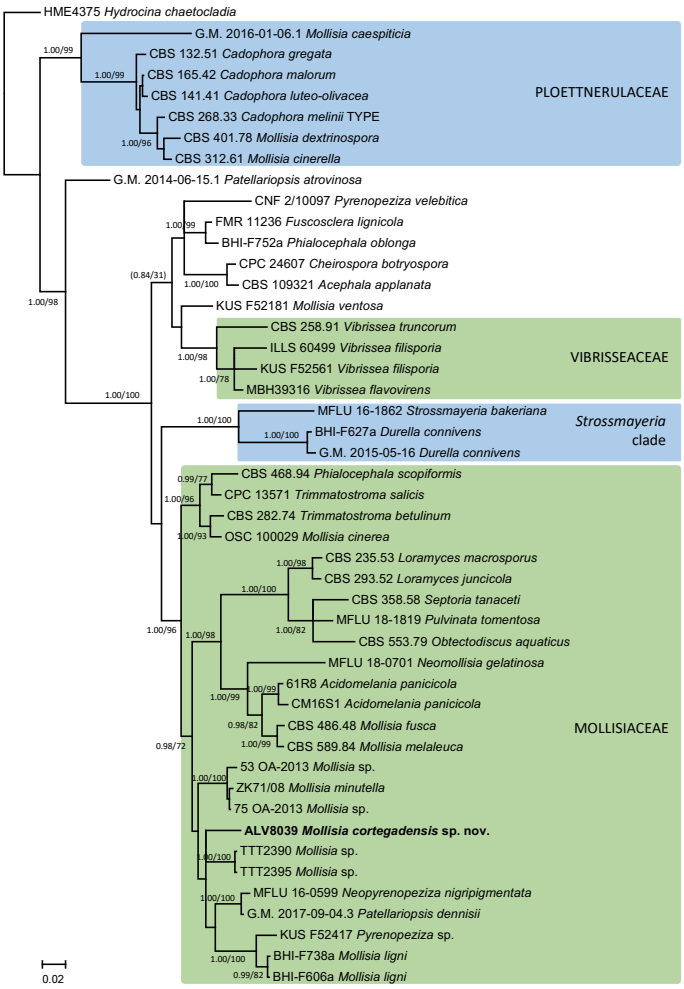
Apothecia gregarious, from 0.5–4 mm diam, first slightly concave and then flattened, irregularly disc-shaped, umbilicated or depressed, sessile, centrally attached to the substrate. *Hymenium* smooth, wavy, gibbous, yellowish grey when fresh and orange-ochre when dry, with the external and central parts dark grey. *Asci* cylindrical-clavate 80–120 × 12–18 µm, 8-spored, with a conical apex and a base gradually narrowed into a medium-sized stalk with croziers, showing no reaction to IKI (Lugol's solution), and turning only slightly yellowish in KOH (no ionomidotic reaction). *Paraphyses* distinctly dimorphic, either cylindrical, inflated (molliform), or slightly broadened at the apex, with refractive vacuolar bodies at the top. In addition, the paraphyses extend beyond the asci. *Ascospores* elliptical with rounded ends, measuring 15–18 × 5.5–7 µm, with 1–2 small (< 1 µm) guttules at the poles. Ectal excipulum consisting of a brownish texture globose at the base, and globose elements in the surface. The margin lacks conspicuous protruding cells. The medullary tissue consists of gelatinized hyphae. Subicular hyphae sparse, hyaline and thick-walled. All observations made on fresh specimens.

Distribution — Currently known only from the type location in north-western Spain.

Phylogeny — The analysis of ITS and 28S rDNA suggests that the sample from Cortegada is related with the monophyletic *Vibrissea-Loramyces* clade (Wang et al. 2006, Hustad & Miller 2011, Han et al. 2014) of the *Mollisiaceae* s.lat. According to the family concepts proposed by Johnston et al. (2019), *M. cortegadensis* belongs to the clade of families *Mollisiaceae, Loramycetaceae* and *Vibrisseaceae*, which could be merged into the oldest name *Mollisiaceae*.

Typus. Spain, Galicia, Pontevedra, Parque Nacional de las Islas Atlánticas de Galicia, Illa de Cortegada, N42°36'59.65" W8°46'59.22", 9.4 m asl, a group of ascomata at the tip of a dead attached twig of *Quercus robur*, 27 Apr. 2016, *S. De la Peña-Lastra* (holotype MSS906, ITS and 28S/LSU sequences GenBank MN129025 and MN129020, MycoBank MB831739).

Notes — *Mollisia cortegadensis* is characterised by its two types of paraphyses: slightly broadened at their tips and others strongly swollen, but all of them have conspicuous refractive vacuolar bodies that stain in cresyl blue. In addition, the fungus is drought-tolerant suggested by the dry photo and the inamyloid asci. *Mollisia spectabilis* has similar spore dimensions about 8–14 × 2.8–3.5 µm, but those of *M. cortegadensis* can be as long as 18 µm. In addition, *M. cortegadensis* is drought-tolerant and growing in clusters in the apical part of small decorticated branches of *Quercus robur*, while *M. spectabilis* grows on rotten leaves of *Q. robur* or underneath rotten *Quercus* logs (Kirschstein 1938). Other species similar to *M. spectabilis* such as *M. elegantior* and *M. olivascens* can be found in the same locality, but they have different spore dimensions and lack the orange ochre tones when dry (Richter & Baral 2008, Le Gal & Mangenot 1958). The putative phylogenetic relationship with *M. ligni* and *M. minutella* is only supported by a few shared ecological or morphological trait, since *M. ligni* has ascospores 6–10 × 2–3 µm, cylindrical paraphyses with low refractive vacuoles (Karsten 1873) and *M. minutella*, which is sometimes considered a synonym of *M. cinerea*, has ascospores 7–14 × 2.5–3 µm and the apices of asci stain blue in IKI (Karsten 1871).



50 % majority rule ITS-28S rDNA consensus phylogram of several lineages in the Mollisioid clade (Johnston et al. 2019), including families *Mollisiaceae*, *Loramycetaceae* and *Vibrisseaceae* obtained in MrBayes from 1650 sampled trees. Nodes were annotated if supported by ≥ 0.95 Bayesian PP (left) or ≥ 70 % ML BP (right). Non-significant support values are exceptionally represented inside parentheses.

Colour illustrations. Location where *M. cortegadensis* was collected on Cortegada Island. Fresh apothecia; dry apothecia; elements of the hymenium; spores (two of them in IKI at the bottom); paraphyses, hymenium in KOH; ascus in IKI (-); ascus in water, base of an ascus showing the crozier, paraphyses; detail of paraphyses in cresyl blue, ectal excipulum; medullary excipulum; medullary excipulum in KOH, medullary excipulum in NH_4OH; ascome margin; marginal cells; flanks. Scale bars = 50 µm (apothecia, ascus in water and medullary excipulum in KOH), 20 µm (other structures).

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Ophiocordyceps khonkaenensis

Fungal Planet 1020 – 18 December 2019

Ophiocordyceps khonkaenensis Tasan., Thanakitp. & Luangsa-ard, *sp. nov.*

Etymology. Named after the location where the species was collected, Khon Kaen Province, Thailand.

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

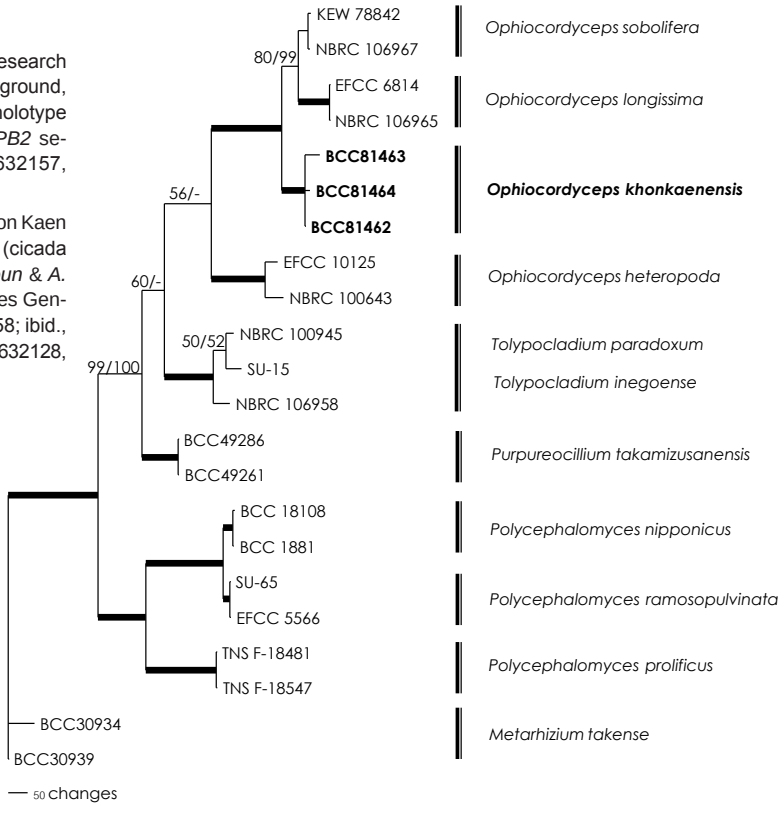
Stromata variable in number, solitary to three, 20–30 mm tall and 2–3 mm wide. *Rhizoids* flexuous, c. 2 cm long, arising from the head of cicada nymphs living underground. Fertile part distinctly terminal, globose, pinkish red, sterile stroma beneath the fertile part cylindrical, pale pink. *Ascomata* perithecial, completely immersed, ovoid, (590–)615–675(–700) × (200–)216–263(–300) µm. *Asci* cylindrical, (237.5–)252–326(–337.5) × 5–5.8(–6) µm with cap, 5 × 5 µm. *Ascospores* filiform, (300–)314–353(–360) × 1.5–2 µm readily breaking into 32 part-spores, (7–)9–11.5(–13) × 1.5–2 µm.

Culture characteristics — Colonies developed from germinating ascospores. The ascospores germinated within 24 h on potato dextrose agar (PDA). Colonies relatively slow-growing, attaining a diameter of 5 mm in 30 d at 25 °C, dark brown with cream edges. Colonies produce brown synnemata after 1 mo with a pruinose area bearing conidiogenous cells and conidia. *Conidiogenous cells* phialidic, hirsutella-like, (5.5–)6.4–8.6 (–11) × 2–2.7(–3) µm. *Conidia* hyaline, fusiform, smooth-walled, (3–)3.7–4.9(–5.5) × (1–)1.5–2.3(–3) µm.

Typus. Thailand, Khon Kaen Province, Khon Kaen Field Crop Research Center, 16.484'N 102.831'E, on *Hemiptera* (cicada nymph) underground, 27 May 2016, *W. Noisripoom, S. Wongkanoun & A. Klaysuban* (holotype BBH45360, culture ex-type BCC81462, SSU, *TEF, RPB1* and *RPB2* sequences GenBank MK632126, MK632075, MK632168 and MK632157, MycoBank MB830259).

Additional materials examined. Thailand, Khon Kaen Province, Khon Kaen Field Crop Research Center, 16.484'N 102.831'E, on *Hemiptera* (cicada nymph) underground, 27 May 2016, *W. Noisripoom, S. Wongkanoun & A. Klaysuban*, BCC81463, SSU, LSU, *TEF, RPB1* and *RPB2* sequences GenBank MK632127, MK632102, MK632076, MK632169 and MK632158; ibid., BCC81464, SSU, LSU, *TEF, RPB1* and *RPB2* sequences GenBank MK632128, MK632103, MK632077, MK632170 and MK632159.

Notes — *Ophiocordyceps khonkaenensis* produces ascomata on the terminal part of the stroma. Their hosts are cicada nymphs that can be found buried in soil. This species was only found in Khon Kaen Field Crops Research Center, Khon Kaen Province during the rainy season. It is nested in a clade together with *O. longissima* and *O. sobolifera* (Sung et al. 2007). It shares similarity with *O. longissima* in the colour of the fertile part. However, in *O. longissima* and also in *O. sobolifera*, the shape of the fertile part is clavate with a pointed end. *Ophiocordyceps khonkaenensis* produces broadly ellipsoidal fertile heads and ovoid perithecia but in *O. sobolifera* the fertile head is cream, not red, and the perithecia are stouter (500–600 × 220–260) compared to *O. khonkaenensis*. It shares similarities with *O. heteropoda* in the ovoid shape of the fertile area (Sung et al. 2007). However, it differs in the colour of the fertile head, which is mustard yellow to dark brown in *O. heteropoda*, and the perithecia are ampullaceous, completely immersed, 610–660 µm long, around 210 µm wide.



Phylogenetic reconstruction using the Maximum Parsimony (MP) and Maxi-mum Likelihood (ML) (RAxML v. 8.2.10, Stamatakis 2006) multi-locus phylogenetic analyses based on nuclear ribosomal small and large subunits (SSU and LSU), the largest and second largest subunits of RNA polymerase II (*RPB1* and *RPB2*) and elongation factor 1-α (*TEF*) revealed that *Ophiocordyceps khonkaenensis* is closely related to *O. sobolifera* and *O. longissima*. Molecular data of these specimens formed a separate clade from other species of *Ophiocordyceps* with full bootstrap support (100 %), thus a new species *Ophiocordyceps khonkaenensis* is introduced.

Colour illustrations. Type locality – a small plot in Khon Kaen Field Crop Research Center. Fungus on cicada nymph producing three stromata; ovoid perithecia; asci; ascospore; part-spores; obverse and reverse of colonies on PDA; hirsutella-like asexual morph on PDA. Scale bars = 10 mm (plate culture), 7 mm (stromata), 110 µm (perithecia), 30 µm (asci and ascospore), 10 µm (part-spores), 8 µm (hirsutella-like asexual morph on PDA).

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Penicillium cuddlyae

Fungal Planet 1021 – 18 December 2019

Penicillium cuddlyae Visagie & I.H. Rong, *sp. nov*.

Etymology. Latin, *cuddlyae*, named after Cuddly the Dachshund; this species was isolated from her dog food.

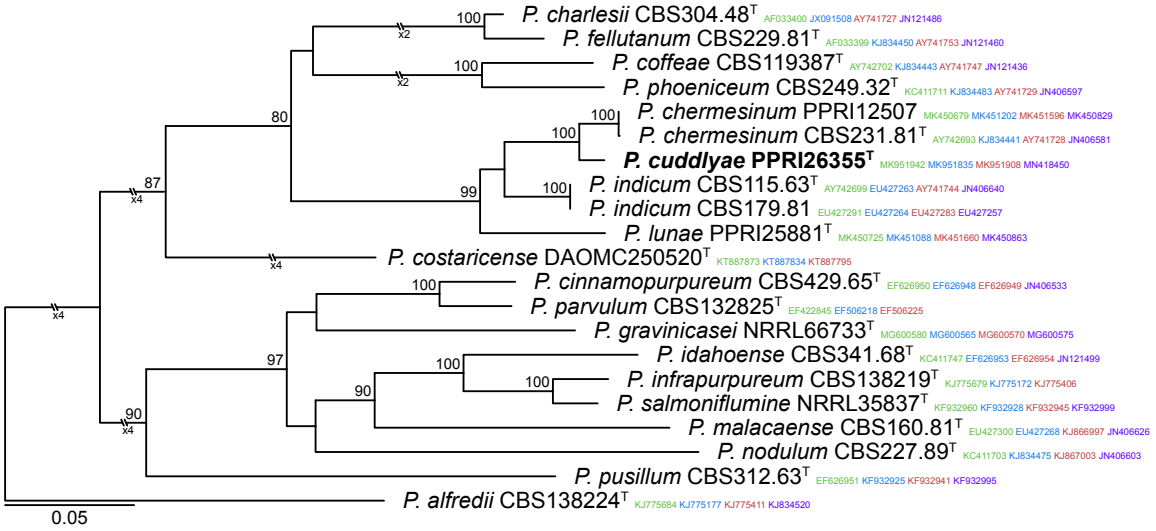
Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetes.*

Conidiophores monoverticillate; *stipes* smooth-walled, 20–45 × 2–3 µm; *vesicle* 5–6 µm wide; *phialides* ampulliform, 10–20 per vesicle, 8–10 × 2–3 µm (9 ± 0.7 × 2.6 ± 0.2); *conidia* smooth-walled, ellipsoid, often almost appearing cylindrical, 2–3 × 2.5–2 µm (2.5 ± 0.2 × 1.8 ± 0.2), average length/width = 0.73, n = 54.

Culture characteristics (25 °C, 7 d) — On Czapek yeast autolysate agar (CYA): Colonies low, radially and concentrically sulcate, raised centrally; margins low, narrow (1 mm), entire; mycelia white to inconspicuously yellow to orange; texture floccose; sporulation very sparse, conidia *en masse* not determined; soluble pigments absent; exudates clear to orange; reverse orange to reddish orange (6A7–7A7; colour code based on Kornerup & Wanscher (1967)), orange (5A6), pale yellow (2A3). On malt extract agar (MEA): Colonies low, plain, raised centrally; margins low, wide (3 mm), entire; mycelia white; texture velutinous and floccose; sporulation sparse to moderately dense, conidia *en masse* greyish green (25B3–26B3); soluble pigments absent; exudates absent; reverse greyish orange (5B6), greyish green (30B4–C4), yellowish white (2A2). On yeast extract sucrose agar (YES): Colonies moderately deep, radially and concentrically sulcate, sunken centrally; margins low, wide (2–3 mm), entire; mycelia white, inconspicuously yellow at centre; texture floccose; sporulation sparse, conidia *en masse* greenish white (25A2); soluble pigments absent; exudates absent; reverse orange (6A7), brownish orange (5C3), pale yellow (3A3). On dichloran 18 % glycerol agar (DG18): Colonies low, radially sulcate, raised centrally; margins low, narrow (1 mm), entire; mycelia white; texture floccose; sporulation sparse to moderately dense, conidia *en masse* greenish white (25A2); soluble pigments absent; exudates absent; reverse light orange (5A5), light yellow (3A5). On creatine sucrose agar (CREA): Colonies weak growth, no acid production. *Colony diam (in mm)*: CYA 24–26; CYA 30 °C 31–33; CYA 37 °C 19–21; CYA with 5 % NaCl 19–20; MEAbl 21–23; DG18 24–25; YES 30–32; oatmeal agar 28–30; CREA 12–14.

Typus. South Africa, Gauteng Province, Pretoria, from dog food, Feb. 2019, coll. *I. Rong*, isol. *C.M. Visagie* (holotype PREM 623302, cultures ex-type PPRI 26355 = CMV016A6, LSU, ITS, *BenA*, *CaM* and *RPB2* sequences GenBank MN388754, MK951942, MK951835, MK951908 and MN418450, MycoBank MB832433).

Notes — A BLAST search against an ex-type reference sequence dataset placed the new species in *Penicillium* sect. *Charlesia* (Visagie et al. 2014). A multigene phylogeny based on ITS, *BenA, CaM* and *RPB2* resolves *Penicillium cuddlyae* as sister to *P. chermesinum, P. indicum* and the recently described *P. lunae* (Crous et al. 2019a). All four genes distinguish these species. Morphologically, *P. lunae* is the only of the three that can grow on CYA at 37 °C. Compared to *P. chermesinum* and *P. indicum*, the new species generally shows more restricted growth (especially on CYA) (Pitt 1980, Peterson et al. 2005). Microscopically they are very similar except for *P. cuddlyae* and *P. lunae* producing longer phialides (up to 10 µm vs 7–8 µm) (Pitt 1980). *Penicillium cuddlyae* produces ellipsoid conidia compared to the subglobose to broadly ellipsoid conidia of *P. lunae*.



Combined phylogeny of representative *Penicillium* species from sections *Charlesia* and *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 in a smaller font after the culture accession number (ITS = green, *BenA* = blue, *CaM* = red, *RPB2* = purple). The tree is rooted to *P. alfredii*.

Colour illustrations. Dog food pellets. Colonies on CYA and MEA; colony texture on MEA; conidiophores; conidia. Scale bars = 10 µm.

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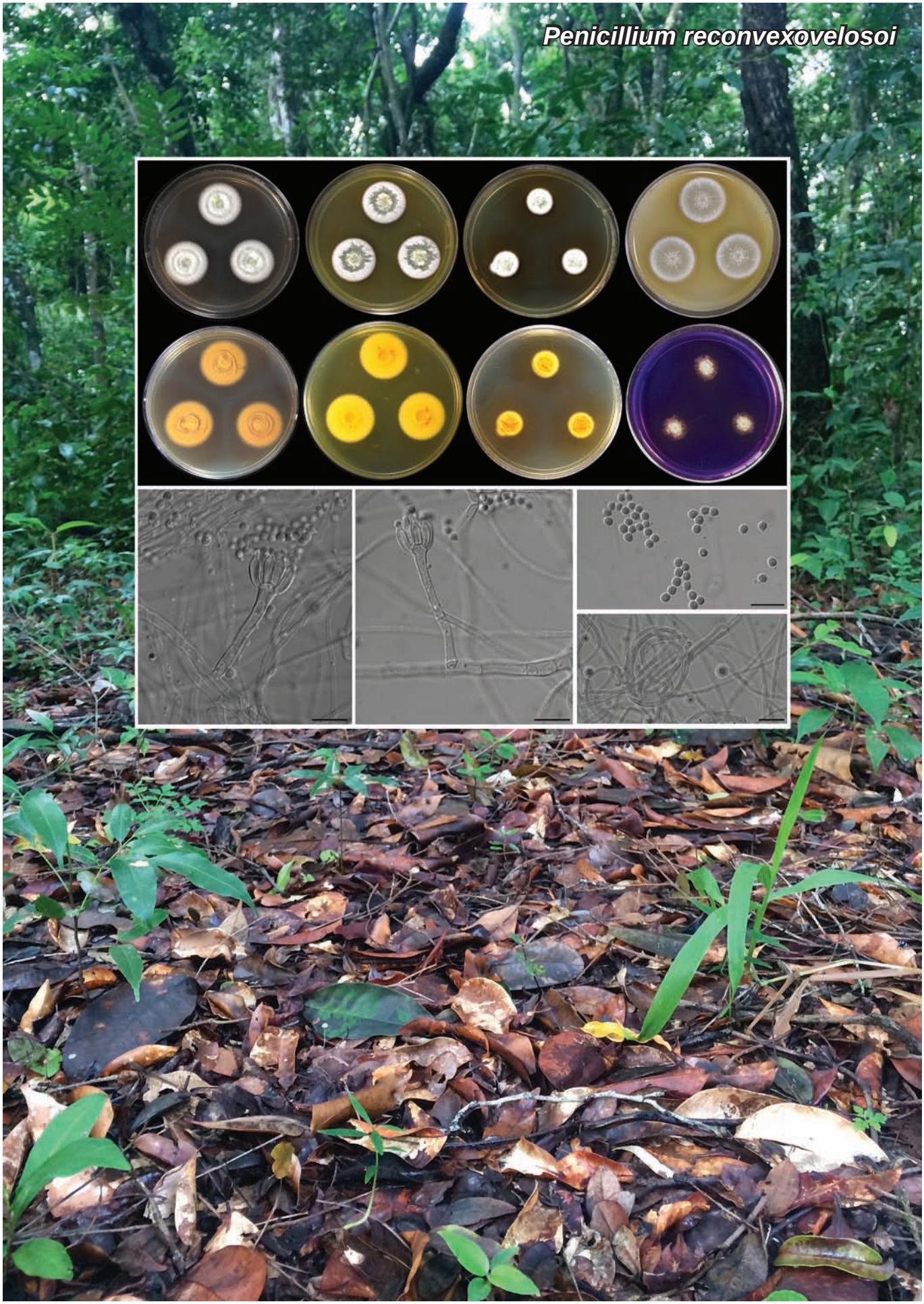

Penicillium reconvexovelosoi

Fungal Planet 1022 – 18 December 2019

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

Etymology. *reconvexovelosoi*, named in honour of the artist Caetano Veloso, an icon of Brazilian culture in the struggle for freedom of expression mainly during the military dictatorship.

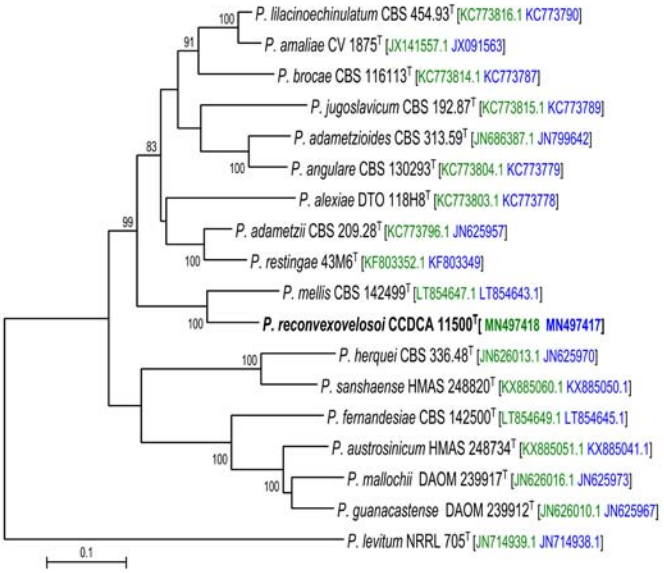
Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetes*.

Conidiophores monoverticillate. *Stipes* smooth to finely rough walled, 27–172 × 1.5–3.0 µm, sometimes *vesicilate,* 2–5 × 3–6 µm. *Phialides* ampulliform, 7–11 × 2–3 µm. *Conidia* finely roughened, ellipsoidal to subglobose, 2–2.5 × 2–3 µm. Mycelial coilings sometimes observed.

Culture characteristics — Colony diam (7 d, in mm): Czapek Yeast Autolysate agar (CYA) 28–29; CYA 30 °C 15–18; CYA 37 °C no growth; MEAbl 26–27; Yeast extract sucrose agar (YES) 21–23; Dichloran 18 % Glycerol agar (DG18) 27–29; Czapek Yeast Autolysate agar with 5 % NaCl (CYAS) 22–25; Oatmeal agar (OA) 28–30; Czapek's agar (CZ) 25–27; Creatine sucrose agar (CREA) 12–15, weak acid production.CYA, 25 °C: Colonies deep, concentrically sulcate, crateriform; margins low, wide, entire; mycelia white; texture floccose; sporulation moderate, conidia *en masse* white to light grey (1A1–D1) (Kornerup & Wanscher 1978); exudate light yellow, soluble pigment light brown; reverse greyish yellow to light orange (4B4–6A4) at centre and light orange (5A5) at margin. MEAbl, 25 °C: Colonies low, slightly raised in the centre, margins low, narrow, entire; mycelia white; texture floccose; sporulation moderate; conidia *en masse* white to olive grey (1A1–E2); exudate absent, soluble pigment golden yellow; reverse greyish yellow (3B5). YES, 25 °C: Colonies deep, radially and concentrically sulcate, crateriform, margins low, narrow, entire; mycelia white; texture floccose; sporulation sparse; conidia *en masse* white to light grey (1A1–D1); exudate absent, soluble pigment golden yellow; reverse greyish orange (5B4) light yellow (4A5) at margin. DG18, 25 °C: Colonies low, raised in the centre, margins low, narrow, entire; mycelia white; texture floccose; sporulation moderate; conidia *en masse* grey (3B1–C1); exudate absent, soluble pigment brilliant yellow; reverse greyish yellow (3B5). CYAS, 25 °C: Colonies radially and concentrically sulcate, crateriform, margins low, narrow, entire; mycelia white; texture floccose; sporulation sparse, conidia *en masse* yellowish white to grey (1A2–C1); exudate absent, soluble pigment light brown; reverse greyish yellow to reddish orange (4B6–7A8) at centre light orange (5A5) at margin. OA, 25 °C: Colonies low, plane; margins low, narrow, entire; mycelia white; texture velutinous; sporulation dense; pale yellow sclerotia present; conidia *en masse* olive grey (2D2); exudate clear, soluble pigment golden yellow. CZ, 25 °C: Colonies low, plane; margins low, wide, entire; mycelia white; texture floccose; sporulation sparse, conidia *en masse* pale grey (1B1); exudate absent, soluble pigment light brown; reverse pale orange (6A3) at centre and light brown (6D6) at margin.

Typus. Brazil, Bahia, in leaf litter from the Guaibim sandbank, S13°18' W38°57', 20 Aug. 2012, *V. de J. Nunes* (holotype HURB 18575 (dried culture on MEA); culture ex-type CCDCA 11500 = 45, LSU, *BenA* and *CaM* sequences GenBank MN497417, MN497418 and MN503515, MycoBank MB 832747).

Notes — *Penicillium reconvexovelosoi* is phylogenetically related to *P. mellis* (Barbosa et al. 2018), both included in the section *Sclerotiora*. *Penicillium mellis* grows faster than *P. reconvexovelosoi* on CYA 30 °C (33–35 mm) and YES (34–36) and grows slower on OA (24–25), DG18 (24–25) and CREA (10–11). *Penicillium reconvexovelosoi* does not grow on CYA 37 °C, but *P. mellis* grows (2–4 mm). *Penicillium reconvexovelosoi* may produce a soluble light brown pigment on CYA and weak acid production on CREA, but *P. mellis* does not produce soluble pigments in CYA and neither acid on CREA. *Penicillium reconvexovelosoi* has longer stipes than *P. mellis* (25–40 × 2–3.5 µm) and produces mycelial coils, but these structures were not reported for *P. mellis*. All macroscopic and microscopic measurements were done twice, independently, for isolate CCDCA 11500.



Maximum likelihood tree obtained by phylogenetic analysis of the combined *BenA* and *CaM* sequences from *Penicillium reconvexovelosoi* and phylogenetically related species in section *Sclerotiora* performed in MEGA v. 6.06 software employing K2+G+I model with 1 000 bootstrap re-samplings. Bootstrap support values (BS > 80 %) are presented at the nodes. *Penicillium levitum* NRRL 705^{T} was used as outgroup. The new species is presented in **bold** font (^{T} = ex-type). GenBank accession numbers are given between square brackets (*CaM* = green, *BenA* = blue).

Colour illustrations. Leaf litter at Guaibim environmental protection area located in Bahia, Brazil. Seven-day-old colonies growing at 25 °C, top row left to right, obverse CYA, MEAbl, YES and OA; bottom row left to right, reverse CYA, MEAbl, YES and obverse CREA, conidiophores, conidia and coiling of mycelia. Scale bars = 10 µm.

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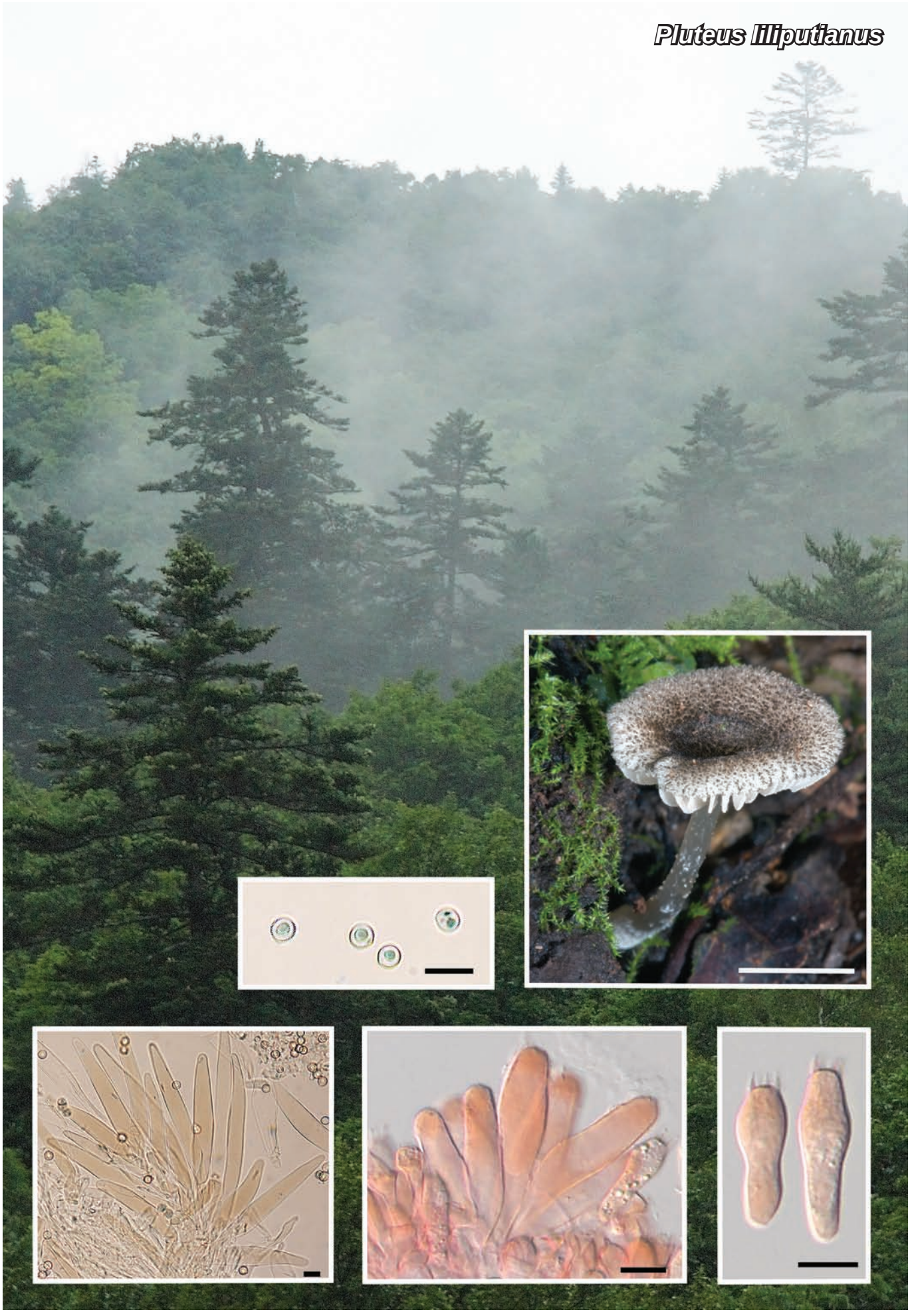

Pluteus liliputianus

Fungal Planet 1023 – 18 December 2019

Pluteus liliputianus E.F. Malysheva & Malysheva, *sp. nov*.

Etymology. The epithet reflects very small, diminutive size of basidiocarps.

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

Basidiocarp tiny. *Pileus* 9 mm diam, infundibular with concave centre; margin serrated, not striated, slightly undulating; not hygrophanous; surface squamulose, covered with small erect dark brown squamules, densely located at centre and scarce towards margin with white context exhibited between them, and the pattern of the squamules arrangement gives the impression of mottle. *Lamellae* free, fairly distant, ventricose, white becoming pink, with serrulated, concolorous edges. *Stipe* 10 × 1–1.5 mm, cylindrical, somewhat broadening towards base, but without basal bulb, whitish or with light ochraceous shades, slightly pruinose. *Context* in pileus and stipe white. *Smell* and *taste* not distinctive. *Basidiospores* 5.3–6.2 × 5–5.8 µm (L_{av} = 5.7, W_{av} = 5.3), Q = 1.00–1.16, Q* = 1.08, globose to subglobose; thick-walled; hyaline in KOH, with one large or numerous small guttules. *Basidia* 19–33 × 7.5–8.5 µm, 4-spored, broadly clavate with a medial constriction at maturity. *Cheilocystidia* rather numerous to abundant, forming sterile layer at the lamella edge, 36–83 × 9–15 µm, mainly clavate or narrowly utriform, rare almost cylindrical, pedicellate (with short to long pedicels), most of them with slimy apical caps or apical drops; slightly thick-walled; hyaline. *Pleurocystidia* absent. *Pileipellis* a cutis, made up of ascending bundles of narrowly fusiform or cylindrical thick-walled elements, with intracellular brown pigment, 70–170 × 10–14 µm. *Stipitipellis* a cutis, made up of long, cylindrical, hyaline hyphae, 4–10 µm wide. *Caulocystidia* absent. *Clamp connections* absent in all parts examined.

Habitat & Distribution — Solitary, on fallen branch of deciduous tree, in mixed coniferous-broadleaf forest. So far known only from type locality.

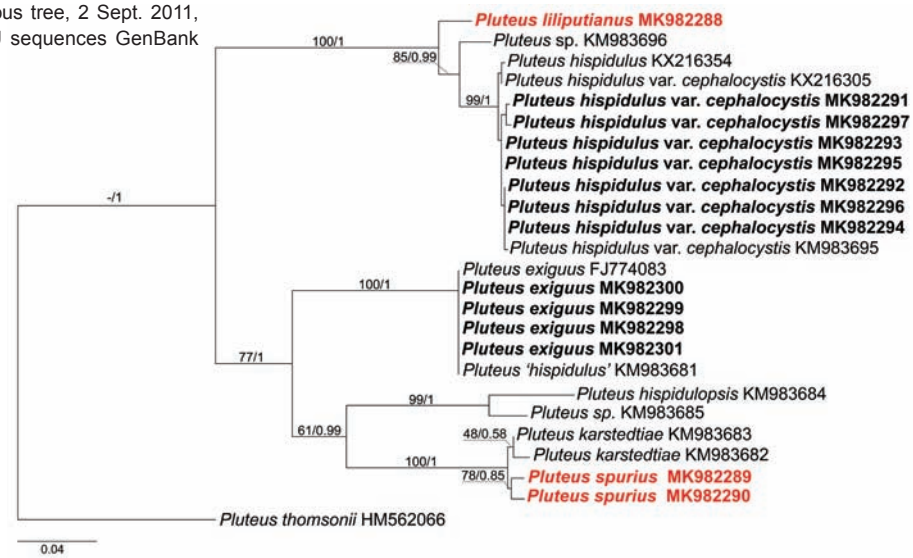
Typus. Russia, Primorye Territory, Land of the Leopard National Park, watershed of Ananievka and Gryaznaya rivers, mixed coniferous-broadleaf forest (with *Abies holophylla, Quercus mongolica, Carpinus cordata, Tilia mandshurica* and *Acer* spp.), on fallen branch of deciduous tree, 2 Sept. 2011, *V. Malysheva* (holotype LE 312868, ITS and LSU sequences GenBank MK982288 and MK982304, MycoBank MB831298).

Notes — *Pluteus liliputianus* is characterised by tiny basidiocarps, squamulose dark brown pileus with a peculiar arrangement pattern of squamules, pileipellis organised as a trichoderm with long fusiform terminal elements, absence of pleuro- and caulocystidia, and globose or subglobose basidiospores. Based on its pileipellis structure *P. liliputianus* is placed in sect. *Celluloderma*.

This new species resembles *P. hispidulus*, *P. exiguus*, *P. karstedtiae*, *P. hispidulopsis* and *P. spurius* by its macroscopic features but can be distinguished from them due to microscopic characters.

Pluteus liliputianus can be distinguished from the first three species listed mainly by the cheilocystidia shape, as well as shape and size of basidiospores (Vellinga 1990). It differs from *P. karstedtiae* by having a smaller basidiocarp, differently coloured pileus with more distinct squamation and non-striate margin, larger cheilocystidia, and the pileipellis structure (Menolli et al. 2015). *Pluteus hispidulopsis* is distinguished by the structure of its pileus surface and colouration, smaller basidiospores (5–5.5 × 4.5–5.5 µm), the presence of pleurocystidia and the pileipellis organised as a cutis (Menolli et al. 2015). *Pluteus spurius*, another species distributed in the same territory and described herein, is characterised by larger basidiocarps, differently shaped cheilocystidia, pileipellis a cutis, and the presence of caulocystidia.

In the phylogenetic analyses, the sequence of *P. liliputianus* forms an individual branch which is placed close to the group of *P. hispidulus*.



Best tree from the ML analysis of the nrITS dataset for *Pluteus hispidulus* and allied taxa with *P. thomsonii* as outgroup, generated on RAxML server v. 0.9.0. Bootstrap support values and Posterior probability (BS/PP) are given above the branches. All tips are labelled with taxon name and GenBank accession number. The newly generated sequences are in **bold**.

Colour illustrations. Russia, Land of the Leopard National Park, mixed coniferous-broadleaf forest. Basidiocarp; basidiospores; pileipellis; cheilocystidia; basidia (all from holotype). Scale bars = 5 mm (basidiocarp), 10 µm (microscopic structures).

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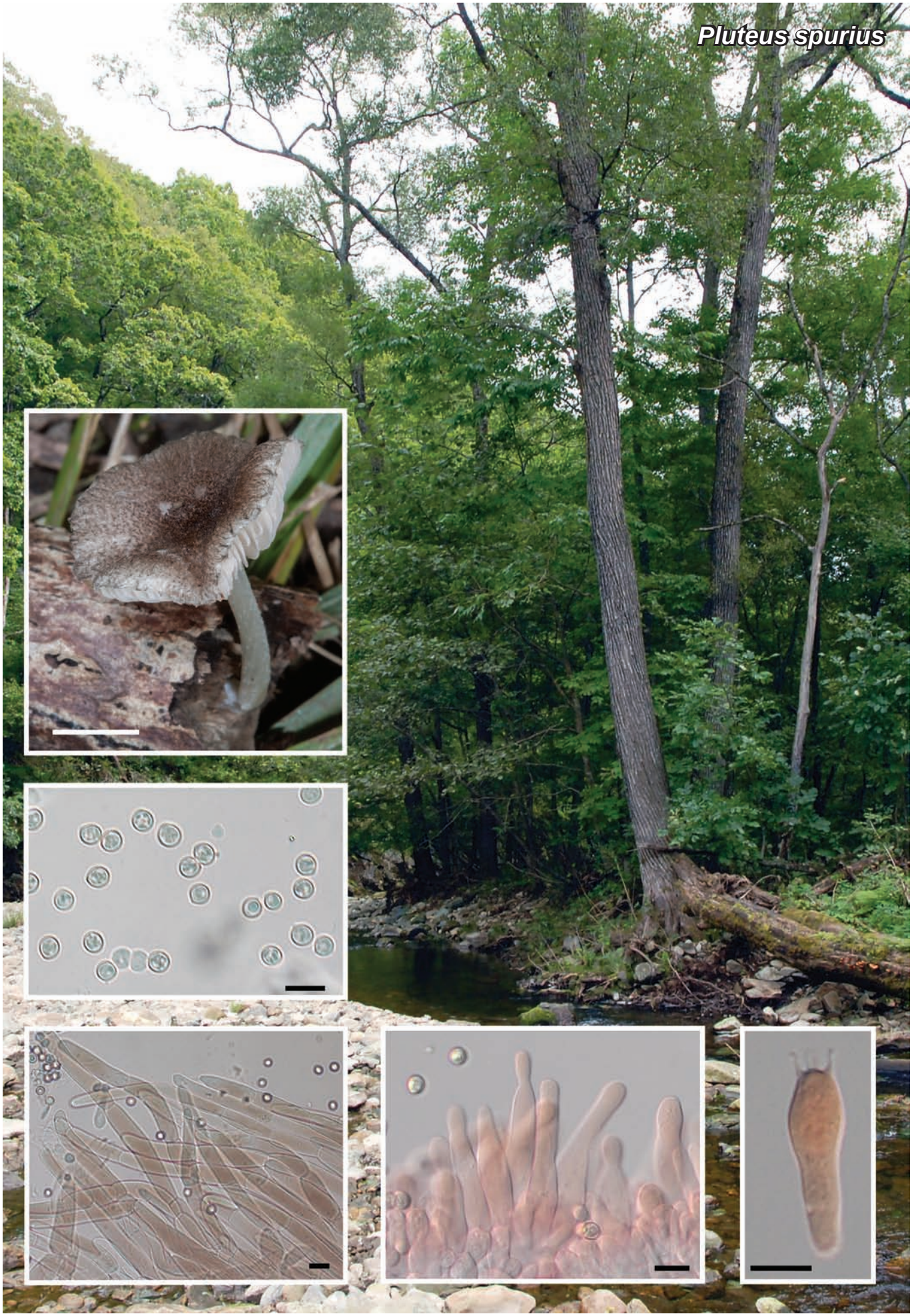
Pluteus spurius

Fungal Planet 1024 – 18 December 2019

Pluteus spurius E.F. Malysheva & Malysheva, *sp. nov*.

Etymology. Name reflects the similarity of the newly described species with a group of closely related taxa and the possibility of confusion when definition is based only on macroscopic features.

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

Basidiocarp small. *Pileus* 10–18 mm diam, at first hemispherical, later applanate and becoming concave, without umbo; margin even, not striated, slightly undulating; not hygrophanous; surface fibrillose-squamulose, covered with small greyish brown or ash brown squamules, densely located at centre, and adpressed fibrils becoming sparse towards margin with white context exhibited between them. *Lamellae* free, fairly distant, ventricose, white becoming pink, with serrulated, concolorous edges. *Stipe* 15–25 × 1–2.5 mm, cylindrical, somewhat broadening towards base, but without basal bulb, whitish or with light ochraceous shades, slightly pruinose and longitudinally fibrillose. *Context* in pileus and stipe white. *Smell* and *taste* not distinctive. *Basidiospores* (5.2–)5.5–6.5(–7) × (4.8–)5–5.6(–6.4) µm (L_{av} = 5.9, W_{av} = 5.3), Q = 1.00–1.22, Q* = 1.10, globose to subglobose; thick-walled; hyaline in KOH, with one large or numerous small guttules. *Basidia* 20–35 × 7–8.5 µm, 4-spored, broadly clavate with a medial constriction at maturity. *Cheilocystidia* rather numerous to abundant, forming sterile layer at the lamella edge, 30–54 × 9.5–15(–17) µm, mainly lageniform, inflated-lageniform or fusiform, rarely utriform or clavate, with short pedicels and often with subglobose apex; thin-walled; hyaline. *Pleurocystidia* absent. *Pileipellis* a cutis, made up of slightly thick-walled hyphae, 10–12 µm wide, with intracellular brown pigment; transforming into a trichoderm at centre of pileus, with bundles of fusiform, usually septate, terminal elements more than 100 µm long and 12–22 µm wide. *Stipitipellis* a cutis, made up of long, cylindrical, hyaline hyphae, 4–8 µm wide. *Caulocystidia* present in all parts of stipe, scarce, in bundles, cylindrical or fusiform, 50–120 × 8–10(–14) µm; thin- or slightly thick-walled; hyaline. *Clamp connections* absent in all parts examined.

Habitat & Distribution — Solitary, on decaying deciduous wood or soil, in floodplain broadleaf or mixed coniferous-broadleaf forests. Known from two localities in the Russian Far East.

Typus. Russia, Primorye Territory, Kedrovaya Pad' Biosphere Nature Reserve, floodplain of Kedrovaya River, broadleaf forest, on decaying wood of deciduous tree, 4 Sept. 2011, *V. Malysheva* (holotype LE 312866; ITS and LSU sequences GenBank MK982290 and MK982303, MycoBank MB831299).

Additional material examined. Russia, Primorye Territory, vicinities of Vladivostok, Ocean Ridge, mixed coniferous-broadleaf forest (*Abies holophylla*, *Pinus koraiensis*, *Juglans mandshurica*, *Acer* spp.), on soil, 9 Sept. 2013, *E. Malysheva* (LE 312869, ITS and LSU sequences GenBank MK982289 and MK982302).

Notes — *Pluteus spurius* is characterised by small-sized basidiocarps, with greyish brown coloured and fibrillose-squamulose pileus, serrulated edges of lamellae, pileipellis as a cutis with long fusiform terminal elements, absence of pleurocystidia, numerous caulocystidia, and globose or subglobose basidiospores. Based on its pileipellis structure *P. spurius* is placed in sect. *Celluloderma*.

Pluteus spurius is morphologically close to *P. hispidulus* var. *hispidulus*, *P. hispidulus* var. *cephalocystis, P. exiguus*, *P. karstedtiae* and *P. hispidulopsis* in terms of basidiocarp size, squamulose pileus of similar colouration, and pileipellis structure, but can be distinguished from them due to other microscopic features (for detailed discussion: see Additional data below).

The molecular data (generated nrITS sequences) confirmed the morphological differences between all species discussed and supported the recognition of *Pluteus spurius* as a separate taxon (see phylogenetic tree on the page with *Pluteus liliputianus* description = FP1023).

Additional data

Pluteus spurius can be distinguished from *P. hispidulus* var. *hispidulus* by the cheilocystidia shape, slightly smaller (vs (5.2–)6–8(–8.5) × (4–)5–6 µm), globose or subglobose basidiospores and the presence of caulocystidia (Vellinga 1990).

Pluteus hispidulus var. *cephalocystis* differs by ellipsoid basidiospores (Vellinga 1990) and the absence of caulocystidia (Malysheva et al. 2016).

Pluteus exiguus differs in the shape of cheilocystidia, ellipsoid or slightly amygdaliform basidiospores, and pileipellis organized as a trichoderm (Vellinga 1990).

Pluteus karstedtiae is distinguished by sulcate-striate margin of pileus, rare cheilocystidia of slightly different shape, and the absence of caulocystidia (Menolli et al. 2015). In the phylogenetic analyses, the sequences of *P. karstedtiae*, including one from the holotype, form a sister clade to *Pluteus spurius*.

Pluteus hispidulopsis differs in the fringed margin of pileus, smaller basidiospores (5–5.5 × 4.5–5.5 µm), the presence of pleurocystidia, differently shaped cheilocystidia and the absence of caulocystidia (Menolli et al. 2015).

Colour illustrations. Russia, Kedrovaya Pad' Biosphere Nature Reserve. Basidiocarp; basidiospores; pileipellis; cheilocystidia; basidia (all from holotype). Scale bars = 5 mm (basidiocarp), 10 µm (microscopic structures).

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Psathyrella ovispora
1 cm

Fungal Planet 1025 – 18 December 2019

Psathyrella ovispora D. Deschuyteneer, Heykoop & G. Moreno, *sp. nov.*

Etymology. Name reflects the unusual morphology of its spores.

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

Cap 9–23 mm broad and 6–13 mm high, convex to conical convex, flattened convex at maturity, with umbo, ochre-brown, hygrophanous, striate when moist, first drying at the margin that adopts a beige straw colour, leaving the central area with a darker ochre colour, finally light beige ochre colour. *Veil* fugacious, consisting of white appressed fibrils at margin of pileus, connecting the upper part of stipe, soon evanescent, leaving remnants on the edge of some gills near the stipe. Gills subventricose, adnate, more or less dark blackish greyish coloured, with white edge, but coloured brown in its half near the margin of the cap; lamellulae present. *Stem* 30–50 × 1.5–3 mm, cylindrical, slightly widened at the base, white to whitish, some with pale creamy ochre tones especially in the lower two thirds. *Odour* not distinctive. *Spores* (9.6–)10.3–12.3(–13.3) × (5.9–)6.3–7.8(–8.1) µm, av. 10.9–11.6 × 6.7–7.1; Q_{av} 1.6, ellipsoid and ovoid in frontal view and even a little rounded, asymmetric and amygdaliform in side-view, smooth, germ pore distinct, central, 1–1.5 µm, hilar appendix very tiny, base sometimes truncate giving a subtriangular look in frontal view, dark brown, not opaque, very granular, containing most often one large oil drop. *Basidia* 4-spored, rarely 2-spored, (21.9–)23.4–29.4(–31) × (10.2–)11.6–13.5(–15.1) µm, av. 26.5 × 12.6 µm, clavate, hyaline with intracellular content. *Pleurocystidia* (39.5–)43.7–66.7(–77.3) × (9.5–)10.4–17.4(–19.4) µm, numerous, mostly lageniform with a long neck, some of them shorter (sub)utriform, ventricose or clavate, apex obtuse, very rarely forked, most often widely pedicellate, always thin-walled, hyaline, some of them covered with mucoid droplets or granular deposits which gradually disappear in exsiccate. The importance of these deposits will have to be reassessed after examination of new fresh specimens. *Cheilocystidia* (23.6–)30.6–43(–55) × (8.2–)9.3–12.4(–14.1) µm, very numerous and densely packed, hyaline, sublageniform, ventricose, clavate, subutriform, often polymorphic, always thin-walled, apex obtuse, sometimes subcapitate, rarely forked. At the half of the lamella-edge close to the cap margin thin-walled cheilocystidia become scattered, fewer in number, intermixed with many clavate marginal cells (= paracystidia), some of them thick-walled and brown coloured. *Veil* fibrillose, consisting of elongated and septate hyaline hyphae with inflated endings. *Clamp connections* present.

Habitat & Distribution — Gregarious on nitrified calcareous loamy soil among grasses under *Conium maculatum*, *Foeniculum vulgare* with *Urtica urens*. So far only known from Spain and Hungary.

Colour illustrations. Spain, Alcalá de Henares, El Gurugú, nitrified calcareous loamy grasslands with *Conium maculatum* where the holotype was collected. Basidiomata; pleurocystidia; spores under LM; smooth spores under SEM (from the holotype). Scale bars = 1 cm (basidiomata), 10 µm (pleurocystidia and spores under LM), 2 µm (spores under SEM).

Typus. Spain, Madrid, Alcalá de Henares, El Gurugú, on nitrified calcareous loamy soil, among grass with *Conium maculatum* and *Urtica urens*, 2 Dec. 2016, *G. Moreno & M. Heykoop* (holotype AH 33724, ITS and LSU sequences GenBank MF966497 and MN190260, MycoBank MB832058).

Notes — *Psathyrella ovispora* is characterised by the unusual if not unique appearance of its spores which vary from ellipsoid to ovoid, with base sometimes truncate giving a subtriangular look in frontal view, asymmetric and amygdaliform in side-view, containing most often one large oil drop. Other characters are the small to medium sized basidiomata and its gregarious fruiting on calcareous nitrified soils.

Psathyrella ovispora was erroneously identified by us as *P. fusca* (Heykoop et al. 2017). A morphological re-evaluation of our material, comparing it with abundant samples of *P. tephrophylla* (= *P. fusca*), has showed that it corresponds to a new species. Moreover, our former cladogram (Heykoop et al. 2017), due to poor sampling, showed a unique *P. fusca* clade. However, new sequences of *P. tephrophylla* generated a cladogram (see Supplementary Fig. FP1025-2) in which two very distinct clades can be differentiated, i.e., *P. tephrophylla* clade A corresponding to *P. tephrophylla* s.str., and *P. tephrophylla* clade B corresponding to *P. ovispora*. The material included by Nagy et al. (2011) in their study as *P. fusca* is conspecific with *P. ovispora*.

The commonly used name *Psathyrella fusca* (Schumach.) A. Pearson is illegitimate, and must be rejected, since its basionym *Agaricus fuscus* Schumach. 1803 is a later homonym of *A. fuscus* Schaeff. 1774, *A. fuscus* Batsch 1783 and many others. Therefore, the correct name for *Psathyrella fusca* s.str. is *P. tephrophylla*. This nomenclatural problem will be discussed by one of us (Deschuyteneer) in a future paper.

Psathyrella ovispora shares with *P. tephrophylla* similar cheilocystidia and pleurocystidia. However, it differs from the latter by its very different spores, the much smaller basidiomata, by fruiting in a different habitat and by being genetically different. Due to its very wide spores *P. ovispora* keys out (key B) as *P. magnispora* in Örstadius et al. (2015). *Psathyrella ovispora*, however, differs from *P. magnispora* by its slightly larger basidiomata, the differently shaped spores and cystidia. Besides, *P. magnispora* is completely different genetically and constitutes the very distinct and monospecific *magnispora* clade, whereas *P. ovispora* belongs to the *pygmaea* clade (Örstadius et al. 2015)

Supplementary material

FP1025-1 Additional specimens examined.

FP1025-2 50 % majority rule ITS-28S rDNA consensus phylogram of the /pygmaea clade of *Psathyrella* (as delimited in Örstadius et al. 2015), with *P. magnispora* as outgroup. It was obtained in MrBayes from 3 900 sampled trees. Values next to nodes represent Bayesian PP and Maximum Likelihood BP. Only nodes supported by > 0.95 PP or > 70 % BP were annotated. Several clades around *P. pygmaea* were condensed (black triangle), and the rooting branch was reduced for publishing. **Bold** names represent samples sequenced in the present work.

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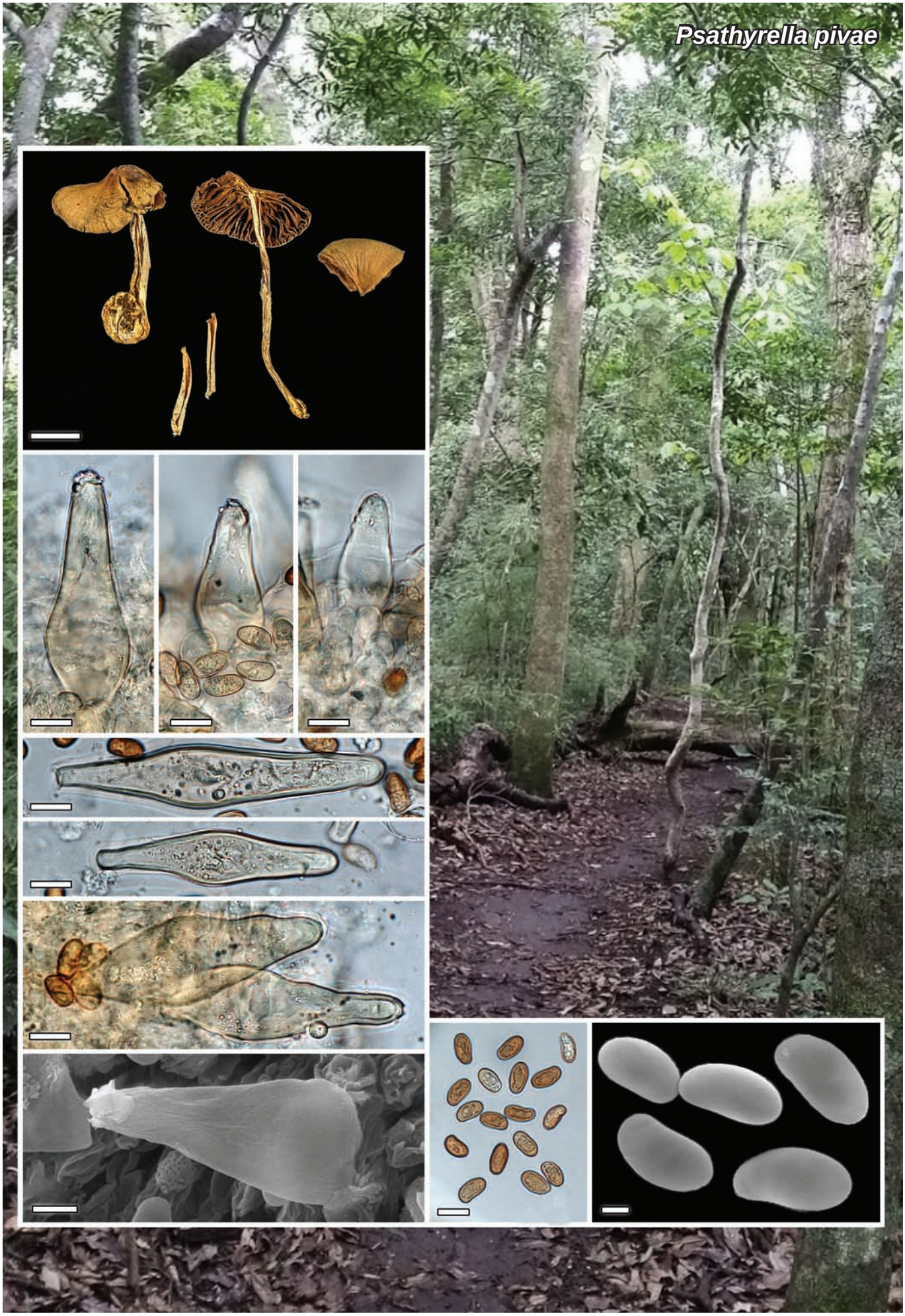

Psathyrella pivae

Fungal Planet 1026 – 18 December 2019

Psathyrella pivae Heykoop, G. Moreno & M. Mata, *sp. nov.*

Etymology. Named for Dr Alfio Piva, former Director of the INBio and ex vice-president of the Republic of Costa Rica, recognising his contribution to the conservation of biodiversity.

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

Cap 30–35 mm broad, applanate to slightly convex, surface fibrillose with appressed fibrils, coffee milky brown coloured. Margin deflexed, hygrophanous, striate when moist. *Context* of pileus 1 mm thick, 2 mm at centre, concolorous to surface. *Veil* forming a fibrillose annulus in the upper half of the stipe. *Gills* up to 5 mm broad, (sub)ventricose, adnate, smooth, coffee brown coloured, lamella-edge white; lamellulae present. *Stem* 50–55 × 4 mm, cylindrical, central, equal, some of them curved, hollow, fibrillose, yellow coffee coloured in the upper part, whitish in the lower part, with some dark brown fibrils at the apex and equipped with a fibrillose ring. *Odour* and *taste* not recorded. *Spores* (8.5–)9.5–11 × 5–6 µm, av. 9.9 × 5.5 (one collection); Q_{av} 1.79, ellipsoid to phaseoliform, smooth, with small apical germ pore (difficult to see), in NH_4OH (10 %) pale brown to orange brown. *Basidia* 4-spored, 22–30 × 9 µm, clavate, hyaline. *Pleurocystidia* 68–90(–100) × 15–27 µm, numerous, lageniform to ventricose-fusoid or fusiform, most of them with wall thickened 1–1.5 µm along entire length, often thickest at apex (up to 4 µm), yellowish refractive, very few thin-walled; apex of most cells encrusted with a cap of crystals and/or crystalline granular material. *Cheilocystidia* 38–50 × 12–14 µm, very abundant, lageniform to fusoid-ventricose, fusiform or even utriform, with walls thickened but thinner than those of pleurocystidia (rarely thin-walled), yellowish refractive, some of them colourless. *Hymenophoral trama* in NH_4OH (10 %) consisting of hyaline thin-walled hyphae, 2–5 µm diam, without encrustations. *Clamp connections* present.

Habitat & Distribution — Caespitose on woody debris. So far only known from Costa Rica.

Typus. Costa Rica, Guanacaste, Parque Nacional de Guanacaste, Rincón de La Vieja, Sector Santa María, Sendero del León, 800–900 m, 10:45:48.0520N–85:18:41.9040W, on wood, 13 Mar. 1996, *M. Mata 360* (holotype INB0003481172, ITS and LSU sequences GenBank MF966507 and MN161533, isotype AH 49110, MycoBank MB831899).

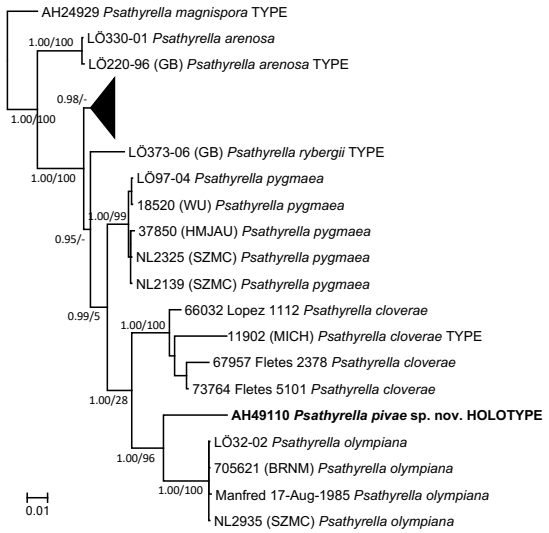
Additional materials examined. ***Psathyrella cloverae***: USA, Texas, Hidalgo County, Mission, scattered on the ground, June, year unknown, *E. Clover*, holotype MICH 11902 (E. Clover 2129), ITS sequence GenBank MF966417. – Costa Rica, Guanacaste, Arenal, Zona Protegida Arenal-Monteverde, A.C Arenal, R.B. Nuboso Santa Elena, Sendero Caño Negro, 900–1000 m; 10:21:17.8908 N–84:46:11.2907 W, on woody debris, 16 Feb. 2000, *I. López*, INB0003407719 (I.López 1112), ITS sequence GenBank MF966508; Puntarenas, Osa, Parque Nacional Corcovado, Sendero Espaveles, 0–100 m; 8:29:21.9637N–83:35:13.9191W, on trunks, 9 May 2003, *E. Fletes*, INB0003718172 (E. Fletes 5101), ITS sequence GenBank MF966510; Puntarenas, Osa, Parque Nacional Corcovado, Sendero Espaveles, 0–100 m; 8:29:21.9637N–83:35:13.9191W, on trunks, 12 May 2001, *E. Fletes*, INB0003752257 (E. Fletes 2376), ITS sequence GenBank MF966509.

Colour illustrations. Costa Rica, Parque Nacional Rincón de la Vieja, where the holotype was collected (photo Mauricio Torres). Basidiomata; cystidia and spores under LM and SEM (all from the holotype). Scale bars = 1 cm (basidiomata), 10 µm (microscopic elements under LM), 5 µm (cystidia under SEM), 2 µm (spores under SEM).

Notes — *Psathyrella pivae* is characterised by its fibrillose ring, abundant and very long thick-walled pleurocystidia and by growing caespitose on woody debris.

In our ITS phylogeny (see below) *Psathyrella pivae* belongs to the *pygmaea* clade (Örstadius et al. 2015) in which it is significantly related to *P. olympiana.* Within this monophyletic assemblage *P. pivae* forms a subclade together with *P. pygmaea*, *P. cloverae* and *P. olympiana*, all of them sharing the presence of more or less thick-walled pleuro- and cheilocystidia, apically covered with a crown of crystals and/or crystalline granular material. This clade has been included by Kits van Waveren (1985) in sect. *Spadiceae*. However, according to Larsson & Örstadius (2008), Vasutová et al. (2008), Nagy et al. (2013) and Örstadius et al. (2015), sect. *Spadiceae* turned out to be a polyphyletic taxon including species from two different genera, viz. *Psathyrella* and *Homophron*, since the presence of muricate pleurocystidia evolved independently at least in three different clades.

Because of the muricate pleurocystidia and the presence of veil *Psathyrella pivae* keys out in Kits van Waveren's monograph (1985) close to *P. olympiana*. *Psathyrella pivae*, however, differs from *P. olympiana* genetically and by the presence of a fibrillose annulus, larger spores and much longer pleurocystidia (up to 100 µm in length). *Psathyrella pivae* is a species with abundant fibrillose veil recalling macroscopically a *Stropharia* species, and as such it was tentatively identified in the field. Kits van Waveren (1985) included in his monograph *P. olympiana* f. *amstelodamensis*, characterised by its strongly developed veil but mentioning "in all other respects this form is identical with *P. olympiana*". Moreover, the illustrations of his f. *amstelodamensis* do not show any annulus on the stipe.



50 % majority rule ITS-28S rDNA consensus phylogram of the /pygmaea clade of *Psathyrella* (as delimited in Örstadius et al. 2015), with *P. magnispora* as outgroup. It was obtained in MrBayes from 3900 sampled trees. Values next to nodes represent Bayesian PP and Maximum Likelihood BP. Only nodes supported by > 0.95 PP or > 70 % BP were annotated. Several clades around *P. panaeoloides* and *P. abieticola* were condensed (black triangle), and the rooting branch was reduced for publishing.

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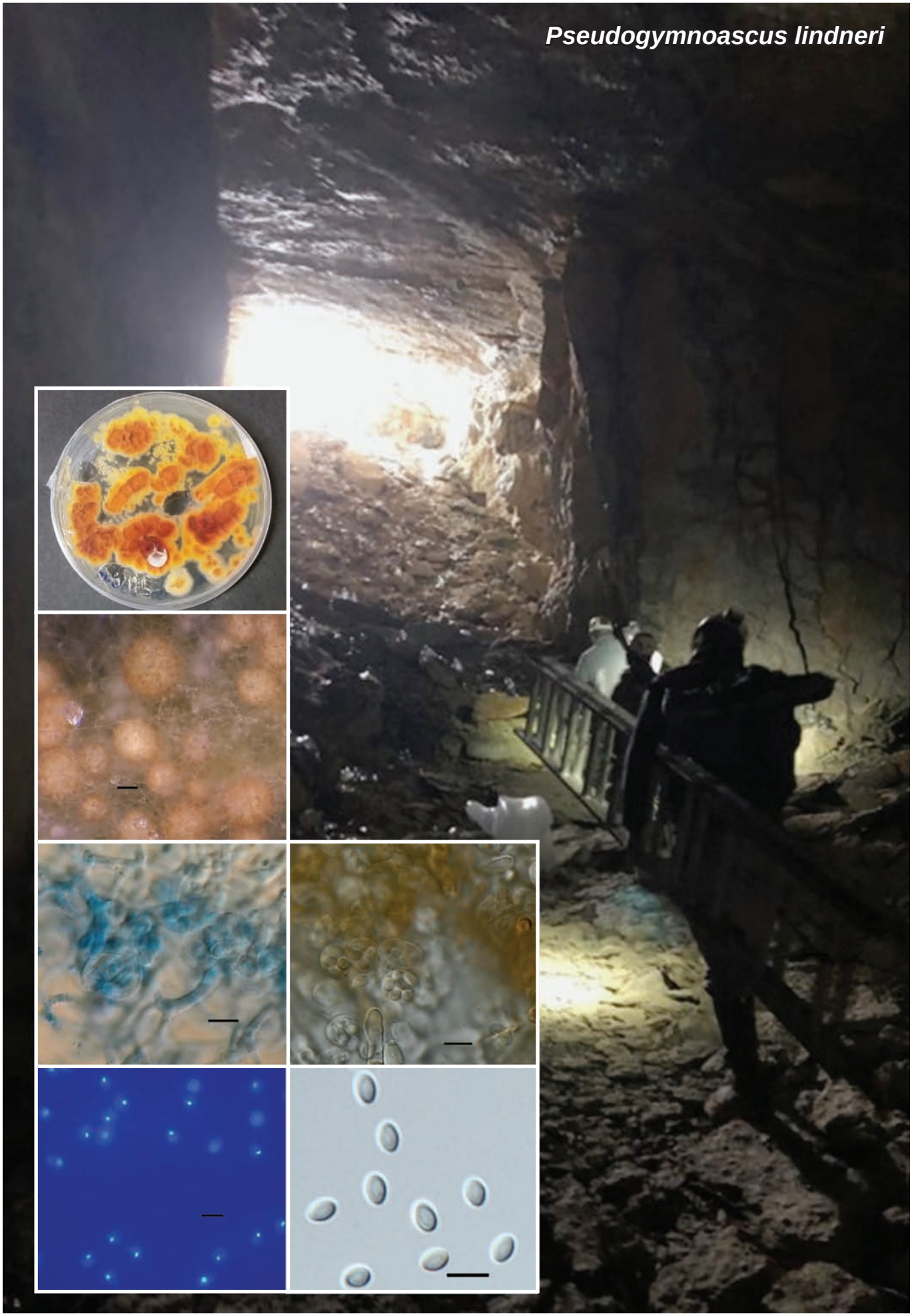

Pseudogymnoascus lindneri

Fungal Planet 1027 – 18 December 2019

Pseudogymnoascus lindneri Rea, Smyth & Overton, *sp. nov.*

Etymology. Named after Daniel Lindner from the United States Forest Service for his significant contributions to the modern taxonomy of *Pseudogymnoascus* and his contributions to White-nose Syndrome research.

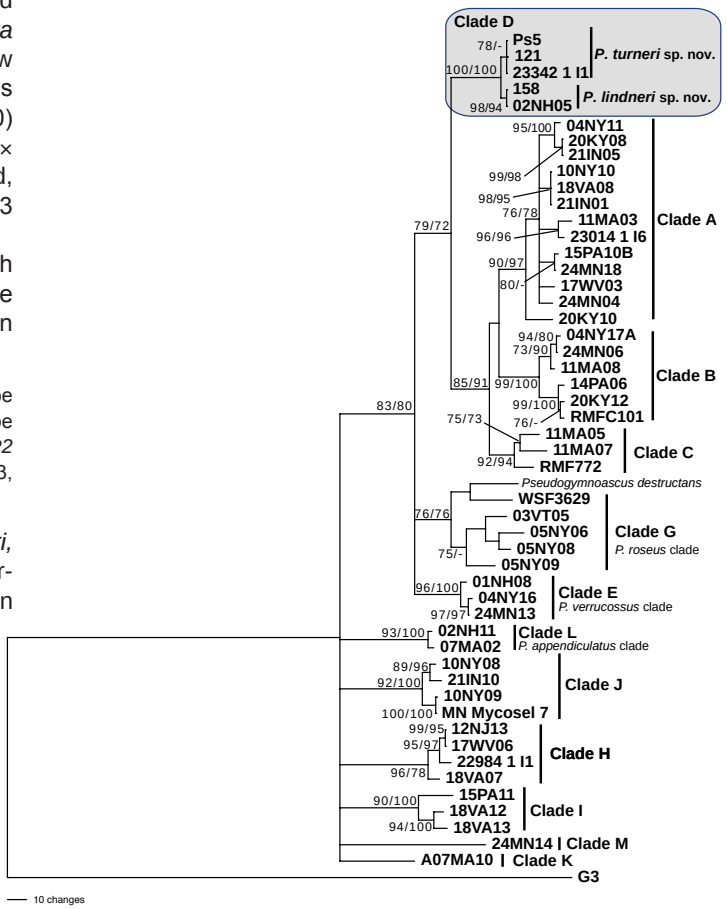
Classification — *Pseudeurotiaceae, incertae sedis, Leotiomycetes.*

On Sabouraud dextrose acidified with 120 µL 85 % lactic acid for optimal pigment production: *Conidia* borne singly at the tips, globose to obovate, smooth, with one abscission scar 2.8–4.1 (3.5, n = 30) µm in length. Intercalary conidia with two abscission scars, globose to truncate, measuring 3–4 (3.5, n = 10) µm in length. On oatmeal salt sediment agar: *Ascomata* gymnothecial, solitary, globose, measuring 181–311 (220, n = 20) µm diam; greyish orange (5B6; Kornerup & Wanscher 1978); developing rapidly and ripening within 10 d at 25 °C (12 h white fluorescent light / 12 h dark). *Ascomatal* initials coiled to irregular; peridium is a gymnothecium composed of *textura intricata*, the peridial hyphae darkly pigmented brownish yellow (5C7), smooth to minutely roughened with distinct appendages measuring 5.1–10.1 (7.6, n = 10) × 1.92–3.24 (2.5, n = 10) µm. *Asci* globose to ovoid, 8-spored, 5.4–8 (6.7, n = 84) × 3–6.1 (4.7, n = 84) µm in size. *Ascospores* aseptate, fusoid, smooth, greyish orange (5B6); 2.6–4 (3.2, n = 216) × 1.6–3 (2.1, n = 216) µm in size.

Culture characteristics — (12 h white fluorescent light / 12 h dark at 25 °C): Colonies at first yellow-orange to dark orange (4A7/8–5A8), in age changing to brown-orange to brown (6C8–6E8) after 10 d.

Typus. USA, Pennsylvania, Blair County, Canoe Creek State Park, Canoe Creek Hartman Mine, from sediment, 2017, *B. Overton* LHU 158 (holotype in Cornell University Plant Pathology Herbarium (CUP-070714), ITS, *RBP2* and *TEF-1α* sequences GenBank MN542212, MN541384 and MN541383, MycoBank MB832750).

Notes — Morphological analyses suggest that *P. lindneri,* and *P. bhattii* could be sister taxa. They are similar in the morphological characteristics of gymnothecial ascomata production and colony colouration. Samson (1972) described *P. bhattii* as being characterised by yellow ascomata and the absence of distinct peridial appendages. However, *P. lindneri* can be distinguished from *P. bhattii* based on conidiogenesis (*P. bhattii* does not produce conidia) and the presence of distinct peridial appendages. Minnis & Lindner (2013), were the first to study many *Pseudogymnoascus* taxa using modern phylogenetic methods using a multigene approach. In their work, they identified multiple clades of *Pseudogymnoascus.* The new species described here is identical in the three genes studied to the same three genes from Minnis & Lindner's 02NH05 isolate deposited in GenBank. Isolate 02NH05 up until this point has remained an undescribed homothallic species since the publication of their work. This work is the first to unite morphological characters used by Samson (1972) with molecular data.



Phylogenetic placement of *Pseudogymnoascus lindneri* on a maximum parsimony tree with maximum likelihood/maximum parsimony bootstrap support values, generated from the concatenated dataset of three loci (rDNA, *TEF* and *RPB2*) using PAUP v. 4.0a build 166 (Swofford 2003). The parsimony analysis generated a single most parsimonious tree via strict consensus. A maximum likelihood analysis was completed using GARLI v. 2.01 (Zwickl 2006) on the CiPRES Science Gateway (Miller et al. 2010). We generated a consensus tree from a single replicate ML analysis with 1000 bootstrap pseudo-replications. The General Time Reversible (GTR) evolutionary model was used with estimate selected for the proportion of invariant sites, and gamma distribution as the model of rate heterogeneity. Bootstrap support values located at nodes are: Maximum Likelihood/Maximum Parsimony. Alignment and tree(s) in TreeBASE (study 25145).

Colour illustrations. Background photo of Canoe Creek Hartman Mine, Canoe Creek State Park. Fluorescence image of nuclei in conidia on SAB; asci and peridial hyphae on oatmeal agar; ascomatal initials on oatmeal agar at 10 d; ascospores on oatmeal agar; gymnothecia on oatmeal agar; colony back colour on SAB at 10 d. Scale bar = 100 µm (gymnothecia), 5 µm (all others).

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Pseudogymnoascus turneri

Fungal Planet 1028 – 18 December 2019

Pseudogymnoascus turneri Rea, Smyth & Overton, *sp. nov.*

Etymology. Named after Gregory G. Turner from the Pennsylvania Game Commission for his many contributions to the study and conservation of hibernating bats affected by White-nose Syndrome, a wildlife disease caused by the invasive fungal pathogen *Pseudogymnoascus destructans*.

Classification — *Pseudeurotiaceae, incertae sedis, Leotiomycetes.*

On Sabouraud dextrose acidified with 120 µL 85 % lactic acid for optimal pigment production: *Conidia* borne singly at the tips, globose to obovate, smooth, with one abscission scar 2.5–4.3 (3.3, n = 30) µm in length. Intercalary conidia with two abscission scars, globose to truncate, measuring 3–5.5 (3.8, n = 30) µm in length. On oatmeal salt sediment agar: *Ascomata* gymnothecial, solitary, globose, measuring 103–263 (173, n = 20) µm diam; greyish orange (5B6; Kornerup & Wanscher 1978); developing rapidly and ripening within 10 d at 25 °C, (12 h white fluorescent light / 12 h dark). *Ascomatal* initials coiled to irregular; peridium is a gymnothecium composed of *textura intricata*, the peridial hyphae darkly pigmented brownish yellow (5C7), smooth to minutely roughened with distinct appendages measuring 4.6–11.4 (7.0, n = 10) × 2.2–2.8 (2.4, n = 10) µm. *Asci* globose to ovoid, 8-spored, 5–7.7 (6.5, n = 84) × 3.2–6 (4.6, n = 84) µm in size. *Ascospores* aseptate, fusoid, smooth, greyish orange (5B6); 2.9–4.8 (3.5, n = 216) × 1.8–2.9 (2.1, n = 216) µm in size.

Culture characteristics — (12 h white fluorescent light / 12 h dark at 25 °C): Colonies at first pastel yellow to light yellow (3A3–5), in age changing to reddish golden to brown-orange (6C7–8) after 10 d.

Typus. USA, Pennsylvania, Clearfield County, Sabula railroad tunnel, from sediment, 2017, *Dr. Barrie Overton* LHU 121 (holotype in Cornell University Plant Pathology Herbarium (CUP-070715), ITS, *RBP2* and *TEF-1α* sequences MN542213, MN541380 and MN541379; MycoBank MB832738).

Additional material examined. USA, Pennsylvania, Blair County, Canoe Creek State Park, Canoe Creek Hartman Mine, from sediment, 2016, *Dr. Barrie Overton*, paratype LHU Ps5 in Cornell University Plant Pathology Herbarium (CUP-070716), ITS, *RBP2* and *TEF-1α* sequences MN542214, MN541382 and MN541381.

Colour illustrations. Background photo of Sabula Railroad Tunnel, Pennsylvania, USA. Conidia on SAB; ascospores on oatmeal agar; SEM image of asci and peridial hyphae from oatmeal agar; DIC image of asci and peridial hyphae on oatmeal agar; colony back colour on SAB at 10 d; gymnothecia on oatmeal agar; ascomatal initials on oatmeal agar at 10 d. Scale bar = 100 µm (gymnotheicia), 10 µm (SEM image), 5 µm (all others).

Notes — Morphological analyses suggest that *P. turneri, P. lindneri* and *P. bhattii* could be sister taxa. They are similar in the morphological characteristics of gymnothecial ascomata production and colony colouration. Samson (1972) described *P. bhattii* as being characterised by yellow ascomata and the absence of distinct peridial appendages. However, *P. turneri* can be distinguished from *P. bhattii* based on conidiogenesis (*P. bhattii* does not produce conidia) and the presence of distinct peridial appendages. *Pseudogymnoascus turneri* can be distinguished from *P. lindneri* based on ascospore dimensions (*P. lindneri* ascospores are smaller in size: 2.6–4 × 1.6–3 (3.2 × 2.1 µm, n = 216) and gymnothecial dimensions (*P. lindneri* gymnothecia are larger, 181–311 µm diam (220, n = 20). Minnis & Lindner (2013) were the first to analyse many *Pseudogymnoascus* taxa using modern phylogenetic methods using a multigene approach. In their work, they identified multiple clades of *Pseudogymnoascus.* The new species described here is identical in the three genes analysed to the same three genes from Minnis & Lindner's 23342-1-I1 isolate. Isolate 23342-1-I1 has remained an undescribed homothallic species since the publication of their work. In addition to the morphological differences elucidated between *P. turneri* and *P. lindneri*, there is strong bootstrap support separating these species based on a three-gene-phylogeny. This work is the first to unite the morphological characters used by Samson (1972) with molecular data.

For phylogenetic tree see FP 1027.

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Pulchroboletus sclerotiorum

Fungal Planet 1029 – 18 December 2019

Pulchroboletus sclerotiorum M.E. Sm., Bessette & A.R. Bessette, *sp. nov.*

Etymology. The epithet *sclerotiorum* is in reference to the subterranean orange sclerotia formed by this species.

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

Basidiomata epigeous, pileate, pileus 4–10 cm wide, hemispheric at first, becoming convex to broadly convex at maturity, surface dry, dull or somewhat shiny, matted-subtomentose, pinkish red to rose-red or purplish red, sometimes with olive tints, becoming dull rose-pink to brownish pink in age, slowly staining blackish blue when bruised, margin bright yellow, often persistent, incurved at first, with a narrow band of sterile tissue; pileipellis tastes slightly acidic, immediately staining grey then fading to orange with red areas bleached with KOH, slowly staining weakly orange with NH_4OH, and olive-grey with $FeSO_4$. *Context* pale yellow, sometimes with a pinkish tinge under the pileipellis, staining blue when exposed, sometimes weakly and erratically, staining pale orange with KOH, negative with NH_4OH on yellow areas, and bleaching blue areas, $FeSO_4$ staining context faintly bluish grey, *odour* not distinctive, *taste* acidic. *Hymenophore* bright yellow at first, becoming dull yellow then brownish yellow at maturity, staining blue when bruised, slightly depressed near the stipe in age, pores angular to irregular, 2–3 per mm, tubes 6–15 mm deep, yellow, staining blue then brown when bruised. *Stipe* 4.5–9 cm long, 1–2 cm thick, enlarged downward or nearly equal, solid, surface dry, longitudinally striate, yellow at apex, red on lower portion, with conspicuous red to reddish brown punctae over a yellow ground colour, staining blue when handled or bruised, sometimes slowly, lacking reticulation or sometimes reticulate on upper portion, reticulation yellow at the apex and reddish below, often with white basal mycelium and yellow rhizomorphs sometimes with orange sclerotia, context brighter and deeper yellow than in the pileus, reddish brown around larval tunnels, staining bluish green, sometimes slowly and erratically. *Spores* olive-brown in fresh deposit, (12–)14–16(–18) × 4–6 µm, n = 20, av. = 15.15 × 4.99 µm, Q = 3.05, subfusoid to fusiform, hyaline to pale brownish yellow, smooth, thin-walled. *Basidia* 24–28 × 6.5–11 µm, clavate, 4-sterigmate, hyaline, lacking dextrinoid contents in Melzer's. Hymenial cystidia not observed. *Hymenophoral trama* boletoid, with lateral elements 4.5–10 µm, moderately divergent, hyaline to pale greyish yellow in KOH, pale greyish yellow in Melzer's. *Pileus* trama hyphae loosely interwoven, hyaline in KOH, pale ochraceous in Melzer's, inamyloid, 5–17.5 µm wide, thin-walled, smooth. *Pileipellis* a suberect trichodermium that becomes a cutis of tangled and interwoven cylindrical hyphae, with red contents in water, hyaline in KOH, with dingy ochraceous contents in Melzer's, inamyloid, 5–9 µm wide, immediately staining orange with KOH, staining slowly and weakly orange with NH_4OH, and staining pale olive-grey or negative with $FeSO_4$. *Stipitipellis* hymeniform with clavate elements 5–13 µm wide, subparallel to interwoven, pinkish red to red in water, ochre in KOH, and yellow-brown to reddish brown in Melzer's, with scattered clavate caulocystidia. *Stipe* trama parallel, vertically oriented, cylindrical, hyaline, inamyloid, with scattered oleiferous elements. *Clamp connections* absent.

Habitat & Distribution — Scattered or in groups, often on sandy soil, with species of *Quercus*, summer to fall (July-November), eastern USA from Massachusetts to Florida.

Typus. USA, Florida, Putnam County, Ordway-Swisher Biological Station, c. 50 m asl, in oak-dominated forest, 14 June 2017, *L. Kaminsky* (holotype FLAS-F-60908, ITS sequence GenBank MH016883, MycoBank MB830772).

Paratypus. USA, Tennessee, Anderson County, Oak Ridge, beneath *Quercus,* 21 Aug. 2015, *H. Hitchcock*, ARB1260 (FLAS-F-60333, ITS, LSU, *rpb1, rpb2* and *tef1* sequences GenBank MF098659, MF614166, MF614168, MF614169 and MF614165).

Notes — *Pulchroboletus sclerotiorum* is characterised by the red pileus with a distinctive yellow margin, yellow hymenophore that stains blue when bruised, yellow and red stipe with conspicuous red to reddish brown punctae over a yellow ground colour, often with white basal mycelium and yellow rhizomorphs and an association with oaks. Among similar species *Boletus rubissimus* also has a pinkish red to rose-red pileus with a bright yellow margin and a similarly coloured stipe, but it has different macrochemical reactions and smaller spores, 9–11 × 3–4.5 µm. *Hortiboletus rubellus* has reddish orange context in the lower stipe, tubes that split lengthwise when torn, and smaller spores, 10–13 × 4–5 µm. *Pulchroboletus rubricitrinus* has a similarly coloured pileus that lacks a bright yellow margin, has a more yellow, longitudinally striate stipe streaked with red, and has different macrochemical reactions. *Aureoboletus mirabilis* is found in the Western USA with conifers, has a dark purplish red to reddish brown pileus, a yellow pore surface and context that does not stain blue. *Xerocomus morrisii* has a brown pileus, yellow context that does not stain blue, a yellow pore surface that becomes brownish orange to brick-red in age, and a punctate stipe. *Hemileccinum subglabripes* has an ochre to reddish brown pileus, a yellow pore surface that does not stain blue, and red to reddish brown punctae on its stipe. *Pulchroboletus sclerotiorum* is also distinct based on molecular characters. BLAST searches based on ITS rDNA did not match closely with any known boletes. The most closely related named taxa in GenBank are *P. roseoalbidus*, *P. rubricitrinus, Boletus smithii* and *Gasteroboletus vividus*. However, sequences of these taxa were < 91 % similar across the ITS. ITS sequences provide important insight into the ecology of this new species because they match a sequence from orange sclerotia collected beneath oaks in Massachusetts (Smith & Pfister 2009). Sclerotia of ectomycorrhizal fungi are rarely reported in the literature (Smith et al. 2015) but several other species of ectomycorrhizal *Boletales* have been shown to form sclerotia, including *B. rubropunctus* (Smith & Pfister 2009) and *Leccinum holopus* (Müller & Agerer 1990).

Colour illustrations. Quercus-dominated forest at the Ordway-Swisher Biological Reserve where *Pulchroboletus sclerotiorum* is found during wet periods in summer and fall. Basidiomata of specimen FLAS-F-60908; orange sclerotia of *P. sclerotiorum* (MES-260) from oak woodland; pale brownish basidiospores in KOH. Scale bars = 1 cm (basidiomata), 3 mm (sclerotia), 5 µm (basidiospores).

Supplementary material

FP1029-1 Additional specimens examined.

FP1029-2 Phylogenetic tree based on Maximum Likelihood analysis of ITS rDNA in RAxML v. 8 shows the placement of *Pulchroboletus sclerotiorum* among *Pulchroboletus* and *Alessioporus* species (*Boletaceae, Boletales*). *Hemileccinum impolitum* served as the outgroup.

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Russula quercus-floribundae

Fungal Planet 1030 – 18 December 2019

Russula quercus-floribundae M. Kiran & Adamčík, *sp. nov.*

Etymology. The name refers to the probable host tree, *Quercus floribunda* (synonym *Q. dilatata*).

Classification — *Russulaceae*, *Russulales*, *Agaricomycetes*.

Pileus medium-sized, 45–60 mm diam, semi-globose, convex, centrally slightly depressed when mature; margin incurved, tuberculate-striate when mature; surface relatively shiny also when dry, smooth near the margin, rugulose and pitted at the centre, near the margin brown-red to orange-red sometimes discolouring to pale orange; towards the centre orange, yellow-brown to reddish brown. *Lamellae* relatively dense, adnate-emarginate, first white, becoming pale yellow; lamellulae very rare, furcations frequent near the stipe, edge even and becoming red-brown, spotted when old or after handling. *Stipe* 40–65 × 5–12 mm, obclavate, central, longitudinally striate, on white background with yellow-brown to brown flush or spots, especially in central part and near the base, without pinkish shades. *Context* white, unchanging, compact. *Spores* (10.3–)10.9–12.3(–13.4) × (8.8–)9.7–11(–11.7) µm, av. 11.6 × 10.4 µm, subglobose to broadly ellipsoid, Q = (1.04–)1.07–1.19(–1.28), av. Q = 1.13; ornamentation of large, distant to moderately distant (3–5(–7) in a 3 µm diam circle) amyloid spines, (1.2–)1.3–1.9(–2.2) µm high, occasionally to frequently fused in branched or unbranched long chains, radially oriented from suprahilar spot ((0–)1–3(–4) fusions in the circle), connected by dispersed fine line connections (0–1(–3) in the circle); suprahilar spot large, amyloid, irregular in shape. *Basidia* (47–)51.5–62(–67) × (14–)16–20.5(–22) µm, av. 56.8 × 18.2 µm, 2–4-spored, broadly clavate, sometimes pedicellate; basidiola first cylindrical or ellipsoid, then clavate, 4.5–11 µm wide. *Hymenial cystidia* on lamellar sides dispersed, 450–600 /mm^2, (75.5–)82.5–107(–125) × (12–)15.5–20.5(–22) µm, av. 94.4 × 17.9 µm, fusiform or rarely clavate, often pedicellate, walls thin or sometimes slightly thickened (0.5–1 µm), apically obtuse or acute and occasionally with 4–12 µm long appendage; contents heteromorphous, crystalline-banded, turning red-brown to almost black in sulfovanillin; abundant near the lamellae edges, (63.5–)73.5–99(–115) × (7–)9–13(–16) µm, av. 86.4 × 10.6 µm, narrower and more frequently clavate and appendiculate. Lamellae edges fertile; marginal cells not well differentiated, 11–20 × 4–5 µm, cylindrical or clavate. *Pileipellis* orthochromatic in Cresyl blue, not sharply delimited from the underlying context, 130–190 µm deep, strongly gelatinised throughout, covered by often disconnected, 50–60 µm deep extra gelatinous matter. Acid-resistant incrustations absent. Hyphal terminations in pileipellis near the pileus margin frequently branched, often slightly flexuous, thin-walled; terminal cells (10–)20.5–42.5(–60) × 2–3.5(–5) µm, av. 31.6 × 3 µm, mainly cylindrical, apically often slightly attenuated; subterminal cells equally wide and sometimes shorter, usually branched. Hyphal terminations near the pileus centre narrower and more flexuous, terminal cells (15–)21.5–38.5(–45) × (1.5–)2–3(–3.5) µm, av. 30 × 2.5 µm. *Pileocystidia* near the pileus margin very abundant, 1–3(–4)-celled, cylindrical to narrowly clavate, thin-walled, terminal cells (12–)25–62(–87) × (3–)4–6.5(–10.5) µm, av. 43.5 × 5.1 µm, mainly cylindrical or clavate, apically mainly obtuse, contents heteromorphous, mainly banded, occasionally also granulose, weakly turning greyish in sulfovanillin. Pileocystidia near the pileus centre similar, terminal cells (14.5–)29.5–72.5(–105) × (3.5–)4–7(–10) µm, av. 51 × 5.5 µm. *Cystidioid hyphae* in subpellis and context dispersed, contents heteromorphous-banded.

Typus. Pakistan, Khyber Pakhtunkhwa province, Malakand division, Swat district, Upper Shawar, alt. 1300 m, on the floor of *Quercus floribunda* dominated forest mixed with a few pines, 29 July 2018, *Z. Ullah BS59* (holotype LAH 36219, ITS, LSU, mtSSU and *rpb2* sequences GenBank MN053395, MN513043, MN053397 and MN053389, MycoBank MB831387).

Additional material examined. Pakistan, Upper Shawar, Malakand division, Swat district, Upper Shawar, alt. 1300 m, on the floor of *Quercus floribunda* dominated forest mixed with a few pines, 29 July 2018, *Z. Ullah BS80* (LAH 36220, ITS, LSU, mtSSU and *rpb2* sequences GenBank MN053391, MN513043, MN053396 and MN053390).

Notes — The type ITS sequence has the closest GenBank BLAST match (98.7 %) with an unidentified *Russula* from China (GenBank JQ991794) and the most similar sequences identified to species are those of *R. tengii* (95.6 %) and *R. dryadicola* (95.6 %). Our multi-locus phylogenetic analysis based on nrITS, *rpb2* and mtSSU clearly places *R. quercus-floribundae* in the *R. globispora* lineage as sister of two sequences of unidentified *Russula* from China (for the phylogenetic tree, see Supplementary Fig. FP1030). They form a well-supported clade with *R. abbottabadensis* from Pakistan and *R. heilongjiangensis* from China. All Asian species share features typical for the *R. globispora* lineage: brownish yellow spots on basidiomata, red and soon discolouring pilei and large spores with prominent spines. *Russula dryadicola*, *R. globispora* and *R. tengii* differ in isolated spines of spore ornamentation that do not form chains (Caboň et al. 2019). *Russula heilongjiangensis* has similar spore ornamentation but has narrower hymenial cystidia on lamellae sides (Li et al. 2018). *Russula quercus-floribundae* has, together with sequestrate species *R. mediterraneensis* and *R. mattiroloana*, the largest spores within the lineage, often exceeding 11 µm (Vidal et al. 2019).

Colour illustrations. Background: *Quercus floribunda* dominated forest in Upper Shawar (Khyber Pakhtunkhwa province, Pakistan) where the holotype was collected. Bottom row: basidiomata of collection LAH 36220 (left) and the type collection (right). Line drawings (top row, all from the holotype). Right: pileocystidia near the pileus centre (left) and near the pileus margin (centre), hyphal terminations near the pileus centre (right top) and near the pileus margin (right bottom). Left: basidia (left top), basidiola (centre top), hymenial cystidia near the lamellae edges (right top) and lamellae sides (left bottom), marginal cells (centre) and spores (right bottom). Scale bars = 10 mm (basidiomes), 5 µm (spores), 10 µm (all other microscopic structures).

Supplementary material

FP1030 Maximum likelihood phylogeny computed in RAxML (Stamatakis et al. 2008) inferred from three loci (nrITS, mtSSU, *rpb2*), rooted to *Russula juniperina*. Bootstrap support values followed by Bayesian posterior probabilities computed in MrBayes v. 3.2 (Ronquist et al. 2012) are indicated at the nodes with the estimated threshold 70 % / 0.95. All analyses (partitioning, RAxML, MrBayes) were computed using CIPRES portal (http://www.phylo.org/sub_sections/portal/). Types are labeled in **bold** and newly sequenced collections in blue. Species names are followed by herbarium code or GenBank accesion numbers in *italics*.

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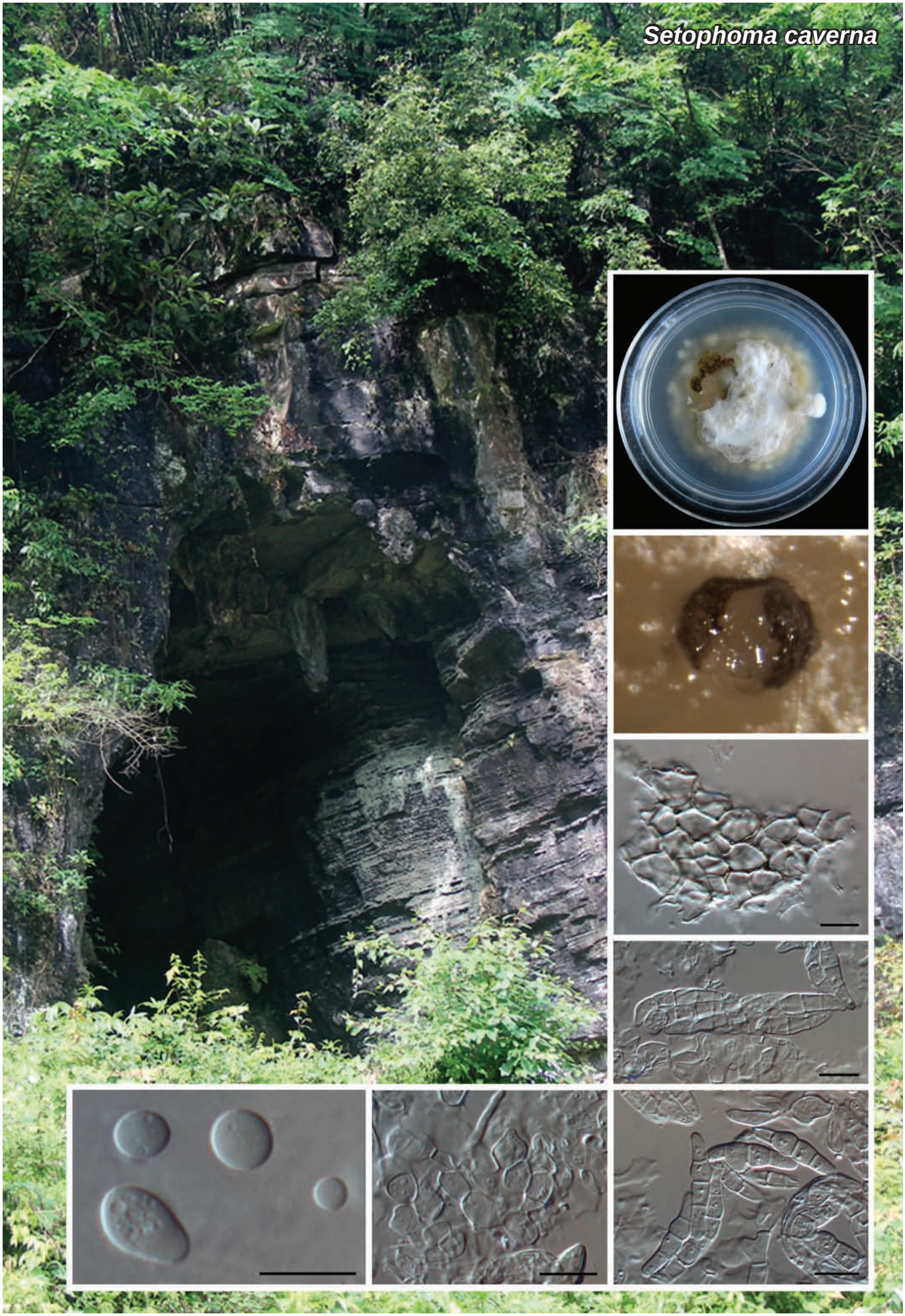
Setophoma caverna

Fungal Planet 1031 – 18 December 2019

Setophoma caverna F. Liu & L. Cai, *sp. nov.*

Etymology. Named after the habitat of this fungus, occurring in a cave.

Classification — *Phaeosphaeriaceae, Pleosporales, Dothideomycetes.*

Ascomata brown to dark brown, solitary or gregarious, globose to subglobose, semi-immersed, usually covered by aerial mycelia, erumpent. *Peridium* hyaline to pale brown, 12–20 µm wide, with 3–5 layers, walls of *textura angularis*. *Asci* cylindrical to cylindrical-clavate, 8-spored, wall easy to dissolve and invisible. *Ascospores* hyaline, fusoid-ellipsoidal with rounded ends, 3-septate and constricted at the first and second septa, the second cell from apex wider than other cells, 17–28.5 × 3.5–6 µm (av. = 22.4 ± 2.8 × 4.6 ± 0.5 µm). *Asexual morph*: *Conidiophores* hyaline, branched, often reduced to *conidiogenous cells* lining in the inner cavity. *Conidiogenous cells* hyaline, smooth, ovoid, ampulliform or subcylindrical, aseptate, 5–7.5 × 2–6 µm (av. = 6.3 ± 0.7 × 3.8 ± 1 µm). *Conidia* aseptate, hyaline, granular to guttulate, surface smooth or roughened, variable in shape and size, globose, ellipsoid or irregularly, 3–16.5 × 2.5–10.5 µm (av. = 7.4 ± 3.8 × 5.4 ± 2.1 µm).

Culture characteristics — On potato dextrose agar, flat with lobate edge, buff, sometimes olivaceous at the edge, reverse buff, reaching 27–30 mm diam after 10 d at 25 °C. On malt extract agar, flat with undulate edge, front and reverse buff, reaching 17–18 mm diam after 10 d at 25 °C.

Typus. China, Guizhou Province, Suiyang, Shuanghe Cave National Geopark, unnamed Karst cave, from carbonatite, 8 May 2015, *Z.F. Zhang* (holotype HMAS 248085, ex-type culture CGMCC 3.19526 = LC7511 = R150, LSU, ITS, *tub2*, *tef-1α* and *gapdh* sequences GenBank MK511965, MK511944, MK525032, MK525105 and MK525066, MycoBank MB829901).

Additional materials examined. China, Guizhou Province, Suiyang, Shuanghe Cave National Geopark, unnamed Karst cave, from carbonatite, 8 May 2015, *Z.F. Zhang*, LC12841 = LF2095, ITS, *tub2*, *tef-1α* and *gapdh* sequences GenBank MK511927, MK525016, MK525088 and MK525049; ibid., LC12842 = LF2096, ITS, *tub2*, *tef-1α* and *gapdh* sequences GenBank MK511928, MK525017, MK525089 and MK525050.

Notes — The oligotrophic fungus *S. caverna* was isolated from carbonatite using 1/2 000 PDA and silica agar (Jiang et al. 2017), and this is the first report of a *Setophoma* species from a Karst cave. It differs from other *Setophoma* species, in that the peridium of *S. caverna* is hyaline, and its ascus wall was difficult to observe, which is probably due to its adaptation to the cave habitat. It is closely related with the tea plant associated species *S. longinqua* (Liu et al. 2019b), but with low sequence similarity (95 % on ITS, 92 % on *tef-1α* and 90 % on *tub2*). Morphologically, they could be easily distinguished from each other by the conidial shape and dimensions (globose or ellipsoid, 3–16.5 × 2.5–10.5 µm in *S. caverna* vs cylindrical or subcylindrical, 4–5.5 × 1.5–2 µm in *S. longinqua*).

Colour illustrations. Karst cave where the type was collected. Colony on PDA; ascomata; vertical section of ascomata; ascus and ascospores; conidiogenous cells and conidia. Scale bars = 10 µm.

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Sorocybe oblongispora

Fungal Planet 1032 – 18 December 2019

Sorocybe oblongispora Tanney & Seifert, *sp. nov.*

Etymology. Refers to the oblong conidia that distinguish this species from the related *S. resinae*.

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

Ascomata not observed. *Conidiomata* mononematous or synnematous and arising from dark brown, well-developed subiculum. *Synnemata* scattered or gregarious, up to about 2 mm tall, dark brown to black, often splayed at the base but with a compact cylindrical stipe c. 60–80 µm wide, and a compact, dry, ellipsoidal conidial head c. 300 × 150 µm. Hyphae of stipe brown to dark brown, strictly parallel in the main part of the stipe, infrequently branched, with some anastomoses between adjacent hyphae, frequently septate, cells about 10–22 µm long, somewhat interwoven and rough-walled towards the base and (2.5–)3.5–5 µm wide, walls 0.5–1 µm thick, uneven in outline, smooth-walled and 2–3 µm wide in the main body of the stipe. *Conidiogenous cells* terminal or in pairs at the ends of the stipe hyphae, cylindrical and very similar in size to the conidia, but with a truncate base the same width as the stipe hyphae, 10–13 × 3.5–4.5 µm, or intercalary and arising as a lateral extension about 7–10.5 × 3.5 µm from a shorter stipe hyphal cell, lacking a basal septum. *Conidia* in sparingly branched acropetal chains, oblong-ellipsoidal to almost fusiform, (8.5–)11.5–15(–18.5) × (2.5–)3–4(–4.5) µm (length: n = 126, av. = 13.2 µm, SD = 1.9 µm, SE = 0.17 µm, 95 % CI = 0.33; width: n = 126, av. = 3.5 µm, SD = 0.4 µm, SE = 0.04 µm, 95 % CI = 0.07), brown, mostly aseptate, fewer than 5 % of the conidia with a ± central septum, with lateral walls 0.5–1 µm thick, with no visible secession scars, connection almost a point to a flat area about 1.5 µm wide, smooth-walled, sometimes adjacent conidia anastomosing; ramoconidia infrequent, 11–15.5 × 3.5–4 µm, usually with just two emerging chains, conidial chains appressed and more or less parallel.

Culture characteristics — Colonies after 4 wk at 20 °C on malt extract agar restricted, coal-black, brittle and wrinkled. Synnemata not produced.

Typus. Canada, New Brunswick, Charlotte County, Campobello Island, Roosevelt Campobello International Park, Fox Farm Trail, 44.849288, -66.966173, on resin on self-pruned branch stub of *Picea rubens* (*Pinaceae*), 26 Sept. 2016, *J.B. Tanney* (holotype DAOM 867433, culture ex-type DAOMC 251618, culture ex-paratype DAOMC 241619; ITS and LSU sequences GenBank MN114116 and MN114118, MycoBank MB831660).

Notes — *Sorocybe oblongispora* differs from the type species, *S. resinae*, by its longer, narrower conidia (mostly 11.5–15 × 3–4 µm vs 5.5–11 × 2.5–3.5 µm in *S. resinae*) and ramoconidia (11–15.5 × 3.5–4 µm vs 7–12 × 4–7 um). Both appear to be restricted to conifer resin, where they produce conspicuous synnemata and a less conspicuous mononematous morph. In North America, *S. oblongispora* occurs on the east coast of Canada on *Picea rubens*, and *S. resinae* in the Pacific Northwest of Canada and the USA on *Abies*, *Picea,* and *Pseudotsuga* spp. *Sorocybe resinae* was described from resin of *Picea abies* in Sweden, and is also known from *Abies* and *Larix* elsewhere in Europe; it is unclear whether the morphologically identical western North American and European fungi are the same phylogenetic species (Seifert et al. 2007). The other two species, *S. indica* with slimy conidia (Pratibha et al. 2005) and the poorly-known *S. tenella* (Hughes 1958), seem unlikely to belong in *Sorocybe* as now circumscribed.

Phylogenetic analyses of ITS and LSU sequences confirm that *S. oblongispora* DAOMC 251618 and *S. resinae* DAOM 239134 are congeneric (ITS: GenBank EU030275; Identities = 479/499 (96 %), 3 gaps (0 %); LSU: GenBank EU030277; Identities = 867/874 (99 %), 1 gap (0 %)). Our LSU phylogeny places *S. oblongispora* and *S. resinae* in a strongly-supported clade sister to *Ceratosporella novae-zelandiae* (*incertae sedis*), potentially a long-branch attraction artefact, a sequence misidentified as *Lasallia pustulata* (*Umbilicariaceae*, *Umbilicariales*), and *Endococcus fusigera* (*incertae sedis*). This well-supported (PP = 0.97) clade is in turn sister to *Verrucaria* (*Verrucariaceae*, *Verrucariales*). Based on an NCBI GenBank BLASTn query of the *S. oblongispora* DAOMC 251618 ITS sequence, the closest related taxon after *S. resinae* is *Endococcus fusigera* (GenBank FJ645262; Identities = 652/748 (87 %), 22 gaps (2 %)).

Seifert et al. (2007) placed *S. resinae* sister to *Capronia villosa* (*Herpotrichiellaceae*, *Chaetothyriales*) from an ITS phylogeny (GenBank EU030275; Identities = 418/492 (85 %), 3 gaps (3 %)). We cannot confidently place *Sorocybe* in a family using the available reference sequences and Vu et al.'s (2019) rDNA taxonomic threshold values as a guide, but tentatively maintain this classification of *Sorocybe* within *Herpotrichiellaceae* pending further investigation.

Sorocybe oblongispora was commonly found in New Brunswick, Canada on *Picea rubens* resin flows associated with self-pruned branch stubs or wounds. The resin was older and blackish in colour from the proliferation of mycelia from *S. oblongispora* and an unidentified sooty mould (*Capnodiales*). *Sorocybe oblongispora* co-occurred with other resinicolous fungi including *Eustilbum aureum*, *Claussenomyces olivaceus*, *Lachnellula resinaria, Sarea difformis, S. resinae*, and hysteriaceous species. Resinicolous fungi have been little studied in recent years and the known species are poorly represented by public DNA sequences. This recent discovery of *Chaenothecopsis claydenii* and now *S. oblongispora* highlights the undiscovered resinicolous fungal diversity of the Acadian forests of eastern Canada.

Colour illustrations. Campobello Island, NB, Canada (photo R. Smith). From left to right (DAOM 867433: synnemata on *Picea rubens* resin, conidial head, mononematous conidiophore, conidia with examples of anastomosis. Scale bars = 100 µm (synnemata), 10 µm (all others).

Supplementary material

FP1032 Bayesian inference (BI) phylogenetic tree based on LSU sequences. The BI analysis was performed with MrBayes v. 3.2.6 using the best-fit nucleotide substitution model (GTR+G) estimated by the Akaike Information Criterion (AIC) using jModelTest v. 2.1.10, with a sampling frequency every 500 generations, three runs consisting of four chains (three heated, one cold), an automated stop value of 0.01, and the first 25 % of the trees discarded as burn-in. Posterior probabilities < 1 are presented in branch nodes. GenBank accession numbers follow the species name and sequences derived from ex-types are denoted with a superscript (ᵀ). The novel species is indicated in **bold** and highlighted in an orange box.

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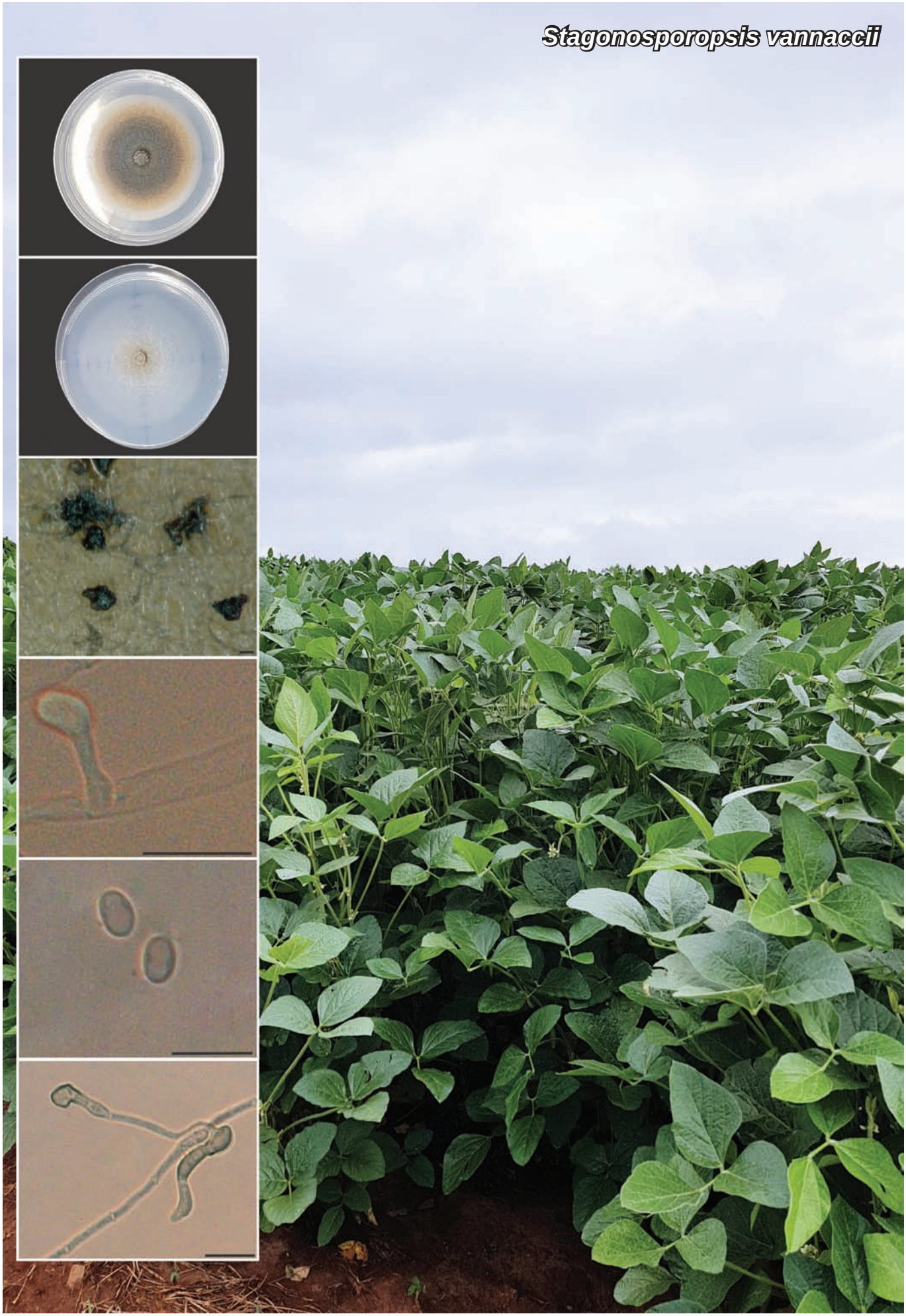

Stagonosporopsis vannaccii

Fungal Planet 1033 – 18 December 2019

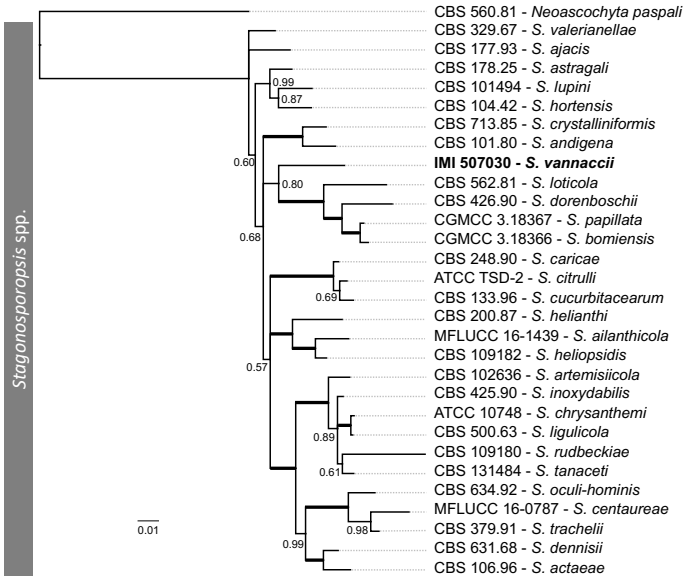
Stagonosporopsis vannaccii Baroncelli, Cafà, Castro, Boufleur & Massola, *sp. nov.*

Etymology. Named in honour of the Italian mycologist Giovanni Vannacci, for his important contributions to the study of fungi.

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

Hyphae hyaline, smooth, thin-walled, septate, 1.3–4 µm wide onto potato-dextrose-agar (PDA). *Conidiomata* pycnidial, black, unilocular, globose to subglobose, solitary or confluent, glabrous, superficial in the culture medium, 152.1–198.7 µm diam. *Ostiole* single and central, slightly papillate to papillate and occasionally rostrate. *Pycnidial wall* pseudoparenchymatous. *Conidiogenous cells* phialidic, hyaline, smooth, ampulliform, 6.7–13.3 × 2–2.7 µm. *Conidia* hyaline, ellipsoidal to cylindrical with rounded ends, aseptate, with two polar guttules after ageing, 3.4–6.4 × 2–2.7 µm. *Appressoria* sepia, obovoid to ovoid, truncate, entire or undulate edges, 2.9–6.6 × 3.2–9.1 µm. *Sexual morph* unknown.

Culture characteristics — On PDA: colonies circular, flattened, reaching 64–66 mm diam after 6 d under 12 h photoperiod and 25 °C, margin entire, aerial mycelium sparse. Colonies surface with concentric circles fusco-black, violet-slate, vinaceus-grey and pale vinaceus-grey (from centre to edge), reverse fusco-black according to Rayner's colour chart (Rayner 1970). On synthetic nutrient-poor agar (SNA): colonies circular, flattened, reaching 65–67 mm diam after 6 d under 12 h photoperiod and 25 °C, margin entire, aerial mycelium sparse, surface grey-sepia in the centre and pale mouse grey at the edge, reverse grey-sepia. No pycnidia were observed on SNA.



Phylogenetic tree of *Stagonosporopsis* spp. obtained with MrBayes v. 3.2.7 (Ronquist & Huelsenbeck 2003) inferred from the concatenated LSU (1340 bp), ITS (481 bp), *tub2* (363 bp), *rpb2* (596 bp) and *act* (314) sequence alignment. The tree is rooted to *Neoascochyta paspali* CBS 560.81. PP values > 0.50 are shown above or below the branches while thicker branches indicate PP values of 1. Sequences used are those reported in Marin-Felix et al. (2019).

Colour illustrations. Piracicaba, Brazil, soybean plants. Colony on PDA and SNA after 6 d at 25 ± 1 °C; conidiomata pycnidia under the dissecting microscope; conidiogenous cells; conidia and appressoria. Scale bars = 10 µm.

Typus. Brazil, S13°18'46,7" W56°02'33,4" (Sinop, MT), from pod of soybean (*Glycine max*), cultivar M8766RR, 2016, *F. Rogério* (holotype IMI 507030, cultures ex-type LFN0148 = IMI 507030, ITS, LSU, *tub2, tef1, act, rpb2* sequences GenBank MK519453, MK519452, MK519454, MK519455, MN534890 and MN534891, MycoBank MB831973).

Notes — *Stagonosporopsis vannaccii* was isolated from anthracnose symptoms on pods of soybean in central Brazil in 2017. Pathogenicity was proved through seed inoculation in accordance with Costa et al. (2003) on different soybean cultivars. Inoculated seeds of BMX Bônus 8579 IPRO and M6210 IPRO cultivars had the germination reduced by 50 % and 70 %, respectively, and gave rise to plantlets with damping-off symptoms. Based on the similarity of symptoms, it is very likely that the disease caused by *S. vannaccii* in soybean is being confused with damping-off caused by *Colletotrichum* spp. in the field. Further studies should show the real importance of this disease to the soybean crop. *Stagonosporopsis* spp. has been reported causing diseases in other cultures in Brazil, such as *S. caricae* in *Carica papaya* (Aveskamp et al. 2010, Vivas et al. 2014) and *S. cucurbitacearum* in *Luffa cylindrica* (Silva et al. 2013b), and also in other countries, such as *S. tanaceti, S. chrysanthemi* and *S. inoxydabilis* in *Asteraceae* in Australia (Vaghefi et al. 2012), *S. cucurbitacearum* in *Cucumis melo* in Thailand (Nuangmek et al. 2018) and *S. cucurbitacearum*, *S. citrulli* and *S. caricae* in *Cucurbita* species (Stewart et al. 2015).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the **LSU** sequence is *Allophoma minor* strain CBS 315.83 (GenBank GU238106.1; Identities = 1 326/1 327 (99.9 %), no gaps). Closest hits using the **ITS** sequence are *Stagonosporopsis trachelii* isolate NJ1-2 and strain CBS 384.68 (GenBank MH062183.2 and GU237856.1, respectively; Identities = 471/475 (99.2 %), no gaps). The closest hits using the ***tub*2** sequence are *S. ligulicola* strain SWJ-6 and strain NB-5 (GenBank KJ868169.1 and KJ868168.1, respectively; Identities = 321/333 (96.44 %), 2 gaps (0.3 %)) and *S. inoxydabilis* strain CBS 425.90 (GenBank GU237693.1; Identities = 321/333 (96.44 %), 2 gaps (0.3 %)). The closest hit using the ***tef*-1α** sequence is *Neodidymella thailandicum* strain MFLUCC 11-0140 (GenBank MG520938.1; Identities = 884/902 (98.0 %), no gaps).

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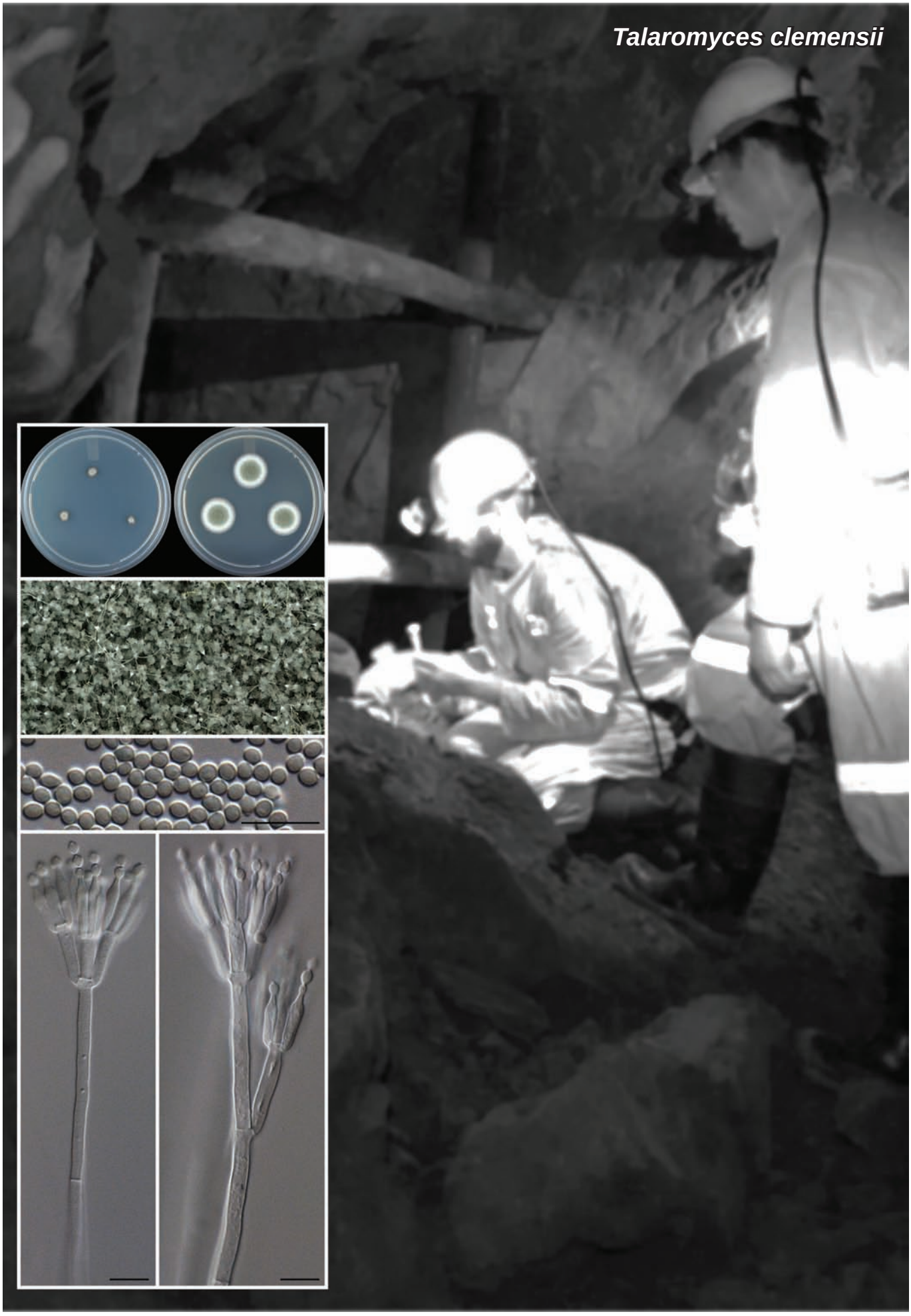

Talaromyces clemensii

Fungal Planet 1034 – 18 December 2019

Talaromyces clemensii Visagie & Yilmaz, *sp. nov*.

Etymology. Latin, *clemensii*, named after Clemens Kiessig of Barberton Mines who assisted with sample collections inside goldmine shaft.

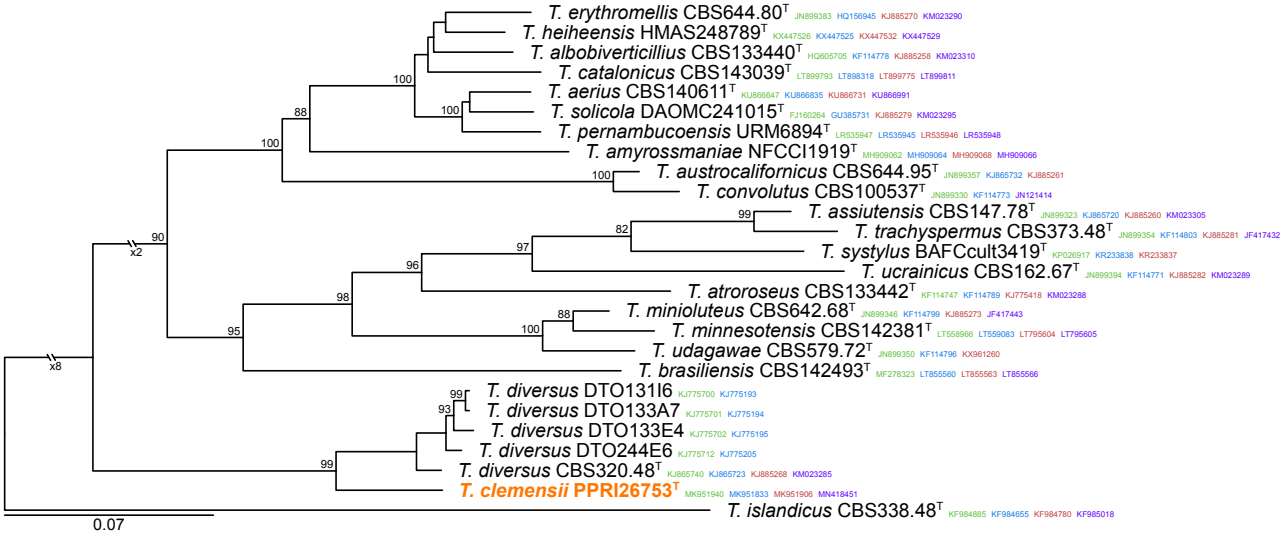
Classification — *Trichocomaceae*, *Eurotiales*, *Eurotiomycetes.*

Conidiophores biverticillate, sometimes subterminal branched; *stipes* smooth walled, 150–520 × 3–4 µm; *branches* 12–35 µm; *metulae* 4–8 per stipe, 10.5–13(–16) × 3–4 µm; *phialides* acerose, 4–6 per metula, 10–12(–13) × 2.5–3 µm (11.4 ± 0.8 × 2.8 ± 0.2); average length metula/phialide 1.1; *conidia* smooth walled, broadly ellipsoid to ellipsoid, 2–3(–5) × 2–2.5(–3.5) µm (2.6 ± 0.1 × 2.2 ± 0.1), av. width/length = 0.8, n = 70.

Culture characteristics (25 °C, 7 d) — On Czapek yeast autolysate agar (CYA): Colonies low, plain, raised centrally, having an olive (2F5; colour code based on Kornerup & Wanscher (1967)) to olive grey (2E2) colour; margins low, narrow (1 mm), entire; mycelia white; texture floccose; sporulation very sparse, conidia *en masse* not determined; soluble pigments absent; exudates absent; reverse black to olive brown (4F3–6). On malt extract agar (MEA): Colonies low, plain, raised centrally; margins low, wide (3 mm), entire; mycelia white; texture velutinous and floccose; sporulation moderately dense, conidia *en masse* greyish green (25D5–E5), dull green (27E4); soluble pigments absent; exudates absent; reverse greyish yellow (2B4), greyish green (30C3–4), yellowish white (2A2). On yeast extract sucrose agar (YES): Colonies moderately deep, plain, slightly sunken centrally, having a greyish colour; margins low, narrow (1 mm), entire; mycelia white; texture velutinous; sporulation sparse, conidia *en masse* turquoise grey (24E2); soluble pigments absent; exudates absent; reverse brownish grey (5F2–6F2), brownish orange (5C3). On dichloran 18 % glycerol agar (DG18): Colonies low to moderately deep, plain, raised centrally; margins low, narrow (1 mm), entire; mycelia white; texture floccose; sporulation absent, conidia *en masse* not determined; soluble pigments absent; exudates absent; reverse yellowish white (3A2). On creatine sucrose agar (CREA): Colonies weak growth, no acid production. *Colony diam (in mm)*: CYA 5–8; CYA 30 °C 3–5; CYA 37 °C no growth; CYA with 5 % NaCl 4–5; MEAbl 30–31; DG18 6–8; YES 6–7; oatmeal agar (OA) 10–11; CREA 6–7.

Typus. South Africa, Mpumalanga, Barberton, from rotting wood in goldmine, Nov. 2018, coll. *C.M. Visagie* & *C. Kiessig*, isol. *C.M. Visagie* (holotype PREM 62301, cultures ex-type PPRI 26753 = CMV016A4, LSU, ITS, *BenA*, *CaM* and *RPB2* sequences GenBank MN388753, MK951940, MK951833, MK951906 and MN418451; MycoBank MB832488).

Notes — A BLAST search against an ex-type reference sequence dataset placed the new species in *Talaromyces* sect. *Trachyspermi* (Yilmaz et al. 2014). A multigene phylogeny based on ITS, *BenA, CaM* and *RPB2* resolves *T. clemensii* as sister to *T. diversus*. All four genes distinguish between these species. Morphologically, both species are distinguished by poor growth on CYA. *Talaromyces clemensii* is distinguished from *T. diversus* by its inability of growth on CYA at 37 °C, and more restricted growth on OA (10–11 vs 25–40 mm).



Combined phylogeny of *Talaromyces* sect *Trachyspermi* 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** orange text, T = ex-type strain. GenBank accession numbers are shown in a smaller font next to the culture accession number (ITS = green, *BenA* = blue, *CaM* = red, *RPB2* = purple). The tree is rooted to *T. islandicus*.

Colour illustrations. Collecting rotting wood in goldmine shaft. Colonies on CYA and MEA; colony texture on MEA; conidiophores; conidia. Scale bars = 10 µm.

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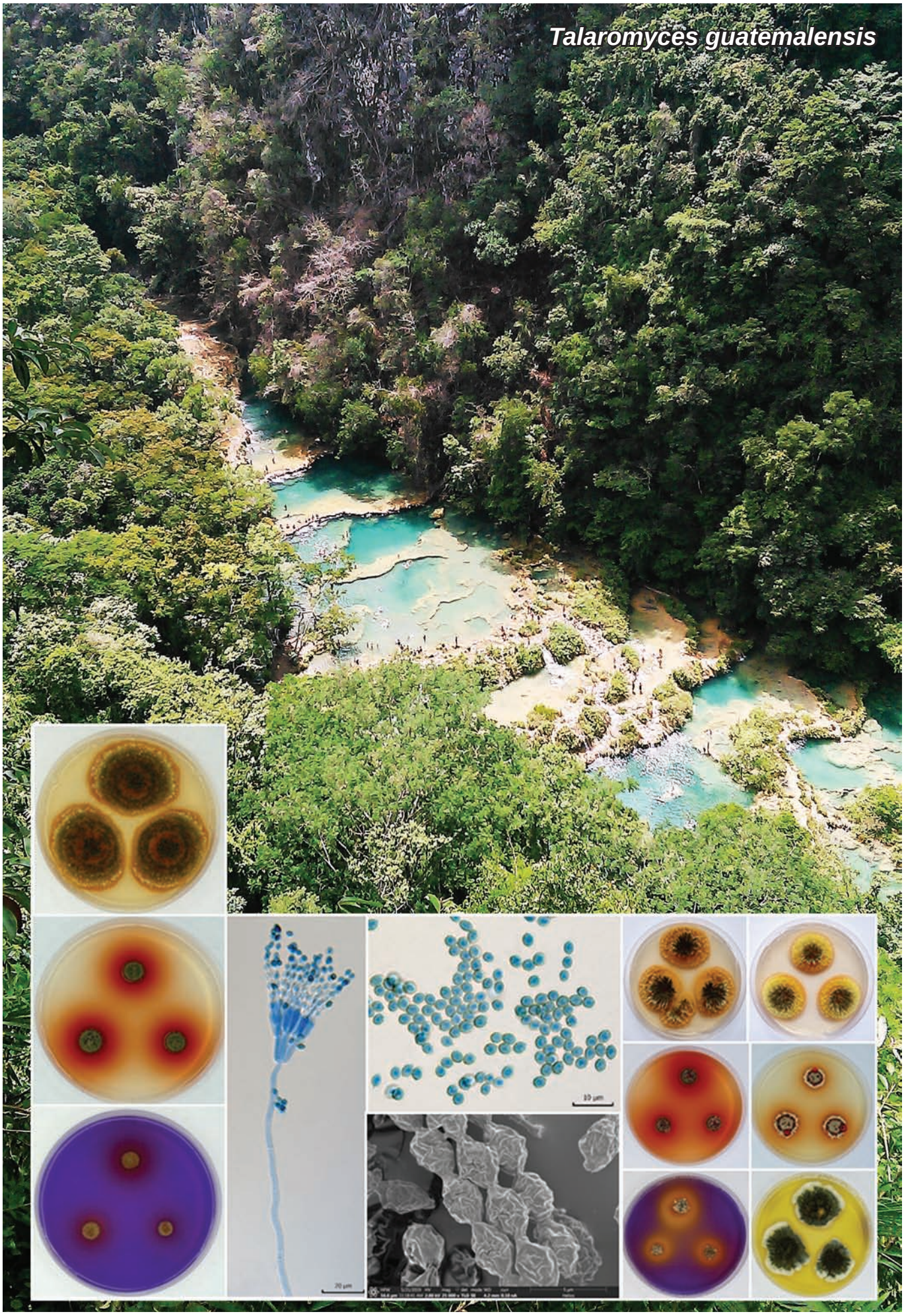

Talaromyces guatemalensis

Fungal Planet 1035 – 18 December 2019

Talaromyces guatemalensis A. Nováková, Svec, F. Sklenar, Kubátová & M. Kolařík, *sp. nov.*

Etymology. Named according to the geographical origin of investigated isolates.

Classification — *Trichocomaceae, Eurotiales, Eurotiomycetes.*

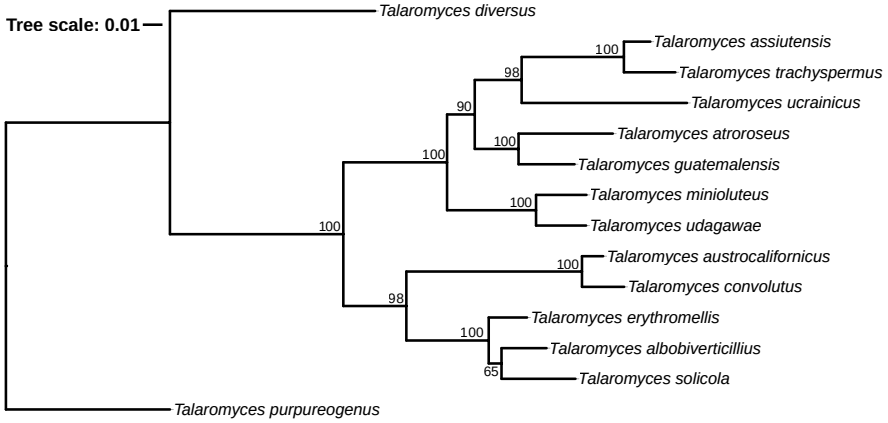
On malt extract agar (MEA). *Conidiophores* biverticillate-symmetrical, stipe smooth, 144–151 × 4.7 µm, under penicillus with spathulate widening. *Metulae* cylindrical, smooth, 4–5 in compact terminal whorls, 17.6 × 3.9–4.7 µm. *Phialides* ampulliform-acerose, 3–4 in whorls, 12–14.4 × 3.6(–4.8) µm. *Conidia* elliptical, rough-walled, 3.1–3.9 × 2.3 µm.

Culture characteristics — (in the dark, 25 °C after 7 d): Colonies on malt extract agar (MEA) synnematal, colony margins brilliant yellow (ISCC–NBS No. 83) with very low acerose synnemata coloured also brilliant yellow, colony centre (15 mm diam) with distinct acerose synnemata up to 6–8 mm high, turn to greyish olive green (No. 127), some with yellowish tops, no exudate, no soluble pigment, reverse vivid yellow (No. 82) to strong orange yellow (No. 68). Colonies on Czapek yeast autolysate agar (CYA) synnematal, synnemata short, brilliant to moderate yellow (No. 83, 87), 1 mm to 2–3 mm high in colony centre and greyish greenish yellow (No. 105) to light greyish olive (No. 109) with 4–5 mm yellowish grey (No. 93) centre and 2 mm submerged colony margin, soluble pigment vivid reddish orange (No. 34) to deep reddish orange (No. 38), reverse deep reddish brown (No. 44) with paler margins. Colonies on Czapek-Dox agar (CZA) synnematal with low synnemata, greyish greenish yellow (No. 105) on margin to greyish olive green (No. 127) with paler tops in the centre, no exudate, delicate to strong (5–8 mm ring) soluble pigment vivid reddish orange (No. 34) missing in any colonies, reverse dark reddish brown (No. 44). Colonies on Czapek yeast autolysate agar with 20 % sucrose (CY20S) plane, low lanose with 1–5 mm submerged margins, acerose synnemata production sporadic, 1–2 mm high, pale yellow (No. 89), more abundant in 10–12 mm centre, where are 5–6 mm high, greyish olive (No. 110) with pale yellow (No. 89) tops, lanose parts of colonies light brown (No. 57) to brownish orange (No. 54), no exudate, no soluble pigment, reverse light brown (No. 57) to brownish orange (No. 54) with darker 3–5 mm centre and pale orange yellow (No. 73) margins and strong orange (No. 50) borderline between submerged and lanose parts. Colonies on creatine sucrose agar (CREA) plane, velutinous-granulose turning distinctly synnematous, sporulation light greyish olive (No. 109), no exudate, no acid production, but pure production of deep reddish orange (No. 38) soluble pigment in some colonies, reverse deep reddish brown (No. 44). No growth at 37 °C.

Typus. Guatemala, Semuc Champey on the Cahabòn river, under small overhang of limestone, ex soil from tropical forest using the soil dilution plate method, 2017, *K. Švec* (holotype PRM 952195, culture ex-type CCF 6215, ITS, *tub2*, *CaM* and *RPB2* sequences GenBank MN322789, MN329687, MN329688 and MN329689, MycoBank MB832313).

Additional material examined. Guatemala, Semuc Champey on the Cahabòn river, under small overhang of limestone, ex soil from tropical forest using the soil dilution plate method, 2017, *K. Švec,* GUA2-1 (= CCF 6214), GUA2-3 and GUA2-4.

Notes — Isolate GUA2-1 (CCF 6214, PRM 952196) is phenotypically different (brilliant yellow to brilliant greenish yellow pigmentation of colonies on BWA and MEA, synnemata 80–100 µm high, no or pure production of soluble pigment on CYA and CZA, big reddish droplets on CZA in 14 d (on the contrary in the ex-type isolate, deep reddish orange (No. 41) soluble pigment with distinct abundant occurrence in colony environs and reddish black (No. 24 reverse were found), very good growth and sporulation as well as massive acid production on CREA). However, the molecular analyses of all tested genes (ITS, *tub2*, *CaM* and *RPB2*) revealed them to be identical.



Phylogenetic tree depicting the position of *Talaromyces guatemalensis* within the section *Trachyspermi*. The tree was inferred in IQ-TREE v. 1.6.5 from a concatenated alignment of DNA sequences from the ITS region of rDNA and partial genes of β-tubulin, calmodulin and *RPB2*. Models of evolution for each partition were calculated in jModeltest v. 2.1.7.

Colour illustrations. Pools in the Cahabòn river in Semuc Champey, Guatemala. Seven-day-old colonies on CYA, MEA, CZA and CREA (column left); conidiophore and conidia (light microscopy) and SEM photography of conidia; columns on the right – colonies of CCF 6215 and CCF 6214 isolates on beer-wort agar (7 d), CZA and CREA (14 d). Scale bars = 20, 10 and 5 µm.

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Terfezia dunensis

Fungal Planet 1036 – 18 December 2019

Terfezia dunensis Ant. Rodr., Cabero, Luque & Morte, *sp. nov.*

Etymology. In accordance with the habitat (coastal dunes).

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

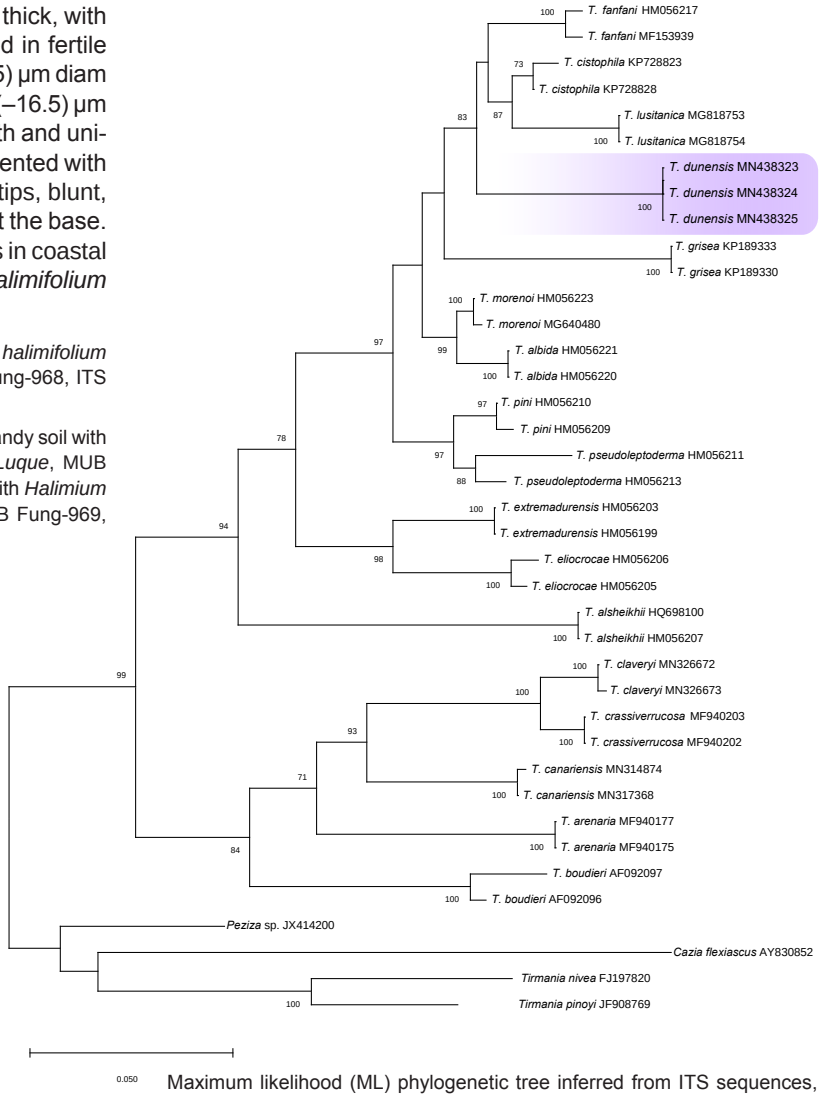
Ascomata hypogeous to partially emergent at maturity, 2–5 cm in size, globose to subglobose, sometimes gibbous or lobed, often with tapered, sterile short base with a thick mycelial cord, cream colour at first, becoming lilac to pale lavender, then ochre brown with black spots, smooth, rough to tuberculate at full maturity. *Peridium* 150–500 µm thick, whitish in cross section, pseudoparenchymatous, composed of subglobose cells, 40–90 µm diam, thin-walled, hyaline, yellowish and angular to oblong in the outermost layers. *Gleba* solid, fleshy, succulent, whitish with small pale grey pockets at first, soon becoming lilac, then brown, maturing to dark grey to black pockets of fertile tissue separated by whitish, sterile veins. Spermatic *odour*. Acidic, unpleasant *taste*. *Asci* inamyloid, subglobose, sessile or short-stipitate, 60–85 × 50–70 µm, walls 1–2 µm thick, with 6–8 irregularly disposed spores, randomly arranged in fertile pockets. *Ascospores* globose, (18–)18.5–19.5(–20.5) µm diam (av. = 19 µm) including ornamentation, (13–)13.5–15(–16.5) µm (av. = 14 µm) without ornamentation, hyaline, smooth and uniguttulate at first, by maturity yellow ochre and ornamented with cylindrical, conical spines with occasional uncinate tips, blunt, separate, (2–)2.5–3.5(–4) µm long, 1–2 µm wide at the base.

Ecology & Distribution — *Terfezia dunensis* grows in coastal sand dunes, acidic soils, associated with *Halimium halimifolium* and *Cistus salvifolius*, from January to March.

Typus. Spain, Huelva, Almonte, in sandy soil with *Halimium halimifolium* and *Cistus salvifolius*, Mar. 2019, *D. Luque* (holotype MUB Fung-968, ITS sequence GenBank MN438324, MycoBank MB831972).

Additional materials examined. Spain, Huelva, Almonte, in sandy soil with *Halimium halimifolium* and *Cistus salvifolius*, Jan. 2019, *D. Luque*, MUB Fung-967, ITS sequence GenBank MN438323; in sandy soil with *Halimium halimifolium* and *Cistus salvifolius*, Mar. 2019, *D. Luque*, MUB Fung-969, ITS sequence GenBank MN438325.

Notes — *Terfezia dunensis* is a spiny-spored *Terfezia* species characterised by its acidic coastal dune habitat, associated with *Halimium halimifolium* and *Cistus salvifolius*, lilac colours of peridium and gleba and spermatic odour. It differs from all other spiny-spored species by its habitat and lilac colour, that is unique in the genus *Terfezia*. *Terfezia cistophila* and *T. albida* have spermatic odour but different habitat, colour and spores (Bordallo et al. 2013, 2015). Moreover, the new taxon is distinguished from all *Terfezia* spp. in its ITS nrDNA sequence.



Maximum likelihood (ML) phylogenetic tree inferred from ITS sequences, using RAxML-HPC v. 8 (Stamatakis 2014) on XSEDE in the CIPRES science gateway (Miller et al. 2010). GTR + G selected as model of evolution for analysis. Bootstrap support values (≥ 70 %) are indicated at the nodes. *Cazia* AY830852, *Peziza* JX414200, *Tirmania* JF908769 and *Tirmania* FJ197820 were used as outgroups. The scale bar indicates the expected changes per site.

Colour illustrations. Spain, Almonte (Huelva), coastal dune in National Park of Doñana. Ascocarps; mature ascospores; *Halimium halimifolium* and *Cistus salvifolius* plants. Scale bar = 20 µm.

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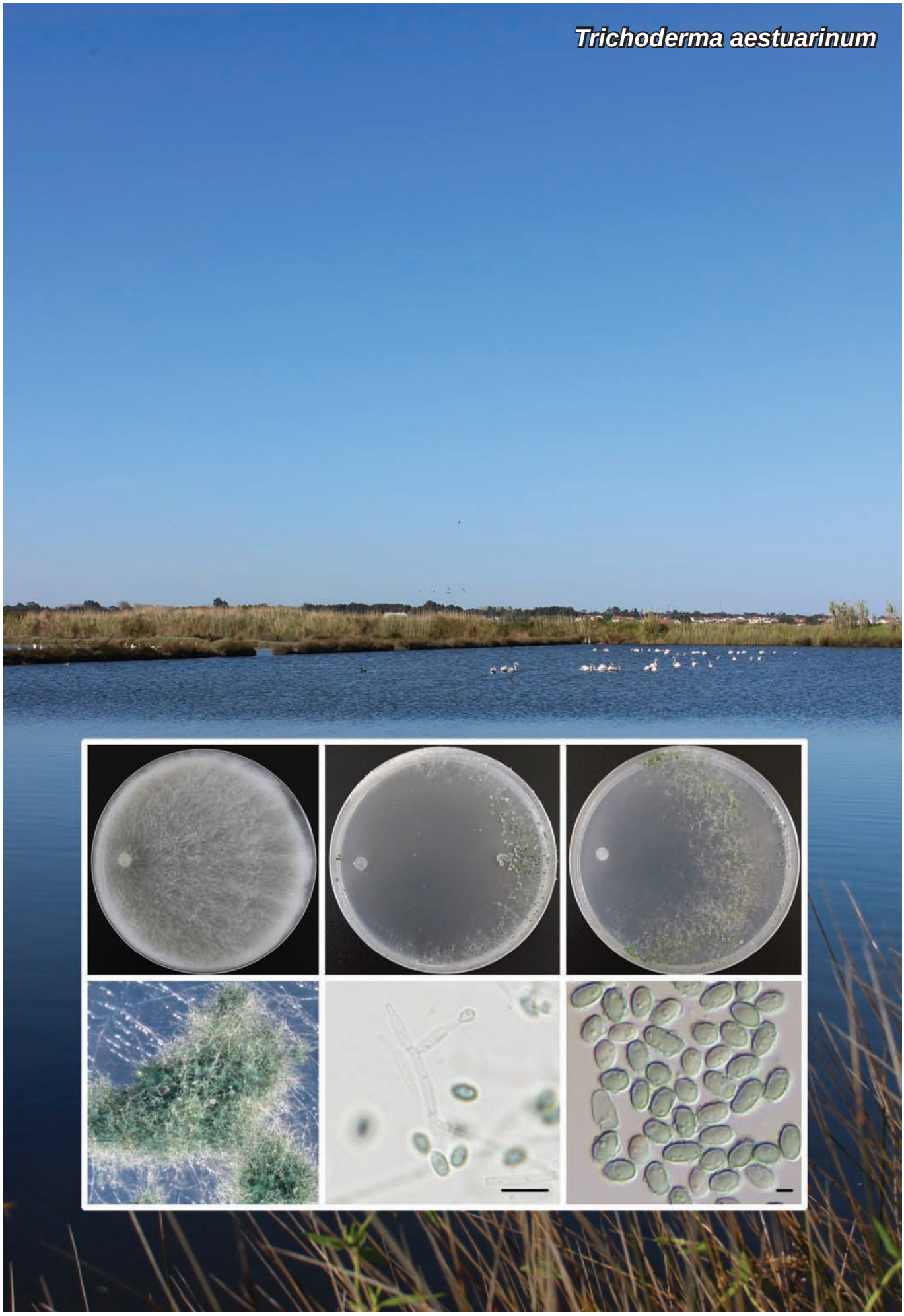

Trichoderma aestuarinum

Fungal Planet 1037 – 18 December 2019

Trichoderma aestuarinum M. Gonçalves & A. Alves, *sp. nov.*

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

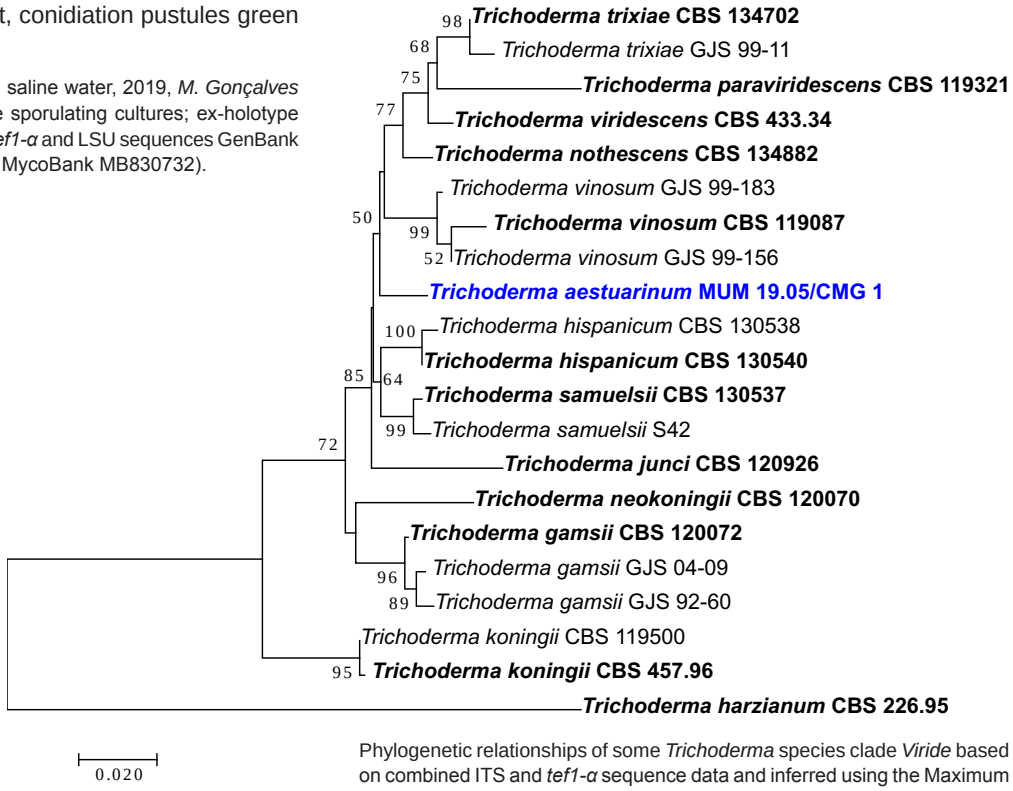
Classification — *Hypocreaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes.*

Mycelium on synthetic low nutrient agar (SNA) smooth, hyaline with aerial hyphae. *Chlamydospores* infrequent. Conidiation starting after 7 d, short effuse and predominantly in small pustules 1–2 mm diam formed mostly in the middle plate. *Conidiophores* variable, irregular. *Phialides* solitary or divergent, (7.7–)13.7(–20.1) × (1.9–)2.5(–3.2) µm (n = 50). *Conidia* ellipsoid to oblong, green, rough, (4.4–)6.1(–7.4) × (2.6–)3.4(–4.4) µm (n = 100).

Culture characteristics — Optimum temperature for growth 25 °C. No growth at 35 °C in potato dextrose agar (PDA), corn meal agar (CMA) and SNA. Colony radius after 2 wk: on PDA, colonies have 75 mm at 25, 20 and 15 °C; 15 mm at 10 °C and 3 mm at 30 °C; colony circular, dense, margin wavy, surface whitish, abundant aerial hyphae, absent autolytic excretions, conidiation pustules and diffusing pigment, odour indistinct, reverse turning slightly yellowish. On CMA, colonies have 75 mm at 25, 20 and 15 °C; 26 mm at 10 °C and 2 mm at 30 °C; colony circular, hyaline, dense, aerial hyphae scant, absent autolytic excretions and diffusing pigment, odour indistinct, conidiation pustules mainly in periphery, green or grey-green. On SNA, colonies have 75 mm at 25, 20 and 15 °C; 6 mm at 10 °C and 3 mm at 30 °C; colony circular, hyaline, dense, with some aerial hyphae from the middle, absent autolytic excretions and diffusing pigment, odour indistinct, conidiation pustules green beginning to form in the centre.

Typus. Portugal, Ria de Aveiro, from saline water, 2019, *M. Gonçalves* (holotype MUM H-19.05, a dried culture sporulating cultures; ex-holotype living culture MUM 19.05 = CMG 1, ITS, *tef1-α* and LSU sequences GenBank MK770830, MK770831 and MN535286, MycoBank MB830732).

Notes — Phylogenetic analysis of *Trichoderma* species based on the ITS and *tef1-α* genes provides highest resolution for identification of species of the genus, particularly in the distinction of species within the *Viride* clade (Jaklitsch et al. 2006, Samuels et al. 2006). Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Trichoderma koningii* (GenBank KY788329; Identities = 568/570 (99 %), no gaps), *Trichoderma koningiopsis* (GenBank MF116301; Identities = 567/570 (99 %), no gaps) and *Trichoderma sp.* (GenBank KP172544; Identities = 567/570 (99 %), no gaps). Closest hits using the *tef1-α* sequence had highest similarity to *Trichoderma paraviridescens* (GenBank MF782846; Identities = 608/646 (94 %), 18 gaps (2 %)), *Trichoderma trixiae* (GenBank MF782847; Identities = 605/646 (94 %), 21 gaps (3 %)) and *Trichoderma vinosum* (GenBank DQ841719; Identities = 587/624 (94 %), 22 gaps (3 %)). Alignment and tree were deposited in TreeBASE (TB2:S24289).



Phylogenetic relationships of some *Trichoderma* species clade *Viride* based on combined ITS and *tef1-α* sequence data and inferred using the Maximum Likelihood method under the Kimura 2-parameter model (MEGA7 v.7.0). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site and rooted to *Trichoderma harzianum* (CBS 226.95). Bootstrap support values (> 50 %) are shown at the nodes. Ex-type strains are in **bold** and the isolate from the current study is in blue.

Colour illustrations. Estuary Ria de Aveiro (Portugal). Colony after 2 wk at 25 °C on PDA, CMA and SNA; conidiation pustules, phialides and conidia on SNA. Scale bars 10 µm (middle), 2.5 µm (right).

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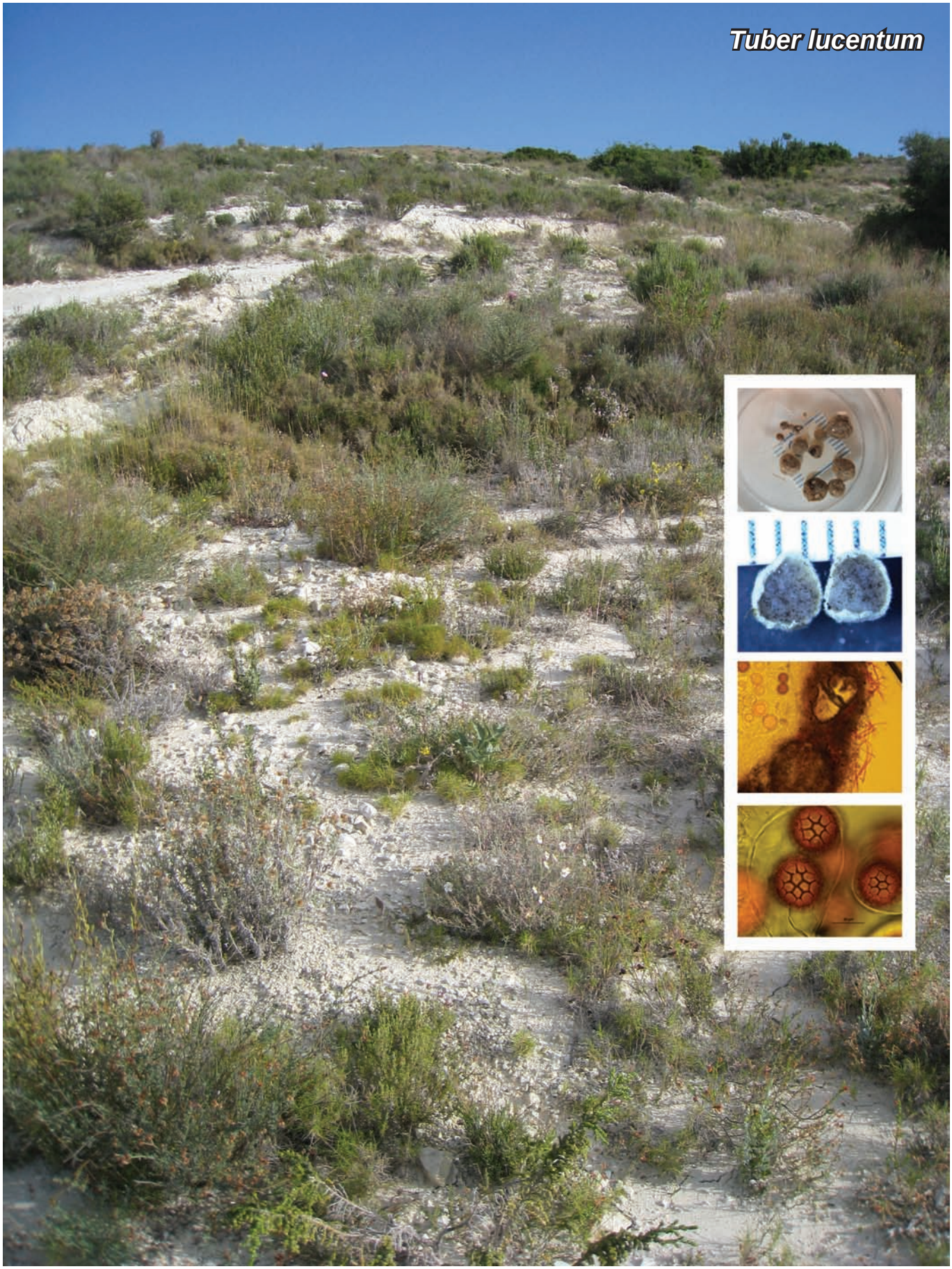

Tuber lucentum

Fungal Planet 1038 – 18 December 2019

Tuber lucentum Bordallo, *sp. nov.*

Etymology. The epithet refers to Lucentum, the old Roman name for the city of Alicante (Spain), the locality where this species was found.

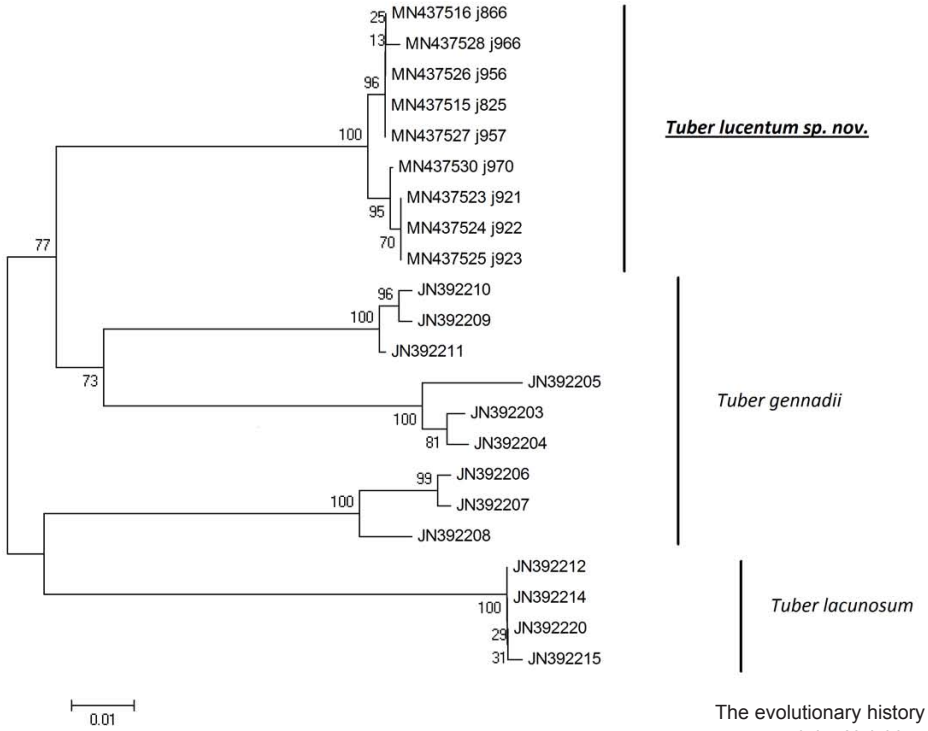
Classification — *Pezizaceae*, *Pezizales, Pezizomycetes.*

Ascomata hypogeous, very small globose, round, regular, < 1 cm diam in size. *Exoperidium* tomentose white to light cream and endoperidium pseudoparenchymatic (< 100 µm). *Gleba* hyaline, vitrea; forming neither isolated locules nor continuous labyrinthine loculated gleba. *Asci* clavate, containing mostly two spores. *Ascospores* globose to citriform (40–60 µm), by maturity ocher and ornamented with reticulum, mostly pentagonal or hexagonal, cells 3 µm high.

Habitat, Distribution & Season — Accompanying *Terfezia claveryi, T. crassiverrucosa,* and other desert truffles. Grows in calcareous, alkaline soils from eastern Spain, associated with *Cistaceae* plants: *Helianthemum violaceum, H. almeriense, H. syriacum, Fumana thymifolia*, etc. Collected in spring (Apr.–June).

Typus. Spain, Alicante, Moralet, 2017, *J.J. Bordallo*, (holotype MUB Fung-j825, ITS sequence GenBank MN437515, MycoBank MB832580); Paratype MUB Fung-j866, ITS sequence GenBank MN437516; Paratype MUB Fung-j921, ITS sequence GenBank MN437523; Paratype MUB Fung-j922, ITS sequence GenBank MN437524; Paratype MUB Fung-j923, ITS sequence GenBank MN437525; Paratype MUB Fung-j956, ITS sequence GenBank MN437526; Paratype MUB Fung-j957, ITS sequence GenBank MN437527; Paratype JJ Fung-j966, ITS sequence GenBank MN437528; Paratype JJ Fung-j970, ITS sequence GenBank MN437530.

Notes — *Tuber lucentum* is distinguished from *T. gennadii* and *T. lacunosum* based on its very small ascomata, its gleba lacking isolated locules or continuous labyrinthine locules, and ITS sequence identity.



The evolutionary history of 22 taxa was inferred using the Maximum Parsimony and the Neighbour-Joining methods. The bootstrap consensus tree inferred from 500 replicates is taken to represent the evolutionary history of the taxa analysed. Branches corresponding to partitions reproduced in less than 50 % bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) are shown next to the branches. The MP tree was obtained using the Close-Neighbour-Interchange algorithm with search level 3. The evolutionary distances were computed using the Maximum Composite Likelihood method. All positions containing gaps and missing data were eliminated from the dataset (Complete Deletion option). There were a total of 487 positions in the final dataset, out of which 114 were parsimony informative. Maximum Parsimony and the Neighbour-Joining were similar in bootstrap support. Phylogenetic analyses were conducted in MEGA 4.

Colour illustrations. Habitat with *Helianthemum violaceum, H. syriacum* and *Fumana thymifolia*. Ascocarps; gleba and mature ascospores (stain Acidic Fuchsina).

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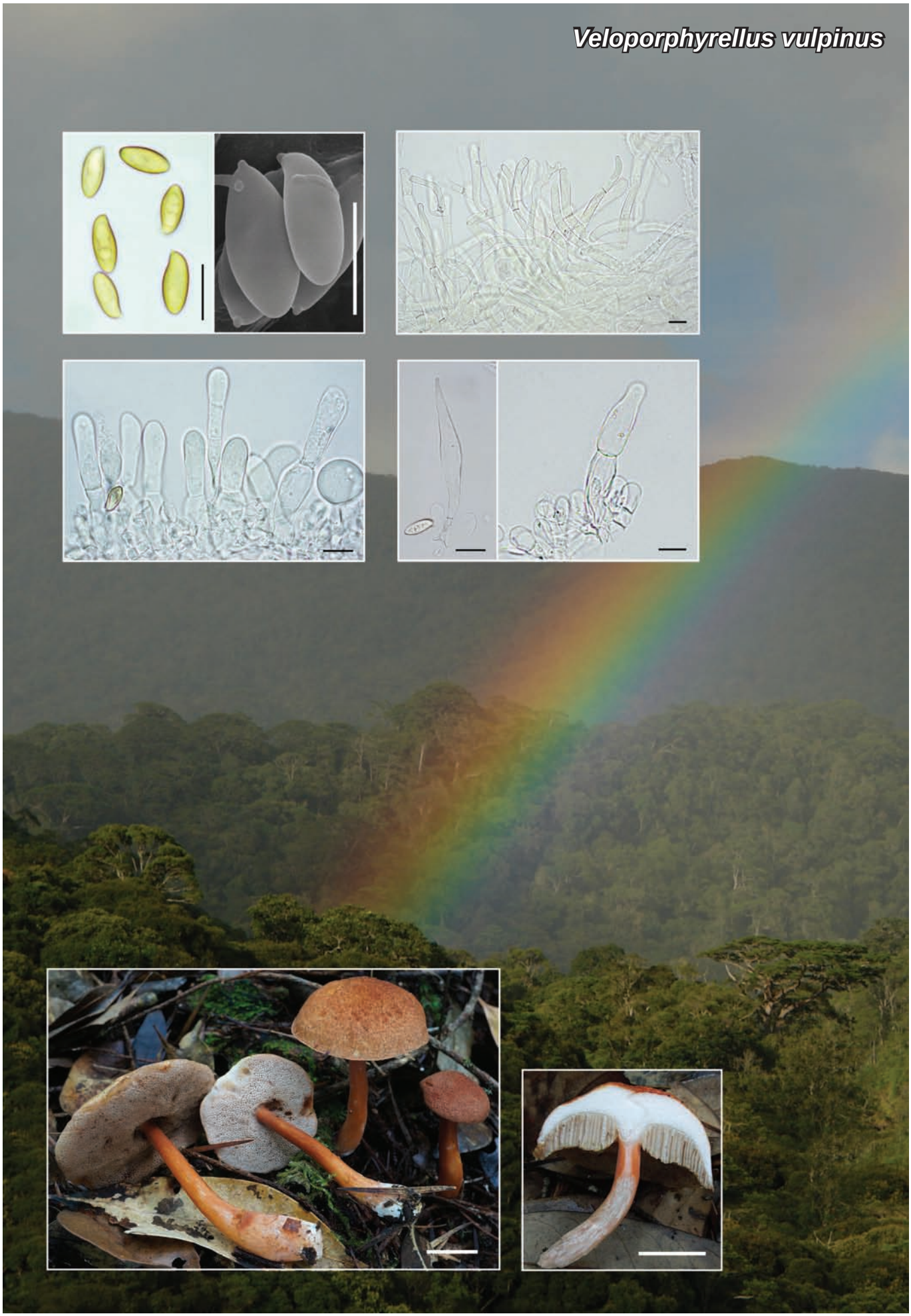
Veloporphyrellus vulpinus

Fungal Planet 1039 – 18 December 2019

Veloporphyrellus vulpinus T.H.G. Pham, O.V. Morozova, A.V. Alexandrova & E.S. Popov, *sp. nov*.

Etymology. The epithet *vulpinus* (Latin for 'of or belonging to a fox') refers to the reddish brown colour of the basidiomata, like fox fur.

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

Basidiomata small to medium sized, boletoid. *Pileus* 25–60 mm diam, hemispherical to convex; reddish brown to orange brown (6C7–8, Kornerup & Wanscher 1978); surface dry, firstly completely fibrillose or tomentose, in mature covered with fibrillose reddish brown squamules on the paler background; the pileus margin slightly extending and does not embrace the apex of the stipe. *Hymenophore* tubular, adnate-emarginate, depressed around apex of stipe, 4–10 mm thick, whitish to creme (4A2–3), unchanging in colour when bruised, pinkish from spores in maturity; pores rounded to angular, 1–2/mm, with slightly fringed edge; tubes concolorous with the hymenophore surface. *Spore print* brownish pink. *Stipe* 40–90 × 5–10 mm, cylindrical, usually significantly broadened up to 20 mm in the basal part, concolorous with the pileal surface; slightly pubescent in the upper part, white tomentose near the stem base. *Context* white in pileus, unchanging, pinkish or turning pink in the stem. *Smell* faint, *taste* bitter. *Basidiospores* (12–)13–15(–16) × (4.5–)5–6(–6.5) µm, Q = (2.1–)2.4–2.8(–3.1), fusoid, subfusoid and inequilateral in side view with weak suprahilar depression, narrowly oblong to subfusoid in ventral view, yellowish to brownish yellow in KOH, smooth. *Basidia* 25–31 × 9–12 µm, 4-spored, sometimes 2-spored, clavate. *Cheilocystidia* 56–77 × 8–11 µm, forming a sterile edge, cylindrical, septate, thin-walled, consist of 2–3 cells, with terminal cells 25–38 × 7–12 µm. *Pleurocystidia* 38–65 × 6–9 µm, cylindrical, fusiform, subfusoid to narrowly lageniform, thin-walled, sparse. *Hymenophoral trama* divergent, boletoid. *Pileipellis* a trichoderm, made up of interwoven cylindrical hyphae 2.5–4 µm wide with narrowly clavate or fusiform terminal cells, 29–75 × 6–16 µm, sometimes with thickened walls in the apex; pigment incrusting, in some hyphae zebra-striped (-verrucose) and additionally pale intracellular. *Pileal trama* composed of interwoven hyphae 3.5–5.5 µm wide. *Stipitipellis* hymeniform. *Caulocystidia* 41–84 × 9–12 µm, as cylindrical, septate hairs with clavate or sometimes rostrate terminal cells. *Clamp connections* absent.

Habit, Habitat & Distribution — In groups on soil and dead wood in primary tropical middle to upper montane evergreen mixed forests. Known from Vietnam.

Typus. Vietnam, Lam Dong Province, Lac Duong District, Bidoup-Nui Ba National Park, vicinities of Giang Ly, 12.18061°N, 108.68442°E, 1 500 m alt., on soil and dead wood in middle montane mixed forest with the participation of *Pinus kempfii*, *P. dalatensis*, 25 May 2014, *O.V. Morozova* (holotype LE315544, ITS, *tef1α* and LSU sequences GenBank MN511177, MN597966 and MN511170, MycoBank MB832742).

Additional materials examined. Vietnam, Lam Dong Province, Lac Duong District, Bidoup-Nui Ba National Park, vicinities of Giang Ly, 12.18442°N, 108.68610°E, 1 520 m alt., on soil in middle montane mixed forest with the participation of *Pinus kempfii*, *P. dalatensis*, 2 July 2010, *E.S. Popov* (LE315549, ITS sequence GenBank MN511180); ibid., 12.18440°N, 108.68988°E, 1 500 m alt., on soil in middle montane mixed forest with the participation of *Pinus kempfii*, *P. dalatensis*, 23 May 2014, *O.V. Morozova* (LE315545); Dak Lak Province, Krong Bong District, Chu Yang Sin National Park, Krong Kmar, 7 km northwest of Chu Yang Sin, 12.40856°N, 108.38856°E, 1 530 m alt., on soil in mountain polydominant rainforest with the participation of *Pinus kempfii*, 21 May 2014, *A.V. Alexandrova* (LE315547, ITS, *tef1α* and LSU sequences GenBank MN511178, MN597965 and MN511171; ibid., LE315546, ITS and *tef1α* sequence GenBank MN511179 and MN597964).

Notes — The genus *Veloporphyrellus* was originally described based on *V. pantoleucus* from Costa Rica (Gómez & Singer 1984). It is characterised by the whitish to pink tubular hymenophore, the pinkish to brownish pink spore print, the smooth, elongate to fusiform basidiospores, trichodermial pileipellis and the extending membranous veil remnants on the pileus margin which often embraces the apex of the stipe (Wu et al. 2016). Li et al. (2014) considered the genus as monophyletic. However, in the work of Wu et al. (2016) its monophyly was questioned because species of this genus nested into two clades. Considering the morphological similarities and following latest work (Wu et al. 2016) we treat our new species as *Veloporphyrellus* until further data are available.

The closest species is *V. gracilioides*, from which the new species differs by the brighter reddish- or orange-brown colour of the basidiomata and less developed pileus margin. Due to macromorphology *V. vulpinus* resembles *Austroboletus gracilis*, with the exception of the non-reticulate stipe surface. But like other *Austroboletus* species *A. gracilis* possesses ornamented pitted spores, while the spores of *Veloporphyrellus* are smooth.

Colour illustrations. Vietnam, Lam Dong Prov., Lac Duong Dist., Bidoup-Nui Ba National Park, vicinities of Giang Ly, middle montane mixed forest with the participation of *Pinus kempfii*. Spores; SEM photos of spores; cheilocystidia; pileipellis; pleurocystidia; caulocystidia; basidiomata *in situ* (all from holotype); cross section of the basidioma (from LE315547). Scale bars = 1 cm (basidiomata), 10 µm (microstructures).

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Venturia submersa

Fungal Planet 1040 – 18 December 2019

Venturia submersa Iturrieta-González, Gené, Dania García, *sp. nov.*

Etymology. Referring to the fungus growing on submerged plant debris.

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

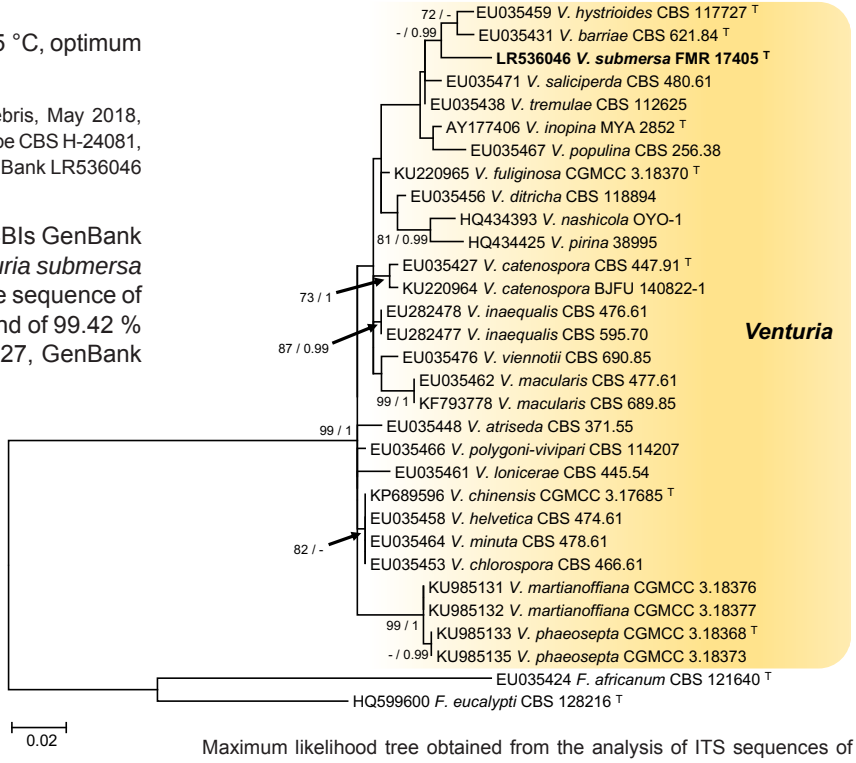
Mycelium consisting of branched, septate, subhyaline to pale olivaceous, smooth-walled 2–5 µm diam hyphae. *Conidiophores* mononematous, growing laterally on hyphae, micronematous, reduced to a conidiogenous cell, or macronematous, erect, unbranched, more rarely branched, subcylindrical, pale olivaceous, smooth-walled, up to 30 µm long. *Conidiogenous cells* terminal, polyblastic, with up to three denticle-like conidiogenous loci, smooth-walled, pale olivaceous, 11–24 × 2–4 µm, forming conidia in simple or branched acropetal chains. *Ramoconidia* 0(–1)-septate, cylindrical, with truncate base, up to three terminal or subterminal conidiogenous loci, smooth-walled, pale olivaceous, 13–24 × 2–4 µm. *Conidia* fusiform, ellipsoidal or cylindrical, 0(–2)-septate, pale olivaceous, smooth-walled, 7–15 × 3–4(–5) µm. *Sexual morph* not observed.

Culture characteristics at 25 °C in 2 wk — Colonies on potato dextrose agar (PDA) reaching 9 mm diam, grey (4F1), velvety, umbonate, aerial mycelium scarce, regular margin; reverse black. On potato carrot agar (PCA) reaching 8–10 mm, brownish grey (4F2), velvety, flat, aerial mycelium scarce, regular margin; reverse black. On oatmeal agar (OA) reaching 8–10 mm diam, grey (4F1), velvety, flat, aerial mycelium scarce, regular margin; reverse dark brown (6F8).

Cardinal temperature for growth — Minimum 5 °C, optimum 20 °C, maximum 25 °C.

Typus. Spain, Segovia, Riaza, on submerged plant debris, May 2018, *I. Iturrieta-González, V. Magaña-Dueñas & D. García* (holotype CBS H-24081, cultures ex-type FMR 17405; ITS and LSU sequences GenBank LR536046 and LR536048, MycoBank MB831789).

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the LSU sequence of *Venturia submersa* showed a similarity of 99.77 % (857/859) with the sequence of *V. barriae* (CBS 621.84, GenBank EU035431) and of 99.42 % (854/859) with that of *V. hystrioides* (CBS 117727, GenBank EU035459); while the ITS sequence was 96.44 % (488/506) similar with that of the latter species (CBS 117727, GenBank EU035459) and 95.46 % (484/507) with *V. barriae* (CBS 621.84, GenBank EU035431). The phylogenetic reconstruction using ITS barcodes of different accepted *Venturia* species, including the type *V. inaequalis*, showed that the new species was located in an unsupported clade together with *V. barriae*, *V. hystrioides, V. inopina*, *V. populina*, *V. tremulae* and *V. saliciperda*, being closely related with the former two species. *Venturia barriae*, formerly *Fusicladium fagi*, and *V. hystrioides,* formerly *Capronia hystrioides,* were described from decaying leaves of *Fagus sylvatica* and from scar of cherry fruit, respectively (Dugan et al. 1995, Crous et al. 2007c, Rossman et al. 2015). Morphologically, our new species differs from *V. barriae* in having longer conidiophores (up to 30 µm long vs up to 15 µm long in *V. barriae*), commonly aseptate and shorter conidia (7–15 µm vs up to 40 µm in *V. barriae*), and slower growth on PDA after 4 wk in darkness (23 mm in *V. submersa* vs 50 mm at 25 °C in *V. barriae*). *Venturia hystrioides* differs from *V. submersa* in the absence of macronematous conidiophores, larger ramoconidia (up to 30 µm long) with more septa (0–3), and by its more rapid growth on PDA and OA (reaching 40 mm after 2 wk at 25 °C in dark) (Crous et al. 2007c).



Maximum likelihood tree obtained from the analysis of ITS sequences of the genus *Venturia*. The alignment included 502 bp and was performed with ClustalW. Both the alignment and tree for ML were constructed with MEGA v. 6 software (Tamura et al. 2013) and Bayesian Inference (BI) approaches under MrBayes v. 3.2.6 (Ronquist et al. 2012). Kimura 2-parameters with Gamma distribution (K2+G) was used as the best nucleotide substitution model for ML and Hasegawa-Kishino-Yano with Gamma distribution (HKY+G) for BI. Bootstrap support values for ML greater than 70 % and Bayesian posterior probabilities greater than 0.95 are given near nodes. The new species proposed in this study is indicated in **bold** face. A superscript T denotes ex-type cultures.

Colour illustrations. Riaza, Segovia, Spain. Colony sporulating on PCA after 2 wk at 25 °C; conidiophores and conidia after 10 d. Scale bars 10 mm (colony), 10 µm (microscopic structures).

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Apenidiella antarctica

Fungal Planet 1041 – 18 December 2019

Apenidiella antarctica Ivanushkina, Kochkina, Vasilenko & Ozerskaya, *sp. nov.*

Etymology. Named after Antarctica, where the fungus was collected.

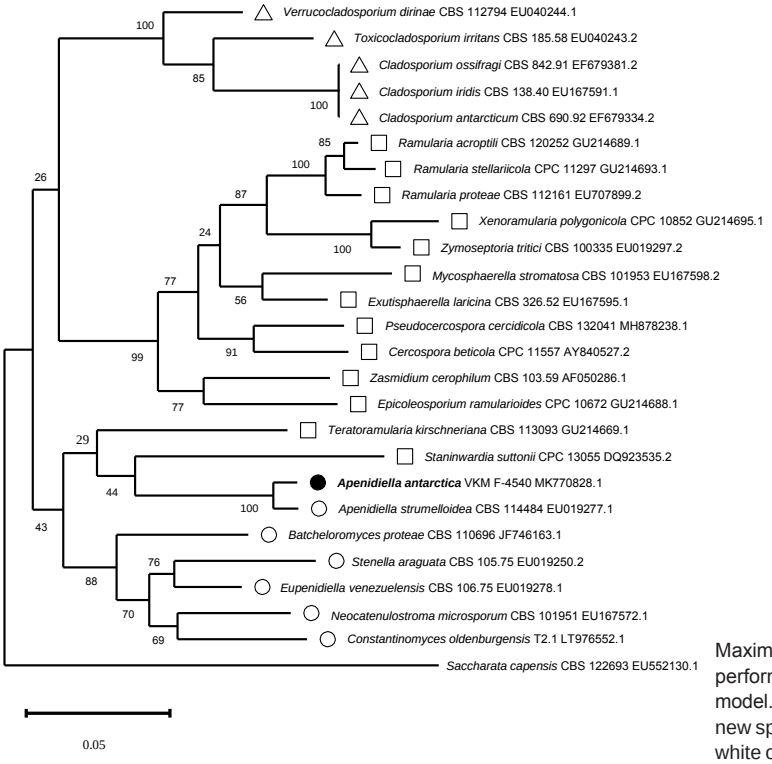
Classification — *Teratosphaeriaceae, Capnodiales, Dothideomycetidae, Dothideomycetes.*

Mycelium consisting of branched, septate, smooth to warty, hyaline to pale olivaceous, 1–4 µm wide hyphae. *Conidiophores* solitary, erect, arising from superficial mycelium, macronematous, subcylindrical, straight to slightly curved, subcylindrical throughout, 30–100 × 2.5–4.5 µm, 0–6-septate, medium to dark brown, paler towards the apex, smooth, wall ≤ 0.75 µm diam, penicillate apex formed by a terminal conidiogenous cell giving rise to a single set of ramoconidia. *Conidiogenous cells* terminal, rarely intercalary integrated, subcylindrical, straight to curved, 8–30 × 2.5–4.5 µm, pale brown, thin-walled, smooth, with several (–10) terminal and intercalary conidiogenous loci, thickened and darkened, scars protuberant, 1–1.5 µm diam. *Conidia* in short (–5), dense penicillate, acropetal chains, ramoconidia subcylindrical, with 1–3 terminal loci, olivaceous brown, smooth, 11–12.5 × 3.5–4.5(–5) µm; secondary conidia ellipsoid to obovoid, (7–)8.5–10(–11) × (3.5–)4–5.5(–6) µm, hila not thickened or almost so to somewhat thickened and darkened, not refractive, 1 µm diam.

Culture characteristics — (in the dark, PDA, 25 °C after 1 mo). Colonies olivaceous grey, dense, aerial mycelium abundant, felty to woolly, growth regular, low convex with an elevated colony centre, sometimes forming few large prominent exudates, reverse iron-grey, margin almost colourless, regular, colonies fertile; colonies reaching 20–22 mm diam (at 25 °C), 26–29 mm diam (at 20 °C), 20–21 mm diam (at 15 °C), 2–3 mm diam (at 5 °C), no growth (at 30 °C).

Typus. Antarctica, Russkaya Station (S74°45'48" W136°47'47", altitude 76 m), hole A8/08, depth 1.3–1.4 m, isolated from permafrost, *N. Ivanushkina* (holotype VKM H-0001, ex-type culture VKM F-4540, SSU/ITS/LSU sequence GenBank MK770828.1, MycoBank MB830584).

Notes — *Apenidiella antarctica* is the second member of the genus *Apenidiella* (Crous et al. 2007a, Quaedvlieg et al. 2014). Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Apenidiella strumelloidea* (GenBank NR_145090.1; Identities = 547/564 (97 %), 2 gaps (0 %)), *Cercosporella dolichandrae* (GenBank NR_156282.1; Identities = 489/574 (85 %), 32 gaps (5 %)), *Hortaea thailandica* (GenBank GU214637.1; Identities = 491/578 (85 %), 26 gaps (4 %)). Closest hits using the partial LSU sequence are *Apenidiella strumelloidea* (GenBank EU019277.1; Identities = 800/805 (99 %), no gaps), *Microcyclospora tardicrescens* (GenBank MH875507.1; Identities = 778/806 (97 %), 2 gaps (0 %)), *M. pomicola* (GenBank MH875506.1 with the same statistics), and *Microcyclospora malicola* (GenBank MH875503.1; Identities = 775/806 (96 %), 2 gaps (0 %)). Closest hits using the contiguous tandem ITS plus LSU (including D1-D3 domains) sequence are *Apenidiella strumelloidea* (GenBank EU019277.1; Identities = 1345/1367 (98 %), 2 gaps (0 %)), *Eupenidiella venezuelensis* (GenBank EU019277.1; Identities = 1228/1351 (91 %), 29 gaps (2 %)), *Teratoramularia kirschneriana* (GenBank GU214669.1; Identities = 1210/1343 (90 %), 26 gaps (1 %)). *Apenidiella antarctica* differs morphologically from *A. strumelloidea* VKM F-2534^T (= CBS 114484^T) in having numerous loci aggregated or spread over the whole conidiogenous cell, short and little branched conidial chains, and wider, not curved conidia.



Maximum likelihood phylogenetic tree inferred from ITS+LSU sequences performed with MEGA-X (Kumar et al. 2018) using the Kimura 2-parameter model. Bootstrap support values (500 replicates) are shown at the nodes. The new species described in this study is marked with the black circle, where as white ones mark the known members of *Teratosphaeriaceae*, white squares mark *Mycosphaerellaceae* and triangles mark *Cladosporiaceae*. *Saccharata capensis* represents the outgroup. The alignment and tree are deposited in TreeBASE (S24413).

Colour illustrations. David Gilichinsky at the Russkaya Station in Marie Byrd Land, Antarctica, busy sampling via the dry drilling technique. Colonies on PDA; conidiophores and conidiogenous cells; conidia. Scale bars = 10 µm.

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REFERENCES

Al-Hatmi AMS, Bonifaz A, De Hoog GS, et al. 2014. Keratitis by Fusarium temperatum, a novel opportunist. BMC Infectious Diseases 14: 1–9.

Andjic V, Carnegie AJ, Pegg GS, et al. 2019. 23 years of research on Teratosphaeria leaf blight of Eucalyptus. Forest Ecology and Management 443: 19–27.

Aveskamp MM, Guyter J, Woudenberg JHC, et al. 2010. Highlights of the Didymellaceae: A polyphasic approach to characterise Phoma and related pleosporalean genera. Studies in Mycology 65: 1–60.

Baral H-O, Rämä T. 2015. Morphological update on Calycina marina (Pezizellaceae, Helotiales, Leotiomycetes), a new combination for Laetinaevia marina. Botanica Marina 58 (6): 523–534.

Barbosa RN, Bezerra JDP, Souza-Motta CM, et al. 2018. New Penicillium and Talaromyces species from honey, pollen and nests of stingless bees. Antonie van Leeuwenhoek 111: 1883–1912.

Batista AC, Bezerra JL, Da Silva MH. 1960. Vonarxia n.gen. e outros imperfecti fungi. Publicações Instituto de Micologia da Universidade do Recife 283: 1–32.

Bensch K, Braun U, Groenewald JZ, et al. 2012. The genus Cladosporium. Studies in Mycology 72: 1–401.

Bensch K, Groenewald JZ, Braun U, et al. 2015. Common but different: The expanding realm of Cladosporium. Studies in Mycology 82: 23–74.

Bessette A, Roody WC, Bessette AR. 1999. North American Boletes: a color guide to the fleshy pored mushrooms. Syracuse University Press.

Boertmann D. 1990. The identity of Hygrocybe vitellina and related species. Nordic Journal of Botany 10: 311–317.

Boertmann D. 2010. The genus Hygrocybe. Fungi of Northern Europe vol. I, 2nd edn. Danish Mycological Society, Denmark.

Bordallo JJ, Rodríguez A, Kaounas V, et al. 2015. Two new Terfezia species from Southern Europe. Phytotaxa 230: 239–249.

Bordallo JJ, Rodríguez A, Muñoz-Mohedano JM, et al. 2013. Five new Terfezia species from the Iberian Peninsula. Mycotaxon 124: 189–208.

Borgen T, Arnolds E. 2004. Taxonomy, ecology and distribution of Hygrocybe (Fr.) P. Kumm and Camarophyllopsis Herink (Fungi, Basidiomycota, Hygrocybeae) in Greenland. Bioscience 54: 1–68.

Bourdot H, Galzin A. 1928. Hyménomycètes de France. M. Bry ed., Sceaux, F.

Braun U, Cook RTA. 2012. Taxonomic manual of the Erysiphales (Powdery Mildews). CBS Biodiversity Series 11. CBS, Utrecht, Netherlands.

Braun U, Shin HD, Takamatsu S, et al. 2019. Phylogeny and taxonomy of Golovinomyces orontii revisited. Mycological Progress 18: 335–357.

Bulliard JBP. 1791. Histoire des champignons de la France I: 1–368.

Caboň M, Li GJ, Saba M, et al. 2019. Phylogenetic study documents different speciation mechanisms within the Russula globispora lineage in boreal and arctic environments of the northern hemisphere. IMA Fungus 1: 1–16.

Cabral TS, Silva BDB, Ishkawa NK, et al. 2014. A new species and new records of gasteroid fungi (Basidiomycota) from Central Amazonia, Brazil. Phytotaxa 183: 239–253.

Cai L, Wu W-P, Hyde KD. 2009. Phylogenetic relationships of Chalara and allied species inferred from ribosomal DNA sequences. Mycological Progress 8: 133–143.

Calonge FD, Demoulin V. 1975. Les Gastéromycètes d'Espagne. Bulletin Trimestriel de la Société Mycologique de France 91: 247–292.

Calonge FD, Mata M. 2004. A new species of Geastrum from Costa Rica and Mexico. Boletín de la Sociedad Micológica de Madrid 28: 331–335.

Candusso M. 1997. Hygrophorus s. l. Fungi Europaei 6: 1–784.

Cheewangkoon R, Groenewald JZ, Summerell BA, et al. 2009. Myrtaceae, a cache of fungal biodiversity. Persoonia 23: 55–85.

Chomnunti P, Ko TWK, Chukeatirote E, et al. 2012. Phylogeny of Chaetothyriaceae in northern Thailand including three new species. Mycologia 104: 382–395.

Consiglio G, Contu M. 2007. Hygrocybe citrinopallida. Rivista di Micologia 1: 57–64.

Cooper J, Leonard P. 2012. Boletopsis nothofagi sp. nov. associated with Nothofagus in the Southern Hemisphere. MycoKeys 3: 13–22.

Corner EJH. 1950. A monograph of Clavaria and allied genera. Oxford University Press, London, UK.

Corner EJH. 1970. Supplement to 'A monograph of Clavaria and allied genera'. Beihefte zur Nova Hedwigia 33: 1–299.

Corner EJH. 1972. Boletus in Malaysia. Botanic Gardens, Singapore.

Costa MLN, Machado JC, Guimarães RM, et al. 2003. Inoculação de Fusarium oxysporum f. sp. phaseoli em sementes de feijoeiro através de restrição hídrica. Ciência e Agrotecnologia 27: 1023–1030.

Crous PW, Braun U. 2003. Mycosphaerella and its anamorphs. 1. Names published in Cercospora and Passalora. CBS Biodiversity Series 1: 1–571. CBS-KNAW Fungal Biodiversity Centre, Utrecht, Netherlands.

Crous PW, Braun U, Groenewald JZ. 2007a. Mycosphaerella is polyphyletic. Studies in Mycology 58: 1–32.

Crous PW, Braun U, Hunter GC, et al. 2013a. Phylogenetic lineages in Pseudocercospora. Studies in Mycology 75: 37–114.

Crous PW, Braun U, Schubert K, et al. 2007b. Delimiting Cladosporium from morphologically similar genera. Studies in Mycology 58: 33–56.

Crous PW, Carnegie AJ, Wingfield MJ, et al. 2019a. Fungal Planet description sheets: 868–950. Persoonia 42: 291–473.

Crous PW, Kendrick WB, Alfenas AC. 1997. New species of hyphomycetes associated with Eucalyptus. South African Journal of Botany 63: 286–290.

Crous PW, Luangsa-ard JJ, Wingfield MJ, et al. 2018a. Fungal Planet description sheets: 785–867. Persoonia 41: 238–417.

Crous PW, Schubert K, Braun U, et al. 2007c. Opportunistic, human-pathogenic species in the Herpotrichiellaceae are phenotypically similar to saprobic or Phytopathogenic species in the Venturiaceae. Studies in Mycology 58: 185–217.

Crous PW, Schumacher RK, Akulov A, et al. 2019b. New and interesting fungi. 2. Fungal Systematics and Evolution 3: 57–134.

Crous PW, Schumacher RK, Wingfield MJ, et al. 2015a. Fungal Systematics and Evolution: FUSE 1. Sydowia 67: 81–118.

Crous PW, Schumacher RK, Wingfield MJ, et al. 2018b. New and interesting fungi. 1. Fungal Systematics and Evolution 1: 169–215.

Crous PW, Shivas RG, Quaedvlieg W, et al. 2014. Fungal Planet description sheets: 214–280. Persoonia 32: 184–306.

Crous PW, Shivas RG, Wingfield MJ, et al. 2012a. Fungal Planet description sheets: 128–153. Persoonia 29: 146–201.

Crous PW, Summerell BA, Shivas RG, et al. 2012b. Fungal Planet description sheets: 107–127. Persoonia 28: 138–182.

Crous PW, Wingfield MJ. 1993. A re-evaluation of Cylindrocladiella, and a comparison with allied genera. Mycological Research 97: 433–448.

Crous PW, Wingfield MJ, Alfenas AC, et al. 1994. Cylindrocladium naviculatum sp. nov., and two new vesiculate Hyphomycete genera, Falcocladium and Vesicladiella. Mycotaxon 50: 441–458.

Crous PW, Wingfield MJ, Burgess TI, et al. 2016a. Fungal Planet description sheets: 232–233. Persoonia 37: 469–557.

Crous PW, Wingfield MJ, Burgess TI, et al. 2017a. Fungal Planet description sheets: 625–715. Persoonia 39: 270–467.

Crous PW, Wingfield MJ, Burgess TI, et al. 2017b. Fungal Planet description sheets: 558–624. Persoonia 38: 240–384.

Crous PW, Wingfield MJ, Burgess TI, et al. 2018c. Fungal Planet description sheets: 716–784. Persoonia 40: 240–393.

Crous PW, Wingfield MJ, Cheewangkoon R, et al. 2019c. Foliar pathogens of eucalypts. Studies in Mycology 94: 125–298.

Crous PW, Wingfield MJ, Guarro J, et al. 2013b. Fungal Planet description sheets: 154–213. Persoonia 31: 188–296.

Crous PW, Wingfield MJ, Guarro J, et al. 2015b. Fungal Planet description sheets: 320–370. Persoonia 34: 167–266.

Crous PW, Wingfield MJ, Richardson DM, et al. 2016b. Fungal Planet description sheets: 400–468. Persoonia 36: 316–458.

Damm U, Cannon PF, Woudenberg JHC, et al. 2012. The Colletotrichum acutatum species complex. Studies in Mycology 73: 37–113.

De Crop E, Nuytinck J, Van de Putte K, et al. 2017. A multi-gene phylogeny of Lactifluus (Basidiomycota, Russulales) translated into a new infrageneric classification of the genus. Persoonia 38: 58–80.

De Hoog GS. 1985. Taxonomy of the Dactylaria complex, IV. Dactylaria, Neta, Subulispora and Scolecobasidium. Studies in Mycology 26: 1–60.

Decock C, Delgado-Rodríguez G, Buchet S, et al. 2003. A new species and three new combinations in Cyphellophora, with a note on the taxonomic affinities of the genus, and its relation to Kumbhamaya and Pseudomicrodochium. Antonie van Leeuwenhoek 84: 209–216.

Demoulin V. 1979. The typification of Lycoperdon described by Peck and Morgan. Beihefte zur Sydowia 8: 139–151.

Dereeper A, Guignon V, Blanc G et al. 2008. Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Research (Web Server issue): W465-9.

Desprez-Loustau M-L, Massot M, Toïgo M, et al. 2018. From leaf to continent: the multi-scale distribution of an invasive cryptic pathogen complex on oak. Fungal Ecology 36: 39–50.

Domsch K, Gams W, Anderson TH. 2007. Compendium of soil fungi, 2 edn. IHW-Verlag, Eching.

Donk MA. 1933. Revisie van de Nederlandse Heterobasidiomyceteae (uitgez. Uredinales en Ustilaginales) en Homobasidiomyceteae-Aphyllophoraceae: II. Mededelingen van het botanisch Museum en Herbarium van de Rijksuniversiteit Utrecht 9: 1–278.

Dugan FM, Roberts RG, Hanlin RT. 1995. New and rare fungi from cherry fruits. Mycologia 87: 713–718.

Ellis MB. 1971. Dematiaceous Hyphomycetes. Commonwealth Mycological Institute, Kew, Surrey, England.
Ellis MB. 1976. More Dematiaceous Hyphomycetes. Commonwealth Mycological Institute, Kew, Surrey, England.
Ellison CA, Sankaran KV. 2017. Profile of an invasive plant: Mikania micrantha. In: Ellison CA, Sankaran KV, Murphy ST (eds), Invasive alien plants: 18–28. CABI Publishing, Wallingford, UK.
Eriksson OE. 1982. Cordyceps bifusispora spec. nov. Mycotaxon 15: 185–188.
Faria CB, Abe CAL, Da Silva CN, et al. 2012. New PCR assays for the identification of Fusarium verticillioides, Fusarium subglutinans, and other species of the Gibberella fujikuroi complex. International Journal of Molecular Sciences 13: 115–132.
Funnell-Harris DL, Scully ED, Sattler SE, et al. 2017. Differences in Fusarium species in brown midrib Sorghum and in air populations in production fields. Phytopathology 107: 1353–1363.
Giraldo A, Crous PW. 2019. Inside Plectosphaerellaceae. Studies in Mycology 92: 227–286.
Giraldo A, Hernández-Restrepo M, Crous PW. 2019. New plectosphaerellaceous species from Dutch garden soil. Mycological Progress 18: 1135–1154.
Gómez LD, Singer R. 1984. Veloporphyrellus, a new genus of Boletaceae from Costa Rica. Brenesia 22: 293–298.
Gouy M, Guindon S, Gascuel O. 2010. SeaView version 4: A multiplatform graphical user interface for sequence alignment and phylogenetic tree building. Molecular Biology and Evolution 27: 221–224.
Guatimosim E, Schwartsburd PB, Barreto RW, et al. 2016. Novel fungi from an old niche: cercosporoid and related sexual morphs on ferns. Persoonia 37: 106–141.
Guindon S, Gascuel O. 2003. A simple, fast and accurate algorithm to estimate large phylogenies by maximum likelihood. Systematic Biology 52: 696–704.
Han J-G, Hosoya T, Sung G-H, et al. 2014. Phylogenetic reassessment of Hyaloscyphaceae sensu lato (Helotiales, Leotiomycetes) based on multigene analyses. Fungal Biology 118: 150–167.
Hausknecht A, Krisai-Greilhuber I, Jaklitsch W. 2003. Rezente Pilfunde aus Osttirol. Österreischiche Zeitschrifte für Pilzkunde 12: 153–192.
Hernández-Restrepo M, Gené J, Castañeda-Ruiz RF, et al. 2017. Phylogeny of saprobic microfungi from Southern Europe. Studies in Mycology 86: 53–97.
Heykoop M, Moreno G, Alvarado P, et al. 2017. El género Psathyrella (Fr.) Quél. S.l. en España. VI. Especies nuevas o raras y reevaluación de otras. Boletín de la Sociedad Micológica de Madrid 41: 71–98.
Holubová-Jechová V. 1974. A revision of the genus Olpitrichum Atk. Folia Geobotanica et Phytotaxonomica 9: 425–432.
Hughes SJ. 1958. Revisiones hyphomycetum aliquot cum appendice de nominibus rejiciendis. Canadian Journal of Botany 36: 727–836.
Hughes SJ, Pirozynski KA. 1971. New Zealand fungi 15. Beltraniella, Circinotrichum, and Gyrothrix (Syn. Peglionia), New Zealand Journal of Botany 9: 39–45.
Hustad VP, Miller AN. 2011. Phylogenetic placement of four genera within the Leotiomycetes (Ascomycota). North American Fungi 6: 1–13.
Isola D, Zucconi L, Onofri S, et al. 2016. Extremotolerant rock inhabiting black fungi from Italian monumental sites. Fungal Diversity 76: 75–96.
Jaklitsch WM, Checa J, Blanco MN, et al. 2018. A preliminary account of the Cucurbitariaceae. Studies in Mycology 90: 71–118.
Jaklitsch WM, Gardiennet A, Voglmayr H. 2016. Resolution of morphology-based taxonomic delusions: Acrocordiella, Basiseptospora, Blogiascospora, Clypeosphaeria, Hymenopleella, Lepteutypa, Pseudapiospora, Requienella, Seiridium and Strickeria. Persoonia 37: 82–105.
Jaklitsch WM, Samuels GL, Dodd SL, et al. 2006. Hypocrea rufa/Trichoderma viride: a reassessment, and description of five closely related species with and without warted conidia. Studies in Mycology 56: 135–177.
Jiang JR, Cai L, Liu F. 2017. Oligotrophic fungi from a carbonate cave, with three new species of Cephalotrichum. Mycology 8: 164–177.
Jiang Y, Dukik K, Muñoz JF, et al. 2018. Phylogeny, ecology and taxonomy of systemic pathogens and their relatives in Ajellomycetaceae (Onygenales): Blastomyces, Emergomyces, Emmonsia, Emmonsiellopsis. Fungal Diversity 90: 245–291.
Johnston PR, Quijada L, Smith CA, et al. 2019. A multigene phylogeny toward a new phylogenetic classification of Leotiomycetes. IMA Fungus 10: 1.
Karsten PA. 1871. Mycologia fennica. Pars prima. Discomycetes. Bidrag till Kännedom av Finlands Natur och Folk 19: 1–264.
Karsten PA. 1873. Mycologia fennica. Pars secunda. Pyrenomycetes. Bidrag till Kännedom av Finlands Natur och Folk 23: 1–252.
Kim JH, Kang MR, Kim HK, et al. 2012. Population structure of the Gibberella fujikuroi species complex associated with rice and corn in Korea. Plant Pathology Journal 28: 357–363.
Kirschstein W. 1938. Über neue, seltene und kritische Ascomyceten und Fungi imperfecti. I. Annales Mycologici 36: 367–400.
Kiss L, Jankovics T, Kovács GM, et al. 2008. Oidium longipes, a new powdery mildew fungus on petunia in the USA: A potential threat to ornamental and vegetable solanaceous crops. Plant Disease 92: 818–825.
Kits van Waveren E. 1985. The Dutch, French and British species of Psathyrella. Persoonia Supplement 2: 1–300.
Kornerup A, Wanscher JH. 1967. Methuen Handbook of Colour. Methuen & Co Ltd, London.
Kornerup A, Wanscher JH. 1978. Methuen Handbook of Colour. 3rd ed. Eyre Methuen, London.
Kreisel H. 1967. Taxonomisch-Pflanzengeographische Monographie der Gattung Bovista. Beiheft Nova Hedwigia 25: 1–244.
Kumar S, Stecher G, Li M, et al. 2018. MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. Molecular Biology and Evolution 35: 1547–1549.
Küppers H. 2002. Atlas de los colores. Blume: 1–165.
Larsson E, Örstadius L. 2008. Fourteen coprophilous species of Psathyrella identified in the Nordic countries using morphology and nuclear rDNA sequence data. Mycological Research 112: 1165–1185.
Le Gal F, Mangenot F. 1958. Revue mycologique (Paris) 23: 54.
Leslie JF, Summerell BA. 2006. The Fusarium Laboratory Manual. Blackwell Publishing, Ames, Iowa, USA.
Li GJ, Zhang CL, Zhao RL, et al. 2018. Two new species of Russula from Northeast China. Mycosphere 9: 431–443.
Li YC, Ortiz-Santana B, Zeng NK, et al. 2014. Molecular phylogeny and taxonomy of the genus Veloporphyrellus. Mycologia 106: 291–306.
Liu F, Bonthond G, Groenewald JZ, et al. 2019a. Sporocadaceae, a family of coelomycetous fungi with appendage-bearing conidia. Studies in Mycology 92: 287–415.
Liu F, Wang J, Li H, et al. 2019b. Setophoma spp. on Camellia sinensis. Fungal Systematics and Evolution 4: 43–57.
Lodge D, Padamsse M, Matheny PB, et al. 2013. Molecular phylogeny, morphology, pigment chemistry and ecology in Hygrophoraceae (Agaricales). Fungal Diversity 10: 311–317.
Lombard L, Shivas RG, To-Anun C, et al. 2012. Phylogeny and taxonomy of the genus Cylindrocladiella. Mycological Progress 11: 835–868.
Luangsa-ard JJ, Tasanathai K, Mongkolsamrit S, et al. 2008. Atlas of Invertebrate-Pathogenic Fungi of Thailand, vol. 2. NSTDA publication. Darnsutha Press Co., Ltd.
Malysheva EF, Malysheva VF, Justo A. 2016. Observation on Pluteus (Pluteaceae) diversity in South Siberia, Russia: morphological and molecular data. Mycological Progress 15: 861–882.
Marin-Felix Y, Groenewald JZ, Cai L, et al. 2017. Genera of phytopathogenic fungi: GOPHY 1. Studies in Mycology 86: 99–216.
Marin-Felix Y, Hernández-Restrepo M, Iturrieta-González I, et al. 2019. Genera of phytopathogenic fungi: GOPHY 3. Studies in Mycology 94: 1–124.
Marin-Felix Y, Stchigel AM, Cano-Lira JF, et al. 2015. Emmonsiellopsis, a new genus related to the thermally dimorphic fungi of the family Ajellomycetaceae. Mycoses 58: 451–460.
Menolli Jr N, Justo A, Capelari M. 2015. Phylogeny of Pluteus section Celluloderma including eight new species from Brazil. Mycologia 107: 1205–1220.
Miller AN, Huhndorf SM. 2004. A natural classification of Lasiosphaeria based on nuclear LSU rDNA sequences. Mycological Research 108: 26–34.
Miller AN, Huhndorf SM, Fournier J. 2014. Phylogenetic relationships of five uncommon species of Lasiosphaeria and three new species in the Helminthosphaeriaceae (Sordariomycetes). Mycologia 106: 505–524.
Miller MA, Pfeiffer W, Schwartz T. 2010. Creating the CIPRES Science Gateway for inference of large phylogenetic trees. In: Proceedings of the Gateway Computing Environments Workshop (GCE), New Orleans, LA: 1–8.
Miller MA, Pfeiffer W, Schwartz T. 2012. The CIPRES science gateway: enabling high-impact science for phylogenetics researchers with limited resources. In: Proceedings of the 1st Conference of the Extreme Science and Engineering Discovery Environment: Bridging from the extreme to the campus and beyond: 1–8. Association for Computing Machinery, USA.
Miller OK, Lodge DJ, Baroni TJ. 2000. New and interesting ectomycorrhizal fungi from Puerto Rico, Mona, and Guana Islands. Mycologia 92: 558–570.
Minnis AM, Lindner DL. 2013. Phylogenetic evaluation of Geomyces and allies reveals no close relatives of Pseudogymnoascus destructans, comb. nov., in bat hibernacula of eastern North America. Fungal Mycology 117: 638–649.
Mongkolsamrit S, Noisripoom W, Thanakitpipattana D, et al. 2018. Disentangling cryptic species with isaria-like morphs in Cordycipitaceae. Mycologia 110: 230–257.
Moyersoen B, Demoulin V. 1996. Les Gastéromycètes de Corse: taxonomie, écologie, chorologie. Lejeunia 152: 1–130.
Müller W, Agerer R. 1990. Studien an Ektomykorrhizen. XXIX, Drei Mykorrhizen aus der Leccinum-scabrum-Gruppe. Nova Hedwigia 51: 381–410.

Nag Raj TR. 1993. Coelomycetous anamorphs with appendage-bearing conidia. Mycologue Publications, Waterloo, Ontario.
Nag Raj TR, Kendrick B. 1976. A monograph of Chalara and allied genera. Wilfrid Laurier University Press, Waterloo, Ontario, Canada.
Nagy LG, Vágvölgyi C, Papp T. 2013. Morphological characterization of clades of the Psathyrellaceae (Agaricales) inferred from a multigene phylogeny. Mycological Progress 12: 505–517.
Nagy LG, Walther G, Házi J, et al. 2011. Understanding the evolutionary processes of fungal fruiting bodies: correlated evolution and divergence times in the Psathyrellaceae. Systematic Biology 60: 303–317.
Nguyen L-T, Schmidt HA, Von Haeseler A, et al. 2015. IQ-TREE: A fast and effective stochastic algorithm for estimating maximum likelihood phylogenies. Molecular Biology and Evolution 32: 268–274.
Niemelä T, Saarenoksa R. 1989. On Fennoscandian polypores 10. Boletopsis leucomelaena and B. grisea described and illustrated. Karstenia 29: 12–28.
Nuangmek W, Aiduang W, Suwannarach N, et al. 2018. First report of gummy stem blight caused by Stagonosporopsis cucurbitacearum on cantaloupe in Thailand. Canadian Journal of Plant Pathology 40: 306–311.
O'Donnell K, McCormick SP, Busman M, et al. 2018. Marasas et al. 1984. 'Toxigenic Fusarium Species: Identity and Mycotoxicology' revisited. Mycologia 110: 1058–1080.
Olariaga I, Jugo BM, Garcia-Etxerbarria K, et al. 2009. Species delimitation in the European species of Clavulina (Cantharellales, Basidiomycota) inferred from phylogenetic analyses of ITS region and morphological data. Mycological Research 113: 1261–1270.
Olariaga I, Salcedo I. 2012. New combinations and notes in clavarioid fungi. Mycotaxon 121: 37–44.
Olson DM, Dinerstein E, Wikramanayake ED, et al. 2001. Terrestrial ecoregions of the world: A new map of life on earth. BioScience 51: 933–938.
Örstadius L, Ryberg M, Larsson E. 2015. Molecular phylogenetics and taxonomy in Psathyrellaceae (Agaricales) with focus on psathyrelloid species: introduction of three new genera and 18 new species. Mycological Progress 14: 25.
Peterson SW, Vega F, Posada F, et al. 2005. Penicillium coffeae, a new endophytic species isolated from a coffee plant and its phylogenetic relationship to P. fellutanum, P. thiersii and P. brocae based on parsimony analysis of multilocus DNA sequences. Mycologia 97: 659–666.
Petrak F, Sydow H. 1934. Kritisch-systematische Originaluntersuchungen über Pyrenomyzeten, Sphaeropsideen und Melanconieen. Annales Mycologici 32: 1–35.
Pham NQ, Barnes I, Chen SF, et al. 2018. New species of Cylindrocladiella from plantation soils in South-East Asia. MycoKeys 32: 1–24.
Pitt JI. 1980. The genus Penicillium and its teleomorphic states Eupenicillium and Talaromyces. Academic Press, London.
Pratibha SJ, Gawas P, Shenoy BD, et al. 2005. Chalara indica sp. nov. and Sorocybe indicus sp. nov. from India. Cryptogamie, Mycologie 26: 97–103.
Quaedvlieg W, Binder M, Groenewald JZ, et al. 2014. Introducing the consolidated species concept to resolve species in the Teratosphaeriaceae. Persoonia 33: 1–40.
Quaedvlieg W, Verkley GJM, Shin H-D, et al. 2013. Sizing up Septoria. Studies in Mycology 75: 307–390.
Rajeshkumar KC, Crous PW, Groenewald JZ, et al. 2016. Resolving the phylogenetic placement of Porobeltraniella and allied genera in the Beltraniaceae. Mycological Progress 15: 1119–1136.
Rayner RW. 1970. A mycological colour chart. Commonwealth Mycological Institute & British Mycological Society, Kew, Richmond.
Rea C. 1918. New or rare British fungi. Transactions of the British Mycological Society 6: 61–64.
Richter T, Baral H-O. 2008. Coronellaria pulicaris, Mollisia luctuosa und Marasmius corelii - seltene Saprobionten an Cyperaceen. Boletus 31: 45–63.
Ronquist F, Huelsenbeck JP. 2003. MrBayes 3: Bayesian phylogenetic inference under mixed models. Bioinformatics 19: 1572–1574.
Ronquist F, Teslenko M, Van der Mark P, et al. 2012. MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61: 539–542.
Rossman AY, Aime MC, Farr DF, et al. 2004. The coelomycetous genera Chaetomella and Pilidium represent a newly discovered lineage of inoperculate discomycetes. Mycological Progress 3: 275–290.
Rossman AY, Crous PW, Hyde KD, et al. 2015. Recommended names for pleomorphic genera in Dothideomycetes. IMA Fungus 6: 507–523.
Samerpitak K, Van der Linde E, Choi H-J, et al. 2014. Taxonomy of Ochroconis, genus including opportunistic pathogens on humans and animals. Fungal Diversity 65: 89–126.
Samson RA. 1972. Notes on Pseudogymnoascus, Gymnoascus and related genera. Acta Botanica Neerlandica 21: 517–527.
Samuels GJ, Dodd SL, Lu B-S, et al. 2006. The Trichoderma koningii aggregate species. Studies in Mycology 56: 67–133.
Sánchez L, Gibert YS. 2015. Chromosera viola (J. Geesink & Bas) Vizzini & Ercole 2012, une spectacular especie localizada en Cataluña. Revista Catalana de Micologia 36: 29–32.
Scauflaire J, Gourgue M, Munaut F. 2011. Fusarium temperatum sp. nov. from maize, an emergent species closely related to Fusarium subglutinans. Mycologia 103: 586–597.
Scholler M, Schmidt A, Siahaan SAS, et al. 2016. A taxonomic and phylogenetic study of the Golovinomyces biocellatus complex (Erysiphales, Ascomycota) using asexual state morphology and rDNA sequence data. Mycological Progress 15: 56.
Schubert K, Groenewald Z, Braun U, et al. 2007. Biodiversity in the Cladosporium herbarum complex (Davidiellaceae, Capnodiales), with standardization of methods for Cladosporium taxonomy and diagnostics. Studies in Mycology 58: 105–156.
Schultes NP, Murtishi B, Li DW. 2017. Phylogenetic relationships of Chlamydomyces, Harzia, Olpitrichum, and their sexual allies, Melanospora and Sphaerodes. Fungal Biology 121: 890–904.
Seifert KA, Hughes SJ, Boulay H, et al. 2007. Taxonomy, nomenclature and phylogeny of three cladosporium-like hyphomycetes, Sorocybe resinae, Seifertia azaleae and the Hormoconis anamorph of Amorphotheca resinae. Studies in Mycology 58: 235–245.
Seifert KA, Morgan-Jones G, Gams W, et al. 2011. The genera of Hyphomycetes. CBS Biodiversity Series 9. CBS-KNAW Fungal Biodiversity Centre, Utrecht, the Netherlands.
Silva BDB, Cabral TS, Marihno P, et al. 2013a. Two new species of Geastrum (Geastraceae, Basidiomycota) found in Brazil. Nova Hedwigia 96: 445–456.
Silva M, Freitas NM, Mendonça HL, et al. 2013b. First report of Stagonosporopsis curcubitacearum causing fruit rot of Luffa cylindrica in Brazil. Plant Disease 97: 1120.
Smith ME, Henkel TW, Rollins JA. 2015. How many fungi make sclerotia? Fungal Ecology 13: 211–220.
Smith ME, Pfister DH. 2009. Tuberculate ectomycorrhizae of angiosperms: the interaction between Boletus rubropunctus (Boletaceae) and Quercus species (Fagaceae) in the United States and Mexico. American Journal of Botany 96: 1665–1675.
Spegazzini CL. 1910. Fungi Chilensis. Contribución al Estudio de los Hongos Chilenos. Revista de la Facultad de Agronomía y Veterinaria, Universidad Nacional de La Plata 6: 1–205.
Stamatakis A. 2006. RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. Bioinformatics 22: 2688–2690.
Stamatakis A. 2014. RAxML version 8: A toll for phylogenetic analysis and post-analysis of large phylogenenies. Bioinformatic 30: 1312–1313.
Stamatakis A, Hoover P, Rougemont J. 2008. A rapid bootstrap algorithm for the RAxML Web servers. Systematic Biology 57: 758–771.
Stewart JE, Turner AN, Brewer MT. 2015. Evolutionary history and variation in host range of three Stagonosporopsis species causing gummy stem blight of cucurbits. Fungal Biology 119: 370–382.
Su CH, Wang HH. 1986. Phytocordyceps, a new genus of the Clavicipitaceae. Mycotaxon 26: 337–344.
Su HY, Hyde KD, Maharachchikumbura SSN, et al. 2016. The families Distoseptisporaceae fam. nov., Kirschsteiniotheliaceae, Sporidesmiaceae and Torulaceae, with new species from freshwater in Yunnan Province, China. Fungal Diversity 80: 375–409.
Suija A, Motiejūnaitė J. 2017. Calycina alstrupii sp. nov. (Pezizellaceae, Helotiales), a new lichenicolous fungus from Norway. Phytotaxa 307: 113–122.
Sung GH, Hywel-Jones NL, Sung JM, et al. 2007. Phylogenetic classification of Cordyceps and the clavicipitaceous fungi. Studies in Mycology 57: 5–59.
Sunhede S. 1989. Geastraceae (Basidiomycotina): Morphology, ecology and systematics with special emphasis on the North European species. Synopsis Fungorum 1: 1–534.
Sutton BC. 1980. The Coelomycetes. Fungi Imperfecti with Pycnidia, Acervuli and Stromata. Commonwealth Mycological Institute, Kew.
Swofford DL. 2003. PAUP*. Phylogenetic analysis using parsimony and other methods. Version 4. Sinauer Associates, Sunderland, Massachusetts.
Tamura K, Stecher G, Peterson D, et al. 2013. MEGA6: Molecular evolutionary genetics analysis version 6.0. Molecular Biology and Evolution 30: 2725–2729.
Tanaka K, Hirayama K, Yonezawa H, et al. 2015. Revision of the Massarineae (Pleosporales, Dothideomycetes). Studies in Mycology 82: 75–136.
Tsui CKM, Sivichai S, Berbee ML. 2006. Molecular systematics of Helicoma, Helicomyces and Helicosporium and their teleomorphs inferred from rDNA sequences. Mycologia 98: 94–104.
Vaghefi N, Pethybridge SJ, Ford R, et al. 2012. Stagonosporopsis spp. associated with ray blight disease of Asteraceae. Australasian Plant Pathology 41: 675–686.

Valenzuela-Lopez N, Cano-Lira JF, Guarro J, et al. 2018. Coelomycetous Dothideomycetes with emphasis on the families Cucurbitariaceae and Didymellaceae. Studies in Mycology 90: 1–69.
Van der Aa HA. 1973. Studies in Phyllosticta I. Studies in Mycology 5: 1–110.
Vasutová M, Antonin V, Urban A. 2008. Phylogenetic studies in Psathyrella focusing on sections Pennatae and Spadiceae – new evidence for the paraphyly of the genus. Mycological Research 112: 1153–1164.
Vellinga EC. 1990. Pluteus. In: Bas C, Kuyper ThW, Noordeloos ME, et al. (eds), Flora Agaricina Neerlandica, vol 2: 31–55. Balkema, Rotterdam.
Verkley GJM, Quaedvlieg W, Shin HD, et al. 2013. A new approach to species delimitation in Septoria. Studies in Mycology 75: 213–305.
Vidal JM, Alvarado P, Loizides M, et al. 2019. A phylogenetic and taxonomic revision of sequestrate Russulaceae in Mediterranean and temperate Europe. Persoonia 42: 127–185.
Videira SIR, Groenewald JZ, Nakashima C, et al. 2017. Mycosphaerellaceae – chaos or clarity? Studies in Mycology 87: 257–421.
Visagie CM, Houbraken J, Frisvad JC, et al. 2014. Identification and nomenclature of the genus Penicillium. Studies in Mycology 78: 343–371.
Vivas M, Silveira SF, Vivas JMS, et al. 2014. Seleção de progênies femininas de mamoeiro para resistência a mancha-de-phoma via modelos mistos. Bragantia 73: 446–450.
Voglmayr H, Aguirre-Hudson MB, Wagner HG, et al. 2019. Lichens or endophytes? The enigmatic genus Leptosillia in the Leptosilliaceae fam. nov. (Xylariales), and Furfurella gen. nov. (Delonicicolaceae). Persoonia 42: 228–260.
Vu D, Groenewald M, De Vries M, et al. 2019. Large-scale generation and analysis of filamentous fungal DNA barcodes boosts coverage for kingdom fungi and reveals thresholds for fungal species and higher taxon delimitation. Studies in Mycology 92: 135–154.
Wanasinghe DN, Hyde KD, Jeewon R, et al. 2017. Phylogenetic revision of Camarosporium (Pleosporineae, Dothideomycetes) and allied genera. Studies in Mycology 87: 207–256.
Wang Z, Binder M, Schoch CL, et al. 2006. Evolution of helotialean fungi (Leotiomycetes, Pezizomycotina): A nuclear rDNA phylogeny. Molecular Phylogenetics and Evolution 41: 295–312.
Watling R, Milne J. 2006. A new species of Boletopsis associated with Pinus sylvestris L. in Scotland. Botanical Journal of Scotland 58: 81–92.
Wu G, Li YC, Zhu XT, et al. 2016. One hundred noteworthy boletes from China. Fungal Diversity 81: 25–188.
Yang H, Chomnunti P, Ariyawansa HA, et al. 2014. The genus Phaeosaccardinula (Chaetothyriales) from Yunnan, China, introducing two new species. Chiang Mai Journal of Science 41: 873–884.
Yilmaz N, Visagie CM, Houbraken J, et al. 2014. Polyphasic taxonomy of the genus Talaromyces. Studies in Mycology 78: 175–341.
Yousaf N, Kreisel H, Khalid AN. 2013. Bovista himalaica sp. nov. (gasteroid fungi; Basidiomycetes) from Pakistan. Mycological Progress 12: 569–574.
Zalar P, De Hoog GS, Schroers H-J, et al. 2007. Phylogeny and ecology of the ubiquitous saprobe Cladosporium sphaerospermum, with descriptions of seven new species from hypersaline environments. Studies in Mycology 58: 157–183.
Zamora JC, Calonge FD, Hosaka K, et al. 2014. Systematics of the genus Geastrum (Fungi: Basidiomycota) revisited. Taxon 63: 477–497.
Zamora JC, Calonge FD, Martín MP. 2015. Integrative taxonomy reveals an unexpected diversity in Geastrum section Geastrum (Geastrales, Basidiomycota). Persoonia 34: 130–165.
Zamora JC, Dios MM, Moreno G. 2017. Clarifying the identity of Geastrum campestre var. famatinum (Geastrales, Basidiomycota). Phytotaxa 328: 159–166.
Zhang H, Brankovics B, Luo W, et al. 2016. Crops are a main driver for species diversity and the toxigenic potential of Fusarium isolates in maize ears in China. World Mycotoxin Journal 9: 701–715.
Zucconi L, Onofri S. 1989. Gyrothrix ramosa sp. nov. and notes on G. citricola. Mycological Research 92: 380–382.
Zwickl DJ. 2006. Genetic algorithm approaches for the phylogenetic analysis of large biological sequence datasets under the maximum likelihood criterion. PhD thesis. University of Texas, Austin, USA.