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RESEARCH ARTICLE

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Fungal Planet description sheets: 558–624

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Key words

ITS nrDNA barcodes
LSU
novel fungal species
systematics

Abstract Novel species of fungi described in this study include those from various countries as follows: **Australia**: *Banksiophoma australiensis* (incl. *Banksiophoma* gen. nov.) on *Banksia coccinea*, *Davidiellomyces australiensis* (incl. *Davidiellomyces* gen. nov.) on *Cyperaceae*, *Didymocyrtis banksiae* on *Banksia sessilis* var. *cygnorum*, *Disculoides calophyllae* on *Corymbia calophylla*, *Harknessia banksiae* on *Banksia sessilis*, *Harknessia banksiae-repens* on *Banksia repens*, *Harknessia banksiigena* on *Banksia sessilis* var. *cygnorum*, *Harknessia communis* on *Podocarpus* sp., *Harknessia platyphyllae* on *Eucalyptus platyphylla*, *Myrtacremonium eucalypti* (incl. *Myrtacremonium* gen. nov.) on *Eucalyptus globulus*, *Myrtapenidiella balenae* on *Eucalyptus* sp., *Myrtapenidiella eucalyptigena* on *Eucalyptus* sp., *Myrtapenidiella pleurocarpae* on *Eucalyptus pleurocarpa*, *Paraconiothyrium hakeae* on *Hakea* sp., *Paraphaeosphaeria xanthorrhoeae* on *Xanthorrhoea* sp., *Parateratosphaeria stirlingiae* on *Stirlingia* sp., *Perthomyces podocarpi* (incl. *Perthomyces* gen. nov.) on *Podocarpus* sp., *Readeriella ellipsoidea* on *Eucalyptus* sp., *Rosellinia australiensis* on *Banksia grandis*, *Tiarosporella corymbiae* on *Corymbia calophylla*, *Verrucoconiothyrium eucalyptigenum* on *Eucalyptus* sp., *Zasmidium commune* on *Xanthorrhoea* sp., and *Zasmidium podocarpi* on *Podocarpus* sp. **Brazil**: *Cyathus aurantogriseocarpus* on decaying wood, *Perenniporia brasiliensis* on decayed wood, *Perenniporia paraguyanensis* on decayed wood, and *Pseudocercospora leandrae-fragilis* on *Leandra fragilis.* **Chile**: *Phialocephala cladophialophoroides* on human toe nail. **Costa Rica**: *Psathyrella striatoannulata* from soil. **Czech Republic**: *Myotisia cremea* (incl. *Myotisia* gen. nov.) on bat droppings. **Ecuador**: *Humidicutis dictiocephala* from soil, *Hygrocybe macrosiparia* from soil, *Hygrocybe sangayensis* from soil, and *Polycephalomyces onorei* on stem of *Etlingera* sp. **France**: *Westerdykella centenaria* from soil. **Hungary**: *Tuber magentipunctatum* from soil. **India**: *Ganoderma mizoramense* on decaying wood, *Hodophilus indicus* from soil, *Keratinophyton turgidum* in soil, and *Russula arunii* on *Pterigota alata.* **Italy**: *Rhodocybe matesina* from soil. **Malaysia**: *Apoharknessia eucalyptorum*, *Harknessia malayensis*, *Harknessia pellitae*, and *Peyronellaea eucalypti* on *Eucalyptus pellita*, *Lectera capsici* on *Capsicum annuum*, and *Wallrothiella gmelinae* on *Gmelina arborea.* **Morocco**: *Neocordana musigena* on *Musa* sp. **New Zealand**: *Candida rongomai-pounamu* on agaric mushroom surface, *Candida vespimorsuum* on cup fungus surface, *Cylindrocladiella vitis* on *Vitis vinifera*, *Foliocryphia eucalyptorum* on *Eucalyptus* sp., *Ramularia vaccinii-cola* on *Vaccinium* sp., and *Rhodotorula ngohengohe* on bird feather surface. **Poland**: *Tolypocladium fumosum* on a caterpillar case of unidentified *Lepidoptera.* **Russia**: *Pholiotina longistipitata* among moss. **Spain**: *Coprinopsis pseudomarcescibilis* from soil, *Eremiomyces innocentii* from soil, *Gyroporus pseudocyanescens* in humus, *Inocybe parvicystis* in humus, and *Penicillium parvofructum* from soil. **Unknown origin**: *Paraphoma rhaphiolepidis* on *Rhaphiolepsis indica.* **USA**: *Acidiella americana* from wall of a cooling tower, *Neodactylaria obpyriformis* (incl. *Neodactylaria* gen. nov.) from human bronchoalveolar lavage, and *Saksenaea loutrophoriformis* from human eye. **Vietnam**: *Phytophthora mekongensis* from *Citrus grandis*, and *Phytophthora prodigiosa* from *Citrus grandis.* Morphological and culture characteristics along with DNA barcodes are provided.

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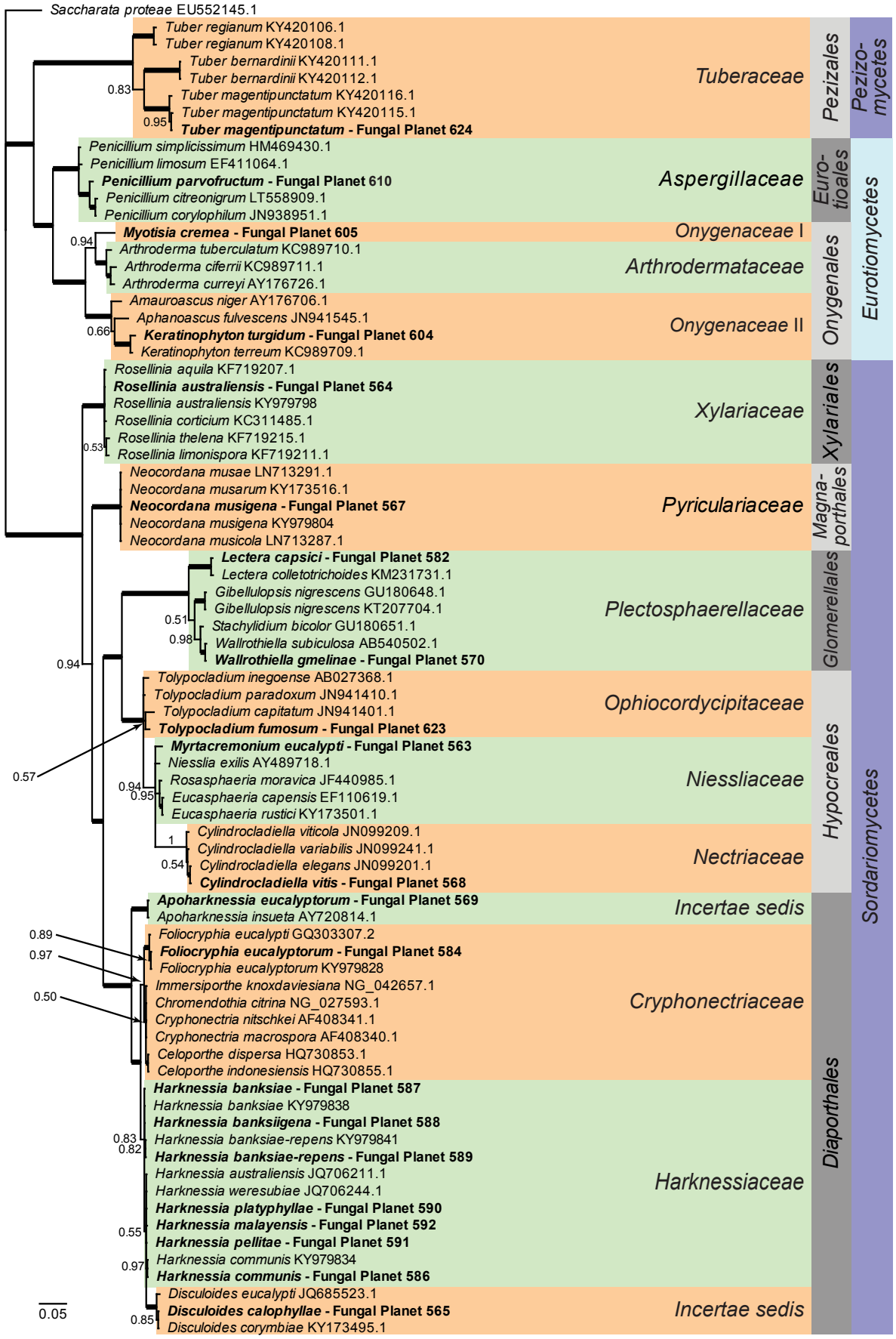

Overview *Pezizomycetes*, *Eurotiomycetes* and *Sordariomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 21 302 trees resulting from a Bayesian analysis of the LSU sequence alignment (78 taxa including outgroup; 825 aligned positions; 368 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) 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 *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 S20946).

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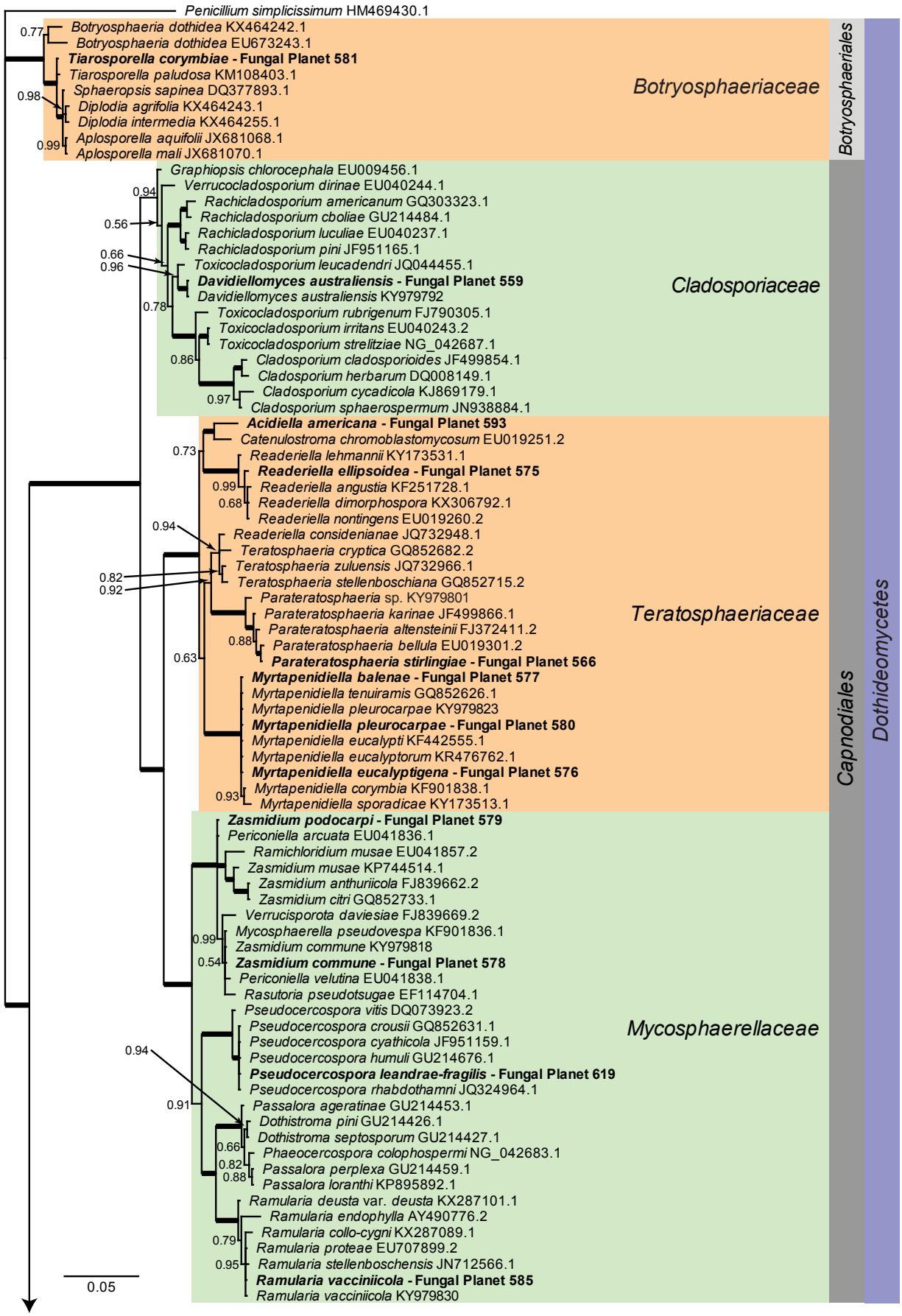
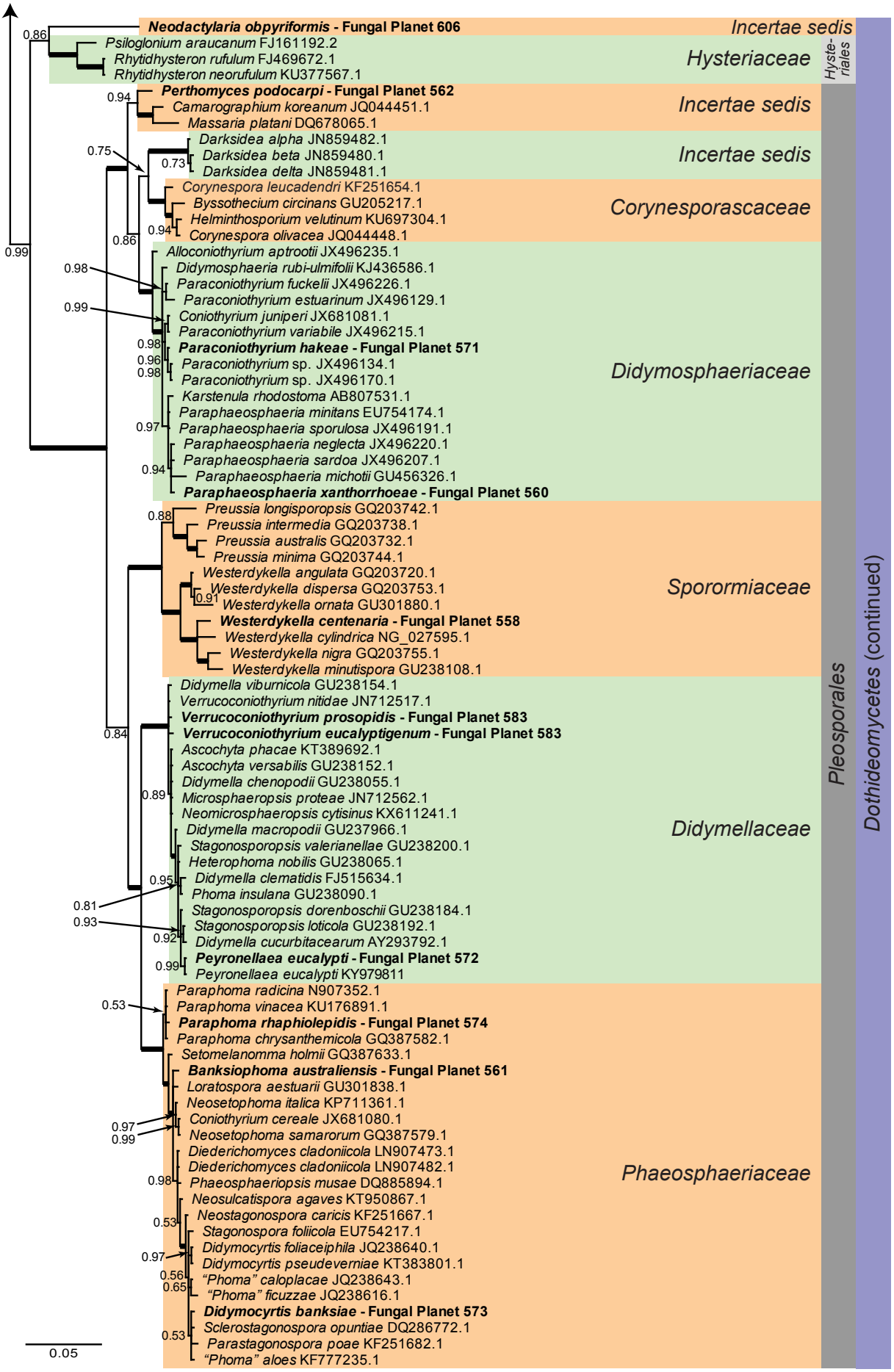


Overview *Dothideomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 16 202 trees resulting from a Bayesian analysis of the LSU sequence alignment (166 taxa including outgroup; 769 aligned positions; 300 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) 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 *Penicillium simplicissimum* (GenBank HM469430.1) 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 S20946).



Overview *Dothideomycetes* phylogeny (cont.)

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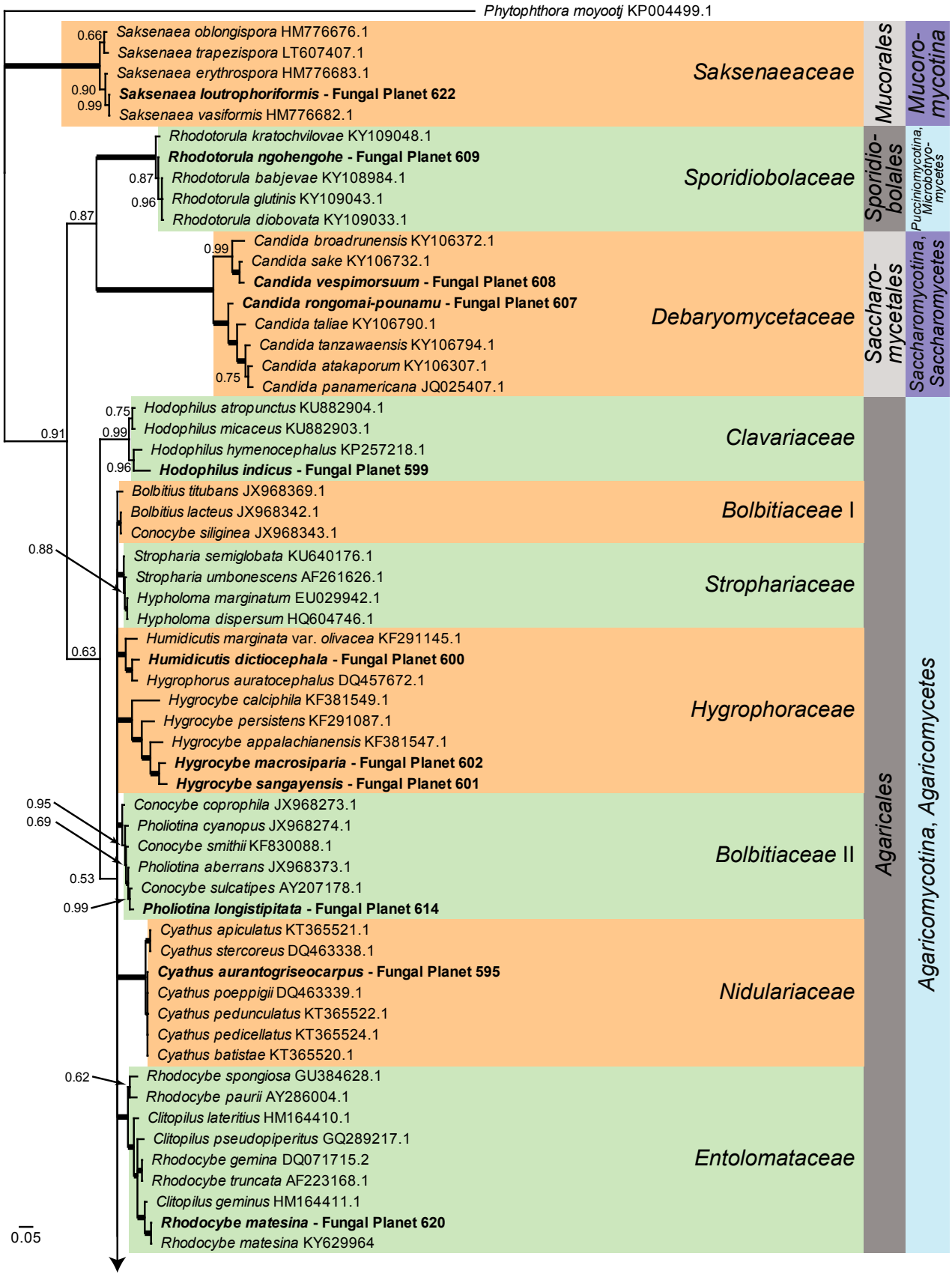
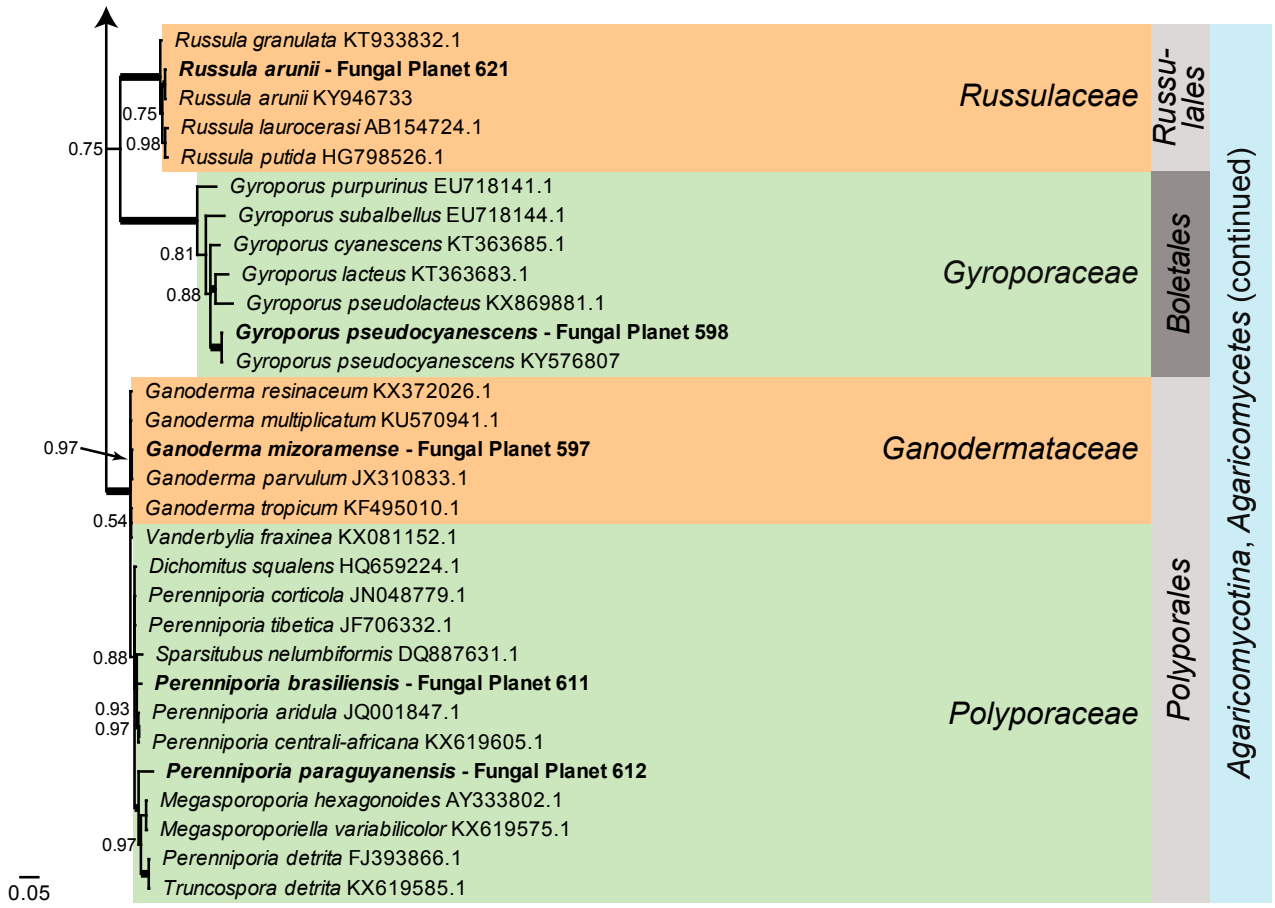


Overview *Mucoromycotina*, *Pucciniomycotina*, *Saccharomycotina* and *Agaricomycotina* phylogeny

Consensus phylogram (50 % majority rule) of 64 278 trees resulting from a Bayesian analysis of the LSU sequence alignment (90 taxa including outgroup; 838 aligned positions; 611 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) 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 *Phytophthora moyootj* (GenBank KP004499.1) 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 S20946).



Overview *Mucoromycotina*, *Pucciniomycotina*, *Saccharomycotina* and *Agaricomycotina* phylogeny (cont.)

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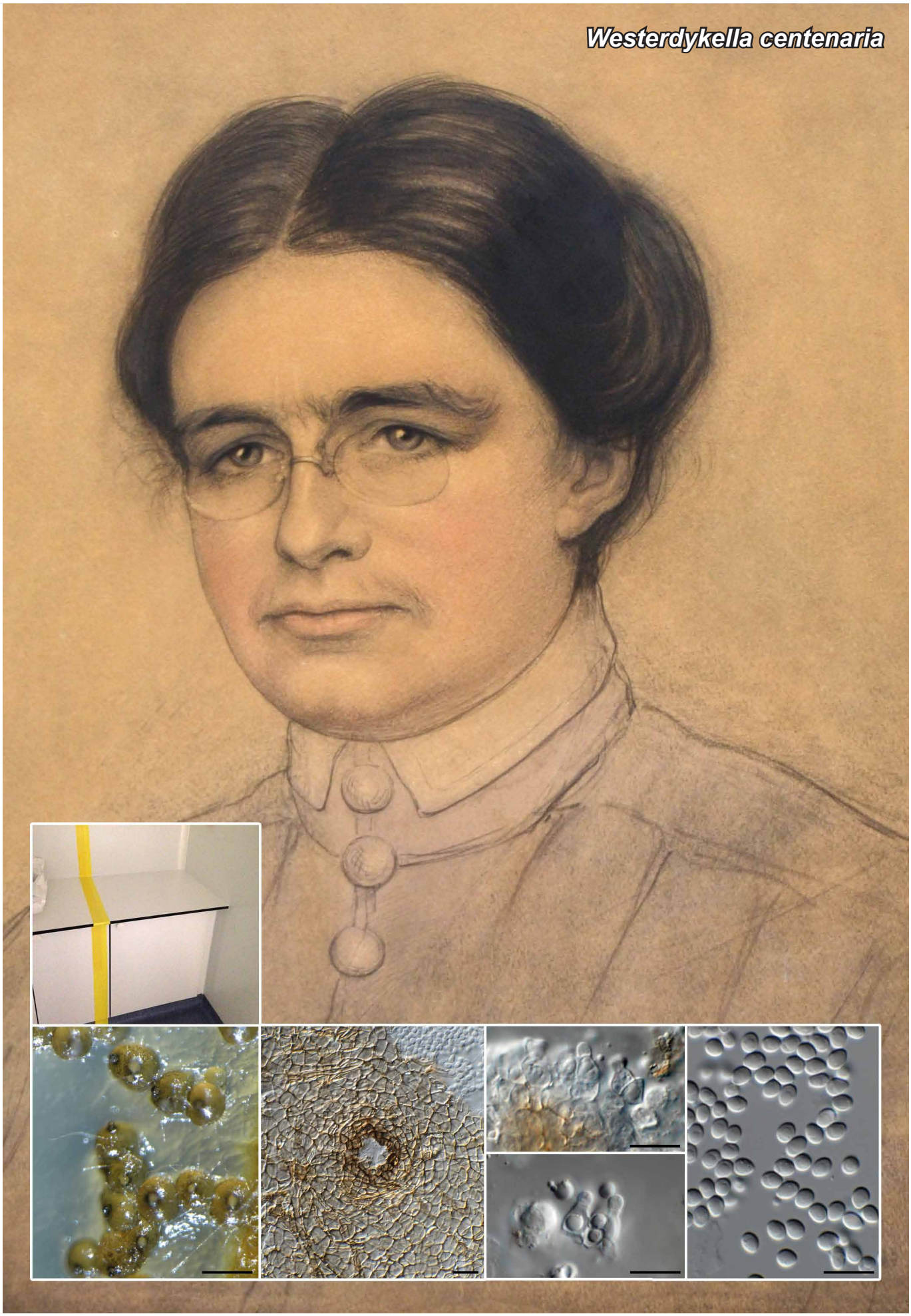
Westerdykella centenaria

Fungal Planet 558 – 20 June 2017

Westerdykella centenaria Crous, van Diepeningen & A.-C. Normand, *sp. nov.*

Etymology. Name reflects the 100th anniversary of the appointment of Prof. dr Johanna Westerdijk, the first female professor in the Netherlands, appointed at Utrecht University on the 10th of February 1917; *centenaria* = 100 years (1917–2017).

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

Conidiomata erumpent, subglobose, 100–200 µm diam on SNA, solitary, or in clusters of 2–3, pale to medium brown, uni- to multilocular, with 1–2 dark brown ostioles, 10–15 µm diam, exuding a creamy conidial mass. On OA conidiomata arranged in concentric circles, aggregated in clusters, dark brown, mostly unilocular, outer wall smooth, lacking setae; wall of 5–8 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, ampulliform to doliiform, 4–6 × 3–5 µm; phialidic with inconspicuous periclinal thickening at apex, or at times with percurrent proliferation. *Conidia* solitary, hyaline, smooth, granular, with large central guttule, clavate to ellipsoid or somewhat irregular, apex obtuse, base truncate, 1.5–2 µm diam, (3–)4(–4.5) × (2.5–)3 µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium, sporulating in brown concentric circles; surface and margins smooth, reaching 60 mm diam after 3 wk at 25 °C. On OA surface umber with patches of orange. On PDA surface isabelline with patches of orange, reverse similar.

Typus. France, Marseille, public hospital, laboratory bench in sterile preparation 'clean room', 2016, *A.-C. Normand* (holotype CBS H-23075, culture ex-type CPC 31368 = CBS 142400, ITS, LSU, and *tub2* sequences GenBank KY979734, KY979790, and KY979908, MycoBank MB820928).

Additional specimen examined. Kuwait, Gulf of Kuwait, from saline soil, Aug. 1973, *A.F. Moustafa*, specimen CBS H-16164, culture CBS 262.74, ITS sequence GenBank KY979735.

Notes — Stolk (1955) introduced the genus *Westerdykella* based on a fungal isolate collected from soil in Mozambique by H.J. Swart. *Westerdykella* was named in honour of the then director of the Centraalbureau voor Schimmelcultures in Baarn (now Westerdijk Fungal Biodiversity Institute in Utrecht), the Netherlands. Species of *Westerdykella* occur on a wide range of substrates, including soil, dung, plant debris, and algae (Ebead et al. 2012), have been shown to exhibit antibiotic activity (Poch & Gloer 1991), but also to cause infections in immunocompromised patients (Sue et al. 2014). Delimitation of species in the genus has traditionally been based on the presence of the sexual morph, although some species (as in the case of *W. centenaria*) are known to produce a phoma-like asexual morph. Ten species are recognised in the genus, and although the majority are sexual, *W. centenaria* is clearly distinct based on its DNA data (ITS: highest similarities are with unnamed isolates from soil in Oman, e.g. 500/508 (98 %) identity, 1 gap (0 %), with GenBank KU945963; closest named species is *Westerdykella reniformis* GenBank KM678366, 409/436 (94 %) identity, 6 gaps (1 %). On LSU, the best match is *Westerdykella cylindrica* GenBank NG_027595, 862/880 (98 %) identity, 1 gap (0 %), and on *tub2*, the best match is *Westerdykella dispersa* GenBank KJ413346, 308/366 (84 %) identity, 5 gaps (1 %)).

Colour illustrations. Portrait of Prof. dr Johanna Westerdijk (by A. Roland Holst); laboratory bench in sterile preparation 'clean room'; conidiomata sporulating on PNA (scale bar = 200 mm); ostiolar region of conidioma, conidiogenous cells and conidia (scale bars = 10 µm).

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Davidiellomyces australiensis

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Davidiellomyces Crous, *gen. nov.*

Etymology. Named for Dr John C. David, recognising his contribution to our knowledge of the genus *Cladosporium* and its sexual morph.

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

Ascomata pseudothecial, on dead leaves, amphigenous, black, subepidermal, globose; apical ostiole; wall consisting of 2–3 layers of medium brown *textura angularis*. *Asci* aparaphysate, fasciculate, bitunicate, subsessile, obovoid to broadly ellipsoid, straight to slightly curved, 8-spored. *Ascospores* multiseriate, overlapping, hyaline, prominently guttulate with angular inclusions, thick-walled, straight, fusoid-ellipsoidal with obtuse ends, widest above septum, medianly 1-septate; enclosed in a mucoid sheath (also visible inside asci), and becoming brown and verruculose in older asci.

Type species. Davidiellomyces australiensis Crous.
MycoBank MB820929.

Davidiellomyces australiensis Crous, *sp. nov.*

Etymology. Name refers to Australia, the country where this fungus was collected.

Ascomata pseudothecial, on dead leaves, amphigenous, black, subepidermal, globose, 70–120 µm diam; apical ostiole 5–10 µm diam; wall consisting of 2–3 layers of medium brown *textura angularis*. *Asci* aparaphysate, fasciculate, bitunicate, subsessile, obovoid to broadly ellipsoid, straight to slightly curved, 8-spored, 30–40 × 7–12 µm. *Ascospores* multiseriate, overlapping, hyaline, prominently guttulate with angular inclusions, thick-walled, straight, fusoid-ellipsoidal with obtuse ends, widest above septum, medianly 1-septate, constricted at the septum, tapering towards both ends, but more prominently towards lower end, (12–)13–15(–16) × (3–)3.5 µm; enclosed in a mucoid sheath (also visible inside asci), and becoming brown and verruculose in older asci.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium; surface folded, margins smooth, lobate, reaching 20 mm diam after 2 wk at 25 °C. On MEA surface ochreous, reverse sienna. On OA surface saffron. On PDA surface luteous, reverse pale luteous. Germinating from both ends, and elsewhere (irregular); ascospores becoming brown, verruculose, constricted at septum, 5–6 µm diam, with prominent mucoid sheath.

Typus. Australia, Western Australia, S35°01.320 E117°16.598, on leaves of *Cyperaceae*, 19 Sept. 2015, *P.W. Crous* (holotype CBS H-23077, culture ex-type CPC 29168 = CBS 142165; ITS, LSU, and *actA* sequences GenBank KY979736, KY979791, and KY979853, MycoBank MB820930); CPC 29170 ITS and LSU sequences GenBank KY979737, KY979792.

Notes — The isolates (sexual morph, no asexual morph observed in culture) included in this study cluster close to *Toxicocladosporium* (Crous et al. 2007b; see phylogeny in Bezerra et al. 2017), but are not congeneric with the genus *Toxicocladosporium* s.str., being separated by clades representing *Cladosporium* and *Neocladosporium.* This suggests that the present collection represents yet another genus in the *Cladosporiaceae* (see Bensch et al. 2012 for generic overview). Interestingly, ascospores of *Davidiellomyces* have angular inclusions such as those observed in ascospores of *Cladosporium* s.str. (see Crous et al. 2007b, Bensch et al. 2010), which appears to be a conserved character in the *Cladosporiaceae*. However, based on a megablast search of the NCBIs GenBank nucleotide database using the ITS sequence, the closest *Cladosporium* sequences have less than 90 % similarity over almost 500 nucleotides.

Colour illustrations. Beach with *Cyperaceae* in foreground; ascomata on leaf, asci, ascospores and germinating ascospores. Scale bars = 10 µm.

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Paraphaeosphaeria xanthorrhoeae

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Paraphaeosphaeria xanthorrhoeae Crous, *sp. nov.*

Etymology. Name refers to *Xanthorrhoea*, the plant genus from which this fungus was collected.

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

Conidiomata erumpent, globose, pycnidial, brown, 80–150 µm diam, with central ostiole; wall of 3–5 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, ampulliform, phialidic with periclinal thickening or percurrent proliferation at apex, 5–8 × 4–6 µm. *Conidia* solitary, golden brown, ellipsoid with obtuse ends, thick-walled, roughened, (6–)7–8(–9) × (3–)3.5 µm.

Culture characteristics — Colonies flat, spreading, covering dish in 2 wk at 25 °C, surface folded, with moderate aerial mycelium and smooth margins. On MEA surface dirty white, reverse luteous. On OA surface dirty white with patches of luteous. On PDA surface dirty white, reverse apricot.

Typus. Australia, Western Australia, Denmark, Lights Beach, on *Xanthorrhoea* sp. (*Xanthorrhoeaceae*), 19 Sept. 2015, *P.W. Crous* (holotype CBS H-23120, culture ex-type CPC 29244 = CBS 142164; ITS, LSU, *rpb2*, *tef1*, and *tub2* sequences GenBank KY979738, KY979793, KY979845, KY979888, and KY979909, MycoBank MB820931).

Notes — The genus *Paraconiothyrium* (based on *P. estuarinum*) was established by Verkley et al. (2004) to accommodate several microsphaeropsis-like coelomycetes, some of which had proven abilities to act as biocontrol agents of other fungal pathogens. In a recent study, Verkley et al. (2014) revealed *Paraconiothyrium* to be paraphyletic, and separated the genus from *Alloconiothyrium*, *Dendrothyrium*, and *Paraphaeosphaeria*. *Paraphaeosphaeria xanthorrhoeae* resembles asexual morphs of *Paraphaeosphaeria*, having pycnidial conidiomata with percurrently proliferating conidiogenous cells and aseptate, brown, roughened conidia. Phylogenetically, it is distinct from all taxa presently known to occur in the genus, the closest species on ITS being *Paraphaeosphaeria sporulosa* (GenBank JX496114; Identities = 564/585 (96 %), 4 gaps (0 %)).

Colour illustrations. Dead *Xanthorrhoea* sp.; conidiomata sporulating on PNA and OA (scale bars = 150 µm); conidiogenous cells and conidia (scale bars = 10 µm).

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Banksiophoma australiensis

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Banksiophoma Crous, *gen. nov.*

Etymology. *Banksia* (host), and *Phoma* (morphology).

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

Conidiomata pycnidial, brown, globose, with central ostiole, somewhat aggregated with a brown stroma on PNA; wall of 3–6 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells or with a supporting cell lining the inner cavity, hyaline, smooth, subcylindrical to ampulliform; proliferating percurrently at apex. *Conidia* solitary, hyaline, smooth, guttulate, aseptate, ellipsoid to globose or subglobose.

Type species. *Banksiophoma australiensis* Crous.
MycoBank MB820932.

Banksiophoma australiensis Crous, *sp. nov.*

Etymology. Name refers to Australia where this fungus was collected.

Conidiomata pycnidial, brown, globose, 90–120 µm diam, with central ostiole, somewhat aggregated with a brown stroma on PNA; wall of 3–6 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells or with a supporting cell lining the inner cavity, hyaline, smooth, subcylindrical to ampulliform, 5–12 × 3–5 µm; proliferating percurrently at apex. *Conidia* solitary, hyaline, smooth, guttulate, aseptate, ellipsoid to globose or subglobose, (3–)4(–5) × (2.5–)3(–3.5) µm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, lobate margins, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface greyish sepia, reverse fulvous to ochreous. On OA surface greyish sepia. On PDA surface and reverse umber.

Typus. Australia, Western Australia, Gull Rock, Albany, on leaves of *Banksia coccinea* (*Proteaceae*), 20 Sept. 2015, *P.W. Crous* (holotype CBS H-23121, culture ex-type CPC 29192 = CBS 142163; ITS, LSU *rpb2*, *tef1*, and *tub2* sequences GenBank KY979739, KY979794, KY979846, KY979889, and KY979910, MycoBank MB820933).

Notes — The *Proteaceae* appears to harbour an unusually large number of new fungal genera (Crous et al. 2011), as was recently shown with the description of a new order of *Dothideomycetes*, namely *Superstratomycetales*, and the phoma-like species *Superstratomyces flavomucosus* occurring on *Hakea* (Van Nieuwenhuijzen et al. 2016). The present collection represents yet another phoma-like genus on *Proteaceae*, this time occurring on *Banksia. Banksiophoma* appears to be distantly related to *Neosetophoma* (De Gruyter et al. 2010). Only distant hits (less than 93 % similarity) with phaeosphaeria-like sequences were obtained from a megablast search of the NCBIs GenBank nucleotide database; the LSU sequence was 99 % identical to species in numerous different genera, e.g. *Loratospora aestuarii* (GenBank GU301838), *Neosetophoma italica* (GenBank KP711361), and *Diederichomyces cladoniicola* (GenBank LN907482).

Colour illustrations. *Banksia coccinea*; conidiomata sporulating on PNA (scale bar = 120 µm), conidiogenous cells and conidia (scale bars = 10 µm).

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Perthomyces podocarpi

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Perthomyces Crous, *gen. nov.*

Etymology. Named for the city of Perth, Australia, where this fungus was collected.

Classification — *Incertae sedis*, *Pleosporales*, *Dothideomycetes.*

Conidiomata solitary, erumpent, globose, dark brown with central ostiole, exuding a white conidial mass; wall of 3–8 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, ampulliform to doliiform or subcylindrical, phialidic with periclinal thickening or tightly aggregated, percurrent proliferations. *Conidia* solitary, hyaline, smooth, guttulate, aseptate, subcylindrical with obtuse ends, straight.

Type species. *Perthomyces podocarpi* Crous.
MycoBank MB820934.

Perthomyces podocarpi Crous, *sp. nov.*

Etymology. Name refers to *Podocarpus*, the host genus from which this fungus was collected.

Conidiomata solitary, erumpent, globose, 200–250 µm diam, dark brown with central ostiole, exuding a white conidial mass; wall of 3–8 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, ampulliform to doliiform or subcylindrical, 4–10 × 2.5–5 µm, phialidic with periclinal thickening or tightly aggregated, percurrent proliferations. *Conidia* solitary, hyaline, smooth, guttulate, aseptate, subcylindrical with obtuse ends, straight, (5–)6(–7) × 2(–2.5) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margins. On MEA surface pale grey olivaceous with diffuse brown pigment, reverse pale olivaceous grey. On OA surface olivaceous grey. On PDA surface and reverse olivaceous grey.

Typus. Australia, Western Australia, Perth, King's Park Botanic Gardens, on leaves of *Podocarpus* sp. (*Podocarpaceae*), 27 Sept. 2015, *P.W. Crous* (holotype CBS H-23122, culture ex-type CPC 28972 = CBS 142162; ITS, LSU, and *tub2* sequences GenBank KY979740, KY979795, and KY979911, MycoBank MB820936).

Notes — *Perthomyces* is a phoma-like genus in the *Pleosporales* (Chen et al. 2015), being phylogenetically related to *Camarographium koreanum* (GenBank JQ044451; Identities = 813/834 (96 %), 2 gaps (0 %)), *Corynespora olivacea* (GenBank JQ044448; Identities = 810/834 (97 %), 1 gap (0 %)), and *Massaria platani* (GenBank DQ678065; Identities = 811/836 (97 %), 2 gaps (0 %)) based on its LSU sequence. Highest similarities based on ITS are for species of *Darksidea*, e.g. *Darksidea alpha* (GenBank JN859354; Identities = 404/441 (92 %), 7 gaps (1 %)).

Colour illustrations. Symptomatic leaves of *Podocarpus* sp.; conidiomata sporulating on PDA (scale bar = 250 µm), conidiogenous cells and conidia (scale bars = 10 µm).

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Myrtacremonium eucalypti

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Myrtacremonium Crous, *gen. nov.*

Etymology. Name reflects the host family *Myrtaceae*, and the fact that the fungus has an acremonium-like morphology.

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

Mycelium consisting of hyaline, smooth, septate, branched, hyphae. *Conidiophores* solitary, erect, straight to flexuous, hyaline, smooth, with basal septum. *Conidiogenous cells* terminal, integrated, hyaline, smooth, thick-walled at base, subcylindrical; apex phialidic, with minute flared collarette. *Conidia* solitary, but accumulating in slimy mass, hyaline, smooth, subcylindrical, straight with obtuse ends.

Type species. *Myrtacremonium eucalypti* Crous.
MycoBank MB820937.

Myrtacremonium eucalypti Crous, *sp. nov.*

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

Mycelium consisting of hyaline, smooth, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* solitary, erect, straight to flexuous, hyaline, smooth, with basal septum, 20–60 × 2–3 µm. *Conidiogenous cells* terminal, integrated, hyaline, smooth, thick-walled at base, subcylindrical, 15–55 × 2–2.5 µm; apex phialidic, 1–1.5 µm diam with minute flared collarette. *Conidia* solitary, but accumulating in slimy mass, hyaline, smooth, subcylindrical, straight with obtuse ends, (5–)6–7(–8) × 1.5 µm.

Culture characteristics — Colonies flat, spreading, reaching 10–20 mm diam after 2 wk at 25 °C, with sparse aerial mycelium, folded surface, and smooth, lobed margins. On MEA surface and reverse buff. On OA surface pale luteous to luteous. On PDA surface and reverse pale luteous.

Typus. Australia, Western Australia, Perth, on leaves of *Eucalyptus globulus* (*Myrtaceae*), 21 Sept. 2015, *P.W. Crous* (holotype CBS H-23123, culture ex-type CPC 29272 = CBS 142161, ITS, LSU, and *tub2* sequences GenBank KY979741, KY979796, and KY979912, MycoBank MB820938).

Notes — *Myrtacremonium* is a new genus in the *Acremonium* complex (Gräfenhan et al. 2011, Lombard et al. 2015). Phylogenetically, it is related to *Eucasphaeria* (e.g. *E. rustici*, LSU GenBank KY173501; Identities = 767/785 (98 %), 2 gaps (0 %)), *Niesslia* (e.g. *N. exilis*, LSU GenBank AY489718; Identities = 782/798 (98 %), 2 gaps (0 %)), and *Rosasphaeria* (e.g. *R. moravica*, LSU GenBank JF440985; Identities = 782/798 (98 %), 2 gaps (0 %)), although it appears to cluster apart (only distant hits were also obtained when the ITS sequences were compared).

Colour illustrations. *Eucalyptus globulus*; colony on SNA, conidiophores and conidia. Scale bars = 10 µm.

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Rosellinia australiensis

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Rosellinia australiensis Crous & Barber, *sp. nov.*

Etymology. Name refers to Australia, the country from which this fungus was collected.

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

Mycelium consisting of superficial to immersed, branched, septate, hyaline to pale brown, smooth, 3–4 µm diam hyphae. *Conidiophores* erect, straight to flexuous, branched, septate, indeterminate, with numerous lateral branches, brown, warty, 4–5 µm diam. *Conidiogenous cells* integrated, terminal or intercalary, subcylindrical to clavate, pale brown, smooth, 5–12 × 4–5.5 µm, with several terminal, hyaline denticles, 0.5 µm diam, inconspicuous, not thickened nor darkened. *Conidia* solitary, rhexolytic conidiogenesis, acrogenous, obovate to broadly ellipsoid, guttulate, thin-walled, aseptate, brown, smooth; hilum truncate, 1.5 µm diam, not thickened nor darkened, (8–)9(–10) × (6.5–)7(–8) µm.

Culture characteristics — Colonies covering dish after 7 d at 25 °C, with fluffy aerial mycelium. On MEA and OA surface olivaceous grey, reverse umber. On PDA surface and reverse dirty white.

Typus. Australia, Western Australia, Perth, Chichester Park, on *Banksia grandis* litter, 15 June 2015, *P.A. Barber* (holotype CBS H-23124, culture ex-type CPC 27694 = CBS 142160, ITS and LSU sequence GenBank KY979742 and KY979797, MycoBank MB820940).

Additional isolates examined. Australia, Western Australia, Perth, Bedford, Bedfordale, *Hakea* sp. (*Proteaceae*), 29 Sept. 2015, *P.W. Crous*, culture CPC 29482 = CBS 142079, ITS and LSU sequence GenBank KY979744 and KY979799; Western Australia, Perth, King's Park Botanic Gardens, on *Eucalyptus lane-poolei* (*Myrtaceae*), 27 Sept. 2015, *M.J. Wingfield*, culture CPC 29422 = CBS 142078, ITS and LSU sequence GenBank KY979743 and KY979798.

Notes — *Rosellinia australiensis* is known only by its asexual morph, which is hansfordia- to nodulisporium-like in morphology. Phylogenetically, however, it clusters among several species of *Rosellinia*, consequently a name in this genus was chosen for it. There is considerable confusion regarding the sexual and asexual morphs in *Xylariales*, and sequence data are required for a greater number of taxa in order to produce a solid taxonomic backbone for the order. Based on a megablast search using the ITS sequence of the ex-type culture, the best matches were with *R. thelena* (GenBank KF719202; Identities = 491/513 (96 %), 9 gaps (1 %)), *R. aquila* (GenBank KY610392; Identities = 494/518 (95 %), 11 gaps (2 %)), and *R. corticium* (GenBank KT149736; Identities = 416/444 (94 %), 10 gaps (2 %)).

Colour illustrations. *Banksia* leaf litter; conidiophores and conidia on PNA. Scale bars = 10 µm.

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Disculoides calophyllae

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Disculoides calophyllae Crous, *sp. nov*.

Etymology. Name refers to *Corymbia calophylla*, the host from which this fungus was collected.

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

Associated with *Corymbia* leaf litter. *Conidiomata* black, amphigenous, subepidermal, acervular, opening by irregular rupture, 200–400 µm diam; wall of 6–10 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells or 1–2-septate, 10–20 × 4–6 µm. *Conidiogenous cells* terminal and intercalary, hyaline, smooth, subcylindrical to ampulliform, tapering to a long thin neck, 10–15 × 3.5–4 µm, proliferating percurrently at apex, with minute flaring collarette. *Conidia* hyaline, smooth, thick-walled, guttulate, ellipsoid to fusoid, straight to curved, (9–)11–13(–15) × (4–)4.5(–5) µm; apex subobtuse, base truncate, 1–1.5 µm diam, with minute marginal frill.

Cultural characteristics — Colonies flat, spreading, covering dish in 2 wk at 25 °C, with sparse aerial mycelium and feathery margins. On MEA surface and reverse buff, on OA surface olivaceous grey. On PDA surface and reverse dirty white with patches of olivaceous grey.

Typus. Australia, Western Australia, near Kojonup, on leaves of *Corymbia calophylla* (*Myrtaceae*), 18 Sept. 2015, *P.W. Crous* (holotype CBS H-23125, culture ex-type CPC 29246 = CBS 142080, ITS, LSU, *cmdA*, and *tub2* sequences GenBank KY979745, KY979800, KY979866, and KY979913, MycoBank MB820941).

Notes — *Disculoides* represents a genus of foliar pathogens of *Corymbia* and *Eucalyptus* (Crous et al. 2012a), which is presently known to accommodate three species. *Disculoides calophyllae* is morphologically most similar to *D. corymbiae* (conidia 10–15 × 3.5–4.5 µm; Crous et al. 2016), although it is only 95 % similar to *D. corymbiae* (ITS GenBank KY173403; Identities = 397/420 (95 %), 9 gaps (2 %)), and 97 % similar to *D. eucalyptorum* (ITS GenBank JQ685518; Identities = 354/365 (97 %), 4 gaps (1 %)) and *D. eucalypti* (ITS GenBank NR_120089; Identities = 353/365 (97 %), 4 gaps (1 %)).

Colour illustrations. *Corymbia* leaf litter; conidiomata sporulating on PNA (scale bar = 350 µm), conidiogenous cells and conidia (scale bars = 10 µm).

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Parateratosphaeria stirlingiae

Fungal Planet 566 – 20 June 2017

Parateratosphaeria stirlingiae Crous, *sp. nov.*

Etymology. Name refers to *Stirlingia*, the host genus from which this fungus was collected.

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

Leaf spots amphigenous, irregular to subcircular, grey-brown with a raised dark brown border, 3–10 mm long, 2–4 mm wide. *Pseudothecia* amphigenous, black subepidermal, erumpent, globose, 70–90 µm diam; apical ostiole 5–10 µm diam; wall consisting of 2–3 layers of brown *textura angularis. Asci* aparaphysate, fasciculate, bitunicate, subsessile, obovoid, straight to slightly curved, 8-spored, 25–30 × 10–11 µm. *Ascospores* tri- to multiseriate, overlapping, hyaline, guttulate, thin-walled, straight, obovoid, with obtuse ends, widest near middle of apical cell, medianly 1-septate, constricted at septum, tapering towards both ends, but with more prominent taper towards lower end, (8–)9–10 × (3–)3.5 µm. *Germinating ascospores* irregular, with ascospores becoming brown, verruculose, with prominent distortion, 6–8 µm diam.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium, and smooth margins, reaching 8 mm diam after 2 wk. On MEA surface and reverse olivaceous grey. On PDA surface olivaceous grey, reverse iron-grey. On OA surface olivaceous grey. Cultures sterile.

Typus. Australia, Western Australia, Albany, Stirling Range National Park, Stirling Range Drive, S34°23'24.4" E118°6'31.7", on leaves of *Stirlingia* sp. (*Proteaceae*), 23 Sept. 2015, *P.W. Crous* (holotype CBS H-23078, culture ex-type CPC 29252 = CBS 142623; ITS, LSU, *tef1*, and *tub2* sequences GenBank KY979747, KY979802, KY979890, and KY979914, MycoBank MB820942.

Notes — Although the *Teratosphaeriaceae* includes several important foliar pathogens of *Proteaceae* (Crous et al. 2008, Quaedvlieg et al. 2014), no species of *Teratosphaeriaceae* have thus far been reported on *Stirlingia*. Furthermore, *Pa. stirlingiae* appears to be phylogenetically distinct from all species of *Parateratosphaeria* thus known from DNA sequence data. This species is consequently introduced as a novel taxon. Based on a megablast search using the ITS sequence, the best matches were to *Pa. bellula* (GenBank EU707860; Identities = 525/531 (99 %), 1 gap (0 %)), *Pa. altensteinii* (GenBank FJ372394; Identities = 498/507 (98 %), 2 gaps (0 %)), and *Pa. persoonii* (GenBank NR_145096; Identities = 512/523 (98 %), 1 gap (0 %)).

Colour illustrations. *Stirlingia* sp.; ascoma (scale bar = 180 µm); asci, ascospores and germinating ascospores (scale bars = 10 µm).

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Neocordana musigena

Fungal Planet 567 – 20 June 2017

Neocordana musigena Crous, *sp. nov.*

Etymology. Name refers to *Musa*, the host genus from which this fungus was collected.

Classification — *Pyriculariaceae*, *Magnaporthales*, *Sordariomycetes*.

Leaf spots pale grey to brown, covering large areas of the leaf lamina. *Mycelium* consisting of pale brown to subhyaline, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* subcylindrical, flexuous, erect, medium brown, smooth, multi-septate, 50–100 × 4–6 µm. *Conidiogenous cells* polyblastic, terminal and intercalary, 15–50 × 4–6 µm, denticulate; denticles up to 1.5 µm long, 0.5–1 µm wide. *Conidia* oblong to obovoid, (15–)16–17(–18) × (7–)8(–9) µm, 1-septate, thick-walled, brown, with truncate base, 1 µm diam.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium, and feathery margins, reaching 30–40 mm diam after 2 wk. On MEA surface dirty white, reverse plate luteous. On PDA surface umber, reverse umber. On OA surface honey.

Typus. Morocco, leaves of *Musa* sp. (*Musaceae*), 2010, *P.W. Crous* (holotype CBS H-23079, culture ex-type 29777 = CBS 142624, ITS, LSU, *actA*, *rpb1*, and *tub2* sequences GenBank KY979748, KY979803, KY979854, KY979885, and KY979915, MycoBank MB820943); CPC 29140, 29777, 29779, ITS, LSU, *actA*, *rpb1*, and *tub2* sequences GenBank KY979749–KY979750, KY979804–KY979805, KY979855–KY979856, KY979886–KY979887, and KY979916–KY979917.

Notes — Hernández-Restrepo et al. (2015) introduced the genus *Neocordana* to accommodate four species of hyphomycetes causing a foliar disease of *Canna* and *Musa*. Crous et al. (2016) added a fifth species, *N. musarum*, causing a foliar disease on bananas in La Réunion. *Neocordana musigena* (conidia 15–18 × 7–9 µm) is most similar to *C. musicola* (conidia 14.5–20 × 6.5–9.5 µm), but is phylogenetically distinct from it. Based on a megablast search using the ITS sequence of the ex-type culture, the best matches were to *Neocordana musae* (GenBank LN713281; Identities = 571/571 (100 %), no gaps), *Neocordana musarum* (GenBank KY173424; Identities = 565/571 (99 %), 1 gap (0 %)), and *Neocordana musicola* (GenBank LN713283; Identities = 544/550 (99 %), 1 gap (0 %)). Based on a megablast search using the *rpb1* sequence of the ex-type culture, the strain is identical to *Neocordana musarum* (GenBank KY173577; Identities = 749/749 (100 %), no gaps), while the *actA* sequence is 99 % identical to *Neocordana musarum* (GenBank KY173568; Identities = 357/358 (99 %), no gaps).

Colour illustrations. *Musa* plants; symptomatic leaf; conidiophores and conidia. Scale bars = 10 µm.

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Cylindrocladiella vitis

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Cylindrocladiella vitis Crous & Thangavel, *sp. nov.*

Etymology. Name refers to *Vitis*, the host genus from which this fungus was collected.

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

Conidiophores dimorphic, penicillate and subverticillate, mononematous and hyaline. *Penicillate conidiophores* comprising a stipe, a penicillate arrangement of fertile branches, a stipe extension and a terminal vesicle; stipe septate, hyaline, smooth, 40–60 × 5–7 µm; stipe extension aseptate, straight, 100–140 µm long, thick-walled with one basal septum, terminating in thin-walled, ellipsoidal to lanceolate vesicles, 4–6 µm wide. *Penicillate conidiogenous apparatus* with primary branches aseptate, 12–17 × 3–4 µm, secondary branches aseptate, 8–12 × 2–3 µm, each terminal branch producing 2–4 phialides; phialides doliiform to reniform to cymbiform, hyaline, aseptate, 10–15 × 2–3 µm, apex with minute periclinal thickening and collarette. *Subverticillate conidiophores* sparse, comprising of a septate stipe, and primary branches terminating in 1–3 phialides; stipe straight, hyaline, 0–1-septate, 30–40 × 2.5–3.5 µm; phialides cymbiform to cylindrical, hyaline, aseptate, 15–30 × 2.5–3 µm, apex with minute periclinal thickening and collarette. *Conidia* cylindrical, rounded at both ends, straight, 1-septate, (12–)13–16(–18) × (2–)2.5(–3) µm (av. = 14 × 2.5 µm), frequently slightly flattened at the base, held in asymmetrical clusters by colourless slime.

Culture characteristics — Colonies covering dish in 2 wk, with abundant aerial mycelium and smooth, lobate margins. On MEA and PDA surface dirty white, reverse sienna on MEA, luteous on PDA. On OA surface ochreous, with patches of pale luteous.

Typus. New Zealand, Ohau Wines, 2 Bishops Road, RD 20, Ohau 5570, Levin, on *Vitis vinifera* (*Vitaceae*), 2014, *D. Davis* (holotype CBS H-23080, culture ex-type CPC 28701 = CBS 142517 = T14_2612P = ICMP 22045, ITS, LSU, *tef1*, and *tub2* sequences GenBank KY979751, KY979806, KY979891, and KY979918, MycoBank MB820944).

Notes — The genus *Cylindrocladiella* accommodates a group of soil-borne fungi that are commonly associated with nursery diseases in subtropical and tropical regions worldwide (Crous 2002). In a recent revision of the genus, Lombard et al. (2012) delineated five species complexes based on morphology and phylogenetic inference. Van Coller et al. (2005) described *C. viticola* (vesicles ellipsoid to clavate, conidia 8–15 × 2–3 µm), a species associated with cutting rot of grapevines. *Cylindrocladiella vitis* is distinct in having ellipsoidal to lanceolate vesicles, and larger conidia (12–18 × 2–3 µm). Furthermore, it is also phylogenetically distinct from all other species known in the genus. Based on a megablast search using the ITS sequence, the best matches were to *Cylindrocladiella elegans* (GenBank JN100609; Identities = 505/512 (99 %), 2 gaps (0 %)) and *Cylindrocladiella novae-zelandiae* (GenBank NR_111055; Identities = 498/506 (98 %), 1 gap (0 %)). The best match based on *tef1* was to *Cylindrocladiella cymbiformis* (GenBank JN098989; Identities = 475/499 (95 %), 7 gaps (1 %)) and based on *tub2* it was closely related to *Cylindrocladiella elegans* (GenBank JN098755; Identities = 607/623 (97 %), no gaps).

Colour illustrations. Vineyard at Ohau Wines; conidiophores sporulating on PNA; conidiophores and conidia. Scale bars = 10 µm.

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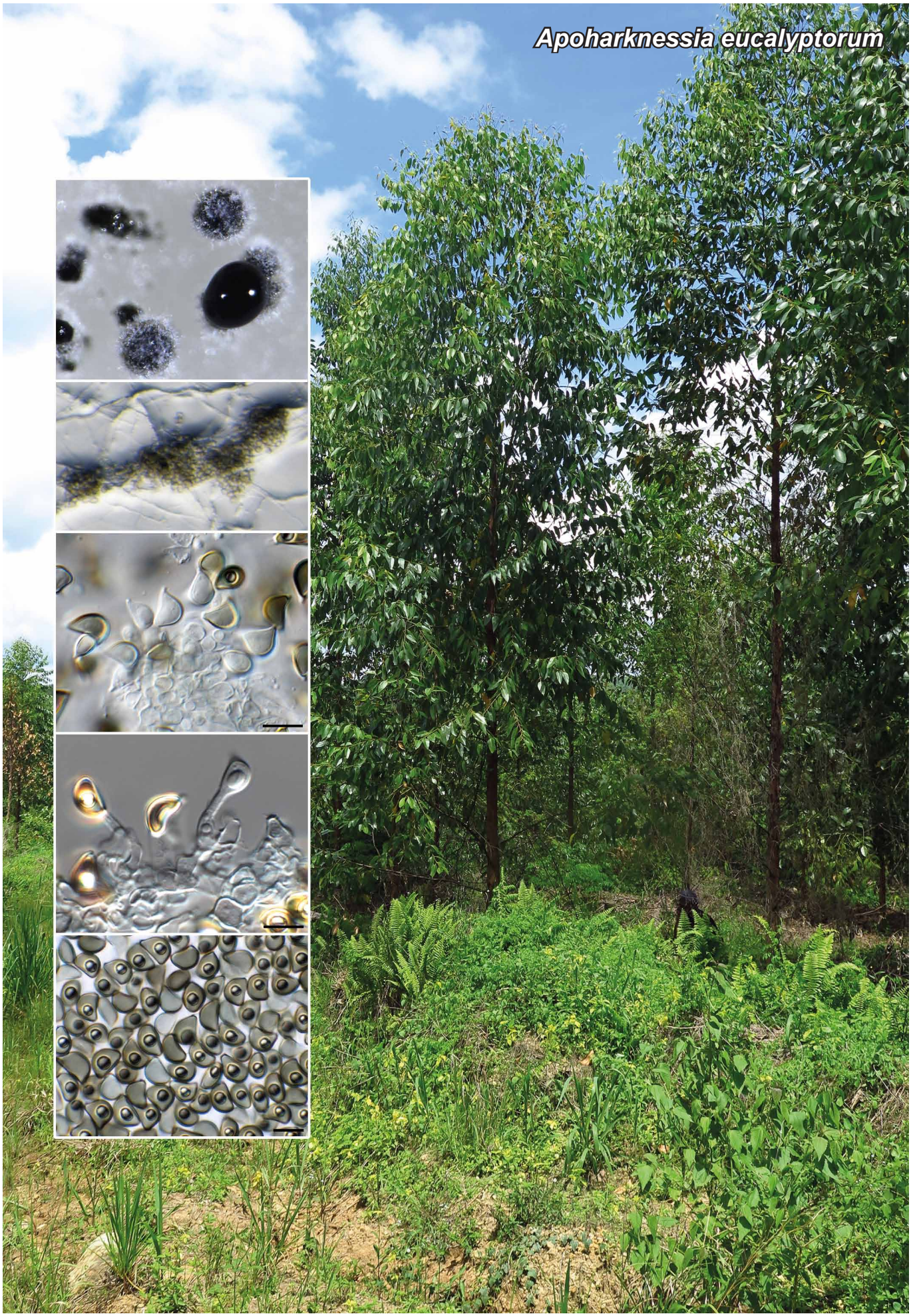
Apoharknessia eucalyptorum

Fungal Planet 569 – 20 June 2017

Apoharknessia eucalyptorum Crous & M.J. Wingf., *sp. nov.*

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

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

Foliicolous, isolated from leaves incubated in moist chambers (presumed endophyte). *Conidiomata* pycnidioid, separate to gregarious, subepidermal, becoming erumpent, stromatic, amphigenous, depressed globose, up to 250 µm diam; opening irregular, with yellowish, furfuraceous cells; wall of *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* 7–20 × 4–7 µm, ampulliform to lageniform, hyaline, smooth, invested in mucilage, percurrently proliferating once or twice near apex. *Conidia* (8–)9–10(–11) × (5–)6–6.5(–7) µm, obliquely gibbose, aseptate, brown, smooth, thick-walled, with prominent central guttule, lacking striations, with conical short apiculus. *Basal appendage* (1.5–)2–3(–3.5) × 2–2.5 µm, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm, 0–2 µm long, 2 µm diam.

Culture characteristics — Colonies reaching 70 mm diam after 2 wk at 25 °C, flat, spreading, with sparse aerial mycelium and lobate, smooth margins. On MEA surface olivaceous black, margin dirty white, reverse olivaceous grey in centre, dirty white in outer region. On PDA surface and reverse dirty white. On OA surface black in centre, grey olivaceous in outer region. Colonies with slimy sporulation on superficial mycelium; sporulating within 1 wk, much faster than *Harknessia* spp., which usually only sporulate after 2–4 wk.

Typus. Malaysia, Sabah, on leaves of *Eucalyptus pellita* (*Myrtaceae*), May 2015, *M.J. Wingfield* (holotype CBS H-23082, culture ex-type CPC 27546 = CBS 142519, ITS, LSU, *cmdA*, and *tub2* sequences GenBank KY979752, KY979807, KY979867, and KY979919, MycoBank MB820946).

Notes — *Apoharknessia eucalyptorum* is morphologically similar to *A. insueta* (conidia 10–11(–12.5) × 7.5–9 µm; Nag Raj 1993), other than the fact that it has smaller conidia (8–11 × 5–7 µm). The ITS sequence of *A. eucalyptorum* is only 93 % similar to that of *A. insueta* (GenBank JQ706083; Identities = 572/616 (93 %), 30 gaps (4 %)).

Colour illustrations. *Eucalyptus pellita* trees growing in Malaysia; conidiomata sporulating on SNA; conidiogenous cells and conidia. Scale bars = 10 µm.

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Wallrothiella gmelinae

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Wallrothiella gmelinae Crous & M.J. Wingf., *sp. nov.*

Etymology. Name refers to *Gmelina*, the host genus from which this fungus was collected.

Classification — *Amplistromataceae*, *Hypocreales*, *Sordariomycetes*.

Mycelium consisting of hyaline, branched, septate, 1.5–2.5 µm diam hyphae. *Conidiophores* solitary, erect, subcylindrical, pale brown, smooth, 0–1-septate, 20–60 × 2.5–3.5 µm. *Conidiogenous cells* pale brown, smooth, subcylindrical to subulate, with prominent taper in upper third, intercalary on conidiophores, or terminal, phialidic, with flared collarette, 2.5–3.5 µm diam, 18–40 × 2.5–3 µm. *Conidia* solitary, aggregating in slimy masses, subcylindrical with obtuse ends, straight, aseptate, minutely guttulate, pale brown, turning medium brown with age, (7–)8–9(–11) × (2.5–)3 µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium, and smooth, lobate margins, reaching 12 mm diam after 2 wk at 25 °C. On MEA surface saffron, reverse pale luteous. On PDA surface pale luteous, reverse dirty white. On OA surface dirty white.

Typus. Malaysia, Sabah, on twigs of *Gmelina arborea* (*Lamiaceae*), May 2015, *M.J. Wingfield* (holotype CBS H-23083, culture ex-type CPC 27584 = CBS 142520; ITS and LSU sequences GenBank KY979753 and KY979808, MycoBank MB820947).

Notes — The genus *Wallrothiella* is commonly isolated from plant litter and soil, although its ecology remains largely unknown. *Wallrothiella* has a phialophora-like asexual morph, *Pseudogliomastix* (Gams & Boekhout 1985). *Wallrothiella gmelinae* is phylogenetically similar to *W. subiculosa* (= *Pseudogliomastix protea*; conidia 3.7–5.6 × 1.6–3 µm; Gams 1971). Based on a megablast search using the ITS sequence, the best match was to *W. subiculosa* (GenBank AB540576; Identities = 549/555 (99 %), no gaps), followed by *Gliomastix murorum* (GenBank JQ354922; Identities = 490/505 (97 %), 2 gaps (0 %)).

Colour illustrations. *Gmelina arborea* trees in Malaysia; conidiophores sporulating on PNA; conidiophores and conidia. Scale bars = 10 µm.

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Paraconiothyrium hakeae

Fungal Planet 571 – 20 June 2017

Paraconiothyrium hakeae Crous & Barber, *sp. nov.*

Etymology. Name refers to *Hakea*, the host genus from which this fungus was collected.

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

Conidiomata solitary, globose, dark brown, up to 250 µm diam, with central papillate ostiole; surface with short brown setae; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* lining the inner cavity, hyaline, smooth, subcylindrical to ampulliform, 0–1-septate, branched or not, 8–12 × 2–3.5 µm. *Conidiogenous cells* terminal and intercalary, subcylindrical with apical taper and a few inconspicuous percurrent proliferations at apex, 4–6 × 2–3 µm. *Conidia* solitary, brown, smooth, thick-walled, subcylindrical, apex obtuse, base truncate, (2.5–)3(–4) × 2 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and even, lobate margins, reaching 50 mm diam after 2 wk. On MEA surface dirty white, reverse ochreous. On PDA surface sienna in centre, pale luteous in outer region. On OA surface pale luteous, with patches of sienna.

Typus. Australia, Western Australia, Perth, Periwinkle Park, on *Hakea* sp. (*Proteaceae*), 23 June 2015, *P.A. Barber* (holotype CBS H-23084, culture ex-type CPC 27651 = CBS 142521, ITS, LSU, *rpb2*, *tef1*, and *tub2* sequences GenBank KY979754, KY979809, KY979847, KY979892, and KY979920, MycoBank MB820948).

Notes — *Paraconiothyrium hakeae* is phylogenetically similar to *P. brasiliense* (from fruit of *Coffee arabica* in Brazil; conidia 3–5 × 1.8–2.5 µm; Verkley et al. 2004; GenBank JX496099; Identities = 579/589 (98 %), 1 gap (0 %)), although its conidia are slightly smaller (2.5–4 × 2 µm). However, the *tub2* sequences are only 93 % similar (GenBank JX496438; Identities = 419/450 (93 %), 1 gap (0 %)). The ecology of *P. hakeae*, which occurs on leaves of *Hakea* sp. in Australia, is unknown.

Colour illustrations. Periwinkle Park; conidiomata sporulating on PNA (scale bar = 250 µm), conidiomatal wall with setae, conidiogenous cells and conidia (scale bars = 10 µm).

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Peyronellaea eucalypti

Fungal Planet 572 – 20 June 2017

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

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

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

Ascomata pseudothecial, solitary, erect, pyriform, 120–200 µm diam; apex dark brown, basal two thirds pale brown, with central papillate ostiole; wall of 3–6 layers of brown *textura angularis. Pseudoparaphyses* absent. *Asci* bitunicate, stipitate, narrowly ellipsoid to subcylindrical with inconspicuous apical chamber, 45–70 × 8–12 µm. *Ascospores* bi- to triseriate, hyaline, smooth, constricted at median septum, prominently guttulate with mucoid sheath, widest just above septum, ends subobtusely rounded, (13–)14–15(–17) × (4–)5–6 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margins, reaching 60 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse chestnut. On PDA surface and reverse isabelline. On OA surface olivaceous grey.

Typus. Malaysia, Sabah, on leaves of *Eucalyptus pellita* (*Myrtaceae*), May 2015, *M.J. Wingfield* (holotype CBS H-23085, culture ex-type CPC 27678 = CBS 142522, ITS, LSU, *rpb2*, *tef1*, and *tub2* sequences GenBank KY979755, KY979810, KY979848, KY979893, and KY979921, MycoBank MB820950); CPC 27682, ITS, LSU, *rpb2*, *tef1*, and *tub2* sequences GenBank KY979756, KY979811, KY979849, KY979894, and KY979922.

Notes — The genus *Peyronellaea* is characterised by species having setose pycnidia and dictyochlamydospores. Aveskamp et al. (2009, 2010) showed that these structures have evolved several times within the *Phoma* complex. *Peyronellaea eucalypti* is phylogenetically related to *Peyronellaea glomerata* (GenBank KM979831; Identities = 523/535 (98 %), 3 gaps (0 %)). It cannot be compared based on morphology because *P. eucalypti* only occurs as a sexual morph. This is interesting, because it links a didymella-like sexual morph to the genus. The protein-coding sequences did not reveal any highly similar sequences in the NCBIs GenBank nucleotide database.

Colour illustrations. Eucalyptus pellita trees growing in Malaysia; ascomata sporulating on PNA (scale bar = 200 µm); asci and ascospores (scale bars = 10 µm).

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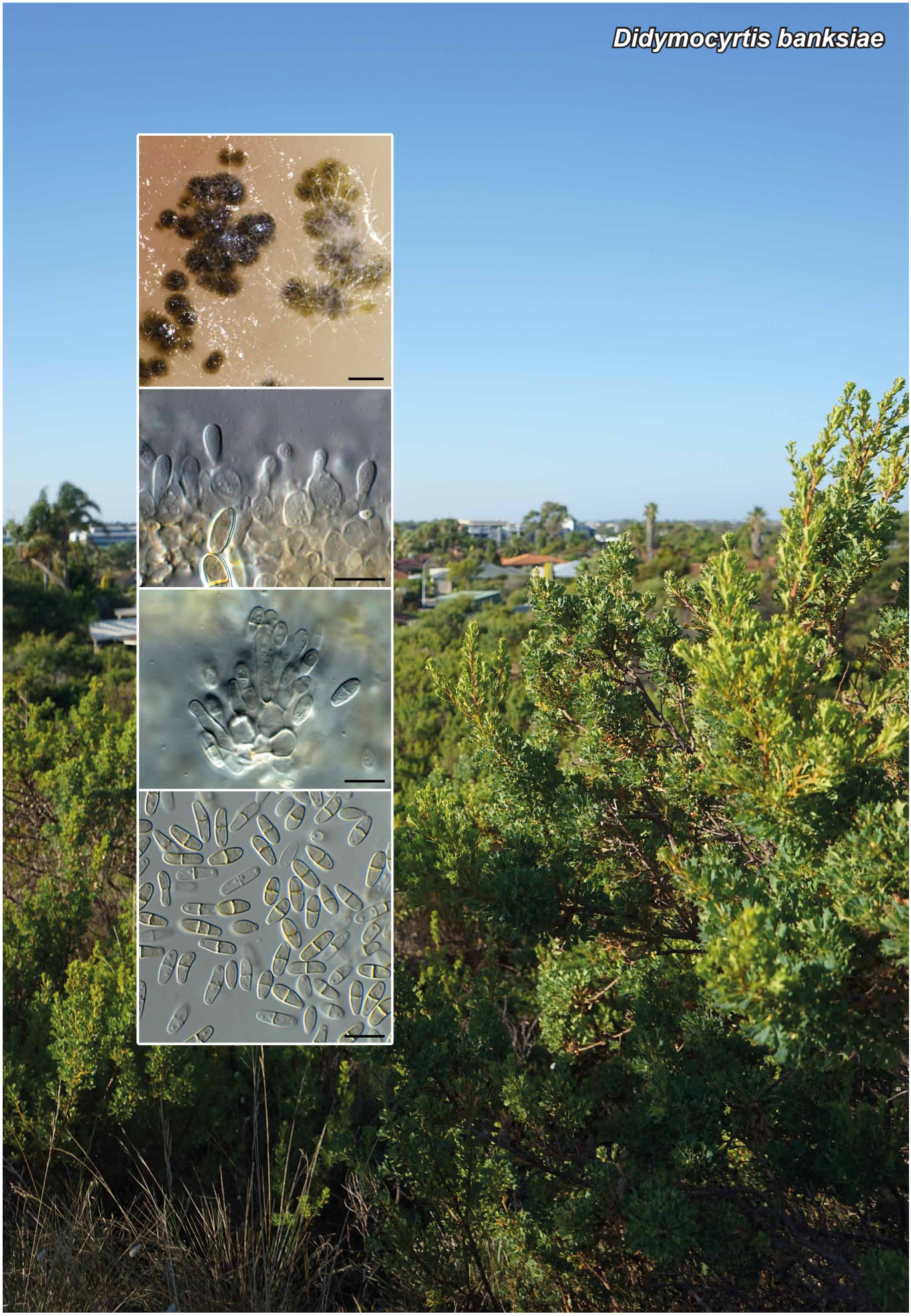
Didymocyrtis banksiae

Fungal Planet 573 – 20 June 2017

Didymocyrtis banksiae Crous & Barber, *sp. nov.*

Etymology. Name refers to *Banksia*, the host genus from which this fungus was collected.

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

Conidiomata pycnidial, dark brown, globose, multilocular, 200–300 µm diam, with 1–2 ostioles exuding a brown conidial mass; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* lining the inner cavity, hyaline, smooth, subcylindrical, 0–3-septate, 8–20 × 4–6 µm. *Paraphyses* intermingled among conidiophores, hyaline, septate, at times branched, apices obtuse, 20–35 × 3–4 µm. *Conidiogenous cells* ampulliform to subcylindrical, hyaline, smooth, terminal and intercalary, 5–13 × 3–4 µm; proliferating percurrently at apex. *Conidia* solitary, subcylindrical to narrowly fusoid-ellipsoid, straight, widest in middle, apex obtuse, base truncate, 2–2.5 µm diam, (0–)1(–3)-septate, guttulate, medium brown, smooth, (8–)10–11(–14) × (3–)4 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium, and smooth, lobate margins, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface dirty white, with patches of red, reverse pale luteous, with patches of red. On PDA surface and reverse isabelline with patches of dirty white. On OA surface dirty white with patches of red.

Typus. Australia, Western Australia, Perth, St. Clair Park, on *Banksia sessilis* var. *cygnorum* (*Proteaceae*), 24 June 2015, *P.A. Barber* (holotype CBS H-23086, culture ex-type CPC 28238 = CBS 142523, ITS, LSU, *rpb2*, *tef1*, and *tub2* sequences GenBank KY979757, KY979812, KY979850, KY979895, and KY979923, MycoBank MB821081).

Notes — The genus *Didymocyrtis* was recently resurrected for lichenicolous species previously assigned to *Diederichia*, *Diederichomyces*, *Leptosphaeria*, and *Phoma* (Trakunyingcharoen et al. 2014, Ertz et al. 2015). *Didymocyrtis banksiae* appears to be a non-lichenicolous species, although it occurs on hard, leathery leaves of *Banksia*, which frequently have some lichen growth on the leaf surface. It is, therefore, quite possible that *D. banksiae* has some lichenicolous association not observed at the time of isolation. Based on a megablast search using the ITS sequence, the best match was to *D. cladoniicola* (GenBank JQ238623; Identities = 563/585 (96 %), 3 gaps (0 %)), followed by *D. foliaceiphila* (GenBank JQ238638; Identities = 562/584 (96 %), 2 gaps (0 %)). The protein-coding sequences did not reveal any highly similar sequences in the NCBIs GenBank nucleotide database.

Colour illustrations. St. Clair Park; conidiomata sporulating on OA (scale bar = 300 µm); conidiogenous cells and conidia (scale bars = 10 µm).

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Paraphoma rhaphiolepidis

Fungal Planet 574 – 20 June 2017

Paraphoma rhaphiolepidis Crous & Toome, *sp. nov.*

Etymology. Name refers to *Rhaphiolepsis*, the host genus from which this fungus was collected.

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

Conidiomata pycnidial to stromatic, globose, 250–350 µm diam, in clusters of 2–5, with darker ostiolar region, 1–2 ostioles per pycnidium; outer surface covered with flexuous, brown, verruculose setae. *Conidiophores* lining the inner cavity, hyaline, smooth, densely aggregated, branched, 1–2-septate, subcylindrical, 10–17 × 3–5 µm. *Conidiogenous cells* hyaline, smooth, subcylindrical to ampulliform, terminal and intercalary, with prominent periclinal thickening at apex, 5–8 × 3–5 µm. *Conidia* solitary, hyaline, straight, smooth, guttulate, subcylindrical, apex obtuse, base truncate, (4.5–)5–6(–6.5) × 2(–2.5) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margins, reaching 40 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 olivaceous grey.

Typus. Origin uncertain, intercepted during post entry quarantine in New Zealand, on *Rhaphiolepsis indica* (*Rosaceae*), June 2015, *M. Toome-Heller* (holotype CBS H-23087, culture ex-type CPC 28707 = CBS 142524 = T15_03251A = ICMP 21068, ITS, LSU, *rpb2*, *tef1*, and *tub2* sequences GenBank KY979758, KY979813, KY979851, KY979896, and KY979924, MycoBank MB820951).

Notes — Members of the genus *Paraphoma* have a wide geographic distribution, and include primary and secondary pathogens of agricultural crops (Moslemi et al. 2016). *Paraphoma rhaphiolepidis* is phylogenetically related, but distinct from *P. chrysanthemicola* (GenBank KF251165; Identities = 524/536 (98 %), 4 gaps (0 %)), a stem and root pathogen of *Chrysanthemum* (De Gruyter et al. 2010). The protein-coding sequences did not reveal any highly similar sequences in the NCBIs GenBank nucleotide database.

Colour illustrations. Quarantine glasshouse; conidiomata sporulating on OA (scale bar = 300 µm); conidiophores and conidia (scale bars = 10 µm).

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Readeriella ellipsoidea

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Readeriella ellipsoidea Crous, *sp. nov.*

Etymology. Name refers to the characteristic narrowly ellipsoid conidia of this fungus.

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

Conidiomata eustromatic, occurring in a stroma of dark brown *textura angularis*, up to 400 µm diam, 150–200 µm diam, with one to several ostioles, uni- to multilocular (resembling the genus *Davisoniella*). *Conidiophores* lining the inner cavity, subcylindrical, pale brown, branched, 0–2-septate, smooth, 10–20 × 3–4 µm. *Conidiogenous cells* integrated, terminal and intercalary, pale brown, smooth, ampulliform to subcylindrical, with 1–2 inconspicuous percurrent proliferations at apex, 4–8 × 3–3.5 µm. *Conidia* solitary, narrowly ellipsoid, apex obtuse, tapering to a narrowly truncate base, 1 µm diam, yellow brown in mass, finely roughened, (4–)5(–6) × (2–)2.5 µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium, and even lobate margins, reaching 20 mm diam after 2 wk. On MEA surface chestnut, reverse umber. On PDA surface greenish black, reverse olivaceous grey. On OA surface olivaceous grey.

Typus. Australia, Western Australia, Albany, Stirling Range National Park, Bluff Knoll, S34°22'3.8" E118°14'313", on leaves of *Eucalyptus* sp. (*Myrtaceae*), 23 Sept. 2015, *P.W. Crous* (holotype CBS H-23088, culture ex-type CPC 29153 = CBS 142525, ITS, LSU, *tef1*, and *tub2* sequences GenBank KY979759, KY979814, KY979897, and KY979925, MycoBank MB820952).

Notes — Crous et al. (2007a, c, 2009a, b) showed that *Readeriella* resides in the *Teratosphaeriaceae*, having *Nothostrasseria* and *Cibiessia* synasexual morphs. *Readeriella ellipsoidea* is phylogenetically related to *R. dimorphospora* (Crous et al. 2007c), though only the *Readeriella* morph was observed in culture. Based on a megablast search using the ITS sequence, the best match was to *R. dimorphospora* (GenBank KF901544; Identities = 477/481 (99 %), 2 gaps (0 %)), followed by *R. nontingens* (GenBank EF394847; Identities = 540/545 (99 %), 1 gap (0 %)). Based on both *tef1* and *tub2*, *R. ellipsoidea* was less than 85 % identical to *R. dimorphospora* (GenBank KF903252 and KF902956, respectively).

Colour illustrations. Eucalyptus sp. in Stirling Range National Park; conidiomata sporulating on OA (scale bar = 200 µm); conidiophores and conidia (scale bars = 10 µm).

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Myrtapenidiella eucalyptigena

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Myrtapenidiella eucalyptigena Crous, *sp. nov.*

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

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

Conidiophores erect, flexuous, mostly unbranched, fasciculate, subcylindrical, thick-walled, finely roughened, medium brown, multiseptate, 50–150 × 5–7 µm. *Conidiogenous cells* integrated, terminal, subcylindrical, medium brown, finely roughened, 10–20 × 4–6 µm; scars thickened, darkened, not refractive, 3–4 µm diam, proliferating sympodially. *Secondary ramoconidia* medium brown, verruculose, thick-walled, 1-septate, subcylindrical, 20–35 × 5–6 µm. *Conidia* occurring in branched chains of up to 10, medium brown, verruculose, thick-walled, 1(–2)-septate, (15–)17–20(–26) × (4–)5(–6) µm; hila thickened, darkened, 2–3 µm diam.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and feathery margins, reaching 15 mm diam after 2 wk at 25 °C. On MEA surface dark mouse grey, reverse mouse grey. On PDA surface violaceous black, reverse dark mouse grey. On OA surface olivaceous grey.

Typus. Australia, Western Australia, Williams Nature Reserve, 10 km north west of the Williams town, on *Eucalyptus* leaf litter (*Myrtaceae*), 18 Sept. 2015, *P.W. Crous* (holotype CBS H-23089, culture ex-type CPC 29184 = CBS 142526, ITS, LSU, *tef1*, and *tub2* sequences GenBank KY979760, KY979815, KY979898, and KY979926, MycoBank MB820953).

Notes — Quaedvlieg et al. (2014) introduced *Myrtapenidiella* to accommodate penidiella-like genera occurring on *Myrtaceae*. *Myrtapenidiella eucalyptigena* is phylogenetically closely related to *M. tenuiramis* (conidia (6–)8–10(–12) × 3–4 µm; Crous et al. 2009a) and *T. corymbiae* (conidia 7–9(–12.5) × 2.5–3(–3.5) µm; Cheewangkoon et al. 2009), but is distinct in having larger conidia. Based on a megablast search using the ITS sequence, the best match was *M. tenuiramis* (GenBank NR_145118; Identities = 476/482 (99 %), 4 gaps (0 %)), followed by *M. corymbia* (GenBank NR_145115; Identities = 470/482 (98 %), 4 gaps (0 %)). Based on both *tef1* and *tub2*, the closest matches in the NCBIs GenBank nucleotide database are equal to or less than 90 % similar.

Colour illustrations. Leaf litter in Williams Nature Reserve; colony sporulating on PNA; conidiophores and conidia. Scale bars = 10 µm.

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Myrtapenidiella balenae

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Myrtapenidiella balenae Crous, *sp. nov.*

Etymology. The name is derived from the Latin word *Balena* for whale, and refers to the fact that whales were present close to the shoreline at the time that this fungus was collected at Point Ann in Western Australia.

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

Conidiophores erect, flexuous, unbranched, solitary (not fasciculate), subcylindrical, thick-walled, finely roughened, medium brown, multiseptate, 70–200 × 4–5 µm. *Conidiogenous cells* integrated, terminal, subcylindrical, medium brown, finely verruculose, 15–25 × 3–4 µm; scars thickened, darkened, 1.5–2 µm diam, proliferating sympodially. *Primary ramoconidia* medium brown, verruculose, 0–1-septate, guttulate, 20–40 × 4–5 µm, frequently with mucoid sheath; hila thickened, darkened, 2.5–3 µm diam. *Secondary ramoconidia* subcylindrical, 0–1-septate, medium brown, verruculose with mucoid sheath, proliferating sympodially, 17–20 × 4–5 µm. *Conidia* in branched chains of up to 7, medium brown, verruculose, with sheath, thick-walled, 0–1-septate, (13–)15–17(–18) × (3–)4 µm; hila thickened and darkened, 1.5–2 µm diam.

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

Typus. Australia, Western Australia, Albany, Fitzgerald River National Park, Point Ann, on leaves of *Eucalyptus* sp. (*Myrtaceae*), at *Phytophthora* site, 22 Sept. 2015, *P.W. Crous* (holotype CBS H-23090, culture ex-type CPC 29235 = CBS 142527, ITS, LSU, *tef1*, and *tub2* sequences GenBank KY979761, KY979816, KY979899, and KY979927, MycoBank MB 820954).

Notes — *Myrtapenidiella balenae* is phylogenetically closely related to *M. tenuiramis* (on *E. tenuiramis*, Tasmania; conidia (6–)8–10(–12) × 3–4 µm; Crous et al. 2009a), but morphologically distinct in having larger conidia, (13–)15–17(–18) × (3–)4 µm. Based on a megablast search using the ITS sequence, the best match was *M. tenuiramis* (GenBank NR_145118; Identities = 474/482 (98 %), 2 gaps (0 %)), followed by *M. corymbia* (GenBank NR_145115; Identities = 472/482 (98 %), 2 gaps (0 %)). Based on a megablast search using the *tub2* sequence, the best match was *M. corymbia* (GenBank KF442481; Identities = 328/349 (94 %), 2 gaps (0 %)).

Colour illustrations. Point Ann, Fitzgerald River National Park; conidiophores sporulating on PNA; conidiophores and conidia. Scale bars = 10 µm.

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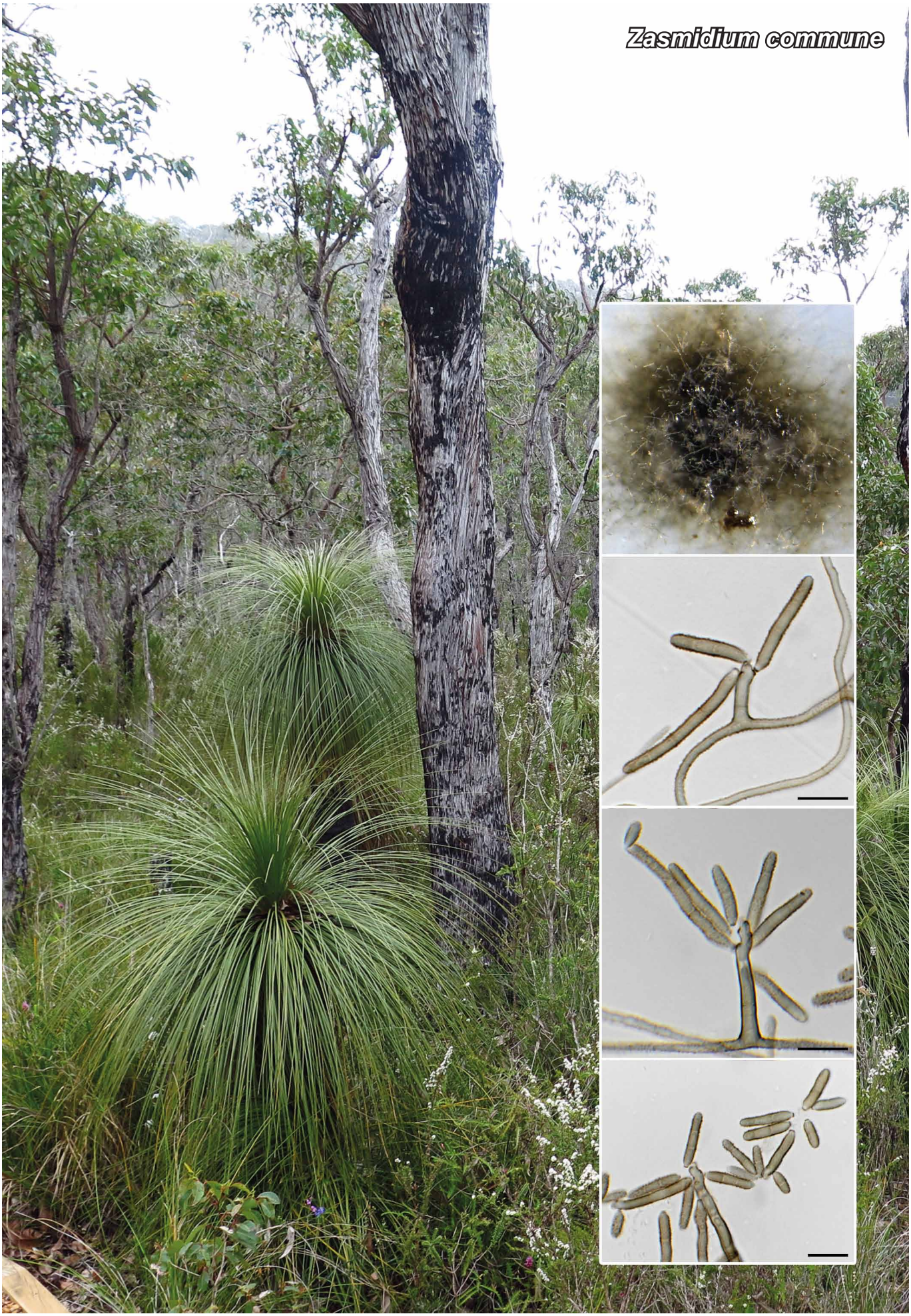
Zasmidium commune

Fungal Planet 578 – 20 June 2017

Zasmidium commune Crous, *sp. nov.*

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

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

Mycelium consisting of branched, septate, medium brown, verruculose, 1.5–2.5 µm diam hyphae. *Conidiophores* solitary, erect, arising from superficial mycelium, 25–100 × 3–5 µm, subcylindrical, somewhat flexuous, medium brown, thick-walled, smooth, 1–8-septate, unbranched. *Conidiogenous cells* integrated, terminal, subcylindrical, medium brown, smooth, 5–20 × 3–4 µm; scars thickened, darkened, sympodial, 1 µm diam, proliferating sympodially. *Secondary ramoconidia* medium brown, verruculose, narrowly obclavate to somewhat subcylindrical, 30–150 × 3 µm, multiseptate; hila thickened, darkened, 0.5 µm diam. *Conidia* in short (1–2) branched chains, medium brown, verruculose, narrowly obclavate to somewhat subcylindrical, apex obtuse, base truncate, hilum 0.5 µm diam, thickened, darkened, (8–)15–35(–45) × (2.5–)3(–4) µm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium, and feathery margins, reaching 15 mm diam after 2 wk at 25 °C. On MEA and PDA surface brown vinaceous, reverse isabelline. On OA surface olivaceous grey.

Typus. Australia, Western Australia, Denmark, Mount Lindesay Walk Trail, on leaves of *Xanthorrhoea* sp. (*Xanthorrhoeaceae*), 19 Sept. 2015, *P.W. Crous* (holotype CBS H-23093, cultures CPC 29725 = CBS 142530, ITS, LSU, and *actA* sequences GenBank KY979765, KY979820, and KY979860, MycoBank MB820955); CPC 29547, CPC 29723, ITS, LSU, *actA*, and *tub2* sequences GenBank KY979763–KY979764, KY979818–KY979819, KY979858–KY979859, and KY979929 (CPC 29547).

Notes — The genus *Zasmidium* (*Mycosphaerellaceae*) as it is presently defined is paraphyletic (Videira et al. in prep.). Most of the known species are associated with leaf spot diseases of various hosts. Some of these are agriculturally important, such as greasy leaf spot disease of *Citrus* (Huang et al. 2015). *Zasmidium commune* appears to be specific to leaves of a *Xanthorrhoea* sp. Phylogenetically, *Z. commune* is distinct from other *Zasmidium* spp. that are presently known based on their DNA sequences. Based on a megablast search using the ITS sequence, the best match was to *Mycosphaerella pseudovespa* (GenBank NR_137548; Identities = 501/507 (99 %), no gaps), followed by *Periconiella velutina* (GenBank EU041781; Identities = 526/547 (96 %), 1 gap (0 %)). Based on the *actA* sequence, *Z. commune* was only 95 % similar to *Mycosphaerella pseudovespa* (GenBank KF903535; Identities = 502/531 (95 %), 10 gaps (1 %)).

Colour illustrations. Xanthorrhoea sp. at the Mount Lindesay Walk Trail; colony sporulating on SNA; conidiophores and conidia. Scale bars = 10 µm.

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Zasmidium podocarpi

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Zasmidium podocarpi Crous, *sp. nov.*

Etymology. Name refers to *Podocarpus*, the host genus from which this fungus was collected.

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

Conidiophores solitary on underside of leaves (litter), erect, flexuous, dark brown, thick-walled, multiseptate, subcylindrical, verruculose to warty, branching in upper third of conidiophore, 200–300 × 9–12 µm; with 1–3 lateral branches, 1–3-septate, 40–70 µm long. *Conidiogenous cells* terminal and lateral, dark brown, verruculose, warty, thick-walled, obtusely rounded, 20–30 × 9–10 µm; scars numerous, darkened, thickened, prominently raised, up to 1 µm high, 3 µm diam. *Conidia* solitary, obclavate to subcylindrical, medium brown, verruculose to warty, apex subobtuse, 1–3-septate, (30–)35–40(–45) × (6–)8 µm; hila truncate, 3–4 µm diam, somewhat thickened and darkened; a few conidia observed in culture were much longer, thinner and flexuous.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margins, reaching 25 mm diam after 2 wk at 25 °C. On MEA surface olivaceous grey, reverse iron grey. On PDA surface iron grey with patches of orange, reverse similar, but with diffuse orange pigment. On OA surface olivaceous grey, and sienna on SNA.

Typus. Australia, Western Australia, Denmark, Mount Lindesay Walk Trail, on leaf litter of *Podocarpus* sp. (*Podocarpaceae*), 19 Sept. 2015, *P.W. Crous* (holotype CBS H-23092, culture ex-type CPC 29284 = CBS 142529, ITS, LSU, *actA*, and *tub2* sequences GenBank KY979766, KY979821, KY979861, and KY979930, MycoBank MB820956).

Notes — *Zasmidium podocarpi* represents a morphologically distinct species of *Zasmidium* that occurs on leaves of *Podocarpus*. At the time of collection, these leaves displayed prominent red leaf spots (devoid of fungal sporocarps). There was no evidence to link the disease to *Z. podocarpi*, as sporulation was observed only on the leaf litter. This suggests that *Z. podocarpi* is an endophyte, which is a common character trait for species of *Zasmidium* (see Huang et al. 2015). Further collections would be required to resolve the ecology of this fungus. Based on a megablast search using the ITS sequence, the best match was to *Mycosphaerella pseudovespa* (GenBank NR_137548; Identities = 497/509 (98 %), no gaps), followed by *Periconiella velutina* (GenBank EU041781; Identities = 525/548 (96 %), 3 gaps (0 %)). Based on both *actA* and *tub2*, the closest matches in the NCBIs GenBank nucleotide database were equal to or less than 93 % similar to species of *Mycosphaerellaceae*.

Colour illustrations. Mount Lindesay Walk Trail; colony on MEA; conidiophores with thickened darkened scars, and conidia. Scale bars = 10 µm.

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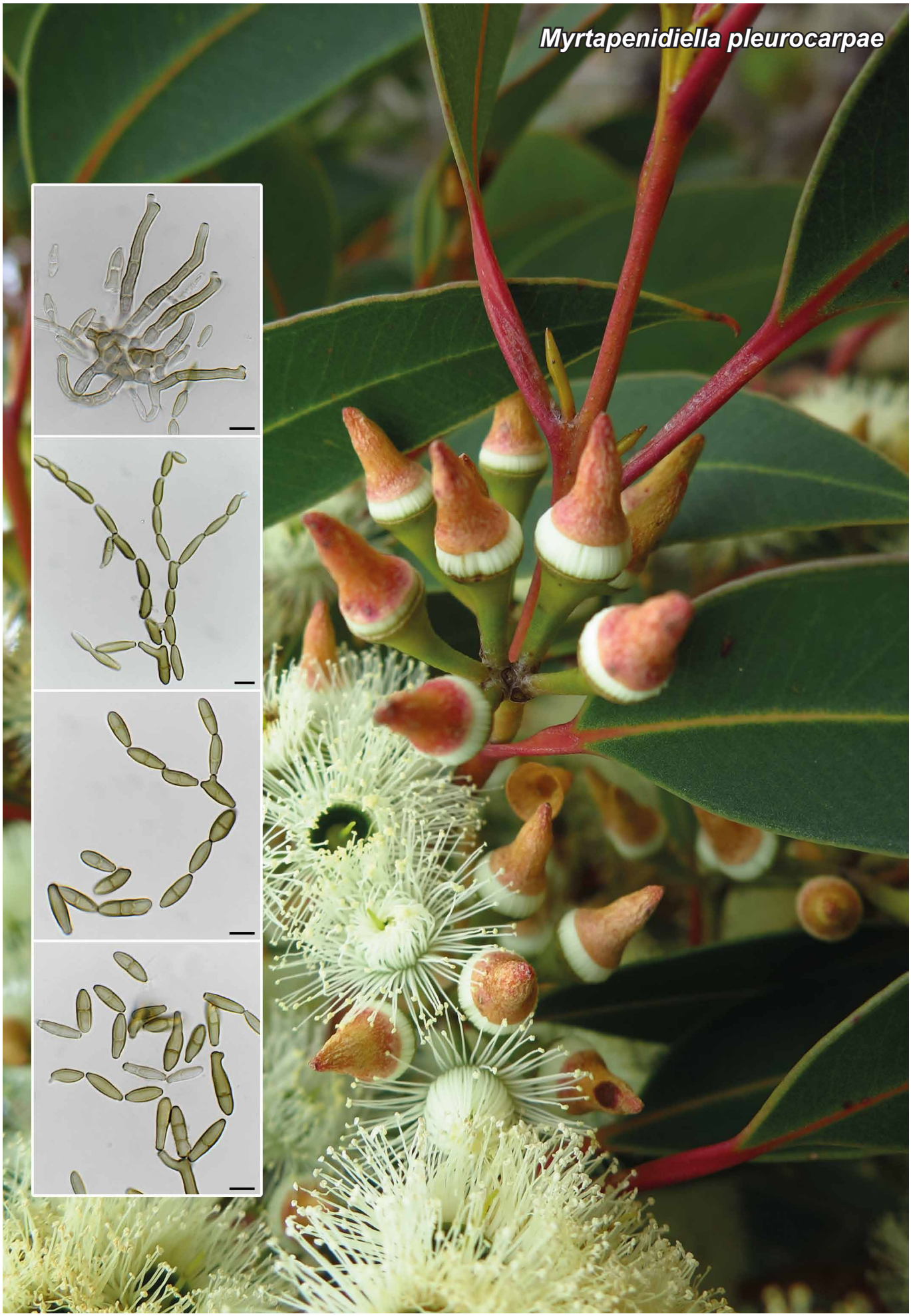
Myrtapenidiella pleurocarpae

Fungal Planet 580 – 20 June 2017

Myrtapenidiella pleurocarpae Crous, *sp. nov.*

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

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

Mycelium consisting of branched, septate, pale brown, smooth, 3–4 µm diam hyphae. *Conidiophores* solitary to fasciculate, arising from superficial hyphae or a small stroma of a few cells, erect, subcylindrical, straight to geniculate-sinuous, 30–90 × 5–6 µm, thick-walled, medium brown, smooth, 1–4-septate. *Conidiogenous cells* terminal, integrated, subcylindrical, medium brown, smooth, 20–35 × 5–6 µm; scars flat, somewhat thickened and darkened, 2.5–3 µm diam; proliferating sympodially. *Secondary ramoconidia* medium brown, finely verruculose, 0–3-septate, 15–35 × 5–7 µm, subcylindrical to fusoid-ellipsoid; hila truncate, 2–2.5 µm diam, somewhat darkened and thickened. *Conidia* in branched chains (–7), medium brown, finely verruculose, thick-walled, fusoid-ellipsoid, (15–)19–22(–25) × (5–)6(–6.5) µm; hila thickened and darkened, 1–2 µm diam.

Culture characteristics — Colonies erumpent, slow growing, with sparse to moderate aerial mycelium and smooth, even margins, reaching 15 mm diam after 2 wk at 25 °C. On MEA and PDA surface and reverse olivaceous grey. On OA surface iron-grey.

Typus. Australia, Western Australia, Albany, Fitzgerald River National Park, Cape Riche Lookout, on leaves of *Eucalyptus pleurocarpa* (*Myrtaceae*), 21 Sept. 2015, *P.W. Crous* (holotype CBS H-23094, culture ex-type CPC 29279 = CBS 142531, ITS, LSU, *tef1*, and *tub2* sequences GenBank KY979767, KY979822, KY979900, and KY979931, MycoBank MB820957); CPC 29234, ITS, LSU, *tef1*, and *tub2* sequences GenBank KY979768, KY979823, KY979901, and KY979932.

Notes — *Myrtapenidiella pleurocarpae* is phylogenetically closely related to *M. tenuiramis* (on *E. tenuiramis*, Tasmania; conidia (6–)8–10(–12) × 3–4 µm; Crous et al. 2009a), but morphologically distinct in having larger conidia, (15–)19–22(–25) × (5–)6(–6.5) µm, which also distinguishes it from *M. balenae* (see FP577 in this paper. It differs 3 nucleotides on ITS and is 89 % similar on *tef1* and 94 % similar on *tub2*). Based on a megablast search using the ITS sequence, the best match was to *M. tenuiramis* (GenBank NR_145118; Identities = 475/481 (98 %), 1 gap (0 %)), followed by *M. corymbia* (GenBank NR_145115; Identities = 473/481 (98 %), 1 gap (0 %)). Based on both *tef1* and *tub2*, the closest matches in the NCBIs GenBank nucleotide database were equal to or less than 93 % similar to species of *Myrtapenidiella*.

Colour illustrations. *Eucalyptus pleurocarpa* in Fitzgerald River National Park; conidiophores and conidia. Scale bars = 10 µm.

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Tiarosporella corymbiae

Fungal Planet 581 – 20 June 2017

Tiarosporella corymbiae Crous & Barber, *sp. nov.*

Etymology. Name refers to *Corymbia*, the host genus from which this fungus was collected.

Classification — *Botryosphaeriaceae*, *Botryosphaeriales*, *Dothideomycetes*.

Conidiomata brown, dark brown at apex, globose, 90–150 µm diam, with central ostiole, solitary on SNA, aggregated in clusters on OA, exuding crystalline conidial mass; wall of 2–4 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity, subcylindrical to doliiform, hyaline, smooth, proliferating percurrently at apex, 5–10 × 3–5 µm. *Conidia* solitary, hyaline, smooth, guttulate, thick-walled, fusoid-ellipsoid to obclavate, base truncate, 3–4 µm diam with marginal frill; apex subobtuse with thickened tip, at times with flared mucoid cap, but rarely observed, (16–)17–18(–20) × (5–)6–7 µm.

Culture characteristics — Colonies covering dish in 2 wk with moderate aerial mycelium at 25 °C. On MEA surface amber, reverse ochreous. On PDA surface iron-grey, reverse olivaceous grey. On OA surface olivaceous grey.

Typus. Australia, Western Australia, Perth, Greenshank Park, on *Corymbia calophylla* (*Myrtaceae*), 26 June 2015, *P.A. Barber* (holotype CBS H-23095, culture ex-type CPC 28201 = CBS 142532, ITS, LSU, *tef1*, and *tub2* sequences GenBank KY979769, KY979824, KY979902, and KY979933, MycoBank MB820958).

Notes — The poly- and paraphyletic nature of *Tiarosporella* was recently addressed by Crous et al. (2015a), who introduced several genera to accommodate tiarosporella-like genera occurring in other families. *Tiarosporella corymbiae* is phylogenetically related to the type species, *T. paludosa* (conidia 22–45 × 4–7 µm; GenBank NR_132907; Identities = 537/559 (96 %), 9 gaps (1 %)), although it is morphologically distinct, having much smaller conidia (16–20 × 5–7 µm).

Colour illustrations. Greenshank Park, Perth; conidiomata sporulating on OA (scale bar = 150 µm); conidiogenous cells and conidia (scale bars = 10 µm).

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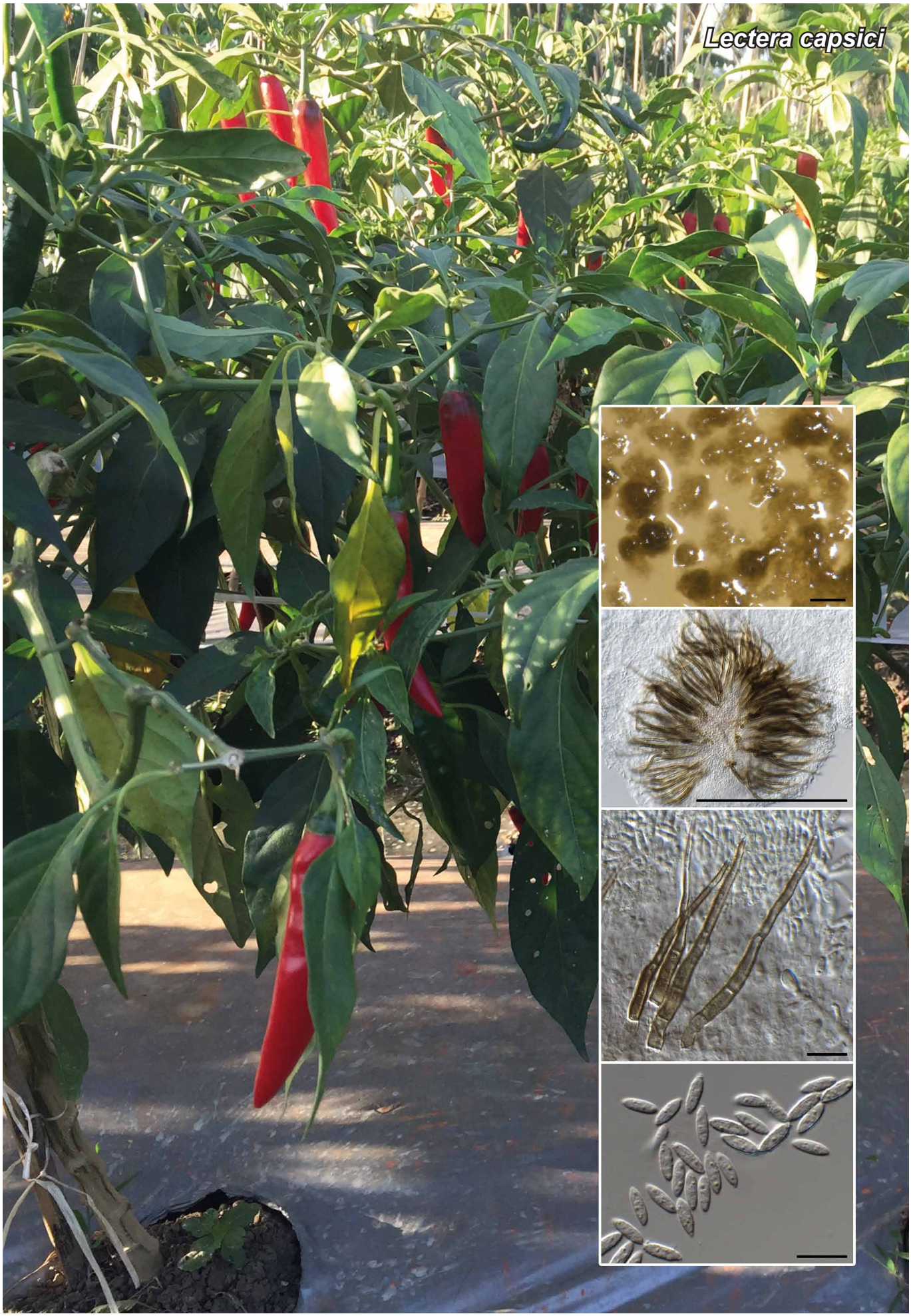
Lectera capsici

Fungal Planet 582 – 20 June 2017

Lectera capsici Crous & P.W.J. Taylor, *sp. nov.*

Etymology. Name refers to *Capsicum*, the host genus from which this fungus was collected.

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

Conidiomata initially closed, brown, globose on OA, but forming sporodochia on SNA, cushion-shaped, 100–200 µm diam, surrounded by grey-brown, verruculose setae, thick-walled, flexuous, 5–7-septate, tapering to acutely rounded apices, 60–80 × 3–4.5 µm. *Conidiogenous cells* cylindrical, proliferating percurrently at apex, 15–30 × 3–4 µm. *Conidia* (on SNA) hyaline, smooth (becoming olivaceous in mass, and appearing somewhat roughened), aseptate, fusoid-ellipsoid to navicular, straight, apex acutely rounded, base truncate, 0.5–1 µm diam, inequilateral, with inner plane flat, and outer plane convex, (6.5–)7–8(–9) × (2–)2.5(–3) µm on SNA.

Culture characteristics — Colonies flat, spreading with sparse aerial mycelium and even, lobate margins, reaching 60 mm diam on PDA and OA, 25 mm diam on MEA after 2 wk at 25 °C. On MEA surface folded, saffron, reverse saffron. On PDA surface apricot, reverse salmon. On OA surface saffron.

Typus. Malaysia, leaf spots of *Capsicum annuum* (*Solanaceae*), 6 Aug. 2015, *P.W.J. Taylor* (holotype CBS H-23097, culture ex-type CPC 28723 = CBS 142534, ITS, LSU, *tef1*, and *tub2* sequences GenBank KY979770, KY979825, KY979903, and KY979934, MycoBank MB820959).

Notes — Cannon et al. (2012) introduced the genus *Lectera* to accommodate two soil-borne plant pathogens associated with diseases of *Fabaceae*. *Lectera capsicum* is phylogenetically related, but distinct from *L. colletotrichoides* (conidia on *Medicago* stem, 6.5–11.5 × 2.5–3 µm, av. 8.35 × 2.67 µm; on PCA and PDA, 6.5–9(–10.5) × 2–3 µm, av. 7.41 × 2.43 µm; Cannon et al. 2012). These two species cannot be distinguished based on their conidial dimensions, and are best separated based on their DNA sequence data. Based on a megablast search using the ITS sequence, the best match was to *L. colletotrichoides* (GenBank JQ647428; Identities = 500/505 (99 %), 2 gaps (0 %)), followed by *L. longa* (GenBank NR_111715; Identities = 494/510 (97 %), 12 gaps (2 %)). The *tef1* and *tub2* sequences were 84 % and 86 % similar to *L. colletotrichoides* (GenBank KM231987 and KM232121), respectively.

Colour illustrations. *Capsicum annuum* plants; conidiomata sporulating on OA; conidioma with setae (scale bar = 200 µm); setae and conidia (scale bars = 10 µm).

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Verrucoconiothyrium eucalyptigenum

Fungal Planet 583 – 20 June 2017

Verrucoconiothyrium eucalyptigenum Crous, *sp. nov.*

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

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

Conidiomata separate, solitary, subglobose, papillate (having a prominent long neck in vivo), 200–250 µm diam, with central ostiole exuding a dark brown conidial mass; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, doliiform, 6–8 × 5–7 µm; proliferating percurrently at apex. *Conidia* solitary, golden brown, finely roughened, thick-walled, granular to finely guttulate, subcylindrical to narrowly ellipsoid, apex subobtuse, base truncate, 2–3 µm diam, (0–)1(–2)-septate, (8–)9–13(–15) × (4–)5(–6) µm (av. 12 × 5 µm).

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margins, covering dish in 2 wk. On PDA surface bay, reverse sienna. On OA surface sienna.

Typus. Australia, Western Australia, Perth, King's Park Botanic Gardens, on *Eucalyptus* leaf litter (*Myrtaceae*), 27 Sept. 2015, *P.W. Crous* (holotype CBS H-23098, culture ex-type CPC 29000 = CBS 142535, ITS, LSU, *rpb2*, *tef1*, and *tub2* sequences GenBank KY979771, KY979826, KY979852, KY979904, and KY979935, MycoBank MB820960).

Colour illustrations. King's Park Botanic Gardens; conidiomata sporulating on PNA (scale bar = 250 µm); conidiogenous cells and conidia (scale bars = 10 µm).

Notes — *Verrucoconiothyrium* was introduced by Crous et al. (2015b) to accommodate *Coniothyrium nitidae*, a foliar pathogen of *Proteaceae*. *Coniothyrium prosopidis* (associated with a bark disease of *Prosopis*; Crous et al. 2013) is allied to *Verrucoconiothyrium*, which is also true for the new species described here from *Eucalyptus* leaves collected in Australia. Based on a megablast search using the ITS sequence, the best match was to *V. nitidae* (GenBank KX306774; Identities = 534/542 (99 %), 1 gap (0 %)), followed by *V. prosopidis* (as *C. prosopidis*, GenBank NR_137604; Identities = 530/543 (98 %), no gaps).

Verrucoconiothyrium prosopidis (Crous & A.R. Wood) Crous, *comb. nov.* — MycoBank MB820961

Basionym. *Coniothyrium prosopidis* Crous & A.R. Wood, Persoonia 31: 207. 2013.

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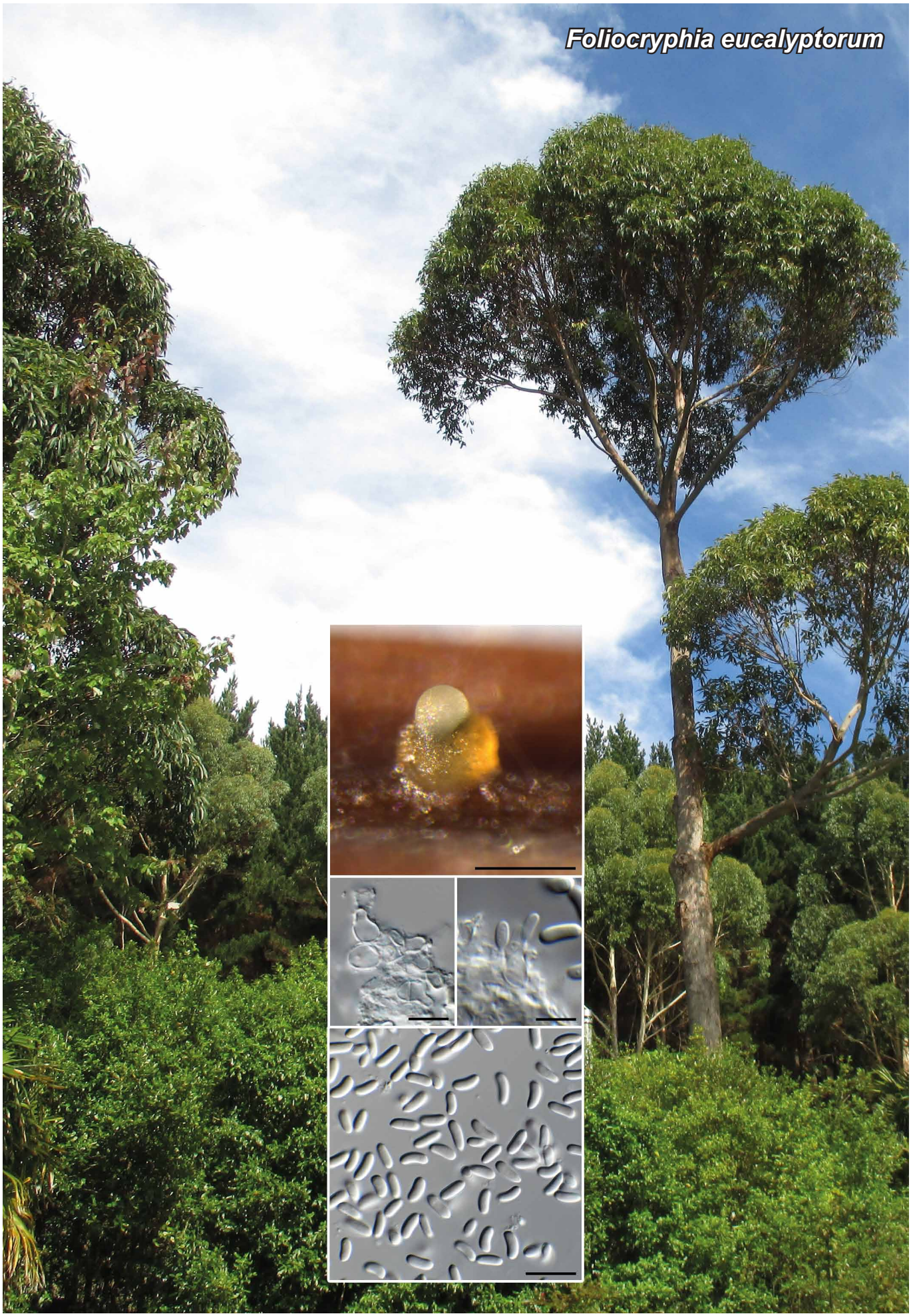
Foliocryphia eucalyptorum

Fungal Planet 584 – 20 June 2017

Foliocryphia eucalyptorum Crous & Thangavel, *sp. nov.*

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

Classification — *Incertae sedis*, *Sordariomycetes*.

Conidiomata eustromatic, separate, pulvinate, subglobose, up to 250 µm diam with central ostiole, pale to medium brown, singular to multilocular. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, subcylindrical to ampulliform with prominent apical taper towards narrowly cylindrical apical part, phialidic, with apical collarette and periclinal thickening, 5–12 × 3–5 µm. *Conidia* aseptate, hyaline, smooth, ellipsoid, straight to irregularly curved, apex obtuse, base truncate with protruding hilum, somewhat off-centre, smooth, thin-walled, (5–)6–8(–9) × (2–)2.5(–3) µm.

Culture characteristics — Colonies flat, spreading, covering dish in 2 wk with sparse aerial mycelium and smooth, even margins. On MEA surface dirty white to luteous, reverse luteous. On PDA surface and reverse pale luteous. On OA surface pale luteous.

Typus. New Zealand, Warkworth, Kaipara coast road, on *Eucalyptus* sp. (*Myrtaceae*), 2015, *R. Thangavel* (holotype CBS H-23099, culture ex-type CPC 29357 = CBS 142536 = T15_06344D = ICMP 21664, ITS, LSU, and *tub2* sequences GenBank KY979772, KY979827, and KY979936, MycoBank MB820962), CPC 29358, ITS, LSU, and *tub2* sequences GenBank KY979773, KY979828, and KY979937.

Notes — The genus *Foliocryphia* was established as monotypic genus by Cheewangkoon et al. (2009) to accommodate a foliicolous fungus occurring on *Eucalyptus*. *Foliocryphia eucalyptorum* can be distinguished from *F. eucalypti* (conidia 8.5–11.5 × 3.3–4.2 µm) by its smaller conidia. The two species are 99 % similar on ITS (GenBank NR_135975; Identities = 571/579 (99 %), no gaps) and 95 % similar on *tub2* (GenBank JQ706128; Identities = 708/742 (95 %), 12 gaps (1 %)).

Colour illustrations. *Eucalyptus* trees along the Kaipara coastal road; conidioma sporulating on PNA (scale bar = 250 µm); conidiogenous cells and conidia (scale bars = 10 µm).

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Ramularia vacciniicola

Fungal Planet 585 – 20 June 2017

Ramularia vacciniicola Crous & Thangavel, *sp. nov.*

Etymology. Name refers to *Vaccinium*, the host genus from which this fungus was collected.

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

Mycelium consisting of hyaline, smooth, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* micronematous, reduced to conidiogenous cells. *Conidiogenous cells* erect on hyphae, subcylindrical, straight, hyaline, smooth, 3–10 × 1.5–2.5 µm; scars thickened, darkened, somewhat refractive, 0.5 µm diam. *Secondary ramoconidia* hyaline, smooth, subcylindrical to narrowly fusoid-ellipsoid, 0(–1)-septate, 10–20(–30) × 2–2.5 µm, with 1–3 apical hila, thickened, darkened, somewhat refractive, 0.5–1 µm diam. *Conidia* in branched chains (–8), hyaline, smooth, guttulate, aseptate, narrowly fusoid-ellipsoid, (5–)8–10(–11) × (2–)2.5(–3) µm; hila thickened, darkened, somewhat refractive, 0.5–1 µm diam.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and even, lobate margins, reaching 20 mm diam after 2 wk at 25 °C. On MEA surface dark violet, reverse sepia. On PDA surface and reverse dark violet. On OA surface dirty white with diffuse dark violet pigment in agar.

Typus. New Zealand, Rotorua, on *Vaccinium* sp. (*Ericaceae*), 2015, *R. Thangavel* (holotype CBS H-23100, culture ex-type CPC 29365 = T15_05165F = CBS 142537 = ICMP 22047, ITS, LSU, *actA*, *his3*, and *tef1* sequences GenBank KY979774, KY979829, KY979862, KY979881, and KY979905, MycoBank MB820963); CPC 29366 = CBS 142537, CPC 29367–29368, ITS, LSU, *actA*, *his3*, and *tef1* sequences GenBank KY979775–KY979777, KY979830–KY979832, KY979863–KY979865, KY979882–KY979884, and KY979906–KY979907.

Notes — The genus *Ramularia* is linked to *Mycosphaerella* sexual morphs (Videira et al. 2015a, b). However, the older name *Ramularia* was selected over that of *Mycosphaerella* (Kirk et al. 2013, Wijayawardene et al. 2014, Rossman et al. 2015) for these fungi. Braun (1998) treated two *Ramularia* spp. known from *Vaccinium*. *Ramularia vacciniicola* is easily distinguished from *R. vaccinii* based on its smaller conidial dimensions (USA, conidia ellipsoid-ovoid, subcylindrical-fusoid, 10–20 × 2–5 µm). Conidia of *R. multiplex* are also somewhat larger (USA, conidia ellipsoid-ovoid, subcylindrical-fusoid, 6–15 × 1.5–5 µm), and further distinct in that the latter species forms well-developed fascicles with conidiophores. Furthermore, *R. vacciniicola* is also phylogenetically distinct from all species presently known from culture (see Videira et al. 2016). Based on a megablast search using the ITS sequence of the ex-type strain, the best match was to *R. proteae* (GenBank NR_145097; Identities = 524/526 (99 %), no gaps), followed by *R. stellenboschensis* (GenBank NR_145101; Identities = 520/526 (99 %), no gaps). Based on a megablast search using the *actA* sequence of the ex-type strain, the best match is *R. stellenboschensis* (GenBank KX287798; Identities = 568/575 (99 %), no gaps), followed by *R. rumicicola* (GenBank KX287786; Identities = 543/576 (94 %), 2 gaps (0 %)). Based on a megablast search using the *his3* sequence of the ex-type strain, the best match was to *R. proteae* (GenBank KX288939; Identities = 374/376 (99 %), no gaps), followed by *R. stellenboschensis* (GenBank KX288966; Identities = 370/376 (98 %), no gaps).

Colour illustrations. Blueberry Cottage berry farm, New Zealand; conidiophores sporulating on PNA; conidiophores and conidial chains. Scale bars = 10 µm.

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Harknessia communis

Fungal Planet 586 – 20 June 2017

Harknessia communis Crous, *sp. nov.*

Etymology. Name refers to the wider host range of this species.

Classification — *Harknessiaceae*, *Diaporthales*, *Sordariomycetes*.

Foliicolous. *Conidiomata* pycnidioid, separate to gregarious, subepidermal, becoming erumpent, stromatic, globose, up to 300 µm diam, with irregular opening and border of yellowish furfuraceous cells; wall of *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* 5–12 × 3–6 µm, ampulliform to subcylindrical, hyaline, smooth, invested in mucilage, proliferating percurrently at apex. *Conidia* (13–)14–15(–16) × (9–)10(–11) µm (av. 14.5 × 10 µm) in vitro, broadly ellipsoid, apex acutely rounded, aseptate, apiculate, pale yellow-brown, thick-walled, smooth, lacking striations, multi-guttulate. Basal appendage (3–)5–8(–11) × 2–2.5 µm in vitro, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm. *Spermatia* not seen.

Culture characteristics — Colonies spreading, fluffy, with moderate to abundant aerial mycelium, covering dish in 2 wk at 25 °C. On MEA surface dirty white, reverse luteous. On PDA surface and reverse dirty white. On OA surface dirty white.

Typus. Australia, Western Australia, Denmark, Mount Lindesay Walk Trail, on leaf litter of *Podocarpus* sp. (*Podocarpaceae*), 19 Sept. 2015, *P.W. Crous* (holotype CBS H-23101, culture ex-type CPC 29028 = CBS 142538, ITS, LSU, and *cmdA* sequences GenBank KY979778, KY979833, and KY979868, MycoBank MB820964).

Additional specimens examined. Australia, Western Australia, Denmark, Lights Beach, on *Leucopogon verticillatus* (*Ericaceae*), 19 Sept. 2015, *P.W. Crous*, HPC 712, CPC 29038; Williams Nature Reserve, 10 km north west of the Williams town, on *Melaleuca* sp. (*Myrtaceae*), 18 Sept. 2015, *P.W. Crous*, HPC 731, CPC 29468; Williams Nature Reserve, 10 km north west of the Williams town, on *Leptospermum* sp. (*Myrtaceae*), 18 Sept. 2015, *P.W. Crous*, HPC 732, CPC 29470, ITS, LSU, and *cmdA* sequences GenBank KY979779–KY979781, KY979834–KY979836, and KY979869–KY979871.

Notes — Species of *Harknessia* have a cosmopolitan distribution and are commonly associated with leaves and twigs of a wide range of plants, but they are especially common on *Myrtaceae* and *Proteaceae* (Crous et al. 2012b). Although they appear to be common endophytes, and several species are regarded as important foliar pathogens, the majority of species appear to be of little economic importance (Park et al. 2000). *Harknessia communis* is phylogenetically related to (see phylogenetic tree in Fungal Planet 591) *H. ravenstreetina* (conidia broadly venticose, (14–)16–18(–20) × (7–)8(–9) µm (av. 17 × 9 µm); Crous et al. 2012b), although it is morphologically distinct in having shorter and wider, broadly ellipsoid conidia. *Harknessia podocarpi* (on *Podocarpus parlatorei* from Argentina) has conidia that are 17.5–26 × 11–15 µm (Nag Raj 1993), thus larger than those of *H. communis* reported here. Based on a megablast search using the ITS sequence of the ex-type strain, the best matches were to numerous species of *Harknessia* with 99 % similarity, e.g. *H. ravenstreetina* (GenBank JQ706113; Identities = 429/431 (99 %), no gaps), followed by *H. spermatoidea* (GenBank JQ706120; Identities = 626/632 (99 %), 6 gaps (0 %)), and *H. uromycoides* (GenBank AY720740; Identities = 597/603 (99 %), 5 gaps (0 %)). However, based on a megablast search using the *cmdA* sequence of the ex-type strain, the best matches were equal to or less than 96 % similar to species of *Harknessia* in the NCBIs GenBank nucleotide database.

Colour illustrations. Mount Lindesay Walk Trail; conidiomata sporulating on PNA (scale bar = 250 µm); conidiogenous cells and conidia (scale bars = 10 µm).

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Harknessia banksiae

Fungal Planet 587 – 20 June 2017

Harknessia banksiae Crous, *sp. nov.*

Etymology. Name refers to *Banksia*, the host genus from which this fungus was collected.

Classification — *Harknessiaceae*, *Diaporthales*, *Sordariomycetes*.

Foliicolous. *Conidiomata* pycnidioid, separate to gregarious, subepidermal, becoming erumpent, stromatic, globose, up to 250 µm diam, with irregular opening and border of yellowish furfuraceous cells; wall of *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* 6–10 × 3–4 µm, ampulliform to subcylindrical, hyaline, smooth, invested in mucilage, proliferating percurrently at apex. *Conidia* (20–)22–26(–28) × (11–)12–13(–14) µm (av. 23 × 12.5 µm) in vitro, broadly fusoid-ellipsoid, apex acutely rounded, aseptate, apiculate, pale yellow-brown, thick-walled, smooth, lacking striations, multi-guttulate. Basal appendage (3–)4–6(–10) × 2–2.5 µm in vitro, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm. *Spermatia* not seen.

Culture characteristics — Colonies spreading, fluffy, with moderate to abundant aerial mycelium, covering dish in 2 wk at 25 °C. On MEA surface dirty white, reverse luteous. On PDA surface dirty white, reverse luteous. On OA surface salmon.

Typus. Australia, Western Australia, Albany, Stirling Range National Park, Stirling Range Drive, S34°22'19.4" E118°1'33.6", on leaves of *Banksia sessilis* (*Proteaceae*), 23 Sept. 2015, *P.W. Crous* (holotype CBS H-23102, culture ex-type CPC 29002 = CBS 142539, ITS, LSU, *cmdA*, and *tub2* sequences GenBank KY979782, KY979837, KY979872, and KY979938, MycoBank MB820965).

Additional specimen examined. Australia, Western Australia, Murray Road (at Ranger Station), on leaves of *Banksia plumosa* (*Proteaceae*), 21 Sept. 2015, *P.W. Crous*, HPC 613, CPC 29443, ITS, LSU, *cmdA*, and *tub2* sequences GenBank KY979783, KY979838, KY979873, and KY979939.

Notes — *Harknessia banksiae* is phylogenetically related to (see phylogenetic tree in Fungal Planet 591) *H. ravenstreetina* (conidia broadly venticose, (14–)16–18(–20) × (7–)8(–9) µm, av. 17 × 9 µm; Crous et al. 2012b), and *H. karwarrae* (conidia ellipsoid to ventricose, (12–)13–16(–19) × (10–)11(–12) µm, av. 15 × 11 µm; Lee et al. 2004), although it is distinct in having larger, broadly fusoid-ellipsoid conidia. Based on a megablast search using the ITS sequence of the ex-type strain, the best matches were to *H. ravenstreetina* (GenBank JQ706113; Identities = 429/431 (99 %), no gaps) and to *H. ellipsoidea* (GenBank JQ706087; Identities = 620/626 (99 %), 4 gaps (0 %)). However, based on a megablast search using the *cmdA* sequence of the ex-type strain, the best matches were to *H. eucalyptorum* (GenBank JQ706178; Identities = 467/483 (97 %), 2 gaps (0 %)) and to *H. ravenstreetina* (GenBank JQ706198; Identities = 463/484 (96 %), 4 gaps (0 %)). Based on a megablast search using the *tub2* sequence of the ex-type strain, the best match was to *H. eucalyptorum* (GenBank JQ706136; Identities = 823/860 (96 %), 17 gaps (1 %)).

Colour illustrations. *Banksia* spp. growing along Murray Road; conidioma sporulating on PNA (scale bar = 250 µm); conidiogenous cells and conidia (scale bars = 10 µm).

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Harknessia banksiigena

Fungal Planet 588 – 20 June 2017

Harknessia banksiigena Crous & Barber, *sp. nov.*

Etymology. Name refers to *Banksia*, the host genus from which this fungus was collected.

Classification — *Harknessiaceae*, *Diaporthales*, *Sordariomycetes*.

Foliicolous. *Conidiomata* pycnidioid, separate to gregarious, subepidermal, becoming erumpent, stromatic, globose, up to 250 µm diam, with irregular opening and border of yellowish furfuraceous cells; wall of *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* 6–10 × 4–6 µm, ampulliform to subcylindrical, hyaline, smooth, invested in mucilage, proliferating percurrently at apex. *Conidia* (19–)21–24(–26) × (13–)14(–15) µm (av. 23 × 14 µm) in vitro, fusoid-ellipsoid, apex acutely rounded, aseptate, apiculate, pale yellow-brown, thick-walled, smooth, lacking striations, multi-guttulate. Basal appendage (1.5–)3–4(–7) × 2–2.5 µm in vitro, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm. *Spermatia* not seen.

Culture characteristics — Colonies spreading, fluffy, with moderate to abundant aerial mycelium, covering dish in 2 wk at 25 °C. On MEA surface dirty white, reverse pale luteous. On PDA surface dirty white, reverse pale luteous. On OA surface dirty white.

Typus. Australia, Western Australia, Perth, St. Claire Park, on leaves of *Banksia sessilis* var. *cygnorum* (*Proteaceae*), 24 June 2015, *P.A. Barber* (holotype CBS H-23103, culture ex-type CPC 28232 = CBS 142540, ITS, LSU, and *cmdA* sequences GenBank KY979784, KY979839, and KY979874, MycoBank MB820966).

Notes — *Harknessia banksiigena* is phylogenetically related to (see phylogenetic tree in Fungal Planet 591) *H. renispora* (conidia reniform, (13–)14–17 × 9–12.5 µm, av. 15.5 × 11 µm; Nag Raj 1993) and *H. ellipsoidea* (conidia broadly ellipsoid to subglobose, (9–)11–12(–13) × 7(–8) µm, av. 11.5 × 7 µm; Crous et al. 2012b), but can be distinguished morphologically by having larger, fusoid-ellipsoid conidia. Based on a megablast search using the ITS sequence, the best matches were to *H. ravenstreetina* (GenBank JQ706113; Identities = 430/431 (99 %), no gaps) and to *H. ellipsoidea* (GenBank JQ706087; Identities = 618/624 (99 %), 2 gaps (0 %)). However, based on a megablast search using the *cmdA* sequence, the best matches were to *H. eucalyptorum* (GenBank JQ706178; Identities = 469/482 (97 %), 1 gap (0 %)) and to *H. ravenstreetina* (GenBank JQ706198; Identities = 465/483 (96 %), 3 gaps (0 %)).

Colour illustrations. St. Claire Park, Perth; conidiomata sporulating on OA; conidiogenous cells and conidia. Scale bars = 10 µm.

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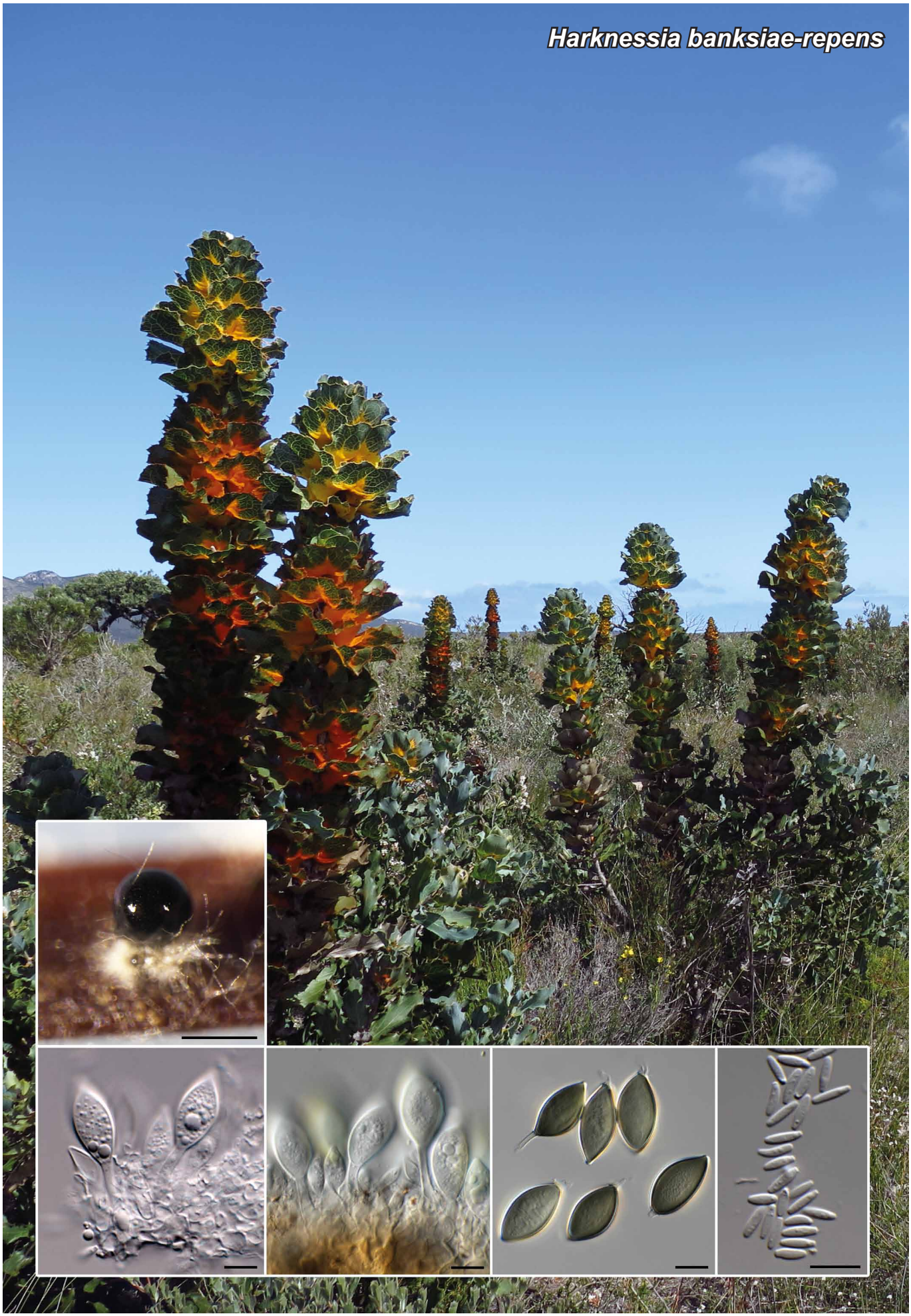
Harknessia banksiae-repens

Fungal Planet 589 – 20 June 2017

Harknessia banksiae-repens Crous, *sp. nov.*

Etymology. Name refers to *Banksia repens*, the host from which this fungus was first collected.

Classification — *Harknessiaceae*, *Diaporthales*, *Sordariomycetes*.

Foliicolous. *Conidiomata* pycnidioid, separate to gregarious, subepidermal, becoming erumpent, stromatic, globose, up to 250 µm diam, with irregular opening and border of yellowish furfuraceous cells; wall of *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* 5–10 × 4–6 µm, ampulliform to subcylindrical, hyaline, smooth, invested in mucilage, proliferating percurrently at apex. *Conidia* (19–)20–23(–26) × (10–)11–12(–13) µm (av. 22 × 12 µm) in vitro, fusoid, apex acutely rounded, aseptate, apiculate, pale yellow-brown, thick-walled, smooth, lacking striations, frequently with central zone of pale pigment along the length of conidium, multi-guttulate. Basal appendage (2–)3–8(–10) × 2–2.5 µm in vitro, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm. *Spermatia* hyaline, smooth, narrowly fusoid-ellipsoid, 4–7 × 2 µm.

Culture characteristics — Colonies spreading, fluffy, with moderate to abundant aerial mycelium, covering dish in 2 wk at 25 °C. On MEA surface dirty white, reverse saffron. On PDA surface and reverse dirty white. On OA surface salmon.

Typus. Australia, Western Australia, Murray Road (at Ranger Station), on leaves of *Banksia repens* (*Proteaceae*), 21 Sept. 2015, *P.W. Crous* (holotype CBS H-23104, culture ex-type CPC 29006 = CBS 142541, ITS, LSU, *cmdA*, and *tub2* sequences GenBank KY979785, KY979840, KY979875, and KY979940, MycoBank MB820967).

Additional specimen examined. Australia, Western Australia, Albany, Stirling Range National Park, Stirling Range Drive, on leaves of *Stirlingia* sp. (*Proteaceae*), 23 Sept. 2015, *P.W. Crous*, HPC 594, CPC 28874, ITS, LSU, and *cmdA* sequences GenBank KY979786, KY979841, and KY979876.

Notes — *Harknessia banksiae-repens* is phylogenetically related to (see phylogenetic tree in Fungal Planet 591) *H. ravenstreetina* (conidia broadly venticose, (14–)16–18(–20) × (7–)8(–9) µm, av. 17 × 9 µm; Crous et al. 2012b) and *H. karwarrae* (conidia ellipsoid to ventricose, (12–)13–16(–19) × (10–)11(–12) µm, av. 15 × 11 µm; Lee et al. 2004), but is distinct in having larger, fusoid conidia. Based on a megablast search using the ITS sequence of the ex-type strain, the best matches were to *H. ravenstreetina* (GenBank JQ706113; Identities = 428/431 (99 %), no gaps) and to *H. ellipsoidea* (GenBank JQ706087; Identities = 613/621 (99 %), 4 gaps (0 %)). However, based on a megablast search using the *cmdA* sequence of the ex-type strain, the best matches were to *H. eucalyptorum* (GenBank JQ706178; Identities = 467/482 (97 %), no gaps) and to *H. ravenstreetina* (GenBank JQ706198; Identities = 465/483 (96 %), 2 gaps (0 %)). Based on a megablast search using the *tub2* sequence of the ex-type strain, the best matches were to *H. eucalyptorum* (GenBank JQ706136; Identities = 655/686 (95 %), 11 gaps (1 %)) and to *H. renispora* (GenBank AY720769; Identities = 653/687 (95 %), 9 gaps (1 %)).

Colour illustrations. Stirling Range National Park, Stirling Range Drive, with a diversity of plant species, including *Banksia victoria*; conidioma sporulating on PNA (scale bar = 250 µm); conidiogenous cells, conidia and spermatia (scale bars = 10 µm).

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Harknessia platyphyllae

Fungal Planet 590 – 20 June 2017

Harknessia platyphyllae Crous, *sp. nov.*

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

Classification — *Harknessiaceae*, *Diaporthales*, *Sordariomycetes*.

Foliicolous. *Conidiomata* pycnidioid, separate to gregarious, subepidermal, becoming erumpent, stromatic, globose, up to 250 µm diam, with irregular opening and border of yellowish furfuraceous cells; wall of *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* 10–20 × 3–4 µm, ampulliform to subcylindrical, hyaline, smooth, invested in mucilage, proliferating percurrently at apex. *Conidia* (16–)17–19(–21) × (11–)12–13(–15) µm (av. 18 × 12.5 µm) in vitro, broadly ellipsoid, apex acutely rounded, aseptate, apiculate, pale yellow-brown, thick-walled, smooth, striations along length of conidium, multi-guttulate. Basal appendage (4–)6–8(–20) × 2–2.5 µm in vitro, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm. *Spermatia* hyaline, smooth, narrowly ellipsoid, 5–7 × 2–3 µm.

Culture characteristics — Colonies spreading, fluffy, with moderate to abundant aerial mycelium, covering dish in 2 wk at 25 °C. On MEA surface and reverse orange. On PDA surface and reverse pale luteous. On OA surface orange.

Typus. Australia, Western Australia, Perth, King's Park Botanic Gardens, on leaves of *Eucalyptus platyphylla* (*Myrtaceae*), 26 Sept. 2015, *M.J. Wingfield* (holotype CBS H-23105, culture ex-type CPC 28862 = CBS 142542, ITS, LSU, and *cmdA* sequences GenBank KY979787, KY979842, and KY979877, MycoBank MB820968).

Notes — *Harknessia platyphyllae* is phylogenetically related to (see phylogenetic tree in Fungal Planet 591) *H. ravenstreetina* and *H. karwarrae*. It is distinct from *H. karwarrae* (conidia ellipsoid to ventricose, (12–)13–16(–19) × (10–)11(–12) µm, av. 15 × 11 µm; Lee et al. 2004) and *H. ravenstreetina* (conidia broadly venticose, (14–)16–18(–20) × (7–)8(–9) µm, av. 17 × 9 µm; Crous et al. 2012b), based on its broadly ellipsoid conidia. Based on a megablast search using the ITS sequence, the best matches were to *H. ravenstreetina* (GenBank JQ706113; Identities = 430/431 (99 %), no gaps) and to *H. karwarrae* (GenBank AY720748; Identities = 593/595 (99 %), no gaps). However, based on a megablast search using the *cmdA* sequence, the best matches were to *H. karwarrae* (GenBank AY720811; Identities = 468/473 (99 %), no gaps) and to *H. eucalyptorum* (GenBank JQ706177; Identities = 510/524 (97 %), no gaps).

Colour illustrations. *Eucalyptus platyphylla* in King's Park Botanic Gardens; conidioma sporulating on PNA (scale bar = 250 µm), conidiogenous cells, conidia and spermatia (scale bars = 10 µm).

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Harknessia pellitae

Fungal Planet 591 – 20 June 2017

Harknessia pellitae Crous & M.J. Wingf., *sp. nov.*

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

Classification — *Harknessiaceae*, *Diaporthales*, *Sordariomycetes.*

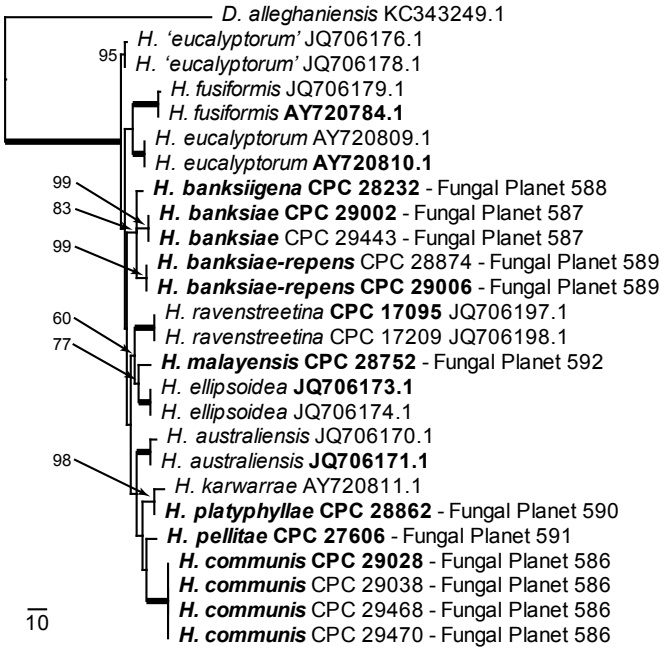
Foliicolous. *Conidiomata* pycnidioid, separate to gregarious, subepidermal, becoming erumpent, stromatic, globose, up to 200–350 µm diam, with irregular opening and border of yellowish furfuraceous cells; wall of *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* 5–10 × 3–5 µm, ampulliform to subcylindrical, hyaline, smooth, invested in mucilage, proliferating percurrently at apex. *Conidia* (12–)13–15(–16) × (8–)9(–10) µm (av. 14 × 9 µm) in vitro, ellipsoid, apex subobtusely rounded, aseptate, non-apiculate, pale yellow-brown, thick-walled, smooth, striations along length of the conidium, multi-guttulate. Basal appendage (3–)4–7(–10) × 2–2.5 µm in vitro, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm. *Spermatia* not seen.

Culture characteristics — Colonies spreading, fluffy, with moderate to abundant aerial mycelium, covering dish in 2 wk at 25 °C. On MEA surface pale luteous, reverse luteous. On OA surface pale luteous.

Typus. Malaysia, Sabah, on leaves of *Eucalyptus pellita* (*Myrtaceae*), May 2015, *M.J. Wingfield* (holotype CBS H-23106, culture ex-type CPC 27606 = CBS 142543, ITS, LSU, and *cmdA* sequences GenBank KY979788, KY979843, and KY979878, MycoBank MB820969).

Colour illustrations. *Eucalyptus pellita* trees growing in Malaysia; conidiomata sporulating on OA (scale bar = 300 µm); conidiogenous cells and conidia (scale bars = 10 µm).

Notes — *Harknessia pellitae* is phylogenetically related to *H. ravenstreetina* (conidia broadly venticose, (14–)16–18(–20) × (7–)8(–9) µm, av. 17 × 9 µm; Crous et al. 2012b), but is distinct in having smaller, ellipsoid conidia. Based on a megablast search using the ITS sequence, the best matches were to *H. ravenstreetina* (GenBank JQ706113; Identities = 428/430 (99 %), no gaps) and to *H. renispora* (GenBank AY720737; Identities = 439/442 (99 %), 1 gap (0 %)). However, based on a megablast search using the *cmdA* sequence, the best matches were to *H. australiensis* (GenBank JQ706171; Identities = 467/482 (97 %), 1 gap (0 %)) and to *H. eucalyptorum* (GenBank JQ706177; Identities = 456/472 (97 %), no gaps).



The first of six equally most parsimonious trees obtained from a parsimony analysis of the calmodulin alignment with PAUP (Swofford 2003; 26 sequences including the ingroup, 470 included characters of which 77 were parsimony-informative). The tree was rooted with *Diaporthe alleghaniensis* (GenBank KC343249.1) and ex-type strains are indicated with the culture of GenBank accession number in **bold**. Novel *Harknessia* species described here are indicated in ***bold italic*** text and their corresponding Fungal Planet numbers are indicated. The scale bar represents the number of changes and parsimony bootstrap support values from 1 000 replicates are indicated at the nodes (thickened lines were fully supported).

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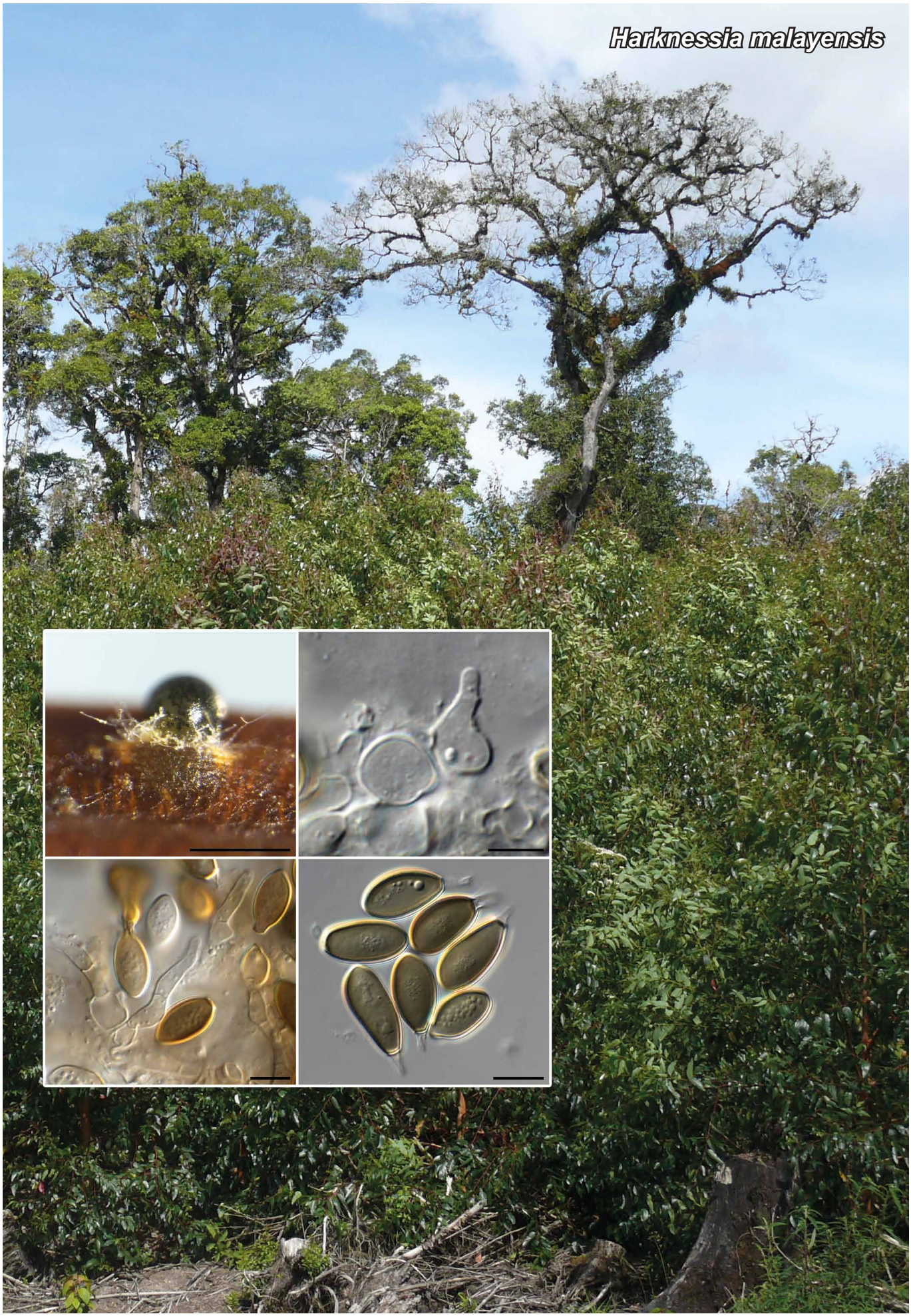
Harknessia malayensis

Fungal Planet 592 – 20 June 2017

Harknessia malayensis Crous & M.J. Wingf., *sp. nov.*

Etymology. Name refers to Malaysia, the country from which this fungus was collected.

Classification — *Harknessiaceae*, *Diaporthales*, *Sordariomycetes.*

Foliicolous. *Conidiomata* pycnidioid, separate to gregarious, subepidermal, becoming erumpent, stromatic, globose, up to 250 µm diam, with irregular opening and border of yellowish furfuraceous cells; wall of *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* 5–10 × 3–5 µm, ampulliform to subcylindrical, hyaline, smooth, invested in mucilage, proliferating percurrently at apex. *Conidia* (15–)16–18(–20) × (7–)8–9(–10) µm (av. 17 × 8.5 µm) in vitro, fusoid-ellipsoid, apex subobtusely rounded, aseptate, non-apiculate, pale yellow-brown, thick-walled, smooth, striations along length of the conidium, multi-guttulate. Basal appendage (1–)2–5(–8) × 2–2.5 µm in vitro, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm. *Spermatia* not seen.

Culture characteristics — Colonies spreading, fluffy, with moderate to abundant aerial mycelium, covering dish in 2 wk at 25 °C. On MEA surface and reverse luteous. On PDA surface and reverse pale luteous. On OA surface orange.

Typus. Malaysia, Sabah, on leaves of *Eucalyptus pellita* (*Myrtaceae*), May 2015, *M.J. Wingfield* (holotype CBS H-23107, culture ex-type CPC 28752 = CBS 142544, ITS, LSU, *cmdA*, and *tub2* sequences GenBank KY979789, KY979844, KY979879, and KY979941, MycoBank MB820970).

Notes — *Harknessia malayensis* is phylogenetically related to (see phylogenetic tree in Fungal Planet 591) *H. ravenstreetina* (conidia broadly venticose, (14–)16–18(–20) × (7–)8(–9) µm, av. 17 × 9 µm; Crous et al. 2012b) and *H. renispora* (conidia reniform, (13–)14–17 × 9–12.5 µm, av. 15.5 × 11 µm; Nag Raj 1993). Although it can be distinguished from *H. renispora* based on its conidial dimensions, it has similar conidial dimensions to that of *H. ravenstreetina*. However, conidia of the latter lack striations, whereas conidia of *H. malayensis* have striations along the length of the conidial body, which can be used to separate these two species if no DNA data were available. Based on a megablast search using the ITS sequence, the best matches were to *H. ravenstreetina* (GenBank JQ706113; Identities = 415/417 (99 %), no gaps) and to *H. ellipsoidea* (GenBank JQ706087; Identities = 608/622 (98 %), 11 gaps (1 %)). However, based on a megablast search using the *cmdA* sequence, the best matches were to *H. ellipsoidea* (GenBank JQ706174; Identities = 460/472 (97 %), 1 gap (0 %)) and to *H. ravenstreetina* (GenBank JQ706198; Identities = 459/473 (97 %), 2 gaps (0 %)). Based on a megablast search using the *tub2* sequence, the best matches were to *H. australiensis* (GenBank JQ706130; Identities = 396/412 (96 %), 1 gap (0 %)) and to *H. ravenstreetina* (GenBank JQ706157; Identities = 395/413 (96 %), 2 gaps (0 %)).

Colour illustrations. *Eucalyptus pellita* trees growing in Malaysia; conidioma sporulating on PNA (scale bar = 250 µm); conidiogenous cells and conidia (scale bars = 10 µm).

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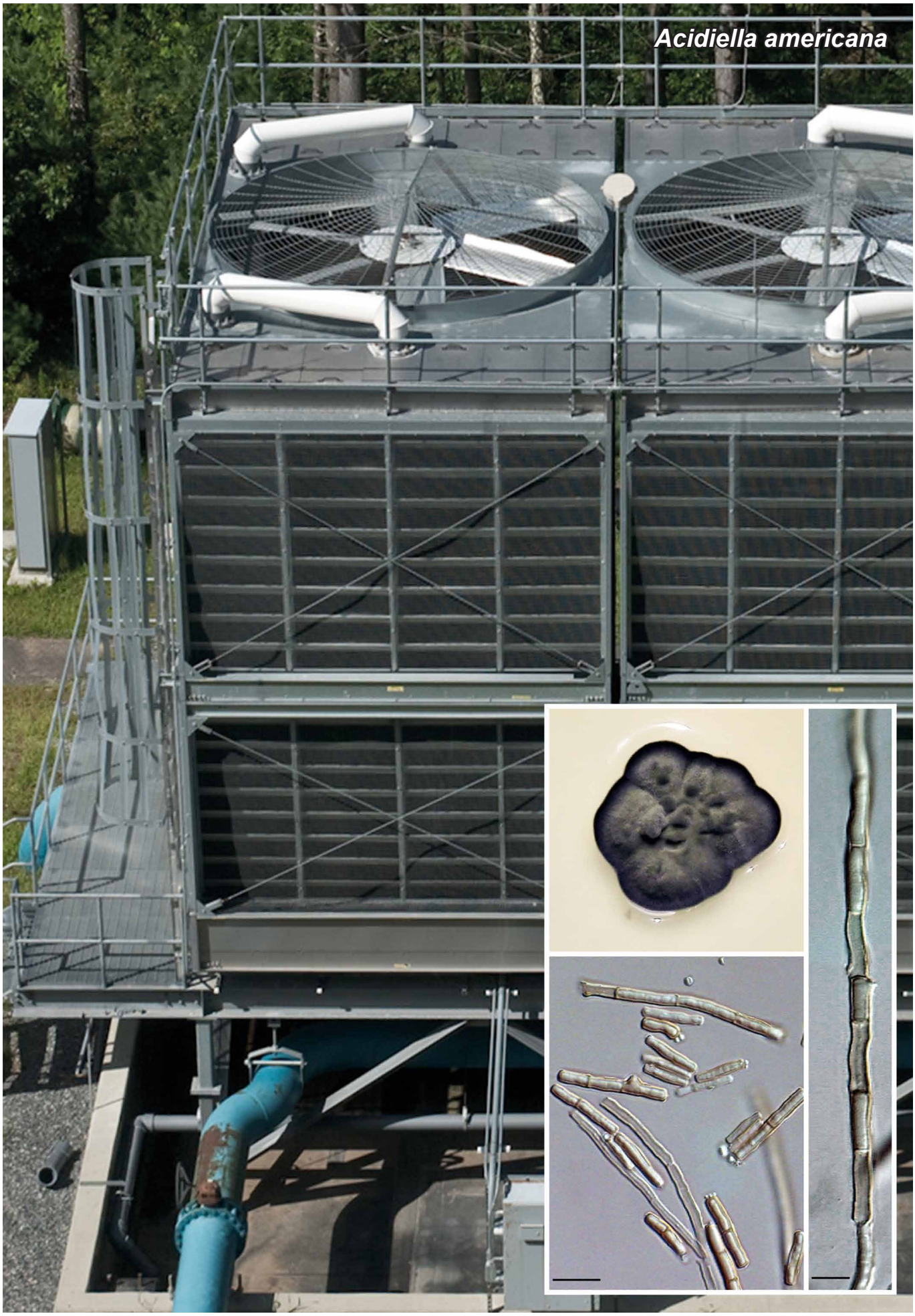

Acidiella americana

Fungal Planet 593 – 20 June 2017

Acidiella americana M. Kolařík, Jurjević & Hubka, *sp. nov.*

Etymology. *americana* (Latin, fem. adj.) from America. Refers to the country of origin.

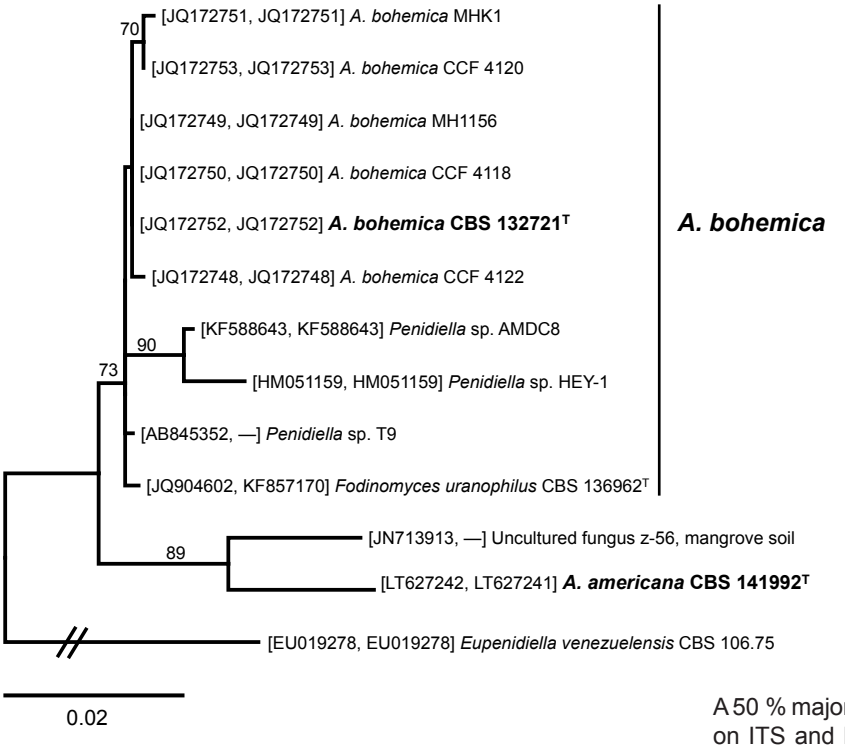
Classification — *Teratosphaeriaceae*, *Capnodiales*, *Dothideomycetes*.

Mycelium 2–3.5 µm diam, smooth, septate, pale to medium brown. *Conidia* produced by fragmentation of hyphae, oblong-elliptical to cylindrical, 7–21 × 2–3.5 µm.

Culture characteristics — (in the dark at 25 °C after 14 d): Colonies on 4 % malt extract agar (MEA, pH 7) attained 25 mm diam; compact, wrinkled, surface velvety, black. Growth optimum at pH 7 and minimum at pH 2. Growth on MEA at pH 3 was 3 mm diam. Growth at 37 °C (MEA, pH 7) was 12 mm diam. Growth in response to the acidity gradient was tested according to Hujslová et al. (2013).

Typus. USA, New Jersey, wall of a cooling tower, June 2014, isol. *Ž. Jurjević* as EMSL No. 2404 (holotype PRM 935805, culture ex-type CCF 5435 = CBS 141992; ITS, LSU, and SSU sequences GenBank LT627242, LT627241, and LT671442, MycoBank MB819188).

Notes — *Acidiella* encompasses two species, *A. bohemica* and *A. uranophila*. They probably represent a single species, that has been isolated from highly acidic soil and mine water (Hujslová et al. 2013, Vázquez-Campos et al. 2014, Kolařík et al. 2015). Their colonies, arthroconidia and mycelium morphology is undistinguishable from *A. americana*. *Acidiella bohemica* and *A. uranophila* have a growth optimum at pH 5 and exhibit growth at pH 2 in contrast to *A. americana*. Based on ITS sequences, *A. americana* is 95 % similar to *A. bohemica* (490/516 bp, GenBank JN713913) and *A. uranophila* (489/515 bp, JQ904602). The LSU sequence shows highest level of similarity to *A. bohemica* (99 %, 740/746 bp, KF901984) and *A. uranophila* (99 %, 815/820 bp, KF857170). SSU sequence differs in a single position (1029/1030 bp) from *A. uranophila* (KF857169) and *A. bohemica* (JQ172750).



A 50 % majority consensus rule maximum likelihood tree based on ITS and LSU rDNA sequences showing the relationships of taxa within the genus *Acidiella*. Partitioning scheme and substitution models for analyses were selected using PartitionFinder v. 1.1.1 (Lanfear et al. 2012): the HKY+I model was proposed for the ITS1 + ITS2 region, and a K80 model for the 5.8S + LSU region. The tree was constructed with IQ-TREE v. 1.4.0 (Nguyen et al. 2015). The dataset contained 13 taxa and a total of 813 characters of which 102 were variable and 23 parsimony-informative. Support values at branches were obtained from 500 bootstrap replicates. Only bootstrap support values ≥ 70 % are shown; ex-type strains are indicated by ^{T}. The tree is rooted with *Eupenidiella venezuelensis* CBS 106.75.

Colour illustrations. Cooling tower in New Jersey; colonies on malt extract agar after 2 wk at 25 °C; mycelium disintegrating into conidia (scale bars = 10 µm).

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Coprinopsis pseudomarcescibilis
1 cm
1 cm

Fungal Planet 594 – 20 June 2017

Coprinopsis pseudomarcescibilis Heykoop, G. Moreno & P. Alvarado, *sp. nov.*

Etymology. Name reflects its morphological similarity to *Coprinopsis marcescibilis.*

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

Cap 12–50 mm broad, 10–30 mm high, convex to conical convex, with prominent umbo, glabrous, sometimes somewhat wrinkled, orange brown when young, then dark beige brown or date colour, hygrophanous, after drying it becomes first pale greyish beige to ochraceous beige, then greyish white. Margin in some specimens somewhat incurved, faintly striate when moist. *Veil* white, abundant in young specimens forming a firm collar, connecting margin of cap with stem and in addition a layer of radially arranged fibrils present in a 1–2 mm broad zone along margin; later, while detaching itself from stem, the collar forms an appendiculate belt soon splitting into more or less irregular flocci; finally, in older specimens veil evanescent and progressively disappearing. *Gills* close, ascending, adnate, first greyish, then blackish, with white fimbriate edge; lamellulae present. *Stem* (25–)65–130 × 2–7 mm, cylindrical, central, hollow, longitudinally striate (more pronounced in the upper part), white with pale ochraceous tinges; apex pruinose, and the lower part covered with small white fibrils. *Odour* not distinctive. *Spores* 11–16.5(–17) × 6–8 µm, av. 13.3–14.5 × 6.9–7.2 µm (4 collections), Q_{av} 1.86–2.08, ellipsoid, smooth, with apical germ pore, in NH_4OH (10 %) reddish brown to orange brown. *Basidia* 4-spored, 20–35 × 11–13 µm, clavate, hyaline; pseudoparaphyses often seen. *Pleurocystidia* not observed. *Marginal cells*: cheilocystidia 25–40 × 11–15 µm, very abundant and densely packed, narrowly utriform, sometimes subcapitate; sphaeropedunculate and clavate cells extremely rare and difficult to observe, e.g. 16 × 12 µm; all cells thin-walled, colourless. *Hymenophoral trama* in NH_4OH (10 %) consisting of hyaline thin-walled hyphae, without encrustations. *Pileipellis* a cutis consisting of a layer of thin elongate hyphae 8–18 µm diam, on top of a much thicker layer of more cellular structure consisting of broadly ellipsoid, subglobose or irregularly shaped cells, up to 40 µm diam. *Clamp connections* present. *Stipitipellis* a cutis consisting of elongate septate hyphae 5–12 µm diam. *Caulocystidia* abundant, similar in size and shape to cheilocystidia. *Veil* fibrillose consisting of elongate and septate hyaline hyphae, 3–11 µm diam; many of these hyphae ending in terminal cystidia, 34–60 × 10–18 µm, utriform to subcapitate or cylindrical, which probably are caulocystidia detached from stem together with veil.

Habitat & Distribution — Growing solitary to gregarious on calcareous loamy soil under *Salsola vermiculata* or different gramineae. So far known from Spain, Germany, Italy (Sicily), and Finland but probably often mistaken for *Coprinopsis marcescibilis*.

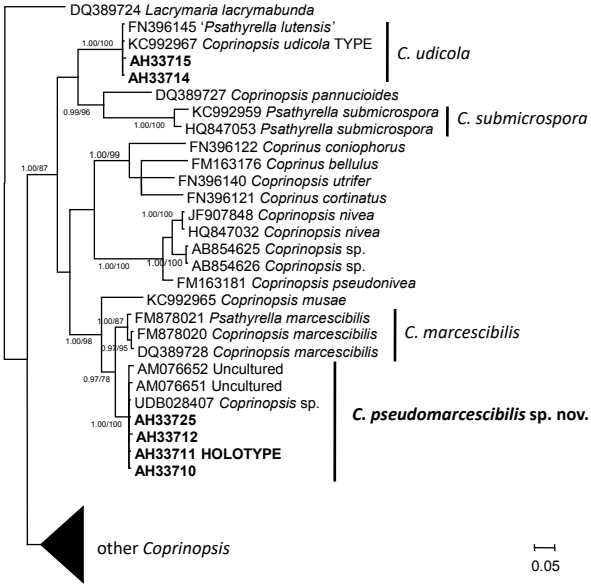
Typus. Spain, Alcalá de Henares, Parque de los Cerros, under *Salsola vermiculata* on calcareous loamy soil, 4 Dec. 2014, *M. Heykoop*, *G. Moreno & M. Lizárraga* (holotype AH 33711, ITS and LSU sequences GenBank KY698008 and MF033345, MycoBank MB820344).

Colour illustrations. Spain, Alcalá de Henares, El Gurugú, calcareous loamy soil with *Salsola vermiculata*, where the holotype was collected; basidiomata; cheilocystidia; cheilocystidia basidium and spores; basidia; spores under LM; smooth spores with central germ pore under SEM (from the holotype); scale bars = 1 cm (basidiomata), 10 µm (cheilocystidia), 10 µm (cheilocystidia, basidium and spores), 10 µm (basidia), 10 µm (spores under LM), 2 µm (spores under SEM).

Additional specimens examined. ***Coprinopsis pseudomarcescibilis***: Spain, Alcalá de Henares, Parque de los Cerros, under *Salsola vermiculata* on calcareous loamy soil, 4 Dec. 2014, *M. Heykoop*, *G. Moreno & M. Lizárraga*, paratype AH 33710, ITS sequence GenBank KY698009; ibid., AH33712, ITS sequences GenBank KY698007; Alcalá de Henares, Campus Universidad de Alcalá, on calcareous soil among grasses, 1 Dec. 2016, *J.A. Picado* (paratype AH 33725, ITS sequence GenBank KY698006). ***Coprinopsis udicola***: Spain, Alcalá de Henares, El Gurugú, under *Ulmus pumila* and *Dactylis glomerata* in border of *Pinus halepensis* wood, 12 Dec. 2014, *G. Moreno & M. Heykoop*, AH 33714, ITS, LSU sequences GenBank KY698004, KY698005; ibid., AH 33715, ITS, LSU sequences GenBank KY698002, KY698003.

Notes — *Coprinopsis pseudomarcescibilis* is characterised by its moderately large basidiocarps with appendiculate veil splitting into more or less irregular flocci, the absence of pleurocystidia, and the large and dark spores (11–16.5(–17) × 6–8 µm).

In our ITS phylogeny *Coprinopsis pseudomarcescibilis* is included in a clade together with *C. marcescibilis* and *C. musae*, the latter recently described by Örstadius et al. (2015). All three species are psathyrelloid members of *Coprinopsis* which share the presence of a pileipellis forming a cutis and the absence of pleurocystidia. *Coprinopsis musae* differs from *C. pseudomarcescibilis* in having smaller and paler spores and smaller basidiomata. *Coprinopsis pseudomarcescibilis* is genetically close to *C. marcescibilis* (2.21 % nucleotide differences in the ITS sequence, 11/497), but it differs from the latter by its slightly longer spores, 13.3–14.5 µm (mean values 4 coll.) vs 11.6–12.8 (mean values 18 coll.; Kits van Waveren 1985), and the veil splitting into more irregular flocci on cap margin instead of triangular denticles. However, *C. pseudomarcescibilis* and *C. marcescibilis* seem to be sibling species (i.e., cryptic sister species; Bickford et al. 2006) which are difficult to separate only based on morphology.



Consensus phylogram obtained in MrBayes v. 3.1 from an ITS alignment of genus *Coprinopsis*. Values next to nodes represent Bayesian PP and maximum likelihood BP (RAxML). Only nodes supported by > 0.95 PP or > 70 % BP are annotated. The main group of sequences has been collapsed for publication.

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Cyathus aurantogriseocarpus

Fungal Planet 595 – 20 June 2017

Cyathus aurantogriseocarpus R. Cruz, J.S. Góis, M.P. Martín, K. Hosaka & Baseia, *sp. nov.*

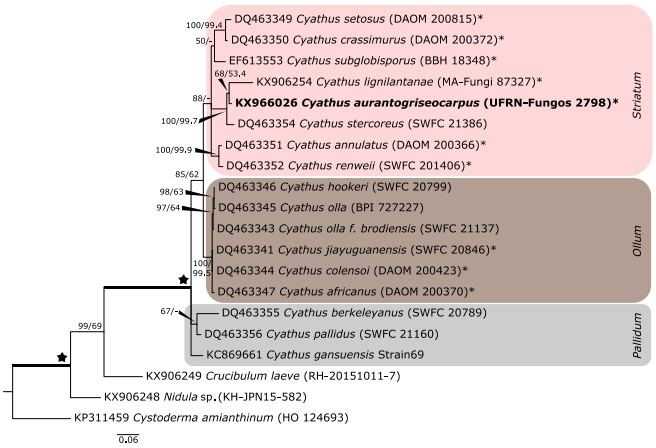
Etymology. Named in reference to the orange-grey colour of the exoperidium.

Classification — *Nidulariaceae*, *Agaricales*, *Agaricomycetes.*

Basidiomata infundibuliform, 5–6 mm in height, 4–6 mm in width at the upper part, not expanded in the mouth or tapering abruptly at the base. *Emplacement* 1.5–2 mm in width, conspicuous, greyish brown (7F3 Kornerup & Wanscher 1978). *Exoperidium* hirsute, orange-grey (5B2), provided with 0.5–0.75 mm long tomentum, arranged in regular and flexible tufts. External wall conspicuously plicated, with 0.3–0.5 mm between the striae. *Mouth* finely fimbriated, in a continuous pattern, 0.2 mm in height, greyish brown (7F3). *Endoperidium* brownish grey to greyish brown (7C2–7D3), conspicuously plicated, with 0.2–0.4 mm between the striae. Perceptible bright contrasting with the exoperidium. Stipe 1 mm long, greyish brown (7F3). *Epiphragm* not observed. *Peridioles* brownish grey (7F2) to black, 1.5–1.75 × 1.2–1.5 mm, in number of 6 (average) in each basidiomata, circular to irregular in shape, smooth surface, tunic indistinct and provided with double layered cortex. *Basidiospores* smooth, hyaline, 32.5–47 × 22.5–28.5 µm (L = 38.9 µm; W = 25.9 µm; n = 30 spores), slightly elliptical to elongated (Q = 1.25–1.79), elliptical in average (Q_m = 1.51), apicule absent and spore wall 2.3–4.9 µm in thickness.

Typus. Brazil, Rio Grande do Norte, Natal, Pitimbu, on decaying wood, 12 Feb. 2013, *A.S. Medeiros* (holotype UFRN-Fungos 2798, ITS and LSU sequences GenBank KX966026 and KX966027, MycoBank MB818580).

Notes — Following Brodie's (1975) classification, *C. aurantogriseocarpus* can be grouped in group VI (*poeppigii*) or in group VII (*striatus*), and in the classification of Zhao et al. (2007) this species belongs to the *striatum* group. Morphologically this species resembles *C. bulleri*, *C. griseocarpus*, and *C. rudis*. However, *C. aurantogriseocarpus* can be distinguished from those species by the strong plication in the external wall, larger spores (5 × 8.5 µm in *C. bulleri*, 7.5–9 × 5–6 µm in *C. griseocarpus*, and 9–12 × 5 µm in *C. rudis*), and the double-layered cortex, unlike the single-layered cortex of these three species (Brodie 1967, 1975, Brodie & Sharma 1980). *Cyathus aurantogriseocarpus* is also similar to *C. poeppigii* since this species also has large spores (30–42 × 20–28 µm), but *C. poeppigii* has small basidiomata (7–10 mm in height × 5–6 mm in width), with paler coloured peridium, and peridioles less than 2 mm diam (Tulasne & Tulasne 1844, Brodie 1975). From the species published after Brodie (1984), *C. aurantogriseocarpus* can be compared with *C. magnomuralis* due to its large spores (28–49.5 × 23–42 µm); however, *C. magnomuralis* differs from *C. aurantogriseocarpus* by having globose to elliptical spores (slightly elliptical to elongated in *C. aurantogriseocarpus*). Additionally, *C. magnomuralis* has thick spore walls up to 6.5 µm, endoperidium with strong bright colour contrasting with the external wall colour, and smaller emplacement (3–6 mm diam) (Cruz & Baseia 2014). In the ITS phylogeny, *C. aurantogriseocarpus* groups in the same clade with *C. stercoreus* and *C. lignilantanae*; all these species possess a double-layer cortex, and spores reaching more than 20 µm diam. However, *C. stercoreus* is distinguished by the absence of striae in the peridium, inconspicuous emplacement, woolly tomentum, endoperidium with platinum bright colour, spores not exceeding 31 µm in length, and spore walls less than 2.5 µm in thickness. *Cyathus lignilantanae* has basidiomata above 7 mm in height, internal wall with platinum bright colour, peridioles with 2–2.5 × 1.5–2 mm, spores smaller than 25.5 µm in length and 17 µm in width, and with thin walls not reaching 2 µm (Martín et al. 2015).



The 50 % majority rule Bayesian tree inferred from ITS sequences with the model T92 + G using MrBayes v. 3.2.6 (Ronquist et al. 2012). A maximum parsimony analysis was done (PAUP v. 4.0a147), and similar topology was obtained (not shown). Bayesian posterior probabilities (PP) from 10 M generations, and maximum parsimony bootstrap (MPbs) support values from 10 000 replications and random addition sequences repeated 10 times, are indicated on the branches. The star (★) represents the nodes with PP = 1.00 and MPbs = 100 %. Sequences from type species are marked with asterisks (*). The new species proposed is shown in **bold**. The scale bar indicates the estimated number of nucleotide substitutions per site. Sequence alignment is available in TreeBASE (submission ID: S20237).

Colour illustrations. Brazil, environment near the locality where the type species was collected in Pitimbu district; peridium (scale bar = 2 mm); cross section showing the double-layered cortex (scale bar = 1 mm); upper view of peridioles (scale bar = 2 mm); basidiospores (scale bar = 40 µm). All from UFRN-Fungos 2798, holotype.

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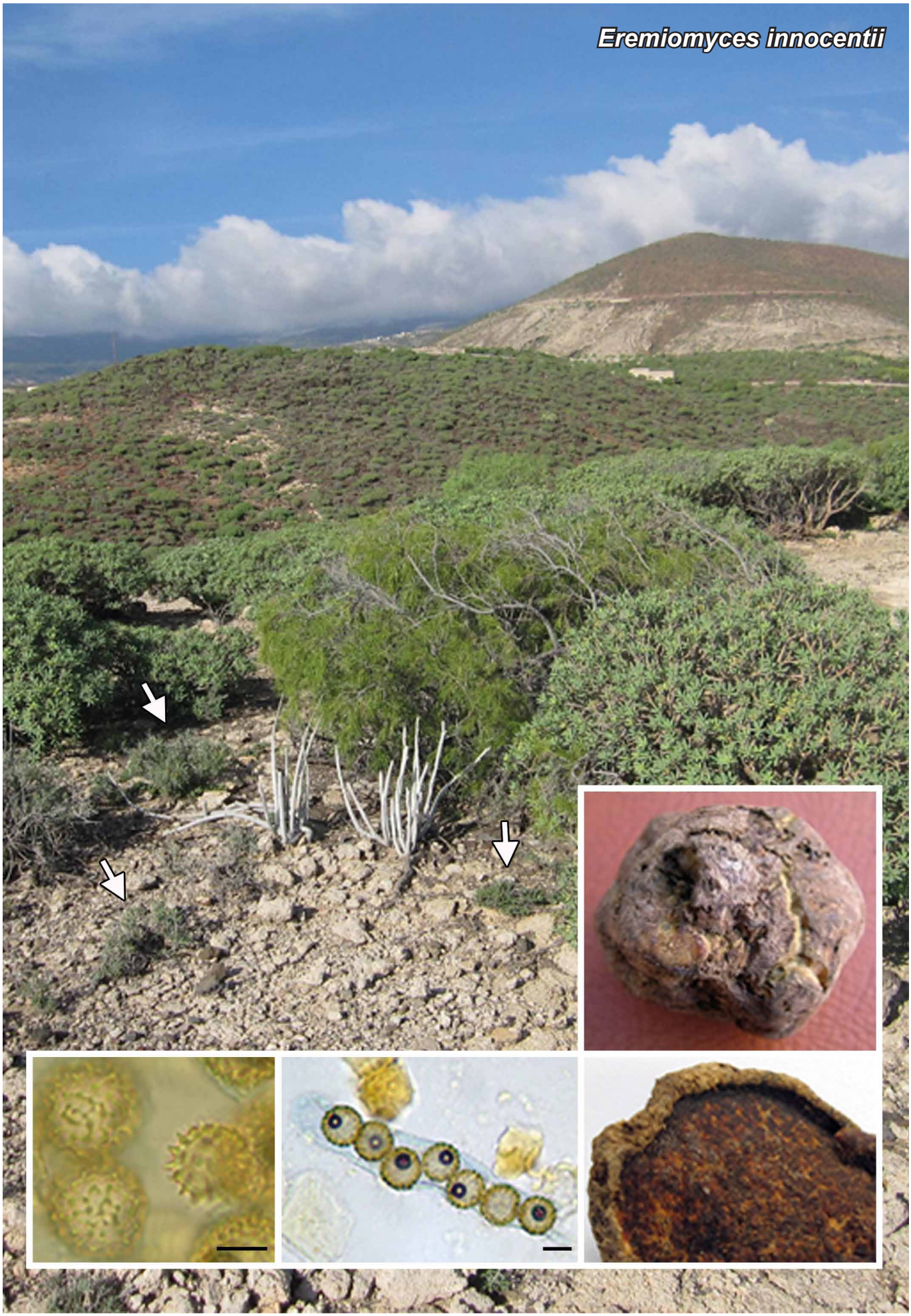

Eremiomyces innocentii

Fungal Planet 596 – 20 June 2017

Eremiomyces innocentii Ant. Rodr. & Bordallo, *sp. nov.*

Etymology. Named after Mauro Innocenti, for his outstanding contribution to knowledge of hypogeous fungi of the Canary Islands.

Classification — *Pezizaceae*, *Pezizales*, *Pezizomycetes.*

Ascomata hypogeous, 2–4 cm diam, subglobose, pale brown colour with pink spots and yellowish cracks in fresh, pale brown colour in exsiccata. *Peridium* 150–400 µm thick, well-defined, concolorous with surface in cross section, prosenchymatous, composed of parallel arranged hyphae, 15–20 µm broad, walls 1–2 µm thick, some hyphal cells inflated to 50 µm diam, yellowish in KOH. *Gleba* composed of dark red pockets of fertile tissue marbled by yellowish, sterile veins of subparallel hyphae 3–5 µm diam. *Odour* faint, not distinctive. *Asci* amyloid, thin-walled, mostly cylindrical, sometimes clavate-cylindrical, sessile or short-stipitate, 150–180(–200) × 30–40 µm, with 6–8 uniseriate spores, randomly arranged in fertile pockets. *Ascospores* globose, (16–)17–20(–21) µm diam (av. = 18.5 µm) including ornamentation, (15–)16–18(–18.5) µm (av. = 17 µm) without ornamentation, by maturity yellow and ornamented with conical, blunt spines, 1–2 µm long, 1 µm diam at the base, sometimes truncated, often joined at the base to form ridges.

Habitat & Distribution — Arid zones of Tenerife (Canary Islands), in calcareous sandy soils, associated with *Helianthemum canariense*. The annual rainfall is about 50–300 mm in the lower levels (Inframediterranean), specifically around 200 mm in the study area. Rainfall can be high in a short period of time in the case of storms from the west or the south of the islands, reaching 200 mm or more in 3–4 d.

Typus. Spain, Canary Islands, Tenerife, Fasnia, 1 Feb. 2006, *M. Innocenti* (holotype MUB Fung-j153, ITS sequence GenBank KY678905, MycoBank MB820114).

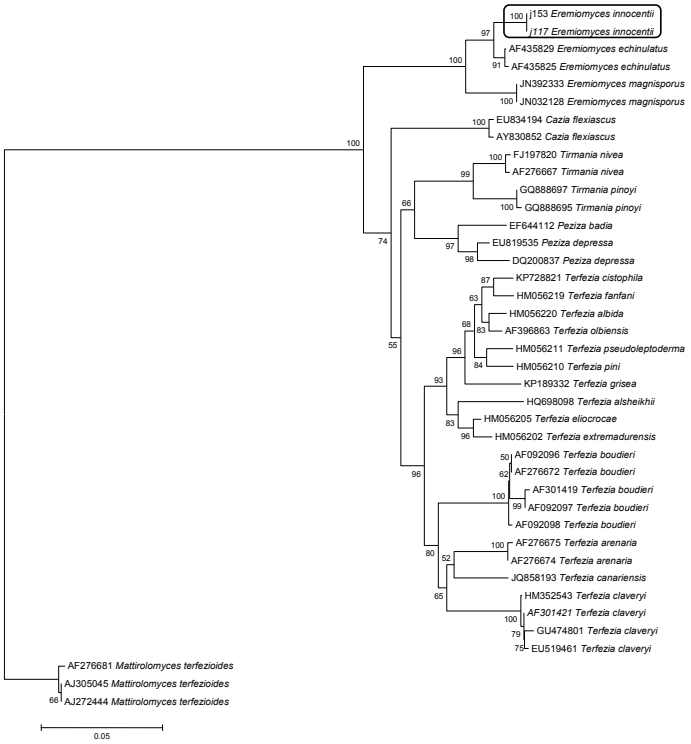
Additional specimen examined. Spain, Canary Islands, Tenerife, Fasnia, Feb. 2006, *M. Innocenti*, MUB Fung-j117.

Notes — The genus *Eremiomyces* was established by Ferdman et al. (2005) to accommodate *E. echinulatus*, a southern African desert truffle originally described as *Choiromyces echinulatus* from the Cape Province in South Africa by Marasas & Trappe (1973). The genus *Eremiomyces* has two accepted species, *E. echinulatus* also collected in the Kalahari Desert of Botswana and Namibia (Ferdman et al. 2005, Trappe et al. 2008, 2010) and *E. magnisporus*, collected in semi-arid hills around Alcalá de Henares, central Spain (Alvarado et al. 2011).

Eremiomyces innocentii is the first *Eremiomyces* species described with amyloid asci. *Eremiomyces magnisporus* was described from a single ascoma where asci could not be found due to the advanced maturity of the sample (Alvarado et al. 2011). However, it differs from all other *Eremiomyces* spp. by its amyloid asci with larger spores (16–18 µm) than *E. echinulatus* (10–14 µm) and *E. magnisporus* (14–17 µm), excluding the ornamentation.

Colour illustrations. Tenerife (Canary Islands), *Helianthemum canariense* plants (arrows); ascocarp, gleba, amyloid asci and mature ascospores. Scale bars = 10 µm.

Eremiomyces innocentii shares the same characteristics of alkaline soils and *Helianthemum canariense* as host plant with *Terfezia canariensis*, another hypogeous mycorrhizal and edible fungus known as a desert truffle. *Cistaceae* species have been associated with a high number of mycorrhizal fungal species (Bordallo et al. 2012, 2013, 2015). However, genera of *Poaceae* have been indicated as the most probable host plants for the other two species of *Eremiomyces* already described in arid (Trappe et al. 2010) and semiarid (Alvarado et al. 2011) areas. Sequence analyses of the ITS-rDNA from the examined samples resulted in a tree based on the Neighbour-Joining (NJ) method, where the two sequences of *E. innocentii* grouped together with 97 % bootstrap support, being closely related to *E. echinulatis* and *E. magnisporus*.



The evolutionary history based on the ITS-rDNA alignment was inferred using the Neighbour-Joining method. 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 tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method and are in the units of the number of base substitutions per site. All positions containing gaps and missing data were eliminated from the dataset (Complete deletion option). There was a total of 432 positions in the final dataset. Phylogenetic analyses were conducted in MEGA v. 4.

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Ganoderma mizoramense

Fungal Planet 597 – 20 June 2017

Ganoderma mizoramense Zothanzama, Blanchette, Held, C.W. Barnes, *sp. nov.*

Etymology. Named after the state of Mizoram, where it was found growing on a tree near Mizoram University in Aizawl, Mizoram, northeast India.

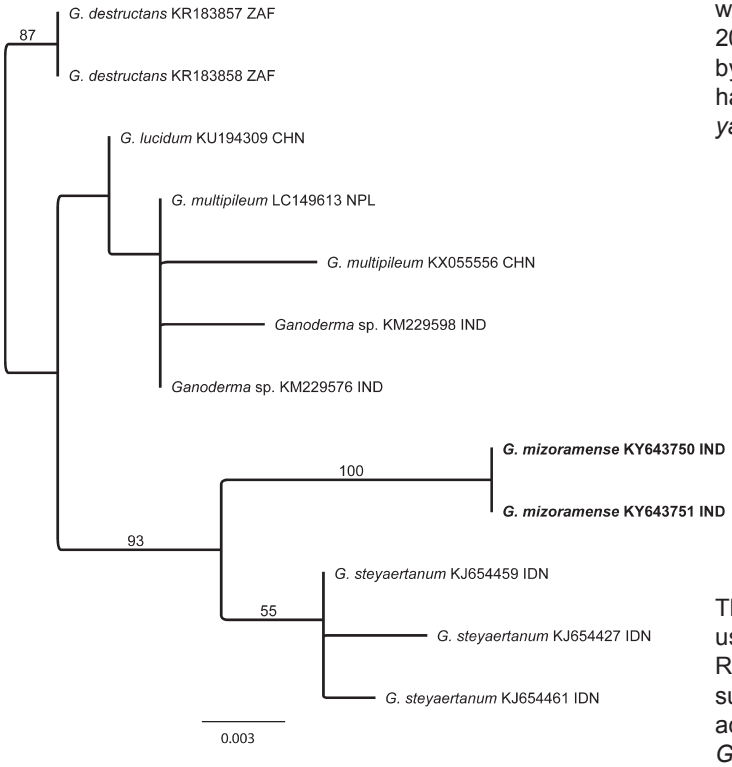
Classification — *Ganodermataceae*, *Polyporales*, *Agaricomycetes*.

Mature *basidiomata* annual, pileate, stipitate, applanate, soft and leathery when fresh and woody to corky when dried, more or less flabelliform, semi-circular, irregular surface; absence of any 'growing zones'; dark brownish to dark reddish brown, homogenous context structure 2–20 mm. *Pileus* upper surface reddish brown when fresh, liver brown when dry, surface hard and glabrous, margin white, rounded, thickened, lower surface white when fresh, pale brown when dry. *Context* uniformly ochraceous or cinnamon, firm; tubes 1–12 mm long, dark brown, not stratified. *Stipe* sometimes absent, but more commonly present and often prominent; twisted and irregular; varnished and coloured like the cap; often bearing pores. *Pore surface* smooth, creamy to snuff brown when dry, *pores* 4–5 per mm, round to somewhat slightly oval, 187–278 × 134–228 µm (av. 229 × 191 µm; SD 19, 20; n = 50), dissepiments 33–88 µm (av. 56 µm; SD 14; n = 50). *Hyphal system* trimitic, generative hyphae hyaline, slightly thicker than skeletal hyphae with clamp connections at very few places, no branching observed; skeletal hyphae most prevalent in the basidiocarp, 1.5–7 µm (av. 4.29 µm; SD 1.14; n = 50); binding hyphae hyaline and highly branched, 2–5.5 µm (av. 3.83 µm; SD 0.92; n = 50). *Basidia* tetrasterigmatic basidium. *Basidiospores* brown, ellipsoid with a truncate base, bitunicate, verruculose, 10–12.5 × 6–9 µm (av. 11.10 × 7.6 µm; SD 0.62, 0.54; n = 30). *Chlamydospores* not observed.

Culture characteristics — No live culture obtained.

Typus. India, Mizoram State, on angiosperm trees in hill country near Aizawl, Mizoram, Apr. 2016, *J.M.C. Vabeikhokhei* & *Zohmangaiha* (holotype MIN 948145, holotype ITS sequence GenBank KY643750 and LSU sequence GenBank KY747490, MycoBank MB818802).

Notes — The complete ITS sequence of the *G. mizoramense* holotype was used for the BLASTn search. The first 22 highest blast hits were to *G. steyaertanum*. The first three were downloaded for phylogenetic analysis (Glen et al. 2014). The next highest scoring other *Ganoderma* species was an isolated *G. lucidum* sequence. The *G. lucidum* sequence plus a few other isolated sequences interspersed among additional *G. steyaertanum* sequences were downloaded for phylogenetic analysis, with *G. destructans* used for the outgroup. The final alignment was edited by hand for alignment errors. Sequences were trimmed to the ITS1, after the CATTA motif (Schoch et al. 2014) and to the end of ITS2 to the CTCT/GACC motif described by Moncalvo & Buchanan (2008). *Ganoderma mizoramense* had 7 to 8 single bp differences, no gaps, from the three *G. steyaertanum* sequences included in the phylogenetic analysis.



Colour illustrations. Native trees and landscape in the Hill Country of Mizoram, India where the fungus was found on a dead tree, photo by Karlyn Eckman (background); young freshly collected basidiocarp; older basidiocarp; basidiospores by light microscopy; skeletal hyphae; Scale bars = 5 cm (basidiocarps), 10 µm (microscopic structures).

The phylogenetic tree with *G. mizoramense* was constructed using the Maximum Likelihood plugin PHYML in Geneious R9 (http://www.geneious.com; Kearse et al. 2012), and the substitution model determined by jModelTest (Posada 2008) according to Corrected Akaike Information Criterion (AICc). *Ganoderma destructans* (KR183857 and KR183858) is the outgroup. Bootstrap support values ≥ 50 % are given above branches. The phylogenetic position of *G. mizoramense* is indicated in **bold**. The *Ganoderma* species is followed by the sample ID and country code, in order of appearance: ZAF = South Africa; CHN = China; NPL = Nepal; IND = India; IDN = Indonesia.

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Gyroporus pseudocyanescens

Fungal Planet 598 – 20 June 2017

Gyroporus pseudocyanescens G. Moreno, Carlavilla, Heykoop, Manjón & Vizzini, *sp. nov.*

Etymology. Name reflects its morphological similarity to *Gyroporus cyanescens*.

Classification — *Gyroporaceae*, *Boletales*, *Agaricomycetes*.

Pileus 4–10 cm diam, at first more or less hemispherical, then becoming convex to applanate convex, sometimes depressed at centre, the surface velutinous, dry, strawish cream to yellow cream, often cracking at maturity becoming more or less brownish to brown yellowish; *context* in pileus whitish, staining strongly dark blue or blue indigo when bruised or cut, this colour being retained in drying and in some herbarium specimens; *margin* straight and regular, somewhat exceeding. *Tubes* short, 5–10 mm in length, free, sometimes emarginated towards the stipe, whitish; *pore surface* concolorous with the tubes when young, at maturity yellowish, very small, circular to angular at maturity, 1–2 per mm. *Stipe* 5–9 × 1.5–2.5 cm, cylindrical to clavate, brittle, developing cavities or becoming hollow at maturity, concolorous with the pileus, with a pseudoannular zone in the upper part where it is paler and smooth, becoming more or less yellowish brown at maturity; *context* in stem whitish, staining dark blue or blue indigo when bruised or cut, less obvious than in the pileus. *Odour* and *taste* not distinctive. *Spore-print* yellowish. *Spores* 8–11 × 4.5–6(–6.5) µm, (av. 9.5 × 5.3 µm, $Q_{av.}$ = 1.75–1.85), cylindrical-ellipsoid to ellipsoid in face view, some of them suballantoid in side view, with strong hilar appendage, without germ-pore, hyaline to yellowish; under the SEM, spores lack any ornamentation. *Basidia* 4-spored, 35–43 × 10–14 µm, sterigmata up to 5.5 µm long, clavate, hyaline. *Cheilocystidia* difficult to observe in dried material, 35–55 × 7–10 µm fusiform, with encrustations at the apex. *Pleurocystidia* infrequent, similar to cheilocystidia. *Caulocystidia*, 50–80 × 8–12 µm, cylindrical with tapering apex. *Pileipellis* a cutis consisting of cylindrical septate hyphae, with obtuse apex, 50–80 × 9–15 µm, slightly yellowish and slightly encrusted. *Clamp connections* present in all tissues.

Typus. Spain, Guadalajara, Campillo de Ranas, in humus of *Quercus pyrenaica*, 28 June 2015, *A. Bernal* (holotype AH 55729, ITS and LSU sequences GenBank KY576808 and KY576806, MycoBank MB819875).

Additional specimens examined. ***Gyroporus pseudocyanescens***: Spain, Coruña, Fragas del Eume, in humus of *Quercus robur*, 10 Nov. 2009, *G. Moreno* (paratype AH 45840, ITS, LSU sequences GenBank KY576809, KY576807). ***Gyroporus ammophilus***: Spain, Pontevedra, Cangas de Morrazo, in littoral dunes with *Pinus pinea*, autumn 2000, *D. Cereijo & J. Parcero*, AH 45842, ITS, LSU sequences GenBank KX869876, KX869890; Girona, Les Dunes, Torroella de Montgrí, Baix Empordà, in littoral dunes with *P. pinea* and *P. pinaster*, 5 Nov. 2000, *M.A. Pérez de Gregorio & J. Carbó*, AH 45843, ITS, LSU sequences GenBank KX869877, KX869891; Coruña, Cabañas, in sandy pine forests of *P. pinaster*, 8 Nov. 2008, *Sociedad Micológica Pan de Raposo*, AH 45814, ITS, LSU sequences GenBank KX869878, KX869892. ***Gyroporus castaneus***: Spain, Cáceres, Jarandilla de la Vera, in sandy pine forest of *P. pinaster*, 9 Oct. 2007, *C. Gelpi*, *J. Muñoz*, *M. Lizárraga & G. Moreno*, AH 45844, ITS, LSU sequences GenBank KX869874, KX869888; Ávila, Piedrahita, in sandy pine forest of *P. pinaster*, 4 Oct. 2010, *L. González*, AH 45841, ITS, LSU sequences GenBank KX869875, KX869889. ***Gyroporus cyanescens***: Spain, Asturias, 16 Nov. 1973, *Sociedad Micológica Aranzadi*, AH 535, ITS, LSU sequences GenBank KX869879, KX869893; Coruña, Berdoias, Vimianzo, in humus of *Castanea sativa*, 18 Aug. 2009, *J.M. Castro-Marcote*, PR1080809636, duplo in AH 46009, ITS, LSU sequences GenBank KY576810, KY576811. ***Gyroporus pseudolacteus***: Spain, Segovia, Coca, in humus of *P. pinaster*, 18 Nov. 2011, *Sociedad Micológica Madrid*, holotype AH 39364, ITS, LSU sequences GenBank KX869866, KX869880; Segovia, in humus of *P. pinaster*, 25 Oct. 1997, *A. Sánchez* (paratype AH 45848, ITS, LSU sequences GenBank KX869867, KX869881); Segovia, Muñoveros, in humus of *P. pinaster*, 26 Oct. 1997, *G. Moreno & J. Díez* (paratype AH 45849, ITS, LSU sequences GenBank KX869868, KX869882); ibid., 25 Oct. 1998 (paratype AH 45811, ITS, LSU sequences GenBank KX869869, KX869883); Cáceres, Pinar de la Bazagona, Malpartida de Plasencia, in humus of *P. pinaster*, 7 Nov. 1999, *C. Gelpi* (paratype AH 45812, ITS, LSU sequences GenBank KX869870, KX869884); ibid., 7 Oct. 2007 (paratype AH 45850, ITS, LSU sequences GenBank KX869871, KX869885); ibid., 10 Nov. 2009 (paratype AH 37878, ITS, LSU sequences GenBank KX869872, KX869886); Segovia, Coca, in humus of *P. pinaster*, 30 Oct. 2014, *J. de Frutos* (paratype AH 44522, ITS, LSU sequences GenBank KX869873, KX869887). ***Gyroporus sulfureus***: Russia, Umpyr, Krasnodarskiy, Caucasus Nature Reserve, on the ground of mixed forest (*Picea*, *Abies*, *Carpinus*, 1200 m, N43°48'00" E40°38'00", 13 Aug. 1976, *L. Pihlik & M. Vaasma* (TAAM095146 holotype).

Colour illustrations. Guadalajara, Campillo de Ranas, in humus of *Quercus pyrenaica*, where the holotype was collected; upper face and underside of basidiomata and longitudinal section of stipe; hymenium clamped basidiole; 4-spored basidia and basidioles; spores under LM, smooth lacking germ-pore and with strong hilar appendage; spores under SEM (holotype AH 55729). Scale bars = 1 cm (basidiomata), 10 µm (basidiole, basidia, spores under LM), 2 µm (spores under SEM).

Notes — *Gyroporus pseudocyanescens* is morphologically characterised by its medium size, the stipe length more or less similar to pileus diameter, the yellowish basidiomata staining deep indigo blue when handled or bruised, and by fruiting on acid soil under different deciduous *Quercus* species.

In our phylogeny (MycoBank supplementary data), *Gyroporus pseudocyanescens* belongs to a clade together with *G. cyanescens*, *G. lacteus*, *G. pseudolacteus*, *G. ammophilus* and *G. castaneus*. The closest species to *G. pseudocyanescens* is *G. cyanescens*, which should be considered a complex of cryptic species (Vizzini et al. 2015). These authors typified *G. cyanescens* by selecting Bulliard's plate 369 (Bulliard 1788) as a lectotype (iconotype) and a collection from Italy under *Pinus sylvestris* as an epitype. Sequences of *G. cyanescens* have been deposited in GenBank. *Gyroporus pseudocyanescens* and *G. cyanescens* seem to be sibling species which are difficult to separate only based on morphology. *Gyroporus lacteus* differs from *G. pseudocyanescens* by its whitish pileus covered by large and irregular scales, and by fruiting in Mediterranean woods with *Pinus pinea* and *Quercus ilex*. *Gyroporus pseudolacteus* differs from *G. pseudocyanescens* by its larger size, longer stipe in relation to the pileus diameter (up to 1.5–2 times longer) and by fruiting under *Pinus pinaster*. *Gyroporus ammophilus*, a species linked to *Pinus* species growing in littoral areas on sandy calcareous soils (Castro & Freire 1995), differs from *G. pseudocyanescens* by its slightly pinkish to salmon coloured context staining light blue when handled or bruised (Muñoz 2005). According to our molecular studies it must be considered an autonomous species. *Gyroporus castaneus* differs from *G. pseudocyanescens* by its chestnut-brown pileus and white context not blueing when handled or bruised. *Gyroporus sulfureus*, known only from the type material (Kalamees 1989), is considered to be a synonym of *G. cyanescens* (Muñoz 2005). We have attempted to sequence this species (holotype) but have not succeeded, so no conclusion on the former can be drawn.

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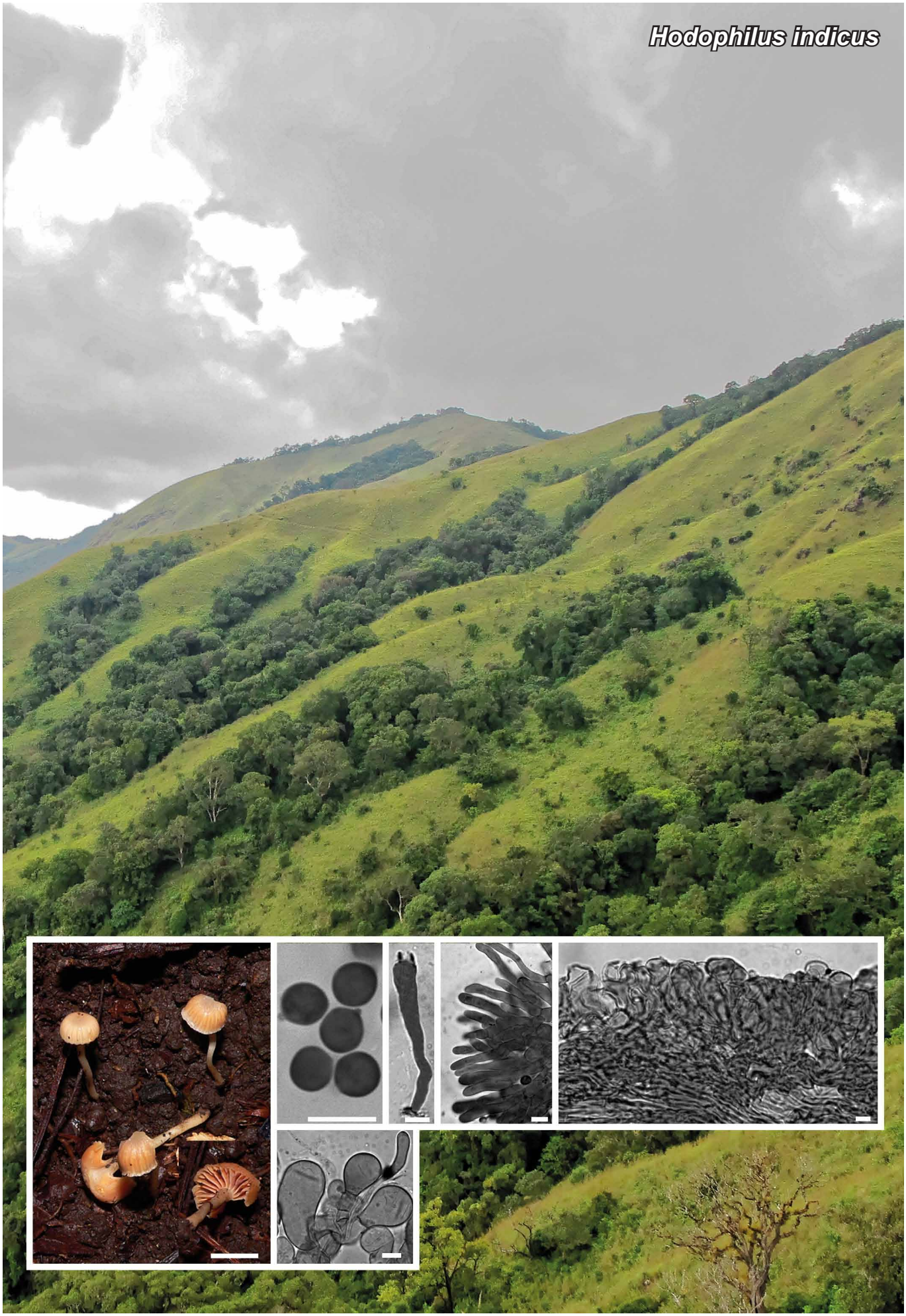
Hodophilus indicus

Fungal Planet 599 – 20 June 2017

Hodophilus indicus K.N.A. Raj, K.P.D. Latha & Manim., *sp. nov.*

Etymology. Name refers to India, the country where this species was first discovered.

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

Basidiocarps small, somewhat omphalinoid. *Pileus* 6–13 mm diam, hemispherical to convex with a very shallow central depression; surface greyish brown (6D3/OAC773) at the centre and on the striations, and brownish orange (6C5/OAC653) elsewhere, strongly hygrophanous and becoming paler soon after collection, finely pellucid-striate, somewhat tacky when wet, smooth or occasionally finely appressed-squamulose at the centre, somewhat plicate towards the margin; margin incurved when young, becoming decurved or slightly reflexed with age, crenate or somewhat wavy. *Lamellae* 16–18, arcuate-subdecurrent, rather waxy, moderately close, pale orange (6A4, 6A5/OAC655), up to 4 mm wide, with lamellulae in 1–3 tiers; edge entire to the naked eye, finely torn under a lens, concolorous with the sides. *Stipe* 12–26 × 1.5–3.5 mm, central, terete, equal, rather flexuous, solid; surface greyish orange (6B3/OAC633) all over, glabrous to the naked eye, weakly pruinose all over under a lens, somewhat tacky when wet; base with scanty basal mycelium. *Odour* and *taste* not distinctive. *Basidiospores* 4–5 × 3–5 (4.57 ± 0.37 × 4.17 ± 0.45) µm, Q = 1.0–1.66, Qm = 1.11, subglobose to globose, smooth, thin-walled, hyaline, inamyloid, hilar appendage up to 1 µm. *Basidia* 32–46 × 4–7 µm, narrowly clavate, often tapered and flexuous towards the base, pale yellow, thin-walled, 4-spored; sterigmata up to 4 µm long. *Basidioles* 29–45 × 3–6 µm, cylindrical to narrowly clavate, often flexuous, thin-walled, pale yellow. *Pleurocystidia* absent. *Lamella-edge* sterile with crowded marginal cells. *Marginal cells* 14–48 × 3–8 µm, cylindrical or flexuous, occasionally septate, hyaline, thin-walled. *Lamellar trama* subregular to somewhat irregular; hyphae 2–16 µm wide, thin-walled, hyaline or pale yellow, inamyloid. *Subhymenium* poorly developed. *Pileus trama* parallel interwoven; hyphae 3–12 µm wide, thin-walled, hyaline, inamyloid. *Pileipellis* a hymeniderm with diverticulate elements; hyphae 3–10 µm wide, thin-walled, hyaline; terminal elements 12–32 × 10–16 µm, diverticulate, broadly clavate or inflated-clavate, thin- to slightly thick-walled, hyaline. *Stipitipellis* a cutis disrupted by patches of ascending or erect, somewhat diverticulate caulocystidia; hyphae 3–7 µm wide, thin- to slightly thick-walled, hyaline or with a pale-yellow wall pigment. *Caulocystidia* multiseptate, terminal elements 14–88 × 4–8 µm, cylindrical-flexuous, clavate, obtuse or at times with apical constrictions, thin- to slightly thick-walled, inamyloid. *Clamp connections* not observed on any hyphae.

Habit, Habitat & Distribution — In small groups, on humus-rich soil. Known only from the type locality in Kerala State, India.

Typus. India, Kerala State, Wayanad District, Tirunelli, Brahmagiri Hill, from a shola forest of rolling shola grasslands of Western Ghats, 17 Nov. 2010, *K.N. Anil Raj* (holotype CAL 1526, ITS and LSU sequences GenBank KY807130 and GenBank KY815097, MycoBank MB820656).

Colour illustrations. Kerala State, Wayanad District, Tirunelli, Brahmagiri Hill shola forest, type locality; basidiocarps, basidiospores, basidium, lamella-edge showing marginal cells, pileipellis, terminal elements of pileipellis. Scale bars = 10 mm (basidiocarps), 10 µm (microscopic structures).

Notes — The combination of characters such as the hymeniderm-type pileipellis composed of clavate or inflated-clavate terminal elements and the absence of clamp connections indicates that this species belongs to the genus *Hodophilus* (Adamčík et al. 2016, Birkebak et al. 2016). *Hodophilus hymenocephalus*, a species originally described from USA by Smith & Hesler (1942, as *Hygrophorus hymenocephalus*), shows similarity with *H. indicus* in having a similar-looking pileus with somewhat similar surface features, almost similar number and attachment of lamellae, similar-sized basidiospores (4–5 µm), an irregular lamellar trama and a similar pileipellis. *Hodophilus hymenocephalus*, however, is distinguished by its pale pinkish cinnamon to brown pileus, hair-brown lamellae, longer stipe (3–4 cm), a hymenium devoid of marginal cells and the geographical location. Additionally, a pairwise comparison of the ITS sequences (GenBank KY807130/DQ484066) of these two species showed only 87 % sequence similarity (with a high e-value). *Hodophilus micacea* shares a few features with *H. indicus* such as a hygrophanous pileus with somewhat similar surface features, rather similarly-attached lamellae, somewhat similar-sized basidiospores ((3.5–)4–5(–5.5) × (3–)3.5–4.5 µm), a hymenium devoid of pleurocystidia, an irregular lamellar trama, similar pileipellis and stipitipellis structure and clamped hyphae. *Hodophilus micacea*, however, differs from *H. indicus* in having slightly larger basidiomata with a dark grey-brown pileus, very distant, dark grey-brown, slightly purple-tinted lamellae with a pale brown edge, a beige-brown stipe with pruinosity confined to the apex, a weak aromatic odour, infrequent presence of ellipsoid or broadly ellipsoid basidiospores, occasional absence of cystidia on the lamella-edge, hyphae of lamellar trama with an encrusting pigment, a pileipellis with larger terminal elements (23–70 × 11–42 µm) and a stipitipellis with smaller (18–50 × 5–14 µm) and inflated-clavate terminal elements (Arnolds 1990).

A BLASTn search using the ITS (593 bp) sequence of *H. indicus* showed *H. micaceus* (GenBank KU882873; 91 % identity) as the closest hit. While using the LSU (706 bp) sequence, *Hodophilus micaceus* (GenBank KP257222; 93 % identity), a collection from Slovakia resulted as the closest hit. ML and BI analyses of the combined ITS and LSU dataset recovered two large clades designated as *Hodophilus micaceus* and *Hodophilus foetens* superclades following Adamčík et al. (2016). *Hodophilus indicus* was found nested inside the *Hodophilus micaceus* superclade with strong posterior probability (0.98 PP) and weak bootstrap support (58 % BS). Within this *Hodophilus micaceus* superclade, *H. indicus* resolved as an independent lineage well-differentiated from other species of the clade with significant support values (0.93 PP/72 % BS) (MycoBank supplementary data).

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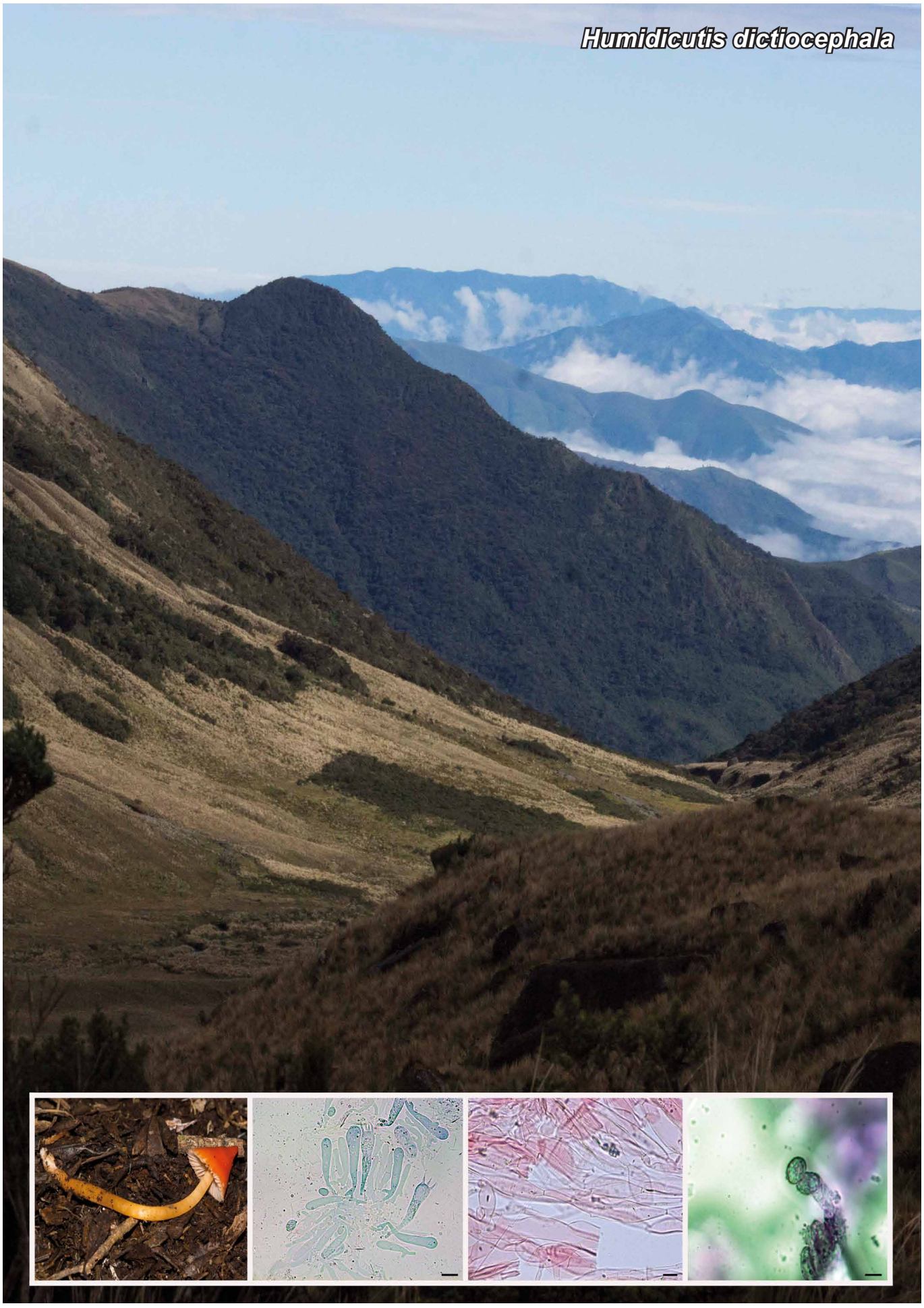

Humidicutis dictiocephala

Fungal Planet 600 – 20 June 2017

Humidicutis dictiocephala A. Barili, C.W. Barnes & Ordoñez, *sp. nov.*

Etymology. Name reflects the morphology of the pileus.

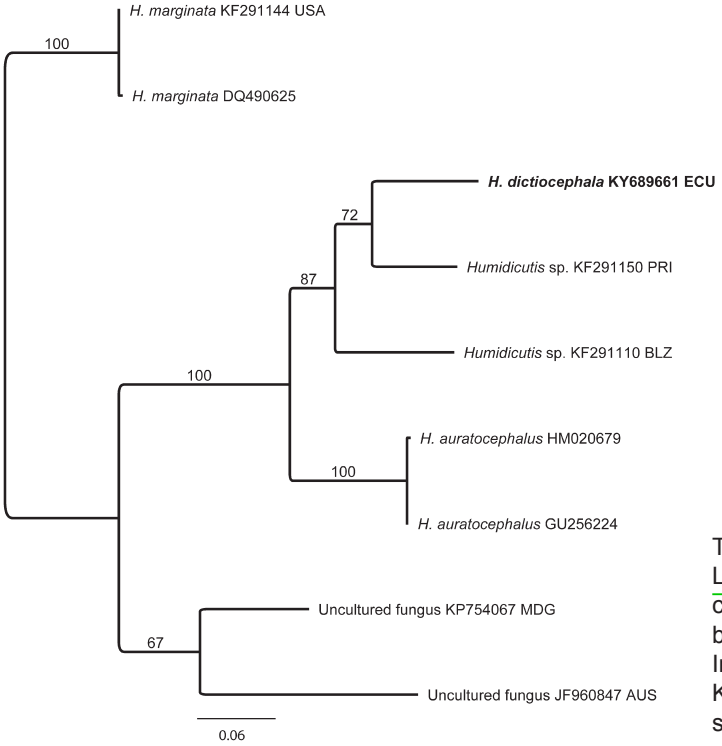
Classification — *Hygrophoraceae*, *Agaricales*, *Agaricomycetes.*

Basidiomata stipitate, pileus conical, umbonate, 20 mm high, 22 mm diam, orange, velvety-rough surface, radially fibrillose, margin rimose. No distinct *odour* or *taste*. *Lamellae* emarginate, thick, waxy, pale orange to whitish, anastomosed, subdistant, with lamellae present, smooth margin. *Stipe* central, 80 × 5 mm, yellowish at the apex, pale orange at the base, hollow, smooth, dry. *Pileipellis* as cutis with cylindrical parallel hyphae, clamp connections absent. *Lamellar trama* irregular to subregular. *Basidia* 36.5–54 × 6–10.5 µm, elongate, clavate, tetrasporic, toruloid clamp connections at the base, sterigmata 5.5–9 µm long. *Basidiospores* 6.5–9 × 4.5–6 µm, ellipsoid, subcylindrical, smooth with subtle wall, hyaline, non-amyloid, non-dextrinoid, not metachromatic, without germ pore, apiculate.

Habit — Solitary, on the ground, high montane forest.

Typus. Ecuador, Zamora Chinchipe province, Yacuri National Park, alt. 3 234 m, May 2015, *C. Vivanco* (holotype QCAM6000, ITS and LSU sequences GenBank KY689661 and KY780120, MycoBank MB820098, TreeBASE Submission ID 20678).

Notes — According to the description of Young (1999), *Humidicutis dictiocephala* belongs to the subgenus *Humidicutis*. However, the combination of observed characters does not lead to a species identification. Horak's (1990) key for *Humidicutis* indicates *H. conspicua* as the closest species, but it differs from *H. dictiocephala* by having a fibrillose, dry pileal surface, margin whole, lamellae not bright orange but whitish in colour, and larger basidia and basidiospores. The description of Lodge et al. (2014) places *H. dictiocephala* within the genus *Humidicutis*, differing from the closely related *Porpolomopsis* by the short hyphae of the lamellar trama and by the adnate lamellae. The complete ITS sequence of 571 bp of the *H. dictiocephala* holotype was used for the BLASTn search. Phylogenetic analysis was done using representative sequences from the top BLASTn hit species. The results gave the two highest scores as *Humidicutis* sp. from Belize (GenBank KF291110), and from Puerto Rico (GenBank KF291150) reported by Lodge et al. (2014). Following the *Humidicutis* sp. in the BLASTn search results were 11 sequences of *Hygrocybe auratocephalus*, but only two representative sequences were used for the sequence alignment. Finally, we included sequences from two uncultured fungal clones, both ectomycorrhizal, and two sequences of *Humidicutis marginata* for the outgroup.



Colour illustrations. Ecuador, Yacuri National Park; basidiocarp, lamellar trama, basidia and basidiospores. Scale bars = 10 µm.

The phylogenetic tree was constructed using the Maximum Likelihood plugin PhyML in Geneious R9 (http://www.geneious.com; Kearse et al. 2012), and the substitution model determined by jModelTest (Posada 2008) according to Corrected Akaike Information Criterion (AICc). *Humidicutis marginata* (GenBank KF291144 and DQ490625) was chosen as outgroup. Bootstrap support values ≥ 50 % are given above branches. The phylogenetic position of *H. dictiocephala* is indicated in **bold**. The species name is followed by the GenBank ID, and where known, the country of origin indicated as: USA = United States; ECU = Ecuador; PRI = Puerto Rico; BLZ = Belize; MDG = Madagascar; AUS = Australia.

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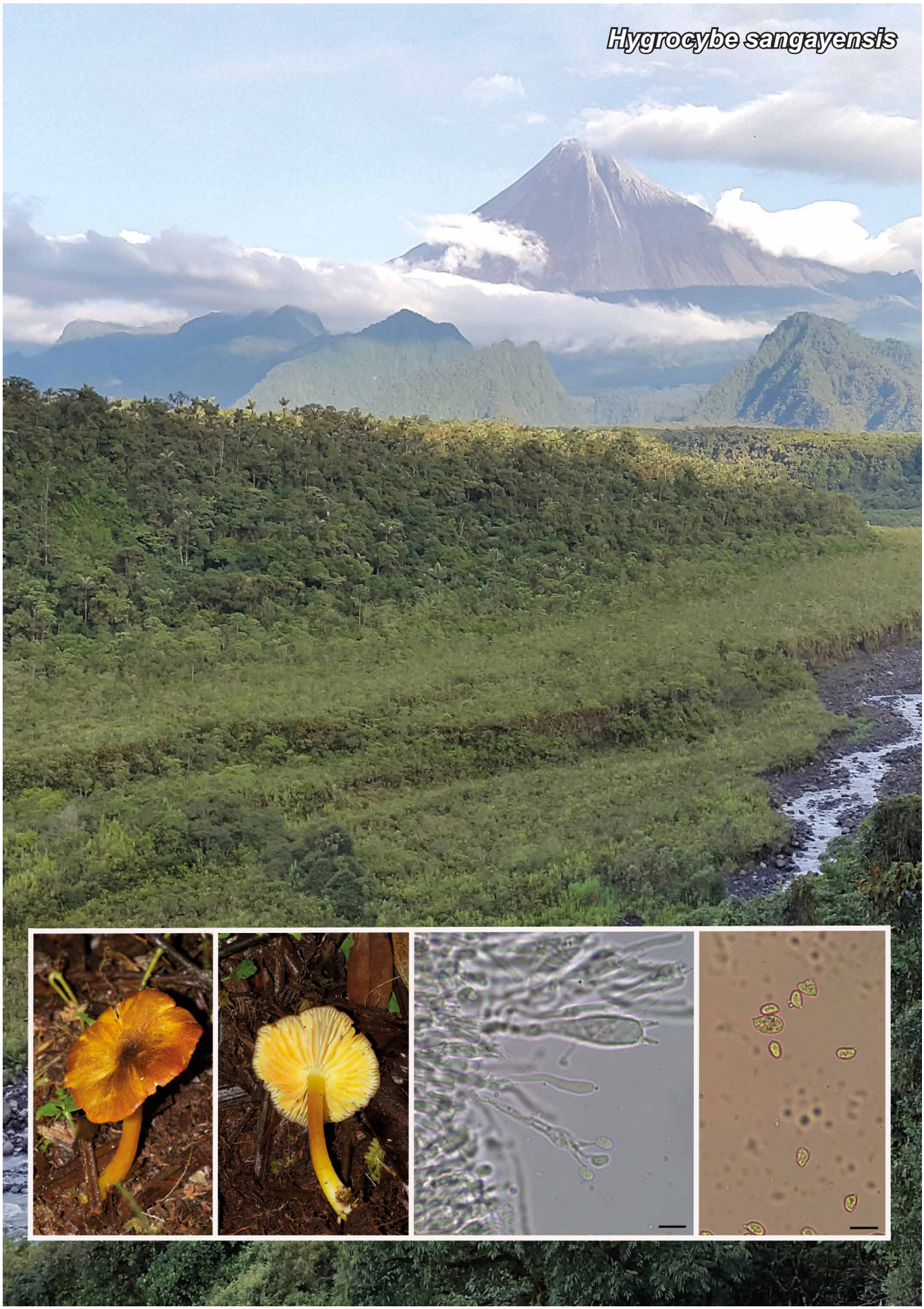

Hygrocybe sangayensis

Fungal Planet 601 – 20 June 2017

Hygrocybe sangayensis A. Barili, C.W. Barnes, J.A. Flores & Ordoñez, *sp. nov.*

Etymology. Name reflects the locality from where the fungus was collected, Sangay National Park.

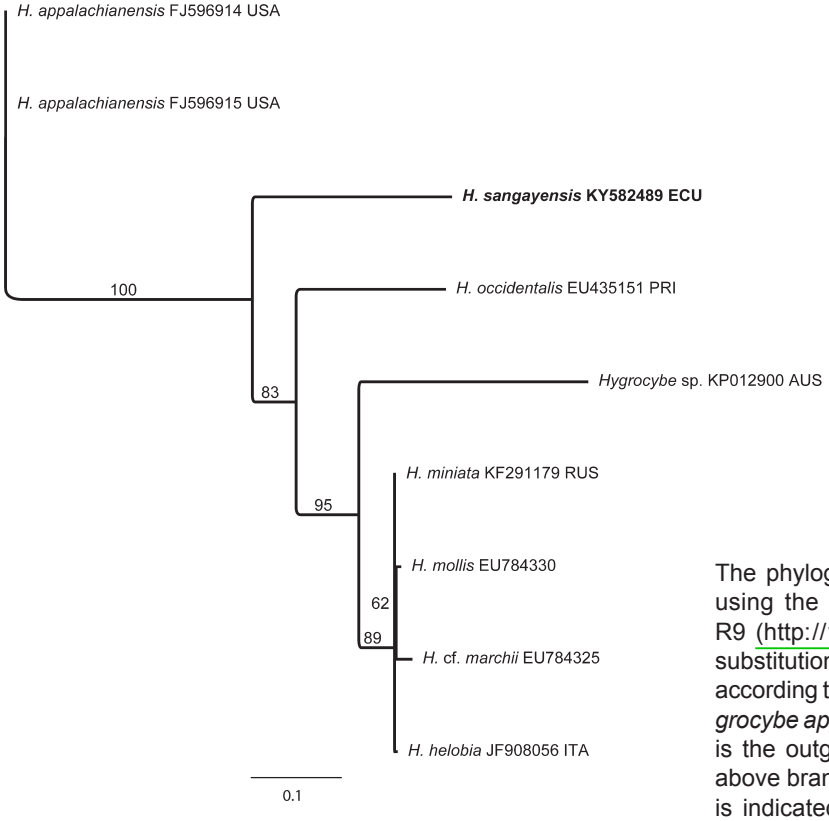
Classification — *Hygrophoraceae*, *Agaricales*, *Agaricomycetes.*

Basidiomata stipitate, pileus flat, 50 mm diam, slightly depressed in the centre, margin smooth, slightly lobate, rimose, dry surface, covered by small dark brown scales, more concentrated towards the centre and dissociating towards the margin, fibrillose. Orange yellowish, slight to fleshy texture, fragile, flesh whitish yellow, with no colour changes upon mechanical injury. No distinct *odour* or *taste*. *Lamellae* adnate to unicate, thick, ventricose, smooth margin, whitish yellow to orange towards the margin, pruinose, with 3–7 lamellae in between. *Stipe* central, 70 × 8–9 mm, yellow at the apex, orange at the centre and yellow to whitish at the base, hollow, fragile. *Pileipellis* filamentous as a cutis to subtrichoderm, elongated hyphae 57 × 14 µm with septa and bifurcations, *clamp connections* present, non-differentiated pileocystidia. *Gill trama* parallel to subregular. *Macrobasidia* 49 × 12 µm, 2- and 4-spored, clavate, elongate, multiguttulate, sterigmata 5.5–10 µm. *Microbasidia* 45 × 7.5 µm 2-, 3- and 4-spored, clavate, elongate, similar to macrobasidia but much narrower, guttulate, sterigma – 8.5 µm. *Macrospores* 12 × 7.5 µm, cylindrical to ellipsoid, sometimes depressed in the centre, smooth, hyaline, non-amyloid, apiculate. *Microspores* 6.5 × 4.5 µm, cylindrical to ellipsoid, sometimes depressed in the centre, smooth, hyaline, non-amyloid, apiculate. *Cheilocystidia* 45.5 × 10 µm, pleurocystidia mucronate to lageniform 39.5 × 6.5 µm.

Habitat — Solitary, on the ground among leaf litter, foothill forest.

Typus. Ecuador, Morona Santiago province, Sangay National Park, alt. 1 510 m, Jan. 2015, *C. Vivanco* (holotype QCAM4254, ITS-LSU sequence GenBank KY582489, MycoBank MB819814).

Notes — According to the description of Pegler & Fiard (1978), *H. sangayensis* belongs to the section *Firmae*, with *H. occidentalis* as the closest species based on morphological characters. However, it differs by having a scaly pilial surface, non-glabrous, non-translucent, non-striated, with the lamellae margin non-heterogeneous. The complete ITS sequence of the *H. sangayensis* holotype was used for the BLASTn search. The results gave the highest score to a *Hygrocybe* sp. (GMB-2014, GenBank KP012900) from Australia, but with only 44 % coverage and 87 % identity. The top seven BLASTn hit species with full ITS sequences were downloaded for the phylogenetic analysis. There were significant indels among the aligned sequences. Noting gaps greater than five bases, ITS1 showed gaps of 7, 13, 6 and 10 bases, and ITS2 had gaps of 16, 6, 6 and 9 bases.



Colour illustrations. Ecuador, Sangay National Park (photo credit S. Ron); basidiocarps; macrobasidia and microbasidia; macrobasidiospores and microbasidiospores. Scale bars = 10 µm.

The phylogenetic tree with *H. sangayensis* was constructed using the Maximum Likelihood plugin PhyML in Geneious R9 (http://www.geneious.com; Kearse et al. 2012), and the substitution model determined by jModelTest (Posada 2008) according to Corrected Akaike Information Criterion (AICc). *Hygrocybe appalachianensis* (GenBank FJ596914 and FJ596915) is the outgroup. Bootstrap support values ≥ 50 % are given above branches. The phylogenetic position of *H. sangayensis* is indicated in **bold**. The *Hygrocybe s*pecies is followed by the GenBank ID, and where known, the country of origin, in order of appearance: USA = United States; ECU = Ecuador; PRI = Puerto Rico; AUS = Australia; RUS = Russia; ITA = Italy.

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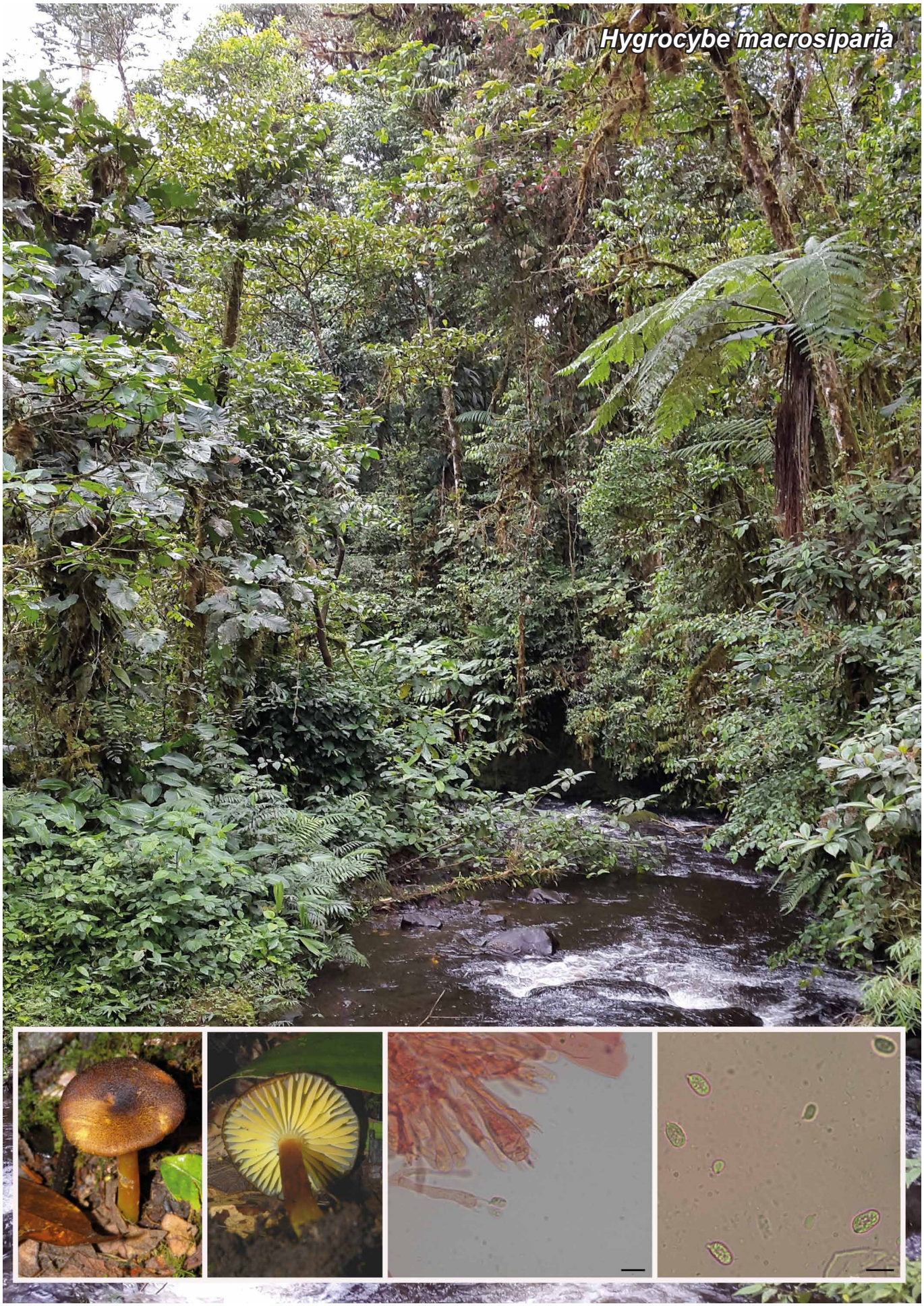

Hygrocybe macrosiparia

Fungal Planet 602 – 20 June 2017

Hygrocybe macrosiparia A. Barili, C.W. Barnes, J.A. Flores & Ordoñez, *sp. nov.*

Etymology. Name reflects the morphological similarity to *Hygrocybe siparia*, but with reference to its larger size.

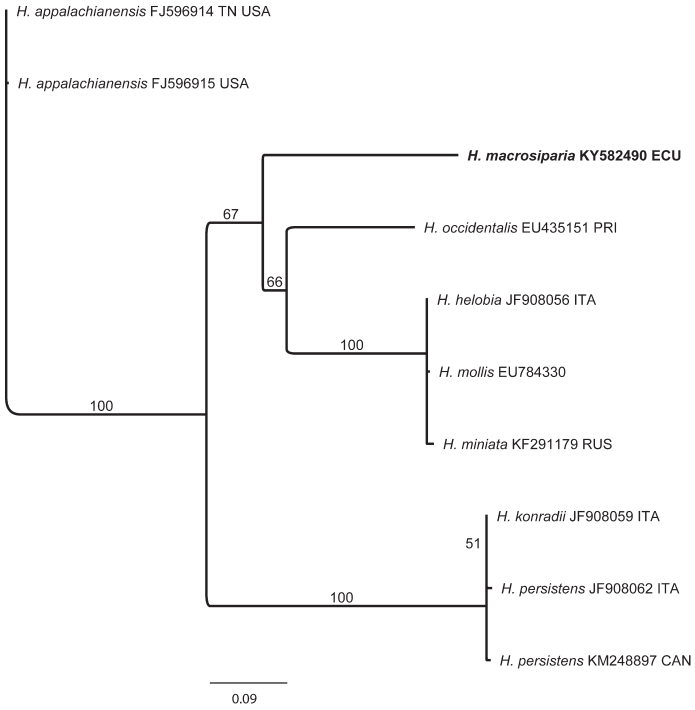
Classification — *Hygrophoraceae*, *Agaricales*, *Agaricomycetes.*

Basidiomata stipitate, pileus flat, 25 mm diam, margin smooth, involute, surface dry, covered by dark brown scales, more concentrated towards the centre and dissociating towards the margin, orange yellowish, slight fleshy texture, with no colour changes upon mechanical injury. No distinct *odour* or *taste*. *Lamellae* adnate, distant, with one lamella in between, thick, ventricose, smooth margin, yellow, lighter in colour towards the margin. *Stipe* central, 70 × 5 mm, yellow at the apex and base, orange at the centre, the orange pigment is distributed in striae parallel to the stipe, cylindrical, hollow, fragile. *Pileipellis* as a cutis subtrichoderm, hyphae 70 × 22.5 µm. *Gill trama* parallel. *Macrobasidia* 51.5 × 13.5 µm, 2- and 4-spored, clavate, elongate, guttulate, sterigmata 6.5 µm. *Microbasidia* 41.5 × 7 µm, 4-spored, clavate, elongate similar to macrobasidia but much more narrow, non-guttulate but if present sparse, sterigmata 6 µm. *Macrospores* 10.5 × 6.5 µm, cylindrical to ellipsoid, sometimes depressed in the centre, smooth, hyaline, non-amyloid, apiculate. *Microspores* 7 × 4.5 µm, cylindrical to ellipsoid, sometimes depressed in the centre, smooth, hyaline, non-amyloid, apiculate. *Cheilocystidia* and *pleurocystidia* absent. *Clamp connections* present.

Habitat — Solitary, on the ground among leaf litter, foothill forest.

Typus. Ecuador, Morona Santiago province, Sangay National Park, alt. 1 524 m, Jan. 2015, *A. Salazar* (holotype QCAM4359, ITS-LSU sequence GenBank KY582490, MycoBank MB819896).

Notes — According to the description of Pegler & Fiard (1978), *H. macrosiparia* belongs to the section *Firmae*. The closest species based on morphological characters is *H. siparia*. However, it differs by having a flat and non-umbilicate pileus which exceeds in 5 mm the maximum size reported, and an orange yellowish colour instead of crimson. The complete 578 bases of ITS sequence of the *H. macrosiparia* holotype was used for the BLASTn search. The results gave the highest score to a *H. occidentalis* (PR-6493, GenBank EU435151) from Puerto Rico, but with only 63 % coverage and 87 % identity. The top seven BLASTn hit species were downloaded for phylogenetic analysis. There were significant indels among the aligned sequences. Noting gaps greater than five bases, ITS1 showed gaps of 10, 6, 7 and 6 bases, and ITS2 had gaps of 10, 10, 6 and 6 bases.



Colour illustrations. Ecuador, Sangay National Park (photo credit S. Ron); basidiocarps; macro- and microbasidia with Congo Red; macro- and microbasidiospores. Scale bars = 10 µm.

The phylogenetic tree with *H. macrosiparia* was constructed using the Maximum Likelihood plugin PhyML in Geneious R9 (http://www.geneious.com; Kearse et al. 2012), and the substitution model determined by jModelTest (Posada 2008) according to Corrected Akaike Information Criterion (AICc). *Hygrocybe appalachianensis* (GenBank FJ596914 and FJ596915) is the outgroup. Bootstrap support values ≥ 50 % are given above branches. The phylogenetic position of *H. macrosiparia* is indicated in **bold**. The *Hygrocybe s*pecies are followed by the GenBank ID, and where known, the country of origin, in order of appearance: USA = United States; ECU = Ecuador, PRI = Puerto Rico; ITA = Italy; RUS = Russia; CAN = Canada.

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Inocybe parvicystis

Fungal Planet 603 – 20 June 2017

Inocybe parvicystis F.J. Rodr.-Campo & Esteve-Rav., *sp. nov.*

Etymology. From Latin *parvus* and *cystidium*, referring to the small size of cystidia.

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

Basidiomata agaricoid and stipitate. *Pileus* 15–40 mm, convex to plano-convex, not or hardly umbonate, not or very slightly hygrophanous; margin deflexed to straight, often wavy with age, in young basidiomes often showing appendiculate rests of the velipellis; colour initially very pale, cream whitish (Mu 7.5Y 9/2), then yellow ochraceous (Mu 10YR 6/6) or pale yellowish brown (Mu 7.5Y 8/4), in old or washed specimens often becoming copperish yellow to orange yellow (Mu 7.5YR 3/6), often paler at the centre or in areas where velipellis is present; surface smooth, becoming radially fibrillose at margin but never rimose, often agglutinating soil remains, when young covered by white to greyish velipellis, often persisting in old specimens, especially towards the centre. *Lamellae* rather crowded (L = 36–44), adnexed to emarginate, ventricose, with lamellulae (l = 1–2), initially pale grey to beige, then yellowish brown with a faint olivaceous reflection at maturity, edge whitish to concolorous, crenulate. *Stipe* 35–55 × 5–8 mm, straight to curved towards base, cylindrical with a bulbous to abruptly bulbous base, less often subbulbous or clearly marginate bulbous, bulb 8–10.2 mm wide; colour whitish (Mu 7.5Y 9/2), ochraceous (Mu 10YR 6/6) or even yellowish brown (Mu 7.5Y 8/4) in old basidiomes, often concolorous to pileus in aged specimens, especially towards base; surface sparsely fibrillose, fibrillose-pruinose towards the apex (descending to 1/6–1/4, rarely –1/3), sometimes covered by abundant fibrillose veil towards the lower half in young basidiomes. *Context* fibrose, whitish, unchanging. *Smell* slightly spermatic, *taste* slightly raphanoid. *Spores* (7.5–)8–9–10 (–11.5) × (4.5–)5–5.5–6(–6.5) µm, Qm: 1.25–1.6–2 (n = 165), smooth, yellowish, ellipsoid to mostly amygdaliform to rhomboid with subogival apex, most often showing a typical 'callus' or sometimes a small and distinct germ pore at the apex, walls –0.5 µm thick. *Basidia* (25.5–)27–31.5–36.5(–46.5) × (6.5–)8–9–10(–12.5) µm (n = 32), (2–)4-spored, clavate. *Lamella edge* practically sterile, composed by numerous cheilocystidia and more or less common clavate to pyriform paracystidia, hyaline to yellowish in some specimens. *Cheilocystidia* very numerous, not protruding, narrow, (30.5–)34–43–46(–54.5) × (8–)8.5–9.5–11.5(–12.5) µm (n = 41), cylindrical, subfusiform or subclavate, often attenuate pedicellate towards base and with sinuose outline, heavily crystalliferous at the apex, walls (1.5–)2–3 µm thick, moderately to pale to distinctly yellow in 5 % NH_4OH. *Pleurocystidia* numerous, similar to cheilocystidia, (35–)37.5–45.5–52(–56) × (7–)8.5–10–12(–13.5) µm (n = 51). *Hymenophoral trama* regular, formed by cylindrical to ellipsoidal cells, 4–20 µm wide. *Stipitipellis* a cutis bearing sparse caulocystidia at the apex (so 1/6–1/4, rarely –1/3), similar to hymenial cystidia and often broader, (34.5–)35.5–42(–43.5) × (9–)9.5–13(–15.5) µm, mostly crystalliferous, accompanied by cylindrical, sublageniform, clavate or pyriform paracystidia. *Pileipellis* a cutis formed by parallel cylindrical cells (< 6 µm) with some yellowish incrusting pigment, slightly gellified in wet condition. *Clamp connections* present in all tissues.

Habitat & Distribution — Gregarious in acidic soils under evergreen Mediterranean oaks (*Quercus ilex*, *Q. suber*), sometimes mixed with *Cistus* bushes; often found half-buried in soft or sandy soils. Known from Spain, but probably widespread in the Mediterranean in similar habitats.

Typus. Spain, Comunidad de Madrid, Madrid, Villa del Prado, 30T 039074–445661, 450 m, in humus of *Quercus ilex* subsp. *ballota* forest, in acidic soil, 29 Dec. 2014, *F.J. Rodríguez-Campo*, *A. Díaz-Fernández & J.A. Rodea-Butragueño* (holotype AH 46600, isotype PRC-141229, ITS sequence GenBank KY349121, MycoBank MB819706).

Additional specimens examined. See MycoBank MB819706.

Notes — Colour codes are taken from Munsell (1994), terminology follows Vellinga (1988) and Kuyper (1986). The presence of a well-developed velipellis, pale yellow-ochraceous colour, bulbous stipe, caulocystidia reduced to the upper 1/4 of the stipe, hymenial cystidia short, narrow, pedicellate and very crystalliferous, and spores provided with a 'pseudopore' in most cases, are distinct features of *I. parvicystis*. It grows in acidic soils in evergreen oak forests (*Quercus ilex*, *Q. suber*), often mixed with maquis (*Cistus* spp.) vegetation in the western Mediterranean areas. Among other leiosporeous species showing short cystidia and a bulbous stipe, *I. mystica* is devoid of velipellis, its colours are warmer orange-ochraceous, the spores are devoid of a germ pore and smaller (7.5–)8.5–9.4(–9.7) × (4.7–)5.2–5.7(–5.8) µm, Qm: 1.45–1.6–1.8 (n = 30), holotype measurements); it develops in frondose temperate forests in Europe (Stangl & Glowinski 1980). Kuyper (1986) considered the American species *I. cryptocystis* conspecific with *I. mystica*, but the results of our ITS analyses from both prove that, though phylogenetically closely related, they are distinct species. *Inocybe cryptocystis* (Stuntz 1954) is also devoid of a distinct velipellis and shows very short, mostly subutriform to oblong-ellipsoid cystidia, with obtuse to truncate, non-pedicellate base. The interpretation of *I. confusa* in Heim (1931), could well be referred to *I. parvicystis*; Heim's description fits the general characters of the new species, and the habitat is said to be 'Mediterranean, under evergreen oaks'; unfortunately, no voucher material has been preserved of Heim's collections.

ITS sequences of *I. parvicystis* do not seem related to those generated from *I. cryptocystis* or *I. mystica* type collections. The most closely related ITS sequences come from ectomycorrhizae studies in Californian oaks (KC791069, Taniguchi et al. 2013) and Pakistani Himalayan pine forests (KF679813, Hanif & Khalid, unpubl.). Both collections gathered under *Abies pinsapo* (AH 18898, 18899) differ from *I. parvicystis* because of their paler colour. They probably represent an independent phylogenetic lineage different from *I. parvicystis*, as the ITS sequence produced from one of them had up to 19/562 bp different from the other *I. parvicystis* samples (including 4-bp and 7-bp insertions, and a 3-bp deletion not observed in any other sequence of the latter species). Collections studied by the authors are indicated in **bold** in the phylogenetic tree for ITS sequences (see figure in MycoBank).

Colour illustrations. Spain, Madrid, Villa del Prado, open forest of *Quercus ilex* subsp. *ballota*, area where the holotype was collected; from top to bottom: basidiomata, spores, pleurocystidia, cheilocystidia, caulocystidia (all from holotype). Scale bars = 1 cm (basidiomata), 10 µm (microscopic elements).

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Keratinophyton turgidum

Fungal Planet 604 – 20 June 2017

Keratinophyton turgidum Rahul Sharma, & Shouche, *sp. nov.*

Etymology. Refers to the swollen nature of conidiogenous cells (Latin-*turgidus* means swollen).

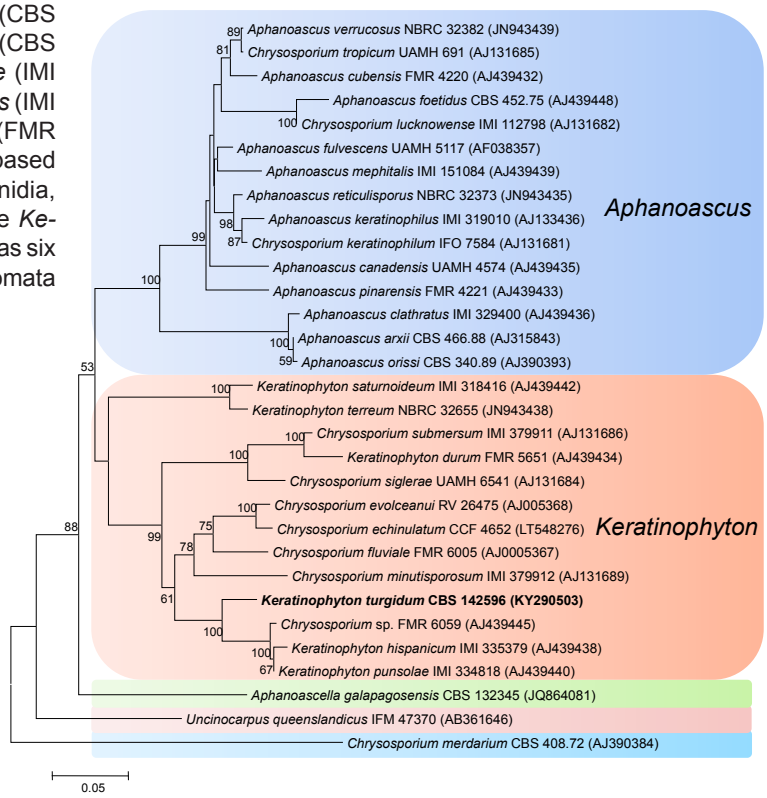
Classification — *Onygenaceae*, *Onygenales*, *Eurotiomycetes*.

Hyphae hyaline, septate, smooth-walled, 1.5–6.5 µm wide, straight, profusely branched. *Conidiophores* made up of swollen hyphae which are otherwise undifferentiated from vegetative hyphae, hyaline, unbranched, 2–18 × 1.5–2 µm. *Conidiogenous cells* non-specialised, swollen, 2.5–4 µm wide and 6.5–8.5 µm long. *Conidia* pyriform to oval, smooth-walled, terminal or lateral aleurioconidia, 5–7 × 3.5–5 µm, borne singly on mostly elongate and swollen fertile hyphae. *Conidia* have a broad basal scar, 1.5–2.5 µm diam, left after rhexolytic dehiscence from conidiophores. Intercalary conidia present, elongated barrel-shaped, 11.5 × 4.5 µm. *Chlamydospores* absent. *Racquet hyphae* present. Keratinolytic. *Sexual morph* not observed.

Culture characteristics — Colony on Sabouraud dextrose agar (SDA) at 28 °C white, circular, cottony with central area having dense sporulation (5–5.5 cm diam after 16 d), reverse pale brown with dark brown central spot. Growth at 37 °C on SDA 3.5 cm diam after 7 d of incubation.

Typus. India, Buldana, barber shop soil, 2016, *R. Sharma* (holotype MCC H-1006, cultures ex-type MS 335 = CBS 142596, ITS and LSU sequences GenBank KY290503 and KY962732, MycoBank MB819848).

Notes — An NCBI BLASTn search of ITS sequences showed closest similarity to be 95 % with *Chrysosporium indicum* (CBS 117.63, NR_145203); 94 % with *Keratinophyton terreum* (CBS 504.63, AJ439443); 93 % with *Keratinophyton punsolae* (IMI 334818, AJ439440); 91 % with *Keratinophyton hispanicus* (IMI 335379, AJ439438); 88 % with *Keratinophyton durum* (FMR 5651, AJ439434). The description of the new species is based on the morphology of its chrysosporium-like aleurioconidia, and the ITS sequence similarity which positions it in the *Keratinophyton* clade. The genus *Keratinophyton* currently has six recognised species which are all sexual and produce ascomata (Sutton et al. 2013). These species can be distinguished on the basis of morphologically different ascospores and genetically by differences in the ITS region (Cano et al. 2002, Guarro et al. 2012). Due to the one-fungus one-name concept asexual species are now placed in genera conventionally comprising only sexual forms. A recent example is the dermatophyte genus *Nannizzia* which previously comprised of species which were all sexual but now contain two asexual species, *N. duboisii* and *N. praecox* (De Hoog et al. 2016). Currently, species within a genus are recognized as entities which are phylogenetically distinct from their neighbours irrespective of whether they are sexual or asexual. Likewise, the monophyletic *Keratinophyton* clade also contains several asexual species which have a *Chrysosporium* morph, and require renaming in *Keratinophyton*. In the present case the name *Keratinophyton* is chosen to represent this new species instead of *Chrysosporium* since it is phylogenetically more distant from the type species of *Chrysosporium* (*C. merdarium*). The two species that produce smooth-walled conidia and form a monophyletic cluster with *K. turgidum* are *K. hispanicum* and *K. punsolae*. Conidia of *K. turgidum* are pyriform and smaller (5–7 × 3.5–5 µm) than those of *K. punsolae* (8.5–13 × 5.5–9 µm) but slightly larger than those of *K. hispanicum* (3.5–8 × 2–3 µm).



Neighbour-Joining phylogram of ITS sequence data using MEGA v. 5.05, showing the phylogenetic position of CBS 142596 in the *Keratinophyton* clade. Branches with bootstrap support values ≥ 50 % are shown (based on 1 000 replicates).

Colour illustrations. A village barber's shop in Maharashtra, India. Macromorphology: Colony after 15 d on SDA (5 cm diam). Micromorphology: conidia attached to swollen conidiophores, intercalary conidium, conidia formed on conidiophores on extensively branched hyphae, smaller conidia on swollen conidiophores formed when grown at 37 °C on SDA. Scale bars = 10 µm.

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Myotisia cremea

Fungal Planet 605 – 20 June 2017

Myotisia Kubátová, M. Kolařík & Hubka, *gen. nov.*

Etymology. Refers to the bat (*Myotis myotis*) on who's excrement the fungus was found.

Classification — *Onygenaceae*, *Onygenales*, *Eurotiomycetes.*

Ascomata gymnothecial, solitary or in clusters, whitish, spherical. *Peridium* consisting of a network of branched hyaline septate hyphae; peridial hyphae undulated or dichotomously branched, asperulate. *Asci* 8-spored, globose; ascospores 1-celled, globose, hyaline, whitish in mass, smooth-walled. *Conidial morph* malbranchea-like.

Type species. *Myotisia cremea* Kubátová, M. Kolařík & Hubka. MycoBank MB819229.

Myotisia cremea Kubátová, M. Kolařík & Hubka, *sp. nov.*

Etymology. Refers to the cream colour of ascomata and mycelium.

Ascomata gymnothecial, solitary or in clusters, whitish, spherical, 320–480 µm diam. *Peridium* consisting of a network of branched hyaline septate hyphae; surface peridial hyphae undulated or dichotomously branched, asperulate, 2.9–4.5 µm thick. *Asci* 8-spored, globose, 6–7 µm diam; *ascospores* 1-celled, globose, hyaline, whitish in mass, smooth walled (delicately reticulate by SEM), 2–3 µm diam. *Conidial morph* malbranchea-like, *arthroconidia* verruculose, terminal arthroconidia obovoid to ellipsoidal, intercalary arthroconidia alternate, barrel-shaped to ellipsoidal, 3.5–6.5 × 2.5–3 µm.

Culture characteristics — (in the dark at 25 °C after 28 d): Colonies on cornmeal agar (CMA) attained 39–48 mm diam, mycelium sparse, granular appearance due to production of ascomata, reverse uncoloured. Colonies on potato dextrose agar (PDA) and yeast extract malt extract agar (YM) similar to CMA, however with apricot-coloured reverse. Colonies at 20, 15 and 10 °C on all three media were similarly coloured. Well-developed ascomata occurred on CMA and PDA at 20 and 25 °C after 2–3 wk. Growth rates at different temperatures on CMA/PDA/YM (in mm): 10 °C 12–14/14–18/10–17; 15 °C 31–34/29–35/23–29; 20 °C 45–48/40–45/25–36; 25 °C 39–48/40–46/35–55; 30 °C 10–16/10–16/8–18; 37 °C no growth.

Typus. Czech Republic, Bohemian Karst, Malá Amerika mine, on bat droppings of *Myotis myotis*, 21 Feb. 2009, coll. *P. Špryňar*, isol. *A. Kubátová* (holotype PRM 935803, isotypes PRM 935804, PRM 935805, PRC 3709, culture ex-type CCF 5407 = CBS 141864; ITS, LSU, and SSU sequences GenBank LT627243, LT627240, and LT671443, MycoBank MB819230).

Additional material examined. Czech republic, Bohemian Karst, Malá Amerika mine, sediment, 2 Mar. 2013, coll. *A. Kubátová*, isol. *A. Kubátová* using hair baiting technique (culture CCF 5406 = CBS 141863, herbarium specimen PRC 3708, ITS sequence GenBank LT627244).

Colour illustrations. Underground tunnel of Malá Amerika mine (Czech Republic) with cluster of *Myotis myotis* individuals; colonies on cornmeal agar after 2 mo at 25 °C; malbranchea-like asexual morph; arthroconidia; gymnothecial ascoma, peridial hyphae; ascospores. Scale bars = 20 µm, scale bar of ascospores = 2 µm.

Notes — CCF 5407 has an identical ITS sequence to that of CCF 5406. Based on ITS sequences, *M. cremea* is 99 % (486/492) similar to strain UAMH 3124 (GenBank KF477240) isolated from a reptile during the study of Sigler et al. (2013); the similarity of the other sequences deposited in GenBank did not exceed 87 %. The LSU rDNA sequence exhibited the highest similarity (95 %) to various species of *Arthroderma*, *Microsporum* and *Onygena*. Sigler et al. (2013) investigated taxonomic position of the strain UAMH 3124 and classified it as an undetermined fungus at generic as well as species level, which belonged to the phylogenetic lineage of *Arachnotheca glomerata*. We used the LSU sequence dataset of onygenalean fungi published by Hirooka et al. (2016) to assess the phylogenetic position of *M. cremea* (data not shown). The fungus was resolved as a member of the family *Onygenaceae* and clustered with members of the '*Onygenaceae* 3' clade together with *Arachnotheca glomerata* UAMH 3551 (NR_111884) with 94 % sequence similarity (553/591). Morphologically, *Myotisia* can be easily distinguished from *Arachnotheca* by smooth-walled ascospores.

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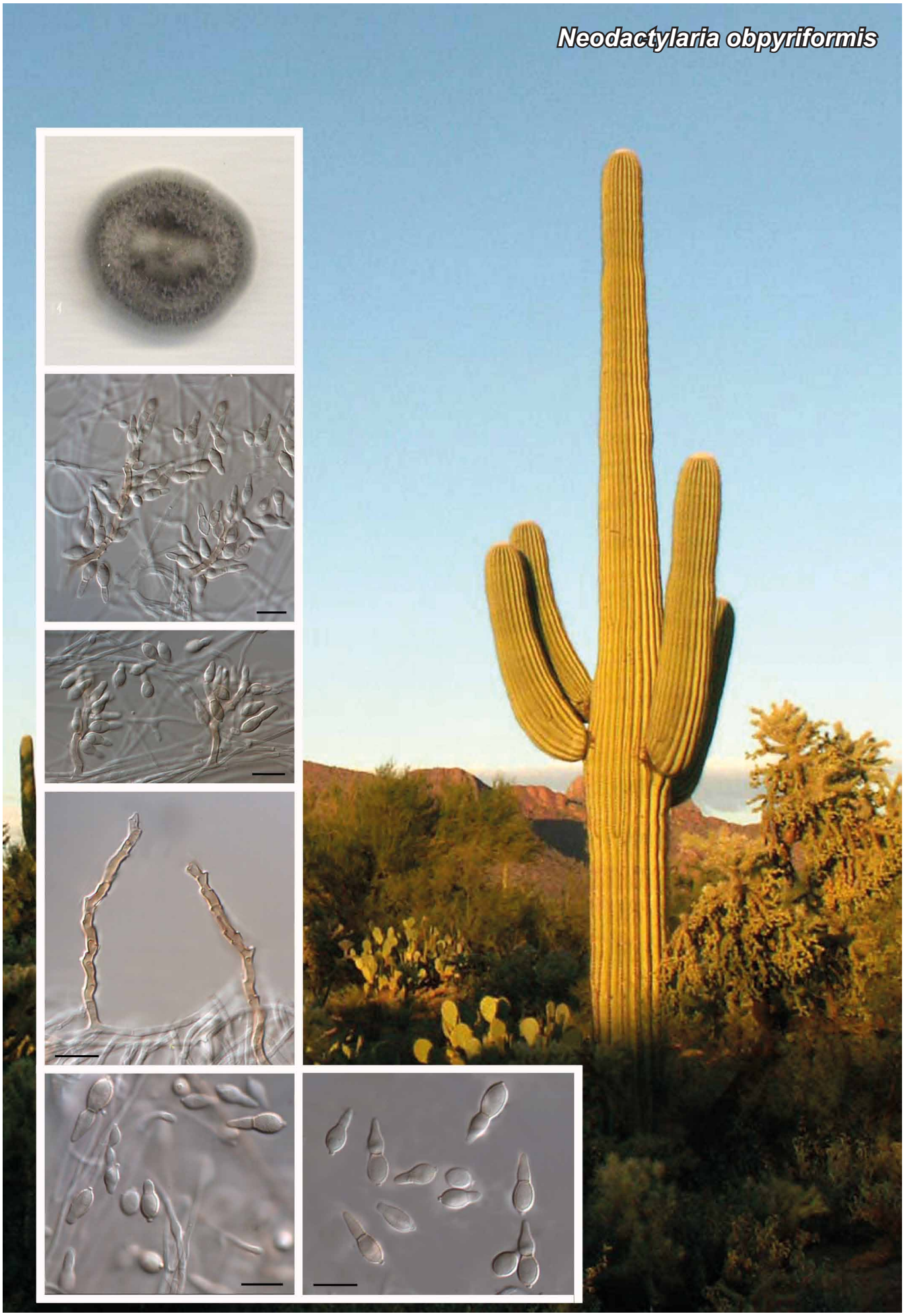

Neodactylaria obpyriformis

Fungal Planet 606 – 20 June 2017

Neodactylaria Guevara-Suarez, Deanna A. Sutton, Wiederhold & Gené, *gen. nov.*

Etymology. *Neo-* meaning new; *-dactylaria* referring to the asexual genus *Dactylaria.* Name reflects its morphological similarity with the genus *Dactylaria*.

Classification — *Incertae sedis*, *Dothideomycetes*.

Mycelium consisting of branched, septate, smooth-walled, hyaline to subhyaline hyphae. *Conidiophores* macronematous, mononematous, erect, straight or flexuous, septate, unbranched, brown. *Conidiogenous cells* integrated, terminal or intercalary, polyblastic, sympodial, with several denticle-like loci. *Conidia* solitary, 1-celled or septate, obpyriform or rostrate, often constricted at the septum, smooth-walled or echinulate, brownish, subhyaline towards the apex, often with a protuberant hilum. *Sexual morph* unknown.

Type species. *Neodactylaria obpyriformis* Guevara-Suarez, Deanna A. Sutton, Wiederhold & Gené.

MycoBank MB820857.

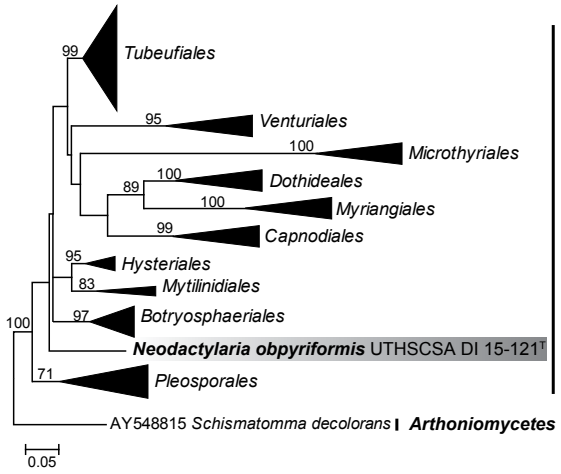
Neodactylaria obpyriformis Guevara-Suarez, Deanna A. Sutton, Wiederhold & Gené, *sp. nov.*

Etymology. Name refers to the conidial shape.

Mycelium superficial or immersed, composed of branched, septate, thin-walled, smooth-walled, hyaline to subhyaline, 1–2 µm wide hyphae. *Conidiophores* solitary, straight or flexuous, septate, unbranched, smooth-walled, pale to mid-brown, 25–40 (–70) × 3–4 µm. *Conidiogenous cells* terminal or intercalary, polyblastic, sympodial, with short-cylindrical denticles. *Conidia* solitary, (0–)1-septate, constricted at the septum, obpyriform to slightly rostrate, 10–14 × 3–5 µm, with an obtuse apex and a hilum up to 1 µm long, finely echinulate, pale brown, subhyaline towards the apex. *Sexual morph* not observed.

Culture characteristics — (in darkness, at 25 °C after 7 d). Colonies attaining 14–19 mm diam on PDA, OA and PCA. On PCA and OA colonies flat, floccose at the centre, cottony towards the periphery, olive grey (3F2), margin smooth and entire; reverse grey (3E1); sporulation abundant. On PDA flat, white to cream-coloured, margin entire; sporulation sparse. The fungus does not grow at 37 °C.

Typus. USA, Arizona, Phoenix, from human bronchoalveolar lavage, *D.A. Sutton*, 2015 (holotype CBS H-23131, cultures ex-type UTHSCSA DI 15-121 = FMR 14604; ITS and LSU sequences GenBank LT839090 and LT839091, MycoBank MB820858).



Maximum likelihood (ML) tree obtained from the analysis of LSU sequence data. Bootstrap support values above 70 % are shown at the nodes. The alignment included 552 bp and was performed with ClustalW. The General Time Reversible model (GTR) with Gamma distribution and invariant sites (G+I) was used as the best nucleotide substitution model. Both the alignment and tree were constructed with MEGA v. 6.06 (Tamura et al. 2013).

Colour illustrations. Saguaro cactus and landscape in Saguaro National Park, Arizona, USA (image credit: https://www.goodfreephotos.com); colonies growing on PCA after 14 d at 25 °C, conidiophores and conidia. Scale bars = 10 µm.

Notes — *Neodactylaria obpyriformis* is morphologically similar to *Dactylaria kumamotoensis* and to *D. madresensis*, two *Dactylaria* species described by Matsushima (1981, 1983) from soil and plant debris in Japan and India, respectively. Although these fungi could be congeneric with *N. obpyriformis*, they are only known from the type collection and no living cultures are available for molecular comparison. Morphologically, both species mainly differ from the novel fungus in having larger conidia which can have more than one septum; i.e., in *D. kumamotoensis* they are 12–40 × 4–8 µm, 1–3-septate, and in *D. madresensis* 9–19 × 4.5–6 µm, 1–2 septa. *Neodactylaria obpyriformis* also resembles some *Pyricularia* species, such as *P. higginsii*, now accommodated in *Pseudopyricularia* (Klaubauf et al. 2014), or *P. valdalurensis.* However, the former has smooth, 2-septate conidia, 17.5–36.5 × 5.3–6.5 µm (Luttrell 1954, Klaubauf et al. 2014), and the latter has larger conidiophores (up to 240 µm long), and hyaline, smaller conidia (9–10 × 3–4 µm) (Subramanian & Vittal 1974). It is noteworthy that *Dactylaria* sensu De Hoog (1985) is a heterogeneous genus with species of different phylogenetic affinities (Crous et al. 2016), although its type species, *D. purpurella*, as well as those of the genera *Pyricularia* and *Pseudopyricularia* belong to the *Magnaporthales* (*Sordariomycetes*) (Bussaban et al. 2005, Klaubauf et al. 2014). Our phylogenetic analysis shows that *Neodactylaria* is related to *Dothideomycetes*, but with uncertain taxonomic position at the ordinal level.

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Candida rongomai-pounamu

Fungal Planet 607 – 20 June 2017

Candida rongomai-pounamu Padamsee, B.S. Weir, Petterson & P.K. Buchanan, *sp. nov.*

Etymology. The specific epithet 'rongomai-pounamu' (Māori), referring to the 'treasure of Rongomai'. The students who discovered this new species and chose the name are in a Science, Technology, Engineering and Maths (STEM) education immersion class at Rongomai School, Otara, Auckland, New Zealand. Pounamu is the Māori word for the treasured greenstone (or jade), representing the students as the school's precious treasure and also the future.

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

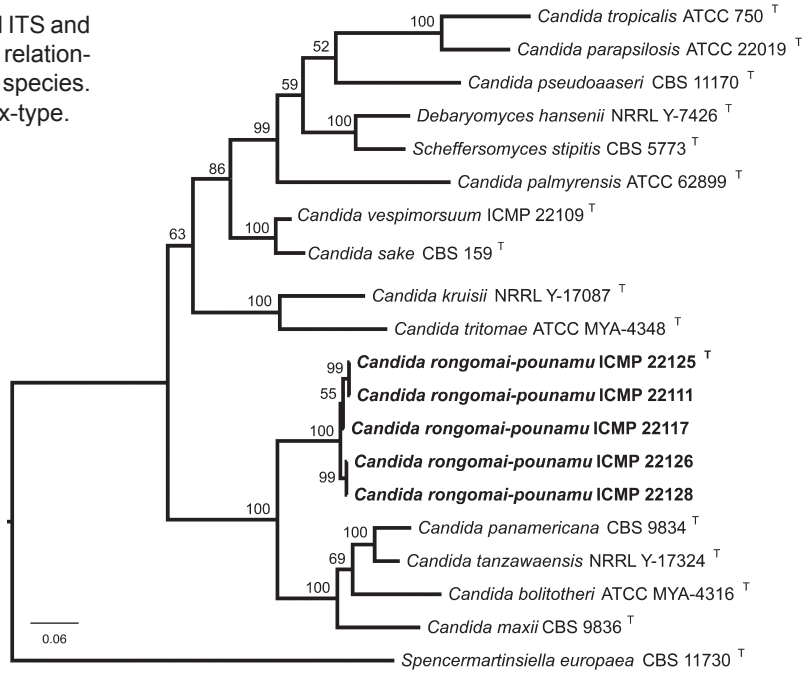
On Yeast extract Malt agar (YM), after 9 d at 22 °C, colony is white, somewhat glistening, apically-hirsute, with a raised undulating, membranous margin. After 6 d growth at 22 °C in YM broth, cells are ellipsoidal and cylindrical, 7–9(–11) × 3–5(–5.5) µm (av. 8.5 × 4 µm), occurring singly, in clusters, as pseudohyphae, and proliferating by budding. Dalmau plate culture after 10 d was white with pseudohyphae and the margin was also fringed with pseudohyphae. Fermentation and assimilation of carbon compounds – see MycoBank MB819344.

Typus. New Zealand, Auckland, The Gardens, Totara Park, on agaric mushroom surface, 8 Mar. 2016 (holotype PDD 105303, culture ex-type ICMP 22125, ITS and LSU sequences GenBank KY285000 and KY285009, MycoBank MB819344).

Notes — This study began as a project to raise awareness of fungal diversity and function among New Zealand school students and teachers. Mycologists at Landcare Research assisted 20 students (9–11 yr) at Rongomai Primary School, Otara, Auckland to collect and identify fungi in a native forest at Totara Park, 5 km from the school. The students' challenge was to discover and describe a fungal species new to science. Students prepared cultures from swabs of the surface of collected specimens; colonies arising were subcultured and sequenced. Students then observed the process to differentiate and publish a new species, and collectively chose the name for the species epithet. The students involved in this project are as follows: Fotu Holikimafua, Serenity Iako, Gina Kavemanu, Michaela Langdon, Julius Marino, Te Rangihau Matthews, Carlos McCabe Davis, Janine Mulipola, James Nansen, Matarii Nicholas, Daychelle Paniani-Tietie, Daize Puaha, Sam Ratahi, Ula Sefo, Micheal Simona, Harlyn Teau-Rewa, Florence Tafaoga, Sheribyn Tiatia, Vanisha Vaeteru, Watson Wilson.

Phylogenetic analyses using an alignment of concatenated sequences of the nuclear large subunit and the internal transcribed spacer regions show that the three conspecific strains, ICMP 22125, 22126, and 22128, represent a novel yeast species and are sister to the *Candida tanzawaensis* clade, which is mainly composed of yeasts isolated from the digestive tract of basidiocarp-feeding beetles (Suh et al. 2004). Physiological profiles further support the separation of the new species as distinct from *C. tanzawaensis* and *C. panamericana*. The new species can be distinguished from *C. tanzawaensis* by its ability to grow in 50 % glucose. The new species can be distinguished from *C. panamericana* by its ability to assimilate arbutin and its inability to ferment either D-xylose or galactose. The new species can be distinguished both from *C. tanzawaensis and C. panamericana* by its inability to grow at 30 °C. All supplementary data including assimilation tests and sequence alignments are available at doi:10.7931/J2XW4GQT, specimen and strain data is available at https://scd.landcareresearch.co.nz.

Bayesian inference phylogenetic tree of concatenated ITS and LSU sequences using MrBayes v. 3.2.6, showing the relationship of *Candida rongomai-pounamu* to closely related species. The novel species is printed in **bold**. All strains are ex-type.



Colour illustrations. Rongomai School students and teacher collecting fungi in Totara Park, Auckland, New Zealand; light micrographs of *Candida rongomai-pounamu* budding cells in YM broth. Scale bar = 10 µm.

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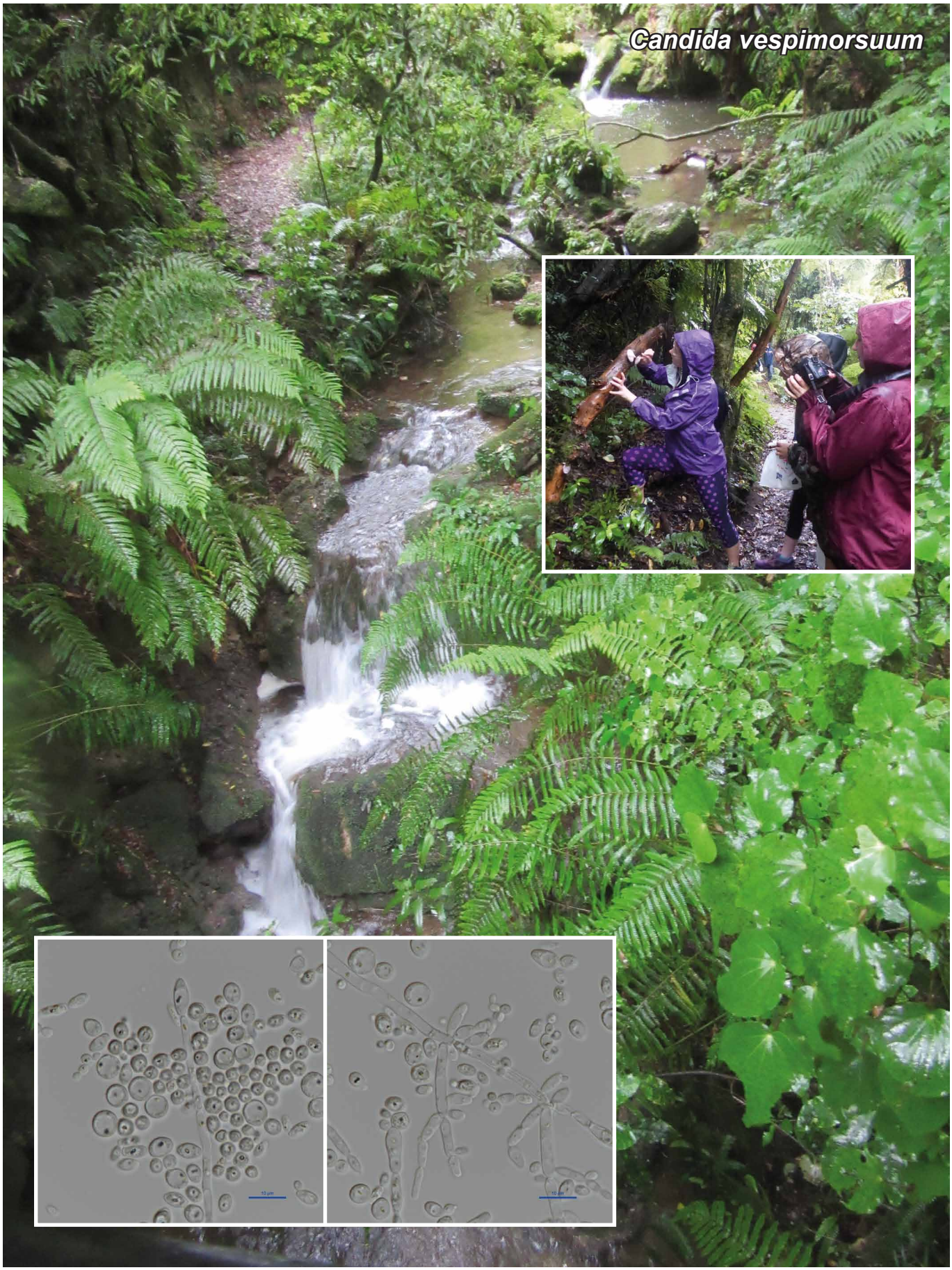

Candida vespimorsuum

Fungal Planet 608 – 20 June 2017

Candida vespimorsuum Padamsee, B.S. Weir, Petterson, P.K. Buchanan, *sp. nov.*

Etymology. The specific epithet '*vespimorsuum*', referring to 'wasp stings'. Five students from the class of 32 at Karamu High School, Hastings, New Zealand who discovered this new species and chose the name were stung by invasive wasps during the fungal collecting trip. Hence 'the *Candida* of the wasp-stings'.

Classification — *Incertae sedis*, *Saccharomycetales*, *Saccharomycetes*, *Saccharomycotina.*

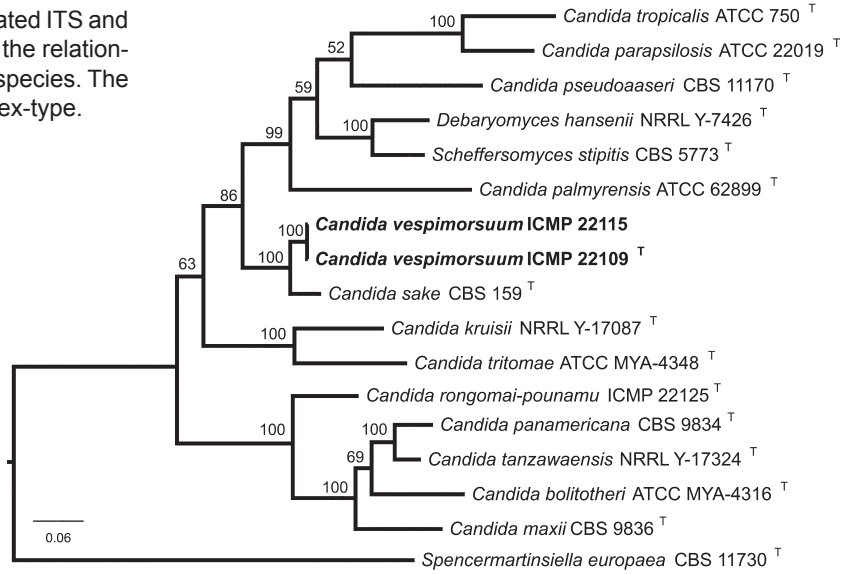
On Yeast extract Malt agar (YM), after 9 d at 22 °C, colony is white, moist and glistening, with a somewhat raised, lobed, membranous margin. After 5 d growth at 22 °C in YM broth, cells are subglobose to globose, ellipsoidal and cylindrical, (3–)4.5–7.5(–8) × (2.5–)3.5–6(–7.5) µm (av. 5.6 × 4.8 µm), occurring singly, in clusters or chains, as pseudohyphae, and proliferating by budding. Dalmau plate culture after 10 d was white with an undulating to entire margin. Fermentation and assimilation of carbon compounds – see MycoBank MB819395.

Typus. New Zealand, Hawke's Bay Region, White Pine Bush Scenic Reserve, on cup fungus surface, 2 Mar. 2016 (holotype PDD 105304, culture ex-type = ICMP 22109, ITS and LSU sequences GenBank KY285004 and KY285007, MycoBank MB819395).

Notes — This study began as a project to raise awareness of fungal diversity and function among New Zealand school students and teachers. Mycologists at Landcare Research assisted 32 students (15–17 yr) at Karamu High School, Hastings, Hawke's Bay to collect and identify fungi in a native forest at White Pine Bush Scenic Reserve, 45 km north of the school. The students' challenge was to discover and describe a fungal species new to science. Students prepared cultures from swabs of the surface of collected specimens; colonies arising were subcultured and sequenced. Students then observed the process to differentiate and publish a new species, and collectively chose the name for the species epithet. The students involved in this project are as follows: Keegan Beets, Gurkamal Bhangal, Tom Black, Zara Blake, Emma Bone, Georgia Boyes, Mia Braddock, Jesca-Lee Bron, Caleb Brothers, Shayne Brown, Isla Christensen, Niels Clayton, Holly Davison, Holly Foulkes, Yvaan Hapuku-Lambert, Dominique Harmer-Higgins, Hannah Hemi-Robinson, Kate Jacobs, Kate Jones, Kevin Karnbach, Ana Marks, Kirsten Rutten, Cerys Sanders-Jones, Bailey Seymour, Reece Sullivan, Mason Templeton, Felix Thornton, Camryn Toki, Liam Urquhart, Sophie Wells, Jaymie Wright, Cameron Young.

Phylogenetic analyses using an alignment of concatenated sequences of the nuclear large subunit and the internal transcribed spacer regions show that the two conspecific strains, ICMP 22109 and 22115, represent a novel yeast species and are sister to *Candida sake*. Physiological profiles further support the separation of the new species as distinct from *C. sake* and *C. parapsilosis*. The new species can be distinguished from *C. sake* by its inability to assimilate L-sorbose or to ferment sucrose. The new species can be distinguished both from *C. sake* and *C. parapsilosis* by its ability to assimilate D-glucosamine and D-arabinose and inability to assimilate D-melezitose. All supplementary data including assimilation tests and sequence alignments are available at doi:10.7931/J2XW4GQT, specimen and strain data is available at https://scd.landcareresearch.co.nz.

Bayesian inference phylogenetic tree of concatenated ITS and LSU sequences using MrBayes v. 3.2.6, showing the relationship of *Candida vespimorsuum* to closely related species. The novel species is indicated in **bold**. All strains are ex-type.



Colour illustrations. White Pine Bush Scenic Reserve, Hawke's Bay, New Zealand; Karamu High School students examining a mushroom; light micrographs of *Candida vespimorsuum* budding cells and pseudohyphae in YM broth. Scale bar = 10 µm.

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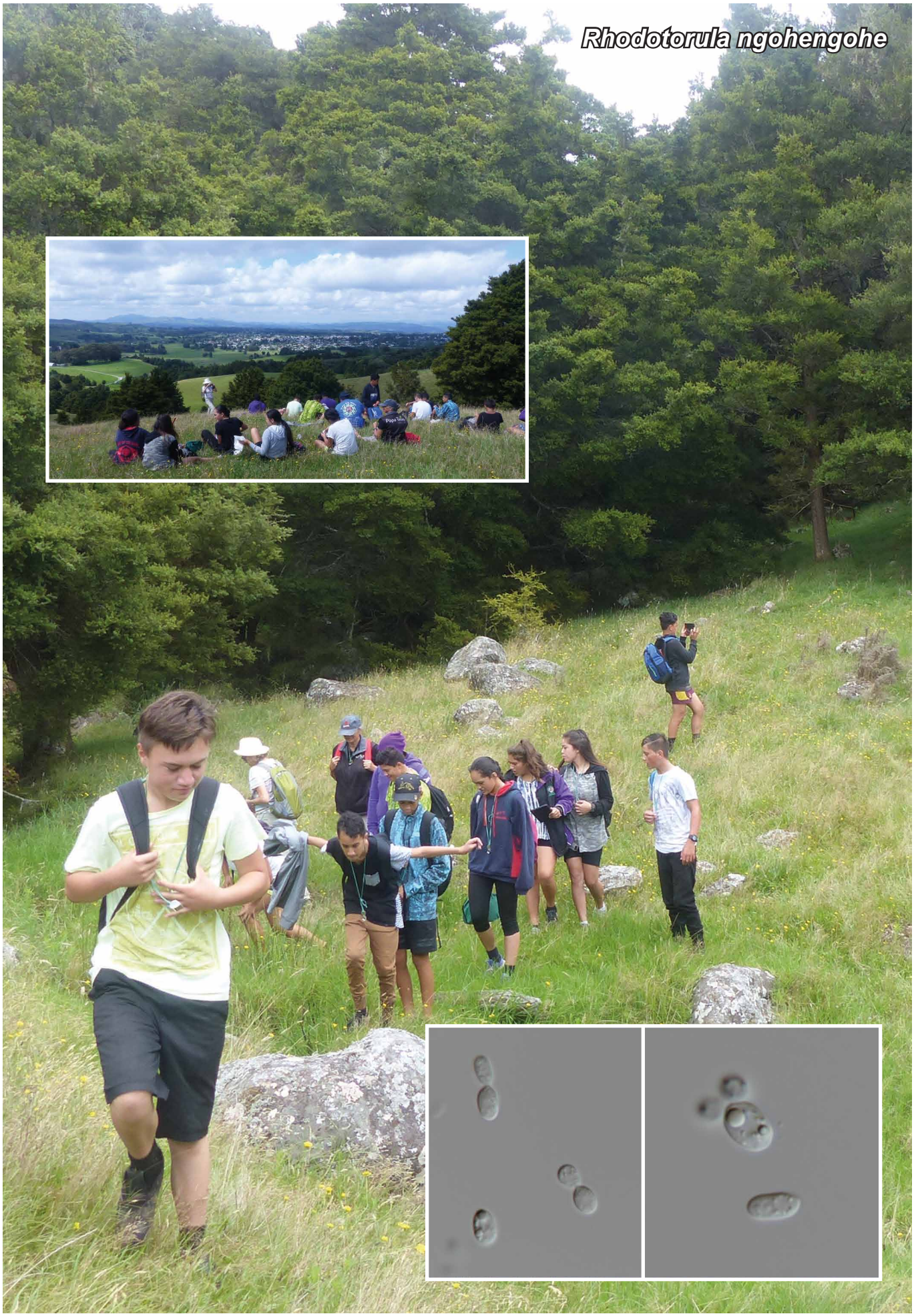

Rhodotorula ngohengohe

Fungal Planet 609 – 20 June 2017

Rhodotorula ngohengohe Padamsee, B.S. Weir, Petterson & P.K. Buchanan, *sp. nov.*

Etymology. The specific epithet 'ngohengohe' (Māori), referring to 'be humble, agreeable'. Students who discovered this new species are from Te Kura Kaupapa Māori o Kaikohe, and chose *ngohengohe* for this species from their school motto E rere, Kia koi, Kia ngohengohe = Fly, Be on to it, Be humble in your successes (pronounced ngohe-ngohe).

Classification — *Sporidiobolaceae*, *Sporidiobolales*, *Microbotryomycetes*, *Pucciniomycotina*.

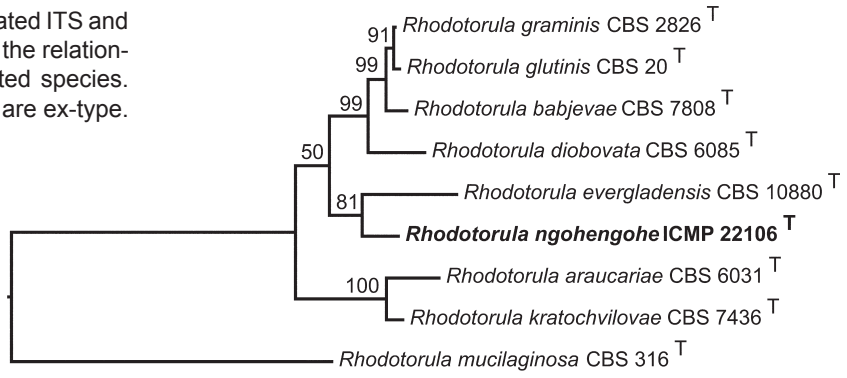
On Yeast extract Malt agar (YM), after 9 d at 22 °C, colony is flat, pink, moist and glistening, with a curved margin. After 5 d growth at 22 °C in YM broth, cells are mostly ellipsoidal and occasionally oval, (4.5–)6.5–8(–9) × 3–4.5(–5.5) µm (av. 7 × 3.8 µm), occurring singly, in clusters, and proliferating by budding. Dalmau plate culture after 10 d was pink with an entire margin. Fermentation and assimilation of carbon compounds – see MycoBank MB819394.

Typus. New Zealand, Northland, Kaikohe water catchment, on bird feather surface, 12 Feb. 2016 (holotype PDD 105305, culture ex-type ICMP 22106, ITS and LSU sequences GenBank KY285005 and KY285006, MycoBank MB819394).

Notes — This study began as a project to raise awareness of fungal diversity and function among New Zealand school students and teachers. Mycologists at Landcare Research assisted 18 students (13–14 yr) at Te Kura Kaupapa Māori o Kaikohe, Kaikohe, Northland to collect and identify fungi in a native forest of the nearby water catchment. The students' challenge was to discover and describe a fungal species new to science. Students prepared cultures from swabs of the surface of collected specimens; colonies arising were subcultured and sequenced. Students then observed the process to differentiate and publish a new species, and collectively chose the name for the species epithet. The students involved in this project are as follows: Jayson Gotz-Edmonds, Kahurangi Hauraki, Awhina Herewini Hona, Temepara Hita, Sean Kaka, Sione Kata, Te Ao Kohatu Kaukau-Troughton, Niki Lawrence, Shaden Marsh, Kahurangi Maxwell, Te Painga Osborne, Reiata Phillips Heihei, Tawauwau Rakete, Tasha Richards, Romeo Tau-Ashby, Vincent Tau-Roberts, Mikaira Te Haara, Monique Terei.

Phylogenetic analyses using an alignment of concatenated sequences of the nuclear large subunit and the internal transcribed spacer regions show that ICMP 22106 represents a novel yeast species and is sister to *Rhodotorula evergladiensis*. Physiological profiles further support the separation of the new species as distinct from *R. evergladiensis* and *R. kratochvilovae*. The new species can be distinguished from *R. evergladiensis* by its ability to assimilate D-arabinose, L-arabinose, and D-ribose as well as its ability to use nitrate as a nitrogen source. The new species can be distinguished from *R. kratochvilovae* by its inability to assimilate D-raffinose, its ability to assimilate xylitol, and its weak growth in 10 % NaCl. All supplementary data including assimilation tests and sequence alignments are available at doi:10.7931/J2XW4GQT, specimen and strain data are available at https://scd.landcareresearch.co.nz.

Bayesian inference phylogenetic tree of concatenated ITS and LSU sequences using MrBayes v. 3.2.6, showing the relationship of *Rhodotorula ngohengohe* to closely related species. The novel species is indicated in **bold**. All strains are ex-type.



Colour illustrations. Students from Te Kura Kaupapa Māori o Kaikohe returning from fungal collecting in Kaikohe water catchment forest, Kaikohe, New Zealand; overlooking town of Kaikohe; light micrographs of *Rhodotorula ngohengohe* budding cells in YM broth. Scale bar = 10 µm.

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Penicillium parvofructum

Fungal Planet 610 – 20 June 2017

Penicillium parvofructum Guevara-Suarez, Cano-Canals, Cano & Stchigel, *sp. nov.*

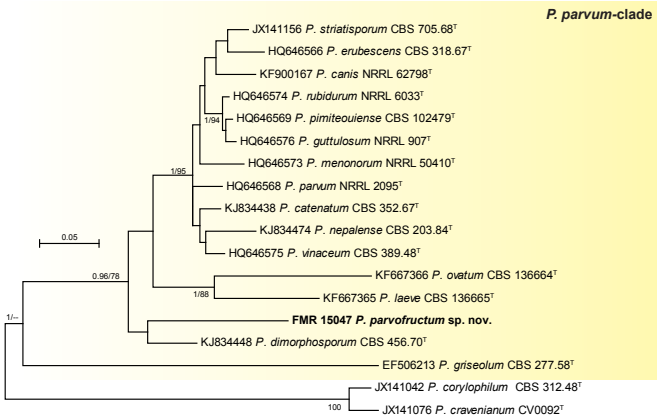
Etymology. From Latin *parvum*-, small, and -*fructum*, fruit, in reference to the small size of the conidiophores.

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

Mycelium sparse, uncoloured, septate, branched. *Conidiophores* typically monoverticillate; stipes 13–18 × 2.5–3 µm, smooth-walled, hyaline. *Conidiogenous cells* phialidic, solitary to in verticils of up to 3, ampulliform, 8–10 × 1.5–2.5 µm, smooth-walled, hyaline. *Conidia* in chains, broadly ovoid to bacilliform, 3–3.5 × 2–2.5 µm, smooth-walled, hyaline to subhyaline.

Culture characteristics — (after 7 d at 25 °C in darkness). On MEA colonies attaining 13–15 mm diam, flat, with a raised centre and a concave edge, radially sulcate, margins entire, whitish (M.2A1); sporulation absent; exudate and soluble pigment absent. On CYA colonies attaining 17–19 mm diam, similar to those on MEA, but light yellow (M.2A5) centrally and at the margins; sporulation poor; exudate and soluble pigment absents. On YES colonies attaining 15–17 mm diam, cerebriform, of raised centre with a concave edge, margins entire edge, greenish grey (M.1B2) at the margins and centrally greyish yellow (M.1B5); sporulation moderately abundant; exudate and soluble pigment absents. Optimum temperature of growth 30–37 °C (CYA at 30 °C, 21–25 mm diam; CYA at 37 °C, 23–26 mm diam; MEA at 30 °C, 19–20 mm diam; MEA at 37 °C, 18–19 mm diam; YES at 30 °C, 21–25 mm diam; YES at 37 °C, 25–28). Does not grow at/above 40 °C.

Typus. Spain, Tarragona province, Prades, from a forest soil sample, 13 June 2015, *J. Cano-Canals* (holotype CBS H-22733, cultures ex-type FMR 15047 = CBS 141690; ITS, LSU, *BenA*, and *CaM* sequences GenBank LT559091, LT559092, LT627645, and LT627646; MycoBank MB819947).



Colour illustrations. Prades, Tarragona, Spain; colonies after 7 d at 25 °C on YES, MEA and CYA, respectively; texture of colonies on YES at 37 °C; conidiophores with conidia. Scale bars = 10 um.

Notes — According to a sequence comparison with available data (ITS, *BenA* and *CaM*), *P. parvofructum* is most closely related with *P. dimorphosporum* in the *P. parvum* clade, section *Exilicaulis* (Visagie et al. 2016).

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Penicillium dimorphosporum* (GenBank NR 121271; Identities = 534/553 (97 %), Gaps = 4/553 (0 %)), *Penicillium erubescens* (GenBank NR 121245; Identities = 532/551 (97 %), Gaps = 6/551 (1 %)), and *Penicillium rubidurum* (GenBank NR 121243; Identities = 531/551 (96 %), Gaps = 5/551 (0 %)).

BenA. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the *BenA* sequence are *Penicillium rubidurum* (GenBank HQ646574; Identities = 408/466 (88 %), Gaps = 4/466 (0 %)), *Penicillium dimorphosporum* (GenBank KF900165; Identities = 383/429 (89 %), Gaps = 5/429 (1 %)), and *Penicillium pimiteouiense* (GenBank KC344994; Identities = 406/467 (87 %), Gaps = 7/467 (1 %)).

CaM. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the *CaM* sequence are *Penicillium dimorphosporum* (GenBank KF900176; Identities = 472/544 (87 %), Gaps = 13/544 (2 %)), *Penicillium vinaceum* (GenBank AY678543; Identities = 452/544 (83 %), Gaps = 18/544 (3 %)), and *Penicillium pimiteouiense* (GenBank HQ646580|; Identities = 454/548 (83 %), Gaps = 25/548 (4 %)).

Penicillium parvofructum differs from *P. dimorphosporum* (the species phylogenetically more closely related) in the size of the stipes of the conidiophores (13–18 µm long in *P. parvofructum* vs 15–30 µm long in *P. dimorphosporum*), in the morphology of the conidia (*P. parvofructum* produces hyaline to subhyaline, smooth-walled, broadly ovoid to bacilliform conidia, which turn brown, ornamented and globose with age in *P. dimorphosporum*) and in the optimum temperature of growth (*P. parvofructum* displays the best growth at 37 °C, while the optimum temperature for *P. dimorphosporum* is 25 °C).

Phylogenetic tree built by using *BenA* (401 bp) nucleotide sequences of *Penicillium* section *Exilicaulis* belonging to the *P. parvum* clade, using Maximum-likelihood and Bayesian inference. The tree was built by using MEGA v. 6. Posterior probabilities and/or bootstrap support values higher than 0.95 and 70 %, respectively, are indicated at the nodes. *Penicillium corylophilum* and *Penicillium cravenianum* were chosen as outgroup. Ex-type strains of the different species are indicated with T. The new species is indicated in **bold**. The alignment and tree is available in TreeBASE (ID 19427).

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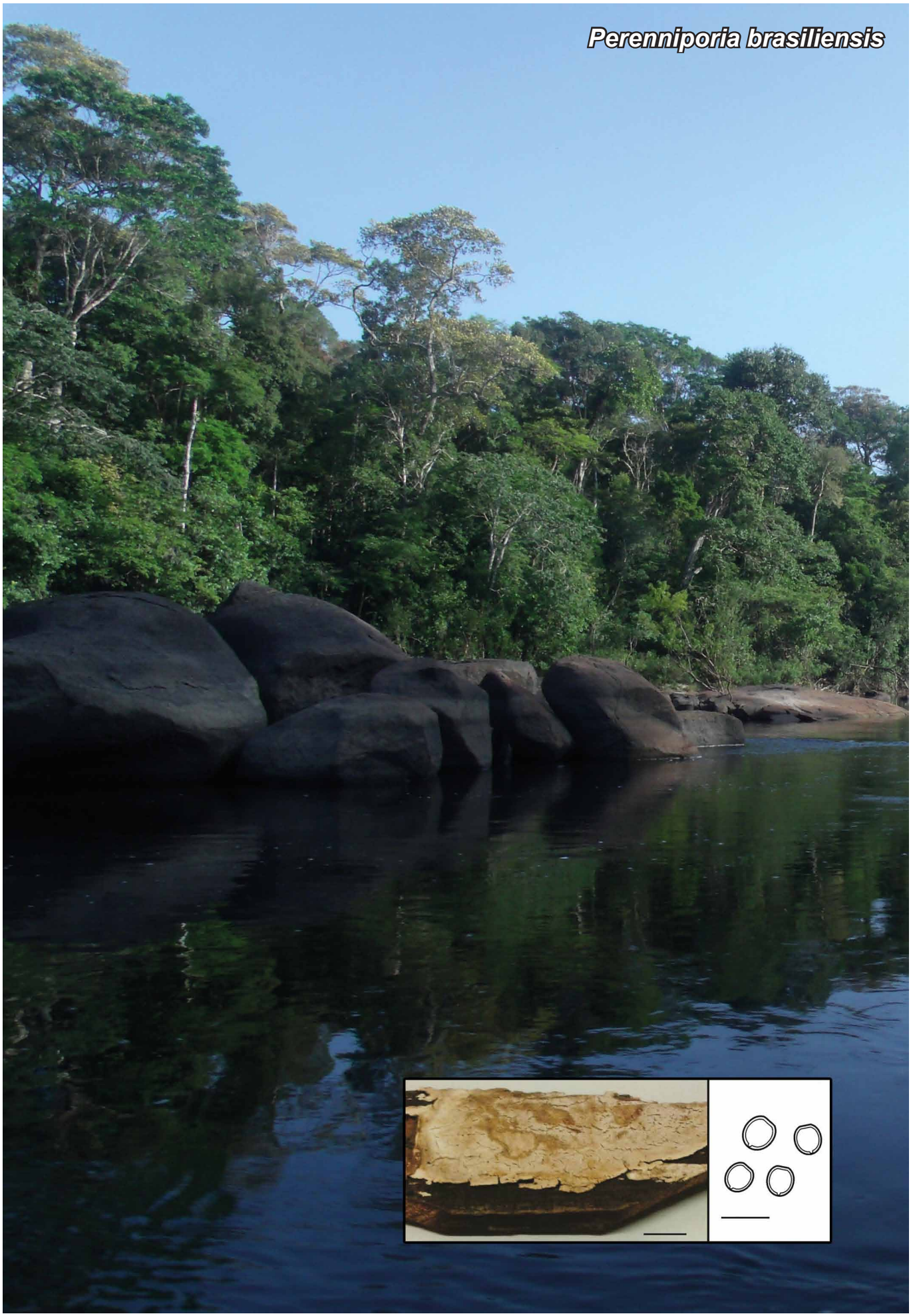

Perenniporia brasiliensis

Fungal Planet 611 – 20 June 2017

Perenniporia brasiliensis Lira, A.M.S. Soares, Ryvarden & Gibertoni, *sp. nov.*

Etymology. Referring to the country where this fungus was collected, Brazil.

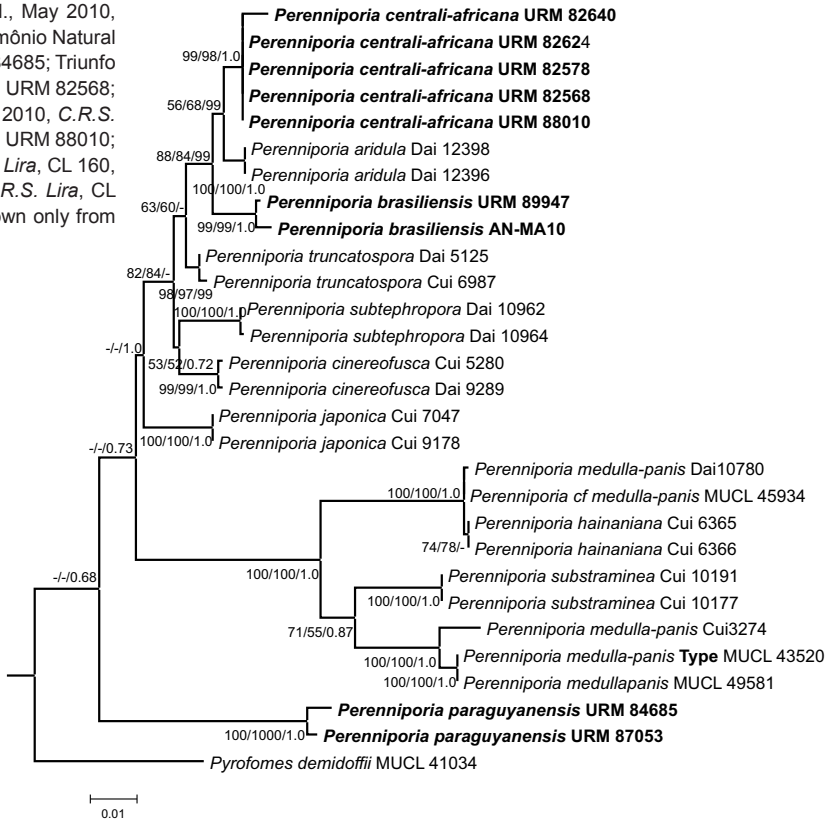
Classification — *Polyporaceae*, *Polyporales*, *Agaricomycetes.*

Basidiomata annual, resupinate, smooth and even, hard to brittle, 10 × 1.5 cm in the holotype and 0.5 mm thick; *pore surface* cream greyish to tan (31 vinaceous buff to 10 cinnamon); *pores* slightly thick-walled, round to angular, mostly 6–7 per mm; *dissepiments* entire, thick; *tubes* concolorous with the pore surface, up to 0.5 mm deep; *context* about 100 mm thick, cottony and concolorous with the pore surface; margin smooth, narrow and concolorous with the pore surface. *Hyphal system* dimitic, generative hyphae thin-walled, smooth and with clamps, 2–4 µm wide, skeletal hyphae weakly dextrinoid, 2–3 µm. *Cystidia* or other sterile elements absent. *Basidia* 14–20 × 4–6 µm, clavate with four sterigmata. *Basidiospores* 3–4 × 2–4 µm, globose to subglobose, hyaline, thick-walled and dextrinoid.

Typus. Brazil, Amapá, Porto Grande, Floresta Nacional do Amapá, on wood decay, Sept. 2013, *A. Soares*, AS 914 (holotype URM 89947, isotype in O, ITS and LSU sequences GenBank KX584437 and KX619595, MycoBank MB816407).

Additional material examined. ***Perenniporia centrali-africana***: Brazil, Ceará, Missão Velha, Cachoeira de Missão Velha, Jan. 2011, *C.R.S. Lira*, PPBio 128, URM 83175; Crato, Floresta Nacional do Araripe, May 2012, *C.R.S. Lira*, PPBio 883, URM 85599; Pernambuco, Cabrobó, Fazenda Mosquito, Jan. 2010, *C.R.S. Lira*, CL 007, URM 82624; ibid., May 2010, *C.R.S. Lira*, CL 007, URM 82640; Jaqueira, Reserva do Patrimônio Natural Frei Caneca, Mar. 2012, *G.S. Nogueira-Melo*, NM 103, URM 84685; Triunfo Triunfo, Sítio Carro Quebrado, Jan. 2010, *C.R.S. Lira*, CL 003, URM 82568; ibid., Mar. 2010, *C.R.S. Lira*, CL 011, URM 82578; ibid., Apr. 2010, *C.R.S. Lira*, CL 23, URM 82584; ibid., July 2012, *C.R.S. Lira*, CL 160, URM 88010; ibid., Sept. 2010, CL 26, URM 82957; ibid., July 2012, *C.R.S. Lira*, CL 160, URM 88010; ibid., CL 699, URM 85597; ibid., Jan. 2014, *C.R.S. Lira*, CL 772, URM 87999; ibid., CL 768, URM 88016 (previously known only from Cameroon).

Notes — Based on a BLASTn search of NCBIs GenBank database, the closest hits using the ITS sequence are *Perenniporia* sp. (GenBank KT156689; Identities = 588/598 (98 %), Gaps = 1/598 (0 %)), *Dichomitus squalens* (GenBank KM411455; Identities = 631/666 (95 %), Gaps = 4/666 (0 %)), and *P. tenuis* (GenBank JQ001859; Identities = 631/667 (95 %), Gaps = 4/667 (0 %)). Using the LSU sequence, the highest similarity was to *P. aridula* (GenBank JQ001847; Identities = 801/817 (98 %), Gaps = 7/817 (0 %)), *P. aridula* (GenBank JQ001846; Identities = 801/817 (98 %), Gaps = 7/817 (0 %)), and *P. tibetica* (GenBank JF706332; Identities = 801/817 (98 %), Gaps = 7/817 (0 %)). Although genetically close to *P. aridula*, *P. tenuis* and *P. tibetica*, *P. brasiliensis* is morphologically different (Table 1 - see FP 612). *Perenniporia brasiliensis* is similar to *P. albo-incarnata*, *P. centrali-africana*, and *P. guyanensis*, sharing the same whitish colour. However, they are micro-morphologically different (Table 1 - see FP 612).



Colour illustrations. Porto Grande, Floresta Nacional do Amapá; basidiomata (scale bar = 1 cm); basidiospores (scale bar = 5 µm).

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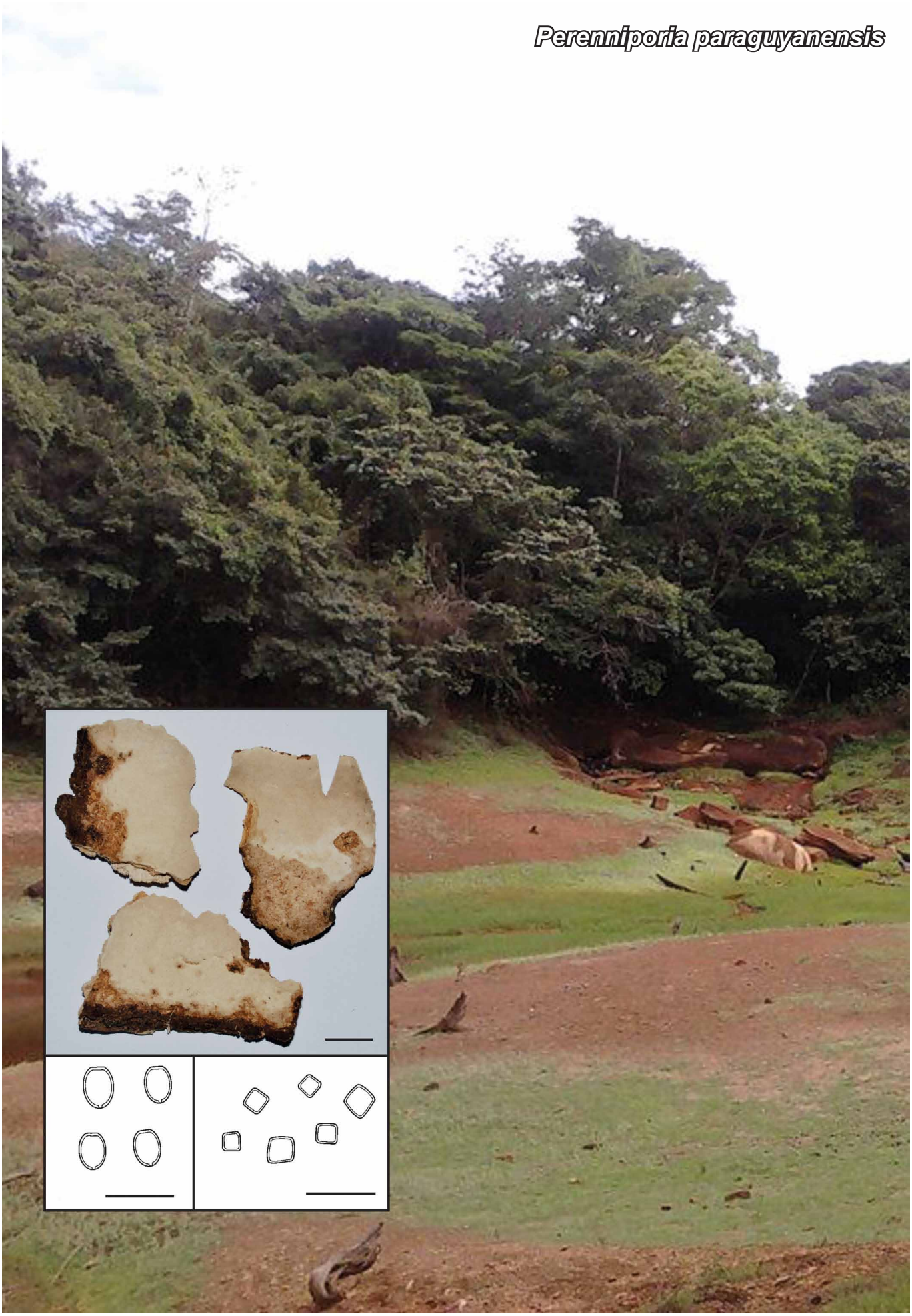
Perenniporia paraguyanensis

Fungal Planet 612 – 20 June 2017

Perenniporia paraguyanensis Lira & Gibertoni, *sp. nov.*

Etymology. Referring to morphological similarity to *P. guyanensis*.

Classification — *Polyporaceae*, *Polyporales*, *Agaricomycetes*.

Basidiomata perennial, resupinate, 5–12 cm long × 1.5–5.5 cm wide, 1–4 mm thick at the margin, with the base strongly adnate to the substrate and hard when dry; *pore surface* cream (D 4); *pores* round to angular 6–8/mm; *dissepiments* thin and entire; *context* reduced to a thin layer above the substrate, less than 1 mm thick, homogeneous and concolorous with the pore surface; *tubes* thin, stratified and concolorous with the pore surface. *Hyphal system* dimitic; *generative hyphae* hyaline, clamped, but difficult to observe think-walled, 1–2 µm wide and branched. *Skeletal hyphae* hyaline to pale yellow, with 1–2(–3) branches, thick-walled, narrow, 1–2.3 µm diam, non- to strongly dextrinoid, often variable in the same basidiomata; pyramidal crystals present in the trama and hymenium. *Cystidia* or other sterile elements absent; *basidia* with 4 sterigmata, clavate with a narrow base, 17–25 × 6–10 µm; *basidiospores* subglobose to broadly ellipsoid, slightly truncate at the apex, slightly thick-walled, smooth, hyaline, non- to weakly dextrinoid, 4.5–5.2 × 3.4–4.7 µm.

Typus. Brazil, Pernambuco, Jaqueira, Reserva do Patrimônio Natural Frei Caneca, on dead wood, Mar. 2012, *G.S. Nogueira-Melo*, NM 103 (holotype URM 84685, isotype in O, ITS and LSU sequences GenBank KX584461 and KX619588, MycoBank MB816440).

Additional specimen examined. Brazil, Amapá, Porto Grande, Floresta Estadual do Amapá, Sept. 2013, *A. Soares*, AS 1054, URM 87053.

Notes — Based on the BLASTn search of GenBank database, according to the LSU sequence, the closest hits are *Perenniporia subacida* (GenBank AY333796; Identities = 900/935 (96 %), Gaps = 7/935 (0 %)), *P. japonica* (GenBank JX141469, Identities = 897/931 (96 %), Gaps = 7/931 (0 %)), and *P. japonica* (GenBank JX141468, Identities = 897/931 (96 %), Gaps = 7/931 (0 %)). Furthermore, using the ITS sequence, the sequence had similarity to *Polyporales* 'sp. 4' (GenBank JQ312166, Identities 531/604 (88 %), Gaps = 26/604 (0 %)), and *P. tenuis* (GenBank JQ001859, Identities = 539/623 (87 %), Gaps = 28/623 (4 %)). Despite the genetic proximity with those three species, *P. japonica* has no crystals in the hymenium, *P. subacida* has larger pores, unbranched skeletal hyphae and no truncate basidiospores and *P. tenuis* has a bright lemon yellow pore surface. Morphologically, *P. paraguyanensis* is also very similar to *P. guyanensis*, but the latter has thinner basidiomata (1–1.2 mm), strongly adhering to the substrate and smaller pores (Decock & Ryvarden 2011) (Table 1).

Table 1 Morphology of resupinate, similar *Perenniporia* species.

Species	Pores/mm	Basidiomata	Basidiospores (µm)	References
P. albo-incarnata	(4–)5–6(–7)	Resupinate	(5.5–)6.0–7.0(–7.5) × (4.5–)5.0–6.0(–6.3)	Decock & Ryvarden (2011)
P. aridula	6–7	Resupinate	6.0–7.0 × 5.1–6.0	Cui & Zhao (2012)
P. brasiliensis	6–7	Resupinate	3.0–4.0 × 2.0–3.0	Present study
P. centrali-africana	(6–)7–8	Resupinate – Effused-reflexed	4.5–6.0(–6.5) × 3.5–5.5	Decock & Mossebo (2001)
P. cinereofusca	4–6	Resupinate	6.5–7.7 × 5.3–6.3	Zhao et al. (2014)
P. guyanensis	(7–)8–9	Resupinate	5.0–5.5(–6.0) × (3.5–)4.0–4.5	Decock & Ryvarden (2011)
P. hainaniana	5–6	Resupinate	4.0–4.5 × 3.0–4.0	Zhao & Cui (2013)
P. japonica	5–6	Resupinate	4.0–5.0 × 2.5–3.5	Ryvarden & Gilbertson (1994)
P. medulla-panis	5–7	Resupinate	4.0–7.0 × 3.5–6.0	Ryvarden & Johansen (1980)
P. paraguyanensis	6–8	Resupinate	4.5–5.2 × 3.4–4.7	Present study
P. parvispora	(6–)7–8	Resupinate	(3.5–)3.7–4.1(–4.5) × 3.0–3.7(–4.0)	Decock & Ryvarden (2000)
P. subacida	(4–)5–6	Effused-reflexed	4.5–6.0 × 3.5–4.5	Ryvarden & Johansen (1980)
P. substraminea	9–12	Resupinate	3.0–3.9 × (2.1–)2.4–3.0	Zhao et al. (2013)
P. subtephropora	6–8	Resupinate	4.0–5.0 × (3.0–)3.5–4.5	Zhao & Cui (2013)
P. tenuis	3–5	Effused-reflexed	4.5–6.0 × 3.5–4.5	Ryvarden & Gilbertson (1994)
P. tibetica	6–10	Pileate	(6–)6.7–8.7(–9) × (5–)5.3–6.8(–7)	Cui & Zhao (2012)

Colour illustrations. Pernambuco, Jaqueira, Reserva do Patrimônio Natural Frei Caneca; basidiomata (scale bar = 1 cm); basidiospores (scale bar = 10 µm); crystals (scale bar = 5 µm).

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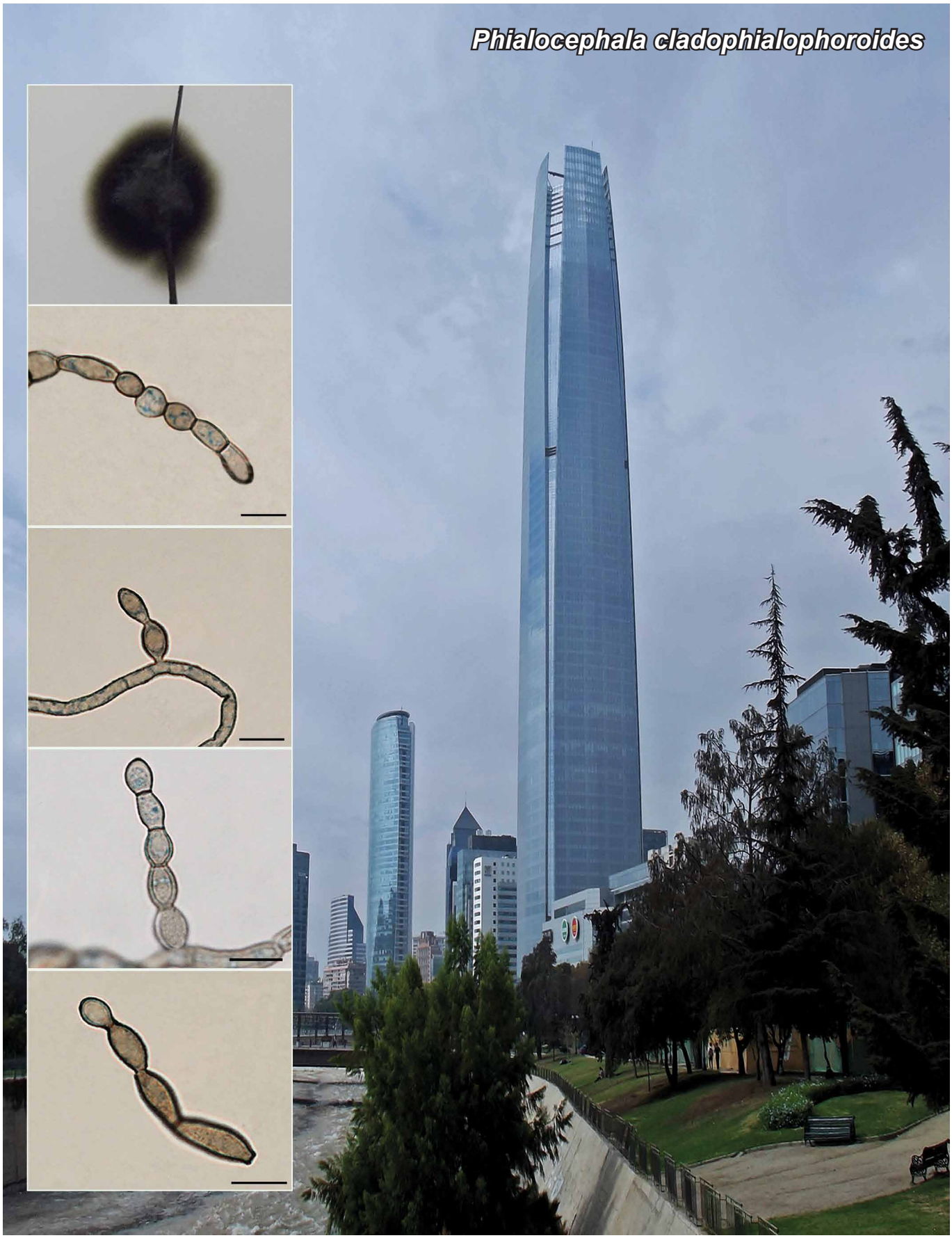
Phialocephala cladophialophoroides

Fungal Planet 613 – 20 June 2017

Phialocephala cladophialophoroides Madrid, C. Tapia, V. Silva & M. Lafourcade, *sp. nov.*

Etymology. The name refers to the morphological similarity between this fungus and members of the genus *Cladophialophora*.

Classification — *Vibrisseaceae*, *Helotiales*, *Leotiomycetes*.

On water agar with sterilised pine needles (PNA): *Mycelium* consisting of septate, branched, subhyaline to dark olivaceous brown, smooth to verruculose, thin- to thick-walled, 1–6 µm wide hyphae, with moniliform segments showing swollen cells up to 8 µm wide. *Conidiophores* micronematous, often reduced to conidiogenous cells, pale to dark olivaceous brown, smooth to verruculose. *Conidiogenous cells* mostly subcylindrical, 12–25 × 4–6 µm. *Conidia* in acropetal, simple, strongly coherent chains, mostly subglobose to subcylindrical, aseptate, pale olivaceous brown to dark brown, smooth-walled to verruculose, 5–17(–22) × (4–)5–6(–7) µm. *Chlamydospores* and *sexual morph* not observed.

Culture characteristics — Colonies after 21 d at 25 °C attaining 26 mm on PNA and 29 mm on MEA, funiculose, with a fimbriate margin, olivaceous black on the former medium, dark grey on the latter; reverse concolorous with obverse on each medium.

Typus. Chile, Santiago, isolated from human toe nail, Nov. 2016, *C. Tapia* (holotype SGO 167659, ex-type culture CCCT 17.04, ITS and LSU sequences GenBank KY798313 and KY798314, MycoBank MB820647).

Notes — This fungus was isolated from toe nail lesions of an immunocompromised patient. The clinical case is currently under study and will be reported elsewhere. The isolate remained sterile or sporulated poorly on routine mycological media, such as malt extract agar or Sabouraud dextrose agar. Therefore, it was grown on PNA in order to stimulate sporulation. On this medium, undifferentiated fertile hyphae produced cladosporioid, coherent chains of aseptate, subglobose to elongate dematiaceous conidia without dark scars. These morphological features closely resembled those of *Cladophialophora* (*Chaetothyriales*), a genus which includes important clinically-relevant species with a broad clinical spectrum, including chromoblastomycosis, phaeohyphomycosis, mycetoma and onychomycosis (Badali et al. 2008, Brasch et al. 2011). BLAST searches with the ITS sequence of isolate CCCT 17.04, however, revealed affinities with species of *Phialocephala* (*Helotiales*), and the closest match was the type species, *P. dimorphospora* (ex-type strain, CBS 300.62, ITS sequence GenBank AF486121, and other strains, 97–98 % identical). Considering that the ITS region provides little resolution for closely related taxa in *Phialocephala* (Tanney et al. 2016), isolate CCCT 17.04 was considered to represent a species different from *P. dimorphospora*.

The genus *Phialocephala* traditionally has been characterised by macronematous conidiophores bearing penicillately arranged, phialidic conidiogenous cells with deep collarettes and aseptate conidia in slimy masses (Kendrick 1961, Seifert et al. 2011). These structures are produced by *P. dimorphospora* in cultures on MEA at 25 °C (Mouton et al. 1993), but were not observed in isolate CCCT 17.04. Several studies have revealed a high degree of morphological plasticity in the asexual morphs of *Phialocephala*, including the occasional presence of an accompanying anavirga-like or diplococcium-like morph in some species, or the production of a synnematous conidial apparatus with blastic, non-phialidic, conidiogenous cells in *P. oblonga* (Descals & Sutton 1976, Tanney et al. 2016). In spite of this morphological variability, no cladophialophora-like morph has been reported previously in *Phialocephala*, supporting the proposal of the novel species described herein.

Colour illustrations. Urban landscape in Santiago de Chile; colony after 21 d at 25 °C on water agar with sterilised pine needles; moniliform hypha; developing and detached conidial chains. Scale bars = 10 µm.

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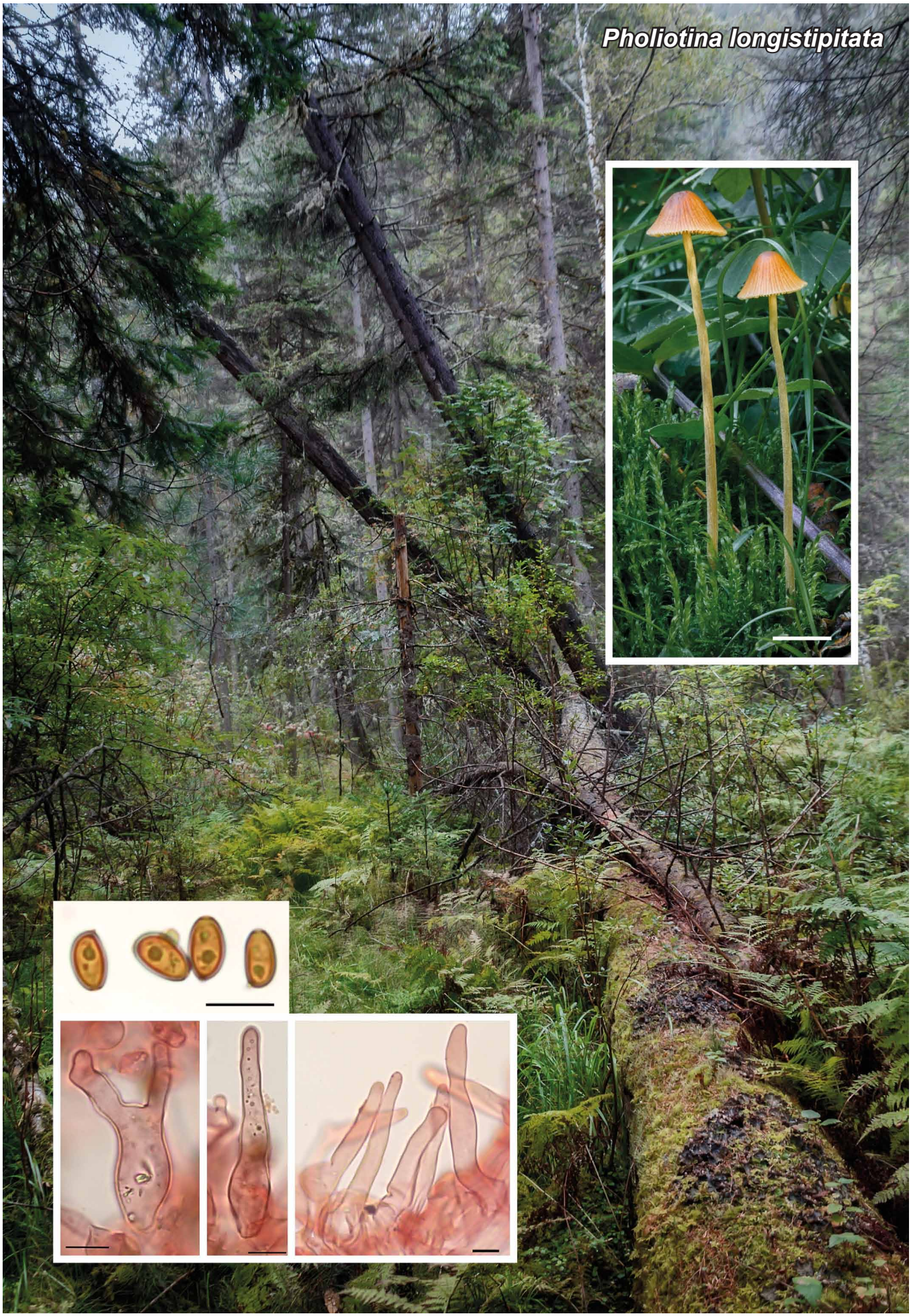

Pholiotina longistipitata

Fungal Planet 614 – 20 June 2017

Pholiotina longistipitata E.F. Malysheva & Kiyashko, *sp. nov.*

Etymology. The epithet emphasises the important character of the new species – basidiocarps with long stipes.

Classification — *Bolbitiaceae*, *Agaricales*, *Agaricomycetes*.

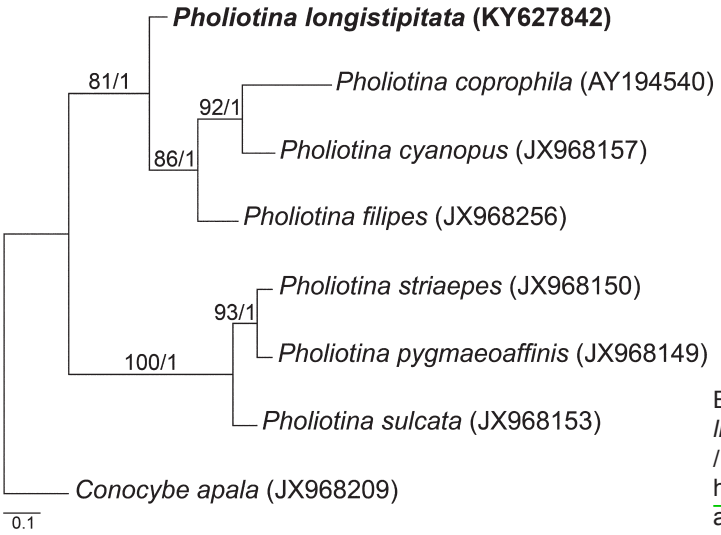
Pileus 5–17 mm, broadly campanulate or obtuse conical, without distinct umbo, with even margin; hygrophanous, up to centre striate; pale brownish orange (7C3–4), sometimes with greyish tint, towards margin paler to cream, towards centre darker – agate or henna (7CE) to reddish brown (8E8) (colour terms according to Kornerup & Wanscher 1978); surface smooth. *Lamellae* moderately distant, narrowly adnate, hardly ventricose, orange-brown to yellow-brown, with concolorous edge. *Stipe* 50–110 × 1–2 mm, cylindrical, subbulbous base; entirely pure white or slightly yellowish; longitudinally fibrillose, minutely pruinose or almost smooth; veil absent. *Basidiospores* 8–9.5 × 4.3–5.4 µm, Q = (1.23–)1.35–2.00, Q* = 1.72, narrowly to broadly ellipsoid, elongate-ellipsoid, yellow-brown in KOH, slightly thick-walled, with distinct germ pore. *Basidia* 18–27 × 8–10 µm, 4-spored, broadly clavate. *Cheilocystidia* 27–55 × 6–11 µm, narrowly to broadly lageniform, fusiform with inflated base and obtuse, occasionally bifurcated, apex, some proportion utriform, thin- or slightly thick-walled. *Pileipellis* a hymeniderm, consisting of clavate to sphaeropedunculate elements, 23–50 × 15–25 µm, slightly thick-walled. *Pileocystidia* numerous, similar to cheilocystidia but larger (up to 110 µm long and 20 µm wide), often pigmented and thick-walled. *Caulocystidia* numerous, often in clusters, similar to cheilocystidia, but larger and more often irregular-shaped, 45–110 × 8–17 µm. *Clamp connections* present.

Habitat & Distribution — In a small group, on litter in mixed forest. Up to now known only from the type locality.

Typus. Russia, Krasnoyarsk Territory, Sayano-Shushenskiy State Biospheric Nature Reserve, floodplain of Malaya Golaya River, mixed forest (*Abies sibirica*, *Pinus sibirica*, *Betula pendula*), among moss, 17 Aug. 2015, *A. Kiyashko* & *E. Malysheva* (holotype LE312984, ITS and LSU sequences GenBank KY627842 and KY627843, MycoBank MB819993).

Notes — *Pholiotina longistipitata* is characterised by the following features: rather slender basidiocarps with conical pilei strongly striated up to the centre, long whitish stipes, relatively small elongate-ellipsoid basidiospores, and numerous pileocystidia in the pileus.

Due to absence of a veil and lageniform cheilocystidia, *Pholiotina longistipitata* can be placed in sect. *Piliferae*. This new species is quite similar to *Ph. striipes* on the basis of a complex of microscopic features, but the latter noticeably differs in habit, forming rather stout basidiocarps that commonly grow in fascicles, having a lower ratio of stipe length to pileus diameter as well as differently shaped and weakly striated pileus (Hausknecht 2009). An additional difference is based on an ITS sequence analysis which demonstrated strong dissimilarity with more than 30 % distance between sequences (in comparison with WU269997 specimen of *Ph. striipes* originated from Austria). *Pholiotina pygmaeoaffinis* differs in having significantly larger basidiospores, smaller caulocystidia and geographical distribution restricted by Europe (Hausknecht 2009).



Best tree from a ML analysis of the ITS dataset of some *Pholiotina* species from sect. *Piliferae*. Support values (BS ≥ 50 % / PP ≥ 0.95) are given above the branches. Maximum likelihood analysis was run in the PhyML server v. 3.0 (http://www.atgc-montpellier.fr/phyml/) under a GTR model, with 100 rapid bootstrap replicates. Bayesian analysis was performed with MrBayes v. 3.1 software (Ronquist & Huelsenbeck 2003) for two independent runs, each with 5 million generations and under the same model. Taxa names are followed by the GenBank accession numbers. The novel species is indicated in **bold**. The tree was rooted to *Conocybe apala* (GenBank JX968209). The scale bar indicates the expected changes per site.

Colour illustrations. Russia, South Siberia, Sayano-Shushenskiy State Biospheric Nature Reserve, site in taiga where fungus was found; basidiocarps, basidiospores, cheilocystidia, caulocystidia (all from holotype). Scale bars = 1 cm (basidiocarps), 10 µm (microscopic structures).

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Phytophthora mekongensis

Fungal Planet 615 – 20 June 2017

Phytophthora mekongensis Cacciola & N.V. Hoa, *sp. nov.*

Etymology. Name refers to the area from where the species was isolated, Mekong River Delta in Vietnam.

Classification — *Peronosporaceae*, *Peronosporales*, *Peronosporomycetes*.

Sporangia produced on V8-agar (V8A) flooded with both distilled water and non-sterile soil extract (Jung et al. 2017), formed in dense sympodia and were limoniform, ovoid-obpyriform, ellipsoid to fusiform, papillate, frequently bi-papillate and bi- or tri-lobed, often caducous (pedicel length 5–15 µm) with a conspicuous basal plug at the point where the pedicel attaches to the sporangium; average size of sporangia was 35 × 24 µm (overall range 25–50 × 20–36 µm) with a mean length/breadth ratio of 1.5. *Gametangia* were not produced in single culture or in dual cultures with A1 and A2 mating type tester strains of *P. nicotianae* and *P. citrophthora* (Puglisi et al. 2017). Minimum, optimum and maximum temperatures for growth were 12 °C, 28 °C and 36 °C, respectively. Radial growth rate on V8A in the dark at 28 °C was 6.7 ± 0.1 mm/d.

Culture characteristics — Colonies are stellate to rosaceous on V8A and stellate on PDA.

Typus. Southern Vietnam, Vĩnh Long province, Mekong Delta region, from *Citrus grandis* (syn.: *C. maxima*) fruit, 2012, *A. De Patrizio & G. Magnano di San Lio* (holotype PF6a2, culture ex-type PF6a2 = CBS 135136, ITS and COI sequences GenBank KC875838 and KT366920, MycoBank MB820796).

Additional specimens examined. Southern Vietnam, Vĩnh Long province, Mekong Delta region, from *Citrus grandis* fruits, 2012, *A. De Patrizio & G. Magnano di San Lio*, 68 isolates; Ben Tre, Mekong Delta region, from *Citrus grandis* roots, five isolates.

Notes — Phylogenetically (phylogenetic tree reported in Puglisi et al. 2017; supplementary figure in MycoBank), *Phytophthora mekongensis* resides in the *Phytophthora* major Clade 2, subclade 2a, and is closely related to *P. meadii* and *P. colocasiae* (Puglisi et al. 2017). In nature, *P. mekongensis* was found associated with root rot and fruit brown rot of pomelo (*C. grandis*). In artificial inoculations it induced brown rot on various *Citrus* species, including pomelo, grapefruit, sweet orange and bergamot as well as gum exudation from the bark of pomelo ‘Chandler’ and sweet orange ‘Lane late’ (Puglisi et al. 2017).

Colour illustrations. Typical environment for recovery of *P. mekongensis*; sympodium of limoniform, papillate sporangia; limoniform, papillate caducous sporangium; limoniform papillate sporangium; bipapillate sporangium with medium-length pedicel; obpyriform, papillate caducous sporangium with medium-length pedicel and curved apex. Scale bars = 10 µm.

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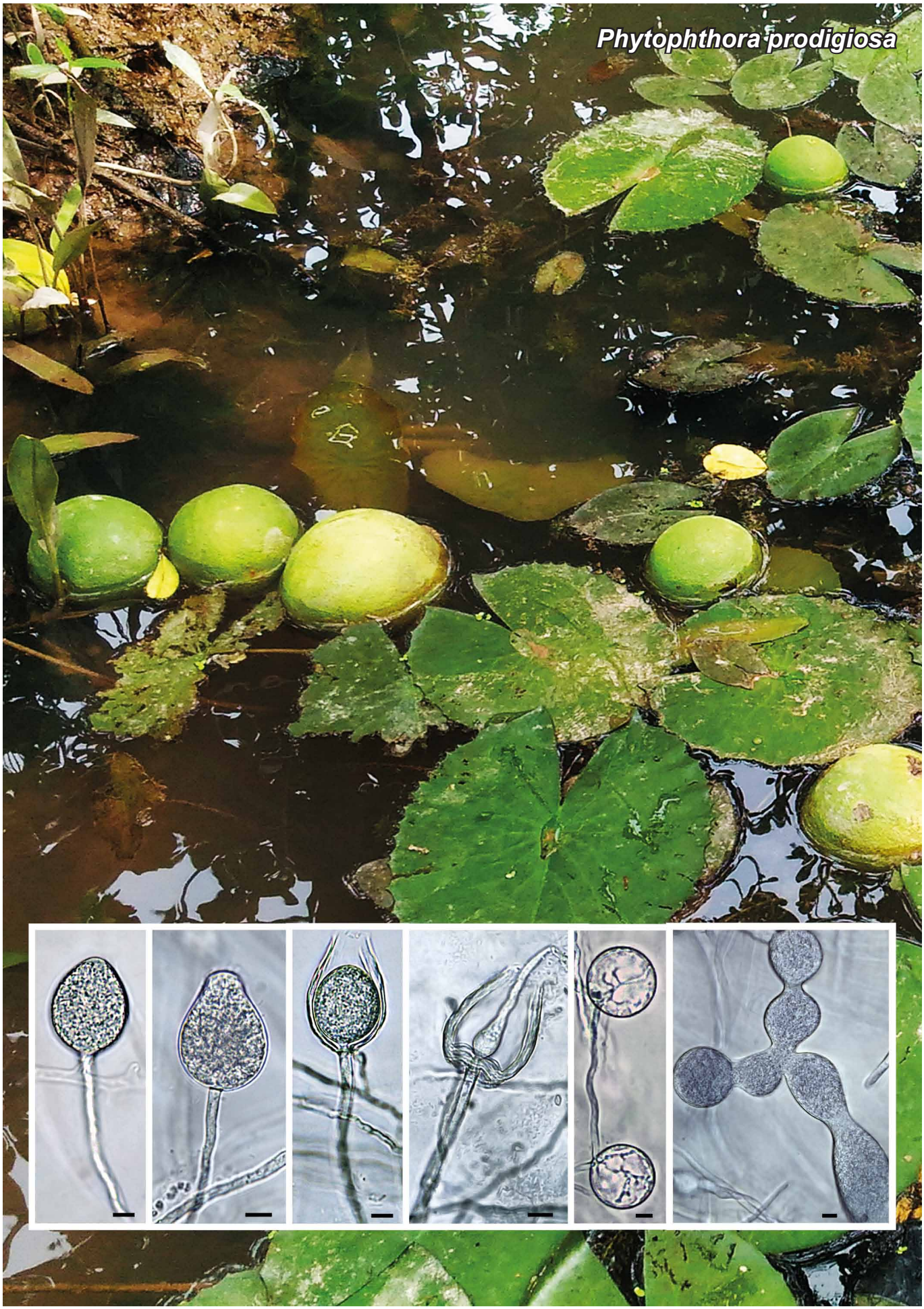
Phytophthora prodigiosa

Fungal Planet 616 – 20 June 2017

Phytophthora prodigiosa Cacciola & M.V. Tri, *sp. nov.*

Etymology. Name refers to the bizarre (*prodigiosum* in Latin) and unusual shape of the hyphal swellings.

Classification — *Peronosporaceae*, *Peronosporales*, *Peronosporomycetes*.

Sporangia produced on V8-agar (V8A) flooded with both distilled water and non-sterile soil extract (Jung et al. 2017), were non-caducous, ovoid to obpyriform, and non-papillate; average size of sporangia was 45 × 32 µm (overall range 30–50 × 19–34 µm) with a mean length/breadth ratio of 1.4. *Sporangia* proliferated internally in both nested and extended way. *Chlamydospores* of variable size (20–48 µm), globose to obpyriform, sometimes laterally attached. Catenulate, elongated to globose *hyphal swellings*, often with a bizarre shape, were abundantly formed on V8A. *Gametangia* not produced in single culture or in dual cultures with A1 and A2 mating type tester strains of *P. nicotianae* and *P. citrophthora* (Puglisi et al. 2017). Minimum, optimum and maximum temperatures for growth were 12 °C, 32 °C and 36 °C, respectively. Radial growth rate on V8A in the dark at 32 °C was 6.5 ± 1.4 mm/d.

Culture characteristics — A rosaceous colony growth pattern was produced on V8A and PDA.

Typus. Southern Vietnam, Vĩnh Long province, Mekong Delta region, from *Citrus grandis* (syn.: *C. maxima*) fruit, 2012, *A. De Patrizio & G. Magnano di San Lio* (holotype PF6e, culture ex-type PF6e = CBS 135138, ITS and COI sequences GenBank KC875840 and KT366918, MycoBank MB820797).

Additional specimens examined. Southern Vietnam, Vĩnh Long province, Mekong Delta region, from *Citrus grandis* fruits, 2012, *A. De Patrizio & G. Magnano di San Lio*, nine isolates; Dong Thap, Mekong Delta region, from Mandarin / Volkamer lemon roots, five isolates.

Notes — Phylogenetically (phylogenetic tree reported in Puglisi et al. 2017; supplementary figure in MycoBank), *Phytophthora prodigiosa* resides in *Phytophthora* major Clade 9 and shows many morphological characteristics corresponding to the original description of *P. insolita* (Ann & Ko 1980). The major difference between the two species is the sterile breeding system of *P. prodigiosa*, whereas *P. insolita* is homothallic. In nature, *P. prodigiosa* was found associated with brown rot of pomelo (*C. grandis*) fruit fallen to the ground or floating on water as well as on rotten rootlets of citrus trees (Puglisi et al. 2017).

Colour illustrations. Typical habitat for the recovery of *P. prodigiosa*; persistent, non-papillate ovoid sporangium; obpyriform, persistent sporangium; sporangium with internal nested proliferation; sporangium with internal nested and extended proliferation; globose, small, sessile chlamydospores; irregularly shaped hyphal swellings. Scale bars = 10 µm.

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Polycephalomyces onorei

Fungal Planet 617 – 20 June 2017

Polycephalomyces onorei Kautman & Kautmanova, *sp. nov.*

Etymology. Named after Giovanni Onore, a great Italian naturalist living in Ecuador and founder of the Otonga foundation.

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

Stromata numerous, irregularly growing in various directions from the whole body of hairy, red-headed caterpillar of undetermined moth species, probably of subfamily *Arctinae* (*Lepidoptera*, *Erebidae*); stromata solitary, simple or 2–3 times branched, 10–25(–45) × 0.5–1.5 mm, ampulliform, thickened at the base, cinnamon brown, darker when wet, fading with age and drying to greyish brown. Fertile parts with perithecia 1–4 mm diam, subapical, forming lateral pads around stipe, pale brown to ochraceous orange. Sterile apical parts whitish, often twisted, simple or 2–3 times branched, in old specimens sometimes missing, probably broken with age. *Perithecia* 854–950 × 330–395 µm, narrowly pyriform, with dark brown protruding apices, close to each other and immersed when young, emerged and apart when mature. *Asci* 450–510 µm long, *ascospores* filiform, cylindrical, breaking to small truncate, bacilliform part-spores (3.5–)4(–5.5) × 0.5–1 µm, sometimes part-spores not divided, then up to 6 µm long.

Habitat & Ecology — Western slopes of Los Andes (Ecuador), mostly secondary pre-montane forest with residues of primary forest. Parasitised caterpillars were found on bare soil, sometimes half buried, or among leaves and debris, in shaded places, one specimen was found on a stem of *Etlingera* sp. plant c. 1 m above ground.

Typus. Ecuador, Prov. Cotopaxi, Union de Toachi village, S0°19.256' W78°57.101', alt. 840 m, on caterpillar of *Lepidoptera* (cf. *Arctinae*), on stem of *Etlingera* sp., in secondary pre-montane rainforest close to Otongachi field station, at the right bank of Toachi River, 27 Mar. 2011, *V. Kautman* (holotype BRA CR23902, ITS sequence GenBank KU898841, MycoBank MB819868).

Additional specimens examined. Ecuador, Prov. Cotopaxi, Union de Toachi village, S0°19.256' W78°57.101', alt. 830 m, on caterpillar of *Lepidoptera* (cf. *Arctinae*), on bare soil among shrubs, 1 Apr. 2011, *V. Kautman*, BRA CR23903, ITS sequence GenBank KU898842; ibid., alt. 840 m, on caterpillar of *Lepidoptera* (cf. *Arctinae*), in soil among herbs and fallen leaves, 2 Mar. 2014, *V. Kautman*, BRA CR23904, ITS sequence GenBank KU898843; ibid., alt. 845 m, on caterpillar of *Leidoptera* (cf. *Arctinae*), buried in soil, 2 Mar. 2014, *V. Kautman*, BRA CR23905, ITS sequence GenBank KU898844; ibid., on caterpillar of undetermined *Lepidoptera*, on ground, 26 Mar. 2016, *V. Kautman*, BRACR25968.

Notes — *Polycephalomyces onorei* belongs to a group of sexual species of *Polycephalomyces* s.l., which until now was unknown to have asexual morphs, as defined by Kepler et al. (2013). It is well distinguished from all other *Polycephalomyces* species by the following combination of characters: lepidopteran host, large stromata up to 3.5 cm tall, perithecia big, pyriform and in maturity protruding, part-spores small.

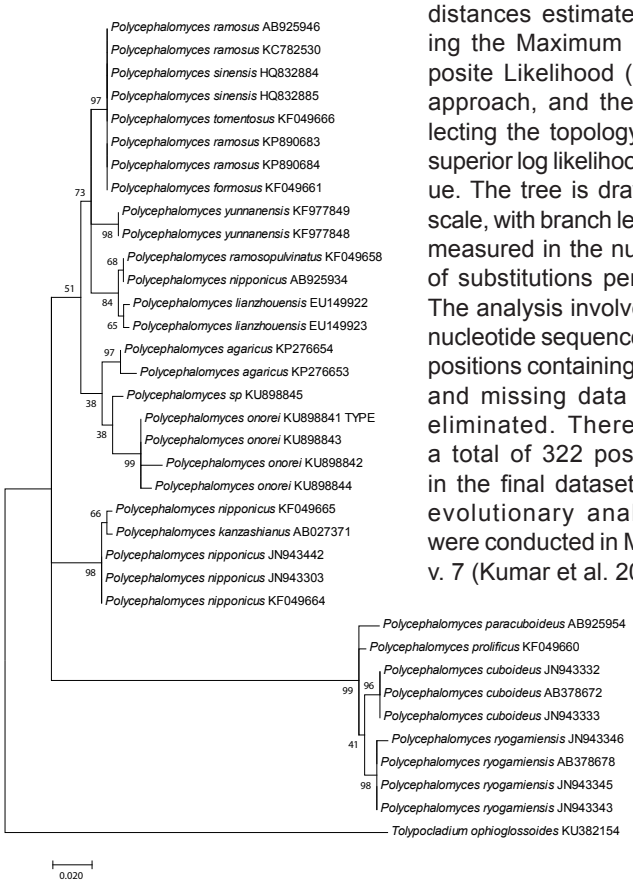
Colour illustrations. Type locality – interior of the secondary pre-montane rainforest at the vicinity of the Otongachi Field Station, Union de Toachi, Cotopaxi Province, Ecuador, holotype; mature stromata; detail of the fertile part with perithecia; immature stromata; perithecia; ascus; part-spores (from holotype). Scale bars: lower row = 1 cm, part-spores = 10 µm, ascus and perithecia = 100 µm.

Macroscopically, *P. onorei* is the most similar to *P. lianzhouensis* which also parasitises lepidopteran caterpillars. However, *P. lianzhouensis* is much smaller (2–12 mm long), with a hemispherical capiform fertile part with very few, immersed, narrowly ovoid perithecia, which are also much smaller (355–473 × 158–197 µm). Part-spores are larger, up to 7.5 µm long. Bare stroma tips characteristic for *P. onorei* were also not observed in *P. lianzhouensis*. In the ML tree of the ITS region (MycoBank supplementary figure) *P. lianzhouensis* is positioned on a distant branch together with the *Cicadidae* nymphs parasite *P. ramosopulvinatus*, with which it shares also similarity in some macro- and micro-characters (Wang et al. 2014).

The closest species to *P. onorei* in the ITS tree is *P. agaricus*, an asexual hyperparasite growing in the form of very small synnemata (0.3–1.2 mm) on an *Ophiocordyceps* sp. parasitising melolonthoid larvae (Wang et al. 2015).

Polycephalomyces onorei is the first published record of a sexual *Polycephalomyces* species from the American continent. Until recently all published records were from Asia, mostly China and Japan.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Tamura-Nei model (Tamura & Nei 1993). The tree with the highest log likelihood (-1013.9878) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbour-Joining and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 36 nucleotide sequences. All positions containing gaps and missing data were eliminated. There was a total of 322 positions in the final dataset. The evolutionary analyses were conducted in MEGA v. 7 (Kumar et al. 2016).



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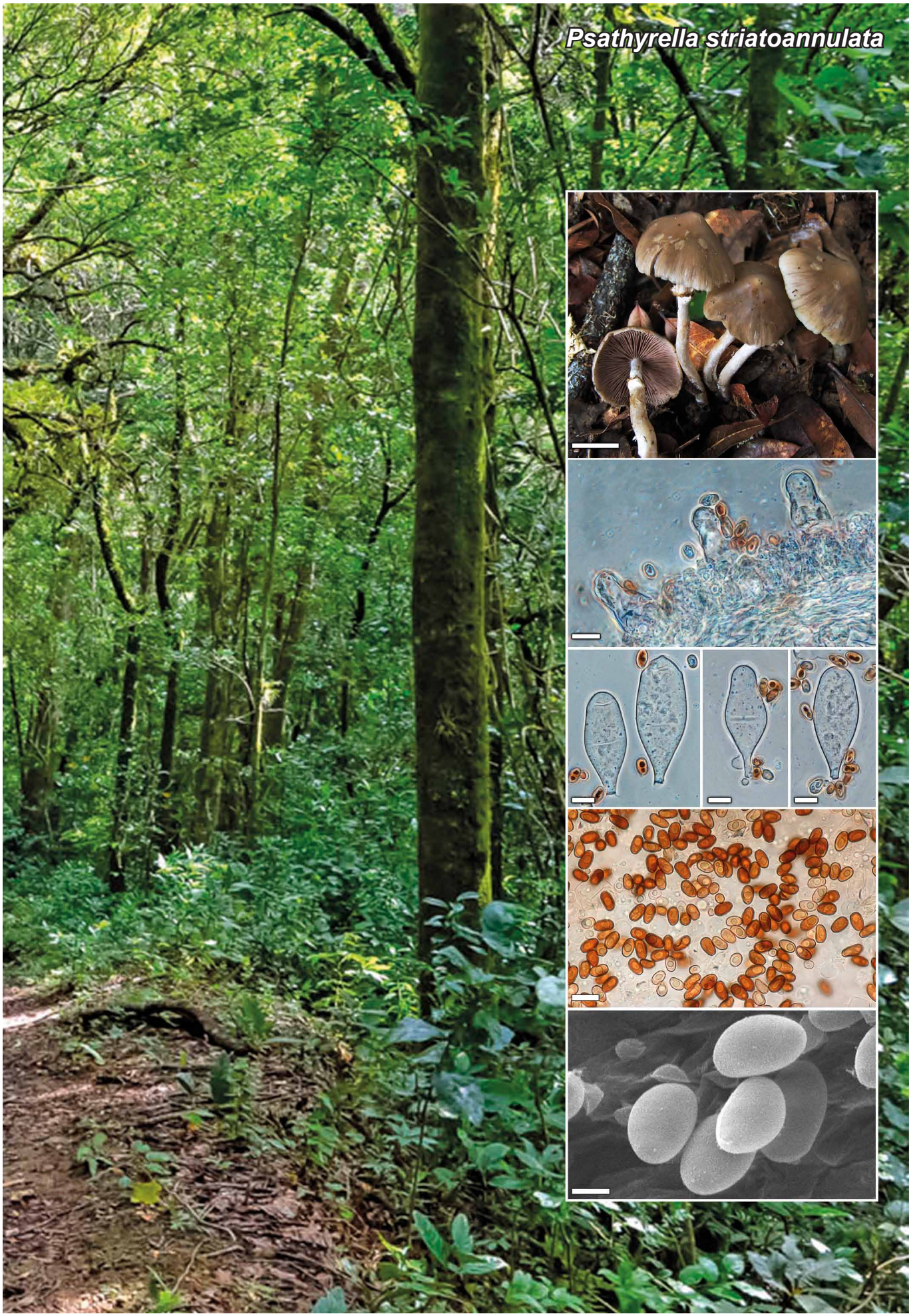
Psathyrella striatoannulata

Fungal Planet 618 – 20 June 2017

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

Etymology. Name refers to the presence of a striate ring on the stipe of this fungus.

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

Cap 12–36 mm broad, convex to applanate convex, with umbo, glabrous, pale brown (121 C, mikado brown) to greyish brown (219 B, army brown), becoming paler brown when drying (223 D tawny olive). Margin deflexed, hygrophanous, striate. *Context* of pileus 1 mm thick, concolorous to whitish. *Veil* white, forming an annulus on stem and fugacious, small, scattered fibrils at margin of cap and lower part of stem. *Gills* 1–4 mm broad, adnate to subdecurrent, close, coffee brown greyish (Mu 9.0 YR 5.5/2.5) to brown (219 B army brown), with entire edge; lamellulae present. *Stem* 42–110 × 1–5 mm, cylindrical, central, hollow, fibrillose, white, with some brownish tinges, especially below the ring, equipped with an apical conspicuous well-developed upright membranous annulus, white to brownish at margin (221 A warm sepia), its margin longitudinally striate. *Odour* and *taste* not distinctive. *Spores* 7.5–9.5(–10) × 4–5.5 µm, av. 8–8.3 × 4.4–4.6 (2 collections), Q_{av} 1.74–1.86, ellipsoid, smooth, with apical germ pore, in NH_4OH (10 %) reddish brown. *Basidia* 4-spored, 18–27 × 7–9 µm, clavate, hyaline. *Pleurocystidia* 45–52 × 14–21 µm, numerous, utriform to cylindrical or clavate, thin-walled, sometimes at the upper part slightly thick-walled and wall refractive, then ochraceous brown to reddish brown, hyaline or frequently with reddish brown granular content in their apical part, at and around apex sometimes covered with mucoid droplets or granular deposits, variable in number and size, staining reddish brown in NH_4OH (10 %) when (still fairly) fresh. *Marginal cells*: sphaeropedunculate and clavate cells 18–32 × 11–16 µm, abundant and almost exclusively forming the cellular lining of gill edge; pleurocystidioid cheilocystidia 25–35 × 11–13 µm, scarce, utriform; all cells thin-walled, colourless. *Hymenophoral trama* in NH_4OH (10 %) consisting of hyaline thin-walled hyphae, without encrustations. *Clamp connections* present (especially in thin hyphae of hymenium) but difficult to observe.

Habitat & Distribution — Growing gregarious on woody debris or terrestrial. So far only known from Costa Rica.

Typus. Costa Rica, Puntarenas, La Amistad Pacífico, unprotected area, Finca Santa Marta, at the base of the Cerro Quijada del Diablo, 1 600–1 700 m; 8:53:51.7890N-82:45:30.1370W, on soil, 12 June 2008, *E. Navarro* (holotype INB0004162132, ITS sequence GenBank KY350220, MycoBank MB819509; isotype AH 46129).

Additional specimens examined. ***Psathyrella striatoannulata***: Costa Rica, Puntarenas, La Amistad Pacífico, unprotected area, Mellizas, near the catholic church, 1400–1500 m, 8:53:09.5830N-82:46:16.0650W, on woody debris, 29 Aug. 2005, *E. Navarro*, paratype INB0003978642, E. Navarro 9454, ITS sequence GenBank KY350221. ***Psathyrella phegophila***: Spain, Navarra, Elzaburu, in dead leaves of *Fagus sylvatica*, 28 Oct. 1978, *L.M. García Bona*, AH 45940, ITS sequence GenBank KY350219. ***Psathyrella fatua***: Spain, Madrid, Alcalá de Henares, El Gurugú, under *Kochia prostrata* close to *Pinus halepensis* wood, 12 Nov. 2014, *G. Moreno & M. Heykoop*, AH 33718, ITS sequence GenBank KY350222. ***Psathyrella ammophila***: Spain, Asturias, Oviedo, in sand on beach, 4 May 1974, *G. López & G. Moreno*, AH 947, ITS sequence GenBank KY350223; Madrid, Alcalá de Henares, El Gurugú, in humus of *Kockia prostrata*, 9 Oct. 1998, *M. Heykoop*, *J. Rejos & G. Moreno*, AH 24456, ITS sequence GenBank KY350224.

Colour illustrations. Costa Rica, vegetation of the Finca Santa Marta 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), 10 µm (spores under LM), 2 µm (spores under SEM).

Notes — For the description of the colours the Naturalist's colour guide of Smithe (1975) as well as the Munsell soil colour charts (Munsell 1975) were used. *Psathyrella striatoannulata* is characterised by its conspicuous well-developed and persistent membranous ring, abundant utriform pleurocystidia, which sometimes are slightly thick-walled and covered with reddish brown mucoid droplets or granular deposits (similar to those of *P. lutensis*), and by growing with gregarious habit on soil or woody debris.

In our ITS phylogeny (MycoBank supplementary data), *P. striatoannulata* belongs to the spadiceogrisea clade in which it is related to *P. phegophila*. The presence of this monophyletic assemblage, corresponding to subsection *Spadiceogriseae* of Kits van Waveren (1985) has already been noted by Vasutová et al. (2008), Larsson & Örstadius (2008), Nagy et al. (2013) and Örstadius et al. (2015). As pointed out by Nagy et al. (2013), in the spadiceogrisea clade the basidiomes are fairly large (more than 3 cm), non-deliquescent with medium-sized, ellipsoid-subphaseoliform spores (7–9 µm), and fibrillose, scanty veil that is visible only on young specimens. The gill edge is lined mainly with poorly developed globose-sphaeropedunculate cells (paracystidia), whereas true, utriform cheilocystidia are very scarce.

Because of the gill-edge lined with large numbers of predominantly sphaeropedunculate and clavate cells and few scattered utriform cheilocystidia, *P. striatoannulata* keys out in Kits van Waveren's monograph (1985) close to *P. phegophila*. *Psathyrella striatoannulata*, however, differs from *P. phegophila* by the presence of a persistent well-developed annulus, the pleurocystidia often covered with reddish brown mucoid droplets or granular deposits and by their slightly thick-walled apices which frequently show reddish brown granular contents, and by its different habitat not restricted to *Fagus sylvatica* woods. The presence of cystidia covered with mucoid droplets or granular deposits is not a constant character since in old specimens they very gradually disappear. If thoroughly searched for, however, some reddish brown deposits may still be found. Other species of *Psathyrella* s.l. with cystidia covered with mucoid droplets or granular deposits are, e.g., *P. lutensis* with bluish green mucoid deposits; *Cystoagaricus sylvestris* (= *P. populina*) with bluish green deposits; *C. hirtosquamulosa* (= *P. hirtosquamulosa*) with greenish deposits; *P. supernula* (= *P. narcotica*) with greenish deposits; *P. jacobssonii* with greenish deposits; and *P. niveobadia* with yellowish brown deposits. However, *P. striatoannulata* differs from all these species by a very different set of macro- and microscopical characters.

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Pseudocercospora leandrae-fragilis

Fungal Planet 619 – 20 June 2017

Pseudocercospora leandrae-fragilis O.L. Pereira & Meir. Silva, *sp. nov.*

Etymology. Name derived from the plant host, *Leandra fragilis*.

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

Leaf spots amphigenous, irregular, initially chlorotic, becoming brown with age, 3–8 mm diam. *Internal mycelium* indistinct. *External mycelium* absent. *Stromata* well-developed, subglobose to irregular, brown, cells of brown *textura subglobosa*. *Conidiophores* hypophyllous, aggregated in sporodochia, arising from the upper cells of the stroma, subcylindrical, 16.5–34 × 3–4.5 µm, 0–2-septate, straight or geniculate, unbranched, brown, smooth, mostly restricted to conidiogenous cells. *Conidiogenous cells* terminal, subcylindrical, brown, smooth. *Conidiogenous loci* inconspicuous, unthickened, not darkened. *Conidia* solitary, guttulate, pale brown, smooth, subcylindrical, straight to curved, 80–164.5 × 4–5 µm, apex obtuse, base truncate, septate, hila unthickened, neither darkened nor refractive.

Culture characteristics — Colonies on PDA 18 mm diam after 2 wk at 25 °C in the dark; slow-growing raised, margins irregular, with aerial mycelium sparse, grey, reverse iron-grey, sterile.

Typus. Brazil, Minas Gerais, Araponga, Parque Estadual da Serra do Brigadeiro, on leaves of *Leandra fragilis* (*Melastomataceae*), 28 Mar. 2015, *O.L. Pereira & M. Silva* (holotype VIC 44202, culture ex-type COAD 1977; ITS and LSU sequences GenBank KY574288 and KY574287, MycoBank MB819904).

Notes — Nineteen *Pseudocercospora* species have been described from hosts in the *Melastomataceae*: *P. aciotidis*, *P. curta*, *P. dissotidis*, *P. erythrogena*, *P. leandrae*, *P. melastomobia*, *P. miconiae*, *P. miconiicola*, *P. miconiigena*, *P. mirandensis*, *P. monochaeticola*, *P. osbeckiae*, *P. oxysporae*, *P. subsynnematosa*, *P. tamoneae*, *P. tibouchina-herbaceae*, *P. tibouchinae*, *P. tibouchinicola* and *P. tibouchinigena* (Parreira et al. 2014, Silva et al. 2016, Farr & Rossman 2017). However, only one species of *Pseudocercospora* is known to occur on a member of *Leandra* (Crous & Braun 2003, Farr & Rossman 2017), namely *P. leandrae* on *Leandra subseriata* from Colombia and Ecuador (Crous & Braun 2003). *Pseudocercospora leandrae* clearly differs from *P. leandrae-fragilis* by having longer conidiophores (20–80 µm) and smaller conidia (40–140 µm) (Braun 1999). Among these species in *Melastomataceae*, *Pseudocercospora melastomobia* is morphologically similar but distinguishable from *P. leandrae-fragilis* by having longer and wider conidiophores (10–50 × 3.5–5.5 µm) and smaller conidia (50–150 µm). Additionally, *P. leandrae-fragilis* does not correspond to any sequences available in GenBank at present. Hence, it is described here as a new species.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Pseudocercospora basitruncata* (GenBank KF901632; Identities = 441/446 (99 %), Gaps = 3/446 (0 %)), *Pseudocercospora* sp. (GenBank DQ303084; Identities = 440/445 (99 %), Gaps = 2/445 (0 %)), and *Pseudocercospora paranaensis* (GenBank KT037523; Identities = 438/445 (98 %), Gaps = 2/445 (0 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Pseudocercospora rhabdothamni* (GenBank JQ324964; Identities = 849/849 (100 %), no gaps), *Pseudocercospora cyathicola* (GenBank JF951159; Identities = 849/849 (100 %), no gaps), and *Pseudocercospora humuli* (GenBank GU214676; Identities = 849/849 (100 %), no gaps).

Colour illustrations. Inflorescence of *Leandra fragilis* growing in the Atlantic rainforest at Parque Estadual da Serra do Brigadeiro, state of Minas Gerais, Brazil; leaf spot symptoms; conidiophores aggregated in sporodochia and conidia. Scale bar = 20 µm.

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Rhodocybe matesina

Fungal Planet 620 – 20 June 2017

Rhodocybe matesina Picillo & Vizzini, *sp. nov.*

Etymology. The epithet refers to the locality, Monti del Matese, where this species was found.

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

Pileus 25–60 mm diam, at first convex, then plane and often shallowly depressed at centre with age; surface hygrophanous, beige-salmon-pink to beige-hazelnut when wet, cream with darker zonations towards the pileus margin when dry, pruinose when young, then smooth, dry; margin slightly inrolled when young, soon plane, strongly undulate, lobate when old, cracking longitudinally at times, not striate. *Lamellae* broadly adnate to shortly decurrent, close, up to 3 mm high, intermixed with 1–4(–5) lamellae of variable length (lamellulae), at first whitish, then beige, finally pinkish when very old, easily detachable from the pileus context (as in *Lepista* species); edge entire or slightly eroded, concolorous. *Stipe* 30–60 × 4–9 mm, central, cylindrical to slightly clavate, straight to somewhat flexuose towards the base, solid; at first whitish, then concolorous with the pileus or slightly paler, white pruinose at apex, fibrillose-flocculent elsewhere; with a white basal mycelial tomentum and white rhizomorphs. *Context* thin, fibrous, whitish, beige in the cortex, unchanging when handled. *Odour* peculiar, pleasant, reminding that of *Hygrophorus penarioides*. *Taste* bitter, astringent, numbing the tongue after long chewing. *Spore-print* pinkish. *Macrochemical reactions* 20 % KOH on context negative; on pileus surface olive green. *Basidiospores* (5.5–)6–7(–7.5) × (3.5–)4–4.5(–5) µm [n = 32], on average 6.6 × 4.2 µm, Q = (1.41–)1.43–1.77(–1.97), Q_m = 1.58, subpyriform, broadly ellipsoid to ellipsoid in frontal view, subamygdaliform with suprahilar depression in side view, angular with 6–8 facets in polar view, clearly undulate-pustulate, gibbous, colourless, thin-walled, mono- to pluriguttulate, walls cyanophilic, inamyloid, non-dextrinoid. *Basidia* 20–28 × 5.5–8 µm, clavate, colourless, thin-walled, usually 4-spored, rarely 2-spored; sterigmata up to 4.5 µm long. *Lamella edge* heterogeneous. *Cheilocystidia* 16.5–23 × 3–6.5 µm, scattered, flexuose-cylindrical, often with a secondary septum in the middle zone, colourless, thin-walled. *Pleurocystidia* absent. *Hymenophoral trama* subregular, consisting of cylindrical hyphae mixed with short, inflated elements, 3.5–16 µm diam, thin-walled, colourless, sometimes secondarily septate. *Subhymenium* filamentous of thin (up to 3.5 µm wide) elements. *Pileipellis*: suprapellis as a xerocutis, made up of subparallel, thin-walled, 2–6 µm wide, tightly packed cylindrical hyphae with a pale cream wall pigment and occasionally with a faint, hyaline encrustation; subpellis not well-differentiated, consisting of cylindrical, up to 12 µm wide hyphae. *Stipitipellis* as a xerocutis of parallel, thin- to moderately thick-walled (up to 0.4 µm), 2–6 µm diam, cylindrical hyphae. *Caulocystidia* absent. *Thromboplerous hyphae* rare, but present in all tissues. *Clamp connections* absent, but in the pileipellis rare pseudoclamps (unfused clamp connections) were observed.

Colour illustrations. *Cupressus sempervirens* var. *horizontalis* forest in the type locality; basidiomata *in situ* (MCVE 29261, MCVE 29262); microscopical features (from MCVE 29262); pileipellis (in ammoniacal Congo red); element of the subpellis with a pseudoclamp (indicated by an asterisk; in ammoniacal Congo red); basidiospores (phase contrast microscopy); cheilocystidia (phase contrast microscopy). Scale bars: left panel = 20 mm; right panel = 10 µm. (Pictures by B. Picillo).

Habit, Habitat & Distribution — Terricolous, gregarious or in small clusters of 2–3 basidiomes, under *Cupressus sempervirens* var. *horizontalis*, in autumn. So far only known from the type locality (Campania, Italy).

Typus. Italy, Campania, Fontegreca (CE), Monti del Matese, loc. Bosco degli Zappini, N41°46'030" E14°19'318", 387 m a.s.l., in a *Cupressus sempervirens* var. *horizontalis* wood, with *Hedera helix*, on calcareous soil, 21 Oct. 2012, *B. Picillo* (holotype MCVE 29262, ITS and LSU sequences GenBank KY629961 and KY629963, MycoBank 820033); ibid., 16 Oct. 2016, *B. Picillo* (paratype MCVE 29261, ITS and LSU sequences GenBank KY629962 and KY629964).

Notes — *Rhodocybe matesina* belongs to sect. *Rufobrunnea*, typified by *R. roseiavellanea*, which encompasses the *Rhodocybe* species characterised by a reddish beige, salmon pink, pinkish brown, ochre or reddish brown pileus, adnate to decurrent lamellae, and the absence of clamp-connections (Baroni 1981). Within this section, the new species is circumscribed by medium-sized basidiomes (up to 60 mm broad), an aromatic odour, bitter taste, a thin-fleshed depressed pileus, broadly ellipsoid to ellipsoid basidiospores, pileipellis hyphae with weakly incrusting pigment, and absence of pileo- and caulocystidia. Phylogenetically (MycoBank supplementary data), the ITS sequence analysis shows it sister (BPP = 1, MLB = 100 %) to a recently described species from Turkey, *R. asanii* which differs by shorter basidiospores, (4.5–)5.5–6.5(–7) × (3–)3.5–4.5(–5) µm (av. 5.8 × 4.1 µm), indistinct odour and taste, and adnexed to sinuate lamellae (Sesli & Vizzini 2017). The LSU sequence analysis (data not shown) also indicates *R. asanii* as its closest species. Morphologically, the most similar species are *R. alutacea*, *R. asyae*, *R. incarnata*, *R. pseudopiperita*, and *R. roseiavellanea*. *Rhodocybe alutacea* from North America has a smaller pileus (up to 35 mm diam), a pileus margin remaining inrolled to incurved, a farinaceous odour and taste (mild), septate cheilocystidia with often capitulate terminal elements, and presence of cylindrical to clavate caulocystidia (Singer 1946, Baroni 1981, Baroni & Horak 1994). *Rhodocybe asyae* from Turkey differs in having smaller basidiomes (pileus up to 30 mm diam and stipe up to 5 mm diam), a mild taste, mainly 2-spored basidia, versiform cheilocystidia and less elongated basidiospores (Q_m = 1.3) (Sesli & Vizzini 2017). *Rhodocybe incarnata* from Venezuela differs by a pileus at first fire red, flame red, flame scarlet than becoming paler, a mild taste, but with latent sharpness in back of throat, shorter basidiospores (5.7 µm long on average), pileipellis as a trichoderm and presence of caulocystidia (Baroni & Halling 1992). *Rhodocybe pseudopiperita* from Tasmania is distinguished by a weakly umbonate pileus with shallow depression around umbo, indistinct odour or like mown grass and mild taste, the presence of scattered cystidioid elements in the pileipellis, and dimorphic basidiospore morphology with most of the them being distinctly undulate-pustulate and smaller (5.5–6.5 × 4–5 µm) while c. 30–45 % of the basidiospores are almost smooth and distinctly larger (7–9 × 5–5.5 µm) (Baroni & Gates 2006, Noordeloos & Gates 2012). Finally, the North American *R. roseiavellanea* is distinguished by a robust habitus (pileus 35–70 mm broad and stipe 30–60 × 10–25 mm), a mild taste, and large ellipsoid to subamygdaliform spores, (6.5–)7–9(–10) × (4–)5–5.5(–7) µm (Baroni 1981).

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Russula arunii

Fungal Planet 621 – 20 June 2017

Russula arunii S. Paloi, A.K. Dutta & K. Acharya, *sp. nov.*

Etymology. Named after Arun Kumar Sharma, the founder of the Botanic Garden at the University of Calcutta, from where the specimen was collected.

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

Pileus 39–68 mm diam, convex when young becoming broadly convex to applanate with slightly depressed towards centre at maturity, surface viscid and smooth at early stages that often becomes slightly velvety when mature, semi moist to moist, translucent, cracked that often extends to the centre, disc greyish brown (5D3) to yellowish brown (5D4) when young, becoming light orange (5A4) to greyish orange (5B4) when old, margin pale orange (5A3), no colour change on bruising turns yellow (2B7) with KOH, reddish white (8A2) with guaiacol, negative in phenol, NH_4OH and SV, context c. 2 mm thick at the centre, gradually thinner towards margin (≤ 1 mm), yellowish white (1A2), turning pale yellow (4A3) when exposed, yellow (2A7) with KOH, reddish brown (8D5) with guaiacol, no colour change with NH_4OH, $FeSO_4$, SV and phenol. *Lamellae* c. 2 mm broad, adnexed, entire, regular, white (1A1), even, concolorous, turns reddish brown (8D5) with guaiacol, negative in phenol and NH_4OH, lamellulae of one series. *Stipe* 20–29 × 5–7 mm, central, cylindrical, more or less equal, white (1A1), smooth, moist, fleshy, no colour change on bruising, turns greyish yellow (4B3) with KOH, light brown with SV and high red (9B8) with guaiacol, context solid when young, becoming multi-chambered at maturity, white (1A1), turns light yellow with KOH and high red (9B8) with guaiacol. *Taste* acrid. *Odour* fishy-like. *Spore print* white. *Basidiospores* (5.5–)6–*6.4*–7(–7.5) × (4.5–)5.5–*5.7*–6(–6.5) µm, Q = 1.07–*1.13*–1.16, globose to subglobose, ornamentation amyloid, composed of short (0.2–0.5 µm) and long (0.7–1.0 µm) warts with obtuse to acute apex, connected with a line between three or more warts, often free from each other, forming incomplete reticulum, suprahilar spot amyloid. *Basidia* (32–)36–*40.1*–44(–49) × (8.5–)9.5–*9.9*–10.5(–11.5) µm, clavate to subclavate, hyaline, thin-walled, oil droplets present when viewed with KOH, 4-spored, sterigmata 4.5–7 × 1–2.5 µm, cylindrical. *Hymenial cystidia* c. (50–)53–56(–61) × 7–8(–9) µm on gill sides, near gill edge c. 39.5–43(–48) × 6.5–7.5 µm, clavate to subclavate with capitate or moniliform apex, hyaline, thin-walled, oil granule present when viewed with KOH. *Pileipellis* orthochromatic in cresyl blue, context composed of densely arranged sphaerocytes, c. 53.5–61 µm deep; subpellis non-gelatinous, c. 247–286 µm deep, composed of loosely arranged hyphae (measuring 1.5–3 µm wide), branched, oil granule present when viewed with KOH; suprapellis 79–122 µm deep, composed of erect to suberect hyphae with acute to obtuse apex, oliferous hyphae measuring 2.5–4 µm wide, more abundant towards pileus centre. *Pileocystidia* (17.5–)19–20(–25.5) × 3–4 µm, abundant towards pileus centre, scattered to absent towards margin, 1-celled, mostly with capitate apex, hyaline, thin-walled, base attached with nodular like cells. *Lamellar trama* composed of loosely arranged sphaerocytes, measuring 9–25.5 × 7.5–23 µm, thin-walled. *Subhymenium* pseudo-parenchymatous. *Stipitipellis* 41–63 µm thick, composed of 3.5–5.5 µm broad, branched, septate, hyaline hyphae, hyphal end subulate, oil granule present when viewed with KOH, caulocystidia abundant, clavate with capitate apex, 2–3-celled, hyaline, dense with cytoplasmic contents. *Stipe trama* composed of almost subglobose sphaerocytes, measuring 14.5–34 × 10.5–26 µm.

Typus. India, West Bengal, Kolkata, Botanical Garden of the Ballygunge Science College campus, N22°31'37.30" E88°21'43.50", alt. 10.6 m, on the base of *Pterigota alata* (*Stercaliaceae*), 28 July 2014, *S. Paloi* (holotype CUH AM261, ITS and LSU sequences GenBank KR872619 and KY946732, MycoBank MB819728).

Additional specimen examined. India, West Bengal, Kolkata, Ballygunge Science College campus, N22°31'37.30" E88°21'43.50", alt. 10.6 m, on the base of *Pterigota alata*, 2 Aug. 2015, *S. Paloi* & *A. K. Dutta*, CUH AM270, ITS and LSU sequences GenBank KY450661 and KY946733.

Notes — The combination of features such as a greyish brown or yellowish brown to greyish orange pileus with translucent margin, adnexed attachment of lamellae, white spore print, fishy-like odour, acrid test, and presence of oliferous hyphae and pileocystidia in the pileipellis undoubtedly place *Russula arunii* in subg. *Ingratula* (Sarnari 1998).

Being a good representative member of subg. *Ingratula*, the newly described species appears morphologically close to *R. pulverulenta*, *R. ventricosipes*, and *R. pectinatoides*. However, *R. ventricosipes* has a pale brownish to pink reddish brown or dark reddish orange pileus, negative reaction of the pileus surface with KOH, much longer basidiospores (7–13.6 µm) coloured pale orange yellow with ornamentation that are never partial reticulate (Shaffer 1972). *Russula pulverulenta* differs from *R. arunii* by its yellowish white to dark orange yellow or moderate brown lamellae, pileus surface that turns deep reddish orange to strong reddish brown with KOH, and dark yellowish green colouration of the pileus and stipe context with guaiacol (Shaffer 1972). *Russula pectinatoides*, commonly encountered throughout Europe and North America, has a much longer stipe (up to 50 mm), broader lamellae (4–7 mm) that are forked and interveined, nauseating odour of the pileus context, bitter taste, somewhat differently sized basidiospores (6.7–8.7 × 5.2–7.5 µm), and much longer hymenial cystidia (65–110 × 7–11.5 µm; Romagnesi 1967). The previously described Indian species *Russula dubdiana* differs by the stipe context that turns dark green with guaiacol, cream spore print, and absence of caulocystidia (Das et al. 2013) (MycoBank supplementary data).

Colour illustrations. India, West Bengal, vegetation cover of the collection site (background); left column: field photograph of the basidiocarp, fresh basidiocarp showing lamellae, SEM microphotograph of the basidiospore; right column: basidia, hymenial cystidia, caulocystidia (all from holotype). Scale bars = 5 mm (basidiocarp), 10 µm (microscopic structures), 1 µm (basidiospore).

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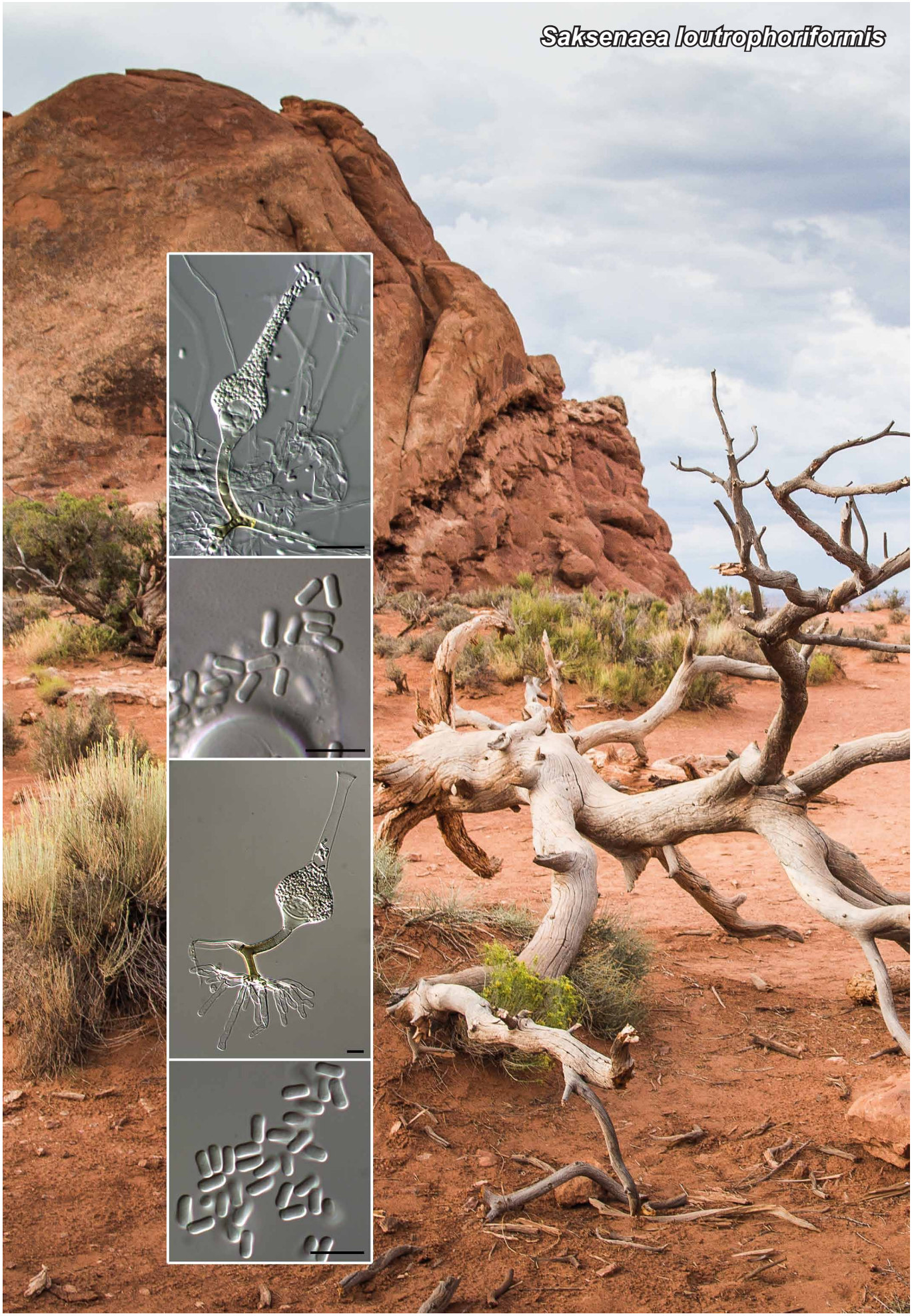

Saksenaea loutrophoriformis

Fungal Planet 622 – 20 June 2017

Saksenaea loutrophoriformis D.A. Sutton, Stchigel, Chander, Guarro & Cano, *sp. nov.*

Etymology. From the ancient Greek λουτροφόρος-, and from the Latin *-forma*, because of the vessel-shape of the sporangiophore.

Classification — *Saksenaeaceae*, *Mucorales*, *Mucoromycotina.*

Hyphae sparsely septate, branched, hyaline, smooth-walled, 3–15 µm wide. *Sporangiophores* erect, generally arising singly, at first hyaline, soon becoming brown, unbranched, 50–75 µm long, 5–10 µm wide, slightly verrucose. *Sporangia* terminal, multi-spored, flask-shaped, asperulate, 70–125 µm long, with a long (60–100 µm) neck; apex of the neck closed with a mucilaginous plug. *Sporangiospores* mostly bacilliform, bilaterally compressed and rounded at both ends, more or less trapezoidal in lateral view, smooth-walled, 3.5–6(–7) × 2–3.5 µm, pale olive brown. *Rhizoids* present, well-developed, terminal or lateral respect to the main axis of the sporangiophore. *Zygospores* not observed.

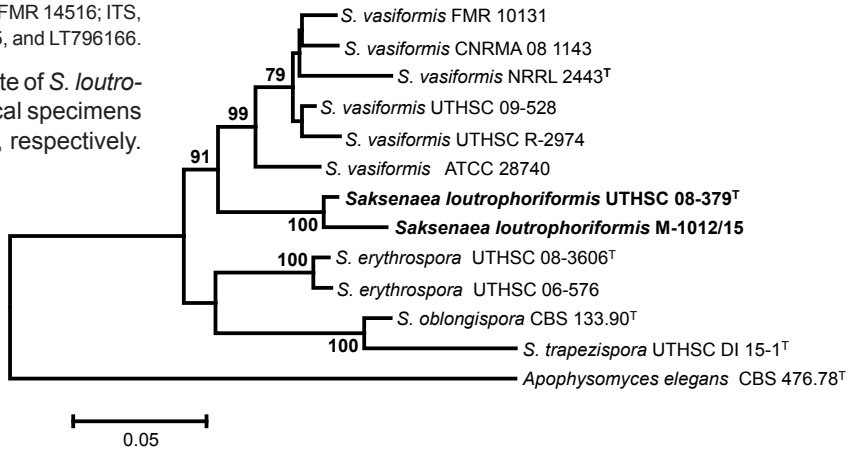
Culture characteristics — *Colonies* on CZA at 37 °C practically filling the Petri dish (90 mm diam) after 4 d of incubation, whitish, with scarce aerial mycelium; reverse concolorous. *Colonies* on MEA, PDA and SAB showing similar features as on CZA, but they were more floccose and white, sporulation absent. The optimum temperature of growth was between 35 and 42 °C (reaching 75–85 mm diam). Minimum growth was observed at 15 °C (colonies of 31–35 mm diam), and the diameter reached at 25 °C was 57–63 mm. The fungus did not grow at 45 °C.

Typus. USA, Utah, from eye, 11 June 2009, *D.A. Sutton* (holotype CBS H-23041, cultures ex-type UTHSC 08-379 = FMR 10674; ITS, LSU, and *EF1-α* sequences GenBank FR687330, HM776682, and HM776693, MycoBank MB820008).

Additional specimens examined. India, Chandigarh, from palate necrotic tissue, 8 Aug. 2015, *J. Chander*, living cultures M-1012/15 = FMR 14516; ITS, LSU, and *EF1-α* sequences GenBank LT796164, LT796165, and LT796166.

Notes — The ex-type strain and a second isolate of *S. loutrophoriformis* have been isolated from human clinical specimens but in two very distant countries, USA and India, respectively.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit with the ex-type strain using the ITS sequence is *Saksenaea vasiformis* PWQ2338 (GenBank KP132601; Identities = 694/739 (94 %), Gaps 27/739 (3 %)); using the LSU sequence it is *Saksenaea erythrospora* strain UTHSC 06-576 (GenBank HM776683; Identities = 714/735 (97 %), Gaps 3/735 (0 %)); and using the *EF1-α* sequence it is *Saksenaea vasiformis* strain FMR 10131 (HM776689; Identities = 465/477 (97 %), no gaps). Our phylogenetic tree, built from the ITS, LSU, and *EF1-α* nucleotide sequences, corroborated that our isolates represent a new species, the closest species being *S. vasiformis*, with 93.6 % similarity with respect to the ex-type strain (NRRL 2443). The sporangiospores of *S. loutrophoriformis* are similar in size to the *S. vasiformis* species complex (5–7 × 2–3 µm), a bit larger than in *S. erythrospora* (5–5.5 × 2–3 µm), but narrower than in *S. oblongispora* (5–6.5 × 3–4.5 µm) and in *S. trapezispora* (av. = 7 × 3.5 µm) (Alvarez et al. 2010, Crous et al. 2016). However, the sporangiospores of *S. loutrophoriformis* appear pale olive brown under the microscope, whereas these are hyaline to subhyaline in *S. vasiformis*; also, the sporangiospores of *S. loutrophoriformis* are bilaterally more compressed at the middle than in *S. vasiformis*. The minimum growth temperature for the *S. vasiformis* species complex has been reported at 15 °C. However, the strains of *S. loutrophoriformis* grew well at that temperature. Also, the optimum growth temperature for *S. vasiformis* has been reported between 25 °C and 37 °C, being higher (35 °C to 42 °C) for both *S. loutrophoriformis* strains.



Maximum likelihood tree obtained from the combined DNA sequences dataset from three loci (ITS, LSU, *EF1-α*) of our isolates and sequences retrieved from GenBank. The tree was built by using MEGA v. 6. Bootstrap support values ≥ 70 % are presented at the nodes. *Apophysomyces elegans* CBS 476.78 was used as outgroup. The new species proposed in this study is indicated in **bold**. T represents the ex-type strains. The scale bar indicates the expected number of changes per site.

Colour illustrations. Typical landscape of Utah (USA); sporangiophore and sporangiospores of both isolates (American and Indian, from top to bottom, respectively). Scale bars = 10 µm.

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Tolypocladium fumosum

Fungal Planet 623 – 20 June 2017

Tolypocladium fumosum Ruszkiewicz-Michalska, Pawłowska & Wrzosek, *sp. nov.*

Etymology. Named after the fumaceous grey colour of the stroma.

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

Stromata connected with a yellowish rhizomorph-like structure to a buried caterpillar case of lepidopteran host belonging to the *Psychidae* family (bagworm moths), unidentified to species level; stroma single, unbranched, with well-defined, rounded apex, pale chalcedony yellow at the base (plate XVII in Ridgway 2005) to dark gull grey at the apex (plate LIII in Ridgway 2005). The stalk slightly twisted, 10 × 1 mm, built with branched, septate hyaline hyphae, cells inflated at the basal septum (up to 3.5 µm). Fertile part of stroma almost 1/5–1/4 of the total length, ellipsoidal when young and capitate when mature, enlarged up to 3.8 mm diam, with stellate appearance due to aggregated perithecia erumpent from stroma (up to one half of the length). *Perithecial apex* partly covered by dense matt of the stroma outer layer (up to 46.5 µm thick), grey in colour, easily peelable. Interior distinctly paler, visible around some ostioles. *Perithecia* ovoid to pear-shaped, 740–760 × 444–558 µm, perithecial wall of brown pigmented *textura angularis* (outer layer, cells thin-walled, 6–10 µm diam) and of paler *textura epidermoidea* (inner layer, hyphae 4–5 µm diam, with wall thick up to 1.2 µm). Ostiolum papillate up to 79 µm long, and 25 µm diam at the apex. *Asci* numerous, cylindrical, narrow, up to 200 × 5–6 µm, non-amyloid, the walls fragile at spore maturity, the apex with conspicuously thickened cup (up to 3 µm), with a narrow, central pore. *Ascospores* eight per ascus, hyaline, filiform, smooth, disarticulating into part-spores within asci. Part-spores short cylindrical to cubic, with flattened ends and wall equally thick, 2–4.5(–6) × 1–1.5(–2) µm, apical part-spores long obovoid, 4–5 × 1 µm. Asexual morph present at the base of the stromatal stalk. *Conidiomata* absent. *Conidiophores* 1(–2)-celled, discrete, micronematic, arranged irregularly, perpendicular to conidiophore, hyaline, monophialidic, flask-shaped with enlarged base and tapering into narrow neck, sometimes bent from the axis, smooth-walled, 8–10(–12) × 1.5–2 µm. *Conidia* produced abundantly, aggregated, in slimy heads, obovate to cylindrical, smooth, hyaline, aseptate, without oil drops, 2–3.5 × 1.5–2 µm. *Chlamydospores* absent.

Culture characteristics — Both part-ascospores and conidia germinate *in vitro* on artificial media (MEA, PDA, OA). Growth of mycelium on mentioned media is sparse, slow, maximum 1 cm / 3 d, white, with abundant aerial mycelium, no soluble pigments present. Numerous anastomoses are formed on the colony edge.

Typus. Poland, Suwałki Lake District (Pojezierze Suwalskie), Wigry National Park, Czarna Hańcza river valley, south-east of Sobolewo village, N54.04849° E23.04272°; alder carr *Ribeso nigri-Alnetum*, at tree base of *Alnus glutinosa*, among mosses, on caterpillar case of unidentified *Lepidoptera* from *Psychidae* family, 1 Oct. 2012, *M. Staniaszek-Kik* (holotype WA 18945, isotype CBS H-22968, ITS and LSU sequences GenBank KU925171 and KU985053, MycoBank MB816126).

Notes — The genus *Tolypocladium* (= *Elaphocordyceps*) was established in 1971 for three species of soil-isolated fungi and currently is defined mainly on a molecular basis (Sung et al. 2007). Quandt et al. (2014) accepted 27 species in the genus and Gazis et al. (2014) described three species isolated from *Hevea* (rubber tree). Diverse ecologies of *Tolypocladium* taxa (parasites of fungi, insects and rotifers, soil saprobes, plant endophytes) are explained by the 'host habitat hypothesis' (Nikoh & Fukatsu 2000, Gazis et al. 2014). Only *T. inflatum* has a known sexual morph. The asexual morph has been also reported for *T. japonicum* (cultural studies by Ke & Ju 2015).

Morphological characters of both morphs of *T. fumosum* agree with the generic concept of the genus (Quandt et al. 2014). It differs from other species in the gross morphology of stromata: they are smoky grey, bereft of brownish, greenish or olivaceous tints that are characteristic for the majority of *Tolypocladium* species. Only two other *Elaphomyces*-associated species have grey stromata: *T. minazukiense* and *T. miomoteanum* (Kobayashi & Shimizu 1982). However, both species form much bigger stromata (50–120 × 5–12 mm and 65 × 6 mm, respectively vs 10 × 3.8 mm) as well as perithecia and part-spores (16–18 × 3 µm and 8–11 × 1.5–2 µm vs 2–4.5 × 1.2–1.5 µm).

In terms of stromatal shape and size of perithecia and part-spores the species seems to be the most similar to *T. inflatum*. However, the asexual morph differs by size and shape of phialides (base inflated, 3–5 × 2–3 µm vs base slightly swollen, 8–10 × 1.5–1.8 µm) and shape of conidia that are ± equal in size (ellipsoidal, 2–2.5 × 1.4–2 µm vs obovate to cylindrical, 2–3.5 × 1.8–2 µm). Both in *T. fumosum* and *T. inflatum* the first phialides produced are acremonium-like (Hodge et al. 1996). The distinctive character of *T. fumosum* is the presence of asexual morph at the base of stromatal stipe, a character that it shares with *T. ophioglossoides* (according to Saccardo (1883), conidia from the initial mycelium of stroma are mentioned in the species description) and *T. inflatum* (asexual morph observed on host body and wood surrounding it; Hodge et al. 1996). Nevertheless, the asexual morphs in the genus seem to be highly variable and the new species is best separated based on its DNA phylogeny. According to the ITS phylogeny (MycoBank supplementary data), *T. fumosum* is different from all other *Tolypocladium* species (96 % similarity to *T. cylindrosporum*, *T. ophioglossoides*, *T. inflatum* and *T. tundrense*).

Colour illustrations. The habitat of the fungus – the alder tree base covered with moss; ascus with disarticulating ascospores; perithecium; part-ascospores; stroma emerging from the mosses; phialides and conidia; the edge of the colony with anastomosing hyphae. Scale bars = 10 µm

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Tuber magentipunctatum
8 µm

Fungal Planet 624 – 20 June 2017

Tuber magentipunctatum Z. Merényi, I. Nagy, Stielow & Bratek, *sp. nov.*

Etymology. The name *magentipunctatum* is derived from '*magenti*' (from Latin '*magentibus*' = magenta) and '*punctatum*' (from Latin patched, punctate, spotted).

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

Ascomata hypogeous globose to subglobose or moderately lobed 5–16(–26) mm diam; smooth, or rarely with some minutely warts in patches but never pubescent, always stained with the following colours: bay (19), purplish chestnut (21), dark brick (20), brown vinaceous (25) and fuscous black (36) in dried state (Royal Botanical Garden, Edinburg (RBGE) 1969). *Peridium* 289 ± 171 µm (127–683 µm) thick in total, with an external layer of 122 ± 45 µm (53–227 µm), composed of cells arranged as a hyaline or pale yellow pseudoparenchyma, while the internal layer 148 ± 98 µm (46–400 µm) thick, intricately interwoven with the hyaline hyphae. The uppermost cells (layer: 106 ± 100 µm) are highly pigmented. The size of the largest isodiametric peridial cells are 19.5 ± 3.4 µm (14.5–24 µm). *Gleba* is whitish at first, becoming hazel (27), milky coffee (28) vinaceous buff (31), clay buff (32), drab (33) (RBGE 1969), marbled with medium spaced white veins. *Odour* resembles *T. aestivum*, pleasant, but slight. *Asci* globose to subglobose, ellipsoid and contain randomly arranged spores. The distribution of spore numbers per asci is 1: 2 ± 1 %, 2: 4 ± 2 %, 3: 8 ± 4 %, 4: 11 ± 3 %, 5: 16 ± 4 %, 6: 20 ± 7 %, 7: 22 ± 5 %, and 8: 18 ± 8 % (these are mean and standard deviation value pairs). Thus, the 6- and the 7-spored asci are the most common. *Ascospores* globose to ellipsoid, Q = 1.03–1.53, yellow to pale brown, 18.3 × 14.9 µm (16.5–21.4 × 12.6–17.4 µm) in 4-spored asci and 18.1 × 14.1 µm (15.8–20.1 × 12.6–16.3 µm), in 8-spored asci excluding ornamentation. Spore volume is 2 178 ± 444 µm^3 (1 524–2 903 µm^3) in 4-spored asci, while 1 895 ± 257 µm^3 (1 561–2 344 µm^3) in 8-spored asci. Spores are ornamented with spines connected by low ridges to form a more or less regularly alveolate reticulum where the spicule height is 1.51 ± 0.39 µm (0.99–2.35 µm) and the average size of meshes is 2.66 ± 0.21 µm (2.38–3.05 µm).

Distribution & Habitat — The fruiting period is almost exclusively in summer (June–July, occasionally August–October). Ascomata can be found under a variety of potential host trees (e.g., *Carpinus betulus*, *Quercus robur*, *Q. cerris*, *Corylus avellana*, *Corylus colurna*, *Ostrya carpinifolia*, *Tilia tomentosa*, *Populus* × *canescens*, *Fagus sylvatica*, and *Picea abies*). The soils of their habitats are slightly basophilous pH (pH_{water} = 7.57 ± 0.10), heavy soil ('sticky point according to Arany' is K_A = 65 ± 7.6). They have been found only in four European countries, from Italy to Romania. Occurs in plains and hilly regions between 80–900 m a.s.l.

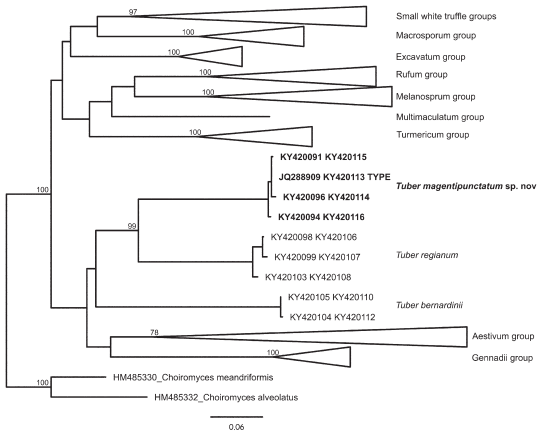
Typus. Hungary, Ásványráró, N47.823414° E17.487609°, 290 m a.s.l., under *C. colurna*, *T. tomentosa*, 6 July 2011, leg. *I. Nagy*, *E. Vajk*, *Z. Bratek*, *B. Baski* (holotype BP107924, ITS, LSU, PKC, and *rpb2* sequences GenBank JQ288909, KY420113, KY420120, and KY420128, MycoBank MB819574).

Colour illustrations. *Tuber magentipunctatum* (ZB4559) growing in mixed forest (*Fagus sylvatica*, *Carpinus betulus*) in Hungary; ascocarp (ZB5221) (scale bar = 1 cm); the smooth surface of peridium with patches bay (CIC 19), dark brick (CIC 20) and fuscous black (CIC 36) (ZB5221) (scale bar = 1 mm); an 8-spored ascus with globose spores (ZB4293) (scale bar = 10 µm); SEM photo of an ellipsoid ascospore (ZB4559) (scale bar = 8 µm).

Notes — *Tuber magentipunctatum* is distinguishable with not only molecular differences, but also with the high rate of 6–8-spored asci, containing small spores with remarkable fine meshes. *Tuber magentipunctatum* is morphologically similar to *Tuber regianum* but differs in the volume of spores, which is larger in *T. magentipunctatum*: 1 895 ± 257 µm^3 (in the range of 1 561–2 344 µm^3) (vs 1 225 ± 146 µm^3 (1 075–1 491 µm^3) in 8-spored asci); additionally, the ratios of 8-spored asci (R8) in *T. magentipunctatum* never exceed 35 % (18 % ± 8 % (8–31 %)) while in *T. regianum* it varies between 38–45 %. *Tuber magentipunctatum* is distinguishable from *T. bernardinii* with the smooth surface of its ascomata (which is often pubescent in *T. bernardinii*) and the excessively small meshes on spores (2.66 ± 0.21 µm vs 6.67 ± 0.3 µm, respectively). There are some other *Tuber* species which were characterised by 6–8-spored asci. *Tuber malenconii* has warts, and its spores are larger (22–26 × 16–18 µm; Montecchi & Sarasini 2000) than *T. magentipunctatum*. The ascoma surface of *T. panniferum* is covered with cottony tomentum and has spiny spores without low ridges to form a reticulum (Montecchi & Sarasini 2000). Ascomata of *T. pseudoexcavatum* always have a basal cavity, its surface is verrucose, warty, and it has larger spores (24–28 × 18–19 µm), and occurs in Asia (Wang et al. 1998).

ITS. Based on a megablast search against the INSDC (GenBank) nucleotide database, the closest hits using the ITS sequence of type material are several sequences originating from *Tuber excavatum* groups: GQ217540: Identities 294/344 (85 %), Gaps 8/344 (2 %); FM205567: 306/361 (85 %), Gaps 13/361 (3 %), with less than 70 % query cover.

LSU. The closest hits using the LSU sequence of type material are *Tuber* species from different species groups: KT067698: Identities 512/566 (90 %), Gaps 6/566 (1 %); KT067703: 511/566 (90 %), Gaps 6/566 (1 %).



Maximum likelihood phylogeny inferred from concatenated internal transcribed spacer (ITS) and 28S rRNA (LSU) regions, rooted to *Choiromyces* spp. Analysis was performed using RAxML through the CIPRES website (http://www.phylo.org) using the GTR+P–Invar model. Bootstrap branch support > 70 % is shown. The scale bar represents 0.06 expected nucleotide changes per site.

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REFERENCES

Adamčík S, Looney BP, Birkebak JM, et al. 2016. Circumscription of species of Hodophilus (Clavariaceae, Agaricales) in North America with naphthalene odours. Botany 94: 941–956.

Alvarado P, Moreno G, Manjón JL, et al. 2011. Eremiomyces magnisporus (Pezizales), a new species from central Spain. Mycotaxon 118: 103–111.

Alvarez E, Garcia-Hermoso D, Sutton DA, et al. 2010. Molecular phylogeny and proposal of two new species of the emerging pathogenic fungus Saksenaea. Journal of Clinical Microbiology 48: 4410–4416.

Ann PJ, Ko WH, 1980. Phytophthora insolita, a new species from Taiwan. Mycologia 72: 1180–1185.

Arnolds E. 1990. Tribus Hygrocybeae (Kühner) Bas & Arnolds. In: Bas C, Kuyper TW, Noordeloos ME, et al. (eds), Flora Agaricina neerlandica, Vol. 2: 71–115. Balkema, Netherlands.

Aveskamp M, De Gruyter H, Woudenberg J, et al. 2010. Highlights of the Didymellaceae: A polyphasic approach to characterise Phoma and related pleosporalean genera. Studies in Mycology 65: 1–60.

Aveskamp MM, Verkley GJM, De Gruyter J, et al. 2009. DNA phylogeny reveals polyphyly of Phoma section Peyronellaea and multiple taxonomic novelties. Mycologia 101: 363–382.

Badali H, Gueidan C, Najafzadeh MJ, et al. 2008. Biodiversity of the genus Cladophialophora. Studies in Mycology 61: 175–191.

Baroni TJ. 1981. A revision of the genus Rhodocybe Maire (Agaricales). Beihefte zur Nova Hedwigia 67: 1–198.

Baroni TJ, Gates GM. 2006. New species and records of Rhodocybe (Entolomataceae, Agaricales) from Tasmania. Australian Systematic Botany 19: 343–358.

Baroni TJ, Halling RE. 1992. New species of Rhodocybe from South America with a key to species. Mycologia 84: 411–421.

Baroni TJ, Horak E. 1994. Entolomataceae in North America III: new taxa, new combinations and notes on species of Rhodocybe. Mycologia 86: 138–145.

Bensch K, Braun U, Groenewald JZ, et al. 2012. The genus Cladosporium. Studies in Mycology 72: 1–401.

Bensch K, Groenewald JZ, Dijksterhuis J, et al. 2010. Species and ecological diversity within the Cladosporium cladosporioides complex (Davidiellaceae, Capnodiales). Studies in Mycology 67: 1–94.

Bezerra JDP, Sandoval-Denis M, Paiva LM, et al. 2017. New endophytic Toxicocladosporium species from cacti in Brazil, and description of Neocladosporium gen. nov. IMA Fungus 8: 77–97.

Bickford D, Lohman DJ, Sodhi NS, et al. 2006. Cryptic species as a window on diversity and conservation. Trends in Ecology and Evolution 22: 148–155.

Birkebak JM, Adamčík S, Matheny PB. 2016. Multilocus phylogenetic reconstruction of the Clavariaceae (Agaricales) reveals polyphyly of the agaricoid members. Mycologia 108: 939–953.

Bordallo JJ, Rodríguez A, Honrubia M, et al. 2012. Terfezia canariensis sp. nov., una nueva especie de trufa encontrada en las Islas Canarias. Cantarela 56: 1–8.

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.

Brasch J, Dressel S, Müller-Wening K, et al. 2011. Toenail infection by Cladophialophora boppii. Medical Mycology 49: 190–193.

Braun U. 1998. A monograph of Cercosporella, Ramularia and allied genera (phytopathogenic Hyphomycetes) 2: 1–493. IHW-Verlag, Eching.

Braun U. 1999. Taxonomic notes on some species of the Cercospora complex (V). Schlechtendalia 2: 1–28.

Brodie HJ. 1967. Cyathus bulleri, a hitherto undescribed fungus of the Nidulariaceae from the West Indies. Bulletin of the Torrey Botanical Club 94: 68–71.

Brodie HJ. 1975. The bird's nest fungi. University of Toronto Press, Toronto, Canada.

Brodie HJ. 1984. More bird's nest fungi (Nidulariaceae) – a supplement to 'The bird's nest fungi' (1975). Lejeunia 112: 1–72.

Brodie HJ, Sharma BM. 1980. Cyathus griseocarpus, a new bird's nest fungus from India. Botaniska Notiser 133: 343–345.

Bulliard JBF. 1788. Herbier de la France 8: 337–384.

Bussaban B, Lumyong S, Lumyong P, et al. 2005. Molecular and morphological characterization of Pyricularia and allied genera. Mycologia 97: 1002–1011.

Cannon P, Buddie A, Bridge P, et al. 2012. Lectera, a new genus of the Plectosphaerellaceae for the legume pathogen Volutella colletotrichoides. MycoKeys 3: 23–36.

Cano J, Sagues M, Barrio E, et al. 2002. Molecular taxonomy of Aphanoascus and description of two new species from soil. Studies in Mycology 47: 153–164.

Castro ML, Freire L. 1995. Gyroporus ammophilus, a new poisonous bolete from the Iberian Peninsula. Persoonia 16: 123–126.

Cheewangkoon R, Groenewald JZ, Summerell BA, et al. 2009. Myrtaceae, a cache of fungal biodiversity. Persoonia 23: 55–85.

Chen Q, Jiang JR, Zhang GZ, et al. 2015. Resolving the Phoma enigma. Studies in Mycology 82: 137–217.

Crous PW. 2002. Taxonomy and pathology of Cylindrocladium (Calonectria) and allied genera. APS Press, MN, USA.

Crous PW, Braun U. 2003. Mycosphaerella and its anamorphs: 1. Names published in Cercospora and Passalora. CBS Biodiversity Series 1: 1–571. Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands.

Crous PW, Braun U, Groenewald JZ. 2007a. Mycosphaerella is polyphyletic. Studies in Mycology 58: 1–32.

Crous PW, Braun U, Schubert K, et al. 2007b. Delimiting Cladosporium from morphologically similar genera. Studies in Mycology 58: 33–56.

Crous PW, Müller M, Sánchez RM, et al. 2015a. Resolving Tiarosporella spp. allied to Botryosphaeriaceae and Phacidiaceae. Phytotaxa 202: 73–93.

Crous PW, Schumacher RK, Wingfield MJ, et al. 2015b. Fungal systematics and evolution: FUSE 1. Sydowia 67: 81–118.

Crous PW, Summerell BA, Alfenas AC, et al. 2012a. Genera of diaporthalean coelomycetes associated with leaf spots of tree hosts. Persoonia 28: 66–75.

Crous PW, Summerell BA, Carnegie AJ, et al. 2007c. Foliicolous Mycosphaerella spp. and their anamorphs on Corymbia and Eucalyptus. Fungal Diversity 26: 143–185.

Crous PW, Summerell BA, Carnegie AJ, et al. 2009a. Novel species of Mycosphaerellaceae and Teratosphaeriaceae. Persoonia 23: 119–146.

Crous PW, Summerell BA, Carnegie AJ, et al. 2009b. Unravelling Mycosphaerella: do you believe in genera? Persoonia 23: 99–118.

Crous PW, Summerell BA, Mostert L, et al. 2008. Host specificity and speciation of Mycosphaerella and Teratosphaeria species associated with leaf spots of Proteaceae. Persoonia 20: 59–86.

Crous PW, Summerell BA, Shivas RG, et al. 2012b. A re-appraisal of Harknessia (Diaporthales), and the introduction of Harknessiaceae fam. nov. Persoonia 28: 49–65.

Crous PW, Summerell BA, Swart L, et al. 2011. Fungal pathogens of Proteaceae. Persoonia 27: 20–45.

Crous PW, Wingfield MJ, Burgess TI, et al. 2016. Fungal Planet description sheets: 469–557. Persoonia 37: 218–403.

Crous PW, Wingfield MJ, Guarro J, et al. 2013. Fungal Planet description sheets: 154–213. Persoonia 31: 188–296.

Cruz RHSF, Baseia IG. 2014. Four new Cyathus species (Nidulariaceae, Basidiomycota, Fungi) from the semi-arid region of Brazil. Journal of the Torrey Botanical Society 141: 173–180.

Cui BK, Zhao CL. 2012. Morphological and molecular evidence for a new species of Perenniporia (Basidiomycota) from Tibet, southwestern China. Mycoscience 53: 365–372.

Das K, Atri NS, Buyck B. 2013. Three new species of Russula (Russulales) from Sikkim (India). Mycosphere 4: 722–732.

De Gruyter J, Woudenberg JHC, Aveskamp MM, et al. 2010. Systematic reappraisal of species in Phoma section Paraphoma, Pyrenochaeta and Pleurophoma. Mycologia 102: 1066–1081.

De Hoog GS. 1985. Taxonomy of the Dactylaria complex, IV. Dactylaria, Neta, Subulispora and Scolecobasidium. Studies in Mycology 26: 1–60.

De Hoog GS, Dukik K, Monad M, et al. 2016. Toward a novel multilocus phylogenetic taxonomy of the dermatophytes. Mycopathologia 182: 5–31.

Decock C, Mossebo DC. 2001. Studies in Perenniporia (Basidiomycetes, Aphyllophorales): African taxa II. Perenniporia centrali-africana, a new species from Cameroon. Systematics and Geography of Plants 71: 607–612.

Decock C, Ryvarden L. 2000. Studies in neotropical polypores. 6. New resupinate Perenniporia species with small pores and small basidiospores. Mycologia 92: 354–360.

Decock C, Ryvarden L. 2011. Additions to the Neotropical Perenniporia: Perenniporia albo-incarnata comb. nov. and Perenniporia guyanensis sp. nov. Cryptogamie, Mycologie 32: 13–23.

Descals CE, Sutton BC. 1976. Anavirga dendromorpha and its Phialocephala phialidic state. Transactions of the British Mycological Society 67: 269–274.

Ebead GA, Overy DP, Berrué F, et al. 2012. Westerdykella reniformis sp. nov., producing the antibiotic metabolites melinacidin IV and chetracin B. IMA Fungus 3: 189–201.

Ertz D, Diederich P, Lawrey JD, et al. 2015. Phylogenetic insights resolve Dacampiaceae (Pleosporales) as polyphyletic: Didymocyrtis (Pleosporales, Phaeosphaeriaceae) with Phoma-like anamorphs resurrected and segregated from Polycoccum (Trypetheliales, Polycoccaceae fam. nov.). Fungal Diversity 74: 53–89.

Farr DF, Rossman AY. 2017. Fungal databases, systematic mycology and microbiology laboratory, ARS, USDA. Retrieved February 1, 2017, from http://nt.ars-grin.gov/fungaldatabases/.

Ferdman Y, Aviram S, Roth-Bejerano N, et al. 2005. Phylogenetic studies of Terfezia pfeilii and Choiromyces echinulatus (Pezizales) support new genera for southern African truffles: Kalaharituber and Eremiomyces. Mycological Research 109: 237–245.
Gams W. 1971. Cephalosporium-artige Schimmelpilze. Fischer Verlag, Stuttgart.
Gams W, Boekhout T. 1985. Pigment localization in dematiaceous hyphomycetes and the segregation of Pseudogliomastix gen. nov. from Acremonium. Proceedings of the Indian Academy of Sciences (Plant Sciences) 94: 273–280.
Gazis R, Skaltsas D, Chaverri P. 2014. Novel endophytic lineages of Tolypocladium provide new insights into the ecology and evolution of Cordyceps-like fungi. Mycologia 106: 1090–1105.
Glen M, Yuskianti V, Puspitasari D, et al. 2014. Identification of basidiomycete fungi in Indonesian hardwood plantations by DNA barcoding. Forest Pathology 44: 496–508.
Gräfenhan T, Schroers HJ, Nirenberg HI, et al. 2011. An overview of the taxonomy, phylogeny, and typification of nectriaceous fungi in Cosmospora, Acremonium, Fusarium, Stilbella, and Volutella. Studies in Mycology 68: 79–113.
Guarro J, Gene J, Stchigel AM, et al. 2012. Atlas of soil ascomycetes. CBS Biodiversity Series 10. Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands.
Hausknecht A. 2009. A monograph of the genera Conocybe Fayod and Pholiotina Fayod in Europe. Fungi Europaei 11: 1–968. Alassio, Candusso.
Heim R. 1931. Le genre Inocybe précédé d'une introduction general à l'étude des Agarics Ochrosporés. Lechevalier & Fils, Paris, France.
Hernández-Restrepo M, Groenewald JZ, Crous PW. 2015. Neocordana gen. nov., the causal organism of Cordana leaf spot of banana. Phytotaxa 205: 229–238.
Hirooka Y, JB Tanney, HD Nguyen, et al. 2016. Xerotolerant fungi in house dust: taxonomy of Spiromastix, Pseudospiromastix and Sigleria gen. nov. in Spiromastigaceae (Onygenales, Eurotiomycetes). Mycologia 108: 135–156.
Hodge KT, Krasnoff SB, Humber RA. 1996. Tolypocladium inflatum is the anamorph of Cordyceps subsessilis. Mycologia 88: 715–719.
Horak E. 1990. Monograph of the New Zealand Hygrophoraceae (Agaricales). New Zealand Journal of Botany 28: 225–309.
Huang F, Groenewald JZ, Zhu L, et al. 2015. Cercosporoid diseases of Citrus. Mycologia 107: 1151–1171.
Hujslová M, Kubatova A, Kostovcik M, et al. 2013. Acidiella bohemica gen. et sp. nov and Acidomyces spp. (Teratosphaeriaceae), the indigenous inhabitants of extremely acidic soils in Europe. Fungal Diversity 58: 33–45.
Jung T, Horta Jung M, Scanu B, et al. 2017. Six new Phytophthora species from ITS Clade 7a including two sexually functional heterothallic hybrid species detected in natural ecosystems in Taiwan. Persoonia 38: 100–135.
Kalamees K. 1989. New and interesting agarics and boletus from East-Europe and Asia. Opera Botanica 100: 135–145.
Ke Y-H, Ju Y-M. 2015. Two rare ophiocordycipitaceous fungi newly recorded in Taiwan. Botanical Studies 56: 30.
Kearse M, Moir R, Wilson A, et al. 2012. Geneious basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics 28: 1647–1649.
Kendrick WB. 1961. The Leptographium complex. Phialocephala gen. nov. Canadian Journal of Botany 39: 1079–1085.
Kepler RM, Ban S, Nakagiri A, et al. 2013. The phylogenetic placement of hypocrealean insect pathogens in the genus Polycephalomyces: an application of one fungus one name. Fungal Biology 117: 611–622.
Kirk PM, Stalpers JA, Braun U, et al. 2013. A without-prejudice list of generic names of fungi for protection under the International Code of Nomenclature for algae, fungi and plants. IMA Fungus 4: 381–443.
Kits van Waveren E. 1985. The Dutch, French and British species of Psathyrella. Persoonia Suppl. 2: 1–300.
Klaubauf S, Tharreau D, Fournier E, et al. 2014. Resolving the polyphyletic nature of Pyricularia (Pyriculariaceae). Studies in Mycology 79: 85–120.
Kobayashi Y, Shimizu D. 1982. Cordyceps species from Japan 5. Bulletin of the National Science Museum, Series B, Botany 8: 111–121.
Kolařík M, Hujslová M, Vázquaz-Campos X. 2015. Acidotolerant genus Fodinomyces (Ascomycota: Capnodiales) is a synonym of Acidiella. Czech Mycology 67: 37–38.
Kornerup A, Wanscher JH. 1978. Methuen handbook of colour. 3rd ed. Eyre Methuen, London.
Kumar S, Stecher G, Tamura K. 2016. MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets. Molecular Biology and Evolution 33: 1870–1874.
Kuyper TW. 1986. A revision of the genus Inocybe in Europe I. Subgenus Inosperma and the smooth-spored species of subgenus Inocybe. Persoonia Suppl. 3: 1–247.
Lanfear R, Calcott B, Ho SY, et al. 2012. PartitionFinder: combined selection of partitioning schemes and substitution models for phylogenetic analyses. Molecular Biology and Evolution 29: 1695–1701.
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.
Lee S, Groenewald JZ, Crous PW. 2004. Phylogenetic reassessment of the coelomycete genus Harknessia and its teleomorph Wuestneia (Diaporthales), and the introduction of Apoharknessia gen. nov. Studies in Mycology 50: 235–252.
Lodge DJ, Padamsee M, Matheny PB, et al. 2014. Molecular phylogeny, morphology, pigment chemistry and ecology in Hygrophoraceae (Agaricales). Fungal Diversity 64: 1–99.
Lombard L, Shivas RG, To-Anun C, et al. 2012. Phylogeny and taxonomy of the genus Cylindrocladiella. Mycological Progress 11: 835–868.
Lombard L, Van der Merwe NA, Groenewald JZ, et al. 2015. Generic concepts in Nectriaceae. Studies in Mycology 80: 189–245.
Luttrell ES. 1954. An undescribed species of Pyricularia on sedges. Mycologia 46: 810–814.
Marasas WFO, Trappe JM. 1973. Notes on southern African Tuberales. Bothalia 11: 139–141.
Martín MP, Cruz RHSF, Dueñas M, et al. 2015. Cyathus lignilantanae sp. nov., a new species of bird's nest fungi (Basidiomycota) from Cape Verde Archipelago. Phytotaxa 236: 161–172.
Matsushima T. 1981. Matsushima Mycological Memoirs 2: 1–68.
Matsushima T. 1983. Matsushima Mycological Memoirs 3: 1–90.
Moncalvo J-M, Buchanan PK. 2008. Molecular evidence for long distance dispersal across the Southern Hemisphere in the Ganoderma applanatum-australe species complex (Basidiomycota). Mycological Research 112: 425–436.
Montecchi A, Sarasini M. 2000. Funghi ipogei d'Europa. Associazione Micologica Bresadola, Fondacione Centro Studi Micologici, Trento, Vicenza
Moslemi A, Ades PK, Groom T, et al. 2016. Paraphoma crown rot of Pyrethrum (Tanacetum cinerariifolium). Plant Disease 100: 2363–2369.
Mouton M, Wingfield MJ, Van Wyk PS. 1993. Conidium development in Phialocephala dimorphospora and a new pattern of wall thickening. Mycological Research 97: 99–104.
Muñoz JA. 2005. Boletus s.l. (excl. Xerocomus). Fungi Europaei 2. Edizioni Candusso, Alassio.
Munsell Color. 1975. Munsell Soil Color Charts. Baltimore, Md., USA.
Munsell Color. 1994. Soil Color Charts (revised edition). Macbeth Division of Kollmorgen Instruments Corporation, New Windsor, New York, USA.
Nag Raj TR. 1993. Coelomycetous anamorphs with appendage bearing conidia. Mycologue Publications, 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.
Nguyen LT, 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.
Nikoh N, Fukatsu T. 2000. Interkingdom host jumping underground: Phylogenetic analysis of entomoparasitic fungi of the genus Cordyceps. Molecular Biology and Evolution 17: 629–638.
Noordeloos ME, Gates GM. 2012. The Entolomataceae in Tasmania. Fungal Diversity Research Series 22. Dordrecht, Springer Science+Business Media BV.
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.
Park RF, Keane PJ, Wingfield MJ, et al. 2000. Fungal diseases of eucalypt foliage. In: Keane PJ, Kile GA, Podger FD, et al. (eds), Diseases and pathogens of eucalypts: 153–239. CSIRO publishing, Australia.
Parreira DF, Silva M, Pereira OL, et al. 2014. Cercosporoid hyphomycetes associated with Tibouchina herbaceae (Melastomataceae) in Brazil. Mycological Progress 13: 691–702.
Pegler DN, Fiard JP. 1978. Hygrocybe sect. Firmae (Agaricales) in tropical America. Kew Bulletin 32: 297–312.
Poch GK, Gloer JB. 1991. Auranticins A and B: two new depsidones from a mangrove isolate of the fungus Preussia aurantiaca. Journal of Natural Products 54: 213–217.
Posada D. 2008. jModelTest: Phylogenetic Model Averaging. Molecular Biology and Evolution 25: 1253–1256.
Puglisi I, De Patrizio A, Schena L, et al. 2017. Two previously unknown Phytophthora species associated with brown rot of Pomelo (Citrus grandis) fruits in Vietnam. PLoS ONE 12: e0172085.
Quaedvlieg W, Binder M, Groenewald JZ, et al. 2014. Introducing the Consolidated Species Concept to resolve species in the Teratosphaeriaceae. Persoonia 33: 1–40.

Quandt CA, Kepler RM, Gams W, et al. 2014. Phylogenetic-based nomenclatural proposals for Ophiocordycipitaceae (Hypocreales) with new combinations in Tolypocladium. IMA Fungus 5: 121–134.
Ridgway R. 2005. Color standards and color nomenclature. Eliborn Classics, Washington.
Romagnesi H. 1967. Les Russules d'Europe et d'Afrique du Nord. Bordas, Paris.
Ronquist F, Huelsenbeck JP. 2003. MrBayes version 3.0: Bayesian phylogenetic inference under mixed models. Bioinformatics 19: 1572–1574.
Ronquist F, Teslenko M, 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, Crous PW, Hyde KD, et al. 2015. Recommended names for pleomorphic genera in Dothideomycetes. IMA Fungus 6: 507–523.
Royal Botanic Garden, Edinburgh, Scotland. 1969. Flora of British fungi (chart): colour identification chart / Royal Botanic Garden, Edinburgh.
Ryvarden L, Gilbertson RL. 1994. European polypores 2. Synopsis Fungorum 7: 394–743.
Ryvarden L, Johansen I. 1980. Preliminary polypore flora of East Africa. Fungiflora, Oslo.
Saccardo PA. 1883. Sylloge Fungorum II: 574. Padua, Italy.
Sarnari M. 1998. Monografia illustrata del genere Russula in Europa. Tomo Primo. Italia.
Schoch CL, Robbertse B, Robert V, et al. 2014. Finding needles in haystacks: linking scientific names, reference specimens and molecular data for Fungi. DATABASE: 1–21, doi: 10.1093/database/bau061.
Seifert K, Morgan-Jones G, Gams W, et al. 2011. The genera of Hyphomycetes. CBS Biodiversity Series 9. Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands.
Sesli E, Vizzini A. 2017. Two new Rhodocybe species (sect. Rufobrunnea, Entolomataceae) from the East Black Sea coast of Turkey. Turkish Journal of Botany 40: 1–11.
Shaffer RL. 1972. North American Russulas of the sub-section Foetentinae. Mycologia 64: 1008–1053.
Sigler L, Hambleton S, Paré JA. 2013. Molecular characterization of reptile pathogens currently known as members of the Chrysosporium anamorph of Nannizziopsis vriesii complex and relationship with some human-associated isolates. Journal of Clinical Microbiology 51: 3338–3357.
Silva M, Barreto RW, Pereira OL, et al. 2016. Exploring fungal mega-diversity: Pseudocercospora from Brazil. Persoonia 37: 142–172.
Singer R. 1946. Two new species in the Agaricales. Mycologia 38: 687–690.
Smith AH, Hesler LR. 1942. Studies in North American species of Hygrophorus – II. Lloydia 5: 1–94.
Smithe FB. 1975. Naturalist's color guide. The American Museum of Natural History, New York.
Stangl J, Glowinski H. 1980. Inocybe mystica nom. nov. (Inocybe confusa Karst. Ss. Heim in Lit.). Zeitschrift für Mykologie 46: 169–172.
Stolk AC. 1955. Emericellopsis minima sp. nov. and Westerdykella ornata gen. nov., sp. nov. Transactions of British Mycological Society 38: 419–424.
Stuntz DE. 1954. Studies on the genus Inocybe II. New and noteworthy species from Michigan. Papers of the Michigan Academy of Science, Arts, and Letters 39: 53–84.
Subramanian CV, Vittal BPR. 1974. Hyphomycetes on litter from India–I. Proceedings of the Indian National Science Academy, part B, 80: 216–222.
Sue PK, Gurda GT, Leec R, et al. 2014. First report of Westerdykella dispersa as a cause of an angioinvasive fungal infection in a neutropenic host. Journal of Clinical Microbiology 52: 4407–4411.
Suh S, McHugh J, Blackwell M. 2004. Expansion of the Candida tanzawaensis yeast clade: 16 novel Candida species from basidiocarp-feeding beetles. International Journal of Systematic and Evolutionary Microbiology 54: 2409–2429.
Sung G-H, Hywel-Jones NL, Sung J-M, et al. 2007. Phylogenetic classification of Cordyceps and the clavicipitaceous fungi. Studies in Mycology 57: 5–59.
Sutton DA, Marin Y, Thomson, EH, et al. 2013. Isolation and characterization of a new fungal genus and species, Aphanoascella galapagosensis, from carapace keratitis of a Galapagos tortoise (Chelonoidis nigra microphyes). Medical Mycology 51: 113–120.
Swofford DL. 2003. PAUP*. Phylogenetic analysis using parsimony (*and their methods). Version 4. Sinauer Associates, Sunderland, Massachusetts.
Tamura K, Nei M. 1993. Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. Molecular Biology and Evolution 10: 512–526.
Tamura K, Stecher G, Peterson D, et al. 2013. MEGA 6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution 30: 2725–2729.
Taniguchi T, Douhan GW, Allen M. 2013. Effect of summer rain pulse on ectomycorrhizal community of Quercus kelloggii in California mixed-conifer forest. International Congress of Mycorrhizae 7, New Delhi, India.
Tanney JB, Douglas B, Seifert KA. 2016. Sexual and asexual states of some endophytic Phialocephala species of Picea. Mycologia 108: 255–280.
Trakunyingcharoen T, Lombard L, Groenewald JZ, et al. 2014. Mycoparasitic species of Sphaerellopsis, and allied lichenicolous and other genera. IMA Fungus 5: 391–414.
Trappe JM, Claridge AW, Arora D, et al. 2008. Desert truffles of the African Kalahari: ecology, ethnomycology, and taxonomy. Economic Botany 62: 521–529.
Trappe JM, Kovács GM, Claridge AW. 2010. Comparative taxonomy of desert truffles of the Australian outback and the African Kalahari. Mycological Progress 9: 131–143.
Tulasne LR, Tulasne C. 1844. Recherches sur l'organisation et le mode de frutification des champignons de la tribu des Nidulariées, suivies d'um essai monographique. Annales des Sciences Naturalles Series 3, 1: 41–107.
Van Coller GJ, Denman S, Groenewald JZ, et al. 2005. Characterisation and pathogenicity of Cylindrocladiella spp. associated with root and cutting rot symptoms of grapevines in nurseries. Australasian Plant Pathology 34: 489–498.
Van Nieuwenhuijzen EJ, Miadlikowska JM, Houbraken JAMP, et al. 2016. Wood staining fungi revealed taxonomic novelties in Pezizomycotina: New order Superstratomycetales and new species Cyanodermella oleoligni. Studies in Mycology 85: 107–124.
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.
Vázquez-Campos X, Kinsela AS, Waite TD, et al. 2014. Fodinomyces uranophilus gen. nov. sp. nov. and Coniochaeta fodinicola sp. nov., two uranium mine-inhabiting Ascomycota fungi from northern Australia. Mycologia 106: 1073–1089.
Vellinga EC. 1988. Glossary. In: Bas C, Kuyper TW, Noordeloos ME, et al. (eds), Flora Agaricina neerlandica vol. 1. Blakema, Rotterdam, The Netherlands: 54–64.
Verkley GJM, Da Silva M, Wicklow DT, et al. 2004. Paraconiothyrium, a new genus to accommodate the mycoparasite Coniothyrium minitans, anamorphs of Paraphaeosphaeria, and four new species. Studies in Mycology 50: 323–335.
Verkley GJM, Dukuk K, Renfurm R, et al. 2014. Novel genera and species of coniothyrium-like fungi in Montagnulaceae (Ascomycota). Persoonia 32: 25–51.
Videira SIR, Groenewald JZ, Braun U, et al. 2016. All that glitters is not Ramularia. Studies in Mycology 83: 49–163.
Videira SIR, Groenewald JZ, Kolecka A, et al. 2015a. Elucidating the Ramularia eucalypti species complex. Persoonia 34: 50–64.
Videira SIR, Groenewald JZ, Verkley GJM, et al. 2015b. The rise of Ramularia from the Mycosphaerella labyrinth. Fungal Biology 119: 823–843.
Visagie CM, Seifert KA, Houbraken J, et al. 2016. A phylogenetic revision of Penicillium sect. Exilicaulis, including nine new species from fynbos in South Africa. IMA Fungus 7: 75–117.
Vizzini A, Angelini C, Ercole E. 2015. Molecular confirmation of Gyroporus lacteus and typification of Boletus cyanescens. Phytotaxa 226: 27–38.
Wang L, Li HH, Chen YQ, et al. 2014. Polycephalomyces lianzhouensis sp. nov., a new species, co-occurs with Ophiocordyceps crinalis. Mycological Progress 13: 1089–1096.
Wang Y, Moreno G, Riousset LJ, et al. 1998. Tuber pseudoexcavatum sp. nov. A new species from China commercialised in Spain, France and Italy with additional comments on Chinese truffles. Cryptogamie, Mycologie 19: 113–120.
Wang YB, Yu H, Dai YD, et al. 2015. Polycephalomyces agaricus, a new hyperparasite of Ophiocordyceps sp. infecting melolonthid larvae in southwestern China. Mycological Progress 14: 70.
Wijayawardene NN, Crous PW, Kirk PM, et al. 2014. Naming and outline of Dothideomycetes – 2014 including proposals for the protection or suppression of generic names. Fungal Diversity 69: 1–55.
Young A. 1999. Additions to the Hygrophoraceae (Fungi, Agaricales) of south-eastern Australia. Muelleria 12: 3–36.
Zhao C, Cui B. 2013. Morphological and molecular identification of four new resupinate species of Perenniporia (Polyporales) from southern China. Mycologia 105: 945–958.
Zhao CL, Cui BK, Dai YC. 2013. New species and phylogeny of Perenniporia based on morphological and molecular characters. Fungal Diversity 58: 47–60.
Zhao CL, Shen LL, Cui BK. 2014. Perenniporia cinereofusca sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis. Mycoscience 55: 417–422.
Zhao RL, Jeewon R, Desjardin DE, et al. 2007. Ribosomal DNA phylogenies of Cyathus: Is the current infrageneric classification appropriate? Mycologia 99: 385–395.