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RESEARCH ARTICLE

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Key words

ITS nrDNA barcodes
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systematics

Abstract Novel species of fungi described in this study include those from various countries as follows: **Australia**: *Apiognomonia lasiopetali* on *Lasiopetalum* sp., *Blastacervulus eucalyptorum* on *Eucalyptus adesmophloia*, *Bullanockia australis* (incl. *Bullanockia* gen. nov.) on *Kingia australis*, *Caliciopsis eucalypti* on *Eucalyptus marginata*, *Celerioriella petrophiles* on *Petrophile teretifolia*, *Coleophoma xanthosiae* on *Xanthosia rotundifolia*, *Coniothyrium hakeae* on *Hakea* sp., *Diatrypella banksiae* on *Banksia formosa*, *Disculoides corymbiae* on *Corymbia calophylla*, *Elsinoë eelemani* on *Melaleuca alternifolia*, *Elsinoë eucalyptigena* on *Eucalyptus kingsmillii*, *Elsinoë preissianae* on *Eucalyptus preissiana*, *Eucasphaeria rustici* on *Eucalyptus creta*, *Hyweljonesia queenslandica* (incl. *Hyweljonesia* gen. nov.) on the cocoon of an unidentified microlepidoptera, *Mycodiella eucalypti* (incl. *Mycodiella* gen. nov.) on *Eucalyptus diversicolor*, *Myrtapenidiella sporadicae* on *Eucalyptus sporadica*, *Neocrinula xanthorrhoeae* (incl. *Neocrinula* gen. nov.) on *Xanthorrhoea* sp., *Ophiocordyceps nooreniae* on dead ant, *Phaeosphaeriopsis agavacearum* on *Agave* sp., *Phlogicylindrium mokarei* on *Eucalyptus* sp., *Phyllosticta acaciigena* on *Acacia suaveolens*, *Pleurophoma acaciae* on *Acacia glaucoptera*, *Pyrenochaeta hakeae* on *Hakea* sp., *Readeriella lehmannii* on *Eucalyptus lehmannii*, *Saccharata banksiae* on *Banksia grandis*, *Saccharata daviesiae* on *Daviesia pachyphylla*, *Saccharata eucalyptorum* on *Eucalyptus bigalerita*, *Saccharata hakeae* on *Hakea baxteri*, *Saccharata hakeicola* on *Hakea victoria*, *Saccharata lambertiae* on *Lambertia ericifolia*, *Saccharata petrophiles* on *Petrophile* sp., *Saccharata petrophilicola* on *Petrophile fastigiata*, *Sphaerellopsis hakeae* on *Hakea* sp., and *Teichospora kingiae* on *Kingia australis*. **Brazil**: *Adautomilanezia caesalpiniae* (incl. *Adautomilanezia* gen. nov.) on *Caesalpina echinata*, *Arthrophiala arthrospora* (incl. *Arthrophiala* gen. nov.) on *Sagittaria montevidensis*, *Diaporthe caatingaensis* (endophyte from *Tacinga inamoena*), *Geastrum ishikawae* on sandy soil, *Geastrum pusillipilosum* on soil, *Gymnopus pygmaeus* on dead leaves and sticks, *Inonotus hymenonitens* on decayed angiosperm trunk, *Pyricularia urashimae* on *Urochloa brizantha*, and *Synnemellisia aurantia* on *Passiflora edulis*. **Chile**: *Tubulicrinis australis* on *Lophosoria quadripinnata*. **France**: *Cercophora squamulosa* from submerged wood, and *Scedosporium cereisporum* from fluids of a wastewater treatment plant. **Hawaii**: *Beltraniella acaciae*, *Dactylaria acaciae*, *Rhexodenticula acaciae*, *Rubikia evansii* and *Torula acaciae* (all on *Acacia koa*). **India**: *Lepidoderma echinosporum* on dead semi-woody stems, and *Rhodocybe rubrobrunnea* from soil. **Iran**: *Talaromyces kabodanensis* from hypersaline soil. **La Réunion**: *Neocordana musarum* from leaves of *Musa* sp. **Malaysia**: *Anungitea eucalyptigena* on *Eucalyptus grandis* × *pellita*, *Camptomeriphila leucaenae* (incl. *Camptomeriphila* gen. nov.) on *Leucaena leucocephala*, *Castanediella communis* on *Eucalyptus pellita*, *Eucalyptostroma eucalypti* (incl. *Eucalyptostroma* gen. nov.) on *Eucalyptus pellita*, *Melanconiella syzygii* on *Syzygium* sp., *Mycophilomyces periconiae* (incl. *Mycophilomyces* gen. nov.) as hyperparasite on *Periconia* on leaves of *Albizia falcataria*, *Synnemadiella eucalypti* (incl. *Synnemadiella* gen. nov.) on *Eucalyptus pellita*, and *Teichospora nephelii* on *Nephelium lappaceum*. **Mexico**: *Aspergillus bicephalus* from soil. **New Zealand**: *Aplosporella sophorae* on *Sophora microphylla*, *Libertasomyces platani* on *Platanus* sp., *Neothyronectria sophorae* (incl. *Neothyronectria* gen. nov.) on *Sophora microphylla*, *Parastagonospora phoenicicola* on *Phoenix canariensis*, *Phaeoacremonium pseudopanacis* on *Pseudopanax crassifolius*, *Phlyctema phoenicis* on *Phoenix canariensis*, and *Pseudoascochyta novae-zelandiae* on *Cordyline australis*. **Panama**: *Chalara panamensis* from needle litter of

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Pinus cf. *caribaea*. **South Africa**: *Exophiala eucalypti* on leaves of *Eucalyptus* sp., *Fantasmomyces hyalinus* (incl. *Fantasmomyces* gen. nov.) on *Acacia exuvialis*, *Paracladophialophora carceris* (incl. *Paracladophialophora* gen. nov.) on *Aloe* sp., and *Umthunziomyces hagahagensis* (incl. *Umthunziomyces* gen. nov.) on *Mimusops caffra*. **Spain**: *Clavaria griseobrunnea* on bare ground in *Pteridium aquilinum* field, *Cyathus ibericus* on small fallen branches of *Pinus halepensis*, *Gyroporus pseudolacteus* in humus of *Pinus pinaster*, and *Pseudoascochyta pratensis* (incl. *Pseudoascochyta* gen. nov.) from soil. **Thailand**: *Neoascochyta adenii* on *Adenium obesum*, and *Ochroconis capsici* on *Capsicum annuum*. **UK**: *Fusicolla melogrammae* from dead stromata of *Melogramma campylosporum* on bark of *Carpinus betulus*. **Uruguay**: *Myrmecridium pulvericola* from house dust. **USA**: *Neoscolecobasidium agapanthi* (incl. *Neoscolecobasidium* gen. nov.) on *Agapanthus* sp., *Polyscytalum purgamentum* on leaf litter, *Pseudopithomyces diversisporus* from human toenail, *Saksenaea trapezispora* from knee wound of a soldier, and *Sirococcus quercus* from *Quercus* sp. Morphological and culture characteristics along with DNA barcodes are provided.

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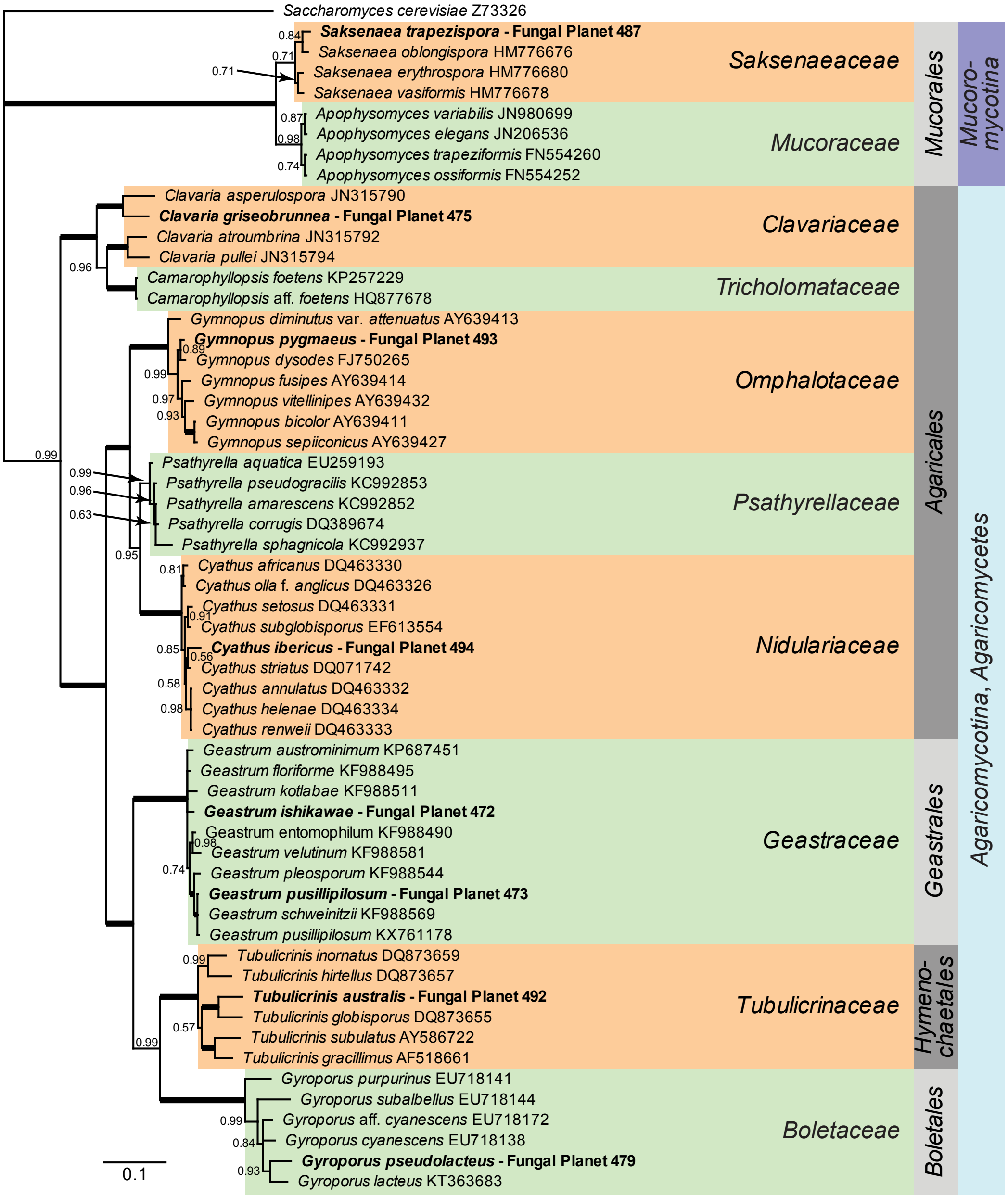

Overview *Mucoromycotina* and *Agaricomycotina* phylogeny

Consensus phylogram (50 % majority rule) of 2 394 trees resulting from a Bayesian analysis of the LSU sequence alignment (58 taxa including outgroup; 874 aligned positions; 507 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 *Saccharomyces cerevisiae* (GenBank Z73326) 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 S20202).

Acknowledgements (cont)

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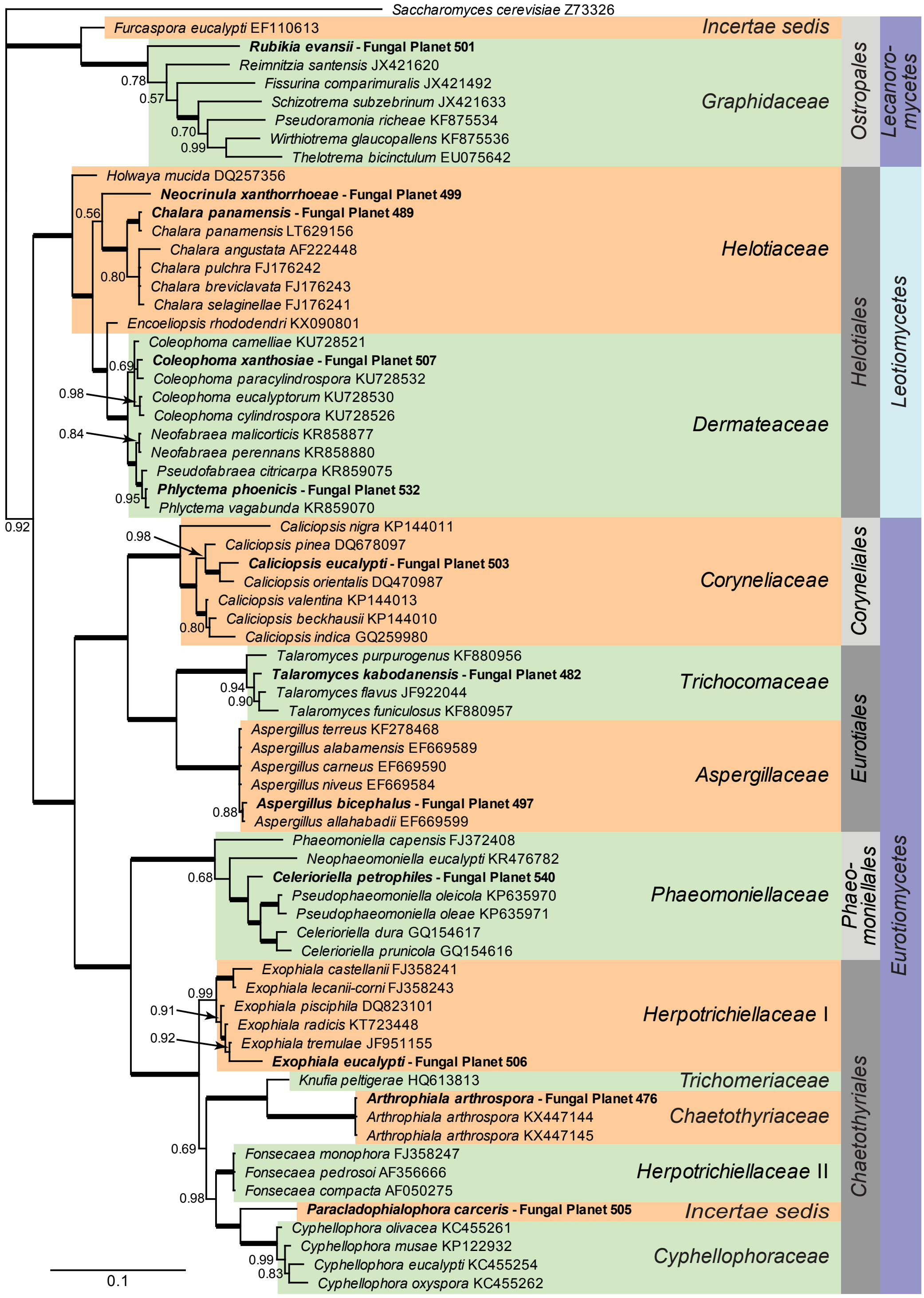
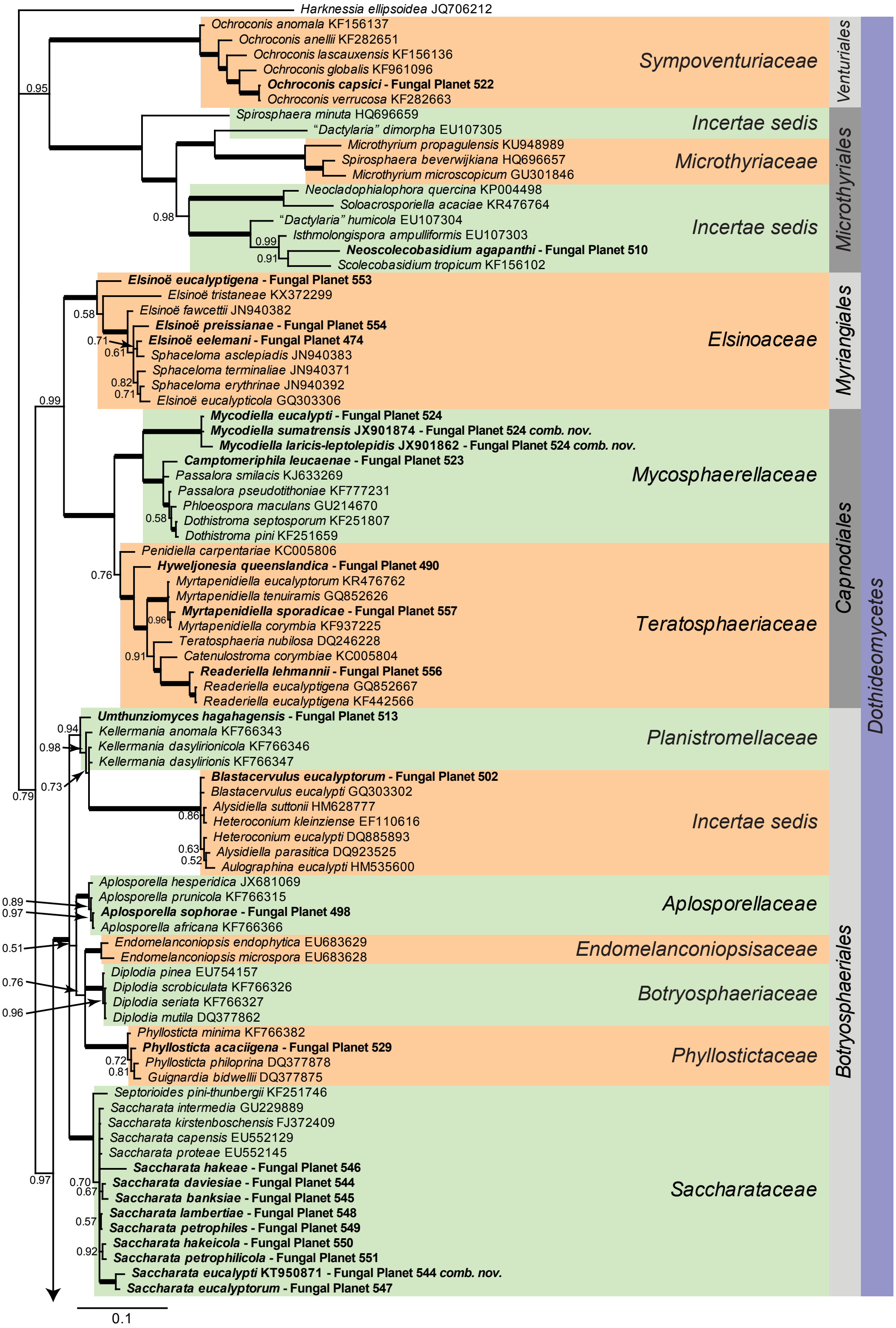


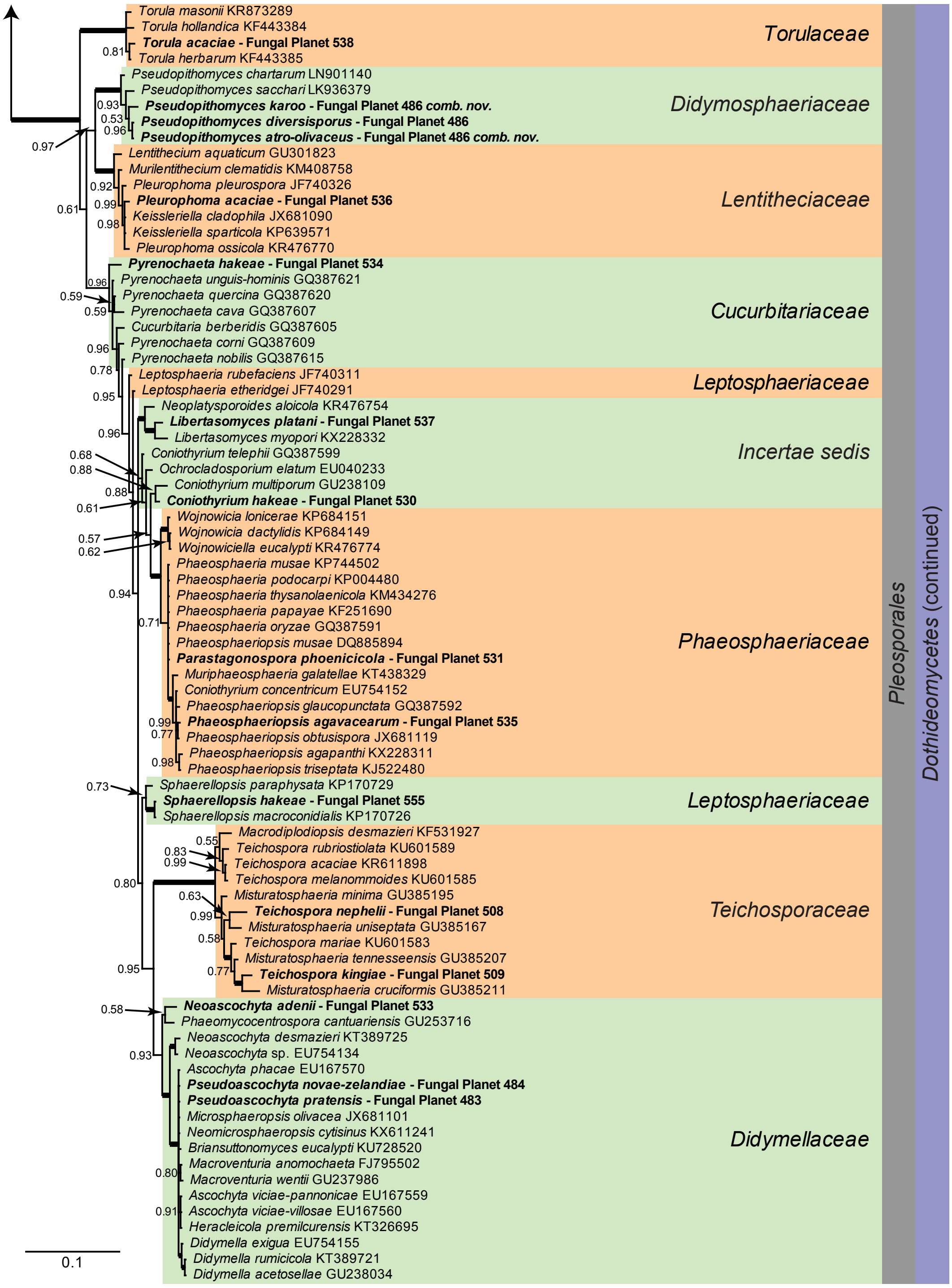
Overview *Lecanoromycetes*, *Leotiomycetes* and *Eurotiomycetes*, phylogeny

Consensus phylogram (50 % majority rule) of 790 trees resulting from a Bayesian analysis of the LSU sequence alignment (70 taxa including outgroup; 808 aligned positions; 386 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 *Saccharomyces cerevisiae* (GenBank Z73326) 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 S20202).

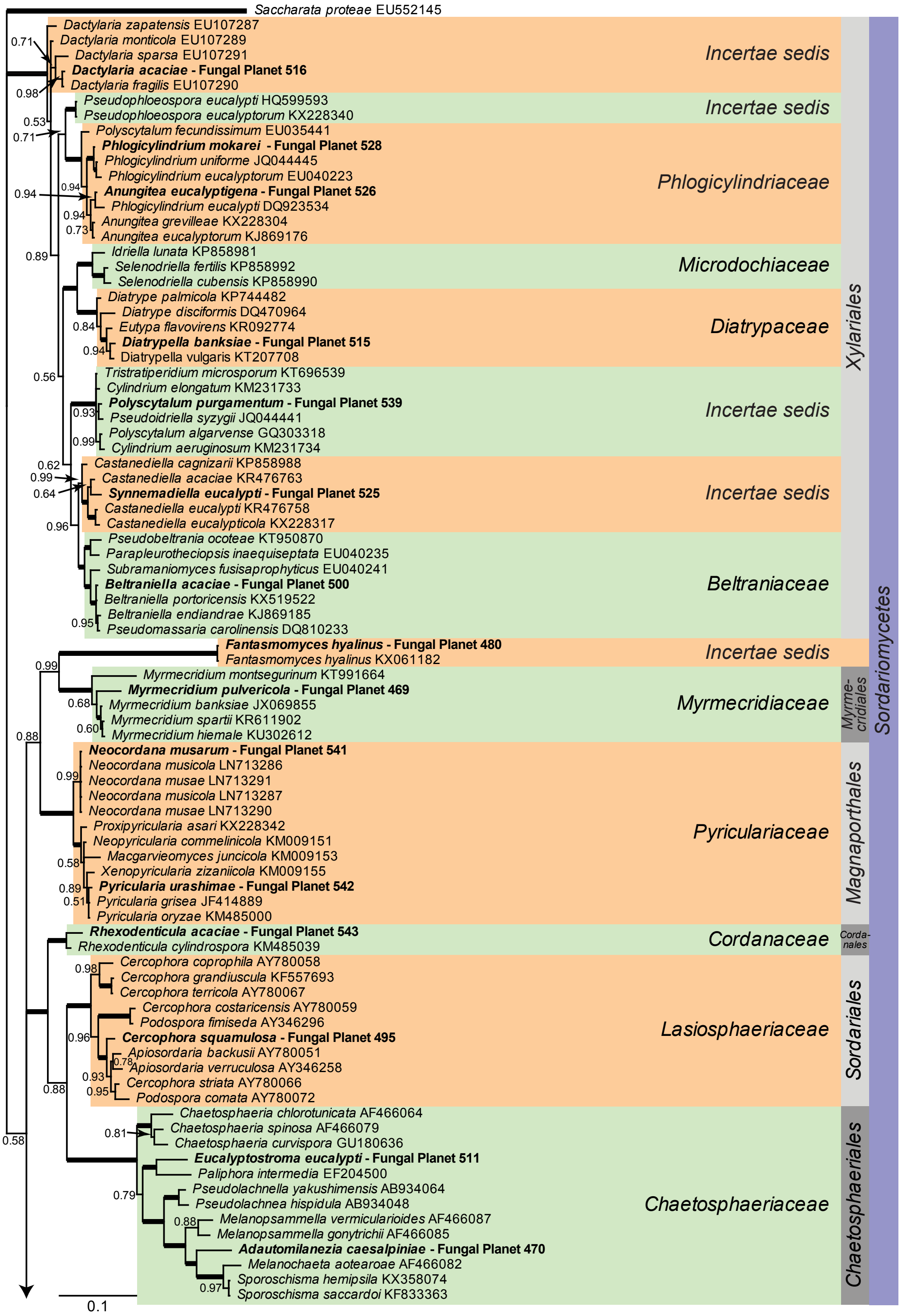


Overview *Dothideomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 10 030 trees resulting from a Bayesian analysis of the LSU sequence alignment (167 taxa including outgroup; 806 aligned positions; 453 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 *Harknessia ellipsoidea* (GenBank JQ706212) 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 S20202).

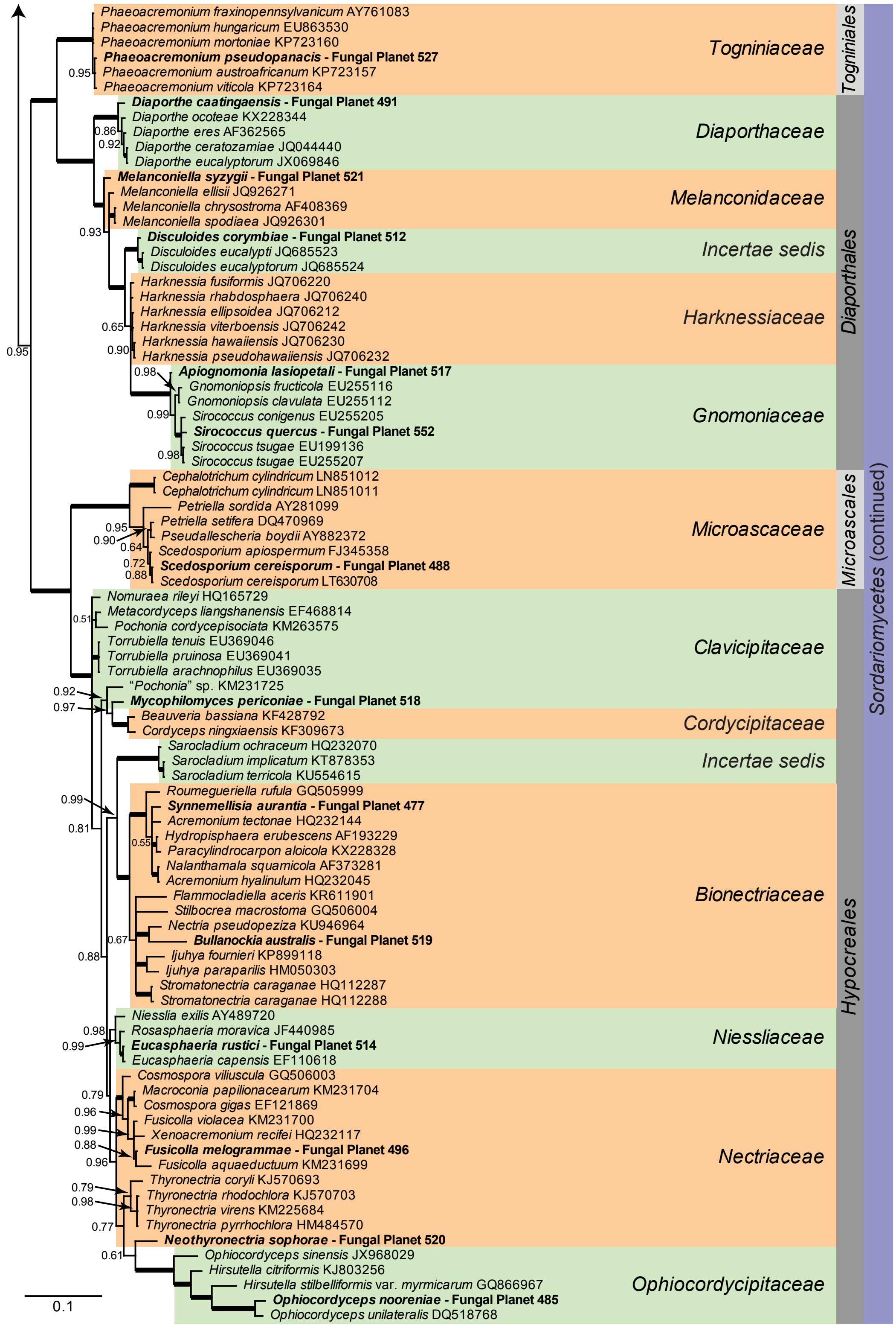


Overview *Dothideomycetes* phylogeny (cont.)

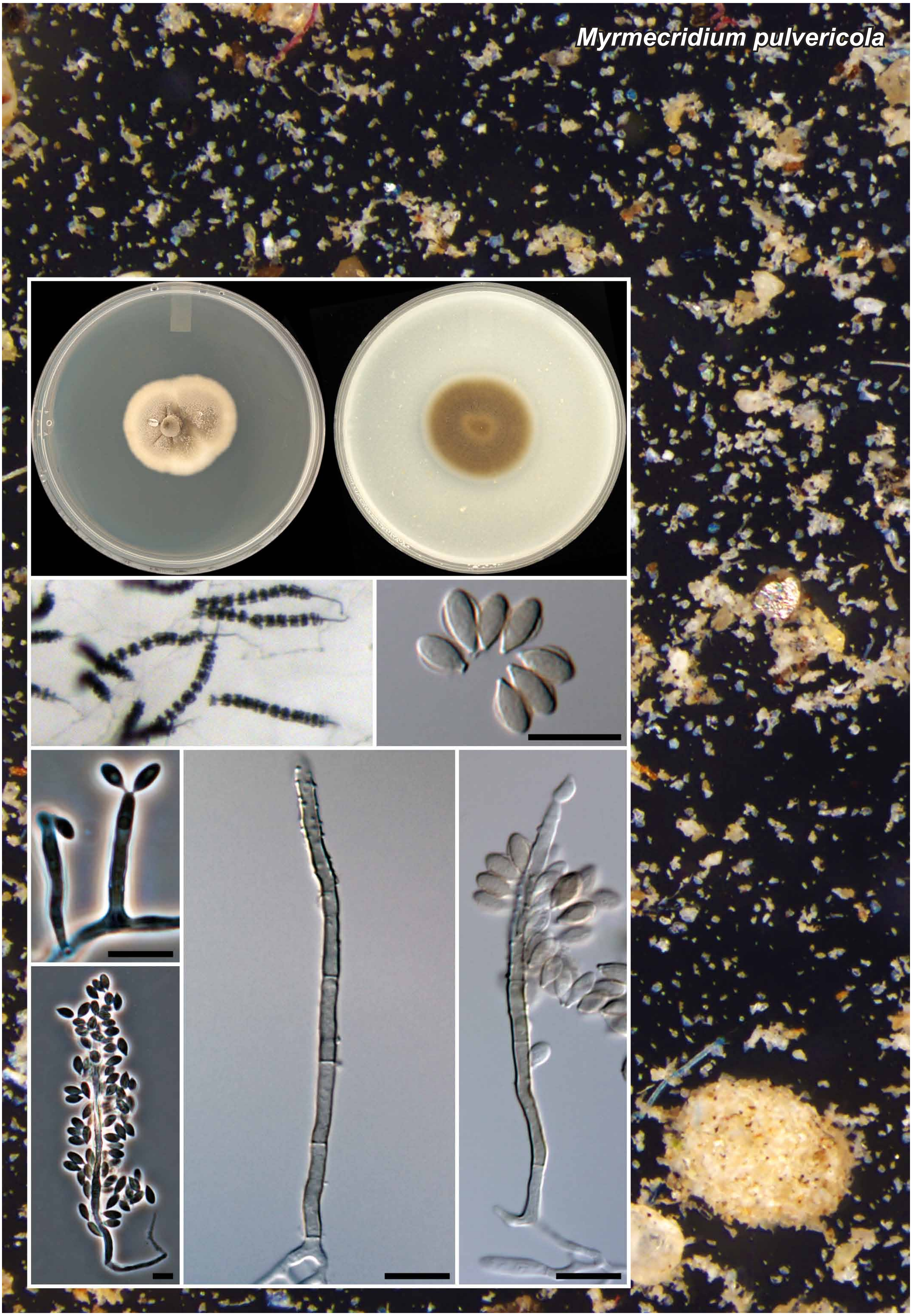


Overview *Sordariomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 8 418 trees resulting from a Bayesian analysis of the LSU sequence alignment (174 taxa including outgroup; 788 aligned positions; 393 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) 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 S20202).



Overview *Sordariomycetes* phylogeny (cont.)


Myrmecridium pulvericola

Fungal Planet 469 – 21 December 2016

Myrmecridium pulvericola Koppel, Visagie, Hirooka & Seifert, *sp. nov.*

Etymology. Latin, *pulvericola*, meaning living in dust.

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

Mycelium consisting of hyaline, thin-walled, smooth, 2–3 µm diam hyphae. *Conidiophores* erect, unbranched, straight, pigmented brown, thick-walled, septate, 22–77 × 2.5–3.5 µm, after 1 mo of incubation up to 350 µm tall, basal cell sometimes inflated, 3–4 µm wide. *Conidiogenous cells* integrated, cylindrical, 10–32 µm long, brownish, becoming reddish brown with age, fertile region forming a rachis with pimple-like denticles arranged in whorls along the conidiogenous axis, less than 0.5 × 0.5 µm, with unpigmented, slightly thickened scars. *Conidia* solitary, hyaline to somewhat pale brown, thin-walled, smooth to finely roughened, wing-like gelatinous sheaths present 0.5–1 µm, ellipsoidal to obovoid or fusiform, 5.5–7(–8) × 2.5–4 µm (6.7 ± 0.7 × 3.5 ± 0.4); tapering from obtuse apex to subtruncate base; hilum unthickened.

Culture characteristics — Colonies on MEA 30 mm diam after 14 d, lightly sulcate; margins entire; sporulation moderately dense, olive-brown (4E5–8) to greyish brown (5D3) near centre; reverse greyish yellow (4C7–4C6). Colonies on OA 36 mm after 14 d.

Typus. Uruguay, Santiago de Auca, Montevideo Dept., from house dust, 2008, coll. *Z. Torrano*, isol. *E. Whitfield & K. Mwange* as ZT01UY-27 (holotype DAOM 675861, cultures ex-type DAOMC 250405, ITS sequence GenBank KU309312, LSU sequence GenBank KU309313, MycoBank MB815486).

Notes — Here we introduce the new species *M. pulvericola*, isolated from house dust collected in Uruguay. *Myrmecridium pulvericola* is distinct from other species and closely related to *M. thailandicum*. Morphologically the mostly smooth-walled conidia of *M. pulvericola* differ from the finely verruculose conidia of *M. thailandicum*. In addition, *M. thailandicum* grows significantly faster than *M. pulvericola* (60 mm vs 30 mm after 2 wk on MEA). Sequence divergence between *M. pulvericola* and *M. thailandicum* is comparable to variation between recently described *Myrmecridium* species. Based on a MegaBLAST search of GenBank's nucleotide database, ITS of *M. pulvericola* is 100 % and 99 % similar to two environmental clones (GenBank JQ081655, JQ081571) from soil collected near a nest of leaf-cutting ants (*Atta bisphaerica*) in Brazil (Rodrigues et al. 2014). A separate analysis (not shown) confirmed the identity of these clones as *M. pulvericola*, suggesting this is a broadly distributed South American species.

Myrmecridium was introduced for *Ramichloridium schulzeri*, when it was found to be phylogenetically distinct from other *Ramichloridium* species (Arzanlou et al. 2007). Based on morphological differences, new combinations were introduced as *M. schulzeri* var. *schulzeri*, *M. schulzeri* var. *tritici* and *M. flexuosum*. In their ITS phylogeny, the taxonomic status of the varieties of *M. schulzeri* was not finalised, mainly because of the lack of ex-type sequences. Although these clades remain unresolved (up to six clades in our phylogeny), several new species were described in recent years (Arzanlou et al. 2007, Crous et al. 2011a, 2012c, 2013, 2015b, c, Jie et al. 2013), including *M. montsegurinum* producing an ascomatal sexual state (Réblová et al. 2016). The genus now includes 10 species that vary in conidial and colony characteristics. For morphological identification, we include a dichotomous key adapted from Jie et al. (2013).

Key to Myrmecridium species

1\. Ascomata present, immersed in wood under a clypeus . . . . . . *M. montsegurinum*
1\. Sexual state not present 2

2\. Conidial hilum pigmented 3
2\. Conidial hilum unpigmented 4

3\. Conidia < 10 µm long. . . . . . . *M. obovoideum*
3\. Conidia 10–20 µm long . . . . *M. iridis*

4\. Conidia typically < 10 µm long. 5
4\. Conidia at least 10 µm long 9

5\. Conidia mostly smooth 6
5\. Conidia textured, finely verruculose or vein-like 7

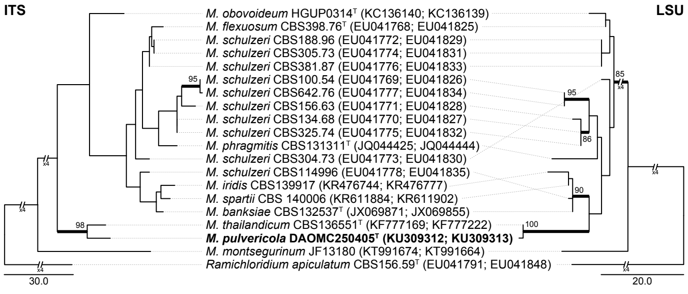
6\. Conidia septate . . . . *M. phragmatis*
6\. Conidia aseptate . . . . ***M. pulvericola***

7\. Colonies reaching 60 mm in 2 wk . . . . . *M. thailandicum*
7\. Colonies not reaching 60 mm in 2 wk 8

8\. Conidia ellipsoid to obovoid, (5–)6–7(–9) µm long. . . . . . . *M. flexuosum*
8\. Conidia obovoid to fusiform (6.5–)8–9(–10) µm long . . . . *M. spartii*

9\. Conidia septate . . . . *M. schulzeri* var. *tritici*
9\. Conidia aseptate 10

10\. Colony surface colour grey olivaceous, conidia up to 14 µm long . . . . *M. banksiae*
10\. Colony surface colour pale orange to orange, conidia up to 12 µm long. . . . . . . *M. schulzeri* var. *schulzeri*



Phylogenetic trees of ITS and LSU. MAFFT aligned datasets were analysed using maximum parsimony. A heuristic search was performed in PAUP* 4.0b.10 with support in nodes calculated using a bootstrap analysis with 1 000 replicates. The new species is indicated by **bold** text, ^{T} = ex-type strain.

Colour illustrations. House dust; colonies on MEA and OA, conidiophores and conidia. Scale bars = 10 µm.

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Adautomilanezia caesalpiniae

Fungal Planet 470 – 21 December 2016

Adautomilanezia Gusmão, S.S. Silva, Fiuza, L.A. Costa, T.A.B. Santos, *gen. nov.*

Etymology. Named Latinised, in honour to the Brazilian mycologist, Dr Adauto Ivo Milanez, who dedicated his life to study the zoosporic fungi.

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

Colonies on natural substrata effuse, black. *Stromata* absent. *Conidiomata* sporodochial, determinate, solitary or in groups, black. *Setae* arising intermixed with conidiogenous cells, straight to curved, acute apex, smooth, septate, inflated at the base, dark brown to black. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* enteroblastic, unilocal, conidiogenous loci lacerate, arising from superficial hyphae, thick-walled, sessile, grouped, globose to subglobose, pale brown. *Conidia* solitary, exogenously produced, dry, smooth, oblong to clavate, multi-septate, pale brown to brown, secession schizolytic.

Type species. Adautomilanezia caesalpiniae Gusmão, S.S. Silva, Fiuza, L.A. Costa, T.A.B. Santos.
MycoBank MB815142.

Adautomilanezia caesalpiniae Gusmão, S.S. Silva, Fiuza, L.A. Costa, T.A.B. Santos, *sp. nov.*

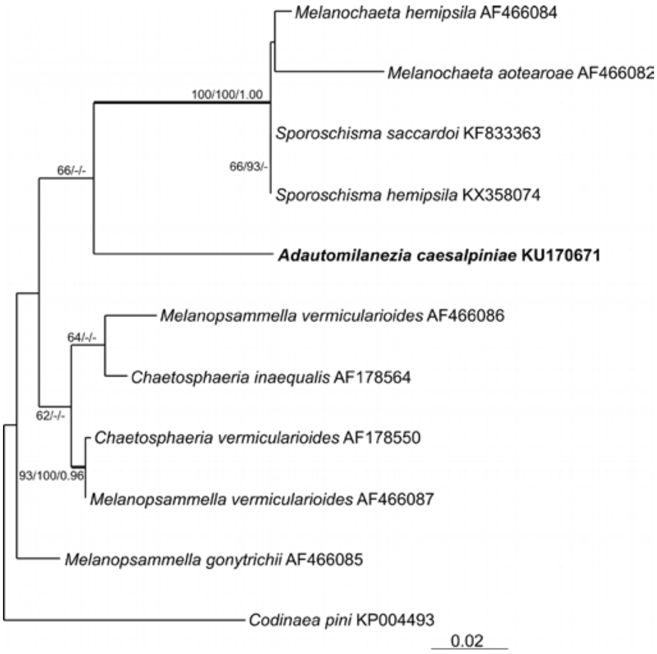
Etymology. Name reflects the host genus *Caesalpinia*, from which the species was isolated.

Colonies on the natural substrate effuse, black. *Mycelium* mostly immersed in substrate. *Stromata* absent. *Conidiomata* sporodochial, determinate, solitary or in groups, black. *Setae* arising from globose basal cells intermixed with conidiogenous cells, straight to curved, acute apex, smooth, septate, dark brown to black, 75–217.5 × 5–10 µm; basal cells 7.5–12.5 µm. *Conidiophores* absent. *Conidiogenous* cells enteroblastic, unilocal, with a large lacerate aperture on conidiogenous loci, 3.8–6.3 µm wide, arising from superficial hyphae, thick-walled, sessile, grouped, globose to subglobose, pale brown, 15–18.8 × 10.5–20 µm. *Conidia* solitary, exogenous, dry, smooth, oblong to clavate, (1–)3-septate, brown, 27.5–42.5 × 12.5–22.5 µm; thick and darkly pigmented at the septa, 2.5–3.7 µm wide.

Culture characteristics — Colonies on AWA (Antibiotic Water Agar), reaching 50 mm diam after 60 d at 25 °C, immersed mycelium, circular, entire edges, dark brown. Reproductive structures and setae present on the surface of the culture medium, and abundant in the centre and the edge of the colony. Colonies on CMA (Corn Meal Agar) attaining 52 mm diam after 15 d at 25 °C, moderate or abundant aerial mycelium, circular, umbonate, entire edges, pale brown.

Typus. Brazil, Bahia, Feira de Santana, Universidade Estadual de Feira de Santana, on decaying twigs of *Caesalpina echinata* (*Caesalpiniaceae*), 23 Nov. 2011, *S.S. Silva* (holotype HUEFS216632, cultures ex-type CC-LAMIC 102/12, ITS sequence GenBank KX821777, LSU sequence GenBank KU170671, TreeBASE ID19855, MycoBank MB815303).

Notes — Based on a megablast search of NCBIs GenBank nucleotide database using the LSU sequence, the closest hits are *Melanochaeta hemipsila* (GenBank AF466084) *M. aotearoae* (GenBank AF466082), *Sporoschisma saccardoi* (GenBank KF833363) and *S. hemipsila* (GenBank KX358074). No data for ITS was deposited in GenBank for either *Melanochaeta* or *Sporoschisma*. Morphologically, *Adautomilanezia* can be compared with *Sporoschisma* (*Melanochaeta*-*Chaetosphaeriaceae*) and *Endogenospora* in conidial ontogeny; in both genera conidia are formed endogenously and successively after schizolytic secession.



Maximum likelihood (ML) tree based on partial sequences of LSU. The Bayesian analysis (MrBayes v. 3.3) was performed under a GTR+G+I model for 2 M generations. The values of maximum parsimony and maximum likelihood bootstrap (BP-MP and BP-ML) and posterior probabilities (PP-BI) were plotted at the nodes for which threshold values (BP-MP: > 50 % / BP-ML: > 70 % / PP: > 0.95) were achieved.

Colour illustrations. Caesalpinia echinata grove at Universidade Estadual de Feira de Santana; general aspect, conidiogenous cells, conidial development, and mature conidia. Scale bars = 10 µm.

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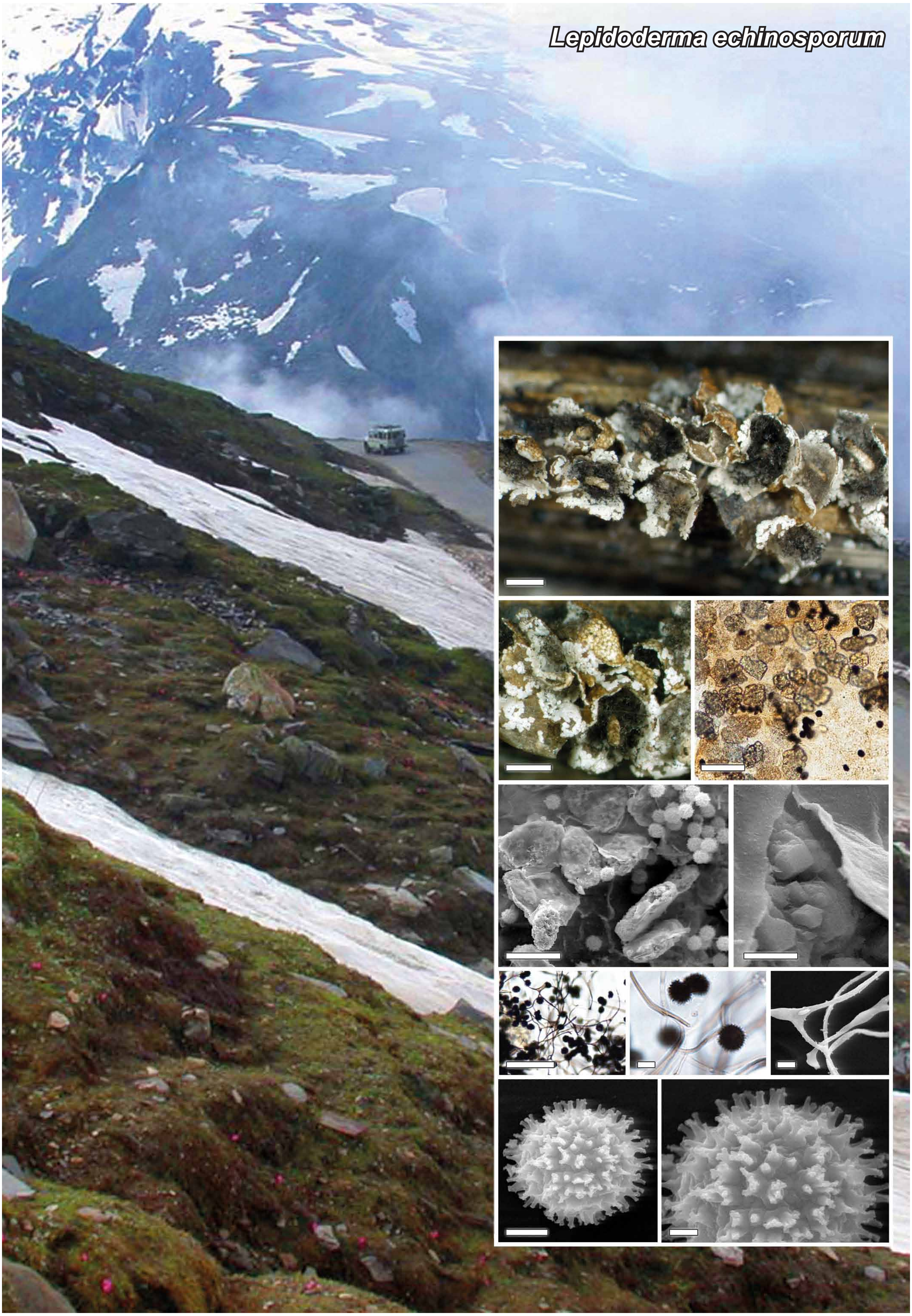
Lepidoderma echinosporum

Fungal Planet 471 – 21 December 2016

Lepidoderma echinosporum G. Moreno, López-Villalba & S.L. Stephenson, *sp. nov.*

Etymology. *Echinosporum* (from Latin *echinos* = spine and *spora* = spore) refers to the conspicuous spines on the spores.

Classification — *Didymiaceae*, *Physarales*, *Myxomycetes*.

Sporocarps sessile, 1–2 mm diam and 1–1.2 mm high. *Peridium* double with apical longitudinal dehiscence, fissures forming stellate radial plates. *Outer layer* membranous, dark brown, the *inner layer* formed by small white flat and prismatic plates of calcium carbonate, which are projected as small lumps on the outer layer, these falling off after dehiscence of the sporocarps. *Columella* well developed, cylindrical, straw-coloured to brown-dark, formed by small plates of calcium carbonate, the latter similar to those of the inner layer, which occupies almost the entire interior of the sporotheca. *Hypothallus* light brown, membranous. *Capillitium* branched and arising along the columella and extending towards the inner peridium, formed by dark brown filaments, 1.5–2 mm diam. *Spores* globose to subglobose, 15–17.7(–18) × 14–17 µm, av. 16.3 × 15.4 µm, Q_{av} = 1.06, brown blackish in transmitted light, with numerous spines, the *spines* very sharp, curved, sometimes dichotomously branched at the apex. Under SEM the *spore ornamentation* is formed by large baculae, these sometimes fused into short ridges and the apices with more or less coralloid branches.

Habitat & Distribution — This is a nivicolous species occurring gregariously in groups of 5–30 sporocarps. It is apparently very rare in the study area.

Typus. India, Himachal Pradesh Province, 50 km N of Manali and S of Rohtang Pass, N32°20'23.9" and E77°13'08.2", elevation 3240 m, on dead semi-woody stems near the margin of a melting snowbank along National Highway 21, 19 May 2006, *S.L. Stephenson* 21862 (holotype AH 46061; isotype in BPI, MycoBank MB818415).

Additional specimens examined. ***Lepidoderma peyerimhoffii***: Spain, Granada, Sierra Nevada, Cauchiles, in *Carduus carlinoides* subsp. *hispanicus* (*Asteraceae*), 14 Aug. 2001, *A. Sánchez* & *M. Sánchez*, AH 29293. ***Lepidoderma trevelyanii***: Spain, Ávila, Aveinte, in bark of *Populus* sp. (*Salicaceae*), 26 Mar. 1977, *G. Moreno*, AH 45471.

Notes — *Lepidoderma echinosporum* is characterised by having sporocarps with stellate dehiscence, a cylindrical columella which occupies almost the entire interior of the sporotheca, an inner layer of the peridium formed by prismatic thick plates of calcium carbonate and spores 16.3 × 15.4 µm on average, with very dark and marked prominent spines. *Lepidoderma trevelyanii* shares a similar morphology but differs in having a smaller and often globose but non-cylindrical columella and warted spores that range in diam from 11–12.5 µm. *Lepidoderma peyerimhoffii* differs by having sporocarps with a tesserae, well-marked, dehiscence with prismatic plates, the latter with whitish edges and smaller (12.0–13.5 µm diam) warted spores. *Lepidoderma takahashii* can be distinguished by its warted spores which are only 9–11.7 × 7.8–9.6 µm diam and its very small globose columella at the base of the sporotheca (Yamamoto 1998).

In order to determine if there were any morphologically similar species in Asia, the monographs of Japan (Yamamoto 1998), India (Thind 1977, Lakhanpal & Mukerji 1981) and China (Li et al. 2007) were reviewed, but no such species were noted.

Colour illustrations. India, 50 km N of Manali and S of Rohtang Pass, 3240 m, on dead semi-woody stems near the margin of a melting snowbank along National Highway 21, where the holotype was collected; sporocarps with a double peridium, cylindrical columella, prismatic plates of calcium carbonate, prismatic plates of calcium carbonate as observed under scanning electron microscope (SEM), detail of a prismatic plate; capillitium; spores and capillitium, capillitium observed under SEM, spore, details of the spore ornamentation (holotype AH 46061). Scale bars = 1 mm (sporocarps), 100 µm (prismatic plates under light microscope), 50 µm (prismatic plates under SEM), 5 µm (detail of prismatic plate under SEM), 100 µm (capillitium), 10 µm (spores and capillitium), 5 µm (capillitium under SEM), 5 µm (spore under SEM), 2 µm (detail of spore ornamentation under SEM).

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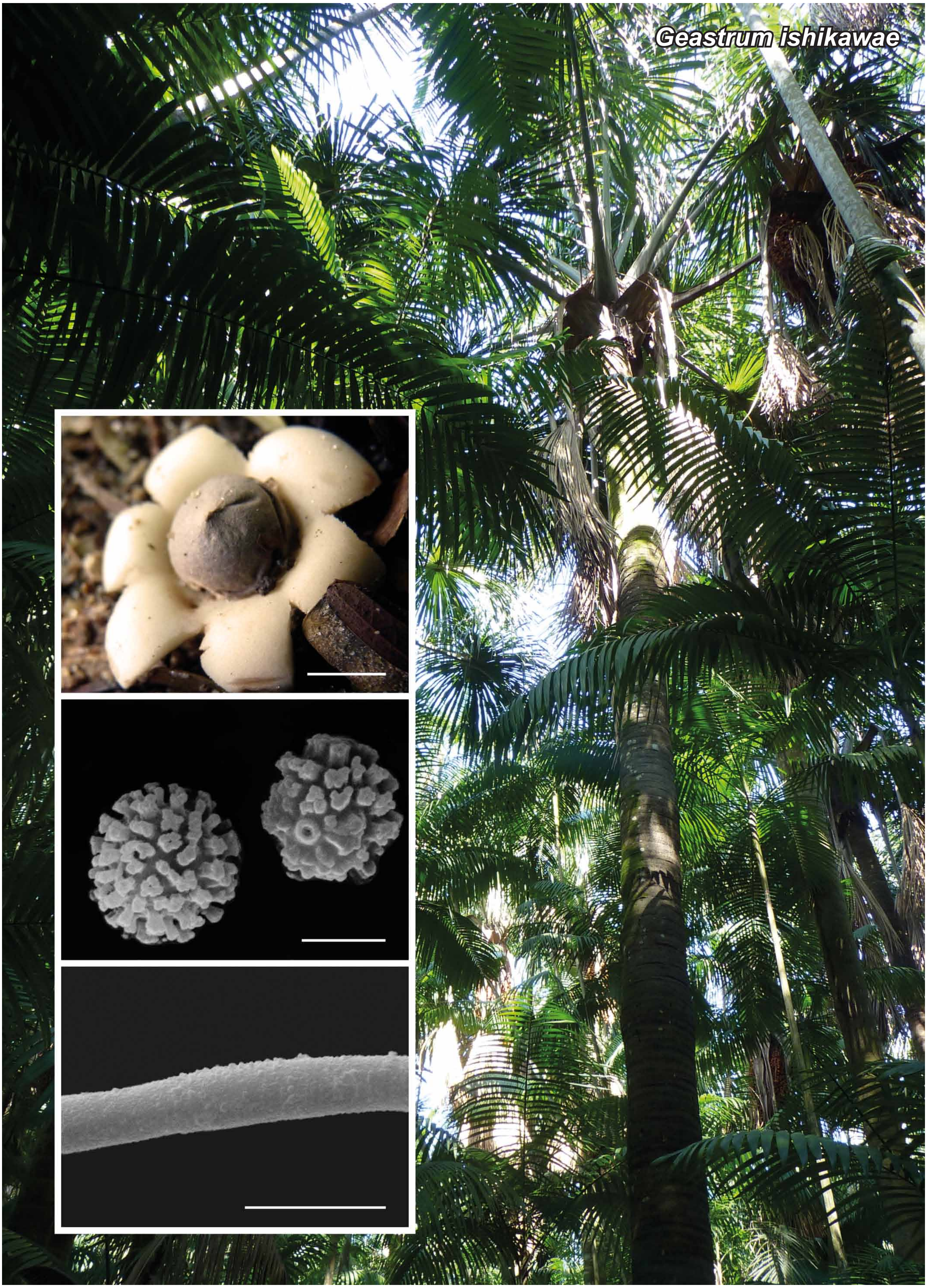

Geastrum ishikawae

Fungal Planet 472 – 21 December 2016

Geastrum ishikawae Accioly, J.O. Sousa, Baseia & M.P. Martín, *sp. nov.*

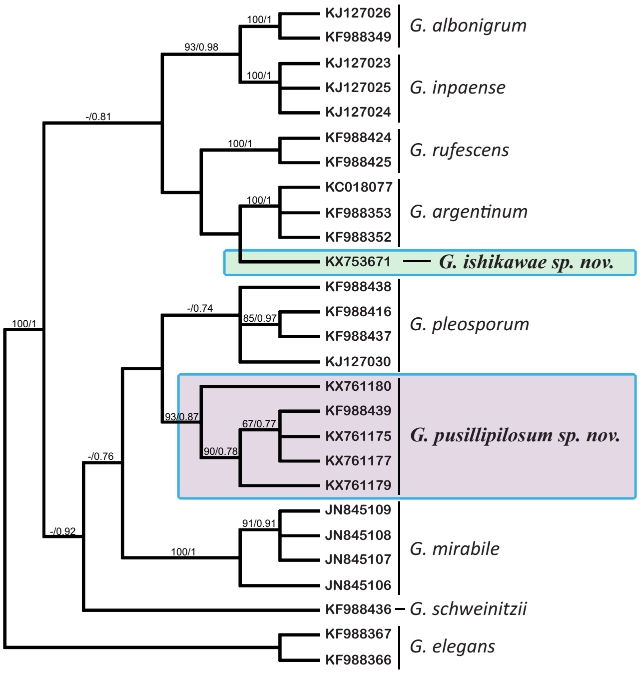
Etymology. In the honour of Noemia Kazue Ishikawa, scientific researcher at INPA for her great contribution to the study of fungi in the Amazon.

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

Basidiomata 12–25 mm diam when mature, rhizomorphs present, white (KW1A1, Kornerup & Wanscher 1978). *Exoperidium* saccate, rays revolute, non-hygroscopic. *Mycelial layer* detaching in patches, cottony to woolly, incrusted with sand debris, white (KW1A1), hyphae 1.2–2.1 µm diam, encrusted, rarely branched, sinuous, hyaline in 5 % KOH. *Fibrous layer* papery to coriaceous, greyish orange (KW5B3), hyphae 2.7–6.4 µm diam, incrusted, not branching, almost hyaline in 5 % KOH. *Pseudoparenchymatous layer* smooth to rimulose, persistent, cracking radially around the endoperidium, dark blond (KW 5D4). *Endoperidium* subglobose, 4–9 mm diam, sessile, felted, pruinose, greyish brown/mouse grey (KW5E3), composed by interwoven, some protruding hyphae. *Peristome* mammiform to flattened, folded, not delimited, concolorous with the endoperidium, mouth fibrillose. *Gleba* greyish brown (KW5F3). *Basidiospores* globose, 4.5–7 µm diam, surface covered with conspicuous columnar warts with truncated tips, some confluent, yellowish brown to brown in 5 % KOH. *Capillitia* 3–5.5 µm diam, verrucose, thick walled (< 4 µm), yellowish brown in 5 % KOH.

Typus. Brazil, Amazonas, Manaus, Instituto Nacional de Pesquisas da Amazônia (INPA), Campus I, alt. 64 m, S3°5'31" W59°59'40", on sandy soil close to palm trees, 12 Jan. 2013, *T. Accioly & N.K. Ishikawa* (holotype UFRN-Fungos 2785; ITS sequence GenBank KX753671, LSU sequence GenBank KX765817, MycoBank MB817951).

Notes — *Geastrum ishikawae* was found growing in an anthropised secondary Amazon Forest, within an urban area. Many other *Geastrum* species also present tiny and non-subiculose basidiomata (*G. kotlabae*, *G. minimum*, G. *schmidelii*, *G. floriforme* and *G. hungaricum*). Although *G. floriforme* and *G. hungaricum* both have very similar mycelial layers to those of *G. ishikawae*, they clearly differ by presenting strongly hygroscopic rays and non-folded peristome. *Geastrum minimum* and *G. schmidelii* also present compatible basidiospore dimensions (up to 7 µm diam) with *G. ishikawae*, but they differ on their stalked endoperidium, and delimited peristome. In the case of *G. kotlabae*, the mycelial layer and basidiospore dimensions (up to 7 µm diam) bring it morphologically close to *G. ishikawae*, but its plicate peristome and strongly hygroscopic rays separate them. An irregularly plicated or folded peristome is also found in *G. rufescens* and *G. morganii*, but they contrast with *G. ishikawae* by exhibiting a brownish coloured and non-woolly mycelial layer, and stalked endoperidium (*G. rufescens*). In the ITS analyses, *G. ishikawae* clustered together with *G. albonigrum*, *G. inpaense* and *G. argentinum*. However, *G. albonigrum* and *G. inpaense* exhibit smaller basidiospores (3–5 µm and 2.6–3.8 µm, respectively) than those of *G. ishikawae*; and *G. argentinum* presents a non-folded fibrillose peristome, and much more regular basidiospore ornamentation. The woolly mycelial layer plus folded peristome are unique characteristics of *G. ishikawae* (Sunhede 1989, Calonge & Mata 2004, Cabral et al. 2014, Zamora et al. 2014).



One of the 19 equally most parsimonious trees of ITS nrDNA sequences obtained after a heuristic search using SeaView v. 4.6 (Gouy et al. 2010). The two new *Geastrum* species described in this issue are marked with rectangles: *G. ishikawae* and *G. pusillipilosum* (see Fungal Planet 473 in this manuscript). The accession numbers from EMBL/GenBank databases are indicated on the tree. Bootstrap support values greater than 50 % are indicated on the branches, as well as posterior probabilities obtained after Bayesian analyses. *Geastrum elegans* was included as outgroup.

Colour illustrations. Brazil, Instituto Nacional de Pesquisas da Amazônia (INPA), Campus I, 'Buriti' palm trees growing at the locality where the type specimens were collected; mature basidiome (UFRN-Fungos 2785, holotype) detailing folded peristome, Scanning Electron Microscopy (SEM) of basidiospores detailing ornamentation (UFRN-Fungos 2785), SEM of capillitium detailing surface (UFRN-Fungos 2785). Scale bars = 5 mm (mature basidiome), 2 µm (basidiospores), 5 µm (capillitium).

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Geastrum pusillipilosum
d
c
a
b

Fungal Planet 473 – 21 December 2016

Geastrum pusillipilosum J.O. Sousa, Alfredo, R.J. Ferreira, M.P. Martín & Baseia, *sp. nov.*

Etymology. Named in reference to reduced size of basidiomata and the hirsute exoperidium.

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

Unexpanded basidiomata epigeous, globose to subglobose, 3–10 mm wide, surface densely hairy, short hair (< 1 mm high), presence of subiculum under some basidiomata, yellowish brown (4C8, 5D5, Kornerup & Wanscher 1978). *Expanded basidiomata* saccate, 4–10 mm high (including peristome) × 6–17 mm wide. *Exoperidium* splitting into 5–9 revolute, triangular rays, non-hygroscopic. *Mycelial layer* not encrusted with debris, persistent, pale yellow (colour 3A3), densely hairy, formed of hyaline to greenish hyphae, 2.5–7 µm diam, lumen evident, hairs formed by brownish, interlaced hyphae, 5.5–9 µm diam, thick-walled (0.5–1.5 µm), lumen evident. *Fibrous layer* papery, yellowish white (colour 4A2), formed of brownish, sinuous hyphae, 3.5–7.5 µm diam, thin-walled (< 1 µm), lumen evident. *Pseudoparenchymatous layer* persistent, glabrous, brown (colour 5E6), formed by brownish hyphal cells, subglobose, oval to pyriform, 15–34 × 15–31.5 µm, thin-walled (< 1 µm). *Endoperidial body* globose, 1–7 mm wide, sessile, glabrous, brown (colour 5E4) to greyish brown (colour 5D3). *Peristome* finally fibrillose, delimited, delimitation dark brown (colour 6F4), concolorous or lighter than endoperidium, up to 1 mm high. *Columella* elliptical, central, inconspicuous, white (colour 4A1). *Mature gleba* greyish brown (colour 5F3). *Basidiospores* globose, 5–6.5 µm diam, dark brown in 5 % KOH, ornamentation densely verrucose, warts columnar, slightly truncated, with planar tips, apiculus reduced. *Basidia* clavate, pyriform to lageniform, 10.5–16.5 × 5–7.5 µm, 3–4 sterigmata, yellowish in 5 % KOH. *Eucapillitium* 2–4.5 µm diam, thin-walled (< 1 µm diam), sinuous, unbranched, surface slightly verrucose, encrusted, lumen not evident, brownish in 5 % KOH.

Ecology & Distribution — The specimens present a gregarious habit and colonise two different types of substrates: leaf-litter and decaying wood. Until now, the distribution of *G. pusillipilosum* is restricted to Brazil and Argentina. In Brazil, this species occurs in the North-east (Paraíba and Ceará States) and South-east (Minas Gerais State) regions. Specimens were found in three Conversation Units of the Brazilian Atlantic Rainforest domain (Reserva Biológica Guaribas and Reserva Biológica Mitzi Brandão), and Caatinga domain (Floresta Nacional do Araripe), in different phytophysiognomies: tropical montane forest low broadleaf; upland, wet forest enclaves and coastal tableland. The Atlantic Rainforest is a 'hotspot' of biodiversity and Caatinga is an endemic vegetation formation of Brazil; however these areas are extremely degraded, and these Conservation Units represent a few remaining of this domain (Galindo-Leal & Câmara 2005, Melo Santos et al. 2007).

Typus. Brazil, Paraíba, Mamanguape, Reserva Biológica Guaribas, alt. 150 m, S06°44'28.0" W35°08'23.8", on soil covered by leaf-litter or decaying wood, 26 June 2014, *J.O. Sousa et al.* (holotype UFRN-Fungos 2315, ITS sequence GenBank KX761175, LSU sequence GenBank KX761176, isotype UFRN-Fungos 2316, ITS sequence GenBank KX761179, MycoBank MB812875).

Notes — *Geastrum pusillipilosum* is recognised by its small basidiomata (up to 17 mm wide), fibrillose, delimited peristome, exoperidium totally covered by short hairs (up to 1 mm in length) and basidiospores 5.0–6.8 µm diam, with columnar warts. The presence of hairs on the exoperidium is a rare feature in the genus *Geastrum*. One species with this characteristic is *G. hirsutum*, which has a morphology closely related to *G. pusillipilosum*. However, it is easily distinguished by its larger basidiomata (25–20 mm wide), subicular base, long, dark-brown hairs (1.5–3 mm in length) and smaller basidiospores (2.5–3 µm diam) (Baseia & Calonge 2006). Other species in the genus *Geastrum* that present an exoperidium with hairs are *G. inpaense* and *G. albonigrun*. However, these species are distinguished by non-delimited peristome, dark brown endoperidium and larger basidiomata, 25–40 mm and 32–40 mm wide, respectively (Calonge & Mata 2004, Cabral et al. 2014). *Geastrum schweinitzii* is another species similar to *G. pusillipilosum*, both having small basidiomata, subiculum, and lignicolous habit, but *G. schweinitzii* differs by not having hairs on the exoperidium and having smaller basidiospores, up to 5 µm diam (Cortez et al. 2008, Sousa et al. 2014). The ITS nrDNA (see tree figure in *G. ishikawae* (FP472)) and LSU sequences of *G. pusillipilosum* show that it is a well-delimited species.

Colour illustrations. Brazil, Paraíba, Reserva Biológica Guaribas, field track where the type species was collected; a. Basidiomata *in situ* (UFRN-Fungos 2316, isotype); b. detail of hairy exoperidium (UFRN-Fungos 2315, holotype); c. basidiospores under the light microscope (UFRN-Fungos 2314); d. verrucose basidiospore with columnar warts (UFRN-Fungos 2314). Scale bars: a = 2.5 mm; b = 0.5 mm; c = 10 µm; d = 1 µm.

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Elsinoë eelemani

Fungal Planet 474 – 21 December 2016

Elsinoë eelemani L.A. Shuttlew., K. Scarlett, Entwistle & R. Daniel, *sp. nov.*

Etymology. Named after the legendary Princess Eelemani of the Bundjalung people. The Bundjalung are Indigenous Australians, the original custodians of coastal areas of northern New South Wales.

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

Leaf spots observed on edges and centre of leaves, circular to subcircular, starting as yellow to red coloured spots, progressing to dark purple to sepia before developing a buff coloured centre surrounded by dark-purple to sepia coloured border, 0.5–1.5 mm diam. Lesions on stems circular to ovate, cream, red to pale-brown centre with raised, scabby margin. *Conidiomatal* walls composed of luteous to orange *textura angularis*. *Conidiophores* hyaline, luteous to orange, smooth, cylindrical to doliiform, unbranched, (11–)15.5(–22.5) × (2.5–)3.5(–4.5) mm. *Conidiogenous cells* hyaline, cylindrical, slight tapering at terminal end, polyphialidic with 1–2 apical loci, (5–)10(–19.5) × (2–)2.5(–4) mm. *Conidia* formed terminally on conidiogenous cells, hyaline, smooth, ovate to subcylindrical, rounded at terminal end, sides tapering toward the base, truncate at base, containing 0–6 guttules, (4.5–)5.5(–8) × (2–)2.5(–3.5) mm. *Chlamydospores* hyaline, luteous to orange, smooth, terminal, intercalary, unbranched or branched, up to 25-septate, produced on PDA after 4–6 wk.

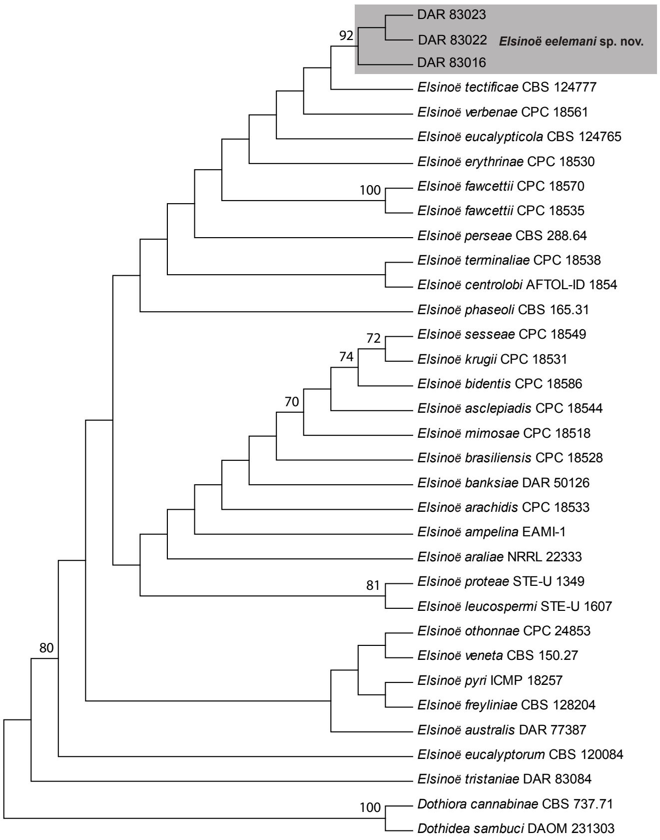
Culture characteristics — Colony colours were determined with Rayner (1970). Colonies after 1 mo in the dark at 25 °C. On PDA: 11 × 17 mm diam, erumpent, subcircular, margins lobed, top surface of colony folded, centre rust to chestnut coloured overlain with dense flesh coloured mycelia with firm, velvet texture, edges luteous and orange overlain with flat velvety flesh coloured mycelia, reverse centre chestnut coloured, edge rust with luteous edge. On MEA: 12.5 × 13 mm diam, top surface velvety and rosy buff in centre, extending to smooth, folded and brick coloured, edge of colony cinnamon, a hyaline gummy substance was produced 1–2 mm around the edge of the colony, reverse centre scarlet and orange, edge cinnamon.

Typus. Australia, New South Wales, Coraki, on leaves and stems of *Melaleuca alternifolia* (*Myrtaceae*), 2014, *R. Daniel & P. Entwistle* (holotype specimen and ex-type culture DAR 83016, ITS sequence GenBank KX372292, LSU sequence GenBank KX372296, *tef1* sequence GenBank KX398203, *rpb2* sequence GenBank KX398204, MycoBank MB817349); Dec. 2015, *R. Daniel & P. Entwistle* (paratype specimen and paratype culture DAR 83022, ITS sequence GenBank KX372293, LSU sequence GenBank KX372297).

Additional specimen examined. Australia, New South Wales, Ruthven, on leaves and stems of *Melaleuca alternifolia*, Dec. 2015, *R. Daniel & P. Entwistle*, culture DAR 83023, ITS sequence GenBank KX372294, LSU sequence GenBank KX372298.

Notes — Species of *Elsinoë* are known as pathogens causing scab diseases and are associated with various hosts including citrus (Miles et al. 2015), cassava (Reeder et al. 2009), legumes (Mchau et al. 1998), *Othonna quinquedentata* (Crous et al. 2015b), mango (Condé et al. 1997), *Eucalyptus* (Cheewangkoon et al. 2009), and *Proteaceae* (Swart et al. 2001, Pascoe et al. 2007). The combined LSU-ITS phylogeny showed that *E. eelemani* forms a distinct clade with 92 % maximum parsimony bootstrap support (MPBS). On ITS, *Elsinoë eelemani* is phylogenetically most closely related to *E. tectificae* from *Eucalyptus tectifica* and *E. eucalypticola* from *Eucalyptus* sp. (Cheewangkoon et al. 2009). However, *E. eelemani* is supported as distinct with 100 % MPBS. On LSU, *E. eelemani* was most closely related to *E. centrolobii* from *Centrolobium robustum* and was distinct with 85 % MPBS. The ITS sequence was not available for *E. centrolobii* on GenBank so could not be compared, however on *tef1 E. eelemani* had 17 polymorphisms when compared to *E. centrolobii*. *Elsinoë tristaniae* DAR 83084 from leaf spots of *Lophostemon confertus* (*Myrtaceae*) collected in Eveleigh, New South Wales, was sequenced in the current study for phylogenetic comparison (ITS sequence GenBank KX372295, LSU sequence GenBank KX372299). *Elsinoë tristaniae* was basal in the LSU-ITS phylogeny to all known *Elsinoë* species, being most closely related to *Elsinoë eucalyptorum* from *Eucalyptus propinqua* from the North Coast, New South Wales, a similar geographic area to *Elsinoë eelemani*. Morphologically, *E. eelemani* has longer conidia than *E. tectificae*. The *Sphaceloma* morph of *E. eucalypticola* was not reported so could not be compared.

Colour illustrations. *Melaleuca alternifolia* infected with *E. eelemani* growing in a plantation, Coraki, New South Wales, Australia; close up of leaf lesion, colony on PDA, conidia. Scale bars = 0.5 mm (lesion), 10 mm (colony), and 20 µm (conidia).



Most parsimonious tree obtained in MEGA v. 7 using a concatenated LSU-ITS dataset with maximum parsimony bootstrap support values ≥ 70 % plotted at the nodes.

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Clavaria griseobrunnea

Fungal Planet 475 – 21 December 2016

Clavaria griseobrunnea Olariaga, Salcedo, Albizu & Kautmanová, *sp. nov.*

Etymology. The epithet refers to the combination of a pale grey clavula and a brown stipe. From Latin 'griseus' (grey) and 'brunneus' (brown).

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

Basidiomata gregarious or fascicled (2–3 basidiomata), 1.5–6 mm long, simple, rarely bifid at apex, stipe well-delimited. *Clavula* 1.1–3.5 × 0.15–0.25 mm, cylindrical to narrowly claviform, often flattened, pale grey (paler than 195A), grey (2.5YR 6/2, 6/3) when dried. *Apex* obtuse, concolorous. *Stipe* 1.3–2.5 × 0.15–0.25 mm, cylindrical, reddish brown (5YR 4/6). *Context* white (155A), taste mild; smell none. *Basidiospores* ellipsoidal to narrowly ellipsoidal in side view, rounded in face view, thin-walled, smooth, with refringent content, non-amyloid, often aggregated in tetrads, with cubic apiculus, 4.5–6(–7) × 2.5(–3) µm (L_m = 5.4; W_m = 2.7; Q_m = 1.99). *Basidia* claviform, 4-spored, clampless, 26–30 × 4.5–6 µm. *Cystidia* absent. *Subhymenium* formed by densely interwoven hyphae, cylindrical to inflated, thin-walled, clampless, 2.5–4.5 µm. *Context hyphae* parallel-arranged, inflated, thin-walled, not closely septate, hyaline, smooth, clampless, 4–12 µm. *Basal mycelium* white, composed of woven hyphae, cylindrical, thick-walled, scarcely septate, hyaline, clampless, 1–2 µm wide.

Distribution — Currently only known from the type location.

Phylogeny — A sequence of the holotype of *C. griseobrunnea* nests in *Clavaria* in the LSU analyses by Olariaga et al. (2015, *as C. guillemini*), holding an isolated position within a supported clade encompassing also *C. asperulospora* and *C. atrofusca*. A megablast search of the NCBIs GenBank nucleotide sequence database using the LSU sequence of *C. griseobrunnea* retrieves as closest hits *C. asperulospora* (GenBank JN315790; Identities = 1295/1381 (94 %), Gaps = 31/1381 (2 %)) and *C. atrofusca* (GenBank HQ606080; Identities = 426/526 (81 %), Gaps = 34/526 (6 %)) when the ITS region is employed.

Typus. Spain, Basque Country, Gipuzkoa, Berastegi, Artaleku, 43.102542, -1.956509, 520 m a.s.l., on bare ground in *Pteridium aquilinum* field, 12 Oct. 2007, *J.L. Albizu & I. Olariaga* (holotype BIO-Fungi 12566, ITS sequence GenBank KY091644, LSU sequence GenBank JQ415939, MycoBank MB817883).

Notes — *Clavaria griseobrunnea* is characterised by producing small-sized basidiomata, its pale grey clavula and a distinct reddish brown stipe. Its clampless basidia, characteristic of *Clavaria* subg. *Clavaria*, and its rather small spores are also distinctive. *Clavaria atrofusca* and *C. asperulospora* differ from *C. griseobrunnea* in having larger dark-coloured basidiomata and ornamented spores. *Clavaria crosslandii*, *C. guilleminii* and *C. corbierei* also have small basidiomata and small spores like *C. griseobrunnea*. *Clavaria crosslandii* differs in having a white stipe and clamped basidia (syntype K(M) 120243!). *Clavaria guilleminii* has basidiomata with truncate apex, a white stipe, clamped basidia and scattered cystidia (holotype PC0094980!), which makes it close to *C. taxophila*. We also attribute *C. corbierei* to *C. taxophila* due to its truncate apex and after observing clamp connections in an authentic specimen from the type locality (leg. Corbière, November 1925, UPS).

Colour illustrations. *Pteridium aquilinum* field where the holotype of *Clavaria griseobrunnea* was encountered; basidiomata growing *in situ* under *Pteridium aquilinum*, basidia and spores aggregated sometimes in tetrads. Scale bars = 10 µm.

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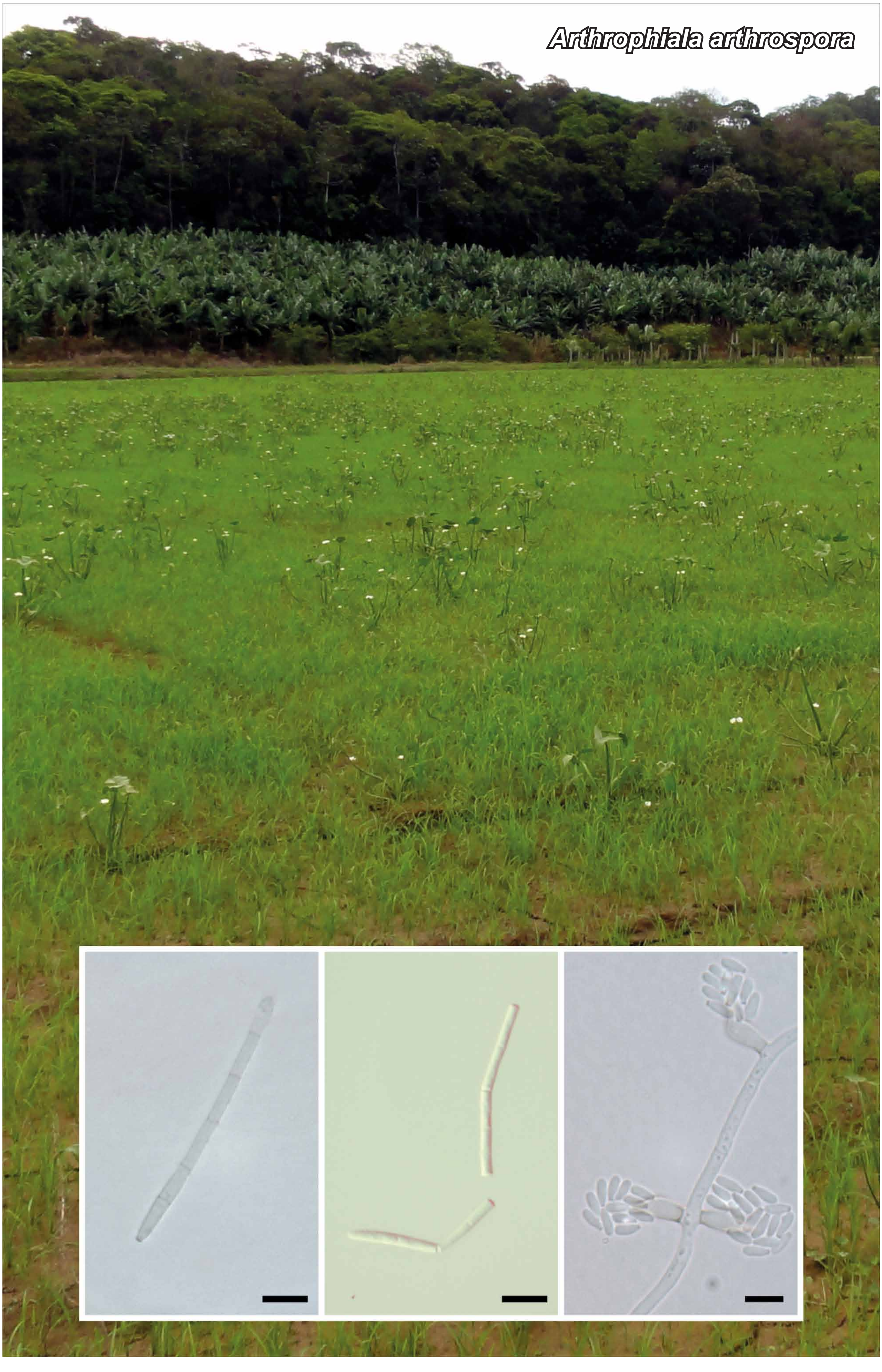
Arthrophiala arthrospora

Fungal Planet 476 – 21 December 2016

Arthrophiala W.S. Lisboa, Meir. Silva & R.W. Barreto, *gen. nov*.

Etymology. Referring to the combination of arthric conidia (from primary conidiophores) and phialoconidia (from secondary conidiophores).

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

Internal mycelium, loosely branched, septate, hyaline to pale olivaceous. *Conidiophores* dimorphic: a) primary – cercosporoid-like, forming dense fascicles on host tissue, epiphyllous, subcylindrical, straight to slightly curved, geniculate, septate, not branched, subhyaline to pale olivaceous or olivaceous brown, paler towards the apex, smooth; b) secondary – restricted to phialidic conidiogenous cells formed on mycelium (only seen in culture), solitary, oblong to subclavate, somewhat narrowed at base and slightly papillate at apical conidiogenous locus, straight or slightly curved, hyaline to subhyaline, smooth. *Conidia* dimorphic: a) on primary conidiophores – mostly entire, or fragmenting as arthroconidia, obclavate to obclavate-cylindrical, thick-walled, straight to curved, septate, septation sometimes almost indistinct, hyaline or subhyaline, smooth, guttulate or eguttulate, hila unthickened, not darkened; b) on secondary conidiophores – phialoconidia formed singly or aggregated in slimy heads, subcylindrical, oval to subclavate, apex rounded, base acute, smooth, hyaline.

Type species: *Arthrophiala arthrospora* (D.J. Soares et al.) W.S. Lisboa, Meir. Silva & R.W. Barreto.
MycoBank MB817842.

Arthrophiala arthrospora (D.J. Soares et al.) W.S. Lisboa, Meir. Silva & R.W. Barreto, *comb. nov.* emend.

Basionym. Pseudocercospora arthrospora D.J. Soares et al., Mycologia 101: 409. 2009.

Internal mycelium 2–3 µm diam, loosely branched, septate, hyaline to pale olivaceous. *Conidiophores* dimorphic. *Primary conidiophores* epiphyllous, cercosporoid-like, forming dense fascicles on host tissue, subcylindrical, straight to slightly curved, geniculate, 20–39 × 2–4 µm, unbranched, 1–3-septate, subhyaline to pale olivaceous or olivaceous-brown, paler towards the apex, smooth. *Conidiogenous cells* terminal, integrated, subcylindrical, 11–21 × 2–3.5 µm, conidiogenous loci almost indistinct to subdenticulate, unthickened or only slightly thickened, somewhat refractive, not darkened, subhyaline, smooth. *Secondary conidiophores* (only seen in culture) restricted to phialidic conidiogenous cells formed on mycelium, solitary, oblong to subclavate, somewhat narrowed at base and slightly papillate at apical conidiogenous locus, straight or slightly curved, narrowed at the base, 3–11 × 1–2.5 µm, hyaline to subhyaline, smooth. *Conidia* dimorphic: a) on primary conidiophores – either entire or as fragment arthroconidia, obclavate to obclavate-cylindrical, straight to curved, 20–190 × 1.5–3.5 µm, thick-walled, apex obtuse, base truncate to obconically truncate, 1–2.5 µm wide, (1–)3–16(–30)-septate, septation almost indistinct, hyaline or subhyaline, smooth, guttulate or eguttulate; hila unthickened, not darkened; b) on secondary conidiophores – phialoconidia formed single or aggregated in slimy heads, subcylindrical, oval to subclavate, 2.5–5 × 1–1.5 µm, apex rounded, base subacute, 0.5–1 µm wide, smooth, hyaline.

Cultural characteristics — On PDA slow-growing, reaching 2 cm diam after 10 d, grey, powdery, sporulating abundantly, velvety to chamois-like, reverse black at centre, dark grey to pale grey towards the edges; on OA aerial mycelium sparse, flat, with irregular edges, pale grey, grey reverse; sporulating abundantly.

Colour illustrations. Brazil, Santa Catarina, Garuva, rice plantation invaded by *Sagittaria montevidensis* bearing leaf spots; COAD 678: primary conidium, primary conidia showing arthric fragmentation, secondary conidia and phialides. Scale bars = 5, 10, 5 µm from left to right.

Typus. Brazil, Santa Catarina, Forquilhinha, rice field at roadside, on leaves of *Sagittaria montevidensis* (*Alismataceae*), 21 Apr. 2005, *D.J. Soares* 172 (holotype VIC 30505, isotype HAL 1884 F, culture ex-type COAD 658 = DJS 172 = CPC 18514); ITS sequence GenBank KY173473, LSU sequence GenBank KX447143, MycoBank MB817842).

Additional specimens examined. All on leaves of *S. montevidensis*. Brazil, Rio de Janeiro, Nova Friburgo, Alto dos Micheis, 30 Oct. 2007, *R.W. Barreto* 814, culture COAD 367 = CPC 19480, ITS sequence GenBank KY173474, LSU sequence GenBank KX447144; Santa Catarina, Itajaí, experimental rice field of EPAGRI, 10 July 2008, *R.W. Barreto* 969 = VIC 30704, culture COAD 368 = CPC 19482; ITS sequence GenBank KY173475, LSU sequence GenBank KX447145.

Notes — *Arthrophiala arthrospora* was previously described as *Pseudocercospora arthrospora* (Soares et al. 2009). At the time of its description there were doubts on its adequate placement and the possibility of describing it as a new species of *Thedgonia* was contemplated. Nevertheless, in the absence of molecular information on this isolate and considering its morphological similarity with *Pseudocercospora* it was placed in this genus. More recently it was observed that the fungus formed phialides in culture and hence its placement in *Pseudocercospora* was regarded to be clearly inadequate. Additionally LSU sequences obtained from COAD 368 were compared in a BLASTn search with GenBank sequences and the highest homology found was with an LSU sequence of *Capronia peltigerae* UAMH 11090 (GenBank HQ613813) – identities 94 %. *Capronia* belongs to the fungal group known as 'black yeasts (*Chaetothyriales*) which includes species of opportunistic vertebrate pathogens (De Hoog et al. 2000, Untereiner et al. 2011). The phylogenetic analysis based on the LSU sequence placed *Arthrophiala* in the *Chaetothyriaceae* close to another genus with phialidic conidial states, *Exophiala.* Nevertheless, fungi in *Exophiala* (Ellis 1971) lack the cercosporoid-like morph which predominates under natural conditions for *Arthrophiala* and the newly described genus is a demonstrated plant pathogenic fungus, hence occupying a different niche from other *Chaetothyriaceae*. For phylogenetic tree see MycoBank.

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Synnemellisia aurantia

Fungal Planet 477 – 21 December 2016

Synnemellisia aurantia D.O. Lisboa, J.L. Alves & R.W. Barreto, *sp. nov.*

Etymology. Referring to the orange coloured mucilaginous head of the synnemata.

Classification — *Bionectriaceae*, *Hypocreales*, *Sordariomycetes.*

Internal mycelium indistinct. *External mycelium* absent. *Stromata* absent. *Synnemata* determinate, conspicuous, superficial, erect, obclavate to obconical, up to 300 µm long, 37.5–150 µm wide at the base, 50–137.5 µm wide at the middle, 75–237.5 µm wide at the convex apex, stem of golden brown *textura intricata*, ending in orange coloured cushion-like head of conidiogenous cells and mucilaginous conidial mass. *Conidiophores* cylindrical, 27.5–62.5 × 2.5–5 µm, septate, unbranched, subhyaline, smooth. *Conidiogenous cells* monoblastic, terminal, integrated, cylindrical, tapering towards the apex, 14–57 × 2–4 µm, hyaline, smooth. *Conidiogenous loci* 2–2.5 µm diam, not thickened nor darkened. *Conidia* aggregated on a cushion-like head, navicular to fusiform, 23–30 × 7–9 µm, apex subacute, base obtuse to subtruncate, aseptate, guttulate, subhyaline, smooth.

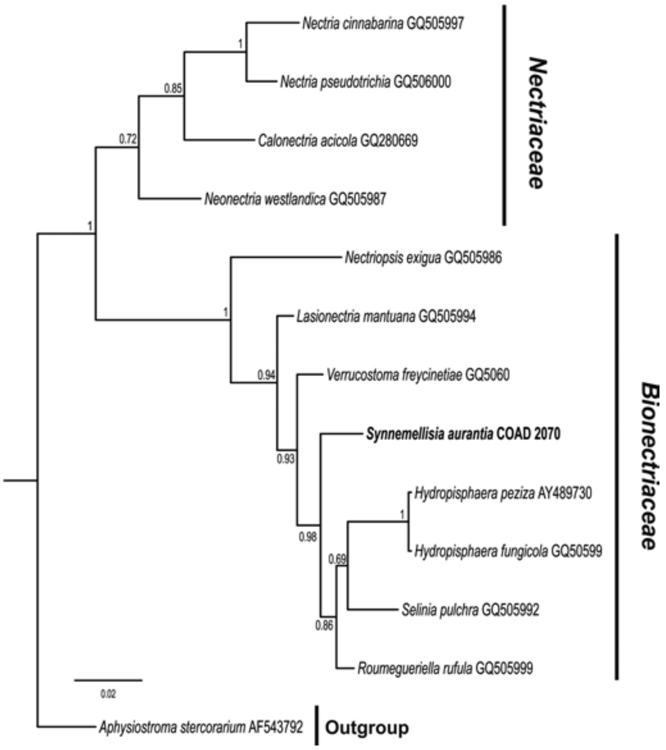
Culture characteristics — Colonies moderately fast-growing, reaching 60 mm diam after 13 d at 25 °C on vegetable broth-agar (VBA according to Pereira et al. 2003); irregular, central zone of aerial mycelium dense and cottony, becoming sparse towards the periphery, white; reverse olivaceous buff (with diurnal zonations on PCA); sporulation absent on VBA but abundant (on synnemata) on PCA.

Typus. Brazil, Minas Gerais, Viçosa, Infectarium - Clinica de Doenças de Plantas, on dead branches of *Passiflora edulis* (*Passifloraceae*), 16 May 2016, *R.W. Barreto* (holotype VIC 44082, culture ex-type COAD 2070, ITS sequence GenBank KX866395, LSU sequence GenBank KX866396, MycoBank MB818371).

Colour illustrations. Fence bearing a dead vine of *Passiflora edulis* with 'disease garden' (Infectarium) in the background; close-up of synnemata distributed over dead stem, numerous and erect orange-headed synnemata, close-up of monoblastic conidiogenous cells, navicular to fusiform conidia. Scale bars = 10 µm.

Notes — *Synnemellisia aurantia* was only found on dead branches of *Passiflora edulis* and is regarded here as probably saprophytic on decaying passion flower stems. This is the second species described for the monotypic genus *Synnemellisia* which was proposed to accommodate the species *S. hyalospora* (Rao et al. 1988) found in India. The size of conidia and synnemata allows for an easy distinction between *S. aurantia* and *S. hyalospora*. Additionally, a megablast search of NCBIs GenBank nucleotide database did not yield any close hits for LSU and ITS sequences. A study of the more closely matching sequences indicated that *S. aurantia* has affinities with members of the families *Nectriaceae* and *Bionectriaceae*. A phylogenetic analysis based on the LSU sequence, placed *S. aurantia* inside the family *Bionectriaceae* and close to the (rather morphologically distinct) genera *Hydropisphaera* (Dumortier 1822), *Selinia* (Karsten 1876) and *Roumegueriella* (Roumeguère 1880).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Hydropisphaera erubescens* (GenBank AF193229; Identities = 832/845 (98 %), Gaps = 1/845 (0 %)), *Verrucostoma freycinetiae* (GenBank GQ506013; Identities = 824/845 (98 %), Gaps = 2/845 (0 %)) and *Roumegueriella rufula* (GenBank GQ505999; Identities = 827/845 (98 %); Gaps= 1/845 (0 %)).



Phylogenetic tree inferred from Bayesian analysis based on LSU sequences. The analysis was performed with 10 M generations in MrBayes v. 3.1.1. The Bayesian posterior probability values are indicated at the nodes. The tree was rooted to *Aphysiostroma stercorarium*. The new species is highlighted in **bold** face.

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Rhodocybe rubrobrunnea

Fungal Planet 478 – 21 December 2016

Rhodocybe rubrobrunnea K.N.A. Raj, K.P.D. Latha & Manim., *sp. nov.*

Etymology. The name refers to the reddish brown pileus of this species.

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

Basidiocarps small to medium-sized, tricholomatoid. *Pileus* 3–21 mm diam, convex when young, becoming somewhat broadly convex with an obscure, low, broad umbo with age; surface pale red (7A4/OAC619) when young, becoming reddish brown (8D6/OAC616) on umbo and pale reddish brown (8B5, 8C5/OAC617) elsewhere with age, not hygrophanous, not striate, velutinous all over, rather pruinose when young; margin somewhat inrolled when young, becoming incurved with age, entire or somewhat wavy, becoming rather lobate with age. *Lamellae* adnate, occasionally furcate, narrow, close, orange white (6A2/OAC683) when young, becoming greyish orange (6B4/OAC654), up to 2 mm wide, with lamellulae in 2–3 tiers; edge entire to the naked eye, finely torn under a lens, concolourous with the sides. *Stipe* 9–25 × 2–12 mm, central, terete or somewhat compressed, equal or tapering towards the apex or the base, solid; initially whitish, becoming pale orange (6A3/OAC682) with age, finely appressed-fibrillose and finely pruinose all over; base slightly enlarged, with profuse, white mycelial mass. *Odour* and *taste* not distinctive. *Basidiospores* 6–7 × 3–5 (av. 6.45 ± 0.51 × 4.07 ± 0.40) µm, Q = 1.2–2, Q_m = 1.59; with 7–8 facets in polar view, ellipsoid in frontal view and subamygdaliform in side view, very subtly undulate-pustulate or nearly smooth, hyaline, thin-walled. *Basidia* 24–48 × 6–7 µm, clavate, hyaline, thin-walled, 4-spored; sterigmata up to 4 µm long. *Lamella edge* heterogeneous. *Cheilocystidia* 18–56 × 4–5 µm, scattered, flexuoso-cylindric, filamentous, often septate. *Pleurocystidia* absent. *Lamellar trama* subregular; hyphae 3–9 µm wide, pale yellow, thin-walled. Subhymenium inconspicuous. *Pileus trama* broad, interwoven; hyphae 5–7 µm, pale yellow, occasionally with faint hyaline encrustations, thick-walled, with a narrow lumen. *Pileipellis* a cutis with transition to a trichoderm towards the margin and almost a trichoderm at the centre, made up of closely septate hyphae; hyphae 4–35 × 3–5 µm wide, with a pale yellow wall pigment and occasionally with a faint, hyaline encrustation, thin- to slightly thick-walled. *Stipitipellis* a cutis often disrupted by flaring-out hyphae; hyphae 3–7 µm wide, hyaline or pale yellow, thin-walled. *Caulocystidia* absent. *Clamp connections* not observed on any hyphae.

Habit, Habitat & Distribution — In small groups, on soil, among leaf litter. Known only from the type locality in Kerala State, India.

Typus. INDIA, Kerala State, Kollam District, Thenmala Forest, Shenduruni Wildlife Sanctuary, 19 Sept. 2014, *K.P. Deepna Latha* (holotype CAL 1387, ITS sequence GenBank KX951452, MycoBank MB818605).

Colour illustrations. *Rhodocybe rubrobrunnea in situ* in Thenmala Forest, Shenduruni Wildlife Sanctuary; the upper inset shows the locality, lower insets show basidiospores, basidium, lamella edge showing cheilocystidia, pileipellis. Scale bars = 10 mm (basidiocarps), 10 µm (microscopic structures).

Notes — This species is characterised by a pileus with a broadly umbonate disc; adnate and furcate lamellae; ellipsoid or subamygdaliform basidiospores; hyaline, filiform and septate cheilocystidia; and a broad pileus trama with thick-walled hyphae showing hyaline encrustations. A combination of characters such as the centrally stipitate basidiocarps, the adnate lamellae, the reddish brown pileus, the absence of hymenial pseudocystidia, the presence of cheilocystidia and the absence of clamp connections indicates that this species belongs to sect. *Rufrobrunnea* (Baroni 1981).

A key to the species belonging to sect. *Rufrobrunnea* (Baroni 1981) leads to *Rhodocybe nuciolens*, a species from the USA. It resembles the present species in having a convex, umbonate pileus with incurved to inrolled margin, a solid stipe, similar-shaped basidiospores of almost similar size (5.5–8 × 4–5 µm), lamella-edges with cheilocystidia, a hymenium devoid of pseudocystidia, pileipellis hyphae with faint encrustations, and hyphae lacking clamp connections. However, *R. nuciolens* differs from the present species in having larger basidiocarps, a differently-coloured pileus with velutinous surface and larger cheilocystidia. *Rhodocybe incarnata* from Venezuela, another species belonging to sect. *Rufrobrunnea*, also has a rather similar-coloured pileus of somewhat similar shape and surface features, almost similar-sized basidiospores (4.5–6.5 × 4–5 µm), similar, occasionally septate cheilocystidia, an interwoven pileus trama, a trichoderm-type pileipellis and hyphae lacking clamp connections. That species, however, has adnexed or sinuate-adnate lamellae with a yellow-white colour, basidiospores with a lower Q-value (Q = 1.4) and more facets in polar view (6–9) and a pileipellis made up of non-encrusted hyphae with pinkish ochraceous intracellular contents (Baroni & Halling 1992).

Based on a megablast search of NCBIs GenBank nucleotide database using ITS sequence of this species, the closest hit was an undescribed collection labelled as *Rhodocybe* sp. 1 GMB-2014 from Australia (GenBank KP012803; 98 % identity) followed by *R. griseoaurantia* (GenBank KX083571; 97 % identity). *Rhodocybe griseoaurantia*, a species recently described from Kerala State, India (Hyde et al. 2016) and also assigned to sect. *Rufrobrunnea*, is similar to *R. rubrobrunnea* in having rather furcate lamellae, similar-sized basidiospores (5–7 × 3.5–4.5 µm), somewhat similar type of cheilocystidia, a hymenium devoid of pleurocystidia, faintly encrusted hyphae of pileipellis and similar stipitipellis. However, *R. griseoaurantia* has smaller basidiocarps with a greyish orange, hygrophanous pileus with different surface features, adnate to short decurrent lamellae, an apically pruinose stipe, ellipsoid basidiospores showing 6–7 facets in polar view, smaller cheilocystidia and a disrupted cutis-type pileipellis. In our ITS phylogeny (MycoBank supplementary data), *R. rubrobrunnea* nested within the clade containing species of *Rhodocybe* s.str. in a subclade composed of *R. griseoaurantia*, *Rhodocybe* sp. GMB-2014, *R. truncata* and two sequences of *R. gemina* with maximum bootstrap support (100 %). Within this subclade, *R. rubrobrunnea* appeared as a lineage distinct from the other two species with full bootstrap support (100 %).

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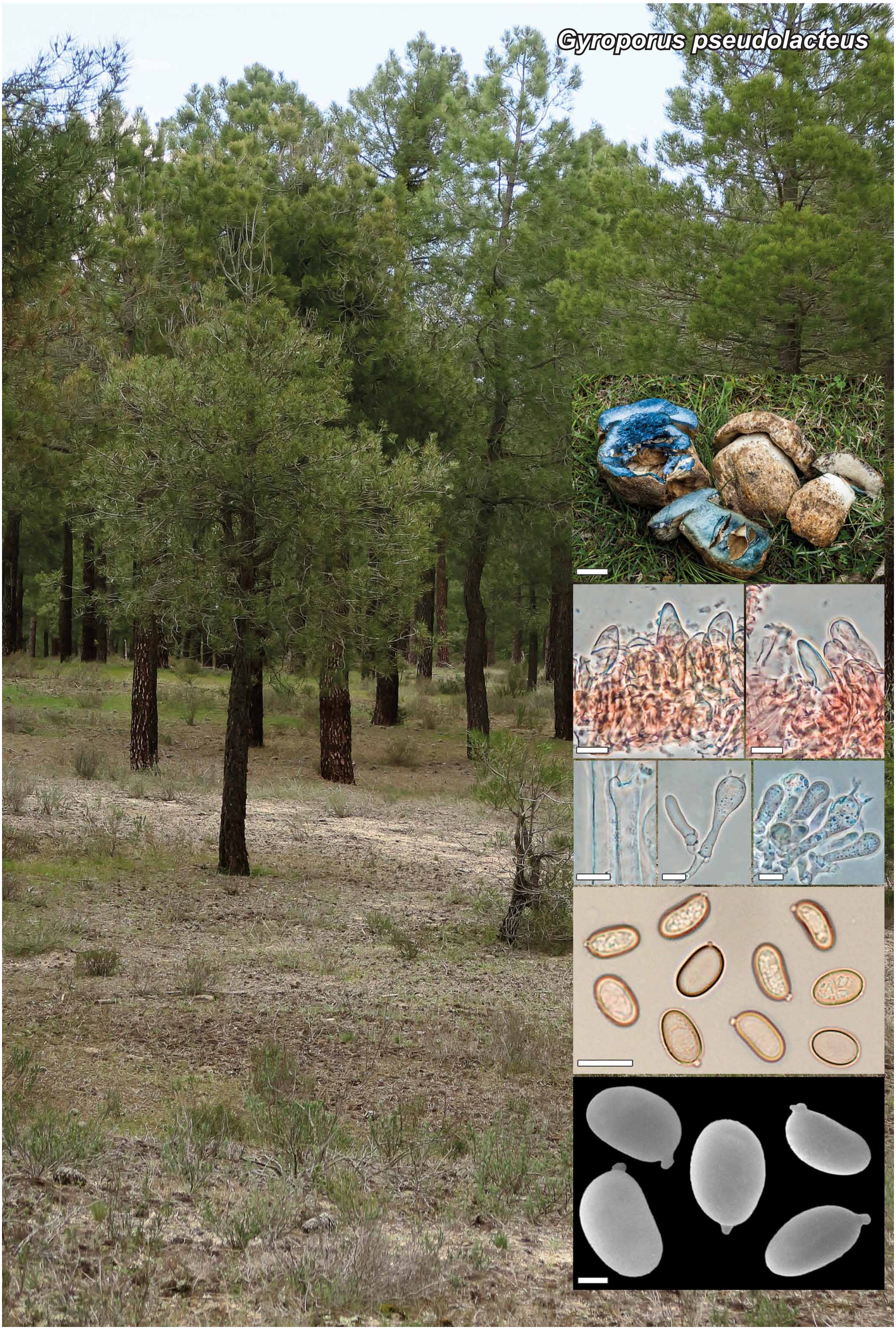
Gyroporus pseudolacteus

Fungal Planet 479 – 21 December 2016

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

Etymology. Name reflects its morphological similarity to the species *Gyroporus lacteus*.

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

Pileus fleshy, 7–15 cm broad, at first more or less hemispherical, then becoming convex to applanate convex, rarely depressed at centre, the surface velutinous, dry, whitish to cream white, at maturity with more or less strong ochraceous tinges, often covered with sand which is difficult to wipe off; *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, exceeding. *Tubes* short, 5–10 mm in length, free, sometimes emarginate towards the stipe, whitish, staining strongly dark blue or blue indigo when bruised or cut; *pore surface* when young concolorous with the tubes, at maturity cream to pale yellowish, very small, circular to angular at maturity, 1–2 per mm. *Stipe* 5–19 × 2–7 cm, cylindrical to clavate, widened at the base, brittle, stuffed with a soft pith, developing several cavities or becoming hollow at maturity, whitish to white cream, becoming more or less ochraceous at maturity, often covered with sand which is difficult to wipe off; *context* in stem whitish, staining strongly dark blue or blue indigo when bruised or cut, this colour being retained in drying and in some herbarium specimens. *Odour* and *taste* not distinctive. *Spore-print* yellowish. *Spores* 8–12 × 4.5–6.5 µm, on average 9.1–10.3 × 4.9–5.5 µm, $Q_{av.}$ = 1.75–1.87 cylindrical-ellipsoid to ellipsoid in face view, some of them slightly phaseoliform to reniform-phaseoliform in side view, with strong hilar appendage, without germ-pore, hyaline to yellowish; under the SEM spores lack any ornamentation. *Basidia* 4-spored, 35–45 × 10–15 µm, sterigmata up to 5.5 µm long, clavate, hyaline. *Cheilocystidia* fusiform, 35–50 × 9–17 µm. *Pleurocystidia* infrequent or absent, similar to cheilocystidia. *Caulocystidia* cylindrical, thinner at the apex, 50–80 × 8–12 µm. *Pileipellis* a cutis of radially arranged hyphae, with some terminal repent elements, up to 20 µm wide. *Pigment* yellowish ochre, both intracellular and parietal, sometimes minutely encrusting. *Clamp-connections* present in all tissues.

Habitat & Distribution — Growing gregarious on sandy acid soil under *Pinus pinaster.* Uncommon in the studied area. So far known only from Spain.

Typus. Spain, Segovia, Coca, in humus of *Pinus pinaster*, 18 Nov. 2011, *Soc. Micol. Madrid* (holotype AH 39364, ITS sequence GenBank KX869866, LSU sequence GenBank KX869880, MycoBank MB818416).

Additional specimens examined. ***Gyroporus pseudolacteus***: Spain, Segovia, in humus of *Pinus pinaster*, 25 Oct. 1997, *A. Sánchez*, paratype AH 45848 (ITS, LSU sequences GenBank KX869867, KX869881); Segovia, Muñoveros, in humus of *Pinus pinaster*, 26 Oct. 1997, *G. Moreno & J. Díez*, paratype AH 45849 (ITS, LSU sequences GenBank, KX869868, KX869882); idem, 25 Oct. 1998, paratype AH 45811 (ITS, LSU sequences GenBank, KX869869, KX869883); Cáceres, Pinar de la Bazagona, Malpartida de Plasencia, in humus of *Pinus pinaster*, 7 Nov. 1999, *C. Gelpi*, paratype AH 45812 (ITS, LSU sequences GenBank, KX869870, KX869884); idem, 7 Oct. 2007, paratype AH 45850 (ITS, LSU sequences GenBank, KX869871, KX869885); idem, 10 Nov. 2009, paratype AH 37878 (ITS, LSU sequences GenBank, KX869872, KX869886); Segovia, Coca, in humus of *Pinus pinaster*, 30 Oct. 2014, *J. de Frutos*, paratype AH 44522 (ITS, LSU sequences GenBank, KX869873, KX869887). ***Gyroporus ammophilus***: Spain, Pontevedra, Cangas de Morrazo, 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, littoral dunes with *Pinus pinea* and *P. pinaster*, 5 Nov. 2000, *M.A. Pérez de Gregorio & J. Carbó*, AH 45843 (ITS, LSU sequences GenBank, KX869877, KX869891); Coruña, Cabañas, sandy pine forests of *Pinus 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, sandy pine forest of *Pinus pinaster*, 9 Oct. 2007, *C. Gelpi*, *J. Muñoz*, *M. Lizárraga & G. Moreno*, AH 45844 (ITS, LSU sequences GenBank, KX869874, KX869888); Ávila, Piedrahita, sandy pine forest of *Pinus 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).

Colour illustrations. Spain, Segovia, Coca, *Pinus pinaster* forest, where the holotype was collected; fresh basidiomata in field, fusiform cheilocystidia, clamped hypha of the hymenium, 4-spored basidia and basidioles, spores under the light microscope (smooth lacking germ-pore and with strong hilar appendage), spores under SEM (holotype AH 39364). Scale bars = 5 cm (basidiomata), 10 µm (pileipellis, cheilocystidia, basidia, spores under the light microscope), 2 µm (spores under SEM).

Notes — *Gyroporus pseudolacteus* is morphologically characterised by its large size, the long stipe in relation to the pileus diameter (1.5–2 times longer), the whitish to cream white basidiomata staining deep and persistently indigo blue when handled or bruised, and by fruiting on sandy soil under *Pinus pinaster*.

In our phylogeny (MycoBank supplementary data) *Gyroporus pseudolacteus* belongs to a clade together with *G. lacteus* and *G. cyanescens*. *Gyroporus lacteus*, a species sister to *G. pseudolacteus*, has been typified recently by Vizzini et al. (2015) selecting Léveillé's plate 9 (1–2) (Léveillé 1848) as a lectotype and a collection from Italy collected on sandy soil with *Pinus pinea* and *Quercus ilex* as an epitype. *Gyroporus lacteus*, however, differs from *G. pseudolacteus* because of the shorter stipe in relation with the pileus diameter (same length or shorter than pileus diameter) and the pileus, which at maturity is ochraceous and covered by large and irregular scales. Several studies (e.g. Vizzini et al. 2015) suggest that *G. cyanescens* should be considered a complex, which appears to represent multiple cryptic species. Vizzini et al. (2015) typified *G. cyanescens* by selecting Bulliard's plate 369 (Bulliard 1788) as a lectotype and a collection from Italy under *Pinus sylvestris* as an epitype. *Gyroporus cyanescens* differs from *G. pseudolacteus* because of its smaller habit, the shorter stipe in relation with the pileus diameter (same length as pileus diameter) and the presence of a typical whitish annular zone at the stipe's apex in contact with the pileus as pointed out by Muñoz (2005). Both species, *G. lacteus* and *G. cyanescens*, have been studied by us and sequences of them have been deposited in GenBank. *Gyroporus ammophilus* and *G. castaneus* belong to a clade sister to the clade including *G. pseudolacteus. Gyroporus ammophilus*, is a species linked to sandy calcareous pine groves, in littoral areas, characterised by its slightly pinkish to salmon coloured context staining light blue when handled or bruised (Castro & Freire 1995, Muñoz 2005). According to our phylogeny it must be considered an autonomous species. *Gyroporus castaneus* differs from *G. pseudolacteus* by its white context not blueing when handled or bruised.

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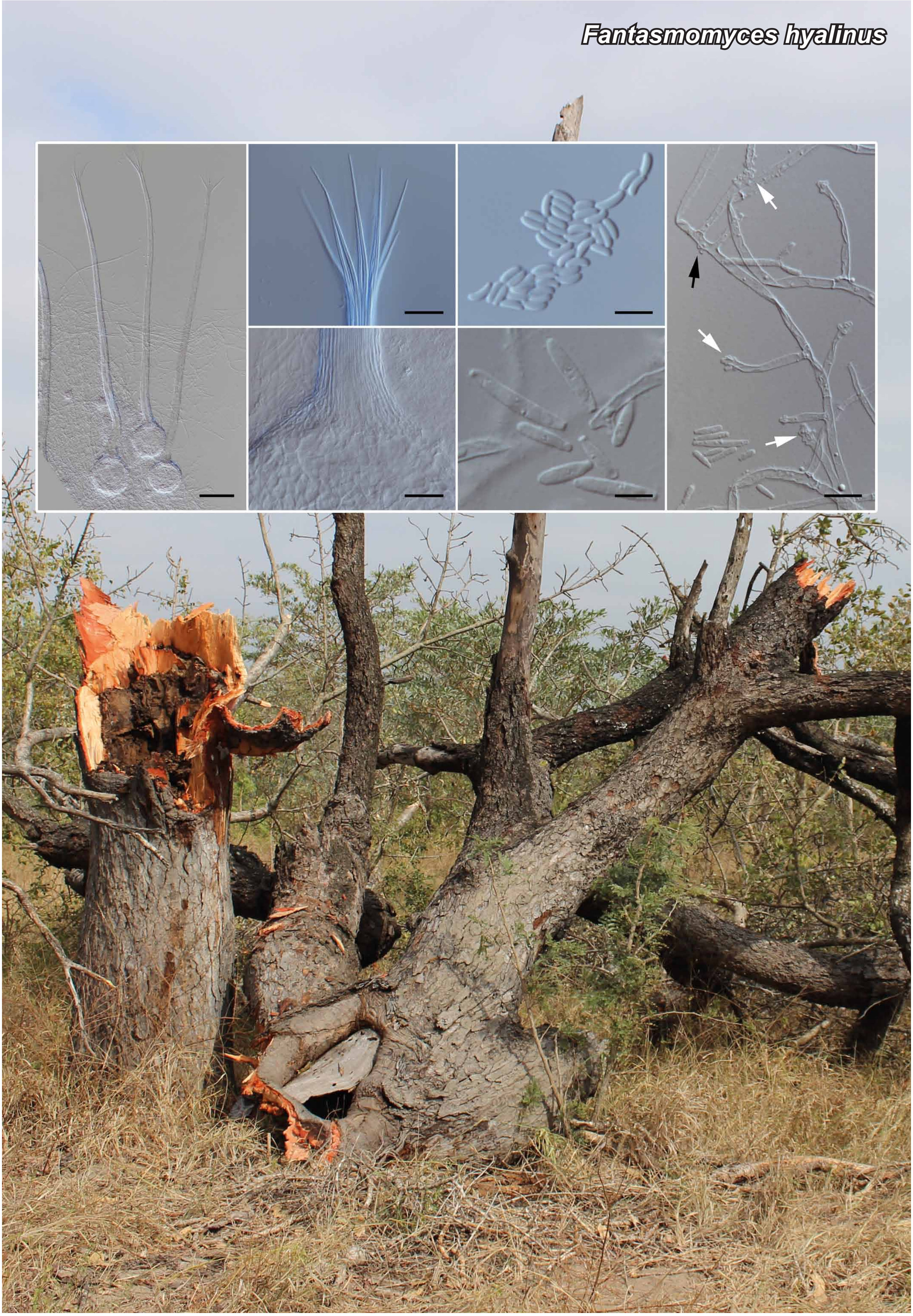
Fantasmomyces hyalinus

Fungal Planet 480 – 21 December 2016

Fantasmomyces DongHyeon Lee, Marinc., Z.W. de Beer, M.J. Wingf., *gen. nov.*

Etymology. Name is reminiscent of the colourless ascomata that can have a 'ghost-like' appearance.

Classification — *Incertae sedis*, *Sordariomycetes*.

Ascomatal base hyaline, globose to subglobose. *Necks* upright, straight, hyaline. *Ostiolar hyphae* divergent. *Ascospores* hyaline, allantoid. *Conidiophores* reduced to conidiogenous cells or semi-macronematous. *Conidiogenous cells* hyaline, blastic, denticulate. *Conidia* hyaline, cylindrical with the rounded apex, tapering towards the base.

Type species. Fantasmomyces hyalinus DongHyeon Lee, Marinc., Z.W. de Beer, M.J. Wingf.

MycoBank MB816620.

Fantasmomyces hyalinus DongHyeon Lee, Marinc., Z.W. de Beer, M.J. Wingf., *sp. nov.*

Etymology. Name refers to the colourless ascomata and hyaline spores.

On 2 % malt extract agar (MEA). *Ascomatal base* entirely hyaline, globose to subglobose, 80–190 µm high, 85–195 µm wide. *Necks* straight, upright, hyaline, gradually tapering towards the apex, 575–1050 µm high, 20–60 µm wide at the base, tapering to 9–22 µm wide near the apex, often reflective when observed under a compound microscope. *Peridium* composed of 3–4 layers of hyaline, thick, compressed cells. *Ostiolar hyphae* divergent, straight, 35–105 µm long, tapering towards the apex. *Asci* not observed. *Ascospores* hyaline, allantoid, 2.5–4.5 × 1–1.5 µm. *Conidiophores* reduced to conidiogenous cells or semi-macronematous. *Conidiogenous cells* hyaline, blastic, 9.5–50 µm high, 2–3 µm wide at the base, 1.5–2 µm wide just below the denticle cluster. *Conidia* hyaline, when terminal ellipsoidal to cylindrical with the rounded apex, tapering towards a truncated base, 3–11.5 × 1.5–2.5 µm, when intercalary, 7.5–25 × 1.5–3 µm.

Culture characteristics — On 2 % MEA with optimum growth at 25 °C in the dark, reaching 73 mm in 14 d, 70.5 mm at 30 °C, 46.3 mm at 20 °C, 28.2 mm at 15 °C. Cultures showing circular growth with smooth margins, aerial mycelium sparse, above semi-transparent to whitish at all temperatures but at 30 °C with an inner zone of yellow pigment 20 mm diam.

Typus. SOUTH AFRICA, Mpumalanga province, Kruger National Park, Tshokwane area, on exposed fresh bark flap on *Acacia exuvialis* (flaky thorn; *Leguminosae*), 24 Apr. 2014, *D.H. Lee* (holotype PREM 61340, dried culture of CBS 139038, living culture ex-holotype CBS 139038 = CMW 42166, ITS sequence GenBank KX061179, LSU sequence GenBank KX061180, MycoBank MB816622)

Colour illustrations. *Lannea schweinfurthii* trees damaged by elephants in Lower Sabie area in the Kruger National Park, South Africa, giving rise to the exposed bark on which the fungus is found; colourless ascomata on 2 % MEA, ostiolar hyphae, base of the neck, ascospores, conidia, denticles on conidiophores (white arrows) and on vegetative hypha (black arrow). Scale bars = 100 µm (ascomata), 5 µm (ascospores and conidia), 10 µm (all others).

Additional specimen examined. SOUTH AFRICA, Mpumalanga province, Kruger National Park, Lower Sabie area, on freshly exposed bark flap of *Lannea schweinfurthii* (false marula; *Anacardiaceae*), 29 May 2014, *D.H. Lee*, paratype PREM 61341, dried culture of CBS 139039, living culture ex-paratype CBS 139039 = CMW 42167, ITS sequence GenBank KX061181, LSU sequence GenBank KX061182.

Notes — The morphological features of *F. hyalinus* are reminiscent of *Ophiostoma*, *Sporothrix* and *Hawksworthiomyces* spp. (*Ophiostomatales*, *Sordariomycetidae*) (De Beer & Wingfield 2013, De Beer et al. 2016a, b). The hyaline, allantoid ascospores resemble those of the sexual morphs of the first two of these genera. Although the shape and size of the ascomata are similar to those in the *Ophiostomatales*, none of the species in that order have entirely hyaline ascomata such as those of *F. hyalinus* (De Beer et al. 2013). The denticulate conidiogenous cells of the asexual morph resemble those of the sporothrix-like asexual morphs in the *Ophiostomatales* (De Beer et al. 2016a, b). However, both LSU and ITS sequences place *F. hyalinus* in a distinct lineage in the *Sordariomycetidae*, distant from the *Ophiostomatales*, and among several lineages of uncertain ordinal placement, including genera such as *Barbatosphaeria* (Réblová et al. 2015), *Papulosa* (Réblová 2013), and *Ceratostomella* (Réblová 2006).

Fantasmomyces hyalinus was discovered during an expedition to search for *Ceratocystis albifundus* (*Microascales*, *Hypocreomycetidae*) that has a hyaline ascomatal base with pigmented long neck and occurs on freshly made wounds on trees (DeVay et al. 1965, Kile 1993, Wingfield et al. 1996). Although *F. hyalinus* is not an ophiostomatoid fungus (Wingfield et al. 1993, Seifert et al. 2013), we assume that it shares a biology similar to those fungi that have evolved to be vectored by insects or mites.

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Inonotus hymenonitens

Fungal Planet 481 – 21 December 2016

Inonotus hymenonitens G. Coelho & Yurchenko, *sp. nov.*

Etymology. Name refers to shining pore surface of basidiomata.

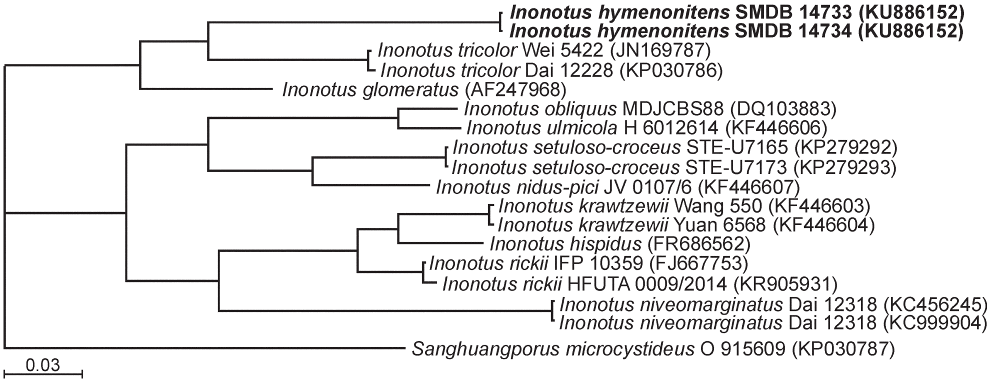
Classification — *Hymenochaetaceae*, *Hymenochaetales*, *Agaricomycetes*.

Basidioma annual, sometimes biennial, almost effused to effused-reflexed, up to 90 mm wide, 65 mm long, and 10 mm thick, firmly attached to the substratum, slightly fragile when fresh, woody and very light when dry. *Pilear surface* concentrically zoned, markedly sulcate, brown to dark brown, tomentous; margin entire, rounded, inflated (up to 3 mm thick), velutinous or tomentous, concolorous to the pileus or slightly paler. *Hymenophore* poroid, distinctly glossy, varying from yellow to olive yellow and yellowish brown; *pores* rounded, rarely polygonal, (4–)5–6(–7)/mm; dissepiments velutinous with projecting setae. *Tube layer* brownish yellow, up to 6 mm thick. *Context* slightly darker than the tube layer, yellowish brown when fresh, up to 4 mm thick, duplex, with a dark line separating an upper tomentum from a lower solid layer. *Hyphal system* monomitic; *generative hyphae* wholly simple-septate, pale yellow to ferruginous brown, in trama moderately branched, intertwined, thin- to moderately thick-walled, (2–)2.5–3.5(–4) µm diam, in context thin- to thick-walled, (2.5–)3–4.5(–5.5) µm diam. *Setal hyphae* lanceolate, dark ferruginous brown, in trama thick-walled, partly projecting into hymenium, (50–)65–200(–245) × (7–)9.5–20(–22.5) µm, with uniform lumen, in context thick-walled, sometimes solid, (65–)85–330(–375) × (8–)10–25(–30) µm. *Hymenial setae* scattered, difficult to find, lanceolate to ventricose, dark ferruginous brown in KOH, thick-walled, sometimes solid, (12–)20–50(–55) × (3–)5.5–10.5(–15) µm. *Basidia* short, clavate, 4-sterigmate, (6.5–)8–10.5(–13) × (5–)5.5–6.5(–7) µm. *Basidiospores* broadly-ellipsoid to mostly ellipsoid, flattened adaxially, ferruginous brown, thick-walled, (4–)4.5–5.5(–6.5) × (3.2–)3.6–4(–4.5) µm, on average 4.80 × 3.86 µm, length/width ratio 1.1–1.5, on average 1.26 (n = 92).

Typus. Brazil, Rio Grande do Sul State, Municipality of Itaara, Balneário Parque Pinhal, on strongly decayed fallen angiosperm trunk, 23 Oct. 2011, *G. Coelho* (holotype SMDB 14733, ITS sequence GenBank KU886152, alignment in TreeBASE S19410, MycoBank MB817740).

Additional specimens examined. The same locality and kind of substratum as holotype, 23 Oct. 2011, *G. Coelho*, SMDB 14734, ITS sequence GenBank KU886153; idem, SMDB 14735, 14736.

Notes — The microscopic measurements were based on two basidiomata. The most morphologically related species to *I. hymenonitens* are *I. glomeratus* and *I. pseudoglomeratus*. *Inonotus glomeratus*, known from north-eastern USA and eastern Canada (Ryvarden 2005), differs by larger pores (3–5/mm), setal hyphae conspicuous in trama only, abundant hymenial setae, and pale yellowish, ovoid to broadly-ellipsoid spores (5–7 × 4.5–5 µm). *Inonotus pseudoglomeratus* differs by dimidiate basidioma with a contracted base, polygonal pores, and spores pale yellow and being only slightly thick-walled (Ryvarden 2002). According to our phylogenetic analysis, the most related species is *I. tricolor*, which differs from the new species by larger, perennial basidiomata, dark brown pore surface with 8–10 pores/mm, narrower setal hyphae and basidia, and smaller spores (4–5 × 3–4 µm; Dai 2010).



Colour illustrations. South-west edge of Atlantic tropical forests in mountains near Santa-Maria, Brazil; basidiomata on rotten angiosperm wood, pore surface, hymenial seta, setal hypha from trama, basidiospores. Scale bars = 5 cm (basidioma), 2 mm (pore surface), 10 µm (all others).

Phylogram of *Inonotus* species inferred from a Bayesian analysis of the ITS dataset (including the new *Inonotus* in **bold** face and most similar sequences, suggested by BLAST). The scale bar denotes the number of substitutions per base. All branches have posterior probability = 1.00 (for parameters of the analysis see TreeBASE S19410).

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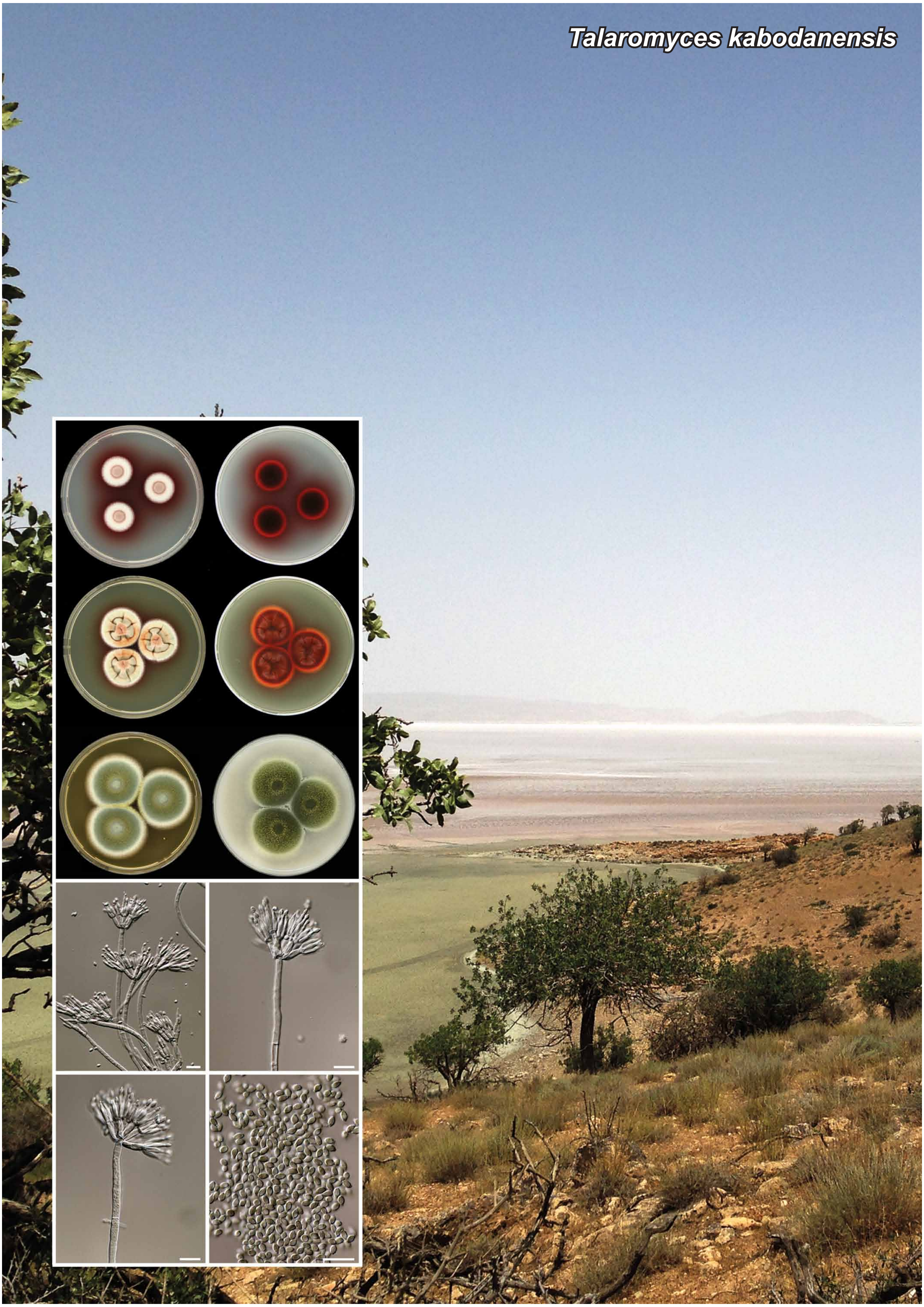

Talaromyces kabodanensis

Fungal Planet 482 – 21 December 2016

Talaromyces kabodanensis Houbraken, Arzanlou, Samadi & M. Meijer, *sp. nov.*

Etymology. Name refers to Kabodan Island, the collection location of the ex-type strain.

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

Conidiophores 100–200 µm long, with smooth walled stipes, non-vesiculate, predominantly biverticillate, occasionally with additional branch up to 20 µm long, stipes 3.0–4.0 µm wide. *Metulae* cylindrical, 4–10, 10–14 × 2.5–3.5 µm. *Phialides* acerose, 3–8 per metula, 10–13 × 2.0–2.5 µm. *Conidia* in long, distorted chains, finely rough to rough, majority with spiral striations, ovoidal to fusiform, often with a connective on one side, 2.5–3.5 × 1.5–2.5 µm. *Sclerotia* absent.

Culture characteristics — Colony diam, 7 d, in mm: CYA 15–25; CYA15°C 5–10; CYA30°C 18–24; CYA37°C no growth; CYAS 2–5; MEA 37–44; OA 36–45; YES 28–35; creatine agar 6–12, poor growth and acid production absent or weak.

CYA, 25 °C: Colonies slightly raised in centre, non-sulcate; colony texture velvety or slightly floccose; sporulation on CYA absent or poor; conidia dull green; mycelium white; exudate absent; soluble pigment deep red; margin entire, becoming irregular in age; reverse blackish red. YES, 25 °C: Colonies raised in centre, concentrical and radial sulcate; colony texture slightly floccose; sporulation on YES absent or poor; conidia grey-green; mycelium white at the margin, pinkish, yellow or red towards the centre; exudate absent or present as red droplets; soluble pigments produced, red; reverse red-brown. MEA, 25 °C: Colonies elevated, non-sulcate; colony texture velvety; sporulation on MEA variable, absent to strong; conidia dull green; mycelium pale yellow or yellow-orange; exudate absent; soluble pigments absent, present after 14 d of incubation; reverse red coloured in centre, becoming red-brown in age.

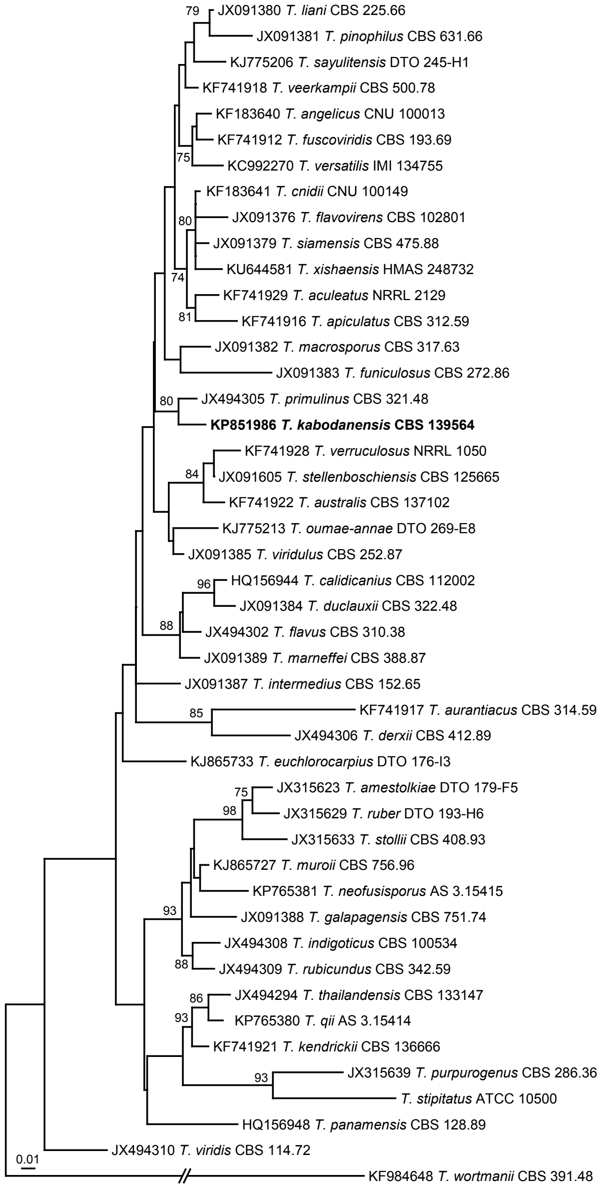
Typus. Iran, Urmia Lake National Park, Kabodan Island, from hypersaline soil, 2011, coll. *Y. Ghosta & R. Samadi*, isol. *R. Samadi* (holotype CBS H-22857, culture ex-type CBS 139564 = DTO 204-F2 = CCTU 850; ITS barcode KP851981, alternative markers: *BenA* = KP851986; *CaM* = KP851995, LSU barcode KY129843, MycoBank MB819001).

Additional specimens studied. Austria, isol. from patient material, 2016, *M. Lackner* (DTO 359-C2). – Czech Republic, Okrouhlo, isol. from bark of *Quercus*, 1991, *A. Kubátová* (DTO 355-A3). – Germany, isol. from sputum, *U. Weidner* (DTO 149-E1, DTO 149-E2); isol. from indoor environment (DTO 281-C1). – Iran, Urmia Lake National Park, Kabodan Island, isol. from hypersaline soil, *R. Samadi* (CBS 139563). – The Netherlands, isol. from CF patient, *C. Klaassen* (DTO 307-B9), isol. from clinical specimen, 2016, *F. Hagen* (DTO 354-G4). – Turkey, Zonguldak, isol. from soil, *R. Demirel* (DTO 307-B9, DTO 308-D2).

Notes — Maximum Likelihood analysis based on partial *BenA* sequences revealed *T. kabodanensis* to be related to *T. primulinus*. *Talaromyces kabodanensis* and *T. primulinus* share various characters, such as the inability to grow at 37 °C and the production of fusiform conidia, but differ in their growth rates on agar media (e.g. CYA, 15–25 vs 5–6; MEA, 37–44 vs 20–25; YES, 28–35 vs 8–10 mm) (Yilmaz et al. 2014).

Colour illustrations. Kabodan Island; from top-left to bottom-right (7-d-old colonies), CYA, observe; CYA, reverse; YES, obverse; YES, reverse; MEA obverse, OA, obverse; conidiophores and conidia. Scale bars = 10 µm.

Talaromyces kabodanensis produces red soluble pigments on CYA, a feature shared with the following members of sect. *Talaromyces*: *T. amestolkiae*, *T. cnidii*, *T. marneffei*, *T. purpurogenus*, *T. ruber* and *T. stollii*. The new species can be differentiated from these species by its inability to grow at 37 °C. Another distinguishing character of *T. kabodanensis* is the production of rough-walled conidia with spiral striations. This feature is shared with *T. calidicanius*, *T. ptychoconidium*, *T. purpureus* and *T. radicus*. *Talaromyces kabodanensis* can be differentiated from *T. calidicanius* and *T. ptychoconidium* by its inability to form synnemata, and from *T. purpureus* and *T. radicus* by its faster growth rate on MEA and YES (Yilmaz et al. 2014).



The *BenA* phylogenetic tree was inferred using the maximum likelihood analysis. Bootstrap support values are indicated at the nodes (1 000 bootstraps). The scale bar indicates the expected number of changes per site.

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Pseudoascochyta pratensis

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Pseudoascochyta Valenzuela-Lopez, Stchigel, Cano-Canals, Guarro & Cano, *gen. nov.*

Etymology. Name reflects the morphological similarity with the genus *Ascochyta*, but from which it is distinct.

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

Hyphae pale to dark brown, smooth- and thin- to thick-walled, septate. *Pycnidia* brown to dark brown, globose, solitary, pycnidial wall of *textura angularis*, neck absent, ostiolated or not. *Conidiogenous cells* enteroblastic, phialidic, globose to flask-shaped, hyaline, thin-walled. *Conidia* hyaline, cylindrical, 1-septate, guttulate. *Chlamydospores* absent.

Type species. *Pseudoascochyta pratensis* Valenzuela-Lopez, Cano-Canals, Stchigel, Guarro & Cano.
MycoBank MB817646.

Pseudoascochyta pratensis Valenzuela-Lopez, Cano-Canals, Stchigel, Guarro & Cano, *sp. nov.*

Etymology. From Latin *pratum*, prairie, referring to the toponymy of the place where the specimen was collected.

Hyphae pale to dark brown, 2–2.5 mm wide, smooth- and thin- to thick-walled, septate. *Pycnidia* dark brown, globose, with hyphal outgrowths, mostly immersed, solitary, 250–330 mm diam, pycnidial wall of *textura angularis* (*textura epidermoidea* on sterile carnation leaves), 30–40 mm thick, outer wall 2–3-layered, composed of dark brown, flattened polygonal cells of 5–25 mm diam, inner wall 4–6-layered, composed of hyaline to subhyaline, flattened polygonal cells, neck absent, ostiole absent (formed very late when the fungus grow on sterile carnation leaves, of 25–35 mm diam). *Conidiogenous cells* enteroblastic, phialidic, globose to flask-shaped, hyaline, thin-walled, 5–8 mm diam. *Conidia* hyaline, cylindrical, 1-septate, (8–)10–12 × 2.5–3 mm, narrowing slightly at the septa, smooth- and thin-walled, guttulate.

Culture characteristics — Colonies on OA reaching 12 mm diam in 7 d at 25 ± 1 °C, flattened, granulose due to the production of pycnidia, dark green (M.30F3); reverse olive brown (M.4F3) to brownish grey (M.4F2). Colonies on MEA reaching 15 mm in 7 d at 25 ± 1 °C, flattened, compact, greyish brown (M.7F3); reverse dark brown (M.8F5). NaOH spot test negative. Crystals absent. Optimal temperature for sporulation, 15 °C; optimal temperature of growth, 25 °C; minimum temperature of growth, 5 °C; maximum temperature of growth, 30 °C.

Typus. Spain, Tarragona, Prades, from soil, 13 Apr. 2015, *J. Cano-Canals* (holotype CBS H-22735, cultures ex-type FMR 14524 = CBS 141688, ITS sequence GenBank LT223130, LSU sequence GenBank LT223131, *tub2* sequence GenBank LT223132, *rpb2* sequence GenBank LT223133, MycoBank MB817647).

Colour illustrations. Prades, Tarragona, Spain; colony on OA after 7 d at 25 ± 1 °C, conidiomata (pycnidia) under the stereomicroscope, pycnidia, conidiogenous cells, conidia. Scale bars = 10 µm.

Notes — The fungus was isolated from a soil sample. Morphologically, *Pseudoascochyta pratensis* resembles species of the genus *Ascochyta* (Chen et al. 2015). Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Ascochyta phacae* (GenBank EU167570; Identities = 841/841 (100 %), no gaps) and *Microsphaeropsis olivacea* (GenBank JX681101; Identities = 840/841 (99 %), no gaps). Closest hits using the ITS sequence are *Ascochyta medicaginicola* (GenBank EU167575; Identities = 550/558 (99 %), gaps 3/558), *Leptosphaerulina australis* (GenBank JN712494; Identities = 537/542 (99 %), gaps 1/542). The closest hit using the *tub2* sequence is *Phoma* sp. (GenBank KT309385; Identities = 330/332 (99 %), no gaps). The closest hit using the *rpb2* (*RPB2*) sequence is *Ascochyta pisi* (GenBank EU874867; Identities = 844/923 (91 %), gaps 2/923). Our phylogenetic tree (see FP484), built by using the combined LSU, ITS, *tub2* and *rpb2* sequence alignment, corroborated that our fungus represents a new genus and a new species. *Pseudoascochyta pratensis* differs from *A. medicaginicola* var. *macrospora* by its lower growth rate on OA, the absence of crystal production, its larger conidia (28 × 6 mm vs (8–)10–12 × 2.5–3 mm) and the number of septa (1–3 vs 1).

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Pseudoascochyta novae-zelandiae

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Pseudoascochyta novae-zelandiae Valenzuela-Lopez, Stchigel, Guarro & Cano, *sp. nov.*

Etymology. Referring to the geographical origin of the fungus.

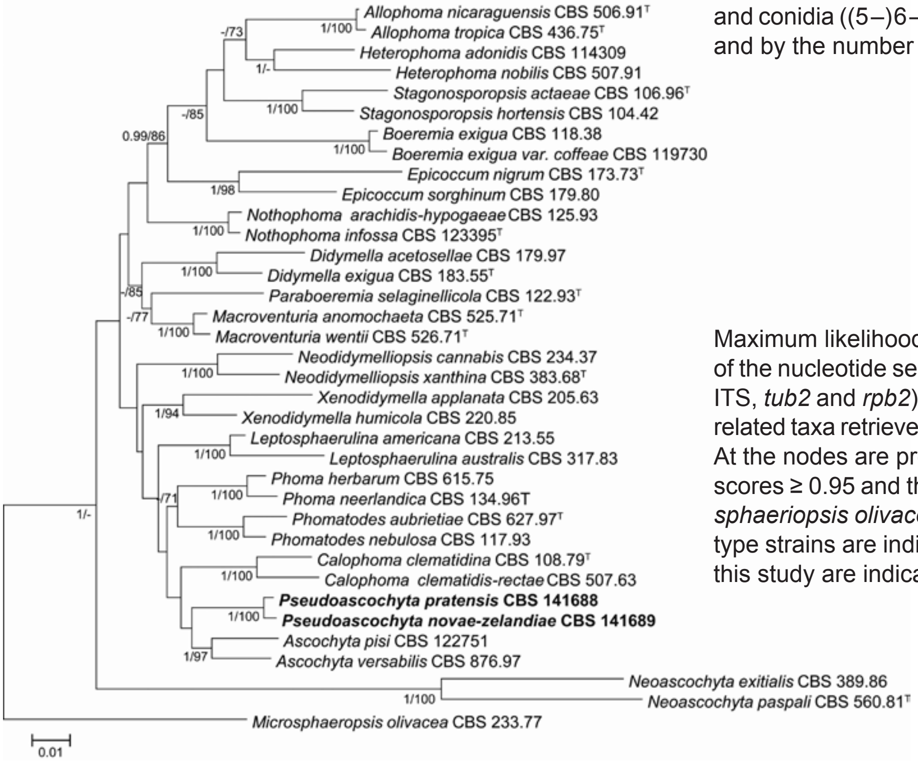
Classification — *Didymellaceae*, *Pleosporales*, *Dothideomycetes*.

Hyphae brown, 2.5–3 mm wide, smooth- and thin- to thick-walled, septate. *Pycnidia* brown to dark brown, globose, immersed, solitary, 120–250 mm diam, pycnidial wall of *textura angularis*, 3-layered, 10–15 mm thick, composed of dark brown polygonal cells of 5–25 mm diam, neck absent, non-ostiolated. *Conidiogenous cells* enteroblastic, phialidic, globose to flask-shaped, hyaline, thin-walled, 5–6 mm diam. *Conidia* hyaline, cylindrical, aseptate, (5–)6–7 × 2–2.5 mm, guttulate.

Culture characteristics — Colonies on OA reaching 50 mm diam in 7 d at 25 ± 1 °C, flattened, granulose due to the production of pycnidia, olive (M.3F2) to olive grey (M.3F4); reverse dark grey (M.1F1). Colonies on MEA reaching 48 mm diam in 7 d at 25 ± 1 °C, flattened, compact, olive (M.2E5) to yellowish white (M.2A2); reverse dark brown (M.6F6) to olive brown (M.4D4). NaOH spot test negative. Crystals absent. Optimal temperature for sporulation, 15 °C; optimal temperature of growth, 25 °C; minimum temperature of growth, 5 °C; maximum temperature of growth, 30 °C.

Typus. New Zealand, Wellington, Titahi Bay, *Cordyline australis* (*Agavaceae*), 1 May 1990, *P.R. Johnston* (holotype CBS H-22734, cultures ex-type FMR 15110 = CBS 141689, ITS sequence GenBank LT592892, LSU sequence GenBank LT592893, *tub2* sequence GenBank LT592894, *rpb2* sequence GenBank LT592895, MycoBank MB817648).

Notes — The fungus was isolated from a cabbage tree, endemic to New Zealand. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Ascochyta phacae* (GenBank EU167570; Identities = 842/842 (100 %), no gaps) and *Microsphaeropsis olivacea* (GenBank JX681101; Identities = 841/842 (99 %), no gaps). Closest hits using the ITS sequence are *Ascochyta medicaginicola* (GenBank EU167575; Identities = 540/546 (99 %), gaps 2/546), *Leptosphaerulina australis* (GenBank JN712494; Identities = 537/542 (99 %), gaps 1/542). The closest hit using the *tub2* sequence is *Phoma* sp. (GenBank KT309385; Identities = 332/332 (100 %), no gaps). The closest hit using the *rpb2* sequence is *Ascochyta pisi* (GenBank EU874867; Identities = 760/835 (91 %), gaps 1/835 (0%)). Our phylogenetic tree, built by using the concatenated LSU, ITS, *tub2* and *rpb2* sequence alignment, corroborated that our fungus represents a new species. *Pseudoascochyta novae-zelandiae* differs from *P. pratensis* (the type species of the genus) by its faster growth rate on OA, smaller pycnidia (130–250 mm vs 250–330 mm) and conidia ((5–)6–7 × 2–2.5 mm vs (8–)10–12 × 2.5–3 mm), and by the number of conidial septa (aseptate vs 1-septate).



Maximum likelihood tree obtained from the combined dataset of the nucleotide sequences of four different nuclear *loci* (LSU, ITS, *tub2* and *rpb2*) of the new proposed species and those of related taxa retrieved from the GenBank (TreeBASE ID 19426). At the nodes are presented the Bayesian posterior probability scores ≥ 0.95 and the bootstrap support values ≥ 70 %. *Microsphaeriopsis olivacea* CBS 233.77 was used as outgroup. Ex-type strains are indicated with ^{T}. The new species proposed in this study are indicated in **bold** face.

Colour illustrations. Titahi Bay, Wellington, New Zealand (image credit: Graeme Simpson, www.graemesimpsonimages.com); colony on OA after 7 d at 25 °C, conidiomata under the stereomicroscope, pycnidia, conidiogenous cells, conidia. Scale bars = 10 µm.

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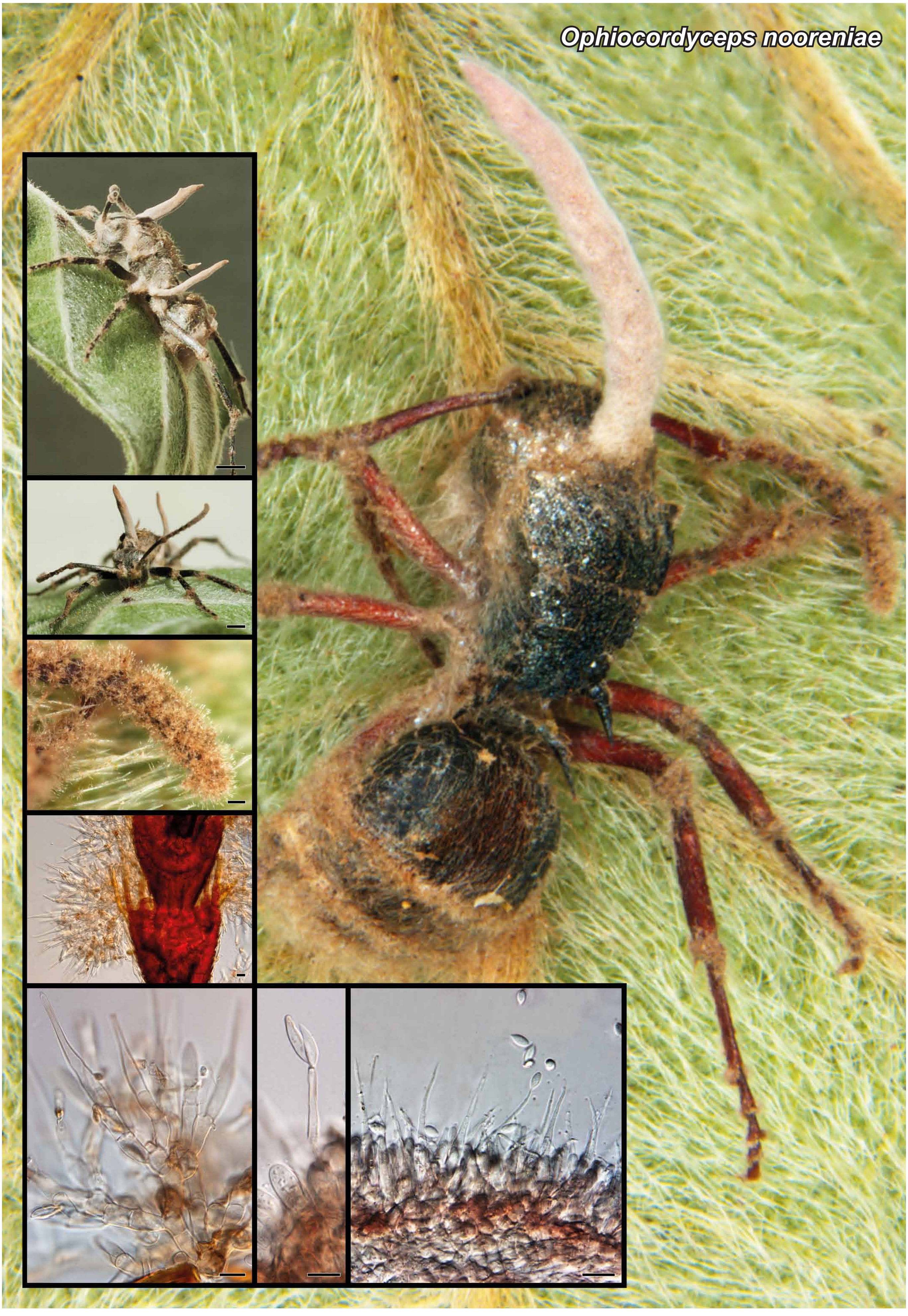

Ophiocordyceps nooreniae

Fungal Planet 485 – 21 December 2016

Ophiocordyceps nooreniae R.G. Shivas, G.F. Claridge & Y.P. Tan, *sp. nov.*

Etymology. Named after Hanneke Nooren, who discovered this fungus on dead ants (*Polyrhachis* (*Hagiomyrma*) *lydiae* and *Polyrhachis* (*Chariomyrma*) cf. *hookeri*) attached to leaves of siratro (*Macroptilium atropurpureum*) growing under a budgeroo tree (*Lysicarpus angustifolia*) in the open woodland garden she shares with Gordon Claridge.

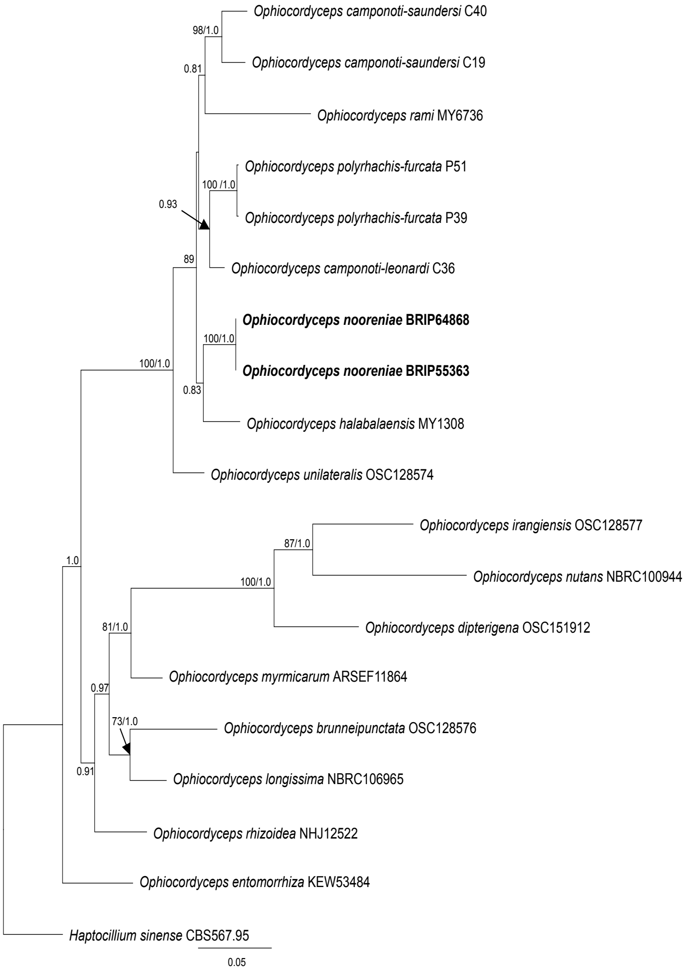
Classification — *Ophiocordycipitaceae*, *Hypocreales*, *Sordariomycetes*.

Mycelium emerges from the joints of legs and antennae of dead ants. *Synnemata* arise from dorsal pronotum and thorax as well as from between sclerites, up to 1 cm long, cylindrical, pale brown. Asexual morphs of two types. Hirsutella A-type morph produced on synnemata; *conidiophores* reduced to phialides, hyaline, smooth, tapering to a long narrow neck from a cylindrical base, 30–55 µm; *conidia* ovoid, 5–6 × 2–3 µm, slightly tapered at base. Hirsutella C-type morph produced at joints on legs and antennae; *conidiophores* on sporodochia, branched in the basal part, septate, subhyaline to pale brown; *conidiogenous cells* phialides, tapering in the upper half to a narrow neck 1.5–2.5 µm wide from a cylindrical base 6–8 µm wide, 35–50 long; conidia formed in groups of 2–4, fusiform with slightly curved apex and refractive base, 13–18 × 2.5–4.5 µm.

Typus. Australia, Queensland, Vinegar Hill, on dead ant (*Polyrhachis* (*Hagiomyrma*) *lydiae* det. J.S. Bartlett) on the underside of a leaf of siratro (*Macroptilium atropurpureum*, *Fabaceae*) in open woodland, 15 Feb. 2012, *H. Nooren* (holotype BRIP 55363a, LSU sequence GenBank KX673810, *rpb2* sequence GenBank KX673809, SSU sequence GenBank KX673811, *tef1* sequence GenBank KX673812, MycoBank MB817944).

Other specimen examined. Australia, Queensland, Vinegar Hill, on dead ant (*Polyrhachis* (*Chariomyrma*) cf. *hookeri* det. J.S. Bartlett) on the underside of a leaf of siratro (*Macroptilium atropurpureum*, *Fabaceae*) in open woodland, 15 Feb. 2012, *H. Nooren*, BRIP 64868a, *rpb2* sequence GenBank KX961141, SSU sequence GenBank KX961142, *tef1* sequence GenBank KX961144.

Notes — *Ophiocordyceps nooreniae* produced Hirsutella A-type (Evans & Samson 1982) and Hirsutella C-type (Evans et al. 2011) asexual morphs. A sexual morph was not found. This new fungus is classified in *Ophiocordyceps* as the generic name *Hirsutella* has been proposed for suppression in favour of *Ophiocordyceps* (Quandt et al. 2014). All *Hirsutella*/*Ophiocordyceps* isolates from formicine ants occupied a monophyletic clade (Simmons et al. 2015a). *Ophiocordyceps nooreniae* produces phialides on sporodochia (Hirsutella C-type) on the legs and antennae of *Polyrhachis* (*Hagiomyrma*) *lydiae* and *Polyrhachis* (*Chariomyrma*) cf. *hookeri* and in this regard is very similar to *Hirsutella sporodochialis* (Evans & Samson 1984). Evans & Samson (1984) also examined two ants from the Northern Territory, which they prudently assigned to *Hirsutella sporodochialis* and warrant comparison with *O. nooreniae*. *Ophiocordyceps nooreniae* is unusual in that it was found in open woodland in the subtropics, rather than tropical forests where most species of *Ophiocordyceps* have been discovered. In recent years several new cryptic species of *Ophiocordyceps* on ants have been discovered by both morphological and molecular phylogenetic studies (Evans et al. 2011, Kobmoo et al. 2012, Araújo et al. 2015, Simmons et al. 2015b).



A maximum likelihood tree of *Ophiocordyceps* based on a concatenated alignment of SSU, *tef1*, LSU and *rpb2* loci. Analyses were performed using RAxML v. 7.2 (Stamatakis & Alchiotis 2010) and MrBayes v. 2.2 on the Geneious v. 9.1.5 platform, both utilised the GTR substitution model with a gamma-distribution rate variation. In the tree, branch lengths are proportional to distance. Bootstrap support values ≥ 70 / Bayesian posterior probability scores ≥ 0.9 are indicated on the nodes. *Hirsutella sinensis* (CBS 567.95) was used as outgroup. The new species proposed in this study is indicated in **bold** face.

Colour illustrations. *Ophiocordyceps nooreniae* on *Polyrhachis* (*Chariomyrma*) cf. *hookeri* (background) and on *Polyrhachis* (*Hagiomyrma*) *lydiae* (other images); sporodochia on antenna, Hirsutella C-type phialides and conidia (lower left and lower middle), Hirsutella A-type phialides and conidia (lower right). Scale bars = 1 mm (ants), 10 µm (microscopic structures).

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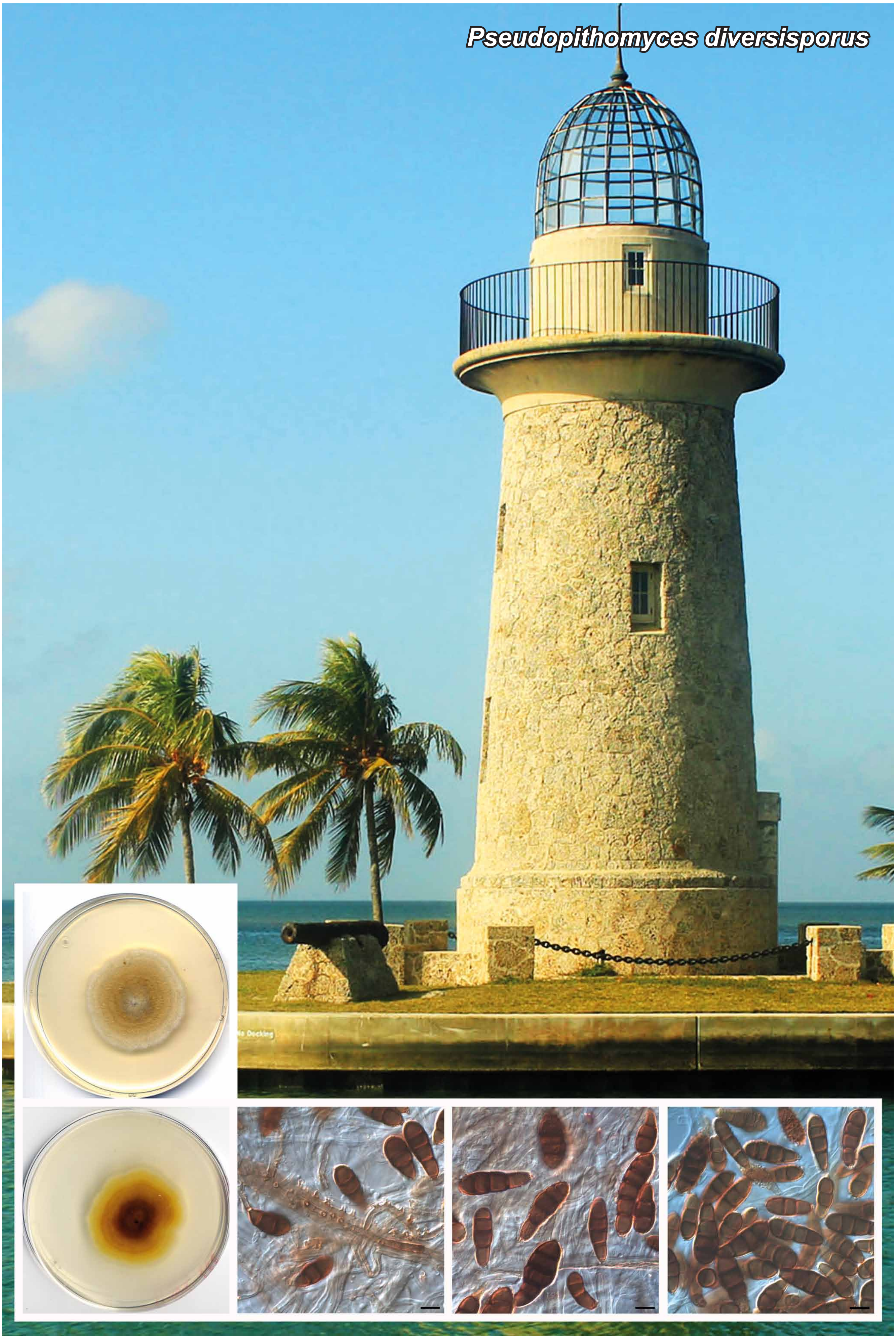

Pseudopithomyces diversisporus

Fungal Planet 486 – 21 December 2016

Pseudopithomyces diversisporus Guevara-Suarez, Da Cunha & Gené, *sp. nov.*

Etymology. Name refers to the different morphology of the conidia.

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

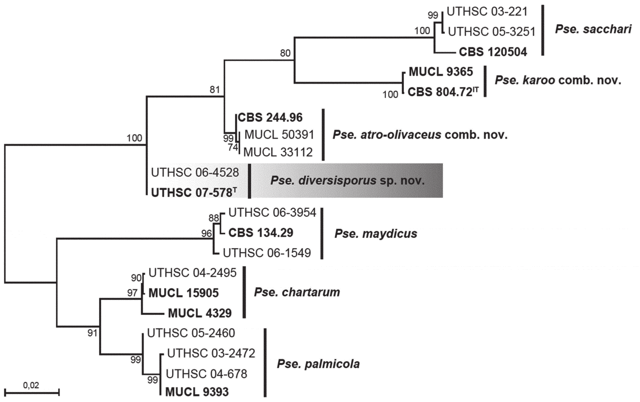
Mycelium (on PDA and PCA) consisting of branched, septate, hyaline to brown, smooth to asperulate, thin-walled, 2–3.5 µm wide hyphae. *Conidiophores* inconspicuous, consisting of lateral, short cylindrical, 2–4.5 × 2–2.5 µm, hyaline to subhyaline pegs, producing terminally blastoconidia liberated rhexolitically. *Conidia* solitary, ellipsoidal, subcylindrical, pyriform or clavate, 20–38 × 7–11 µm, brown to dark brown, verruculose to tuberculate, with (1–)2–3(–5) transverse septa, occasionally with some oblique or longitudinal septum, often with constricted wall at the basal septum, basal cell usually longer than the others, 5–8(–15) × 5–7(–9) µm. *Sexual morph* not observed.

Culture characteristics — (in darkness, at 25 °C after 7 d): Colonies attaining 38–45 mm diam on PDA and PCA. On PDA cottony, with concentric areas, greyish yellow (4C6) to brownish orange (5C6) (Kornerup & Wanscher 1978), with white and undulate margin; reverse reddish brown (8D7) at the centre, yellowish orange (4A8) towards the periphery.

Typus. USA, Florida, from human toenail, 2007, *D.A. Sutton* (holotype CBS H-22809, culture ex-type CBS 141846 = UTHSCSA 07-578 = FMR 12460, ITS sequence GenBank LK936373, LSU sequence GenBank LK936381, *gpdh* sequence GenBank LK936407, *rpb2* sequence GenBank LK936436, MycoBank MB818727).

Additional material examined. USA, Florida, from human foot, 2006, *D.A. Sutton* (UTHSCSA 06-4528 = FMR 12459, ITS sequence GenBank HG933810, LSU sequence GenBank HG933827, *gpdh* sequence GenBank LK936406, *rpb2* sequence GenBank LK936435).

Notes — The genus *Pseudopithomyces* (*Pse.*) was established by Ariyawansa et al. (2015) to accommodate four species, i.e. *Pse. chartarum*, *Pse. maydicus*, *Pse. sacchari* and *Pse. palmicola*; the first three species having been classified previously in the genus *Pithomyces* (*P.*). Morphological features of *Pseudopithomyces* are similar to *Pithomyces*, but phylogenetically they are clearly two distinct genera; while the type species of the former, *Pse. chartarum*, belongs to the family *Didymosphaeriaceae*, that of the latter genus, *P. flavus*, is related to the family *Astrosphaeriellaceae* (Pratibha & Prabhugaonkar 2015, Ariyawansa et al. 2015). Other *Pithomyces* species not yet formally transferred to *Pseudopithomyces* but phylogenetically related to the latter genus are *P. atro-olivaceus* and *P. karoo* (Da Cunha et al. 2014). The present analysis confirms that these species as belonging to *Pseudopithomyces*; therefore their respective new combinations are proposed below. *Pseudopithomyces diversisporus* morphologically resembles *Pse. atro-olivaceus*, but the conidia of the novel fungus are verruculose to tuberculate, concolorous, and usually show an elongated basal cell, while those of *Pse. atro-olivaceus* are verruculose to echinulate and exhibit end cells that are often paler than the others (Ellis 1960). Our phylogenetic results using ITS, LSU, *gpdh* and *rpb2* sequences show that *Pse. diversisporus* forms an independent distant branch with the clades of isolates identified as *Pse. atro-olivaceus*, *Pse. karoo* and *Pse. sacchari* within the genus *Pseudopithomyces*.



Colour illustrations. Lighthouse at Biscayne National Park, Florida, USA (image credit: https://www.goodfreephotos.com); colonies growing on PDA after 7 d at 25 °C, conidiogenous cells and conidia. Scale bars = 10 µm.

Pseudopithomyces atro-olivaceus (Cooke & Harkn.) Guevara-Suarez, Da Cunha & Gené, *comb. nov.* — MycoBank MB819007

Basionym. *Helminthosporium atro-olivaceum* Cooke & Harkn., Grevillea 12, 64: 95. 1884.

≡ *Pithomyces atro-olivaceus* (Cooke & Harkn.) M.B. Ellis, Mycol. Pap. 76: 8. 1960.

Specimens examined. Malawi, from dead twig, 1991, *C. Decock* (MUCL 33112 = FMR 13106). – USA, Florida, from human skin scrapings, 1996, *M.R. Rinaldi* (CBS 244.96 = MUCL 54968 = FMR 13083). – Zimbabwe, from dead twig, 1996, *C. Decock* (MUCL 50391 = FMR 13113). Sequences of ITS, LSU, *gpdh* and *rpb2* have been deposited in GenBank.

Pseudopithomyces karoo (Marasas & I.H. Schumann) Guevara-Suarez, Da Cunha & Gené, *comb. nov.* — MycoBank MB819013

Basionym. *Pithomyces karoo* Marasas & I.H. Schumann, Bothalia 10: 511. 1972.

Specimens examined. South Africa, Colesberg, Cape Province, from dead stem of *Gnidia polycephala*, 1972, *W.F.O. Marasas* (isotype: CBS H-7655; ex-isotype cultures: MUCL 54970 = CBS 804.72 = ATCC 24322 = IMI 155881 = PRE 44605 = FMR 13088, ITS sequence GenBank HG933811, LSU sequence GenBank HG933828, *gpdh* sequence GenBank LK936394, *rpb2* sequence GenBank LK936423); Potchefstroom, Transvaal, from litter under *Acacia karrroo*, 1966, *M. Papendorf* (as *P. quadratus*, MUCL 9365 = FMR 13112; ITS sequence GenBank HG933812, LSU sequence GenBank HG933829, *gpdh* sequence GenBank LK936395, *rpb2* sequence GenBank LK936424).

Maximum likelihood (ML) tree obtained from the combined of ITS, LSU, *gpdh* and *rpb2* sequences. Bootstrap support values above 70 % are shown at the nodes. The alignment included 2205 bp and was performed with ClustalW and MUSCLE. Tamura-Nei with Gamma distribution was used as the best nucleotide substitution model. Both the alignment and tree were constructed with MEGA v. 6.06 (Tamura et al. 2013). The ex-type/isotype and reference strains are in **bold** and the new species proposed is shown in dark box.

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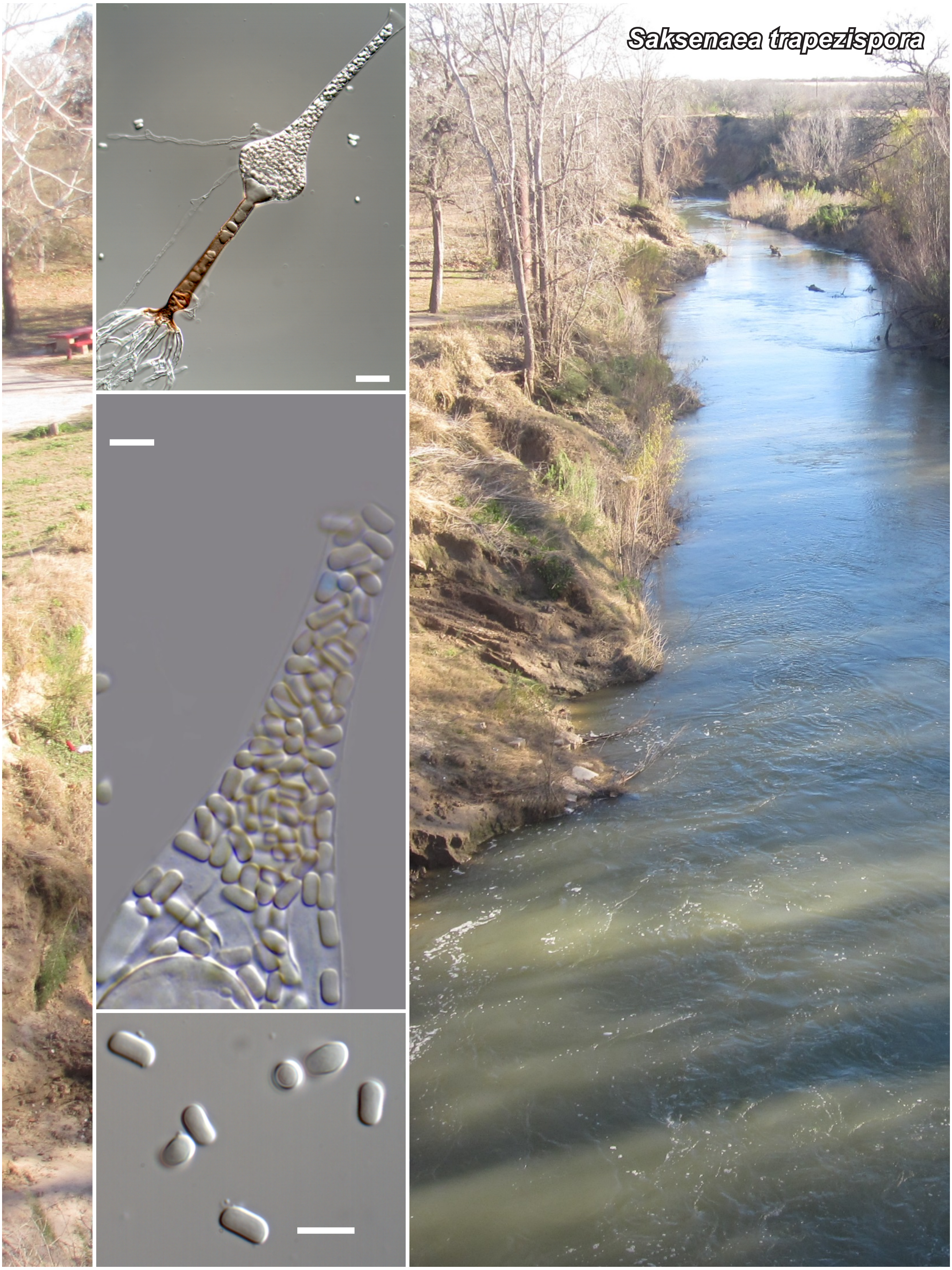

Saksenaea trapezispora

Fungal Planet 487 – 21 December 2016

Saksenaea trapezispora D.A. Sutton, Stchigel, Wiederhold, Guarro & Cano, *sp. nov.*

Etymology. From the Latin *trapeze*- and -*spora*, because of the trapezoid shape of the sporangiospores.

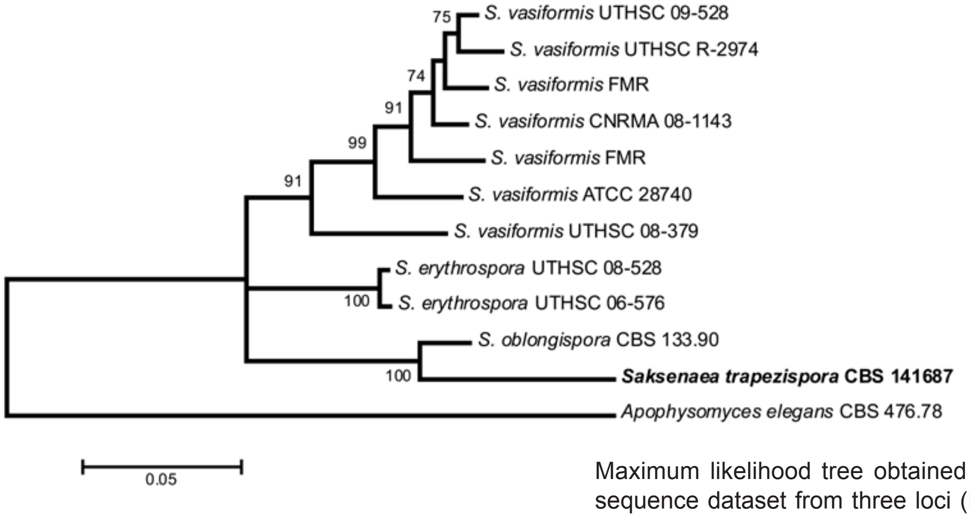
Classification — *Saksenaeaceae*, *Mucorales*, *Mucoromycotina*.

Hyphae sparsely septate, branched, hyaline, smooth- and thin-walled, up to 25 µm wide. *Sporangiophores* erect, generally arising singly, brown, stipe spinulose, unbranched, 150 – 230 µm long, 12 – 15 µm wide (at the stipe), with a profuse dichotomously branched rhizoidal complex. *Sporangia* terminal, multispored, hyaline, flask-shaped, asperulate, 50 – 140 µm long; with a long (30 – 100 µm) neck; apex of the neck closed with a mucilaginous plug, which is gradually dissolved when mature. *Sporangiospores* bacilliform at low magnification, trapezoid-shaped in lateral view because they are flattened on one side and convex on the opposite side, broadly ellipsoidal in frontal view, subhyaline to pale brown in mass, smooth- and moderately thick-walled, (4 –)5.5 – 7.5(– 8) × (2.5 –)3.5 – 4 µm (av. = 7 × 3.5 µm). *Zygospores* not observed.

Culture characteristics — Colonies reaching 35 – 40 mm after 4 d of incubation at 35 °C on CZA, whitish, with very scarce aerial mycelium and abundant sporangiophores; reverse concolorous. Colonies at 35 °C on MEA, PDA and SDA showing features similar to those on CZA, but they were very floccose and whitish, filling the diameter of the Petri dish without sporulation. At 37 °C the fungal growth is similar to that at 35 °C, but with the sporangiophores on CZA remaining sterile (without sporangiospores). The optimum growth was between 25 °C and 35 °C. The growth at 15 °C was moderately fast, reaching 40 – 45 mm in 4 d on MEA, PDA and SDA. The fungus did not grow at 40 °C.

Typus. USA, Texas, San Antonio, from knee wound of a soldier, 14 Dec. 2014, *D.A. Sutton* (holotype Herb. FMR 14359, cultures ex-type UTHSC DI 15-1 = FMR 14359 = CBS 141687, ITS sequence GenBank LT607406, LSU sequence GenBank LT607407, *tef1* sequence GenBank LT607408, MycoBank MB817644).

Notes — This fungus was isolated from human skin lesions in the USA. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Saksenaea vasiformis* (GenBank HQ010423; Identities = 633 / 687 (92 %), Gaps 20 / 687 (2 %)) and *S. oblongispora* (GenBank NR_137569; Identities = 594 / 646 (92 %), Gaps 22 / 646 (3 %)); by using LSU sequence are *S. oblongispora* CBS 133.90 (GenBank HM776676; Identities = 708 / 723 (98 %), Gaps 1 / 723 (0 %)) and *S. erythrospora* UTHSC 08-3606 (GenBank HM776680; Identities = 687 / 722 (95 %), Gaps 4 / 722 (1 %)); and by using *tef1* sequence are *S. oblongispora* CBS 133.90 (GenBank HM776687; Identities = 469 / 477 (98 %), no gaps) and *S. vasiformis* ATCC 60625 (GenBank HM776686; Identities = 489 / 512 (96 %), no gaps). Our phylogenetic tree, built by using the ITS, LSU and *tef1* nucleotide sequences, corroborated that our fungus represents a new species, being closest to the species *S. oblongispora*. *Saksenaea trapezispora* is easily distinguished from all the other species of the genus due to its moderately fast growth at 15 °C (the other species do not grow, or grow poorly at this temperature), and by the larger size of the sporangiospores (5 – 5.5 × 2 – 3 µm in *S. erythrospora*, 5 – 6.5 × 3 – 4.5 µm in *S. oblongispora*, and 5 – 7 × 2 – 3 µm in *S. vasiformis*), as well as by its shape (trapezoid-shaped in lateral view vs ellipsoid and biconcave in *S. erythrospora*, oblong in *S. oblongispora*, and barrel-shaped with rounded ends in *S. vasiformis*; Alvarez et al. 2010).



Maximum likelihood tree obtained from the combined DNA sequence dataset from three loci (ITS, LSU and *tef1*) of our isolate and sequences retrieved from GenBank. Bootstrap support values ≥ 70 % are presented above the nodes. *Apophysomyces elegans* CBS 476.78 was used as outgroup. The new species proposed in this study is indicated in **bold** face.

Colour illustrations. San Antonio's river, San Antonio, Texas, USA; sporangiophore, detail of the sporangium, sporangiospores. Scale bars = 20 µm (sporangiophore), 5 µm (all others).

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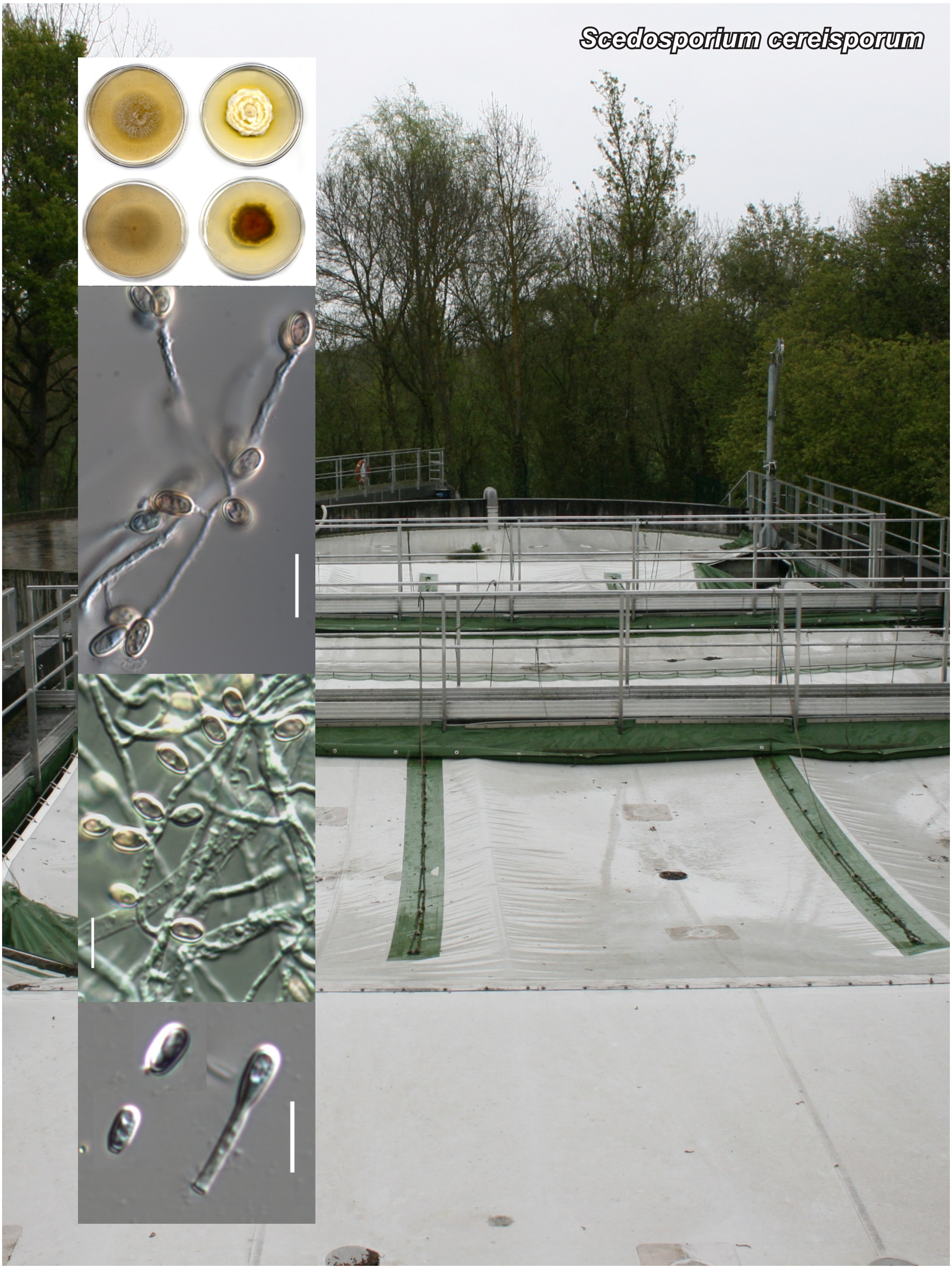

Scedosporium cereisporum

Fungal Planet 488 – 21 December 2016

Scedosporium cereisporum Rougeron, Stchigel, S. Giraud, Bouchara & Cano, *sp. nov.*

Etymology. From Latin *cereus*-, wax light, and -*spora*, spore, because of the shape of one of the fungal propagules produced by the fungus.

Classification — *Microascaceae*, *Microascales*, *Sordariomycetes*.

Hyphae pale to dark brown, 3–10 µm wide, thin- to thick-walled, smooth to granulose due to the production of dark granules, septate, anastomosing. *Conidiophores* solitary, consisting of a single conidiogenous cell, or arranged in verticilles of 2–3 conidiogenous cells, disposed laterally on undifferentiated hyphae or in side branches. *Conidiogenous cells* enteroblastic, percurrent (annellides), hyaline, thin- and smooth-walled, cylindrical or slightly broad at the base and with several broad scars at the upper part, 4–30 × 1.5–3 µm, producing conidia singly, or in slimy masses similar in shape and size to the sessile conidia, but with a broader basal scar. *Conidia* sessile or on short, cylindrical to conical denticles directly from the hyphae, arranged in palisade at both sides or at the end of lateral branches of sympodial growth, at first hyaline, later becoming pale brown, thick- and smooth-walled, ellipsoid to obovoid to subcylindrical, but bilaterally compressed, rounded at the ends, but with a small flattened area at the base or with a hyaline scar, 6–8 × 3–5 µm; *thallic propagules* of wax, light-shaped, scarce, truncate at the base, 25–35 × 3–6 µm. *Synnemata* and *sexual morph* not observed.

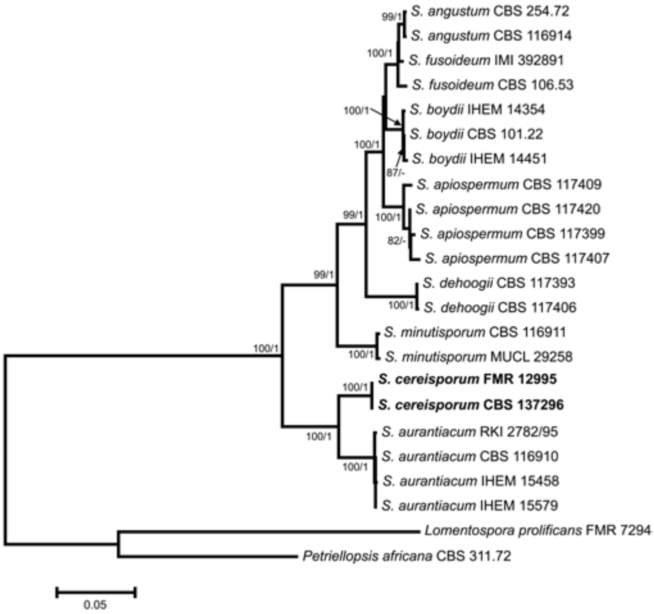
Culture characteristics — Colonies on potato dextrose agar (PDA) attaining 43–50 mm diam after 14 d at 25 °C, cottony, irregularly zoned, margins lobed, white and yellowish orange (M. 4A7 to 4B7); reverse brownish orange (6C8) and olive (2F8) to white to the margins, with a yellow (3A7) diffusible pigment. Colonies on oatmeal agar (OA) attaining 50–55 mm diam after 14 d at 25 °C, sparsely cottony to hairy, pale to light grey (1C1 to 1D1); reverse concolorous. At 5 °C and 40 °C the fungus does not grow.

Typus. France, Mûrs-Erignés, Maine-et-Loire, from fluids of a wastewater treatment plant, 13 Jan. 2012, *A. Rougeron* (holotype CBS H-21597, cultures ex-type 120008812-01/4 = FMR 12996 = CBS 137296; ITS sequence GenBank KJ599660, LSU sequence GenBank LT630707, *cmdA* sequence GenBank KJ599658 and *tub2* sequence GenBank KC779496, MycoBank MB817375).

Additional specimen examined. France, Mûrs-Erignés, Maine-et-Loire, from fluids of a wastewater treatment sample, 13 Jan. 2012, *A. Rougeron*, living cultures 120008812-01/3 = FMR 12995; ITS sequence GenBank KJ599669, LSU sequence GenBank LT630708, *cmdA* sequence GenBank KJ599664, *tub2* sequence GenBank KC779497.

Notes — This fungus was isolated from a wastewater sludge sample. Morphologically, *Scedosporium cereisporum* resembles *S. aurantiacum* (Gilgado et al. 2005). Both produce a yellow diffusible pigment leading to specific-coloured colonies on PDA. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using ITS sequences are *S. aurantiacum* UOA/HCPF 12709 (GenBank KC254094; Identities = 608/624 (97 %), gaps 5/624 (0 %)) and *S. aurantiacum* IHEM 23571 (GenBank JQ690909; Identities = 607/623 (97 %), gaps 5/623 (0 %)). The closest hits using exons 4 to 6 of the *tub2* sequence are *S. aurantiacum* CBS 101725 (GenBank GU126389; Identities = 550/581 (95 %), gaps 11/581 (1 %)) and other strains of the same species, and by using exons 5 and 6 of the *tub2* sequence are *S. aurantiacum* IHEM 15460 and 15461 (GenBank KC812570 and KC812570, respectively; Identities = 626/658 (95 %), gaps 4/658 (0 %)) and other strains of the same species. By using the *cmdA* sequence, the two closest hits are *S. apiospermum* isolate IHEM 15458 (GenBank JQ691080; Identities = 680/743 (92 %), gaps 26/743 (3 %)) and *S. aurantiacum* IHEM 23068 (GenBank JQ691115; Identities = 672/733 (92 %), gaps 26/733 (3 %)). Our phylogenetic tree, built by using the ITS, *tub2* and *cmdA* sequences, corroborated that both fungal isolates represents a new species of the genus *Scedosporium* (Lackner et al. 2014), *S. aurantiacum* being the most phylogenetically and morphologically related species. *Scedosporium cereisporum* differs from *S. aurantiacum* by the absence of growth at 40 °C, and by the production of sessile conidia arranged in palisade and wax light-shaped thallic propagules (two specific traits never reported within the *S. apiospermum* complex) (Gilgado et al. 2005, 2008).

Colour illustrations. Wastewater treatment plant, Mûrs-Erignés, Maine-et-Loire; colonies on OMA (left) and on PDA (right) after 14 d at 25 °C, conidiophores bearing conidia, sessile conidia, common conidia (to the left) and a wax light-shaped propagule. Scale bars = 10 µm.



Maximum likelihood tree obtained from the combined DNA sequence dataset from three loci (ITS, *tub2* and *cmdA*) of our isolate and sequences retrieved from GenBank. At the nodes are presented the bootstrap support values ≥ 70 % before the slash, and the Bayesian posterior probability scores ≥ 0.95 after the slash. *Lomentospora prolificans* FMR 7294 and *Petriellopsis africana* CBS 311.72 were used as outgroup. The new species proposed in this study is indicated in **bold** face.

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Chalara panamensis

Fungal Planet 489 – 21 December 2016

Chalara panamensis Koukol, T.A. Hofm. & M. Piepenbr., *sp. nov.*

Etymology. Named after the country of origin, Panama.

Classification — *Incertae sedis*, *Helotiales*, *Leotiomycetes*.

Description on substrate — *Colonies* effuse, superficial, mycelium composed of pale brown, septate, branched hyphae forming an indistinct net on the needles. *Conidiophores* reduced to a single cell bearing a phialide, slightly swollen up to 8 µm with thick cell wall, distinctly darker than the phialide. *Phialides* straight with gradual transition from venter to collarette, (82–)85–93 µm long and 5–6.5(–7.5) µm wide. *Venter* cylindrical, with smooth wall, (22.5–)24–28.5(–31) µm long. *Collarette* with distinct small warts covering the wall (at least upper two thirds), 59–69 µm long and 3.5–4 µm wide, ratio of the mean lengths of collarette and venter 2.4 : 1. Proliferation not observed. *Conidia* cylindrical with both ends rounded, 1-septate, hyaline, with smooth wall, (11–)14.5–20.5 µm long and 2.5–3 µm wide, the mean conidium length/width ratio 6 : 1. Conidia do not form chains, but rather assemble into bunches on top of the phialides.

On MEA: *Conidiophores* apical or intercalary, multicellular, up to 150 µm long and 4–5.5 µm wide terminated by a single phialide. *Phialides* straight to slightly bent with gradual transition from venter to collarette, (72–)74–83.5(–87) µm long and 4.5–5.5 µm wide. *Venter* subcylindrical, straight to slightly bent, with smooth wall, (25–)26.5–34.5(–37) µm long. *Collarette* with distinct warts covering at least upper third of its length, (43.5–)47.5–55(–56.5) µm long and 3–3.5 µm wide, ratio of the mean lengths of collarette and venter 1.7 : 1. Proliferation not observed. *Conidia* cylindrical with both ends rounded, 1-septate, hyaline, with smooth wall, (11.5–)12.5–15.5(–18) µm long and 3–3.5 µm wide, the mean conidium length/width ratio 4.6 : 1.

Culture characteristics — (in the dark, 25 °C after 14 d): colonies on MEA dense, yellowish white, intensively sporulating (sporulating regions turning dark brown due to mass of conidiophores), reaching 22–25 mm, on OA and PCA yellowish white, reaching 16–19 mm and 11–12 mm, respectively.

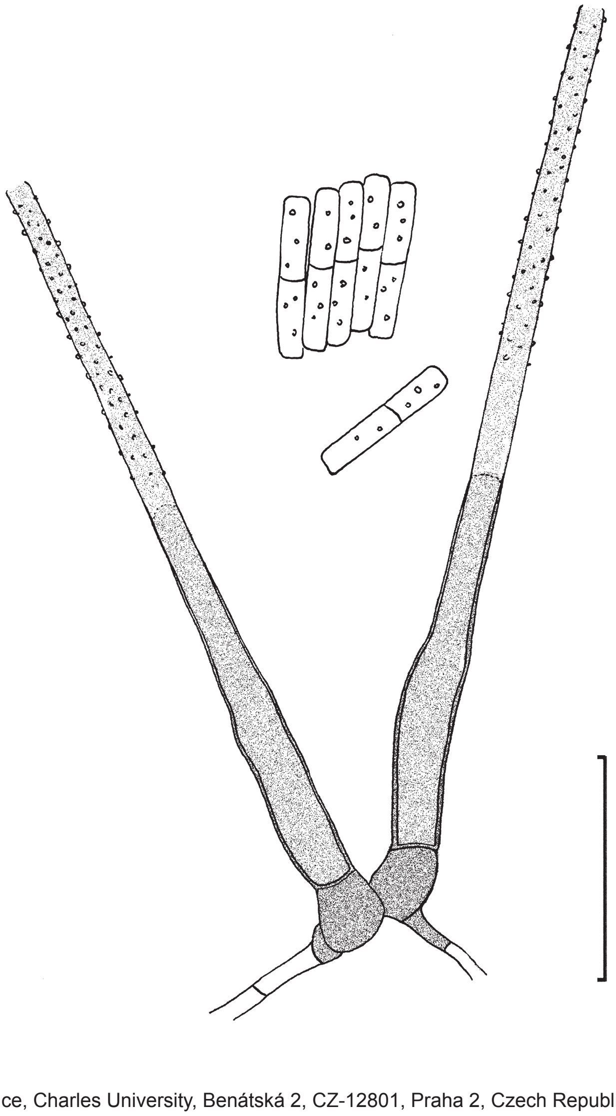
Typus. Panama, Chiriquí province, Boquete, Lago La Estrella, forest path to Caldera, southern part of forest, N8°43'45.4" W82°22'45.8", 1003 m a.s.l., needle litter of *Pinus* cf. *caribaea*, 7 July 2015, *O. Koukol* (holotype PMA; isotypes UCH, PRM 944173, PRC 3714; living culture ex-type CCF 5444 = PANC 16; ITS and LSU sequence GenBank LT629155, MycoBank MB818092).

Additional specimen examined. Panama, Chiriquí province, road from David to Boquete, km 26, N8°37'39.1" W82°25'43.7", 450 m a.s.l., needle litter of *Pinus* sp., 16 Jan. 2014, leg. *M. Piepenbring* & *O. Cáceres* 5202, isol. *O. Koukol*, living culture NK388; ITS and LSU sequence GenBank LT629156.

Colour illustrations. Needle litter of *Pinus* cf. *caribaea* above Lago La Estrella; 14-d-old cultures of *Chalara panamensis* cultivated at 25 °C on MEA (top, dark areas are caused by intensive sporulation) and on PCA (bottom), phialides on the substrate (left), phialide in culture (middle), conidia (right). Scale bars = 20 µm.

Drawing. Phialides and conidia on natural substrate. Scale bar = 20 µm.

Notes — This species is distinct from known *Chalara* spp. by having rather large phialides with asperate collarettes. It is morphologically most similar to the asexual morph of *Calycellina aspera*. This asexual morph treated by Nag Raj & Kendrick (1976) as *Chaetochalara aspera* also has asperate collarettes and produces 1-septate conidia of similar size (10–27 µm) as *Chalara panamensis*. However, *Chalara panamensis* does not produce setae and its phialides are longer than those of *Chaetochalara aspera* (48–77 µm) due to a much longer collarette (59–69 compared to 30–47 µm). Molecular data confirmed that the newly described species does not have any affinity to *Calycellina*; the closest GenBank match on ITS was *Calycellina populina* (GenBank JN033382) with only 87 % similarity. Further species with a verrucose collarette include only *Chalara verruculosa*, but this species produces only 1-celled conidia (McKenzie et al. 2002). A megablast search in GenBank using the ITS sequence revealed multiple hits with uncultured helotialean clones and also endophyte strains associated with leaves or roots of ericaceous plants with similarities ≤ 94 %. Closest hits using the LSU sequence revealed uncultured clones from soil in coniferous forests with similarities ≤ 98 %.



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Hyweljonesia queenslandica

Fungal Planet 490 – 21 December 2016

Hyweljonesia R.G. Shivas, Y.P. Tan, Marney & Abell, *gen. nov.*

Etymology. Named after the peripatetic mycologist Dr Nigel Hywel-Jones, who is a world authority on entomopathogenic fungi and taught us all how to recognise and identify these fungi in the tropical forests of Australia and Thailand. Although *Hyweljonesia* may not be entomopathogenic, it was collected during a search for such fungi.

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

Mycelium white, consisting of branched, septate, smooth subhyaline to hyaline hyphae. *Conidiophores* often on hyphal tufts, unbranched, integrated, lateral, straight, light brown, smooth walled, with an apical whorl of conidiogenous cells. *Conidiogenous cells* pale brown, clavate, smooth walled, minutely verruculose at the apex from inconspicuous conidial scars, with an apical whorl of conidia. *Conidia* subhyaline, cuneiform with rounded apices, smooth walled, with a refractive basal scar.

Type species. *Hyweljonesia queenslandica* R.G. Shivas, Y.P. Tan, Marney & Abell.
MycoBank MB817134.

Hyweljonesia queenslandica R.G. Shivas, Y.P. Tan, Marney & Abell, *sp. nov.*

Etymology. Named after Queensland, the Australian State where the fungus was collected.

Mycelium covers cocoon of an unidentified microlepidoptera, forming clavate or irregularly branched hyphal tufts up to 3 mm long, white. *Conidiophores* arising from the hyphal tufts, unbranched, integrated, lateral, straight, 0–1 septate, light brown, smooth walled, 7–13 µm long, flared at base to 3–7 µm wide, narrowing to 2–4 µm wide at apex, with an apical whorl of (1–)2–4(–5) conidiogenous cells. *Conidiogenous cells* pale brown, clavate, 6–8 × 2–3.5 µm, smooth walled, minutely verruculose at the apex from inconspicuous conidial scars, with an apical whorl of 10–30 conidia. *Conidia* subhyaline, cuneiform with rounded apices, 3–4 × 1–2 µm, smooth walled, with a refractive basal scar.

Culture characteristics — Colonies (on potato-dextrose agar (PDA) at 25 °C in the dark after 4 wk) circular, up to 5.5 cm diam, central 2 cm diam with abundant hyphal tufts up to 300 × 20–150 µm, umber, outer margin flat, mucoid, ochreous, margin diffuse; reverse honey in centre becoming paler and straw coloured at margin.

Typus. AUSTRALIA, Queensland, Babinda, on the cocoon of an unidentified microlepidoptera on the underside of a leaf in tropical forest, 7 July 2014, *T.S. Marney*, *R.G.*, *M.D.E. & M.A. Shivas* (holotype BRIP 61322b incl. ex-type culture, ITS sequence GenBank KY173476, LSU sequence GenBank KY173562, MycoBank MB817135).

Colour illustrations. *Hyweljonesia queenslandica* on the cocoon of a microlepidoptera in northern Queensland; conidiophores on hyphal tufts with conidia, growth on PDA. Scale bars = 1 mm (on host), 10 µm (microscopic structures), 1 cm (cultures).

Notes — *Hyweljonesia* is unlike any other genus in the *Capnodiales* by having conidiophores, arranged on hyphal tufts, with an apical whorl of conidiogenous cells that are minutely verruculose from inconspicuous conidial scars. Based on a megablast search of NCBIs GenBank nucleotide database, the LSU sequence of *H. queenslandica* was closest to those of ex-type cultures of *Penidiella carpentariae* (GenBank NG_042758; Identities = 850/883 (96 %), Gaps = 3/883 (0 %)), *Teratosphaeria* (as *Mycosphaerella*) *nubilosa* (GenBank DQ246228; Identities = 847/886 (96 %), Gaps = 9/886 (1 %)) and *Catenulostroma corymbiae* (GenBank KC005804; Identities = 845/884 (96 %), Gaps = 7/884 (0 %)), which all belong to the *Teratosphaeriaceae* (Quaedvlieg et al. 2014). Morphology and analysis of ITS and LSU sequence data did not reveal any close associations with other known genera of fungi (Seifert et al. 2011).

Hyweljonesia queenslandica has only been recovered once from the cocoon of an unidentified microlepidoptera parasitised by a chalcidoid wasp (*Hymenoptera*: *Chalcoidea*) on the underside of a leaf of a dicotyledonous plant in tropical forest in northern Queensland. It is not known whether *H. queenslandica* is an entomopathogen or merely saprobic, possibly competing with the chalcidoid wasp for the pupal nutrients.

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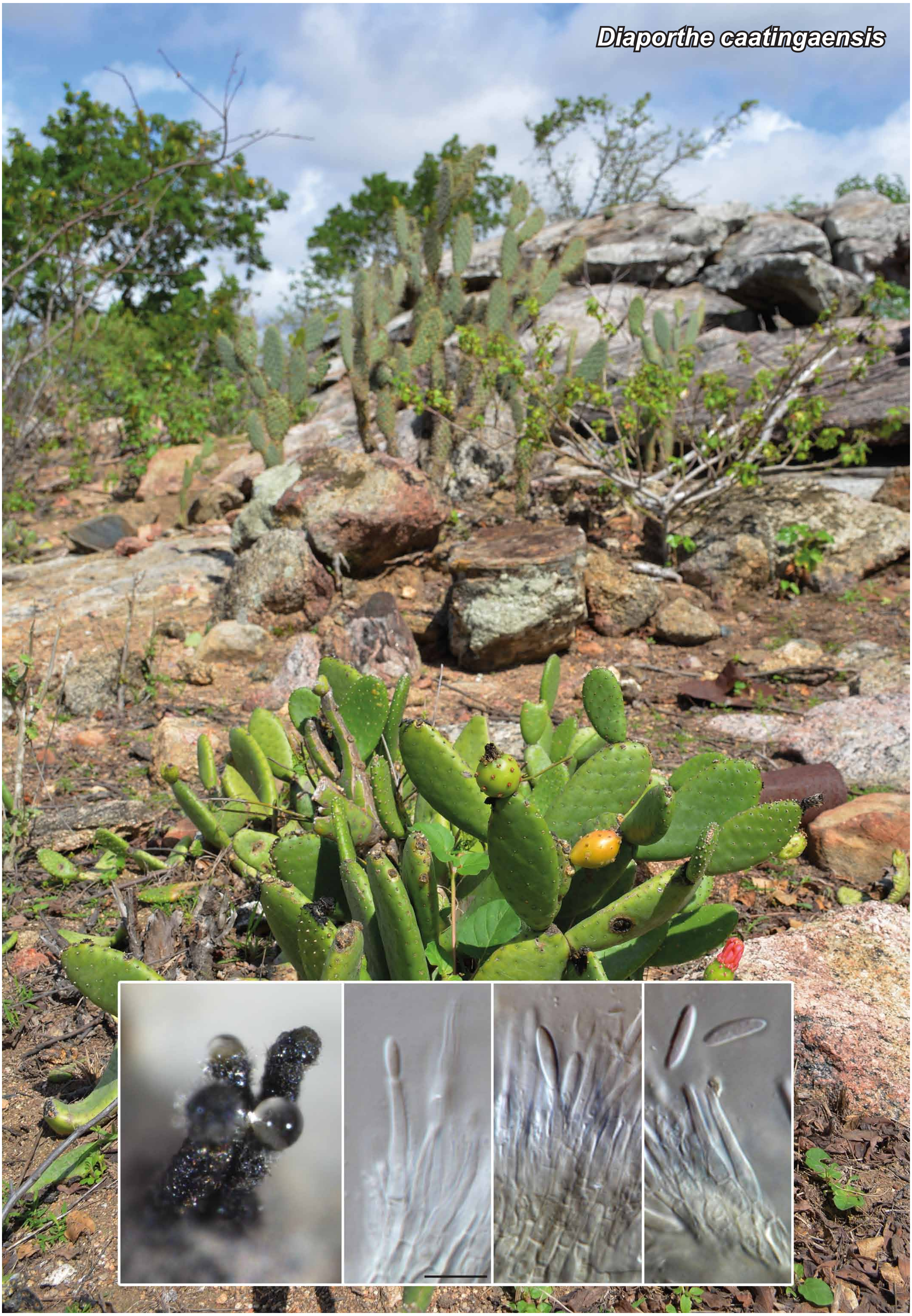

Diaporthe caatingaensis

Fungal Planet 491 – 21 December 2016

Diaporthe caatingaensis J.D.P. Bezerra, L.M. Paiva, G.A. Silva, Souza-Motta & Crous, *sp. nov.*

Etymology. Name refers to the Caatinga, the Brazilian tropical dry forest where this fungus was isolated as endophyte from cacti species.

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

Conidiomata pycnidial, solitary or aggregated, dark brown to black, erumpent, globose to subglobose-conical, up to 465 µm diam, with long black neck (up to 510 µm tall) sometimes hairy at apex, conidial masses hyaline to pale at neck apex; medium brown thick-walled cells of *textura angularis*. *Conidiophores* hyaline, smooth, 3–5-septate, densely aggregated, cylindrical, straight to sinuous, sometimes branched, 30–37.5 × 2(–2.5) µm. *Conidiogenous cells* 16–23.5 × 1–2(–2.5) µm, phialidic, cylindrical, terminal, with slight periclinal thickening; distinct collarette at apex. *Paraphyses* not observed. *Alpha conidia* aseptate, hyaline, smooth, guttulate, fusoid-ellipsoid, tapering towards both ends, apex subobtuse to obtuse, base subtruncate to truncate, (6.5–)8.5–9.5(–10.5) × (1.5–)2(–2.5) µm. *Beta* and *gamma conidia* not observed.

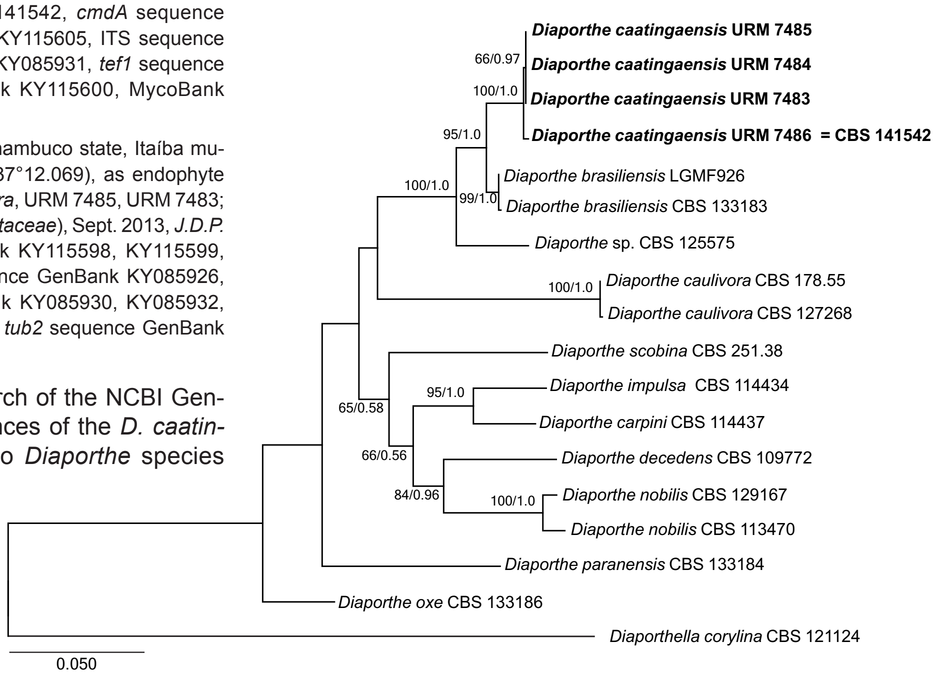
Culture characteristics — Colonies covering Petri dishes after 2 wk at 25 °C. On PDA, colonies with smooth margins, and fluffy aerial mycelium, surface and reverse dark grey to black. On MEA, surface dark grey to black and reverse amber to buff. On OA surface and reverse dark grey to black.

Typus. Brazil, Pernambuco state, Itaíba municipality, Curral Velho farm (S9°08.895 and W37°12.069), as endophyte from *Tacinga inamoena* (*Cactaceae*), Sept. 2013, *J.D.P. Bezerra* (holotype URM 90021, isotype CBS H-22862, culture ex-type URM 7486 = CBS 141542, *cmdA* sequence GenBank KY115597, *his3* sequence GenBank KY115605, ITS sequence GenBank KY085927, LSU sequence GenBank KY085931, *tef1* sequence GenBank KY115603, *tub2* sequence GenBank KY115600, MycoBank MB818928).

Additional specimens examined. Brazil, Pernambuco state, Itaíba municipality, Curral Velho farm (S9°08.895 and W37°12.069), as endophyte from *Tacinga inamoena*, Sept. 2013, *J.D.P. Bezerra*, URM 7485, URM 7483; from *Pilosocereus gounellei* subsp. *gounellei* (*Cactaceae*), Sept. 2013, *J.D.P. Bezerra* URM 7484 (*cmdA* sequence GenBank KY115598, KY115599, *his3* sequence GenBank KY115606, ITS sequence GenBank KY085926, KY085928, KY085925, LSU sequence GenBank KY085930, KY085932, KY085929, *tef1* sequence GenBank KY115604, *tub2* sequence GenBank KY115601, KY115602).

Notes — Based on a megablast search of the NCBI GenBank nucleotide database, LSU sequences of the *D. caatingaensis* has high identity (98–99 %) to *Diaporthe* species (e.g. *D. ocoteae*; CBS 141330; GenBank KX228344.1). On ITS sequences, *D. caatingaensis* is 98 % (532/543) similar to *D. brasiliensis* (CBS 133183; GenBank NR_111844.1), amongst others. Using *his3* sequences *D. caatingaensis* is 98 % (404/412) identical to *D. brasiliensis* (CBS 133183; GenBank KC343526.1), 96 % (396/411) to *Diaporthe* sp. (CBS 125575; GenBank KC343691.1) and has low identity to *Diaporthe* species (e.g. *D. paranensis*; CBS 133184; GenBank KC343655.1, 93% (377/405)). The *tub2* sequences are 97 % (687/708) similar to *D. brasiliensis* (CBS 133183; GenBank KC344010.1) and 95 % (667/701) to *Diaporthe* sp. (CBS 125575; GenBank KC343691.1) and has low identity to *D. oxe* (CBS 133186; GenBank KC344132.1, 93 % (418/450)). On *cmdA* sequences, *D. caatingaensis* is 96 % (483/501) similar to *D. brasiliensis* (CBS 133183; GenBank KC343284.1) and *Diaporthe* sp. (CBS 125575; GenBank KC343449.1). On *tef1* sequences *D. caatingaensis* has low identity to *D. brasiliensis* (CBS 133183; GenBank KC343768.1, 93 % (286/308)). Morphologically, *D. caatingaensis* is different from *D. brasiliensis* in the size of its picnidia (up to 465 µm vs 70–160 µm diam in *D. brasiliensis*), pycnidial necks (up to 510 µm vs 60–130 µm tall in *D. brasiliensis*), conidiophores (30–37.5 × 2(–2.5) µm, 3–5-septate vs (17–)20–27(–30) × 2(–4) µm, 1–3-septate in *D. brasiliensis*, alpha conidia ((6.5–)8.5–9.5(–10.5) × (1.5–)2(–2.5) µm vs 6–7(–8) × 2–3 µm in *D. brasiliensis*) (Gomes et al. 2013).

Colour illustrations. *Tacinga inamoena* in the Brazilian tropical dry forest (Caatinga); pycnidial conidiomata, conidiogenous cells and conidia. Scale bar = 10 µm.



Maximum likelihood tree obtained by phylogenetic analyses of the combined ITS rDNA, *cmdA*, *his3*, *tef1*, and *tub2* datasets. Bootstrap support values from Maximum Likelihood and Bayesian posterior probabilities, respectively, are indicated at the nodes. The new species is indicated in **bold** face. *Diaporthella corylina* (CBS 121124) was used as outgroup.

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Tubulicrinis australis

Fungal Planet 492 – 21 December 2016

Tubulicrinis australis M. Dueñas, Telleria & M.P. Martín, *sp. nov.*

Etymology. The name refers to the southern South America, where this species was collected.

Classification — *Tubulicrinaceae*, *Hymenochaetales*, *Agaricomycetes*.

Basidioma resupinate, effuse, loosely adnate, thin, furfuraceous; hymenophore porose-reticulate, sometimes tuberculate, white to cream; margin not especially differentiated. *Hyphal system* monomitic; hyphae hyaline, thin-walled, ramified, with clamps, 2–2.5 µm wide; subicular hyphae branching sometimes at right angles, subhymenial hyphae short-celled and densely interwoven. *Cystidia* cylindrical capitate, generally bi- or multi-radicate, projecting for the greater part of their length, 70–90 µm long and 7–10 µm wide in the middle part, narrowing slightly towards the neck, then abruptly widened to a distinct head, 7–8 µm diam; apex initially encrusted, the crystals opening and lost, except around the neck; capillary lumen widening abruptly to the thin-walled apex; weakly amyloid, surrounded by ascending unbranched hyphae. *Basidia* subclaviform, 9–12 × 4–5 µm. *Spores* narrowly ellipsoid, adaxially concave, 6–7.5 × 3–3.5 µm, thin-walled, smooth, guttulate, inamyloid and non cyanophilous.

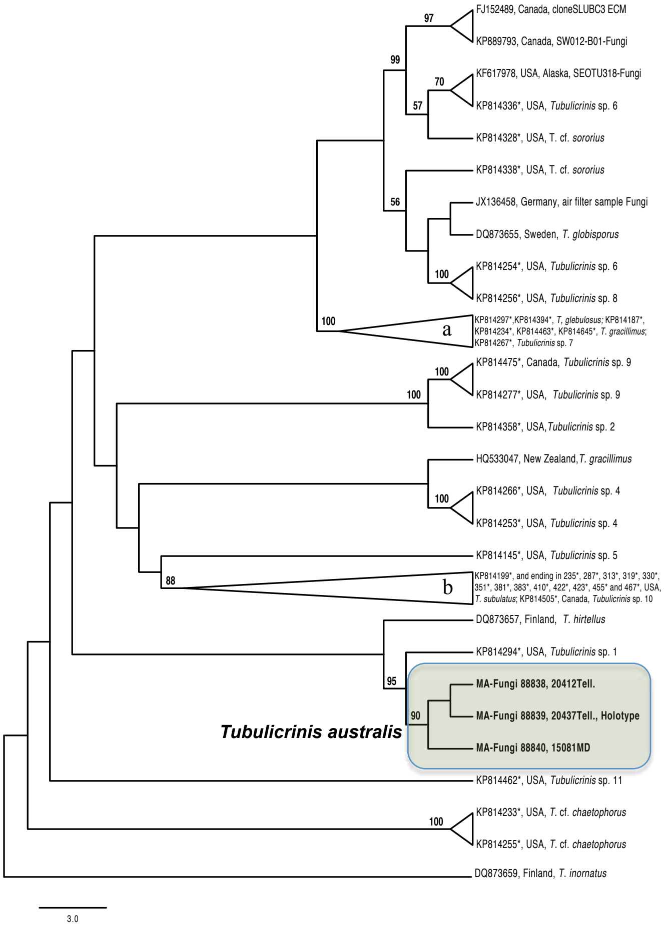
Habitat — On *Lophosoria.*

Typus. Chile, Los Lagos (X Region), Palena, Comuna Hualaihué, Comau fjord, Huinay, path to geyser, S42°24'55.9" W72°27'16.1", on *Lophosoria quadripinnata* (*Dicksoniaceae*), alt. 55 m, 14 Oct. 2014, *M. Dueñas & M.T. Telleria*, 20437Tell. (holotype MA-Fungi 88839, ITS sequence GenBank KX017593, LSU sequence GenBank KX017596, MycoBank MB816887).

Additional specimens examined. Chile, Los Lagos (X Region), Palena, Comuna Hualaihué, Comau fjord, Huinay, forest behind the hydroelectric station, S42°22'53.3" W72°24'55.9", on *Lophosoria quadripinnata*, alt. 24 m, 13 Oct. 2014, *M. Dueñas & M.T. Telleria*, 20412Tell., MA-Fungi 88838, ITS sequence GenBank KX0175916, LSU sequence GenBank KX017594; idem, path to geyser, S42°24'55.9" W72°27'16.1", on *L. quadripinnata*, alt. 55 m, 14 Oct. 2014, *M. Dueñas & M.T. Telleria*, 15081MD, MA-Fungi 88840, ITS sequence GenBank KX017592, LSU sequence GenBank KX017595.

Notes — Based on morphology, *Tubulicrinis australis* is related to *T. cinctus*, described from New Zealand (Cunningham 1963) and *T. regificus*, from Europe and North America (Hjortstam et al. 1988), both with capitate cystidia. *Tubulicrinus cinctus* has cystidia with incrusted neck and capillar lumen that ends abruptly as in *T. australis*, but the spores are smaller and subglobose, 4–4.5(–5) × (3.5–)4–4.5 µm; whereas, *T. regificus* has longer cystidia, 80–120 µm, without crystals around the neck and ellipsoid spores, adaxially straight to convex 6.5–9 × 3.5–5 µm. The presence of ascending hyphae in the cystidia is a typical character of the genera *Litschauerella* and *Tubulicium*, but we do not know any species of *Tubulicrinis* presenting them. Based on three collections of *T. australis*, and all *Tubulicrinis* ITS nrDNA sequences available in GenBank (46 sequences), the maximum parsimony analyses under a heuristic search, clearly grouped the new sequences as a sister clade to '*Tubulicrinis* sp. 1' (GenBank KP814294, collected on litter or well decayed wood in pine forest in Michigan, USA; Rosenthal & Bruns, unpubl. data). In GenBank, only seven *Tubulicrinis* LSU nrDNA sequences are available, and the phylogenetic analysis (parsimony; exhaustive search), grouped the three new sequences as a sister group of a clade formed by *Tubulicrinis globisporus* (GenBank DQ873655) and *Tubulicrinis* sp. (GenBank AJ406447).

Colour illustrations. *Lophosoria quadripinnata* in Huinay, along the path to the geyser (photo credit M.T. Telleria); cystidia and spores of *Tubulicrinis australis*. Scale bars = 10 µm.



Strict consensus parsimony tree (100 equal MPTs) obtained from the *Tubulicrinis* ITS sequence analysis (PAUP v. 4.0a147). A sequence of *Tubulicrinis inornatus* was used as outgroup. Two major clades were collapsed ('a' and 'b' in the triangles), both including more than one species. Percentage of bootstrap support values (> 50 %) is indicated on the branches (10 000 replicates under fast swap option). The *T. australis* clade is marked with a green square; the accession number from the EMBL/GenBank database are indicated at the terminal nodes. The asterisk (*) after the EMBL/GenBank accession number are sequences obtained by Rosenthal & Bruns (unpubl. data) on litter or well-decayed wood in pinaceous forest from Canada and USA.

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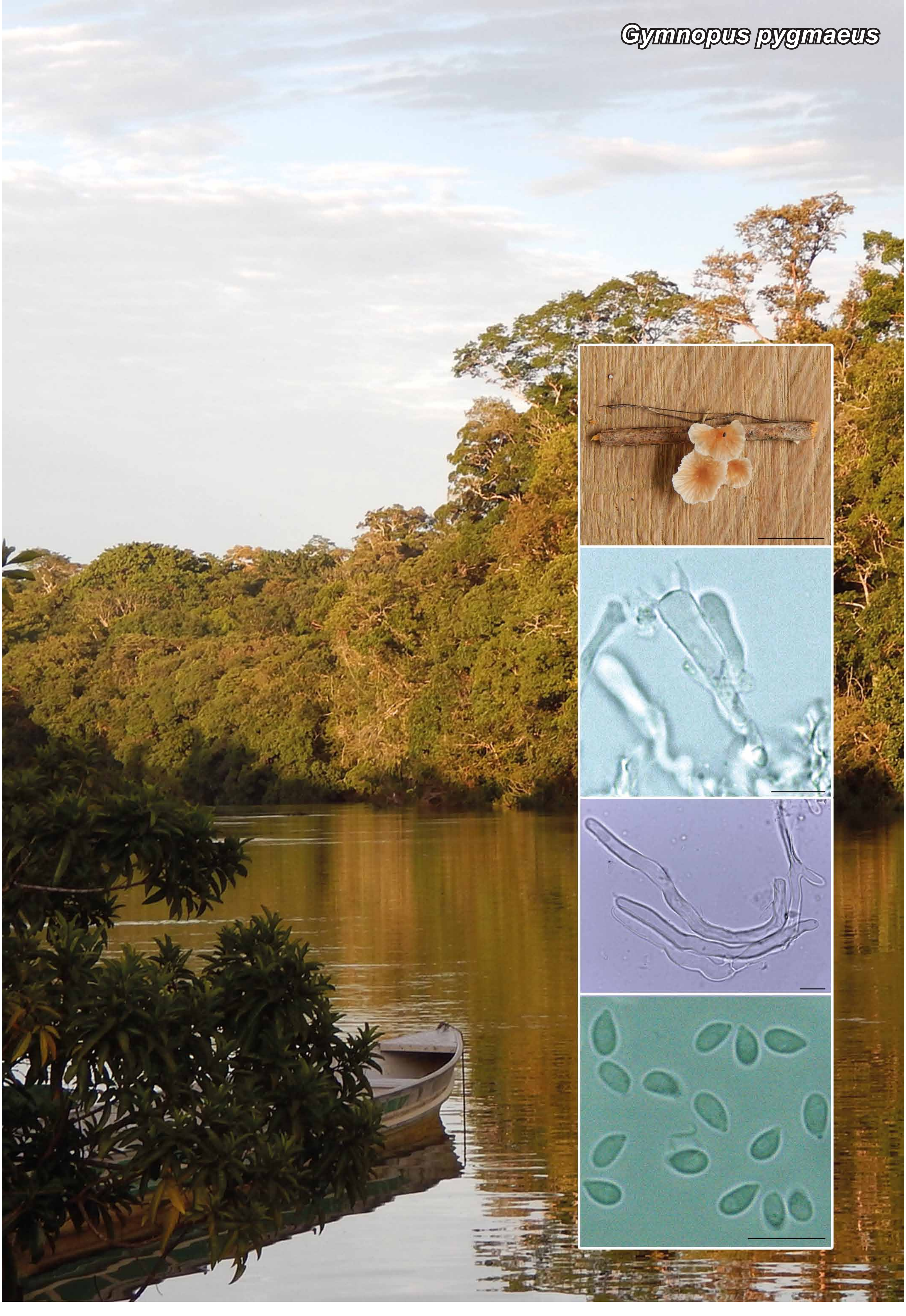

Gymnopus pygmaeus

Fungal Planet 493 – 21 December 2016

Gymnopus pygmaeus V. Coimbra, E. Larss., Wartchow & Gibertoni, *sp. nov.*

Etymology. The name refers to the small size of basidiomata.

Classification — *Omphalotaceae*, *Agaricales*, *Agaricomycetes*.

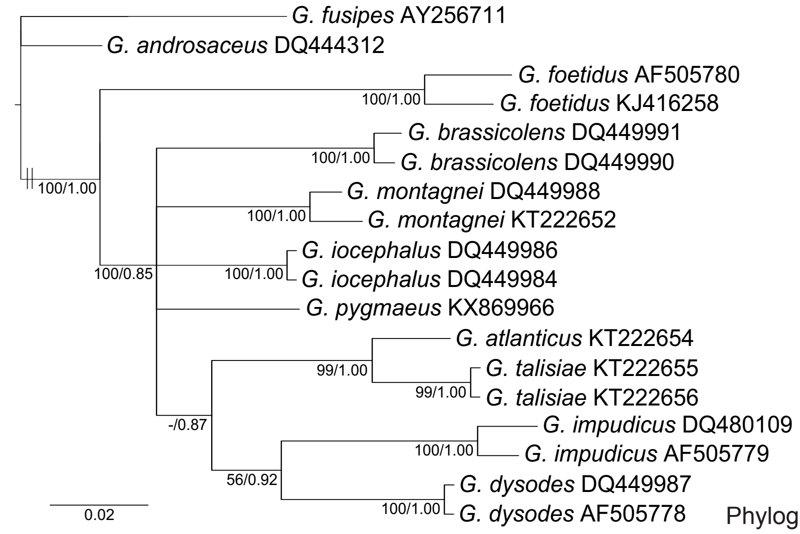
Basidiomata collybioid, gregarious. *Pileus* 4–9 mm diam, plane-convex to plane, smooth, hygrophanous, greyish orange (5B2/3, 6B3/4/5), becoming light orange (6A5), orange (6A6) to brownish orange (6C6) at the disk, margin sulcate. *Lamellae* adnexed to adnate, orange white (5A2, 6A2), close, thin, lamellulae of one length, edge smooth. *Stipe* 4–8 × 0.5–1 mm, cylindrical, central, equal, insititious, finely furfuraceous overall, becoming hirsute at the base (under ×30 lens), greyish orange (5B2/3), solid. *Context* orange white (5A2, 6A2), unchanging. *Odour* not noted. *Taste* not noted. *Basal mycelium* absent. *Basidiospores* 5–6 × 2.5–4 µm (5.3 × 3.2 µm, Q = 1.42–2.00, Q_m = 1.67), broadly ellipsoid, smooth, hyaline, thin-walled. *Basidia* 17–27(–30) × 4–7 µm, clavate, hyaline, thin-walled, 4-sterigmata. *Cheilocystidia* inconspicuous. *Pleurocystidia* absent. *Pileipellis* a cutis made of smooth to usually poorly diverticulate hyphae of 4–7 µm, with weak and yellowish encrusted pigment, hyaline, thin-walled. *Caulocystidia* 48–107(–140) × 5–7 µm, narrowly cylindrical to flexuous, rarely lobate, smooth, hyaline, thin-walled. *Lamellae trama* regular, made of cylindrical hyphae of 3–8 µm, hyaline, thin-walled. *Clamp-connections* present.

Typus. BRAZIL, Amapá, Porto Grande, Floresta Estadual do Amapá, on dead leaves and sticks, 4 Feb. 2014, *V.R.M. Coimbra* VRMC 89 (holotype URM 90003, ITS sequence GenBank KX869966, LSU sequence GenBank KY088273, MycoBank MB818634).

Notes — *Gymnopus pygmaeus* is found in the Brazilian Amazon, mainly characterised by its orange coloured and small basidiomata, insititious stipe, small basidiospores, inconspicuous cheilocystidia and a pileipellis mostly composed of poorly diverticulate hyphae.

Phylogenetic analyses were performed using the obtained ITS sequence of the holotype of *G. pygmaeus* (KX869966) and 17 sequences downloaded from GenBank. Both the Maximum Likelihood and Bayesian analyses placed *G. pygmaeus* with members of *Gymnopus* sect. *Impudicae* in a strongly supported clade (100/1.00), and equivalent to the clade /impudicae (Coimbra et al. 2015). Despite of its negligible smell and pileipellis as a cutis made of smooth to poorly diverticulate hyphae, in contrast to the diagnostic features of that section (Antonín & Noordeloos 2010), the phylogenetic data suggest the placement of *G. pygmaeus* within *Gymnopus* sect. *Impudicae*.

Other species in the section that are characterised by having small basidiomata are *G. bisporiger* and *G. montagnei* (Antonín & Noordeloos 2010, Coimbra et al. 2015). The former, known only to the Netherlands, differs from *G. pygmaeus* by having larger basidiospores (7–8.5 × 4–5 µm), mostly 2-spored basidia, the pileipellis a thick ixocutis with nodulose hyphae and absence of clamp-connections (Antonín & Noordeloos 2010). *Gymnopus montagnei* is widely distributed in the Neotropics and differs from *G. pygmaeus* mainly by its conical to goblet-like basidiomata with a hard consistency, hymenium lacking true lamellae, inconspicuous basidia and a pileipellis resembling a trichoderm, made of strongly diverticulate and coralloid terminal cells (Coimbra et al. 2015).



Phylogenetic tree topology derived from a Bayesian analysis, based on ITS rDNA (ITS1-5.8S-ITS2) sequence data. The Maximum Likelihood (ML) analysis was performed using PAUP v. 4.0b10 (Swofford 2003), for 1 000 generations under the TrN+G model. The Bayesian analysis (BA) was run on TOPALi v. 2 (Milne et al. 2009) under the HKY+G model, for 5 M generations. Bootstrap support and Bayesian Posterior Probability values are presented as ML/BA to the left of nodes.

Colour illustrations. Floresta Estadual do Amapá, Porto Grande, Brazil; basidiomata growing on wood stick, basidium, caulocystidia, basidiospores in mass. Scale bars = 10 mm (for basidiomata) and 10 µm (for microstructures).

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Cyathus ibericus
a
b
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Fungal Planet 494 – 21 December 2016

Cyathus ibericus J.C. Zamora & Poveda-Molero, *sp. nov.*

Etymology. Adjectival epithet meaning 'from *Iberia*', referring to the Iberian Peninsula, the geographical area where the species has been found.

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

Basidiomata clavate when young, obconic to infundibuliform after opening, 2.5–5.5(–7) mm high × 2.5–5(–5.5) mm wide at the top; sides more or less straight in side view, margin straight or slightly flaring out. *Base* gradually to abruptly attenuated, but normally not forming a true stalk. *Peridium* 3-layered; external peridium shaggy/woolly to hairy, whitish to pale brownish grey; internal peridium without plications, smooth to slightly cracked near the margin, brownish grey to dark brown. *Epifragm* membranaceous, whitish to pale cream, cracking during the maturation process and persisting as small fragments on some peridioles and around the inner margin of the peridium. *Peridioles* 0.8–1.2 mm diam, rounded to slightly angular, with clearly convex sides, dark brownish grey to blackish (often slightly darker than the internal peridium); cortex single-layered, but with some differentiation between the internal (more prosoplectenchymatous) and the external (more paraplectenchymatous) parts; tunica present, often inconspicuous. *Basidiospores* hyaline, thick-walled, ovoid, 7–9 × 5–6 µm; hilar appendix often visible.

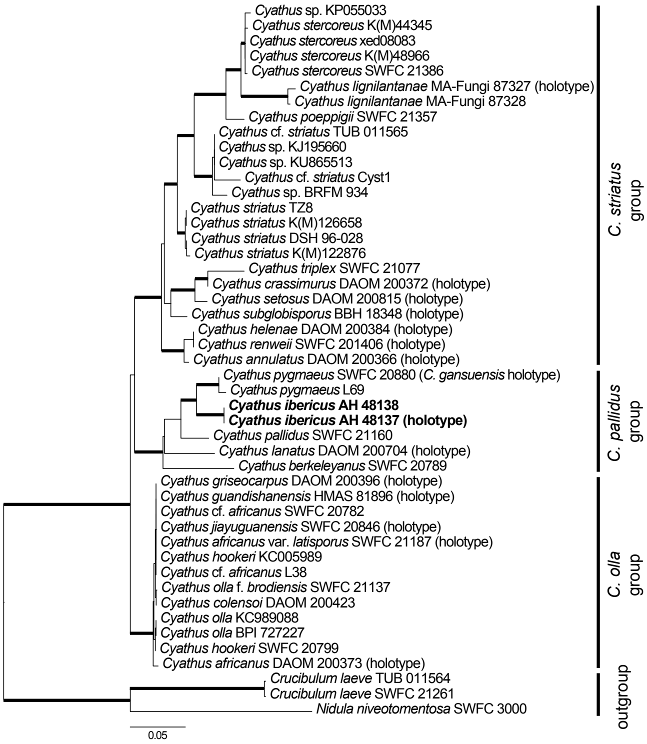
Ecology & Distribution — Saprotrophic on lignified small fragments (small branches, parts of cones) of *Pinus halepensis*, but probably also on other woody substrates such as dead branches of *Rhamnus lycioides*. Known from few localities in the Thermomediterranean area of the Eastern and South-eastern Iberian Peninsula, which belong to the 'Iberian sclerophyllous and semi-deciduous forests' ecoregion of the 'Mediterranean forests, woodlands and scrub' biome (Olson et al. 2001).

Typus. Spain, Comunidad Valenciana, Valencia, Riba-roja de Túria, La Vallesa de Mandor, on small fallen branches and semidecomposed cones of *Pinus halepensis* (*Pinaceae*), 25 Oct. 2015, *J.C. Poveda* (holotype AH 48137, isotypes in MA-Fungi and UPS, ITS and LSU sequence GenBank KX858597, MycoBank MB818296).

Additional specimens examined. Spain, Comunidad Valenciana, Valencia, Riba-roja de Túria, on small fallen branches and semidecomposed cones of *Pinus halepensis*, Apr. 2010, *J.C. Poveda*, AH 48138, ITS sequence GenBank KX858598; La Vallesa de Mandor, on small fallen branches of *Pinus halepensis*, Oct. 2015, *J.C. Poveda*, AH 48139.

Notes — This species was first published as *Cyathus pygmaeus* based on a single basidioma (Honrubia et al. 1982), and kept as such in the Iberian revision of epigaean gasteroid fungi performed by Calonge (1998). No more published records are known, so the species seems to be very rare. Fortunately, some rich collections have been gathered during the last years (more than 100 basidiomata are present in the type collection), allowing a detailed study of the intraspecific variation and the diagnostic characters. Following Brodie (1966, 1975, 1977, 1984) and Zhao et al. (2006), *C. pygmaeus* is indeed the morphologically and phylogenetically closest species, but can be readily separated by the clearly larger basidiospores (7–9 × 5–6 µm in *C. ibericus* vs 10–15 × 7–12 µm in *C. pygmaeus*); in addition, the cortex is uniform in section, the external peridium is tomentose-woolly instead of shaggy-hairy, the internal peridium is often slightly darker than the peridioles (the opposite in *C. ibericus*), the margin tends to be more conspicuously flaring out, and has not been found in the Mediterranean biome. Both taxa belong to the *C. pallidus* group ('*pallidum* group' of Zhao et al. 2007, see included phylogenetic tree). Indeed, *C. pallidus* is another morphologically close species. This taxon differs by the slightly larger and more ellipsoid basidiospores (8–15 × 4–8 µm), cortex more uniform in section, paler and bigger basidiomata (5–6 mm diam), and external peridium with tufts of hairs oriented downwards (Brodie 1977). Furthermore, *C. pygmaeus* and *C. pallidus* are phylogenetically well-separated from the new *C. ibericus* based on ITS and nrLSU molecular data (see included phylogenetic tree).

Colour illustrations. *Pinus halepensis* forest in the type locality; a: mature basidiomata; b, c. detail of the external peridium; d. thin section of a peridiolum; e. detail of the peridiolum wall with a fragment of the tunica; f–h. basidiospores. Scale bars: a = 5 mm; b, c = 1 mm; d, e = 100 µm; f–h = 5 µm.



Maximum likelihood (ML) phylogenetic tree of the genus *Cyathus*, based on an alignment of ITS1, 5.8S nrDNA, ITS2, and first part of the nrLSU (TreeBASE S19862). Statistical support was assessed by non-parametric bootstrapping for ML analysis (bs, following Zamora et al. 2014) and additionally by the posterior probability (pp) of a Bayesian analysis (according to Zamora et al. 2015, but using model jumping as indicated in Ronquist et al. 2012). Thickened branches received > 70 % bs and > 0.95 pp.

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Cercophora squamulosa

Fungal Planet 495 – 21 December 2016

Cercophora squamulosa A.N. Mill., J. Fourn., Raja & Lechat, *sp. nov.*

Etymology. The specific epithet refers to the ascomatal vestiture.

Classification — *Lasiosphaeriaceae*, *Sordariales*, *Sordariomycetes*.

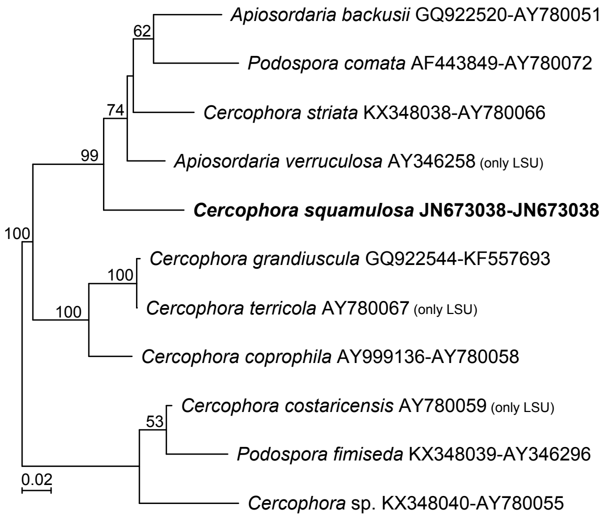
Ascomata subglobose to obpyriform with a conical neck, 320–500 µm diam × 390–580 µm high, superficial, clustered in small groups, at times in contact, young ascomata with white hyphae radiating from the lower part of ascomata, covering the ascomata and becoming grey with age then wearing away, surface of older ascomata covered with white to greyish granules or crystalline flakes below the neck, most noticeable upon drying, sometimes laterally collapsed; neck papillate, broadly conical to bluntly rounded, 60–200 µm high, ostiolate, black, slightly sulcate or roughened, at times not clearly differentiated from the venter. *Ascomatal wall* 40–50 µm thick, upper part 10–24 µm thick, covered by a fugacious pseudoparenchymatous tissue of *textura angularis*, composed of hyaline thin-walled cells, sloughing off into greyish flakes, base 30–120 µm thick, embedded in a dense prosenchymatous tissue of *textura intricata*, composed of olivaceous brown hyphae 2–4 µm wide, areolate in surface view, roughened, black, pseudoparenchymatous, 3-layered: outermost layer 15–20 µm thick, composed of patches of dark brown, entirely melanised cells separated by hyaline thin-walled cells; middle layer 15–20 µm thick, composed of hyaline thin-walled cells interspersed with dark brown opaque hyphae 1.5–2 µm wide; inner layer 10–15 µm thick, composed of flattened, thin-walled hyaline to pale brown cells. *Ascomatal apex* periphysate, wall entirely melanised. *Centrum* hyaline. *Paraphyses* filiform, 2.5–7 µm wide, tapering above asci, hyaline, thin-walled, abundant, septate, slightly constricted at the refractive septa, unbranched, persistent. *Asci* unitunicate, cylindrical becoming slightly fusiform, 280–360 × 10–13 µm, apex rounded, long-stipitate, with eight bi- to triseriate ascospores, apical ring refractive, 4.5–5 µm wide × 0.5 µm high, inamyloid, subapical globule absent. *Ascospores* cylindrical, 50–80 × 4–6 µm, sigmoid, geniculate in lower quarter, hyaline, aseptate, guttulate; bipolar appendages 30–50 µm long, lash-like, centrally attached on ascospores ends, fragile; ascospore becoming differentiated into an apical swollen head and a basal tail while inside the ascus; head ellipsoid, 17–21 × 8–10 µm, hyaline, rarely pigmented, pale brown; tail 30–43 × 4–6 µm, 0–4-septate, hyaline, rarely pigmented, pale brown.

Culture characteristics — Colonies (of holotype) moderately fast-growing on all media, covering the PDA and WA plates in 14 d and the CMA plate in 21 d, downy to silky on all media, appressed, hyaline on WA and CMA, brown (5F8) at centre, becoming olive brown (4E8) towards margin on PDA; margin even, appressed, hyaline on all media; reverse same as the mat. *Asexual morph*: Hyphae largely undifferentiated, 2–3 µm wide, thin-walled, hyaline to pale brown. *Conidiogenous cells* phialides, commonly produced from hyphae as single terminal or several lateral phialides, delimited by a basal septum, mono- or polyphialidic, cylindrical to lageniform, 7–12 × 1.5–4 µm at widest part, hyaline to pale brown, constricted below the collarette, 1–1.5 µm just below the collarette; collarette short, slightly flaring, inconspicuous, same colour as phialide. *Conidia* subglobose to pyriform, truncate at base, 2–2.5 × 2.5–3 µm, hyaline to pale greenish brown.

Typus. France, Ariège, Clermont, Le Pujol stream, along road D 119, c. 360 m elev., on submerged wood, 31 July 2009, incubated in moist chamber until 11 Aug. 2009, *J. Fournier*, JF 09214 (holotype ILLS 79803, cultures ex-type ANM Acc#323-1 = CBS 125293, ITS-LSU sequence GenBank JN673038, *mcm7* sequence GenBank JN672980, MycoBank MB817292).

Additional material examined. France, Ariège, Rimont, Peyrau brook, 400 m elev., on driftwood of *Alnus glutinosa* and *Salix* sp. in the bed of the stream, likely long submerged and recently out of the water, 26 July 2006, collected immature and incubated in moist chamber, *J. Fournier* (JF 06159); on *Alnus glutinosa* driftwood, 8 Aug. 2006, *J. Fournier* (JF 06174); on submerged wood of *Alnus glutinosa*, 26 June 2009, *M. Fournier* (JF 09171, ILLS 79954).

Notes — *Cercophora squamulosa* is distinguished by its ascomata that develop whitish flakes with age, cephalothecoid ascomatal wall, asci that lack a subapical globule, long ascospores with long, lash-like appendages, and aquatic habitat. Only one other species in the genus, *C. striata* is known to produce ascomata with whitish flakes (Miller & Huhndorf 2001) and these two species occur in a well-supported clade (see tree) along with two species of *Apiosordaria* and *Podospora comata*. However, *C. striata* is a terrestrial taxon that is only known from the tropics and possesses a striate neck but lacks a subiculum. A typical phialophora-like asexual morph was produced in culture (JF 09214; CBS 125293).



Maximum likelihood tree generated using PhyML in Seaview v. 4.5.4 (Gouy et al. 2010). *Cercophora squamulosa* is in **bold**. Numbers above branches refer to bootstrap support values. GenBank accession numbers for the ITS and LSU regions are given after taxon names.

Colour illustrations. Background photo of Peyrau stream in the Ariège region of south-western France; ascomata, longitudinal section through ascoma, longitudinal section through ascomal wall, squash mount of ascomal wall, ascospore, and phialides. Photos: Jacques Fournier, Huzefa Raja, Andrew Miller and Christian Lechat. Scale bars: 500 µm (ascomata), 100 µm (ascomal section), 10 µm (all others).

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Fusicolla melogrammae

Fungal Planet 496 – 21 December 2016

Fusicolla melogrammae Lechat & Aplin, *sp. nov.*

Etymology. The epithet refers to the host fungus *Melogramma*.

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

Diagnosis — Differs from *Fusicolla matuoi* in having larger ascomata turning orange in lactic acid, larger ascospores, asexual morph with smaller macroconidia and its occurrence on *Melogramma campylosporum*.

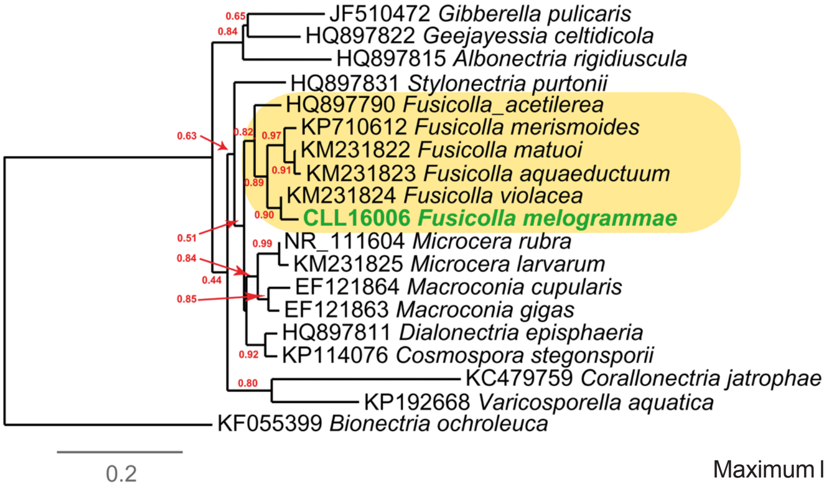
Ascomata perithecial, superficial, solitary or in groups of 2–4, crowded on host surface or sometimes on bark around stromata, with base remaining slightly immersed in substratum, nonstromatic, obpyriform, (230–)250–290(–300) µm high × (190–)220–250(–260) µm diam (av. = 280 × 245 µm, n = 10), uniloculate, smooth, pale yellow to pale orange, laterally collapsing when dry, not changing colour in 3 % KOH, but turning orange in lactic acid, with a broadly conical, rounded apex 40–60 µm high, 60–80 µm diam at base, composed of cylindrical, pale yellow cells narrowly clavate at tip. Perithecial surface cells forming a *textura angularis* in surface view with cells up to 20 µm in greatest dimension, covered by thick-walled (1.5 µm), hyphal elements arising from base of perithecium, pale yellow, aseptate, 5–6 µm diam, rounded at free end, developing to form a crown around ostiolar region, thick-walled (0.6–1.2 µm), cylindrical, pale yellow, aseptate, 3–4.5 µm diam, rounded at tip. *Ascomatal wall* 20–25 µm thick, composed of a single region of globose to ellipsoidal cells 4–10 × 2.5–4.5 µm with very pale orange wall 1–2 µm thick, becoming flattened and hyaline inwardly. *Asci* unitunicate, shortly stipitate (60–)70–80(–85) × (9–)10–12(–14) µm (av. = 76.5 × 11.5 µm, n = 20), cylindrical to narrowly clavate, with eight obliquely uniseriate ascospores, apically truncate when immature, becoming rounded when mature, with a faint apical ring-like thickening, interspersed with early deliquescing, slightly moniliform paraphyses 6–8 µm wide at base. *Ascospores* ellipsoidal, rounded at ends, 1-septate, (10–)12–14(–15) × 4.5–5(–5.5) µm (av. = 13 × 5 µm, n = 30), hyaline to pale golden brown when mature, slightly constricted at septum, spinulose. *Asexual morph* fusarium-like.

Culture characteristics — After 2 wk on 2 % PDA with 5 mg/L streptomycin: colony reaching 12–15 mm diam, slimy, aerial hyphae rare to absent, white to cream in centre; middle area orange with carmine, radiating strands; white at margin, producing a fast growing fusarium-like asexual morph. No microconidia produced; macroconidia hyaline, smooth, (0–)1–3-septate, long-fusiform, falcate, acute at both ends; 8–22 × 2–3.5 µm when 0–1-septate, (25–)30–38(–44) × (4–)4.5–5.5 µm when 3-septate.

Typus. UK, West Sussex, River Mole Woodland, near Gatwick Airport, on dead stromata of *Melogramma campylosporum* on bark of *Carpinus betulus*, 24 Jan. 2016, *N. Aplin* (CLL16006, holotype LIP, ex-type culture CBS 141092, ITS sequence GenBank KX897140, LSU sequence GenBank KX897141, MycoBank MB818573).

Additional material examined. France, Peyrau, Rimont (09), on *Melogramma campylosporum* on bark of *Corylus avellana*, 29 Nov. 2011, leg. J. Fournier JF11178 (LIP).

Notes — The placement of this species in the *Nectriaceae* is confirmed by phylogenetic comparison of its ITS sequence with those of 10 other nectriaceous species (included phylogeny) having a fusarium-like asexual morph. As *Fusicolla* features ascomata with hairs around the ostiolar region, an ascomatal wall less than 25 µm thick of a single region composed of thick-walled cells not changing colour in 3 % KOH, it appeared to closely resemble *Nectriopsis*. However, *Nectriopsis* belongs to the *Bionectriaceae*.



Colour illustrations. UK, West Sussex, River Mole Woodland, near Gatwick Airport, where the sample was collected; ascomata on host substratum, vertical section through lateral, ascomatal wall, asci and ascospores. Scale bars = 200, 10 and 10 µm.

Maximum likelihood phylogeny of *Fusicolla* inferred from ITS sequences, rooted with *Bionectria ochroleuca*. Analysis performed online at www.phylogeny.fr (alignments edited with GBlocks v. 0.91b), run in PhyML v. 3.0aLRT using the GRT+I+Γ model. Branch supports assessed by the SH-aLRT statistical test. The novel species described here is highlighted in green text.

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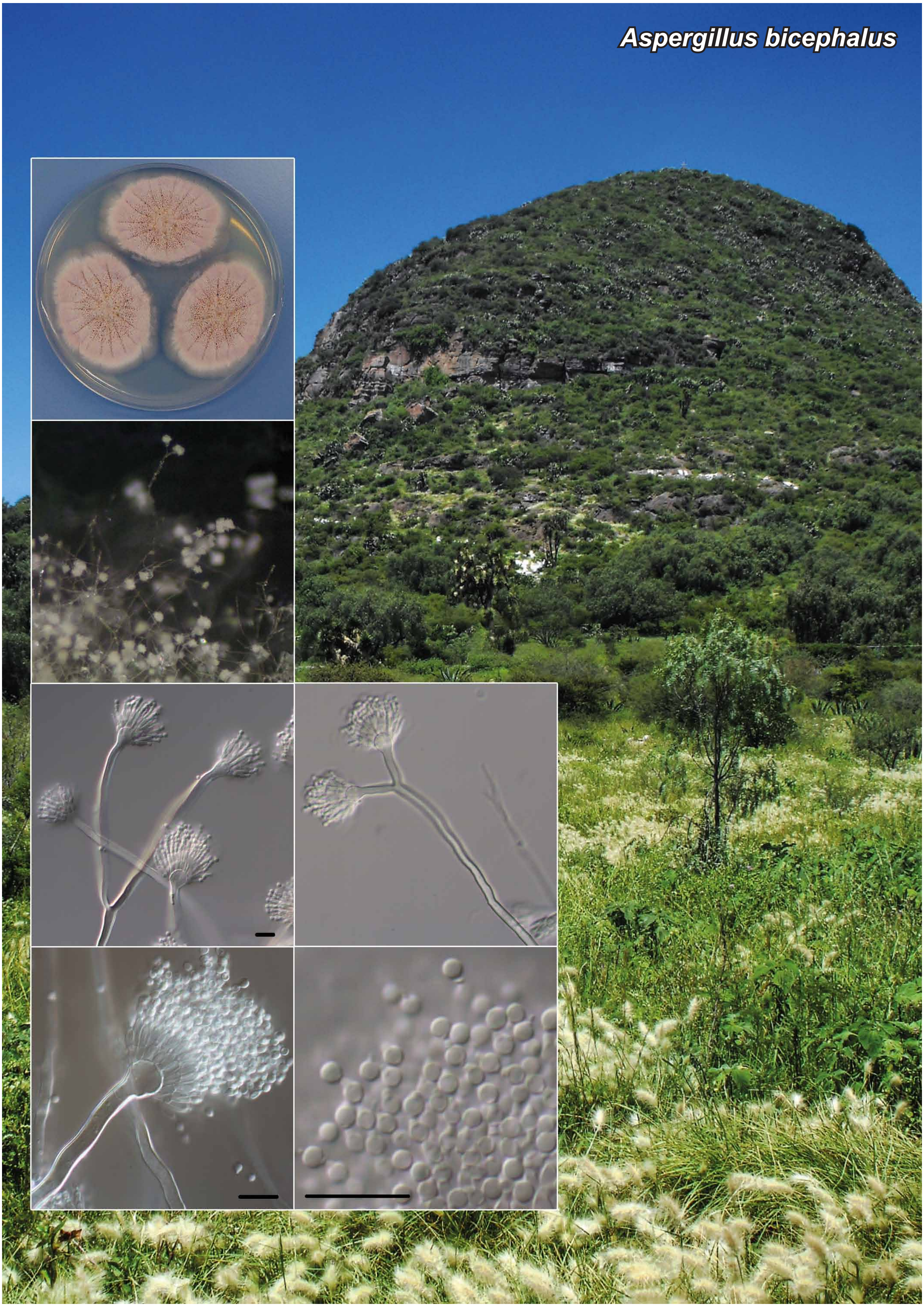

Aspergillus bicephalus

Fungal Planet 497 – 21 December 2016

Aspergillus bicephalus J.P.Z. Siqueira, Gené & Guarro, *sp. nov.*

Etymology. Name refers to the production of conidiophores with two conidial heads.

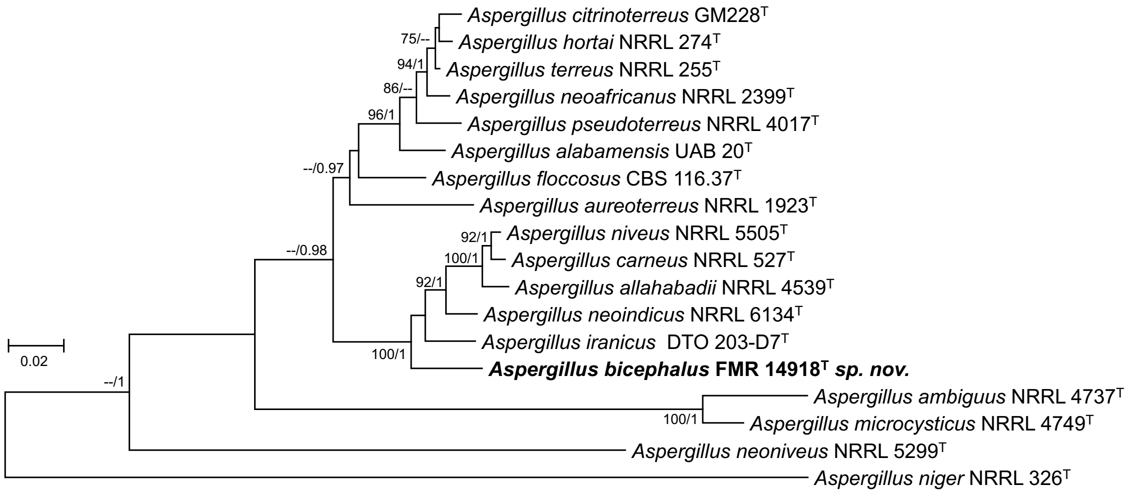
Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetes*.

Conidiophores on MEA hyaline, septate, smooth, thick-walled, often bifurcately branched, producing a terminal conidial head on each branch, 300–950 × 3–9.5 µm. *Conidial heads* columnar, biseriate. *Vesicles* subglobose or pyriform, 8–12 µm wide. *Metulae* cylindrical, covering about 2/3 of the vesicle, 3.5–6.5 × 2–3 µm. *Phialides* ampulliform, 5–8.5 × 2–3 µm. *Conidia* globose to ellipsoidal, hyaline, smooth-walled, 2–2.5 × 1.5–2.5 µm.

Culture characteristics — (in the dark, at 25 °C after 7 d): Colonies on CYA attaining 28–31 mm diam, colony texture velvety to powdery with a floccose centre, sulcate, sporulation strong with conidial mass reddish white (8A2) (Kornerup & Wanscher 1978); reverse light yellow (4A4); exudate colourless; soluble pigments absent. On MEA reaching 20–24 mm diam, velvety to densely floccose, with an elevated centre, sporulation strong with conidial mass reddish white (8A2) to pale red (7A3), mycelium white to yellowish white (4A2) towards the periphery; reverse yellowish white (4A2) to light yellow (4A4); exudate colourless; soluble pigments absent. On YES reaching 32–34 mm diam, velvety to floccose with elevated centre, sulcate, conidial mass white to reddish white (8A2); reverse light yellow (4A4) to greyish yellow (4B4); exudate absent; soluble pigments absent. On OA reaching 19–20 mm diam, colony texture powdery to slightly granular, strong sporulation in centre, conidial mass white; reverse colourless; exudate absent; soluble pigments absent. On CREA, 18–19 mm diam, velvety to powdery, strong sporulation in the centre with conidial mass pale red (9A3), white towards the periphery; acid production absent, even after 14 d. Colonies, mainly on MEA, CYA and YES showing darker shades of rose (11A3 to 11A5) after 14 d. On CYA after 7 d, the colonies reached up to 7.5 mm diam at 15 °C, 44–45 mm diam at 30 °C, 44–47 mm diam at 37 °C, and 32–37 mm diam at 40 °C; growth absent at 45 °C.

Typus. Mexico, Ecatepec de Morelos, from soil, June 2015, coll. *E. Rosas*, isol. *J. Siqueira* (holotype CBS H-22807, culture ex-type FMR 14918; DNA barcode: ITS LT601380 (other barcodes: LSU LT630488; β-tubulin (*BenA*) LT601381; calmodulin (*CaM*) LT601382; RNA polymerase II second largest subunit gene (*RPB2*) sequence LT601383, MycoBank MB818290).

Notes — A BLAST search of the GenBank nucleotide database shows that the sequences of *A. bicephalus* are unique for all the tested markers and confirms that it belongs to *Aspergillus* sect. *Terrei*. This species is clearly differentiated from the others of the section by its bifurcate conidiophores with a terminal conidial head on each branch and by the reddish colour of the conidial mass. *Aspergillus carneus*, a species of the section with similar macroscopic features, has paler colonies, and its vesicles and conidia are slightly larger (9–15 µm wide and 2.5–3 µm diam, respectively) (Klich 2002). The closest phylogenetically related species are *A. iranicus* and *A. neoindicus*. However, the former has white colonies which change to peach after 3 wk and produces accessory conidia (Arzanlou et al. 2016), and the latter species has colonies with yellow-green mycelial tufts and conidiophores with spatulate vesicles (Samson et al. 2011).



Colour illustrations. Hill of Ecatepec de Morelos, Mexico State (available at https://www.flickr.com/photos/13383617@N05); 14-d-old colony on CYA showing the characteristic colours of the mature conidial heads, closer look of the conidial heads, detailed conidiophores showing the bifurcation to form two conidial heads, conidia. Scale bars = 10 µm.

Maximum Likelihood tree inferred from the combined ITS, *BenA* and *CaM* regions from all the type strains (^{T}) of the species currently accepted in *Aspergillus* sect. *Terrei*, rooted to *Aspergillus niger* NRRL 326 (section *Nigri*). Maximum likelihood bootstrap support values ≥ 70 % (MEGA v. 6) and Bayesian posterior probabilities ≥ 0.95 (MrBayes v. 3.1.2) are displayed at the nodes. The novel species is indicated in **bold** face.

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Aplosporella sophorae

Fungal Planet 498 – 21 December 2016

Aplosporella sophorae Crous & Thangavel, *sp. nov.*

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

Classification — *Aplosporellaceae*, *Botryosphaeriales*, *Dothideomycetes.*

Conidiomata solitary, erumpent, globose, 200–250 µm diam, dark brown, exuding a black conidial mass; ostiole central, wall of 3–6 layers of brown *textura angularis*. *Paraphyses* intermingled among conidiophores, hyaline, smooth, aseptate, 25–80 × 2–3 µm. *Conidiophores* reduced to conidiogenous cells, doliiform, hyaline, smooth, with inconspicuous percurrent proliferation at apex, 10–15 × 10–12 µm. *Conidia* solitary, aseptate, ellipsoid to subcylindrical, straight, rarely slightly curved, apex and base obtusely rounded, verruculose, guttulate, hyaline, becoming honey-brown, eventually dark brown, 18–20(–30) × 8–9(–13) µm.

Culture characteristics — Colonies covering dish in 2 wk at 25 °C, with fluffy aerial mycelium and feathery margins. On MEA surface pale olivaceous grey, reverse umber, on PDA surface and reverse grey olivaceous, on OA surface olivaceous grey.

Typus. New Zealand, Okoia, Whanganui, on *Sophora microphylla* (*Fabaceae*), 2015, *R. Thangavel* (holotype CBS H-22858, culture ex-type CPC 29688 = CBS 142061; ITS sequence GenBank KY173388, LSU sequence GenBank KY173482, MycoBank MB819050).

Notes — Species of *Aplosporella* are commonly associated with cankers on twigs of woody plants (Damm et al. 2007, Trakunyingcharoen et al. 2015). The genus accommodates multilocular pycnidial coelomycetous fungi with hyaline paraphyses, and phialides with percurrent proliferation giving rise to brown, aseptate conidia that become thick-walled and verruculose (Sutton 1980). Slippers et al. (2013) placed *Aplosporella* in its own family, *Aplosporellaceae*, together with its purported sexual morph, *Bagnisiella*. The first confirmed sexual link was published by Ekanayaka et al. (2016), suggesting that *Bagnisiella* may be a synonym of *Aplosporella* as suggested by Slippers et al. (2013). *Aplosporella sophorae* is phylogenetically closely related to *A. africana*, from which it can easily be distinguished based on the smaller conidia in the latter species, 10.5–19 × 5.5–13 µm (Slippers et al. 2014). Our ITS sequence is identical to an unpublished sequence (GenBank EU931111) from dead wood in New Zealand, published as '*Aplosporella* sp.'. The closest known species is *A. africana* (GenBank KF766196; Identities = 584/588 (99 %), Gaps = 2/588 (0 %)), followed by *A. prunicola* (GenBank KF766147; Identities = 573/587 (98 %), Gaps = 9/587 (1 %)).

Colour illustrations. *Sophora microphylla* (image credit Peter Grant); conidioma sporulating on PNA, conidiophores and conidia. Scale bars = 10 µm.

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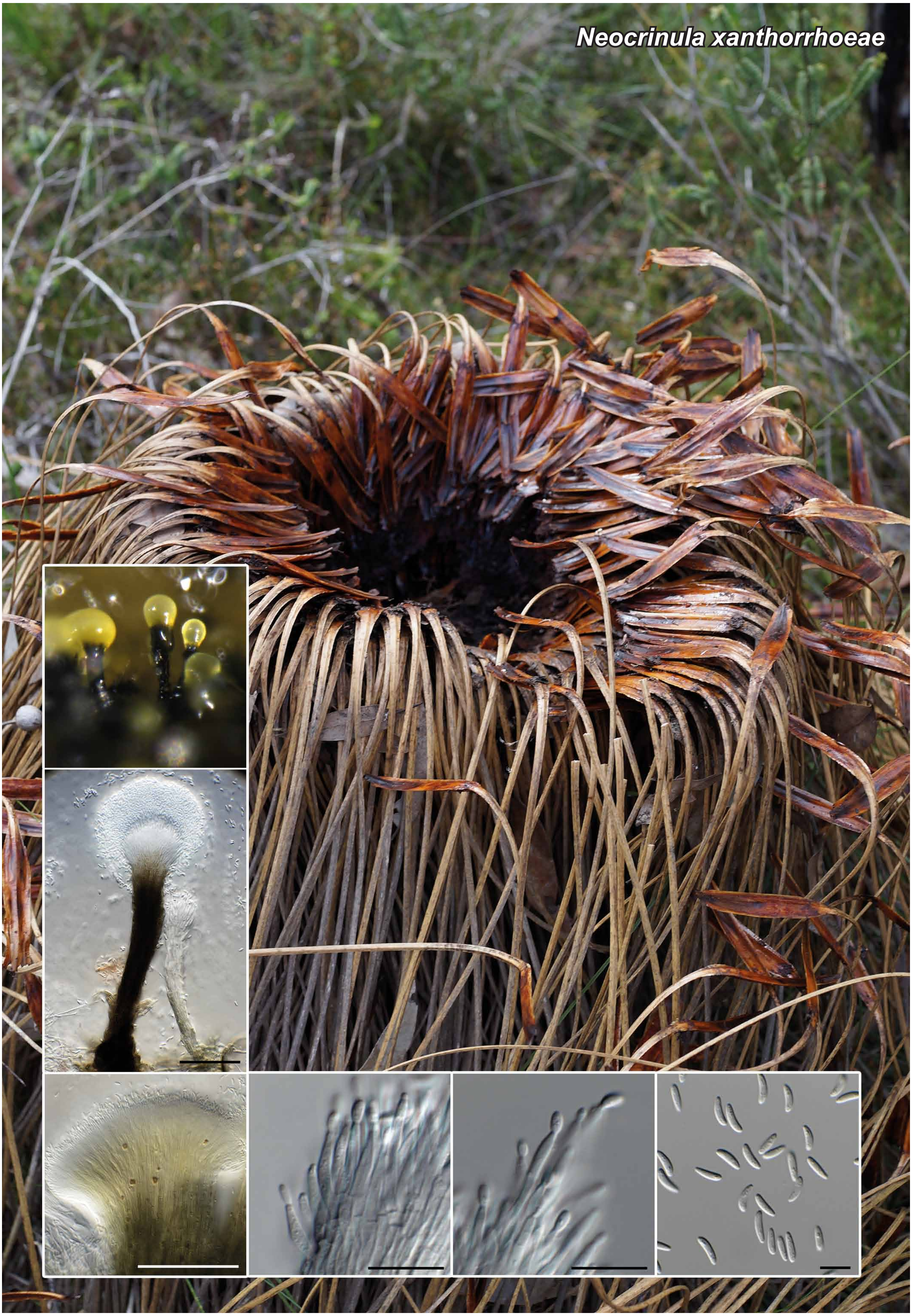
Neocrinula xanthorrhoeae

Fungal Planet 499 – 21 December 2016

Neocrinula Crous, *gen. nov.*

Etymology. Name reflects its morphological similarity to the genus *Crinula.*

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

Mycelium consisting of septate, branched, smooth, hyaline to verruculose, brown, hyphae, giving rise to erect synnemata. *Synnemata* solitary or in a cluster, erect, straight, with flared apex, brown; stalk consisting of numerous brown, septate, verruculose hyphae that form a flared conidiogenous apparatus at the apex, pale brown, becoming hyaline at conidiogenous region. *Conidiogenous cells* terminal and intercalary on subapical cell, subcylindrical, hyaline, smooth, phialidic. *Conidia* solitary, aseptate, hyaline, smooth, fusoid-ellipsoid, inequilaterally curved, apex subobtuse, base truncate.

Type species. *Neocrinula xanthorrhoeae* Crous.
MycoBank MB819051.

Neocrinula xanthorrhoeae Crous, *sp. nov.*

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

Mycelium consisting of septate, branched, smooth, hyaline to verruculose, brown, 2–3 µm diam hyphae, giving rise to erect synnemata. *Synnemata* solitary or in a cluster, erect, straight, with flared apex, brown, 180–300 × 15–50 µm; stalk consisting of numerous brown, septate, verruculose hyphae that form a flared conidiogenous apparatus at the apex, pale brown, becoming hyaline at conidiogenous region, 40–150 µm diam. *Conidiogenous cells* terminal and intercalary on subapical cell, subcylindrical, hyaline, smooth, phialidic, 5–15 × 1–2.5 µm. *Conidia* solitary, hyaline, smooth, fusoid-ellipsoid, inequilaterally curved, apex subobtuse, base truncate, 0.5 µm diam, aseptate, (4–)6–7(–8) × (1.5–)2 µm.

Culture characteristics — Colonies flat, spreading, somewhat erumpent on MEA, with sparse to moderate aerial mycelium and smooth, lobate margins. On PDA surface and reverse olivaceous grey, on MEA surface olivaceous grey, reverse pale olivaceous grey, on OA surface iron-grey.

Typus. Australia, Western Australia, Denmark, Mount Lindesay Walk Trail, on *Xanthorrhoea* sp. (*Xanthorrhoeaceae*), 19 Sept. 2015, *P.W. Crous* (holotype CBS H-22859, culture ex-type CPC 29474 = CBS 142136; ITS sequence GenBank KY173412, LSU sequence GenBank KY173503, MycoBank MB819052).

Additional specimen studied. Australia, Western Australia, Denmark, Mount Lindesay Walk Trail, on *Xanthorrhoea* sp., 19 Sept. 2015, *P.W. Crous*, CPC 29842 = CBS 142062, CPC 29845 = CBS 142063; ITS sequences GenBank KY173413–KY173414, LSU sequences GenBank KY173504–KY173505.

Colour illustrations. *Xanthorrhoea* sp.; synnemata sporulating on PNA, synnemata, conidiogenous cells and conidia. Scale bars = 50 and 100 µm (synnemata), 10 µm (other structures).

Notes — The genus *Holwaya* is congeneric with *Crinula* (its synnematous hyphomycetous asexual morph), and is the name to be used for this holomorph (Johnston et al. 2014). *Neocrinula* resembles *Crinula* in general morphology, but is phylogenetically distinct. *Neocrinula xanthorrhoeae* commonly occurs on *Xanthorrhoea*, which is phylogenetically distant from *Holwaya mucida* (= *Crinula caliciiformis*) (Seifert & Okada 1990). A megablast search of NCBIs GenBank nucleotide database with our ex-type strain ITS sequence did not provide a better match than 90 % with species in the *Helotiales*. A blast2 comparison between our sequence and the only available *Holwaya* sequence identified to species level on GenBank (*H. mucida*, GenBank DQ257357) revealed a similarity of 86 % (478/557, Gaps = 24/557 (4 %)). Likewise, a comparison with the only ITS sequence deposited under the name *Crinula* (*C. caliciiformis*; GenBank KT225524) revealed a similarity of 84 % (429/508, Gaps = 24/508 (4 %)). GenBank accessions DQ257357 and KT225524 are identical (492/492, no gaps). The best similarity obtained from a megablast search with the type strain LSU sequence was 95 % with *Encoeliopsis rhododendri* (GenBank KX090801; 782/826, Gaps = 13/826 (1 %)) and *H. mucida* (GenBank DQ257357; 775/820, Gaps = 9/820 (1 %)).

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Beltraniella acaciae

Fungal Planet 500 – 21 December 2016

Beltraniella acaciae Crous, *sp. nov.*

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

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

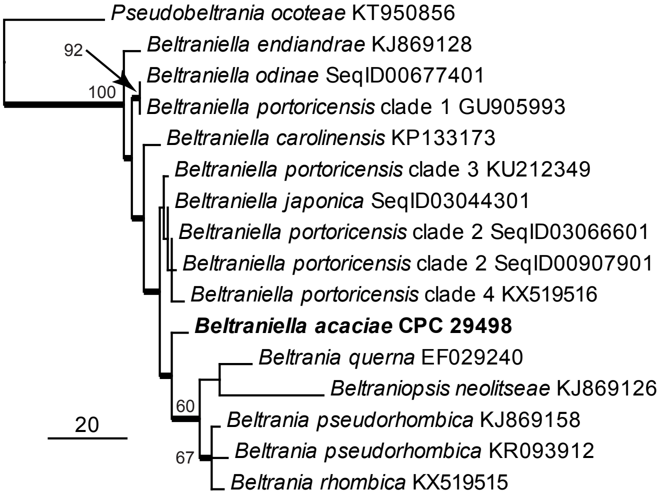
Conidiophores erect, medium brown, smooth, multiseptate, flexuous, branched at apex, very long in culture. *Setae* erect, dark brown, thick-walled, indistinctly septate, with prominent warts, straight, becoming flexuous when longer, tapering to an acute apex, 120–350 × 4–10 µm, with radially lobed basal foot cell, 16–30 µm diam. *Conidiogenous cells* subcylindrical, terminal and intercalary, 6–20 × 4–6 µm, pale brown, smooth, polyblastic, with several flat-tipped denticles, 1 × 1 µm, separating cells subhyaline, smooth, 7–11 × 3–4 µm, with a single flat-tipped denticle, 1 × 1 µm. *Conidia* solitary, turbinate to pyriform, distal end truncate, subhyaline, smooth, aseptate, with median transverse band of lighter pigment, (18–)20–22(–24) × (5–)6(–6.5) µm, apical appendage tapering to an acutely rounded tip.

Culture characteristics — Colonies covering dish after 2 wk at 25 °C, with sparse aerial mycelium and smooth, even margins. On MEA, OA and PDA surface and reverse fuscous black.

Typus. USA, Hawaii, Oahu, on leaves of *Acacia koa* (*Fabaceae*), 30 Sept. 2015, *J.J. Le Roux* (holotype CBS H-22860, culture ex-type CPC 29498 = CBS 142064; ITS sequence GenBank KY173389, LSU sequence GenBank KY173483, MycoBank MB819053).

Colour illustrations. *Acacia koa* in Hawaii; setae, conidiophores and conidia. Scale bars = 10 µm.

Notes — The genus *Beltrania* is characterised by having brown setae with radially lobed basal cells, conidiophores with separating cells, and turbinate to pyriform conidia with a hyaline, transverse band (Ellis 1971, Crous et al. 2014, Rajeshkumar et al. 2016). *Beltraniella acaciae* is allied to the *B. portoricensis* species complex (conidia 20–25(–31) × 5.5–7 µm, see Rajeshkumar et al. 2016), but differs in being phylogenetically distinct. A phylogenetic analysis of our ITS sequence in the dataset of Rajeshkumar et al. (2016) reveals that the species described here is intermediate between *Beltraniella* and *Beltrania*.



The first of 69 equally most parsimonious trees obtained from a heuristic search of a reduced version of the ITS alignment of Rajeshkumar et al. (2016). The analysis was conducted with PAUP* v. 4.0b10 with 100 random taxon additions and 1 000 bootstrap replicates. Bootstrap support values are shown at the nodes and strict consensus branches are thickened. The novel species described here is shown in **bold** face and the scale bar represents the number of changes. The tree was rooted to *Pseudobeltrania ocoteae* (GenBank KT950856).

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Rubikia evansii

Fungal Planet 501 – 21 December 2016

Rubikia evansii Crous, *sp. nov.*

Etymology. Named for Harry C. Evans, who established the genus, and named *R. samsonii* for his colleague, Robert A. Samson.

Classification — *Graphidaceae*, *Ostropales*, *Lecanoromycetes*.

Conidiomata foliicolous, solitary, scattered, immersed, 200–300 µm diam, globose, pycnidial with apical ostiole, black, unilocular, exuding a black conidial mass, ostiole splitting with age, or forming a weakly developed black clypeus at apex; conidiomatal wall of 3–4 layers of hyaline to pale brown, thin-walled *textura angularis*, that give rise to a dense mass of conidiophores. *Conidiophores* hyaline, branched, septate, 1.5–2 µm diam, forming a dense hyphal-like network filling the cavity, forming terminal and lateral conidiogenous cells, 2–10 µm long, with truncate ends, attaching to conidial base, but at times also to one of the central cells. *Conidia* initially hyaline, globose to somewhat globose-ellipsoid in side view, flattened on both sides, coin-shaped when viewed from above, 7–9 µm diam, brown, smooth, central area consisting of a block of four square cells, each cell 3–5 µm tall and broad, surrounded by a layer of 8–10 slightly curved brown cells, 3–5 µm tall, 4–5 µm wide in outer layer, that give the conidia a globose to globose-ellipsoid shape, 16–21 µm diam.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium, and smooth, lobate margin. On MEA surface dirty white with patches of greyish sepia, reverse greyish sepia. On PDA surface and reverse greyish sepia with patches of dirty white. On OA surface ochreous.

Typus. USA, Hawaii, Oahu, on leaves of *Acacia koa* (*Fabaceae*), 30 Sept. 2015, *J.J. Le Roux* (holotype CBS H-22861, culture ex-type CPC 29752 = CBS 142083; ITS sequence GenBank KY173448, LSU sequence GenBank KY173538, MycoBank MB819054).

Additional specimens studied. USA, Hawaii, Oahu, on leaves of *Acacia koa* (*Fabaceae*), 30 Sept. 2015, *J.J. Le Roux*, CPC 29741, 29743, 29744, 29748, 29750; ITS sequences GenBank KY173443–KY173447, LSU sequences GenBank KY173533–KY173537.

Colour illustrations. Conidiomata on leaves of *Acacia koa*; conidiomata sporulating on OA, conidiophores and conidia. Scale bars = 10 µm.

Notes — Evans & Minter (1985) introduced the genus *Rubikia* for a coelomycetous fungus occurring on *Pinus caribaea* needle litter collected in Honduras. *Rubikia evansii* is the third species to be described in the genus, distinguished from *R. samsonii* (conidia 14–16 × 6.5–8 µm) and *R. splendida* (on *Pandanus rigidifolius* in Mauritius, conidia 21–28 × 9.5–12.5 µm; Dulymamode et al. 1998) by its conidial dimensions, being intermediary between the two presently known taxa. The sequences of *R. evensii* represent the first DNA sequences for this genus in the NCBIs nucleotide database. A megablast search of the NCBIs nucleotide database using the type strain ITS sequence gave similarities of less than 87 %; these included *Sarea resinae* (*Lecanoromycetes*, *incertae sedis*; GenBank FJ903329; Identities = 337/391 (86 %), Gaps = 17/391 (4 %)), *Lambiella insularis* (*Lecanoromycetes*, *Ostropomycetidae*, *Trapeliales*, *Trapeliaceae*; GenBank KJ462268; Identities = 365/433 (84 %), Gaps = 26/433 (6 %)) and *Umbilicaria lyngei* (*Lecanoromycetes*, *Umbilicariomycetidae*, *Umbilicariales*, *Umbilicariaceae*; GenBank AF297669; Identities = 364/433 (84 %), Gaps = 23/433 (5 %)). A megablast search of the NCBIs nucleotide database using LSU sequence data for the ex-type strain obtained similarities of maximum 91 %; these included *Schizotrema subzebrinum* (*Lecanoromycetes*, *Ostropomycetidae*, *Ostropales*, *Graphidaceae*; GenBank JX421633; Identities = 701/767 (91 %), Gaps = 3/767 (0 %)), *Furcaspora eucalypti* (*Lecanoromycetes*, *Lecanoromycetidae*, *incertae sedis*; GenBank EF110613; Identities = 751/822 (91 %), Gaps = 6/822 (0 %)), *Reimnitzia santensis* (*Lecanoromycetes*, *Ostropomycetidae*, *Ostropales*, *Graphidaceae*; GenBank JX421620; Identities = 698/769 (91 %), Gaps = 5/769 (0 %)) and *Wirthiotrema glaucopallens* (*Lecanoromycetes*, *Ostropomycetidae*, *Ostropales*, *Graphidaceae*; GenBank KF875536; Identities = 695/767 (91 %), Gaps = 4/767 (0 %)). The results of the LSU megablast searches suggest that this genus is best placed in *Graphidaceae*. However, given the diversity of the results obtained with the ITS megablast it might warrant its own family and order in the OSLEUM clade sensu Miadlikowska et al. (2014).

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Blastacervulus eucalyptorum

Fungal Planet 502 – 21 December 2016

Blastacervulus eucalyptorum Crous, *sp. nov.*

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

Classification — *Asterinaceae*, *Asterinales*, *Dothideomycetes*.

Leaf spots not extending through leaf lamina; circular to subcircular or irregular, 2–8 mm diam, becoming confluent, brown, with red-purple margin. *Conidiomata* acervular, up to 350 µm diam, brown, subcuticular with a single layer of brown epidermal cells; *conidioma* with brown hyphal threads, verruculose, septate, 3–4 µm diam, giving rise to conidia sympodially or percurrently. *Conidia* in a dry powdery mass, globose to ellipsoidal, medium brown, thick-walled, verruculose, guttulate, frequently in chains of two, at times with a thin mucoid sheath, base truncate, unthickened, 2–3 µm diam, apex obtuse, aseptate conidia, 5–6 × 4–5 µm, 1-septate (7–)8–9(–10) × 4–5 µm, 2-septate (10–)12–14(–17) × 4–5 µm.

Culture characteristics — Colonies erumpent with sparse aerial mycelium; slow growing, with uneven margin. On MEA, OA and PDA surface sepia to fuscous black.

Typus. Australia, Western Australia, Kalgan, Gull Rock National Park, S35°00.520 E118°02.329, on leaves of *Eucalyptus adesmophloia* (*Myrtaceae*), 22 Sept. 2015, *P.W. Crous* (holotype CBS H-22862, culture ex-type CPC 29450 = CBS 142065; ITS sequence GenBank KY173390, LSU sequence GenBank KY173484, MycoBank MB819055).

Notes — The genus *Blastacervulus* is monotypic, based on *B. eucalypti* (Swart 1988). *Blastacervulus eucalypti* is closely related to *Aulagraphina eucalypti* and *Alysidiella* species, with all three genera causing 'chocolate spot' disease on *Eucalyptus* (Cheewangkoon et al. 2012). *Blastacervulus eucalyptorum* can be distinguished from *B. eucalypti* (aseptate conidia (4–)6–7(–8) × (4–)5–6 µm) in having larger, 1- and 2-septate conidia (Giraldo et al. in prep.). In addition, the two species are 96 % identical in their ITS sequence (GenBank GQ303271; 764/796, Gaps = 8/796 (1 %)). A megablast search of the NCBIs nucleotide database using the ITS sequence revealed high level of identity with *Blastacervulus eucalypti* (GenBank GQ303271; Identities = 764/796 (96 %), Gaps = 8/796 (1 %)), *Alysidiella suttonii* (GenBank HM628774; Identities = 690/719 (96 %), Gaps = 6/719 (0 %)) and *Aulographina eucalypti* (GenBank HM535599; Identities = 354/370 (96 %), no gaps). A megablast search of the NCBIs nucleotide database using the LSU sequence revealed high identity with *Alysidiella suttonii* (GenBank HM628777; Identities = 795/799 (99 %), no gaps), *Blastacervulus eucalypti* (GenBank GQ303302; Identities = 794/799 (99 %), no gaps) and *Heteroconium eucalypti* (GenBank DQ885893; Identities = 794/800 (99 %), Gaps = 1/800 (0 %)). These genera have long been recorded as *incertae sedis*, but Giraldo et al. (in prep.) showed that they are associated with *Asterinaceae*.

Colour illustrations. Symptomatic leaves of *Eucalyptus decipiens*; leaf spot with conidiomata; conidiophores and conidia. Scale bars = 10 µm.

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Caliciopsis eucalypti

Fungal Planet 503 – 21 December 2016

Caliciopsis eucalypti Crous, *sp. nov.*

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

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

Conidiomata solitary, erumpent, globose, brown, 150–200 µm diam, with central ostiole, exuding a creamy conidial mass; wall of 2–3 layers of brown *textura angularis*. *Conidiophores* lining the inner cavity, at times reduced to conidiogenous cells, ampulliform to doliiform, hyaline, smooth, 4–7 × 3–4 µm, or elongated, branched, 1–4-septate, with terminal, and lateral conidiogenous loci, 10–40 × 2–3 µm. *Conidiogenous cells* subcylindrical, reduced to inconspicuous loci or up to 10 µm long, 2–2.5 µm wide. *Paraphyses* intermingled among conidiophores, hypha-like, hyaline, smooth, septate, 20–30 × 2–3 µm. *Conidia* solitary, hyaline, smooth, bean-shaped, ends obtuse, mostly slightly curved, 3–4 × 1.5 µm.

Culture characteristics — Colonies spreading, with moderate aerial mycelium, folded surface, and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface brown vinaceous with patches of hazel, reverse umber. On PDA surface and reverse umber. On OA surface brown-vinaceous.

Typus. Australia, Western Australia, Albany, Stirling Range National Park, Mt Hassell walk, on leaves of *Eucalyptus marginata* (*Myrtaceae*), 23 Sept. 2015, *P.W. Crous* (holotype CBS H-22863, culture ex-type CPC 28872 = CBS 142066; ITS sequence GenBank KY173391, LSU sequence GenBank KY173485, MycoBank MB819056).

Notes — The genus *Caliciopsis* belongs to the *Coryneliaceae* (*Coryneliales*, *Coryneliomycetidae*) (Wood et al. 2016), and has phoma-like asexual morphs (Garrido-Benavent & Pérez-Ortega 2015). Phylogenetically, *C. eucalypti* is related to but distinct from *C. beckhausii* (conidia 3.5–4.5 × 1–1.5 µm; ITS GenBank KP144005, Identities = 538/581 (93 %), Gaps = 19/581 (3 %)), *C. calicioides* (conidial dimensions unknown; ITS GenBank JX968549; Identities = 547/596 (92 %), Gaps = 20/596 (3 %)) and *C. valentina* (conidia 4–5 × 1–1.5 µm; ITS GenBank KP144008; Identities = 490/527 (93 %), Gaps = 17/527 (3 %)) (Garrido-Benavent & Pérez-Ortega 2015) and has smaller conidia.

Colour illustrations. *Eucalyptus marginata*; conidiomata sporulating on OA, conidioma, conidiogenous cells and conidia. Scale bars = 200 µm (conidioma), 10 µm (other structures).

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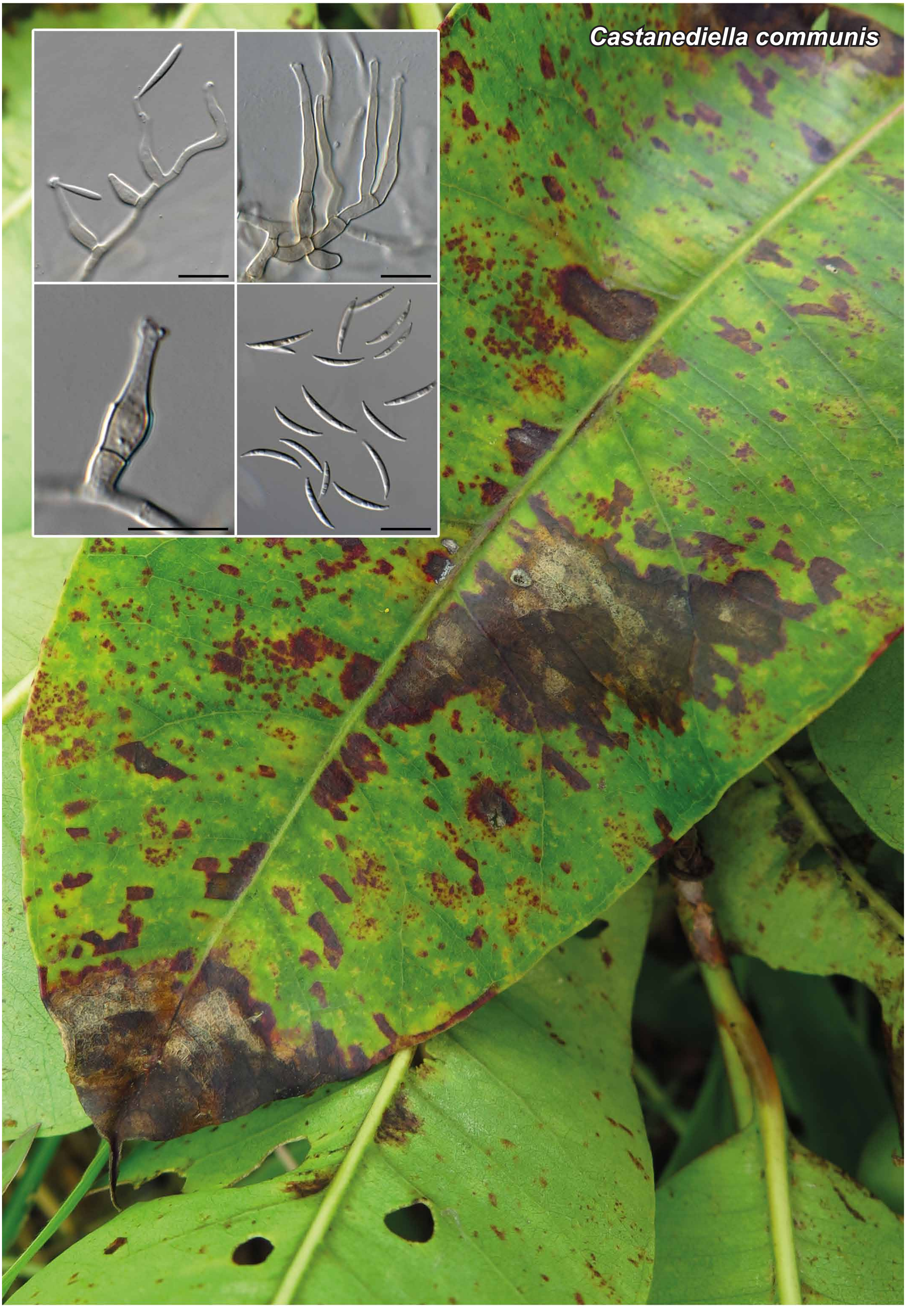
Castanediella communis

Fungal Planet 504 – 21 December 2016

Castanediella communis Crous & M.J. Wingf., *sp. nov.*

Etymology. Name refers to its common occurrence on *Eucalyptus* leaves.

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

Mycelium pale brown, smooth, consisting of branched, septate, 2–3 µm diam hyphae, forming chains of globose, brown, 4–9 µm diam chlamydospores. *Conidiophores* subcylindrical, branched, 1–4-septate, medium brown, smooth, 20–60 × 3–4 µm. *Conidiogenous cells* solitary, terminal and intercalary, subcylindrical to ampulliform, pale brown, smooth, apex swollen, polyblastic with minute flat-tipped scars, 0.5–1 µm diam at apex, 10–35 × 2–4 µm. *Conidia* solitary, hyaline, smooth, falcate with subobtuse ends, guttulate, (13–)17–20(–22) × (2–)2.5(–3) µm.

Culture characteristics — Colonies spreading, erumpent, with moderate aerial mycelium and smooth, lobate margins. On MEA surface fuscous-black, reverse greyish sepia. On OA surface mouse grey. On PDA surface and reverse mouse grey.

Typus. MALAYSIA, Sabah, on leaves of *Eucalyptus pellita* (*Myrtaceae*), May 2015, *M.J. Wingfield* (holotype CBS H-22864, culture ex-type CPC 27631 = CBS 142067; ITS sequence GenBank KY173393, MycoBank MB819057).

Notes — The genus *Castanediella* was introduced for species with sporodochial conidiomata, pale brown, branched conidiophores, denticulate conidiogenous cells, and falcate, 0–1-septate conidia (Crous et al. 2015c, 2016). *Castanediella communis* is closely related to *C. eucalypticola* (conidia (15–)20–26(–30) × (2.5–)3 µm; Crous et al. 2016; ITS GenBank KX228266, Identities = 554/564 (98 %), Gaps = 3/564 (0 %)) and *C. couratarii* (conidia 9.5–19 × 2–3 µm; Hernández-Restrepo et al. 2016; ITS GenBank KP859050, Identities = 522/552 (95 %), Gaps = 9/552 (1 %)), but is phylogenetically distinct, and has longer conidia.

Colour illustrations. Symptomatic leaves of *Eucalyptus pellita*; conidiophores and conidia. Scale bars = 10 µm.

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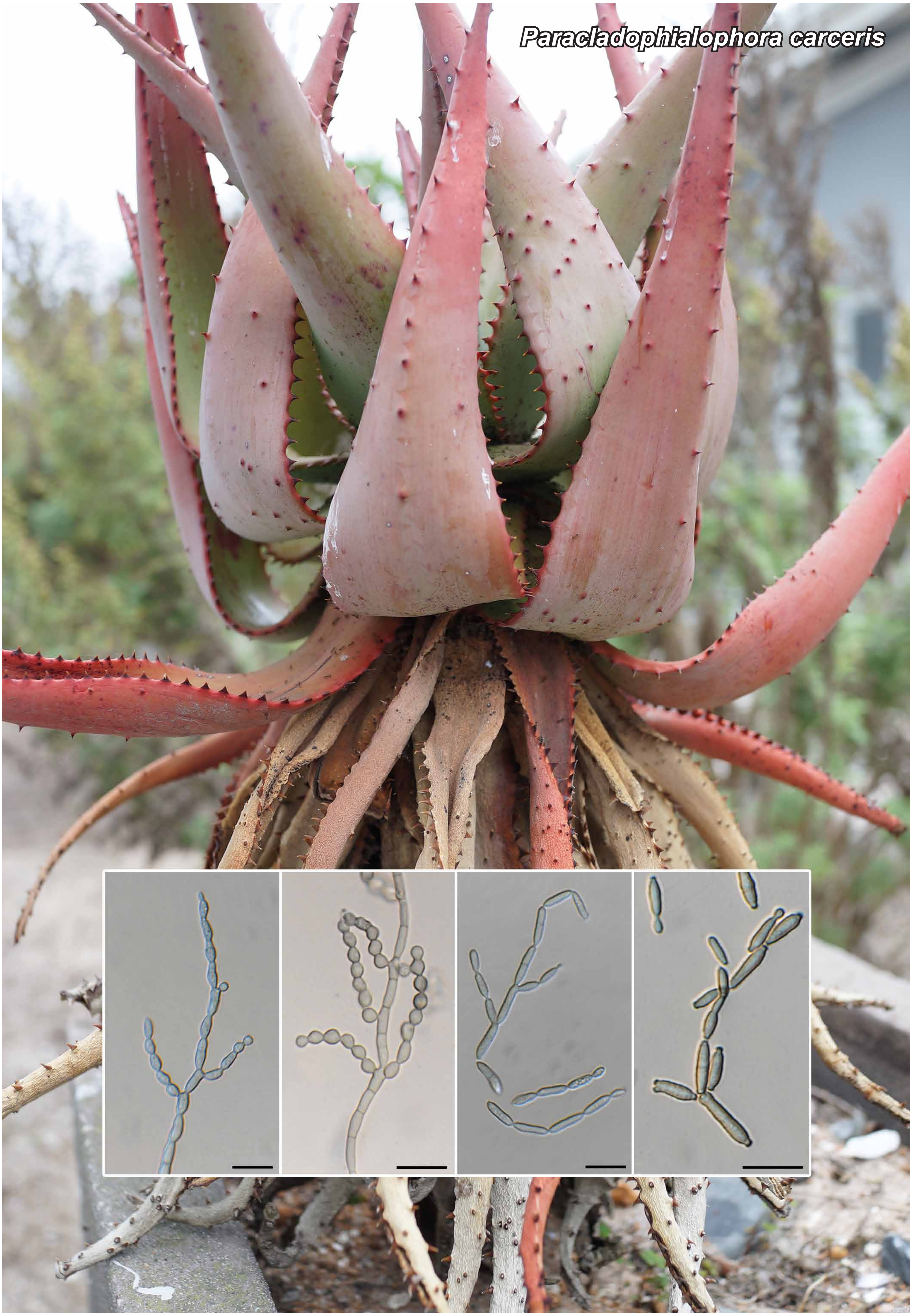
Paracladophialophora carceris

Fungal Planet 505 – 21 December 2016

Paracladophialophora Crous, *gen. nov.*

Etymology. Name reflects morphological similarity to the genus *Cladophialophora*.

Classification — *Incertae sedis*, *Chaetothyriales*, *Eurotiomycetes*.

Mycelium consisting of pale brown, smooth, septate, branched, hyphae. *Conidiophores* solitary, erect, macronematous, grey-brown, straight to irregularly curved, apical apparatus tuft-like due to extremely long conidial chains; conidiophores pale brown, smooth, septate. *Conidiogenous cells* pale brown, smooth, terminal and lateral, subcylindrical with truncate loci, not darkened and thickened, mono- and polyblastic, proliferating sympodially. *Conidia* pale brown, smooth, guttulate, in long branched chains; hila not thickened nor darkened; ramoconidia subcylindrical, septate; conidia ellipsoid to fusoid-ellipsoid.

Type species. *Paracladophialophora carceris* Crous & Roets.
MycoBank MB819058.

Paracladophialophora carceris Crous & Roets, *sp. nov.*

Etymology. Name refers to the prison courtyard (carcer), where this fungus was collected.

Mycelium consisting of pale brown, smooth, septate, branched, 2–2.5 µm diam hyphae. *Conidiophores* solitary, erect, macronematous, grey-brown, straight to irregularly curved, apical apparatus tuft-like due to extremely long conidial chains; conidiophores pale brown, smooth, septate. *Conidiogenous cells* pale brown, smooth, terminal and lateral, subcylindrical with truncate loci, 1 µm diam, not darkened and thickened, mono- and polyblastic, proliferating sympodially. *Conidia* pale brown, smooth, guttulate, in long branched chains; hila not thickened nor darkened, 0.5 µm diam; ramoconidia subcylindrical, 0–3-septate, (7–)9–15(–17) × (2–)2.5(–3) µm; conidia ellipsoid to fusoid-ellipsoid, (6–)7–8 × (2.5–)3 µm.

Culture characteristics — Colonies erumpent, slow-growing, spreading, with sparse to moderate aerial mycelium, and smooth, lobate margins. On MEA surface olivaceous grey, reverse iron grey. On OA and PDA surface and reverse olivaceous grey.

Typus. South Africa, Robben Island, prison courtyard, on leaves of *Aloe* sp. (*Asphodelaceae*), 23 May 2015, *P.W. Crous* (holotype CBS H-22865, culture ex-type CPC 27596 = CBS 142068; ITS sequence GenBank KY173395, LSU sequence GenBank KY173488, MycoBank MB819059).

Notes — The genus *Cladophialophora* accommodates black, yeast-like fungi frequently encountered in human infections (Badali et al. 2008). Several species have, however, been associated with living plants (Crous et al. 2007d, De Hoog et al. 2007). *Paracladophialophora* resembles *Cladophialophora* in morphology, although based on phylogeny, the two genera are distinct within the *Herpotrichiellaceae*. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were found with *Cyphellophora reptans* (as *Phialophora reptans* GenBank AB190380; Identities = 373/429 (87 %), Gaps = 23/429 (5 %)), *Cyphellophora laciniata* (GenBank EU035416; Identities = 370/427 (87 %), Gaps = 18/427 (4 %)) and *Bagliettoa cazzae* (GenBank KM371448; Identities = 373/419 (89 %), Gaps = 16/419 (3 %)). The LSU sequence was most similar to *Cyphellophora olivacea* (GenBank KC455261; Identities = 789/836 (94 %), Gaps = 5/836 (0 %)), *Fonsecaea monophora* (GenBank FJ358247; Identities = 788/835 (94 %), Gaps = 7/835 (0 %)) and *Cyphellophora musae* (GenBank KP122932; Identities = 789/837 (94 %), Gaps = 7/837 (0 %)).

Colour illustrations. Symptomatic leaves of *Aloe* sp. in prison courtyard; conidiophores and conidia in culture. Scale bars = 10 µm.

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Exophiala eucalypti

Fungal Planet 506 – 21 December 2016

Exophiala eucalypti Crous & Roets, *sp. nov.*

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

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

Mycelium consisting of pale brown, smooth, septate, branched, 2–3 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* as separate phialidic loci on hyphae, 1 × 1 µm, giving rise to solitary conidia, guttulate, ellipsoid, apex obtuse, base truncate, 1 µm diam, (3–)4–5 × 2(–3) µm; older conidia becoming swollen, up to 5 µm diam and 7 µm long.

Culture characteristics — Colonies slow growing, erumpent, with moderate aerial mycelium, folded surface, and smooth, even margins. On MEA surface smoke grey, reverse olivaceous grey. On OA surface olivaceous grey. On PDA surface and reverse iron-grey.

Typus. South Africa, Robben Island, on leaves of *Eucalyptus* sp. (*Myrtaceae*), 25 May 2015, *P.W. Crous* (holotype CBS H-22866, culture ex-type CPC 27630 = CBS 142069; ITS sequence GenBank KY173411, LSU sequence GenBank KY173502, MycoBank MB819060).

Colour illustrations. Symptomatic leaves of *Eucalyptus* sp.; hyphae, conidiogenous loci and conidia. Scale bars = 10 µm.

Notes — *Exophiala eucalypti* is phylogenetically related to *Exophiala capensis* (Crous & Groenewald 2011), which has a *Cladophialophora* synasexual morph. Species of *Exophiala* have also been linked to *Capronia* sexual morphs (De Hoog et al. 2000), and although they are commonly isolated as human pathogens, some are associated with plants and other niches (Crous et al. 2007d). Several species are known from *Eucalyptus*, namely *E. eucalyptorum* and *E. placitae* (Crous et al. 2007b). However, the latter two species have ITS sequences that are less than 90 % identical to our ITS sequence (GenBank KC455245; Identities = 287/336 (85 %), Gaps = 20/336 (5 %) and GenBank EU040215; Identities = 307/374 (81 %), Gaps = 22/374 (5 %), respectively).

Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were found with *Exophiala salmonis* (GenBank AF050274; Identities = 713/801 (89 %), Gaps = 25/801 (3 %)), *Cladophialophora chaetospira* (GenBank EU035406; Identities = 710/817 (87 %), Gaps = 41/817 (5 %)) and *Capronia leucadendri* (GenBank EU552108, Identities = 725/823 (88 %), Gaps = 36/823 (4 %)).

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Coleophoma xanthosiae

Fungal Planet 507 – 21 December 2016

Coleophoma xanthosiae Crous, *sp. nov.*

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

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

Conidiomata pycnidial, dark brown to black, globose, immersed to erumpent, up to 400 µm diam; wall of 2–3 layers of brown *textura angularis. Paraphyses* intermingled among conidiophores, hyaline, subcylindrical, septate, branched, extending above conidiophores. *Conidiophores* hyaline, smooth, subcylindrical, 1–2-septate, 10–45 × 3–4 µm. *Conidiogenous cells* hyaline, smooth, subcylindrical to doliiform, apical and intercalary, 5–10 × 3–4 µm; phialidic with periclinal thickening. *Conidia* solitary, hyaline, smooth, guttulate, aseptate, subcylindrical, apex obtuse, base truncate with flattened scar, 0.5–1 µm diam, (17–)18–19(–20) × 3(–3.5) µm.

Culture characteristics — Colonies spreading with sparse to moderate aerial mycelium, and even, smooth margins, reaching 60 mm diam after 2 wk at 25 °C. On MEA surface pale mouse grey, reverse dark mouse grey. On OA surface umber. On PDA surface isabelline, reverse chestnut.

Typus. AUSTRALIA, Western Australia, Denmark, Mount Lindesay Walk Trail, Southern Cross, on leaves of *Xanthosia rotundifolia* (*Mackinlayaceae*), 19 Sept. 2015, *P.W. Crous* (holotype CBS H-22867, culture ex-type CPC 29214 = CBS 142070; ITS sequence GenBank KY173396, LSU sequence GenBank KY173489, *tub2* sequence GenBank KY173598, MycoBank MB819061).

Notes — The genus *Coleophoma* accommodates coelomycetous fungi with pycnidial conidiomata, hyaline conidiophores intermingled among hyaline, collapsing paraphyses, and discrete, integrated phialidic conidiogenous cells, and smooth, hyaline, cylindrical, straight conidia with obtuse ends (Crous & Groenewald 2016). *Coleophoma xanthosiae* is closely related to *C. cylindrospora* (= *C. empetri*), which has conidia of similar dimensions (15–)18–20(–22) × (2.5–)3 µm (Crous & Groenewald 2016). These two species can be distinguished only based on their DNA data. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were found with *Coleophoma ericicola* (GenBank KU728488; Identities = 526/543 (97 %), Gaps = 2/543 (0 %)), *Coleophoma cylindrospora* (GenBank KU728486; Identities = 524/543 (97 %), Gaps = 3/543 (0 %)) and *Coleophoma paracylindrospora* (GenBank KU728492; Identities = 520/543 (96 %), Gaps = 1/543 (0 %)).

Colour illustrations. Leaves of *Xanthosia rotundifolia*; conidiomata sporulating on OA, conidiophores, paraphyses and conidia. Scale bars = 10 µm.

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Teichospora nephelii

Fungal Planet 508 – 21 December 2016

Teichospora nephelii Crous & M.J. Wingf., *sp. nov.*

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

Classification — *Teichosporaceae*, *Pleosporales*, *Dothideomycetes.*

Conidiomata solitary, erumpent, globose, brown, 150 – 200 µm diam, with central ostiole, exuding a pale yellow conidial mass; wall of 3 – 8 layers of brown *textura angularis*. *Conidiophores* hyaline, smooth, subcylindrical, branched, 1 – 2-septate, 15 – 20 × 3 – 4 µm. *Conidiogenous cells* ampulliform to subcylindrical, hyaline, smooth, with several percurrent proliferations at apex, 7 – 12 × 2 – 3 µm. *Conidia* solitary, ellipsoid, apex acutely rounded, base truncate, 1 µm diam, hyaline, smooth, granular to guttulate, (3.5 –)4 – 5(– 5.5) × 2 µm.

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

Typus. Malaysia, Kota Kinabalu, on leaf spots and twigs of *Nephelium lappaceum*, 'Rambutan' (*Sapindaceae*), 30 May 2015, *M.J. Wingfield* (holotype CBS H-22868, culture ex-type CPC 27539 = CBS 142071; ITS sequence GenBank KY173469, LSU sequence GenBank KY173558, MycoBank MB819062).

Notes — In a recent treatment by Jaklitsch et al. (2016), species described in the genus *Curreya* (1883) were allocated to *Teichospora* (1870), and that assessment is also followed here. *Teichospora nepheliae* is introduced as a new species, phylogenetically distinct but closely related to *T. parva* (= *T. minima*), a species known only by its sexual morph (Mugambi & Huhndorf 2009). Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were found with *Teichospora austroafricana* (GenBank HQ428123; Identities = 389/421 (92 %), Gaps = 11/421 (2 %)), *Teichospora melanommoides* (GenBank KU601585; Identities = 451/494 (91 %), Gaps = 10/494 (2 %)) and *Teichospora rubriostiolata* (GenBank KU601590; Identities = 449/493 (91 %), Gaps = 7/493 (1 %)).

Colour illustrations. *Nephelium lappaceum*; conidiomata sporulating on OA, conidiophores and conidia. Scale bars = 10 µm.

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Teichospora kingiae

Fungal Planet 509 – 21 December 2016

Teichospora kingiae Crous & M.J. Wingf., *sp. nov.*

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

Classification — *Teichosporaceae*, *Pleosporales*, *Dothideomycetes.*

Conidiomata erumpent, black, solitary on host, but in culture eustromatic, aggregated, multilocular, with ostiole exuding black conidial mass; wall of 6–12 layers of brown *textura angularis. Paraphyses* intermingled among conidiophores, hyaline, septate, branched, up to 60 µm long, 2.5–3 µm diam. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, subcylindrical, hyaline, smooth, with several indistinct percurrent proliferations at apex, 5–10 × 2.5–5 µm. *Conidia* solitary, golden-brown, verruculose, subcylindrical, apex obtuse, base truncate, 2.5–3 µm diam, transversely 3-septate, thick-walled, (13–)14–15(–16) × (5–)6(–6.5) µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium, reaching 40 mm diam after 2 wk at 25 °C on OA, 15 mm diam on PDA, and 30 mm diam on MEA. On MEA surface dirty white, reverse leaden grey. On OA surface dirty white. On PDA surface dirty white, reverse umber with diffuse brown pigment in agar.

Typus. Australia, Western Australia, Denmark, Mount Lindesay National Park, S34°51'027" E117°16'455", on leaves of *Kingia australis* (*Dasypogonaceae*), 19 Sept. 2015, *P.W. Crous* (holotype CBS H-22869, culture ex-type CPC 29104 = CBS 142072; ITS sequence GenBank KY173468, LSU sequence GenBank KY173557, MycoBank MB819063).

Colour illustrations. Leaves of *Kingia australis*; conidiomata sporulating on PDA, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — *Teichospora kingiae* is phylogenetically distinct and distantly related to *T. viticola*, *T. proteae* and *T. grandicipis*. Morphologically, it has larger conidia than these species, except for *T. proteae*, which is known only by its sexual morph (Marincowitz et al. 2008, Crous et al. 2011b, Ariyawansa et al. 2015). Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were found with *Teichospora mariae* (GenBank KU601580; Identities = 540/566 (95 %), Gaps = 8/566 (1 %)), *Teichospora viticola* (GenBank KT305997; Identities = 486/528 (92 %), Gaps = 15/528 (2 %)) and *Teichospora grandicipis* (GenBank JN712456; Identities = 502/568 (88 %), Gaps = 24/568 (4 %)).

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Neoscolecobasidium agapanthi

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Neoscolecobasidium Crous, *gen. nov.*

Etymology. Name reflects a morphological similarity to the genus *Scolecobasidium*.

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

Mycelium consisting of branched, septate, hyaline, smooth, hyphae, frequently forming hyphal coils. *Conidiophores* solitary, erect, subcylindrical, straight to flexuous, unbranched, hyaline, smooth, septate. *Conidiogenous cells* terminal, subcylindrical, hyaline, smooth, tapering to an acute truncate apex; with several truncate denticle-like loci; scars unthickened, nor darkened. *Conidia* solitary, fusoid-ellipsoid, apex obtuse, constricted at central septum, hyaline, smooth, guttulate, tapering from middle to truncate hilum. Older conidia appear somewhat pale brown and finely roughened. A separating cell exists between the conidiogenous cell and the conidium (rhexolytic conidiogenesis), and a marginal frill is visible at the conidium hilum and scar on the conidiogenous cell.

Type species. *Neoscolecobasidium agapanthi* Crous.
MycoBank MB819064.

Neoscolecobasidium agapanthi Crous, *sp. nov.*

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

Mycelium consisting of branched, septate, hyaline, smooth, 2–2.5 µm diam hyphae, frequently forming hyphal coils. *Conidiophores* solitary, erect, subcylindrical, straight to flexuous, unbranched, hyaline, smooth, 1–2(–4)-septate, 20–60(–100) × 2–2.5 µm. *Conidiogenous cells* terminal, subcylindrical, hyaline, smooth, tapering to an acute truncate apex, 10–30 × 2–2.5 µm; with several truncate denticle-like loci, 1–2 × 1 µm; scars unthickened, nor darkened. *Conidia* solitary, fusoid-ellipsoid, apex obtuse, constricted at central septum, hyaline, smooth, guttulate, tapering from middle to truncate hilum, 1 µm diam, (11–)13–15(–17) × (3–)4 µm. Older conidia appear somewhat pale brown and finely roughened. A separating cell exists between the conidiogenous cell and the conidium (rhexolytic conidiogenesis), and a marginal frill is visible at the conidium hilum and scar on the conidiogenous cell.

Culture characteristics — Colonies erumpent, spreading, reaching 15 mm diam after 2 wk at 25 °C, with moderate aerial mycelium and smooth, lobed margins. On MEA, OA and PDA surface dirty white, reverse saffron to ochreous.

Typus. USA, Texas, Austin, on dead leaves of *Agapanthus* sp. (*Alliaceae*), Aug. 2013, *P.W. Crous* (holotype CBS H-22870, culture ex-type CPC 28778 = CBS 142073; ITS sequence GenBank KY173426, LSU sequence GenBank KY173517, MycoBank MB819065).

Notes — The *Ochroconis* complex was recently revised by Samerpitak et al. (2014), resolving the status of the genera *Ochroconis* and *Scolecobasidium*. In this study, *S. tropicum* (CBS 360.87) was shown to be unrelated to these two genera, clustering in *Pezizomycotina*. The fungus isolated from *Agapanthus* in this study was closely related to '*Scolecobasidium*' *tropicum*, although additional isolates and species are required to determine whether these two taxa are indeed congeneric. A new genus, *Neoscolecobasidium*, is introduced here to accommodate the fungus from *Agapanthus*, which resembles *Scolecobasidium* in general morphology. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarity for a full-length sequence was found only with *Dactylaria ampulliformis* (GenBank AY265336; Identities = 418/527 (79 %), Gaps = 41/527 (7 %)); all other matches were with 5.8S nrRNA gene sequences only. Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were found with *Isthmolongispora ampulliformis* (GenBank EU107303; Identities = 748/792 (94 %), Gaps = 3/792 (0 %)), '*Scolecobasidium*' *tropicum* (GenBank KF156102; Identities = 708/768 (92 %), Gaps = 3/768 (0 %)) and *Dactylaria humicola* (GenBank EU107304; Identities = 734/798 (92 %), Gaps = 12/798 (1 %)).

Colour illustrations. Flowering *Agapanthus* sp.; conidiophores and conidia. Scale bars = 10 µm.

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Eucalyptostroma eucalypti

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

Etymology. Name reflects the host plant *Eucalyptus*, and the characteristic basal stroma giving rise to conidiophores.

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

Conidiomata scattered to gregarious, superficial, sporodochial, cupulate, orange-yellow; basal stroma of *textura intricata*. *Setae* absent. *Conidiophores* arising from a stroma, septate, branched, pale orange-brown; forming a penicillate conidiogenous apparatus. *Conidiogenous cells* integrated, terminal, lageniform to cylindrical, in whorls, orange-brown, finely roughened to warty, thin-walled, with apical percurrent proliferations, 7–16 × 2.5–4 µm, apex 1–1.5 µm diam. *Conidia* (3–)4(–4.5) × 2 µm, aseptate, hyaline, smooth, thin-walled, ellipsoid, apex subobtuse, base truncate, 1 µm diam, widest in upper third, lacking appendages.

Type species. *Eucalyptostroma eucalypti* Crous & M.J. Wingf.
MycoBank MB819066.

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

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

Conidiomata scattered to gregarious, superficial, sporodochial, cupulate, orange-yellow, 70–300 µm diam; basal stroma of *textura intricata*. *Setae* absent. *Conidiophores* arising from a stroma, septate, branched, pale orange-brown, 30–60 × 2.5–3.5 µm; forming a penicillate conidiogenous apparatus. *Conidiogenous cells* integrated, terminal, lageniform to cylindrical, in whorls, orange-brown, finely roughened to warty, thin-walled, with apical percurrent proliferations, 7–16 × 2.5–4 µm, apex 1–1.5 µm diam. *Conidia* (3–)4(–4.5) × 2 µm, aseptate, hyaline, smooth, thin-walled, ellipsoid, apex subobtuse, base truncate, 1 µm diam, widest in upper third, lacking appendages.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium and even, lobate margins, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface umber to apricot, reverse rust with diffuse apricot pigment. On OA surface pale luteous in outer region, orange in centre. On PDA surface and reverse apricot, with diffuse apricot pigment in agar.

Typus. MALAYSIA, Kota Kinabalu, on leaf spots of *Eucalyptus pellita* (*Myrtaceae*), 30 May 2015, *M.J. Wingfield* (holotype CBS H-22871, culture ex-type CPC 28764 = CBS 142074; ITS sequence GenBank KY173408, LSU sequence GenBank KY173500, MycoBank MB819067); idem, CPC 28748 = CBS 142075; ITS sequence GenBank KY173407, LSU sequence GenBank KY173499.

Colour illustrations. *Eucalyptus pellita* trees; conidiomata, conidiophores and conidia. Scale bars = 10 µm.

Notes — The isolates obtained from *Eucalyptus pellita* in the present study are phylogenetically distinct, but allied to the genus *Pseudolachnella* (see Hashimoto et al. 2015). However, they cannot be accommodated in this genus as the conidiomata lack marginal setae, conidiophores are pigmented and in a penicillate arrangement, and conidia are aseptate. We could also not find a suitable genus of hyphomycetes to accommodate this fungus. A new genus, *Eucalyptostroma*, is therefore introduced to accommodate this fungus. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence of the ex-type culture, the best similarities were less than 90 % with species of *Chaetosphaeriaceae*; the highest similarity was found with *Codinaea pini* (GenBank KP004465; Identities = 349/398 (88 %), Gaps = 15/398 (3 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence of the ex-type culture, the highest similarities were found with species of *Chaetosphaeria* such as *C. spinosa* (GenBank AF466079; Identities = 775/817 (95 %), no gaps), with *Paliphora intermedia* (GenBank EF204500; Identities = 765/811 (94 %), Gaps = 4/811 (0 %)) and with species of *Pseudolachnella* such as *P. yakushimensis* (GenBank AB934064; Identities = 770/818 (94 %), Gaps = 2/818 (0 %)).

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Disculoides corymbiae

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Disculoides corymbiae Crous, *sp. nov.*

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

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

Leaf spots prominent, amphigenous, as broad bands running across from the leaf margin to the midrib, medium brown, with red-purple margin, 5–15 mm diam. *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 with a supporting cell. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, subcylindrical to ampulliform, tapering to a long thin neck, 10–20 × 2.5–3.5 µm, proliferating percurrently at apex, with minute flaring collarette. *Conidia* hyaline, smooth, thick-walled, guttulate, ellipsoid to fusoid, straight to curved, (10–)12–14(–15) × (3.5–)4(–4.5) µm; apex subobtuse, base truncate, 1–1.5 µm diam, with minute marginal frill.

Culture 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, Denmark, Mount Lindesay Walk Trail, on leaves of *Corymbia calophylla* (*Myrtaceae*), 19 Sept. 2015, *P.W. Crous* (holotype CBS H-22872, culture ex-type CPC 28864 = CBS 142076; ITS sequence GenBank KY173403, LSU sequence GenBank KY173495, *cmdA* sequence GenBank KY173574, *tub2* sequence GenBank KY173602, MycoBank MB819068).

Colour illustrations. *Corymbia calophylla*; leaf spots, conidiomata sporulating on MEA, conidiophores and conidia. Scale bars = 10 µm.

Notes — The genus *Disculoides* was recently established for two species associated with leaf spots on *Eucalyptus* in Australia (Crous et al. 2012b). *Disculoides corymbiae* adds a third species to the genus, distinguished from *D. eucalypti* (conidia (16–)17–20(–23) × (5–)6–6.5(–7) µm; GenBank JQ685517, Identities = 568/587 (97 %), Gaps = 2/587 (0 %)) and *D. eucalyptorum* (conidia (12–)14–18(–20) × (4.5–)5(–5.5) µm; GenBank JQ685518, Identities = 568/586 (97 %), Gaps = 2/586 (0 %)) based on its smaller conidia. Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the two existing *Disculoides* species were found with 99 % similarity, followed at 98 % with species of *Harknessia*.

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Umthunziomyces hagahagensis

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

Etymology. Composed of *Umthunzi* = the Xhosa name for the red wilkwood tree, which grows along the coastal dune vegetation in southern Africa, and -myces (fungus).

Classification — *Planistromellaceae*, *Botryosphaeriales*, *Dothideomycetes.*

Conidiomata globose, solitary, dark brown to black, erumpent with central ostiole; wall of 2–4 layers of pale brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells, or with a single supporting cell, in which case it can be branched below. *Conidiogenous cells* tightly aggregated, lining the inner cavity, hyaline, smooth, ampulliform, holoblastic. *Conidia* solitary, hyaline, smooth, prominently guttulate, thin-walled, narrowly long obclavate, transversely euseptate, apex subobtuse, base truncate, not thickened nor darkened.

Type species. *Umthunziomyces hagahagensis* Crous & M.J. Wingf. MycoBank MB819069.

Umthunziomyces hagahagensis Crous & M.J. Wingf., *sp. nov.*

Etymology. Named for the small village of Haga Haga on the Eastern Cape wild coast of South Africa.

Conidiomata globose, solitary, dark brown to black, 200–300 µm diam, erumpent with central ostiole; wall of 2–4 layers of pale brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells, or with a single supporting cell, in which case it can be branched below. *Conidiogenous cells* tightly aggregated, lining the inner cavity, hyaline, smooth, ampulliform, holoblastic, 8–15 × 2.5–3.5 µm. *Conidia* solitary, hyaline, smooth, prominently guttulate, thin-walled, narrowly long obclavate, 0–3-euseptate, apex subobtuse, base truncate, 3 µm diam (not thickened nor darkened), (63–)65–68(–75) × 3.5(–4) µm.

Culture characteristics — Colonies covering dish after 2 wk at 25 °C, with fluffy aerial mycelium, and even lobed margins. On MEA surface mouse grey to pale mouse grey, reverse dark mouse grey. On OA surface dark mouse grey. On PDA surface and reverse dark mouse grey.

Typus. South Africa, Eastern Cape Province, Haga Haga, on dead leaves of *Mimusops caffra* (*Sapotaceae*), Dec. 2015, *M.J. Wingfield* (holotype CBS H-22873, culture ex-type CPC 29917 = CBS 142084; ITS sequence GenBank KY173472, LSU sequence GenBank KY173561, MycoBank MB819070).

Colour illustrations. *Mimusops caffra*; conidiomata sporulating on PNA, conidiophores and conidia. Scale bars = 300 µm (conidiomata), 10 µm (all others).

Notes — The genus *Umthunziomyces* is reminiscent of septoria-like genera treated by Quaedvlieg et al. (2013). Although morphologically septoria-like, the genus is allied to the *Planistromellaceae*, which is rather unusual. It was collected on leaf litter, and is probably an endophyte of this host. Its potential role as pathogen appears unlikely, as leaves of *Mimusops caffra* are typically devoid of leaf spots. However, members of *Planistromellaceae* are often associated with dead leaves (Minnis et al. 2012). Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the best hits of 89 % were mainly with species of *Endomelanconiopsis*, such as *E. endophytica* (GenBank GQ469968, Identities = 523/588, Gaps = 19/588 (3 %)). Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the best hits of 89 % were mainly with species of *Kellermania*, such as *K. yuccigena* (GenBank KJ710450, Identities = 825/838, no gaps).

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Eucasphaeria rustici

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Eucasphaeria rustici Crous & T.I. Burgess, *sp. nov.*

Etymology. The term refers to 'bogan' (rusticus), a derogatory Australian and slang word used to describe a person whose speech, clothing, attitude and behaviour exemplify values and behaviour considered unrefined or unsophisticated. While collecting the second isolate of this fungus in a park in Willagee, Perth, a bogan man accosted the authors, leaving a lasting impression.

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

On SNA. *Conidiomata* in culture sporodochial, up to 300 µm diam, appearing orange-pink on OA, MEA, PDA and SNA, hyaline under compound microscope. *Conidiophores* hyaline, subcylindrical, apically branched, 1–2-septate, 30–35 × 3–4 µm, giving rise to 1–2 conidiogenous cells. *Conidiogenous cells* phialidic, hyaline, smooth, fusoid-ellipsoid, tapering to a truncate apex with visible periclinal thickening, 10–17 × 2–3 µm. *Conidia* hyaline, guttulate, falcate, widest in middle, 0–1-septate, base subtruncate, apex subobtusely rounded, (12–)17–22(–25) × (2.5–)3(–4) µm, covered in mucus.

Culture characteristics — Colonies spreading, erumpent, aerial mycelium absent, margins smooth, lobate, reaching 15 mm diam after 1 wk at 25 °C. On MEA, OA and PDA surface luteous to orange, reverse luteous.

Typus. Australia, Western Australia, Perth, King's Park Botanic Gardens, on leaves of *Eucalyptus creta* (*Myrtaceae*), 27 Sept. 2015, *M.J. Wingfield* (holotype CBS H-22874, culture ex-type CPC 28946 = CBS 142085; ITS sequence GenBank KY173409, LSU sequence GenBank KY173501, MycoBank MB819071).

Additional specimen examined. Australia, Western Australia, Perth, Willagee, on leaves of *Corymbia ficifolia* (*Myrtaceae*), 29 Sept. 2015, *P.W. Crous*, CPC 29570 = CBS 142140; ITS and LSU sequence GenBank KY173410.

Notes — The monotypic genus *Eucasphaeria* was introduced by Crous et al. (2007c) for a genus of Ascomycetes occurring on leaves of *Eucalyptus* in South Africa. *Eucasphaeria rustici* is similar to *E. capensis* (conidia 0–2-septate, (22–)25–30(–40) × 3(–4) µm; GenBank EF110618, Identities = 561/567 (99 %), Gaps = 3/567 (0 %)), although it can be distinguished by having smaller conidia.

Colour illustrations. Symptomatic leaves of *Eucalyptus creta*; conidiomata sporulating on OA, conidiophores and conidia. Scale bars = 10 µm.

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Diatrypella banksiae

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Diatrypella banksiae Crous, *sp. nov.*

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

Classification — *Diatrypaceae*, *Xylariales*, *Sordariomycetes*.

Associated with branch cankers of *Luteocirrhus shearii*. *Conidiomata* solitary, brown, pycnidial, 200–400 µm diam, exuding a long white conidial cirrhus; wall of several layers of brown *textura intricata*. *Paraphyses* intermingled among conidiophores, subcylindrical, branched, septate, extending above conidiophores. *Conidiophores* hyaline, smooth, lining the inner cavity, subcylindrical, branched, 1–3-septate, 15–30 × 2.5–3.5 µm. *Conidiogenous cells* integrated, terminal and intercalary, smooth, hyaline, 10–15 × 2–2.5 µm, proliferating sympodially at apex, with flat-tipped loci, 0.5 µm diam. *Conidia* solitary, hyaline, smooth, spindle-shaped, apex subobtuse, base truncate, (25–)27–30(–35) × 1.5(–2) µm.

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

Typus. Australia, Western Australia, Gull Rock National Park, Albany, on leaves of *Banksia formosa* (*Proteaceae*), 20 Sept. 2015, *P.W. Crous* (holotype CBS H-22875, culture ex-type CPC 29118 = CBS 142086; ITS sequence GenBank KY173402, LSU sequence GenBank KY173494, MycoBank MB819072).

Additional specimen examined. Australia, Western Australia, Gull Rock National Park, Albany, on leaves of *Banksia coccinia* (*Proteaceae*), 20 Sept. 2015, *P.W. Crous*, CPC 29054 = CBS 142170; ITS and LSU sequence GenBank KY173401.

Notes — *Diatrypella banksiae* is phylogenetically allied to *D. vulgaris*, a species occurring on *Citrus paradisi*, *Fraxinus angustifolia* and *Schinus molle* var. *areira* in Australia (Trouillas et al. 2011). Morphologically, it can be distinguished from *D. vulgaris* (conidia 25–40(–55) × (1–)1.5–2 µm) by its smaller conidia. *Diatrypella banksiae* was found to occur in association with *Luteocirrhus shearii* (Crane & Burgess 2013) on *Banksia* stem cankers and leaves, and may thus also play a role as plant pathogen. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence of the ex-type culture, the highest similarities were with *Eutypella caricae* (GenBank JX241652; Identities = 545/555 (98 %), no gaps), *Diatrype macowaniana* (GenBank AJ302431; Identities = 514/524 (98 %), no gaps) and *Diatrype enteroxantha* (GenBank KM396622; Identities = 570/591 (96 %), Gaps = 3/591 (0 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence of the ex-type culture, the highest similarities were with *Diatrypella vulgaris* (GenBank KT207708; Identities = 814/821 (99 %), no gaps), *Eutypa flavovirens* (GenBank KR092774; Identities = 809/821 (99 %), Gaps = 1/821 (0 %)) and *Diatrype palmicola* (GenBank KP744481; Identities = 797/810 (98 %), Gaps = 1/810 (0 %)).

Colour illustrations. *Banksia formosa*; conidioma sporulating on PNA, conidiophores and conidia. Scale bars = 10 µm.

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Dactylaria acaciae

Fungal Planet 516 – 21 December 2016

Dactylaria acaciae Crous, *sp. nov.*

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

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

Mycelium consisting of hyaline, smooth, branched, septate, 2–2.5 µm diam hyphae. *Conidiophores* solitary, erect, micro- to macronematous, subcylindrical, straight to geniculate-sinuous, 0–7-septate, brown, smooth, 7–60 × 2–3.5 µm. *Conidiogenous cells* brown, smooth, subcylindrical, terminal or intercalary, apex frequently slightly swollen, with flat-tipped denticles, 0.5–1.5 × 0.5 µm, with unthickened nor darkened scars, 7–25 × 2–3.5 µm. *Conidia* solitary, hyaline, smooth, guttulate, narrowly fusoid-ellipsoid, apex subobtuse, base truncate, 1–1.5 µm diam, 2-septate, (one third from apex and base, respectively), (16–)25–34(–37) × 2(–2.5) µm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium reaching up to 25 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse luteous. On OA surface umber. On PDA surface and reverse umber with patches of pale luteous.

Typus. USA, Hawaii, Oahu, on leaves of *Acacia koa* (*Fabaceae*), 30 Sept. 2015, *J.J. Le Roux* (holotype CBS H-22876, culture ex-type CPC 29771 = CBS 142087; ITS sequence GenBank KY173400, LSU sequence GenBank KY173493, MycoBank MB819073).

Notes — The genus *Dactylaria* is heterogeneous, and includes isolates with a range of different ecologies, and phylogenetic affinities (De Hoog 1985). *Dactylaria acaciae* is phylogenetically closely related to *D. fragilis* (conidia 18–26 × 1.5 µm; De Hoog 1985), though the two species can easily be distinguished based on the larger conidial dimensions of *D. acaciae*. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence of the ex-type culture, the highest similarities were with *Fusidium griseum* (GenBank EF029217; Identities = 502/555 (90 %), Gaps = 28/555 (5 %)), *Pseudapiospora corni* (GenBank KT949908; Identities = 505/591 (85 %), Gaps = 42/591 (7 %)) and *Phlogicylindrium uniforme* (GenBank JQ044426; Identities = 503/589 (85 %), Gaps = 36/589 (6 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence of the ex-type culture, the highest similarities were with species of *Dactylaria* such as *D. fragilis* (GenBank EU107290; Identities = 816/818 (99 %), no gaps) and *D. monticola* (GenBank EU107289; Identities = 807/818 (99 %), no gaps) and species of *Pseudophleospora* such as *P. eucalypti* (GenBank HQ599593; Identities = 796/823 (97 %), Gaps = 5/823 (0 %)) and *P. eucalyptorum* (GenBank KX228340; Identities = 788/815 (97 %), Gaps = 5/815 (0 %)) as well as species of *Castanediella* such as *C. acaciae* (GenBank KR476763; Identities = 788/818 (96 %), no gaps).

Colour illustrations. *Acacia koa* in Hawaii; conidiogenous cells and conidia. Scale bars = 10 µm.

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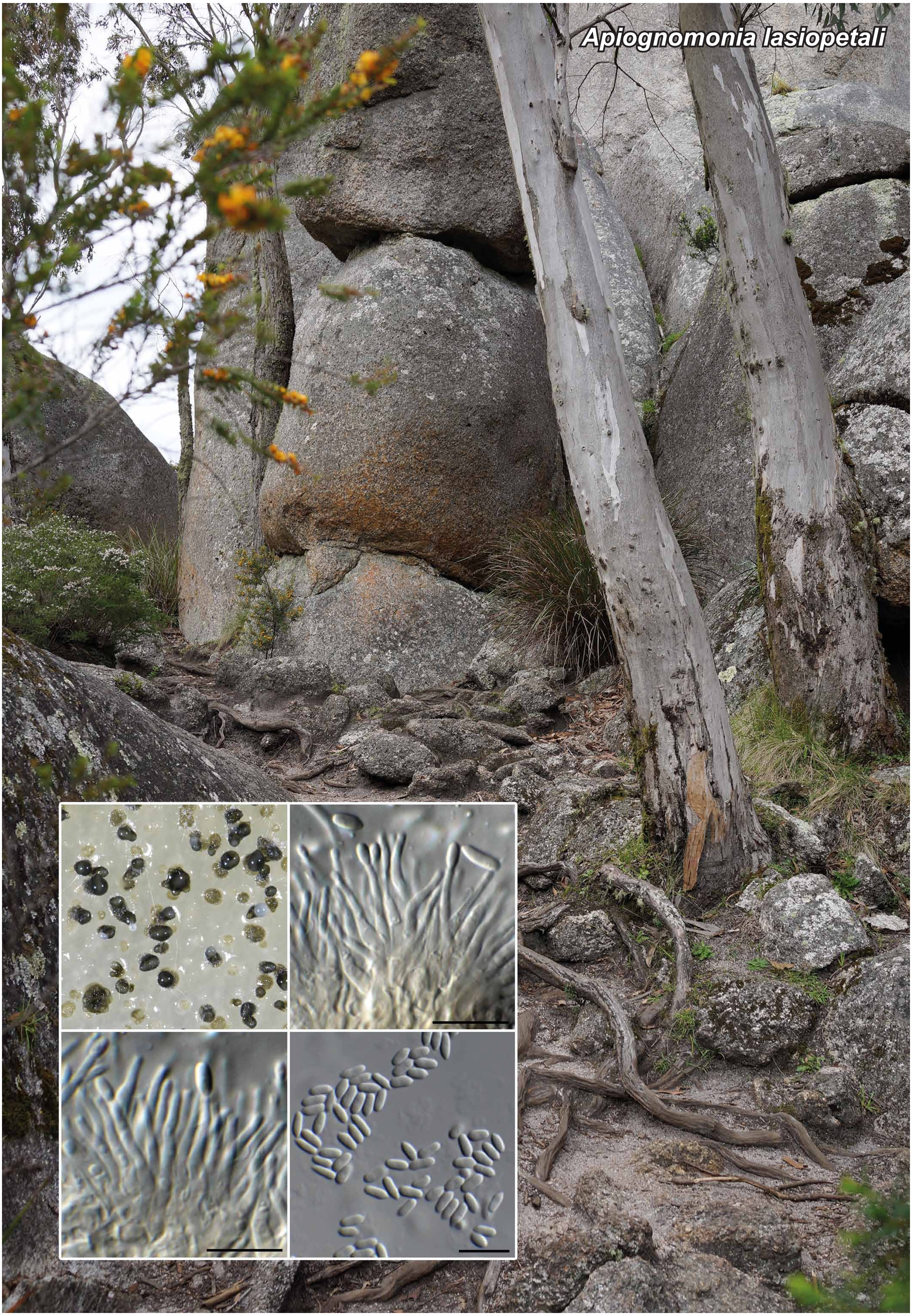
Apiognomonia lasiopetali

Fungal Planet 517 – 21 December 2016

Apiognomonia lasiopetali Crous, *sp. nov.*

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

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

Conidiomata separate, erumpent, elongated, subcylindrical with obtuse apex, 100–150 µm diam, 300–350 µm tall, base dark brown, mid section and apex pale brown to creamy, with central ostiole. *Conidiophores* subcylindrical, hyaline, smooth, branched, 1–4-septate, 10–25 × 2.5–3.5 µm. *Conidiogenous cells* integrated, phialidic, hyaline, smooth, terminal and intercalary, 5–10 × 2–2.5 µm; collarette minute, not flared, 1 µm long, apex 1 µm diam. *Conidia* solitary, hyaline, smooth, subcylindrical, apex obtuse, base tapered with minute flat hilum, 0.5 µm diam, (4–)5–6 × (1.5–)2 µm.

Culture characteristics — Colonies fast growing, covering the dish in 2 wk at 25 °C, flat, with sparse to moderate aerial mycelium. On MEA surface dirty white, reverse luteous. On OA and PDA surface and reverse dirty white.

Typus. Australia, Western Australia, Porongurup, Porongurup National Park, Castle Rock Skywalk, on leaves of *Lasiopetalum* sp. (*Sterculiaceae*), 24 Sept. 2015, *P.W. Crous* (holotype CBS H-22877, culture ex-type CPC 29084 = CBS 142088; ITS sequence GenBank KY173385, LSU sequence GenBank KY173479, MycoBank MB819074); idem, CPC 29158 = CBS 142089; ITS sequence GenBank KY173386, LSU sequence GenBank KY173480.

Additional specimens examined. Australia, Western Australia, on leaves of *Spiridium* sp., 19 Sept. 2015, *P.W. Crous*, CPC 29018 = CBS 142090; Denmark, Mount Lindesay Walk Trail, on leaves of *Trymalium* sp. (*Rhamnaceae*), 19 Sept. 2015, *P.W. Crous*, CPC 29180 = CBS 142091; ITS sequences GenBank KY173384, KY173387, LSU sequences GenBank KY173478, KY173481, respectively.

Notes — The genus *Discula* (based on *D. quercina*), is a synonym of *D. umbrinella*, which is the asexual morph of *Apiognomonia errabunda.* Rossman et al. (2015) recommended the use of *Apiognomonia* over that of *Discula*. *Apiognomonia lasiopetali* appears to occur on several hosts in Western Australia, and even though there are differences in conidial size (e.g. CPC 29018 has larger conidia, (6.5–)7(–8) × (2–)2.5 µm), these isolates appear identical on ITS sequence data (exception being CPC 29018 which differs with 1/583 nucleotides on ITS). *Apiognomonia lasiopetali* is related, but phylogenetically distinct from *A. errabunda*, and therefore introduced here as new species. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence of the ex-type culture, the highest similarities were with *Gnomoniopsis smithogilvyi* (GenBank KC145890; Identities = 547/589 (93 %), Gaps = 12/589 (2 %)), *Amphiporthe leiphaemia* (GenBank HQ608140; Identities = 536/578 (93 %), Gaps = 15/578 (2 %)) and *Discula quercina* (GenBank GQ452264; Identities = 547/591 (93 %), Gaps = 15/591 (2 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence of the ex-type culture, the highest similarities were with *Gnomoniopsis smithogilvyi* (GenBank JX069842; Identities = 815/821 (99 %), no gaps), *Gnomoniopsis paraclavulata* (GenBank EU255118; Identities = 775/781 (99 %), no gaps) and *Gnomonia petiolorum* (GenBank AY818963; Identities = 814/821 (99 %), no gaps).

Colour illustrations. Castle Rock Skywalk; conidiomata sporulating on OA, conidiophores and conidia. Scale bars = 10 µm.

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Mycophilomyces periconiae

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

Etymology. Name indicating its mycophylic growth habit.

Classification — *Clavicipitaceae*, *Hypocreales*, *Sordariomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate, hyphae. *Conidiophores* solitary, erect, flexuous, hypha-like, 1- to multiseptate, with integrated terminal conidiogenous cells. *Conidiogenous cells* terminating in a truncate apex with holoblastic conidiogenesis. *Conidia* solitary, hyaline, smooth, granular, obclavate, apex subobtusely rounded, base obconically truncate, transversely euseptate.

Type species. *Mycophilomyces periconiae* Crous & M.J. Wingf.
MycoBank MB819075.

Mycophilomyces periconiae Crous & M.J. Wingf., *sp. nov.*

Etymology. Name refers to *Periconia*, the fungal genus from which this fungus was isolated.

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* solitary, erect, flexuous, hypha-like, 25–150 × 1.5–2 µm, 1- to multiseptate, with integrated terminal conidiogenous cells. *Conidiogenous cells* 25–80 × 1.5–2 µm, terminating in a truncate apex with holoblastic conidiogenesis. *Conidia* solitary, hyaline, smooth, granular, obclavate, apex subobtusely rounded, base obconically truncate, 1 µm diam, 3–6-septate, (27–)31–34(–43) × 3.5(–4) µm.

Culture characteristics — Colonies erumpent, spreading, reaching 15 mm diam on PDA, 40 mm on OA and MEA after 2 wk at 25 °C, with abundant aerial mycelium and feathery margins. On MEA, OA and PDA surface and reverse dirty white.

Typus. Malaysia, Sabah, hyaline hyperparasite on *Periconia* growing on leaves of *Albizia falcataria* (*Fabaceae*), May 2015, *M.J. Wingfield* (holotype CBS H-22878, culture ex-type CPC 27558 = CBS 142092; ITS sequence GenBank KY173418, LSU sequence GenBank KY173509, *tef1* sequence GenBank KY173595, *tub2* sequence GenBank KY173605, MycoBank MB819076).

Notes — This fungus is mycophylic growing on the conidiophore apparatus of a *Periconia* sp. growing on *Albizia falcataria* leaves. It is morphologically similar to *Dactylella*, a genus of nematode trapping fungi residing in the *Orbiliaceae*. However, our fungus clusters in *Clavicipitaceae*, being related to genera such as *Pochonia* (e.g. *Pochonia* sp. ITS GenBank KM231844, Identities = 548/601 (91 %), Gaps = 27/601 (4 %)), *Calcarisporium* (e.g. *C. arbuscula* ITS GenBank AY271809, Identities = 550/607 (91 %), Gaps = 28/607 (4 %)), *Aphanocladium* (e.g. *A.* aff. *album* ITS GenBank KT316743, Identities = 485/540 (90 %), Gaps = 21/540 (3 %)) and *Sarcopodium* (e.g. *S. circinatum* ITS GenBank KM231787, Identities = 542/609 (89 %), Gaps = 25/609 (4 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with *Metacordyceps liangshanensis* (GenBank EF468814; Identities = 799/821 (97 %), Gaps = 5/821 (0 %)), *Pochonia* sp. (GenBank KM231725; Identities = 797/817 (99 %), Gaps = 3/819 (0 %)) and *Torrubiella tenuis* (GenBank EU369046; Identities = 796/821 (97 %), Gaps = 5/821 (0 %)). A new genus is therefore introduced to accommodate this mycophylic fungus.

Colour illustrations. *Albizia falcataria*; conidiophores and conidia. Scale bars = 10 µm.

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Bullanockia australis

Fungal Planet 519 – 21 December 2016

Bullanockia Crous, *gen. nov.*

Etymology. Named after the Noongar (indigenous Australian people who live in the south-west corner of Western Australia) name 'bullanock' for the genus *Kingia.*

Classification — *Bionectriaceae*, *Hypocreales*, *Sordariomycetes.*

Mycelium consisting of septate, branched, hyaline, smooth, hyphae. *Conidiophores* solitary, erect, straight or flexuous, subcylindrical, septate. *Conidiogenous cells* hyaline, smooth, terminal; phialidic with minute non-flared collarette; conidia aggregating in slimy mass, or as a dry chain. *Conidia* solitary, hyaline, smooth, granular to guttulate, subcylindrical with obtuse ends, but base somewhat truncate at times, straight to slightly curved.

Type species. *Bullanockia australis* Crous.
MycoBank MB819077.

Bullanockia australis Crous, *sp. nov.*

Etymology. Name refers to the host species *Kingia australis*, from which the fungus was collected.

Mycelium consisting of septate, branched, hyaline, smooth, 1–1.5 µm diam hyphae. *Conidiophores* solitary, erect, straight or flexuous, subcylindrical, 1–2-septate, 15–60 × 2 µm. *Conidiogenous cells* hyaline, smooth, terminal, 15–40 × 1.5–2 µm; phialidic with minute non-flared collarette, 1 µm long; conidia aggregating in slimy mass, or as a dry chain. *Conidia* solitary, hyaline, smooth, granular to guttulate, subcylindrical with obtuse ends, but base somewhat truncate at times, straight to slightly curved, (5–)6–8(–10) × 1.5(–2) µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium, surface folded, margin smooth, lobate, reaching 30–45 mm diam after 2 wk at 25 °C. On MEA and PDA surface and reverse saffron. On OA surface dirty white with patches of saffron.

Typus. Australia, Western Australia, Denmark, Mount Lindesay National Park, S34°51'027" E117°16'455", on leaves of *Kingia australis* (*Dasypogonaceae*), 19 Sept. 2015, *P.W. Crous* (holotype CBS H-22879, culture ex-type CPC 28976 = CBS 142093; ITS sequence GenBank KY173415, LSU sequence GenBank KY173506, *tub2* sequence GenBank KY173603, MycoBank MB819078).

Notes — Phylogenetically *Bullanockia australis* from leaves of *Kingia australis* is related to, but distinct from species of *Ijuhya* (Rossman et al. 1999), which have acremonium-like asexual morphs (Lechat et al. 2015). It is therefore proposed as a phylogenetically distinct acremonium-like genus. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *Peristomialis corynospora* (*Bionectriaceae*, GenBank LC146752; Identities = 498/563 (88 %), Gaps = 25/563 (4 %)), *Acremonium salmoneum* (*Incertae sedis*, GenBank HM747162; Identities = 503/572 (88 %), Gaps = 18/572 (3 %)) and *Alfaria spartii* (*Stachybotriaceae*, GenBank KX822125; Identities = 481/552 (87 %), Gaps = 20/552 (3 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with *Nectria pseudopeziza* (*Nectriaceae*, GenBank KU946964; Identities = 747/785 (95 %), Gaps = 2/785 (0 %)), *Ijuhya fournieri* (*Bionectriaceae*, GenBank KP899118; Identities = 741/788 (94 %), Gaps = 7/788 (0 %)) and *Hirsutella thompsonii* (*Ophiocordycipitaceae*, GenBank KJ524692; Identities = 744/792 (94 %), Gaps = 9/792 (1 %)).

Colour illustrations. Kingia australis; conidiophores sporulating on PNA, conidiophores and conidia. Scale bars = 10 µm.

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Neothyronectria sophorae

Fungal Planet 520 – 21 December 2016

Neothyronectria Crous & Thangavel, *gen. nov.*

Etymology. Named after its morphological similarity to the asexual morph of *Thyronectria.*

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

Conidiomata pycnidial, exuding a creamy mucoid conidial mass. *Conidiophores* lining the inner surface, forming rosettes with apical conidiogenous cells, septate, subcylindrical, hyaline, smooth, branched. *Conidiogenous cells* hyaline, smooth, ampulliform to subcylindrical with prominent apical taper, phialidic. *Conidia* solitary, subcylindrical with obtuse ends, straight to slightly curved, hyaline, smooth.

Type species. *Neothyronectria sophorae* Crous & Thangavel.
MycoBank MB819079.

Neothyronectria sophorae Crous & Thangavel, *sp. nov.*

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

Conidiomata pycnidial, exuding a creamy mucoid conidial mass. *Conidiophores* lining the inner surface, forming rosettes with apical conidiogenous cells, 1–2-septate, subcylindrical, hyaline, smooth, branched, 15–30 × 3–5 µm. *Conidiogenous cells* hyaline, smooth, ampulliform to subcylindrical with prominent apical taper, phialidic, apex 1.5 µm diam, 10–15 × 2–3 µm. *Conidia* solitary, subcylindrical with obtuse ends, straight to slightly curved, hyaline, smooth, (3.5–)4–5(–6) × 1.5(–2) µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium. On OA surface luteous. On MEA surface and reverse sienna with patches of luteous. On PDA surface and reverse dirty white to pale luteous.

Typus. New Zealand, Okoia, Whanganui, on *Sophora microphylla* (*Fabaceae*), 2015, *R. Thangavel* (holotype CBS H-22880, culture ex-type CPC 29690 = CBS 142094; ITS sequence GenBank KY173470, LSU sequence GenBank KY173559, *tub2* sequence GenBank KY173619, MycoBank MB819080).

Notes — *Neothyronectria sophorae* described here is known from a pycnidial asexual morph phylogenetically allied to species of *Pleonectria* (Hirooka 2012), a genus which was later shown to be a synonym of *Thyronectria* (Jaklitsch & Voglmayr 2014, Lombard et al. 2015). *Neothyronectria* is allied to, but phylogenetically distinct from *Thyronectria.* Although the species of *Thyronectria* presently known have mostly been described from their sexual morphs, making a morphological comparison difficult, none of the known species are similar to *N. sophorae.* Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *Thyronectria virens* (GenBank KM225684; Identities = 509/561 (91 %), Gaps = 15/561 (2 %)), *Thyronectria aquifolii* (GenBank HM534891; Identities = 504/556 (91 %), Gaps = 11/556 (1 %)) and *Allantonectria miltina* (GenBank KM231835; Identities = 503/556 (90 %), Gaps = 10/556 (1 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with *Thyronectria rhodochlora* (GenBank KJ570703; Identities = 787/816 (96 %), Gaps = 2/816 (0 %)), *Thyronectria virens* (GenBank KM225684; Identities = 786/816 (96 %), Gaps = 2/816 (0 %)) and *Thyronectria pyrrhochlora* (GenBank HM484570; Identities = 780/810 (96 %), Gaps = 2/810 (0 %)).

Colour illustrations. *Sophora microphylla*; conidiomata sporulating on OA, conidiophores and conidia. Scale bars = 10 µm.

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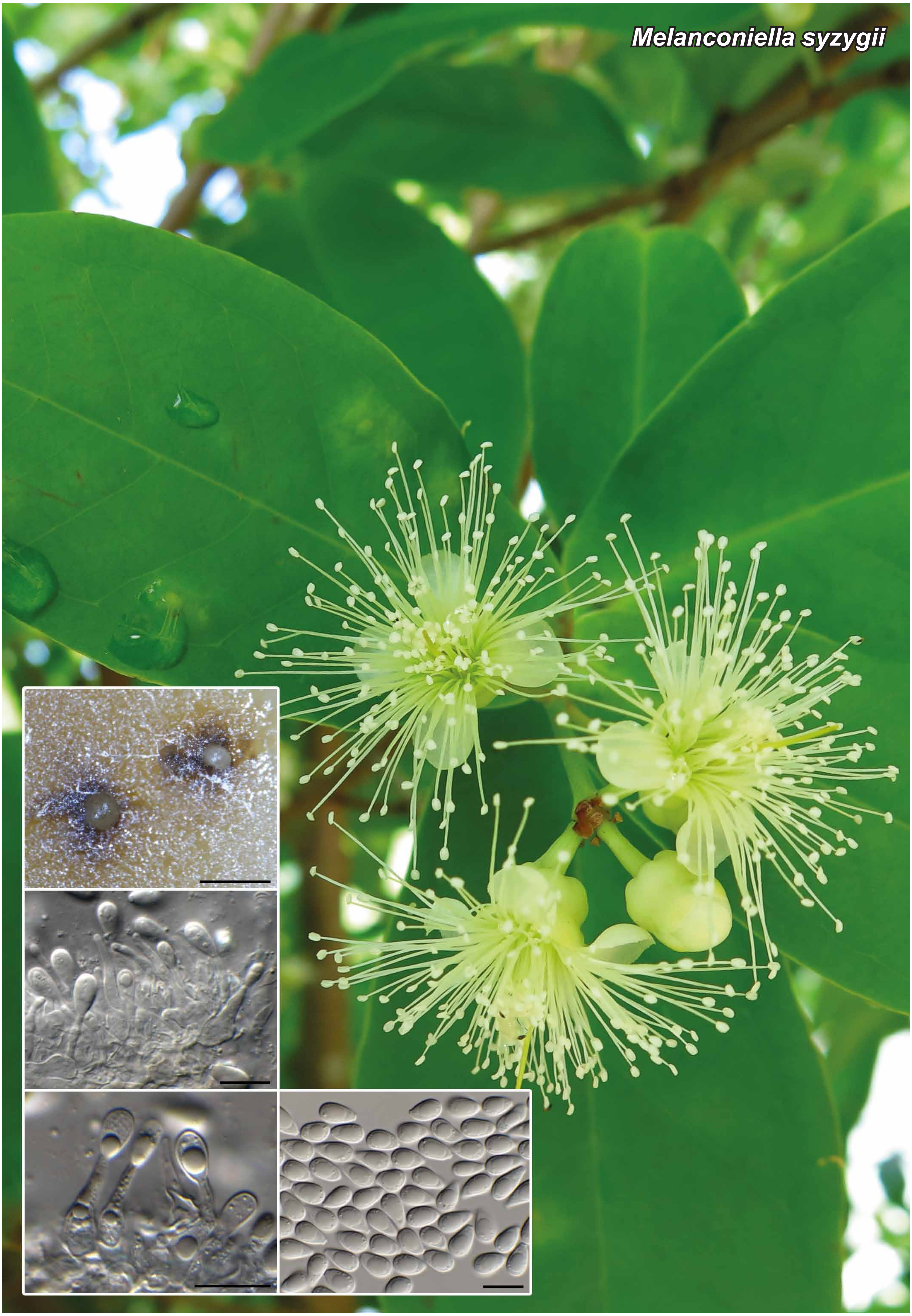
Melanconiella syzygii

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

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

Classification — *Melanconidaceae*, *Diaporthales*, *Sordariomycetes.*

Leaf spots amphigenous, subcircular, brown with a raised red-brown border, 5–30 mm diam. *Conidiomata* solitary, acervular to pycnidial, erumpent on agar, globose, up to 300 µm diam; wall of 3–6 layers of pale brown *textura angularis*. *Conidiophores* lining the inner cavity, hyaline, smooth, ampulliform, 1–2-septate, unbranched, 12–30 × 4–6 µm. *Conidiogenous cells* integrated, terminal, subcylindrical, hyaline, smooth, 7–18 × 1.5–3.5 µm, proliferating several times percurrently at apex. *Conidia* solitary, hyaline, smooth, granular, with large central guttule, thin-walled, apex obtuse, base truncate, 2 µm diam, (8–)9–10(–11) × 5(–6) µm, becoming pale brown with age, and hilum appearing slightly refractive.

Culture characteristics — Colonies flat, spreading, immersed, with sparse aerial mycelium and feathery margins, reaching 60 mm diam after 2 wk at 25 °C. On MEA surface buff, reverse cinnamon. On OA surface buff. On PDA surface honey to isabelline, reverse honey.

Typus. Malaysia, Kota Kinabalu, on leaf spots of *Syzygium* sp. (*Myrtaceae*), 30 May 2015, *M.J. Wingfield* (holotype CBS H-22882, culture ex-type CPC 28750 = CBS 142095; ITS sequence GenBank KY173417, LSU sequence GenBank KY173508, MycoBank MB819081).

Notes — *Melanconiella syzygii* is phylogenetically related to other species of *Melanconiella*, and fits the general morphology as outlined by Voglmayr et al. (2012). The fungus is associated with a prominent leaf spot disease of *Syzygium*, and as far as we could establish, no species of *Melanconiella* has been described from this host. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *Melanconiella ellisii* (GenBank JQ926271; Identities = 544/615 (88 %), Gaps = 25/615 (4 %)), *Melanconiella spodiaea* (GenBank JQ926301; Identities = 552/632 (87 %), Gaps = 34/632 (5 %)) and *Greeneria uvicola* (GenBank JN547715; Identities = 521/602 (87 %), Gaps = 23/602 (3 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with *Melanconiella spodiaea* (GenBank JQ926301; Identities = 803/815 (99 %), Gaps = 2/815 (0 %)), *Melanconiella ellisii* (GenBank JQ926271; Identities = 803/815 (99 %), Gaps = 2/815 (0 %)) and *Melanconiella chrysostroma* (GenBank AF408369; Identities = 803/815 (99 %), Gaps = 2/815 (0 %)).

Colour illustrations. *Syzygium* sp.; conidiomata sporulating on OA, conidiophores and conidia. Scale bars = 10 µm.

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Ochroconis capsici

Fungal Planet 522 – 21 December 2016

Ochroconis capsici Crous & Cheew., *sp. nov.*

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

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

Mycelium consisting of smooth, pale brown, septate, branched, 1.5–3 µm diam hyphae. *Conidiophores* solitary, erect, brown, smooth, arising from superficial hyphae, subcylindrical, straight to geniculous-sinuous, unbranched, 0–2-septate, 8–20 × 3–4.5 µm. *Conidiogenous cells* brown, smooth, terminal on conidiophores, 5–15 × 3–4.5 µm, containing several apical, cylindrical denticles, 0.5–2 × 1 µm. *Conidia* solitary, subcylindrical with obtuse ends, pale brown, verruculose, (1–)3(–5)-septate, hilum with protruding marginal frill, 0.5–1 × 1 µm, (10–)19–22(–27) × (3–)3.5(–4) µm.

Culture characteristics — Colonies reaching 10 mm diam after 2 wk at 25 °C, with moderate aerial mycelium. On MEA surface isabelline, reverse sepia. On OA surface sepia. On PDA surface umber, reverse isabelline.

Typus. Thailand, Chiang Rai, N19°48'01" E99°41'27", on *Capsicum annuum* (*Solanaceae*), 2013, *R. Cheewangkoon* (holotype CBS H-22883, culture ex-type CPC 28782 = CBS 142096; ITS sequence GenBank KY173427, LSU sequence GenBank KY173518, MycoBank MB819082).

Colour illustrations. Forest undergrowth in Thailand; conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — *Ochroconis capsici* is related to *Ochroconis verrucosa* (GenBank KF156015, Identities = 662/701 (94 %), Gaps = 6/701 (0 %); conidia 3(–4)-septate, 7.5–20 × 2.5–4 µm, conidiophores 6.3–22.5 × 2.5–3 µm; Samerpitak et al. 2014), although conidia of *O. capsici* are larger and its conidiophores are wider.

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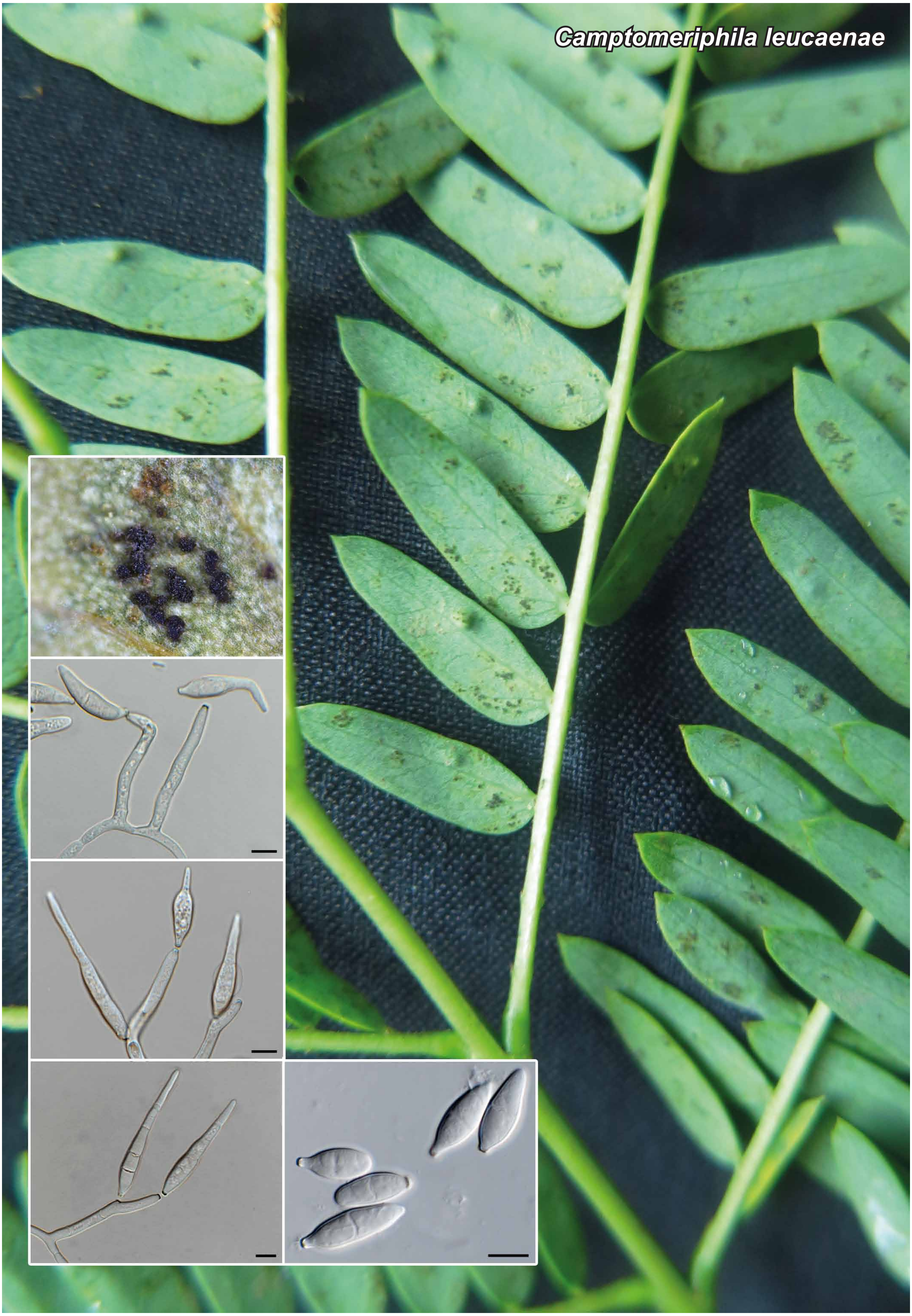
Camptomeriphila leucaenae

Fungal Planet 523 – 21 December 2016

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

Etymology. Indicating a love (mycophylic growth habit) for *Camptomeris*.

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

Mycelium consisting of branched, septate, smooth, pale brown, hyphae, forming thick-walled, brown, verruculose, intercalary chlamydospores. *Conidiophores* in loose fascicles, erect, branched, flexuous, multiseptate, pale brown, smooth. *Conidiogenous cells* integrated, terminal and lateral, subcylindrical, pale brown, smooth; scars thickened, darkened, refractive. *Conidia* solitary, fusoid-ellipsoid, becoming obclavate when mature, subhyaline to pale brown, smooth, apex subobtuse, hilum protruding, truncate, thickened, darkened, refractive.

Type species. *Camptomeriphila leucaenae* Crous & M.J. Wingf.
MycoBank MB819083.

Camptomeriphila leucaenae Crous & M.J. Wingf., *sp. nov.*

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

Description based on SNA. *Mycelium* consisting of branched, septate, smooth, pale brown, 3–5 µm diam hyphae, forming thick-walled, brown, verruculose, intercalary chlamydospores. *Conidiophores* in loose fascicles, erect, branched, flexuous, multiseptate, pale brown, smooth, 50–180 × 4–5 µm. *Conidiogenous cells* integrated, terminal and lateral, subcylindrical, pale brown, smooth, 15–35 × 4–5 µm; scars thickened, darkened, refractive, 1.5–2.5 µm. *Conidia* solitary, fusoid-ellipsoid, becoming obclavate when mature, subhyaline to pale brown, smooth, apex subobtuse, hilum protruding, truncate, thickened, darkened, refractive, 1.5–2 µm diam, (18–)26–35(–45) × (6–)7(–8) µm.

Culture characteristics — Colonies slow growing, with sparse to moderate aerial mycelium and smooth, lobate margins. On MEA surface smoke grey, reverse olivaceous grey. On OA surface olivaceous grey. On PDA surface and reverse smoke grey.

Typus. Malaysia, Sabah, on leaves of *Leucaena leucocephala* (*Fabaceae*), 29 May 2015, *M.J. Wingfield* (holotype CBS H-22884, culture ex-type CPC 27608 = CBS 142135; ITS sequence GenBank KY173392, LSU sequence GenBank KY173486, *actA* sequence GenBank KY173563, *rpb2* sequence GenBank KY173581, MycoBank MB819084).

Notes — All attempts to culture species of *Camptomeris* have thus far proven unsuccessful. In an attempt to culture a recent collection of *Camptomeris leucaenae*, which causes a leaf spot disease on *Leucaena leucocephala*, a passalora-like mycophylic fungus growing on its sporodochia was cultured. That fungus is described here as *Camptomeriphila.* Morphologically, it would not be possible to distinguish *Camptomeriphila* from the numerous other passalora-like genera that are now known to exist (Videira et al., in prep.). Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *Sirosporium diffusum* (GenBank KX344494; Identities = 501/544 (92 %), Gaps = 9/542 (1 %)), *Passalora bougainvilleae* (GenBank KF539412; Identities = 498/542 (92 %), Gaps = 7/544 (1 %)) and *Passalora capsicicola* (GenBank KJ633263; Identities = 487/531 (92 %), Gaps = 4/531 (1 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with species of *Passalora* (e.g. *P. smilacis* GenBank KJ633269; Identities = 774/792 (98 %), Gaps = 3/792 (0 %)), species of *Dothistroma* (e.g. *D. septosporum* GenBank KF251807; Identities = 771/792 (97 %), Gaps = 3/792 (0 %)) and *Phloeospora maculans* (GenBank GU214670; Identities = 773/792 (98 %), Gaps = 3/792 (0 %)).

Colour illustrations. *Leucaena leucocephala*; conidiomata of *Camptomeris leucaenae* sporulating on leaf (gets colonised by *Camptomeriphila leucaenae*), conidiophores and conidia. Scale bars = 10 µm.

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Mycodiella eucalypti

Fungal Planet 524 – 21 December 2016

Mycodiella Crous, *gen. nov.*

Etymology. Similar to the genus *Mycosphaerella*.

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

Ascomata pseudothecial, brown, erumpent, globose; wall consisting of 2–3 layers of medium brown *textura angularis*. *Asci* aparaphysate, fasciculate, bitunicate, subsessile, obovoid, straight to slightly curved, 8-spored. *Ascospores* multiseriate, overlapping, hyaline, guttulate, thin-walled, straight to slightly curved, fusoid-ellipsoidal with obtuse ends, widest in middle of apical cell, medianly 1-septate.

Type species. *Mycodiella eucalypti* Crous.
MycoBank MB819085.

Mycodiella eucalypti Crous, *sp. nov.*

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

Leaf spots on *E. diversifolia* amphigenous, irregular to subcircular, 5–10 mm diam, medium brown, slightly grey in middle with raised red-purple margin, medium brown underneath. *Ascomata* pseudothecial, amphigenous but predominantly epiphyllous, brown, characteristically bursting through epidermis, erumpent, globose, 70–120 µm diam; wall consisting of 2–3 layers of medium brown *textura angularis*. *Asci* aparaphysate, fasciculate, bitunicate, subsessile, obovoid, straight to slightly curved, 8-spored, 30–37 × 9–12 µm. *Ascospores* multiseriate, overlapping, hyaline, guttulate, thin-walled, straight to slightly curved, fusoid-ellipsoidal with obtuse ends, widest in middle of apical cell, medianly 1-septate, not constricted at the septum, tapering towards both ends, but more prominently towards lower end, (11–)12–13(–15) × (2.5–)3(–3.5) µm.

Culture characteristics — Colonies spreading, erumpent, reaching 12 mm diam after 2 wk at 25 °C, with moderate aerial mycelium and smooth, lobate margins. On MEA surface pale olivaceous grey, reverse iron-grey. On OA surface pale olivaceous grey. On PDA surface pale olivaceous grey, reverse olivaceous grey. *Ascospores* germinating from both ends, with germ tubes parallel to the long axis, remaining hyaline, becoming slightly constricted at septum, 3.5–4 µm diam.

Typus. AUSTRALIA, Western Australia, Porongurup, Porongurup National Park, S34°41'18.6" E117°55'56", on leaves of *Eucalyptus diversicolor* (*Myrtaceae*), 24 Sept. 2015, *P.W. Crous* (holotype CBS H-22885, culture ex-type CPC 29226 = CBS 142097; ITS sequence GenBank KY173419, LSU sequence GenBank KY173510, *actA* sequence GenBank KY173564, MycoBank MB819123); idem, CPC 29458 = CBS 142098; ITS sequence GenBank KY173420, LSU sequence GenBank KY173511, *actA* sequence GenBank KY173565, *rpb2* sequence GenBank KY173586.

Additional specimen examined. AUSTRALIA, Western Australia, Denmark, Mount Lindesay Walk Trail, Southern Cross, on leaves of *Xanthosia rotundifolia* (*Apiaceae*), 19 Sept. 2015, *P.W. Crous*, CPC 29525 = CBS 142099; ITS sequence GenBank KY173421, LSU sequence GenBank KY173512, *actA* sequence GenBank KY173566.

Colour illustrations. Path at Porongurup National Park; leaf spot, asci, ascospores and germinating ascospores. Scale bars = 10 µm..

Notes — The genus *Mycosphaerella* is a synonym of *Ramularia*, and clusters apart from the clade of fungi treated here (Videira et al. 2015a, b, 2016). The DNA sequences generated for these isolates are not 100 % identical (differ with up to 3 nucleotides on ITS) from one another, and additional loci may eventually show the isolate from *Xanthosia rotundifolia* to represent an additional distinct species. These isolates cluster with other known species such as '*Mycosphaerella*' *sumatrensis* (a pathogen of *Eucalyptus* in Sumatra, Indonesia; e.g. GenBank DQ303049, Identities = 470/484 (97 %), Gaps = 2/484 (0 %)), '*M.*' *laricis-leptolepidis* (e.g. GenBank JX901770, Identities = 444/468 (95 %), Gaps = 3/468 (0 %)), a quarantine organism in the EPPO region, occurring on *Larix* spp. in Asia, and '*M.*' *polygoni-cuspidati* (e.g. GenBank AB434910, Identities = 476/498 (96 %), Gaps = 3/498 (0 %)), a biological control agent of *Fallopia japonica* and recently neotypified by Kurose et al. (2009). A new genus, *Mycodiella*, is therefore introduced to accommodate these taxa. Morphologically, however, it is mycosphaerella-like, and lacks any known asexual morph. *Mycodiella* can only be distinguished from other genera in this complex based on DNA data, as they are morphologically very similar.

Mycodiella laricis-leptolepidis (Kaz. Itô, K. Satô & M. Ota) Crous, *comb. nov.* — MycoBank MB819086

Basionym. *Mycosphaerella laricis-leptolepidis* Kaz. Itô, K. Satô & M. Ota, Bull. Govt. Forest Exp. Stn Meguro 96: 84. 1957.

Description and illustration — Ito et al. (1957).

Mycodiella sumatrensis (Crous & M.J. Wingf.) Crous, *comb. nov.* — MycoBank MB819087

Basionym. *Mycosphaerella sumatrensis* Crous & M.J. Wingf., Stud. Mycol. 55: 124. 2006.

Description and illustration — Crous et al. (2006).

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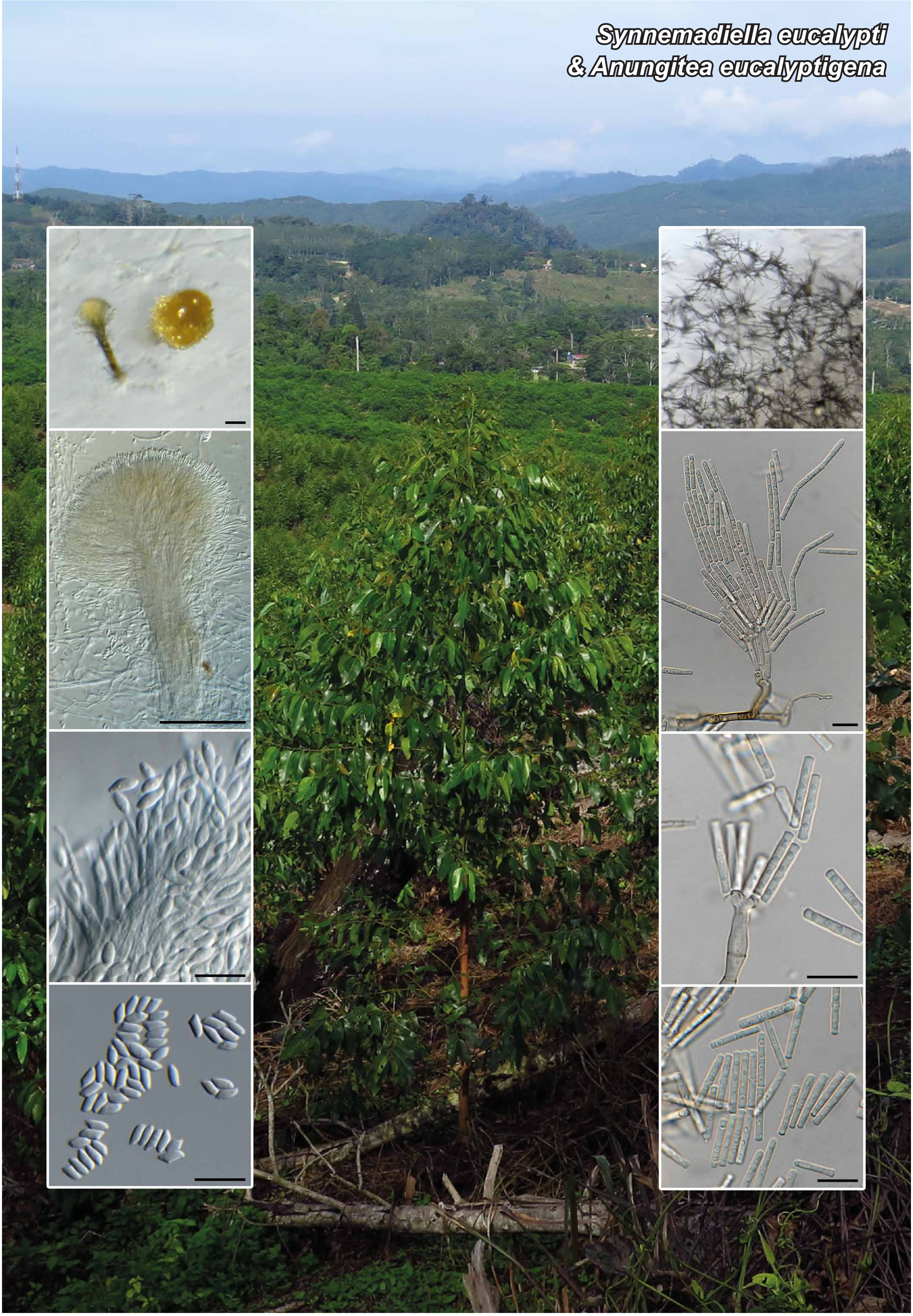
Synnemadiella eucalypti
& Anungitea eucalyptigena

Fungal Planet 525 & 526 – 21 December 2016

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

Etymology. Named after its synnematous conidiophores.

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

Mycelium consisting of hyaline, smooth, branched, septate, hyphae. *Hyphae* aggregating to form erect, solitary synnemata, consisting of numerous conidiophores, hyaline, becoming pale brown with age, forming a flaring head of conidiogenous cells, hyaline, smooth, subcylindrical with apical taper; conidiogenesis phialidic, at times with percurrent proliferation. Synasexual morph subverticillium-like, on superficial hyphae, conidiophores erect, hyaline, smooth, subcylindrical, septate. *Conidiogenous cells* subcylindrical with apical taper, hyaline, smooth, phialidic with minute collarette at apex. *Conidia* solitary, hyaline, smooth, granular, ellipsoid, but inequilateral, one side with distinct bump a third of the conidium length from the basal hilum, apex subobtuse, base truncate.

Type species. *Synnemadiella eucalypti* Crous & M.J. Wingf.
MycoBank MB819088.

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

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

Mycelium consisting of hyaline, smooth, branched, septate, 1–4 µm diam hyphae. *Hyphae* aggregating to form erect, solitary synnemata, 120–300 × 20–40 µm, consisting of numerous conidiophores, 2–3 µm diam, hyaline, becoming pale brown with age, forming a flaring head (120–200 µm diam) of conidiogenous cells, hyaline, smooth, subcylindrical with apical taper, 30–60 × 1.5–2 µm; conidiogenesis phialidic, at times with percurrent proliferation. *Synasexual morph* subverticillium-like, on superficial hyphae, conidiophores erect, hyaline, smooth, subcylindrical, 1–3-septate, 30–60 × 2–3 µm. *Conidiogenous cells* subcylindrical with apical taper, hyaline, smooth, 10–40 × 1.5–2 µm, phialidic with minute collarette at apex, 1 µm diam. *Conidia* solitary, hyaline, smooth, granular, ellipsoid, but inequilateral, one side with distinct bump a third of the conidium length from the basal hilum, apex subobtuse, base truncate, 0.5 µm diam, (9–)10–11 × 3–4 µm.

Culture characteristics — Colonies spreading, flat, with sparse to moderate aerial mycelium, and smooth, even margins. On MEA surface dirty white, reverse umber. On OA surface ochreous. On PDA surface umber in middle with dirty white outer region, and umber in reverse.

Typus. Malaysia, Kota Kinabalu, on leaf spots of *Eucalyptus pellita* (*Myrtaceae*), 1 July 2015, *M.J. Wingfield* (holotype CBS H-22886, culture ex-type CPC 27637 = CBS 142100; ITS sequence GenBank KY173467, LSU sequence GenBank KY173556, MycoBank MB819089).

Notes — *Synnemadiella* is phylogenetically related to *Castanediella* (Crous et al. 2015c, 2016). Morphologically, however, they can be distinguished from *Castanediella* by having solitary to sporodochial conidiophores, polyblastic conidiogenous cells with minute apical scars, and falcate conidia. In contrast, *Synnemadiella* forms synnemata, has phialidic conidiogenous cells with percurrent proliferation, and inequilateral, ellipsoid conidia. As we were unable to find a genus for this fungus, a new genus, *Synnemadiella*, is introduced to accommodate it. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with species of *Neopestalotiopsis* (e.g. *N. eucalypticola*, GenBank KM199376; Identities = 499/547 (91 %), Gaps =17/547 (3 %)) and *Pestalotiopsis* (e.g. *P. microspora*, GenBank AF377292; Identities = 500/549 (91 %), Gaps =19/549 (3 %)).

Anungitea eucalyptigena Crous & M.J. Wingf., *sp. nov.*

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

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

Conidiomata sporodochial in older cultures, visible as hyphal tufts on younger growth. *Conidiophores* arising from superficial mycelium on SNA, erect, unbranched. *Conidiogenous cells* terminal, integrated, subcylindrical, 7–20 × 3–4 µm, pale brown, smooth, with several flat-tipped sympodially arranged loci, 2–2.5 µm diam, not thickened nor darkened. *Ramoconidia* pale brown, smooth, 0–1-septate, subcylindrical with truncate base and several sympodially arranged truncate apical loci, 2 µm diam, 16–20 × 2.5–3 µm. *Conidia* cylindrical, hyaline, smooth, guttulate, 0–1-septate, in long, unbranched chains, (11–)14–16(–18) × (2–)2.5(–3) µm; hila truncate, not thickened nor darkened.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margins. On MEA surface ochreous with diffuse umber pigment in agar, reverse umber. On OA surface chestnut. On PDA surface and reverse chestnut.

Typus. Malaysia, Kota Kinabalu, on leaf spots of *Eucalyptus grandis* × *pellita* (*Myrtaceae*), 30 May 2015, *M.J. Wingfield* (holotype CBS H-22888, culture ex-type CPC 28762 = CBS 142102; ITS sequence GenBank KY173383, LSU sequence GenBank KY173477, MycoBank MB819090).

Notes — *Anungitea eucalyptigena* is similar to *A. eucalyptorum* (conidia 0–1-septate, (13–)14–15(–17) × 2.5(–3) µm; Crous et al. 2014) and *A. grevilleae* (conidia 0–1-septate, (10–)13–16(–22) × (2–)2.5–3 µm; Crous et al. 2016), and is best distinguished based on its DNA sequence data.

Colour illustrations. Eucalyptus pellita; *Synnemadiella eucalypti* (left column), synnemata, conidiogenous cells and conidia; *Anungitea eucalyptigena* (right column), conidiophores sporulating on PNA, conidiophores and conidia. Scale bars = 100 µm (synnemata), 10 µm (all others).

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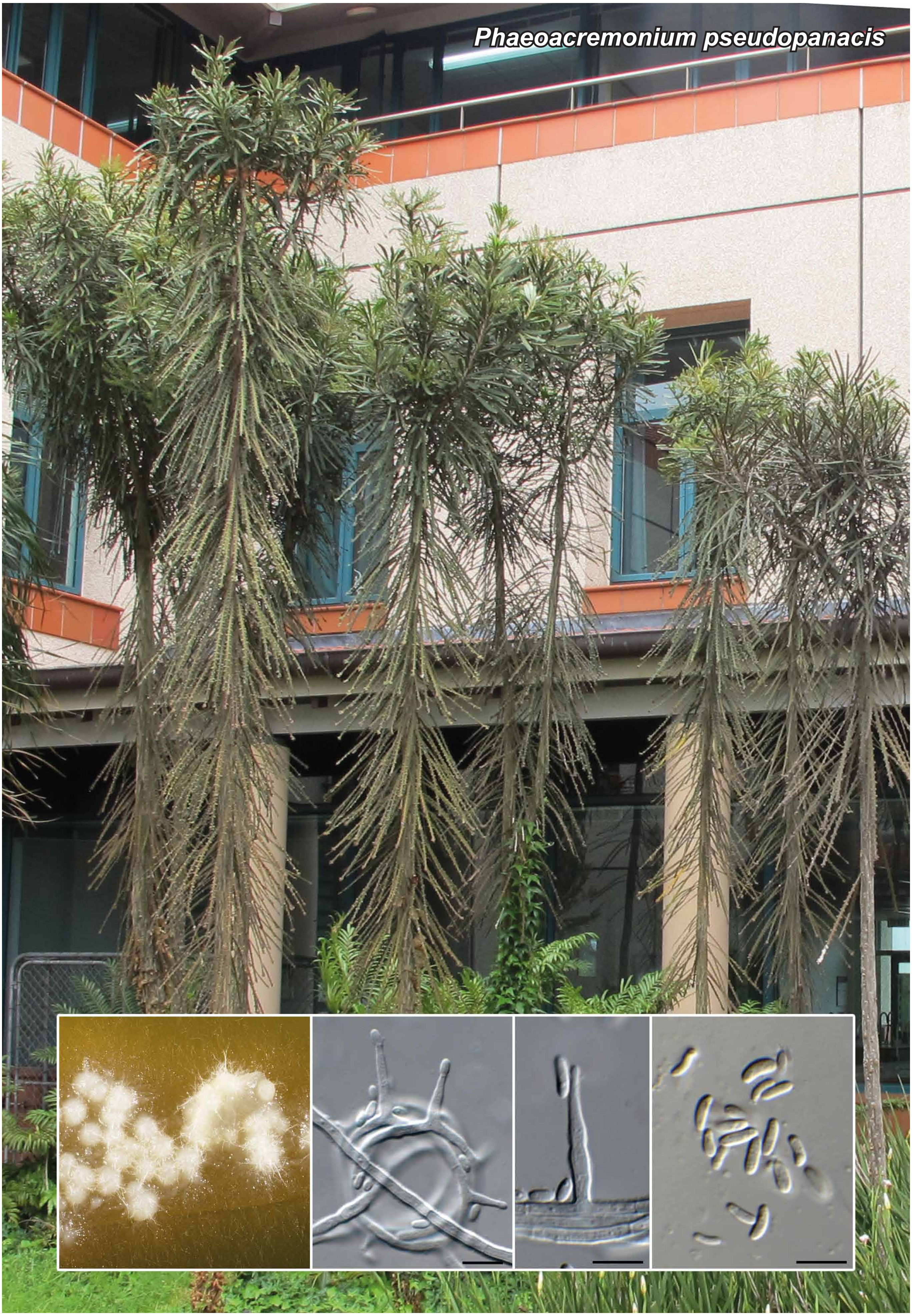
Phaeoacremonium pseudopanacis

Fungal Planet 527 – 21 December 2016

Phaeoacremonium pseudopanacis Crous & Thangavel, *sp. nov.*

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

Classification — *Togniniaceae*, *Togniniales*, *Sordariomycetes.*

Mycelium consisting of branched, septate, 2–2.5 µm diam smooth, hyaline hyphae that form hyphal strands. *Conidiophores* arising from aerial hyphae, erect, simple, or 1–3-septate, branched or not, at times reduced to conidiogenous cells (adelophialides), smooth, hyaline. *Conidiogenous cells* phialidic, terminal and intercalary, monophialidic, naviculate to subcylindrical, smooth, hyaline, collarettes 1–2 µm long, 1 µm wide, 5–25 × 2.5–3 µm. *Conidia* allantoid, subcylindrical with obtuse ends, hyaline, smooth, guttulate, aseptate, (4–)5–6(–7) × (2–)2.5(–3) µm.

Culture characteristics — Colonies erumpent, with sparse aerial mycelium, and feathery margins, reaching 10 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white, buff in reverse.

Typus. New Zealand, Hunua range, Auckland, on *Pseudopanax crassifolius* (*Araliaceae*), 2015, *R. Thangavel* (holotype CBS H-22887, culture ex-type CPC 28694 = CBS 142101; ITS sequence GenBank KY173429, LSU sequence GenBank KY173519, *actA* sequence GenBank KY173569, *tub2* sequence GenBank KY173609, MycoBank MB819091).

Notes — More than 40 species of *Phaeoacremonium* (= *Togninia*) are recognised, many of which are associated with Petri disease of grapevines, brown wood streaking, or phaeohyphomycosis in humans (Mostert et al. 2005, 2006, Gramaje et al. 2015). Presently, species are best distinguished via a comparison of DNA sequence data (www.cbs.knaw.nl/phaeoacremonium/), which shows *P. pseudopanax* to be closely related to, but distinct from *P. angustius*, *P. austroafricanum*, *P. roseum* and *P. viticola*. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *P. angustius* (GenBank KU060813; Identities = 587/592 (99 %), Gaps = 2/592 (0 %)), *P. viticola* (GenBank EU128045; Identities = 549/554 (99 %), Gaps = 2/554 (0 %)) and *P. roseum* (GenBank KF764534; Identities = 573/579 (99 %), Gaps = 2/579 (0 %)). Based on a megablast search of the NCBIs nucleotide database using the *actA* sequence, the highest similarities were with *P. viticola* (GenBank EU863506; Identities = 235/245 (99 %), Gaps = 4/245 (1 %)), *P. austroafricanum* (GenBank DQ173122; Identities = 233/245 (95 %), Gaps = 3/245 (1 %)) and *P. angustius* (GenBank DQ173126; Identities = 229/245 (93 %), Gaps = 4/245 (1 %)). Based on a megablast search of the NCBIs nucleotide database using the *tub2* sequence, the highest similarities were with *P. roseum* (GenBank KF764658; Identities = 653/679 (96 %), Gaps = 3/679 (0 %)), *P. viticola* (GenBank EU128093; Identities = 668/695 (96 %), Gaps = 3/695 (0 %)) and *P. angustius* (GenBank AF246815; Identities = 505/530 (95 %), Gaps = 3/530 (0 %)).

Colour illustrations. *Pseudopanax crassifolius*; colony on MEA, conidiogenous cells and conidia. Scale bars = 10 µm.

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Phlogicylindrium mokarei

Fungal Planet 528 – 21 December 2016

Phlogicylindrium mokarei Crous, *sp. nov.*

Etymology. Name refers to 'Mokare' (c. 1800–26 June 1831), an indigenous Australian Noogar from the south-west corner of Australia, who was pivotal in aiding European exploration of the area, and showed explorers the various walking trails in the area where this fungus was collected.

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

Conidiomata sporodochial (rarely as hyphal tufts with solitary conidiophores), with conidiophores arising from a brown stroma up to 60 µm diam. *Conidiophores* aggregated in clusters, medium brown, smooth, erect, subcylindrical, 17–40 × 3–4 µm, 1–4-septate. *Conidiogenous cells* terminal and intercalary, integrated, subcylindrical to doliiform with apical taper, 10–20 × 3–4 µm, with several flat-tipped sympodially arranged loci, 2 µm diam, not thickened nor darkened; at times proliferating percurrently. *Conidia* cylindrical, straight, hyaline, smooth, guttulate, 1(–3)-septate, becoming pale brown with age, in long, unbranched chains, (17–)18–21(–23) × (2–)2.5 µm; hila truncate, not thickened nor darkened.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium; surface folded, margins smooth, lobate. On MEA surface chestnut with spots of dirty white, reverse chestnut. On OA surface chestnut. On PDA surface and reverse umber.

Typus. Australia, Western Australia, Denmark, Mount Lindesay Walk Trail, on *Eucalyptus* sp. (*Myrtaceae*), 19 Sept. 2015, *P.W. Crous* (holotype CBS H-22889, culture ex-type CPC 29306 = CBS 142103; ITS sequence GenBank KY173431, LSU sequence GenBank KY173521, MycoBank MB819092).

Notes — The genus *Phlogicylindrium* was introduced for a genus of hyphomycetes occurring on *Eucalyptus*, with sporodochia to flame-like conidial tufts, conidiophores with percurrent proliferation, and 0–1-septate, hyaline, cylindrical conidia (Summerell et al. 2006). *Phlogicylindrium mokarei* is related to *P. uniforme* (conidia 1-septate, (14–)16–20(–21) × (1.5–)2(–2.5) µm; Crous et al. 2011a), and *P. eucalyptorum* (conidia 1(–3)-septate, (27–)40–50(–55) × 2–2.5(–3) µm; Crous et al. 2007a). Morphologically, it is closest to *P. uniforme* in conidial dimensions, and the two species are best separated based on their DNA sequence data. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *P. eucalyptorum* (GenBank EU040222; Identities = 584/590 (99 %), no gaps), *P. uniforme* (GenBank JQ044426; Identities = 571/578 (99 %), no gaps) and *P. eucalypti* (GenBank DQ923534; Identities = 580/592 (98 %), Gaps = 3/592 (0 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with *P. uniforme* (GenBank JQ044445; Identities = 816/818 (99 %), no gaps), *P. eucalyptorum* (GenBank EU040223; Identities = 812/818 (99 %), no gaps) and *Anungitea eucalyptorum* (GenBank KJ869176; Identities = 807/818 (99 %), Gaps = 1/818 (0 %)).

Colour illustrations. Mount Lindesay Walk Trail; conidiophores and conidia. Scale bars = 10 µm.

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Phyllosticta acaciigena

Fungal Planet 529 – 21 December 2016

Phyllosticta acaciigena Crous & J. Edwards, *sp. nov.*

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

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

Conidiomata pycnidial, solitary, black, erumpent, globose, exuding colourless conidial masses; pycnidia up to 250 µm diam; wall of several layers of brown *textura angularis*. *Ostiole* central, up to 30 µm diam. *Conidiophores* subcylindrical to ampulliform, reduced to conidiogenous cells. *Conidiogenous cells* terminal, subcylindrical, hyaline, smooth, coated in a mucoid layer, 7–15 × 3–5 µm, proliferating several times percurrently near apex. *Conidia* (10–)12–15(–16) × 7(–8) µm, solitary, hyaline, aseptate, thin- and smooth-walled, coarsely guttulate, ellipsoid to obovoid, tapering towards a truncate base, 3 µm diam, enclosed in a mucoid sheath, 2–3 µm thick, and bearing a hyaline apical mucoid appendage, (7–)15–20(–22) × 1.5(–2) µm, tapering towards an acute tip.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and feathery, lobate margins, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface and reverse iron-grey. On PDA surface olivaceous grey. On OA surface olivaceous grey with diffuse yellow pigment in agar.

Typus. Australia, Victoria, near Anglesea, on *Acacia suaveolens* (*Fabaceae*), 9 Apr. 1986 (holotype CBS H-22890, culture ex-type CPC 28295 = VPRI 13730 = CBS 142104; ITS sequence GenBank KY173433, LSU sequence GenBank KY173523, *actA* sequence GenBank KY173570, MycoBank MB819093).

Colour illustrations. Beach area near Anglesea; conidiomata sporulating on PDA, conidiophores and conidia. Scale bars = 10 µm.

Notes — *Phyllosticta acaciigena* is distinct, but phylogenetically related to *P. aloeicola* (on *Aloe*; Wikee et al. 2013b), *P. aristolochiicola* (on *Aristolochia*; Crous et al. 2012a) and *P. capitalensis* (a common saprobe with a wide host range; Wikee et al. 2013a). It must also be compared with *P. acaciicola* (on *Acacia*, conidia 5–8 × 3–3.5 µm; Van der Aa & Vanev 2002), but the latter species is clearly distinct, having much smaller conidia. A new species is thus introduced to accommodate this taxon occurring on *Acacia* leaves in Australia. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *P. aristolochiicola* (GenBank KT072733; Identities = 532/554 (96 %), Gaps = 6/554 (1 %)), *Guignardia mangiferae* (GenBank JF261459; Identities = 552/580 (95 %), Gaps = 15/580 (2 %)) and *P. carochlae* (GenBank KJ847422; Identities = 608/645 (94 %), Gaps = 21/645 (3 %)). Based on a megablast search of the NCBIs nucleotide database using the *actA* sequence, the highest similarities were with *P. conjac* (GenBank AB704239; Identities = 197/205 (96 %), Gaps = 1/205 (0 %)), *P. sphaeropsoidea* (GenBank AB704227; Identities = 197/205 (96 %), Gaps = 1/205 (0 %)) and *P. harai* (GenBank AB704219; Identities = 197/205 (96 %), Gaps = 1/205 (0 %)).

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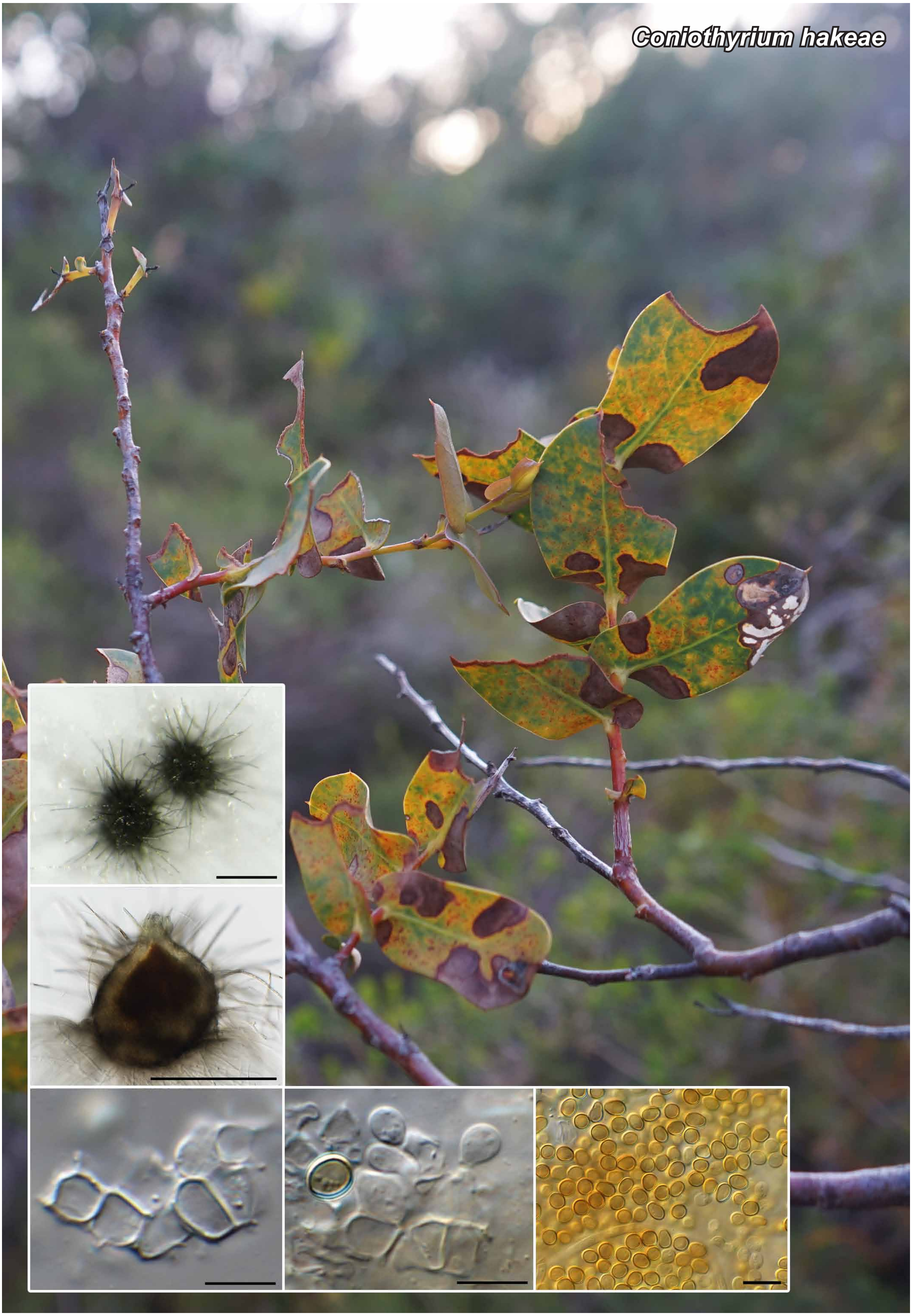
Coniothyrium hakeae

Fungal Planet 530 – 21 December 2016

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

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

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

Conidiomata erumpent, solitary, brown, globose, uniloculate, 100–170 µm diam, with central ostiole that is slightly papillate, 20–35 µm diam; wall of 2–3 layers of brown *textura angularis*; wall covered with brown, flexuous setae, thick-walled, unbranched, 1–12-septate, base smooth, apex slightly roughened, tapering to subobtuse apex, 50–170 × 4–7 µm. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, ampulliform to doliiform, 5–7 × 3–6 µm; phialidic with periclinal thickening, or percurrent proliferation at apex. *Conidia* solitary, globose to broadly ellipsoid or slightly clavate, apex obtuse, base truncate, becoming golden brown, finely verruculose, (5–)6(–7) × (3–)4(–4.5) µm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium, and smooth, lobate margins, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface pale olivaceous grey, reverse smoke grey. On OA surface olivaceous grey. On PDA surface olivaceous grey with patches of pale olivaceous grey, reverse olivaceous grey.

Typus. Australia, Western Australia, Perth, Periwinkle Park, on *Hakea* sp. (*Proteaceae*), 15 June 2015, *P.A. Barber* (holotype CBS H-22891, culture ex-type CPC 27620 = CBS 142105; ITS sequence GenBank KY173398, LSU sequence GenBank KY173491, *rpb2* sequence GenBank KY173583, *tub2* sequence GenBank KY173600, MycoBank MB819094).

Additional specimen examined. Australia, Western Australia, Perth, Fernwood Park, on leaves of *Banksia attenuata* (*Proteaceae*), 15 June 2015, *P.A. Barber*, CPC 27616 = CBS 142106. – New Zealand, Auckland, Browns Bay, on *Metrosideros excelsa* (*Myrtaceae*), 2015, *R. Thangavel*, CPC 29612; ITS sequences GenBank KY173397, KY173399, LSU sequences GenBank KY173490, KY173492, *rpb2* sequences GenBank KY173582, KY173584, *tub2* sequences GenBank KY173599, KY173601, respectively.

Colour illustrations. Symptomatic leaves of *Hakea* sp.; conidiomata (note setae) sporulating on PNA, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — Phylogenetically, *Coniothyrium hakeae* clusters with species of *Coniothyrium*, such as *C. telepathii* and *C. multiporum* (see De Gruyter et al. 2013). Morphologically, however, these isolates do not fit the concept of *Coniothyrium palmarum*, as they have conidiomata covered by prominent, flexuous, brown setae. It is possible that this clade will eventually be shown to represent a sister genus to *Coniothyrium* s.str., but for the present it is best accommodated in *Coniothyrium*. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *Ochrocladosporium elatum* (GenBank EU040233; Identities = 475/504 (94 %), Gaps = 5/504 (0 %)), *Coniothyrium carteri* (GenBank KF251209; Identities = 532/564 (94 %), Gaps = 9/564 (1 %)) and *Ochrocladosporium frigidarii* (GenBank EU040234; Identities = 475/504 (94 %), Gaps = 5/504 (0 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with *Wojnowicia dactylidis* (GenBank KP684149; Identities = 822/832 (99 %), Gaps = 4/832 (0 %)), *Coniothyrium telephii* (GenBank GQ387599; Identities = 820/830 (99 %), no gaps) and *Ochrocladosporium elatum* (GenBank EU040233; Identities = 820/830 (99 %), Gaps = 1/830 (0 %)).

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Parastagonospora phoenicicola
& Phlyctema phoenicis

Fungal Planet 531 & 532 – 21 December 2016

Parastagonospora phoenicicola Crous & Thangavel, *sp. nov.*

Etymology. Name refers to *Phoenix*, the host genus from which this fungus was collected ('inhabitant of *Phoenix*').

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

Conidiomata pycnidial, solitary, immersed to erumpent, globose, brown with central ostiole, 120–300 µm diam; wall of 3–5 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* subhyaline, smooth, ampulliform to doliiform, 5–7 × 5–6 µm; proliferating inconspicuously percurrently at apex. *Conidia* solitary, pale brown, smooth, guttulate, subcylindrical, straight or curved, apex obtuse, base truncate with flat scar, 0.5 µm diam, 1–3-septate, (8–)12–14(–16) × (2–)2.5(–3) µm.

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

Typus. New Zealand, Auckland, Botany road, *Phoenix canariensis* (*Arecaceae*), 2015, *R. Thangavel* (holotype CBS H-22892, culture ex-type CPC 28711 = CBS 142107; ITS and LSU sequence GenBank KY173428, MycoBank MB819095).

Notes — *Parastagonospora phoenicicola* is related to, but phylogenetically distinct from *P. nodorum* (see Quaedvlieg et al. 2013). As no species of *Parastagonospora* is presently known from *Phoenix canariensis*, a new species is introduced to accommodate this isolate. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *Parastagonospora nodorum* (GenBank KF512822; Identities = 485/494 (98 %), no gaps), *Neosulcatispora strelitziae* (GenBank KX228253; Identities = 531/543 (98 %), Gaps = 3/543 (0 %)) and *Phaeosphaeria podocarpi* (GenBank KP004452; Identities = 533/553 (96 %), Gaps = 9/553 (1 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with *Phaeosphaeriopsis musae* (GenBank DQ885894; Identities = 941/943 (99 %), no gaps), *Parastagonospora nodorum* (GenBank JX681113; Identities = 901/906 (99 %), no gaps) and *Didymocyrtis foliaceiphila* (GenBank JQ318010; Identities = 882/887 (99 %), no gaps).

Phlyctema phoenicis Crous & Thangavel, *sp. nov.*

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

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

Conidiomata eustromatic, superficial to immersed, separate, 200–300 µm diam, initially closed, spherical, buff, becoming more cinnamon in colour once open. *Conidiophores* hyaline, smooth, subcylindrical, branched, 1–4-septate, 10–70 × 2–3 µm, with *conidiogenous cells* terminal and intercalary, phialidic, subcylindrical to cymbiform, 8–15 × 2–3 µm; frequently with minute collarette and periclinal thickening, encased in mucoid layer. *Conidia* solitary, hyaline, smooth, guttulate, aseptate, subcylindrical to fusiform with rounded ends, curved, (17–)24–26(–27) × 2(–2.5) µm.

Culture characteristics — Colonies erumpent, spreading, reaching 35 mm diam after 2 wk at 25 °C, with moderate aerial mycelium, and smooth, feathery, lobate margins. On MEA surface dirty white, reverse ochreous. On OA surface dirty white. On PDA surface bay with diffuse scarlet pigment in agar, reverse chestnut.

Typus. New Zealand, Auckland, Botany road, *Phoenix canariensis* (*Arecaceae*), 2015, *R. Thangavel* (holotype CBS H-22881, culture ex-type CPC 29372 = CBS 142134 = T15_05353B; ITS sequence GenBank KY173432, LSU sequence GenBank KY173522, *tub2* sequence GenBank KY173611, MycoBank MB819096).

Notes — The *Neofabraea* complex was recently revised by Chen et al. (2016), who resurrected the genus *Phlyctema*. *Phlyctema phoenicis* is allied to but phylogenetically distinct from presently known species. No species of *Phlyctema* have thus far been described from *Phoenix*. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *Neofabraea* sp. (GenBank KF251242; Identities = 510/510 (100 %), no gaps), *Neofabraea kienholzii* (GenBank KR859083; Identities = 542/544 (99 %), no gaps) and *Neofabraea inaequalis* (GenBank KR859081; Identities = 543/548 (99 %), Gaps = 1/548 (0 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with *Neofabraea alba* (GenBank AY064705; Identities = 826/827 (99 %), no gaps), *Phlyctema vagabunda* (GenBank KR859069; Identities = 825/826 (99 %), no gaps) and *Pseudofabraea citricarpa* (GenBank KR859075; Identities = 824/827 (99 %), no gaps).

Colour illustrations. *Phoenix canariensis* growing at Pakuranga Golf course, New Zealand. *Parastagonospora phoenicicola* (left column); conidioma on OA, conidiogenous cells and conidia. *Phlyctema phoenicis* (right column); conidiomata sporulating on OA, conidiophores and conidia. Scale bars = 300 µm (conidioma of *Parastagonospora phoenicicola*), 10 µm (all others).

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Neoascochyta adenii

Fungal Planet 533 – 21 December 2016

Neoascochyta adenii Crous & Cheew., *sp. nov.*

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

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

Conidiomata solitary, uniloculate, brown, erumpent, globose, 120–200 µm diam with central ostiole, papillate, 20–30 µm diam; apical region covered by brown, straight, thick-walled, roughened setae, 1–12-septate, 50–220 × 7–11 µm; conidiomatal wall of 3–4 layers of brown *textura angularis. Conidiophores* subcylindrical, hyaline, smooth, branched, 1–3-septate, 15–45 × 4–7 µm. *Conidiogenous cells* subcylindrical with slight apical taper, hyaline, smooth, 12–17 × 3–4 µm, phialidic, with prominent periclinal thickening at apex. *Conidia* solitary, hyaline, smooth, guttulate, subcylindrical to narrowly obclavate, medianly 1-septate, apex subobtuse, base truncate, 2 µm diam, (21–)23–25(–27) × (2.5–)3(–3.5) µm.

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

Typus. THAILAND, Chiang Mai, Baan Kooh Dang, Nong Fag district, Sarapee, on *Adenium obesum* (*Apocynaceae*), 2013, *R. Cheewangkoon* (holotype CBS H-22893, culture ex-type CPC 28795 = CBS 142108; ITS sequence GenBank KY173423, LSU sequence GenBank KY173514, *rpb2* sequence GenBank KY173587, *tub2* sequence GenBank KY173607, MycoBank MB819097).

Notes — *Neoascochyta adenii* is related to several species of *Neoascochyta*, but is the first species to be described from *Adenium*. Morphologically, it fits the concept of *Neoascochyta* other than the fact that it has conidiomatal setae, whereas the original description (Chen et al. 2015) mentions only hyphal outgrowths associated with conidiomata. Based on its phylogenetic position, however, we have elected to allocate this fungus to *Neoascochyta.* Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *Phoma pereupyrena* (GenBank KJ767076; Identities = 488/547 (89 %), Gaps = 13/547 (2 %)), *Neoascochyta exitialis* (GenBank EU167564; Identities = 494/554 (89 %), Gaps = 15/554 (2 %)) and *Stagonosporopsis cucurbitacearum* (GenBank KT989559; Identities = 492/552 (89 %), Gaps = 13/552 (2 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with *Phaeomycocentrospora cantuariensis* (GenBank GU253716; Identities = 806/821 (98 %), Gaps = 1/821 (0 %)), *Neoascochyta desmazieri* (GenBank KT389725; Identities = 804/821 (98 %), Gaps = 1/821 (0 %)) and *Neoascochyta* sp. (GenBank EU754134; Identities = 804/821 (98 %), Gaps = 1/821 (0 %)).

Colour illustrations. *Adenium obesum* growing in Chiang Mai; conidioma sporulating on PNA, conidiophores, setae and conidia. Scale bars = 200 µm (conidioma), 10 µm (all others).

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Pyrenochaeta hakeae

Fungal Planet 534 – 21 December 2016

Pyrenochaeta hakeae Crous, *sp. nov.*

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

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

Conidiomata solitary, erumpent, globose, with central ostiole, 50–90 µm diam, with central ostiole, 15–25 µm diam; wall of 3–4 layers of brown *textura angularis*. *Conidiophores* hyaline to pale brown, lining the inner cavity, branched, 1–3-septate, 7–25 × 2–3 µm. *Conidiogenous cells* terminal and intercalary, subcylindrical, hyaline, smooth to pale brown (on OA with age), 4–6 × 2.5–3.5 µm, with visible periclinal thickening. *Conidia* solitary, hyaline, smooth, guttulate, subcylindrical with obtuse ends, 3–3.5(–4) × 2 µm.

Culture characteristics — Colonies spreading, flat, with sparse to moderate aerial mycelium and lobate, feathery margins, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface olivaceous grey to pale olivaceous grey, reverse sienna. On OA surface olivaceous grey. On PDA surface and reverse olivaceous grey.

Typus. Australia, Western Australia, Denmark, Lights Beach, on leaves of *Hakea* sp. (*Proteaceae*), 19 Sept. 2015, *P.W. Crous* (holotype CBS H-22894, culture ex-type CPC 28920 = CBS 142109; ITS sequence GenBank KY173436, LSU sequence GenBank KY173526, *rpb2* sequence GenBank KY173593, *tub2* sequence GenBank KY173613, MycoBank MB819098).

Colour illustrations. Beach area in Denmark, Australia; conidiomata sporulating on OA, conidiomata, conidiogenous cells and conidia. Scale bars = 100 µm (conidiomata), 10 µm (all others).

Notes — This phoma-like fungus occurring on leaves of *Hakea* in Australia is phylogenetically allied to species of *Pyrenochaeta*. Morphologically, it also fits the concept well, and as no species are known from *Hakea*, a new taxon, *P. hakeae*, is introduced to accommodate it. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *Pyrenochaeta cava* (GenBank JF440610; Identities = 462/482 (96 %), Gaps = 4/482 (0 %)), *Ochrocladosporium frigidarii* (GenBank FJ755255; Identities = 448/469 (96 %), Gaps = 4/469 (0 %)) and *Ochrocladosporium elatum* (GenBank GU248334; Identities = 485/515 (94 %), Gaps = 7/515 (1 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with *Pyrenochaeta unguis-hominis* (GenBank GQ387621; Identities = 824/836 (99 %), Gaps = 2/836 (0 %)), *Pyrenochaeta quercina* (GenBank GQ387620; Identities = 823/836 (98 %), Gaps = 2/836 (0%)) and *Fenestella fenestrata* (GenBank GU205220; Identities = 820/836 (99 %), Gaps = 2/836 (0%)).

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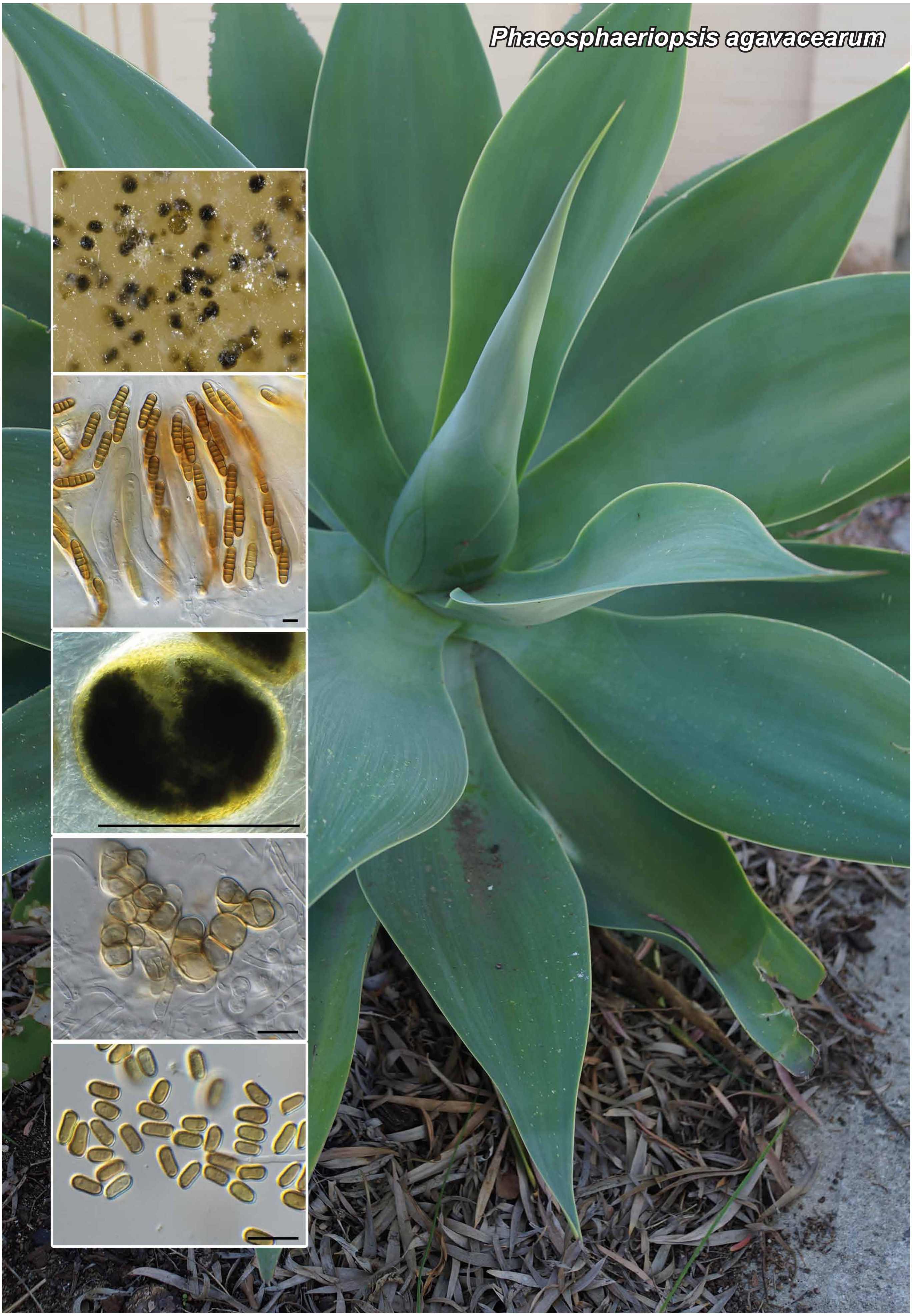
Phaeosphaeriopsis agavacearum

Fungal Planet 535 – 21 December 2016

Phaeosphaeriopsis agavacearum Crous, *sp. nov.*

Etymology. Name refers to the family *Agavaceae* (now considered a subfamily of the *Asparagaceae*), the host family from which this fungus was collected.

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

Ascomata immersed, subepidermal, 200–300 µm diam, somewhat erumpent, globose, unilocular, dark brown, solitary, papillate, with central ostiole, 20–30 µm diam; wall of several layers of brown *textura angularis*. *Paraphyses* intermingled among asci, hyphae-like, hyaline, smooth, septate, 2.5–3.5 µm diam. *Asci* fasciculate, stipitate, subcylindrical, bitunicate, 8-spored, 80–100 × 8–11 µm. *Ascospores* bi- to triseriate in asci, subcylindrical with obtuse ends, 5-septate, 4th cell from apex somewhat swollen, golden brown, verruculose, (16–)19–20(–22) × (5–)6(–7) µm. *Mycelium* consisting of hyaline, smooth, branched, septate, 2–4 µm diam hyphae, forming chains of brown, globose chlamydospores, 7–10 µm diam. *Conidiomata* pycnidial, immersed, mostly solitary, globose to subglobose, 120–180 µm diam, with central ostiole, 20–30 µm diam; wall of 2–4 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, ampulliform, 5–10 × 3–5 µm, phialidic with periclinal thickening or aggregated percurrent proliferations. *Conidia* solitary, golden brown, verruculose, subcylindrical, apex obtuse, base truncate, straight to slightly curved, (5–)6–7(–9) × 3(–4) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium, and even, lobate margins. On MEA surface dirty white, reverse umber with patches of dirty white. On OA surface dirty white with patches of grey olivaceous (due to sporulation). On PDA surface and reverse dirty white.

Typus. AUSTRALIA, Western Australia, Fremantle, Suffolk Street, leaves of *Agave* sp. (*Agavaceae* = *Asparagaceae* subg. *Agavoideae*), 15 Sept. 2015, *P.W. Crous* (holotype CBS H-22895, culture ex-type CPC 29122 = CBS 142110; ITS sequence GenBank KY173430, LSU sequence GenBank KY173520, *rpb2* sequence GenBank KY173591, *tub2* sequence GenBank KY173610, MycoBank MB819099).

Colour illustrations. Agave sp.; conidiomata sporulating on OA, conidioma, chlamydospores and conidia. Scale bars = 300 µm (conidioma), 10 µm (all others).

Notes — *Phaeosphaeriopsis agavacearum* is the second species in this genus to be described from *Agave.* However, the other species *P. agavensis* has conidia that are smaller (4–6.5 × 1.5–2.5 µm) and ascospores that are larger (28.5–36.5 × 8.5–11 µm; Ramaley 1997), and based on ITS sequence data, cultures identified as *P. agavensis* (GenBank AF250828 and AF250823; 501/564 (89 %) and 465/528 (88 %), respectively) are only 88–89 % identical to *P. agavacearum.* Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *Phaeosphaeriopsis obtusispora* (GenBank AF250822; Identities = 544/563 (97 %), Gaps = 1/563 (0 %)), *Coniothyrium vitivorum* (GenBank EU520058; Identities = 559/583 (96 %), Gaps = 5/583 (0 %)) and *Phaeosphaeriopsis triseptata* (GenBank KJ522476; Identities = 545/570 (96 %), Gaps = 5/570 (0 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with *Phaeosphaeriopsis obtusispora* (GenBank JX681119; Identities = 826/827 (99 %), no gaps), *Coniothyrium concentricum* (GenBank EU754152; Identities = 825/827 (99 %), no gaps) and *Leptospora rubella* (GenBank DQ195792; Identities = 823/827 (99 %), no gaps).

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Pleurophoma acaciae

Fungal Planet 536 – 21 December 2016

Pleurophoma acaciae Crous, *sp. nov.*

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

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

Conidiomata globose, erumpent, mostly aggregated in small clusters (3–5), uni- to multilocular, 70–160 µm diam, pale brown, apical region dark brown, ostiole papillate, 20–35 µm diam. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, subcylindrical to ampulliform, 5–12 × 3–4 µm; phialidic with periclinal thickening or percurrent proliferation (inconspicuous). *Conidia* solitary, subcylindrical, aseptate, hyaline, smooth, mostly straight, granular with obtuse ends, (4–)5–6(–6.5) × 2(–2.5) µm.

Culture characteristics — Colonies spreading, with moderate aerial mycelium (MEA), sparse aerial mycelium on PDA and OA, with even, lobate margins, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse luteous. On OA surface pale luteous. On PDA surface and reverse pale luteous.

Typus. Australia, Western Australia, Williams, Williams Nature Reserve, on leaves of *Acacia glaucoptera* (*Fabaceae*), 18 Sept. 2015, *P.W. Crous* (holotype CBS H-22896, culture ex-type CPC 29188 = CBS 142111; ITS sequence GenBank KY173434, LSU sequence GenBank KY173524, *rpb2* sequence GenBank KY173592, *tub2* sequence GenBank KY173612, MycoBank MB819100).

Notes — Crous et al. (2015c) reported a sexual morph for *Pleurophoma*, and commented on the potential link with the genus *Keissleriella*, which is also apparent in the phylogenetic relationships emerging for the present fungus. Presently, no *Pleurophoma* spp. are known from *Acacia*, and no species deposited in GenBank are identical to our fungus, and thus the latter is described as new. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *Camarosporium brabeji* (GenBank LN714529; Identities = 516/554 (93 %), Gaps = 14/554 (2 %)), *Coniothyrium nitidae* (GenBank EU552112; Identities = 517/555 (93 %), Gaps = 13/555 (2 %)) and *Microdiplodia hawaiiensis* (GenBank DQ885897; Identities = 517/555 (93 %), Gaps = 16/555 (2 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with *Keissleriella cladophila* (GenBank JX681090; Identities = 829/833 (99 %), Gaps = 4/833 (0 %)), *Keissleriella sparticola* (GenBank KP639571; Identities = 814/819 (99 %), Gaps = 5/819 (0 %)) and *Pleurophoma ossicola* (GenBank KR476770; Identities = 826/833 (99 %), Gaps = 4/833 (0 %)).

Colour illustrations. Acacia glaucoptera; conidiomata sporulating on OA, conidioma, conidiogenous cells and conidia. Scale bars = 160 µm (conidioma), 10 µm (all others).

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Libertasomyces platani

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Libertasomyces platani Crous & Thangavel, *sp. nov.*

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

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

Conidiomata solitary, immersed to erumpent, globose, medium brown, 80–160 µm diam, with central ostiole, slightly papillate, ostiole dark brown, 15–25 µm diam. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* solitary, hyaline, smooth, ampulliform to doliiform, 4–6 × 4–5 µm; phialidic with periclinal thickening. *Conidia* solitary, aseptate, hyaline, smooth, granular, narrowly ellipsoid to subcylindrical with obtuse ends, (4.5–)5(–6) × (2–)2.5(–3) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and feathery margins, reaching 20–30 mm diam after 2 wk at 25 °C. On MEA surface olivaceous grey with dirty white outer region, reverse grey olivaceous. On OA surface smoke grey. On PDA surface and reverse olivaceous grey.

Typus. New Zealand, Auckland, Papakura, Hanua road, on *Platanus* sp. (*Platanaceae)*, 2015, *R. Thangavel* (holotype CBS H-22897, culture ex-type CPC 29609 = CBS 142112; ITS sequence GenBank KY173416, LSU sequence GenBank KY173507, *rpb2* sequence GenBank KY173585, *tub2* sequence GenBank KY173604, MycoBank MB819101).

Notes — The genus *Libertasomyces* was recently introduced for a phoma-like genus occurring on twigs of *Myoporum serratum* in South Africa (Crous et al. 2016). Morphologically, its relatively nondescript, with pycnidial conidiomata lacking setae, conidiophores reduced to phialidic conidiogenous cells with periclinal thickening, and hyaline, aseptate ellipsoid conidia. *Libertasomyces platani* is morphologically similar to *L. myopori*, and the two species are best distinguished based on their DNA data. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *Neoplatysporoides aloicola* (GenBank KR476719; Identities = 530/570 (93 %), Gaps = 8/570 (1 %)) and *Libertasomyces myopori* (GenBank KX228281; Identities = 516/566 (91 %), Gaps = 14/566 (2 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with '*Camarosporium quaternatum*' (GenBank DQ377883; Identities = 801/803 (99 %), Gaps = 1/803 (0 %)), *Libertasomyces myopori* (GenBank KX228332; Identities = 782/798 (98 %), Gaps = 4/798 (0 %)) and *Subplenodomus drobnjacensis* (GenBank JF740285; Identities = 787/804 (98 %), Gaps = 3/804 (0 %)).

Colour illustrations. *Platanus occidentalis* (image credit Bob McLain); conidiomata sporulating on PNA, conidioma and conidia. Scale bars = 200 µm (conidioma), 10 µm (conidia).

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Torula acaciae

Fungal Planet 538 – 21 December 2016

Torula acaciae Crous, *sp. nov.*

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

Classification – *Torulaceae*, *Pleosporales*, *Dothideomycetes.*

Mycelium consisting of brown, smooth, septate, branched, 3–5 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells, or with one brown supporting cell, 5–10 × 4–5 µm. *Conidiogenous cells* solitary on mycelium, erect, doliiform to ellipsoid, brown, 5–15 × 4–5 µm, verruculose at apex, proliferating mono- or polyblastically. *Conidia* phragmosporous, in branched chains, acrogenous, brown, apex subhyaline, dry, constricted at septa, verrucose, fragmenting into segments; cells subglobose, 2-septate conidia, 14–16 × 5–6 µm; 3-septate conidia, 18–20 µm long, 4-septate conidia, 25–28 µm long; conidia up to 15-septate, frequently with lateral branches, individual cells (4–)5(–6) × 5–6 µm.

Culture characteristics — Colonies flat, spreading, reaching 40 mm diam after 2 wk at 25 °C, with moderate aerial mycelium and smooth, lobate margins. On MEA surface olivaceous grey, reverse pale olivaceous grey. On OA surface dirty white. On PDA surface and reverse olivaceous grey.

Typus. USA, Hawaii, Oahu, on leaves of *Acacia koa* (*Fabaceae*), 30 Sept. 2015, *J.J. Le Roux* (holotype CBS H-22898, culture ex-type CPC 29737 = CBS 142113; ITS sequence GenBank KY173471, LSU sequence GenBank KY173560, *rpb2* sequence GenBank KY173594, *tub2* sequence GenBank KY173620, MycoBank MB819102).

Colour illustrations. Acacia koa in Hawaii; conidiophores sporulating on PNA, conidiophores and conidia. Scale bars = 10 µm.

Notes — *Torula* and morphologically similar genera were recently treated by Crous et al. (2015a) and Crane & Miller (2016). Based on ITS sequence data, *T. acaciae* is similar to *T. masonii*. Although both species could have multiseptate conidia, in general *T. masonii* has longer and wider conidia (3-septate conidia 19–30 × 6–7 µm, 4-septate conidia 23–35 × 6–7 µm; Crous et al. 2015a). Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *Torula caligans* (GenBank JX156379; Identities = 452/495 (91 %), Gaps = 14/495 (2 %)) and *Torula masonii* (GenBank KR873261; Identities = 486/536 (91 %), Gaps = 12/536 (2 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with *Torula herbarum* (GenBank KF443385; Identities = 777/781 (99 %), no gaps), *Torula hollandica* (GenBank KF443384; Identities = 752/761 (99 %), no gaps) and *Torula masonii* (GenBank KR873289; Identities = 791/801 (99 %), Gaps = 1/801 (0 %)).

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Polyscytalum purgamentum

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Polyscytalum purgamentum Crous, *sp. nov.*

Etymology. Occurring on leaf litter (waste, debris), *purgamentum*.

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

Mycelium consisting of hyaline, smooth, septate, branched, 2.5–3.5 µm diam hyphae. *Conidiophores* solitary, erect, hyphae and basal part of conidiophores becoming pale brown, smooth; subcylindrical, erect, 1–2-septate, 20–40 × 2.5–3.5 µm. *Conidiogenous cells* terminal, subcylindrical, hyaline, smooth, 15–25 × 2–2.5 µm, apex frequently slightly clavate, with several sympodial flat-tipped loci, 1–1.5 µm diam, unthickened, not darkened. *Ramoconidia* hyaline, smooth, guttulate, subcylindrical, 15–25 × 2 µm. *Conidia* aseptate, hyaline, smooth, arranged in long, branched chains, with lateral branches arising below the septum at the apex of each primary conidium, (12–)18–20(–22) × 2 µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and feathery, lobate margins, reaching 20 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse pale luteous. On OA surface chestnut. On PDA surface and reverse olivaceous grey.

Typus. USA, Texas, Austin, on leaf litter, Aug. 2013, *P.W. Crous* (holotype CBS H-22899, culture ex-type CPC 29580 = CBS 142114; ITS sequence GenBank KY173435, LSU sequence GenBank KY173525, MycoBank MB819103).

Notes — *Polyscytalum purgamentum* clusters in a clade among species of *Cylindrium* and *Polyscytalum*, but is phylogenetically distinct from those taxa presently available in GenBank. It is placed in *Polyscytalum* because of its pigmented stipe, and flat tipped, sympodial loci that give rise to ramoconidia. Morphologically it is allied to *P. algarvense*, although the latter has much smaller conidia (11–13.5(–15) × 2–2.5 µm; Cheewangkoon et al. 2009). Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *Polyscytalum algarvense* (GenBank GQ303287; Identities = 512/529 (97 %), Gaps = 2/529 (0 %)), *Cylindrium aeruginosum* (GenBank KM231854; Identities = 528/549 (96 %), Gaps = 3/549 (0 %)) and *Cylindrium elongatum* (GenBank KM231852; Identities = 511/549 (93 %), Gaps = 11/549 (2 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with *Tristratiperidium microsporum* (GenBank KT696539; Identities = 732/736 (99 %), no gaps), *Pseudoidriella syzygii* (GenBank JQ044441; Identities = 817/822 (99 %), no gaps) and *Cylindrium elongatum* (GenBank KM231733; Identities = 814/820 (99 %), Gaps = 1/820 (0 %)).

Colour illustrations. Walking trail in Austin, Texas; conidiophores and conidia. Scale bars = 10 µm.

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Celerioriella petrophiles

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Celerioriella petrophiles Crous, *sp. nov.*

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

Classification – *Phaeomoniellaceae*, *Phaeomoniellales*, *Eurotiomycetes.*

Dimorphic, forming conidiomatal pycnidia as well as a hyphomycetous morph in agar. *Conidiomata* brown, erumpent, globose, 60–120 µm diam, with central ostiole. *Mycelium* 3–4 µm diam, hyaline, smooth, frequently surrounded by a thick mucoid sheath, giving rise to erect conidiogenous cells. *Conidiogenous cells* hyaline, smooth, subcylindrical to elongated doliiform, phialidic with minute collarette, 3–12 × 2–3 µm. *Conidia* solitary, hyaline, smooth, subcylindrical with obtuse ends, 3–5 × 2 µm, becoming ellipsoid, swollen, up to 6 µm long, 5 µm diam, eventually budding like a yeast to form secondary conidia; older conidia can also turn brown and verruculose.

Culture characteristics — Colonies flat, spreading, slimy, with sparse aerial mycelium and even, lobed margins, reaching 20 mm diam after 2 wk at 25 °C. On MEA surface and reverse smoke grey. On OA surface grey olivaceous with patches of pale luteous. On PDA surface pale olivaceous with patches of sienna, reverse ochreous.

Typus. Australia, Western Australia, Kojaneerup South, Chillinup Road, on leaves of *Petrophile teretifolia* (*Proteaceae*), 22 Sept. 2015, *P.W. Crous* (holotype CBS H-22900, culture ex-type CPC 29256 = CBS 142115; ITS sequence GenBank KY173394, LSU sequence GenBank KY173487, MycoBank MB819104).

Colour illustrations. *Petrophile teretifolia*; conidiomata sporulating on OA, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — The genus *Celerioriella* was established by Crous et al. (2015c) for two species occurring in prunus wood in South Africa, and being associated with brown streaking in the wood of this host. Phylogenetically and morphologically *C. petrophiles* is distinct in that it has larger conidia than those of *C. dura* ((2.5–)3–3.5(–4) × 1(–1.5) µm) and *C. prunicola* ((2–)2.5–4(–4.5) × 1–1.5(–2) µm). Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *Phaeomoniella chlamydospora* (GenBank AB278179; Identities = 691/781 (88 %), Gaps = 26/781 (3 %)), *Celerioriella prunicola* (GenBank GQ154590; Identities = 524/564 (93 %), Gaps = 16/564 (2 %)) and *Pseudophaeomoniella oleae* (GenBank KP635972; Identities = 686/747 (92 %), Gaps = 16/747 (2 %)).

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Neocordana musarum

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Neocordana musarum 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, 70–300 × 4–7 µm. *Conidiogenous cells* polyblastic, terminal and intercalary, 20–40 × 4–6 µm, denticulate; denticles up to 1.5 µm long, 0.5–1 µm wide. *Conidia* oblong to obovoid, (15–)17–19(–20) × (9–)10(–13) µm, 1-septate, thick-walled, pale brown, base darker, truncate, 1.5 µm diam.

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

Typus. FRANCE, La Réunion, site no. 1, Riviere Langevin, leaves of *Musa* sp. (*Musaceae*), 7 July 2015, *A. Viljoen* (holotype CBS H-22901, culture ex-type CPC 28529 = CBS 142116; ITS sequence GenBank KY173425, LSU sequence GenBank KY173516, *actA* sequence GenBank KY173568, *rpb1* sequence GenBank KY173577, *tub2* sequence GenBank KY173608, MycoBank MB819105); idem, CPC 28525; ITS sequence GenBank KY173424, LSU sequence GenBank KY173515, *actA* sequence GenBank KY173567, *rpb1* sequence GenBank KY173576.

Notes — The genus *Neocordana* was established to accommodate a clade of cordana-like fungi that cause leaf spot diseases of *Canna* and *Musa*. Four species are presently known, namely *C. musae* (conidia obclavate to pyriform, 14–18 × 8–10 µm), *C. johnstonii* (conidia ellipsoidal to subglobose, 19–26 × 14–16 µm), *C. versicolor* (conidia ellipsoid, 15–25 × 10–15 µm) and *C. musicola* (conidia oblong to obovoid, 14.5–20 × 6.5–9.5 µm) (Hernández-Restrepo et al. 2015). *Neocordana musarum* resembles *N. musae* and *N. musicola*, but it has wider conidia. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *Neocordana musae* (GenBank HE971730, as '*Pyricularia* sp.'; Identities = 345/345 (100 %), no gaps), *Neocordana musae* (GenBank LN713277; Identities = 559/567 (99 %), Gaps = 1/567 (0 %)) and *Neocordana musicola* (GenBank LN713285; Identities = 514/516 (99 %), Gaps = 2/516 (3 %)).

Colour illustrations. Neocordana leaf spots on banana leaves; conidiophores and conidia on PNA. Scale bars = 10 µm.

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Pyricularia urashimae

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Pyricularia urashimae V.L. Castroagudín, J.L.N. Maciel, Crous & P.C. Ceresini, *sp. nov.*

Etymology. Name recognises Dr Alfredo Seiiti Urashima, who has dedicated his entire career as plant pathologist to work with the wheat blast disease in Brazil since the first outbreaks in 1989.

Classification – *Pyriculariaceae*, *Magnaporthales*, *Sordariomycetes.*

On SNA on sterile barley seeds. *Mycelium* consisting of smooth, hyaline, branched, septate hyphae, 3–4 µm diam. *Conidiophores* solitary, erect, straight or curved, unbranched, medium brown, smooth, 60–200 × 4–5 µm, 1–4-septate; base arising from hyphae, not swollen, lacking rhizoids. *Conidiogenous cells* 40–100 × 3–5 µm, integrated, terminal, pale brown, smooth, forming a rachis with several protruding denticles, 1–4 µm long, 2–2.5 µm diam. *Conidia* solitary, pyriform to obclavate, pale brown, verruculose, granular to guttulate, 2-septate, (18–)20–24(–27) × (7–)8(–9) µm; apical cell 5–10 µm long, basal cell 5–7 µm long; hilum truncate, protruding, 0.5–1 µm long, 2 µm diam, unthickened, not darkened.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium, smooth margins and folded surface (on MEA). On MEA and OA surface and reverse olivaceous grey. On PDA surface and reverse iron grey.

Typus. Brazil, Amambai, Mato Grosso do Sul, on leaves of *Urochloa brizantha* (*Poaceae*), 2012, *J.L.N. Maciel* (holotype CBS H-22902, culture ex-type CPC 29414 = CBS 142117 = CML 3520 = URM 7373 = isolate 12.0.148 = isolate 12.0.149; ITS sequence GenBank KY173437, LSU sequence GenBank KY173527, *actA* sequence GenBank KX524119, *cmdA* sequence GenBank KX524100, *rpb1* sequence GenBank KY173578, *tub2* sequence GenBank KY173614, MycoBank MB819106).

Additional specimens examined. Brazil, Londrina, Paraná, on leaves of *Chloris distichophylla* (*Poaceae*), 2012, *J.L.N. Maciel*, CPC 29421 = CBS 142166 = CML 3519 = URM 7374 = isolate 12.0.595i; ITS sequence GenBank KY173439, LSU sequence GenBank KY173529, *actA* sequence GenBank KX524121, *cmdA* sequence GenBank KX524102, *rpb1* sequence GenBank KY173580, *tub2* sequence GenBank KY173616; Aral Moreira, Mato Grosso do Sul, on leaves of *Panicum maximum* (*Poaceae*), 2012, *J.L.N. Maciel*, CPC 29419 = CBS 142118, isolate 12.0.212; ITS sequence GenBank KY173438, LSU sequence GenBank KY173528, *actA* sequence GenBank KX524120, *cmdA* sequence GenBank KX524101, *rpb1* sequence GenBank KY173579, *tub2* sequence GenBank KY173615.

Notes — The type species of the genus *Pyricularia* was recently epitypified, fixing its phylogenetic position (Crous et al. 2015a), while the family *Pyriculariaceae* was revised by Klaubauf et al. (2014). Isolates of *P. urashimae* are allied to *P. oryzae*, and were formerly treated as *P. zingibericola* (Castroagudín et al. 2016, Reges et al. 2016), which is a phylogenetically distinct species. *Pyricularia urashimae* causes blast disease on leaves and heads of *Triticum aestivum* (Reges et al. 2016, Dorigan & Ceresini, unpubl. data) and leaves of *Hordeum vulgare* and *Urochloa brizantha* (Reges et al. 2016). Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with '*Pyricularia* sp.' (GenBank KM484940; Identities = 462/461 (100 %), no gaps), *Pyricularia angulata* (GenBank GU066873; Identities = 495/504 (98 %), Gaps = 2/504 (0 %)) and *Pyricularia penniseticola* (GenBank KM484927; Identities = 454/464 (98 %), Gaps = 2/464 (0 %)).

Colour illustrations. *Urochloa brizantha* cv. Marandu; inoculated wheat cv. Anahuac head (left), barley cv. BRS Korbel leaf (middle) and *Urochloa* cv. Piatã leaf (right), conidiophores and conidia. Scale bars = 10 µm.

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Rhexodenticula acaciae

Fungal Planet 543 – 21 December 2016

Rhexodenticula acaciae Crous, *sp. nov.*

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

Classification – *Cordanaceae*, *Cordanales*, *Sordariomycetes*.

Mycelium consisting of hyaline, smooth, septate, branched, 2.5–3.5 µm diam hyphae. *Conidiophores* solitary, erect, medium brown, smooth, subcylindrical, mostly unbranched, 1–3-septate, 10–40 × 4–5 µm. *Conidiogenous cells* integrated, terminal, rarely intercalary on conidiophores, subcylindrical or clavate, straight or hooked, medium brown, smooth, 10–15 × 3–5 µm, with several cylindrical denticles, 1–1.5 × 1 µm. *Conidia* solitary, fusoid-ellipsoid, guttulate, medium brown, verruculose, apex subacute, base tapered, with prominent tubular marginal frill, 0.5–1 × 1 µm; 2-septate with septa a third from apex and base, respectively, median cell somewhat darker brown than apical and basal cell, and at times appearing to have a mucoid sheath, (16–)20–23(–25) × (4–)5 µm.

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

Typus. USA, Hawaii, Oahu, on leaves of *Acacia koa* (*Fabaceae*), 30 Sept. 2015, *J.J. Le Roux* (holotype CBS H-22903, culture ex-type CPC 29590 = CBS 142119; ITS sequence GenBank KY173442, LSU sequence GenBank KY173532, MycoBank MB819107).

Notes — The genus *Rhexodenticula* (based on *R. cylindrospora*; Klaubauf et al. 2014), accommodates three species. *Rhexodenticula acaciae* can easily be distinguished from these taxa, as it is the only species that has 2-septate, rather than 3-septate conidia (Mel'nik et al. 2004, Li et al. 2011). Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *Rhexodenticula cylindrospora* (GenBank KM484942; Identities = 462/461 (100 %), no gaps), *Spadicoides bina* (GenBank JF340260; Identities = 392/448 (88 %), Gaps = 14/448 (3 %)) and *Pseudobotrytis terrestris* (GenBank KF733463; Identities = 479/553 (87 %), Gaps = 19/553 (3 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with *Rhexodenticula cylindrospora* (GenBank KM485039; Identities = 819/835 (98 %), no gaps), *Pseudobotrytis bisbyi* (GenBank KF746880; Identities = 790/828 (95 %), Gaps = 1/828 (0 %)) and *Pseudobotrytis terrestris* (GenBank KF746879; Identities = 788/828 (95 %), Gaps = 1/828 (0 %)).

Colour illustrations. *Acacia koa* in Hawaii; conidiophores sporulating on PNA, conidiophores and conidia. Scale bars = 10 µm.

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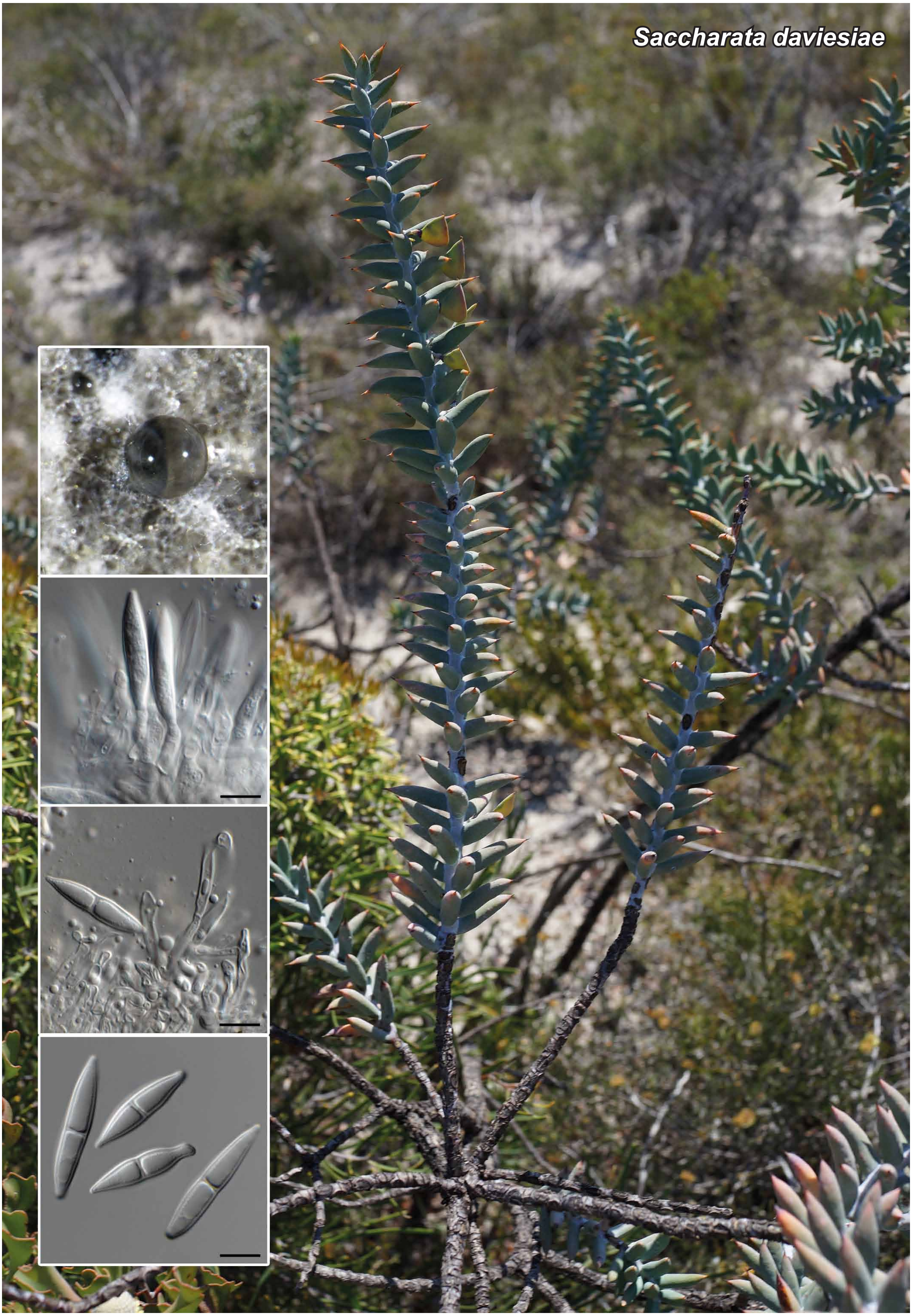
Saccharata daviesiae

Fungal Planet 544 – 21 December 2016

Saccharata daviesiae Crous, *sp. nov.*

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

Classification – *Saccharataceae*, *Botryosphaeriales*, *Dothideomycetes.*

Conidiomata pycnidial, eustromatic, to 350 µm diam, immersed, subepidermal, erumpent in culture, separate, or aggregated, dark brown, uni- to multi-locular, walls consisting of dark brown *textura angularis*, ostiolate. *Conidiophores* hyaline, smooth, branched, subcylindrical, 1–3-septate, formed from the inner layer of the locule, 15–40 × 3–5 µm, intermingled with hyaline, septate paraphyses. *Conidiogenous cells* phialidic, discrete or integrated, hyaline, smooth, cylindrical, enteroblastic, proliferating percurrently with numerous apical annellations, 7–25 × 3–4 µm. *Conidia* hyaline, thick-walled, medianly 1-septate, constricted at septum, smooth, fusoid, widest in the middle of the conidium, prominently guttulate, with a bluntly subobtuse apex, and a truncate base, 3 µm diam, (27–)33–38(–42) × (4–)6 µm. *Spermatia* occurring in separate or the same conidiomata. *Spermatophores* hyaline, smooth, branched, cylindrical, 1–3-septate, formed from the inner layers of the locule, 10–20 × 2.5–3 µm. *Spermatogenous cells* phialidic, discrete or integrated, terminal and lateral, hyaline, smooth, cylindrical, determinate, with prominent periclinal thickening, 5–10 × 2.5–3.5 µm. *Spermatia* hyaline, thin-walled, smooth, aseptate, subcylindrical with rounded ends, 3–5 × 1.5–2 µm.

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

Typus. Australia, Western Australia, Albany, Fitzgerald River National Park, on *Daviesia pachyphylla* (*Fabaceae*), 22 Sept. 2015, *P.W. Crous* (holotype CBS H-22904, culture ex-type CPC 29174 = CBS 142120; ITS sequence GenBank KY173450, LSU sequence GenBank KY173540, *rpb2* sequence GenBank KY173589, MycoBank MB819108).

Colour illustrations. *Daviesia pachyphylla*; conidiomata sporulating on PNA, conidiophores and conidia. Scale bars = 10 µm.

Notes — The genus *Neoseptorioides* (based on *N. eucalypti*) was established for a species occurring on leaf litter of *Eucalyptus radiata* collected in Victoria, Australia (Crous et al. 2015d). Although *Neoseptorioides* is morphologically distinct from the genus *Saccharata*, numerous isolates were collected in this study that cluster between these two genera. It is consequently convenient to expand the generic circumscription of *Saccharata* to also include *Neoseptorioides. Neoseptorioides* is monotypic, and a new combination is proposed for *N. eucalypti*.

Saccharata eucalypti (Crous et al.) Crous, *comb. nov*. — MycoBank MB819109

Basionym. Neoseptorioides eucalypti Crous et al., Persoonia 35: 291. 2015.

Saccharata daviesiae is easily distinguished from *S. eucalypti* in that the latter has cylindrical, 0(–3)-euseptate conidia, (18–)35–42(–50) × (3.5–)4(–4.5) µm. The two species are only 88 % similar based on their ITS sequences (Identities = 316/359 (88 %), Gaps = 17/359 (4 %), based on an ITS comparison to GenBank KT950857). Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *S. kirstenboschensis* (GenBank FJ372392; Identities = 565/596 (95 %), Gaps = 6/596 (1 %)), *S. proteae* (GenBank KF766226; Identities = 553/585 (95 %), Gaps = 8/585 (1 %)) and *S. capensis* (GenBank EU552130; Identities = 563/596 (94 %), Gaps = 4/596 (0 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with *Saccharata proteae* (GenBank JX556251; Identities = 809/815 (99 %), no gaps), *S. capensis* (GenBank KF766390; Identities = 808/815 (99 %), no gaps) and *S. intermedia* (GenBank GU229889; Identities = 808/815 (99 %), no gaps).

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Saccharata banksiae

Fungal Planet 545 – 21 December 2016

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

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

Classification – *Saccharataceae*, *Botryosphaeriales*, *Dothideomycetes.*

Conidiomata pycnidial, eustromatic, to 150–250 µm diam, immersed, subepidermal, erumpent in culture, separate, dark brown, unilocular, walls consisting of dark brown *textura angularis*, ostiolate. *Conidiophores* hyaline, smooth, branched, subcylindrical, 0–1-septate, formed from the inner layer of the locule, 10–15 × 3–6 µm; paraphyses not seen. *Conidiogenous cells* phialidic, discrete or integrated, hyaline, smooth, cylindrical, enteroblastic, proliferating percurrently at apex, 7–12 × 3–4 µm. *Conidia* hyaline, thick-walled, guttulate, aseptate, smooth, fusoid, widest in the middle of the conidium, with a bluntly subobtuse apex, and a truncate base, (13–)15–17(–20) × 6(–6.5) µm. *Spermatia* occurring in separate or the same conidiomata. *Spermatophores* hyaline, smooth, branched, cylindrical, 1–3-septate, formed from the inner layers of the locule, 9–15 × 4–5 µm. *Spermatogenous cells* phialidic, discrete or integrated, terminal and lateral, hyaline, smooth, cylindrical, determinate, with prominent periclinal thickening, 7–10 × 2–3 µm. *Spermatia* hyaline, thin-walled, smooth, aseptate, subcylindrical with rounded ends, 3–5 × 1.5–2 µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium, and lobate, feathery margins. On MEA, PDA and OA surface and reverse olivaceous grey. On OA and PDA surface dirty white, reverse pale olivaceous grey in centre, buff in outer region.

Typus. Australia, Western Australia, Perth, Chichester Park, on *Banksia grandis* leaf litter (*Proteaceae*), 15 June 2015, *P.A. Barber* (holotype CBS H-22905, culture ex-type CPC 27698 = CBS 142137; ITS sequence GenBank KY173449, LSU sequence GenBank KY173539, *rpb2* sequence GenBank KY173588, *tef1* sequence GenBank KY173596, MycoBank MB819110).

Colour illustrations. *Banksia grandis*; conidiomata sporulating on PNA, conidiophores and conidia. Scale bars = 10 µm.

Notes — *Saccharata banksiae* is distinct from *S. daviesiae* (conidia fusoid, 1-septate, (27–)33–38(–42) × (4–)6 µm; Identities = 550/573 (96 %), Gaps = 5/573 (0 %), based on an ITS comparison to CPC 29174) and *S. eucalypti* (conidia cylindrical, 0(–3)-septate, (18–)35–42(–50) × (3.5–)4(–4.5) µm; Identities = 326/357 (91 %), Gaps = 14/357 (4 %), based on an ITS comparison to GenBank KT950857) by having smaller, aseptate conidia. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *S. kirstenboschensis* (GenBank FJ372392; Identities = 556/571 (97 %), Gaps = 3/571 (0 %)), *S. capensis* (GenBank EU552130; Identities = 554/573 (97 %), Gaps = 5/573 (0 %)) and *S. proteae* (GenBank EU552145; Identities = 557/578 (96 %), Gaps = 10/578 (1 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with *S. proteae* (GenBank JX556251; Identities = 824/830 (99 %), no gaps), *S. intermedia* (GenBank GU229889; Identities = 823/830 (99 %), no gaps) and *S. kirstenboschensis* (GenBank FJ372409; Identities = 823/830 (99 %), no gaps).

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Saccharata hakeae

Fungal Planet 546 – 21 December 2016

Saccharata hakeae Crous, *sp. nov.*

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

Classification – *Saccharataceae*, *Botryosphaeriales*, *Dothideomycetes.*

Associated with brown leaf spots on *Hakea baxteri. Conidiomata* pycnidial, eustromatic, to 200–250 µm diam, immersed, subepidermal, erumpent in culture, separate, or aggregated, dark brown, unilocular, walls consisting of 6–8 layers of dark brown *textura angularis*, ostiolate. *Conidiophores* hyaline, smooth, branched, below or not, subcylindrical, 0–1-septate, formed from the inner layer of the locule, 10–25 × 2.5–3.5 µm. *Conidiogenous cells* phialidic, discrete or integrated, hyaline, smooth, cylindrical, enteroblastic, proliferating percurrently with several apical annellations, 7–20 × 2.5–3.5 µm. *Conidia* hyaline, thick-walled, aseptate, smooth, fusoid, widest in the middle of the conidium, with a subobtuse apex, and a truncate base, 4–5 µm diam, (24–)28–31(–33) × (6.5–)7–8 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium, and feathery, even margins, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface dirty white with patches of pale olivaceous grey, reverse olivaceous grey. On OA and PDA surface and reverse olivaceous grey.

Typus. Australia, Western Australia, Albany, Stirling Range National Park, Mt Hassell walk, on *Hakea baxteri* (*Proteaceae*), 23 Sept. 2015, *P.W. Crous* (holotype CBS H-22906, culture ex-type CPC 29250 = CBS 142121; ITS sequence GenBank KY173454, LSU sequence GenBank KY173544, MycoBank MB819111); idem, CPC 29210 = CBS 142167; ITS sequence GenBank KY173453, LSU sequence GenBank KY173543; idem, CPC 29251.

Additional specimens examined. Australia, Western Australia, Albany, Stirling Range National Park, Mt Hassell walk, on *Hakea pandanicarpa* (*Proteaceae*), 23 Sept. 2015, *P.W. Crous*, HPC 582, CPC 29204 = CBS 142168; ITS sequence GenBank KY173452, LSU sequence GenBank KY173542; Denmark, Lights Beach, on *Hakea* sp. (*Proteaceae*), 19 Sept. 2015, *P.W. Crous*, HPC 659, CPC 29704 = CBS 142169; ITS sequence GenBank KY173455, LSU sequence GenBank KY173545.

Notes — *Saccharata hakeae* is distinct from *S. banksiae* (conidia aseptate, fusoid, (13–)15–17(–20) × 6(–6.5) µm; Identities = 524/563 (93 %), Gaps = 10/563 (1 %), based on an ITS comparison to CPC 27698), *S. daviesiae* (conidia fusoid, 1-septate, (27–)33–38(–42) × (4–)6 µm; Identities = 515/566 (91 %), Gaps = 13/566 (2 %), based on an ITS comparison to CPC 29174) and *S. eucalypti* (conidia cylindrical, 0(–3)-septate, (18–)35–42(–50) × (3.5–)4(–4.5) µm; Identities = 319/350 (91 %), Gaps = 9/350 (2 %), based on an ITS comparison to GenBank KT950857) by having aseptate, fusoid conidia that are larger than those of *S. banksiae*, but smaller than those of the other species. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence of the ex-type culture, the highest similarities were with *Septorioides strobi* (GenBank KT884694; Identities = 405/435 (93 %), Gaps = 5/435 (1 %)), *Saccharata kirstenboschensis* (GenBank FJ372392; Identities = 521/564 (92 %), Gaps = 11/564 (1 %)) and *Saccharata capensis* (GenBank EU552130; Identities = 519/566 (92 %), Gaps = 13/566 (2 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence of the ex-type culture, the highest similarities were with *Saccharata proteae* (GenBank EU552145; Identities = 818/841 (97 %), Gaps = 2/841 (0 %)), *Saccharata intermedia* (GenBank GU229889; Identities = 813/836 (99 %), Gaps = 2/836 (0 %)) and *Saccharata capensis* (GenBank KF766390; Identities = 815/841 (97 %), Gaps = 2/841 (0 %)).

Colour illustrations. Leaves of *Hakea baxteri*; conidiogenous cells and conidia. Scale bars = 10 µm.

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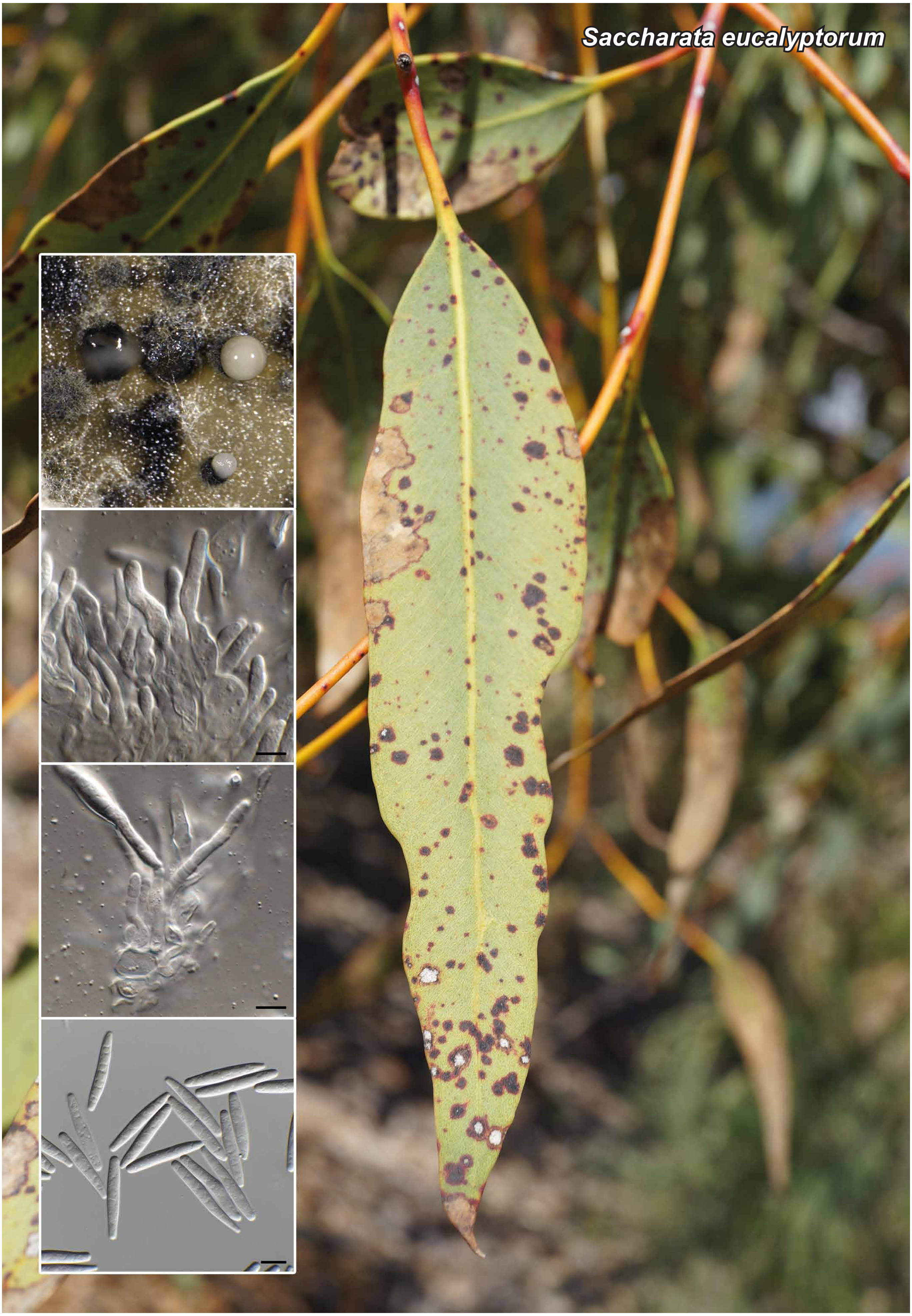
Saccharata eucalyptorum

Fungal Planet 547 – 21 December 2016

Saccharata eucalyptorum Crous, *sp. nov.*

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

Classification – *Saccharataceae*, *Botryosphaeriales*, *Dothideomycetes.*

Conidiomata pycnidial, eustromatic, to 200–300 µm diam, immersed, subepidermal, erumpent in culture, separate, or aggregated, dark brown, unilocular; walls consisting of 6–8 layers of dark brown *textura angularis*, ostiolate. *Conidiophores* hyaline, smooth, branched, below or not, subcylindrical, 0–3-septate, formed from the inner layer of the locule, 20–40 × 2.5–3.5 µm, intermingled with hyaline, septate paraphyses up to 60 µm tall. *Conidiogenous cells* phialidic, discrete or integrated, hyaline, smooth, cylindrical, enteroblastic, proliferating percurrently with numerous apical annellations, 15–25 × 2.5–3.5 µm. *Conidia* hyaline, thick-walled, guttulate, aseptate, smooth, fusoid, widest in the middle of the conidium, with a subobtuse apex, and a truncate base, 2–3 µm diam, (25–)30–33(–35) × (4–)5 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 and reverse olivaceous grey. On OA and PDA surface and reverse iron-grey.

Typus. Australia, Western Australia, Perth, King's Park Botanic Gardens, on *Eucalyptus bigalerita* (*Myrtaceae*), 27 Sept. 2015, *P.W. Crous* (holotype CBS H-22907, culture ex-type CPC 29222 = CBS 142122; ITS sequence GenBank KY173451, LSU sequence GenBank KY173541, MycoBank MB819112).

Colour illustrations. Symptomatic leaves of *Eucalyptus bigalerita*; conidiomata sporulating on OA, conidiophores and conidia. Scale bars = 300 µm (conidiomata), 10 µm (all others).

Notes — Of the *Saccharata* species presently known that lack a synasexual morph with brown conidia, several species have fusoid, aseptate conidia, namely *S. banksiae* ((13–)15–17(–20) × 6(–6.5) µm; Identities = 524/568 (92 %), Gaps = 17/568 (2 %), based on an ITS comparison to CPC 27698) and *S. hakeae* ((24–)28–31(–33) × (6.5–)7–8 µm; Identities = 516/557 (93 %), Gaps = 13/557 (2 %), based on an ITS comparison to CPC 29250). *Saccharata eucalyptorum* is distinct from these two species by having narrower conidia. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence of the ex-type culture, the highest similarities were with *S. eucalypti* (GenBank KT950857; Identities = 336/346 (97 %), Gaps = 3/346 (0 %)), *S. proteae* (GenBank AF452562; Identities = 373/397 (94 %), Gaps = 4/397 (1 %)) and *Septorioides strobi* (GenBank KT884694; Identities = 407/440 (93 %), Gaps = 6/440 (1 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence of the ex-type culture, the highest similarities were with *Saccharata capensis* (GenBank EU552129; Identities = 805/819 (98 %), Gaps = 2/819 (0 %)), *S. kirstenboschensis* (GenBank FJ372409; Identities = 800/814 (98 %), no gaps) and *S. eucalypti* (GenBank KT950871; Identities = 1107/1127 (98 %), Gaps = 4/1127 (0 %)).

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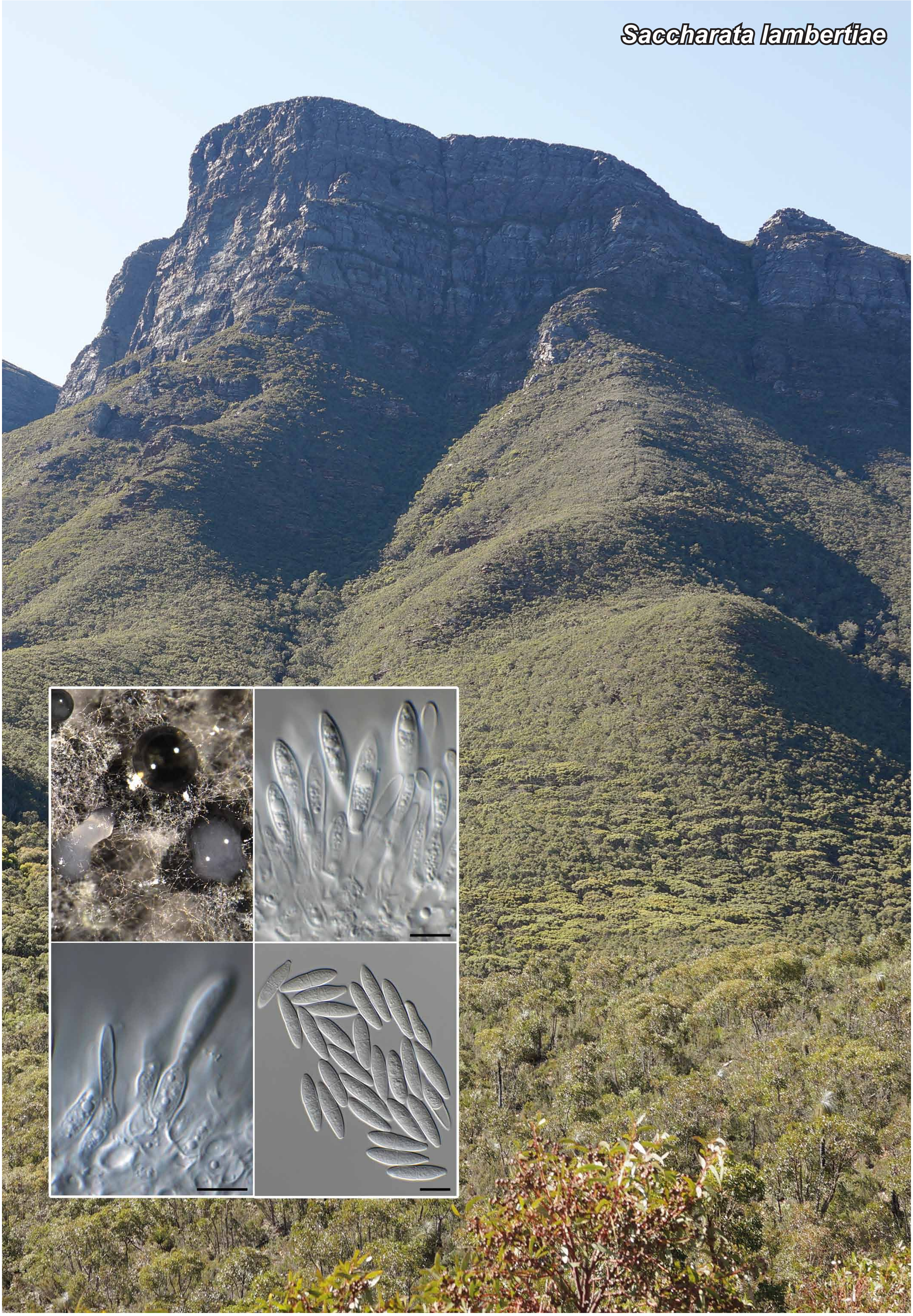
Saccharata lambertiae

Fungal Planet 548 – 21 December 2016

Saccharata lambertiae Crous, *sp. nov.*

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

Classification – *Saccharataceae*, *Botryosphaeriales*, *Dothideomycetes.*

Conidiomata pycnidial, eustromatic, to 200–300 µm diam, immersed, subepidermal, erumpent in culture, separate, or aggregated, dark brown, unilocular; walls consisting of 6–12 layers of dark brown *textura angularis*, ostiolate. *Conidiophores* hyaline, smooth, branched, below or not, subcylindrical, 1–2-septate, formed from the inner layer of the locule, 10–20 × 2.5–3.5 µm, intermingled with hyaline, aseptate paraphyses up to 40 µm tall. *Conidiogenous cells* phialidic, discrete or integrated, hyaline, smooth, cylindrical, enteroblastic, proliferating percurrently with several apical annellations, 7–12 × 2.5–3.5 µm. *Conidia* hyaline, thin-walled, guttulate, (0–)1(–2)-septate, smooth, fusoid, widest in the middle of the conidium, frequently constricted at septum, with a subobtuse apex, and a truncate base, 2 µm diam, (9–)20–23(–25) × (4–)5–6(–7) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium, and feathery, lobate margins, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface and reverse olivaceous grey. On OA and PDA surface and reverse pale olivaceous grey to olivaceous grey.

Typus. Australia, Western Australia, Albany, Stirling Range National Park, Central lookout, on *Lambertia ericifolia* (*Proteaceae*), 23 Sept. 2015, *P.W. Crous* (holotype CBS H-22908, culture ex-type CPC 29216 = CBS 142123; ITS sequence GenBank KY173459, LSU sequence GenBank KY173549, *rpb2* sequence GenBank KY173590, *tef1* sequence GenBank KY173597, MycoBank MB819113).

Colour illustrations. Central lookout at Stirling Range National Park; conidiomata sporulating on PDA, conidiophores and conidia. Scale bars = 10 µm.

Notes — Of the *Saccharata* species presently known with fusoid, septate conidia lacking an asexual morph, *S. lambertiae* needs to be compared with *S. daviesiae* (conidia 1-septate, (27–)33–38(–42) × (4–)6 µm; Identities = 482/510 (95 %), Gaps = 4/510 (0 %), based on an ITS comparison to CPC 29174), which has much larger conidia. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence of the ex-type culture, the highest similarities were with '*Saccharata* sp. 1' (GenBank JN225922; Identities = 487/506 (96 %), Gaps = 1/506 (0 %)), *S. kirstenboschensis* (GenBank FJ372392; Identities = 488/509 (96 %), Gaps = 4/509 (0 %)) and *S. capensis* (GenBank EU552130; Identities = 489/512 (96 %), Gaps = 8/512 (1 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence of the ex-type culture, the highest similarities were with *S. proteae* (GenBank JX556251; Identities = 824/827 (99 %), no gaps), *S. capensis* (GenBank KF766390; Identities = 823/827 (99 %), no gaps) and *S. intermedia* (GenBank GU229889; Identities = 823/827 (99 %), no gaps).

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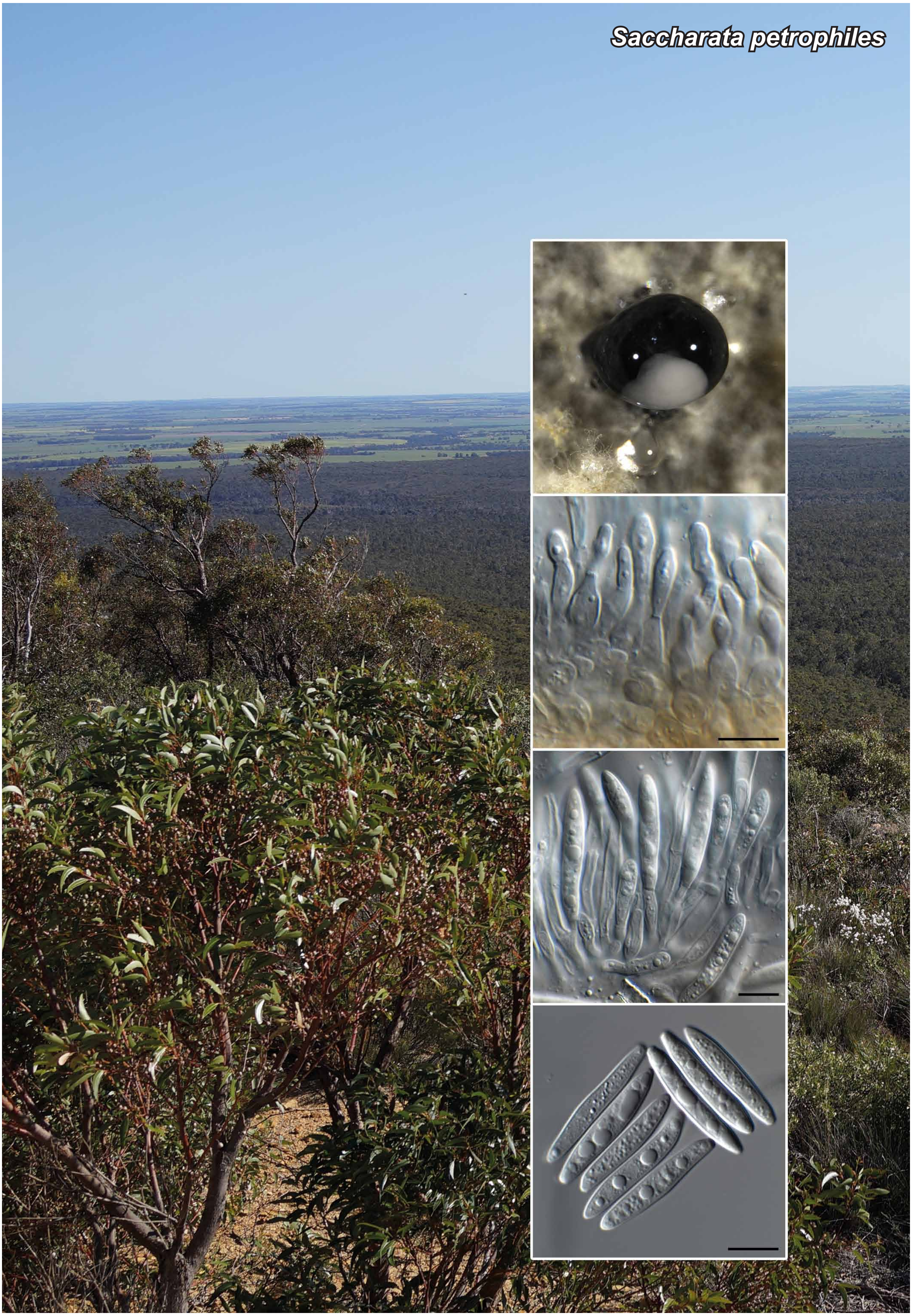
Saccharata petrophiles

Fungal Planet 549 – 21 December 2016

Saccharata petrophiles Crous, *sp. nov.*

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

Classification – *Saccharataceae*, *Botryosphaeriales*, *Dothideomycetes.*

Conidiomata pycnidial, eustromatic, to 150–250 µm diam (on SNA), immersed, subepidermal, erumpent in culture, separate, or aggregated (on PDA, OA), dark brown, unilocular; walls consisting of 6–10 layers of dark brown *textura angularis*, ostiolate. *Conidiophores* hyaline, smooth, unbranched below or not, subcylindrical, 0–1-septate, formed from the inner layer of the locule, 8–15 × 3–5 µm; intermingled with hyaline, septate paraphyses up to 70 µm tall. *Conidiogenous cells* phialidic, discrete or integrated, hyaline, smooth, ampulliform, doliiform to subcylindrical, enteroblastic, proliferating percurrently at apex, 7–12 × 2.5–5 µm. *Conidia* hyaline, thin-walled, guttulate, aseptate, smooth, fusoid, widest in the middle of the conidium, with a subobtuse apex, and a truncate base, 2–2.5 µm diam, (15–)28–33(–35) × (4.5–)5(–5.5) µm.

Culture characteristics — Colonies flat, spreading, with moderate fluffy aerial mycelium, and feathery, lobate margins. On MEA, OA and PDA surface grey olivaceous, reverse olivaceous grey.

Typus. Australia, Western Australia, S34°22'19.4" E118°1'33.6", on *Petrophile* sp. (*Proteaceae*), 23 Sept. 2015, *P.W. Crous* (holotype CBS H-22909, culture ex-type CPC 29151 = CBS 142138; ITS sequence GenBank KY173463, LSU sequence GenBank KY173553, MycoBank MB819114).

Additional specimen examined. Australia, Western Australia, Mari Road Ranger Station, on leaves of *Isopogon polycephalus* (*Proteaceae*), 21 Sept. 2015, *P.W. Crous*, HPC 612, CPC 29441 = CBS 142171; ITS and LSU sequence GenBank KY173464.

Colour illustrations. Australian bush; conidiomata sporulating on PNA, conidiogenous cells, paraphyses and conidia. Scale bars = 10 µm.

Notes — *Saccharata petrophiles* contributes an additional species with fusoid, aseptate conidia, being similar to *S. banksiae* ((13–)15–17(–20) × 6(–6.5) µm; Identities = 541/557 (97 %), Gaps = 2/557 (0 %), based on an ITS comparison to CPC 27698), *N. hakeae* ((24–)28–31(–33) × (6.5–)7–8 µm; Identities = 515/557 (92 %), Gaps = 10/557 (1 %), based on an ITS comparison to CPC 29250), and *S. eucalyptorum* ((25–)30–33(–35) × (4–)5 µm; Identities = 511/557 (92 %), Gaps = 13/557 (2 %), based on an ITS comparison to CPC 29222). Morphologically, it is very similar to *S. hakeae*, other than the fact that its conidia are narrower. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence of the ex-type culture, the highest similarities were with *S. kirstenboschensis* (GenBank FJ372392; Identities = 545/558 (98 %), Gaps = 3/558 (0 %)), '*Saccharata* sp. 1' (GenBank JN225922; Identities = 542/555 (98 %), no gaps) and *S. capensis* (GenBank EU552130; Identities = 540/560 (96 %), Gaps = 5/560 (0 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence of the ex-type culture, the highest similarities were with *S. proteae* (GenBank JX556251; Identities = 802/805 (99 %), no gaps), *S. capensis* (GenBank KF766390; Identities = 799/802 (99 %), no gaps) and *S. intermedia* (GenBank GU229889; Identities = 801/805 (99 %), no gaps).

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Saccharata hakeicola

Fungal Planet 550 – 21 December 2016

Saccharata hakeicola Crous, *sp. nov.*

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

Classification – *Saccharataceae*, *Botryosphaeriales*, *Dothideomycetes.*

Ascomata amphigenous, separate, unilocular, solitary and discrete, immersed, substomatal, globose, 200–300 µm diam; wall consisting of numerous layers of dark brown pseudoparenchymatous *textura angularis*, up to 80 µm thick. *Asci* 8-spored, cylindrical, stipitate, bitunicate, 90–150 × 12–17 µm; apical chamber visible as small notch, 2 µm diam. *Pseudoparaphyses* filamentous, hyaline, septate, branched, frequently attached to top and base of ascoma, 2–3 µm diam. *Ascospores* uni- to biseriate, hyaline, guttulate, smooth, ellipsoid, clavate to fusoid, (18–)19–20(–21) × (7–)9–10 µm. *Conidiomata* pycnidial, eustromatic, to 150–250 µm diam, immersed, subepidermal, erumpent in culture, separate, or aggregated, dark brown, unilocular; walls consisting of 6–10 layers of dark brown *textura angularis*, ostiolate. *Conidiophores* hyaline, smooth, unbranched below or not, subcylindrical, formed from the inner layer of the locule, reduced to conidiogenous cells or with a single supporting cell; paraphyses not seen. *Conidiogenous cells* phialidic, discrete or integrated, hyaline, smooth, cylindrical, enteroblastic, proliferating percurrently with several apical annellations, 5–15 × 3–4(–5) µm. *Conidia* hyaline, thick-walled, guttulate, aseptate, smooth, fusoid, widest in the middle of the conidium, with a subobtuse apex, and a truncate base, 2.5–3 µm diam, (23–)27–29(–32) × (5–)5.5(–6) 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 and reverse smoke grey. On OA and PDA surface and reverse smoke grey to pale olivaceous grey.

Typus. Australia, Western Australia, Albany, Fitzgerald River National Park, Point Ann, on *Hakea victoria* (*Proteaceae*), 21 Sept. 2015, *P.W. Crous* (holotype CBS H-22910, culture ex-type CPC 29706 = CBS 142124; ITS sequence GenBank KY173458, LSU sequence GenBank KY173548, MycoBank MB819115).

Additional specimens examined. Australia, Western Australia, Wellstead, Cape Riche lookout, on *Hakea marginata* (*Proteaceae*), 21 Sept. 2015, *P.W. Crous*, HPC 657, CPC 29531 = CBS 142173; Albany, Fitzgerald River National Park, on *Hakea corymbosa* (*Proteaceae*), 22 Sept. 2015, *P.W. Crous*, HPC 680, CPC 29274 = CBS 142172; ITS sequences GenBank KY173457, KY173456, LSU sequences GenBank KY173547, KY173546, respectively.

Notes — Several species of *Saccharata* are known from Australia with fusoid, aseptate conidia. Of these, *S. hakeicola* is most similar to *S. hakeae* ((24–)28–31(–33) × (6.5–)7–8 µm; also occurring on *Hakea*; Identities = 512/566 (90 %), Gaps = 20/566 (3 %), based on an ITS comparison to CPC 29250), but can be distinguished by having narrower conidia. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence of the ex-type culture, the highest similarities were with '*Saccharata* sp. 1' (GenBank JN225922; Identities = 530/564 (94 %), Gaps = 10/564 (1 %)), *S. kirstenboschensis* (GenBank FJ372392; Identities = 532/567 (94 %), Gaps = 13/567 (2 %)) and *S. capensis* (GenBank EU552130; Identities = 528/567 (93 %), Gaps = 11/567 (1 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence of the ex-type culture, the highest similarities were with *S. capensis* (GenBank KF766390; Identities = 811/815 (99 %), no gaps), *S. kirstenboschensis* (GenBank FJ372409; Identities = 811/815 (99 %), no gaps) and *S. capensis* (GenBank EU552130; Identities = 811/815 (99 %), no gaps).

Colour illustrations. *Hakea victoria*; conidiomata sporulating on OA, asci, ascospores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Saccharata petrophilicola

Fungal Planet 551 – 21 December 2016

Saccharata petrophilicola Crous, *sp. nov.*

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

Classification – *Saccharataceae*, *Botryosphaeriales*, *Dothideomycetes.*

Conidiomata pycnidial, eustromatic, to 200–300 µm diam, immersed, subepidermal, erumpent in culture, separate, dark brown, uni- to multi-locular; walls consisting of 6–12 layers of dark brown *textura angularis*, ostiolate, exuding a crystalline conidial mass. *Conidiophores* hyaline, smooth, branched, below or not, subcylindrical, 1–3-septate, formed from the inner layer of the locule, 20–30 × 2.5–4 µm, intermingled with hyaline, septate paraphyses up to 50 µm tall. *Conidiogenous cells* phialidic, discrete or integrated, hyaline, smooth, cylindrical, enteroblastic, proliferating percurrently with numerous apical annellations, 7–15 × 2.5–4 µm. *Conidia* hyaline, thick-walled, guttulate, aseptate, smooth, narrowly fusoid, curved to sigmoid, with a subobtuse apex, tapering towards a truncate base, 1.5–2 µm diam, (45–)60–70(–80) × (3–)3.5(–4) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium, and feathery, lobate margins, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface and reverse olivaceous grey with patches of smoke grey. On OA and PDA surface and reverse olivaceous grey with patches of pale olivaceous grey.

Typus. Australia, Western Australia, Albany, Fitzgerald River National Park, on *Petrophile fastigiata* (*Proteaceae*), 22 Sept. 2015, *P.W. Crous* (holotype CBS H-22911, culture ex-type CPC 29160 = CBS 142125; ITS sequence GenBank KY173460, LSU sequence GenBank KY173550, MycoBank MB819116); idem, CPC 29264; ITS sequence GenBank KY173462, LSU sequence GenBank KY173552, *cmdA* sequence GenBank KY173575.

Additional specimen examined. Australia, Western Australia, Albany, Fitzgerald River National Park, on *Petrophile fastigiata*, 22 Sept. 2015, *P.W. Crous*, HPC 646, CPC 29230; ITS sequence GenBank KY173461, LSU sequence GenBank KY173551.

Colour illustrations. *Petrophile fastigiata*; conidiomata sporulating on OA, conidiophores and conidia. Scale bars = 10 µm.

Notes — Of the species of *Saccharata* presently known, none have aseptate conidia as large as those of *S. petrophilicola*. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence of the ex-type culture, the highest similarities were with '*Saccharata* sp. 1' (GenBank JN225922; Identities = 532/574 (93 %), Gaps = 16/574 (2 %)), *S. proteae* (GenBank EU552145; Identities = 536/580 (92 %), Gaps = 18/580 (3 %)) and *S. intermedia* (GenBank GU229888; Identities = 532/576 (92 %), Gaps = 13/576 (2 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence of the ex-type culture, the highest similarities were with *S. kirstenboschensis* (GenBank FJ372409; Identities = 830/834 (99 %), no gaps), *S. proteae* (GenBank EU552145; Identities = 834/839 (99 %), no gaps) and *S. capensis* (GenBank KF766390; Identities = 833/839 (99 %), no gaps).

Key to the known Australian species of Saccharata

1. Conidia hyaline, fusoid, with synasexual morph having brown, subcylindrical to ellipsoid conidia . . . . *S. proteae*
1. Conidia hyaline, lacking synasexual morph with brown conidia 2

2. Conidia fusoid 3
2. Conidia cylindrical, 0(–3)-euseptate, (18–)35–42(–50) × (3.5–)4(–4.5) µm . . . . *S. eucalypti*

3. Conidia septate 4
3. Conidia aseptate 5

4. Conidia 1-septate, (27–)33–38(–42) × (4–)6 µm . . . . *S. daviesiae*
4. Conidia (0–)1(–2)-septate, (9–)20–23(–25) × (4–)5–6(–7) µm . . . . *S. lambertiae*

5. Conidia up to 20 µm long, (13–)15–17(–20) × 6(–6.5) µm . . . . *S. banksiae*
5. Conidia longer than 20 µm 6

6. Conidia up to 80 µm long, (45–)60–70(–80) × (3–)3.5(–4) µm . . . . *S. petrophilicola*
6. Conidia shorter 7

7. Mean conidial length 27–29 µm, (23–)27–29(–32) × (5–)5.5(–6) µm . . . . *S. hakeicola*
7. Mean conidial length 28–35 µm 8

8. Conidia (6.5–)7–8 µm wide . . . . *S. hakeae*
8. Conidia narrower 9

9. Conidia (4–)5 µm diam, occurring on *Eucalyptus* . . . . *S. eucalyptorum*
9. Conidia (4.5–)5(–5.5) µm diam, occurring on *Petrophile* and *Isopogon* . . . . *S. petrophiles*

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Sirococcus quercus

Fungal Planet 552 – 21 December 2016

Sirococcus quercus Crous, *sp. nov.*

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

Classification – *Gnomoniaceae*, *Diaporthales*, *Sordariomycetes*.

Leaf spots amphigenous, dark brown, irregular. *Conidiomata* immersed, becoming erumpent, solitary, medium brown, globose, unilocular, thick-walled, of 6–10 layers of brown *textura angularis*, opening by irregular rupture. *Conidiophores* subcylindrical, hyaline, smooth, branched at base, 0–1-septate, or reduced to conidiogenous cells, 10–15 × 2.5–3.5 µm. *Conidiogenous cells* hyaline, smooth, ampulliform to subcylindrical, tapered, apex phialidic with periclinal thickening, 1.5 µm diam, 7–12 × 2.5–3 µm. *Conidia* solitary, hyaline, smooth, guttulate, fusoid, straight to curved, apex subobtuse, base truncate, 1 µm diam, medianly 1-septate, (10–)13–15(–17) × 3(–3.5) µm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium and even, smooth margins, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface and reverse pale luteous. On OA and PDA surface and reverse pale luteous.

Typus. USA, Texas, Austin, on leaves of *Quercus* sp. (*Fagaceae*), Aug. 2013, *P.W. Crous* (holotype CBS H-22912, culture ex-type CPC 29512 = CBS 142126; ITS sequence GenBank KY173465, LSU sequence GenBank KY173554, MycoBank MB819117).

Notes — The taxonomy of the genus *Sirococcus*, which is commonly associated with shoot infections and cankers on woody plants, is unresolved. Many of the taxa presently accommodated in this genus will eventually be relocated elsewhere (Sutton 1980). *Sirococcus quercus*, isolated from brown leaf spots on *Quercus*, is phylogenetically related to species such as *S. pineicola* (on *Picea*), *S. tsugae* (on *Tsugae*) and *S. conigenus* (shoot blight of conifers) (Rossman et al. 2008). Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *S. tsugae* (GenBank HQ256769; Identities = 530/551 (96 %), Gaps = 3/551 (0 %)), *S. piceicola* (GenBank EF512480; Identities = 523/547 (96 %), Gaps = 5/547 (0 %)) and *S. conigenus* (GenBank AY437753; Identities = 523/547 (96 %), Gaps = 5/547 (0 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with *S. tsugae* (GenBank EU255207; Identities = 747/752 (99 %), no gaps), *Plagiostoma conradii* (GenBank AF408381; Identities = 743/748 (99 %), no gaps) and *Gnomonia petiolorum* (GenBank AY818963; Identities = 786/793 (99 %), no gaps).

Colour illustrations. Symptomatic leaves of *Quercus* sp.; conidiomata sporulating on PNA, conidiophores and conidia. Scale bars = 10 µm.

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Elsinoë eucalyptigena

Fungal Planet 553 – 21 December 2016

Elsinoë eucalyptigena Crous, *sp. nov.*

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

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

Leaf spots on *E. kingsmillii* mostly epiphyllous, round, 1–3 mm diam, dark brown, developing grey centres with conidiomata; on *E. pachyphylla* mostly epiphyllous, round, 1–4 mm diam, grey with irregular red-purple margins. *Conidiomata* acervular, brown, erumpent, solitary or somewhat aggregated, 50–120 µm diam; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells, or with a supporting cell. *Conidiogenous cells* hyaline, smooth or pale brown, and somewhat roughened, lining the inner cavity, polyphialidic, pale brown, subcylindrical, 5–10 × 2.5–3.5 µm. *Conidia* solitary, subcylindrical with obtuse ends, straight, base with truncate hilum, 0.5 µm diam, guttulate, 7(–8) × 2.5(–3) µm.

Culture characteristics — Colonies erumpent, folded, with sparse aerial mycelium, and smooth, lobed margins, reaching 5 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse saffron.

Typus. AUSTRALIA, Western Australia, Perth, King's Park Botanic Gardens, on leaves of *Eucalyptus kingsmillii* (*Myrtaceae*), 27 Sept. 2015, *P.W. Crous* (holotype CBS H-22913, culture ex-type CPC 29529 = CBS 142127; ITS sequence GenBank KY173404, LSU sequence GenBank KY173496, MycoBank MB819118).

Additional specimen examined. AUSTRALIA, Western Australia, Perth, King's Park Botanic Gardens, on leaves of *Eucalyptus pachyphylla* (*Myrtaceae*), 27 Sept. 2015, *P.W. Crous*, CPC 29565= CBS 142128; ITS sequence GenBank KY173405, LSU sequence GenBank KY173497.

Notes — Although several species of *Elsinoë* have been described from leaf spots of *Eucalyptus*, namely *E. eucalypti*, *E. eucalypticola*, *E. eucalyptorum* and *E. tectificae* (Summerell et al. 2006, Cheewangkoon et al. 2009), *E. eucalyptigena* is phylogenetically distinct from them. These species remain difficult to compare based on morphology, as some are known only based on their sexual morph. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *Elsinoë australis* (GenBank FJ010328; Identities = 442/505 (88 %), Gaps = 27/505 (5 %)), *Elsinoë othonnae* (GenBank KR476726; Identities = 439/512 (86 %), Gaps = 35/512 (6 %)) and *Sphaceloma coryli* (GenBank KT001428; Identities = 446/525 (85 %), Gaps = 34/525 (6 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with *Elsinoë fawcettii* (GenBank JN940385; Identities = 756/792 (95 %), Gaps = 2/792 (0 %)), *Elsinoë eucalypticola* (GenBank GQ303306; Identities = 756/792 (95 %), Gaps = 2/792 (0 %)) and *Elsinoë eucalyptorum* (GenBank DQ923530; Identities = 756/794 (95 %), Gaps = 4/794 (0 %)).

Colour illustrations. *Eucalyptus pachyphylla*; leaf spots, conidiogenous cells and conidia. Scale bars = 10 µm.

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Elsinoë preissianae

Fungal Planet 554 – 21 December 2016

Elsinoë preissianae Crous, *sp. nov.*

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

Classification – *Elsinoaceae*, *Myriangiales*, *Dothideomycetes*.

Associated with corky brown leaf spots, but occurring in association with other fungi. Sporulation on PDA. *Conidiophores* hyaline, smooth, subcylindrical, ampulliform to doliiform, 0–1-septate, 10–20 × 3–4 µm. *Conidiogenous cells* integrated, terminal, polyphialidic, hyaline, smooth, ampulliform to subcylindrical or doliiform, 5–10 × 3–4 µm. *Conidia* hyaline, smooth, aseptate, granular, narrowly ellipsoid to subcylindrical, apex obtuse, base truncate, 1–1.5 µm diam, (10–)11–12(–13) × (3–)3.5(–4) µm.

Culture characteristics — Colonies slow growing, reaching 3–4 mm diam after 2 wk at 25 °C, erumpent, with sparse aerial mycelium; surface folded, margin irregular. On MEA, PDA and OA surface scarlet red with diffuse red pigment in agar.

Typus. Australia, Western Australia, Albany, Stirling Range National Park, Central lookout, on leaves of *Eucalyptus preissiana* (*Myrtaceae*), 23 Sept. 2015, *P.W. Crous* (holotype CBS H-22914, culture ex-type CPC 29787 = CBS 142129; ITS sequence GenBank KY173406, LSU sequence GenBank KY173498, MycoBank MB819119).

Notes — Based on its ITS sequence, *E. preissianae* is related but phylogenetically distinct from species such as *E. araliae* (on *Aralia*), *E. ampelina* (on *Citrus*) and *E. verbenae* (on *Verbena*). A new species is therefore introduced to accommodate this taxon. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *Elsinoë eucalypticola* (GenBank GQ303275; Identities = 528/607 (87 %), Gaps = 35/607 (5 %)), *Sphaceloma arachidis* (GenBank JN943485; Identities = 461/528 (87 %), Gaps = 31/528 (5 %)) and *Sphaceloma perseae* (GenBank HM191256; Identities = 339/364 (93 %), Gaps = 6/364 (1 %)). Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with *Sphaceloma erythrinae* (GenBank JN940392; Identities = 821/836 (98 %), Gaps = 1/836 (0 %)), *Elsinoë fawcettii* (GenBank JN940382; Identities = 819/835 (98 %), no gaps) and *Sphaceloma terminaliae* (GenBank JN940371; Identities = 818/835 (98 %), no gaps).

Colour illustrations. *Eucalyptus preissiana*; culture with diffuse red pigment, conidiogenous cells and conidia. Scale bars = 10 µm.

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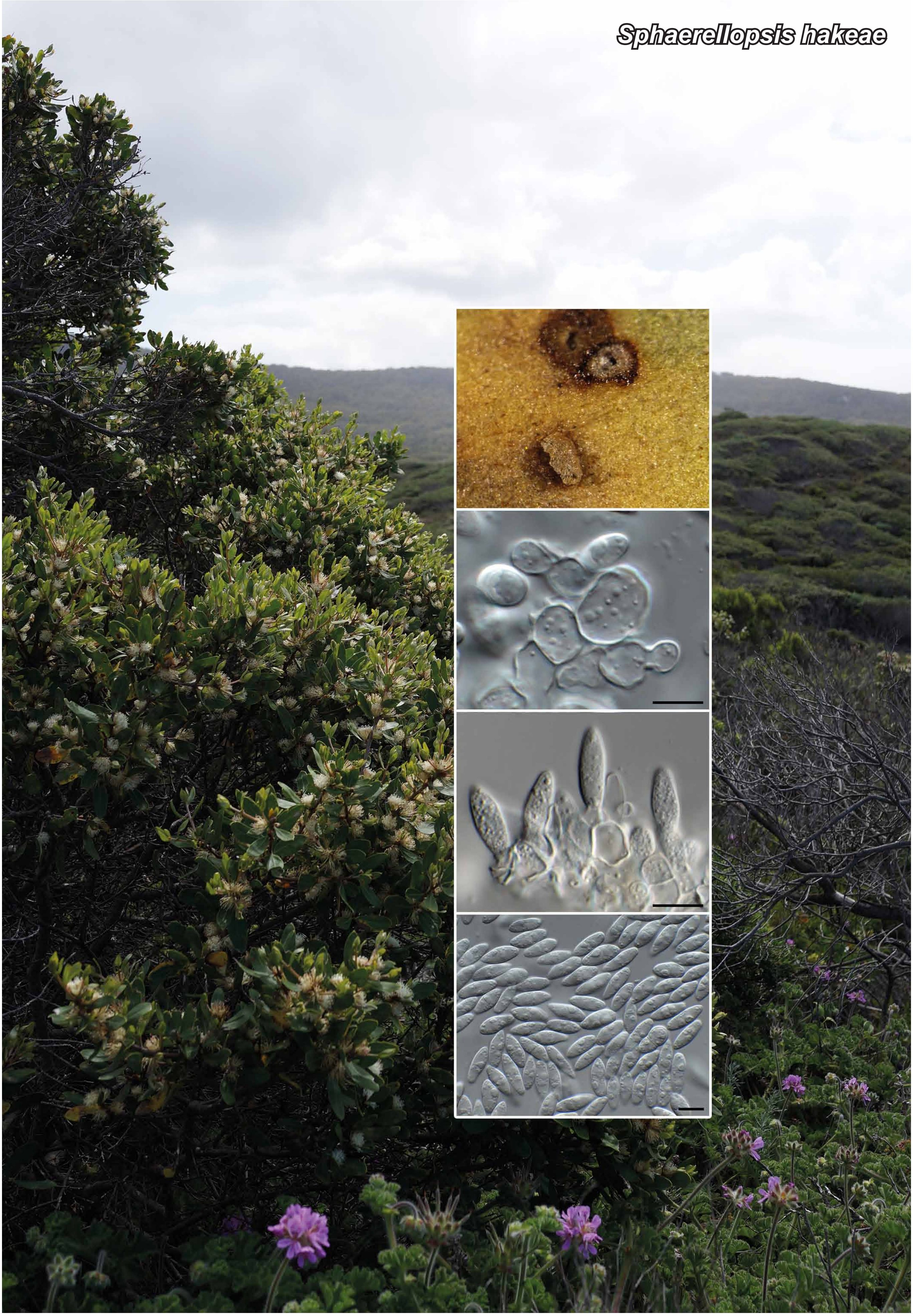
Sphaerellopsis hakeae



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Sphaerellopsis hakeae Crous, *sp. nov.*

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

Classification – *Leptosphaeriaceae*, *Pleosporales*, *Dothideomycetes.*

Conidiomata associated with rust pustules, but also occurring separately without any association to the rust. *Conidiomata* pycnidial, erumpent, aggregated, globose, 90–150 µm diam, with central ostiole, exuding crystalline conidial mass; wall of 2–3 layers of medium brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, smooth, hyaline, ampulliform to doliiform, 5–6 × 3–7 µm, with prominent periclinal thickening or several percurrent proliferations at apex. *Conidia* hyaline, smooth, guttulate, fusoid-ellipsoid, rarely Y-forked, medianly 1-septate, prominently constricted at septum, apex subobtuse, tapering to truncate hilum, 2–2.5 µm diam, with mucoid appendages at both ends, (11–)12–14(–15) × (4–)5(–6) µm.

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

Typus. Australia, Western Australia, Denmark, Lights Beach, on leaves of *Hakea* sp. (*Proteaceae*), 19 Sept. 2015, *P.W. Crous* (holotype CBS H-22915, culture ex-type CPC 29566 = CBS 142130; ITS sequence GenBank KY173466, LSU sequence GenBank KY173555, MycoBank MB819120).

Notes — Species of *Sphaerellopsis* are mycoparasites of rust fungi, with conidiomata and ascomata frequently occurring in rust pustules. The genus *Sphaerellopsis* was recently treated by Trakunyingcharoen et al. (2014). *Sphaerellopsis hakeae* is phylogenetically closely related to *S. macroconidialis* (conidia 1(–3)-septate, (13–)17–20(–27) × (3.5–)4.5(–5) µm; Trakunyingcharoen et al. 2014; Identities = 525/539 (97 %), no gaps, based on ITS sequence GenBank KP170660), which is easily distinguishable based on its much larger conidia. Based on a megablast search of the NCBIs nucleotide database using the LSU sequence, the highest similarities were with *Sphaerellopsis macroconidialis* (GenBank KP170726; Identities = 830/830 (100 %), no gaps), *Plenodomus enteroleucus* (GenBank JF740287; Identities = 825/833 (99 %), no gaps) and *Plenodomus libanotidis* (GenBank JF740300; Identities = 824/834 (99 %), Gaps = 1/834 (0 %)).

Colour illustrations. *Hakea* sp.; leaf spots, conidiogenous cells and conidia. Scale bars = 10 µm.

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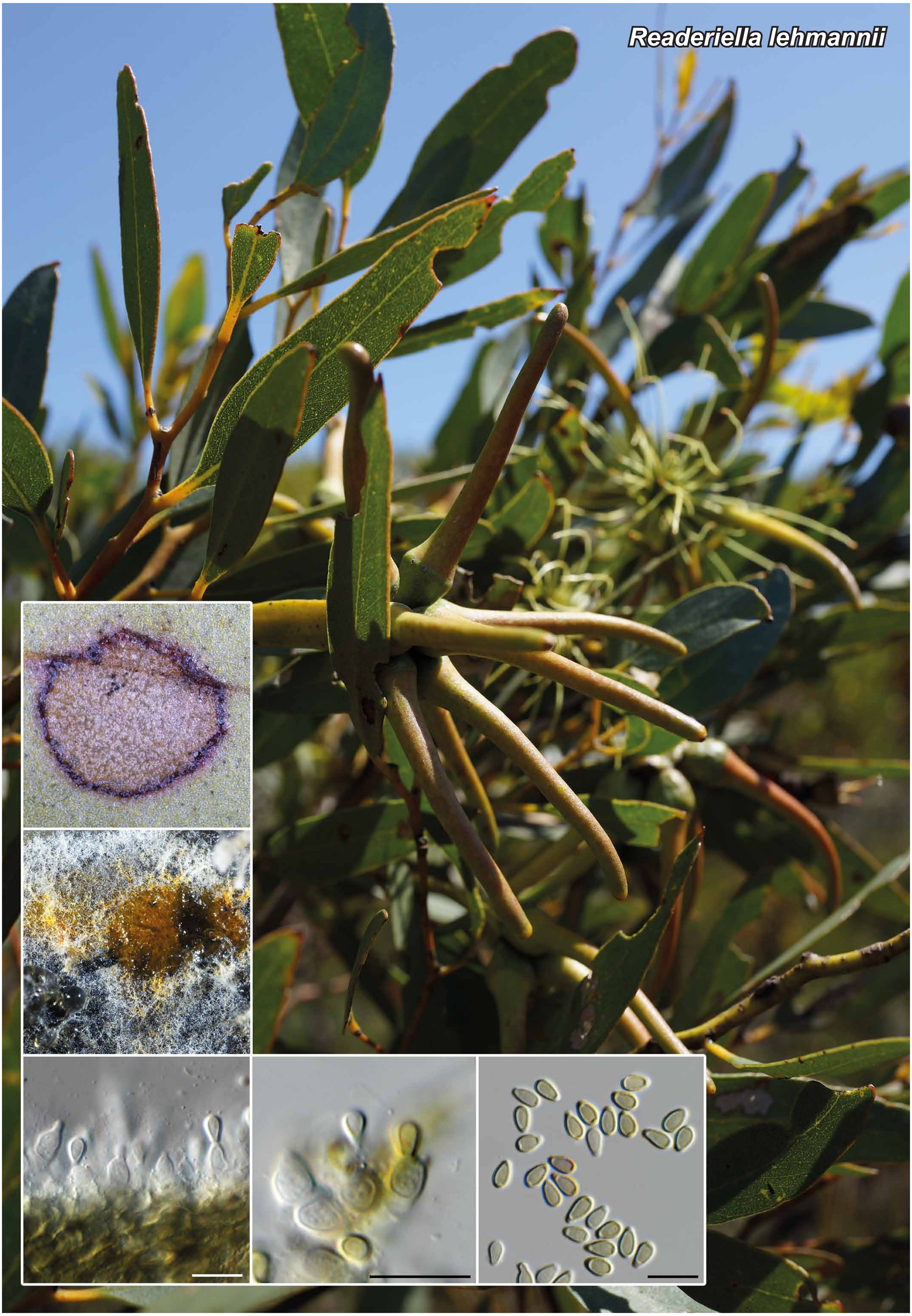
Readeriella lehmannii

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Readeriella lehmannii Crous, *sp. nov.*

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

Classification – *Teratosphaeriaceae*, *Capnodiales*, *Dothideomycetes.*

Leaf spots amphigenous, circular, medium brown, with raised red-brown margin, 2–5 mm diam. On PDA: *Conidiomata* globose, solitary, 180–250 µm diam; wall of 3–6 layers of brown *textura angularis. Conidiophores* hyaline to pale brown, smooth to finely verruculose, 0–3-septate, subcylindrical, branched or not, 5–20 × 3–4 µm, with terminal and intercalary conidiogenous cells. *Conidiogenous cells* doliiform, hyaline, proliferating percurrently at apex, 5–7 × 3–4 µm. *Conidia* solitary, medium brown, aseptate, granular, verruculose, thick-walled, ellipsoid to clavate, apex obtuse, base truncate, 1 µm diam, apex and base frequently slightly thickened, (5–)6(–7) × (2.5–)3(–3.5) µm, lacking a sheath.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface dark brick, reverse brown vinaceous. On OA surface brick. On PDA surface hazel with patches of brick, reverse isabelline.

Typus. Australia, Western Australia, Albany, Stirling Range National Park, Central lookout, on leaves of *Eucalyptus lehmannii* (*Myrtaceae*), 23 Sept. 2015, *P.W. Crous* (holotype CBS H-22916, culture ex-type CPC 28935 = CBS 142131; ITS sequence GenBank KY173440, LSU sequence GenBank KY173530, *tub2* sequence GenBank KY173617, MycoBank MB819121).

Additional specimen examined. Australia, Western Australia, Bridal Creek, on leaves of *Corymbia calophylla* (*Myrtaceae*), 20 Sept. 2015, *P.W. Crous*, HPC 717, culture CPC 29298 = CBS 142132; ITS sequence GenBank KY173441, LSU sequence GenBank KY173531, *tub2* sequence GenBank KY173618.

Colour illustrations. *Eucalyptus lehmannii*; leaf spot, conidiomata sporulating on PDA, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — Species of *Readeriella* are commonly encountered pathogens causing leaf spots on *Eucalyptus*, and several species have *Cibiessia* synasexual morphs (Crous et al. 2009). *Readeriella lehmannii* is phylogenetically closely related to *R. patrickii* (conidia (6–)7–8(–9) × (2.5–)3(–3.5) µm, covered in a persistent mucilaginous sheath; Crous et al. 2009), but can be distinguished in that it has smaller conidia, lacking a sheath. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *Readeriella patrickii* (GenBank KF901662; Identities = 475/481 (99 %), no gaps), *Readeriella dimorphospora* (GenBank EF394850; Identities = 546/555 (98 %), no gaps) and *Readeriella tasmanica* (GenBank FR667977; Identities = 431/439 (98 %), no gaps).

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Myrtapenidiella sporadicae

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Myrtapenidiella sporadicae Crous, *sp. nov.*

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

Classification – *Teratosphaeriaceae*, *Capnodiales*, *Dothideomycetes.*

Mycelium consisting of branched, septate, brown, smooth, 2–3 µm diam hyphae. *Conidiophores* solitary, erect, rarely branched, straight to geniculate-sinuous, 50–100 × 5–7 µm, 3–7-septate, brown, roughened, thick-walled. *Conidiogenous cells* terminal and intercalary, subcylindrical, thick-walled, straight, brown, roughened, 10–20 × 5–6 µm, with 1–2 apical, flat-tipped loci, 2.5–3 µm, darkened and thickened. *Ramoconidia* brown, thick-walled, roughened to warted, subcylindrical to ellipsoid-fusoid, 0–2-septate, 15–25 × 5–6 µm, with 1–2 hila, thickened and darkened, 2–2.5 µm diam. *Conidia* occurring in branched chains (–15), acropetal, brown, thick-walled, roughened, 0–1-septate, (15–)17–19(–25) × (2.5–)3–4 µm; hila thickened darkened, 2–2.5 µm diam.

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

Typus. Australia, Western Australia, Perth, King's Park Botanic Gardens, on leaves of *Eucalyptus sporadica* (*Myrtaceae*), 27 Sept. 2015, *M.J. Wingfield* (holotype CBS H-22917, culture ex-type CPC 29200 = CBS 142133; ITS sequence GenBank KY173422, LSU sequence GenBank KY173513, *tub2* sequence GenBank KY173606, MycoBank MB819122).

Colour illustrations. Symptomatic leaves of *Eucalyptus sporadica*; conidiophores sporulating on PNA, conidiophores and conidia. Scale bars = 10 µm.

Notes — There are four species of *Myrtapenidiella* and all occur on *Myrtaceae* (Quaedvlieg et al. 2014, Crous et al. 2015b). Phylogenetically, *M. sporadicae* is closely related to *M. eucalyptorum* (conidia (10–)12–14(–16) × (3–)3.5–4 µm; Crous et al. 2015b), but the latter has much smaller conidia. Based on a megablast search of the NCBIs nucleotide database using the ITS sequence, the highest similarities were with *M. tenuiramis* (GenBank GQ852750; Identities = 518/538 (96 %), Gaps = 2/538 (0 %)), *M. corymbia* (GenBank KF442520; Identities = 472/495 (95 %), Gaps = 2/495 (0 %)), *M. eucalypti* (GenBank EU882131; Identities = 513/538 (95 %), Gaps = 5/538 (0 %)) and *M. eucalyptorum* (GenBank KR476727; Identities = 515/543 (95 %), Gaps = 7/543 (0 %)).

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