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RESEARCH ARTICLE

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Key words

ITS DNA barcodes
LSU
novel fungal species
systematics

Abstract Novel species of fungi described in the present study include the following from Australia: *Neoseptorioides eucalypti* gen. & sp. nov. from *Eucalyptus radiata* leaves, *Phytophthora gondwanensis* from soil, *Diaporthe tulliensis* from rotted stem ends of *Theobroma cacao* fruit, *Diaporthe vawdreyi* from fruit rot of *Psidium guajava*, *Magnaporthiopsis agrostidis* from rotted roots of *Agrostis stolonifera* and *Semifissispora natalis* from *Eucalyptus* leaf litter. Furthermore, *Neopestalotiopsis egyptiaca* is described from *Mangifera indica* leaves (Egypt), *Roussoella mexicana* from *Coffea arabica* leaves (Mexico), *Calonectria monticola* from soil (Thailand), *Hygrocybe jackmanii* from littoral sand dunes (Canada), *Lindgomyces madisonensis* from submerged decorticated wood (USA), *Neofabraea brasiliensis* from *Malus domestica* (Brazil), *Geastrum diosiae* from litter (Argentina), *Ganoderma wiiroense* on angiosperms (Ghana), *Arthrinium gutiae* from the gut of a grasshopper (India), *Pyrenochaeta telephoni* from the screen of a mobile phone (India) and *Xenoleptographium phialoconidium* gen. & sp. nov. on exposed xylem tissues of *Gmelina arborea* (Indonesia). Several novelties are introduced from Spain, namely *Psathyrella complutensis* on loamy soil, *Chlorophyllum lusitanicum* on nitrified grasslands (incl. *Chlorophyllum arizonicum* comb. nov.), *Aspergillus citocrescens* from cave sediment and *Lotinia verna* gen. & sp. nov. from muddy soil. Novel foliicolous taxa from South Africa include *Phyllosticta carissicola* from *Carissa macrocarpa, Pseudopyricularia hagahagae* from *Cyperaceae* and *Zeloasperisporium searsiae* from *Searsia chirindensis*. Furthermore, *Neophaeococcomyces* is introduced as a novel genus, with two new combinations, *N. aloes* and *N. catenatus*. Several foliicolous novelties are recorded from La Réunion, France, namely *Ochroconis pandanicola* from *Pandanus utilis, Neosulcatispora agaves* gen. & sp. nov. from *Agave vera-cruz*, *Pilidium eucalyptorum* from *Eucalyptus robusta*, *Strelitziana syzygii* from *Syzygium jambos* (incl. *Strelitzianaceae* fam. nov.) and *Pseudobeltrania ocoteae* from *Ocotea obtusata* (*Beltraniaceae* emend.). Morphological and culture characteristics along with ITS DNA barcodes are provided for all taxa.

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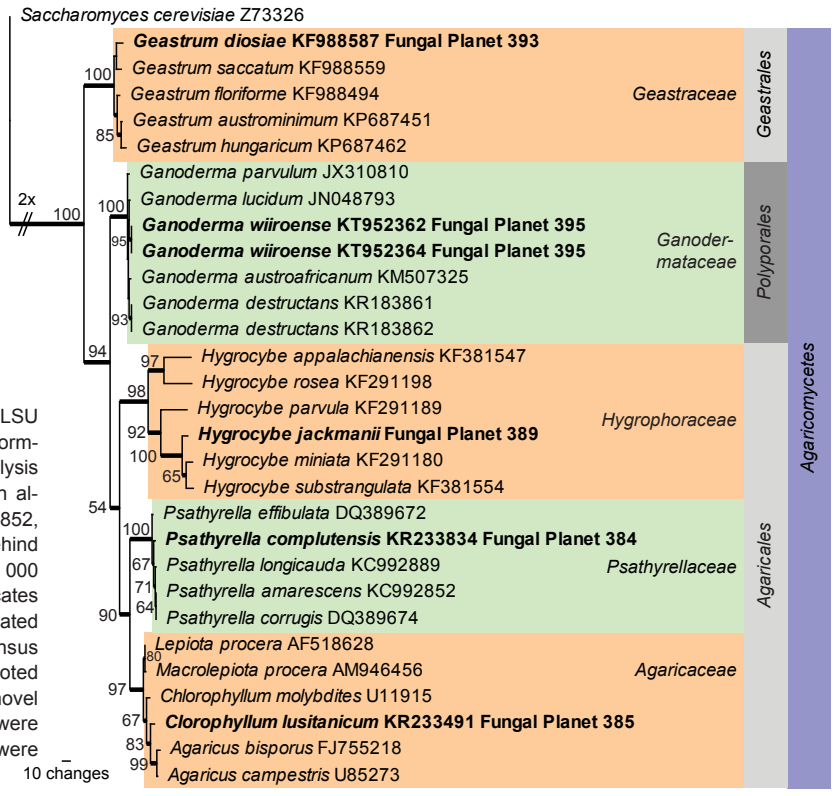
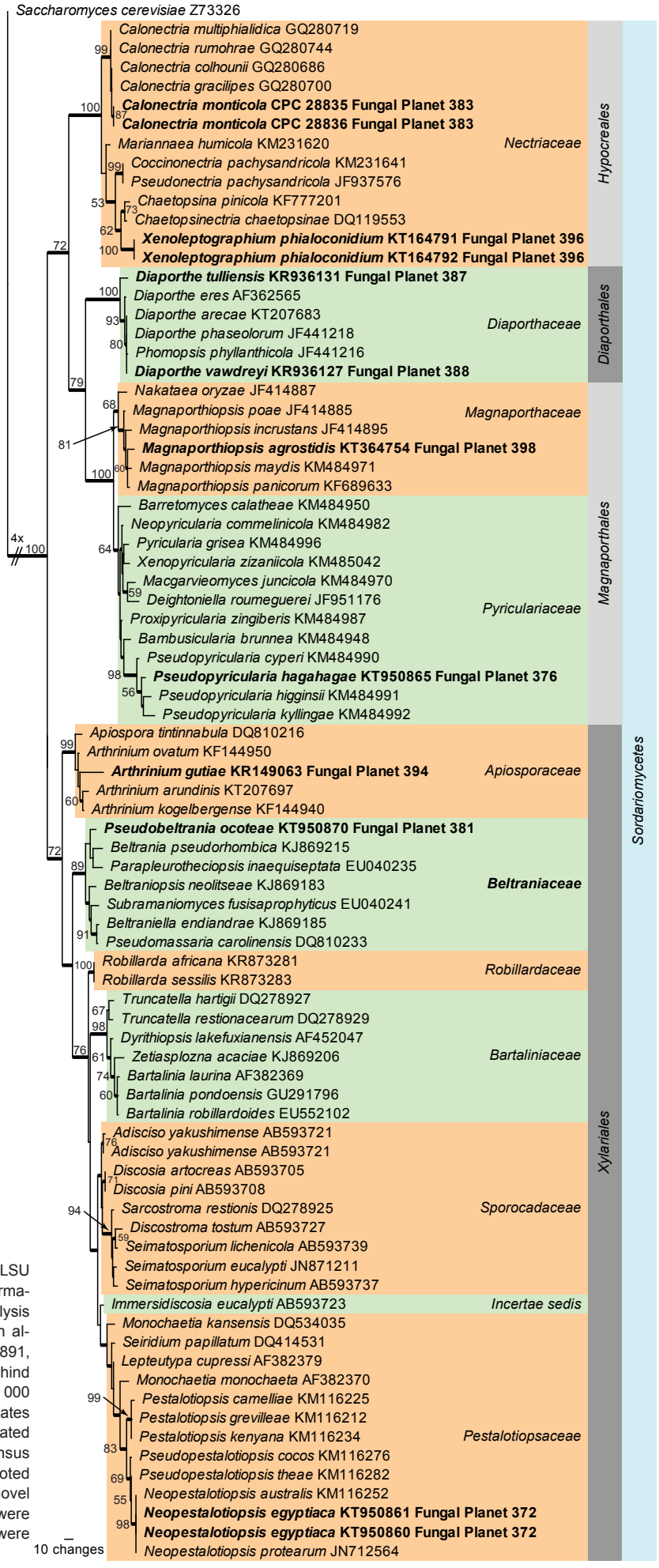
Overview *Basidiomycota* phylogeny

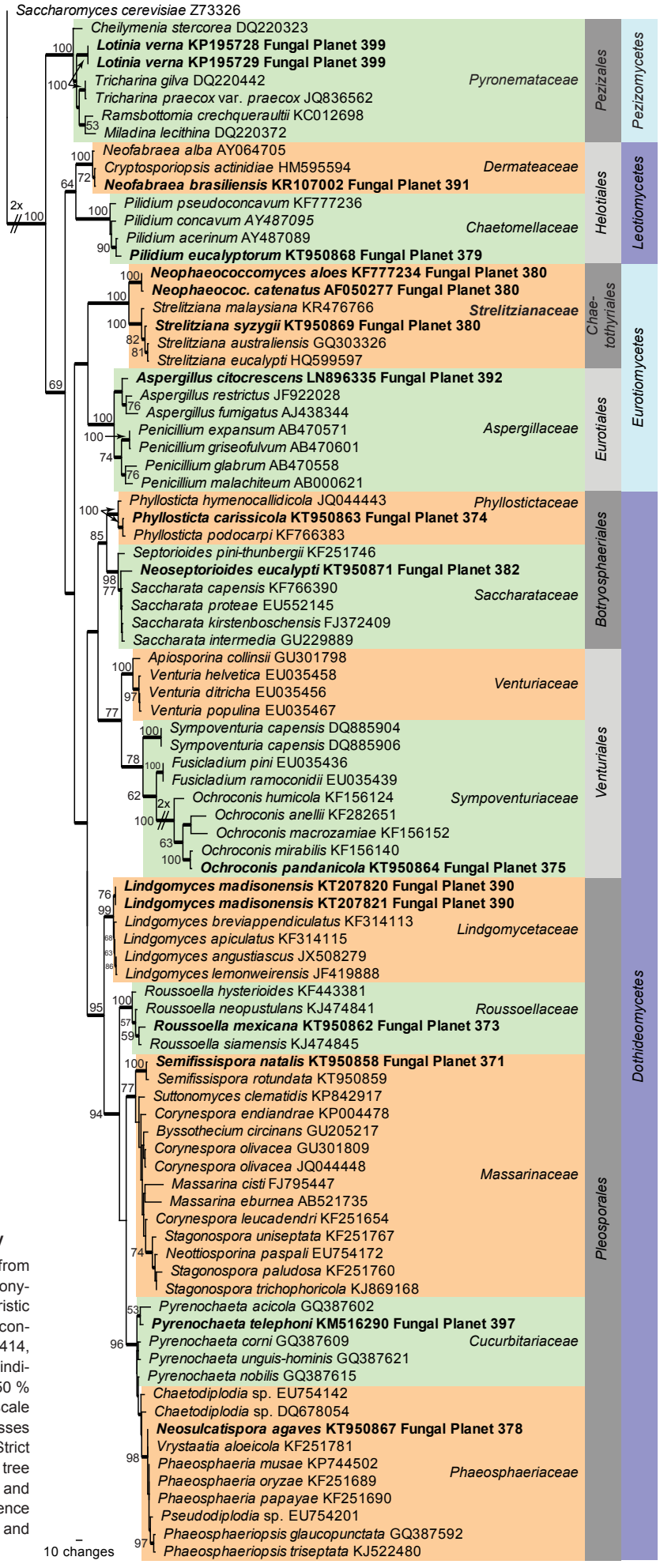
First of 12 equally most parsimonious trees obtained from the LSU alignment (215 parsimony-informative, 131 parsimony-uninformative and 463 constant characters) based on a heuristic analysis with simple taxon additions and tree-bisection-reconnection algorithm using PAUP v. 4.0b10 (TL = 673, CI = 0.719, RI = 0.852, RC = 0.613). GenBank accession numbers are indicated behind the species names. Bootstrap support values > 50 % from 100 000 fast replicates are shown at the nodes and the scale bar indicates the number of changes. Families, orders and classes are indicated with coloured blocks to the right of the tree. Strict consensus branches are indicated with thickened lines. The tree was rooted to *Saccharomyces cerevisiae* (GenBank Z73326) and the novel species 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 18408).





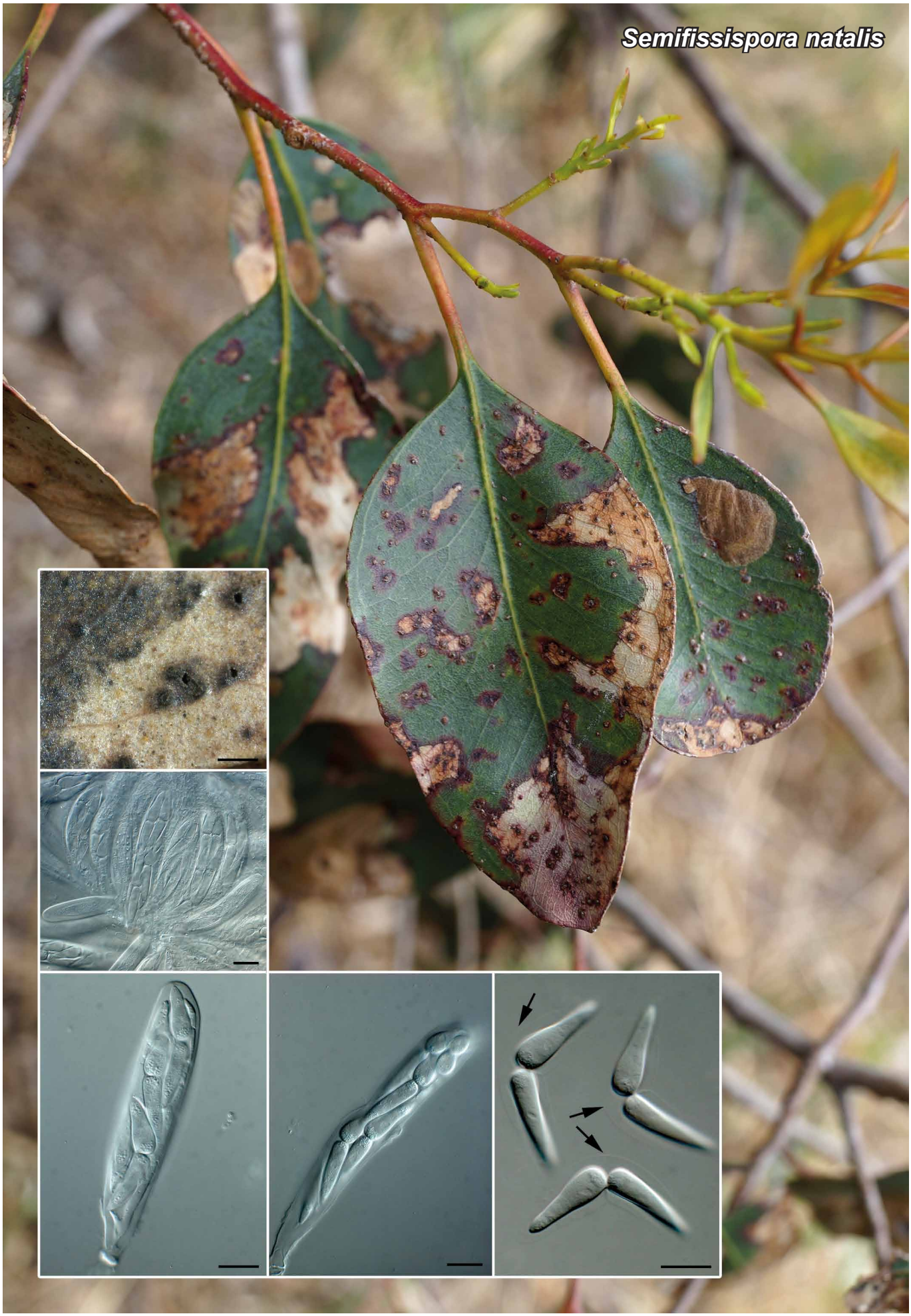
Overview *Sordariomycetes* phylogeny

First of 260 equally most parsimonious trees obtained from the LSU alignment (213 parsimony-informative, 115 parsimony-uninformative and 453 constant characters) based on a heuristic analysis with simple taxon additions and tree-bisection-reconnection algorithm using PAUP v. 4.0b10 (TL = 939, CI = 0.520, RI = 0.891, RC = 0.463). GenBank accession numbers are indicated behind the species names. Bootstrap support values > 50 % from 100 000 fast replicates are shown at the nodes and the scale bar indicates the number of changes. Families, orders and classes are indicated with coloured blocks to the right of the tree. Strict consensus branches are indicated with thickened lines. The tree was rooted to *Saccharomyces cerevisiae* (GenBank Z73326) and the novel species 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 18408).



Overview *Dothideomycetes* and other classes phylogeny

First of 1 000 equally most parsimonious trees obtained from the LSU alignment (308 parsimony-informative, 44 parsimony-uninformative and 417 constant characters) based on a heuristic analysis with simple taxon additions and tree-bisection-reconnection algorithm using PAUP v. 4.0b10 (TL = 1 536, CI = 0.414, RI = 0.844, RC = 0.349). GenBank accession numbers are indicated behind the species names. Bootstrap support values > 50 % from 100 000 fast replicates are shown at the nodes and the scale bar indicates the number of changes. Families, orders and classes are indicated with coloured blocks to the right of the tree. Strict consensus branches are indicated with thickened lines. The tree was rooted to *Saccharomyces cerevisiae* (GenBank Z73326) and the novel species 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 18408).


Semifissispora natalis

Fungal Planet 371 – 1 December 2015

Semifissispora natalis Crous, J. Edwards & P.W.J. Taylor, *sp. nov.*

Etymology. *natalis* (Latin genitive noun), refers to the birth date of the first author, on which this fungus was collected.

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

Ascomata pseudothecial, immersed in leaf tissue (litter), separate, globose, brown, to 350 µm diam, with central ostiole, 40–50 µm diam (but frequently rupturing the epidermis via irregular split); wall of 3–6 layers of brown *textura angularis*, becoming thin-walled and hyaline towards the centrum. *Pseudoparaphyses* intermingled among asci, hyaline, smooth, with clavate terminal cells, constricted at septa, hyphae-like, 3.5–6 µm diam, extending above asci. *Asci* stipitate, bitunicate, 8-spored, fusoid-ellipsoid, hyaline, smooth, with visible apical chamber, 2–3 µm diam, 90–140 × 16–22 µm. *Ascospores* bi- to triseriate, fusoid, hyaline, smooth, guttulate, with minute fine guttules concentrated at polar ends of each cell, 1-septate, prominently constricted at septum, bending at maturity, surrounded by a prominent mucoid sheath, 2–4 µm diam; apical cells (22–)24–27(–28) × (7–)8–9(–10) µm, basal cells (23–)26–28(–31) × (6.5–)7(–7.5) µm.

Culture characteristics — Colonies reaching up to 20 mm diam after 2 wk at 25 °C spreading, with surface folded, margins feathery, lobate, and sparse aerial mycelium. On 2 % malt extract agar (MEA) surface smoke grey with patches of sepia, reverse sepia. On oatmeal agar (OA) surface isabelline. On 2 % potato dextrose agar (PDA) surface and reverse isabelline.

Typus. Australia, Melbourne, cycle path alongside Moonee Ponds Creek, on leaf litter of *Eucalyptus* sp. (*Myrtaceae*), 2 Nov. 2014, *P.W. Crous, J. Edwards & P.W.J. Taylor* (holotype CBS H-22394, culture ex-type CPC 25383 = CBS 140659; ITS sequence GenBank KT950846, LSU sequence GenBank KT950858, *gapdh* sequence GenBank KT950875, *tef1* sequence GenBank KT950878, MycoBank MB814924); CPC 25384.

Notes — Swart (1982) introduced the genus *Semifissispora* (based on *S. fusiformis*) to accommodate three species found on *Eucalyptus* leaf litter, which he suspected to play a role in breakdown of litter under semi-arid conditions. There have subsequently been two additional reports of *Semifissispora* spp. from South Africa, namely *S. elongata* and *S. rotundata* (Crous 1993, Crous & Van der Linde 1993). The genus has remained obscure, although Swart (1982) correctly place it in the *Pleosporales*, suspecting that it was a member of *Pleosporaceae*. Based on the LSU sequences generated in this study, *Semifissispora* resides in the *Massarinaceae*, a position that is also supported by its morphology.

Of the three species presently known in *Semifissispora*, *S. natalis* differs from the other species in having longer and wider ascospores, the largest ascospores found in *S. elongata*, with apical cells being 18–25 × 4–6 (av. 20.7 × 5.1) and basal cells 22–26 × 3.5–5 (av. 23.7 × 4.4) µm.

Colour illustrations. Symptomatic *Eucalyptus* leaves along cycle path next to Moonee Ponds Creek; ascomata, asci and ascospores with sheath. Scale bars: ascomata = 350 µm, all others = 10 µm.

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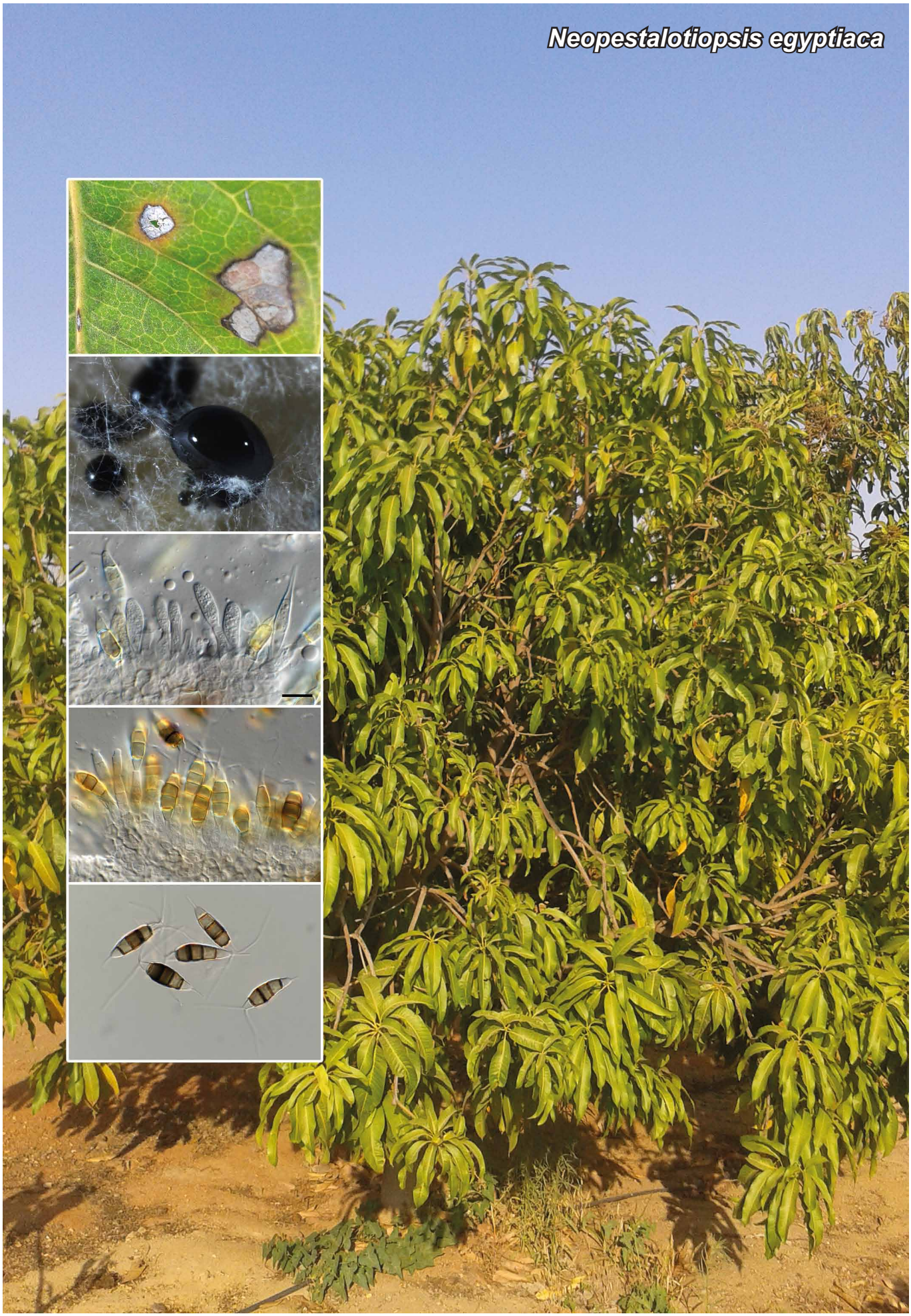
Neopestalotiopsis egyptiaca

Fungal Planet 372 – 1 December 2015

Neopestalotiopsis egyptiaca A.M. Ismail, G. Perrone & Crous, *sp. nov.*

Etymology. Name reflects the country Egypt where the fungus was collected.

Classification — *Sporocadaceae, Xylariales, Sordariomycetes.*

Conidiomata pycnidial, globose, formed on PDA within 7 d, mostly solitary, scattered, semi-immersed or erumpent, to 300 µm diam; releasing slimy, black conidial masses. *Conidiophores* septate, branched at base, sometimes reduced to conidiogenous cells, hyaline, smooth-walled, septate, up to 42 µm long. *Conidiogenous cells* discrete, cylindrical, hyaline, smooth, proliferating 2–3 times percurrently at apex, 15–25 × 3–5 µm. *Conidia* smooth, fusiform, straight and sometimes slightly curved, 4-septate consisting of three thick-walled pale to dark brown median cells, of which the upper two are darker brown than the lower cell (these cells also tend to be finely roughened), and two thin-walled pale to dark olivaceous apical and basal cells, (22.5–)23–26(–28) × 6–7.5 µm. Apical cell giving rise to 2–3 unbranched, tubular, hyaline appendages, (16.5–)15–21(–25) µm long; basal cell with a single, hyaline, centric, unbranched appendage, 4.5–7.5 µm long.

Culture characteristics — On PDA colonies reached up to 90 mm diam after 10 d at 25 °C with smooth edge, whitish, slightly raised, circular appearance, with sparse to moderate aerial mycelium on the surface with black, scattered conidiomata. On reverse, olivaceous, with distinct zonation.

Typus. Egypt, Ismailia, on leaves of *Mangifera indica* (*Anacardiaceae*), Apr. 2014, *A.M. Ismail* (holotype CBS H-22294, culture ex-type CBS 140162 = CPC 26132, CBS 140163 = CPC 26133; ITS sequence GenBank KP943747, LSU sequences GenBank KT950860, KT950861, *tub2* sequence GenBank KP943746, *tef1* sequence GenBank KP943748, MycoBank MB813837).

Notes — Based on a recent multi-locus phylogenetic study of *Pestalotiopsis,* Maharachchikumbura et al. (2014) divided the complex into three genera: *Pestalotiopsis, Neopestalotiopsis* and *Pseudopestalotiopsis*. Morphologically, *Neopestalotiopsis* can be easily distinguished from *Pseudopestalotiopsis* and *Pestalotiopsis* by its versicolorous median cells. Conidiophores in *Neopestalotiopsis* are indistinct and often reduced to conidiogenous cells. Based on the phylogenetic analysis of the sequence data of (*tub2*, *tef1* and ITS), *N. egyptiaca* is phylogenetically closely related to *N. australis.* However, the conidia of *N. australis* are wider and the median cells are darker than those of *N. egyptiaca*.

Colour illustrations. *Mangifera indica* in Egypt; symptomatic leaf, colony on PDA, conidiophores giving rise to conidia and appendaged conidia. Scale bar = 10 µm.

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Roussoella mexicana

Fungal Planet 373 – 1 December 2015

Roussoella mexicana Crous & Yáñez-Moral., *sp. nov.*

Etymology. Name refers to the country from where this species was collected.

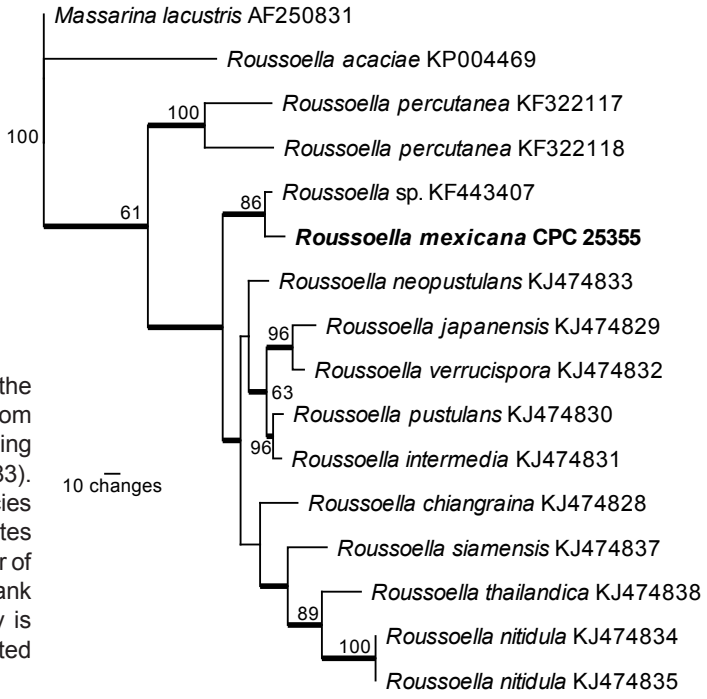
Classification — *Roussoellaceae*, *Pleosporales*, *Dothideomycetes*.

Conidiomata pycnidial, globose, solitary to aggregated, brown, to 150 µm diam, with central ostiole, to 20 µm diam, exuding a brown, globoid conidial mass; wall of 2–3 layers of brown *textura angularis*; forming red crystals intermingled among conidiomata on OA. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* phialidic, lining the inner cavity, subhyaline, smooth, depressed globose to ampulliform, 3–4 × 3–4 µm, with inconspicuous apical locus with minute periclinal thickening. *Conidia* solitary, brown, smooth- and thick-walled, aseptate, granular to minutely guttulate, ellipsoid, apex acutely rounded, base truncate, hilum 0.5 µm diam, (3–)3.5(–4) × 2(–2.5) µm.

Culture characteristics — Colonies reaching up to 60 mm diam after 2 wk at 25 °C, with spreading, flat, folded surface; margins smooth, lobate and moderate aerial mycelium. On MEA surface olivaceous grey, reverse iron-grey. On OA surface olivaceous grey. On PDA surface olivaceous grey, reverse iron-grey.

Typus. Mexico, Pozo del Tigre, Mpio. de Jalpan, Puebla State, on leaf spots of *Coffea arabica* (*Rubiaceae*), Caturra Rojo variety plantations, 23 Oct. 2014, *M. de Jesús Yáñez-Morales* (holotype CBS H-22402, culture ex-type CPC 25355; ITS sequence GenBank KT950848, LSU sequence GenBank KT950862, MycoBank MB814925).

Notes — The LSU sequence confirmed the placement of *R. mexicana* in the *Roussoellaceae*, where it is allied to *R. intermedia*. Unfortunately the latter species is known only from its sexual morph and hence a morphological comparison is not possible (Ju et al. 1996). We isolated only the *Cytoplea* asexual morph, which is also frequently found on woody hosts (Crous et al. 2014) and not restricted to monocotyledons, as previously believed. Based on ITS sequences, *R. mexicana* is also phylogenetically allied to *Roussoella* sp. (GenBank KF443407) with *R. siamensis* (GenBank KJ474837) being the second-closest species.



First of five equally most parsimonious trees obtained from the ITS alignment based on a heuristic analysis with 100 random taxon additions and tree-bisection-reconnection algorithm using PAUP v. 4.0b10 (TL = 481, CI = 0.644, RI = 0.594, RC = 0.383). GenBank accession numbers are indicated behind the species names. Bootstrap support values > 50 % from 1 000 replicates are shown at the node and the scale bar indicates the number of changes. The tree was rooted to *Massarina lacustris* (GenBank AF250831) and the novel species described in this study is indicated in **bold** face. The alignment and tree were deposited in TreeBASE (S18408).

Colour illustrations. *Coffea arabica* in Mexico; colony on PDA, conidioma with central ostiole, conidiogenous cells and conidia. Scale bars: conidioma = 75 µm, all others = 10 µm.

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Phyllosticta carissicola

Fungal Planet 374 – 1 December 2015

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

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

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

Conidiomata (on pine needle agar; PNA) pycnidial, solitary, black, erumpent, globose, exuding a hyaline conidial mass; pycnidia to 250 µm diam; pycnidial wall of several layers of *textura angularis*, 15–30 µm thick; inner layers of hyaline *textura angularis*. *Ostiole* central, to 45 µm diam. *Conidiophores* subcylindrical, reduced to conidiogenous cells, or with one supporting cell, that can be branched at the base, 10–20 × 4–6 µm. *Conidiogenous cells* terminal, subcylindrical, hyaline, smooth, coated in mucoid layer, 7–12 × 3–5 µm; proliferating several times percurrently at apex. *Conidia* (11–)12–14(–15) × (9–)10(–11) µm, solitary, hyaline, aseptate, thin- and smooth-walled, granular, or with a single large, central guttule, ellipsoid, tapering towards a narrow truncate base, 3–4 µm diam, enclosed in a persistent mucoid sheath, 2–3 µm thick, and bearing a hyaline, apical mucoid appendage, (10–)12–17(–25) × 1.5(–2) µm, flexible, unbranched, tapering towards an acutely rounded tip.

Culture characteristics — Colonies reaching up to 15 mm diam after 2 wk at 25 °C, with spreading, flat, folded surface; margins smooth, lobate and sparse aerial mycelium. On MEA surface iron-grey, reverse olivaceous grey. On OA surface olivaceous grey. On PDA surface grey olivaceous, reverse olivaceous grey.

Typus. South Africa, Eastern Cape Province, Haga Haga, on leaves of *Carissa macrocarpa* (*Apocynaceae*), Dec. 2014, *M.J. Wingfield* (holotype CBS H-22399, culture ex-type CPC 25665; ITS sequence GenBank KT950849, LSU sequence GenBank KT950863, *actA* sequence GenBank KT950872, *gapdh* sequence GenBank KT950876, *tef1* sequence GenBank KT950879, MycoBank MB814926).

Notes — *Phyllosticta carissicola* is a novel member of the *Phyllostictaceae*, which contains numerous plant pathogens, several of which are endophytes (Glienke et al. 2011, Wikee et al. 2013). Van der Aa & Vanev (2002) found that the holotype of *Phyllosticta carissae*, which was described from *Carissa arduina* in South Africa, was representative of a species of *Asteromella*, and is therefore not comparable to *P. carissicola*.

The *actA* sequence confirmed that there are no matches on GenBank, closest matches being with *P. podocarpi* (GenBank KF289235), *P. pseudotsugae* (GenBank KF289236) and *P. owaniana* (GenBank FJ538484). The *gapdh* and *tef1* sequences confirmed this association. No *Phyllosticta* species are known on *Carissa* (Crous et al. 2000), and *P. carissicola* also differs morphologically from *P. podocarpi* in that the latter species has somewhat longer and narrower conidia, (10–)14(–17) × (8–)9(–10) µm, and longer appendages, 10–40 µm (Crous et al. 1996).

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

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Ochroconis pandanicola

Fungal Planet 375 – 1 December 2015

Ochroconis pandanicola Crous & M.J. Wingf., *sp. nov.*

Etymology. Name refers to the host genus *Pandanus* from which this species was collected.

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

On synthetic nutrient poor agar (SNA). *Mycelium* consisting of branched, septate, hyaline to pale brown, smooth-walled, 2–3 µm diam hyphae. *Conidiophores* clearly differentiated, erect, arising at right angles from creeping hyphae, branched at lower septum or not, with 1–3 septa, straight to geniculate-sinuous, brown, thick-walled, 7–30 × 2–4 µm. *Conidiogenous cells* 4–10 × 2–3 µm, terminal or lateral, integrated, subcylindrical, brown with one to several apical conidium bearing denticles, subcylindrical, 1–3 × 0.5–1 µm. *Conidia* solitary, subhyaline to hazel brown, finely verruculose, thin-walled, medianly 1-septate, becoming constricted at septum, obovoid to broadly fusiform or ellipsoid, (6–)7–8.5(–10) × 3(–4.5) µm. *Synasexual morph*. *Hyphae* starting to fragment, giving rise to cladophialophora-like synasexual morph. *Ramoconidia* subcylindrical, 0–2-septate, with 1–2 apical denticles, 1–2 µm long, 1–1.5 µm diam, pale brown, smooth, 10–25 × 2–3 µm, giving rise to chains of subcylindrical conidia (–10), smooth, guttulate, pale brown, 0–1-septate, (8–)12–15(–17) × (2.5–)3 µm.

Culture characteristics — Colonies reaching up to 20 mm diam after 2 wk at 25 °C, margins smooth, lobate and sparse aerial mycelium. On MEA surface grey olivaceous, reverse olivaceous grey. On OA surface grey olivaceous with diffuse red pigment at margin. On PDA surface grey olivaceous, reverse olivaceous grey.

Typus. France, La Réunion, S21°21'30.7" E55°44'32.3", Route Forestiere Mare Longue, on leaves of *Pandanus utilis* (*Pandanaceae*), 6 Mar. 2014, *P.W. Crous & M.J. Wingfield* (holotype CBS H-22397, culture ex-type CPC 26317 = CBS 140660; ITS sequence GenBank KT950850, LSU sequence GenBank KT950864, MycoBank MB814927).

Notes — There are no species of *Ochroconis* known from *Pandanus* (Whitton et al. 2012). Based on the LSU sequence, *O. pandanicola* clusters with other species of *Ochroconis*, being most closely related to *O. musae* (= *O. mirabilis*), which differs morphologically in having larger conidia (9–13.5 × 4.8–6.7 µm; Samerpitak et al. 2014).

Colour illustrations. *Pandanus utilis* at the seashore in La Réunion; conidiophores and conidia; cladophialophora-like synasexual morph. Scale bars = 10 µm.

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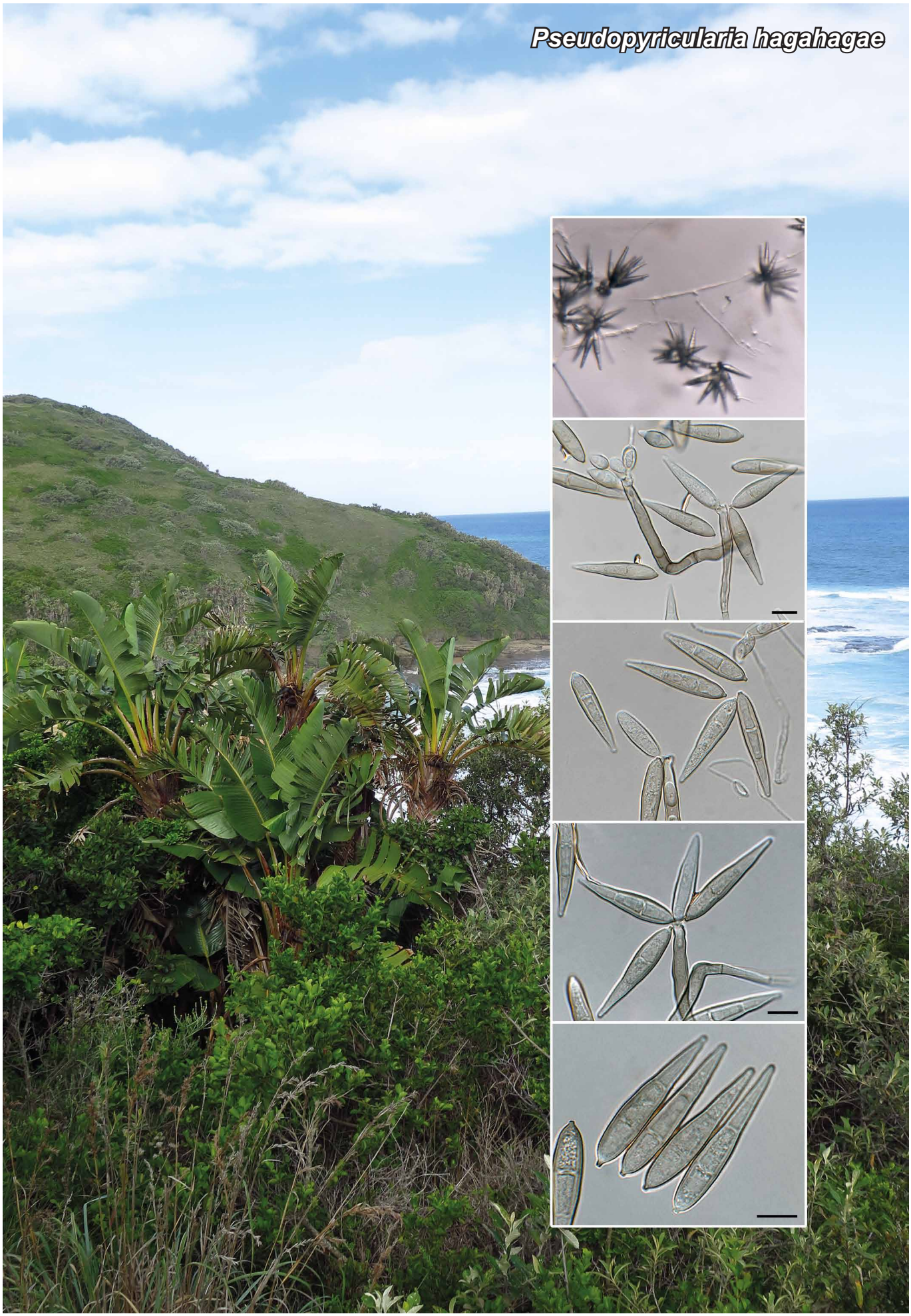
Pseudopyricularia hagahagae

Fungal Planet 376 – 1 December 2015

Pseudopyricularia hagahagae Crous & M.J. Wingf., *sp. nov.*

Etymology. Name refers to the village of Haga Haga in the Eastern Cape Province of South Africa, where this fungus was collected.

Classification — *Pyriculariaceae, Magnaporthales, Sordariomycetes.*

On OA. *Mycelium* consisting of smooth, hyaline, branched, septate, 2.5–3.5 µm diam hyphae. *Conidiophores* solitary, erect, straight or curved, branched above or not, medium brown, smooth, 40–200 × 5–7 µm, 1–10-septate. *Conidiogenous cells* subcylindrical, 30–50 × 5–7 µm, integrated, terminal, rarely intercalary, medium brown, smooth, with 1–7 apical, protruding, flat-tipped denticles, 1–4 µm long, 1–2 µm diam. *Conidia* solitary, obclavate, medium brown, guttulate, 2-septate, (38–)41–45(–49) × (7–)8(–9) µm; apical cell 13–17 µm long, basal cell 10–14 µm long, hilum truncate, slightly protruding, 1.5–2 µm diam, unthickened, not darkened.

Culture characteristics — Colonies reaching up to 25 mm diam on MEA, 40 mm diam on OA after 2 wk at 25 °C, with spreading, flat surface; margins feathery, sparse aerial mycelium. On MEA surface dirty white with patches of greyish sepia, reverse dirty white with patches of mouse grey. On OA surface greyish sepia. On PDA surface and reverse greyish sepia.

Typus. South Africa, Eastern Cape Province, Haga Haga, on leaves of unidentified *Cyperaceae*, Dec. 2014, *M.J. Wingfield* (holotype CBS H-22400, culture ex-type CPC 25635; ITS sequence GenBank KT950851, LSU sequence GenBank KT950865, *actA* sequence GenBank KT950873, *rpb1* sequence GenBank KT950877, *tef1* sequence GenBank KT950880, MycoBank MB814928).

Notes — Based on morphology and DNA-based phylogeny, this species is best accommodated in *Pseudopyricularia* (Klaubauf et al. 2013). In the *rpb1* sequence, the highest level of similarity (92 %; 899/972 nucleotides) was to *Pseudopyricularia higginsii* (GenBank KM485095), although the conidia in the latter species are smaller, 17.5–36.5 × 5.3–6.5 µm (av. 28 × 6 µm), in culture 26.1–28.6 × 6–6.1 µm (av. 26.1 × 6.1 µm) (Luttrell 1954).

Colour illustrations. Coastline at Haga Haga, South Africa; sporulating conidiophores giving rise to 2-septate conidia. Scale bars = 10 µm.

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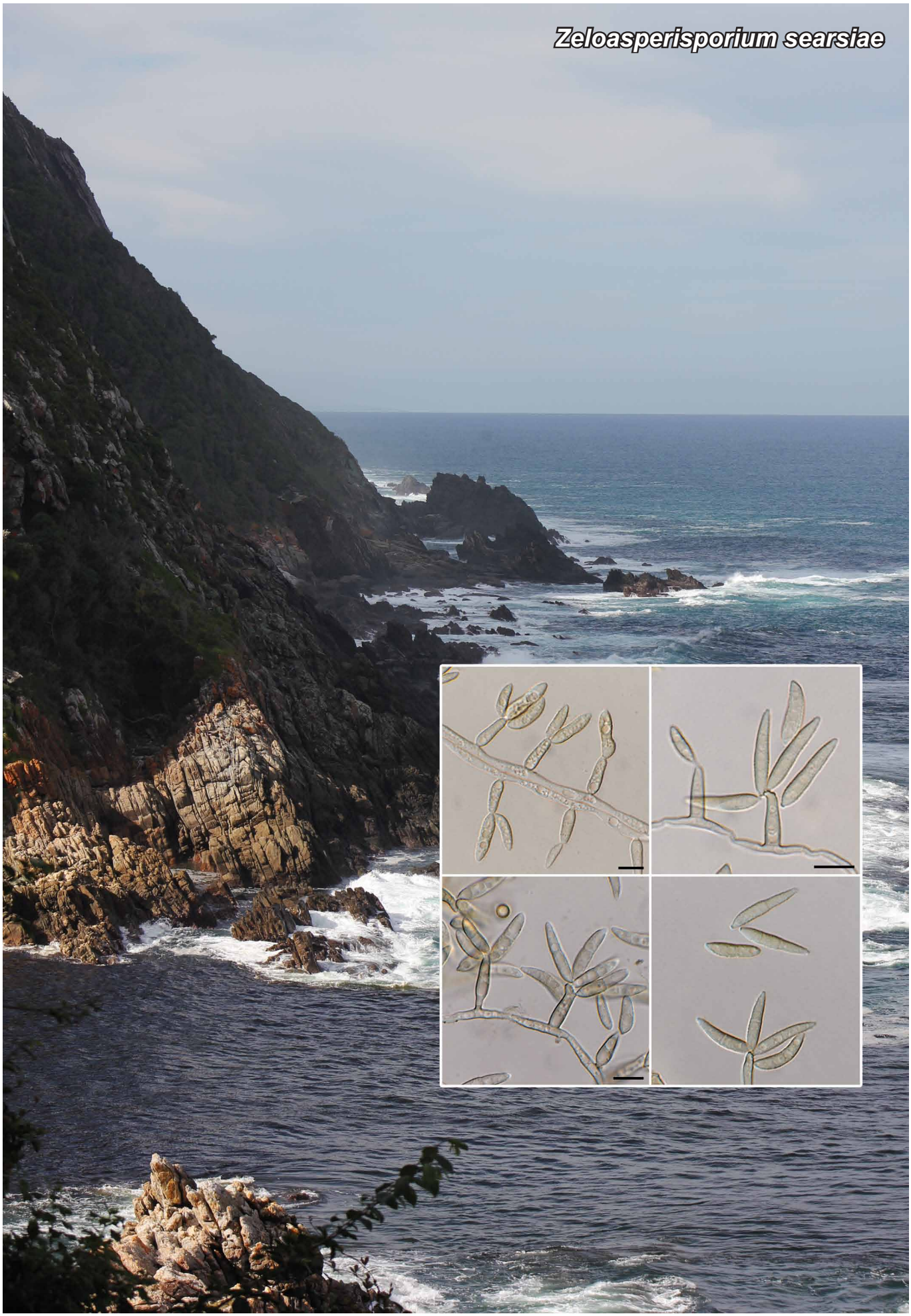
Zeloasperisporium searsiae

Fungal Planet 377 – 1 December 2015

Zeloasperisporium searsiae Crous & A.R. Wood, *sp. nov.*

Etymology. Name refers to the host genus *Searsia* from which this species was collected.

Classification — *Zeloasperisporiaceae, Zeloasperisporiales, Dothideomycetes.*

Mycelium internal to superficial, consisting of sparingly branched, septate, pale brown, finely verruculose, thin-walled, 2–3 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells, arising as lateral hyphal branches, erect, straight, subcylindrical or conical, not geniculate, unbranched, 10–15 × 3.5–5 µm, tapering towards the apex, medium-brown, minutely verruculose, slightly thick-walled, somewhat constricted at the apex below the conidiogenous loci; conidial proliferation sympodial, with one to several subdenticulate to flat conidiogenous loci, mostly crowded at the apex, protuberant; conidial scars thickened-refractive, appearing as thickened circles when viewed from directly above, 1 µm wide. *Conidia* solitary, straight to curved, fusiform, tapered towards the subobtuse apex, 1(–3)-septate, distinctly constricted at the median septum, pale to medium brown, verruculose, somewhat thick-walled, (12–)15–18(–28) × (3–)4–5 µm; hila truncate, 1.5–2 µm diam.

Culture characteristics — Colonies reaching up to 7 mm diam after 2 wk at 25 °C, with spreading, flat, folded surface; margins smooth, lobate and sparse aerial mycelium. On MEA surface isabelline, reverse fuscous black. On OA surface isabelline. On PDA surface isabelline, reverse dark mouse grey.

Typus. South Africa, Western Cape, George, Victoria Bay, on leaf spots of *Searsia chirindensis* (*Anacardiaceae*), 16 July 2014, *A.R. Wood* (holotype CBS H-22403, culture ex-type CPC 25880; ITS sequence GenBank KT950852, LSU sequence GenBank KT950866, MycoBank MB814929).

Notes — *Zeloasperisporium searsiae* is a member of the *Zeloasperisporiaceae* (*Zeloasperisporiales*) (Crous et al. 2015, Hangsanan et al. 2015). It is closely related to *Z. eucalyptorum* and *Z. hyphopodioides*. *Zeloasperisporium searsiae* differs from *Z. eucalyptorum* ((15–)17–22(–25) × 4.5–6(–7) µm; Cheewangkoon et al. 2009), based on its smaller, 1(–3)-septate conidia. It is more difficult to distinguish *Z. searsiae* from *Z. hyphopodioides* (conidia (12–)15–32 × 3.5–5.5 µm, (0–)1–2(–3)-septate; Crous et al. 2007), although the average conidial dimensions tend to be somewhat shorter. Nevertheless, the latter two species are best separated based on their DNA phylogeny. The placement of *Z. searsiae* as sister to *Neomicrothyrium siamense* suggests that *Neomicrothyrium* may be the sexual morph of *Zeloasperisporium*, a hypothesis that has recently been proven by Hangsanan et al. (2015).

Colour illustrations. Rocky coastline along the southern South African coast near Victoria Bay; conidiogenous cells and conidia. Scale bars = 10 µm.

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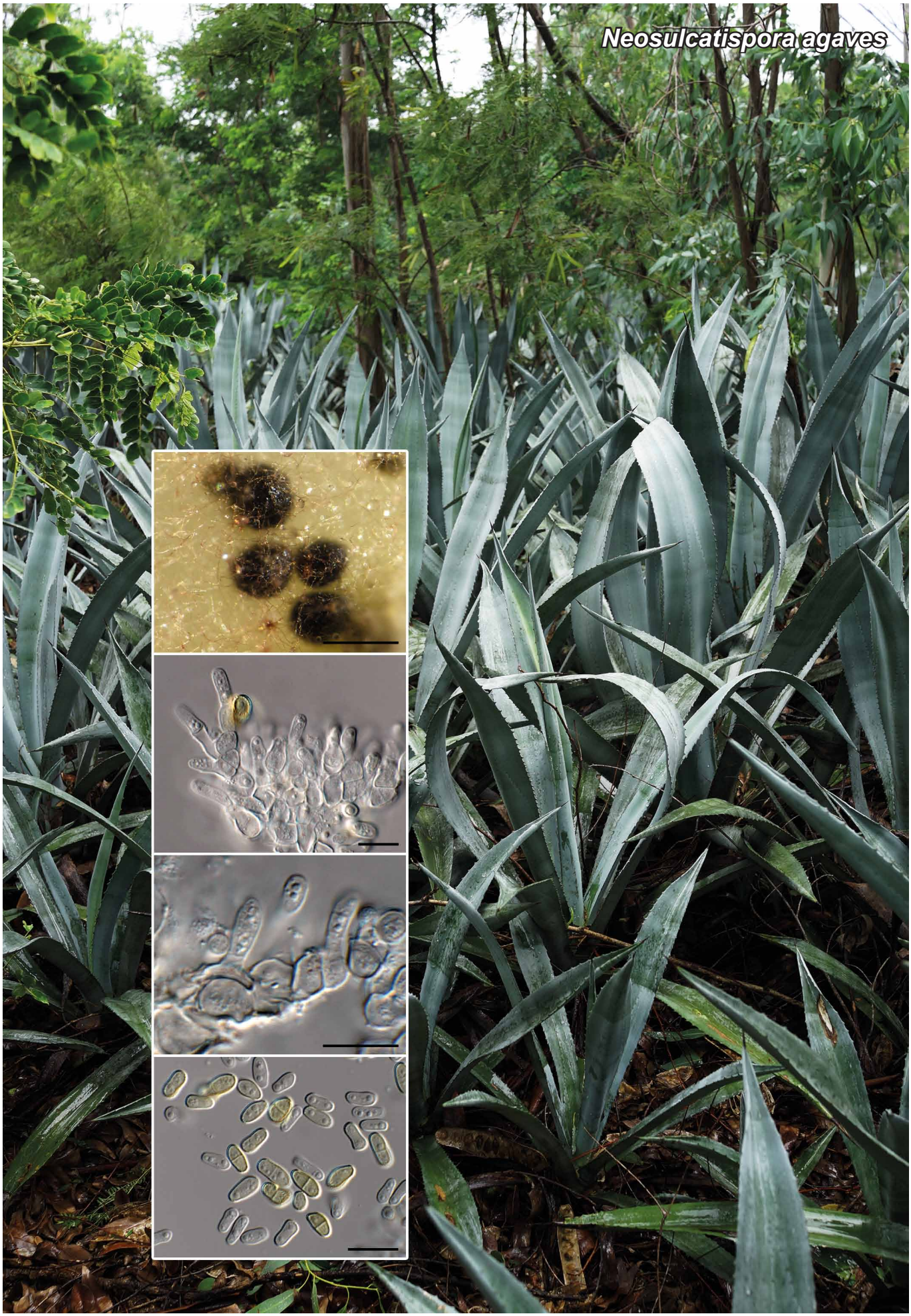
Neosulcatispora agaves

Fungal Planet 378 – 1 December 2015

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

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

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

Conidiomata pycnidial, solitary, becoming aggregated, linked by a stroma, erumpent, globose, dark brown, with central red-brown ostiole; wall of 3–4 layers of brown *textura angularis*; conidiomatal surface covered with red-brown, verruculose hyphae. *Conidiophores* lining the inner cavity, hyaline, smooth, septate, subcylindrical, straight to curved, unbranched or branched below. *Conidiogenous cells* integrated, terminal, subcylindrical, hyaline, smooth, straight to geniculate; proliferating percurrently near apex. *Conidia* solitary, subcylindrical, straight to irregularly curved, apex obtuse, base truncate to bluntly rounded, initially hyaline, with two large polar guttules and various smaller guttules, becoming medianly 1-euseptate, golden-brown, and prominently striate, with striations covering the length of the conidium, becoming dark brown after discharge.

Type species. *Neosulcatispora agaves* Crous & M.J. Wingf. MycoBank MB814930.

Neosulcatispora agaves Crous & M.J. Wingf., *sp. nov.*

Etymology. Name refers to the host genus *Agave* from which this species was collected.

Conidiomata pycnidial, solitary, becoming aggregated, linked by a stroma, erumpent, globose, dark brown, to 300 µm diam, with central red-brown ostiole, 20–40 µm diam; wall of 3–4 layers of brown *textura angularis*; conidiomatal surface covered with red-brown, verruculose, 4–5 µm diam hyphae. *Conidiophores* lining the inner cavity, hyaline, smooth, 0–1-septate, subcylindrical, straight to curved, unbranched or branched below, 5–15 × 3–6 µm. *Conidiogenous cells* integrated, terminal, subcylindrical, hyaline, smooth, straight to geniculate, 5–12 × 3–6 µm; proliferating percurrently near apex. *Conidia* solitary, subcylindrical, straight to irregularly curved, apex obtuse, base truncate to bluntly rounded, initially hyaline, with two large polar guttules and various smaller guttules, becoming medianly 1-euseptate, golden-brown, and prominently striate, with striations covering the length of the conidium, becoming dark brown after discharge, (7–)9–11(–12) × (3.5–)4(–4.5) µm.

Culture characteristics — Colonies reaching 30–40 mm diam after 2 wk at 25 °C, with spreading, flat surface; margins smooth, lobate and sparse aerial mycelium. On MEA surface purple-grey, reverse vinaceous-grey. On OA surface fuscous black to greyish sepia. On PDA surface and reverse greyish sepia.

Typus. France, La Réunion, S21°15'44" E55°20'21.7", Avenue de l'Ocean, on leaves of *Agave vera-cruz* (*Agavaceae*), 10 Mar. 2014, *P.W. Crous & M.J. Wingfield* (holotype CBS H-22404, culture ex-type CPC 26407 = CBS 140661; ITS sequence GenBank KT950853, LSU sequence GenBank KT950867, *tub2* sequence GenBank KT950883, MycoBank MB814931).

Notes — Based on the LSU sequence, *Neosulcatispora* (named after the genus *Sulcatispora*, which clusters in *Sulcatisporaceae*; Tanaka et al. 2015) appears to be a species of *Vrystaatia* (*tub2* sequence is 89 % (261/293 nucleotides) identical to *Vrystaatia aloeicola* (GenBank KF252759). However, *Vrystaatia* is a hyaline septoria-like genus (Quaedvlieg et al. 2013) and thus morphologically quite distinct from *Neosulcatispora.* Similar genera include *Chaetodiplodia, Placodiplodia* and *Pseudodiplodia*, although all three genera have smooth-walled conidia lacking striations (Sutton 1980). The DNA sequences available for some of these species on GenBank suggest that they are not congeneric. A single LSU sequence of '*Chaetodiplodia* sp. CBS 568.88' (GenBank EU754142) is 98 % (841/855 nucleotides, 3 gaps) similar to the LSU sequence of *Neosulcatispora,* and the single LSU sequence of '*Pseudodiplodia* sp. CBS 255.86' (GenBank EU754201) is 99 % (848/853 nucleotides, no gaps) similar to the LSU sequence of *Neosulcatispora*. There are no sequences listed as *Placodiplodia* in the NCBI GenBank nucleotide database and also no cultures listed under this name in the CBS culture collection database.

Colour illustrations. *Agave vera-cruz* growing in La Réunion; conidiomata forming on OA, conidiogenous cells and conidia. Scale bars: conidiomata = 300 µm, all others = 10 µm.

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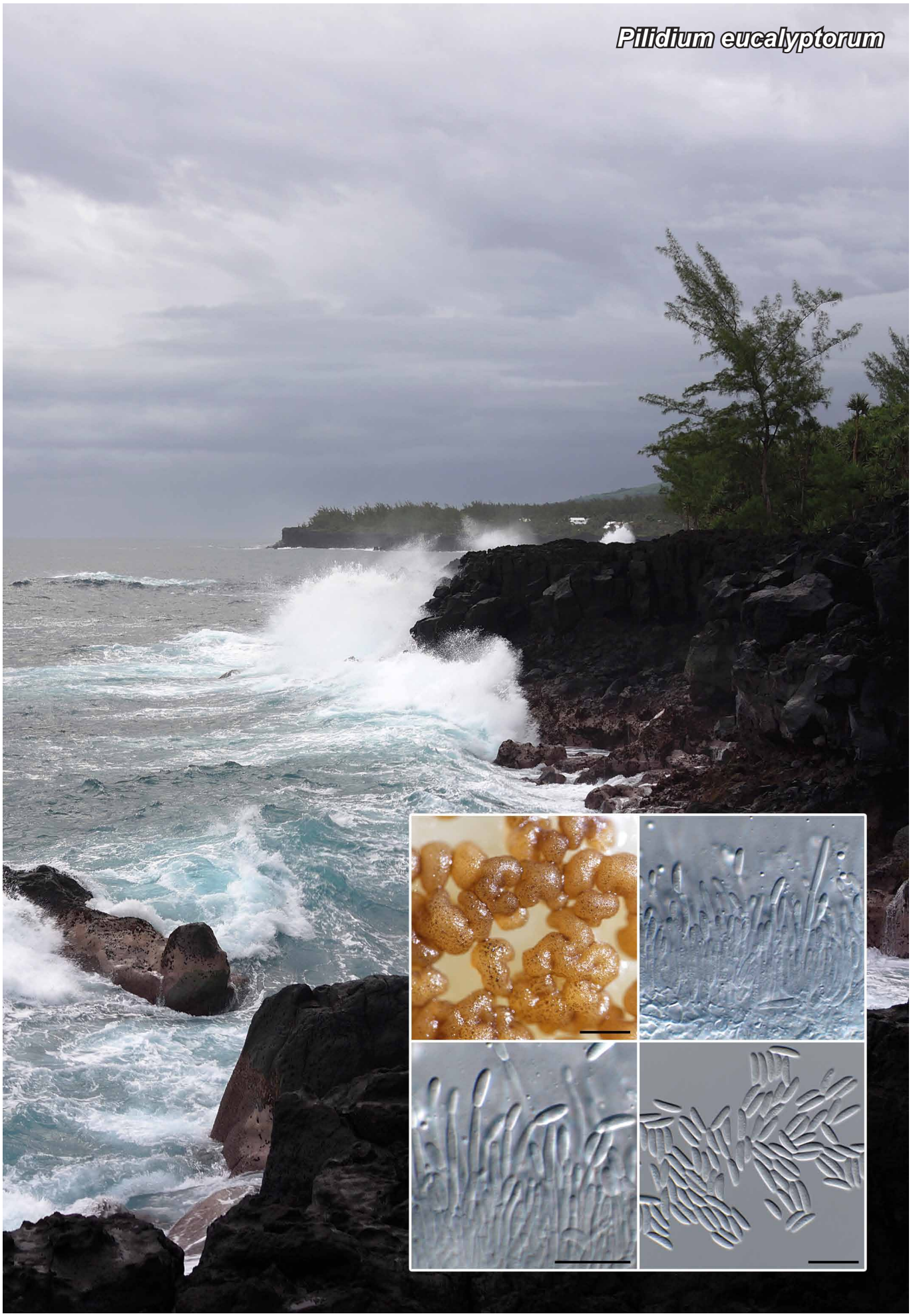
Pilidium eucalyptorum

Fungal Planet 379 – 1 December 2015

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

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

Classification — *Chaetomellaceae*, *Helotiales, Leotiomycetes.*

On SNA. *Conidiomata* pycnidial, globose to oblong, pale brown, smooth, up to 300 µm diam, superficial, aggregated, uniloculate; wall of pale brown *textura angularis*, opening via irregular rupture, exuding a creamy conidial mass. *Conidiophores* hyaline, smooth, branched, septate, filiform, up to 35 µm long, 1.5–2.5 µm diam. *Conidiogenous cells* terminal and lateral, monophialidic, subcylindrical, straight to curved, smooth, hyaline, with minute periclinal thickening and collarette, 5–12 × 1.5–2 µm. *Conidia* hyaline, smooth, aseptate, cymbiform, guttulate, ends acute, (5–)6–7(–8) × (1.5–)2(–2.5) µm.

Culture characteristics — Colonies reaching up to 50 mm diam after 2 wk at 25 °C, with spreading, flat surface; margins smooth, lobate and sparse aerial mycelium. On MEA surface isabelline with patches of smoke grey, reverse isabelline. On OA surface isabelline. On PDA surface dirty white with patches of smokey grey, reverse isabelline.

Typus. France, La Réunion, S21°15'52.4" E55°36'3.3", Cd 36 Nd de la Paix, on leaves of *Eucalyptus robusta* (*Myrtaceae*), 8 Mar. 2014, *P.W. Crous & M.J. Wingfield* (holotype CBS H-22398, culture ex-type CPC 26594 = CBS 140662; ITS sequence GenBank KT950854, LSU sequence GenBank KT950868, MycoBank MB814932).

Notes — The genus *Pilidium* has *Hainesia* synasexual, and *Discohainesia* sexual morphs (Rossman et al. 2004). *Pilidium eucalyptorum* is most similar to *Pilidium acerinum* (GenBank AY487091; identity 449/470 (96 %), gaps 7/470 (1 %) and *Pilidium concavum* (GenBank KF255414; identity 439/466 (94 %), gaps 2/466 (0 %) based on ITS sequence data. The species commonly associated with diseased cutting in *Eucalyptus* nurseries is *Pilidium concavum* (synasexual morph *Hainesia lythri*; Crous et al. 1989).

Colour illustrations. Coastline in La Réunion; conidiomata forming on OA, conidiogenous cells and conidia. Scale bars: conidiomata = 300 µm, all others = 10 µm.

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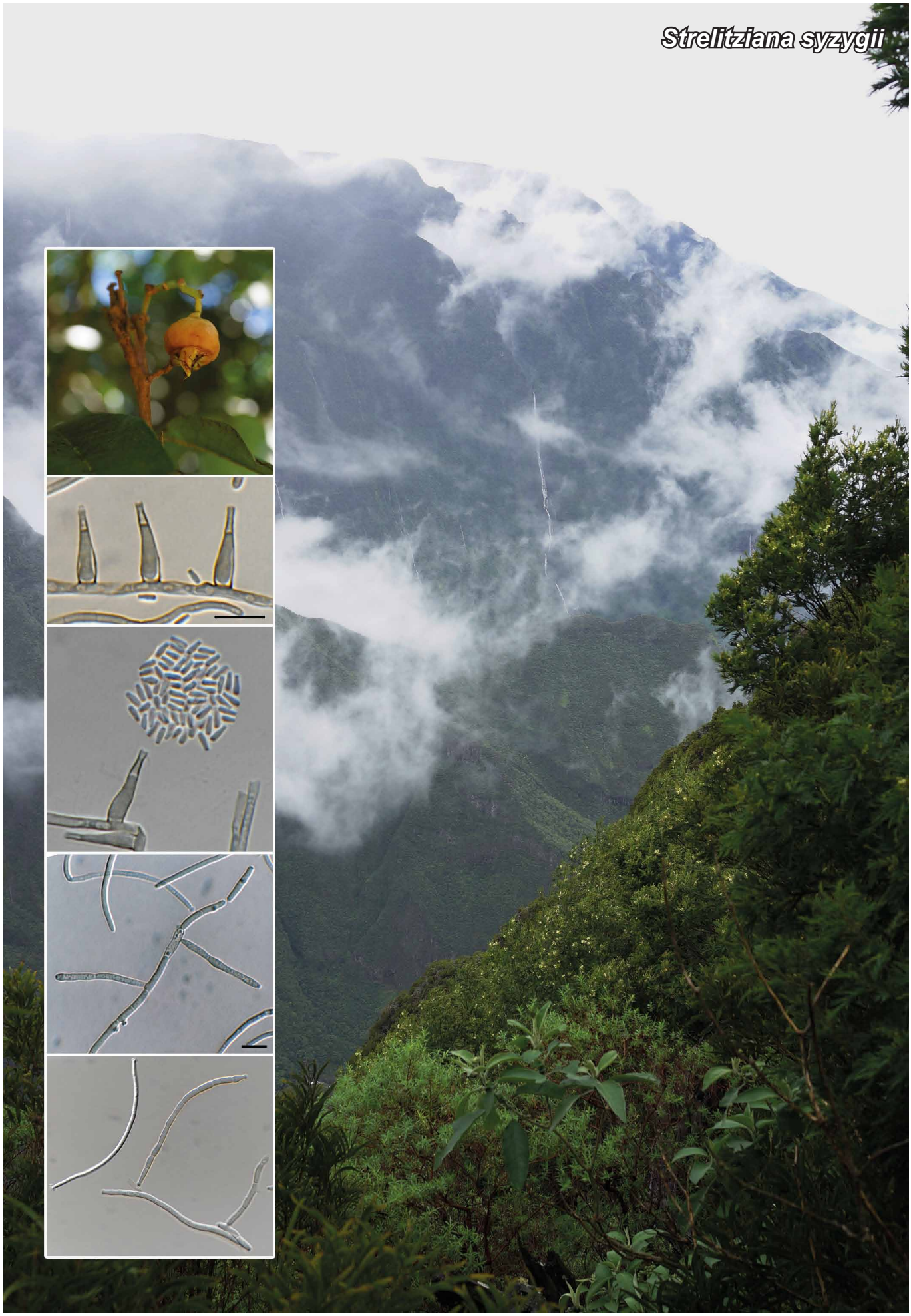
Strelitziana syzygii

Fungal Planet 380 – 1 December 2015

Strelitzianaceae Crous & M.J. Wingf., *fam. nov.*

Classification — *Strelitzianaceae, Chaetothyriales, Eurotiomycetes.*

Colonies lacking mycelium, consisting of a globular mass of chlamydospore-like cells; cells aseptate, brown, covered in mucus, globose, thin-walled, ellipsoid to globose. *Mycelium* when present consisting of pale brown, septate, branched, smooth hyphae, forming sterile, brown, globose, muriformly septate sclerotium-like bodies. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* integrated, lateral or terminal on hyphae, phialidic with small collarette, solitary. *Conidia* pale brown, smooth, subcylindrical with obtuse ends, 5–17-septate, frequently constricted at septa, apex and base with prominent mucoid caps, and conidia undergoing microcyclic conidiation in older cultures. Chalara-like synasexual morph present in some species.

Type genus: *Strelitziana* Arzanlou & Crous.
MycoBank MB814933.

Genera included in family — *Neophaeococcomyces, Strelitziana.*

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

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

On SNA. *Mycelium* consisting of pale brown, septate, branched, smooth, 3–4 µm diam hyphae, frequently constricted at septa, forming sterile, brown, globose, muriformly septate sclerotium-like bodies, 20–40 µm diam. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* integrated, lateral or terminal on hyphae, phialidic with small collarette, solitary, 2–5 µm high, 2–2.5 µm wide. *Conidia* pale brown, smooth, subcylindrical, ends obtuse, 5–17-septate, frequently constricted at septa, (65–)110–130(–150) × (2–)3 µm, apex and base with prominent mucoid caps, and conidia undergoing microcyclic conidiation in older cultures. Chalara-like synasexual morph. *Conidiophores* reduced to conidiogenous cells or with basal supporting cell, erect, ampulliform, unbranched, brown, smooth, 0–1-septate, to 22 µm tall, 3–4 µm wide. *Conidiogenous cells* terminal, long ampulliform, 12–15 × 3–4 µm; collarette 1–2 µm long, apex cylindrical, 1–1.5 µm wide, with visible ring wall building at base of collarette. *Conidia* subcylindrical, apex obtuse, tapering to truncate base, 1 µm diam, 3–4 × 1.5–2 µm, hyaline, smooth, occurring in short chains.

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

Typus. France, La Réunion, S21°5'10.5" E55°41'47.9", Chemin Beaumont, on leaves of *Syzygium jambos* (*Myrtaceae*), 12 Mar. 2014, *P.W. Crous & M.J. Wingfield* (holotype CBS H-22401, culture ex-type CPC 26591 = CBS 140663; ITS sequence GenBank KT950855, LSU sequence GenBank KT950869, *actA* sequence GenBank KT950874, *tef1* sequence GenBank KT950881, *tub2* sequence GenBank KT950884, MycoBank MB814934).

Notes — The genus *Strelitziana* forms part of an undefined clade in the *Chaetothyriales*, for which the family *Strelitzianaceae* is introduced. *Strelitziana syzygii* differs *from S. australiensis* (conidia 4–8-septate, (30–)50–60(–73) × 2.8–3.2 µm; Cheewangkoon et al. 2009) in having longer, pluriseptate conidia.

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

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

Colonies lacking mycelium but consisting of a globular mass of chlamydospore-like cells; cells aseptate, hyaline, becoming brown, covered in mucus, globose, thin-walled, remaining attached to one another through younger end cells at colony margin, which remain attached, detaching only during slide preparation; ellipsoid to globose, hyaline, thin-walled, covered in mucus, smooth.

Type species: *Neophaeococcomyces aloes* (Crous & M.J. Wingf.) Crous & M.J. Wingf.
MycoBank MB814935.

Neophaeococcomyces aloes (Crous & M.J. Wingf.) Crous & M.J. Wingf., *comb. nov.* — MycoBank MB814936

Basionym. *Phaeococcomyces aloes* Crous & M.J. Wingf., Persoonia 31: 237. 2013.

Colour illustrations. Mountain gorge in La Réunion; symptomatic flower of *Syzygium jambos*, chalara-like synasexual morph with small conidia, and hyphae giving rise to long, flexuous conidia of *Strelitziana syzygii*. Scale bars = 10 µm.

Specimen examined. South Africa, Western Cape Province, Clanwilliam, on dark lesions on dead bark of *Aloe dichotoma* (*Xanthorrhoeaceae*), Sept. 2012, *M.J. Wingfield* (holotype CBS H-21441, culture ex-type CPC 21873 = CBS 136431).

Neophaeococcomyces catenatus (de Hoog & Herm.-Nijh.) Crous & M.J. Wingf., *comb. nov.* — MycoBank MB814937

Basionym. *Phaeococcus catenatus* de Hoog & Herm.-Nijh., Stud. Mycol. 15: 126. 1977.
≡ *Phaeococcomyces catenatus* (de Hoog & Herm.-Nijh.) de Hoog, Taxon 28, 4: 348. 1979.

Specimen examined. Switzerland, Lusanne, isolated from air, Dec. 1976, *H. Clémençon* (holotype CBS H-7550, culture ex-type ATCC 42183 = UAMH 4357 = CBS 650.76).

Notes — *Phaeococcomyces* tends to also have some hyphal growth, while in *Neophaeococcomyces* colonies have chains of brown, budding cells that frequently remain attached to one (Moreno-Rico et al. 2014).

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Pseudobeltrania ocoteae

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Beltraniaceae Nann., Repert. mic. uomo: 498. 1934. **emend.**

Classification — *Beltraniaceae, Xylariales, Sordariomycetes*.

Mycelium immersed to superficial, composed of subhyaline to brown, thin-walled hyphae. *Stromata* usually present, parenchymatous to pseudoparenchymatous, hyaline to brown, often confined to epidermal cells. *Setae* present or absent, straight, thick-walled, dark brown, smooth or verrucose, with radially lobed basal cell, tapering to acute apex. *Conidiophores* simple, erect, septate, pale brown, arising from the base of setae or separate. *Conidiogenous cells* pale brown, integrated, denticulate. *Separating cells* present or absent, pale brown, thin-walled, oval to subglobose, with one to several denticles. *Conidia* biconic, lageniform to navicular, subhyaline to red-brown, with transverse band of pale pigment at widest part of the conidium, rounded or 1-denticulate or rostrate at base, apex spicate or apiculate or truncate.

Type genus. *Beltrania* Penz.

Genera included in family — *Beltrania, Beltraniella,* ?*Beltraniomyces, Beltraniopsis, Parapleurotheciopsis,* ?*Porobeltraniella, Pseudobeltrania,* ?*Subramaniomyces*.

Pseudobeltrania ocoteae Crous & M.J. Wingf., *sp. nov.*

Etymology. Name refers to the host genus *Ocotea* on which this fungus was collected.

Mycelium immersed, consisting of hyaline, septate, branched, 1.5–2.5 µm diam hyphae. *Conidiophores* solitary, stipe unbranched, straight to flexuous, (0–)1-septate, 20–50 × 5–8 µm, medium brown, smooth, with radially lobed basal cell, 6–8 µm diam. *Conidiogenous cells* terminal, integrated, 12–40 × 6–8 µm, medium brown, polyblastic, with a whorl of terminal, discrete, cicatrized, cylindrical denticles, 1–3 × 2 µm. *Conidia* solitary, dry, simple, biconic to pyriform, pale olivaceous, smooth, aseptate, with indistinct transverse median hyaline band in vivo (absent when studied in vitro), apex obtuse, tapering from middle to truncate, slightly darkened hilum, 2 µm diam, (21–)23–27(–29) × (9–)10(–11) µm. *Ascomata* pale yellow, solitary to aggregated on OA and PDA, globose to somewhat papillate, with central ostiole, up to 250 µm diam; wall of 3–4 layers of subhyaline *textura angularis* to *intricata*. *Pseudoparaphyses* hyaline, septate, cellular, anastomosing, distributed among asci. *Asci* 8-spored, sessile, unitunicate, hyaline, subcylindrical, 70–90 × 11–16 µm, with obtuse apex that does not stain in Meltzer's reagent. *Ascospores* tri- to multiseriate, obovoid, hyaline, granular, smooth, aseptate with non-persistent mucoid sheath, (19–)20–22(–24) × (5.5–)6–7(–8) µm.

Culture characteristics — Colonies reaching up to 55 mm diam after 2 wk at 25 °C, with spreading, flat surface; margins smooth, lobate and moderate aerial mycelium. On MEA surface dirty white, reverse cream. On OA surface dirty white. On PDA surface and reverse dirty white.

Typus. France, La Réunion, S21°14'34.7" E55°47'55.9", RN2, on leaf spots of *Ocotea obtusata* (*Lauraceae*), 6 Mar. 2014, *P.W. Crous & M.J. Wingfield* (holotype CBS H-22396, culture ex-type CPC 26219 = CBS 140664; ITS sequence GenBank KT950856, LSU sequence GenBank KT950870, MycoBank MB814938).

Colour illustrations. Symptomatic leaves of *Ocotea obtusata* in La Réunion; colony sporulating on OA, conidiophores and conidia, ascomata forming on OA, asci in Meltzer's reagent and in clear lactic acid, ascospores. Scale bars: ascomata = 250 µm, all others = 10 µm.

Notes — *Beltraniaceae* is an old and mostly forgotten family name. Here we provide the first DNA evidence to support the fact that this name can be applied to genera in the *Beltrania*-complex. We also introduce a new species of *Pseudobeltrania*. Important generic characteristics include pigmented conidia with a hyaline transverse band, arising directly from denticulate conidiogenous cells, without an intervening cell, and the absence of setae (Pirozynski 1963). Based on the key to species provided for *Pseudobeltrania* by Heredia et al. (2002), *P. ocoteae* is clearly distinct based on its conidiophore and conidial dimensions. This is also the first time that a sexual morph has been recorded for the genus and for the *Beltraniaceae*.

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Neoseptorioides eucalypti

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Neoseptorioides Crous, J. Edwards & Pascoe, *gen. nov.*

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

Classification — *Saccharataceae*, *Botryosphaeriales*, *Dothideomycetes*.

Conidiomata black, unilocular, globose, flattened, opening by means of irregular rupture; wall consisting of 3–6 layers of pale brown *textura irregularis* to *angularis*, exuding a crystal conidial mass. *Paraphyses* intermingled among conidiophores, hyaline, cylindrical, septate with obtuse ends. *Microconidiophores* hyaline, smooth, subcylindrical, septate, straight to flexuous, with conidiogenous cells terminal and lateral; proliferating percurrently or with periclinal thickening. *Microconidia* hyaline, smooth, subcylindrical, straight or curved, apex obtuse, base truncate, frequently swollen. *Macroconidiophores* reduced to conidiogenous cells or with a supporting cell. *Macroconidiogenous cells* lining the inner cavity in basal layer, hyaline, smooth, subcylindrical to ampulliform. *Macroconidia* hyaline, smooth, guttulate, subcylindrical, straight to irregularly curved, tapering in apical cell to subobtuse apex, base truncate, transversely euseptate.

Type species. *Neoseptorioides eucalypti*.
MycoBank MB814939.

Neoseptorioides eucalypti Crous, J. Edwards & Pascoe, *sp. nov.*

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

Conidiomata black, unilocular, globose, flattened, up to 300 µm diam, opening by means of irregular rupture; wall consisting of 3–6 layers of pale brown *textura irregularis* to *angularis*, exuding a crystal conidial mass. *Paraphyses* intermingled among conidiophores, hyaline, cylindrical, 1–3-septate with obtuse ends, up to 40 µm tall, 3–4 µm wide. *Macroconidiophores* reduced to conidiogenous cells or with a supporting cell. *Macroconidiogenous cells* lining the inner cavity in basal layer, hyaline, smooth, subcylindrical to ampulliform, 8–15 × 3–6 µm, proliferating several times percurrently at the apex. *Macroconidia* hyaline, smooth, guttulate, subcylindrical, straight to irregularly curved, apical cell obtuse, base truncate, 0(–3)-euseptate, (18–)35–42(–50) × (3.5–)4(–4.5) µm. *Microconidiophores* hyaline, smooth, subcylindrical, 1–3-septate, straight to flexuous, with conidiogenous cells terminal and lateral, up to 50 µm tall, 3–5 µm wide; proliferating percurrently or with periclinal thickening. *Microconidia* hyaline, smooth, guttulate, subcylindrical, straight or curved, apex obtuse, base truncate, frequently swollen, (5–)11–18(–25) × (2–)2.5(–3) µm.

Culture characteristics — Colonies reaching up to 15 mm diam after 2 wk at 25 °C, with spreading, flat, folded surface; margins smooth, lobate, and sparse aerial mycelium. On MEA surface iron-grey, reverse olivaceous grey. On OA surface olivaceous grey. On PDA surface grey olivaceous, reverse olivaceous grey.

Typus. Australia, Victoria, S38°22'49" E145°34'14", The Gurdies, Gurdies-St. Heliers Rd, on leaf litter of *Eucalyptus radiata* (*Myrtaceae*), 7 Nov. 2014, *P.W. Crous, J. Edwards & I.G. Pascoe* (holotype CBS H-22395, culture ex-type CPC 25529 = CBS 140665; ITS sequence GenBank KT950857, LSU sequence GenBank KT950871, *tef1* sequence GenBank KT950882, MycoBank MB814940).

Notes — It is not possible to distinguish *Neoseptorioides* from *Septorioides* based on morphology (Quaedvlieg et al. 2013) because both genera have similar conidiomatal anatomy (opening via irregular rupture), the presence of paraphyses, and they have cylindrical macro- and microconidia. The LSU sequence is 97 % (786/814 nucleotides, 2 gaps) similar to *Septorioides pini-thunbergii* strain CBS 473.91 (GenBank KF251746), the ITS sequence only has a partial match of 94 % (223/236 nucleotides, 3 gaps) to the ITS sequence of the same strain (GenBank DQ019397). There are no *tef1* sequences available for this species / strain for comparison; the *tef1* sequence is 87 % (332/383 nucleotides, 17 gaps) similar to *Saccharata capensis* (GenBank EU552094), the ITS sequence 90 % (321/357 nucleotides, 13 gaps) to GenBank KF766224 and the LSU 98 % (811/831 nucleotides, no gaps) to GenBank KF766390. Based on an inspection of LSU phylogeny, the novel genus described here is more closely related to *Saccharata* (*Saccharataceae, Botryosphaeriales*, Slippers et al. 2013, Phillips et al. 2013) than to *Septorioides*.

Colour illustrations. *Eucalyptus* trees growing in The Gurdies, Victoria; acervuli forming on OA, conidiophores, macro- and microconidia. Scale bars: conidiomata = 300 µm, all others = 10 µm.

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Calonectria monticola

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Calonectria monticola L. Lombard & Crous, *sp. nov.*

Etymology. Name reflects the environment, a mountain, from which this fungus was collected.

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

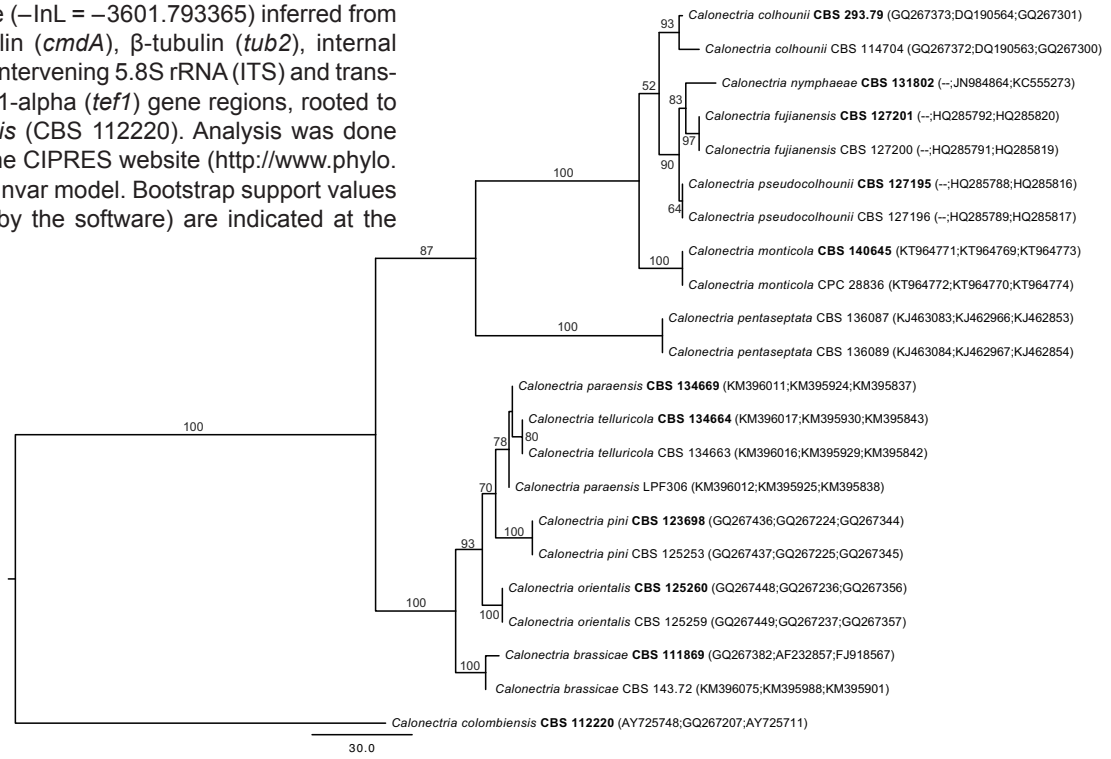
Ascomata not observed. *Macroconidiophores* consist of a stipe bearing a penicillate arrangement of fertile branches, and a stipe extension terminating in a vesicle; stipe septate, hyaline, smooth, 35–100 × 5–10 µm; stipe extension septate, straight to flexuous, 160–220 µm long, 4–8 µm wide at the apical septum, terminating in a broadly clavate vesicle, 4–6 µm diam. *Conidiogenous apparatus* 40–70 µm long and 55–90 µm wide; primary branches aseptate, 16–25 × 4–6 µm; secondary branches aseptate, 10–20 × 3–7 µm; tertiary branches aseptate, 9–15 × 3–5 µm; quaternary and additional branches (–6) aseptate, 7–14 × 2–5 µm, each terminal branch producing 2–6 phialides; phialides doliiform to reniform, hyaline, aseptate, 7–11 × 2–5 µm, apex with minute periclinal thickening and inconspicuous collarette. *Macroconidia* cylindrical, rounded at both ends, straight, 46–51(–56) × 4–6(–7) µm (av. 49 × 5 µm), 3-septate, lacking a visible abscission scar, held in parallel cylindrical clusters by colourless slime. *Mega-* and *microconidia* not observed.

Culture characteristics — Colonies fast growing at 24 °C on MEA, producing abundant white to buff aerial mycelium and sporulating profusely on the medium surface; reverse sienna to umber after 7 d; chlamydospores formed abundantly throughout the medium, forming microsclerotia.

Typus. Thailand, Chaing Mai, from soil collected on Doi Suthep mountain, Nov. 2012, *P.W. Crous* (holotype CBS H-22376, culture ex-type CBS 140645 = CPC 28835; ITS sequence GenBank KT964775, LSU sequence GenBank KT983443, *tub2* sequence GenBank KT964769, *tef1* sequence GenBank KT964773, *cmdA* sequence GenBank KT964771, MycoBank MB814941), CPC 28836 (ITS sequence GenBank KT964776, LSU sequence GenBank KT983444, *tub2* sequence GenBank KT964770, *tef1* sequence GenBank KT964774, *cmdA* sequence GenBank KT964772).

Notes — *Calonectria monticola* is a new member of the *C. colhounii* species complex (Chen et al. 2011, Xu et al. 2012, Alfenas et al. 2015, Lombard et al. 2015a). Macroconidia of *C. monticola* (av. 49 × 5 µm) are smaller than those of *C. colhounii* (av. 55 × 5 µm), *C. eucalypti* (av. 72 × 6 µm), *C. fujianensis* (av. 52.5 × 4 µm), *C. nymphaeae* (61 × 6 µm) and *C. pseudocolhounii* (av. 60 × 4.5 µm). All members of the *C. colhounii* complex are considered homothallic as they readily produce yellow to orange perithecia in axenic cultures, which was not observed for *C. monticola*, even after 6 wk incubation.

Maximum likelihood tree (–lnL = –3601.793365) inferred from the combined calmodulin (*cmdA*), β-tubulin (*tub2*), internal transcribed spacer and intervening 5.8S rRNA (ITS) and translation elongation factor 1-alpha (*tef1*) gene regions, rooted to *Calonectria colombiensis* (CBS 112220). Analysis was done using RAxML through the CIPRES website (http://www.phylo.org) using the GTR+P–Invar model. Bootstrap support values (replicates determined by the software) are indicated at the nodes.



Colour illustrations. River on Doi Suthep mountain in Chiang Mai; conidiophores, vesicles, conidiogenous apparatus and conidia. Scale bars = 10 µm.

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Psathyrella complutensis
1 cm

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Psathyrella complutensis Heykoop & G. Moreno, *sp. nov.*

Etymology. Derived from *Complutum*, Roman name for Alcalá de Henares, the locality where this species was found for the first time.

Classification — *Psathyrellaceae, Agaricales, Agaricomycetes*.

Cap 3–12 mm broad and 2–4 mm high, primordium globose, ellipsoid, then semiglobose, convex, somewhat flattened, with umbo or not, finally totally flat, dark reddish brown when young (Munsell 2.5YR 3/4), sometimes dusky red to dark red (Mu. 10R 3/4, 3/6), in some specimens even darker (Mu. 10R 2.5/2) at centre, elsewhere dark brown (Mu. 7.5 YR 3/4), becoming reddish brown (Mu. 2.5/YR 4/4) or reddish yellow (Mu. 7.5 YR 6/6). Margin paler, hygrophanous, faintly striate, after drying it becomes first strongly ochraceous then cream; in primordium stage entirely covered by a fibrillose white veil, appearing later as dispersed fibrils half-way to centre, evanescent. *Gills* distant, L = 11–17, broadly adnate, ventricose, very pale brown when young (Mu. 10YR 8/4), reddish grey (Mu. 5YR 5/2) to dark reddish brown (Mu. 5YR 3/2) at maturity, with white fimbriate edge; lamellulae present. *Stem* 10–30 × 0.5–1 mm, cylindrical, sometimes curved and slightly widened at base, sometimes united with other stipes forming small bundles, fragile, whitish to pale brown (Mu. 10YR 6/3), top 1/4 part very pruinose, below fibrillose because of veil remnants, and white tomentose at the base. Taste mild, smell none. *Spore-print*: reddish black (Mu. 10R 2.5/1). *Spores* 9–12.5(–14.5) × 5–6.5(–8) µm, av. 10.3–11.3 × 5.4–6 µm (7 collections), Q_{av} = 1.82–1.97, oblong, ellipsoid, smooth, with a well-defined germ pore (up to 2 µm), in NH_4OH 10 % reddish brown. *Basidia* 4-spored, 17–25 × 9.5–12 µm, sterigmata up to 5 µm in height, clavate, hyaline, but sometimes with brownish intracellular pigment. *Cheilocystidia* numerous, very variable, utriform (some subcapitate) to fusiform or lageniform, 25–35 × 7–15 µm, hyaline, intermixed with more or less abundant clavate cells, 15–22 × 10–16 µm, hyaline. *Pleurocystidia* absent. *Caulocystidia* present in the upper part of the stem, similar to cheilocystidia. *Hymenophoral trama* in NH_4OH 10 % sub micr. distinctly yellowish brown from membranal pigment, with yellowish hyphal septa and some encrustations. *Clamp-connections* not seen.

Habitat & Distribution — Growing solitary, gregarious or even fasciculate (small groups consisting of 2–5 united basidiomata) on calcareous loamy soil under *Kochia prostrata*, with *Urtica*, among mosses and *Nostoc*. So far known from Spain and Sweden, but probably often mistaken for *P. effibulata*.

Typus. Spain, Alcalá de Henares, Parque de los Cerros, on slopes with *Kochia prostrata* on loamy soil among mosses, 4 Dec. 2014, *M. Heykoop, G. Moreno & M. Lizárraga* (holotype AH 33713, ITS sequence GenBank KR261441, LSU sequence GenBank KR233834, MycoBank MB812345).

Additional specimens examined. ***Psathyrella complutensis***: Spain, Alcalá de Henares, Parque de los Cerros, under *Kochia prostrata* on slopes on loamy soil among mosses, 4 Dec. 2014, *M. Heykoop, G. Moreno & M. Lizárraga*, paratype AH 45541; ibid., paratype AH 45542 (ITS, LSU sequences GenBank KR261442, KR233835); ibid., paratype AH 45543; Alcalá de Henares, El Gurugú, in open areas under *Kochia prostrata*, on loamy soil among *Nostoc* and mosses, *M. Heykoop & J. Álvarez*, 8 Nov. 1997, paratype AH 23895 (ITS sequence GenBank KR261444); ibid., AH 23896 (ITS sequence GenBank KR261443). – Sweden, Skåne, Kristianstad, Näsby fält, on loamy soil, 19 Aug. 2004, *L. Örstadius*, Herb. Örstadius 92-04 (ITS, LSU sequences GenBank KR261440, KR233833). ***Psathyrella effibulata***: Sweden, Skåne. Ö. Sönnarslöv, Kristinelund, in a nitrophilous pasture 27 Aug. 2008, *L. Örstadius*, Herb. Örstadius 103-08 (ITS, LSU sequences GenBank KR261439, KR233832); Skåne, Trolle-Ljungby. Tosteberga, in a pasture on sandy calcareous soil, in a thicket of *Crataegus* and *Corylus,* 2 Aug. 2011, *L. Örstadius*, Herb. Örstadius 99-11 (ITS, LSU sequences GenBank KR261438, KR233831); Skåne, Ravlunda, Klammersbäck, in a pasture with *Crataegus,* 5 Oct. 2012, *L. Örstadius*, Herb. Örstadius 149-12 (ITS, LSU sequences GenBank KR261437, KR233830). ***Psathyrella purpureobadia***: Spain, Alcalá de Henares, in calcareous pasture under *Kochia prostrata*, 12 Dec. 1991, *A. Altés & G. Moreno,* AH 23690 (ITS sequence GenBank KR261436).

Colour illustrations. Spain, Madrid, Alcalá de Henares, Parque de los Cerros, slope on loamy soil with *Kochia prostrata* and mosses where the holotype was collected; basidiomata, cheilocystidia, basidioles and cells of the subhymenium lacking clamp-connections, spores (all from the holotype). Scale bars = 1 cm (basidiomata), 10 µm (microscopic elements), 2 µm (spores under SEM).

Notes — *Psathyrella complutensis* is characterised by its small size, the reddish brown colour of its caps, the absence of pleurocystidia and by growing with gregarious to subcaespitose habit on loamy calcareous soils.

In our phylogeny *P. complutensis* is included in a clade together with *P. purpureobadia* and *P. effibulata*, all of which lack clamp-connections. *Psathyrella complutensis* keys out in sect. *Spintrigerae* (Kits van Waveren 1985), because of the lack of pleurocystidia, though its average spore length is longer than 10 µm. According to this feature and the small size of its basidiomata it could also be placed within sect. *Atomatae*. However, Kits van Waveren (1985) stated that carpophores in this section are never caespitose or subcaespitose. In the phylogeny of Larsson & Örstadius (2008), *P. effibulata* and *P. purpureobadia* are sometimes included together in a clade sister to the calcarea clade (≈ sect. *Atomatae*) defined by Nagy et al. (2013). In our phylogeny, however, this relationship could not be supported.

Psathyrella purpureobadia differs from *P. complutensis* because of its larger size, vinaceous brownish colours of the caps (similar to those observed in *P. bipellis*), numerous pleurocystidia, differently shaped and much longer cheilocystidia (up to 58 µm in length), and much darker and slightly longer spores. Arnolds (2003) stated spores of *P. purpureobadia* measure on average 10.4–10.8 × 5.4–5.6 µm; however, our material (AH 23690) has longer spores measuring 11.9 × 6.8 µm on average. *Psathyrella effibulata* differs from *P. complutensis* because of the presence of pleurocystidia, different colours of the cap, slightly larger basidiomata which are not fasciculate and smaller spores, measuring on average 8.5–9.9 × 4.3–5 µm vs 10.3–11.3 µm × 5.4–6 µm in *P. complutensis*.

The ITS phylogenetic tree of *Psathyrellaceae* was constructed in MrBayes, and both Bayesian posterior probability and maximum likelihood bootstrap support are annotated. In the resulting tree, most infrageneric nodes were not resolved, providing little information about the phylogenetic affiliation of the new species. *Psathyrella complutensis* is closely related to *P. effibulata* and *P. purpureobadia*. All three species display some degree of intraspecific variability (only 1/567 bp in *P. complutensis*). The low interspecific variability of the ITS region between these taxa could be causing the relatively low Bayesian support for *P. complutensis* (0.77), although this could probably be improved by sequencing additional markers (for phylogenetic tree, see MycoBank).

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Chlorophyllum lusitanicum

Fungal Planet 385 – 1 December 2015

Chlorophyllum lusitanicum G. Moreno, Mohedano, Manjón, Carlavilla & Altés, *sp. nov.*

Etymology. From Lusitania (ancient Iberian Roman province including the southern part of Portugal and mainly the autonomous community of Extremadura in the west of Spain), the geographic area where this species has been collected.

Classification — *Agaricaceae, Agaricales, Agaricomycetes*.

Epigeous basidiomata 1.5–3.5 × 1.2–3.4 cm (measurements taken from herbarium material), irregularly globose or subglobose, rarely obpyriform, not lobed, white with light pink tones when young and after friction, but dark brown at maturity. *Peridium* smooth, breaking into polygonal patches at maturity (similar to *Lycoperdon utriforme*), c. 0.2–0.5 mm thick, formed by cylindrical, septate, thin-walled, smooth hyphae lacking incrustations, 4–8 µm diam, clamp connections not seen. *Stipe* absent or rudimentary with a thick whitish mycelial cord. *Columella* well-developed, reaching half to the fruiting body, up to 1 cm wide, and whitish in colour. *Gleba* whitish to pale yellowish, frequently presenting small cavities and with a scaly appearance in herbarium material, breaking easily. *Basidia* 35–43 × 15–18 µm, clavate to broadly ellipsoid, with 1–4 sterigmata, variable in length, c. 8–16 × 1.4–2 µm, forming a true hyaline hymenium. *Clamp connections* rarely observed at the base of the basidia and basidioles. *Basidiospores* globose to subglobose, more rarely ovoid to ellipsoid (abnormal spores frequently illustrated in gastroid fungi also seen), 10–14(–15) × 10–13(–14) µm, (L/W = 1.0–1.08), germ pore absent, hyaline, smooth, dextrinoid, with a large lipid droplet and hilar appendix, 2–3(–5) × 1.5–2 µm. Smell and taste not recorded.

Habitat & Distribution — Grassland areas used for cattle grazing (dehesa or montado anthropogenic agro-sylvo-pastoral system), where oaks as holm (*Quercus ilex* subsp. *ballota*) and cork oak (*Q. suber*) are the dominant trees. Currently known only from Cáceres, Spain.

Typus. Spain, Extremadura, Cáceres, Navalmoral de la Mata, Jaral del Romeral, beside the reservoir Arroyo de Barrancas Altas, 280 m asl, nitrified grasslands with cow manure, 16 Nov. 2011, *J.M. Mohedano & J.A. Suárez* (holotype AH 45540, ITS sequence GenBank KR233482, LSU sequence GenBank KR233491, MycoBank MB 812380).

Additional specimens examined. ***Chlorophyllum lusitanicum***: Spain, beside the reservoir Arroyo de Barrancas Altas, Jara del Romeral, Navalmoral de la Mata, Cáceres, grassland of *Quercus suber,* 23 Nov. 2011, *J.M. Mohedano, C. Gelpi, J.A. Suárez & G. Moreno*, AH 43927 (ITS, LSU sequences GenBank KR233483, KR233492); Turuñuelo farm, Navalmoral de la Mata, Cáceres, dehesa grassland, Nov. 2011, *J.A. Suárez,* AH 45643; Navalmoral de la Mata, Cáceres, dehesa grassland, 12 Nov. 2012, *J.M. Mohedano*, AH 45539 (ITS, LSU sequences GenBank KR233484, KR233493); dehesa grassland, beside the reservoir Arroyo de Barrancas Altas, Jara del Romeral, Cáceres, 5 Apr. 2012, *J.M. Mohedano & A. Rodríguez*, AH 45644. ***Chlorophyllum agaricoides***: Spain, Toros de Guisando, beside the Cañada Real, El Tiemblo, Ávila, prairie, 1 June 2008, *R. González*, AH 42972 (ITS, LSU sequences GenBank KR233485, KR233494); Añe, Segovia, prairie, 31 Oct. 2008, *F. Gracia*, AH 45645; Valdecañas de Tajo, Cáceres, prairie frequented by sheep, 10 Nov. 2011, *J.M. Mohedano*, AH 43926 (ITS, LSU sequences GenBank KR233486, KR233495); ibid., AH 43924 (ITS, LSU sequences GenBank KR233487, KR233496) and AH 43925 (ITS, LSU sequences GenBank KR233488, KR233497); Millanes de la Mata, Cáceres, prairie, 8 Nov. 2011, *J.A. Suárez*, AH 43928 (ITS, LSU sequences GenBank KR233489, KR233498); Navalmoral de la Mata, Cáceres, prairie of holm oak, 10 Nov. 2011, *Soc. Micol. Extremadura*, AH 45646; Moncalvillo dehesa, San Agustín de Guadalix, Madrid, prairie of holm oak, 9 Nov. 2013, *F. Melgar*, AH 44060; Madrid, prairie of holm oak, 15 Nov. 2013, *Soc. Micol. Madrid*, AH 44064. ***Chlorophyllum arizonicum***: Mexico, km 31 Hermosillo-Yécora, La Colorada, Sonora, thorny bushes, 11 Nov. 1996, *M. Esqueda, A. Armenta, A. Núñez, R. Rodríguez & R. Santos*, AH 31724 (ITS, LSU sequences GenBank KR233490, KR233499).

Colour illustrations. Spain, Navalmoral de la Mata, nitrified grasslands with cow manure where the holotype was collected; basidiomata; fruit body section and gleba detail and columella; tetrasporic, bisporic and monosporic basidia, basidiospores in water, ammoniacal congo red and Melzer reactive (holotype AH 45540). Scale bars = 1 cm (basidiomata), 10 µm (basidia, spores, basidiole by LM), 2 µm (spores by SEM).

Notes — *Chlorophyllum lusitanicum* is characterised by the globose to subglobose basidiomata, whitish to pink hues when young, whitish short columella, reaching a maximum of half of the fruiting body, gleba white to yellowish white at maturity, globose to subglobose spores, 10–14(–15) × 10–13(–14) µm, hyaline, smooth and dextrinoid, with few clamps at the base of the basidia and basidioles.

The position and composition of *Macrolepiota* within the *Agaricaceae* and its phylogenetic relationships with other members of the family were investigated, using both molecular (ITS and LSU rDNA sequences) and morphological characters. The molecular data separate the genus into two clades *Macrolepiota* and *Chlorophyllum* (Vellinga et al. 2003). The secotioid genus *Endoptychum* typified by *E. agaricoides*, must belong to *Chlorophyllum* as *C. agaricoides* (Vellinga 2002, 2003). However, the phylogenetic position of *Endoptychum arizonicum* is unresolved, being sister to *Agaricus* and *Chlorophyllum* (Vellinga 2002, Lebel & Syme 2012).

Chlorophyllum agaricoides is a species close to *C. lusitanicum,* but differs by its stipitate to percurrent basidiomata, well-developed columella, dark brown gleba at maturity, and greenish to yellowish brown, ellipsoid spores, not larger than 10 µm long (Moreno et al. 2007).

Chlorophyllum arizonicum (Shear & Griffiths) G. Moreno & Altés, *comb. nov*. — MB814884

Basionym. Secotium arizonicum Shear & Griffiths, Bull. Torrey Bot. Club 29: 450. 1902.

Notes — *Chlorophyllum arizonicum* is a similar species, differing by its smaller basidiomata, 1–1.3 cm diam in our collections, 2–4 × 1.5–3 cm diam in the original description (Shear 1902), with not fully developed columella, smaller spores, 7–12 µm diam and growing in xerophilous areas. A morphological study of the Arizona type material and other collections of desert areas from USA and Mexico (Hermosillo, San Luis Potosi, Sonora) was conducted by Moreno et al. (2007).

Other species described as *Endoptychum* have affinities with *Agaricus* and they have been transferred to that genus, for example, *Endoptychum depressum* (≡ *Agaricus inapertus*; Vellinga et al. 2003). Similarly, the Australian species as *Endoptychum melanosporum*, *E. moongum* and *E. wariatodes* are also morphologically related to *Agaricus* (Lebel & Syme 2012).

The phylogenetic tree was based on a maximum likelihood (ML) analysis of ITS and LSU sequences with the program MEGA v. 6.05. *Lepiota cristata* was used as outgroup. Bootstrap support values ≥ 75 % are given above the branches (for phylogenetic tree, see MycoBank).

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Phytophthora gondwanensis

Fungal Planet 386 – 1 December 2015

Phytophthora gondwanensis L.A. Shuttlew., K. Scarlett, R. Daniel & D.I. Guest, *sp. nov.*

Etymology. Name refers to Gondwana Rainforests of Australia World Heritage Area where this species was collected.

Classification — *Peronosporaceae, Peronosporidae, Oomycota.*

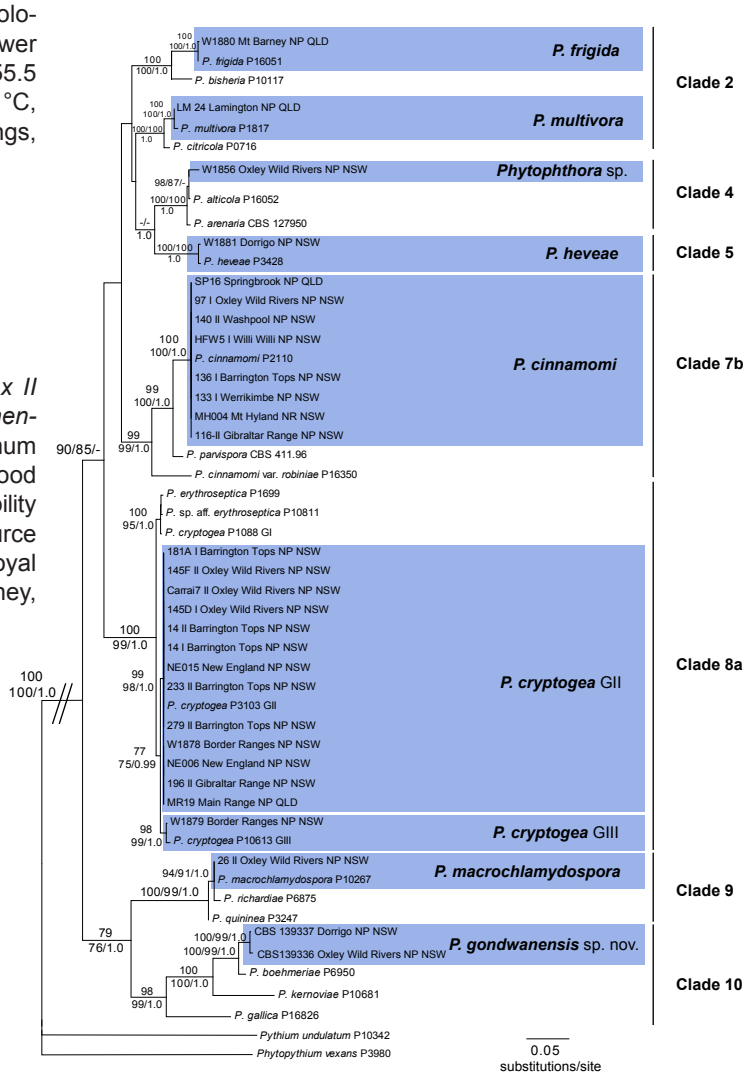
Mycelia often gnarled and tortuous. *Sporangia* initially abundant after isolation from soil, and on 10 % V8 agar after 5 d, caducous, papillate, papilla sometimes elongated, mainly globose to ovoid, sometimes limoniform, obturbinate, obpyriform, 39.3 ± 5.2 × 30.5 ± 3.4 µm (range 26.1–57.1 × 22.5–38.6 µm), length/breadth ratio 1.2 ± 0.1, pedicel length less than 5 µm. *Sporangiophores* sympodial. *Sporangial* production in culture decreased over time. *Chlamydospores* not observed. Sex organs: homothallic, amphigynous, hyaline to yellow. *Oospores* formed abundantly in soil. *Oogonia* abundant on V8 after 5 d, globose, smooth, borne laterally and terminally, mainly monosporous and plerotic, 23.6–32.1 (av. 28.4) µm diam, wall ranging from 1.5–4.5 (av. 2.7) µm. *Antheridia* monoclinous, elongate, 9.6–13.9 (av. 11.5) µm diam. Radial growth rates on 10 % V8 agar, optimum temperature 25–30 °C, no growth at 35 °C.

Culture characteristics — On carrot agar and V8 agar colonies are flat, on PDA they are more aerial, dense and slower growing. Optimum temperatures for growth 25–30 °C (55.5 mm and 55.3 mm diam in 5 d, respectively), 1–2 mm at 5 °C, no growth at 35 °C. Species is pathogenic to lupin seedlings, causing root rot after 3–4 wk.

Typus. Australia, New South Wales, Oxley Wild Rivers National Park, collected from soil, coll. *L.A. Shuttleworth & B.L. Freedman*, 28 Nov. 2011, isol. *K. Scarlett*, Mar. 2014 (holotype a dried 10 % V8 agar disc CBS H-22283; culture ex-type W 1858 = CBS 139336 = CMW 42633, ITS sequence GenBank KP070695, *coxII* sequence GenBank KP070638, *tub2* sequence GenBank KP070605, MycoBank MB812576).

Additional specimen examined. Australia, New South Wales, Dorrigo National Park, coll. *R. Daniel & D.I. Guest*, isol. *K. Scarlett*, Mar. 2014, paratype dried 10 % V8 agar disc CBS H-22284, culture ex-paratype W 1857 = CBS 139337 = CMW 42634, ITS sequence GenBank KP070696, *coxII* sequence GenBank KP070637, *tub* sequence GenBank KP070598.

Notes — Phylogenetically, *P. gondwanensis* is a strongly supported species residing in clade 10 with maximum likelihood bootstrap support, maximum parsimony bootstrap support and Bayesian posterior probability 100 %, 99 % and 1.0, respectively (Scarlett et al. 2015). This species is most closely related to *P. boehmeriae* but differs by 16 fixed polymorphisms on ITS, 17 on *coxII* and 22 on *tub2*. Morphologically, *P. gondwanensis* has smaller sporangial dimensions and smaller antheridia than *P. boehmeriae* (Erwin & Ribeiro 1996).



Maximum likelihood phylogeny of the combined ITS/*cox II* dataset (−ln 9986.75) showing the position of *P. gondwanensis* in clade 10. Values displayed at branches are maximum parsimony bootstrap ≥ 70 % (1st value), maximum likelihood bootstrap ≥ 70 % (2nd value) and Bayesian posterior probability ≥ 0.95 (3rd value). P = World *Phytophthora* Genetic Resource Collection, University of California, Riverside, USA; W = Royal Botanic Gardens and Domain Trust culture collection, Sydney, Australia.

Colour illustrations. Australia, New South Wales, Oxley Wild Rivers National Park, Apsley Falls (photo: L.A. Shuttleworth). L to R: ex-type culture on 10 % V8 agar, globose papillate sporangium, amphigynous oospore. Scale bars = 20 µm.

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Diaporthe tulliensis

Fungal Planet 387 – 1 December 2015

Diaporthe tulliensis R.G. Shivas, Vawdrey & Y.P. Tan, *sp. nov.*

Etymology. Name refers to the town Tully, near where the fungus was collected.

Classification — *Diaporthaceae, Diaporthales, Sordariomycetes*.

Sporulates on PDA and wheat straw pieces on WA after 4 wk. *Conidiomata* pycnidial, scattered, aggregated in small groups up to 4 mm diam, subglobose, up to 500 µm diam, ostiolate, beaks absent or up to 1 mm long, cream to pale yellow conidial droplets exuded from ostioles; walls thin, composed of an inner layer of yellowish brown *textura angularis* and an outer layer of darker yellowish brown *textura epidermoidea*. *Conidiophores* formed from the inner layer of the locular wall, reduced to conidiogenous cells, hyaline, cylindrical, tapered towards the apex, 15–20 × 1.5–2.5 µm. *Alpha conidia* oval to cylindrical, rounded at the apex, obconically truncate at base, hyaline, (4.5–)5–7 × 2–2.5(–3) µm. *Beta conidia* scarce amongst the alpha conidia, flexuous, hamate, hyaline, 25–30 × 1.0(–1.5) µm.

Culture characteristics — (after 1 wk in the dark and a further 3 wk under 12 h ultraviolet light / 12 h dark cycle, at 23 °C): Colonies on PDA cover the entire plate, flat with no aerial mycelium, white, reverse off-white. On OA agar colonies cover the entire plate, flat with sparse aerial mycelium, olivaceous grey diffused with grey olivaceous patches (Rayner 1970), reverse greyish sepia with irregular stromatic patches bordered by narrow dark margins.

Typus. Australia, Queensland, Tully, from rotted stem end of fruit of *Theobroma cacao*, 10 Feb. 2015, *M. Smith* (holotype BRIP 62248a (includes extype culture); ITS sequence GenBank KR936130, LSU sequence GenBank KR936131, *tub2* sequence GenBank KR936132, *tef1* sequence GenBank KR936133, MycoBank MB812896).

Notes — At least two other species, *Phomopsis folliculicola* and *P. theobromae*, have been isolated and described from *Theobroma cacao* (Uecker 1988). One of these species, *P. folliculicola*, causes cacao pod rot, whereas the other, *P. theobromae*, inhabits cacao leaves (Punithalingam 1974). These two species, as well as *D. tulliensis*, all possess morphologically similar alpha conidia in the range 5–8 × 2–3 µm. DNA sequence data is not available from the holotype specimens of either *P. folliculicola* or *P. theobromae*. For taxonomic stability and clarity, the fungus from northern Queensland is described as new. Although *D. tulliensis* was isolated from the rotting stem end of a cacao pod, it is not known whether this fungus is a pathogen, an opportunistic saprobe or an endophyte.

Colour illustrations. *Theobroma cacao* cultivated in northern Queensland, Australia (image by Yan Diczbalis); colonies on PDA (left) and OA (right), surface (top) and reverse (bottom); conidiomata on wheat straw pieces; conidia and conidiophores. Scale bars = 1 cm, 1 mm, 10 µm and 10 µm.

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Diaporthe vawdreyi

Fungal Planet 388 – 1 December 2015

Diaporthe vawdreyi Y.P. Tan & R.G. Shivas, *sp. nov.*

Etymology. Name recognises Lynton Leslie Vawdrey, an eminent and respected Australian plant pathologist, who first isolated this fungus.

Classification — *Diaporthaceae, Diaporthales, Sordariomycetes*.

Sporulates on PDA, OA and wheat straw pieces on WA after 4 wk. *Conidiomata* pycnidial, scattered, aggregated in small groups up to 2 mm diam, subglobose, up to 250 µm diam, ostiolate, beaks up to 1 mm long, abundant cream to pale yellow conidial droplets exuded from ostioles; walls composed of an inner layer of yellowish brown *textura angularis* and an outer layer of darker yellowish brown *textura epidermoidea*. *Conidiophores* formed from the inner layer of the locular wall, ampulliform to lageniform, mostly reduced to conidiogenous cells or 1-septate, hyaline, 6–15 × 1.5–3 µm at base. *Alpha conidia* cylindrical, rounded at the apex, sometimes tapered towards the base, hyaline, (5.5–)6–8 × 1.5–2(–2.5) µm. *Beta conidia* abundant, flexuous, mostly hamate, hyaline, (18–)25–33 × 1.0(–1.5) µm.

Culture characteristics — (after 1 wk in the dark and a further 2 wk under 12 h ultraviolet light / 12 h dark cycle, at 23 °C): Colonies on PDA 6–7 cm diam, flat with no aerial mycelium, margin undulate, off white to faintly mauve, agar darkens, reverse irregularly zonate, pale hazel at margin becoming darker towards centre. On OA colonies cover the entire plate, flat, rosy buff with irregular grey patches, reverse cinnamon with irregular stromatic patches bordered by narrow dark margins (Rayner 1970).

Typus. Australia, Queensland, East Feluga, from fruit rot of *Psidium guajava*, 18 Sept. 2014, *Y. Diczbalis* (holotype BRIP 57887a (includes ex-type culture); ITS sequence GenBank KR936126, LSU sequence GenBank KR936127, *tub2* sequence GenBank KR936128, *tef1* sequence GenBank KR936129, MycoBank MB812895).

Notes — At least two other species, *Phomopsis destructa* (as '*destructum*') and *P. psidii*, have been isolated from *Psidium* (Uecker 1988). One of these two species, *P. destructa*, was associated with pulpy fruit rot of *Psidium guajava* in India (Rao et al. 1976). *Diaporthe vawdreyi* has alpha conidia that are shorter than those of *P. destructa* (11–30 µm) and beta conidia that are longer than those of *P. psidii* (14.5–18.5 µm). Although *D. vawdreyi* was isolated from a specimen of rotted fruit, it is not known whether this fungus is a pathogen, opportunistic saprobe or endophyte.

Colour illustrations. Psidium guajava cultivated in northern Queensland, Australia; colonies on PDA (top) and OA (bottom), surface (left) and reverse (right); conidiophores, beta conidia, conidioma and alpha conidia. Scale bars = 1 cm, 1 cm, 10 µm, 10 µm, 100 µm and 10 µm.

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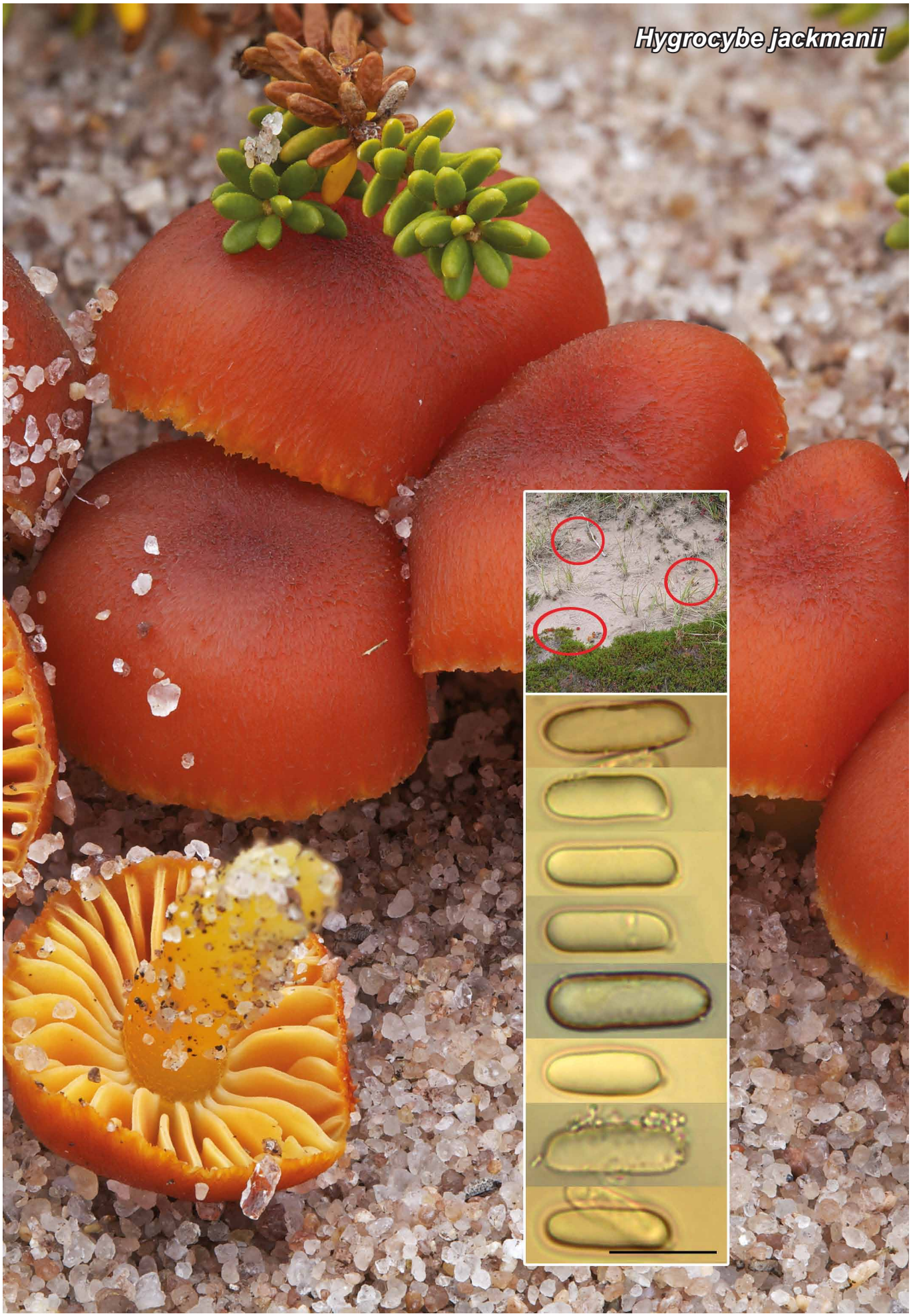

Hygrocybe jackmanii

Fungal Planet 389 – 1 December 2015

Hygrocybe jackmanii Lebeuf, Thorn, Boertm. & Voitk, *sp. nov.*

Etymology. Name is a tribute to Captain William Jackman, who swam back and forth from shore 27 times to save 27 persons from a storm-grounded ship. *Hygrocybe jackmanii* fruits during the same stormy early October on the same Labrador shores where Jackman's heroic feat took place.

Classification — *Hygrophoraceae, Agaricales, Agaricomycetes.*

Macroscopic: *Pileus* 10–40 mm diam, convex, decurved margin, plane with age, centre plane to depressed, margin slightly crenulate; radially adpressed fibrillose approaching squamulose in the centre; opaque, only edge of margin slightly translucent; orange-red, central squamules brown-grey, margin fringed with yellow fibrils. *Lamellae*: distant to moderately spaced, up to 3 mm wide; sinuous, adnate; yellow, turning orange with maturity; lamellulae 0–3. *Stipe*: 12–45 × 3–6 mm; even; smooth with sparse yellow flocculation at apex; ringless; solid to pithy; apex orange-yellow, lighter toward base, no staining; usually half-buried in sand. Context: yellow; smell nonspecific; taste nonspecific. *Sporeprint* white. Entire fruitbody slightly waxy to sticky.

Microscopic: *Spores* (type collection, 3 sporocarps, n = 96) (10.4–)11.8–15.1(–18) × (3.6–)4.2–5.5(–6.2) µm (mean = 13.5 × 4.8), Q = (2.1–)2.5–3.1(–3.5) (mean 2.8); evenly cylindrical, at times slightly constricted with concave side and occasionally distally swollen; walls smooth, thin, inamyloid; contents amorphous. *Basidia* 51–65 × 7–9 µm, 4-spored, basidioles numerous, some segmented with short basal cells. *Cystidia* none seen. *Clamp-connections* present in all tissues, with medallion-clamps on some basidia and basidioles. *Lamellar trama* subregular, of non-inflated cells with perpendicular cross walls, 55–172 × 5–8 µm. *Pileipellis* a trichoderm in young fruitbodies, in older a cutis, end cells 28–96 × 7–10 µm, some with grey-brown content.

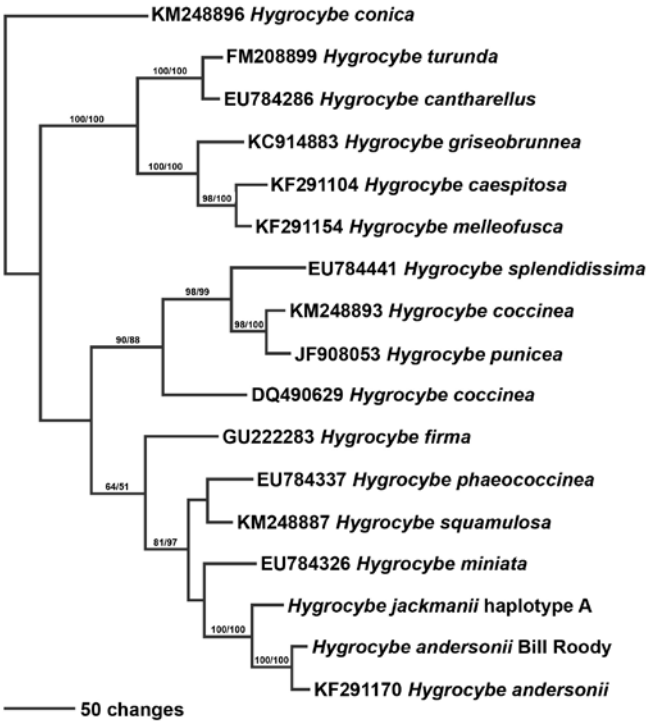
Habitat — In groups in shifting sand adjacent to heath or vascular plants, but not among them; of nearby moss, dune grass, *Alnus viridis* ssp. *crispa*, and *Empetrum nigrum* nearby, *E. nigrum* seems the most consistent; fruits together with *Alpova cinnamomea* and *Sabuloglossum arenarium*.

Distribution — Currently only known from the type location.

Phylogeny — The ITS sequence of the holotype collection (amplified with primers ITS8-F and ITS6-R) was heterozygotic, with one haplotype having two insertions totalling 3 bases in ITS1 plus a single heterozygous site (C/T) early in ITS2. In contrast, the sequence of our material of *H. andersonii* lacked indels but had two separate C/T heterozygosities in the 5.8S and ITS2 regions. Neighbour-joining and maximum parsimony analyses placed both haplotypes of *H. jackmanii* as sister to the two available sequences of *H. andersonii*, but differing sufficiently (12.7 %) to consider *H. jackmanii* as a separate species. Both species were placed in subg. *Pseudohygrocybe*, sect. *Firmae*, in a clade with *H. miniata*. However, sect. *Coccineae* and its subsect. *Squamulosae* were not resolved as monophyletic by these ITS data, so a conclusive placement of *H. andersonii* and *H. jackmanii* awaits further sequence data.

Typus. Canada, Forteau, Labrador, Newfoundland and Labrador, in littoral sand dunes, 2 Oct. 2011, *A. Voitk* (holotype DAOM 574886, ITS sequence GenBank KT207630 (haplotype A) and KT207631 (haplotype B), alignment in TreeBASE S17881; MycoBank MB812924); isotypes *Renée Lebeuf* HRL1060, UWO-F1, *David Boertmann* 11.10.02 (av 15).

Notes — Long, cylindrical spores set *Hygrocybe jackmanii* apart from all other species of *Hygrocybe* with dark squamules on the disc, except the recently described *H. andersonii*. The latter is a southern species growing along the US Gulf Coast with *Ceratiola ericodes*. That plant is not known north of southern South Carolina. In contrast, *H. jackmanii* is a northern fungus, seemingly associated with *Empetrum nigrum*, an ericaceous inhabitant of northern sand dunes. Phylogeny has shown these two fungal species to be distinct. Segmented basidioles are an unusual character found in sect. *Firmae*. For an additional description of *H. jackmanii*, see Lebeuf et al. (2016).



A Muscle alignment of 50 *Hygrocybe* sequences selected from GenBank based on Lodge et al. (2014), with *Hygroaster nodulisporus* and *Hygroaster albellus* as outgroups, was analysed in PAUP v. 4.0b10 using both maximum parsimony and BioNJ algorithms, then pared down to the monophyletic group containing members of sections *Firmae* and *Coccineae*. The single most parsimonious tree is shown; numbers at nodes represent bootstrap support from a bootstrapped heuristic maximum parsimony analysis with 100 random additions of taxa (first number) and from BioNJ (second number).

Colour illustrations. Hygrocybe jackmanii in situ in Labrador sand dune. Upper insert shows characteristic growth in sand, on the border of heath, but not in the heath. Close to moss, dune grass, alder and crowberry; the last (*Empetrum nigrum*) is the most consistent close potential partner. Lower insert shows elongated spores, 11.8–15.1 µm in length. Among red species of *Hygrocybe* with a dark disc, only *H. andersonii* as longer spores. Scale bar = 10 µm.

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Lindgomyces madisonensis

Fungal Planet 390 – 1 December 2015

Lindgomyces madisonensis Raja & Oberlies, *sp. nov.*

Etymology. Name refers to 'Madison' town in North Carolina where the type species was collected.

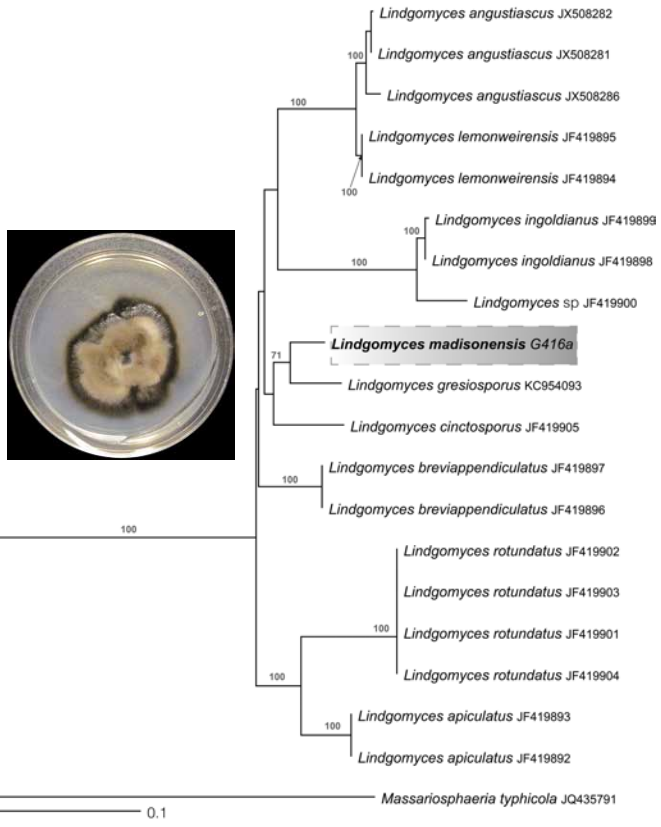
Classification — *Lindgomycetaceae, Pleosporales, Dothideomycetes*.

Ascomata on wood 248–276 × 295–326 µm, black, superficial to partially immersed, scattered, globose to subglobose, ostiolate, short papillate; papilla 37 × 47 µm. *Peridium* c. 25–35 µm wide, composed of dark irregularly shaped cells. *Pseudoparaphyses* cellular, abundant, c. 2 µm wide, covered with gelatinous material, septate, anastomosing above the asci. *Asci* 100–157 × 14–16 µm (mean and SD = 125 ± 16 × 15 ± 1 µm, n = 20), clavate to cylindrical, narrow at the apex, fissitunicate, tapering to a short stipe at the base, with eight overlapping biseriate ascospores at ascus apex becoming uniseriate at ascus base. *Ascospores* 36–43 × 6–9 µm (mean and SD = 39 ± 2 × 7 ± 1 µm, n = 45), fusiform, straight or slightly curved, tapering at the apices, 1-septate, constricted at the septum; primary septum supra-median to mostly median (0.43–0.5; average 0.5, n = 40), hyaline when young; ascospores become 3-septate and brown with age, multiguttulate, equipped with short bipolar appendages, c. 2 µm long; appendages ephemeral in water and not clearly visible in glycerin and lactic acid.

Culture characteristics — Colonies on PDA (Difco, Detroit, MI, USA) growing slowly (~ 25–30 mm diam in 4 wk), irregular, filamentous, raised, cottony, filiform margin, opaque, grey at the centre and black towards the periphery, occasionally colourless guttates/exudates forming on the surface of the colony.

Typus. A specimen derived from a culture isolated from submerged decorticated wood and grown on alfalfa (*Medicago* sp.) stems. USA, North Carolina, Rockingham County, Big Beaver Island Creek, Madison, N36°27'40.0" W80°01'46.0", water 10 °C, pH 5, 26 Apr. 2013, *Huzefa A. Raja & Nicholas H. Oberlies*, G416a (holotype ILLS 73408, ex-type culture DSM 100629 = CBS 140367, single ascospore isolate from holotype; SSU sequences GenBank KT207822, KT207823, ITS sequences GenBank KT207818, KT207819, LSU sequences GenBank KT207820, KT207821, alignment in TreeBASE S17851, MycoBank MB812940).

Notes — Morphological features of this species, such as globose to subglobose, scattered, ostiolate and papillate ascomata; numerous cellular pseudoparaphyses; 8-spored, bitunicate, fissitunicate, cylindrical asci with short, furcate pedicel; narrowly fusiform, hyaline, 1-septate ascospores bearing bipolar mucilaginous appendages, becoming brown and 3-septate with age, agree with the generic concept of the recently circumscribed genus *Lindgomyces* (Hirayama et al. 2010). *Lindgomyces* currently includes eight species, *L. ingoldianus* (type species), *L. angustiascus*, *L. apiculatus, L. brevappendiculatus, L. cinctosporus, L. griseosporus*, *L. lemonweirensis* and *L. rotundatus* (Hirayama et al. 2010, Raja et al. 2011, 2013, Zhang et al. 2014). All species of *Lindgomyces* described thus far have been reported from submerged wood in freshwater habitats. *Lindgomyces madisonensis* is morphologically most similar to *L. apiculatus* in having biapiculate gelatinous appendages. The former, however, differs from the latter in having narrow asci (100–157 × 14–16 µm in *L. madisonensis* vs 85–125 × 17–25 µm in *L. apiculatus*) and ascospores (36–43 × 6–9 µm in *L. madisonensis* vs 33–43 × 8–11 µm in *L. apiculatus*). In addition, molecular phylogenetic analyses of combined SSU and LSU as well as ITS clearly separate the two species. Other species in the genus that have biapiculate appendages include: *L. biappendiculatus* and *L. angustiascus. Lindgomyces madisonensis* differs from these taxa in both morphology and size of asci and ascospores. Molecular phylogenetic analysis also clearly distinguishes the aforementioned biapiculate spp. Raja et al. (2011) provided a key to six species of *Lindgomyces* described previously.



Phylogram of the most likely tree (-lnL = 4216.43) from a RAxML analysis of 20 taxa based on ITS nrDNA sequence data (1 071 bp). Numbers refer to RAxML bootstrap support values ≥ 70 % based on 1 000 replicates. Strain G416 is identified as having phylogenetic affinities to members of the freshwater ascomycete genus *Lindgomyces.* Scale bar indicates number of nucleotide substitutions per site. A 30-d-old colony of G416 on PDA media is shown.

Colour illustrations. Background photo of a stream in Piedmont region of North Carolina. Arrows on apical apices of ascospores show biapiculate appendages; arrow on ascus tip showing gelatinous material. Photos: Huzefa A. Raja. Scale bars = 200 µm (ascoma), 20 µm(pseudoparaphyses, ascospores and asci).

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Neofabraea brasiliensis
10 µm

Fungal Planet 391 – 1 December 2015

Neofabraea brasiliensis Sanhueza & Bogo, *sp. nov.*

Etymology. Name reflects the location where original isolates were collected.

Classification — *Dermateaceae, Helotiales, Leotiomycetes*.

Conidiogenous cells straight or sinuous, 8–14 × 3–5 µm, more or less cylindrical, tapering to narrow apex; usually held on irregularly branched conidiophores, sometimes arising directly from hyphae, sometimes with acropleurogenous conidiogenous loci. *Macroconidia* 12–22 × 2.5–3.7 µm, aseptate, oblong-ellipsoidal, apex rounded to more or less pointed, base slightly conical. *Microconidia* mostly 2.5–3.5 × 1–1.5 µm, ellipsoidal to oblong-ellipsoidal, base slightly conical then truncated; microconidia can be produced in conidial masses with a white, cottony appearance.

Culture characteristics — Colonies on MA, PDA and V8 are 28, 31 and 32 mm diam, respectively, after 15 d at 22 °C. On PDA the diameters are 12, 15, 12 and 12 mm after 3 wk at 4, 5, 30 and 31 °C, respectively. Aerial mycelium more or less lacking, slimy in appearance, surface covered with copious conidial zone. Cultures on PDA and V8 observed from above are intense reddish purple to reddish orange.

Typus. Brazil, Santa Catarina, Fraiburgo/SC, isolated from canker of *Malus domestica* cv. 'Fuji', 2003, *Empresa Brasileira de Pesquisa Agropecuária* (EMBRAPA - Brazilian Corporation of Agricultural Research) (holotype metabolically inert CNPUV499, culture ex-type CNPUV499, both held in CNPUV (Centro Nacional de Pesquisa de Uva e Vinho, Bento Gonçalves, RS, Brazil); ITS sequence GenBank KR107002, LSU sequence GenBank KR107002, *tub2* sequence GenBank KR107011, MycoBank MB812129).

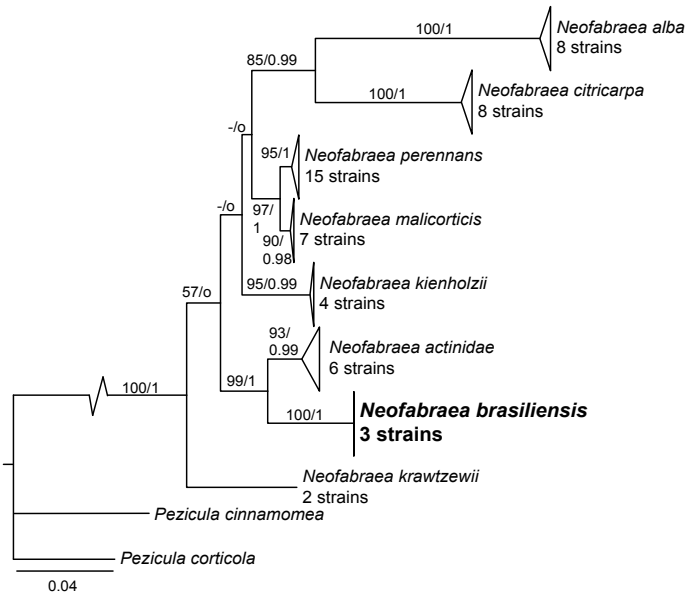
Additional specimens examined. Brazil, Santa Catarina State, Fraiburgo Municipality, isolated from *Malus domestica* cv. 'Fuji', 2002, CNPUV503 (ITS sequence GenBank KR107003, *tub2* sequence GenBank KR107012); Rio Grande do Sul State, Vacaria Municipality, isolated from *Malus domestica* cv. 'Fuji', 2002, CNPUV506 no longer viable in collection (ITS sequence GenBank KR107001, *tub2* sequence GenBank KR107010).

Notes — This species was previously treated as *Cryptosporiopsis perennans* in Bogo et al. (2008). However, upon investigation of morphological and DNA sequence data collected from this strain it was recognised as phylogenetically distinct from all described *Neofabraea*/*Cryptosporiopsis* species (Chen et al. 2015). Three isolates from Brazil were identified as *N. brasiliensis,* and upon analyses of available ITS sequences in GenBank two further strains from Ecuador were found to group with this taxon (GenBank accessions JN546212 and HQ007246).

Besides sequence differences, particularly for *tub2*, the most evident difference between *N. brasiliensis* and its most closely related species, *N. actinidae*, is the rate of growth which is significantly lower in *N. brasiliensis*. The mycelium growth index (average daily growth over the first 7 d) on PDA at the temperatures 4, 5, 30 and 31 °C for *N. brasiliensis* is 0.50, 0.54, 0.88 and 0.65 mm/d and for *N. actinidae* is 1.67, 1.75, 1.57 and 1.38 mm/d.

Colour illustrations. Apple orchard in Brazil where this new species was isolated, macroconidia, microconidia and conidiogenous cell, 21-d-old colony on PDA, bull's eye rot caused by *N. brasiliensis* on Fuji apple fruits, canker caused by *N. brasiliensis* on Fuji apple branch. Scale bar = 10 µm.

ITS and β-tubulin II sequences — Sequence data for *tub2* and ITS retrieved from GenBank was reviewed for all available strains with more than 88 % homology for ITS and 82 % for *tub2*. Including the sequences generated in this study, this amounted to 343 available strains for the ITS region and 108 strains for *tub2*. Strains with sequences available for both regions were selected for phylogenetic analyses and only the sequences belonging to the *Neofabraea* genus concept were kept, including those *Cryptosporiopsis* species that were recently introduced as new combinations for *Neofabraea*. The two regions were then concatenated into a single dataset in the order of ITS–*tub2*. *Pezicula cinnamomea* and *Pezicula corticola* were included as the outgroup. There were 55 strains available to be included in the concatenated alignment including the outgroup; once the identical sequences were removed this left 34 unique sequences representing eight *Cryptosporiopsis*/*Neofabraea* species and the two *Pezicula* species.



The phylogenetic tree with *N. brasiliensis* was constructed with maximum likelihood (ML) analysis of concatenated ITS–*tub2* sequences under the GTR+I+G model using PhyML v. 3.0 and with Bayesian inference (BI) using MrBayes v. 3.2.1. Support values were generated as nonparametric ML bootstraps with 100 bootstrap replicates and as Bayesian probabilities. Bootstrap support values (BV) over 50 percent or posterior probabilities (PB) greater than 0.5 are shown on the tree as BV/PB, BVs that were below 50 % in the PhyML tree are noted as (–) and clades that were absent in the MrBayes tree are noted as (o) (TreeBASE S17434).

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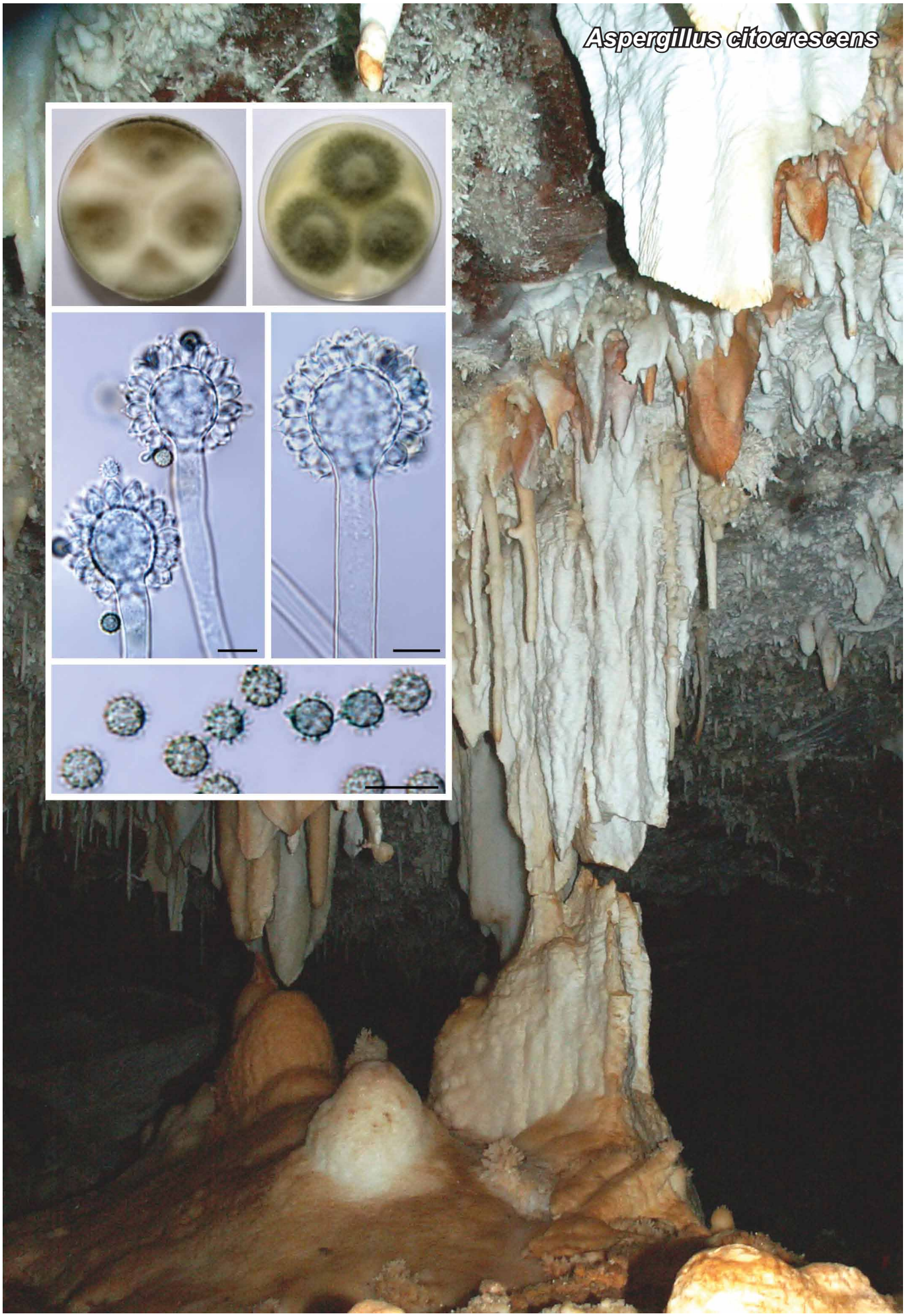
Aspergillus citocrescens

Fungal Planet 392 – 1 December 2015

Aspergillus citocrescens Hubka, A. Nováková & M. Kolařík, *sp. nov.*

Etymology. Name refers to rapid growth of this fungus (from the Latin adverb *cito* and verb *cresco*, *crescere*, *crevi*, *cretus*).

Classification — *Aspergillaceae, Eurotiales, Eurotiomycetes*.

On MEA: *Stipes* hyaline, smooth, 4–10(–12) µm diam; *conidial heads* loosely radiate; uniseriate; *vesicle* globose or subglobose, occasionally subclavate or clavate, 10–30 µm diam; *phialides* lageniform, covering entire surface of vesicle, 5.5–9.5 × 4–6 µm; *conidia* globose, strongly spinulose, sometimes persisting in chains, often with distinct connectives after detachment, green-brown in mass, spore body 4.5–6 µm diam, 6–8 with spines.

Culture characteristics — (in the dark, 25 °C after 7 d): Colonies on MEA 55–68 mm diam, lanose, mycelium white (ISCC−NBS No. 263), sporulation mainly in colony margins near plate walls and in colony centre, greyish yellowish green (No. 122) to greyish green (No. 150), no exudate, no soluble pigment, reverse colourless. Colonies on Czapek yeast autolysate agar (CYA) 65−68 mm diam, densely lanose, raised in centre, yellowish white (No. 92), sporulation in margins of raised colony parts and near the plate wall, greenish grey (No. 155) to dark greyish green (No. 151), no exudate, brilliant greenish yellow (No. 98) soluble pigment, reverse brilliant greenish yellow (No. 98). Colonies on yeast extract sucrose agar (YES) 65−70 mm diam, densely lanose with raised centre, yellowish white (No. 92), sporulation in colony margins, greenish grey (No. 155) to dark greyish green (No. 151), no exudate, no soluble pigment, reverse colourless. Colonies on Czapek agar (CZA) 58–60 mm diam, sparsely floccose to lanose, mycelium white (colony margins), abundant sporulation on the colony surface, greyish yellowish green (No. 122) to greyish olive green (No. 127), no exudate, no soluble pigment, reverse light yellowish green (119) with light greenish yellow (No. 101) centre. Colonies on Czapek yeast extract agar (CY20S) 60–70 mm diam, lanose, yellowish white (No. 92), without visible sporulation or with light greyish olive (109) to greyish olive green (No. 127) sporulation in colony margins, no exudate, no soluble pigment, reverse pale greenish yellow (No. 104). Colonies on Harrold's agar (M40Y) 62–72 mm diam, sparsely lanose with white mycelium and sporulation nearly on the whole surface of colonies, light greyish olive (No. 109) to greyish olive (No. 110), no exudate, no soluble pigment, reverse colourless. Colonies on creatine sucrose agar (CREA) growing more slowly compared with other media, 38–45 mm diam, white (No. 263), sparsely lanose, no sporulation, strong production of acid compounds, no marked production of base compounds. No growth on MEA and CYA at 37 °C.

Typus. Spain, Extremadura, Castañar de Ibor Cave, ex cave sediment, 2009, *A. Nováková* (holotype PRM 934413, isotypes PRM 934414−934417, culture ex-type CCF 4001 = CBS 140566; ITS sequence GenBank FR727121, LSU sequence GenBank LN896335, *tub2* sequence GenBank FR775317, *cmdA* sequence GenBank LN878969, MycoBank MB814680).

Notes — BLAST analysis with the ITS, β-tubulin and calmodulin sequences of *A. citocrescens* with the reference sequences published by Samson et al. (2014) showed greatest number of hits with *A. brunneo-uniseriatus* NRRL 4273^{T}: ITS 98 %; β-tubulin 96 %; calmodulin 91 %.

The species belongs to *Aspergillus* sect. *Cremei. Aspergillus brunneo-uniseriatus* is the only species with somewhat similar growth parameters and phenotype and can be differentiated by its smaller and mostly clavate vesicles. The colonies of *A. brunneo-uniseriatus* on MEA and CZA are almost identical (Raper & Fennell 1965) in contrast to *A. citocrescens* with more intensive sporulation on CZA. The sporulation colour of *A. brunneo-uniseriatus* on CZA is pale grey but grey-green in *A. citocrescens*.

Colour illustrations. Spain, Extremadura, Castañar de Ibor Cave; 7-d-old cultures of *Aspergillus citocrescens* on MEA (left) and CZA (right); conidiophores and conidia on MEA. Scale bars = 10 µm.

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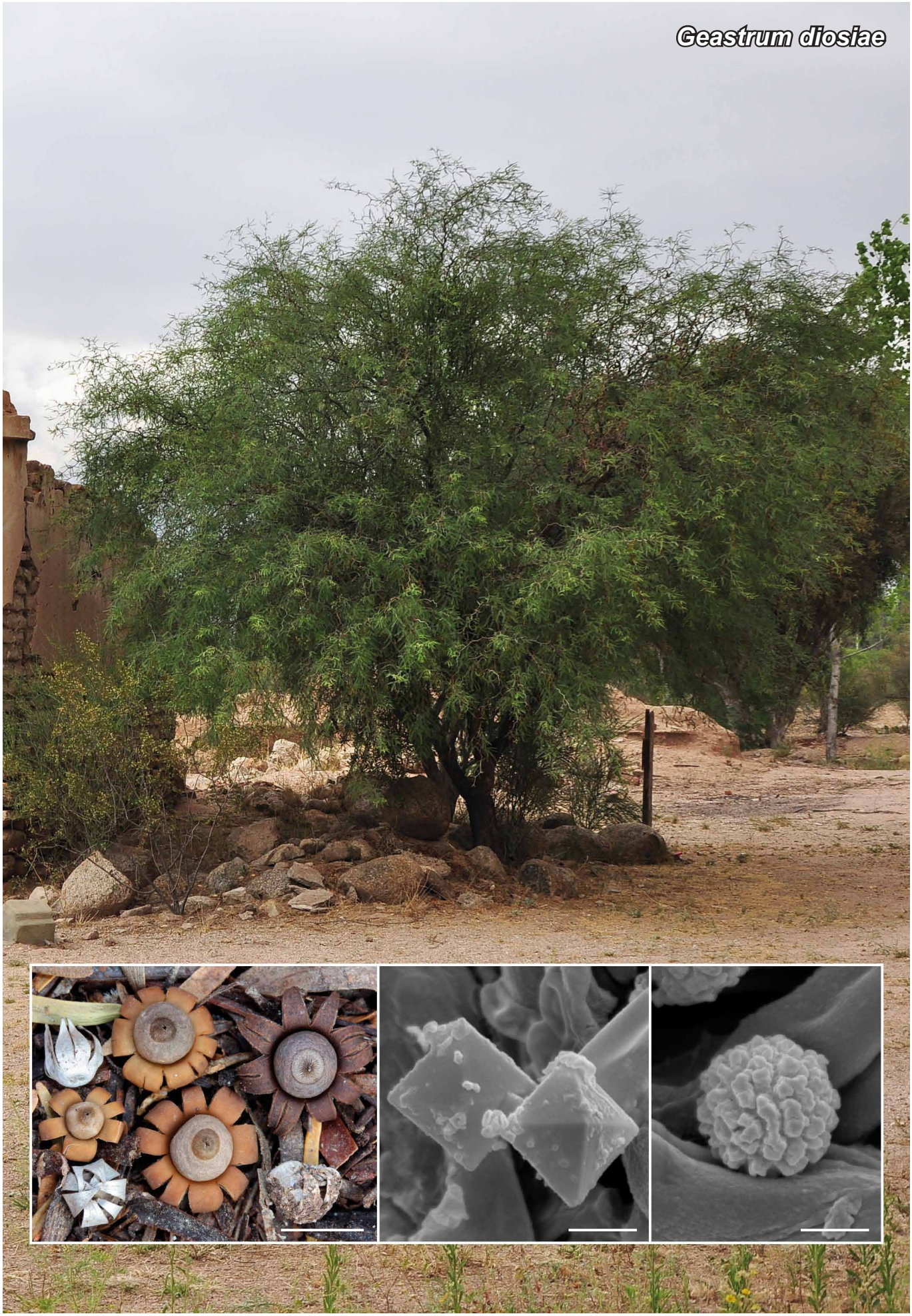
Geastrum diosiae

Fungal Planet 393 – 1 December 2015

Geastrum diosiae J.C. Zamora, *sp. nov.*

Etymology. Named for Maria Martha Dios recognising her contribution to the knowledge of Argentinian gasteroid fungi.

Classification — *Geastraceae, Geastrales, Agaricomycetes*.

Unexpanded basidiomata 5–10 mm diam, subglobose to ovoid, normally with a distinct apical umbo. *Exoperidium* splitting in 6–13 more or less equal to unequal rays, 5–14 mm diam when closed in dry state, 14–33 mm diam when hydrated and forced in horizontal position, saccate, strongly hygrometric. *Mycelial layer* thin, whitish, intermixed with deciduous debris, easily peeling-off leaving its innermost part or the fibrous layer exposed, double-layered; inner layer whitish, formed by rather indistinct, thin-walled, hyaline, clamped, generative hyphae, outer layer formed by comparatively thick-walled and aseptate, hyaline, skeletal hyphae, 1–2.5 µm diam, with indistinct lumen. *Fibrous layer* papyraceous, pale-cream to more or less brown, formed by thick-walled, aseptate, brownish, skeletal hyphae, 2–4.5 µm diam. *Pseudoparenchymatous layer* pale-cream to yellowish when young, soon ochraceous to orange, dark brown when old, normally not cracked, very persistent even in very old basidiomata, composed of thick-walled (walls 2–3 µm thick) cells of various sizes and shapes, about 15–30 µm diam. *Endoperidial body* globose to subglobose, 4–10 mm diam, pale grey to brownish grey; endoperidial surface glabrous and naked or covered with a very inconspicuous pruina, sessile; endoperidium consisting of brownish skeletal hyphae, (2.5–)3–6 µm diam. *Mesoperidium* inconspicuous, reduced to few generative hyphae and some 3–10 µm diam, bipyramidal, calcium oxalate dihydrate crystals on the endoperidial surface. *Peristome* fibrillose, often darker or of the same colour than the endoperidial body, sometimes slightly lighter, flat to broadly conical, distinctly delimited, thickened, formed by up to 12 µm diam, brownish, skeletal hyphae. *Stalk* absent. *Apophysis* absent. *Columella* weak, intruding about 1/3–1/2 in the glebal mass. *Mature gleba* brown to blackish. *Basidiospores* globose, 4.0–5.0 µm diam; ornamentation baculate, consisting of 0.3–0.5(–0.6) µm in height, brown, low, truncate warts, sometimes fused to form short crests. *Broadest capillitial hyphae* 6–7 µm wide, aseptate, brown to dark brown, very rarely branched, thick-walled, with narrow lumen, mostly visible; tips often acute; surface covered with debris or not. *Rhizomorphs* deciduous, only a few studied, covered with some acicular to horn-like calcium oxalate monohydrate crystals.

Ecology & Distribution — This species grows in rather disturbed places, on patches of denuded soil among *Prosopis* spp. ('algarrobos'). It is currently known from rather wooded zones of the Monte ecoregion in Argentina, which is part of the Temperate grasslands, savannas and shrublands biome of the Neotropic ecozone (Olson et al. 2001). These places are not far from the ecotone with the Arid Chaco ecoregion (tropical and subtropical grasslands, savannas and shrublands biome), and some specimens seem to have been found in the Arid Chaco (M.M. Dios, pers. com., not studied by the author and therefore not included here), so the species should probably be looked for in both ecoregions.

Typus. Argentina, La Rioja, Castro Barros, Anjullón, on the ground, with *Prosopis* spp. (*Leguminosae*) litter, growing close to old adobe buildings, 8 Apr. 2012, *L. Papinutti* & *J.C. Zamora* (holotype AH 47602, isotypes in MA-Fungi 83788 and UPS; ITS sequence GenBank KF988452, LSU sequence GenBank KF988587, *rpb1* sequence GenBank KF988722, *atp6* sequence GenBank KF988853, MycoBank MB812569).

Additional specimens examined. Argentina, La Rioja, Castro Barros, Anjullón, on *Prosopis* spp. (*Leguminosae*) litter, growing close to old adobe edifications, 8 Apr. 2012, *L. Papinutti* & *J.C. Zamora*, MA-Fungi 83789, duplo AH 47603 (ITS sequence GenBank KF988453, LSU sequence GenBank KF988588, *rpb1* sequence GenBank KF988723, *atp6* sequence GenBank KF988854); ibid., AH 47604.

Notes — The morphological description is based on c. 70 fruitbodies in different degrees of development. *Geastrum diosiae* is a well-defined species, characterised by the small basidiomata, strongly hygrometric exoperidium, mycelial layer encrusting debris and peeling-off, sessile endoperidial body, fibrillose and distinctly delimited peristome, and basidiospores with baculate ornamentation. This species belongs to *Geastrum* sect. *Corollina* and was included in the phylogenetic analyses of the entire genus *Geastrum* by Zamora et al. (2014), but left undescribed as '*Geastrum* sp.1'. The morphologically closest taxon is *G. hungaricum*, but this species is included in *G.* sect. *Geastrum* by molecular data and by the more distinct mesoperidium, with numerous crystalline aggregates of calcium oxalate monohydrate crystals, having also thinner capillitial hyphae and bigger basidiospores (5.0–6.0 µm) with an irregularly verrucose ornamentation (Sunhede 1989, Zamora et al. 2015). *Geastrum arenarium* is another hygrometric species recorded from the same Argentinian biome, but the endoperidium is subsessile to slightly stalked, the exoperidium is subsaccate to arched, the mycelial layer is rather persistent, and the basidiospores have a very irregularly verrucose ornamentation; it also belongs to *Geastrum* sect. *Geastrum*, being phylogenetically distinct (Zamora et al. 2014, 2015). *Geastrum floriforme* has much larger basidiospores (5–7 µm), an indistinctly delimited peristome, and the endoperidial surface is not completely smooth, but normally rough due to groups of fused hyphae; it is also very different based on molecular data, belonging to *Geastrum* sect. *Papillata* (Zamora et al. 2014). Among the Argentinian species described by C. Spegazzini, only *G. platense* has an hygrometric exoperidium and a fibrillose peristome (Spegazzini 1898) but, after revising the type material (LPS 13345), the specimen was found to be very close to *G. floriforme*, and thus it also has larger basidiospores, an indistinctly delimited peristome and a rough endoperidial surface. Finally, *G. corollinum* is distinguished by the larger basidiomata and mycelial layer not encrusting debris (Sunhede 1989); this species is the type of *Geastrum* sect. *Corollina* and it is further differentiated from *G. diosiae* based on molecular data, each species forming independent and well-separated clades (Zamora et al. 2014).

Colour illustrations. Anthropised the Monte ecosystem in Castro Barros (La Rioja, Argentina) showing *Prosopis* sp. growing close to an old adobe building (photo: G. Rolón, IAA, FADU-UBA); mature basidiomata on *Prosopis* litter; mesoperidial bipyramidal crystals on the endoperidial surface; basidiospore. Scale bars = 10 mm (mature basidiomata), 2 µm (microscopic structures).

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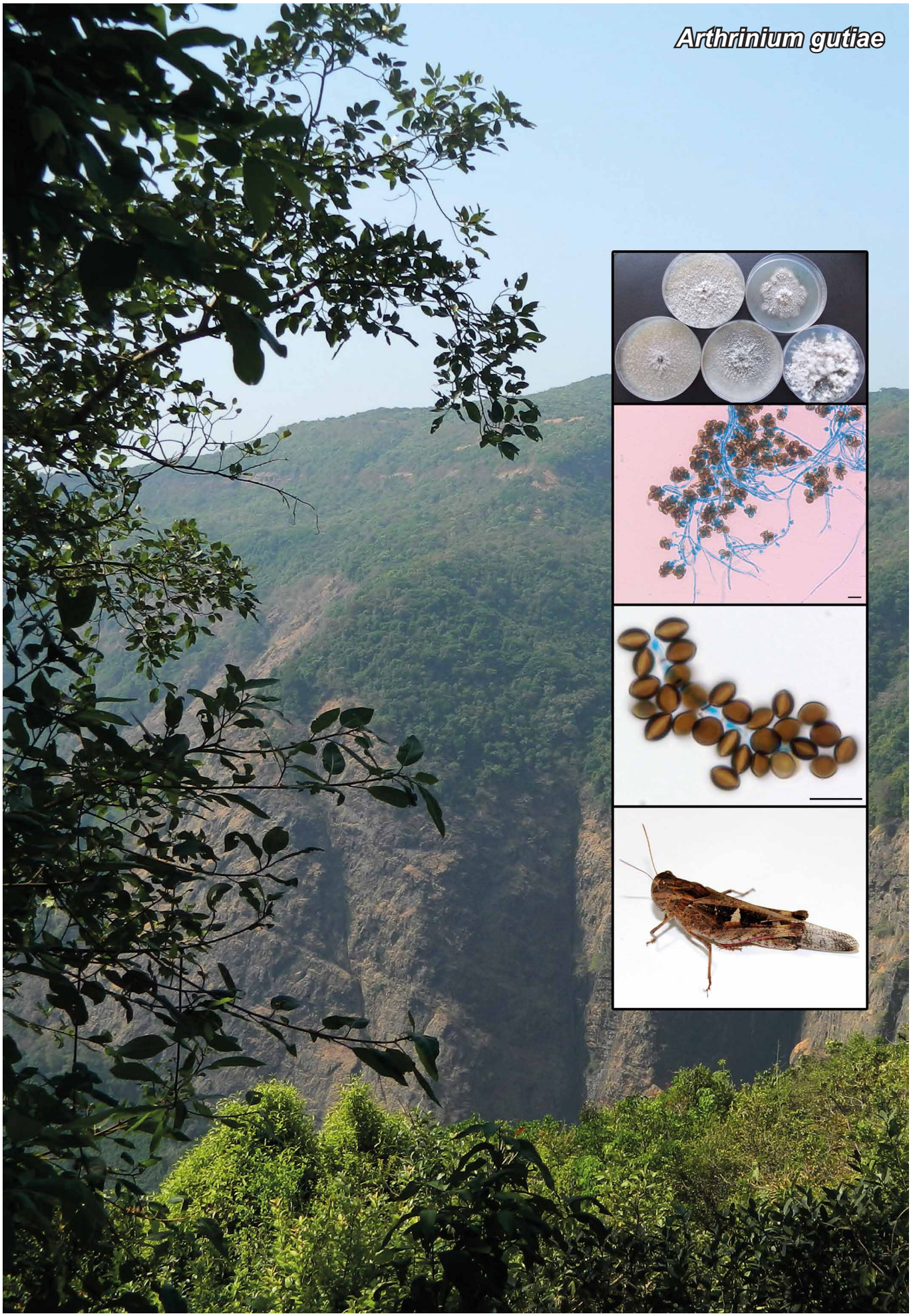

Arthrinium gutiae

Fungal Planet 394 – 1 December 2015

Arthrinium gutiae Kajale, Sonawane & Rohit Sharma, *sp. nov.*

Etymology. Name refers to the gut of an insect from which this species was isolated.

Classification — *Apiosporaceae, Xylariales, Sordariomycetes*.

Mycelium on MEA consisting of smooth, hyaline, branched, septate, 1–2.5 µm diam hyphae, partly immersed and partly superficial; sporulation not uniform, occurring in patches. Sporulation was observed on MEA and OA after 15–20 d incubation at 25 °C. *Conidiophores* hyaline, macronematous, mononematous, arising from long, ampulliform conidiophore mother cells, transversely septate, thick-walled, brown, 21.5–50 × 2–2.5 µm. The conidiophore cells are usually narrow, but broaden at the point of septation. *Conidiophore mother cells* borne directly on hyphae are hyaline, smooth, lageniform, 3–7 × 2–4 µm. *Conidia* borne as bunches on conidiophores, lateral and terminal, brown, smooth, aseptate, globose in surface view, lenticular in side view, with pale equatorial slit, (4.5–)5.5(–6) µm diam in surface view, (2–)4(–6) µm diam in side view, with a central scar. Anomalous conidia not observed.

Culture characteristics — Colonies on MEA at 25 °C were fast growing and spreading, flat, with moderate aerial mycelium, covering the dish after 7–10 d. The fungus grows optimally at 20 to 25 °C.

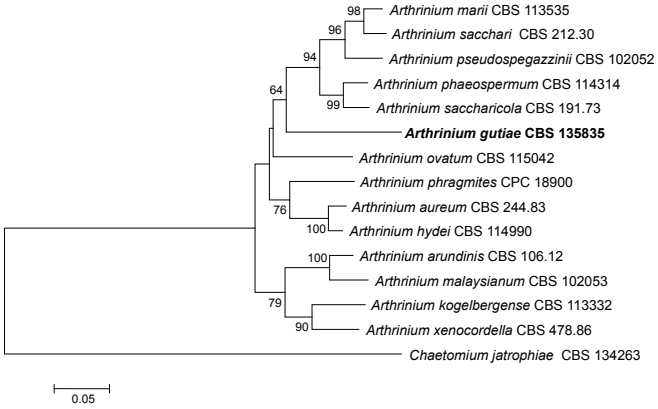
Habitat — Gut of grasshopper.

Distribution — India (Bhimashankar, Pune, Maharashtra).

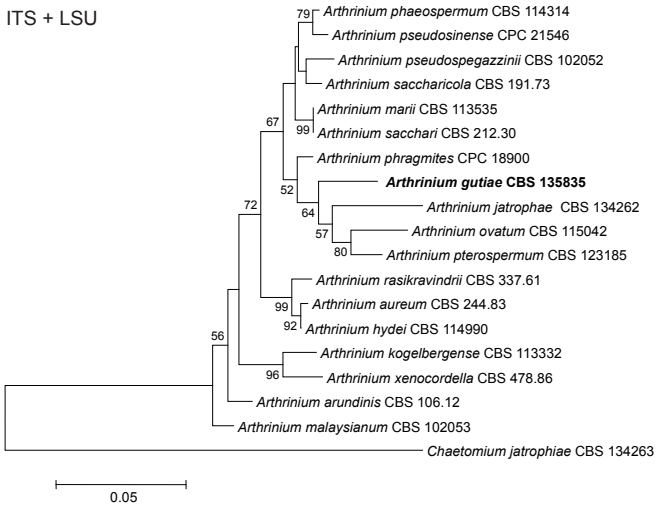
Typus. India, Pune, Western Ghats, Maharashtra, from gut of a grasshopper, 10 Jan. 2013, *S. Kajale & M.S. Sonawane* (holotype MCC H1002, culture ex-type MCC 1077 = CBS 135835; ITS sequence GenBank KR011352, LSU sequence GenBank KR149063, *tef1* sequence GenBank KR011351, *tub2* sequence GenBank KR011350, MycoBank MB812319).

Notes — Based on the concatenated sequence analysis of the internal transcribed spacers (ITS) and large subunit nrDNA (LSU), *A. gutiae* is phylogenetically closely related to *A. jatrophiae,* forming a separate monophyletic branch within *Arthrinium.* This finding is also supported by the *tef1* and *tub2* concatenated sequence analysis that also shows *A. gutiae* to cluster on a separate branch. *Arthrinium gutiae* is morphologically similar to *A. jatrophiae* in the formation of circular or nearly circular lenticular conidia. However, the conidia and conidiophores of *A. gutiae* are small in comparison to *A. jatrophiae.* Furthermore, it does not form anomalous conidia as observed in *A. jatrophiae* (Sharma et al. 2013). Although the genus *Arthrinium* is widespread, occurring as plant pathogen, endophyte or saprobe (Ellis 1971, 1976, Crous et al. 2013), the habitat of *A. gutiae* is unique as it was isolated from the gut of a grasshopper.

BTUB + TEF



ITS + LSU



Neighbour-joining phylogram of ITS/LSU and *tef1/tub2* sequence analysis, showing the clades and subclades, with *Chaetomium jatrophiae* as outgroup. The phylogenetic position of *Arthrinium gutiae* is indicated in **bold**. Branches with bootstrap support (BS) values ≥ 50 % (based on 1 000 replicates) are shown. The alignments were submitted to TreeBASE (S17561, S17562).

Colour illustrations. Collection site in Western Ghats, Maharashtra state, India; colony of *Arthrinium gutiae* on PDA, PCA, CDA, OA, MEA (clockwise), conidiophore mother cells, conidia, grasshopper host. Scale bars = 10 µm.

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Ganoderma wiiroense

Fungal Planet 395 – 1 December 2015

Ganoderma wiiroense E.C. Otto, Blanchette, C. Barnes & Held, *sp. nov.*

Etymology. Named after the village of Wiiro where the fungus was found in the Sissala West District of the Upper West Region of Ghana.

Classification — *Ganodermataceae, Polyporales, Agaricomycetes*.

Mature *basidiomata* annual, pileate, sessile, dimidiate, applantate, woody to corky when dried, not completely homogeneous context structure, zonate, pileus surface hard and glabrous, yellowish brown to dark reddish brown when dry, margin rounded, thickened, yellowish brown to dark reddish brown when dry. *Pore surface* smooth, white to creamy yellow when dry, pores 3–5 mm, round to somewhat irregular and slightly elongated, 122–292 × 80–240 µm (av. 206.1 × 154.9), dissepiments 47–182 µm wide (av. 83.1); tubes 0.1–1 mm long, brown. *Hyphal system* trimitic, generative hyphae slightly inconspicuous, hyaline, thin-walled 2–4 µm diam, branched, clamped and hyaline; skeletal hyphae occasionally branched, pale to dark brown, 2.5–7.5 µm thick; binding and skeleton-binding hyphae hyaline, highly branched, tapering towards the end. *Basidia* not observed. *Basidiospores* ellipsoid to cylindrical-ellipsoid with a truncate base, bitunicate, verruculose, 10–13.5 × 6–8 µm (av. 11.8 × 7.1 µm), perisporium thin, smooth, exosporium with intermediate thick inter-walled pillars, endosporium thick, brown. *Chlamydospores* not observed.

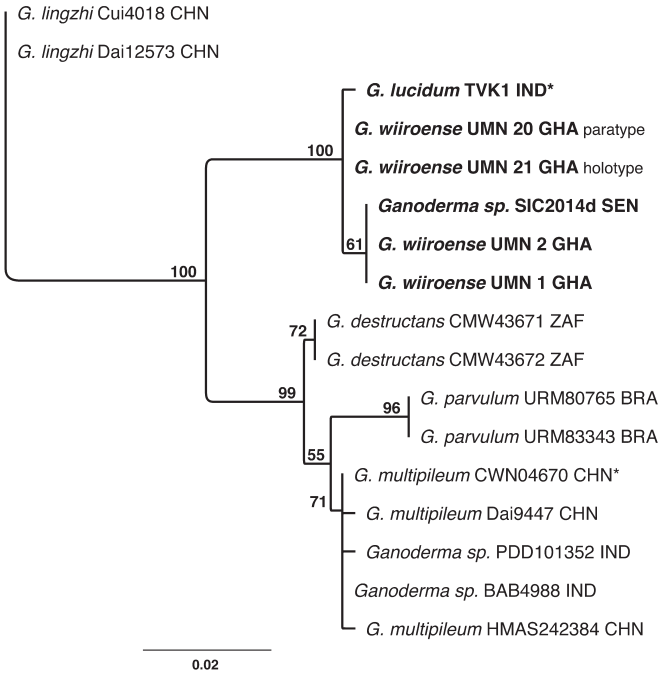
Culture characteristics — Colonies on MEA, showing optimum growth at 30 °C exceeding 40 mm in the dark in 7 d, followed by 35 mm at 35 °C, 33 mm at 25 °C, 20 mm at 20 °C; mycelial mats circular with entire edge, flat, white above and slight creaminess reverse at all temperatures, woolly to felty, superficial mycelium with medium density.

Typus. Ghana, Upper West Region, Sissala West District, Wiiro, on angiosperms, Aug. 2015, *A.B. Wibonto & H.B. Babilwie* (holotype MIN 938704, paratype MIN 938705, cultures ex-type UMN-21-GHA (also deposited at CBS), holotype ITS sequence GenBank KT952363, LSU sequence GenBank KT952364, paratype ITS sequence GenBank KT952361, LSU sequence GenBank KT952362, MycoBank MB814840).

Phylogenetic analysis was done using the Maximum Likelihood plugin PHYML in Geneious v. R7 (http://www.geneious.com) (Kearse et al. 2012), and the substitution model was determined by jModelTest (Posada 2008) according to the Corrected Akaike Information Criterion (AICc). *Ganoderma lingzhi* (GenBank JQ781855 and JQ781856) is the outgroup. Bootstrap support values ≥ 50 % are given above branches. The phylogenetic position of *G. wiiroense* is indicated in **bold**. The *Ganoderma* species is followed by the sample ID and the three letter United Nations country code. The * indicates the country is not specified in the Features section of the Blastn search and is assumed from author affiliations.

Colour illustrations. Field of cotton (*Gossypium hirsutum*) with shea trees (*Vitellaria paradoxa*) and other tree species dispersed throughout the field located near Wiiro, Ghana (background); basidiocarp; basidiocarp; basidiospores; skeletal hyphae. Scale bars = 3 cm (basidiocarp), 10 µm (microscopic structures).

Notes — *Ganoderma wiiroense* causes decay in the roots and trunks of angiosperm trees in the Upper West Region of Ghana in the village of Wiiro (a Sissali name). For Blastn ITS sequence comparisons, 530 bases were used from the *G. wiiroense* holotype sequence, starting at ITS1, after the CATTA motif (Schoch et al. 2014). The Blastn results gave the highest score to an isolate *Ganoderma lucidum* (TVK1, GenBank FJ982798) submitted in 2009 by the Centre for Advanced Studies in Botany, University of Madra, Tamil Nadu, India, with three nucleotide differences. A second sequence from a collection in Senegal (SIC-2014d, GenBank KJ510534) has two nucleotide differences, but was 38 bases shorter at the 3' end than the holotype. Subsequently, two representative sequences of the next highest seven Blastn scores were downloaded for phylogenetic analysis. The sequence alignment was edited by hand to limit differences between sequences. The final alignment, ITS1-5.8S-ITS2, was trimmed at the 3' end following other ITS2 annotations from GenBank and being as conservative as possible not to lose any variable bases. Two additional DNA samples of *G. wiiroense*, along with the top two Blastn hits, showed two heterozygous sites in the alignment, thus forming two groups. The next closest species to *G. wiiroense* is *G. destructans*, with 30–33 nucleotide and gap differences. Eighty to ninety percent of the sequence variability occurs in ITS1.



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Xenoleptographium phialoconidium

Fungal Planet 396 – 1 December 2015

Xenoleptographium Marinc., T.A. Duong, Z.W. de Beer & M.J. Wingf., *gen. nov.*

Etymology. Name reflects a morphological similarity to species in *Leptographium*.

Classification — *Nectriaceae, Hypocreales, Sordariomycetes*.

Conidiophores macronematous, mostly single, upright. *Conidiogenous cells* phialidic, cylindrical, tapering towards the apex, hyaline, collarettes inconspicuous. *Conidia* hyaline, ellipsoid, asymmetric, with truncated base, aseptate, smooth, in yellowish slimy droplets.

Type species. *Xenoleptographium phialoconidium*.
MycoBank MB812683.

Xenoleptographium phialoconidium Marinc., T.A. Duong, Z.W. de Beer & M.J. Wingf., *sp. nov.*

Etymology. Name refers to the phialides from which the conidia are produced.

Conidiophores macronematous, mostly single, straight or occasionally undulated, (252–)301–335(–451) µm in length. *Basal cells* brown or paler at the lower half, club-shaped or foot cell-like, with rhizoid and bubble-like cells around. *Stipes* brown, smooth, cylindrical tapering towards the top, (192–)254–279(–343) µm long, (11–)13–14(–15.5) µm wide at base and (5.5–)7–7.5(–9.5) µm wide close to the apex, with 3–6-septa. *Conidiogenous apparatus* (40–)53–60(–75.5) µm in length, with 3–4 series of cylindrical branches. *Conidiogenous cells* phialidic, cylindrical tapering towards the apex, hyaline, (8.5–)12–14(–18) × (1.5–)2 µm, collarettes inconspicuous. *Conidia* hyaline, ellipsoidal, asymmetric, with truncated base, aseptate, smooth, (6–)6.5–7(–8) × (1.5–)2 µm (av. 6.8 × 1.8 µm), in yellowish slimy droplets. *Synasexual morph* acremonium-like, conidiophores micro- or macronematous, conidiogenous cells hyaline, cylindrical tapering gradually towards the apex with distinct collarette; conidia hyaline, fusiform with truncated base, (8–)9(–11) × 1.5–2 µm (av. 9.4 × 1.7 µm), in colourless slimy droplets which is smaller than the yellowish slimy droplets.

Culture characteristics — On MEA growing in circular, flat, mostly submerged with undulate edge and medium sparse, cartridge buff with whitish aerial hyphae near the edge, optimum growth at 25 °C reaching 42 mm in 21 d, then at 20 °C reaching 33 mm and at 15 °C and 30 °C reaching 21 mm, no growth at 35 °C. No growth occurred at all temperatures on 0.05 % cycloheximide-amended MEA.

Typus. Indonesia, Northern Kalimantan, near to the town of Berau, isolated from the exposed xylem tissues of *Gmelina arborea* (*Lamiaceae*), Dec. 2010, *M.J. Wingfield* (holotype PREM 61244, dried culture of CBS 134694, culture ex-holotype CBS 134694 = CMW 37146; isotype PREM 61245, dried culture of CBS 134695, culture ex-isotype CBS 134695 = CMW 37140; *tub2* sequences GenBank KT164794 (CBS 134694), KT164793 (CBS 134695), *rpb2* sequences GenBank KT164796 (CBS 134694), KT164795 (CBS 134695), *tef1* sequences GenBank KT164798 (CBS 134694), KT164797 (CBS 134695), LSU sequences GenBank KT164792 (CBS 134694), KT164791 (CBS 134695), MycoBank MB814898).

Colour illustrations. Plantation of *Gmelina arborea* in Northern Kalimantan (background); conidia of *Xenoleptographium phialoconidium* in yellow slimy droplets (black arrow) and conidia of acremonium-like synasexual morph in colourless droplets (white arrow), upright conidiophore, conidiogenous cells, conidia, conidiogenous cells of synasexual morph, conidia of synasexual morph. Scale bars = 25 µm (upright conidiophore), 10 µm (all other microscopic structures).

Additional specimens examined. Indonesia, Northern Kalimantan, near to the town of Berau, isolated from the exposed xylem tissues of *Gmelina arborea* (*Lamiaceae*), Dec. 2010, *M.J. Wingfield*, cultures CMW 37138, 37139, 34141–37145.

Notes — *Xenoleptographium phialoconidium* was isolated from artificially induced wounds used to 'trap' species of *Ceratocystis*, where xylem tissues were exposed to the environment after a block of bark had been removed. Six weeks after wounds were made, the exposed tissues were cut from the trunk, sealed in a plastic bag and brought to the laboratory for examination. Yellowish slimy spore droplets at the tips of upright stalks were observed among other ophiostomatoid fungi, *Cornuvesica magnispora* (Marincowitz et al. 2015) and a *Ceratocystis* sp. Culture extracts of *X. phialoconidium* were shown to enhance the growth of *Cornuvesica magnispora*.

The overall appearance of isolates was typical of *Leptographium* species: mononematous conidiophores with upright, brown stipes, verticillately branched conidiogenous apparatuses and slimy conidial droplets. However, the presence of enteroblastic conidiogenous cells (phialides) and an inability to tolerate the antibiotic cycloheximide in culture distinguishes these isolates from *Leptographium* spp. that have percurrent blastic conidiogenous cells and can tolerate high levels of cycloheximide in culture (Jacobs & Wingfield 2001).

Xenoleptographium phialoconidium is morphologically similar to *Phialocephala* spp. (*Leotiomycetes*, *Helotiales*), also previously confused with *Leptographium* spp. due to the overall morphological similarity of these genera, but having conidia produced in phialides with periclinal thickening and prominent collarettes (Wingfield et al. 1987, Jacobs et al. 2003). Multi-gene phylogenies confirmed the placement of *Xenoleptographium* in the *Nectriaceae* (*Hypocreales*) and in which asexual genera generally have phialidic conidiogenous cells (Rossman 1996).

RaxML analyses of the combined dataset of LSU, *tub2*, *tef1* and *rpb2* gene regions showed that *X. phialoconidium* was most closely related to *Volutella*, *Chaetopsina* and *Coccinonectria*. These genera, together with several others, were referred to as clade VIII by Lombard et al. (2015b).

RaxML phylogram resulting from analyses of a combined dataset of LSU, *tub2*, *tef1* and *rpb2* gene regions. Bootstrap support values (1 000 replicates) above 70 % are indicated at nodes. Taxa included and sequence accession numbers were similar to those from Lombard et al. (2015b). All major clades (except clade VIII) were collapsed (refer to Lombard et al. 2015b for more details on these clades) (for phylogenetic tree, see MycoBank)..

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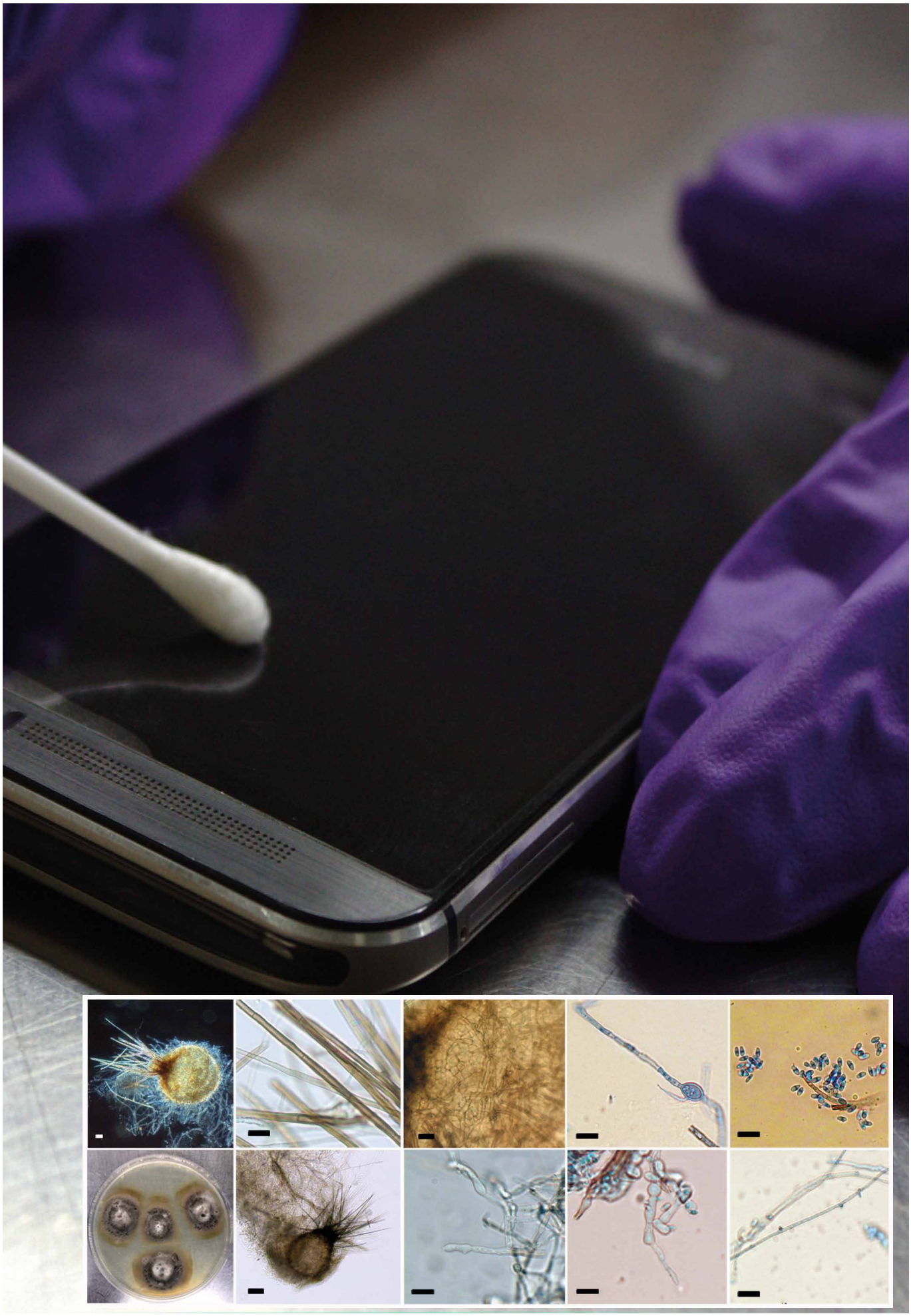


Fungal Planet 397 – 1 December 2015

Pyrenochaeta telephoni Rohit Sharma, Kurli, Sonawane, Shouche & Rahi, *sp. nov.*

Etymology. Name refers to the substrate, the surface of a mobile phone, from which this species was isolated.

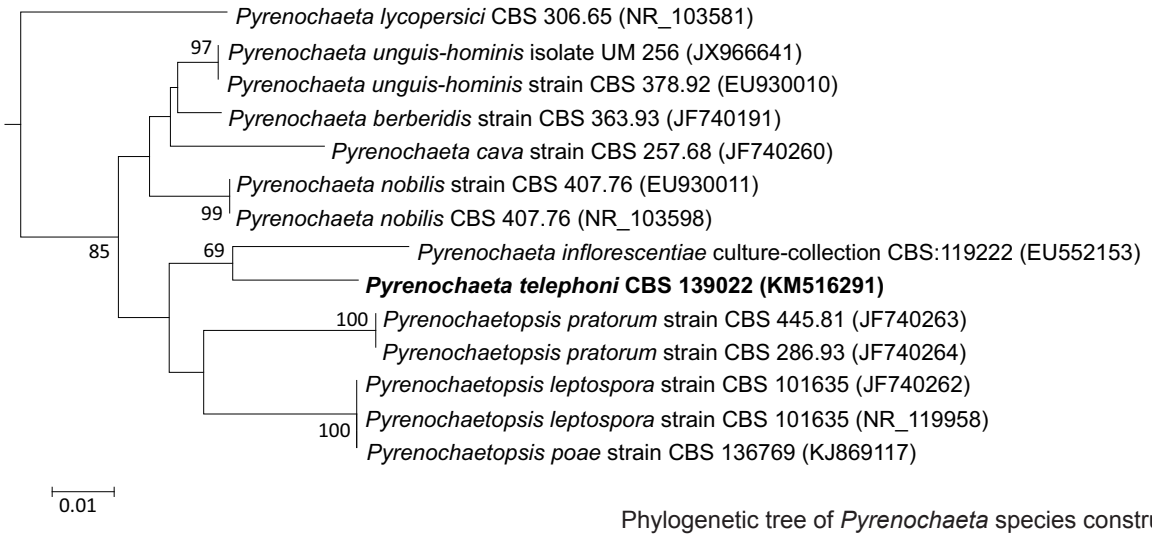
Classification — *Cucurbitariaceae*, *Pleosporales*, *Dothideomycetes*.

Conidiomata pycnidial, formed on MEA after 30–35 d; immersed in media (not superficial) and few in number. *Pycnidia* fuscous, olivaceous brown to fuscous brown, globose or subglobose, single or confluent, simple, (107–)160(–272) × (100–)186(–226) µm diam, setose. *Setae* are of two types. One type formed on the outer wall, long, (1.5–)3.25(–4) µm diam, (108–)171(–268) µm in length, mainly concentrated around the ostiole, stiff, needle-shaped, inflexible, septate, brown coloured, ends obtuse, smooth, 15–18 in number, thick-walled. The other portion of pycnidia have non-stiff hairs or setae-like outgrowths, distributed on all sides, (1.5–)3(–4) µm diam and (15.5–)26(–40) µm in length, hyaline; pycnidia with single central ostiole, non-papillate, or slightly papillate, (54–)60(–73) µm diam; pycnidial wall 3–8 cells thick; conidial matrix white/cream. *Micropycnidia* present. *True chlamydospores* absent, but chlamydospore-like hyphal swollen cells were observed in old MEA cultures. They were intermediate, hyaline, globose, 8–10 µm diam, sooth and thick-walled. *Sexual morph* on OA absent. *Conidiogenous cells* is formed from entire inner surface of pycnidial wall, mostly cylindrical, (3–)4(–5.5) × (9.5–)12(–18) µm mostly integrated in conidiophores, branched at the base, acropleurogenous (having terminal and apical apertures). *Conidia* ellipsoid, (4–)5(–6) × (1.5–)2(–3) µm, straight or slightly curved, whitish in mass, sometimes one end broad, the other narrow, some are uniformly narrow, hyaline, smooth, with granular content inside, usually biguttulate.

Culture characteristics — On Czapek dox agar (CDA) surface pale mouse grey to pale olivaceous grey; margins greyish sepia, margin regular, 13 mm diam (at 25, 30, 35 °C) after 3 d, colony floccose, felty, woolly. Reverse black to fuscous black in centre, margins greyish sepia. On potato carrot agar (PCA) surface mouse grey, margin greyish sepia, colony circular, aerial mycelia present in old cultures; margin regular, 13 mm diam (at 25, 30, 35 °C) after 3 d; reverse black to fuscous black, margin greyish sepia. On MEA surface mouse grey to dark mouse grey, margin greyish sepia, colony circular; colony border regular, 13 mm diam (25, 30, 35 °C) after 3 d; reverse black to fuscous, margin greyish sepia.

Typus. India, Maharashtra, Pune, on screen of a mobile phone, 2013, *R.R. Kurli* (holotype MCC H1001, culture ex-type MCC 1159 = CBS 139022; ITS sequence GenBank KM516291, LSU sequence GenBank KM516290, SSU sequence KR260987, alignments in TreeBASE S17500, S17501, MycoBank MB812301).

Notes — The genus *Pyrenochaeta* is characterised by having species with distinct elongated, septate, acropleurogenous conidiophores produced in pycnidia usually covered by long setae, 200 µm or more, whereas *Pyrenochaetopsis* is characterised by setose pycnidia similar to those in *Pyrenochaeta*, but the conidiogenesis is usually phoma-like (De Gruyter et al. 2010). This isolate forms septate setae which are 200 µm long, septate, elongate acropleurogenous conidiophores and therefore belong to genus *Pyrenochaeta*. Phylogenetically, *Pyrenochaeta telephoni* is close to *P. acicola* and *P. inflorescentiae* (*Cucurbitariaceae*) along with other members of *Pyrenochaeta* and *Pyrenochaetopsis*.



Phylogenetic tree of *Pyrenochaeta* species constructed using Neighbour-Joining (NJ) analysis of ITS region sequences. Bootstrap support values ≥ 65 % are given above branches. The phylogenetic position of *Pyrenochaeta telephoni* is indicated in **bold**.

Colour illustrations. Mobile phone with fungus on screen. Upper row: globose pycnidium of *Pyrenochaeta telephoni* with long setae around ostiole, setae, pycnidial wall, chlamydospore, conidia. Bottom row: font view of fungal colonies on CzD agar, pycnidium with setae, mycelium and hyphae with chlamydospore-like cells. Scale bars = 50 µm (conidiomata), all others = 10 µm.

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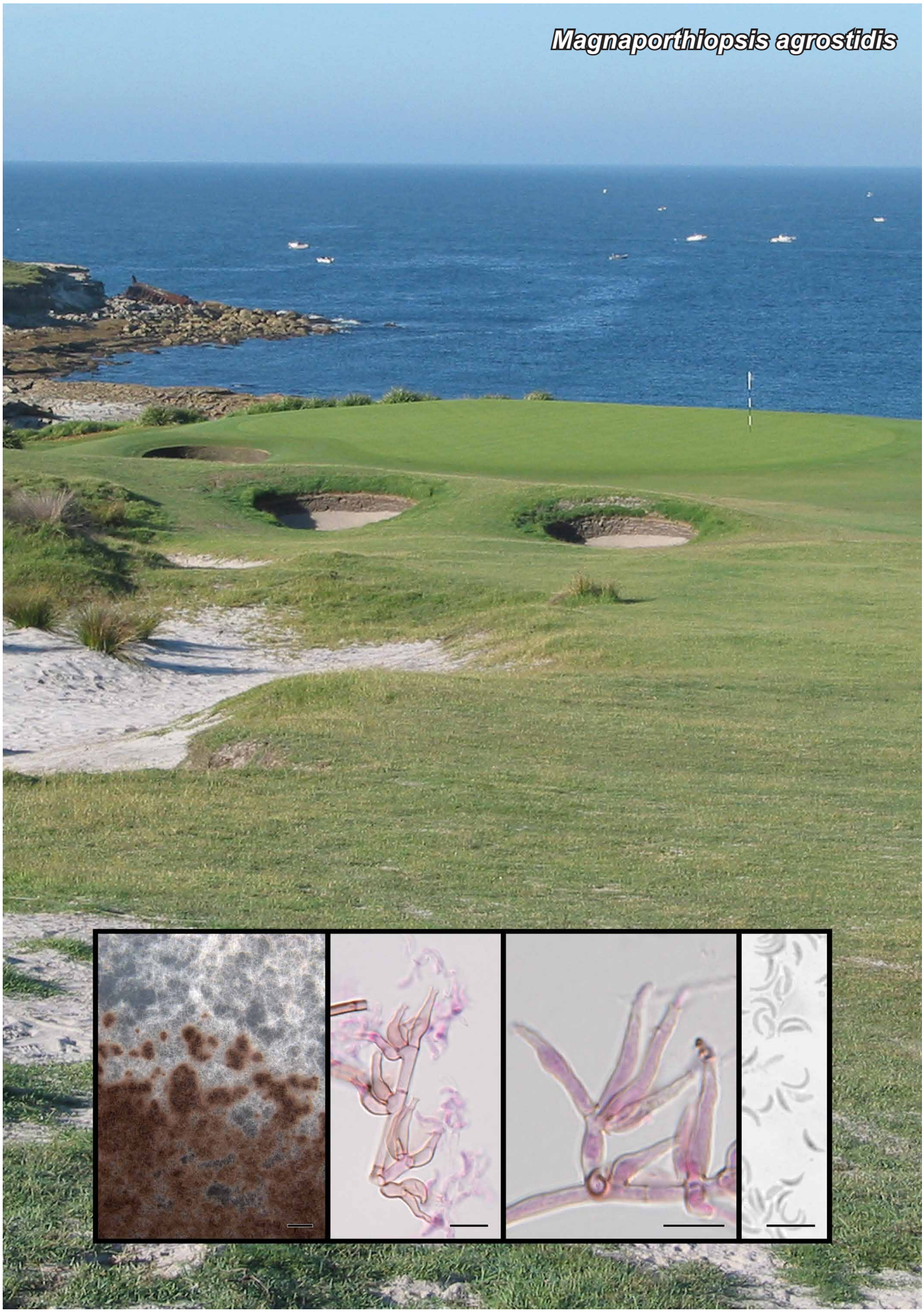

Magnaporthiopsis agrostidis

Fungal Planet 398 – 1 December 2015

Magnaporthiopsis agrostidis P. Wong, Khemmuk & R.G. Shivas, *sp. nov.*

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

Classification — *Magnaporthaceae*, *Magnaporthales*, *Sordariomycetes*.

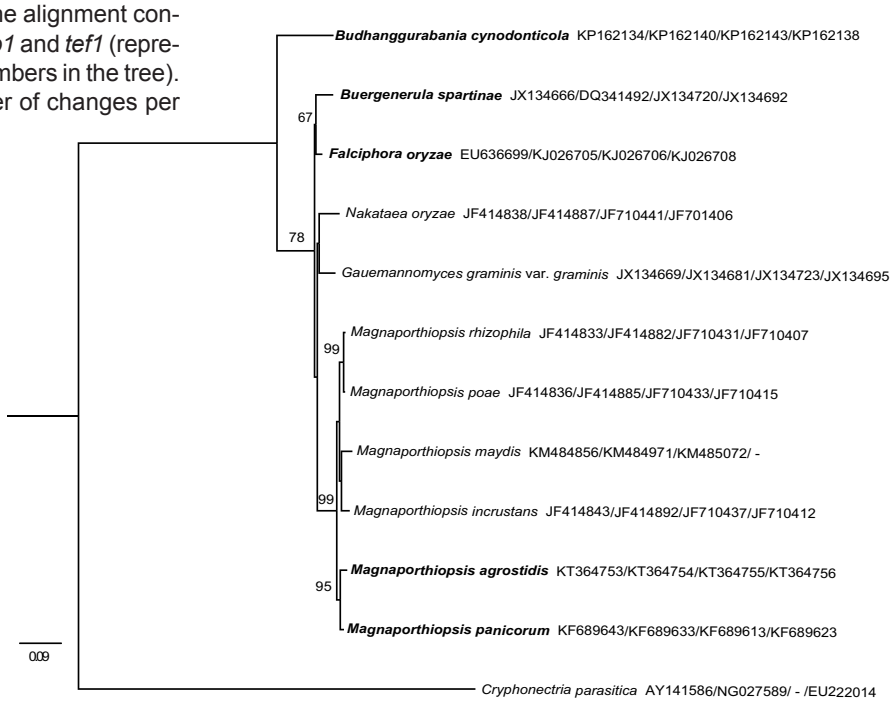
Mycelium hyaline, becoming dark grey to dark brown with age; hyphae septate, branched, smooth, 1–4 µm wide, forming mycelial strands and fans at the margins. *Conidiophores* brown, single and terminal or penicillate and integrated. *Conidiogenous cells* brown or slightly pigmented, phialidic, cylindrical to lageniform, 5–20 × 1.5–3 µm, tapering to a conspicuous flared collarette c. 3 µm high × 1.5 µm wide. *Conidia* hyaline, aseptate, smooth, filiform, rounded at the apex and narrowed towards the base, curved to lunate, 4–6 × 1 µm, aggregated in slimy heads. *Ascomata* not observed in culture.

Culture characteristics — On PDA, colonies reaching 7.5 cm diam after 1 wk at 25 °C in the dark; moderately abundant grey aerial mycelium, becoming olivaceous brown with age and forming dark grey to dark brown crust-like mycelial aggregations on the agar surface in older cultures (> 4 wk); reverse dark grey to olivaceous brown, paler at the margin. The crust-like mycelial aggregations were formed more commonly on quarter-strength PDA amended with novobiocin (100 mg/L).

Typus. Australia, New South Wales, La Perouse, New South Wales Golf Club, from rotted roots of *Agrostis stolonifera*, May 2013, *P.T.W. Wong PW13010* (holotype BRIP 59300, includes ex-type culture; ITS sequence GenBank KT364753, LSU sequence GenBank KT364754, *rpb1* sequence GenBank KT364755, *tef1* sequence GenBank KT364756, MycoBank MB814222).

Notes — Phylogenetic analysis placed *Magnaporthiopsis agrostidis* in a monophyletic clade that includes the type species of the genus, *M. poae* (*Magnaporthaceae*). It is the sixth known species of *Magnaporthiopsis* (Luo & Zhang 2013, Luo et al. 2014). All species of *Magnaporthiopsis* are root-inhabiting fungi or root-infecting pathogens of grasses. *Magnaporthiopsis agrostidis* produces harpophora-like conidia (Gams 2000), which differ from other *Magnaporthiopsis* species by being smaller, filiform, and more curved. They have not been shown to germinate on PDA and may have a role as spermatia in sexual reproduction (Wong & Walker 1975). *Magnaporthiopsis agrostidis* produces superficial crust-like mycelial aggregations that become dark grey to dark brown in older cultures, similar to those of *M. incrustans* (Landschoot & Jackson 1989). *Magnaporthiopsis agrostidis* was isolated from diseased roots of *Agrostis stolonifera* from a golf green with symptoms of a patch disease. It has been shown to be pathogenic to *A. stolonifera* in glasshouse pathogenicity tests.

The multilocus phylogenetic tree was inferred using the maximum likelihood estimation method, as implemented with RAxML v. 7.2.6 using the GTRGAMMA model of evolution. Bootstrap support values are indicated at the nodes. The alignment consisted of four partial loci, namely ITS, LSU, *rpb1* and *tef1* (represented by respective GenBank accession numbers in the tree). The scale bar indicates the expected number of changes per site. Ex-type species are in **bold**.



Colour illustrations. Australia, New South Wales, La Perouse, New South Wales Golf Club; crust-like mycelial aggregations, conidiophores and conidia from ex-holotype culture. Scale bars = 1 mm (left), 10 µm (others).

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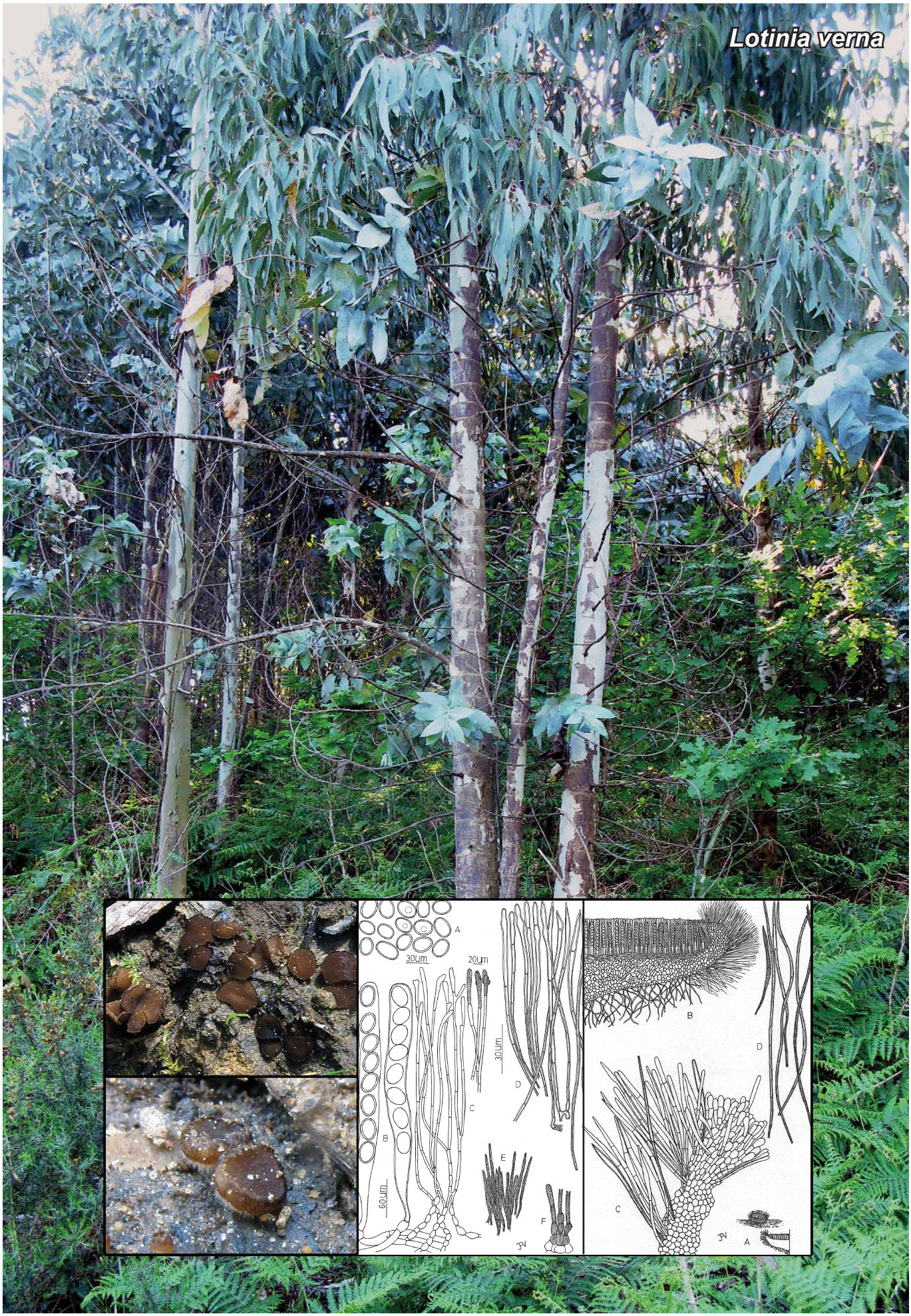
Lotinia verna
A
30µm
20µm
B
C
D
30µm
60µm
E
F
JV
B
D
C
JV
A

Fungal Planet 399 – 1 December 2015

Lotinia Pérez-Butrón, Fern.-Vic. & P. Alvarado, *gen. nov.*

Etymology. The name honours the basque mycologist Dr Roberto Lotina Benguria (1912–1997).

Classification — *Pyronemataceae, Pezizales, Pezizomycetes.*

Ascomata discoidal, brownish, with the external surface covered with flexuose hairs from the base to the top. *Ectal excipulum* arranged as a *textura prismatica*. *Asci* 8-spored, operculate, not amyloid. *Ascospores* smooth, not guttulated, globose to ellipsoid.

Type species. Lotinia verna.
MycoBank MB814887.

Lotinia verna Pérez-Butrón, Fern.-Vic. & P. Alvarado, *sp. nov.*

Etymology. The epithet *verna*, from Latin *vernus* (spring), refers to the fact that this species fruits exclusively in Spring.

Ascoma 2–5 mm diam, sessile, isolated or gregarious over a narrow base, discoidal, flattened, pulvinulate, sometimes with a wavy or elevated margin because of compression. *Hymenium* brownish or ochre, granulose due to the outstanding asci. Soft flesh consistency. Outer surface paler and covered with brownish hairs. Hymenium section measuring 480 µm diam. *Hairs* originating in the surface, deriving from external cells of the excipulum, brownish in colour although pigments dilute at the apex, flexuose, multiseptate, fasciculate, forming dense and compact mats of long filiform hairs from the bottom of the apothecium, becoming compressed or even incrusted at the top, where they can exceed the apothecium's margin, (250–)328–510(–528) × 4–6 µm, with a cell wall 0.8–1(–1.6) µm diam. There are shorter hairs near the margin, usually fusiform and wider, 5–8.4 µm diam, and cell wall measuring 1–2(–2.5) µm diam, with thin septa. Hairs can have an obtuse or acute apex, and become narrower at the base. In rare cases they can be bifid. *Ascospores* measuring 20–27(–30) × (15–)17–20(–22) µm (av. 24.7 × 18.1 µm); Q = 1.36 (measures taken in distilled water from 50 spores from holotype), smooth, hyaline, globose to ellipsoid, frequently with a diffuse central core up to 6 µm diam. They have thick walls about 1.8 µm diam, but sometimes reaching up to 3 µm diam when immature. *Asci* eight-spored, uniseriate, cylindrical, narrowed at the base, operculate, not amyloid, pleurorhynchous, measuring 240–460 × 19–32 µm. *Paraphyses* single, ramified, abundant, hyaline, multiseptate, measuring 4 µm diam in the middle portion, becoming inflated at the apex, where they can reach up to 10 µm diam. Externally, these are covered by a brownish encrusting amorphous matter at the apex. *Hyphal hairs* numerous at the base of the ascomata. *Subhymenium* slightly or not differentiated at all from medullar excipulum. *Medullar excipulum* arranged as *textura intricata*, measuring about 175 µm diam, formed by hyaline hyphae, 12–20 µm diam. *Ectal excipulum* measuring 465 µm thick, with cells 14–20 µm diam at the base appearing as a *textura globosa-angularis*, and prismatic cells 6–18 µm diam at the apex.

Habitat & Distribution — So far known only from *Eucalyptus nitens* and *Pinus radiata* plantations in Basque Country (Spain).

Typus. Spain, Bizkaia, Muskiz, Mount Posadero, in muddy soil, under moss, with *Eucalyptus nitens* and *Pinus radiata*, 4 Apr. 2003, *J.L. Pérez-Butrón* (holotype Herbarium Sociedad Ciencias Naturales Sestao, SESTAO 2003040401; ITS sequence GenBank KP195730, LSU sequence GenBank KP195729, *tef1* sequence GenBank KP195727, MycoBank MB814903).

Additional specimens examined. Spain, Bizkaia, Muskiz, Mount Posadero, UTM 30TVN8896, 310 m, growing isolated or in dense groups in muddy soil of a forest track, with presence of *Eucalyptus nitens* and *Pinus radiata*, 15 Mar. 2001, *J.L. Pérez-Butrón & J. Fernández-Vicente*, SESTAO 2001031501; ibid., 23 Apr. 2002, *J.L. Pérez-Butrón & J. Fernández-Vicente*, SESTAO 2002042301; ibid., 30 May 2002, *J.L. Pérez-Butrón*, SESTAO 2002053001; ibid., 11 June 2002, *J.L. Pérez-Butrón*, SESTAO 2002061101 (LSU sequence GenBank KP195728, *tef1* sequence GenBank KP195726); ibid., 20 Mar. 2003, *J.L. Pérez-Butrón*, SESTAO 2003032001.

Notes — *Lotinia verna* is characterised by the *textura prismatica* and *globosa-angularis* of the ectal excipulum, the external hairs, thin and flexuose, growing in dense mats from the base to the top of the apothecium, a really uncommon feature, hairs obtuse or acute, becoming narrower at the base, and exceptionally bifid, paraphyses presenting an encrusting matter at their top, and fruiting season is spring. Overall morphology can recall many genera in the *Pyronemataceae*, but some of them such as *Cheilymenia*, *Scutellinia*, *Parascutellinia* or *Kotlabaea*, present carotenoid pigments, which are absent in *Lotinia*. Genus *Humaria* has cupuliform ascomata much larger in size, and biguttulate verrucose spores. *Trichophaea* has rigid hairs emerging from the base, and spores are guttulated (Kanouse 1958, Calonge et al. 1988, Bronckers 2003). *Trichophaeopsis* (Korf & Erb 1972, Gamundi 1973) has an ectal excipulum formed by vertical cells arranged in perpendicular rows as a *textura prismatica*, flexuose hairs becoming thin and bifurcating at the base, spores not guttulate, and sometimes containing warts as in *T. latispora* (Moravec 1979). Despite the similarities with *Lotinia*, molecular data separates both lineages. *Paratrichophaea* has white-coloured ascomata, rigid hairs with often radicant base, epidermic texture in the excipulum and subfusiform spores (Trigaux 1985, Bronckers 2002a, b, 2003). *Tricharina* has cupuliform apothecia, subfusiform, depressed, refringent, ascospores with minute guttules at the poles, becoming yellowish with cotton blue, and paraphyses and spore nuclei react with carmine acetic acid (Yang & Korf 1985, Dougoud 2002). These reactions are not observed in *Lotinia*.

Colour illustrations. Ascomata in different developmental stages, ascocarps, ascocarp section, excipulum partial section, hairs, ascospores, asci, paraphyses, external hairs, margin hairs, base of hairs. Scale bars = 60 and 30 µm.

Bayesian consensus tree (LSU-*rpb2*-*tef1*) depicting the phylogenetic position of the new genus *Lotinia* (for phylogenetic tree, see MycoBank).

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