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RESEARCH ARTICLE

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Key words

ITS nrDNA barcodes
LSU
new taxa
systematics

Abstract Novel species of fungi described in this study include those from various countries as follows: **Australia**, *Chaetopsina eucalypti* on *Eucalyptus* leaf litter, *Colletotrichum cobbittiense* from *Cordyline stricta* × *C. australis* hybrid, *Cyanodermella banksiae* on *Banksia ericifolia* subsp. *macrantha, Discosia macrozamiae* on *Macrozamia miquelii, Elsinoë banksiigena* on *Banksia marginata, Elsinoë elaeocarpi* on *Elaeocarpus* sp., *Elsinoë leucopogonis* on *Leucopogon* sp., *Helminthosporium livistonae* on *Livistona australis*, *Idriellomyces eucalypti* (incl. *Idriellomyces* gen. nov.) on *Eucalyptus obliqua*, *Lareunionomyces eucalypti* on *Eucalyptus* sp., *Myrotheciomyces corymbiae* (incl. *Myrotheciomyces* gen. nov., *Myrotheciomycetaceae* fam. nov.), *Neolauriomyces eucalypti* (incl. *Neolauriomyces* gen. nov., *Neolauriomycetaceae* fam. nov.) on *Eucalyptus* sp., *Nullicamyces eucalypti* (incl. *Nullicamyces* gen. nov.) on *Eucalyptus* leaf litter, *Oidiodendron eucalypti* on *Eucalyptus maidenii*, *Paracladophialophora cyperacearum* (incl. *Paracladophialophoraceae* fam. nov.) and *Periconia cyperacearum* on leaves of *Cyperaceae*, *Porodiplodia livistonae* (incl. *Porodiplodia* gen. nov., *Porodiplodiaceae* fam. nov.) on *Livistona australis*, *Sporidesmium melaleucae* (incl. *Sporidesmiales* ord. nov.) on *Melaleuca* sp., *Teratosphaeria sieberi* on *Eucalyptus sieberi*, *Thecaphora australiensis* in capsules of a variant of *Oxalis exilis.* **Brazil**, *Aspergillus serratalhadensis* from soil, *Diaporthe pseudoinconspicua* from *Poincianella pyramidalis*, *Fomitiporella pertenuis* on dead wood, *Geastrum magnosporum* on soil, *Marquesius aquaticus* (incl. *Marquesius* gen. nov.) from submerged decaying twig and leaves of unidentified plant, *Mastigosporella pigmentata* from leaves of *Qualea parviflorae*, *Mucor souzae* from soil, *Mycocalia aquaphila* on decaying wood from tidal detritus, *Preussia citrullina* as endophyte from leaves of *Citrullus lanatus*, *Queiroziella brasiliensis* (incl. *Queiroziella* gen. nov.) as epiphytic yeast on leaves of *Portea leptantha*, *Quixadomyces cearensis* (incl. *Quixadomyces* gen. nov.) on decaying bark, *Xylophallus clavatus* on rotten wood. **Canada**, *Didymella cari* on *Carum carvi* and *Coriandrum sativum.* **Chile**, *Araucasphaeria foliorum* (incl. *Araucasphaeria* gen. nov.) on *Araucaria araucana*, *Aspergillus tumidus* from soil, *Lomentospora valparaisensis* from soil. **Colombia**, *Corynespora pseudocassiicola* on *Byrsonima* sp., *Eucalyptostroma eucalyptorum* on *Eucalyptus pellita*, *Neometulocladosporiella eucalypti* (incl. *Neometulocladosporiella* gen. nov.) on *Eucalyptus grandis* × *urophylla*, *Tracylla eucalypti* (incl. *Tracyllaceae* fam. nov., *Tracyllalales* ord. nov.) on *Eucalyptus urophylla.* **Cyprus**, *Gyromitra anthracobia* (incl. *Gyromitra* subg. *Pseudoverpa*) on burned soil. **Czech Republic**, *Lecanicillium restrictum* from the surface of the wooden barrel, *Lecanicillium testudineum* from scales of *Trachemys scripta elegans.* **Ecuador**, *Entoloma yanacolor* and *Saproamanita quitensis* on soil. **France**, *Lentithecium carbonneanum* from submerged decorticated *Populus* branch. **Hungary**, *Pleuromyces hungaricus* (incl. *Pleuromyces* gen. nov.) from a large *Fagus sylvatica* log. **Iran**, *Zymoseptoria crescenta* on *Aegilops triuncialis.* **Malaysia**, *Ochroconis musicola* on *Musa* sp. **Mexico**, *Cladosporium michoacanense* from soil. **New Zealand**, *Acrodontium metrosideri* on *Metrosideros excelsa, Polynema podocarpi* on *Podocarpus totara, Pseudoarthrographis phlogis* (incl. *Pseudoarthrographis* gen. nov.) on *Phlox subulata.* **Nigeria**, *Coprinopsis afrocinerea* on soil. **Pakistan**, *Russula mansehraensis* on soil under *Pinus roxburghii.* **Russia**, *Baoran-*

Abstract (cont.)

gia alexandri on soil in deciduous forests with *Quercus mongolica.* **South Africa**, *Didymocyrtis brachylaenae* on *Brachylaena discolor.* **Spain**, *Alfaria dactylis* from fruit of *Phoenix dactylifera, Dothiora infuscans* from a blackened wall, *Exophiala nidicola* from the nest of an unidentified bird, *Matsushimaea monilioides* from soil, *Terfezia morenoi* on soil. **United Arab Emirates**, *Tirmania honrubiae* on soil. **USA**, *Arxotrichum wyomingense* (incl. *Arxotrichum* gen. nov.) from soil, *Hongkongmyces snookiorum* from submerged detritus from a fresh water fen, *Leratiomyces tesquorum* from soil, *Talaromyces tabacinus* on leaves of *Nicotiana tabacum.* **Vietnam**, *Afroboletus vietnamensis* on soil in an evergreen tropical forest, *Colletotrichum condaoense* from *Ipomoea pes-caprae.* Morphological and culture characteristics along with DNA barcodes are provided.

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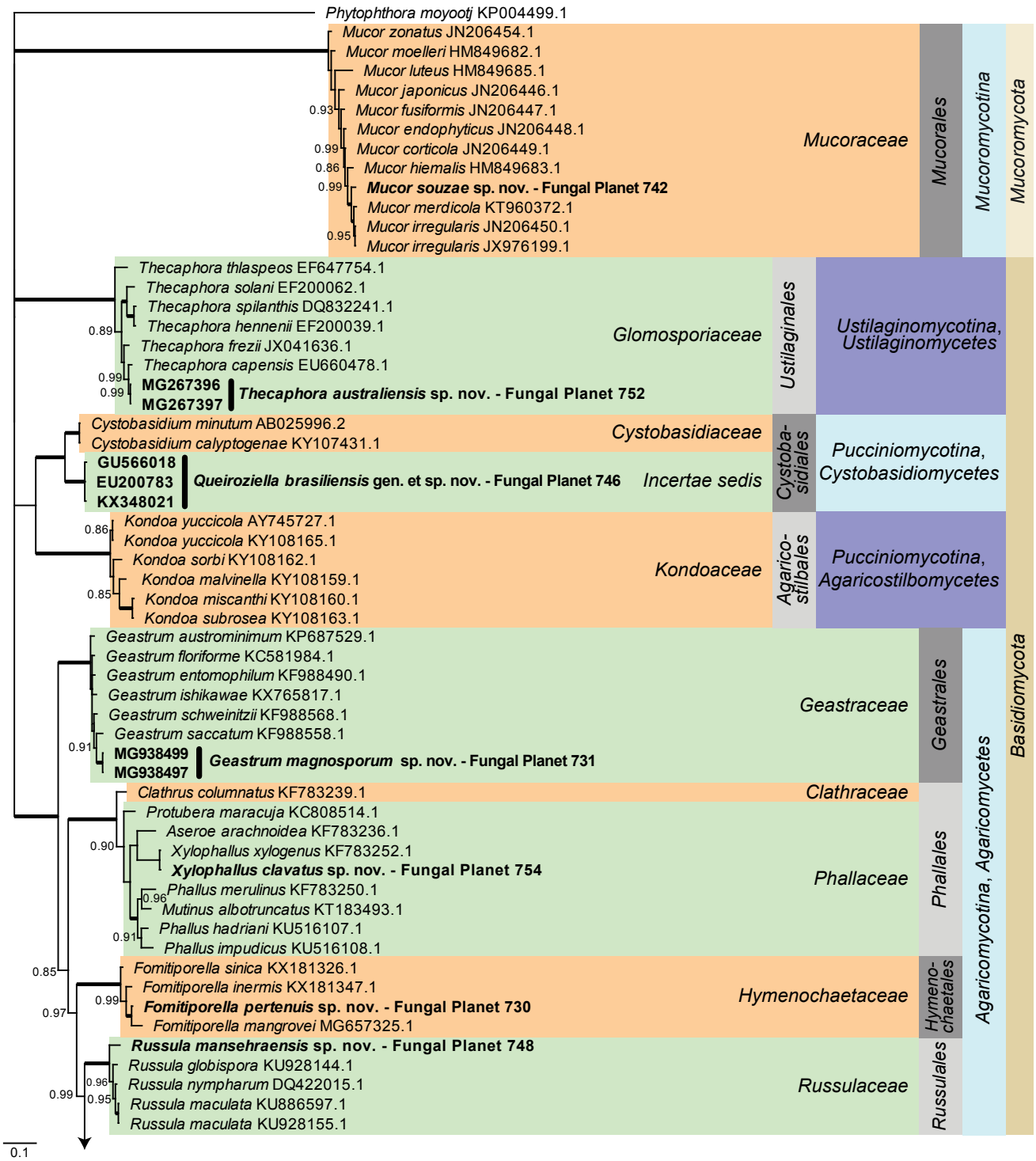
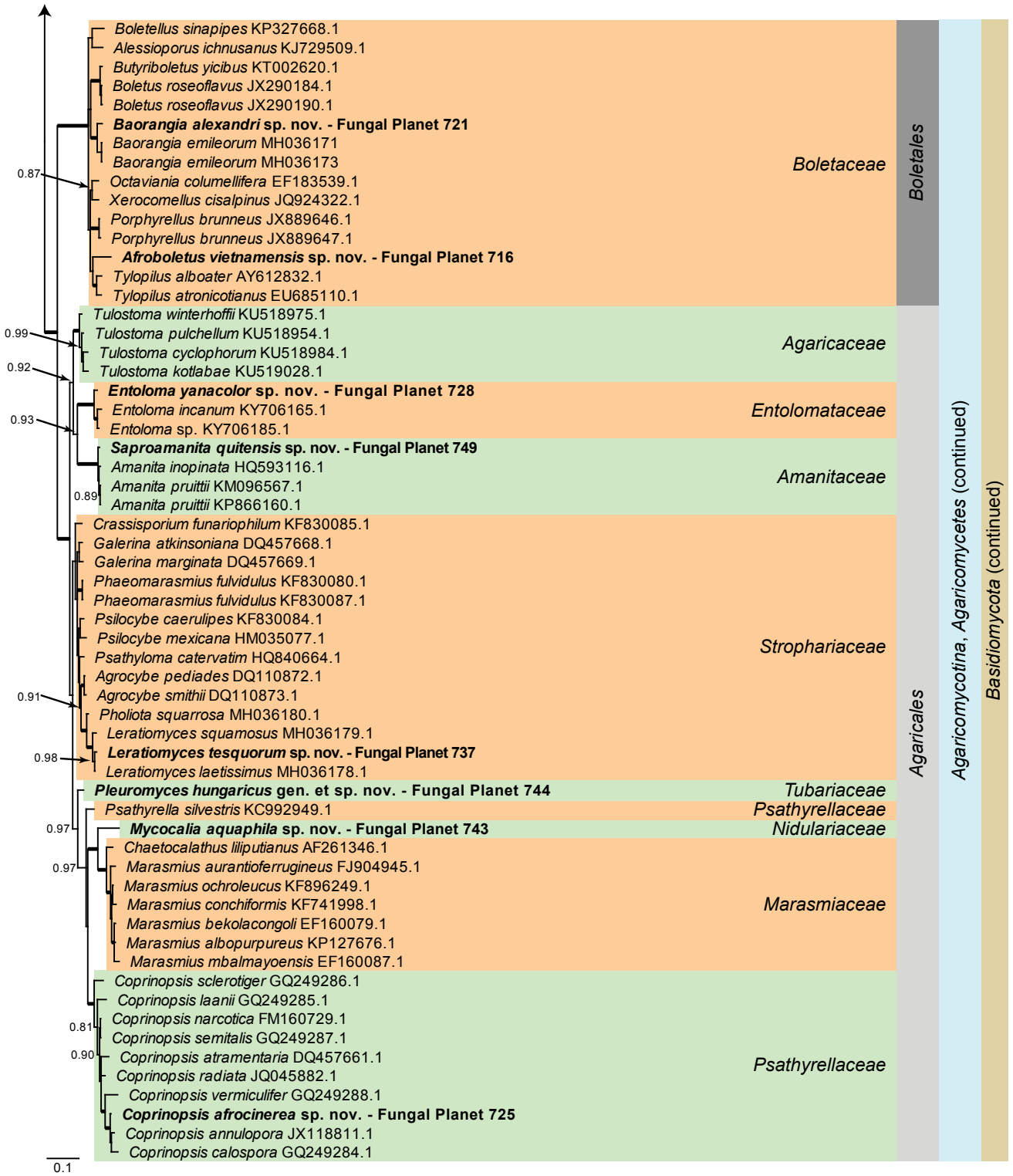
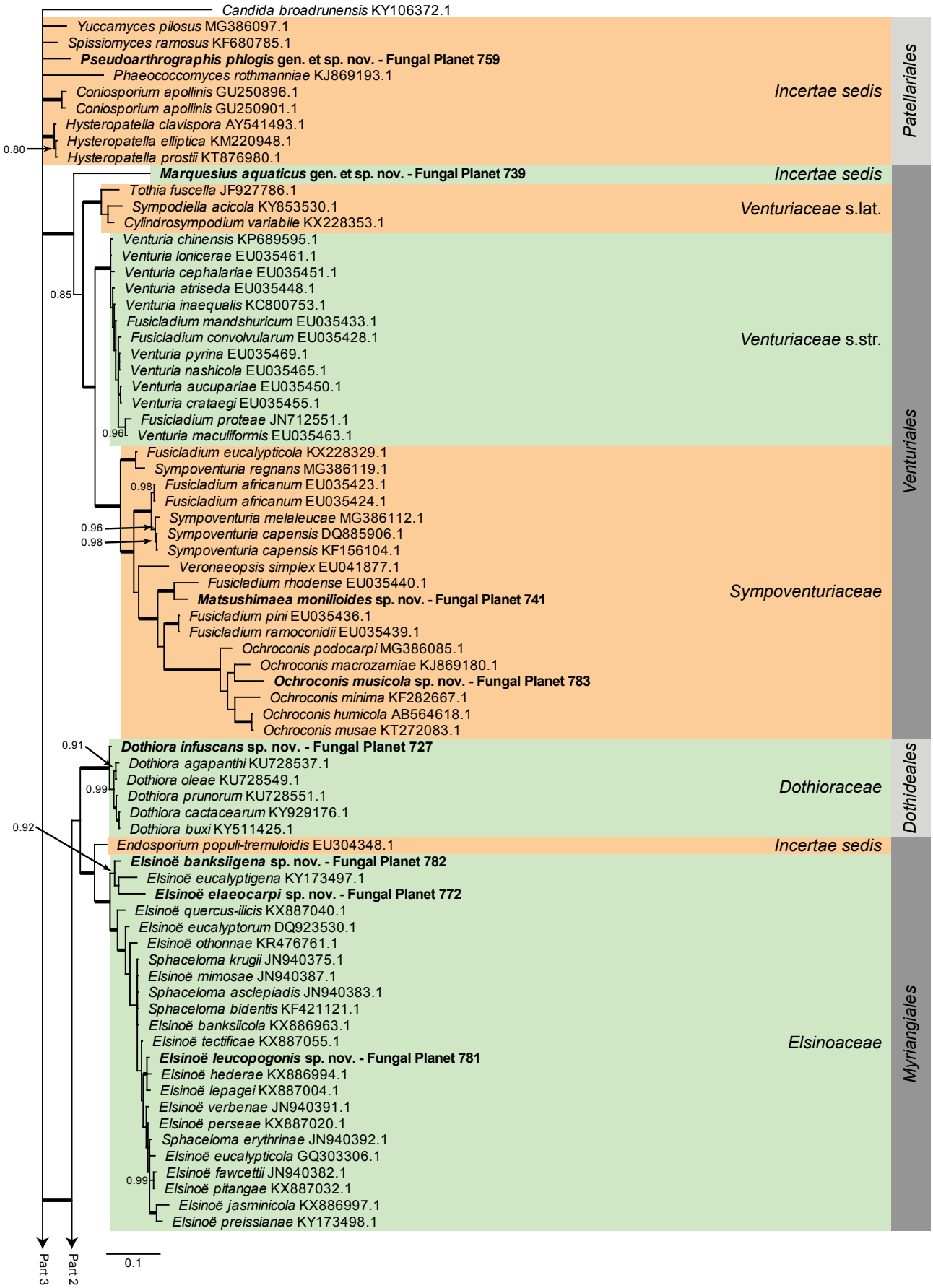


Overview *Mucoromycotina* and *Basidiomycota* phylogeny

Consensus phylogram (50 % majority rule) of 57752 trees resulting from a Bayesian analysis of the LSU sequence alignment (118 taxa including outgroup; 862 aligned positions; 551 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families, orders, classes, subdivisions and phyla are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Phytophthora moyootj* (GenBank KP004499.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID S22745).

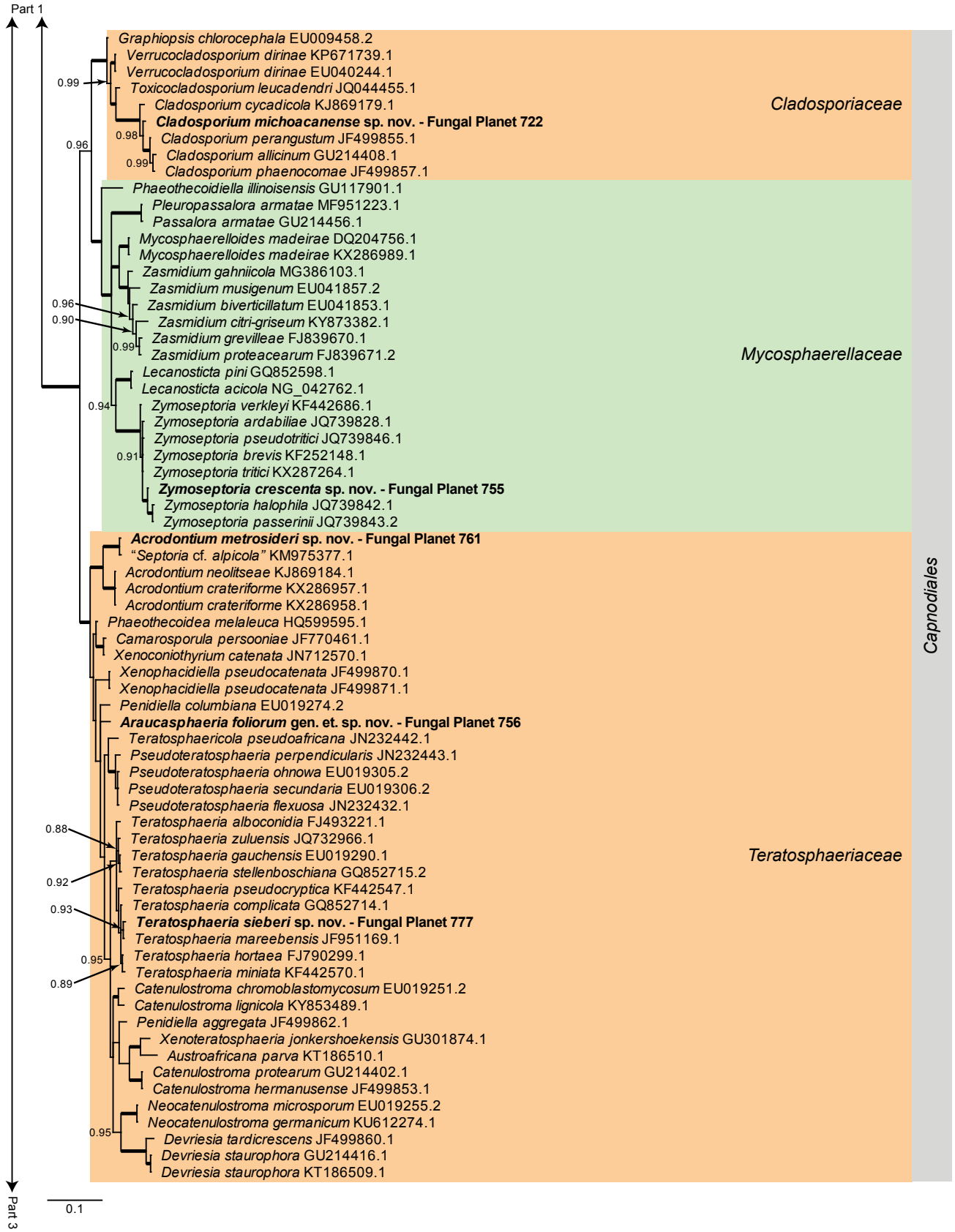


Overview *Mucoromycotina* and *Basidiomycota* phylogeny (cont.)

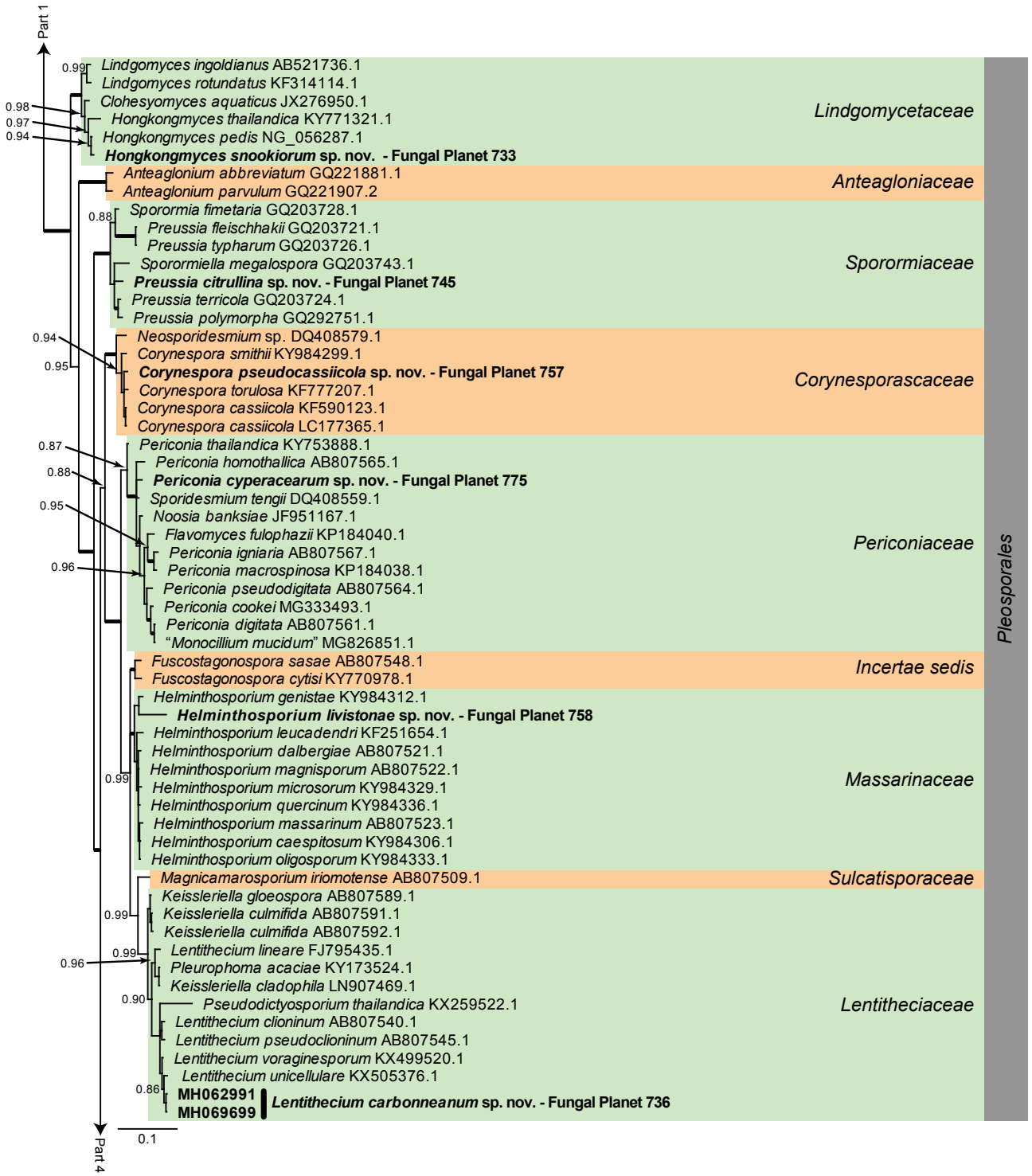


Overview *Dothideomycetes* phylogeny – part 1

Consensus phylogram (50 % majority rule) of 23402 trees resulting from a Bayesian analysis of the LSU sequence alignment (255 taxa including outgroup; 805 aligned positions; 450 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Candida broadrunensis* (GenBank KY106372.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID S22745).

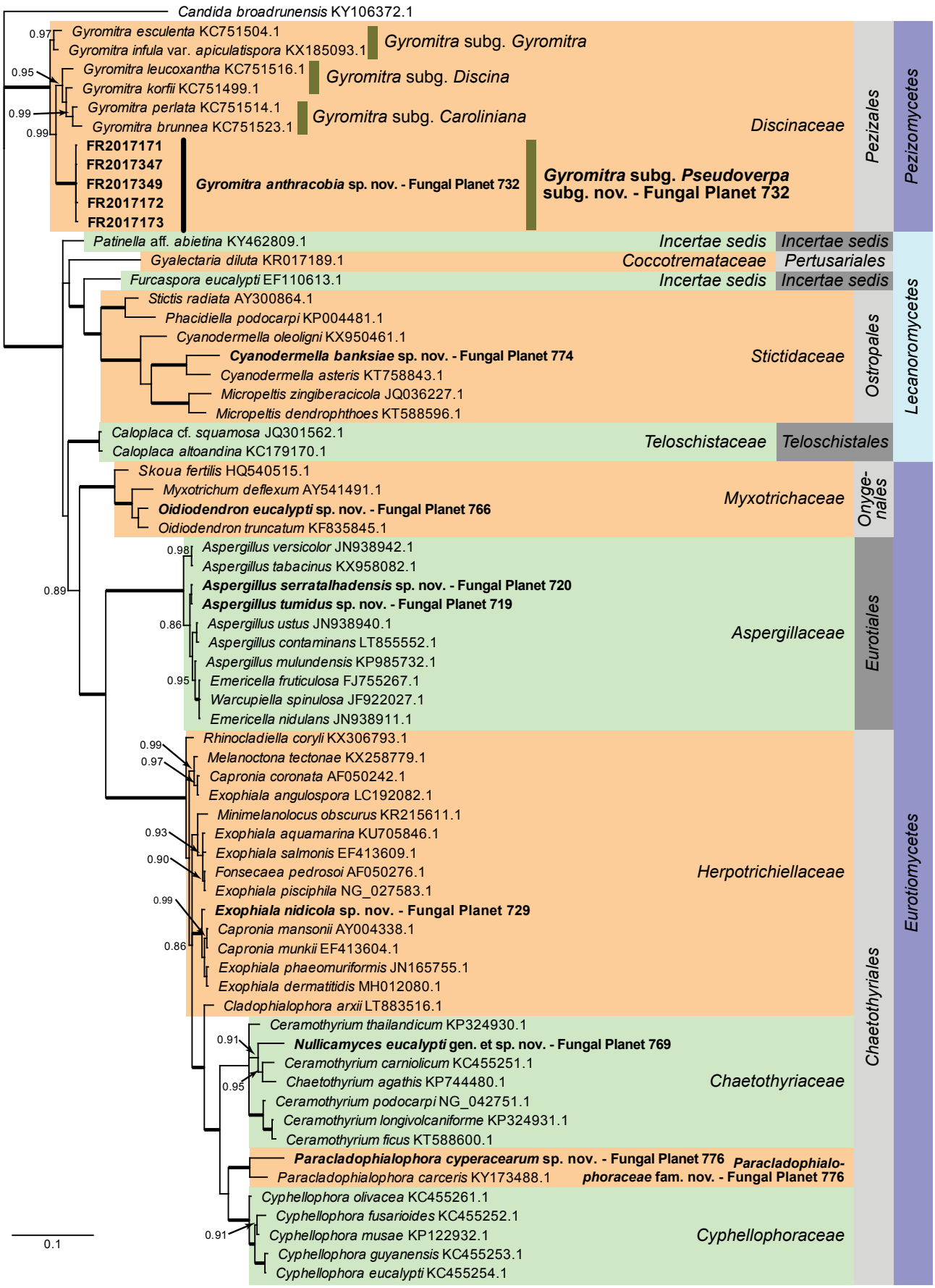


Overview *Dothideomycetes* phylogeny (cont.) – part 2



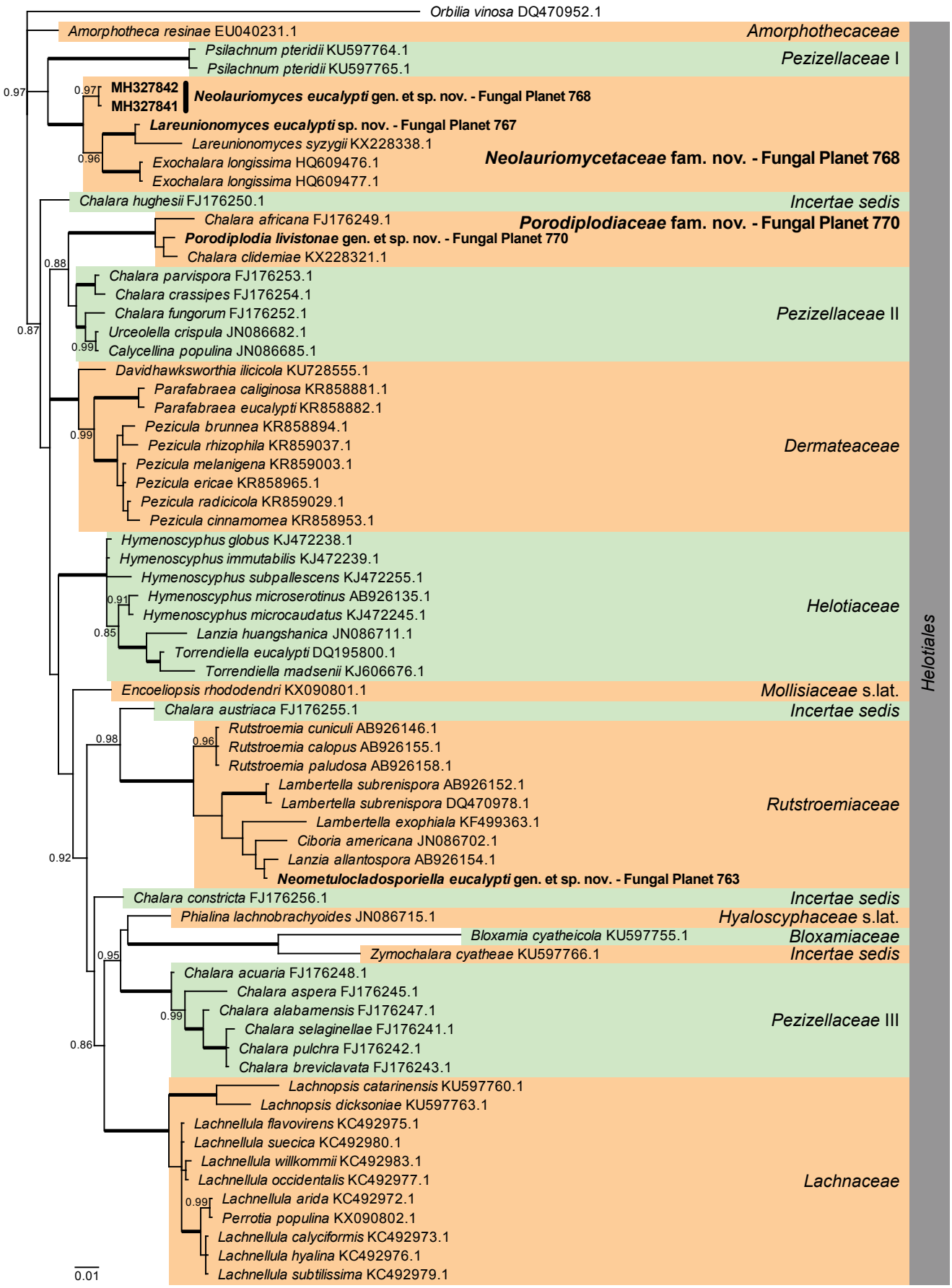
Overview *Dothideomycetes* phylogeny (cont.) – part 3

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



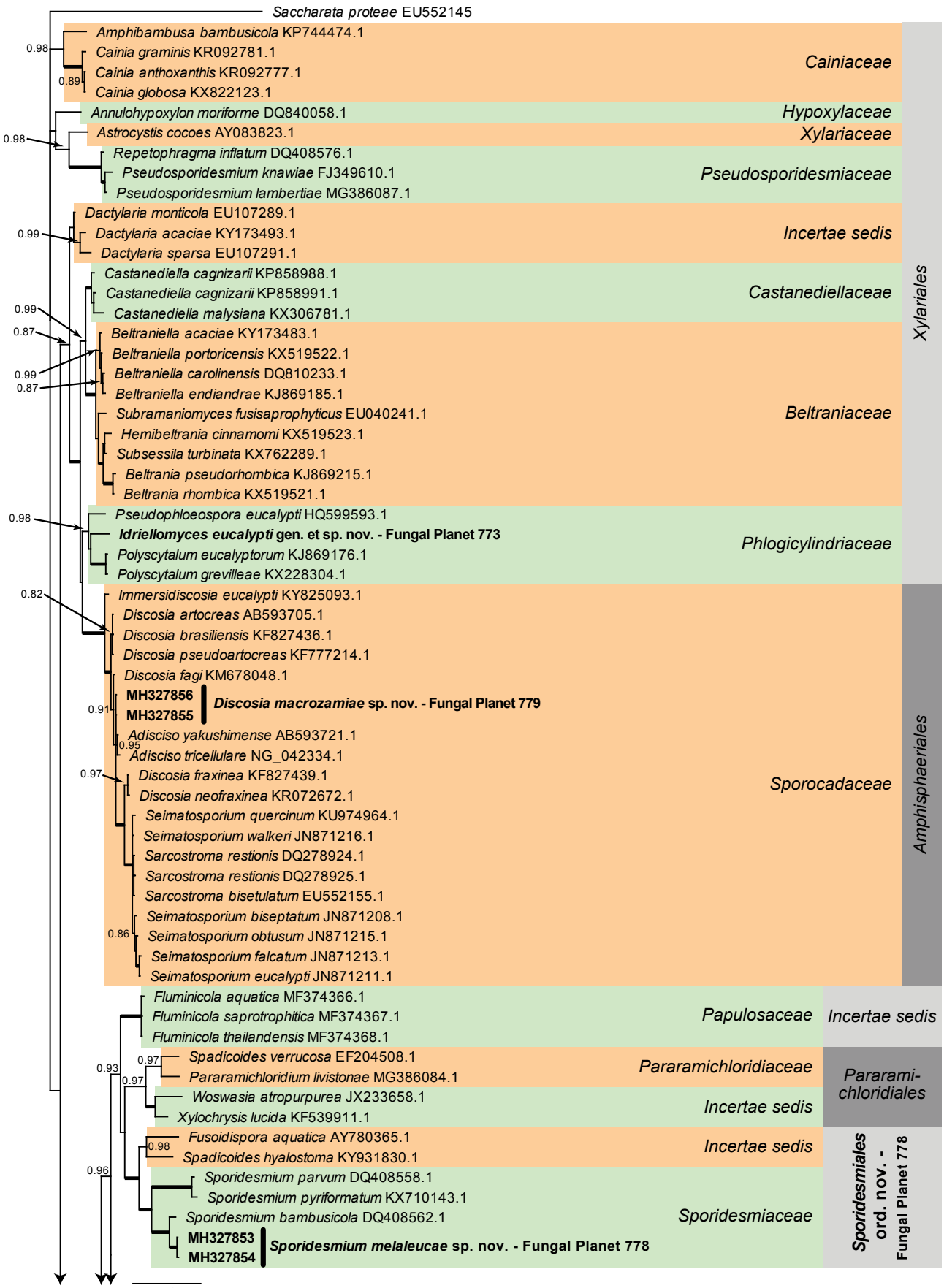
Overview *Pezizomycetes*, *Lecanoromycetes* and *Eurotiomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 6602 trees resulting from a Bayesian analysis of the LSU sequence alignment (67 taxa including outgroup; 805 aligned positions; 380 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families, orders and classes are indicated with coloured blocks to the right of the tree. GenBank accession or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Candida broadrunensis* (GenBank KY106372.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID S22745).



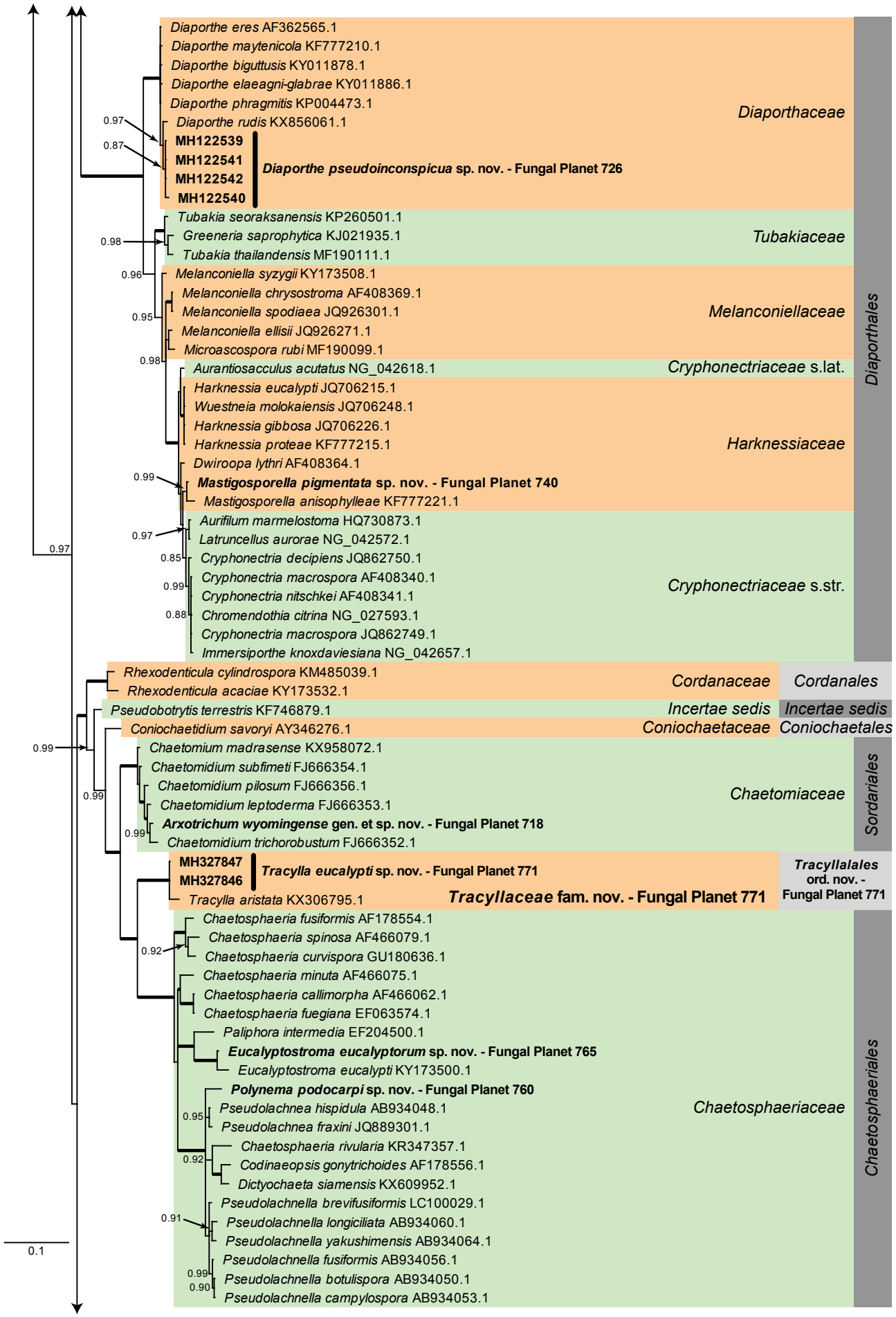
Overview *Leotiomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 18 152 trees resulting from a Bayesian analysis of the LSU sequence alignment (68 taxa including outgroup; 781 aligned positions; 227 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Orbilia vinosa* (GenBank DQ470952.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID S22745).

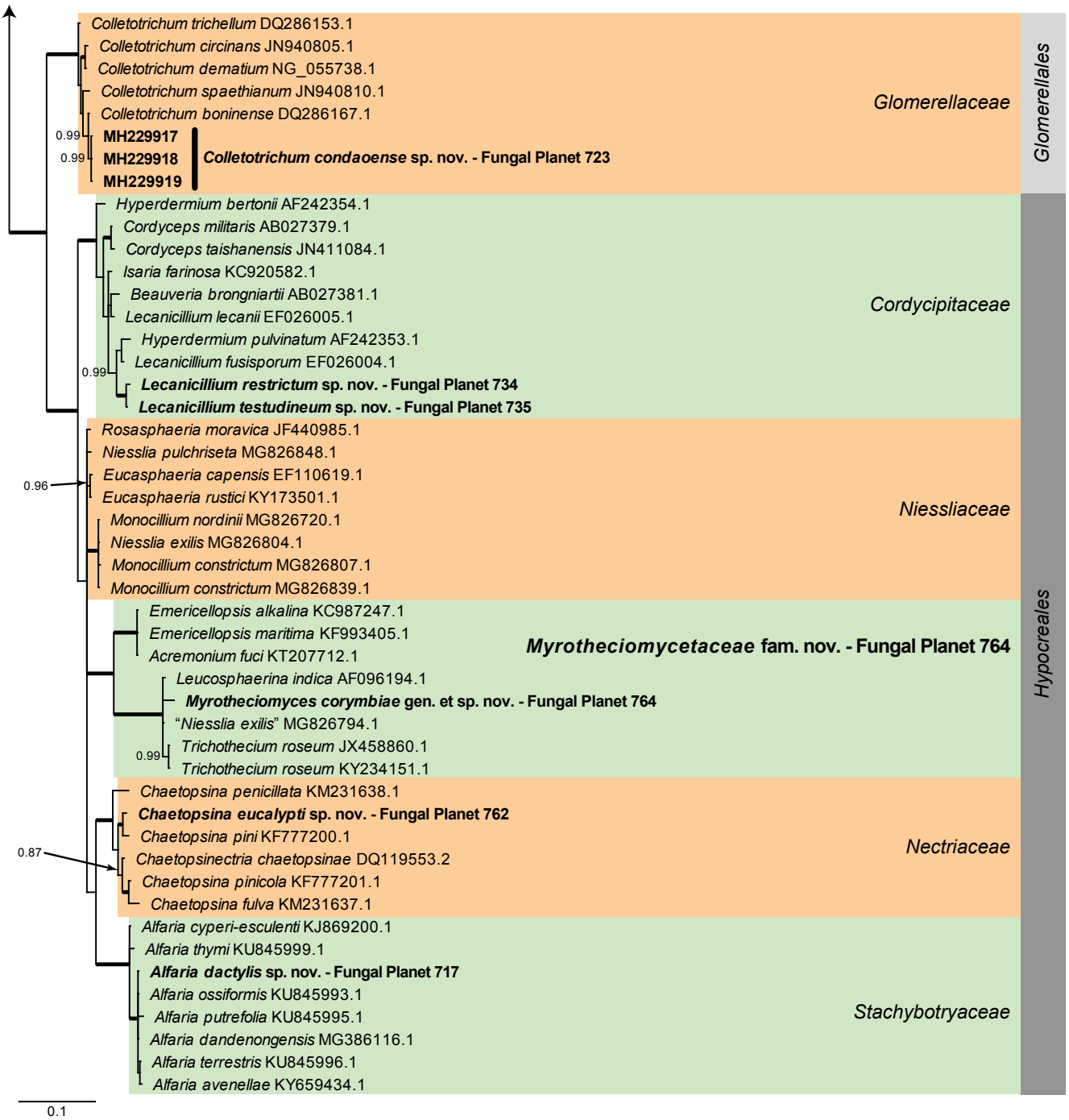


Overview *Sordariomycetes* phylogeny – part 1

Consensus phylogram (50 % majority rule) of 115 202 trees resulting from a Bayesian analysis of the LSU sequence alignment (179 taxa including outgroup; 785 aligned positions; 340 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Saccharata proteae* (GenBank EU552145.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID S22745).



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



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


Afroboletus vietnamensis

Fungal Planet 716 – 13 July 2018

Afroboletus vietnamensis T.H.G. Pham, A.V. Alexandrova, O.V. Morozova, *sp. nov.*

Etymology. The epithet refers to the country Vietnam where the species was collected.

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

Basidiomata medium large sized, boletoid. *Pileus* 30–80 mm diam, initially hemispherical, becoming convex, greyish yellow (2B3–4, 2C3–4, Kornerup & Wanscher 1978), darker in the centre (2D3–4, 3D3–4), paler towards the margin (up to 2A2–3), surface dry, velutinous, tomentous or felted. *Hymenophore* adnate to shortly decurrent to the stipe, 6–8 mm thick, light yellow to greenish yellow (1A4–6), becoming greyish yellow (2B4–5, 3B5–6, 4B4–5); pores irregular, 1–2 mm diam. *Stipe* 60–90 × 10–20 mm, cylindrical or fusiform, often tapered towards the base, dry, deeply broadly alveolate-reticulate, pale yellow (2A3–4), staining pale orange near the base (5A3–5). *Context* pale yellow (2A2–4), staining in the stipe brownish red when bruised, with reddish spots in the stipe base. *Smell* weak, taste not reported. *Spores* (11–)12–12.5(–15) × (8–)8.5–9.5(–11) µm, Q = (1.2–)1.3–1.4(–1.5), dark brown, ellipsoid in outline: amygdaliform with 1–2 µm broad longitudinal wings, sometimes with outgrowths and crystals (SEM). *Basidia* 38–48 × 11–12 µm, 4-spored, narrowly clavate to clavate, clampless. *Cheilocystidia* 52–99 × 5–18 µm, fusoid to lageniform with more or less long neck, *pleurocystidia* similar. *Hymenophoral trama* regular, made up of long, thin, cylindrical hyphae, 70–250 × 4–6 µm. *Pileipellis* a trichoderm, made up of cylindrical hyphae, 5–9 µm wide, with brown intracellular and in some hyphae also incrusting pigment. *Dermatocystidia* of two types: simple lageniform, 37–52 × 8–10 µm, with intracellular light brown pigment, and complex, abundant in the central part, 18–80 × 6–10 µm, fusiform, lageniform, septate: basal part with light brown diffuse intracellular pigment and apical – with bluish black agglutinate intracellular and sometimes additionally incrusting pigment. *Stipitipellis* a hymeniderm of basidiolae-like clavate cells, 19–30 × 7–10 µm. *Caulocystidia* 68–130 × 11–16 µm, lageniform, sometimes septate. *Clamp connections* absent.

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

Typus. Vietnam, Dak Lak Province, Yok Don National Park, 40 km to the northwest of Buon Ma Thuot city, N12.941306° E107.788167°, h = 212 m, on soil in evergreen tropical forest on the top of the hill dominated by *Fagaceae*, *Euphorbiaceae*, *Sapindaceae*, *Ebenaceae* and *Meliaceae*, 13 May 2014, *A. Alexandrova* (holotype LE311973, ITS and LSU sequences GenBank MH087059 and MH087058, MycoBank MB824736).

Colour illustrations. Vietnam, Dak Lak Province, Yok Don National Park, type locality; spores; cheilocystidia; elements of pileipellis; dermatocystidium and caulocystidia; SEM photos of spores; basidioma *in situ*; longitudinal section of the stipe and basidiomata *in situ*. Scale bars = 1 cm (basidiomata), 10 µm (microstructures).

Additional material examined. Vietnam, Binh Phuoc Province, Bu Gia Map District, Bu Gia Map National Park, N12.204509° E107.204415°, h = 346 m, on soil in foothill polydominant tropical forest dominated by *Dipterocarpaceae*, *Lythraceae*, *Rubiaceae*, *Theaceae*, *Lauraceae* and *Arecaceae*, 3 May 2013, *A. Alexandrova*, LE311972, ITS sequence GenBank MH087060.

Notes — The genus *Afroboletus* has been described based on material from equatorial Africa (Pegler & Young 1981). It is characterised first of all by the dark brown ellipsoid spores with a complex eusporial ornamentation of 8–12 large, winged, longitudinal costae, intercostal ridging, and basal thickened rim. *Afroboletus vietnamensis* resembles *A. malaysianus,* which was invalidly described from the Peninsular Malaysia (Chan 2010). However, *A. vietnamensis* differs from *A. malaysianus* by the paler colour of the pileus, by lageniform cheilocystidia with narrow neck, and by the pileipellis structure with characteristic dermatocystidia containing three types of pigment – diffuse brown intracellular, agglutinated dark-blue intracellular and incrusting. Although *A. vietnamensis* does not cluster in the phylogenetic tree with representatives of any known boletoid genera, including African *Afroboletus*, we consider the introduction of a new genus as premature.

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Alfaria dactylis

Fungal Planet 717 – 13 July 2018

Alfaria dactylis Valenz.-Lopez, Cano, Guarro & Stchigel, *sp. nov.*

Etymology. From Latin *dactylus*, date, due to the nature of the substrate (date, the fruit of *Phoenix dactylifera*) from which the fungus was isolated.

Classification — *Stachybotryaceae*, *Hypocreales*, *Sordariomycetes*.

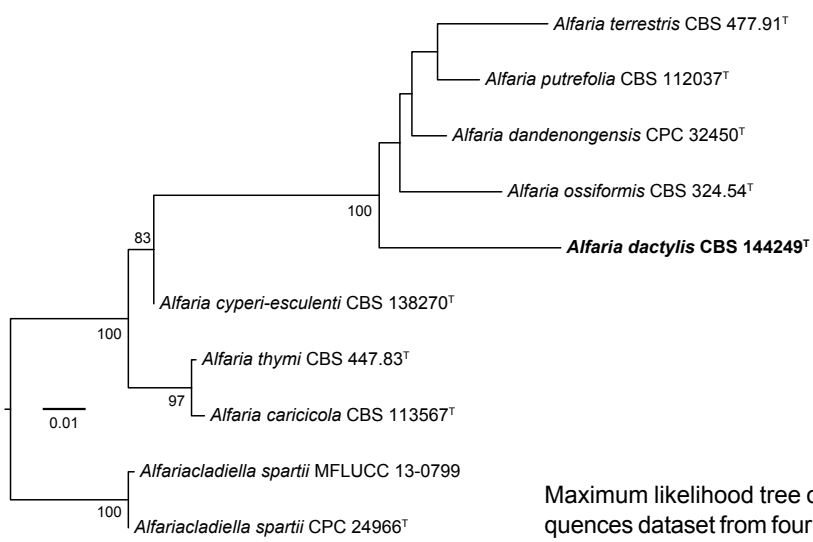
Hyphae hyaline to pale green, smooth- and thin- to thick-walled, septate, 2.5-5 µm wide. *Conidiomata* discrete, cupulate, stromatic, unilocular, non-ostiolate, superficial, solitary or confluent, greenish black, covered by setae, broadly lenticular, 177–275 × 133–242 µm, filled with black mass of slimy conidia; *conidioma wall* 10–27 µm broad, pseudoparenchymatous, of *textura globulosa* and *textura angularis*, composed of 2–4 layers of pale green to dark green, globose to flattened polygonal cells of 5–7.5 µm diam; *setae* greenish black, smooth- and thick-walled, multi-septate, unbranched, straight, narrowing towards the acute apices, 60–200 µm long, 4–8 µm wide at the base. *Conidiophores* densely aggregated, arising from the basal part of the locule, unbranched or branched at the base with 2–4 supporting cells, pale green, smooth-walled, up to 47 µm long, bearing 1–3 conidiogenous cells. *Conidiogenous cells* phialidic, cylindrical, elongate, hyaline to pale green, smooth-walled, 7–16 × 1.5–2.5 µm. *Conidia* hyaline to pale green, aseptate, smooth- and thin-walled, guttulate, lanceolate, 8.5–11.5 × 2–2.5 µm, with an obtuse apex and truncate at the base.

Culture characteristics — Colonies on OA reaching 19–21 mm diam after 7 d at 25 ± 1 °C, margin regular, flattened, with sparse aerial mycelium, surface white (M. 4A1); reverse white (M. 4A1). Colonies on MEA reaching 18–20 mm diam after 7 d at 25 ± 1 °C, margin regular, flattened, covered by dense white felty aerial mycelia, surface white (M. 4A1) to pale yellow (M. 4A3); reverse white (M. 4A1) to yellowish orange (M. 4A6). NaOH test negative.

Typus. Spain, Tarragona, from palm fruit of *Phoenix dactylifera* (*Arecaceae*), Feb. 2017, coll. *I.A. Iturrieta-González*, isol. *N. Valenzuela-Lopez* (holotype CBS H-23398, cultures ex-type FMR 16398 = CBS 144249, ITS, LSU, *tub2* and *tef*-1α sequences GenBank LT984556, LT984557, LT984555 and LT984553, MycoBank MB824149).

Notes — *Alfaria dactylis* is characterised by the production of large, lanceolate, pale green conidia and discrete, cupulate, stromatic conidiomata covered by abundant setae, being morphologically similar to *A. dandenongensis* but differing in aspect of their conidia (cylindrical, granular and verruculose in *A. dandenongensis*) and setae (smooth-walled in *A. dactylis* vs verruculose in *A. dandenongensis*) (Crous et al. 2017). Despite the fact of *A. dactylis* is phylogenetically closely related to *A. ossiformis*, it is morphologically distinct from the latter species by its setose conidiomata (lacking of setae in *A. ossiformis*) (Lombard et al. 2016).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the LSU sequence is *A. ossiformis* CBS 324.54 (GenBank KU845993; Identities = 810/810 (100 %), no gaps). Closest hits using the ITS sequence are *A. putrefolia* CBS 112037 (GenBank KU845985; Identities = 533/544 (98 %), 6 gaps (1 %)) and *A. ossiformis* CBS 324.54 (GenBank NR_145068; Identities = 534/547 (98 %), 7 gaps (1 %)). The closest hits using the *tub*2 sequence are *C. terrestris* CBS 477.91 (GenBank KU846019; Identities = 288/308 (94 %), 4 gaps (1 %)) and *C. putrefolia* CBS 112038 (GenBank KU846017; Identities = 285/307 (93 %), 2 gaps (0 %)). The closest hits using the *tef*-1α sequence are *A. terrestris* CBS 127305 (GenBank KU846012; Identities = 315/362 (87 %), 14 gaps (3 %)) and *A. ossiformis* CBS 324.54 (GenBank KU846009; Identities = 313/360 (87 %), 17 gaps (4 %)).



Maximum likelihood tree obtained from the combined DNA sequences dataset from four loci (ITS, LSU, *tef*-1α and *tub2*) of our isolate and sequences retrieved from the GenBank database. Ex-type strains of the different species are indicated with T. The new species proposed in this study is indicated in **bold**. The RAxML v. 8.2.10 (Stamatakis 2014) bootstrap support values (≥ 70 %) are provided at the nodes. *Alfariacladiella spartii* CPC 24966 and MFLUCC 13-0799 were used as outgroup.

Colour illustrations. Tarragona, Spain; colony on MEA and OA after 14 d at 25 ± 1 °C; conidiomata under the stereomicroscope; cupulate stromatic conidiomata, conidiophores, conidiogenous cells and conidia. Scale bars = 50 µm (conidiomata), 10 µm (conidiophores and conidia).

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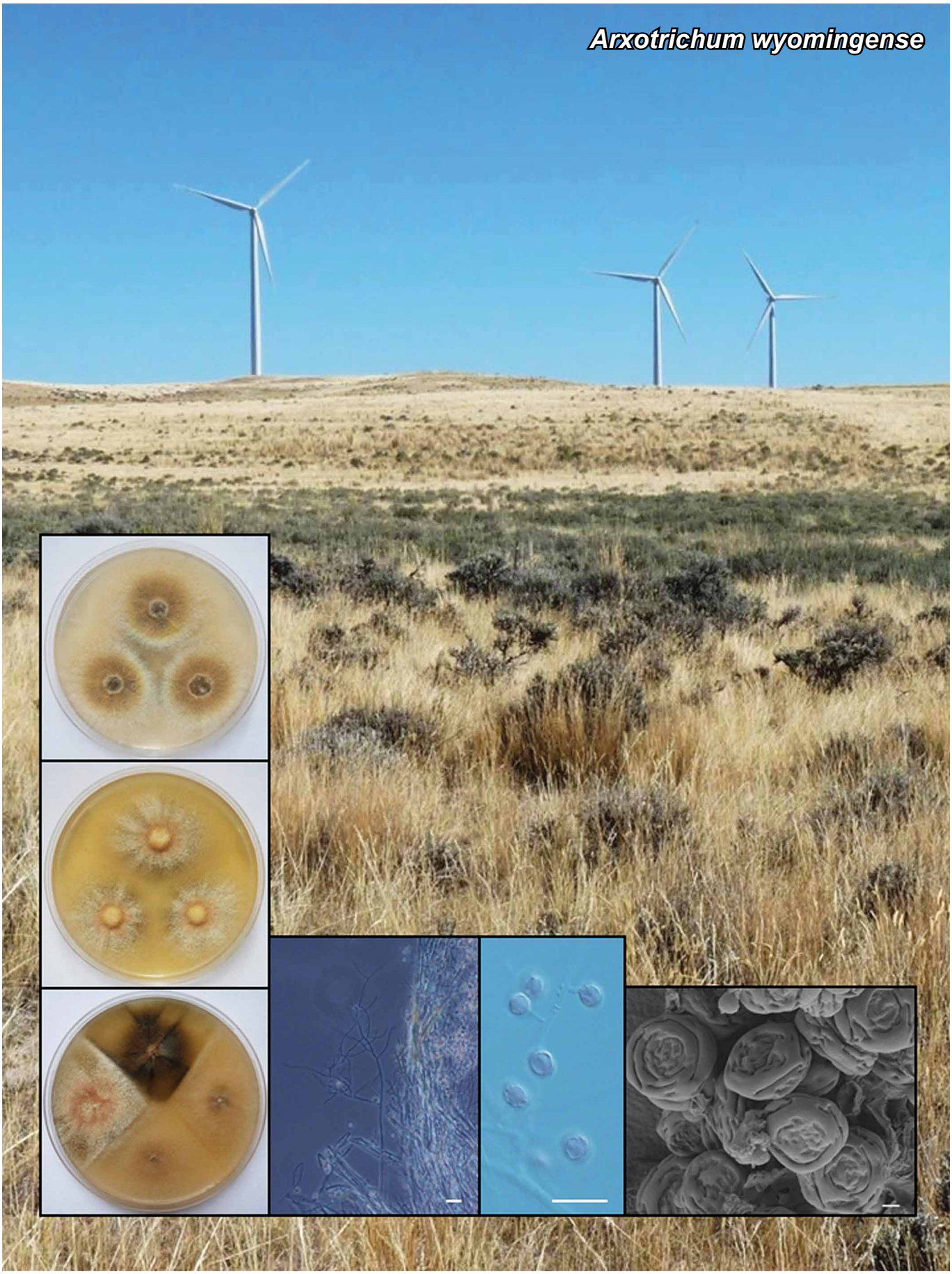
Arxotrichum wyomingense

Fungal Planet 718 – 13 July 2018

Arxotrichum A. Nováková & M. Kolařík, *gen. nov.*

Etymology. Named after Josef Adolf von Arx (1922–1988), honouring his work on the genus *Chaetomium* and according to the morphological similarity with the genus *Staphylotrichum*.

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

Mycelium sterile or producing conidiophores. *Conidiophores* septate, stipe with basal part yellowish brown, upper part colourless, ramified, branches racemose. *Conidiogenous cells* borne on the ends of branches, hyaline. *Conidia* solitary, aseptate, subglobose, rough-walled to rugose. *Ascomata* absent or pale ochraceous to olivaceous grey, superficial, spherical to ovate, 140–240 µm with distinct ostiolar opening, wall angular or irregular; ascomatal hairs numerous, flexuous, undulate or spirally coiled, verrucose or finally echinulate, septate, pale ochraceous or brown. *Asci* obovate-clavate, with short stalks, 34–45 × 16–20 µm, 8-spored, evanescent; *ascospores* ellipsoidal-fusoid, at both ends attenuated and rounded, brown, 12–17 × 6–8.5 µm, with distinct apical germ pore (Von Arx et al. 1986). Good growth to 37 °C, limited at 40 °C (2–3 mm diam in 7 d), no growth at 42 °C. Phylogenetically distinct from related genera of *Chaetomium* and *Myceliophthora*.

Type species. Arxotrichum wyomingense A. Nováková & M. Kolařík. MycoBank MB824080.

Arxotrichum wyomingense A. Nováková & M. Kolařík, *sp. nov.*

Etymology. Latin 'wyomingense' = relating to the state Wyoming, USA, referring to the type locality.

On MEA. *Conidiophores* septate, 250–400 µm long, stipe with basal part yellowish brown, smooth to finely rough, 3 µm wide, upper part colourless, smooth, 2.5 µm wide, ramified, branches racemose. *Conidiogenous cells* borne on the ends of branches, hyaline. *Conidia* solitary, aseptate, 5(–7) µm diam, hyaline to pinkish coloured, subglobose, rough-walled to rugose, flattened from side view with distinct spiral (bands) and visible scars. *Ascomata* not observed.

Culture characteristics — (in the dark, 25 °C after 7 d): Colonies on MEA 56–60 mm diam, plane, with scanty aerial mycelium, radial sporulation yellowish white (ISCC–NBS no. 92; Anon. 1964) to pale yellowish pink (no. 31), but moderate yellowish pink (no. 29) in colony centre, colourless exudate, no soluble pigment, reverse colourless with black (no. 267) colony centre. Colonies on V8 agar 55–60 mm diam, plane, with scanty aerial mycelium, sporulation yellowish white (no. 92) to pale yellowish pink (no. 31) with light orange (no. 52) to light yellowish brown (no. 76) in colony centre, colourless exudate, no soluble pigment, reverse colourless to pale orange yellow (no. 73), colony centre light yellowish brown to brownish black (no. 65).

Typus. USA, Wyoming, Converse Country, Powder River Basin, Glenrock-Rolling Hills Wind Plant (former Dave Johnson Coal Mine), site without a reclamation and plant seedlings (natural plant succession – shortgrass sagebrush prairie), N 42.856372, W 105.862719, isolated from soil using keratin bait technique, 2010, *A. Nováková* (holotype PRM 945788, culture ex-type CCF 5691, ITS, *tub2*, *tef1-α* and LSU sequences GenBank LT968153, LT971393, LT971395 and LT968143, MycoBank MB824081).

Additional material examined. USA, Wyoming, Converse Country, Powder River Basin, Glenrock-Rolling Hills Wind Plant (former Dave Johnson Coal Mine), site without a reclamation and plant seedlings (natural plant succession – shortgrass sagebrush prairie), isolated in 2010 from soil using the cellulose bait technique, CCF 5688 = PRM 945789, ITS sequence GenBank LT968155, and CCF 5689, ITS sequence GenBank LT968157, and using the dilution plate method, CCF 5690, ITS sequence GenBank LT968159.

Colour illustrations. USA, Wyoming, Rolling Hills Wind Plant, shortgrass sagebrush prairie; 7-d-old colonies of *Arxotrichum wyomingense* (CCF 5691) on V8 agar and MEA and colonies of all studied strains growing together on MEA; conidiophores and conidia on MEA. Scale bars = 20 µm (conidiophores), 10 µm (conidia), 1 µm (SEM).

Arxotrichum succineum (L.M. Ames), A. Nováková & M. Kolařík, *comb. nov.* — MycoBank 824082

Basionym. Chaetomium succineum L.M. Ames, Mycologia 41: 645. 1950 '1949'.

Notes — *Arxotrichum wyomingense* is typified by well-defined conidiophores with pigmented bases and a branched hyaline apical part bearing whorls of ornamented conidia. No sexual morph was observed in culture. Crossing of all possible combinations of four strains did not result in the sexual morph, and therefore this species is assumed to be asexual. These characters are not presented in the set of related genera such as *Chaetomium* or *Myceliophthora*, but fit the characteristics of the genus *Staphylotrichum*. Phylogenetically, the type of *Staphylotrichum*, *S. coccorum*, is unrelated to *Arxotrichum*. *Arxotrichum wyomingense* resembles *Staphylotrichum subramaniani* isolated from hare dung in Chile (Udagawa 1997), from which it differs by its smaller conidia, absence of ellipsoidal or pyriform conidia and rather different conidial ornamentation. The living culture of *S. subramanii* does not exist (S. Udagawa, in let.), and the herbarium voucher deposited in the Natural History Museum and Institute, Chiba (CBM) is unavailable for molecular study, and therefore its generic status remains uncertain. *Arxotrichum wyomingense* clusters with *Chaetomium succineum* (ITS rDNA similarity 99 %, 412/418 bp), which is a sexual species lacking an asexual morph (Doveri 2013). Thus, the two species included here in *Arxotrichum* have a few shared phenotypic characters, and the genus as a whole is delimited based on phylogeny only.

The genus *Chaetomium* is a large and polyphyletic taxon (De Hoog et al. 2013, Wang et al. 2016). Based on the current concept of narrow, monophyletic genera, *Chaetomium* was split into several distinct genera (Van den Brink et al. 2012, Marin-Felix et al. 2015). Following this concept, *A. wyomingense* cannot be attributed to any known genus, and thus a new genus is herewith introduced to accommodate it.

Legend and tree added to MycoBank.

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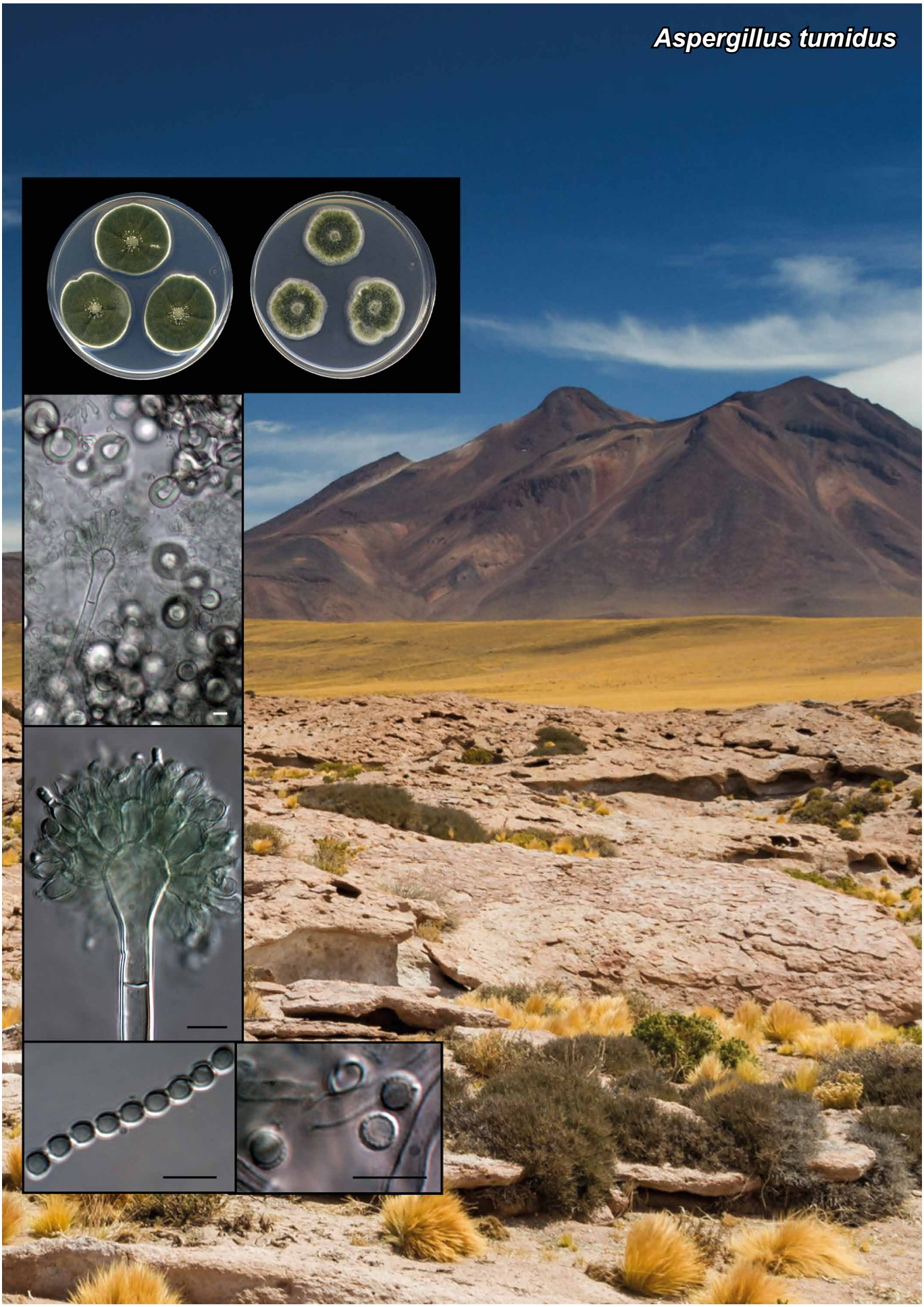

Aspergillus tumidus

Fungal Planet 719 – 13 July 2018

Aspergillus tumidus J.P.Z. Siqueira, Gené, Dania García & Guarro, *sp. nov.*

Etymology. Name refers to the swollen metulae on its conidiophores.

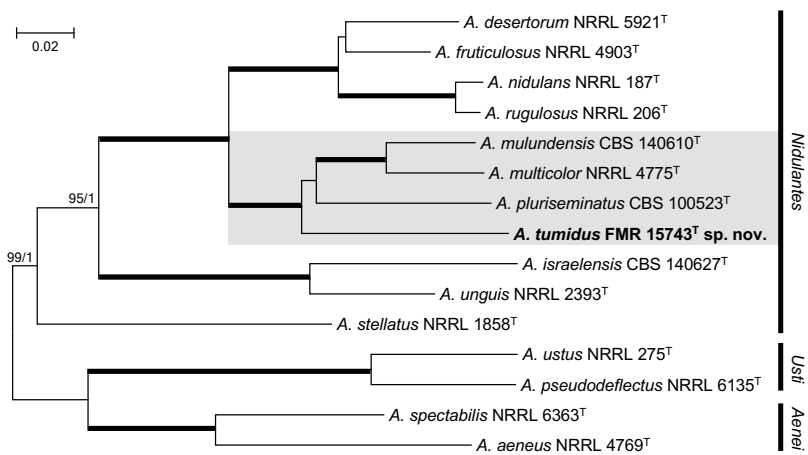
Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetes*.

Conidiophores on MEA hyaline, commonly septate, smooth, 80–400 × 3–5.5 µm. *Conidial heads* biseriate, radiate, in shades of green. *Vesicles* subglobose, 5.5–15 µm wide. *Metulae* usually inflated, covering 75–100 % of the vesicle, 5.5–9.5 × 2.5–8 µm. *Phialides* flask-shaped, 6.5–10 × 2.5–5 µm. *Conidia* globose to subglobose, in shades of green, smooth-walled to finely roughened, 3–8 µm. *Hülle cells* frequently observed, mostly globose, sometimes irregularly shaped, 12–28 µm. *Ascomata* not observed.

Culture characteristics — (in the dark, at 25 °C after 7 d): Colonies on CYA attaining 34–37 mm diam, velvety to floccose, slightly radially sulcate, with elevated centre, mycelium white, margin entire to slightly lobulate; reverse light green (28A4) to dark brown (6F6) (Kornerup & Wanscher 1978); sporulation dense; with conidial masses dark green (29F7); soluble pigment absent; exudate absent. On MEA, colonies reaching 22–23 mm diam, floccose to loosely cottony, mycelium white to greenish white (28A2), margin slightly lobulate; reverse light orange (5A4); sporulation dense, with conidial masses pale green (28A3) to dark green (28F8); soluble pigment absent; exudate light green (28A4). On DG18, colonies reaching 22–23 mm diam, floccose to powdery, mycelium white to greenish white (28A2), margin slightly lobulate; reverse light orange (5A4); sporulation dense, with conidial masses pale green (28A3) to dark green (28E8); soluble pigment absent; exudate light green (28A4). On YES, colonies reaching 33–35 mm diam, floccose to slightly cottony, radially sulcate, mycelium white to greyish green (29B3), margin lobulate; reverse light yellow (4A4) to dark brown(6F6); sporulation dense, with conidial masses greyish green (27C3 to 27E7); soluble pigment absent; exudate yellowish white (3A2) to light yellow (3A4). On OA, colonies reaching 29–31 mm diam, cottony at centre, powdery towards the periphery, mycelium white, margin slightly lobulate and with submerged mycelium; reverse white to dull green (28D4); sporulation moderately dense, with conidial masses deep green (29E8); soluble pigment absent; exudate absent. On CREA, colonies reaching 20–22 mm diam, loosely cottony, dense at the centre, mycelium white, margin irregular; sporulation moderately dense, with conidial masses greyish green (28B4); acid production absent. On CYA after 7 days, the colonies reached 32–34 mm diam at 30 °C; growth absent at 37 °C.

Typus. Chile, Atacama desert, from soil, 2014, coll. *A.M. Stchigel*, isol. *J.P.Z. Siqueira* (holotype CBS H-23244, cultures ex-type FMR 15743 = CBS 143587, ITS, LSU, *BenA*, *CaM* and *RPB2* sequences GenBank LT903691, LT992011, LT903682, LT903685 and LT903688, MycoBank MB823690).

Notes — A multilocus phylogenetic analysis based on ITS, *BenA*, *CaM* and *RPB2* revealed that this species belongs to the *A. multicolor* clade in section *Nidulantes*, together with *A. multicolor*, *A. mulundensis* and *A. pluriseminatus* (Chen et al. 2016). Species in this clade show low genetic similitude, being easier to distinguish by sequence comparison. Nonetheless, phenotypic differences could be observed in order to differentiate the new species from others. *Aspergillus multicolor* has pink to purple drab mycelium and pink Hülle cells; *A. mulundensis* presents conidial masses pale green to blue green (Chen et al. 2016); and *A. pluriseminatus* produces only the sexual morph (Stchigel & Guarro 1997).



Maximum Likelihood tree inferred with MEGA v. 6 software (Tamura et al. 2013) from the combined ITS, *BenA*, *CaM* and *RPB2* regions from the ex-type strains (T) of the species included in the *A. multicolor* clade of section *Nidulantes* and selected *Aspergillus* sections *Nidulantes*, *Usti* and *Aenei* species. Maximum likelihood bootstrap support values ≥ 70 % and Bayesian posterior probabilities ≥ 0.95 are displayed at the nodes. Thickened branches correspond to fully supported clades (100/1). The *A. multicolor* clade is indicated in the grey box and the novel species in **bold** face.

Colour illustrations. Chile, Atacama desert, from soil, 2014, coll. *A.M. Stchigel*, isol. *J.P.Z. Siqueira* (holotype CBS H-23244, cultures ex-type FMR 15743 = CBS 143587, ITS, LSU, *BenA*, *CaM* and *RPB2* sequences GenBank LT903691, LT992011, LT903682, LT903685 and LT903688, MycoBank MB823690).

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Aspergillus serratalhadensis

Fungal Planet 720 – 13 July 2018

Aspergillus serratalhadensis L.F. Oliveira, R.N. Barbosa, G.M.R. Albuquerque, Souza-Motta, Viana Marques, *sp. nov.*

Etymology. *serratalhadensis*, refers to the Brazilian city Serra Talhada, the location of the ex-type strain of this species.

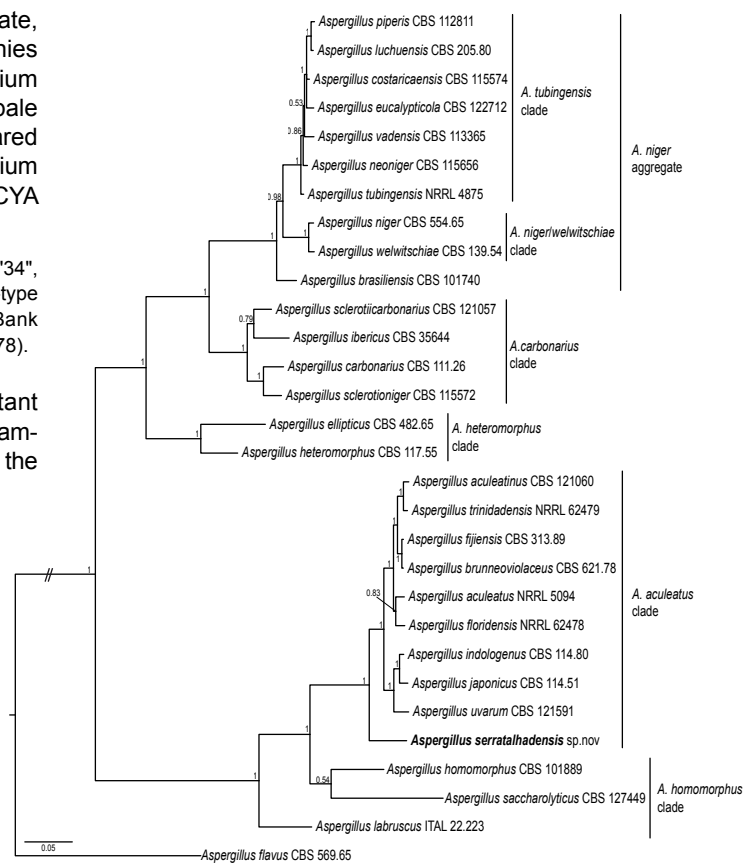
Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetes*.

On MEA: *Stipes* brown, smooth, (200–)250–400(–500) × 8–9(–10) µm; *conidial heads* pale to dark brown; uniseriate; *vesicle* subglobose to globose, (32–)50 × 50(–42) µm diam; *phialides* flask-shaped and covering the entire surface of the vesicle, measuring (1.5–)2 × 1.5(–2) µm; *conidia* globose occasionally subglobose, rough-walled to echinulate, brown-black in mass, 5(–6.5) µm diam including ornamentation.

Culture characteristics — (in the dark, 25 °C after 7 d): Colonies on MEA 54–56 mm diam, sporulating dark brown to black, mycelium white, floccose, exudate absent, no soluble pigments, reverse brownish to buff. Colonies on CYA 60–68 mm diam, dark brown to black, mycelium white, floccose, exudate absent, no soluble pigments, reverse brownish to buff. Colonies on OA 38–40 mm diam, sporulating dark brown to black, mycelium white to pale, floccose, exudate absent, no soluble pigments, reverse darkness. Colonies on YES 60–65 mm diam, sporulating dark brown to black, mycelium white, floccose, sulcate, exudate absent, no soluble pigments, reverse pale. Colonies on CY20S 60–65 mm diam, with black sporulation, mycelium white, floccose, no exudate, no soluble pigments, reverse pale to pale buff. Colonies on CREA growing more slowly compared with other media, 19–20 mm diam, poor sporulation, mycelium white, production of acid positive. No growth on MEA and CYA at 37 °C.

Typus. Brazil, Pernambuco state, Serra Talhada, S7°57'21" W38°17'34", isolated from soil, Sept. 2015, *L.F. Oliveira* (holotype URM 91189, ex-type culture URM 7866, ITS, *BenA*, *CmD* and *RPB2* sequences GenBank MH169127, LT993222, LT993223 and LT995971, MycoBank MB824978).

Notes — ITS, *CmD* and *BenA* sequences are important identification markers for *Aspergillus* (Fungaro et al. 2017, Samson et al. 2014). Based on the current phylogenetic analysis, the new species *Aspergillus serratalhadensis* is a distinct lineage which belongs to *Aspergillus* section *Nigri*, clustering in the *A. aculeatus* clade. The BLASTn analysis showed low similarity of *BenA* sequences: *A. aculeatus* (GenBank HE577806.1; 93 %) and *A. brunneoviolaceus* (GenBank EF661105.1; 92 %). For *CmD* low similarities were found to *A. aculeatus* (GenBank FN594542.1; 90 %) and *A. brunneoviolaceus* (GenBank EF661147.1; 90 %). *Aspergillus serratalhadensis* and these two species are uniseriate. However, in *A. brunneoviolaceus* the conidia are globose to ellipsoidal, smooth, slightly roughened, 3.5–4.5(–6) × 3.5–4.5(–5) µm diam, with a spherical vesicle, (30–)35–70(–90) µm diam. In *A. aculeatus* conidia were spherical, smooth, slightly roughened, 4.9–5.4 µm diam, with a spherical vesicle, 60–63 µm diam (Klich 2002, Jurjević et al. 2012).The new species described also differs in growth rate on the various media tested. *Aspergillus serratalhadensis* was isolated from soil collected in the Brazilian tropical dry forest (Caatinga) in the city of Serra Talhada, Pernambuco state.



Bayesian inference tree obtained by phylogenetic analyses of the combined ITS, *BenA* and *CmD* sequences conducted in MrBayes on XSEDE in the CIPRES science gateway. Bayesian posterior probability values are indicated at the nodes. The new species is indicated in **bold** face. *Aspergillus flavus* (CBS 569.65) was used as outgroup.

Colour illustrations. Caatinga's soil, isolation source of *Aspergillus serratalhadensis*; conidia; conidiophores from 7-d-old colonies on MEA. Scale bars = 10 µm.

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Baorangia alexandri

Fungal Planet 721 – 13 July 2018

Baorangia alexandri Svetash., Simonini & Vizzini, *sp. nov.*

Etymology. Named in honour of the collector of the species, the Russian mycologist Alexander Kovalenko, for his important contributions to the study of *Agaricales* and *Boletales* in Russia.

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

Pileus 40–100 mm diam, at first hemispherical, then convex to almost flat; surface dry, velutinous when young, almost smooth and shining with age, carmine red, pinkish red to dark pink, slowly turning blue when injured; pileus margin involute, then relaxed, slightly lobate, sharp. *Hymenophore* surface from concave to flat or only slightly convex, bright yellow, dark blue indigo when injured, then dingy orange-yellow or olive; tubes at the beginning decurrent, very short (1–2 mm), then slowly well-developed, up to 7 mm in length, sinuate adherent to the stipe; pores small, round or slightly angular. *Stipe* 30–70 × 10–25 mm, usually shorter than pileus width, stout, more or less cylindrical or clavate with enlarged lower part, often tapered to the base, yellow at the apex, below carmine-red, usually without reticulum but sometimes with a very thin reticulation at the very apex, dotted with reddish granules throughout its lower part or only in the middle part; surface slowly turning blue when injured. *Context* yellow, slowly turning blue. *Odour* and *taste* indistinct. *Spore-print* olive-brown. *Spores* (*n* = 54, one collection) (8–)9.5–10.5(–11.5) × (3.5–)4–4.5(–5) µm, Q = 2.35–2.67, Qm = 2.51, Vm = 81, slightly oblong to ventricose in face view; in profile view somewhat inequilateral to oblong, and showing a shallow suprahilar depression; nearly hyaline to pale dingy ochraceous when mounted in potassium hydroxide solution (3 % KOH), with smooth surface. *Basidia* 25.5–30.5 × 8–9.5 µm, mostly 4-spored. *Hymenophoral (tube) trama* divergent and gelatinous, of the 'boletus-type'. *Cheilocystidia* fusiform, hyaline, 47–55 × 9.5–10.5 µm. *Pleurocystidia* fusiform, hyaline, 47–61.5 × 10–12 µm. *Pileipellis* a trichoderm of interwoven hyphae, from suberected tending to prostrate, not gelatinised, smooth, hyaline or weak yellow in 3 % KOH; terminal elements (17–)33–67.5(–78) × (6–)6.5–10(–13) µm. *Caulohymenium* a layer of sterile elements, cylindrical to inflated, often forming chains, 17.5–25 × 4–11.5 µm, hyaline to yellowish, with scattered basidia. *Clamp connections* absent.

Habit, Habitat & Distribution — Solitary or in small groups, in deciduous forests with *Quercus mongolica*, undergrowth of *Corylus heterophilla* and *Lespedeza bicolor*. Rare, so far known only from a single station in Asiatic Russia.

Typus. Russia, Primorsky Krai, Sikhote-Alin Nature Reserve, deciduous forest with *Quercus mongolica* (*Fagaceae*), N44°57'24" E136°33'35", 19 Aug. 2013, *A. Kovalenko* (holotype LE 254266, ITS and LSU sequences GenBank MH043611 and MH036169, MycoBank MB 825173).

Colour illustrations. Russia, Sikhote-Alin Nature Reserve, deciduous forest with *Quercus mongolica*, where the holotype was collected (photo by O. Morosova); basidiomata (photo by A. Kovalenko); spores, basidia, elements of the pileipellis, cheilocystidia, pleurocystidia and caulocystidia (all from the holotype, photos by T. Svetasheva). Microscopic elements observed in 3 % KOH. Scale bars = 20 mm (basidiomata), 10 µm (microscopic elements).

Additional material examined. ***Baorangia alexandri***. Russia, Primorsky Krai, Sikhote-Alin Nature Reserve, vic. of Blagodatnoye, deciduous forest with *Quercus mongolica*, 19 Aug. 2013, *A. Kovalenko*, LE 254265, ITS and LSU sequences GenBank MH043612 and MH036170. ***Baorangia emileorum***. Italy, Lazio, Latina, wood of Valle Fredda, loc. S. Martino, Priverno, in a mixed broadleaved wood with *Quercus suber*, *Q. ilex* and *Q. cerris*, under *Q. cerris*, N41°72'379" E12°32'175", 17 Nov. 2012, *A. Vizzini*, GS 10213, ITS and LSU sequences GenBank MH043613 and MH036171; Liguria, Savona, Borgio Verezzi, under *Q. ilex*, 13 Nov. 2014, *A. Vizzini*, TO HG131114, ITS and LSU sequences GenBank MH043617 and MH036175; Sardinia, Parco del Sulcis, Nuxis (CA), Monte Tiriccu, loc. Arcu su Fixi, under *Q. ilex*, 17 Oct. 2015, *A. Tatti*, TO HG171015, ITS and LSU sequences GenBank MH043615 and MH036173; ibid., 19 Oct. 2015, *A. Tatti*, TO HG191015, ITS and LSU sequences GenBank MH043614 and MH036172. – Portugal, Madeira Island, Levada do Furado, near Ribeiro Frio, on the slope under the path, under *Quercus* sp., 26 Sept. 2015, *J. Borovička*, PRM 934960, ITS and LSU sequences GenBank MH043616 and MH036174. ***Lanmaoa fragrans***. Italy, Piemonte, Torino, Venaria Reale, Parco Naturale La Mandria, under *Q. robur*, 6 Oct. 2002, *A. Vizzini*, TO HG061002, LSU sequence GenBank MH036176.

Notes — GS refers to the personal herbarium of G. Simonini. The phylogenetic hypotheses were constructed using the Maximum likelihood (ML) approach (RAxML v. 7.3.2, Stamatakis 2006). Based on the ITS and LSU analyses, the two collections of *Baorangia alexandri* represent a new species. *Baorangia alexandri* clusters sister (bs = 57 %) to *B. pseudocalopus* (the type species of the genus) in the ITS analysis and, with low support, to a clade consisting of *B. emileorum* and *B. pseudocalopus* and two *Baorangia* sp. (GenBank KF112355 and KF112356) in the LSU analysis.

Baorangia pseudocalopus, so far known from China, Japan (Wu et al. 2016) and India, is the phylogenetically closest species to *B. alexandri* according to the ITS analysis. However, morphologically it is quite different, since its basidiome exhibits not so bright colours, pileus shows predominantly grey, pale reddish grey, light brown or pinkish brown colours, stipe is slightly paler, spores are slightly bigger (9–12.5 × 4–5 µm) and less elongated, hyphae of pileipellis are coloured in brown or yellowish brown tinges. *Baorangia bicolor* and *B. emileorum* (the orthographically correct species epithet for *emilii*, Parra et al. 2017) are morphologically quite similar to *B. alexandri*. Since *B. bicolor* was firstly interpreted in a wide sense including some cryptic species, it is currently problematic to separate some morphological features which distinguish strictly *B. bicolor* from its relatives. Probably the only distinguishing character (besides the genetic one) is the geographical distribution: until now *B. bicolor* is known only from North America (Bessette et al. 2010, 2016). *Baorangia emileorum* is characterised by a more massive and fleshy basidiome than *B. alexandri*, with stouter stipe and more decurrent hymenophore, pileus margin more irregular and undulate, colouration of pileus and stipe surface with usually brighter tints of red: purplish red, carmine red, garnet red, currant red; its spores are statistically longer and narrower, Q = (2.7–)2.8–3.4(–3.6) (according to Muñoz 2005), Q = 2.65–3.27 based on our observations on 132 spores from 4 collections; *B. emileorum* is until now only known from the Mediterranean area (France, Greece, Italy, Portugal (Madeira) and Spain) (Muñoz 2005 and pers. obs.).

For supplementary information see GenBank.

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Cladosporium michoacanense

Fungal Planet 722 – 13 July 2018

Cladosporium michoacanense Iturrieta-González, Gené & Dania García, *sp. nov.*

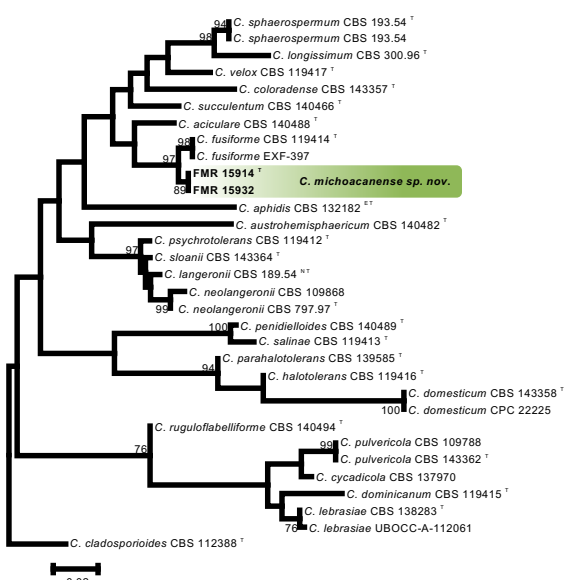
Etymology. Name refers to Michoacán, the geographical area where the fungus was collected.

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

Colonies sporulating on synthetic nutrient-poor agar. *Mycelium* consisting of branched, septate, smooth, brown, 2–3 µm wide hyphae. *Conidiophores* macronematous, erect to slightly flexuous, 1–16-septate, branched or unbranched, pale to medium olivaceous brown, smooth, verruculose to tuberculate 24–552 × 3–3.5 µm. *Conidiogenous cells* terminal, cylindrical, 14–20 × 2–3 µm, bearing 2–4 subdenticulate loci, 1 µm wide, thickened, darkened and refractive. *Primary ramoconidia* 0–1-septate, pale brown, smooth to somewhat tuberculate, cylindrical to subcylindrical, 11–31 × 2–3 µm, with up to three distal hila; hilum thickened, darkened and refractive. *Secondary ramoconidia* aseptate, pale brown, smooth, cylindrical to subcylindrical, 10–15 × 2–3 µm, with up to 4 distal hila. *Conidia* in branched chains, with up to 4 conidia in the terminal unbranched part, aseptate, pale brown, smooth, with protuberant and darkened hila; intercalary conidia, ellipsoidal and obovoid, 5–12.5 × 2–3.5 µm; small terminal conidia subglobose, obovoid, pyriform, ellipsoidal, occasionally fusiform, 2.5–6.5 × 1.5–2 µm.

Culture characteristics — (at 25 °C in 2 wk): Colonies on PDA up to 34 mm diam, slightly dusty to velvety, radially folded, olive to dull green (3F3/28E4) (Kornerup & Wanscher 1978), aerial mycelium scarce, margin regular; reverse dark green (28F8); exudate scarce, consisting of small colourless droplets on the colony surface. On OA, up to 23 mm diam, slightly dusty, flat, olive to dark green (2F4/29F8), aerial mycelium scarce, margin irregular; reverse dark green (29F8) to black. On SNA, up to 22 mm diam, slightly dusty, flat, olive (3F4-8), aerial mycelium scarce, margin regular; reverse olive (2F4).

Cardinal temperature for growth — Optimum 20 °C, maximum 30 °C, minimum 5 °C.



Colour illustrations. Villa Jiménez, Michoacán (Imagen Credit Marco A. Ambris), Mexico; colony sporulating on PDA after 2 wk at 25 °C; conidiophores and conidia on SNA after 7 d at 25 °C. Scale bars = 10 µm.

Typus. Mexico, Michoacán, Villa Jiménez, from soil, Sept. 2016, leg. *E. Rodriguez-Andrade* (holotype CBS H-23245, cultures ex-type FMR 15914 = CBS 143588, ITS, LSU, *actA* and *tef1* sequences GenBank LT907958, LT934506.1, LT907961 and LT907945, MycoBank MB823063).

Additional material examined. Mexico, Michoacán, Morelia, from soil, Sept. 2016, leg. *E. Rodriguez-Andrade*, FMR 15932, ITS, *actA* and *tef1* sequences GenBank LT907944, LT907960 and LT907959.

Notes — *Cladosporium michoacanense* belongs to the *C. sphaerospermum* complex (Bensch et al. 2018). Based on the combined analysis of ITS, *actA* and *tef1* markers, its closest relative is *C. fusiforme.* However, the lineage formed by the two isolates of *C. michoacanense* received a high statistical support and showed a phylogenetic distance of 1 % with respect to the lineage of the ex-type strain of *C. fusiforme* (CBS 119414). *Cladosporium fusiforme* differs from our novel species in several morphological aspects, such as in having shorter conidiophores (up to 200 µm long), larger primary (15–40 µm long) and secondary ramoconidia ((7–)8–24(–31) µm long), and terminal conidia commonly being fusiform (Zalar et al. 2007). *Cladosporium michoacanense* exhibits small conidia of varied shape (subglobose, ellipsoidal, obovoid, pyriform), but rarely fusiform.

Based on a megablast search of NCBIs GenBank nucleotide database using LSU sequences, the closest species were *C. sphaerospermum* (GenBank DQ780351.2; Identities = 840/844 (99 %), Gaps = 1/844 (0 %)), *C. longissimum* (GenBank DQ780352.2; Identities = 838/844 (99 %), Gaps = 1/844 (0 %)) and *C. langeronii* (GenBank DQ780380.2; Identities = 836/844 (99 %), Gaps = 1/844 (0 %)). The closest hits using ITS sequences were *C. cladosporioides* (GenBank JF911745.1; Identities 499/500 (99 %), Gaps = 0/500 (0 %)), *C. succulentum* (GenBank LN834434.1; Identities = 501/511 (98 %), Gaps = 5/511 (0 %)) and *C. crousii* (GenBank NR_148192.1; Identities = 500/511 (98 %), Gaps = 3/511 (0 %)). The closest hits using the *actA* sequences were *C. fusiforme* (GenBank KJ596640.1; Identities = 205/216 (95 %), Gaps = 4/216 (1 %)), *C. aciculare* (GenBank KT600607.1; Identities = 214/232 (92 %), Gaps = 0/232 (0 %)) and *C. velox* (GenBank KT600654.1; Identities = 202/225 (90 %), Gaps = 2/225 (0 %)). The closest hits with *tef1* sequences were *C. fusiforme* (GenBank KJ596595.1; Identities = 236/252 (94 %), Gaps = 3/252 (1 %)), *C. aciculare* (GenBank KT600509.1; Identities = 236/263 (90 %), Gaps = 1/262 (0 %)) and *C. velox* (GenBank KT600556.1; Identities = 216/258 (84 %), Gaps = 4/258 (1 %)).

Maximum likelihood tree obtained from the combined analysis of ITS, *actA* and *tef1* sequences of the *C. sphaerospermum* species complex (Bensch et al. 2018). Bootstrap support values above 70 % are indicated on the nodes. The alignment included 977 bp and was performed with ClustalW. The Kimura 2-parameter with Gamma distribution (G) was used as the best nucleotide substitution model. Both the alignment and tree were constructed with MEGA v. 6.0 (Tamura et al. 2013). The new species proposed herein is in the green box and ex-type, ex-epitype and ex-neotype strains are indicated with ^{T}, ^{ET} and ^{NT}, respectively.

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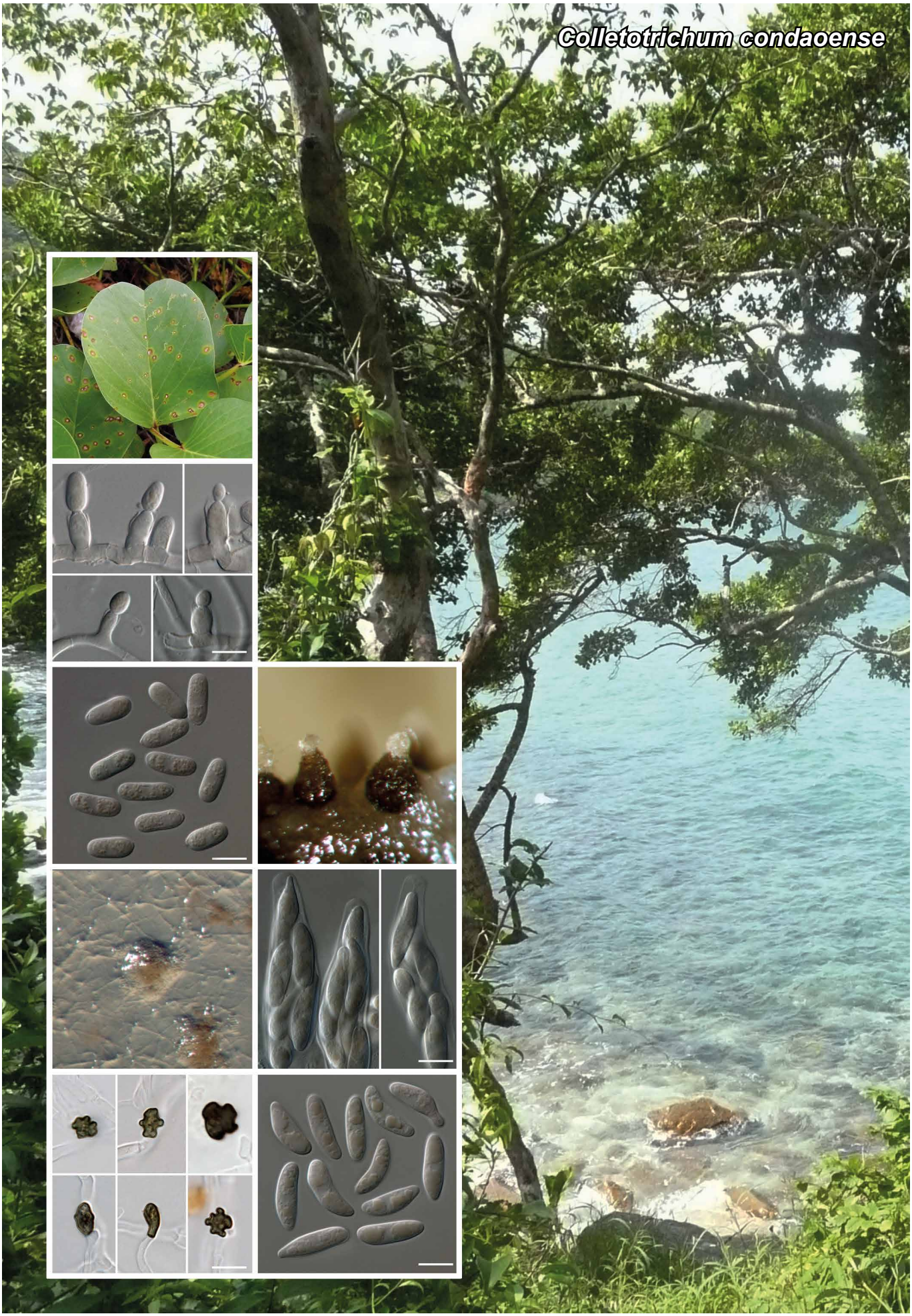
Colletotrichum condaoense

Fungal Planet 723 – 13 July 2018

Colletotrichum condaoense Damm, *sp. nov.*

Etymology. The species epithet is derived from the locality where it was collected, Côn Đảo Islands, Vietnam.

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

Sexual morph on *SNA*. *Ascomata* ovoidal to obpyriform, medium to dark brown, glabrous, 170–260 × 150–180 µm, ostiolate, wall 10–14 µm (4–6 cells) thick, outer layer composed of flattened pale brown angular cells, 5–17.5 µm diam. *Interascal tissue* composed of paraphyses, hyaline, septate, branched at the base, disintegrating quickly, 35–70 µm long, base 3–5 µm diam, apically free, the apex rounded. *Asci* cylindrical to clavate, 55–72 × 11–15.5 µm, 8-spored. *Ascospores* biseriately arranged, hyaline, smooth-walled, aseptate, fusoid, usually more tapering towards one end than to the other, straight or slightly curved, both ends rounded or one end rounded and other end ± acute, (12.5–)15–18.5(–21.5) × (4.5–)5.5–7(–9) µm, mean ± SD = 16.6 ± 1.7 × 6.2 ± 0.8 µm, L/W ratio = 2.7. *Asexual morph on SNA. Vegetative hyphae* 1–8 µm diam, hyaline, smooth-walled, septate, branched. *Chlamydospores* not observed. *Conidiomata* consisting of conidiophores and setae formed directly on hyphae. *Setae* (few observed) pale brown, smooth-walled, 14–50 µm long, 3–4-septate, base cylindrical, 5–5.5 µm diam, tip ± rounded. *Conidiophores* hyaline, smooth-walled, septate, branched, to 20 µm long. *Conidiogenous cells* hyaline, smooth-walled, ovoid to doliiform, with a double gelatinous layer, sometimes integrated, 7–19 × 5–6 µm, opening 1.5–2 µm diam, collarette ≤ 0.5 µm long, periclinal thickening distinct. *Conidia* hyaline, smooth-walled, aseptate, straight, sometimes very slightly curved, apex and base rounded, hilum sometimes visible, 12.5–14(–15) × 5–5.5(–6) µm, av. ± SD = 13.4 ± 0.8 × 5.4 ± 0.3 µm, L/W ratio = 2.5. *Appressoria* single, pale to medium brown, smooth-walled, elliptical, clavate, subglobose or irregular outline, with an undulate or lobate margin, (4.5–)7.5–13(–15) × (3–)4.5–8.5(–12) µm, av. ± SD = 10.3 ± 2.6 × 6.4 ± 1.9 µm, L/W ratio = 1.6.

Culture characteristics — (near UV light with a 12 h photoperiod, 20 °C after 10 d): Colonies on SNA flat with entire margin, hyaline to cinnamon, agar medium, filter paper and *Anthriscus* stem partly covered with grey fruiting bodies (ascomata) and sparse whitish aerial mycelium, reverse same colours; growth 12.5–15 mm in 7 d (19–21.5 mm in 10 d). Colonies on OA flat with entire margin; buff, salmon, ochreous to isabelline, partly covered with grey ascomata, salmon to ochreous conidiomata and sparse whitish aerial mycelium, reverse olivaceous grey, growth 14–16 mm in 7 d (23–24.5 mm in 10 d). Conidia in mass rosy buff to pale salmon.

Typus. Vietnam, Côn Đảo Islands, Côn Sơn, sea shore, from leaf spots on *Ipomoea pes-caprae* (*Convolvulaceae*), 12 Dec. 2012, *U. Damm* (CBS H-21508 holotype, culture ex-holotype CBS 134299; ITS, *gapdh*, *tub2*, *chs-1*, *his3* and LSU sequences GenBank MH229914, MH229920, MH229923, MH229926, MH229927 and MH229917, MycoBank MB825023).

Colour illustrations. Sea shore of Côn Sơn (Vietnam); left: leaf of *Ipomoea pes-caprae* with leaf spots; conidiophores; conidia; conidiomata; appressoria; right: ascomata; asci; ascospores. Scale bars = 10 µm.

Additional material examined. Vietnam, Côn Đảo Islands, Côn Sơn, sea shore, from leaf spots on *Ipomoea pes-caprae*, 12 Dec. 2012, *U. Damm*, culture CBS 135823, ITS, *gapdh*, *tub2* and LSU sequences GenBank MH229915, MH229921, MH229924 and MH229918; idem, culture CBS 135989, ITS, *gapdh*, *tub2* and LSU sequences GenBank MH229916, MH229922, MH229925 and MH229919.

Notes — *Ipomoea pes-caprae*, called bayhops, beach morning glory or goat's foot, is a creeping vine that grows worldwide at tropical beaches; it is one of the most common and most widely distributed salt tolerant plants and one of the first colonisers of dunes (https://en.wikipedia.org/).

Two *Colletotrichum* species were described from *Ipomoea*, none from *I. pes-caprae*. *Colletotrichum ipomoeae* was described from stems of *I. batatas* in Portugal (De Sousa da Câmara 1931) with conidia that are larger than those of *C. condaoense* 16–25 × 3.5–5 µm, while *C. ipomoeicola* (Rao 1963) from leaves of *I. batatas* in India, has curved conidia. There are several *Colletotrichum* species on *Ipomoea* listed in Farr & Rossman (2018): *C. truncatum* (syn. *C. capsici*), *C. circinans*, *C. dematium*, *C. dematium* f. *ipomoaea*, *C. gloeosporioides*, *C. ipomoeicola* and *Colletotrichum* sp. However, there is no report from *Ipomoea pes-caprae*, and most of the species listed are species with curved conidia (Rao 1963, Damm et al. 2009), except for *C. gloeosporioides* (Weir et al. 2012). All reports were from disease indexes/lists or from references prior to the molecular era, and therefore most of the identifications are not reliable.

There is no sequence of a *Colletotrichum* species from *I. pes-caprae* in GenBank, but six sequences of five strains from other *Ipomoea* spp. Three of them (GenBank KT185055 and KT185056, Huang et al., unpubl. data, and JN672591, Hipol 2012) could be assigned to the *C. orchidearum and C. magnum* species complexes, respectively (Damm et al. 2019), while the other two strains (GenBank JN672598, Hipol 2012, and DQ117967/DQ119125, Steiner et al. 2006), belong to the *C. boninense* species complex but are not conspecific with *C. condaoense* (95 % and 98 % sequence identity). In contrast, the ITS of the ex-type strain of *C. condaoense* is 100 % identical with '*C. hippeastri*' strain TV-06 (GenBank KR704574) from a leaf of *Croton bonplandianus* (*Euphorbiaceae*) probably in India (U. Nagajyothi et al., unpubl. data). It is possible that this is also *C. condaoense*; however, sequences of more loci are necessary to confirm this.

The closest species in BLASTn searches with ITS, *gapdh*, *tub2*, *chs-1* and *his3* sequences of the ex-holotype of *C. condaoense*, CBS 134299, in NCBIs GenBank nucleotide database restricted to ex-type strains, is *C. parsonsiae* (*C. boninense* species complex) with four (99 %), seven (97 %), six (99 %), one (99 %) and four (99 %) nucleotides different, respectively. There are several morphological differences between *C. condaoense* and *C. parsonsiae.* For example, conidia of *C. condaoense* are shorter than those of *C. parsonsiae* (18.5 × 5.4 µm on average on SNA), and the shapes of appressoria and ascospores are different (Damm et al. 2012). Based on these results we regard the strains from *I. pes-caprae* as a new species belonging to the *C. boninense* species complex.

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Colletotrichum cobbittiense

Fungal Planet 724 – 13 July 2018

Colletotrichum cobbittiense S. Luo, G. Dong & P. Wong, *sp. nov.*

Etymology. Named after the location, Cobbitty, where it was found.

Classification — *Glomerellaceae, Glomerellales, Sordariomycetes.*

Sexual morph not observed. Asexual morph on PDA. *Hyphae* 1–4 µm diam, hyaline, darkening with age, smooth-walled, septate, branched. *Mycelium* hyaline, becoming grey and dark grey in patches with age. *Conidiomata* cream to pale brown. *Conidiophores* hyaline, septate, single or branched. *Conidiogenous cells* hyaline, smooth-walled, mostly cylindrical, 8–14 × 2–4 µm. *Conidia* hyaline, smooth-walled, aseptate, cylindrical with rounded ends, sometimes tapering to a rounded end or narrowed at the centre, (11–)12(–17) × (4–)5(–6) µm. *Appressoria* single or in clusters, pale to dark brown, smooth-walled, subglobose to ellipsoidal or broadly cylindrical, sometimes tapering to apex, with entire, undulate or lobate margin, 8–18 × 4–8 µm.

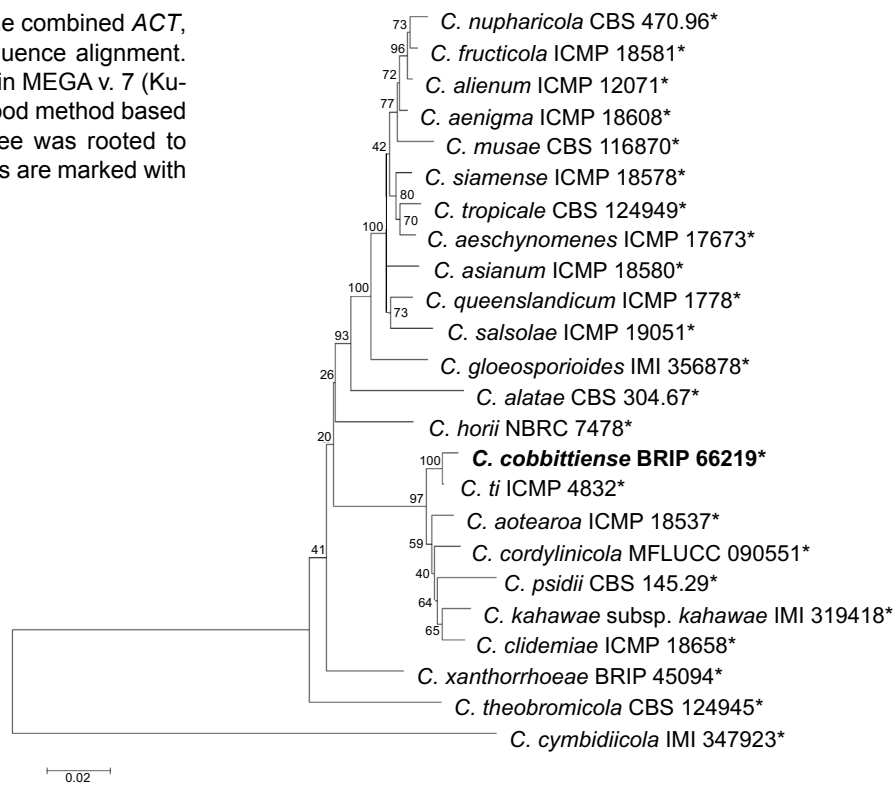
Culture characteristics — Colonies on PDA reaching 55 mm diam in 5 d at 25 °C in the dark; moderate white aerial mycelium, becoming grey to dark grey at the centre or in patches, with moderate sporulation on cream to pale brown conidiomata. Reverse grey to dark grey at centre and in patches after 10 d incubation. Setae not observed. Appressoria abundant, adhering to the plastic surface of the agar plate.

Typus. Australia, New South Wales, Cobbitty, from leaf lesions of a *Cordyline* interspecific hybrid (*C. stricta* × *C. australis*) (*Asparagaceae*), Jan. 2016, *S. Luo & G. Dong* (holotype BRIP 66219, includes ex-type culture, ITS, *GAPDH, ACT, CHS-1, HIS3* and *TUB2* sequences GenBank MH087016, MH094133, MH094134, MH094135, MH094136 and MH094137, MycoBank MB824862).

Notes — Leaf spots were observed on the leaves of a *Cordyline* interspecific hybrid (*C. stricta* × *C. australis*) tree in the garden of the Plant Breeding Institute, Cobbitty, New South Wales, Australia. The leaf lesions were characterised by bleached centres and diffuse brownish margins around the lesions (see photo plate). The leaf spots were generally small (5–10 mm) and discrete. This pathogen has not been previously recorded in Australia (Shivas et al. 2016).

Phylogenetic analyses based on sequence data from six loci (*ACT, CHS-1, GAPDH, HIS3*, ITS and *TUB2*) place the fungus in the Kahawae clade of the *C. gloeosporioides* complex (Weir et al. 2012). It is closest to *C. ti* but differs in having smaller conidia (mean length of 12 µm vs 16 µm), a growth rate of about twice as fast on PDA (55 mm diam after 5 d vs 50–55 mm after 10 d) and in not producing ascomata in culture. *Colletotrichum ti* has only been found in New Zealand on *Cordyline* spp. while *C. cobbittiense* was isolated from lesions on leaves of a *Cordyline* interspecific hybrid (*C. stricta* × *C. australis*).

Multilocus phylogenetic tree inferred from the combined *ACT*, *CHS-1*, *GAPDH*, *HIS3*, ITS and *TUB2* sequence alignment. The evolutionary analyses were conducted in MEGA v. 7 (Kumar et al. 2016) using the Maximum Likelihood method based on the Kimura 2-parameter model. The tree was rooted to *C. cymbidiicola* IMI: 347923*. Ex-type strains are marked with an asterisk (*).



Colour illustrations. Cordyline trees; leaf spot symptom on a *Cordyline* interspecific hybrid (*C. stricta* × *C. australis*); conidiophores and conidia; appressoria adhering to the plastic surface of agar plate. Scale bars (from left to right) = 10 mm, 10 µm, 10 µm.

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Coprinopsis afrocinerea

Fungal Planet 725 – 13 July 2018

Coprinopsis afrocinerea Mešić, Tkalčec, Čerkez, I. Kušan & Matočec, *sp. nov.*

Etymology. Named after the continent on which the type material was found and its similarity to *Coprinopsis cinerea*.

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

Pileus up to 28 mm wide when expanded, ellipsoid to paraboloid at first, later conical to convex, finally applanate or planoconcave with revolute margin, strongly plicate-sulcate except in the central disc, light to medium brown at centre and whitish to light brown towards the edge when young, later light grey to brownish grey except brownish to brown central disc, mostly with serrated edge at maturity. *Veil* on young pileus composed of dense, loosely adpressed hairs, easily detaching, more scattered and floccose at maturity, completely white or light rusty brown in the central zone. *Lamellae* free, moderately crowded, L = c. 45, l = c. 1–3, white at first, later grey, finally brown-black and deliquescent. *Stipe* 30–70 × 1.5–2.5 mm, central, cylindrical or gradually thickened towards the base, not rooting, hollow, dry, hairy-fibrillose at first, later hairy-floccose (more pronounced towards the base), sometimes becoming glabrous in the upper part, hairs white, underneath the surface brownish to light brown. *Odour* and *taste* not observed. *Spore print* brown-black. *Basidiospores* (250/5/3) (9.5–)10–*11.6*–13.3 × 6.8–*7.9*–9.1 µm (in KOH 2.5 %), in average (among different basidiomata) 11.3–12 × 7.7–8.1 µm, Q = (1.28–)1.35–*1.47*–1.59(–1.64), Qav = 1.43–1.5, ellipsoid to ovoid in frontal view, ellipsoid to (sub)amygdaliform in side view, with rounded to slightly conical base and rounded apex, not flattened, smooth, dark reddish brown in H_2O, dark brown in KOH, non-amyloid and non-dextrinoid, slightly transparent, thick-walled (up to 1.5 µm); germ-pore central with inner diam of 1–1.6 µm and outer diam of 2–3.5 µm, covered with disk- to plate-shaped, transparent, red-brown lid, (2.2–)2.6–3.2(–3.6) × 0.3–0.6(–0.8) µm (measured in H_2O), mostly attached to the spore in H_2O, profusely releasing from the spore surface in KOH, expanding (up to 6 µm wide) and shaped like contact lens. *Basidia* 15–30 × 8.5–11 µm, clavate, 4-spored, thin-walled, hyaline, surrounded by 3–6 hymenophysalides (pseudoparaphyses). *Cheilocystidia* probably present, but totally collapsed and unrecognizable in our material (even in young basidiomata). *Pleurocystidia* of trabecular type (anchored in two neighbouring lamellae), abundant, elongated, c. 40–100 µm long, hyaline, rather collapsed in our material (not fully recovered in KOH). *Veil cells* on the pileus 20–200 × 2.5–25(–30) µm, cylindrical to (somewhat) inflated, in chains, often constricted at the septa, with cylindrical, inflated, conical or fusiform terminal elements, not diverticulate, exceptionally with individual and simple excrescences, not branched, thin-walled (up to 0.5 µm), at the centre of the pileus sometimes moderately thick-walled (up to 0.8 µm) or rarely thick-walled at places (up to 2 µm), glabrous, less frequently finely encrusted, rarely coarsely encrusted at the centre, hyaline or pale yellow-brown at the centre. *Pileipellis* a cutis, composed of repent, hyaline, thin-walled, 1.5–25 µm wide hyphae, often constricted at septa, with narrowest hyphae on the surface. *Stipitipellis* a cutis, composed of repent, cylindrical, hyaline, thin-walled, 2–10 µm wide hyphae. *Clamp connections* present and abundant.

Colour illustrations. Heavily disturbed secondary tropical forest in vicinity of Akure, Nigeria; basidiomata (top); basidiospores (top first three in H_2O, all other basidiospores in KOH); veil on the pileus (phase contrast). Scale bars = 10 mm (basidiomata), 5 µm (basidiospores), 20 µm (veil).

Distribution & Habitat — Nigeria, Lagos and Ondo States, two localities 182 km apart; gregarious on sandy/gravel soil with some plant remnants in a courtyard (typus) and on the same substrate in a heavily disturbed secondary tropical forest (*Theobroma cacao*, *Elaeis guineensis*, *Musa* sp., *Khaya ivorensis*), and on rotten log of *Elaeis guineensis* in a courtyard; saprotrophic. India (GenBank KR155115).

Typus. Nigeria, Ondo State, 11 km NW from Akure, N07°19'28" E05°07'31", 400 m a.s.l., on soil, 21 July 2008, *M. Čerkez* (holotype CNF 1/5838, ITS and LSU sequences GenBank MG662162 and MG662158, MycoBank MB823829).

Additional material examined. Nigeria, Ondo State, 11 km NW from Akure, N07°19'28" E05°07'31", 400 m a.s.l., on soil, 21 July 2008, *M. Čerkez*, CNF 1/5836, ITS sequence GenBank MG662164; Lagos State, 6 km W from Imota, N06°39'58" E03°37'05", 50 m a.s.l., on rotten log of *Elaeis guineensis*, 4 July 2008, *M. Čerkez*, CNF 1/5811, ITS sequence GenBank MG662163.

Notes — *Coprinopsis afrocinerea* is morphologically very similar to *C. cinerea*. According to our study, the only constant morphological difference between them are the somewhat smaller basidiospores in the latter. Based on our measurement of 350 spores (from seven basidiomata, in four collections from different localities in Croatia) and data from Uljé (2005), *C. cinerea* has an average spore length less then 11 µm (9–10.9 µm) and an average spore breadth less than 7.5 µm (6.1–7.3 µm), while *C. afrocinerea* has an average spore length more than 11 µm (11.3–12 µm) and an average spore breadth larger than 7.5 µm (7.7–8.1 µm). Another difference is in their ecology. While *C. cinerea* lives on heaps of herbivorous dung (mixed with straw, grass or wood chips), on rotten straw or grass, or on other herbaceous refuse, *C. afrocinerea* was found on sandy/gravel soil with some plant remnants and on rotten wood. Another morphologically similar species is *C. annulopora* which differs by its more robust basidiomata (pileus up to 70 mm wide, stipe up to 18 mm wide), strongly rooting stipe, somewhat larger and more elongated basidiospores (average spore length more than 12.5 µm (12.8–13.2 µm) and an average Q of more than 1.6 (1.61–1.65)), and by a different substrate (heaps of herbivorous dung). The peculiar character shared by all three species is a lid covering the germ pore of the basidiospores, which only partially releases from the spores in H_2O but profusely in KOH. While *C. annulopora* was named after that structure (Enderle 2004), only some authors observed it in *C. cinerea*, at least in some collections or spores (e.g., Citerin 1994, Doveri 2004, Enderle 2004, Gierczyk et al. 2014, Bender 2017, Melzer 2017). However, they described it as annuliform bulge around a germ pore. None of them noticed that this structure was not hollow but shaped like a contact lens.

A megablast search in GenBank using the ITS sequence from holotype of *Coprinopsis afrocinerea* showed that the closest three species were *C. cinerea* (e.g., GenBank AY461825, Identities = 673/696 (97 %), 7 gaps (1 %)), *C. calospora* (GenBank GQ249275, Identities = 616/638 (97 %), 7 gaps (1 %); GenBank JX118675 (holotype), Identities = 524/534 (98 %), 3 gaps (0 %)) and *C. annulopora* (GenBank HQ847017, Identities = 624/653 (96 %), 7 gaps (1 %)). For full phylogenetic analysis, see MycoBank.

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Diaporthe pseudoinconspicua

Fungal Planet 726 – 13 July 2018

Diaporthe pseudoinconspicua T.G.L. Oliveira, J.D.P. Bezerra, A.R. Machado, Souza-Motta & O.M.C. Magalhães, *sp. nov.*

Etymology. The name refers to its morphological similarity to *Diaporthe inconspicua*.

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

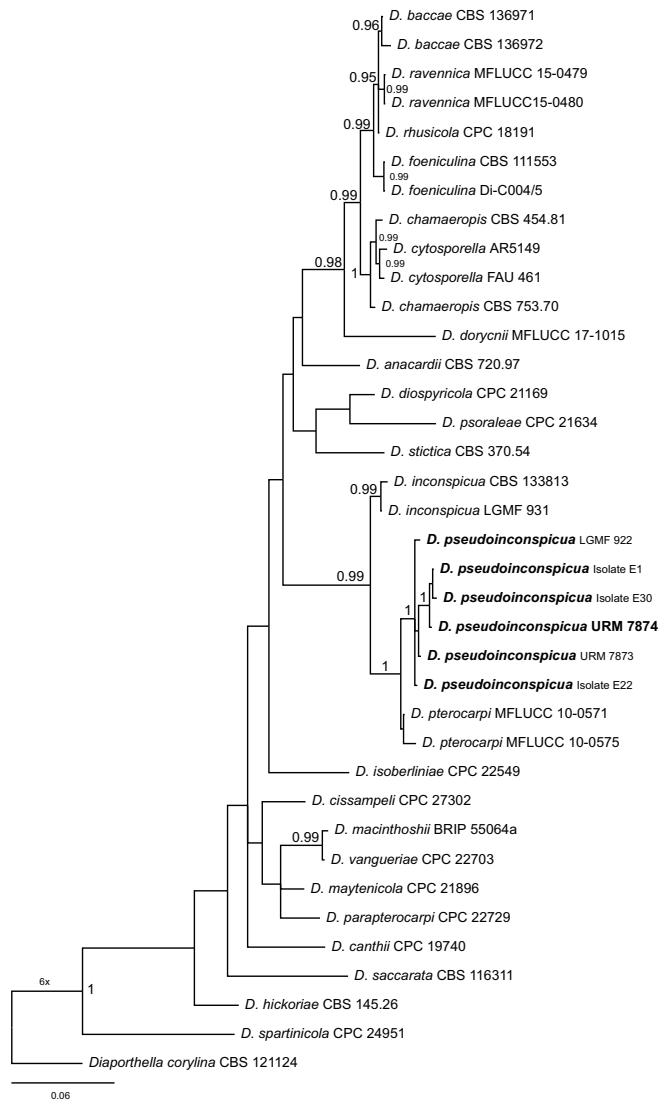
Conidiomata pycnidial on PDA in culture, globose to subglobose, lacking a neck, solitary or aggregated, dark brown to black, 200–320 × 160–190 µm, with yellowish conidial drops exuding from the ostioles. *Alpha conidiophores* hyaline, branched, straight to sinuous, aggregated, 14.5–21.5(–23.5) × 2.5–3 µm. *Beta conidiophores* hyaline, septate, branched, smooth, straight to sinuous, aggregated, 10.5–16(–18) × 2–2.5(–3) µm. *Conidiogenous cells* phialidic, hyaline, bifurcate, straight to sinuous, (9–)10.5–13.5 × 2–2.5(–3) µm. *Alpha conidia* aseptate, hyaline, bi- to multiguttulate, fusoid, rounded at one end, and with acute ends, 5–7.5(–8.5) × 2–2.5(–3.5) µm. *Beta conidia* hyaline, aseptate, filiform, straight to curved, with one end obtuse, the other truncate, 18–21(–25.5) × 1–1.5(–2) µm. *Sexual morph* not observed.

Culture characteristics — On PDA, colonies are initially white, becoming greyish, reverse pale brown with brownish and black dots, fluffy aerial mycelium, covering Petri dishes after 7 d at 25 °C with concentric zonation. Pycnidia forming after 30 d. On MEA, colonies are initially white with slow growth, becoming greyish, reverse pale brown with brownish to black dots, fluffy aerial mycelium, with concentric zonation. Pycnidia forming after 15 days.

Typus. Brazil, Paraíba state, Santa Teresinha, Tamanduá farm (S07°1.524 W037°23.518), as endophyte from branches of *Poincianella pyramidalis* (*Fabaceae*), May 2013, *J.D.P. Bezerra* (holotype URM 91188, culture ex-type URM 7874, ITS, LSU, *CaM*, *his3*, *tef1-α* and *tub2* sequences GenBank MH122538, MH122541, MH122528, MH122517, MH122533 and MH122524, MycoBank MB824820).

Additional material examined. Brazil, Paraíba state, Santa Teresinha, Tamanduá farm (S07°1.524 W037°23.518), as endophyte from branches of *P. pyramidalis*, May 2013, *J.D.P. Bezerra*, URM 7873, isolates E22, E1 and E30. GenBank sequences URM 7873: ITS MH122535, LSU MH122540, *CaM* MH122525, *his3* MH122518, *tef1-α* MH122530, *tub2* MH122521. GenBank sequences E22: ITS MH122534, LSU MH122539, *tef1-α* MH122529, *tub2* MH122520. GenBank sequences E1: ITS MH122536, *CaM* MH122526, *tef1-α* MH122531, *tub2* MH122522. GenBank sequences E30: ITS MH122537, LSU MH122542, *CaM* MH122527, *his3* MH122519, *tef1-α* MH122532, *tub2* MH122523.

Notes — Based on the current phylogenetic analysis, the new species *Diaporthe pseudoinconspicua* is closely related to *D. inconspicua* and *D. pterocarpi*. Gomes et al. (2013) circumscribed the strain LGMF922 as *D. inconspicua* isolated as endophytic fungus from *Spondias mombin* in Brazil. Our phylogenetic inference placed the strain LGMF922 together with some endophytic fungi isolated from *P. pyramidalis* in Brazil, and here they are proposed as a new species, *D. pseudoinconspicua*. Morphologically, *D. pseudoinconspicua* differs from *D. inconspicua* based on the size of pycnidia (424–954 × 371–742 µm), conidiophores (11–21.5 × 2–2.5 µm), alpha (5.5–6.5 × 1.5–2 µm) and beta ((17.5–)20–26(–28) × 1–1.5 µm) conidia (Bezerra et al. 2018). Furthermore, *D. pseudoinconspicua* also differs from *D. pterocarpi* by the size of its pycnidia (100–120 µm diam), conidiophores (10–15 × 1–2 µm), alpha conidia (6–7 × 2.5 µm), and by the absence of beta conidia (Udayanga et al. 2012).



Bayesian inference tree obtained by phylogenetic analyses of the combined ITS rDNA, *tef1-α* and *tub2* sequences conducted in MrBayes on XSEDE in the CIPRES science gateway. Bayesian posterior probability values are indicated at the nodes. The new species is indicated in **bold** face. *Diaporthella corylina* (CBS 121124) was used as outgroup.

Colour illustrations. Brazilian tropical dry forest; colony on PDA; conidiomata pycnidial; alpha and beta conidiophores; alpha and beta conidia. Scale bars = 10 µm.

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Dothiora infuscans

Fungal Planet 727 – 13 July 2018

Dothiora infuscans Rodr.-Andrade, Stchigel, Guarro & Cano*, sp. nov.*

Etymology. From Latin *infusco*, to make dark, referring to the black fungal growth on the substrate it was isolated from.

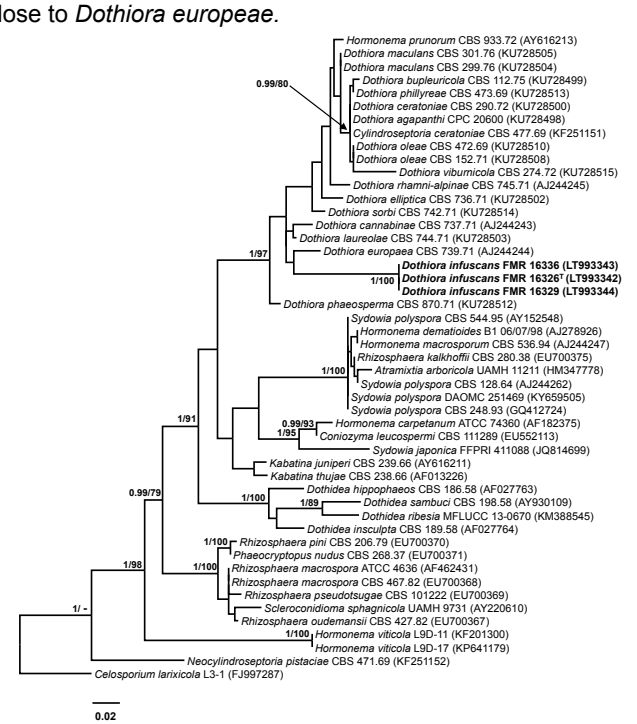
Classification — *Dothioraceae, Dothideales, Dothideomycetes.*

Mycelium composed of subhyaline, smooth-, thin-walled, septate hyphae, 5–7 µm wide, later becoming thick-walled, increasing the number of septa and the volume of their cells to give them a moniliform appearance, and finally the hyphae turn dark brown and produce chains of holothallic (chlamydospore-like) conidia of up to 20 µm diam, which also develop longitudinal/oblique secondary septa over time, giving consequently a 'muriform' aspect to these propagules. *Conidiophores* micronematous, reduced to conidiogenous cells, mostly intercalary, producing conidia on lateral, short to long conic-truncate denticles, with 1–3 per conidiogenous cell. *Conidia* holoblastic, solitary, but attached to one another by a mucilaginous substance; mostly aseptate, smooth- and thin- to thick-walled, hyaline, becoming dark brown, thick-walled, roughened and mostly 1-septate, occasionally 2–3-septate, globose, ellipsoid or irregularly-shaped, prominently constricted at septa when old; unicellular conidia 8–9 × 4–5 µm; 2-celled conidia 10–13 × 6–7 µm; multi-celled conidia 18–19 × 5–7 µm. *Microcyclic conidia* produced by budding of the hyaline or pigmented conidia, solitary or in chains of up to 5 elements on inconspicuous denticles when the conidiogenous cell is young, but on protruding conical-truncate denticles when old, at one or both ends but also laterally, being smaller than the primary conidia. *Endoconidia*, *conidiomata* and *sexual morph* not observed.

Culture characteristics — Colonies on MEA reaching 27–29 mm diam after 3 wk at 25 °C, flattened, light yellow (4A5; Kornerup & Wanscher 1978) at centre, and successively greyish yellow (4B5), pale yellow (4A3) and reddish yellow (4A7) towards the edge, exudates absent, sporulation sparse; reverse light yellow (4A4), diffusible pigment absent. Colonies on PDA reaching 28–29 mm diam after 3 wk at 25 °C, flat and slimy at centre and sulcate at edge, yellowish brown (5D8) at centre, brownish black (6H8) at edge and light yellow (3A5) at the margins, exudates absent, sporulation abundant; reverse light orange (5A4) at centre, brownish grey (5E2) at the edge, and a pale yellow (4A3) margin, diffusible pigment absent. Colonies on OA 6–7 mm diam after 3 wk of incubation at 25 °C, slightly elevated, compact, margins irregular, blackish blue (20F8), exudates absent, abundant yeast-like conidia; reverse blackish brown (6G8) at centre and brownish orange (5C3) at edge, diffusible pigment absent. Colonies on PCA reaching 18–19 mm diam after 3 wk at 25 °C, flat and slimy at centre and filamentous (because of the submerged mycelium) at edge, black (18G2) at centre and olive brown (4E6) at edge, exudates absent, yeast-like conidia abundant; reverse orange white (5A2) at centre, brownish grey (6D2) at the edge, and yellowish white (4A2) at the margins, diffusible pigment absent. Minimum, optimal and maximum temperature of growth: 15 °C, 25 °C and 30 °C, respectively.

Typus. Spain, Tarragona province, Els Pallaresos village, isolated from the blackened wall of an industrial warehouse, 10 July 2017, *J. Cano* & *A.M. Stchigel* (holotype CBS H-23480, cultures ex-type FMR 16326 = CBS 144317; ITS and LSU sequences GenBank LT993342 and LT993345; MycoBank MB824999).

Notes — *Dothiora infuscans* was recovered by a wall surface swab taken in Els Pallaresos village, Tarragona province, Catalonia, Spain. Species of *Dothiora* produce a dothichiza-like asexual morph, as well as a hormonema-like synasexual morph (Crous & Groenewald 2016, 2017). *Dothiora infuscans* can be distinguished from other *Dothiora* spp. with a hormonema-like sexual morph by the production of 'muriform' thalloconidia. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the ITS sequence is with the ex-type strain of *Dothiora europeae* CBS 739.71 (GenBank NR_145339; Identities = 445/470 (95 %), Gaps 5/470 (1 %)); and using the LSU sequence it is with *Dothiora oleaea* (GenBank KU728549; Identities = 834/842 (99 %), no gaps). Our ITS phylogenetic tree corroborated the placement of our isolate as a new species of the genus *Dothiora*, being phylogenetically close to *Dothiora europeae.*



Maximum likelihood tree obtained from the ITS alignment of our isolate and sequences retrieved from GenBank. The tree was built by using RAxML CIPRES (http://www.phylo.org/sub_sections/portal/) and the analysis of probability was run in MrBayes v. 3.2.1 (Huelsenbeck & Ronquist 2001). Bootstrap support values ≥ 70 % and Bayesian posterior probability values ≥ 0.95 are presented at the nodes. *Neocylindroseptoria pistaciae* CBS 471.69 and *Celosporium larixicola* L3-1 were used as outgroups. The new species proposed in this study is indicated in **bold**. ^{T} represents the ex-type strain of the novel species.

Colour illustrations. Wall with chromatic alteration in Els Pallaresos village, Tarragona province, Spain (background picture); colonies growing on different culture media (MEA, PDA, OA and PCA at 25 °C; upper picture); conidia, conidiogenous cells and denticles (black arrows), and 'muriform' propagules (inner pictures); detail of the wall with chromatic alterations (picture inside the black box). Scale bars = 10 µm.

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Entoloma yanacolor

Fungal Planet 728 – 13 July 2018

Entoloma yanacolor A. Barili, C.W. Barnes & Ordoñez, *sp. nov.*

Etymology. Named refers to the black colour of the fruiting body (*yana*) in the native Quichua Andean language.

Classification — *Entolomataceae, Agaricales, Agaricomycetes.*

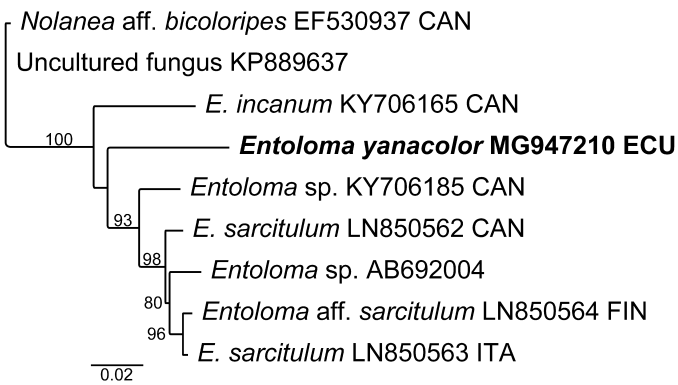
Basidiomata small, convex. *Pileus* 20 mm diam, smooth waxy surface, black, entire margin, slightly fleshy texture. *Lamellae* moderately close, adnate to adnate with decurrent teeth, whitish becoming pink with age, thick with entire and concolorous translucent edge. *Stipe* central, 23 × 2 mm, cylindrical, pale concolorous with pileus, smooth surface with white mycelium at the base. *Context* hollow, fragile. Indistinctive *odour* and taste. *Pileipellis* as a trichoderm, extended fusiform to subclaviform pileocystidia. *Lamellar trama* regular with cylindrical septate hyphae. *Basidia* 30–50 × 8–4 µm, claviform, 4-spored, *clamp connections* absent, fertile lamellae edge. *Basidiospores* 9–11 × 6.5–7.5 µm, ellipsoid, mostly with 6 angles, hyaline to pale pink, non-amyloid, non-dextrinoid, cyanophylic, metachromatic, Q = 1.5. *Pleurocystidia* subcylindrical, hyaline with thin wall. *Cheilocystidia* absent. *Caulocutis* as subtrichoderm with fusiform caulocystidia. *Clamp connections* absent.

Habitat — Gregarious on soil, among *Azorella* sp. in the Andean paramo.

Typus. Ecuador, Chimborazo province, Sangay National Park, alt. 3770 m, May 2016, *J. Flores* (holotype QCAM6312, Fungarium QCAM, ITS-LSU sequence GenBank MG947210, MycoBank MB824642, TreeBASE Submission ID 22308).

Notes — *Entoloma yanacolor* is a small species of Collybioid habit, that belongs to subg. *Leptonia* and to sect. *Cyanula* (Boccardo et al. 2008), the only difference being it is glabrous and not fibrillous / tomentose. Morphologically *E. yanacolor* is very similar to *E. corvinum* (Breitenbach & Kränzlin 1991), differing only by the glabrous surface of the pileus and stipe. However, the DNA sequence analysis excludes it being that species.

The megablast search using the full ITS sequence of *E. yanacolor* was truncated due to a unique 14-base gap near the end of the ITS2, giving only 91 % coverage for the top seven hits. Therefore, 14 ambiguous (n) bases were inserted at the site of the gap, increasing the coverage of the top six megablast results to 100 %. The results of the adjusted megablast search of the NCBI GenBank nucleotide database showed *E. yanacolor* was distinct from other species presently available for the genus with the closest species based on ITS sequence being an *Entoloma* sp. (GenBank KY706185; Identities = 569/624 (91 %), 22 gaps (4 %), adjusted for the 14-base gap insert). The ITS phylogenetic tree includes the top eight megablast hits for the *E. yanacolor* sequence.



The phylogenetic tree was constructed using the Maximum Likelihood plugin PHYML in Geneious R9 (http://www.geneious.com; Kearse et al. 2012), and the substitution model determined by jModelTest (Posada 2008) according to the Corrected Akaike Information Criterion (AICc). *Nolanea* aff. *bicoloripes* (GenBank EF530937) is the outgroup. Bootstrap support values ≥ 80 % are given above branches. The phylogenetic position of *E. yanacolor* is indicated in **bold**. The species name is followed by the GenBank accession number, and when the country of origin was indicated, the three letter United Nations country code was used, in order of appearance CAN: Canada, ECU: Ecuador, FIN: Finland, ITA: Italy.

Colour illustrations. Ecuador, Sangay National Park; basidiocarp; pleurocystidia; basidiospores in cresyl blue. Scale bars = 10 µm.

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Exophiala nidicola

Fungal Planet 729 – 13 July 2018

Exophiala nidicola Gené, Madrid & Guarro, *sp. nov.*

Etymology. The name refers to the habitat where this fungus was found, the nest of a bird.

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

On oatmeal agar (OA): *Mycelium* consisting of septate, branched, subhyaline, smooth, thin-walled hyphae mostly up to 4 µm wide, with moniliform segments consisting of swollen, verruculose, thick-walled cells up to 8 µm wide; the swollen cells can show meristematic growth and form microsclerotia up to 40 µm wide. *Conidiophores* poorly differentiated, simple or rarely branched, mostly formed by 2–3 cells. *Conidiogenous cells* intercalary, terminal or lateral, cylindrical, ellipsoidal or lageniform, annellidic, with one or rarely two conidiogenous loci up to 1 µm wide and inconspicuous annellations; intercalary conidiogenous cells 9–12 × 2–3 µm; terminal and lateral conidiogenous cells 5–9 × 2.5–4 µm. *Conidia* narrowly obovoidal to allantoid, hyaline, smooth, thin-walled, 3–5 × 1–1.5 µm. *Yeast cells* abundant, subcylindrical, ellipsoidal or reniform, 0–1-septate, subhyaline, thick-walled, 6–8 × 2–4 µm, with one or rarely two conidiogenous loci 0.5–1 µm wide, with inconspicuous annellations. *Sexual morph* not observed.

Culture characteristics — Colonies after 14 d at 24 °C attaining 13 mm on OA, floccose to lanose, brownish grey, raised at the centre, with an entire margin and a dark brown to grey reverse; colonies on MEA and SNA attaining 16 mm. On rich media such as Sabouraud dextrose agar and PDA, the fungus formed yeast-like colonies with an abundant cream-coloured mucilaginous exudate and a brownish diffusible pigment at room temperature. Growth positive in the range 6–37 °C, optimum temperature 30 °C, no growth observed at 40 °C.

Typus. Spain, Tarragona Province, L'Arbolí, isolated from the nest of an unidentified bird, Jan. 1990, *J. Gené* (holotype CBS H-21834, ex-type culture CBS 138589 = FMR 3889, ITS and LSU sequences GenBank MG701055 and MG701056, MycoBank MB823878).

Notes — The genus *Exophiala* includes common agents of phaeohyphomycosis and occasional agents of chromoblastomycosis and mycetoma in humans (Zeng et al. 2007, Revankar & Sutton 2010), as well as pathogens of various other warm- and cold-blooded animals (De Hoog et al. 2011, Seyedmousavi et al. 2013). It also includes numerous environmental, apparently non-pathogenic taxa occurring as saprophytes in soil and on plant material, and extremotolerant colonizers of nutrient-poor or polluted habitats (De Hoog et al. 2006, Isola et al. 2016, Madrid et al. 2016).

BLAST searches with the ITS sequence of isolate CBS 138589 revealed affinities with members of the '*Exophiala dermatitidis* clade' (De Hoog et al. 2003), such as *E. heteromorpha* CBS 232.33 ex-type (GenBank ITS: AY857524) and other strains 95–96 % identical, *E. phaeomuriformis* CBS 131.88 ex-type (GenBank ITS: AJ244259) 90 % identical, and *E. dermatitidis* CBS 207.35 ex-type (GenBank ITS: KF928444) and other strains 90 % identical. Considering that *Exophiala* spp. are widely represented in GenBank and that the cut-off for ITS-based species identifications in this genus is 99 % (Zeng et al. 2007, Madrid et al. 2016), strain CBS 138589 is regarded as a novel taxon. The distinguishing characters of *E. nidicola* are the production of some allantoid conidia and the absence of growth at 40 °C. However, its ability to grow at 37 °C and the production of strongly mucoid colonies on sugar-rich media are remarkable. Since extracellular polysaccharides, often forming slimy capsules, are considered putative virulence factors in *Exophiala* (Yurlova & De Hoog 2002), *E. nidicola* might represent another potential opportunistic pathogen. However, this hypothesis should be tested experimentally.

Colour illustrations. L'Arbolí, Tarragona, Spain, where the sample was collected; colony sporulating on OA after 14 d at 25 °C; yeast cells and conidiogenous cells (scale bars = 10 µm); conidia (scale bar = 5 µm) and microsclerotia (scale bars = 20 µm).

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Fomitiporella pertenuis
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Fungal Planet 730 – 13 July 2018

Fomitiporella pertenuis V. Xavier de Lima & J.R. Oliveira-Filho, *sp. nov.*

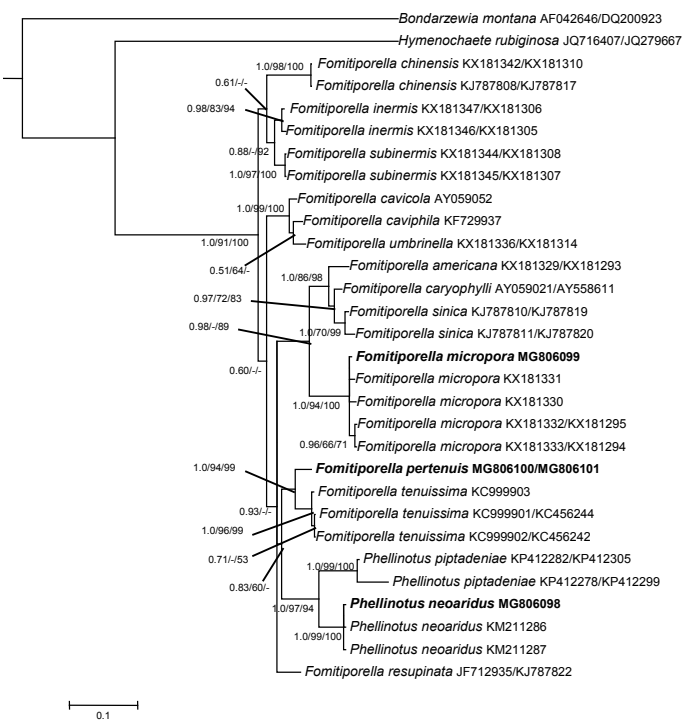
Etymology. Pertenuis (Gr.), referring to the very thin basidioma.

Classification — *Hymenochaetaceae, Hymenochaetales, Agaricomycetes*.

Basidioma annual, resupinate, up to 1.8 mm thick, margin thin; pore surface hazel (27; Watling 1969) when dry, pores angular, 6–8 per mm; dissepiments thin and entire; context reduced to a thin layer above the substrate, less than 0.5 mm thick, homogeneous hazel (27) to snuff brown (17) with the pore surface, sometimes with a darker line just above the tubes; tubes concolorous with the pore surface. Hyphal system monomitic; generative hyphae hyaline to rust (13), thick-walled with a wide lumen, simple septate, 2.5–4 µm diam, IKI-. Cystidia or other sterile elements absent; basidia not seen; basidiospores ellipsoid to ovoid, thick-walled, smooth, rust (13) to rusty tawny (14), IKI-, 4–5.5 × 3–4 µm.

Typus. Brazil, Alagoas, Biological Reserve of Pedra Talhada, on dead wood, July 2017, *V. Xavier de Lima*, PPT 111 (holotype URM 91181, ITS and LSU sequences GenBank MG806101 and MG806100, MycoBank MB824040).

Additional material examined. ***Fomitiporella micropora***. Brazil, Maranhão, São José de Ribamar, Panaquatira beach, on dead branch of living angiosperm, Jan. 2017, *J.R.C. Oliveira-Filho*, JRF135, URM 91186, LSU sequence GenBank MG806099. ***Phellinotus neoaridus***. Brazil, Sergipe, Poço Redondo, Apr. 2016, *T.B. Gibertoni*, PH5, URM 91187, LSU sequence GenBank MG806098.



Colour illustrations. Environment where the type specimen was collected in Biological Reserve of Pedra Talhada, AL, Brazil; close-up showing the thin dissepiments and rather angular pores (scale bar = 1 mm); transversal view of the basidioma: substrate (S), context (C), darker line (L) and tube layer (T) are visible (scale bar = 1 mm); photomicrographs of a septate generative hyphae and basidiospores (scale bar = 10 µm).

Notes — According to our phylogenetic analyses (ITS+LSU), *F. pertenuis* clustered in a clade with high support with specimens of *F. tenuissima* from China (GenBank KC999901, KC999902, KC999903), but diverged significantly from the Chinese specimens and it is distantly related from other species of *Fomitiporella*. Both *F. pertenuis* and *F. tenuissima* have thin basidiomata and lack sterile elements, but *F. pertenuis* has smaller pores (6–8 per mm vs 3–4 per mm in *F. tenuissima*) and monomitical hyphal system (both monomitic and dimitic hyphal system in *F. tenuissima*; Yu et al. 2013). The clade of *F. tenuissima* and *F. pertenuis* shows relation to *Phellinotus* (Dreschler-Santos et al. 2016), which is placed in *Fomitiporella* in our analyses. Thus, synonymising *Phellinotus* under *Fomitiporella* is suggested; however, both species of *Phellinotus* (*P. neoaridus* and *P. piptadeniae*) are pileate and are host-specific on living *Ceasalpinia* and *Piptadeniae*, and *Fomitiporella*, a resupinate genus whose species occur mostly on dead trees, would have to be emended. Another specimen collected in Brazil was identified as *F. micropora*; the specimen is morphologically very similar to the type description, but it has larger pores (4–5 per mm in the Brazilian specimen, 8–10 per mm in the type). *Fomitiporella micropora* is only superficially similar to the new species, from which it differs by the perennial, thicker basidioma (up to 10 mm), smaller pores (8–10 per mm), dimitical hyphal system, and slightly smaller basidiospores, (3–)3.5–4(–4.5) × (2–)2.5–3(–3.5) µm. Besides, *F. micropora* clustered in a clade with specimens collected in the type locality (Virgin Islands) and Costa Rica, distantly related from the new species.

The 50 % majority rule Bayesian tree inferred from ITS+LSU sequences with the model K80 + G using MrBayes v. 3.2.6 (Ronquist et al. 2012). Maximum parsimony (PAUP v. 4.0b10, Swofford 2003) and maximum likelihood (MEGA5, Tamura et al. 2011) analyses were done and similar topologies were obtained (not shown). Bayesian posterior probabilities (PP) from 10 M generations; Maximum parsimony bootstrap (MPbs) and Maximum likelihood bootstrap (MLbs) support values from 1 000 replications. Values next to nodes represent PP/MLbs/MPbs. Sequences generated in this study are shown in **bold**. *Bondarzewia montana* represents the outgroup. The alignment is deposited in TreeBASE (Submission ID 22272).

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Geastrum magnosporum

Fungal Planet 731 – 13 July 2018

Geastrum magnosporum J.O. Sousa, B.D.B. Silva, P. Marinho, M.P. Martín & Baseia, *sp. nov.*

Etymology. Referring to the size of basidiospores, being larger than the mean size in the genus *Geastrum*.

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

Unexpanded basidioma hypogeous, orange white (5A2; Kornerup & Wanscher 1978), subglobose, 7 × 6 mm, surface papery to cottony, strongly encrusted with sand. *Expanded basidiomata*, arched, rarely saccate, 6–16 mm (including peristome) × 10–19 mm. *Exoperidium* splitting into 6–8 rays, arched, revolute, some involute, rolling up under endoperidial body, non-hygroscopic. *Mycelial layer* yellowish white (4A2), surface papery to cottony, strongly encrusted with sand and debris, persistent or peeling away in irregular patches, composed of yellowish, thin-walled (< 1 µm) hyphae, 2–2.5 µm diam, surface not encrusted, lumen not seen. *Fibrous layer* orange white (5A2), surface coriaceous, composed of hyaline, thick-walled hyphae (> 1 µm), surface encrusted, lumen seen. *Pseudoparenquimatous layer*, dark brown (7F4, 6F4), rimose, absent in some basidiomata, composed of brownish, thick-walled (> 1 µm) hyphae cells, subglobose, pyriform to ovoid, 30.5–63 × 27–46.5 µm. *Endoperidial body* orange grey (6B2), depressed-globose to subglobose, 3–5 × 6–9 mm, subsessile, surface furfuraceous. *Apophysis* absent or inconspicuous. *Pedicel* absent or very short (up to 0.6 mm high). *Peristome* fibrillose, lacerate with age, non-delimited to weakly delimited, mammiform to flattened (< 1 mm high), lighter or concolorous with endoperidium. *Columella* circular, central, white (4A1). *Mature gleba* greyish brown (5F3). *Eucapillitium* brownish, thin-walled (< 1 µm diam), 2–5 µm diam, surface encrusted, warts absent, lumen seen, branch absent. *Basidia* clavate to pyriform, 19–24.5 × 8.8–6.3 µm, 2–3 sterigmata. *Basidiospores* brownish to yellowish in 5 % KOH, globose to subglobose, 6–8.5 µm ($x = 6.8 \pm 0.7$, $Q_m = 1.02$, n = 30), densely verrucose, warts long (up to 1.3 µm high), truncate; apiculous reduced.

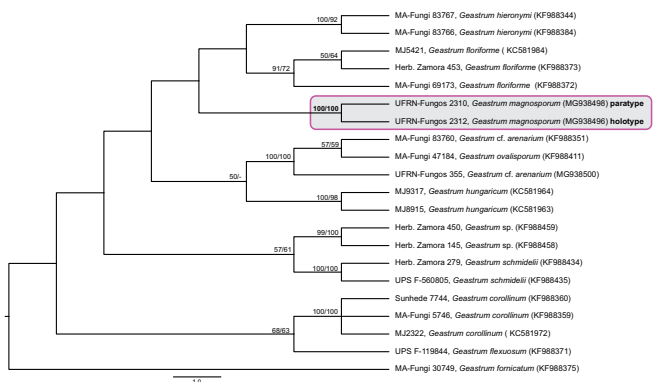
Ecology & Distribution — The specimens were found in the biome Atlantic Rainforest (Tropical & Subtropical Moist Broadleaf Forests of Brazil – Pernambuco interior forests ecoregion) (Dinerstein et al. 2017), growing on sandy soil, without forest cover (exposed to sun), with gregarious or solitary habit.

Typus. Brazil, Paraíba, Mamanguape, Reserva Biológica Guaribas, S6°44'32.1" W35°08'25.8", on sandy soil, 26 June 2014, *J.O. Sousa* et al. (holotype UFRN Fungos–2312, ITS and LSU sequences GenBank MG938496 and MG938497, MycoBank MB824254).

Colour illustrations. Brazil, Paraíba, Reserva Biológica Guaribas, SEMA II, open area of Atlantic rainforest where the type species was collected; expanded basidiomata *in situ* (UFRN–Fungos 2312, holotype); expanded basidiomata *ex situ* (UFRN–Fungos 2312, holotype); basidiospores under LM; basidiospores under SEM; eucapillitium under SEM. Scale bars = 2.5 mm (basidiomata *in situ*), 2 mm (basidiomata *ex situ*), 10 µm (basidiospores under LM), 1 µm (basidiospores and eucapillitium under SEM).

Additional material examined. Brazil, Paraíba, Mamanguape, Reserva Biológica Guaribas, 11 July 2013, *J.O. Sousa* et al., UFRN Fungos–2309; ibid., 27 July 2012, *B.D.B. Silva* et al., paratype UFRN Fungos–2310, ITS and LSU sequences GenBank MG938498 and MG938499.

Notes — *Geastrum magnosporum* is morphologically close to *Geastrum floriforme.* However, *G. floriforme* has strongly hygroscopic rays, a sessile endoperidium and smaller basidiospores (up to 7 µm diam) (Sunhede 1989, Calonge 1998). Another similar species is *G. arenarium*, although, the latter differs in its well-delimited peristome, hygroscopic rays and smaller basidiospores (up to 4 µm diam) (Bates 2004). *Geastrum hieronymi* and *G. minimum* also resemble *G. magnosporum*, but these two species have a longer pedicel (up to 3 mm long) and smaller basidiospores (up to 5 µm and 6.5 µm, respectively) (Bates 2004, Kuhar et al. 2012). Other species with large basidiospores in the genus are *G. laevisporum* (up to 10 µm diam), *G. campestre* (up to 8 µm diam) and *G. platense* (up to 8 µm diam). *Geastrum laevisporum* is distinct due to its smooth basidiospores and hygroscopic rays; *G. campestre* in the plicate peristome and verrucose endoperidium; and *G. platense* in the larger basidiomata (up to 26 mm wide), hygroscopic rays and sessile endoperidium (Sunhede 1989, Soto & Wright 2000, Bates 2004, Sousa et al. 2015).



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

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Gyromitra anthracobia

Fungal Planet 732 – 13 July 2018

Gyromitra subg. *Pseudoverpa* P.-A. Moreau, Bellanger & Loizides, *subg. nov.*

Etymology. Due to the resemblance of species in the genus *Verpa*.

Classification — *Discinaceae*, *Pezizales*, *Pezizomycetes*.

Ascomata carbonicolous, gyromitroid or verpoid in aspect, stipitate, occasionally rufescent, comprised of a grey-brown, purple-brown or black cerebriform pileus and a smooth, white hollow stipe attached to the pileus only at the apex; spores smooth, cyanophilic, mostly biguttulate; paraphyses brown-pigmented.

Type species. *Gyromitra anthracobia* Loizides, P.-A. Moreau & Bellanger. MycoBank MB824545.

Gyromitra anthracobia Loizides, P.-A. Moreau & Bellanger, *sp. nov.*

Etymology. *Anthracobia* = ανθρακόβια (carbon-dwelling); from the Greek ἄνθραξ = carbon, and βίος = life.

Pileus cerebriform, moderately to strongly lobate, 1–4(–6) cm diam, 1–2.5(–3) cm in height, finely tomentose and irregularly variegated, ranging from pale red-brown, olive-brown, purple-brown, purple-grey, or charcoal-grey, becoming black when fully mature or dry; margin deeply involuted but completely detached from the stipe, thick, white, gradually expanding outwards at maturity. *Excipulum* decurrently attached to the stipe, blue-grey under pileus, chalk-white elsewhere, smooth to subtomentose, sometimes with a faintly ochraceous tomentum towards the margin. *Stipe* 1.5–4(–5) cm long by 0.5–1 cm across, cylindrical, attached to the pileus only at the apex, stuffed with a cottony substance when young but soon hollow, pure white and finely tomentose, tomentum sometimes becoming ochraceous-pink to ochraceous-orange. *Context* white, unchanging when bruised, but ascomata occasionally developing prominent red or orange stains. *Odour* somewhat herbaceous. *Ascospores* (16–)18–21(–22.5) × (9–)10–11.5(–12) µm (Me = 19.7 × 11; Q = 1.5–2.2; Qm = 1.79), cyanophilic, ellipsoid, mostly biguttulate in water, sometimes also microguttulate at the poles, thick-walled, hyaline and smooth. *Asci* 150–270 × 13–16 µm, inamyloid, monoseriate, aporhynchus, often flexuous. *Paraphyses* 45–125 µm long, fasciculate, mostly bifurcate and 2–3-septate, with a slightly thickened wall and brown intraparietal pigment all along, often minutely incrusted at the lower part; apices slightly enlarged, cylindrical to clavate, 5–9.5 µm wide. *Subhymenium* 250–300 µm thick, a *textura epidermoidea* composed of small, intricate, jigsaw-like elements with yellowish thickened wall (< 1 µm). *Context* 400–700 µm thick, a mixture of subglobose, ellipsoid, polygonal or filamentous elements, all pale and slightly thick-walled. *Excipulum* 2-layered: inner layer slightly gelatinised, 40–50 µm thick, composed of thick-walled (< 1 µm), pale yellow hyphae, partly slender, 4–5 µm thick, partly globose or ellipsoidal 16–25 µm wide; outer layer hymenidermoid, made of clusters of erect or adpressed, 1(–2)-septate clavate hyphae 35–60 × 8–15 µm, with weakly thickened but bright yellow wall, embedded in pale yellow resinaceous matrix. *Stipitipellis* a cutis of slender, smooth, or rarely incrusted hyphae, 3–6 µm wide, with locally protruding, fasciculate cylindrical terminal elements. *Medulla* predominantly of broad, hyaline ellipsoid elements 12–30 µm wide.

Colour illustrations. Holotype collection area at Kourdali, Cyprus; ascomata *in situ*, holotype coll. LIP 0001407 (scale bar = 10 mm); coll. ML71382VE *in situ* (scale bar = 10 mm); paraphyses and asci in water (scale bar = 50 µm); naturally discharged spores in water (scale bar = 10 µm); stipitipellis hyphae in Floxina aquosa + KOH (scale bar = 100 µm); coll. ML71322V5 *in situ* (scale bar = 10 mm).

Habit, Habitat & Distribution — Carbonicolous, fruiting in small or large groups between mid-March and mid-April, typically the first and second springs following a forest fire.

Typus. Cyprus, Kourdali, in 6-mo-old burned forest, 18 Mar. 2017, *M. Loizides* (holotype in Herbarium of the Faculty of Pharmacy of Lille: LIP 0001407, ITS and LSU sequences GenBank MH014751 and MH014750, MycoBank MB824544).

Additional material examined. Cyprus, Platania, on burned patch, 18 Apr. 2012, *M. Loizides,* ML21481VE, LSU and ITS sequences GenBank H014748 and MH014755; Kourdali, in 6-mo-old burned forest, 22 Mar. 2017, *M. Loizides* & *P.-A. Moreau*, ML71322V5, LSU and ITS sequences GenBank MH014746 and MH014753; Argaka, in 7-mo-old burned forest, 28 Mar. 2017, *M. Loizides*, ML71382VE, LSU and ITS sequences GenBank MH014747 and MH014754; Kourdali, in 7-mo-old burned forest, 22 Apr. 2017, *M. Loizides*, ML71422V2, LSU and ITS sequences GenBankMH014749 and MH014752.

Notes — Based on current phylogenetic inferences, the ITS locus is very divergent within *Gyromitra*, making analyses strongly biased towards the evolution of the 5.8S rDNA. Contrastingly, the LSU locus allows for the recognition of a monophyletic genus, conveniently divided into five subgenera: *Gyromitra*, *Discina*, *Pseudorhizina*, *Melaleucoides* and *Caroliniana* (Methven et al. 2013). Our rDNA (ITS and LSU) phylogenetic analyses place collections from Cyprus in a well-supported clade within *Gyromitra*, distant from its closest neighbour (*G. esculenta*) by 26 positions (3 % of sequence length) at the LSU locus. Considering the phylogenetic distances between presently accepted subgenera and unique morphoecological profile of the Cypriot collections, a new species and subgenus are here proposed.

Because of the cylindrical, elongated hollow stipe attached to the pileus only at the apex, *G. anthracobia* can strongly resemble a *Verpa* species in the field. However, the cerebriform pileus, brown-pigmented paraphyses and biguttulate cyanophilic spores, are all typical gyromitroid features. Although *G. esculenta* has similarly shaped and sized spores, it can be readily distinguished by its glabrous, chestnut-red pileus, its stout, lacunose stipe, attached to the pileus at several points forming chambers, and larger asci reaching 330–350 µm (Boudier 1909, Harmaja 1979, Breitenbach & Kränzlin 1984). *Gyromitra infula* has occasionally been reported from post-fire environments (Egger & Paden 1986), but has a saddle- or mitre-shaped pileus and narrowly ellipsoidal spores (measuring 19–23 × 7–8 µm acc to Dennis 1978, 19–26 × 7–10 µm acc to Van Vooren & Moreau 2009, or 20–30 × 7–9 µm acc to Medardi 2006). The rare *G. fastigiata* is typically associated with deciduous trees and has an intricately corrugated saddle-shaped pileus and ornamented triguttulate spores with polar appendages, measuring 24–32 × 11–15 µm (Svrček & Moravec 1972, Kotlaba & Pouzar 1974).

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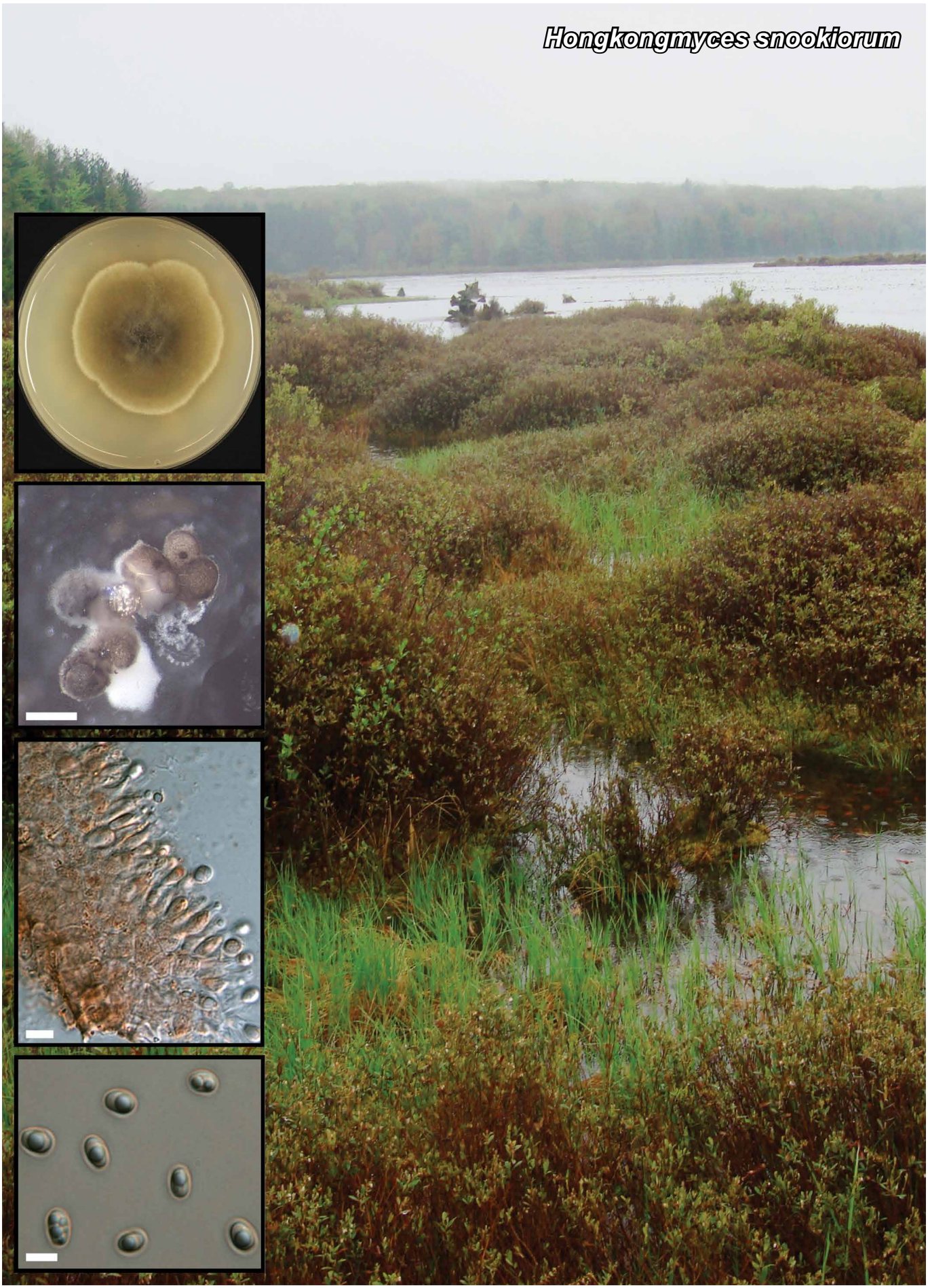

Hongkongmyces snookiorum

Fungal Planet 733 – 13 July 2018

Hongkongmyces snookiorum Raudabaugh, Iturr., & A.N. Mill., *sp. nov.*

Etymology. Named after Lucien and Shirley Snook for permitting research to be conducted on their property, which contributed to the discovery of this new species.

Classification — *Lindgomycetaceae*, *Pleosporales*, *Dothidiomycetes*.

On potato dextrose agar (PDA). *Conidiomata* pycnidial, globose to ampulliform, hyaline turning dark brown with age, up to 500 µm diam, with central ostiole to multiple ostioles, 10–15 µm diam; *outer wall* one cell layer of brown *textura prismatica* to *textura angularis*, inner wall 2–3 cell layers of brown *textura angularis*. *Conidiogenous cells* discrete, phialidic, hyaline, smooth, tightly aggregated, subulate to ampulliform, 7.5–10 × 4–4.5 µm, with sympodial proliferations. *Conidia* white in mass, hyaline, solitary, ellipsoid to ovoid, 4.5–5.5 × 3.5–4 µm, 1–2 central guttules when mature, several small guttules when young.

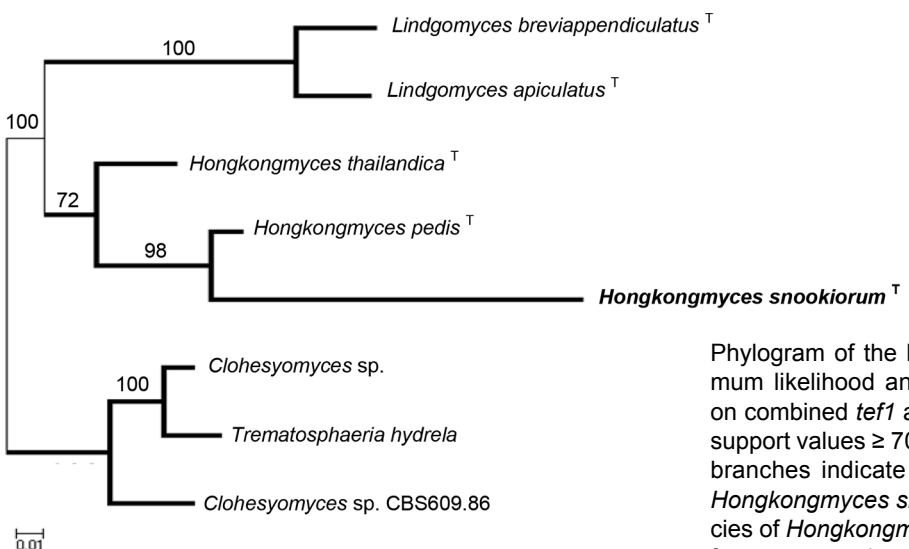
Culture characteristics — Colonies (holotype, 25 °C after 2 wk) moderately slow-growing on water agar (WA), cornmeal agar (CM), and potato dextrose agar (PDA). Colonies reaching 38–40 mm diam on WA, 18–21 mm diam on CMA, and 28–32 mm diam on PDA. Silky, hyaline on WA, felty, hyaline to white on CMA, and felty, greyish brown (D3–D5) (Kornerup & Wanscher 1978) with hyaline margin on PDA; margin even, appressed; reverse same as the mat.

Habitat — Submerged detritus from a fresh water fen.

Distribution — Known only from Pennsylvania, USA.

Typus. USA, Pennsylvania, Center County, near Philipsburg, Black Moshannon State Park, 40.9008, -78.0604, isolated from submerged detritus from a fresh water fen, 11 Aug. 2014, *D.B. Raudabaugh & M. Woodley* (holotype ILLS81638, ex-type strain DAOMC 251900, ITS-LSU and *tef1* sequences GenBank MH161189 and MH161190, MycoBank MB825179).

Notes — Phylogenetic analyses employing ML and Bayesian criteria of individual and concatenated *tef1* and ITS-LSU nrDNA sequences suggest that *H. snookiorum* and *H. pedis* are sister taxa. *Hongkongmyces snookiorum* can be distinguished from *H. pedis* based on habitat (fresh water fen vs human tissue), geography (USA vs Japan), and lack of a yellow to red pigment around the colony on PDA and oatmeal agar (OA) (Tsang et al. 2014).



Phylogram of the RAxML v. 8.2.10 (Stamatakis 2014) maximum likelihood analysis of *Hongkongmyces* species based on combined *tef1* and ITS-LSU nrDNA sequences. Bootstrap support values ≥ 70 % are shown above branches. Thickened branches indicate Bayesian posterior probabilities ≥ 95 %. *Hongkongmyces snookiorum* is shown in **bold**. The type species of *Hongkongmyces* is *H. pedis*. T = sequences generated from type specimens.

Colour illustrations. Background photo of freshwater fen; 14-d-old culture on OA; mature conidiomata with conidia in mass; conidiogenous cells with immature conidia; conidia. Photos: D. Raudabaugh and T. Iturriaga. Scale bars = 400 µm (conidiomata), 5 µm (all others).

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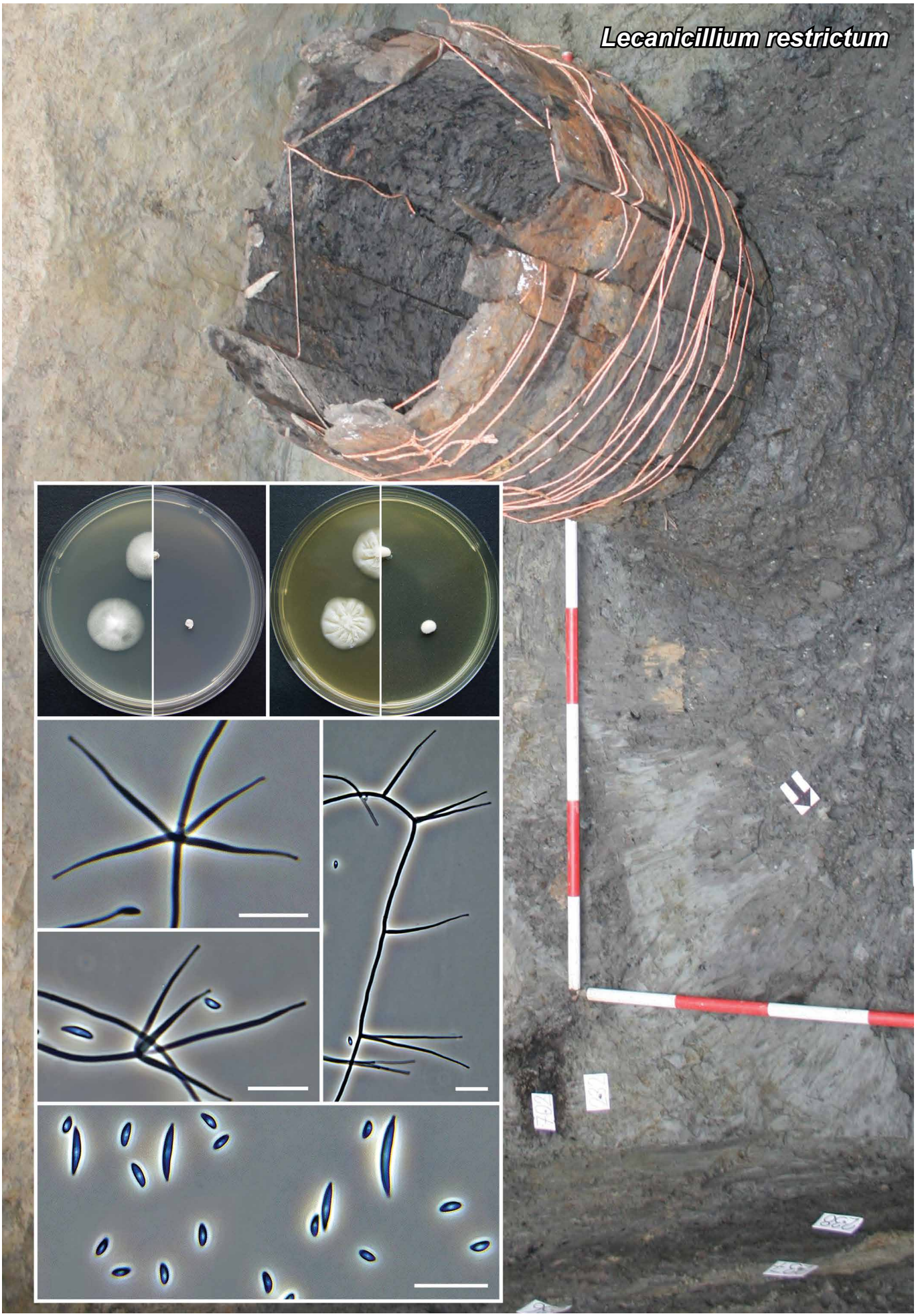
Lecanicillium restrictum

Fungal Planet 734 – 13 July 2018

Lecanicillium restrictum Hubka, Kubátová, Nonaka, Čmoková & Řehulka, *sp. nov.*

Etymology. *restrictum* (res.tric´tum. L. neut. part. adj.); limited, restricted, referring to the slow growth at room temperature (25 °C).

Classification — *Cordycipitaceae, Hypocreales, Sordariomycetes.*

On PCA: *Phialides* produced on aerial hyphae, solitary or aggregated in whorls of 2–5 phialides, tapering toward the tip, (12–)17–30(–36) µm long (mean ± standard deviation; 22.4 ± 4.8), basal part 0.5–1.5 (1.1 ± 0.2) µm wide, 0.3–0.5 µm wide on the tip. *Conidia* dimorphic, macroconidia with pointed ends, fusiform or slightly falcate, smooth-walled, 1-celled, (5–)6–10(–12) × 1–1.5 µm (7.5 ± 1.3 × 1.1 ± 0.1), microconidia usually without sharply pointed ends, ovate, ellipsoidal, obovate or fusoid, frequently slightly curved, smooth-walled, 1-celled, 2.5–3 × 1–1.5 µm (3 ± 0.4 × 1.1 ± 0.1). No microscopic crystals observed.

Culture characteristics — (in the dark, at 20 °C after 14 d): Colonies on PCA 20–23 mm diam (10–12 mm after 7 d), white, cottony, centrally raised, margin entire, no exudate and soluble pigments, reverse yellowish white (4A2; Kornerup & Wanscher 1967). Colonies on MEA 19–22 mm diam (10–12 mm after 7 d), yellowish white (4A2), waxy, delicately funiculose, umbonate, radially wrinkled, margin entire, no exudate and soluble pigments, reverse pale yellow (4A3). Colonies on PDA 21–25 mm diam (11–13 mm after 7 d), yellowish white (4A2), floccose to delicately funiculose, umbonate, radially wrinkled, margin entire, no exudate and soluble pigments, reverse yellowish white (4A2) to pale yellow (4A3). Growth rates at 15 °C on PCA/MEA/PDA: 8–10/8–10/9 mm after 7 d and 17–21/17–20/18–21 mm after 14 d, respectively. Growth rates at 25 °C on PCA/MEA/PDA: 1–3/2–4/2–4 mm after 7 d and 2–4/4–5/3–6 mm after 14 d, respectively. No growth to microcolonies on PCA and MEA at 27 °C; no growth at 30 °C.

Typus. Czech Republic, Starý Bohumín, surface of the wooden barrel found during archaeological excavations, 3 Mar. 2014, coll. *M. Kiecoň & P. Malík*, isol. *J. Řehulka* (holotype PRM 946543, isotype PRM 946544, culture ex-type CCF 5252 = CBS 143072; SSU-ITS-LSU, *tef1-α* and *tub2* sequences GenBank LT548279, LT626943 and LT989952, MycoBank MB824887).

Notes — BLAST analysis with the ITS rDNA region sequence gave closest hits to *L. testudineum* CCF 5201^{T} (99 %, 497/499 bp, GenBank LT548278), *L. kalimantanense* NBRC 105406^{T} (94 %, 465/494 bp, GenBank AB360356), *L. wallacei* CBS 101237^{T} (93 %, 448/484 bp, GenBank EF641891) and *Verticillium indonesiacum* BTCC-F36^{T} (93 %, 462/495 bp, GenBank AB378516). LSU rDNA showed 99 % similarity to *L. testudineum* (99 %, 589/592 bp, GenBank LT548278) and *L. wallacei* (541/548 bp, GenBank AY184967), and 98 % similarity to *L. kalimantanense* (580/589 bp, GenBank AB360356) and *V. indonesiacum* (580/589 bp, GenBank AB378516). The *tub2* sequence showed 91 % similarity to *L. testudineum* (1 225/1 348 bp, GenBank LT548284) and the *tef1-α* sequence 94 % similarity to *L. testudineum* (936/992 bp, GenBank LT626942).

Lecanicillium restrictum is characteristic by having slow growth at 25 °C, optimum temperature for growth around 20 °C and the production of dimorphic conidia. *Lecanicillium testudineum* has an optimum temperature for growth around 25 °C and smaller macroconidia than *L. restrictum*. Microconidia of *L. restrictum* are smaller than conidia produced by *L. kalimantanense* (3.5–12 × 1–2 µm) (Sukarno et al. 2009). Phialides of *V. indonesiacum* are most frequently produced in a single whorl at the end of erect hyphae (Sukarno et al. 2009). *Lecanicillium wallacei* grows more rapidly than *L. restrictum* on PCA at 20 and 25 °C (Zare & Gams 2001).

The best scoring maximum likelihood tree calculated from ITS rDNA and *tef1-α* sequences shows the species relationships within the genus *Lecanicillium*. The optimal partitioning scheme (PartitionFinder v. 1.1.1; Lanfear et al. 2012) divided the dataset into four partitions with the following substitution models: the GTR+G substitution model was used for ITS1 and ITS2 regions, JC+I model for the 5.8S nrDNA region and the 2nd codon positions of *tef1-α*, F81+I+G model for the 1st codon positions of *tef1-α*, and HKY+G model for the 3rd codon positions of *tef1-α*. The tree was constructed with IQ-TREE v. 1.4.0 (Nguyen et al. 2015). The dataset contained 30 taxa and a total of 1 583 characters of which 478 were variable and 357 parsimony-informative. Bootstrap support values at branches were obtained by generating 1 000 bootstrap replicates. Only bootstrap support values ≥ 70 % are shown; ex-type strains are indicated by a superscript ^{T}. The tree is rooted with *Simplicillium lanosoniveum* CBS 704.86 and *S. obclavatum* CBS 311.74^{T}.

For phylogenetic tree see Fungal Planet 735.

Colour illustrations. Wooden barrel found during archaeological excavations, Starý Bohumín, Czech Republic; 14-d-old colonies of *L. restrictum* on PCA (left) and MEA (right), left half of Petri dish: colony at 20 °C, right half: 25 °C; whorls of phialides and solitary phialides; micro- and macroconidia. Scale bars = 10 µm.

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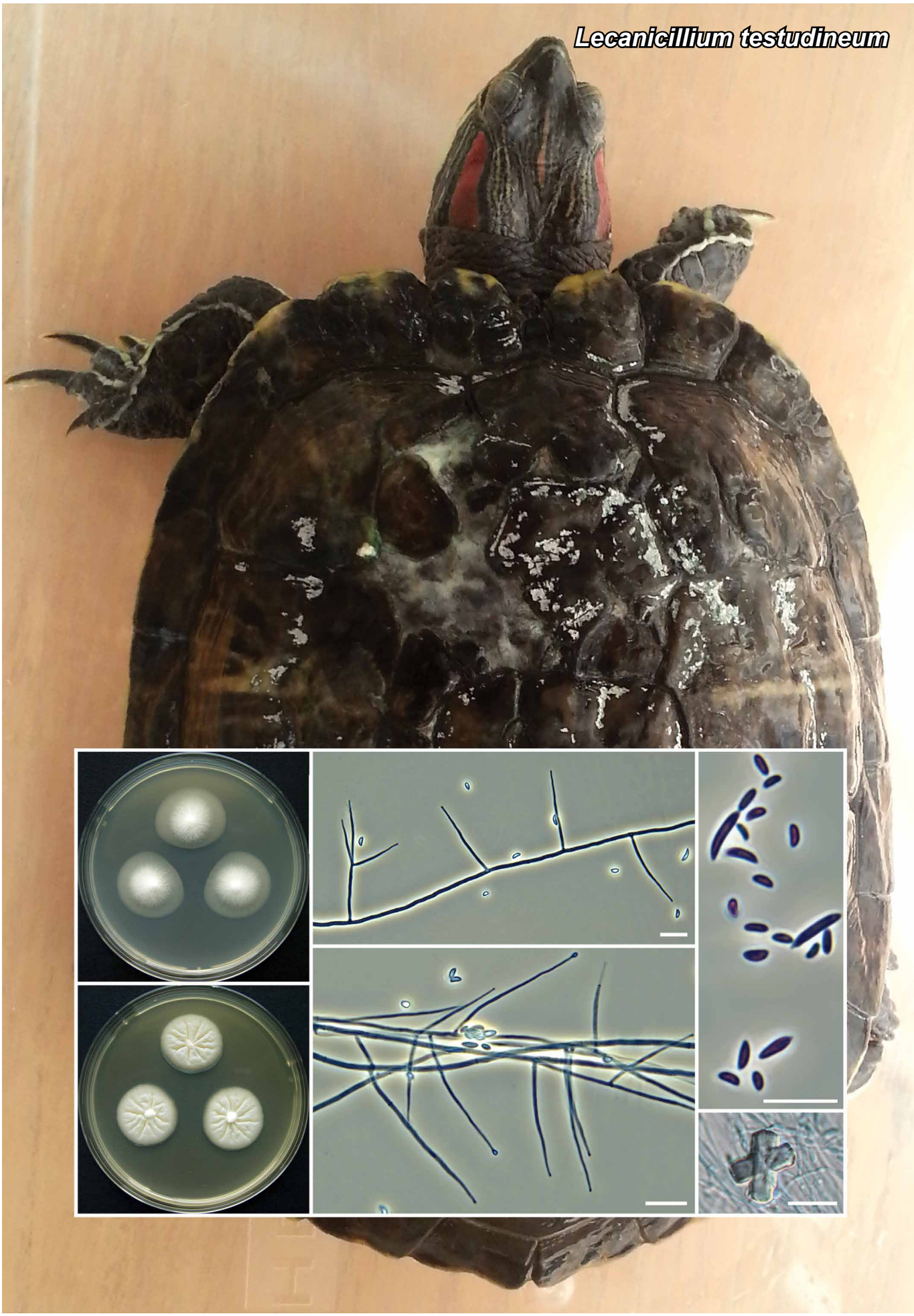

Lecanicillium testudineum

Fungal Planet 735 – 13 July 2018

Lecanicillium testudineum Hubka, Kubátová, Schauflerová, Déniel & Jany, *sp. nov.*

Etymology. *testudineum* (tes.tu.din'e.um. L. neut. adj.); referring to the turtle, the source of isolation of the ex-type strain.

Classification — *Cordycipitaceae, Hypocreales, Sordariomycetes.*

On PCA: *Phialides* produced on aerial hyphae, solitary or aggregated in whorls of 2–4 phialides, tapering toward the tip, (13–)16–45(–53) µm long (mean ± standard deviation; 25.9 ± 8.4), exceptionally up to 80 µm long, basal part 0.5–1 (0.8 ± 0.2) µm wide, 0.5–1 µm wide on the tip. *Conidia* dimorphic, macroconidia with pointed ends, fusiform or slightly falcate, smooth-walled, 1-celled, 3.5–6(–6.5) × 1–1.5 µm (4.8 ± 0.7 × 1.3 ± 0.1), microconidia usually with rounded ends, ovate, ellipsoidal, or fusoid, frequently asymmetric, curved to reniform, smooth-walled, 1-celled, 2–3.5 × 1–1.5 µm (2.7 ± 0.3 × 1.2 ± 0.1). Microscopic prismatic crystals occasionally present in culture, single or twinned (cruciform penetration twinning), up to 16 × 6 µm; no octahedral crystals observed.

Culture characteristics — (in the dark, at 25 °C after 14 d): Colonies on PCA 16–41 mm diam (9–21 mm after 7 d), white, cottony, centrally raised, margin entire, submerged, no exudate and soluble pigments, reverse yellowish white (4A2; Kornerup & Wanscher 1967). Colonies on MEA 16–33 mm diam (9–21 mm after 7 d), white, cottony and raised (ex-type strain CCF 5201) or yellowish white (4A2) to pale yellow (4A3), waxy and radially wrinkled (strains UBOCC-A-116026 and UBOCC-A-112180), margin entire, no exudate and soluble pigments, reverse yellowish white (4A2) to light yellow (4A4). Colonies on PDA 20–41 mm diam (9–21 mm after 7 d), white, cottony, centrally raised, colony surface or at least marginal parts radially wrinkled, margin entire, no exudate and soluble pigments, reverse pale yellow (4A3) to greyish yellow (4B5). Growth rates at 15 °C on PCA/MEA/PDA: 5–7/4–8/4–6 mm after 7 d and 9–15/8–14/8–12 mm after 14 d, respectively. Growth rates at 20 °C on PCA/MEA/PDA: 7–13/8–13/8–13 mm after 7 d and 15–25/13–19/17–25 mm after 14 d, respectively. Growth at 27 and 30 °C slower than at 25 °C; no growth at 37 °C.

Typus. Czech Republic, Prague, scales from the carapace of the captive red-eared slider (*Trachemys scripta elegans*), Aug. 2015, coll. *A. Schauflerová*, isol. *J. Koubková* (holotype PRM 935078, isotype PRM 935079, culture ex-type CCF 5201 = CBS 141096; SSU-ITS-LSU, *tef1-α* and *tub2* sequences GenBank LT548278, LT626942 and LT548284, MycoBank MB824886).

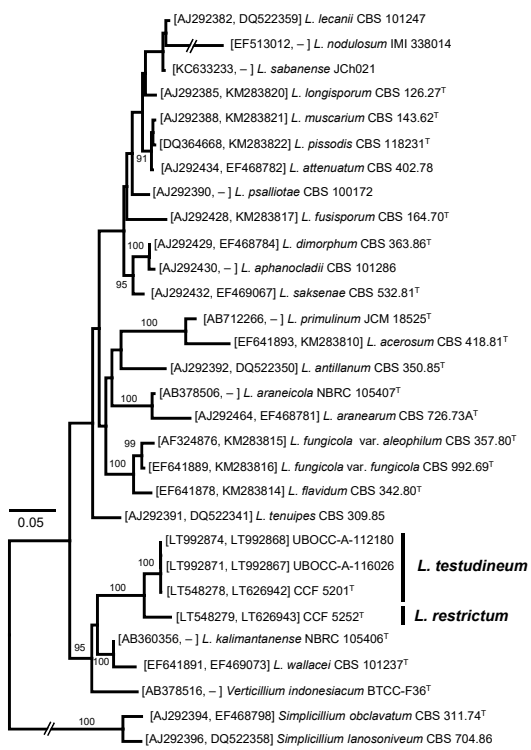
Additional material examined. France, Tours, chemical solution of nickel, Feb. 2012, isol. *F. Déniel*, UBOCC-A-112180 = CCF 5545, ITS, LSU, SSU, *tef1-α* and *tub2* sequences GenBank LT992874, LT992876, LT992875, LT992868 and LT992870; chemical solution of nickel, Oct. 2016, isol. *F. Déniel*, UBOCC-A-116026 = CCF 5546, ITS, LSU, SSU, *tef1-α* and *tub2* sequences GenBank LT992871, LT992873, LT992872, LT992867 and LT992869.

Colour illustrations. A red-eared slider (*Trachemys scripta elegans*) with superficial lesions on the carapace; 14-d-old colonies of *L. testudineum* on PCA (upper Petri dish) and MEA at 25 °C; whorls of phialides and solitary phialides; micro- and macroconidia; twinned prismatic crystals occasionally present in culture. Scale bars = 10 µm.

Notes — For BLAST analysis results see description of *Lecanicillium restrictum*. *Lecanicillium testudineum* has a higher optimum temperature for growth and smaller macroconidia than *L. restrictum*. Both micro- and macroconidia of *L. kalimantanense* and *L. wallacei* are longer than those of *L. testudineum* (Zare & Gams 2001, Sukarno et al. 2009). Phialides of *V. indonesiacum* are most frequently produced in a single whorl at the end of erect hyphae (Sukarno et al. 2009).

Intraspecific variability among isolates of *L. testudineum* was observed in colony morphology on MEA and PDA (see above) and growth parameters. Colony diameters of UBOCC-A-116026 were smaller on all media by 20–40 % compared to UBOCC-A-112180, and by 25–55 % compared to CCF 5201^T. The isolates UBOCC-A-116026 and UBOCC-A-112180 sporulated less intensively compared to CCF 5201^T, but otherwise there was a low degree of phenotypic variability in micromorphology, similarly to a low genetic variability in all five examined loci.

Lecanicillium testudineum has been isolated from nickel-containing solution and superficial lesions on carapaces of two captive red-eared sliders (*Trachemys scripta elegans*). We believe that the species was a causal agent of these infections, because it was isolated in pure culture during two subsequent examinations and fungal hyphae were observed in the direct microscopic examination. A more detailed case report will be published elsewhere. Infections due to *Lecanicillium* spp. in reptiles are rare and have only been reported in captive Guthega skinks (*Liopholis guthega*) (Scheelings et al. 2015).



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Lentithecium carbonneanum

Fungal Planet 736 – 13 July 2018

Lentithecium carbonneanum J. Fourn., Raja & Oberlies, *sp. nov.*

Etymology. Named after 'Carbonne' a commune in the Haute-Garonne department in south-western France where the type species was collected.

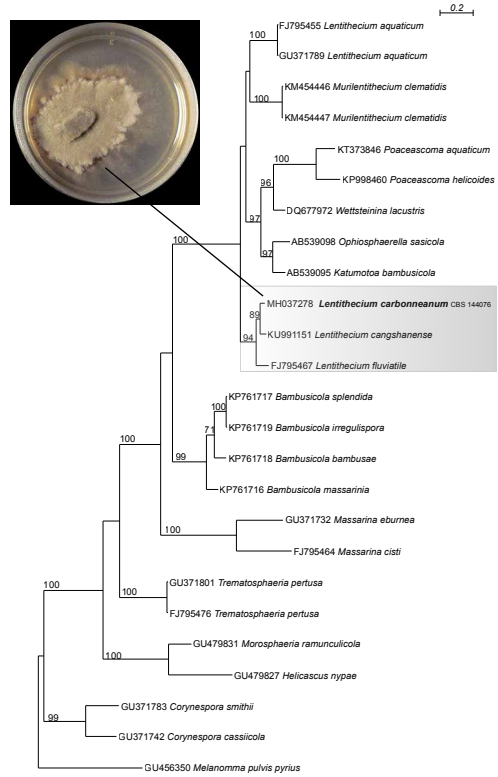
Classification — *Lentitheciaceae*, *Pleosporales*, *Dothideomycetes*.

Ascomata subglobose to depressed-spherical, scattered, 290–340 µm high, 380–420 µm diam, immersed to slightly erumpent, with a non-papillate porate ostiole, blackening host surface. *Peridium* 22–35 µm thick, pale to dark brown, pseudoparenchymatous, beneath a blackish brown clypeus 30–45 µm thick. *Asci* bitunicate, fissitunicate, narrowly clavate, 100–110 × 13.5–16 µm, with eight ascospores; uniseriate in lower half, irregularly biseriate in upper half, including a short straight to contorted stipe, 15–22 µm long, furcate at base; hamathecium of cellular pseudoparaphyses, 1.5–3 µm wide with free rounded tips, sparsely guttulate, embedded in mucilage. *Ascospores* (14.5–)17–19.5(–22) × (5.5–)6–7(–8) µm, quotient length/width (Q) = (2.4–)2.5–2.9(–3); n = 60 (mean = 18.2 × 6.7 µm; mean value of quotient length/width (Qe) = 2.7), ellipsoid-fusiform, 1-septate, strongly constricted at median septum, upper cell wider and slightly constricted at mid height, usually more obtusely rounded than lower one, with 3–4 large guttules, eventually 3-septate; wall 1 µm thick, yellowish brown, verrucose, with remnants of slimy material visible in Indian ink but without well-defined sheath.

Culture characteristics — Colonies on Potato Dextrose Agar (PDA; Difco, Detroit, MI, USA) attaining 30 mm diam after 4 wk at 25 °C, irregular, somewhat raised. Aerial mycelium appearing finely flocculose, colony surface dark to mouse grey, hyaline towards the margin with purple, vinaceous buff, filamentous; reverse black.

Typus. France, Haute-Garonne, Carbonne, SW of route du Lançon, 43.317932, 1.217286, artificial lake in a gravel pit, c. 200 m a.s.l., on submerged decorticated branch of *Populus*, 4 Apr. 2017, *J. Fournier* JF 17012 (holotype ILLS 81639, ex-holotype culture CBS 144076 = G951, single ascospore isolate from holotype, ITS-LSU, partial LSU and partial *rpb2* sequences GenBank MH062991, MH069699 and MH037278, MycoBank MB824593).

Notes — The genus *Lentithecium* was established for *L. fluviatile* (Zhang et al. 2009a). Although this genus was characterised by the lenticular ascomata, later work by Hyde et al. (2013) upon re-examination based on the holotype of *L. fluviatile* revealed that the species has globose ascomata, which agrees with the description of *L. carbonneanum*. Morphologically, the new species from France agrees well with the generic concept of *Lentithecium* in having globose ascomata, fissitunicate, short pedicellate asci, and hyaline, 1–3-septate fusiform ascospores with obtuse ends (Zhang et al. 2009a). More recently, species with brown ascospores (*L. cangshanense* and *L. voraginesporum*) have also been placed within *Lentithecium* (Su et al. 2016, Hyde et al. 2016). The genus *Lentithecium* currently includes six species, *L. cangshanense*, *L. clioninum*, *L. fluviatile*, *L. pseudoclioninum*, *L. unicellulare* and *L. voraginesporum* (Zhang et al. 2009a, b, Hyde et al. 2013, 2016, Tanaka et al. 2015, Su et al. 2016). *Lentithecium carbonneanum* is morphologically similar to *L. cangshanense*, and *L. voraginesporum* in having brown ascospores. *Lentithecium carbonneanum* is, however, different from *L. cangshanense* in having larger ascomata (290–340 µm high, 380–420 µm diam in *L. carbonneanum* vs 210–310 µm high, 220–320 µm diam in *L. cangshanense*). The asci in *L. carbonneanum* are also larger than in *L. cangshanense* (100–110 × 13.5–16 µm in *L. carbonneanum* vs 65–78 × 11–13 µm in *L. cangshanense*) (Su et al. 2016). *Lentithecium carbonneanum* differs from *L. voraginesporum* in habitat type; the former was described and isolated from submerged wood in a freshwater lake, while the latter was described and isolated from submerged, decayed *Phragmites australis* in the Arabian Gulf mangroves (Hyde et al. 2016). A molecular phylogenetic analysis of partial LSU sequences also clearly separates the two species from *L. carbonneanum* (see MycoBank). In addition, a phylogenetic analysis using partial *rpb2* sequences places the new species along with the type species, *L. fluviatile,* and *L. cangshanense*. In our analyses (partial LSU and partial *rpb2*), *L. aquaticum*, does not cluster with other sequenced species of *Lentithecium* including the type species, *L. fluviatile*.



Phylogram of the most likely tree (-lnL = 8822.39) from a PHYML analysis of 25 taxa based on partial *rpb2* sequence data (914 bp). Numbers refer to PHYML bootstrap support values ≥ 70 % based on 1 000 replicates. Strain G951 (CBS 144076) is indicated in **bold** and is identified as having phylogenetic affinities to members of the genus *Lentithecium.* Scale bar indicates nucleotide substitutions per site. A 30-d-old culture of G951 (CBS 144076) on PDA media is shown.

Colour illustrations. Background photo of the artificial lake in France where the fungus was collected (photo credit Marie Fournier); ascoma (scale bars = 1 mm in top photo, 100 µm in others); asci (scale bars = 50 µm); ascospores (scale bars = 10 µm).

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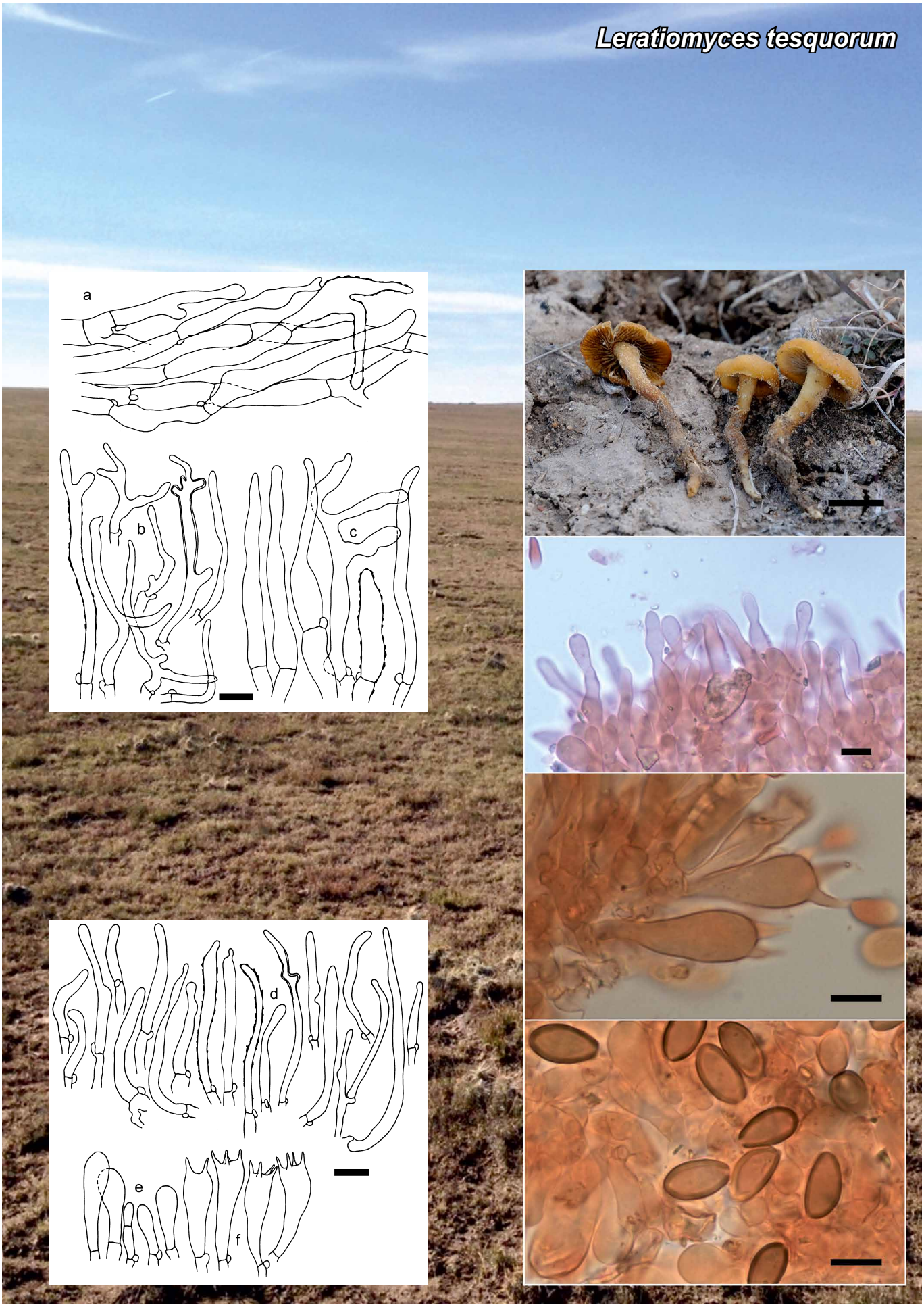
Leratiomyces tesquorum
a
b
c
d
e
f

Fungal Planet 737 – 13 July 2018

Leratiomyces tesquorum Adamčík & Vizzini, *sp. nov.*

Etymology. The specific epithet is the genitive plural of the Latin word *tesquum* (= desert place) and refers to the growing of the fungus in desert and arid areas.

Classification — *Strophariaceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata pileostipitate, with lamellar hymenophore. *Pileus* 14–18 mm wide, plano-convex, without or with low indistinct umbo in the centre, margin not striated (not even when wet), long involuted, surface hygrophanous, matt and shiny when wet, not viscid, near the pileus margin smooth and becoming rugulose towards centre, when wet Sahara-brown (6D5; Kornerup & Wanscher 1974) to yellowish brown (5D8) and dark brown towards centre (6F8), dry uniformly pale yellowish (more reddish than 4A3–4A4), no veil remnants observed. *Lamellae* adnate-emarginate, L = 32–46, l = 1–3, c. 3 mm broad, first ivory-yellow (4B3), later grey-brown (6E3) to brown (6E4). *Stipe* 30–40 × 3.5–6 mm, tapering towards base and rooting deep (20–30 mm) in substrate (sandy soil), often fusiform, surface strongly fibrillose especially near lamellae, without veil remnants, interior hollow, above yellowish brown (4C5 – chamois to 4B6 – amber-yellow), towards base darker brown (6E5). *Context* elastic, concolorous with surface, not changing after bruising or air-exposure, without distinctive *odour* (or faint radish like). *Spore-print* not obtained, probably dark brown. *Spores* (*n* = 32) (11–)11.5–*12.4*–13(–13.5) × (6–)6.5–*6.9*–7.5(–8) µm, Q = (1.63–)1.7–*1.79*–1.90(–2.01), ellipsoid, oblong or amygdaloidal, in frontal view ellipsoid, smooth, dark brown in 10 % KOH solution, walls 1 µm thick, truncate with large germ pore (1–1.5 µm wide), hilar appendage inconspicuous and hyaline. *Basidia* (31–)32.5–*34.5*–36.5(–39) × (9.5–)10–*11*–11.5(–12) µm broadly clavate, mainly 4-spored, occasionally 2- or 3-spored, mainly thin-walled but occasionally with slightly thickened walls, basidiola first cylindrical, then clavate, c. 3.5–10.5 µm wide. *Subhymenium* 25–30 µm thick, of 2–5 µm wide, intricate hyphae forming a pseudoparenchymatic structure, sharply delimited from parallel hyphae of lamellae trama, composed of < 50 µm long and c. 3–10 µm wide elements, often anastomosed and occasionally branched. *Cheilocystidia* abundant, (19.5–)25.5–*31.7*–37.5(–40) × (4.5–)5–*6*–6.5(–7) µm, thin-walled or with slightly thickened walls (< 0.5 µm), narrowly lageniform to subcylindrical, often moniliform, apically mainly subcapitate rounded, occasionally tapering. *Pleurocystidia* absent. *Pileipellis* ixocutis, c. 20–30 µm thick, composed of densely packed, horizontally oriented hyphae with intracellular yellow pigments, with mainly slightly or distinctly thickened walls, near the surface gelatinised and strongly incrusted by yellow-brown pigments, terminal elements near the pileus margin dispersed, narrowly lageniform, subulate or subcylindrical, apically often attenuated or constricted, occasionally with nodules or lateral branches, often flexuous, (32–)44–*62.2*–80(–91) × (4.5–)6–*8.7*–11(–12.5) µm; hyphal terminations near the pileus centre embedded in thick gelatinous matter that does not colour in Congo red, more attenuated, narrower and more nodulose-branched than those near the pileus margin, terminal elements look like ixohyphidia of *Flammulina velutipes*, measuring (32–)38.5–*52*.7–67(–92) × (2.5–)3–*4.1*–5(–5.5) µm. *Pileitrama* composed of irregularly oriented, branched, loose, intricate hyphae composed of c. 40–120 × 2–25(–30) µm elements, often nodulose. *Caulocystidia* present and abundant on stipe surface near just under the lamellae, (22–)32–*47.3*–62.5(–92) × (2.5–)3.6–*4.4*–5(–6) µm, often fasciculate in dense cluster, repent or ascending, subcylindrical, apically often constricted, occasionally nodulose or with lateral branches, towards apices usually flexuous, thin-walled or with slightly thickened walls, with yellow intracellular pigments and brownish yellow incrustations; caulocystidia completely disappear in lower part of the stipe. *Stipititrama* of parallel hyphae composed of c. 30–100 × 4–10(–15) µm large elements that are often nodulose, branched or anastomosed, often with thickened walls. *Clamp connections* present everywhere.

Habit, Habitat & Distribution — Solitary or gregarious, in arid and semi-arid grasslands, associated with *Poaceae* (*Bouteloua dactyloides*, *B. gracilis*, *Stipa hymenoides*). So far known only from USA, viz. Colorado (based on the presence of basidiomes), New Mexico and Utah (based on environmental sequences).

Typus. USA, Colorado, Weld Co., Great Plains prairies, Pawnee National grassland, N40°39'40" W104°5'17", short-grass prairie, cattle pasture, terrestrial on naked sandy soil, among scattered vegetation of *Opuntia* sp., buffalo grass (*Bouteloua dactyloides*) and other plants, 19 Oct. 2013, *S. Adamčík* (holotype SAV F-4052, ITS and LSU sequences GenBank MH043618 and MH036177, MycoBank MB 825174).

Additional material examined. ***Leratiomyces laetissimus***. Czech Republic, Prague-Spořilov, Chodovská street, 26 Sept. 2012, *J. Borovička*, PRM860990, ITS and LSU sequences GenBank MH043619 and MH036178. ***Leratiomyces squamosus***. Czech Republic, Malonty - Bělá, 28 Sept. 2008, *O. Jindřich*, PRM922211, ITS and LSU sequences GenBank MH043620 and MH036179. ***Pholiota squarrosa***. Czech Republic, Bílina, Bořeň, 15 Oct. 2013, *M. Kříž*, PRM923259, ITS and LSU sequences GenBank MH043621 and MH036180.

Notes — A phylogenetic estimation using Maximum likelihood (ML) on the nrITS sequences revealed that a major clade, here named as the *Leratiomyces laetissimus* complex, is highlighted within the genus *Leratiomyces*. This clade encompasses the minor clades 1–3 and the *Psilocybe calongei* lineage. Clade 1 consists of environmental sequences of an uncultured root-associated (endophyte) fungus of *Bouteloua gracilis* (USA, New Mexico; Porras-Alfaro et al. 2008); clade 2 of *L. tesquorum*, two sequences of an uncultured mycorrhizal fungus (endophyte) of *Stipa hymenoides* (USA, Utah; Hawkes et al. 2006) and several sequences of an uncultured root-associated (endophyte) fungus of *Bouteloua gracilis* (USA, New Mexico; Porras-Alfaro et al. 2008); clade 3 of *L. laetissimus* and *Leratiomyces* sp. SC5F2-1.

For supplementary information see MycoBank.

Colour illustrations. Great Plains prairies, Pawnee National grassland, short-grass dry prairie with *Opuntia* sp. and *Bouteloua dactyloides*, where the holotype was collected. Right: Basidiomes; cheilocystidia; basidia and spores (all from holotype). Left: Structure of pileipellis near the pileus margin (a), hyphal terminations in pileipellis near the pileus centre (b) and margin (c); caulocystidia (d), basidiola (e) and basidia (f, all from holotype). Microscopic elements were observed in Congo red. Scale bars = 10 mm (basidiomes), 10 µm (microscopic structures). All photos and drawings by S. Adamčík.

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Lomentospora valparaisensis

Fungal Planet 738 – 13 July 2018

Lomentospora valparaisensis E. Álvarez, *sp. nov.*

Etymology. Referring to Valparaiso, where this fungus was collected, Italy Park, Valparaiso, Chile.

Classification — *Microascaceae, Microascales, Sordariomycetes*.

Hyphae hyaline to pale brown, 1–3 µm wide, thin- to thick-walled, smooth, and septate. Conidiogenous cells of two types: i) solitary, consisting of a single conidiogenous cell disposed laterally on undifferentiated hyphae or in side branches. *Conidiogenous cells* enteroblastic, percurrent (annellides), thin- and smooth-walled, cylindrical or slightly broad at the base and with several broad scars at the upper part, 6–40 × 1.5–4 µm, producing conidia singly, or in slimy masses similar in shape and size to the sessile conidia, but with a broader basal scar. This type of conidiogenous cells resembles those observed in *Scedosporium apiospermum*; ii) aggregated in small brushes, flask-shaped, often bearing a long, inconspicuously annellated zone, inflated at base. This type resembles those observed in *Lomentospora prolificans*. Morphologically, these strains seem to be intermediate between these previously cited species. *Conidia* sessile or situated on conidiogenous cells, at first hyaline, later becoming pale brown, thick- and smooth-walled, regularly ellipsoid, rounded at the ends, but with a small flattened area at the base, 5.5–6.5 × 4–5 µm. *Synnemata* and *sexual morph* not observed.

Culture characteristics — Colonies on Potato Dextrose Agar (PDA) attaining 15 mm diam after 14 d at 25 °C, velvety, olivaceous green, reverse blackish. Colonies on Sabouraud Dextrose Agar (SDA) attaining 12–15 mm diam after 14 d at 25 °C, velvety, olivaceous green; reverse black. Growth observed at 15, 25, 37, 40 and 42 °C, but no growth at 5 and 48 °C.

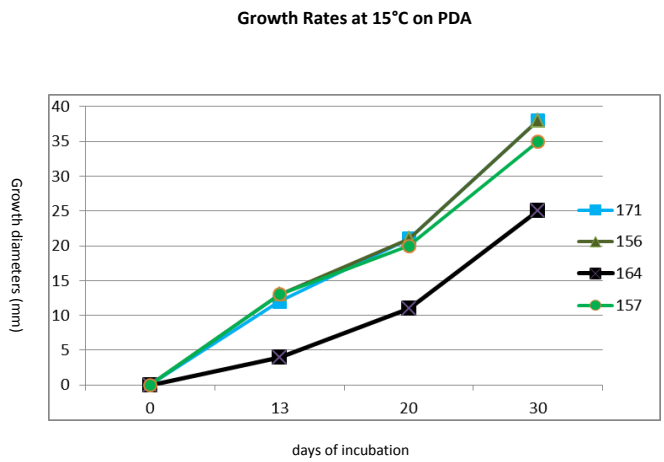
Typus. Chile, Valparaiso, Italy Park, from soil, 2016, *F. Salas* (holotype Vlpo164, culture ex-type ChFC-164, ITS and *tub2* sequences GenBank MG495075 and MG544878, MycoBank MB824509).

Additional material examined. Chile, Valparaiso, O'Higgins Square, from soil, 2017, *E. Álvarez*, specimen Vlpo505, culture ChFC-505, ITS and *tub2* sequences GenBank MG495076 and MG544879.

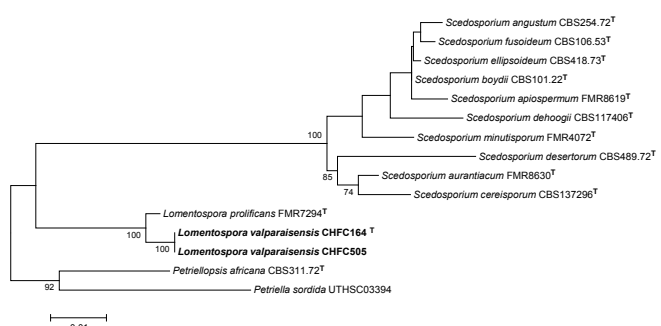
Notes — This fungus was isolated from soil samples from parks and squares of Valparaiso. Macroscopically, *L. valparaisensis* resembles *L. prolificans* (Hennebert & Desai 1974). Both species have dematiaceous colonies in all media tested. However, *L. valparaisensis* has green colonies, while *L. prolificans* exhibits olivaceous grey colonies that become olivaceous green with age. Microscopically, *L. valparaisensis* presents two types of conidiogenous cells; one of them resembling *L. prolificans*, and the other type resembles those observed in *S. apiospermum*. In fact, *L. valparaisensis* seems to be intermediate between *L. prolificans* and *S. apiospermum*.

Based on BLAST search results, the closest hits with ITS sequences was *L. prolificans* (GenBank KC254095; Identities = 528/528 (100 %), no gaps) and *Petriella setifera* (GenBank KX449497; Identities = 489/533 (92 %), 14 gaps (2 %)); by using *tub2* the closest hits were *L. prolificans* (GenBank AJ890127; Identities = 470/481 (98 %), 3 gaps (0 %)) and *Pseudallescheria africana* (GenBank AJ890132; Identities 437/484 (90 %); 16 gaps (3 %)).

Our phylogenetic inference, performed using the ITS and *tub2* sequences, demonstrated that our fungus represents a new species of the genus *Lomentospora*, being closely related to *L. prolificans*. *Lomentospora valparaisensis* can be distinguished from *L. prolificans* based on its slow growth at 15 °C compared to that of *L. prolificans*. They can also be distinguished based on the homogeneous size and shape of the sporangiospores (5.5–6.5 × 4–5 µm) compared with those observed in *L. prolificans* (3–7 × 2–5 µm). In addition, our strains showed mixed conidiogenous cells: i) those arising from undifferentiated hyphae, cylindrical to somewhat flask-shaped (*S. apiospermum* group-like); and ii) those flask-shaped, locally aggregated in small brushes (*L. prolificans*-like). Moreover, *L. valparaisensis* can be differentiated from *Scedosporium* spp. by its colony colour on various culture media.



156: *Lomentospora prolificans;* 157: *Lomentospora prolificans;*
171: *Lomentospora prolificans;* 164: *Lomentospora valparaisiensis*



Maximum Likelihood tree obtained from the concatenated DNA sequences from two loci (ITS and *tub2*) of our isolates and sequences retrieved from GenBank database. Tree was built by using PhyML 3.0. Bootstrap support values (≥ 70 %) are given above the branches. *Petriellopsis africana* CBS 311.72 and *Petriella sordida* UTHSC 03-394 were used as outgroup. The new species proposed in the present study is indicated in **bold** face. T = ex-type.

Colour illustrations. Italy Park, Valparaiso; colony after 15 d at 25 °C on PDA; two types of conidiogenous cells and conidia. Scale bars = 10 µm.

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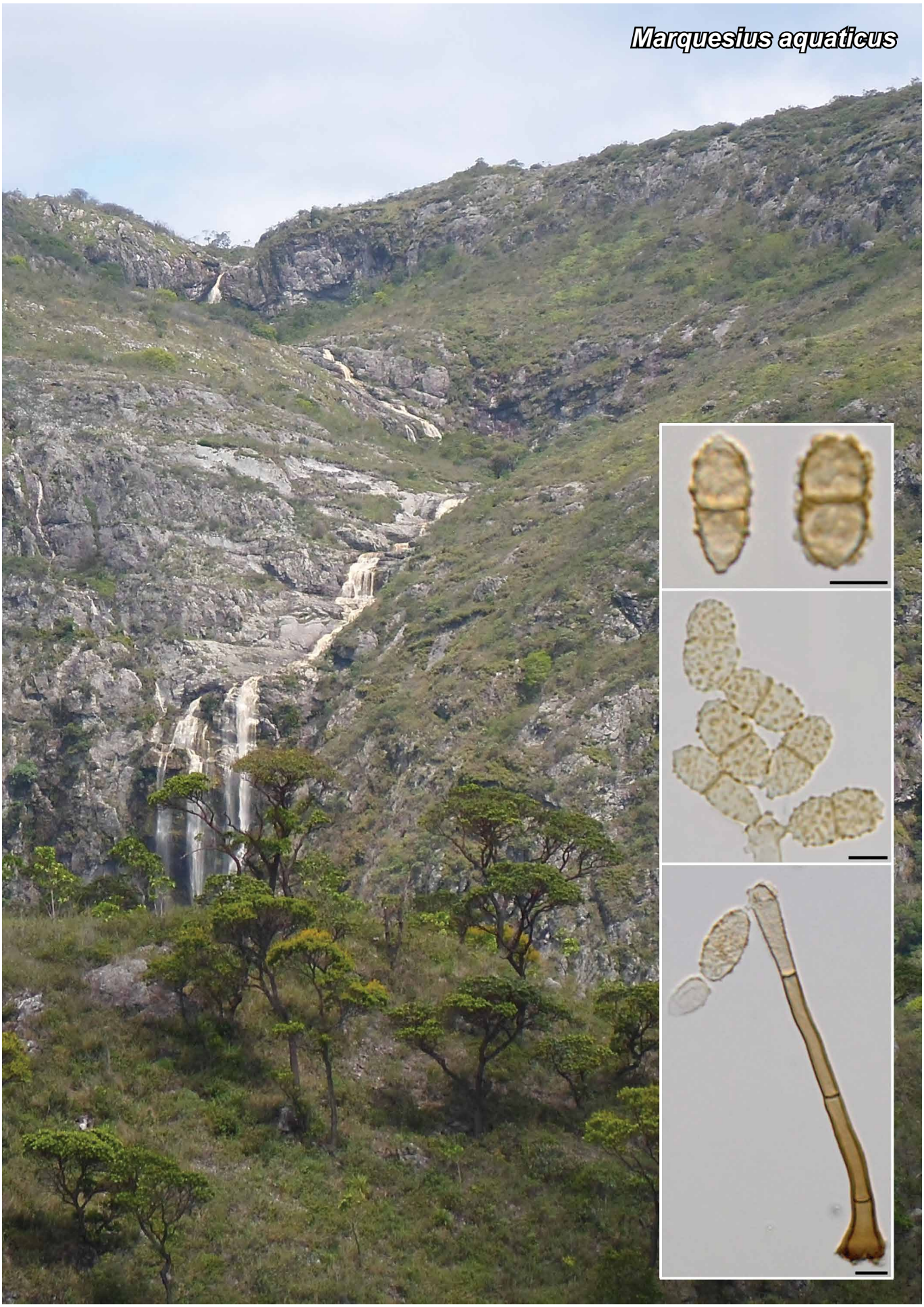
Marquesius aquaticus

Fungal Planet 739 – 13 July 2018

Marquesius L.B. Conç., R.F. Castañeda & Gusmão, *gen. nov.*

Etymology. Named for Dr Marcos F.O. Marques (in memoriam), recognising his contribution to popularisation of mycology in the northeast of Brazil.

Classification — *Incertae sedis, Dothideomycetes*.

Colonies on the natural substrate effuse. *Mycelium* partly superficial, partly immersed. *Conidiophores* macro- and mononematous, erect, simple or branched, straight or slightly curved, cylindrical, sometimes with percurrent extension, septate, smooth or rarely verrucose, brown to pale brown, basal cells lobed or sometimes inflated. *Conidiogenous cells* mono- or polyblastic, denticulate, integrated. *Denticles* conspicuous, cylindrical, truncate at apex. Conidial secession schizolytic. *Conidia* acropleurogenous, holoblastic, simple, in acropetal chains, dry, septate, constricted or not at septa, thick-walled, verrucose, brown to pale brown, sometimes with a conspicuous hilum at base.

Type species. Marquesius aquaticus L.B. Conç., R.F. Castañeda & Gusmão.

MycoBank MB823622.

Marquesius aquaticus L.B. Conç., R.F. Castañeda & Gusmão, *sp. nov.*

Etymology. Name refers to the aquatic habitat, from which this fungus was collected.

Colonies on the natural substrate effuse, sparse, hairy, pale brown. *Mycelium* partly superficial, partly immersed, composed of septate, branched, smooth, pale brown hyphae, 2–3 µm wide. *Conidiophores* macro- and mononematous, erect, simple or rarely with apical branched, straight or slightly curved, cylindrical, sometimes with percurrent extension by regenerative growth unrelated to conidiation, 3–7-septate, thick-walled, smooth, brown to pale brown toward the apex, basal cells lobed or sometimes inflated, 45–202.5 × 3–4.5 µm. *Conidiogenous cells* mono- or polyblastic, denticulate, determinate or with several, short sympodial extension, integrated, terminal or rarely subterminal, smooth, verruculose to verrucose, where terminal, usually inflated at apex, 11–20 × 3–6 µm, 1.5–3 µm wide at base, where subterminal, cylindrical, 16–18 × 2–3 µm. *Denticles* predominately at apex of conidiogenous cells, cylindrical, truncate, slightly melanised margin, 0.5–1.5 × 0.5–1 µm. Conidial secession schizolytic. *Conidia* acropleurogenous, holoblastic, simple, in short acropetal chains (1–2 on natural substrate; 4–5 on culture), dry, 0–1-septate, constrict or not at septa, ellipsoidal to narrowly clavate, thick-walled, verrucose, pale brown, 9–15 × 4–8 µm (on Corn Meal Agar (CMA) ellipsoidal to clavate, 9–14 × 4–6 µm), sometimes with a conspicuous hilum at base.

Culture characteristics — Colonies on CMA with slow development (attaining 25 mm diam in 7 wk at 25 °C), circular, sparse aerial mycelium, raised to umbonate, entire edges, surface with central brown and black margins, reverse black.

Typus. Brazil, Bahia, Pindobaçu, Serra da Fumaça, on submerged decaying twig and leaves of unidentified plant, 26 July 2016, *L.B. Conceição* (holotype HUEFS-216710, culture ex-type CCLAMIC 153/16, ITS and LSU sequences GenBank MG572717 and MG572718, MycoBank MB823623).

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Dothideomycetes* sp. KO-groupB 2014 (GenBank AB986428.1; Identities = 616/616 (100 %), no gaps), *Dothideomycetes* sp. genotype 377 isolate FL0753 (GenBank JQ760416.1; Identities = 523/559 (94 %), 7 gaps (1 %)) and *Sympodiella acicola* strain CBS 487.82 (GenBank KY853530.1; Identities = 563/631 (89 %), 18 gaps (2 %)). Closest hits using the ITS sequence had highest similarity to *Dothideomycetes* sp. KO-groupB 2014 (GenBank AB986428.1; Identities = 555/559 (99 %), no gaps), *Dothideomycetes* sp. genotype 377 isolate FL0753 (GenBank JQ760416.1; Identities = 458/547 (84 %), 29 gaps (5 %)) and *Cylindrosympodium lauri* strain CBS 240.95 (GenBank EU035414.1; Identities = 319/366 (87 %), 13 gaps (3 %)). *Castanedaea minor* (Partridge et al. 2001) represents a monotypic genus and it resembles *Marquesius* morphologically, although the presence of conspicuous denticles distinguishes it. The conidiogenous cells of *Marquesius* are more similar to *Cylindrosympodium* than *Sympodiella*. Apparently, the OTUs (GenBank AB986428 and JQ760416.1) isolated from *Cenococcum* 'black sclerotia' (Obase et al. 2014), are specimens of the same genus.

Colour illustrations. Serra da Fumaça, Pindobaçu, Brazil; general aspect; conidiogenous cells and conidia. Scale bars = 5 µm.

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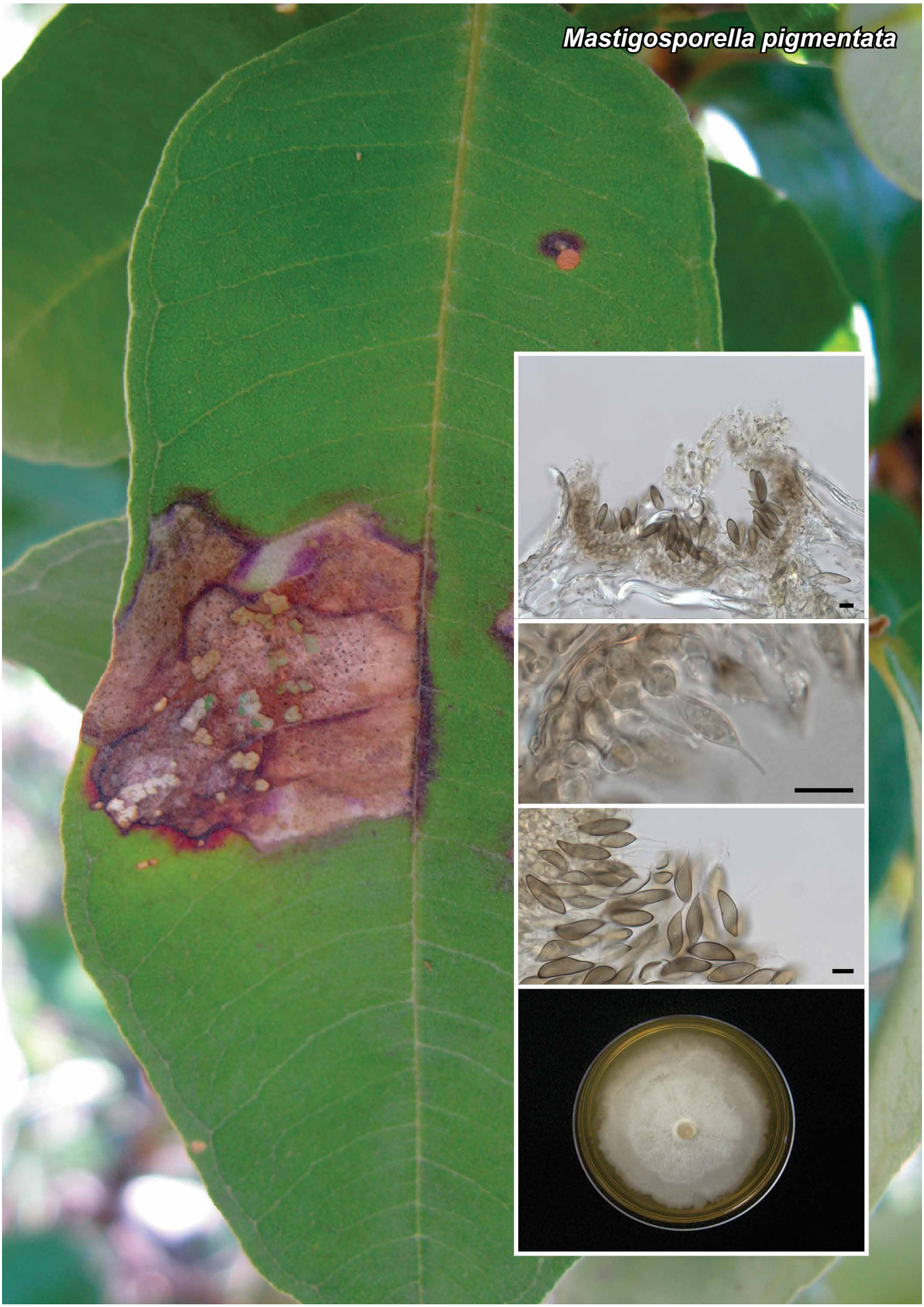
Mastigosporella pigmentata

Fungal Planet 740 – 13 July 2018

Mastigosporella pigmentata V.P. Abreu & O.L. Pereira, *sp. nov.*

Etymology. Refers to the pigmented conidia of the species.

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

Conidiomata immersed, pycnidial, up to 160 µm diam, pale brown on host tissue; wall of 4–6 layers of pale brown to brown *textura globulosa* to *subglobosa*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* pale brown, smooth, ampulliform or doliiform, 4.5–9 × 4–7 µm. *Conidia* solitary, aseptate, ellipsoid to fusiform, unicellular, pale brown, sometimes slightly darker at the ends, smooth, thick-walled, developing a solitary apical appendage (cellular, type A1 *sensu* Nag Raj 1993), which is part of the conidial body, developing while still attached to the conidiogenous cell, attenuating into an acutely rounded tip; conidium body 21–33 × 6.5–9.5 µm (excluding appendage); basal hilum truncate, 1.5–2 µm diam, apical appendage developing as continuation of conidium body, containing cytoplasm, 11–28 µm.

Culture characteristics — Colonies on malt extract agar 63 mm diam after 5 d at 25 °C with a photoperiod of 12 h, margins irregular, white aerial mycelium, colonies fertile.

Typus. Brazil, Minas Gerais, Paraopeba, Floresta Nacional de Paraopeba (FLONA-Paraopeba), on leaves of *Qualea parviflora* (*Vochysiaceae*), 31 Jan. 2016, *V. P. Abreu & O.L. Pereira* (holotype VIC 44383, culture ex-type COAD 2370; ITS, LSU and *tef1* sequences GenBank MG587929, MG587928 and MH020056, MycoBank MB823670).

Notes — Species of the coelomycete genus *Mastigosporella* are characterised by yellowish brown to dark brown pycnidial conidiomata and hyaline conidiogenous cells with enteroblastic-percurrent proliferation to produce additional narrowly ellipsoid to fusiform conidia bearing an appendage of type A1 (appendage initially arising as a tubular extension of the conidium body) (Nag Raj 1993). Presently, the genus *Mastigosporella* is known from three species, *M. hyalina*, *M. anisophylleae* and *M. georgiana* (Nag Raj 1993, Crous et al. 2013, Rossman et al. 2015, Senanayake et al. 2017). Only one species of *Mastigosporella* (*M. anisophylleae*) is known from culture and DNA sequence data (Crous et al. 2013, Senanayake et al. 2017). *Mastigosporella pigmentata* clearly differs from *M. hyalina*, *M. anisophylleae* and *M. georgiana* by having pale brown conidia and conidiogenous cells. *Mastigosporella pigmentata* presents larger and wider conidia than *M. hyalina* and *M. georgiana*. *Mastigosporella pigmentata* has conidia similar in length to *M. anisophylleae*, but distinguishable from it by being wider. In addition, the conidia of *M. pigmentata* presents apical appendages longer than *M. anisophylleae* and *M. hyalina.* Members of this genus were reported from the USA and Zambia on leaves of *Quercus coccinea*; on leaves and petioles of *Nyssa biflora* and *Nyssa sylvatica* and on *Anisophyllea* sp. (Nag Raj 1993, Crous et al. 2013, Senanayake et al. 2017). To our knowledge this is the first report of the occurrence of the genus *Mastigosporella* in Brazil. Phylogenetic analysis and morphological comparisons support the introduction of *M. pigmentata* as a new species within this genus.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Mastigosporella anisophylleae* (GenBank NR_137844; Identities = 508/568 (89 %), 16 gaps (2 %)), *Harknessia communis* (GenBank KY979780; Identities = 517/580 (89 %), 23 gaps (3 %)) and *Harknessia eucalyptorum* (GenBank AY720747; Identities = 501/564 (89 %), 23 gaps (4 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Harknessia lythri* (GenBank AF408364; Identities = 809/815 (99 %), no gaps), *Cryphonectria decipiens* (GenBank JQ862750; Identities = 807/815 (99 %), no gaps) and *Latruncellus aurorae* (GenBank NG_042572; Identities = 807/815 (99 %), no gaps).

tef1. On a megablast search of NCBIs GenBank nucleotide database, no significant hits were obtained.

Morphological characteristics (in µm) of *Mastigosporella* spp.

Species	Conidia	Conidiogenous cells	Apical appendage	References
Mastigosporella anisophylleae	(21–)27–30(–32) × (4.5–)5–5.5(–6)	5–12 × 3–5	(5–)6–7(–8)	Crous et al. (2013)
Mastigosporella georgiana	16–25 × 5–7	5–10 × 2.5–6	12–26 × 1	Nag Raj (1993), Rossman et al. (2015)
Mastigosporella hyalina	18–28 × 3.5–5	7–11 × 3–4(–5)	5–10(–12)	Nag Raj (1993)
Mastigosporella pigmentata	**21–33 × 6.5–9.5**	**4.5–9 × 4–7**	**11–28**	**This study**

Colour illustrations. Leaf spot symptoms on *Qualea parviflora* (*Vochysiaceae*) in Floresta Nacional de Paraopeba, state of Minas Gerais, Brazil; vertical section of conidiomata; conidiogenous cell with developing pigmented conidia; mature pale brown conidia with apical appendages; colony on MEA after 5 d at 25 °C. Scale bars = 10 µm.

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Matsushimaea monilioides

Fungal Planet 741 – 13 July 2018

Matsushimaea monilioides Iturrieta-González, Dania García & Gené*, sp. nov.*

Etymology. Name refers to the moniliform filaments in conidia.

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

Mycelium consisting of branched, septate, olive, smooth-walled, 1–2 µm diam hyphae, frequently forming hyphal coils, occasionally with irregular swellings not constricted at the septa. *Conidiophores* micronematous, often reduced to conidiogenous cells with conidia arising directly on hyphae. *Conidiogenous cells* integrated, mono- or polyblastic, intercalary or terminal, elongated, 7–14.5 × 2–4 µm, pale brown, smooth-walled. *Conidia* solitary, sessile or on short protrusions, irregularly shaped, composed of a basal cell from which arise acropetal chains of cells, giving place to moniliform, septate, often branched filaments, up to 46 µm long and 2–4.5 µm wide, remaining attached at maturity; cells globose, subglobose, ellipsoidal to somewhat pyriform, 2.5–5.5 × 2–4.5 µm, brown, smooth-walled. *Sexual morph* not observed.

Culture characteristics — Colonies on PDA reaching up to 13 mm diam after 14 d at 25 °C, yellowish brown, velvety, flat, aerial mycelium scarce, margin entire; reverse dark brown. On OA up to 14 mm diam after 14 d at 25 °C, dark brown, dusty, flat; reverse dark brown. No growth at 37 °C.

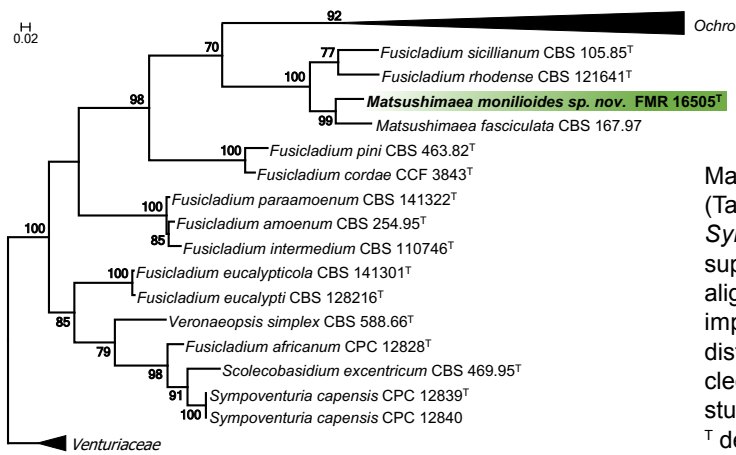
Typus. Spain, Catalonia, Tarragona, Parc Samà, garden soil, Feb. 2017, *J. Gené & I. Iturrieta-González* (holotype CBS H-23392; cultures ex-type FMR 16505 = CBS 143867, ITS and LSU sequences GenBank LT883468 and LT883469, MycoBank MB823930).

Notes — The genus *Matsushimaea* was erected by Subramanian (1977) to accommodate *Torula fasciculata*, a fungus described by Matsushima (1975) and characterised by the production of sessile branched conidia arising directly from vegetative hyphae. In addition to the type, *M. fasciculata*, the genus currently includes two other species, *M. fertilis* (Castañeda-Ruiz et al. 1996) and *M. magna* (Matsushima 1996). The three species were found on leaf litter from Japan, Cuba and South Africa, respectively. Considering the lack of molecular data for *Matsushimaea* and that only for *M. fertilis* ex-type cultures were available for comparison, we selected a reference strain of *M. fasciculata* (CBS 167.97), which morphological features fit with those of the protologue of the species, in order to elucidate the phylogenetic position of the genus among ascomycetes and determine its relationships with our fungus. A phylogenetic analysis with the rDNA operon (ITS and LSU) placed the CBS strain of *M. fasciculate* in the family *Sympoventuriaceae* and it was closely related to our strain. However, both strains showed genetic differences (99 % similar with LSU, 86 % with ITS) enough to be considered distinct species.

Matsushimaea monilioides morphologically resembled *M. fertilis*. However, a megablast search with ITS and LSU sequences of the ex-type strain (INFAT C93/204 = IMI 358617) of this latter species showed it was related to the genus *Cladophialophora* (*Herpotrichiellaceae*, *Chaetothyriales*), being highly similar to the sequences of the ex-type of *C. boppii* (CBS 126.86; LSU 100 % similar with GenBank FJ358233 and ITS 98 % similar with GenBank NR_131297). Therefore, *M. fertilis* was excluded in the present phylogenetic analysis.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using LSU sequence of *M. monilioides* with other sympoventuriaceous species were *Fusicladium sicillianum* (CBS 105.85; GenBank FN398150.1) with a similarity of 95 % (531/557) and *Fusicladium rhodense* (CBS 121641; GenBank EU035440.1) also 95 % (812/855) similar. The closest hits using the ITS sequence were *F. rhodense* (CBS 121641; GenBank EU035440.1) and *F. sicillianum* (CBS 105.85; GenBank FN549914.1) with a similarity of 86 % (402/470) and 85 % (390/459), respectively.

Matsushimaea fasciculata and *M. magna* morphologically differ from our fungus in conidial morphology; while the conidia of the former are more regularly shaped, obconical to cupulate and measure 30–45 µm long (Matsushima 1975), those of *M. magna* are larger, up to 100 µm long (Matsushima 1996).



Maximum likelihood tree inferred with MEGA v. 6 software (Tamura et al. 2013) from the analysis of ITS sequences of *Sympoventuriaceae* and *Venturiaceae* families. Bootstrap support values above 70 % are indicated on the nodes. The alignment included 665 bp and was performed with ClustalW implemented in MEGA. Tamura 3-parameter with Gamma distribution and Invariant sites (G+I) was used as the best nucleotide substitution model. The new species proposed in this study is indicated in **bold** face in the green box. A superscript T denotes ex-type cultures.

Colour illustrations. Parc Samà, Tarragona, Spain; colony sporulating on OA and conidia after 14 d at 25 °C. Scale bars = 10 µm.

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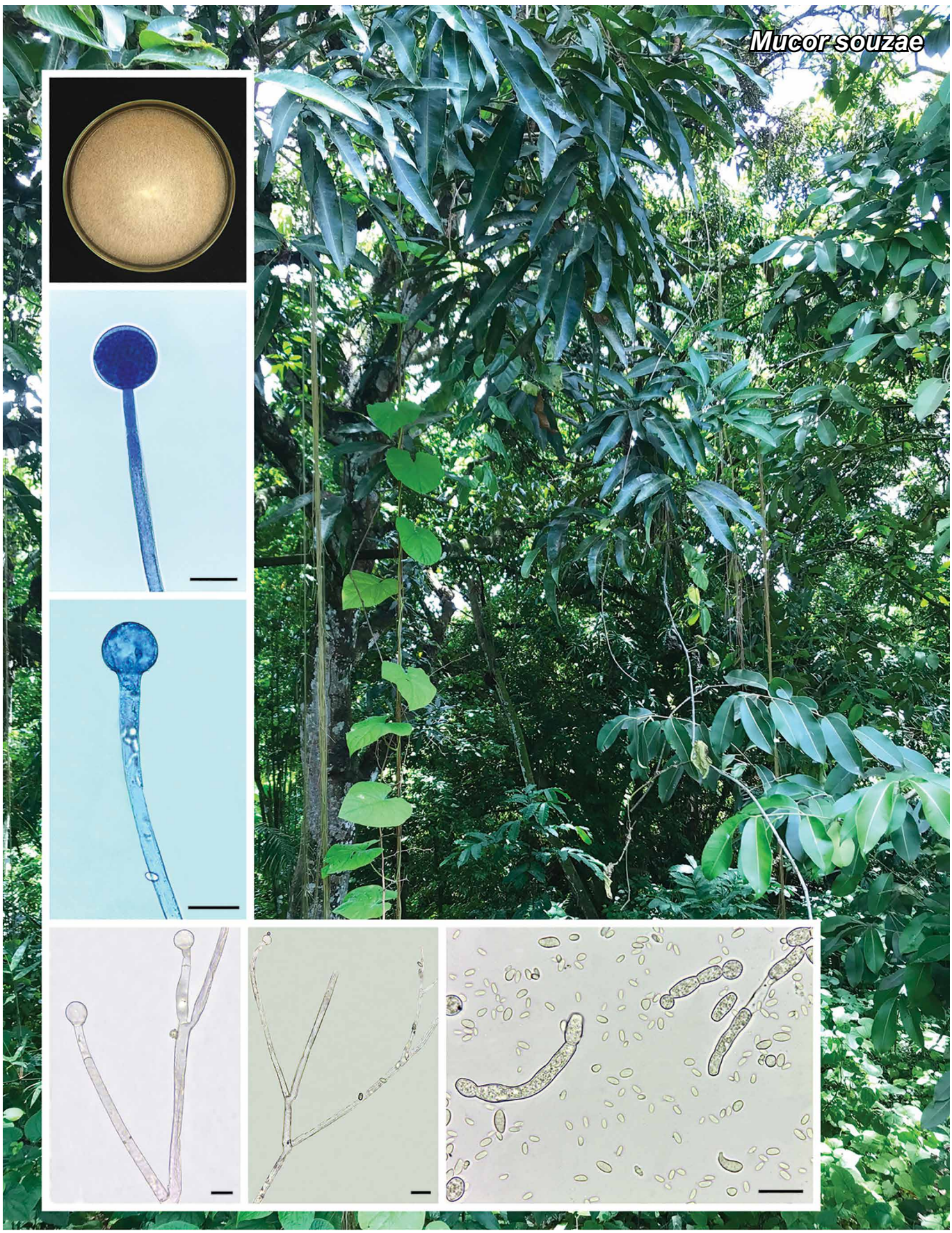
Mucor souzae

Fungal Planet 742 – 13 July 2018

Mucor souzae C.A. de Souza, D.X. Lima & A.L. Santiago, *sp. nov.*

Etymology. The specific epithet honours Dr José Ivanildo de Souza, for his many contributions to our knowledge of mucoralean fungi in Brazil.

Classification — *Mucoraceae*, *Mucorales*, *Mucoromycota.*

Mycelium presents dilated rhizoid-like hyphae with yellow contents as well as randomly distributed globose, subglobose and doliiform swellings, 12.5–22 µm diam. *Odour* acid, strong and unpleasant. *Sporangiophores* arising from aerial mycelia, simple or repeatedly sympodially branched, with long or short branches, erect, some slightly curved, smooth-walled, hyaline, (3–)5–11(–12.5) µm diam. Distance between sporangium and the next lateral branch is sometimes reduced, so that the sporangia appear to be sessile. One or two septa may be formed below the sporangia, mainly in those with short branches. *Sporangia* first yellow then becoming yellow to pale brown, globose, subglobose, 30–50 µm diam, subsmooth to very shortly echinulate; wall evanescent, some leaving small collars. *Columellae* hyaline to pale grey, smooth-walled, globose, subglobose, 15–35 µm diam or applanate, 12–25 × 15–25 µm, some with an evident collar. *Sporangiospores* variable in shape and size, hyaline, smooth-walled, mostly ellipsoid, (6–)7.5–20 × 4.5–7(–10) µm, some ellipsoid to fusoid, 2.5–7.5 × 1.5–2.5 µm, reniform, 6–15 × 3.5–7.5 µm, and some bizarre in shape, 7.5–22 × 5–10 µm. *Oidia* often observed. *Zygosporangia* not observed.

Culture characteristics and cardinal temperatures for growth — Colonies firstly white then turning yellow due to the presence of numerous cytoplasmic oil droplets, silken-like, low and exhibiting fast growth (9 cm diam and 0.5 cm in height) after 3 d on MEA at 25 °C. Reverse yellowish with irregular margins. On MEA: At 10 °C lack of growth and sporulation. At 12 °C limited growth, reaching 3.1 cm diam after 96 h; poor sporulation. At 15 °C slow growth, reaching 4.5 cm diam after 120 h; poor sporulation. At 20 °C good growth (7.5 cm diam in 96 h); excellent sporulation. Mostly sporangiophores with simple branches. At 25 °C better growth (9 cm diam in 72 h); excellent sporulation. At 30 °C good growth (7 cm diam in 72 h); good sporulation. At 35 °C limited growth (0.8 mm diam after 96 h); poor sporulation. At 40 °C growth and sporulation lacking. The growth of *M. souzae* on PDA was slightly slower than on MEA at all the temperatures tested.

Typus. Brazil, Triunfo municipality, Pernambuco state, S7°52'29.42" W38°06'12.07", isolated from soil samples, 6 Nov. 2015, *C.A.F de Souza* (holotype URM 91186, culture ex-type URM 7553, ITS and LSU sequences GenBank KY992878 and KY992879, MycoBank MB824580).

Notes — Based on phylogenetic relationships inferred from LSU and ITS nrDNA loci and morphophysiological analysis, *M. souzae* differs from the other accepted species of the genus. *Mucor souzae* produces sporangiophores arising from aerial mycelia, simple or repeatedly sympodially branched, with long or short branches and sporangiospores that are variable in shape and size. One or two septa may sometimes be formed below the sporangia. In the LSU tree (data not shown), *M. souzae* was nested in a subclade close to *M. hiemalis*, *M. merdicola* and *M. irregularis*. *Mucor hiemalis* is characterised as producing tall sporangiophores that are slightly sympodially branched as well as ellipsoidal columellae with a truncate base, differing from those observed in *M. souzae*, which presents simple or repeatedly sympodially branched sporangiophores, and globose, subglobose or applanate columellae. In contrast to *M. souzae*, *M. irregularis* produces ellipsoidal, cylindrical and pyriform columellae, and rhizoids, which are absent in *M. souzae*. The production of ellipsoid and ellipsoid to fusiform sporangiospores is very common in both *M. souzae* and *M. merdicola*. However, the former is distinguished from *M. merdicola* by the production of larger and bizarre shape of its sporangiospores, 7.5–22 × 5–10 µm, in contrast with those observed in *M. merdicola,* which are ellipsoid to fusiform, ellipsoid or subglobose. The ITS tree showed the new species formed a separate clade between *M. nidicola* and *M. irregularis*. At first, *M. souzae* may be morphologically confused with *M. nidicola* (Madden et al. 2012), as the colour and height of colonies of both can be similar. However, the branching pattern of the sporangiophores of *M. nidicola* reported by Madden et al. (2012), which are simple or 1–2 branched, does not correspond to that observed here. Additionally, *M. souzae* exhibits subsmooth to very shortly echinulate, globose or subglobose sporangia, 30–50 µm diam, whereas *M. nidicola* sporangia are globose, 30–70 µm diam, and smooth-walled to warty. Both ITS and LSU nrDNA sequences of *M. souzae* revealed a close genetic relationship to the *M. hiemalis* group, although it presents a sporangiophore branching pattern different from those described by Schipper (1973) for this group, in which species are characterised as producing tall and weakly sympodially branched sporangiophores. According to Madden et al. (2012), the morphological differences among species within the *M. hiemalis* group are not obvious, although differences between *M. irregularis* and *M. merdicola* were supported (Álvarez et al. 2011).

Legend and tree are in MycoBank.

Colour illustrations. Fragment of an Upland Atlantic Forest within the semi-arid region in Triunfo municipality, Pernambuco state of Northeast Brazil; colony surface on MEA; simple sporangiophore with sporangium; simple sporangiophore with columellae; sympodially branched sporangiophores with columella; sporangiospores and oidia. Scale bars = 25 µm.

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Mycocalia aquaphila
sb
mb
tb
qb

Fungal Planet 743 – 13 July 2018

Mycocalia aquaphila R. Cruz, L.T. Carmo, M.P. Martín, Gusmão & Baseia, *sp. nov.*

Etymology. Named in reference to the submerged substrate where it was found growing, on decaying wood coming from the tidal detritus.

Classification — *Nidulariaceae, Agaricales, Agaricomycetes.*

Basidiomata globose to subglobose, 1.1–1.5 mm height × 1.4–2.2 mm width, covered by a thin whitish peridium when young. *Peridioles* dark brown (7F3; Kornerup & Wanscher 1978), 0.5–0.7 × 0.5–0.6 mm, angular, circular or irregular in shape, with smooth to slightly rugose surface, 0.1–0.2 mm thick. *Cortex* 1-layered, reticulate with brownish hyphal branches, main branch 6–9.5 µm thick, secondary branches 4–6 µm thick, tertiary branches 2.5–4.5 µm thick, quaternary branches 1.5–2 µm thick, gleba dark greyish brown, and intermediate layer spongy, bronze. *Basidiospores* smooth, hyaline, (6.5–)7.5–10.5 × 4–5.5 µm (L = 8.8 µm; W = 4.9 µm; n = 30 spores), ellipsoid to cylindrical, rarely slightly ellipsoid (Q = (1.30–)1.54–2.26), elongated on average (Q_m = 1.82), apicule absent and spore wall 0.5–1 µm thick.

Typus. Brazil, Pará, Belém, Mosqueiro Island, Marahú Beach, S01°04'24.4" W48°24'00.4", solitaire to gregarious on decaying wood from tidal detritus, 7 Apr. 2017, *L.T. Carmo* (holotype UFRN-Fungos 2944, isotype HUEFS 234860, ITS and LSU sequences GenBank MG836281 and MG836282, MycoBank 823882).

Additional material examined. HUEFS 234861.

Notes — Among the bird's nest fungi, *Mycocalia* is one of the genera least reported by researchers (Brodie 1975), and much of it is due to the fact that their species had been described as *Nidularia* until the proposition of *Mycocalia* by Palmer (1961). All new species identifications, five in total, excluding synonyms, occurred in the first half of the 1960s, and no new species had been proposed since *Mycocalia sphagneti* (Cejp & Palmer 1963). Together with *M. denudata* and *M. reticulata,* the new species *M. aquaphila* is one of the few taxa of the genus reported for South America, and the first described and recorded exclusively in Brazil. The new species shows a basidiome covered by a thin and whitish peridium during the initial development; dark brown peridioles, single layered cortex in a reticulated pattern; and hyaline, ellipsoid to cylindrical spores, 7.5–10.5 × 4–5.5 µm. Comparing it with the species that occur in South America, *M. denudata* differs from the new species in the presence of an ephemeral yellowish white peridium (thin but almost persistent, and white in young basidiomata of *M. aquaphila*), peridioles connected in a hyaline gelatinous mass, provided with double layered cortex (single layered in *M. aquaphila*), besides the 7.5 × 5 µm spores. The species *M. reticulata* presents the same reticular pattern of cortex as *M. aquaphila*, but differs in the yellowish brown to pale brown peridiole, thick spore wall (without values defined in the literature), and the main reticulum hyphae branch up to 20 µm in thickness (6–9.5 µm in *M. aquaphila*). A species of the genus that grows in submerged substrates is *M. minutissima*, recorded on submerged leaves of *Juncus effuses*, but *M. minutissima* is distinguished from other *Mycocalia* species by having a double layered cortex and smaller spores (6 × 4 µm). However, Brodie (1975) considered that it may represent an aberrant uniperidiolar variation of some multiperidiolar species, probably *M. denudata*. From the other species of *Mycocalia, M. aquaphila* is distinguished by the following characteristics (Brodie 1975): *M. duriaeana* presents dark blood-red to black peridioles, 0.3 mm diam, and spores of 7 × 5.5 µm; *M. sphagneti* shows a white peridium, initially woolly and later smooth, cortex in labyrinthiform pattern, and pale yellowish brown spores, 13 × 5.5 µm, presenting small droplets of oil inside the spores.

The species with legitimated names in MycoBank, *M. arundinaceae* (MycoBank MB334666) and *M. fusispora* (MycoBank MB334669) were not compared because, according to Cejp & Palmer (1963), they were synonymised under the name *M. denudata*.

Mycocalia aquaphila is the first species of this genus proposed since the 1960s. The ITS sequence obtained in this study has 93 % similarity to the only ITS *Mycocalia* sequence available in GenBank (DQ911596 under *M. denudata*). Moreover, as mentioned above, morphological characters are enough to separate *M. aquaphila* from the already known species.

Colour illustrations. Brazil, environment near the locality where the type species was collected on Marahú Beach, Mosqueiro Island; young basidiomata covered by a thin whitish peridium (scale bar = 1 mm); upper view of isolated peridioles (scale bar = 1 mm); spores (scale bar = 10 µm); reticulated cortex, showing the main branch (mb), secondary branches (sb), tertiary branches (tb) and quaternary branches (qb) (scale bar = 20 µm) (all: UFRN-Fungos 2944, holotype).

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Pleuromyces hungaricus
5 mm

Fungal Planet 744 – 13 July 2018

Pleuromyces Dima, P.-A. Moreau & V. Papp, *gen. nov.*

Etymology. *Pleuromyces* is a compound name, reflecting the morphological similarity to *Pleuroflammula* and *Phaeomyces*.

Classification — *Tubariaceae, Agaricales, Agaricomycetes*.

Basidiomata pleurotoid with short central to eccentric stipe; pileus small size (> 1 cm), yellowish brown, fibrillose, not hygrophanus. *Lamellae* ventricose, yellowish to rusty brown. *Spores* yellowish brown, ovate to ellipsoid, thick-walled, smooth. *Basidia* 2- or 4-spored. *Cheilocystidia* slender or heteromorphous, not encrusted, thin-walled, hyalin. *Pileipellis* a thin trichocutis with coarsely incrusted slender hyphae, inflate at septa. Wood-inhabiting, saprobic.

Type species. *Pleuromyces hungaricus* V. Papp, Dima & P.-A. Moreau. MycoBank MB824585.

Pleuromyces hungaricus V. Papp, Dima & P.-A. Moreau, *sp. nov.*

Etymology. Name reflects the country (Hungary) where the species was collected.

Basidiocarp pleurotoid, pileus 5–8 mm diam, flabelliform, yellowish brown, densely covered with fibrillose squamules, turning ferruginous with age, dry, not hygrophanous. *Lamellae* ventricose, yellowish when young, rusty brown on dry specimens, edge serrulate, slightly darker. *Stipe* short, up to 1.5 × 3 mm, eccentric or lateral, concolorous with pileus or darker, flocculose-fibrillose, dry, solitary. Context yellow brown, spore deposit not noted. *Basidiospores* in side view (6.5–)7(–7.5) × (4–)4.5(–5) µm, Q = 1.4–1.8, mean 7.19 × 4.5 µm, Q = 1.6 (n = 30), ovoid to ellipsoid, somewhat amygdaliform in side view, smooth, thick-walled, yellowish brown, often with one or two guttules, apex usually blunt and subpored. *Basidia* 23–26 × 5–6 µm (excluding sterigma), subclavate, 2- or 4-spored. *Cheilocystidia* abundant, in clusters on lamella edge, variable in shape (heteromorphous, from slender fusiform to ± lageniform), not incrusted, thin-walled, hyaline, up to 85 µm long. *Pleurocystidia* not observed. *Hymenophoral trama* regular, made of slender hyphae 2–4.5 µm wide, pale, mostly smooth. *Pileipellis* a thin adpressed trichocutis made of 1–2 layers of hyphae 2.5–5.5 µm wide, coarsely incrusted, with cylindrical elements 35–60 µm long, mostly filled with oily droplets, terminal element usually rounded to slightly inflated at apex, thick-walled and smooth at apex. *Pileitrama* made of cylindrical hyphae 2–4 µm wide, pale, smooth or incrustate-zebrate, sometimes thickened and darker at septa. *Clamp connections* present at all septa.

Habitat — On large *Fagus sylvatica* log, in a lowland old-growth beech forest (Vértes Mts, Hungary). So far only known from the type locality.

Typus. Hungary, Fejér County, near Csákberény (Vértes Mts), Juhdöglövölgy Forest Reserve, N47°22.662' E18°19.485', 28 Oct. 2013. *V. Papp* (holotype LIP0001404, ITS and LSU sequences GenBank MH036002 and MH036003, MycoBank MB824586).

Notes — Based on a BLAST search of NCBIs GenBank nucleotide databases, the closest hits using the LSU sequence are *Romagnesiella clavus* (as *Pachylepyrium* sp., GenBank HQ832461; Identities = 1 333/1 361 (98 %), 2 gaps (0 %)), *Phaeomarasmius fulvidulus* (GenBank KF830080; Identities = 1 330/1 361 (98 %), 5 gaps (0 %)), *Agrocybe pediades* (GenBank DQ110872; Identities = 1 339/1 372 (98 %), 4 gaps (0 %)) and *Galerina* sp. (GenBank HQ827183; Identities = 1 341/1 374 (98 %), 8 gaps (0 %)). The closest hit by BLAST using the ITS sequence had highest similarity to an 'uncultured fungus' which was sequenced from soil in Illinois, USA (GenBank KX195359); the ITS2 of this environmental sample is very similar to *Pleuromyces hungaricus* (Identities = 323/327 (99 %), 2 gaps (0 %)). The second closest hit using the ITS sequence is *Tubaria* sp. (GenBank KY462443; Identities = 475/556 (85 %), 29 gaps (5 %)), with low query cover (85 %). Based on a discontinuous megablast search the closest hits by best query cover (100 %) are *Flammulaster* cf. *carpophilus* (as *Phaeomyces dubiosus*, unconfirmed, P.-A. Moreau unpubl. data; GenBank KF830099; Identities = 543/644 (84 %), 42 gaps (6 %)) and *Crassisporium carbonicola* (as *Pachylepyrium carbonicola*; GenBank LN714579; Identities = 541/645 (84 %), 39 gaps (6 %)). *Pleuromyces hungaricus* forms a distinct clade in our phylograms, well separated from other genera of *Tubariaceae*. Microscopical observations (spores smooth, thick-walled and subpored; pileipellis with coarsely incrusted hyphae) suggest closest affinities with species of *Phaeomarasmius* and *Flammulaster* pp. (*F. muricatus*/*F. limulatus*), but the weak differentiation of the pileipellis is a distinctive feature for species of these genera. The holotype of *Phaeomyces dubiosus* was not available for revision but its description shows strong affinities with *P. hungaricus*; however, distant lamellae and the pileipellis with branching and erected terminal hyphae suggest that it represents a distinct species of still unclear systematic position.

Colour illustrations. Juhdöglő-völgy Forest Reserve (Vértes Mts, Hungary), substrate of the type material; basidiocarp; cheilocystidia and spores (all from holotype). Scale bars = 5 mm (basidiocarp), 10 µm (elements of hymenium).

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Preussia citrullina

Fungal Planet 745 – 13 July 2018

Preussia citrullina R.M.F. Silva, R.J.V. Oliveira, Souza-Motta, J.L. Bezerra & G.A. Silva, *sp. nov*.

Etymology. The name refers to the host plant, *Citrullus lanatus*.

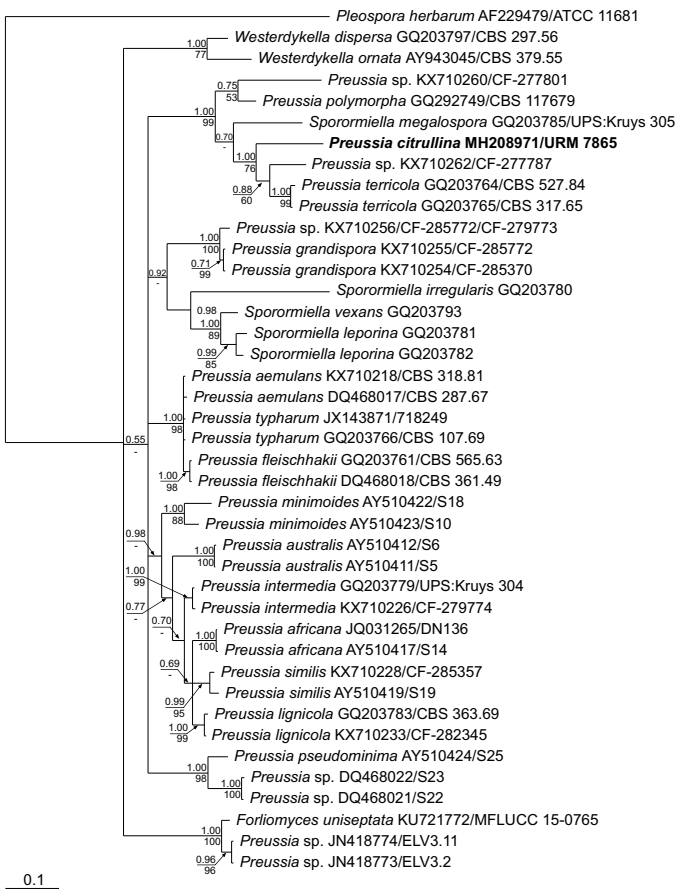
Classification — *Sporormiaceae*, *Pleosporales*, *Dothideomycetes*.

Conidiomata pycnidial on juice agar medium (V8), first immersed then erumpent, brown, glabrous, solitary or aggregated, globose to subglobose, ostiolate, 75–150 × 50–125 µm; walls of 2–3 layers of medium brown cells of *textura angularis*. *Conidiogenous cells* phialidic, hyaline, smooth, ampulliform to doliiform, 6.5–9.5 × 5 µm. *Conidia* ellipsoid to oblong, hyaline, aseptate, sometimes guttulate, 2–3 × 2 µm.

Culture characteristics — Colonies after 7 d at 23 °C on V8, 20 mm diam, irregular margin, cottony, surface greyish, reverse olivaceous buff. Colonies on MEA, 20 mm diam, sterile, irregular margin, sulphur yellow surface, reverse straw coloured. Colonies on OA, 20 mm diam, sterile, regular margin, floccose, surface sulphur yellow, reverse straw coloured. Colonies on PDA, 18 mm diam, sterile, surface sulphur yellow, reverse straw coloured.

Typus. Brazil, Petrolândia municipality, Pernambuco state, isolated as endophyte from leaves of *Citrullus lanatus* (*Cucurbitaceae*), 25 July 2016, *R.M.F. Silva* (holotype URM 91190, culture ex-type URM 7865, ITS and LSU sequences GenBank MH208971 and MH208972, MycoBank MB825032).

Notes — The genus *Preussia* was established by Fuckel (1867). Members of this genus are predominantly coprophilous, although a few species have been isolated from soil, wood, plant debris and as endophytes (Mapperson et al. 2014, Gonzalez-Menendez et al. 2017). Based on morphological analysis and phylogenetic relationships using ITS rDNA sequences, the new species, *P. citrullina*, differs from other species of *Preussia* based on its phoma-like asexual morph. The asexual morphs of *Sporormiaceae* genera, when found, are phoma-like in morphology (Von Arx & Storm 1967, Cannon & Kirk 2007). Based on ITS, *Preussia citrullina* is 93 % similar to *Sporormiella megalospora* (GenBank GQ203785) and *P. terricola* (CBS 317.65, GenBank GQ203765), amongst others. The LSU sequence is 98 % similar to *P. terricola* (CBS 317.65, GenBank GQ203725) and 97 % to *Sporormiella megalospora* (GenBank GQ203743). In the present phylogenetic analyses, *P. citrullina* is closest to *P. terricola* and *Sporormiella megalospora*.



Bayesian inference tree using ITS rDNA sequences of *Preussia* and related genera. The new species is in **bold** face. Support values of at least 50 % are shown at the nodes. *Pleospora herbarum* (ATCC 11681, GenBank AF229479) was used as outgroup. Bayesian inference and Maximum Likelihood (ML) analyses were performed in MrBayes (Ronquist & Huelsenbeck 2003) and PhyML (Guindon & Gascuel 2003), respectively, launched from Topali (Milne et al. 2004).

Colour illustrations. Watermelons for sale, Pernambuco, Brazil; pycnidial conidiomata; conidiogenous cells and conidia. Scale bars = 10 µm.

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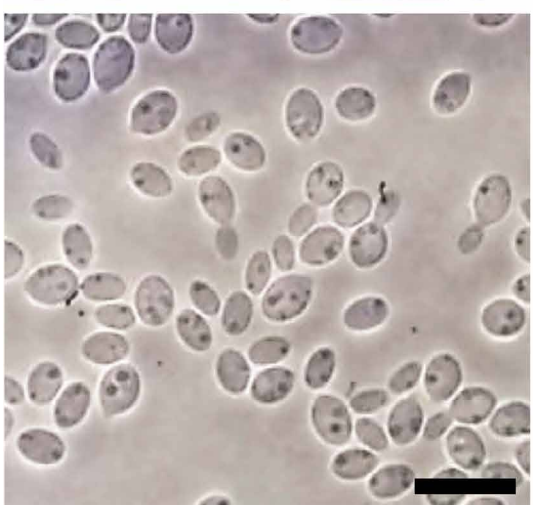
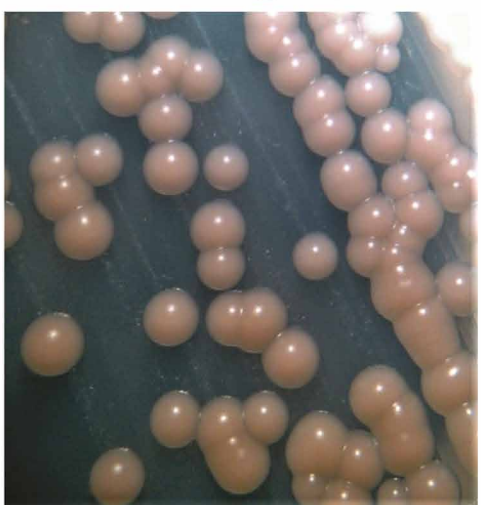
Queiroziella brasiliensis





Fungal Planet 746 – 13 July 2018

Queiroziella C.R. Félix, J.D.P. Bezerra, R.P. Neves & Landell, *gen. nov.*

Etymology. Named for Luzinete Acioli de Queiroz, in acknowledgement for her contributions to the study of yeasts in the former Institute of Mycology of the University of Recife, Brazil.

Classification — *Incertae sedis*, *Cystobasidiomycetes*, *Pucciniomycotina*, *Basidiomycota*.

Pseudohyphae and *true hyphae* not formed. *Sexual reproduction* not observed. *Ballistoconidial* production absent. *Colonies* are pink to salmon, smooth, butyrous to mucoid and glistening. *Budding cells* present. *Fermentation* not observed.

Type species. Queiroziella brasiliensis C.R. Félix, P. Valente & Landell. MycoBank MB822321.

Queiroziella brasiliensis C.R. Félix, P. Valente & Landell, *sp. nov*.

Etymology. Name refers to the country, Brazil, where this yeast was isolated.

On YEPD agar after 3 d at 22–25 °C, cells are globose to oval (4–6 × 3–4 µm) , and the colonies are pink to salmon, smooth, butyrous to mucoid and glistening. *Vegetative reproduction* is by single budding. After 3 wk in Dalmau plate culture on cornmeal agar, *pseudohyphae* or *true hyphae* are not formed. *Sexual reproduction* is not observed. *Ballistoconidia* production is absent. *Fermentation ability* is negative. The following carbon compounds are assimilated: N-Acetylglucosamine, D-arabinose, erythritol, galactose, D-mannitol, raffinose, soluble starch, sorbitol, inulin (slow), D-glucose (slow), DL-lactate (slow), melezitose (slow), melibiose (slow), D-ribose (slow), D-trehalose (slow), tween 80 (slow), xylitol (slow), cellobiose (variable), glycerol (variable), lactose (variable), D-maltose (variable), sodium gluconate (variable), sucrose (variable) and tween 20 (variable). No assimilation of L-arabinose, galacturonate, myo-inositol, L-arabinitol, L-rhamnose, xylose, succinate, galactitol, citrate and salicin. Assimilation of nitrogen compound L-lysine is variable and no assimilation of potassium nitrate, sodium nitrite, ethylamine and cadaverine. Growth at 22, 25 and 30 °C and no growth was observed at 35 °C. Growth is not observed on YPD with 50 % glucose. No growth in the presence of 10 % sodium chloride. After 21 d, growth is observed in the presence of 0.01 % and 0.1 % cycloheximide. Urease activity and diazonium blue B reaction are positive.

Typus. Brazil, União dos Palmares municipality, Alagoas state, Serra da Barriga, S09°10'11" W36°05'19", as epiphytic yeast on leaves of *Portea leptantha* (*Bromeliaceae*), 31 July 2013, *C.R. Félix & M.F. Landell* (holotype as metabolically inactive culture, CBS 14582 = UFMG-CM-Y6102 = BSB 15, ITS, LSU and *rpb2* sequences GenBank KY305143, KX348021 and MH187958, MycoBank MB824924).

Additional material examined. Brazil, Viamão municipality, Rio Grande do Sul state, Parque de Itapuã, S30°21'19" W51°01'57", as epiphytic yeast on leaves of *Tillandsia geminiflora* (*Bromeliaceae*), 5 Apr. 2004, *P. Valente & M.F. Landell*, cultures CBS 11152 = MYA-4544 = BI 02, ITS, LSU and *rpb2* sequences GenBank MH244424, EU200783 and MH187959; on *Vriesea gigantea* (*Bromeliaceae*), 25 May 2007, *P. Valente & M.F. Landell*, cultures CBS 11151 = MYA-4543 = BI 327, ITS and LSU sequences GenBank MH244425 and GU566018.

Colour illustrations. Bromeliad *Tillandsia* sp. in the Serra da Barriga, União dos Palmares, Alagoas, Brazil (photo credit H.M.N. Casanova); microscopy showing the yeast microstructures and colonial macromorphology. Scale bar = 10 µm.

Notes — The new genus *Queiroziella* is proposed based on a phylogenetic analysis and physiological and biochemical features. Phylogenetic inferences of LSU (D1/D2 domain) and ITS rDNA and *rpb2* sequences of *Queiroziella* placed the new genus in a single clade with high support values related to *Sakaguchia*, *Cystobasidium* and *Occultifur*. According to the BLASTn searches (9 Apr. 2018) the LSU rDNA sequences have low identity (93 %) to sequences deposited as *Cystobasidium* spp. (e.g., GenBank FJ515245), *Buckleyzyma armeniaca* (GenBank AF189920), *Symmetrospora* spp. (e.g., GenBank AF189984) and *Occultifur* sp. (GenBank KC698874), amongst others. The ITS rDNA sequences have low identity (90–91 %) to some sequences deposited as *Occultifur* sp. (e.g., GenBank KC698874) and *Cystobasidium* spp. (e.g., *C. minutum*, CBS 2177, GenBank AF190010). The *rpb2* sequences have low identity (77–78 %) to sequences deposited as *Cystobasidium* spp. (e.g., GenBank KJ708214), *Sakaguchia* spp. (e.g., GenBank KJ708346.1), *Microsporomyces bloemfonteinensis* (e.g., GenBank KJ708215), amongst others. *Queiroziella brasiliensis* differs physiologically and biochemically from *Sakaguchia* species by inulin assimilation, from *Cystobasidium* species by assimilation of melibiose and from *Occultifur* species by assimilation of soluble starch and raffinose (Libkind et al. 2010, Fell et al. 2011, Kurtzman et al. 2011, Laich et al. 2013, Wang et al. 2015, Yurkov et al. 2015).

Legend and tree are in MycoBank.

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Quixadomyces cearensis

Fungal Planet 747 – 13 July 2018

Quixadomyces Cantillo & Gusmão, *gen. nov.*

Etymology. Named refers to Quixadá, the locality where the fungus was collected.

Classification — *Parapyrenochaetaceae*, *Pleosporales, Dothideomycetes.*

On natural substrate: *Mycelium* superficial or somewhat immersed in the substrate, composed of warty, sinuous, criss-crossed or stringing, verrucose or verruculose, brown, septate hyphae. *Stroma* composed of tightly clustered and fused hyphae. *Conidiophores* absent. *Conidiogenous cells* absent. *Propagules* rising up directly from interwoven hyphal strands, often globose to subglobose, ovoid to pyriform during development, but may become, ellipsoid-fusoid to obclavate, wall consisting on anastomosed brown to dark olivaceous brown hyphae, *textura epidermoidea similis*, with some peripheral hyphae around propagule body, smooth or warty, approached at the tip.

Type species. Quixadomyces cearensis Cantillo & Gusmão. MycoBank MB824358.

Quixadomyces cearensis Cantillo & Gusmão, *sp. nov.*

Etymology. Name refers to the state (Ceará), where this taxon was collected.

On natural substrate: *Mycelium* superficial or somewhat immersed in substrate, warty, sinuous, criss-crossed or stringing, verrucose or verruculose, brown to dark brown, septate, hyphae 3–5 µm diam. *Conidiophores* absent. *Conidiogenous cells* absent. *Propagules* rising up directly from interwoven hyphal strands, globose at first, ellipsoid to ovoid when mature, 82.5–150 × 45–85 µm, wall consisting of anastomosed brown to dark olivaceous brown hyphae, *textura epidermoidea similis*, with thick-walled peripheral hyphae around the propagule body, 12–18 × 3–5 µm width, smooth or warty, approached at the tip.

Culture characteristics — Colonies on PDA fast-growing, attaining 60 mm in 7 d, immersed mycelium dark olivaceous to black, somatic hyphae verrucose or verruculose, 3–5 µm diam, aerial mycelium coarse due to the abundant sporulation occurring from the third day. In culture, propagules are bigger (85–300 µm long) and frequently fused.

Typus. Brazil, Ceará, Quixadá, near of 'Açude do Cedro', S04°58' W39°, on decaying bark, 28 Apr. 2016, *T. Cantillo* (holotype HUEFS 238438, isotype HUEFS 238439, ex-type culture LAMIC103-16, ITS and LSU sequences GenBank MG970694 and MG970695, MycoBank MB824398).

Notes — This fungus somewhat resembles setose pycnidia common in some species of *Pleosporales*, but no internal structures were observed in any stage of development. In appearance, this fungus also resembles *Akenomyces* (Hornby 1984). *Akenomyces* is characterised by black elliptical-lenticular sclerotia, with pale warty marginal hyphae, brown, consisting of a complex three-layer hyphal structure and, inside the cortex, a tightly interwoven mass of hyaline, thin-walled, much branched hyphae (Voglmayr & Krisai-Greilhuber 1997) a feature that is not present in *Quixadomyces*. Furthermore, the presence of clamp connexions is evidence that *Akenomyces* belongs to the phylum *Basidiomycota* and clearly separates it from *Quixadomyces,* which belongs to *Ascomycota*. Another morphologically similar genus with ovoid to obclavate propagules, *Megacapitula* also has mycelium often being verruculose, forming mycelial cords from which conidia arise; but in this case, integrated or terminal conidiogenous cells are present and the conidia form a beak-like structure at apex from which dense hairy appendages arise, and also its outer wall breaks and starts peeling off after mounting.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Parapyrenochaeta acacia* (GenBank NR_155674 from type material, Identities = 546/592 (92 %), 20 gaps = 20/542 (3 %)), *Pyrenochaetopsis microspora* (GenBank HM751085; Identities = 533/574 (93 %), 18 gaps (3 %)) and *Camarosporium aloes* (GenBank NR_137821 from type material; Identities = 566/635 (89 %), 32 gaps (5 %)).

LSU. Using the LSU sequence, the closest hits on a megablast search of NCBIs GenBank nucleotide database are *Pyrenochaeta protearum* (GenBank JQ044453; Identities = 625/629 (99 %), no gaps) and *Leptosphaeria maculans* (GenBank FO905981; Identities = 621/629 (99 %), no gaps).

Colour illustrations. Pedra da Galinha Choca, Quixadá, CE; propagules on natural substrate and on pure culture with different stages of development. Scale bar = 50 µm.

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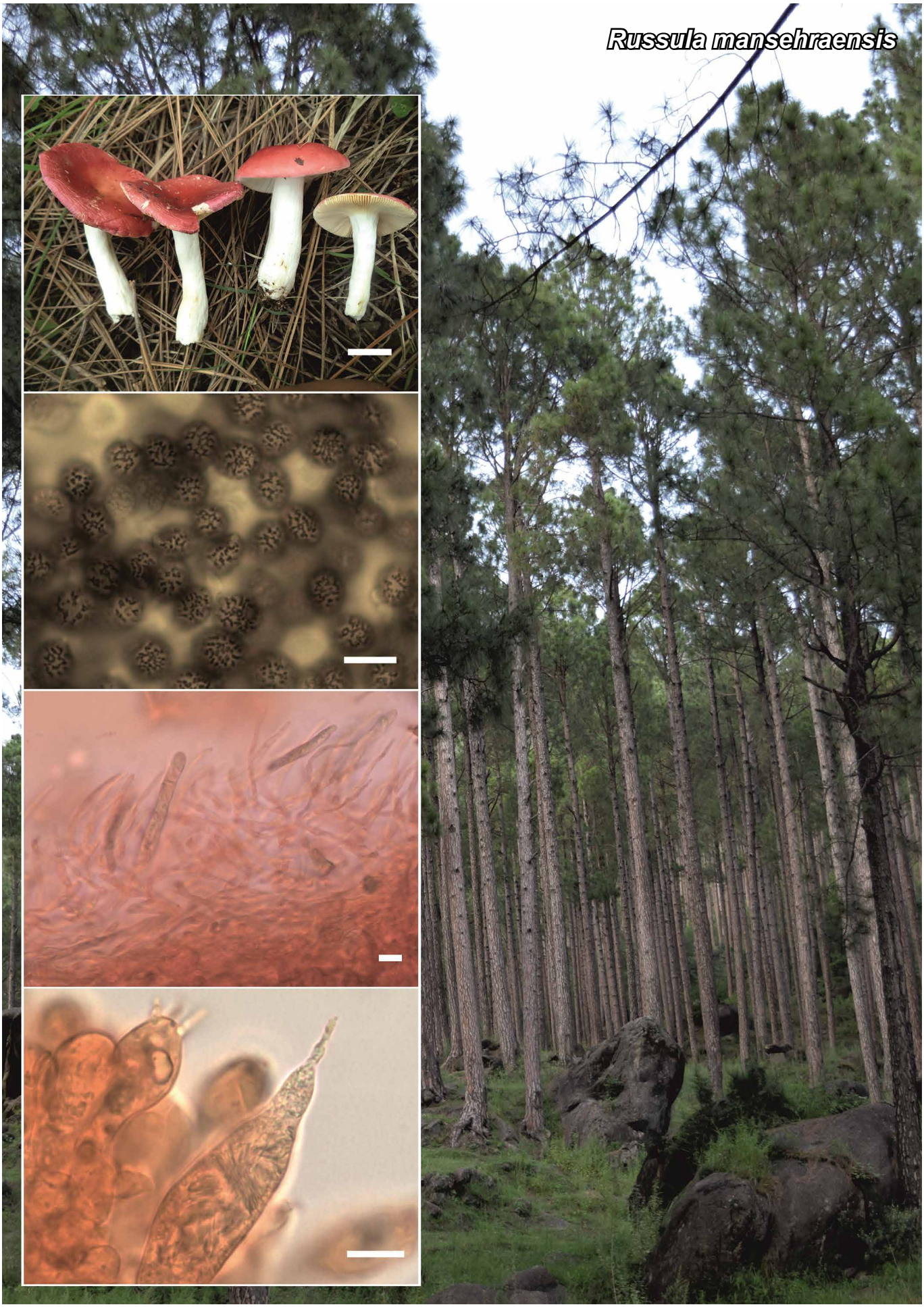
Russula mansehraensis

Fungal Planet 748 – 13 July 2018

Russula mansehraensis Saba, Caboň & Adamčík, *sp. nov.*

Etymology. The name refers to Mansehra, the province where the species was collected for the first time.

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

Basidiomata small to medium sized, 40–45 mm tall. *Pileus* 27–34 mm diam, convex, centrally slightly depressed, surface dry, smooth, matt, vivid red or strong red with centre reddish orange (10R6/12 colour chart of Munsell 1975) and rusty spotted with spots sometimes concentrically arranged; margin even, or slightly involute, without striations. *Lamellae* regular, adnate, crowded, light yellow, pale yellow or light orange yellow, brittle, edge entire, concolorous. *Stipe* 35–40 × 8–10 mm, central, cylindrical to subcylindrical, stuffed, slightly longitudinally wrinkled, white, towards base with light yellow-brownish or moderate yellow-brownish spots, without pinkish shades. *Context* compact, not firm, odour indistinct and taste strongly acrid. *Spores* (7.5–)8–8.5(–9.5) × (5.5–)6.5–7(–7.5) µm, av. 8.3 × 6.7 µm, Q = (1.13–)1.17–1.29(–1.4), av. 1.23, ornamentation consisting of (4–)5–8(–10) moderately large and distant amyloid warts in the circle 3 µm diam on spore surface, warts 0.5–1 µm high, connected with occasional to frequent short or longer fine line connections ((0–)1–3(–5) line connections in the circle), occasionally fused in short or longer chains ((0–)2–5(–7) fusions in the circle), chains and crests often branched, but rarely forming a reticulate structure, isolated warts rare. Suprahilar plage amyloid, large. *Basidia* (29–)31.5–38.8(–47) × (10–)11.5–13.5(–15) µm, av. 35.1 × 12.5 µm, 4-spored, clavate, sometimes pedicellate. *Hymenial cystidia* on lamellar sides widely dispersed to dispersed, 300–400 per mm^2, fusiform or rarely clavate, pedicellate, thin-walled, measuring (49–)54–74(–84) × (10–)11.5–16(–20) µm, av. 64 × 13.7 µm, apically acute to acute-pointed and with 2–7(–9) µm long appendage, contents heteromorphous, granular-banded, yellowish, turning brownish red to almost black in sulfovanillin. Lamellar edges covered with abundant marginal cells, occasional cheilocystidia and dispersed basidia; *marginal cells* not well differentiated, similar to the basidiola on lamellar sides, but smaller, measuring (9–)12–17.5(–19) × (4–)4.5–7(–7.5) µm, av. 15 × 5.8 µm; *cheilocystidia* narrower than pleurocystidia, clavate or fusiform, pedicellate, thin-walled, measuring (42–)50.5–66(–73) × (8–)9.5–14(–16) µm, av. 58.3 × 11.9 µm, apically with mainly acute tips and usually with 1–6 µm long appendages, contents similar as in pleurocystidia. *Pileipellis* orthochromatic in Cresyl blue, 115–135 µm deep, sharply delimited from the underlying spherocytes of the context; distinctly divided in a 60–75 µm deep, strongly gelatinised suprapellis of loose, erect or ascending hyphal terminations and, near surface, with some repent, longer pileocystidia; and a 55–65 µm deep subpellis of less gelatinised, dense, irregularly, but near the trama horizontally oriented, intricate, branched, 2–5 µm wide hyphae. Acidoresistant incrustations absent. Hyphal terminations in pileipellis near the pileus margin slender and branched, thin-walled, with terminal cells measuring (11–)18–33(–48) × 2.5–3.5(–4) µm, av. 25.6 × 3.1 µm, mainly narrowly subulate or fusiform, partly subcylindrical, usually apically attenuated or constricted, often moniliform; near the pileus centre with mainly cylindrical, often flexuous terminal cells, measuring (12–)16–26(–32) × (2–)2.5–3.5(–4.5) µm, av. 21.1 × 3 µm, apically obtuse; subterminal cells mainly branched or not, often with lateral branches or nodules, equally wide as terminal cells. Pileocystidia near the pileus margin numerous, narrowly clavate or fusiform, mainly 2- or more-celled (1–4(–6)-celled), thin-walled, with terminal cells measuring (18–)32.5–85.5(–150) × (3–)4.5–7(–8) µm, av. 59 × 5.8 µm, apically obtuse, subterminal cells equally wide or narrower, often shorter, contents in Congo red heteromorphous, granulose or crystalline, turning dark reddish brown to black in sulfovanillin; near the pileus centre smaller and narrower, with terminal cells measuring (25–)31.5–89.5(–160) × (3.5–)4.5–6.5(–8.5) µm, av. 60.5 × 5.6 µm more frequently 1-celled, with more granular and yellow-coloured contents. Cystidioid hyphae in subpellis and pileus trama dispersed, with heteromorphous-granulose, yellowish, often oleiferous contents.

Colour illustrations. *Russula mansehraensis* (HUP-SUR180) growing in mono-dominant forest of *Pinus roxburghii*; basidiomata; spores; pileipellis near the pileus margin; hymenial elements. Scale bars = 10 mm (basidiomes), 10 µm (microscopic structures).

Typus. Pakistan, four collections from Khyber Pakhtunkhwa, Shangla district, Puran, on soil under *Pinus roxburghii* (*Pinaceae*), alt. 1500 m, 5 Sept. 2013, *S. Ullah* (holotype HUP-SUR180, ITS, LSU, mtSSU and *rpb2* sequences GenBank MG948636, MG944280, MG944266 and MG944255, MycoBank MB816290).

For additional material examined, see MycoBank.

Notes — The type specimen of *R. mansehraensis* was morphologically described as '*Russula* sp.' and its phylogenetic position as member of *R. maculata* lineage was resolved in our previous study (Adamčík et al. 2016). In this study we supported both morphology and phylogeny by more collections from Pakistan, more observations and more sequences including additional loci (for phylogenetic tree, see MycoBank). We confirmed the placement of *R. mansehraensis* in *Russula* subsect. *Maculatinae*, where it clustered in the strongly supported clade together with European species *R. maculata* and *R. nympharum*. Our phylogeny showed strong support for recognising of *R. mansehraensis* as a new species. The other ITS sequences retrieved from GenBank (https://www.ncbi.nlm.nih.gov/genbank) and UNITE (http://unite.ut.ee) databases originate from Papua New Guinea and Southern and Northern China and apparently represent different species associated probably with other host trees (e.g., *Castanopsis* and *Keteleeria*).

The *R. maculata* lineage is morphologically defined by a red pileus cuticle discolouring to yellow or white, yellow spore print, acrid taste of the flesh and yellow brownish spots on surface of the pileus and the stipe. Our field observations on *R. mansehraensis* agree well with this morphological delimitation of the group. Contrary to above-mentioned European species, the Pakistani species does not show any distinct pink shades on the stipe surface and basidiomata are distinctly smaller and thin-fleshed. All studied collections of *R. mansehraensis* were collected in mono-dominant *Pinus roxburghii* forests, contrary to both European species known only as associates of deciduous trees. Our study confirms that relatively small spores (up to 8.5 × 7 µm) and mainly 2- and more-celled pileocystidia are micromorphological characters that define *R. mansehraensis*.

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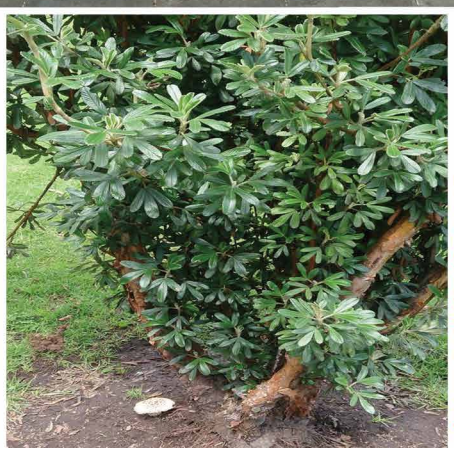
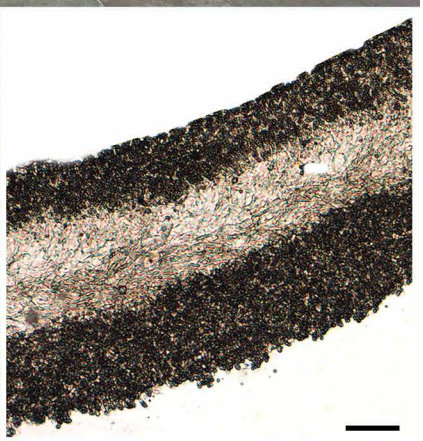
Saproamanita quitensis





Fungal Planet 749 – 13 July 2018

Saproamanita quitensis E. Caicedo, A. Barili, C.W. Barnes & Ordoñez, *sp. nov.*

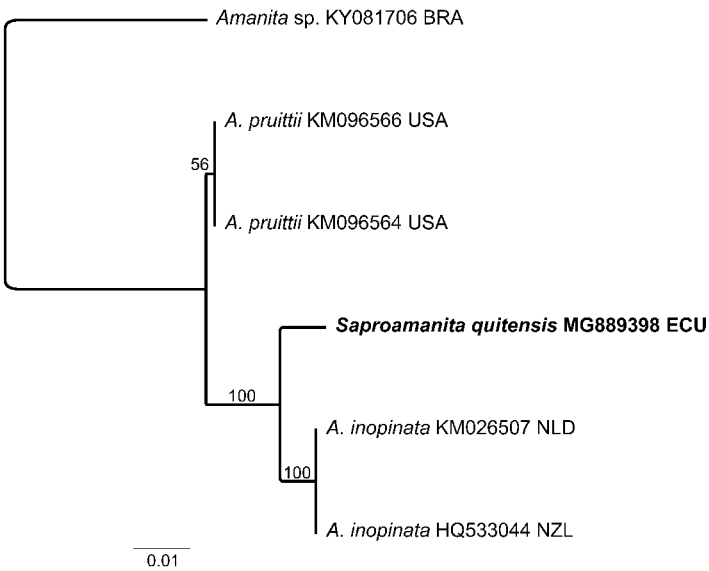
Etymology. Named reflects the locality where the species was collected.

Classification — *Amanitaceae, Agaricales, Agaricomycetes.*

Basidiomata small to medium size, pileus 90 mm diam, broadly convex, whitish, warts on the surface, margin whole, slightly revolute, rimose, thick texture, fleshy. *Warts* thick, dense, hard, scale-shaped, persistent, bigger and thicker towards the centre, pointy. Towards the margin warts thinner and truncated, from whitish to cream until dark brown on the tips, tending to get darker. *Lamellae* free, tall, ventricose, crowded, white with cream tones, slightly wavy margin and very finely serrate. *Stipe* 60 × 30 mm, short, thick, cylindrical with a slight wider base, white, smooth. *Annulus* remnant adhered, cream colour, disappears during drying process. *Volva* dissociated with reddish brown pearls. *Odour* not distinctive when fresh, strong fungal odour when dry. *Pileipellis* pseudocutis. *Lamellar trama* bilateral, divergent, with mostly clavate hyphae 9–14 µm wide, septate, thin cell wall, occasionally little differentiated filamentous hyphae. *Caulocutis* with acrophysalids, clavate hyphae with longitudinal clamp connections. *Veil trama* predominance of filamentous hyphae, ellipsoid and pyriform hyphae less abundant. *Basidia* 34–52.5 × 8–13.5 µm, four sterigmata, sometimes two, 3 µm long. Clamp connections occasionally present at the base. *Basidiospores* 6–12 × 6.5–9.5 µm, globose or rarely subglobose, apiculate, hyaline, thin cell wall or slightly thickened, amyloid, acyanophilic, non-metachromatic, Q = 1.04.

Habitat — Solitary, on the ground near *Polylepis racemosa* in an urban park.

Typus. Ecuador, Pichincha province, Itchimbia Metropolitan Park, alt. 2882 m, Jan. 2017, *E. Caicedo* (holotype QCAM7047, ITS-LSU sequence GenBank MG889398, MycoBank MB824231, TreeBASE Submission ID 22306).



Colour illustrations. Ecuador, Itchimbía Metropolitan Park; close-up of basidiocarp; basidiocarp next to *Polylepis racemosa*; lamellar trama. Scale bar = 100 µm.

Notes — Phylogenetically, *Saproamanita quitensis* is distinct from other *Amanita* spp. available in the NCBI GenBank nucleotide database. The closest species based on a megablast search of the full ITS sequence is *Amanita inopinata,* currently *Saproamanita inopinata*, from the Netherlands (GenBank KM026507) and from New Zealand (GenBank HQ533044) both with 100 % coverage and a 97 % Identity score from 18 base differences and 9 gaps. Only one other species, *A. pruittii*, currently *Saproamanita pruittii* (Redhead et al. 2016), had 100 % coverage for the full ITS sequence in the megablast search, with a 96 % Identity score from 24 base differences and 10 gaps. Following the above-mentioned species, the highest megablast search was to an *Amanita* sp. (GenBank KY081706) from Brazil with 99 % coverage and an 88 % Identity score from 75 base differences and 22 gaps. The percent coverage of the full ITS in the megablast search dropped significantly thereafter.

According to the description of Tulloss (2009), *S. quitensis* belongs to the subgenus *Lepidella*, sect. *Lepidella*, subsect. *Vittadinae*, and according to Tulloss (2003) it belongs to the stirps Nauseosa due to the presence of clamp connections at the base of the basidia, the spore morphology and the characteristics of the remnants of the universal veil on the stipe. Morphologically, the closest species based on the description of Tulloss (2003) is *A. nauseosa* but it differs notably by the larger pileus size, presence of umbo, and strong odour when fresh and dry. Other close species are *S. pruittii*, but it differs by the odour, and shape and size of basidiospores (Tulloss et al. 2014); *A. prairiicola* differs by the presence of a persistent ring, and size and shape of the basidiospores, additionally the latter species belongs to the Vittadinii stirps (Tulloss 1998).

The phylogenetic tree was constructed using the Maximum Likelihood plugin PHYML in Geneious R9 (http://www.geneious.com; Kearse et al. 2012), and the substitution model determined by jModelTest (Posada 2008) according to Corrected Akaike Information Criterion (AICc). The genus *Amanita* is used based on current nomenclature in NCBI nucleotide database. *Amanita* sp. (GenBank KY081706) is the outgroup. Bootstrap support values ≥ 50 % are given above branches. The phylogenetic position of *S. quitensis* is indicated in **bold**. The species name is followed by the accession number, and the three letter United Nations country code, in order of appearance BRA: Brazil, USA: United States, ECU: Ecuador, NLD: Netherlands, NZL: New Zealand.

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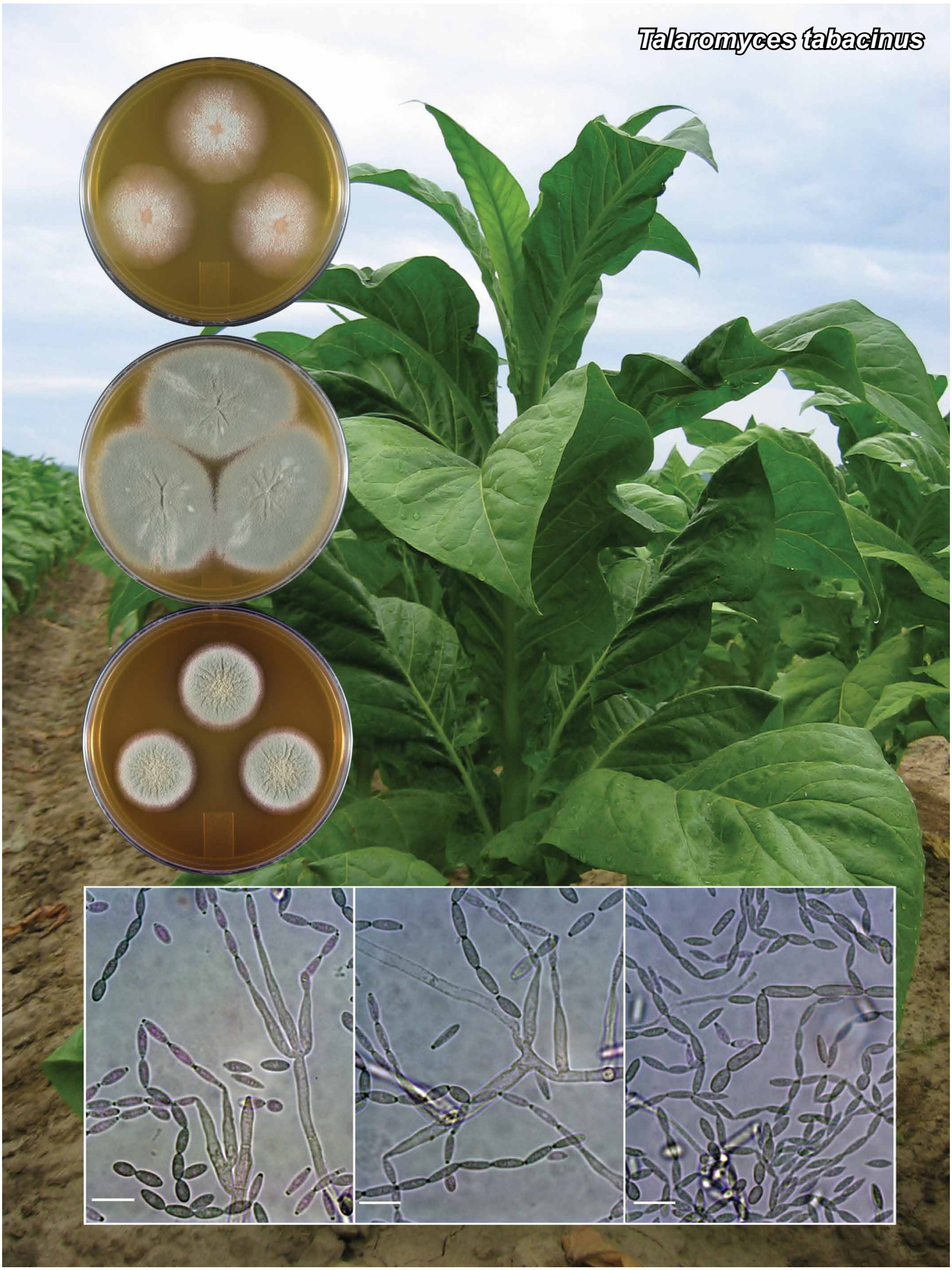

Talaromyces tabacinus

Fungal Planet 750 – 13 July 2018

Talaromyces tabacinus Jurjević, S.W. Peterson & G. Perrone, *sp. nov.*

Etymology. Named for tobacco, the host from which it was isolated.

Classification — *Trichocomaceae, Eurotiales, Eurotiomycetes.*

On MEA: *Conidiophores* with solitary phialides, 15–45(–65) × 3–4(–5.5) µm diam, or monoverticillate, occasionally biverticillate, rarely with subterminal branches; stipes smooth, (3–)10–40(–70) × 2.5–4 µm diam; metulae 2–3, 12–21 × 3–4 µm diam; phialides 2–5, acerose, (9–)14–20(–26) × 3–3.5(–5) µm diam, with gradually tapering collula, occasionally minutely roughened; conidia ellipsoidal to fusiform, rarely small and nearly subglobose, smooth, (4.5–)6–10(–19) × (2.5–)3–3.5(–4.5) µm diam. Borne in long disordered chains. No sexual morph observed.

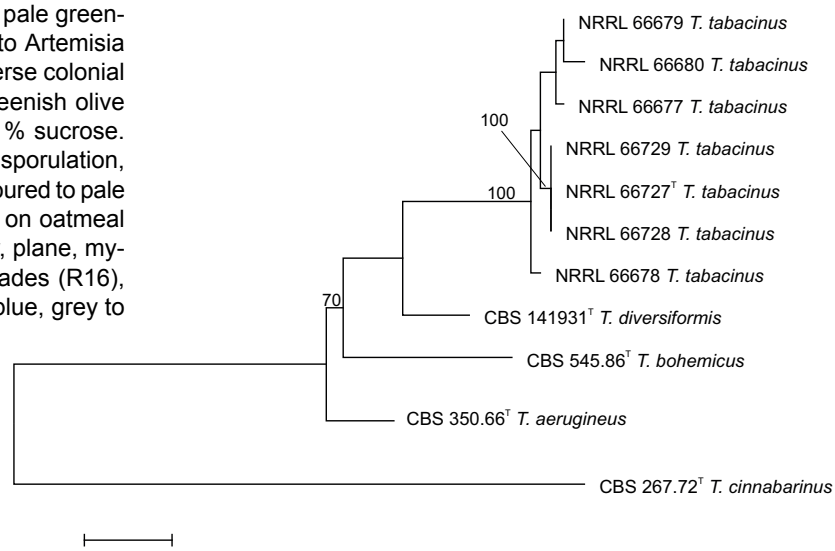
Culture characteristics — Cultured in darkness at 25 °C for 7 d unless otherwise noted. Colonies on malt extract agar (MEA) 27–40 mm diam, floccose to funiculose, low, plane, occasional shallow radial sulci, mycelium white, subsurface hyphae extending c. 4–12 mm from margin, sporulation moderate to very good, conidia *en masse* pale green-blue grey to deep green-blue, grey-blue (R48; Ridgway 1912), no exudate or soluble pigments, reverse cream-buff to deep colonial buff to primrose yellow (R30). Colonies on Czapek yeast autolysate agar (CYA) 14–24 mm diam, floccose to funiculose, rising c. 3–4 mm, mycelium white to yellow ochre (R15), subsurface hyphae extending c. 2–3 mm from margin, sporulation moderate, conidia *en masse* pale Medici blue to deep green-blue grey (R48), no exudate or soluble pigments, reverse cream-buff to chamois to light yellowish olive (R30). Colonies on potato dextrose agar 28–39 mm diam, floccose to funiculose, plane, light to deep radial sulci, mycelium white to deep colonial buff (R30), subsurface hyphae extending c. 3–12 mm from margin, sporulation moderate to heavy, conidia *en masse* pale green-blue, grey to deep green-blue, grey-blue (R48), to Artemisia green (R47), no exudate or soluble pigments, reverse colonial buff to olive-ochre to light olive yellow to dark greenish olive (R30). No growth on Czapek yeast agar with 20 % sucrose. Dichloran 18 % glycerol agar, 2–4 mm diam, no sporulation, mycelium white, largely submerged, reverse uncoloured to pale buff. No growth on CYA with 5 % NaCl. Colonies on oatmeal agar 38–43 mm diam, floccose to funiculose, low, plane, mycelium white, occasionally with Naples yellow shades (R16), heavy sporulation, conidia *en masse* pale green-blue, grey to deep green-blue, grey (R48), exudate when present clear, small droplets, soluble pigments absent. Colonies on creatine sucrose agar up to 4 mm diam, very poor growth. On CYA/MEA (colony diam in mm) at 30 °C 20–30/43–67; 35 °C 22–36/40–67; 37 °C 23–30/30–67; 41 °C 13–30/18–48; no growth at 45 °C.

Typus. USA, North Carolina, Durham, leaves of *Nicotiana tabacum* (*Solanaceae*) from a greenhouse, 17 Sept. 2013, *Ž. Jurjević* (holotype BPI 910533, cultures ex-type NRRL 66727 = EMSL 2174; barcode: ITS, *benA*, *CaM* and *rpb2* sequences GenBank MG182613, MG182627, MG182606 and MG182620, MycoBank MB823318).

Additional material examined. USA, North Carolina, Durham, tobacco leaves from a greenhouse, *Ž. Jurjevic*, 17 Sept. 2013, NRRL 66728 = EMSL 2175, NRRL 66729 = EMSL 2176; 19 July 2016, NRRL 66677; 9 Aug. 2016, NRRL 66678, NRRL 66679. Sequences deposited as GenBank MG182602–MG182629.

Notes — BLAST searches of the sequences of *T. tabacinus* showed ß-tubulin similarity to *T. aerugineus*, *T. bohemicus* and *T. diversiformis*; calmodulin similarities were to *T. bohemicus* and *T. diversiformis*. The ITS barcode was 98–99 % similar to *Talaromyces ryukyuensis, T. aerugineus, T. bohemicus* and *T. diversiformis*.

Talaromyces tabacinus is distinguished by the production of (4.5–)6–10(–19) × (2.5–)3–3.5(–4.5) µm diam ellipsoidal or fusiform conidia, and growth on CYA at 37 °C of 23–30 mm diam. The closely related *T. diversiformis* produces 4–6(–8) × 2–4 µm diam ellipsoidal or fusiform conidia, and growth at 37 °C is 17–19 mm diam. *Talaromyces bohemicus* has 7–9 × 2.5–3 µm fusiform conidia with encrusted cell walls, while *T. aerugineus* has 3–8.5 × 2.5–5 µm smooth conidia, in various shapes, subglobose to ellipsoidal to fusiform. *Talaromyces tabacinus* causes no disease symptoms on tobacco.



Maximum likelihood tree of *T. tabacinus* and closely related species based on a concatenated *benA*, *CaM* and *rpb2* DNA sequence alignment was calculated using MEGA (Kumar et al. 2016). Support values at branches were obtained from 1 000 bootstrap replicates. Bootstrap values greater than 70 % are shown; ex-type strains are indicated by T.

Colour illustrations. Tobacco plant; 7-d-old cultures of *Talaromyces tabacinus* on MEA (top: 25 °C, middle: 37 °C, bottom: 41 °C), conidia and conidiophores on MEA. Scale bars = 10 µm.

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Terfezia morenoi

Fungal Planet 751 – 13 July 2018

Terfezia morenoi Bordallo, Ant. Rodr. & Morte, *sp. nov.*

Etymology. Named after Prof. Gabriel Moreno, from Universidad de Alcalá de Henares (Madrid, Spain), for his long and illustrious career in Spanish Mycology and his outstanding contribution to the knowledge of hypogeous fungi.

Classification — *Pezizaceae, Pezizales, Pezizomycetes*.

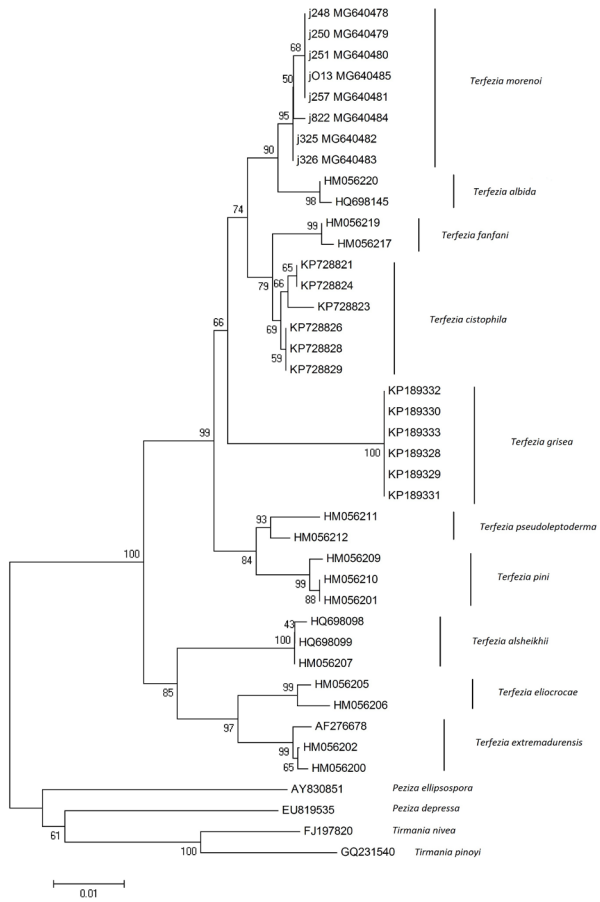
Ascomata hypogeous to partially emergent at maturity, 2–5 cm in size, subglobose, short base, cream colour at first, becoming brown, black spots on the sun-exposed parts or when manipulated, smooth. *Peridium* 300–500 µm thick, whitish in cross section, pseudoparenchymatous, composed of subglobose cells, 20–50 µm diam, thin-walled, hyaline, yellowish and angular to oblong in the outermost layers. *Gleba* solid, fleshy, succulent, whitish with small pale grey pockets at first, maturing to greyish green pockets of fertile tissue separated by whitish, sometimes with salmon pink spots, sterile veins. Often with small holes indicating mycophagous activity. Strong *odour*, more remarkable in mature specimens becoming unpleasant. Mild *taste*. *Asci* nonamyloid, ellipsoid to ovate, citriform, sessile or short-stipitate, 60–90 × 50–60 µm, walls 1–2 µm thick, with 6–8 irregularly disposed spores, randomly arranged in fertile pockets. *Ascospores* globose, (16–)16.5–19(–19.5) µm diam (median = 18 µm) including ornamentation, (13.5–)14–16 (–16.5) µm (median = 15 µm) without ornamentation, hyaline, smooth and uni-guttulate at first, by maturity yellow ochre and ornamented with conical spines, pointed, straight, separate, 1–2(–2.5) µm long, 1 µm wide at the base.

Ecology & Distribution — *Terfezia morenoi* grows in calcareous, clayey, alkaline soils, associated with *Pinus* spp. and *Quercus ilex*, with no presence of *Cistaceae*, it fructifies from March to April. A circular brûlé or burnt area, with scanty vegetation, is usually observed in the ground around its mycorrhizal host plant. This burnt area is very similar to those described for some *Tuber* species and can be widely interpreted as allelopathic phenomena due to volatile secondary metabolites emitted in the course of their life cycle (Streiblova et al. 2012). The fact that this species has a strong odour could be related to the formation of this burnt area, not found in other *Terfezia* species with light spermatic odour or without odour.

Typus. Spain, Albacete, Jorquera, 2013, leg. *Ant. Rodríguez* (holotype MUB Fung-j251, ITS sequence GenBank KY678905, MycoBank MB823725).

Additional material examined. Spain, Albacete, Cilleruelo, 2009, *A. Rodríguez*, MUB Fung-jO12, MUB Fung-jO13, MUB Fung-jO14; Pozohondo, 2013, *A. Rodríguez*, MUB Fung-j257; Lezuza, 2017, *A. Rodríguez*, MUB Fung-j822; Jorquera, 2013, *C. Rodríguez*, MUB Fung-j248, MUB Fung-j250, MUB Fung-j251; Valencia, Onteniente, 2009, *A. Rodríguez*, MUB Fung-jO39; La Rioja, 2013, *A. Rodríguez*, MUB Fung-j325, MUB Fung-j326; Valladolid, Santa Espina, 1998, *A. García*, MUB Fung-jO34.

Notes — *Terfezia morenoi* is a spiny-spored *Terfezia* species characterised by its strong odour attractive for animals, greyish green gleba, growing in alkaline clay soils in spring, associated with *Pinus* spp. and *Quercus ilex* without presence of *Cistaceae*. It differs from *T. albida*, the other spiny-spored species growing in alkaline clay soils in having a spermatic odour, white peridium, larger spores and different host plant (Bordallo et al. 2013). *Terfezia cistophila* has a spermatic odour, different host and grows in acidic soil (Bordallo et al. 2015). *Terfezia olbiensis* is odourless and grows in winter (Tulasne & Tulasne 1851). *Terfezia grisea* is odourless, has blackish grey gleba and different host plant (Bordallo et al. 2015). *Terfezia fanfani*, *T. pseudoleptoderma*, *T. extremadurensis*, *T. pini* and *T. leptoderma*, the other spiny-spored species, differ in growing in acidic soil, having no distinctive odour and larger spores. Moreover, the new taxon is distinguished from the other species based on ITS sequence identity in the phylogenetic tree based on the Neighbour-Joining method, that was topologically identical to the Maximal Parsimony tree (data not shown).



The evolutionary history was inferred using the Neighbour-Joining method. The bootstrap consensus tree inferred from 500 replicates is taken to represent the evolutionary history of the taxa analysed. Branches corresponding to partitions reproduced in less than 50 % bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) are shown next to the branches. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method and are in the units of the number of base substitutions per site. All positions containing gaps and missing data were eliminated from the dataset (Complete deletion option). There were a total of 452 positions in the final dataset. Phylogenetic analyses were conducted in MEGA4 (Tamura et al. 2007).

Colour illustrations. Habitat with *Pinus halepensis* and a burnt area around; ascocarp; gleba and mature ascospores. Scale bar = 10 µm.

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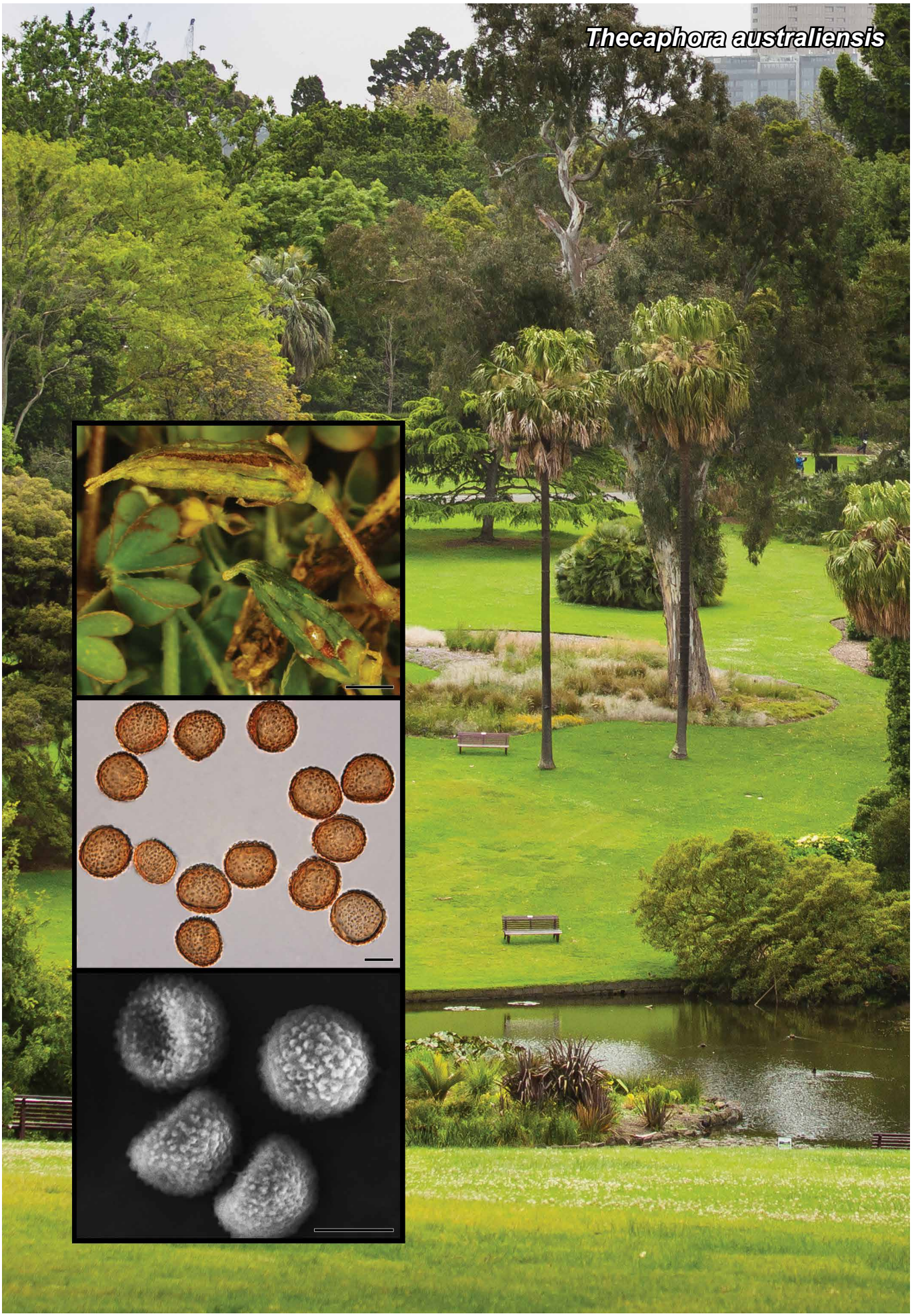

Thecaphora australiensis

Fungal Planet 752 – 13 July 2018

Thecaphora australiensis Stajsic, Y.P. Tan & R.G. Shivas, *sp. nov.*

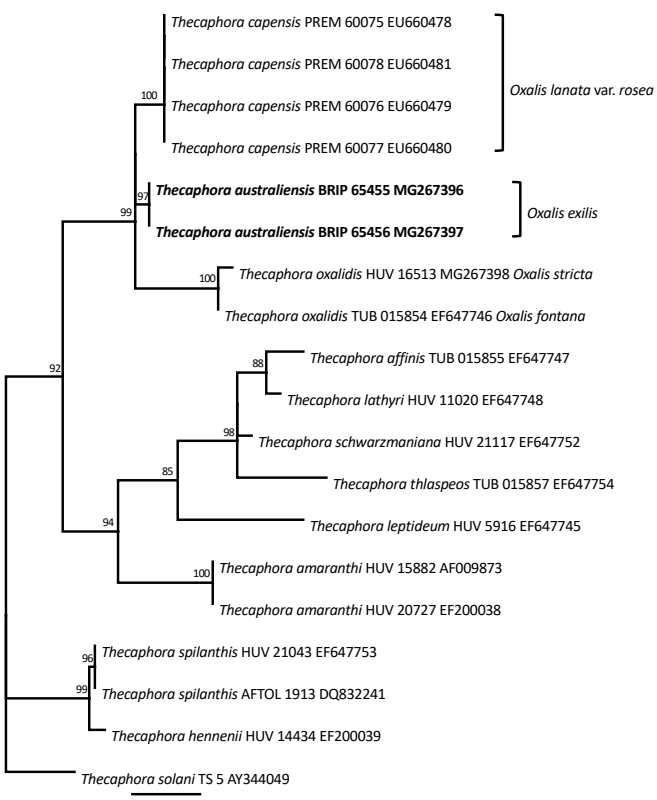
Etymology. Name refers to the country from where this fungus was collected, Australia.

Classification — *Glomosporiaceae*, *Ustilaginales*, *Ustilaginomycetes*.

Sori in all or most capsules on an infected plant, infected capsules slightly swollen and all of the seeds are replaced by a powdery, cinnamon-brown spore mass. *Spores* solitary when mature, subglobose to broadly ellipsoid, 14–26 × 14–19 µm, pale to medium yellowish brown; wall even, 1–2 µm thick including surface ornamentation, densely verruculose, warts c. 1 µm high. *Asexual morph* not seen.

Typus. Australia, Victoria, Beaumaris, Melbourne, Balcombe Road, north side of road, at intersection with Balcombe Park Lane, S37°58'37.7" E145°01'51.7", alt. 27 m, in capsules of a variant of *Oxalis exilis* (*Oxalidaceae*), 7 Feb. 2017, *V. Stajsic 8369* (holotype BRIP 65455, LSU sequence GenBank MG267396, MycoBank MB822652; isotype MEL 2406589A).

Additional material examined. Australia, Victoria, Melbourne, Royal Botanic Gardens, lawn near the National Herbarium of Victoria building, alt. 30 m, in capsules of a variant of *Oxalis exilis*, 10 Feb. 2017, *V. Stajsic 8379*, BRIP 65456, MEL 2406590A, LSU sequence GenBank MG267397; Beaumaris, Fairleigh Avenue, 20 Apr. 2017, *V. Stajsic 8513*, MEL 2417667A.



Colour illustrations. Gardens of the Royal Botanic Gardens Victoria (photo credit Adrian Vittorio); infected capsule of *Oxalis exilis*; spores. Scale bars = 1 mm (infected capsule), 10 µm (spores).

Notes — The smut genus *Thecaphora* contains approximately 60 species, which infect hosts in 16 eudicot families (Vánky 2011). Four species have been found in Australia, two of which are endemic, none of which occur on *Oxalis* (Vánky & Shivas 2008). Only two species, *Thecaphora oxalidis* and *T. capensis*, are known to infect *Oxalis*. *Thecaphora oxalidis* occurs on *Oxalis corniculata*, *O. dillenii*, *O. fontana* and *O. stricta* (all in sect. *Corniculatae*) and *O. laxa* (sect. *Alpinae*) in Asia, Europe, North and South America (Vánky et al. 2008). The second species, *T. capensis* is only known on *O. lanata* f. var. *rosea* (sect. *Oppositae*) from the type locality in South Africa (Salter 1944, Roets et al. 2008). *Thecaphora australiensis* is the only smut fungus known to occur on *Oxalis* in Australia. *Thecaphora australiensis* is morphologically very similar to *T. oxalidis*, but it has longer spores than those of *T. oxalidis*, which are 12–17 × 13.5–21(–24) µm (Vánky 2011). Phylogenetic analyses of the LSU sequences show that it clusters with *T. oxalidis* and *T. capensis*. *Thecaphora australiensis* infects a variant of *Oxalis exilis* (sect. *Corniculatae*), a species which is indigenous to Australia, New Caledonia and New Zealand. This variant occurs mainly in lawns, nature-strips, gardens, edges of paths, parkland and ditches. The origin status of this form of *O. exilis* is uncertain. The discovery of a novel *Thecaphora* species on this variant of *O. exilis* lends support to the likelihood that the host may be indigenous to Australia. An examination of all the Australian-collected specimens from *Oxalis* sect. *Corniculatae* held at MEL did not yield any specimens with *T. australiensis*.

A maximum likelihood tree of *Thecaphora* based on an alignment of LSU sequences. Analyses were performed using RAxML v. 7.2 (Stamatakis & Alachiotis 2010) on the Geneious v. 9.1.8 platform (Biomatters Ltd.) based on the GTR substitution model with gamma-distribution rate variation. In the tree, branch lengths are proportional to distance. Bootstrap support values ≥ 70 % are indicated on the nodes. *Thecaphora solani* TS5 was used as outgroup. The *Oxalis* hosts are indicated after the *Thecaphora* spp. names. The new species proposed in this study is indicated in **bold**.

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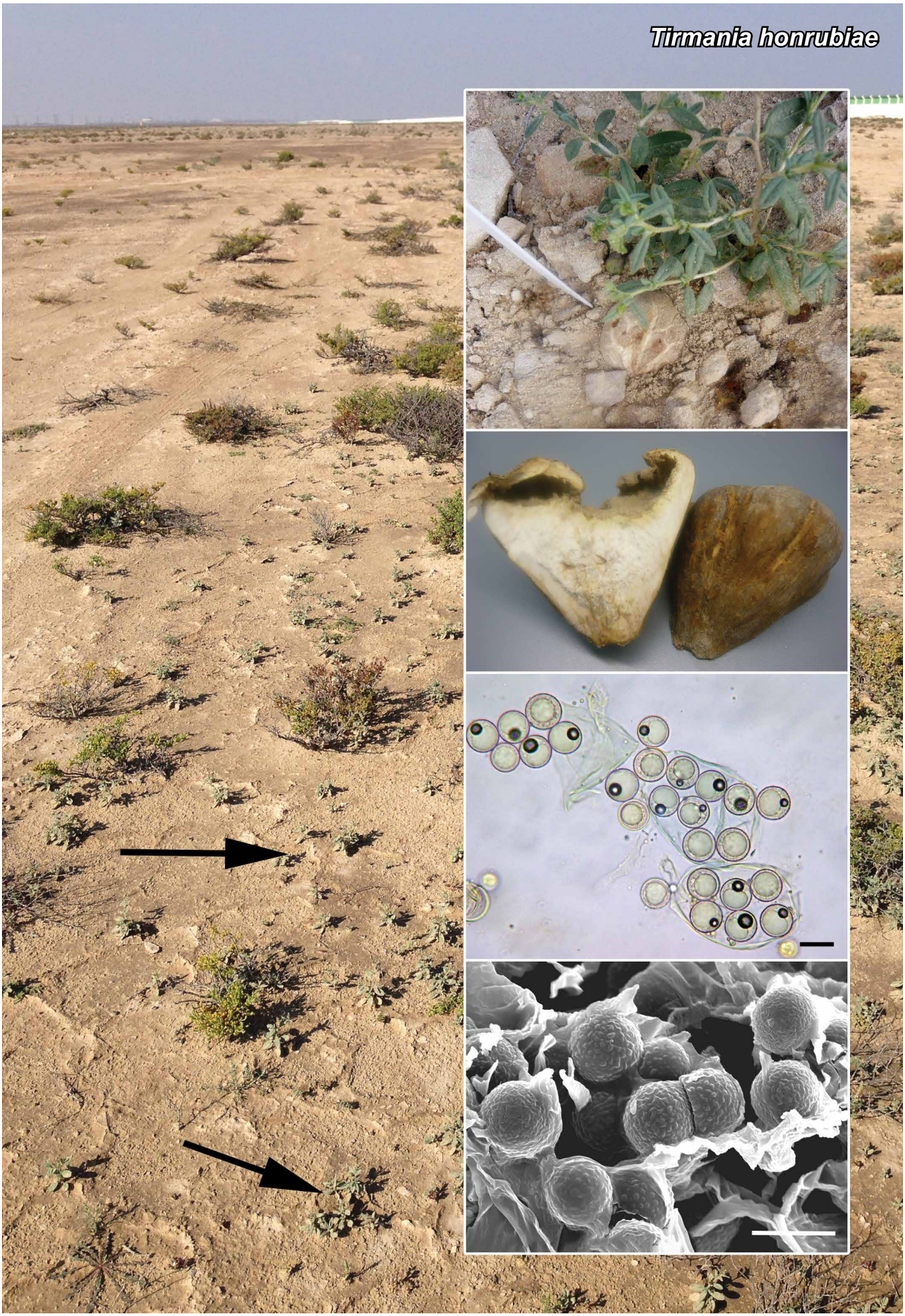

Tirmania honrubiae

Fungal Planet 753 – 13 July 2018

Tirmania honrubiae Morte, Bordallo & Ant. Rodr., *sp. nov.*

Etymology. Named after Prof. Mario Honrubia, from Universidad de Murcia (Murcia, Spain), for his valuable contributions in the fields of mycology and mycorrhizal research.

Classification — *Pezizaceae, Pezizales, Pezizomycetes.*

Ascomata hypogeous to partially emergent at maturity, 5–10 × 4–9 cm, subglobose to turbinate, with basal mycelial attachment, whitish to pale brown, yellowish brown, becoming dark brown with age, smooth. *Peridium* 1 mm thick, thinner or discontinuous in places, 2-layered: the outermost being 100 µm thick, composed of appressed interwoven hyphae, more or less parallel with surface of ascocarp, 5–12 µm diam, thick-walled, yellowish; the inner layer not differentiable from the gleba, composed of subglobose cells, inflated up to 40 µm diam, hyaline and thin-walled. *Gleba* solid, fleshy, with thin, whitish to yellowish sterile veins enclosing cream to pale pink pockets of fertile tissue. *Odour* pleasant. *Taste* not recorded. *Asci* faintly amyloid, ellipsoid to pyriform, short-stipitate, 70–110 × 40–60 µm, walls 1–1.5 µm thick, with 6–8 irregularly disposed spores, randomly arranged in fertile pockets. *Ascospores* globose, 15–19 µm diam, hyaline to pale yellow, with a single guttule, 2-layered: outer layer smooth; inner layer roughened, with low rounded warts (up to 1 µm high) and ridges, protruding into the outer wall layer with age or not fully hydrated, sometimes forming a pseudoreticulum.

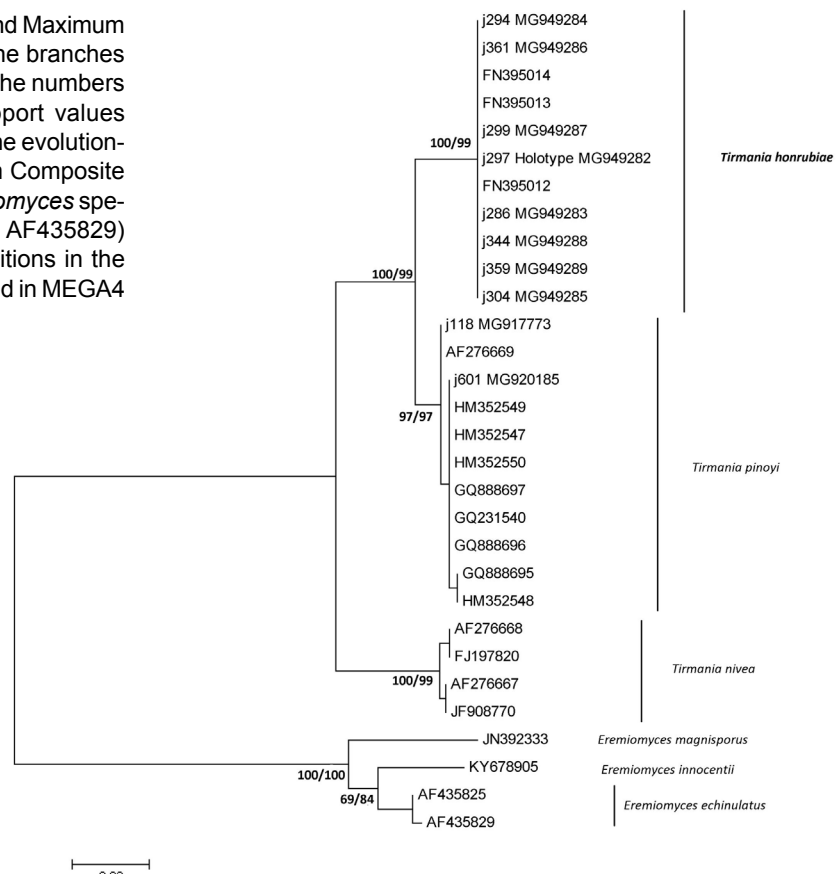
Phylogeny inferred using Neighbour-Joining (NJ) and Maximum Parsimony (MP) methods. The first numbers on the branches are the NJ bootstrap support values (≥ 50 %) and the numbers after the slash represent the MP bootstrap support values (≥ 50 %) based on 500 bootstrapping replicates. The evolutionary distances were computed using the Maximum Composite Likelihood analysis of ITS rDNA sequences. *Eremiomyces* species (GenBank JN392333, KY678905, AF435825, AF435829) were the outgroup. There was a total of 491 positions in the final dataset. Phylogenetic analyses were conducted in MEGA4 (Tamura et al. 2007).

Ecology & Distribution — *Tirmania honrubiae* grows in sandy, calcareous and alkaline soils of arid areas, associated with *Helianthemum lippii*. Sporocarps are observed from January to the beginning of April.

Typus. United Arab Emirates, Abu Dhabi, Ghantoot, 2013, leg. *A. Morte* (holotype MUB Fung-j297, ITS sequence GenBank MG949282, MycoBank MB824243).

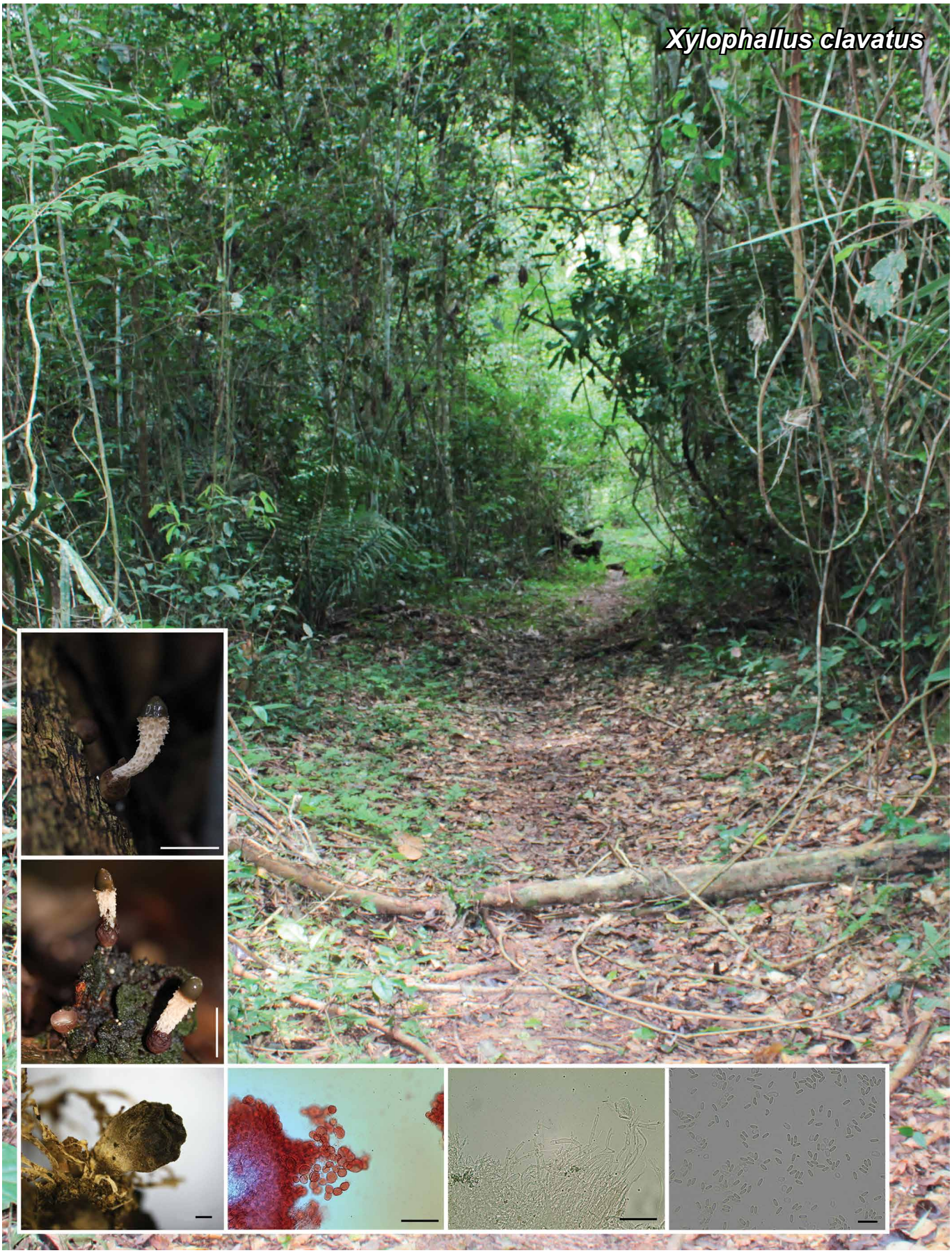
Additional material examined. United Arab Emirates, Abu Dhabi, Ghantoot, 2013, leg. *A. Morte*, MUB Fung-j286, ITS sequence GenBank MG949283, MUB Fung-j294, ITS sequence GenBank MG948294, MUB Fung-j299, ITS sequence GenBank MG949287, MUB Fung-j304, ITS sequence GenBank MG949285; Ghantoot, 2014, leg. *A. Morte*, MUB Fung-j359, ITS sequence GenBank MG949289, MUB Fung-j361, ITS sequence GenBank MG949286; Seih Sadira, 2014, leg. *A. Morte*, MUB Fung-j344, ITS sequence GenBank MG949288, MUB Fung-j348.

Notes — The genus *Tirmania* has only two accepted species, *T. nivea* and *T. pinoyi*, which are mainly distributed in arid areas with alkaline soils, from the north of Africa and west of Asia (Malençon 1973, Kagan-Zur et al. 2014). *Tirmania honrubiae* differs from *T. nivea* and *T. pinoyi* based on its ITS sequence data and the spore ornamentation. *Tirmania nivea* has spores that are smooth or minutely roughened and broadly ellipsoid in shape. *Tirmania pinoyi* has spores that are more conspicuously ornamented, but are clearly shorter than those of *T. honrubiae* when they are observed under a scanning electron microscope.



Colour illustrations. Arid zones of Seih Sadira (Abu Dhabi, UAE), calcareous sandy soils, with *Helianthemum lippii* plants (arrows); ascocarp under *H. lippii*; gleba; amyloid asca with ascospores and scanning electron micrograph of mature ascospores. Scale bars = 20 µm.

Asunción Morte, Juan Julián Bordallo & Antonio Rodríguez, Departamento de Biología Vegetal (Botánica), Facultad de Biología, Universidad de Murcia, 30100 Murcia, Spain; e-mail: amorte@um.es, juanjulian.bordallo@um.es & antonio@trufamania.com


Xylophallus clavatus

Fungal Planet 754 – 13 July 2018

Xylophallus clavatus T.S. Cabral, M.P. Martín, C.R. Clement, K. Hosaka & Baseia, *sp. nov.*

Etymology. In reference to its basidiome shape.

Classification — *Phallaceae, Phallales, Agaricomycetes*.

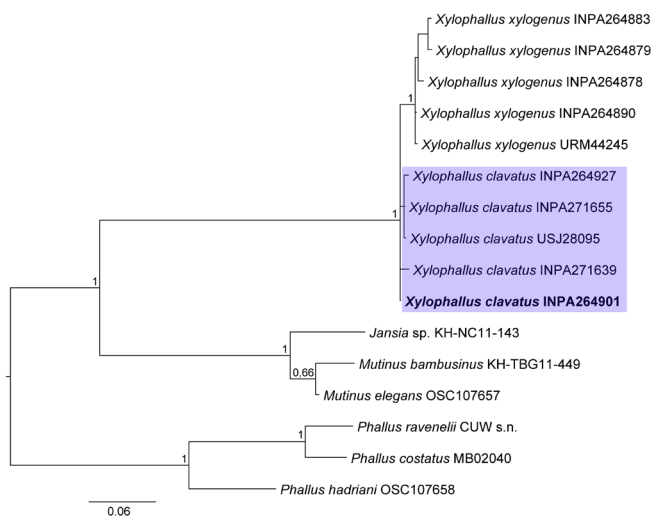
Immature *basidiome* globose to subglobose, with protuberances on the surface, up to 8 × 6 mm, pale brown (N40A99M20; Küppers 1979) on base to brown (N90A99M99) to the apex, rhizomorphs on the base. Mature basidiome up to 38 × 7 mm in its thickest portion when fresh, clavate shape. Receptacle campanulate, smooth, with an umbilicated depression or minutely perforated at apex, adnate to pseudostipe, up to 6 × 7 mm. *Pseudostipe* up to 21 × 7 mm, cylindrical, hollow, not attached to the volva, reticulated surface with reticulations deeper when closer to receptacle, white (N00A00M00), composed of ovoid to pyriform pseudoparenchymatous hyphae 20–35 × 20–27 µm, hyaline in 5 % KOH (same hyphae of receptacle). *Volva* pale brown (N40A99M20) to brown (N90A99M99), with irregular dehiscence, rhizomorphs at base forming a net spreading through substrate, interconnecting basidiomes; external layer composed of filamentous hyphae, 2.5–3.5 µm wide, hyaline in 5 % KOH, sinuous, septate and with clamp connections; internal gelatinous layer composed of pseudoparenchymatous hyphae, 19–34 × 19–27 µm, hyaline in 5 % KOH. *Rhizomorphs* composed of filamentous hyphae, 1.5–3.5 µm wide, thick-walled, septate, hyaline in 5 % KOH. *Gleba* olive-brown (N99A50M10), mucilaginous. *Basidium* clavate, bearing 6–8 spores. *Basidiospores* bacillar, smooth, (4–)4.5–5(–5.5) × 1.5–2(–2.5) µm, greenish to hyaline in 5 % KOH.

Typus. Brazil, Pará, Belterra, National Forest of the Tapajós, -2.94166667, -54.92972222, on rotten wood, 2014, *T.S. Cabral & D.L. Komura* (holotype INPA 264901, ITS, *rpb2* and *tef-1α* sequences GenBank KU871795, KU871723 and KU871513, MycoBank MB824521; isotype INPA 264902).

Additional material examined. Brazil, Amazonas, São Gabriel da Cachoeira, Itacoatiara-Mirim Community, S0°07'43.4" W66°58'24.4", 2014, *T.S. Cabral*, paratype INPA 264927, ITS, *rpb2* and *tef-1α* sequences GenBank KU871800, KU871716 and KU871497; Barcelos, 2015, *T.S. Cabral*, paratype INPA 271655, ITS, *rpb2* and *tef-1α* sequences GenBank KU871814, KU871742 and KU871515; Parintins, Açaí Community, -2.64750000, -56.54833333, 2015, *T.S. Cabral*, paratype INPA 271639, ITS, *rpb2* and *tef-1α* sequences GenBank KU871803, KU871719 and KU871506. – Costa Rica, Heredia, Sarapiquí, La Selva, 1986, *C. Ovrebo*, USJ 28095, ITS, *rpb2* and *tef-1α* sequences GenBank KU871815, KU871715 and KU871514.

Colour illustrations. Brazil, Pará, Belterra, National Forest of the Tapajós; fresh basidiomes of INPA 271639 and INPA 264901 (top, scale bar = 10 mm); immature basidiome with protuberances on surface (bottom, scale bar = 1 mm); pseudoparenchymatous hyphae of pseudostipe (scale bar = 100 µm); filamentous hyphae from volva (scale bar = 50 µm); basidiospores (scale bar = 10 µm).

Notes — To date, the genus *Xylophallus* has been considered monospecific with *X. xylogenus*, the smallest phalloid yet described (up to 15 mm high), as the type of the genus. The immature basidiomes of *X. xylogenus* have a smooth surface, and mature basidiomes are fusiform, with reticulate pseudostipes. However, *X. clavatus* is macroscopically characterised by its large basidiome size, the immature basidiome surface with protuberances, the clavate shape of the mature basidiomes, and the pseudostipe with relatively shallow reticulations. Microscopically, they differ mainly in basidiospore size: in *X. clavatus* the basidiospores are 4.5–5 µm in length, while in *X. xylogenus* basidiospores are 3–4 µm (Trierveiler-Pereira & Da Silveira 2012). Sáenz et al. (1972) provided a very detailed description of specimens from Costa Rica. In our analysis, the Costa Rican specimen (USJ 28095) grouped in the new species clade. We found morphological similarities between the author's description and the specimens of *X. clavatus* analysed here, such as mature and immature basidiomatal sizes, immature basidiomatal surface with protuberances, and basidiospore sizes. In fact, Sáenz et al. (1972) state that their results are somewhat different from those previously published, which now can be explained by the fact that previous papers were dealing with *X. xylogenus*. The species tree indicates that the previous taxonomy of *Xylophallus* does not reflect its evolutionary history. This genus is actually composed of at least two evolutionary units, with *X. xylogenus* being a sister species to the clade representing *X. clavatus*.



Phylogenetic tree obtained with MrBayes v. 3.1.2 (Ronquist & Huelsenbeck 2003) using ITS nrDNA, *tef-1α* and *rpb2* concatenated genes, under GTR+G, TRN+G and SYM+G models, for 3 M generations. Both type and paratype of the new species are marked with a coloured rectangle. Posterior probabilities values are indicated on the branches. TreeBASE submission ID 22365.

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Zymoseptoria crescenta

Fungal Planet 755 – 13 July 2018

Zymoseptoria crescenta Abrinbana, Abdollahz. & Crous, *sp. nov.*

Etymology. Named after its characteristic crescent-shaped conidia.

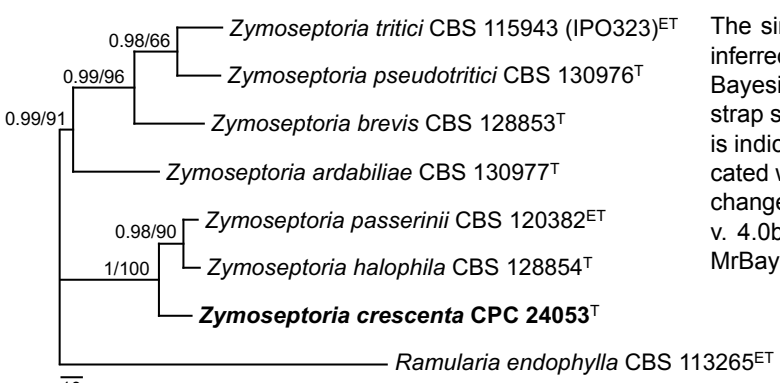
Classification — *Mycosphaerellaceae, Capnodiales, Dothideomycetes*.

Phytopathogenic. *Conidiomata* pycnidial, substomatal, immersed to erumpent, globose, dark brown, up to 120 µm diam, with central ostiole, up to 20 µm diam; wall of 3–4 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells, or with one supporting cell, lining the inner cavity. *Conidiogenous cells* hyaline, smooth, tightly aggregated, subcylindrical to ampulliform, straight to curved, 6–13 × 2–3 µm, with 1–2 inconspicuous, percurrent proliferations at apex, 1–1.5 µm diam. Type I conidia solitary, hyaline, smooth, guttulate, crescent or sickle-shaped, tapering towards acutely rounded apex, with tapering subtruncate or mostly acute base, 0(–1)-septate, (11–)15–21(–25) × 2(–2.5) µm; hila not thickened nor darkened, 1–2 µm diam. On OA and PDA yeast-like growth and microcyclic conidiation (Type III conidia) are observed, and aerial hyphae disarticulate into phragmospores (Type II conidia).

Culture characteristics — Colonies on PDA erumpent, spreading, with sparse aerial mycelium, lobate margins, greenish black, reverse olivaceous grey. On OA erumpent, spreading, with sparse aerial mycelium, olivaceous grey margin; reaching 10 mm diam after 30 d at 25 °C.

Typus. Iran, East Azarbaijan province, Kaleybar, N38°36'43" E47°14'21", on living leaves of *Aegilops triuncialis* (*Poaceae*), May 2012, *M. Abrinbana* (holotype CBS H-23592, cultures ex-types CPC 24053 = CBS 144410, ITS, LSU, *tef1* and *rpb2* sequences GenBank MH259304, MH267287, MH271694 and MH271695, MycoBank 825300).

Notes — The genus *Zymoseptoria* (based on *Z. tritici*) was established by Quaedvlieg et al. (2011) for septoria-like species that occur on graminicolous hosts. With the introduction of *Z. crescenta*, the genus presently contains eight species, including *Z. tritici* (causal agent of septoria tritici blotch on wheat) and *Z. passerinii* (causal agent of septoria speckled leaf blotch of barley) (Stukenbrock et al. 2012, Videira et al. 2017). *Zymoseptoria crescenta* is phylogenetically closely related to *Z. halophila* and *Z. passerinii*. However, it is easily distinguished from all known *Zymoseptoria* species by having crescent-shaped conidia *in vivo*.



The single most parsimonious tree of *Zymoseptoria* species inferred from concatenated ITS, LSU, *tef1* and *rpb2* sequences. Bayesian posterior probability and maximum parsimony bootstrap support values are given at the nodes. The new species is indicated in **bold**. All strains are ex-type or ex-epitype (indicated with T and ET, respectively). The scale bar represents 10 changes. The parsimony analysis was performed using PAUP* v. 4.0b10 (Swofford 2003) and the Bayesian analysis using MrBayes v. 3.2 (Ronquist & Huelsenbeck 2003).

Colour illustrations. Symptomatic leaf of *Aegilops triuncialis*; colony sporulating on potato dextrose agar; conidiogenous cells and conidia. Scale bars = 10 µm.

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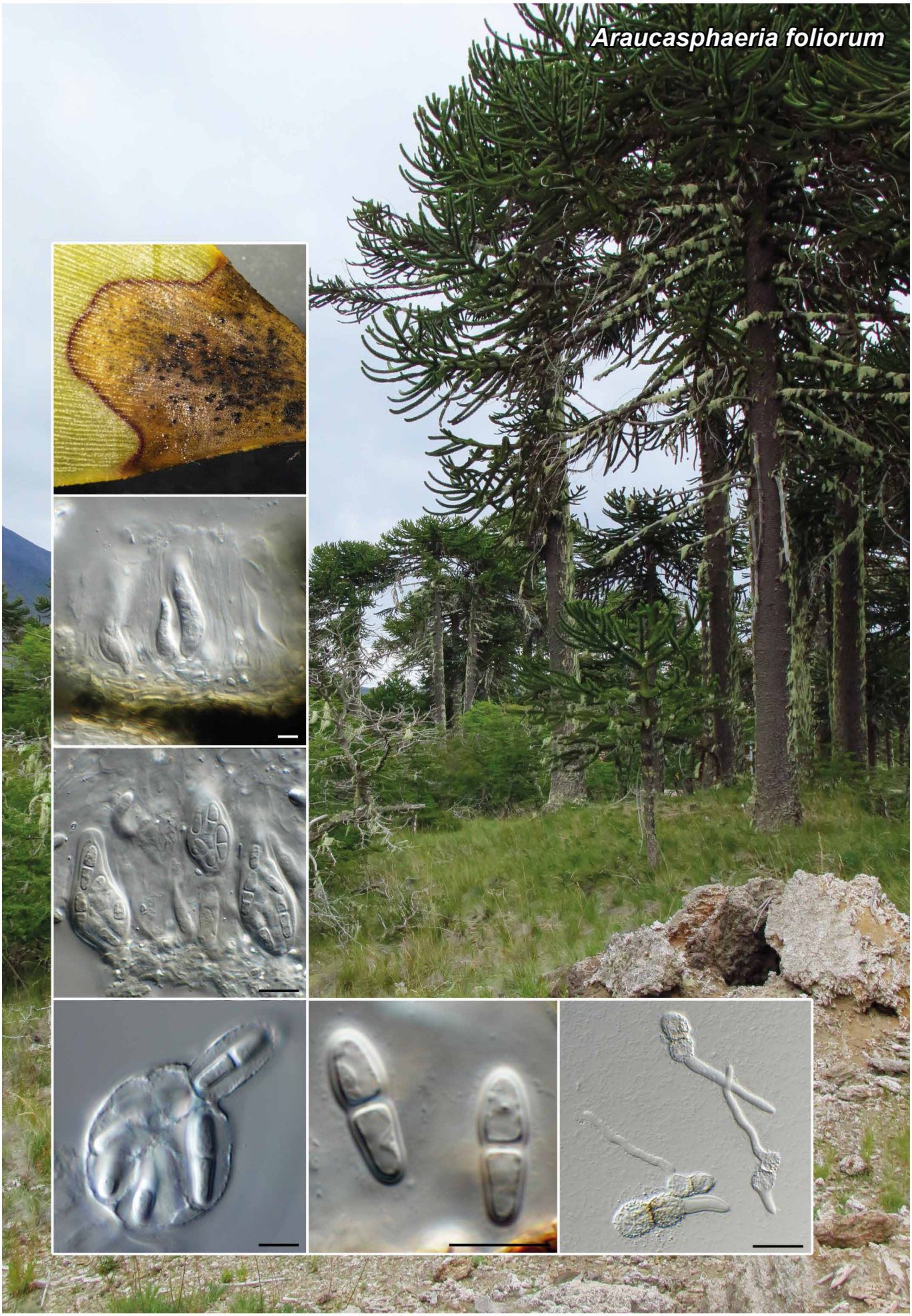
Araucasphaeria foliorum

Fungal Planet 756 – 13 July 2018

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

Etymology. Name combines the host genus, *Araucaria*, and the related fungal genus, *Teratosphaeria*.

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

Phytopathogenic. *Ascomata* pseudothecial, aggregated in a brown stroma, immersed to erumpent, globose, with central ostiole, filled with hyaline, branched, septate periphysoids; wall of 3–8 layers of dark brown *textura angularis. Asci* aparaphysate, fasciculate, bitunicate, subsessile, obovoid, straight to slightly curved, 8-spored. *Ascospores* multiseriate, overlapping, hyaline, guttulate, thick-walled, fusoid-ellipsoid with obtuse ends, medianly 1-septate, encased in a mucoid sheath.

Type species. *Araucasphaeria foliorum* Crous & M.J. Wingf. MycoBank MB825397.

Araucasphaeria foliorum Crous & M.J. Wingf., *sp. nov.*

Etymology. Name refers to the fact that the fungus occurs on leaves.

Leaf spots amphigenous, irregular to subcircular, 5–20 mm diam, brown, with dark brown margins. *Ascomata* pseudothecial, amphigenous, aggregated in a brown stroma, dark brown, immersed to erumpent, globose, 70–100 µm diam, with central ostiole, filled with hyaline, branched, septate periphysoids, 5–15 × 2–3.5 µm; wall of 3–8 layers of dark brown *textura angularis. Asci* aparaphysate, fasciculate, bitunicate, subsessile, obovoid, straight to slightly curved, 8-spored, 25–45 × 12–17 µm. *Ascospores* multiseriate, overlapping, hyaline, guttulate, thick-walled, straight, fusoid-ellipsoid with obtuse ends, widest just above septum, medianly 1-septate, constricted at septum, tapering towards both ends, but more prominently towards lower end, encased in a mucoid sheath up to 5 µm diam, (12–)14–15 × (4–)4.5–5 µm. Ascospores germinating primarily from one end, with germ tubes at an angle to the long axis of the spore, becoming constricted at septum, medium brown, verruculose, 5(–7) µm diam.

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

Typus. Chile, Rio Puesco, near Pucon, on symptomatic leaves of *Araucaria araucana* (*Araucariaceae*), Mar. 2010, *M.J. Wingfield* (holotype CBS H-23591, culture ex-type CPC 33084 = CBS 144411, ITS and LSU sequences GenBank MH327793.1 and MH327829.1, MycoBank MB825398).

Notes — A common ascomycete found on the leaves of *Araucaria* in South America is *Mycosphaerella araucariae* (Rehm 1901, Von Arx 1958, Aptroot 2006). *Araucasphaeria foliorum* is distinct from *Mycosphaerella araucariae,* which has larger ascomata (100–140 µm diam), asci (65–90 × 12–17 µm) and ascospores (19–26 × 5–6 µm) (Von Arx 1958). *Araucasphaeria* differs from *Pseudoteratosphaeria* (Quaedvlieg et al. 2014) in having ascomata aggregated in a stroma, ostioles that are lined with hyaline, branched, septate periphysoids, and ascospores encased in a prominent mucoid sheath.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Pseudotaeniolina globosa* (GenBank KC311489.1; Identities = 482/548 (88 %), 20 gaps (3 %)), *Phaeothecoidea proteae* (GenBank EU707898.1; Identities = 483/553 (87 %), 27 gaps (4 %)) and *Xenophacidiella pseudocatenata* (GenBank JF499851.1; Identities = 485/555 (87 %), 35 gaps (6 %)). Closest hits using the LSU sequence are *Pseudoteratosphaeria secundaria* (GenBank EU019306.2; Identities = 847/868 (98 %), 1 gap (0 %)), *Pseudoteratosphaeria flexuosa* (GenBank JN232432.1; Identities = 846/868 (97 %), 1 gap (0 %)) and *Pseudoteratosphaeria ohnowa* (GenBank EU019305.2; Identities = 846/868 (97 %), 1 gap (0 %)).

Colour illustrations. *Araucaria* trees growing in Chile; symptomatic leaf, asci in ascomata, ascospores with and without sheath, germinating ascospores. Scale bars = 10 µm.

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Corynespora pseudocassiicola

Fungal Planet 757 – 13 July 2018

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

Etymology. Name refers to the morphological similarity to *Corynespora cassiicola*.

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

Leaf spots amphigenous, but more prominent on upper leaf surface, medium brown with broad, dark brown border, circular to subcircular, 5–20 mm diam. *Mycelium* immersed, stromata absent. *Conidiophores* 200–400 × 5–7 µm, septate, dark brown, smooth, cylindrical, flexuous, thick-walled, solitary, at times arising in clusters of 3–6 from a reduced stroma consisting of a few brown, globose cells, 10–13 µm diam. *Conidiogenous cells* terminal, integrated, dark brown, smooth, cylindrical, with obtuse apex with tretic central pore, 12–50 × 5–7 µm. *Conidia* medium brown, finely roughened, subcylindrical to obclavate, apex obtuse, base obconically truncate, with slightly darkened hilum, (3–)4–5(–7) µm diam, (4–)8–12(–17)-distoseptate, straight to flexuous, frequently in short, unbranched chains, (70–)95–160(–230) × (7–)9–10 µm.

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

Typus. Colombia, Llanos, on leaves of *Byrsonima* sp. (*Malpighiaceae*), July 2010, *M.J. Wingfield* (holotype CBS H-23590, culture ex-type CPC 31708 = CBS 144412, ITS, LSU, *actA*, *tef1* and *tub2* sequences GenBank MH327794.1, MH327830.1, MH327864.1, MH327877.1 and MH327888.1, MycoBank MB825399).

Notes — *Corynespora cassiicola* (from leaves of *Cassia* sp. in Cuba) is a common pathogen of a range of crops in the tropics, which is morphologically and phylogenetically highly diverse (Dixon et al. 2009), including several different species. *Corynespora pseudocassiicola* is morphologically similar to several species that are presently treated as *C. 'cassiicola',* but is associated with leaf spots of *Byrsonima* in Colombia, and is herewith distinguished based on its phylogenetic placement, and described as new.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Corynespora cassiicola* (GenBank FJ852587.1; Identities = 520/553 (94 %), 11 gaps (1 %)), *Corynespora torulosa* (GenBank NR_145181.1; Identities = 517/551 (94 %), 10 gaps (1 %)) and *Corynespora smithii* (GenBank KY984300.1; Identities = 513/551 (93 %), 9 gaps (1 %)). Closest hits using the LSU sequence are *Corynespora cassiicola* (GenBank LC177365.1; Identities = 805/809 (99 %), no gaps), *Cory-nespora torulosa* (GenBank KF777207.1; Identities = 847/855 (99 %), no gaps) and *Corynespora smithii* (GenBank KY984299.1; Identities = 845/855 (99 %), no gaps). Closest hits using the *actA* sequence had highest similarity to *Parastagonospora nodorum* (GenBank CP022803.1; Identities = 474/523 (91 %), 10 gaps (1 %)), *Phaeosphaeria podocarpi* (GenBank KP004502.1; Identities = 458/503 (91 %), 5 gaps (0 %)) and *Alternaria intercepta* (GenBank JQ671651.1; Identities = 469/521 (90 %), 8 gaps (1 %)). Closest hits using the *tef1* sequence had highest similarity to *Corynespora smithii* (GenBank KY984436.1; Identities = 372/431 (86 %), 14 gaps (3 %)), *Neocucurbitaria juglandicola* (GenBank MF795861.1; Identities = 351/440 (80 %), 23 gaps (5 %)) and *Protofenestella ulmi* (GenBank MF795879.1; Identities = 351/440 (80 %), 30 gaps (6 %)). The best hit using the *tub2* sequence was with *Corynespora cassiicola* (GenBank KU605248.1; Identities = 360/404 (89 %), 6 gaps (1 %)).

Colour illustrations. *Byrsonima* sp. growing in Colombia; symptomatic leaf, conidiogenous cells and conidia. Scale bars = 10 µm.

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Helminthosporium livistonae

Fungal Planet 758 – 13 July 2018

Helminthosporium livistonae Crous, *sp. nov.*

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

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

Mycelium consisting of hyaline, septate, branched, 2.5–3 µm diam hyphae. *Conidiophores* arising from superficial mycelium, erect, flexuous, medium brown, cylindrical, smooth to rough-walled, multiseptate, up to 500 µm tall, with obtuse apex, 4–6 µm diam. *Conidiogenous cells* integrated along length of conidiophore, terminal and intercalary, pores inconspicuous. *Conidia* subcylindrical, straight, medium brown, smooth, apex obtuse, base somewhat obconic, hilum thickened and darkened, 2–3 µm diam, (3–)4–6(–7)-distoseptate, (25–)40–55(–65) × (7–)8–9 µm; conidia solitary, terminal and lateral, or in short unbranched chains of up to three.

Culture characteristics — Colonies flat, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 65 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse sienna. On PDA surface saffron, reverse peach. On OA surface ochreous to salmon with diffuse salmon pigment.

Typus. Australia, New South Wales, Murramarang National Park, on leaves of *Livistona australis* (*Arecaceae*), 27 Nov. 2016, *P.W. Crous* (holotype CBS H-23589, culture ex-type CPC 32158 = CBS 144413, ITS and LSU sequences GenBank MH327795.1 and MH327831.1, MycoBank MB825400).

Notes — The *Helminthosporium* complex was recently treated by Voglmayr & Jaklitsch (2017). *Helminthosporium livistonae* must to be compared to *Exosporium livistonicola*, which is distinct in having inconspicuous conidiogenous loci, and conidia that are solitary, obclavate, 20–85 × 4–7 µm, 2–5-distoseptate (Braun et al. 2014, Videira et al. 2017). *Exosporium livistonae* is distinct in having obclavate conidia that are solitary, 5-distoseptate, (45–)60–70(–80) × (7–)8(–10) µm, with distinct scars on the conidiophores (Crous et al. 2011b); in addition, its LSU sequence (GenBank JQ044446.1) is only 85 % identical to that of *Helminthosporium livistonae* (760/891, 29 gaps).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Helminthosporium juglandinum* (GenBank NR_155197.1; Identities = 485/542 (89 %), 20 gaps (3 %)), *Helminthosporium quercinum* (GenBank NR_155198.1; Identities = 483/543 (89 %), 22 gaps (4 %)) and *Corynespora proliferata* (GenBank FJ852596.1; Identities = 482/543 (89 %), 23 gaps (4 %)). Closest hits using the LSU sequence are *Helminthosporium genistae* (GenBank KY984312.1; Identities = 855/885 (97 %), 2 gaps (0 %)), *Helminthosporium microsorum* (GenBank KY984329.1; Identities = 853/884 (96 %), no gaps) and *Helminthosporium quercinum* (GenBank KY984338.1; Identities = 852/884 (96 %), no gaps).

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

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Pseudoarthrographis phlogis

Fungal Planet 759 – 13 July 2018

Pseudoarthrographis Crous & Thangavel, *gen. nov.*

Etymology. Name reflects a similarity to the genus *Arthrographis*.

Classification — *Incertae sedis*, *Dothideomycetes.*

Mycelium consisting of smooth, pale brown, septate, branched, hyphae. *Conidiophores* solitary, arising directly from superficial hyphae, subcylindrical, pale brown, smooth, erect, 0–1-septate, or reduced to conidiogenous loci directly on hyphae. *Conidiogenous cells* solitary, loci on hyphae or terminal on conidiophores, integrated. *Arthroconidia* occurring in chains, cylindrical with truncate ends, smooth, pale olivaceous in mass, 0–1-septate, in branched or unbranched chains, hila inconspicuous, truncate. *Chlamydospores* developing in culture, occurring in chains, globose, medium brown, smooth.

Type species. *Pseudoarthrographis phlogis* Crous & Thangavel. MycoBank MB825401.

Pseudoarthrographis phlogis Crous & Thangavel, *sp. nov.*

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

Mycelium consisting of smooth, pale brown, septate, branched, 2–2.5 µm diam hyphae. *Conidiophores* solitary, arising directly from superficial hyphae, subcylindrical, pale brown, smooth, erect, 0–1-septate, or reduced to conidiogenous loci directly on hyphae, 10–25 × 2.5 µm. *Conidiogenous cells* solitary, loci on hyphae or terminal on conidiophores, integrated, 1–10 × 2.5 µm. *Arthroconidia* occurring in chains, cylindrical with truncate ends, smooth, pale olivaceous in mass, (3–)8–12(–15) × 2.5 µm, 0–1-septate, in branched or unbranched chains, hila inconspicuous, truncate, 2–2.5 µm diam. *Chlamydospores* developing in culture, occurring in chains, globose, medium brown, smooth, 5–7 µm diam.

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

Typus. New Zealand, Prebbleton, Trents Rd., RD6, on *Phlox subulata* (*Polemoniaceae*), 10 June 2016, *R. Thangavel,* T16_02340G (holotype CBS H-23588, culture ex-type CPC 32759 = CBS 144414, ITS and LSU sequences GenBank MH327796.1 and MH327832.1, MycoBank MB825402).

Notes — *Pseudoarthrographis* is morphologically similar to the genus *Arthrographis*, which also resides in the *Dothideomycetes* (*Eremomycetaceae*). Species of *Arthrographis* have been isolated from the air, compost, marine sediments, soil, wood and also from opportunistic human infections (Giraldo et al. 2014). Another genus to consider in this description is *Arthropsis*, which accommodates species with dark arthroconidia, joined by adjacent connectives and developing from undifferentiated conidiogenous hyphae (Sigler et al. 1982).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Neodactylaria obpyriformis* (GenBank NR_154267.1; Identities = 476/571 (83 %), 29 gaps (5 %)), *Hormococcus conorum* (GenBank KF993412.1; Identities = 477/577 (83 %), 33 gaps (5 %)) and *Oncopodiella trigonella* (GenBank KY853455.1; Identities = 348/397 (88 %), 6 gaps (1 %)). Closest hits using the LSU sequence are *Spissiomyces ramosus* (GenBank KF680785.1; Identities = 830/877 (95 %), 5 gaps (0 %)), *Hysteropatella clavispora* (GenBank AY541493.1; Identities = 831/880 (94 %), 7 gaps (0 %)) and *Coniosporium apollinis* (GenBank GU250896.1; Identities = 818/867 (94 %), 2 gaps (0 %)).

Colour illustrations. *Phlox subulata* in New Zealand; hyphae forming chains of disarticulating conidia, chlamydospore-like structures and conidia. Scale bars = 10 µm.

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Polynema podocarpi

Fungal Planet 760 – 13 July 2018

Polynema podocarpi Crous & Thangavel, *sp. nov.*

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

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

Conidiomata stromatic, acervuloid, separate, superficial on agar, globose in outline, 200–350 µm diam, brown with creamy conidial mass in centre, surrounded by setae. *Setae* arising from basal stroma, straight to slightly curved, with basal septum, medium brown, smooth, thick-walled, unbranched, 90–200 µm long, apex acute, 3–4 µm diam at the base. *Conidiophores* lining the basal stroma, cylindrical, hyaline, smooth, branched, 1–3-septate, 20–65 × 2–2.5 µm. *Conidiogenous cells* phialidic, cylindrical, hyaline, smooth, 12–20 × 2–2.5 µm. *Conidia* fusoid to subcylindrical, subobtuse at apex, with single central appendage, truncate at base, (1–)3-septate, not constricted at septa, hyaline, smooth, (12–)14–15(–16) × 2.5(–3) µm, bearing appendages at each end; three basal appendages (10–)15–16 µm long, apical appendage central, 6–8 µm long.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and folded surface with smooth, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse sienna. On PDA surface pale luteous to dirty white, reverse umber in centre, luteous in outer region. On OA surface pale luteous with diffuse luteous pigment in agar.

Typus. New Zealand, Auckland, Princes Street, on *Podocarpus totara* (*Podocarpaceae*), 7 July 2016, *R. Thangavel,* T16_02618G (holotype CBS H-23587, culture ex-type CPC 32761 = CBS 144415 = ICMP 22363, ITS and LSU sequences GenBank MH327797.1 and MH327833.1, MycoBank MB825403).

Colour illustrations. *Podocarpus totara* tree in New Zealand; conidioma sporulating on SNA (scale bar = 300 µm), setae, conidiophores, conidiogenous cells and conidia (scale bars = 10 µm).

Notes — Based on morphology this fungus is best accommodated in the genus *Polynema* as defined by Nag Raj (1993), being allied to *Pseudolachnea*, and clustering in *Chaetosphaeriaceae* (Crous et al. 2012). Morphologically, *Polynema podocarpi* is quite distinct from the presently known species, having 3-septate conidia (Nag Raj 1993). *Polynema podocarpi* is the first species of the genus that has been subjected to DNA sequencing, and thus adds a new lineage to the *Chaetosphaeriaceae.*

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Pseudolachnea fraxini* (GenBank NR_155628.1; Identities = 484/536 (90 %), 29 gaps (5 %)), *Pseudolachnea hispidula* (GenBank AB934071.1; Identities = 477/528 (90 %), 28 gaps (5 %)) and *Pseudolachnella longiciliata* (GenBank AB934081.1; Identities = 469/528 (89 %), 29 gaps (5 %)). Closest hits using the LSU sequence are *Pseudolachnella fusiformis* (GenBank AB934056.1; Identities = 817/835 (98 %), no gaps), *Pseudolachnella botulispora* (GenBank AB934050.1; Identities = 811/830 (98 %), no gaps) and *Pseudolachnea hispidula* (GenBank AB934048.1; Identities = 811/830 (98 %), no gaps).

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Acrodontium metrosideri

Fungal Planet 761 – 13 July 2018

Acrodontium metrosideri Crous & Thangavel, *sp. nov.*

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

Classification — *Teratosphaeriacea*e, *Capnodiales*, *Dothideomycetes*.

Mycelium consisting of hyaline, smooth, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* arising from superficial hyphae, medium brown, smooth, the lower third being cylindrical, and the upper section tapering prominently to a subacute apex; upper half consisting of a rachis with tightly aggregated loci, visible as small pimple-like scars, 0.5 µm diam, slightly darkened and refractive, 25–35 × 2.5–3 µm. *Conidia* solitary, aseptate, hyaline, smooth, ellipsoid to clavate, apex obtuse, tapering in lower third to truncate base, 0.5–1 µm diam, (3–)4(–5) × 1.5(–2) µm.

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

Typus. New Zealand, Auckland, Bucklands Beach, 22 Wells Rd, on *Metrosideros excelsa* (*Myrtaceae*), 8 Dec. 2016, *R. Thangavel,* T16_03926D (holotype CBS H-23586, culture ex-type CPC 32783 = CBS 144416, ITS and LSU sequences GenBank MH327798.1 and MH327834.1, MycoBank MB825404).

Notes — Videira et al. (2016) showed that *Acrodontium* resides in the *Teratosphaeriaceae*. Furthermore, her data also showed several other species reside in different orders, and are not congeneric with the type, *A. crateriforme*. The present collection, however, clusters within *Acrodontium* s.str. where it represents a distinct lineage, known from *Metrosideros excelsa* in New Zealand, clustering with another strain from New Zealand (PDD 105475) originally identified as *Septoria alpicola*, occurring on *Fuchsia excorticata* (conidia 60 × 2 µm, 1–7 septate on the specimen). It is apparent that the culture PDD 105475 became contaminated with the fungus described here as *Acrodontium podocarpi*, which due to its sticky, minute conidia, tends to be a common contaminant in culture collections.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to '*Septoria* cf. *alpicola*' (GenBank KM975402.1; Identities = 528/532 (99 %), no gaps), *Acrodontium crateriforme* (GenBank GU214682.1; Identities = 507/538 (94 %), 13 gaps (2 %)) and *Acrodontium crateriforme* (GenBank KX287268.1; Identities = 507/538 (94 %), 13 gaps (2 %)). Closest hits using the LSU sequence are '*Septoria* cf. *alpicola*' (GenBank KM975377.1; Identities = 862/864 (99 %), no gaps), *Acrodontium crateriforme* (GenBank KX286957.1; Identities = 842/870 (97 %), 1 gap (0 %)) and *Acrodontium neolitseae* (GenBank KJ869184.1; Identities = 816/844 (97 %), 1 gap (0 %)).

Colour illustrations. Bucklands Beach, New Zealand; conidiophores sporulating on SNA, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Chaetopsina eucalypti

Fungal Planet 762 – 13 July 2018

Chaetopsina eucalypti Crous, *sp. nov.*

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

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

Conidiomata sporodochial, hyaline, globose, 100–300 µm diam, with crystalline to creamy mucoid conidial mass. *Setae* dispersed throughout sporodochia, at times developing from a brown basal stroma of *textura angularis*, erect, flexuous, unbranched, brown, smooth, thick-walled, tapering to acute apex, multi-septate, 150–300 × 6–7 µm. *Conidiophores* densely aggregated, arising from a central stroma, hyaline, smooth, subcylindrical, 3–6-septate, 20–40 × 2.5–3 µm. *Conidiogenous cells* terminal and intercalary, subcylindrical to fusoid-ellipsoid, hyaline, smooth, phialidic, 7–12 × 2.5–3 µm. *Conidia* aseptate, hyaline, smooth, guttulate, cylindrical, straight, apex obtuse, base truncate, 1 µm diam, (13–)14–15(–18) × (1.5–)2 µm.

Culture characteristics — Colonies flat, spreading, with folded surface and sparse aerial mycelium and even, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA surface saffron, reverse luteous. On PDA surface ochreous, reverse sienna. On OA surface pale luteous.

Typus. Australia, New South Wales, Nullica State Forest, on *Eucalyptus* leaf litter (*Myrtaceae*), 29 Nov. 2016, *P.W. Crous* (holotype CBS H-23585, culture ex-type CPC 32857 = CBS 144417, ITS and LSU sequences GenBank MH327799.1 and MH327835.1, MycoBank MB825405).

Notes — *Chaetopsina eucalypti* is phylogenetically related to *C. pini*, known from needle litter of *Pinus caribaea* collected in Thailand (Crous et al. 2013). The genus *Chaetopsina* has nectria-like sexual morphs, and although the culture examined in this study formed ascomatal initials, these did not become fertile. Some species of *Chaetopsina* have been reported from *Eucalyptus*, namely *C. fulva* (Hawaii; conidia 7–11 × 1 µm) and *C. splendida* (Australia and Brazil; conidia 9.5–12 × 1.5 µm) (Sutton & Hodges 1976, Crous et al. 1989). *Chaetopsina eucalypti* is easily distinguished from these species based on its larger conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Chaetopsina pini* (GenBank NR_137822.1; Identities = 528/588 (90 %), 24 gaps (4 %)) and *Chaetopsina pinicola* (GenBank NR_137823.1; Identities = 524/595 (88 %), 36 gaps (6 %)). Closest hits using the LSU sequence are *Chaetopsina pini* (GenBank KF777200.1; Identities = 872/881 (99 %), no gaps), *Chaetopsinectria chaetopsinae* (GenBank DQ119553.2; Identities = 877/889 (99 %), no gaps) and *Chaetopsina pinicola* (GenBank KF777201.1; Identities = 875/891 (98 %), no gaps).

Colour illustrations. *Eucalyptus* leaf litter next to a dead *Xanthorrhoea* at collection site; conidiomata sporulating on OA (scale bar = 300 µm), setae, conidiogenous cells and conidia (scale bars = 10 µm).

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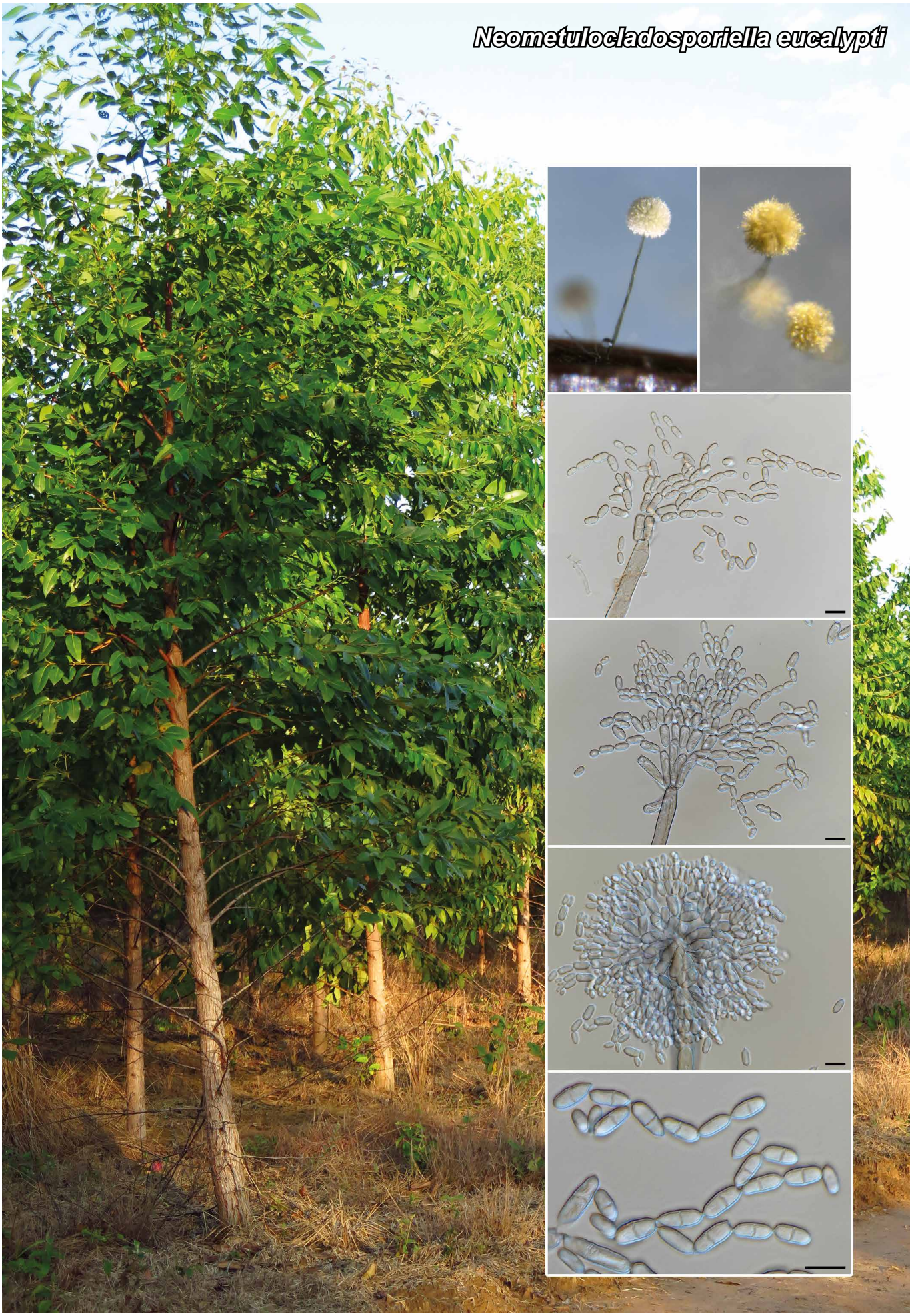
Neometuloclados poriella eucalypti

Fungal Planet 763 – 13 July 2018

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

Etymology. Name refers to the fact that it is similar to *Metulocladosporiella*.

Classification — *Rutstroemiaceae*, *Helotiales*, *Leotiomycetes*.

Conidiophores dimorphic. *Microconidiophores* erect, pale brown, smooth, solitary, subcylindrical, straight to flexuous, septate, giving rise to a single, terminal conidiogenous cell. *Conidiogenous cells* pale brown, smooth, clavate, with 1–3 flat-tipped apical loci, unthickened, not darkened, giving rise to ramoconidia. *Macroconidiophores* solitary, erect, straight to flexuous, unbranched, subcylindrical, medium brown, smooth, arising from superficial mycelium, base narrow but becoming significantly wider and darkened brown in second cell from the base, septate, medium brown, smooth, clavate, giving rise to a series of metulae or branches, which are medium brown, smooth, subcylindrical to clavate, aseptate, base abruptly tapered to flat-tipped locus, apex with 2–4 denticles, unthickened, not darkened, giving rise to secondary ramoconidia. *Primary ramoconidia* fusoid-ellipsoid to subcylindrical, medium brown, smooth, septate, with 1–3 apical flat-tipped loci, unthickened, not darkened. *Secondary ramoconidia* straight, pale brown, smooth, septate, subcylindrical with obtuse ends, base with abrupt taper to truncate hilum, apex with 1–3 denticles, not thickened nor darkened, giving rise to branched, dry chains of acropetal conidia, pale brown, smooth to finely verruculose, subcylindrical with obtuse ends, septate, with a flat-tipped basal hilum and 1–3 apical denticles, not thickened nor darkened.

Type species. *Neometulocladosporiella eucalypti* Crous & M.J. Wingf. MycoBank MB825406.

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

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

Conidiophores dimorphic. *Microconidiophores* erect, pale brown, smooth, solitary, subcylindrical, straight to flexuous, 1–3-septate, 30–70 × 3–4 µm, giving rise to a single, terminal conidiogenous cell. *Conidiogenous cells* 10–50 × 3–4 µm, pale brown, smooth, clavate, with 1–3 flat-tipped apical loci, 2 µm diam, unthickened, not darkened, giving rise to ramoconidia. *Macroconidiophores* solitary, erect, straight to flexuous, unbranched, subcylindrical, medium brown, smooth, arising from superficial mycelium, base narrow but becoming significantly wider and darkened brown in second cell from the base, 200–600 × 10–16 µm, 5–10-septate, medium brown, smooth, clavate, giving rise to a series of up to 20 metulae or branches, 15–25 × 5–9 µm, which are medium brown, smooth, subcylindrical to clavate, aseptate, base abruptly tapered to flat-tipped locus, 2 µm diam, apex with 2–4 denticles, 1 × 1 µm, unthickened, not darkened, giving rise to secondary ramoconidia. *Primary ramoconidia* fusoid-ellipsoid to subcylindrical, medium brown, smooth, 0–1-septate, 12–22 × 4–5 µm, with 1–3 apical flat-tipped loci, 1 µm diam, unthickened, not darkened. *Secondary ramoconidia* straight, pale brown, smooth, 0–1-septate, subcylindrical with obtuse ends, 13–15 × 5–7 µm, base with abrupt taper to truncate hilum, 1–1.5 µm diam, apex with 1–3 denticles, 1 µm diam, not thickened nor darkened, giving rise to branched, dry chains of acropetal conidia, pale brown, smooth to finely verruculose, subcylindrical with obtuse ends, 0–1-septate, (9–)10–11(–12) × (4–)5(–6) µm, with a flat-tipped basal hilum and 1–3 apical denticles, 0.5–1 µm diam, not thickened nor darkened.

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

Typus. Colombia, Cali, on leaves of *Eucalyptus grandis* × *urophylla* (*Myrtaceae*), 26 June 2010, *M.J. Wingfield* (holotype CBS H-23584, culture ex-type CPC 31787 = CBS 144419, ITS and LSU sequences GenBank MH327800.1 and MH327836.1, MycoBank MB825407).

Notes — *Neometulocladosporiella* resembles *Metulocladosporiella* (*Herpotrichiellaceae*), a genus associated with speckle disease on banana leaves (Crous et al. 2006, 2014, Marin-Felix et al. 2019). The fungus from *Eucalyptus* leaves is, however, phylogenetically distinct, being allied to *Helotiales* and clustering with genera such as *Ciboria* and *Lanzia*. A new genus, *Neometulocladosporiella,* is therefore introduced to accommodate the fungus occurring on *Eucalyptus*, and to distinguish it from *Metulocladosporiella*, which occurs on *Musa* spp. (Bensch et al. 2012, Marin-Felix et al. 2019).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Lanzia allantospora* (GenBank AB926099.1; Identities = 526/557 (94 %), 8 gaps (1 %)), *Roseodiscus sinicus* (GenBank NR_154394.1; Identities = 494/529 (93 %), 6 gaps (1 %)) and *Ciboria americana* (GenBank JN033399.1; Identities = 515/552 (93 %), 13 gaps (2 %)). Closest hits using the LSU sequence are *Lanzia allantospora* (GenBank AB926154.1; Identities = 855/859 (99 %), no gaps), *Ciboria americana* (GenBank JN086702.1; Identities = 792/803 (99 %), no gaps) and *Lambertella subrenispora* (GenBank AB926152.1; Identities = 831/851 (98 %), no gaps).

Colour illustrations. *Eucalyptus* trees in Colombia; conidiophores sporulating on pine needle agar, conidiogenous apparatus, conidiogenous cells and conidia. Scale bars = 10 µm.

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Myrotheciomyces corymbiae

Fungal Planet 764 – 13 July 2018

Myrotheciomycetaceae Crous, *fam. nov.*

Classification — *Myrotheciomycetaceae*, *Hypocreales*, *Sordariomycetes.*

Conidiomata superficial on media, solitary conidiophores to sporodochia, with crystalline to white or orange conidial mass; with or without basal stroma. Conidiophores, hyaline, smooth to warty, unbranched to branched, subcylindrical, with terminal and lateral conidiogenous cells. *Conidiogenous cells* hyaline, smooth, phialidic, or with retrogressive conidiogenesis. *Conidia* aggregated in slimy mass, 0–1-septate, hyaline, smooth, fusoid-ellipsoid, apex subobtuse, base truncate, unthickened.

Type genus. *Myrotheciomyces* Crous.
MycoBank MB825408.

Notes — The family *Myrotheciomycetaceae* presently includes *Emericellopsis, Leucosphaerina, Myrotheciomyces* and *Trichothecium*.

Myrotheciomyces Crous, *gen. nov.*

Etymology. Name reflects a similarity to the genus *Myrothecium*.

Conidiomata superficial on media, sporodochial, round to irregular, white with slimy orange conidial mass, surrounded by a loose hyphal network; basal stroma giving rise to densely aggregated conidiophores, hyaline, smooth to warty, excessively branched, subcylindrical, with terminal and lateral conidiogenous cells. *Conidiogenous cells* hyaline, smooth, fusoid-ellipsoid, curved with prominent taper in upper third to a phialidic apex, with minute collarette. *Conidia* solitary, aggregated in slimy mass, hyaline, smooth, thick-walled, granular, aseptate, fusoid-ellipsoid, apex subobtuse, base truncate, unthickened.

Type species. *Myrotheciomyces corymbiae* Crous.
MycoBank MB825409.

Myrotheciomyces corymbiae Crous, *sp. nov.*

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

Conidiomata superficial on media, sporodochial, round to irregular, 200–400 µm diam, white with slimy orange conidial mass, surrounded by a loose hyphal network; basal stroma giving rise to densely aggregated conidiophores, hyaline, smooth to warty, excessively branched, subcylindrical, up to 150 µm long, 3–5 µm diam, with terminal and lateral conidiogenous cells. *Conidiogenous cells* hyaline, smooth, fusoid-ellipsoid, curved with prominent taper in upper third to a phialidic apex, 2 µm diam, with minute collarette, 20–27 × 4–5 µm. *Conidia* solitary, aggregated in slimy mass, hyaline, smooth, thick-walled, granular, aseptate, fusoid-ellipsoid, apex subobtuse, base truncate, 2 µm diam, unthickened, (13–)16–18(–20) × (5–)6 µm.

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

Typus. Australia, New South Wales, Dyraaba, Dyraaba plantation, S28°47'20.5" E152°49'03", on leaves of *Corymbia variegata* (*Myrtaceae*), 14 Mar. 2015, *A.J. Carnegie* (holotype CBS H-23583, culture ex-type CPC 33206 = CBS 144420, ITS and LSU sequences GenBank MH327801.1 and MH327837.1, MycoBank MB825410).

Notes — Morphologically, the present collection resembles species accommodated in the *Myrothecium* complex. The *Myrothecium* generic complex was recently treated by Lombard et al. (2016), none of which cluster with the fungus from *Corymbia*, which is allied to hypocrealean isolates identified as *Trichothecium*, *Niesslia* and *Leucosphaerina*. The new genus, *Myrotheciomyces*, is therefore introduced to accommodate the fungus occurring on *Corymbia*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Niesslia exilis* (GenBank MG826991.1; Identities = 552/636 (87 %), 56 gaps (8 %)), *Trichothecium ovalisporum* (GenBank NR_111321.1; Identities = 539/623 (87 %), 52 gaps (8 %)) and *Trichothecium roseum* (GenBank EU552162.1; Identities = 546/638 (86 %), 44 gaps (6 %)). Closest hits using the LSU sequence are *Niesslia exilis* (GenBank MG826794.1; Identities = 854/866 (99 %), 1 gap (0 %)), *Trichothecium roseum* (GenBank JX458860.1; Identities = 773/786 (98 %), no gaps) and *Leucosphaerina indica* (GenBank AF096194.1; Identities = 854/869 (98 %), 2 gaps (0 %)).

Colour illustrations. Eucalyptus trees; conidiomata sporulating on pine needle agar (scale bar = 400 µm), conidiogenous cells and conidia (scale bars = 10 µm).

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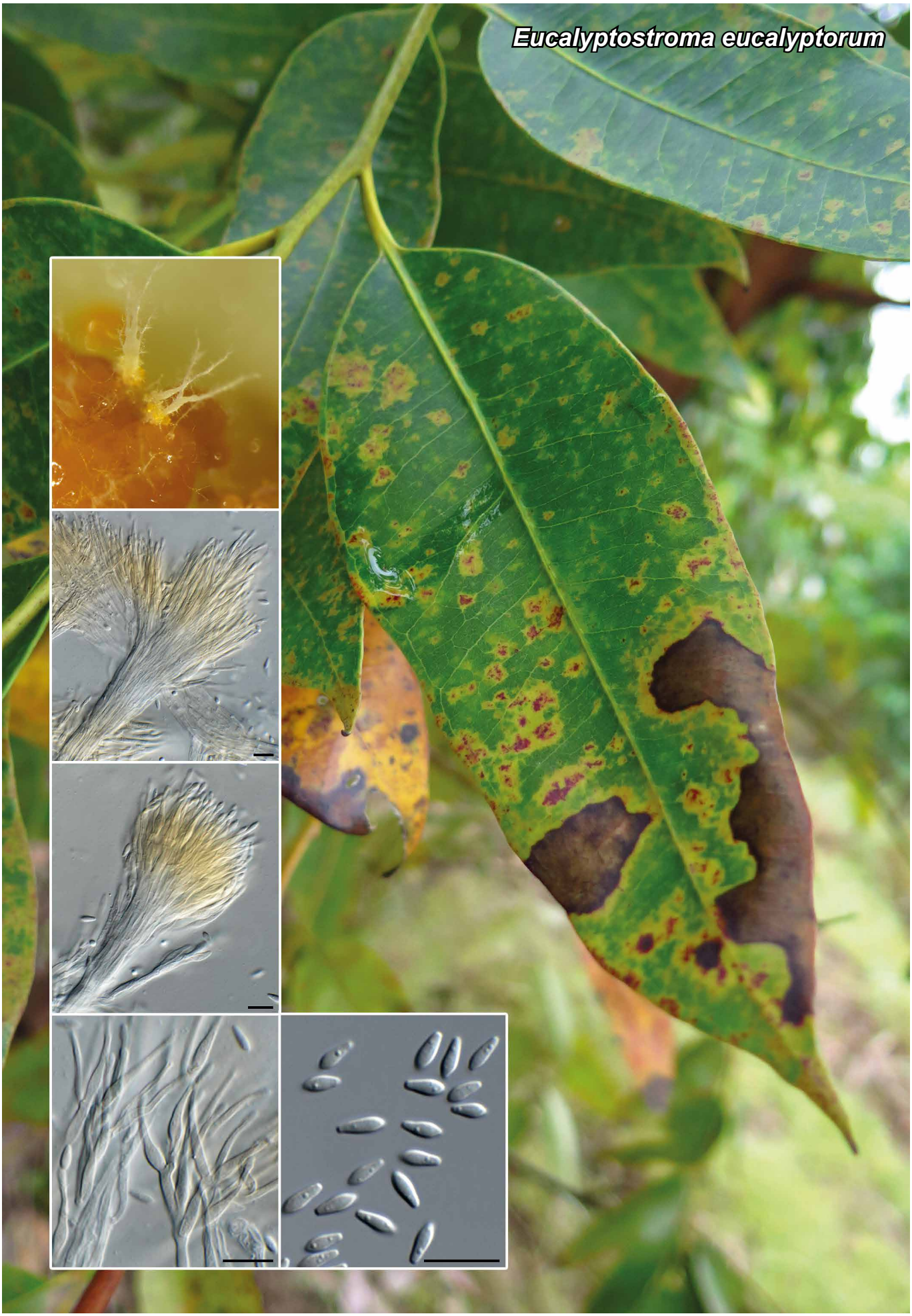
Eucalyptostroma eucalyptorum

Fungal Planet 765 – 13 July 2018

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

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

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

Conidiomata scattered to gregarious, consisting of dense synnemata, 100–300 × 20–70 µm; stem consisting of aggregated conidiophores, hyaline, smooth, 2–3 µm diam, flaring outwards in upper conidiogenous region to form a yellow-orange slimy conidial mass. *Conidiogenous region* consisting of a series of branches (up to 6), giving rise to lateral and terminal conidiogenous cells; branches subcylindrical, aseptate, hyaline, smooth, 9–12 × 2–3 µm. *Conidiogenous cells* elongated ampulliform, pale luteous, smooth, phialidic at apex, 1.5 µm diam, with short collarette, 1–2 µm long, 13–16 × 2–3 µm. *Conidia* solitary, smooth, aseptate, fusoid-ellipsoid in upper third, apex subobtuse, base truncate, 1 µm diam, (4–)5(–6) × (1.5–)2(–2.5) µm.

Culture characteristics — Colonies erumpent, spreading, with sparse to moderate aerial mycelium and smooth, even margin, reaching 12 mm diam after 2 wk at 25 °C. On MEA surface pale luteous, reverse luteous. On PDA surface and reverse umber in centre, pale luteous in outer region. On OA surface luteous in centre, pale luteous in outer region.

Typus. Colombia, Llanos, on leaves of *Eucalyptus pellita* (*Myrtaceae*), July 2010, *M.J. Wingfield* (holotype CBS H-23582, culture ex-type CPC 31800 = CBS 144421, ITS and LSU sequences GenBank MH327802.1 and MH327838.1, MycoBank MB825411).

Notes — The monotypic genus *Eucalyptostroma* was recently introduced for a hyphomycete occurring on *Eucalyptus* leaves in Malaysia (Crous et al. 2016a). *Eucalyptostroma eucalyptorum* which also occurs on *Eucalyptus* leaves, but in Colombia, is distinguished by forming more synnematal conidiomata, and having slightly larger conidia than *E. eucalypti* (3–4.5 × 2 µm). *Eucalyptostroma* is recognized on leaves by forming slimy, yellow-orange conidial massed on either synnemata or sporodochia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Eucalyptostroma eucalypti* (GenBank NR_154027.1; Identities = 517/536 (96 %), 7 gaps (1 %)), *Chaetosphaeria myriocarpa* (GenBank JF340253.1; Identities = 403/474 (85 %), 32 gaps (6 %)) and *Codinaea pini* (GenBank NR_137943.1; Identities = 351/401 (88 %), 13 gaps (3 %)). Closest hits using the LSU sequence are *Eucalyptostroma eucalypti* (GenBank KY173500.1; Identities = 806/818 (99 %), 3 gaps (0 %)), *Paliphora intermedia* (GenBank EF204500.1; Identities = 790/827 (96 %), 1 gap (0 %)) and *Chaetosphaeria curvispora* (GenBank GU180636.1; Identities = 796/838 (95 %), no gaps).

Colour illustrations. Symptomatic *Eucalyptus* leaves; agar colony with sporulation, synnemata, conidiogenous cells and conidia. Scale bars = 10 µm.

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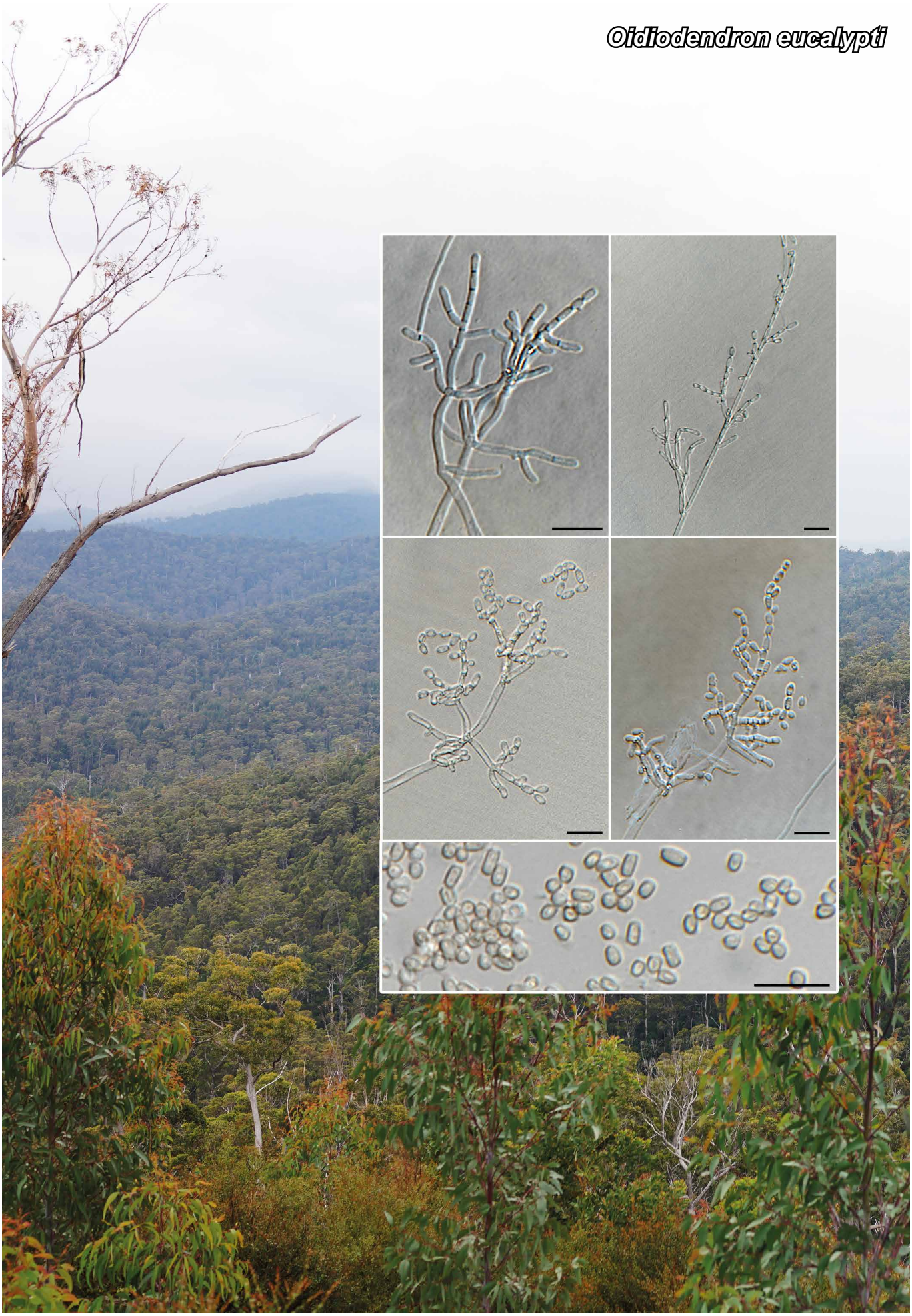
Oidiodendron eucalypti

Fungal Planet 766 – 13 July 2018

Oidiodendron eucalypti Crous, *sp. nov.*

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

Classification — *Myxotrichaceae*, *Onygenales, Eurotiomycetes.*

Conidiophores solitary, erect, flexuous, unbranched, with dry conidial masses, 80–160 × 2–2.5 µm, 4–6-septate. *Fertile hyphae* developing in upper third of conidiophore, 2–2.5 µm diam, dichotomously branched, fragmenting to form long chains of up to 10 conidia in a dry conidiogenous head. *Conidia* thin-walled, subhyaline, subglobose to cylindrical, (2–)3–4(–5) × (1.5–)2 µm, with asperulate perispore.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and even lobate margin, reaching 7 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface smoke-grey, reverse umber with diffuse umber pigment.

Typus. Australia, New South Wales, Gnupa State Forest, on leaves of *Eucalyptus maidenii* (*Myrtaceae*), 29 Nov. 2016, *P.W. Crous* (holotype CBS H-23579, culture ex-type CPC 32659 = CBS 144423, ITS and LSU sequences GenBank MH327803.1 and MH327839.1, MycoBank MB825412).

Notes — The genus *Oidiodendron*, which commonly occurs in soil and on plant litter, was treated by Rice & Currah (2005), who provided keys to 23 species. Phylogenetically, *O. eucalypti* is related to *O. truncatum*, from which it can be distinguished based on its conidia. *Conidia* of *O. truncatum* are dark at maturity, barrel-shaped, truncate with distinct apical scars and reticulate ornamentation, (2–)3.5(–5) × (1–)2.5(–3.5) µm (Rice & Currah 2005).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Oidiodendron tenuissimum* (GenBank AF307773.1; Identities = 489/503 (97 %), 3 gaps (0 %)), *Oidiodendron griseum* (GenBank AF062797.1; Identities = 495/510 (97 %), 1 gap (0 %)) and *Oidiodendron fuscum* (GenBank NR_111035.1; Identities = 495/510 (97 %), 3 gaps (0 %)). Closest hits using the LSU sequence are *Oidiodendron truncatum* (GenBank KF835845.1; Identities = 860/877 (98 %), 1 gap (0 %)), *Myxotrichum deflexum* (GenBank AY541491.1; Identities = 857/885 (97 %), no gaps) and *Eremascus fertilis* (GenBank HQ540515.1; Identities = 807/838 (96 %), 2 gaps (0 %)).

Colour illustrations. Eucalyptus trees in Gnupa State Forest; conidiophores, conidiogenous cells with conidial chains, and conidia. Scale bars = 10 µm.

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Lareunionomyces eucalypti

Fungal Planet 767 – 13 July 2018

Lareunionomyces eucalypti Crous, *sp. nov.*

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

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

Conidiophores solitary, erect, dark brown, finely roughened towards basal region, thick-walled, straight to slightly flexuous, unbranched, subcylindrical, arising from superficial hyphae, base lacking rhizoids, 60–160 × 5–6 µm, 2–7-septate. *Conidiogenous region* consisting of a penicillate series of branches. Primary branches brown, smooth, aseptate, subcylindrical to clavate, 6–15 × 4–5 µm. Secondary and tertiary branches pale brown, subcylindrical, smooth, 6–8 × 2–3 µm, giving rise to 1–4 conidiogenous cells. *Conidiogenous cells* subcylindrical, pale brown, smooth, 7–20 × 2–3 µm; apex proliferating inconspicuously percurrently, collarettes if present cylindrical, inconspicuous. *Conidia* aggregating in mucoid mass, hyaline, smooth, cylindrical, apex obtuse, base truncate, (3.5–)5–6(–7) × 2(–2.5) µm.

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

Typus. Australia, Victoria, Drummer Forest, on leaves of *Eucalyptus* sp. (*Myrtaceae*), 30 Nov. 2016, *P.W. Crous* (holotype CBS H-23578, culture ex-type CPC 32621 = CBS 144424, ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MH327804.1, MH327840.1, MH327867.1, MH327878.1 and MH327889.1, MycoBank MB825413).

Notes — The monotypic genus *Lareunionomyces* was established for a genus of hyphomycetes occurring on leaves of *Syzygium jambos* in La Réunion (Crous et al. 2016b). *Lareunionomyces eucalypti* is allied to *L. syzygii*, but distinct from it in that the latter species has shorter conidiophores, 50–100 × 5–8 µm, up to 8 series of branches in the conidiogenous head, and smaller conidia, (3.5–)4(–5) × (1.5–)2 µm (Crous et al. 2016b). For details on *Neolauriomycetaceae* see *Neolauriomyces eucalypti* in Fungal Planet 768.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Lareunionomyces syzygii* (GenBank NR_145315.1; Identities = 529/542 (98 %), 2 gaps (0 %)), *Neofabraea inaequalis* (GenBank NR_155470.1; Identities = 498/545 (91 %), 14 gaps (2 %)) and *Phlyctema vagabunda* (GenBank KT923789.1; Identities = 497/546 (91 %), 17 gaps (3 %)). Closest hits using the LSU sequence are *Lareunionomyces syzygii* (GenBank KX228338.1; Identities = 861/875 (98 %), no gaps), *Exochalara longissima* (GenBank HQ609476.1; Identities = 856/875 (98 %), no gaps) and *Davidhawksworthia ilicicola* (GenBank KU728555.1; Identities = 847/884 (96 %), 10 gaps (1 %)). Closest hits using the *rpb2* sequence had highest similarity to *Trichoderma* cf. *stilbohypoxyli* (GenBank EU241502.1; Identities = 214/265 (81 %), 4 gaps (1 %)), *Trichoderma hispanicum* (GenBank JN715600.1; Identities = 212/265 (80 %), 4 gaps (1 %)) and *Trichoderma paraviridescens* (GenBank KT343762.1; Identities = 213/267 (80 %), 4 gaps (1 %)). Closest hits using the *tef1* sequence had highest similarity to *Acephala applanata* (GenBank DQ274571.1; Identities = 217/251 (86 %), 9 gaps (3 %)), *Ulocladium alternariae* (GenBank AY375370.1; Identities = 219/255 (86 %), 8 gaps (3 %)) and *Cadophora viticola* (GenBank HQ661081.1; Identities = 206/236 (87 %), 7 gaps (2 %)). Closest hits using the *tub2* sequence had highest similarity to *Amorphotheca resinae* (GenBank XM_024862766.1; Identities = 679/776 (88 %), 2 gaps (0 %)), *Hymenoscyphus subsymmetricus* (GenBank KJ472286.1; Identities = 651/743 (88 %), 4 gaps (0 %)) and *Hymenoscyphus subpallescens* (GenBank KJ472284.1; Identities = 638/733 (87 %), 2 gaps (0 %)).

Colour illustrations. Eucalyptus trees at Drummer Forest; conidiophores sporulating on SNA, showing conidiogenous cells and conidia. Scale bars = 10 µm.

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Neolauriomyces eucalypti

Fungal Planet 768 – 13 July 2018

Neolauriomycetaceae Crous, *fam. nov.*

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

Conidiophores solitary, erect, subcylindrical, straight, slightly flexuous, unbranched, medium brown, smooth, septate, terminating in a phialide, or in a penicillate head: primary branches subcylindrical to doliiform, medium brown, smooth. Secondary branches doliiform to subcylindrical, medium brown, smooth, giving rise to phialides. *Conidiogenous cells* phialidic, ampulliform, medium brown, smooth, including the apical collarette, cylindrical, medium brown. *Conidia* occurring in chains, unbranched, hyaline, smooth-walled, cylindrical, aseptate, ends truncate.

Type genus. *Neolauriomyces* Crous.
MycoBank MB825414.

Notes — The family *Neolauriomycetaceae* presently contains three genera, namely *Exochalara, Lareunionomyces* and *Neolauriomyces*.

Neolauriomyces Crous, *gen. nov.*

Etymology. Named reflects a similarity to the genus *Lauriomyces*.

Conidiophores solitary, erect, subcylindrical, straight, slightly flexuous, unbranched, medium brown, smooth, septate. *Conidiogenous head* penicillate, primary branches subcylindrical to doliiform, medium brown, smooth. Secondary branches doliiform to subcylindrical, medium brown, smooth, giving rise to 1–2 phialides. *Conidiogenous cells* phialidic, ampulliform, medium brown, smooth, including the apical collarette, cylindrical, medium brown. *Conidia* occurring in long dry chains, unbranched, hyaline, smooth-walled, cylindrical, aseptate, ends truncate.

Type species. *Neolauriomyces eucalypti* Crous.
MycoBank MB825415.

Neolauriomyces eucalypti Crous, *sp. nov.*

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

Conidiophores solitary, erect, subcylindrical, straight, slightly flexuous, unbranched, medium brown, smooth, 4–8-septate, 40–120 × 5–6 µm. *Conidiogenous head* penicillate, primary branches subcylindrical to doliiform, medium brown, smooth, 4–6 × 4–5 µm. Secondary branches doliiform to subcylindrical, medium brown, smooth, 3–5 × 4–5 µm, giving rise to 1–2 phialides. *Conidiogenous cells* phialidic, ampulliform, medium brown, smooth, 10–14 × 3–5 µm, including the apical collarette, cylindrical, medium brown, 4–7 × 1.5–2 µm. *Conidia* occurring in long dry chains (20–40), unbranched, hyaline, smooth-walled, cylindrical, aseptate, ends truncate, 4(–5) × 1.5 µm.

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

Typus. Australia, Victoria, Drummer Forest, on leaves of *Eucalyptus* sp. (*Myrtaceae*), 30 Nov. 2016, *P.W. Crous* (holotype CBS H-23577, culture ex-type CPC 32623 = CBS 144425, ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MH327805.1, MH327841.1, MH327868.1, MH327879.1 and MH327890.1, MycoBank MB825416).

Additional material examined. Australia, New South Wales, Nullica State Forest, on *Eucalyptus* leaf litter (*Myrtaceae*), 29 Nov. 2016, *P.W. Crous*, CPC 32613, ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MH327806.1, MH327842.1, MH327869.1, MH327880.1 and MH327891.1.

Colour illustrations. Symptomatic *Eucalyptus* leaves; conidiophores sporulating on SNA, conidiogenous cells and long conidial chains. Scale bars = 10 µm.

Notes — Although *Neolauriomyces* resembles *Lauriomyces* morphologically (Crous et al. 2009), the genus *Neolauriomyces* is phylogenetically related to *Exochalara* and *Lareunionomyces. Exochalara* is quite distinct from *Neolauriomyces* in having solitary conidiophores with percurrent proliferation that terminate in a phialide giving rise to chains of conidia (Gams & Holubová-Jechová 1976). *Neolauriomyces* is also distinct from *Lareunionomyces* because its phialides are widely dispersed (not densely aggregated) and have prominently ampulliform phialides with long collarettes. Based on the *tef1* and *tub2* sequences, the two isolates of *Neolauriomyces eucalypti* considered in this study might actually represent two cryptic species but additional strains are required to resolve this question.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Lareunionomyces syzygii* (GenBank NR_145315.1; Identities = 521/543 (96 %), 7 gaps (1 %)), *Neofabraea inaequalis* (GenBank NR_155470.1; Identities = 496/545 (91 %), 13 gaps (2 %)) and *Pseudofabraea citricarpa* (GenBank NR_154319.1; Identities = 491/539 (91 %), 14 gaps (2 %)). The ITS sequences of CPC 32613 and 32623 are identical (539/539). Closest hits using the LSU sequence are *Exochalara longissima* (GenBank HQ609476.1; Identities = 857/875 (98 %), no gaps), *Lareunionomyces syzygii* (GenBank KX228338.1; Identities = 846/875 (97 %), no gaps) and *Davidhawksworthia ilicicola* (GenBank KU728555.1; Identities = 852/884 (96 %), 10 gaps (1 %)). The LSU sequences of CPC 32613 and 32623 are identical (875/875).

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Nullicamyces eucalypti

Fungal Planet 769 – 13 July 2018

Nullicamyces Crous, *gen. nov.*

Etymology. Name refers to Nullica State Forest, Australia, where this fungus was collected.

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

Mycelium consisting of pale brown, smooth, branched, septate hyphae. *Conidiophores* reduced to conidiogenous cells on hyphae. Pseudocercospora-like morph: *Conidiogenous cells* inconspicuous on hyphae, not thickened nor darkened. *Conidia* solitary, long flexuous, obclavate, apex obtuse, base obconically truncate, multiseptate, pale brown, smooth; frequently giving rise to secondary conidia via microcyclic conidiation. Matsushimaea-like morph: *Conidiogenous cells* reduced to loci on hyphae, inconspicuous. *Conidia* solitary, pale brown, smooth, initial cell ellipsoid, aseptate, forming acropetal chains of conidia that bud irregularly; conidia appearing star-shaped with radiating arms of ellipsoid cells all linked to the basal, initial cell.

Type species. Nullicamyces eucalypti Crous.
MycoBank MB825417.

Nullicamyces eucalypti Crous, *sp. nov.*

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

Mycelium consisting of pale brown, smooth, branched, septate, 2–2.5 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells on hyphae. Pseudocercospora-like morph: *Conidiogenous cells* inconspicuous on hyphae, 2–3 µm diam, not thickened nor darkened. *Conidia* solitary, long flexuous, obclavate, apex obtuse, base obconically truncate, multiseptate, pale brown, smooth, 25–150 × 2–3 µm; frequently giving rise to secondary conidia via microcyclic conidiation. Matsushimaea-like morph: *Conidiogenous cells* reduced to loci on hyphae, inconspicuous, 2–3 µm diam. *Conidia* solitary, pale brown, smooth, initial cell ellipsoid, aseptate, forming acropetal chains of conidia that bud irregularly; conidia appearing star-shaped with radiating arms of ellipsoid cells all linked to the basal, initial cell; cells 5–12 × 2.5–5 µm.

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

Typus. Australia, New South Wales, Nullica State Forest, on *Eucalyptus* leaf litter (*Myrtaceae*), 29 Nov. 2016, *P.W. Crous* (holotype CBS H-23576, culture ex-type CPC 32942 = CBS 144426, ITS and LSU sequences GenBank MH327807.1 and MH327843.1, MycoBank MB825418).

Notes — *Nullicamyces* is a new genus in the *Chaetothyriaceae* that is unique due to the fact that it is dimorphic, forming matsushimaea-like and pseudocercospora-like morphs in culture.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Chaetothyrium brischoficola* (GenBank NR_132849.1; Identities = 432/496 (87 %), 29 gaps (5 %)), *Aphanophora eugeniae* (GenBank NR_132829; Identities = 523/602 (87 %), 36 gaps (5 %)) and *Ceramothyrium ficus* (GenBank NR_154800.1; Identities = 469/543 (86 %), 28 gaps (5 %)). Closest hits using the LSU sequence are *Ceramothyrium podocarpi* (GenBank NG_042751.1; Identities = 785/818 (96 %), 2 gaps (0 %)), *Ceramothyrium carniolicum* (GenBank KC455251.1; Identities = 783/818 (96 %), 1 gap (0 %)) and *Ceramothyrium thailandicum* (GenBank KP324930.1; Identities = 781/818 (95 %), no gaps).

Colour illustrations. *Eucalyptus* trees at Nullica State Forest; dimorphic conidiophores, with matsushimaea-like conidia at the top, and long, slender pseudocercospora-like conidia at the bottom. Scale bars = 10 µm.

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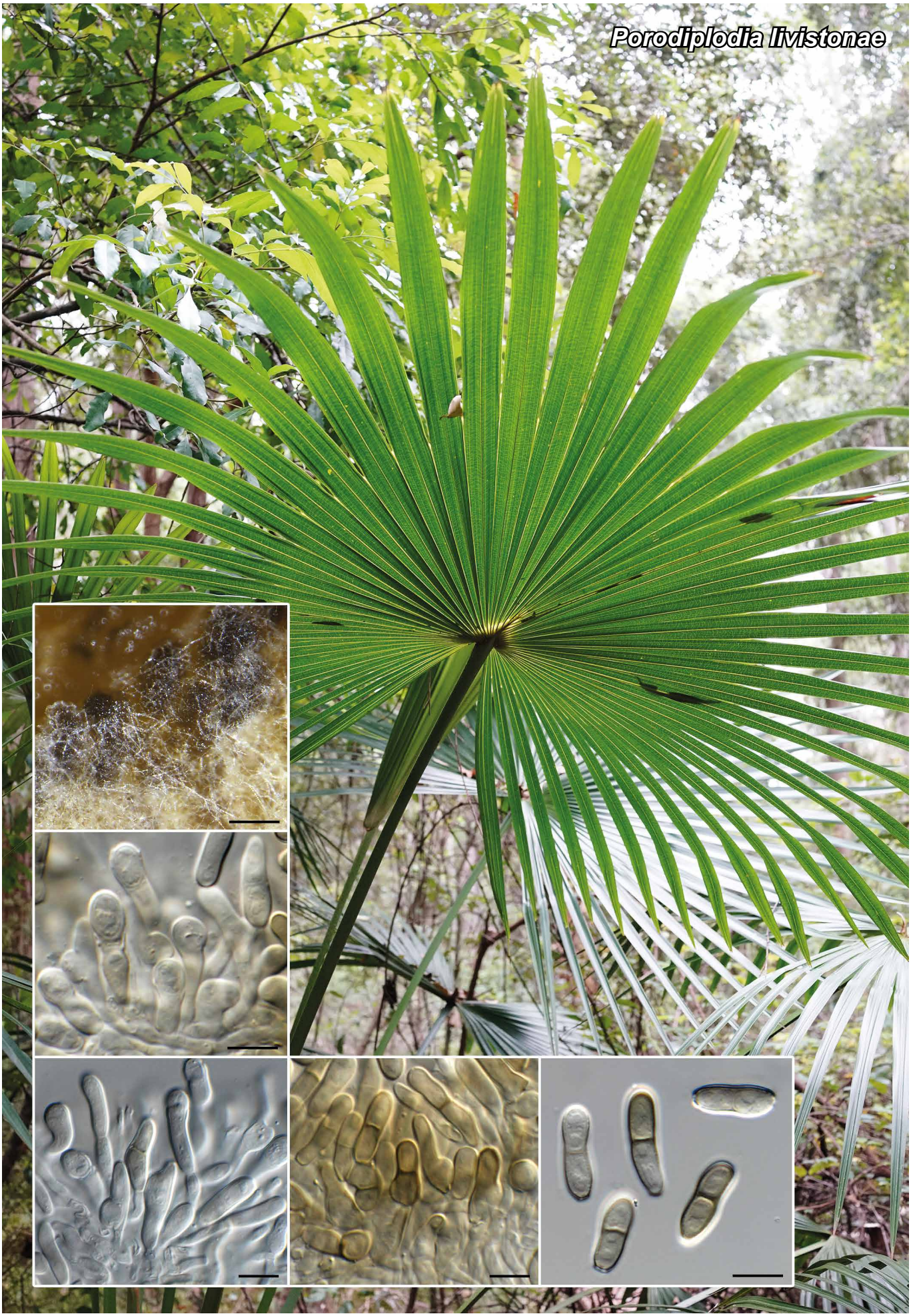
Porodiplodia livistonae

Fungal Planet 770 – 13 July 2018

Porodiplodiaceae Crous, *fam. nov.*

Classification — *Porodiplodiaceae*, *Helotiales*, *Leotiomycetes.*

Conidiomata eustromatic, uni- to multilocular, brown, globose, aggregated on agar, ostiolate, or hyphomycetous, forming clusters of conidiophores. *Conidiophores* lining inner cavity of conidioma, subcylindrical, hyaline, smooth, branched, septate, proliferating percurrently near apex, or occurring in clusters on hyphae, septate, subcylindrical, with upper cells pigmented; conidiogenous cells proliferating percurrently, or phialidic, with prominent collarettes. *Conidia* in chains, fusoid-ellipsoid to subcylindrical, hyaline to medium brown, smooth to finely verruculose, guttulate, 0–1-septate.

Type genus. *Porodiplodia* Crous.
MycoBank MB825419.

Notes — The family *Porodiplodiaceae* presently contains two genera, namely *Porodiplodia* and a chalara-like fungus, *Chalara clidemiae* (see Crous et al. 2016b), as well as a strain identified as *Chalara africana* (OC0018).

Porodiplodia Crous, *gen. nov.*

Etymology. Name refers to a morphological similarity to the genus *Diplodia*, but with conidia having a minute basal pore in the hilum.

Conidiomata eustromatic, uni- to multilocular, brown, globose, aggregated on agar, ostiolate. *Conidiophores* lining inner cavity, subcylindrical, hyaline, smooth, branched, septate, proliferating percurrently near apex. *Paraphyses* intermingled among conidiophores, hyaline, smooth, septate, subcylindrical with obtuse ends. *Conidia* in short chains (–3), fusoid-ellipsoid to subcylindrical, medium brown, finely verruculose, guttulate, thick-walled, 1-septate, apex obtuse (at times with central pore), base truncate with central pore, 2 µm diam.

Type species. *Porodiplodia livistonae* Crous.
MycoBank MB825420.

Porodiplodia livistonae Crous, *sp. nov.*

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

Conidiomata eustrommatic, uni- to multilocular, brown, globose, 180–250 µm, aggregated on agar, ostiolate. *Conidiophores* lining inner cavity, subcylindrical, hyaline, smooth, 1–3-septate, 15–25 × 2.5–3.5 µm, proliferating percurrently near apex. *Paraphyses* intermingled among conidiophores, hyaline, smooth, septate, subcylindrical with obtuse ends, 25–35 × 3–4 µm. *Conidia* in short chains (–3), fusoid-ellipsoid to subcylindrical, medium brown, finely verruculose, guttulate, thick-walled, 1-septate, apex obtuse, base truncate with central pore, 2 µm diam, (14–)15–17(–20) × 5(–6) µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 17 mm diam after 2 wk at 25 °C. On MEA surface cinnamon to buff, reverse sienna. On PDA surface saffron, reverse cinnamon. On OA surface cinnamon, with diffuse cinnamon pigment.

Typus. Australia, New South Wales, Murramarang National Park, on leaves of *Livistona australis* (*Arecaceae*), 27 Nov. 2016, *P.W. Crous* (holotype CBS H-23574, culture ex-type CPC 32154 = CBS 144428, ITS and LSU sequences GenBank MH327809.1 and MH327845.1, MycoBank MB825421).

Notes — A genus that should be compared to *Porodiplodia* is the monotypic genus *Hendersonina*, based on *H. sacchari*. *Hendersonina sacchari* is a fungus that has been implicated with collar rot of sugarcane, though it is accepted to be of minor importance (Nyvall 2013). The morphology of the monotypic genus *Hendersonina* has remained somewhat confused. Sutton (1980) described the conidiomata as eustromatic, but showed conidia as being fusoid to somewhat cylindrical, 1-septate, with a dark, thickened scar at each end (conidia from different specimens given as 21–28 × 5.5–9.5 µm, 19–29 × 4–5 µm, 17–24 × 4–5 µm). The conidiogenesis was described and illustrated as (not observed in original material) enteroblastic, phialidic, with prominent periclinal thickening. The matter was further confused in that Butler & Khan (1913) also referred to hyaline, aseptate secondary conidia.

The two species of *Porodiplodia* studied here in culture are characterised by eustromatic conidiomata, and conidia occurring in short chains. Although a pore was observed at both ends in several conidia, this was rather uncommon. They were never thickened and darkened, and were found only in secondary and tertiary conidia. *Porodiplodia* differs from *Hendersonina* due to its branched conidiophores, conidia lacking scars, and being conspicuously 1-septate (septa in *Hendersonina* are thin-walled). It differs from other genera allied to *Diplodia* (Phillips et al. 2013, Yang et al. 2017) in having conidia occurring in short chains, with visible central pores in their hila.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Chalara clidemiae* (GenBank NR_145313.1; Identities = 521/540 (96 %), 1 gap (0 %)), *Mollisia caespiticia* (GenBank KY965813.1; Identities = 496/531 (93 %), 2 gaps (0 %)) and *Pezizella discreta* (GenBank JF908571.1; Identities = 509/550 (93 %), 3 gaps (0 %)). Closest hits using the LSU sequence are *Chalara clidemiae* (GenBank KX228321.1; Identities = 864/871 (99 %), no gaps), *Chalara africana* (GenBank FJ176249.1; Identities = 840/855 (98 %), 2 gaps (0 %)) and *Urceolella crispula* (GenBank JN086682.1; Identities = 859/892 (96 %), 1 gap (0 %)).

Colour illustrations. *Livistona australis* at Murramarang National Park; conidiomata sporulating on PDA (scale bar = 250 µm), conidiogenous cells and conidia (scale bars = 10 µm).

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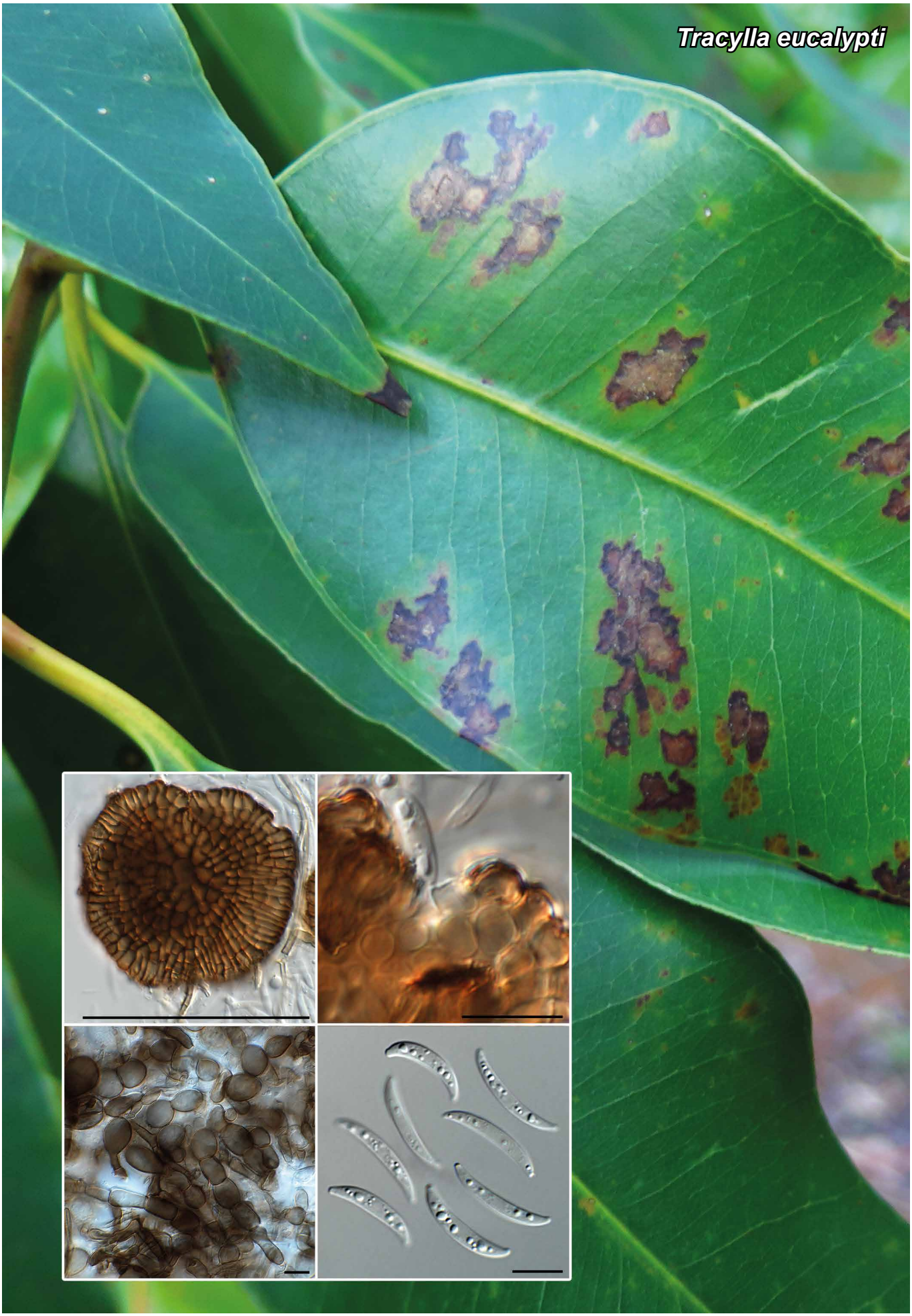
Tracylla eucalypti

Fungal Planet 771 – 13 July 2018

Tracyllalales Crous, *ord. nov*.

MycoBank MB825422.

Tracyllaceae Crous, *fam. nov.*

Classification — *Tracyllaceae*, *Tracyllalales*, *Sordariomycetes.*

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

Type genus. *Tracylla* (Sacc.) Tassi.
MycoBank MB825423.

Notes — *Tracyllalales* presently only includes *Tracylla*.

Tracylla eucalypti Crous, *sp. nov.*

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

Pycnothyria superficial on leaves, round, brown, surface of *textura epidermoidea*, 50–80 µm diam; ostiole lacking, margin of catenate, darker brown cells. *Conidiophores* reduced to conidiogenous cells arising from a central columella, doliiform to ellipsoid, with a single conidiogenous locus, phialidic, 4–5 × 3–4 µm. *Conidia* solitary, hyaline, aseptate, smooth, guttulate, falcate, apex subobtusely rounded, base truncate, 1–1.5 µm diam, (12–)17–19(–20) × (2.5–)3 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and feathery margin, reaching 60 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey to leaden black, forming long ropes of ellipsoid, brown, smooth chlamydospores. Cultures sterile.

Typus. Colombia, Cali, on leaves of *Eucalyptus urophylla* (*Myrtaceae*), July 2010, *M.J. Wingfield* (holotype CBS H-23573, culture ex-type CPC 31806 = CBS 144429, ITS and LSU sequences GenBank MH327810.1 and MH327846.1, MycoBank MB825424).

Additional material examined. Colombia, Cali, on leaves of *Eucalyptus urophylla* (*Myrtaceae*), July 2010, *M.J. Wingfield,* CPC 31777 = CBS 144430, ITS and LSU sequences GenBank MH327811.1 and MH327847.1.

Notes — The genus *Tracylla* (based on *T. spartinae*, occurring on *Spartina patens*, and several other grasses) was considered by Hernández-Restrepo et al. (2016b). *Tracylla eucalypti*, which lacks conidial appendages, clusters with *T. aristata*, which was originally described from *Eucalyptus* leaf litter collected in Australia (Nag Raj 1993). By adding the present collection to the genus, we expand the circumscription of *Tracylla* to include taxa lacking conidial appendages. Unfortunately, cultures of *T. eucalypti* were sterile, and the conidiomatal development could not be fully elucidated.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence of CPC 31777 had highest similarity to *Tracylla aristata* (GenBank NR_154519.1; Identities = 533/575 (93 %), 15 gaps (2 %)). The ITS sequences of CPC 31777 and CPC 31806 were identical (565/565). Closest hits using the LSU sequence are *Tracylla aristata* (GenBank KX306795.1; Identities = 825/835 (99 %), no gaps), *Rhexodenticula cylindrospora* (GenBank KM485039.1; Identities = 815/866 (94 %), no gaps) and *Coniochaetidium savoryi* (GenBank AY346276.1; Identities = 837/891 (94 %), no gaps). The LSU sequences of CPC 31777 and CPC 31806 were identical (817/817).

Colour illustrations. Symptomatic leaves of *Eucalyptus urophylla*; conidioma, conidiogenous cells *in vivo* (top right), chlamydospore-like cells *in vitro* (lower left) and conidia. Scale bars = 10 µm.

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Elsinoë elaeocarpi

Fungal Planet 772 – 13 July 2018

Elsinoë elaeocarpi Crous, *sp. nov.*

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

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

Leaf spots primarily epiphyllous, irregular in outline, 1–3 mm diam, grey with feathery, dark brown border, containing brown to black ascomata. *Ascomata* round to ellipsoid, 150–250 µm diam. *Asci* obovoid, hyaline, smooth, bitunicate, 30–55 × 20–25 µm, 8-spored, with well-defined apical chamber, 4–5 µm diam. *Ascospores* hyaline, smooth, fusoid-ellipsoid, constricted at median septum, widest just above septum with 5–7 transverse and 3–4 vertical septa, (22–)25–28 × (6–)7(–8) µm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 5–7 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse iron-grey.

Typus. Australia, Victoria, close to Eden, on leaves of *Elaeocarpus* sp. (*Elaeocarpaceae*), 29 Nov. 2016, *P.W. Crous* (holotype CBS H-23572, culture ex-type CPC 32853 = CBS 144431, ITS, LSU and *rpb2* sequences GenBank MH327812.1, MH327848.1 and MH327870.1, MycoBank MB825425).

Notes — The genus *Elsinoë* was recently treated by Fan et al. (2017), providing an overview phylogeny for the majority of the species presently known from culture. *Elsinoë elaeocarpi* is phylogenetically allied to *E. banksiigena* (see Fungal Planet 782) and *E. eucalyptigena* (both only known from Australia), and represents a phylogenetically distinct taxon on *Elaeocarpus*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Elsinoë verbenae* (GenBank KX887299.1; Identities = 439/532 (83 %), 37 gaps (6 %)), *Elsinoë fawcettii* (GenBank KF010881.1; Identities = 439/533 (82 %), 43 gaps (8 %)) and *Elsinoë tiliae* (GenBank KX887296.1; Identities = 435/530 (82 %), 35 gaps (6 %)). Closest hits using the LSU sequence are *Elsinoë fawcettii* (GenBank JN940382.1; Identities = 686/730 (94 %), 2 gaps (0 %)), *Sphaceloma erythrinae* (GenBank JN940392.1; Identities = 686/731 (94 %), 3 gaps (0 %)) and *Elsinoë eucalypticola* (GenBank GQ303306.1; Identities = 685/730 (94 %), 2 gaps (0 %)). Closest hits using the *rpb2* sequence had highest similarity to *Myriangium hispanicum* (GenBank GU371744.1; Identities = 771/1 045 (74 %), 4 gaps (0 %)), *Mendogia macrostroma* (GenBank KU940162.1; Identities = 767/1 047 (73 %), 4 gaps (0 %)) and *Strangospora pinicola* (GenBank AY641080.1; Identities = 761/1 046 (73 %), 6 gaps (0 %)).

Colour illustrations. Forest in Victoria, close to Eden; foliar lesion on *Elaeocarpus* sp., asci with ascospores (*in vivo*). Scale bars = 10 µm.

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Idriellomyces eucalypti

Fungal Planet 773 – 13 July 2018

Idriellomyces Crous, *gen. nov.*

Etymology. Name reflects a similarity to the genus *Idriella*.

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

Mycelium consisting of hyaline to olivaceous, smooth, septate, branched hyphae. *Conidiophores* arising from superficial mycelium, brown, smooth, septate, branched, aggregated into thick, erect synnemata, consisting of branched conidiophores with apical and intercalary conidiogenous cells; lateral conidiophores arising from synnemata, septate. *Conidiogenous cells* medium brown, smooth, subcylindrical with apical taper to a rachis containing several darkened scars. *Conidia* aseptate, solitary, dry, hyaline, smooth, guttulate, fusoid, apex subobtuse, base truncate.

Type species. Idriellomyces eucalypti Crous.
MycoBank MB825426.

Idriellomyces eucalypti Crous, *sp. nov.*

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

Mycelium consisting of hyaline to olivaceous, smooth, septate, branched hyphae, 1.5–2 µm diam. *Conidiophores* arising from superficial mycelium, brown, smooth, septate, branched, aggregated into thick, erect synnemata, up to 200 µm tall and 60 µm diam, consisting of branched conidiophores with apical and intercalary conidiogenous cells; lateral conidiophores arising from synnemata, 15–40 × 2–2.5 µm, 1–3-septate. *Conidiogenous cells* medium brown, smooth, subcylindrical with apical taper to a rachis containing several darkened scars, 0.5 µm diam, 8–20 × 2–2.5 µm. *Conidia* aseptate, solitary, dry, hyaline, smooth, guttulate, fusoid, apex subobtuse, base truncate, 0.5 µm diam, (5–)6.5–7(–8) × 1.5(–2) µm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and even, smooth margin, reaching 12 mm diam after 2 wk at 25 °C. On MEA surface and reverse umber. On PDA surface sepia, reverse isabelline. On OA surface cinnamon with patches of sienna.

Typus. Australia, Victoria, Silvan Reservoir Park, on leaves of *Eucalyptus obliqua* (*Myrtaceae*), 1 Dec. 2016, *P.W. Crous* (holotype CBS H-23571, culture ex-type CPC 32632 = CBS 144432, ITS, LSU, *tef1* and *tub2* sequences GenBank MH327813.1, MH327849.1, MH327881.1 and MH327893.1, MycoBank MB825427).

Notes — The genus *Idriella* (based on *I. lunata*) was treated by Hernández-Restrepo et al. (2016a) and shown to reside in the *Microdochiaceae*. The genus *Idriellomyces* is somewhat similar to *Idriella* in morphology, but represents a distinct genus in the family. *Idriellomyces* is morphologically distinct in that it lacks chlamydospores, conidiophores are pigmented and frequently aggregated in synnemata.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Cylindrium elongatum* (GenBank KM231853.1; Identities = 457/540 (85 %), 37 gaps (6 %)), *Neopestalotiopsis piceana* (GenBank KM199372.1; Identities = 464/549 (85 %), 37 gaps (6 %)) and *Neopestalotiopsis aotearoa* (GenBank KM199369.1; Identities = 464/549 (85 %), 37 gaps (6 %)). Closest hits using the LSU sequence are *Castanediella cagnizarii* (GenBank KP858988.1; Identities = 818/849 (96 %), 1 gap (0 %)), *Anungitea eucalyptorum* (GenBank KJ869176.1; Identities = 853/886 (96 %), 2 gaps (0 %)) and *Pseudophloeospora eucalypti* (GenBank HQ599593.1; Identities = 832/866 (96 %), 5 gaps (0 %)). No significant hits were obtained when the *tef1* and *tub2* sequences were used in BLASTn and megablast searches.

Colour illustrations. *Eucalyptus obliqua* trees at Silvan Reservoir Park; synnema on SNA, conidiogenous cells and conidia. Scale bars = 10 µm.

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Cyanodermella banksiae

Fungal Planet 774 – 13 July 2018

Cyanodermella banksiae Crous, *sp. nov.*

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

Classification — *Stictidaceae*, *Ostropales*, *Lecanoromycetes.*

Mycelium consisting of hyaline, smooth, branched, septate, 2–3 µm diam hyphae, immersed, forming a hyaline stroma that gives rise to brown, erect, cylindrical to slightly obpyriform ascomata (circular in outline), brown, with single locule, 150–300 × 250–300 µm; wall of crustose, medium brown cells with dark brown exudate. Asci intermingled among hyaline, smooth, septate hypha-like paraphyses, 1.5 µm diam. *Asci* unitunicate, cylindrical with apical mechanism, stipitate, 130–150 × 8–10 µm. *Ascospores* parallel in ascus, twisted, number undetermined, hyaline to olivaceous, smooth, guttulate, cylindrical, ends obtuse to subobtuse, multiseptate, and breaking into part-spores, each section (12–16 × 2.5–3 µm) containing 3 septa, with age disarticulating into aseptate phragmospores, 5–6 × 3 µm. Sterile in culture.

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

Typus. Australia, New South Wales, Australian Botanical Garden Mount Annan, on leaves of *Banksia ericifolia* subsp. *macrantha* (*Proteaceae*), 25 Nov. 2016, *P.W. Crous* (holotype CBS H-23570, culture ex-type CPC 32105 = CBS 144433, ITS, LSU and *rpb2* sequences GenBank MH327814.1, MH327850.1 and MH327871.1, MycoBank MB825428).

Notes — The sexual morph of *Cyanodermella* (based on *C. viridula*) forms erumpent, subconical ascocarps, the upper parts of which are covered in a grainy white-'mealy' substance. Asci are numerous, thin-walled, cylindrical, gradually tapering towards base. Ascospores are parallel, spirally twisted, filiform, multiseptate, c. 1 µm diam, and paraphyses are sparse (Eriksson 1967). The present collection clusters basal to species identified as *Cyanodermella*, and is consequently placed in this genus, as it is also morphologically similar to other taxa presently accommodated in *Cyanodermella*. Based on Van Nieuwenhuijzen et al. (2016), *Cyanodermella* could have phoma-like asexual morphs, although cultures of *C. banksiae* were sterile and this could not be confirmed.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Cyanodermella asteris* (GenBank KT758843.1; Identities = 492/587 (84 %), 23 gaps (3 %)), *Cyanodermella oleoligni* (GenBank NR_153930.1; Identities = 346/406 (85 %), 11 gaps (2 %)) and *Xylographa septentrionalis* (GenBank KJ462316.1; Identities = 307/356 (86 %), 13 gaps (3 %)). Closest hits using the LSU sequence are *Cyanodermella asteris* (GenBank KT758843.1; Identities = 799/846 (94 %), 4 gaps (0 %)), *Cyanodermella oleoligni* (GenBank KX950461.1; Identities = 763/833 (92 %), 10 gaps (1 %)) and *Micropeltis zingiberacicola* (GenBank JQ036227.1; Identities = 749/825 (91 %), 6 gaps (0 %)). No significant hits were obtained when the *rpb2* sequence was used in a megablast search; however, a BLASTn search yielded as best hits *Cyanodermella asteris* (GenBank KU934214.1; Identities = 635/872 (73 %), 10 gaps (1 %)) and *Cyanodermella viridula* (GenBank HM244792.1; Identities = 626/877 (71 %), 29 gaps (3 %)).

Colour illustrations. Banksia ericifolia subsp. *macrantha* at Australian Botanical Garden Mount Annan; ascomata (*in vivo*) (scale bars = 300 µm), asci and ascospores (scale bars = 10 µm).

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Periconia cyperacearum
& Paracladophialophora cyperacearum

Fungal Planet 775 & 776 – 13 July 2018

Periconia cyperacearum Crous, *sp. nov.*

Etymology. Name refers to *Cyperaceae*, the host family from which this fungus was collected.

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

Conidiophores solitary, erect, subcylindrical, unbranched with branches in conidiogenous head bearing a cluster of dry conidia; thick-walled (1–2 µm diam), dark brown, finely roughened, septa 40–60 µm apart, base bulbous, 12–25 µm diam, stipe 150–350 µm tall (with percurrent rejuvenation), 10–13 µm diam. *Conidiogenous head* penicillate, primary branches dark brown, subcylindrical to doliiform, curved to straight, thick-walled, finely roughened, 0–1-septate, (10–)14–18(–22) × (6–)8–10(–12) µm, giving rise to 1–3 secondary branches, aseptate, doliiform to subcylindrical, medium brown, finely roughened, 8–12 × 6–7 µm; tertiary branches aseptate, doliiform to subcylindrical, medium brown, finely roughened, 5–7 × 5–6 µm, giving rise to monoblastic (rarely polyblastic) *phialides*, doliiform to ellipsoid, pale to medium brown, finely roughened, 5–6 × 3–4 µm. *Conidia* occurring in short, unbranched chains (–6), aseptate, ellipsoid to subcylindrical, medium brown, verruculose, thick-walled, (6–)7–9(–12) × (4.5–)5–6(–7) µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and even, lobate margin, reaching 12 mm diam on PDA, and 35 mm diam on MEA and OA after 2 wk at 25 °C. On MEA surface dirty white to buff, reverse cinnamon. On PDA surface buff, reverse isabelline. On OA surface isabelline with patches of dirty white.

Typus. Australia, New South Wales, Fitzroy Falls, Morton National Park, on leaves of *Cyperaceae*, 26 Nov. 2016, *P.W. Crous* (holotype CBS H-23569, culture ex-type CPC 32138 = CBS 144434, ITS, LSU and *tef1* sequences GenBank MH327815.1, MH327851.1 and MH327882.1, MycoBank MB825429).

Notes — The genus *Periconia* is paraphyletic and is in urgent need of revision. For the present however, we will treat this collection as part of *Periconia* s.lat. *Periconia cyperacearum* is phylogenetically distinct from all species presently known based on their DNA sequence data, being allied to *P. cookei* and *P. homothallica* (Tanaka et al. 2015). Using the key provided by Ellis (1971) it is easily distinguished from other species based on the number of conidiophore branches as well as the shape, ornamentation and conidial dimensions.

Paracladophialophoraceae Crous, *fam. nov.*

Classification — *Paracladophialophoraceae*, *Chaetothyriales*, *Eurotiomycetes.*

Mycelium consisting of pale brown, smooth, septate, branched, hyphae. *Conidiophores* reduced to conidiogenous cells on hyphae, pale brown, smooth, subcylindrical, proliferating sympodially. *Conidia* pale brown, smooth, guttulate, fusoid-ellipsoid to subcylindrical, aseptate, occurring in branched chains; hila not thickened nor darkened.

Type genus. *Paracladophialophora* Crous.
MycoBank MB825430.

Notes — *Paracladophialophoraceae*, which presently only includes the type genus, is allied to *Cyphellophoraceae*, which is distinct in having solitary conidia arising from phialides and aggregating in a mucoid droplet.

Paracladophialophora cyperacearum Crous, *sp. nov.*

Etymology. Name refers to *Cyperaceae*, the host family from which this fungus was collected.

Mycelium consisting of pale brown, smooth, septate, branched, 2.5–3 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells on hyphae, pale brown, smooth, subcylindrical, 5–10 × 2.5–3 µm, proliferating sympodially. *Conidia* pale brown, smooth, guttulate, fusoid-ellipsoid to subcylindrical, aseptate, occurring in branched chains (–20); ramoconidia 8–10 × 2–2.5 µm; conidia 4–9 × (1.5–)2(–2.5) µm; hila not thickened nor darkened.

Colour illustrations. Cyperaceae at Fitzroy Falls, Morton National Park; *Periconia cyperacearum* (left column), conidiophores, *in vivo* (top), and *in vitro* (bottom). *Paracladophialophora cyperacearum* (right column), conidiophores sporulating on SNA, with conidiogenous cells and conidia. Scale bars = 10 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 5 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus. Australia, New South Wales, Fitzroy Falls, Morton National Park, on leaves of *Cyperaceae*, 26 Nov. 2016, *P.W. Crous* (holotype CBS H-23575, culture ex-type CPC 33046 = CBS 144427, ITS, LSU and *tub2* sequences GenBank MH327808.1, MH327844.1 and MH327892.1, MycoBank MB825431).

Notes — The monotypic genus *Paracladophialophora* was established for *P. carceris* (on leaves of *Aloe* sp., collected in the prison courtyard on Robben Island, South Africa). *Paracladophialophora cyperacearum* is allied to *P. carceris*, but distinct in that the latter species has well-defined conidiophores, and longer ramoconidia (0–3-septate, (7–)9–15(–17) × (2–)2.5(–3) µm), and conidia ((6–)7–8 × (2.5–)3 µm; Crous et al. 2016a).

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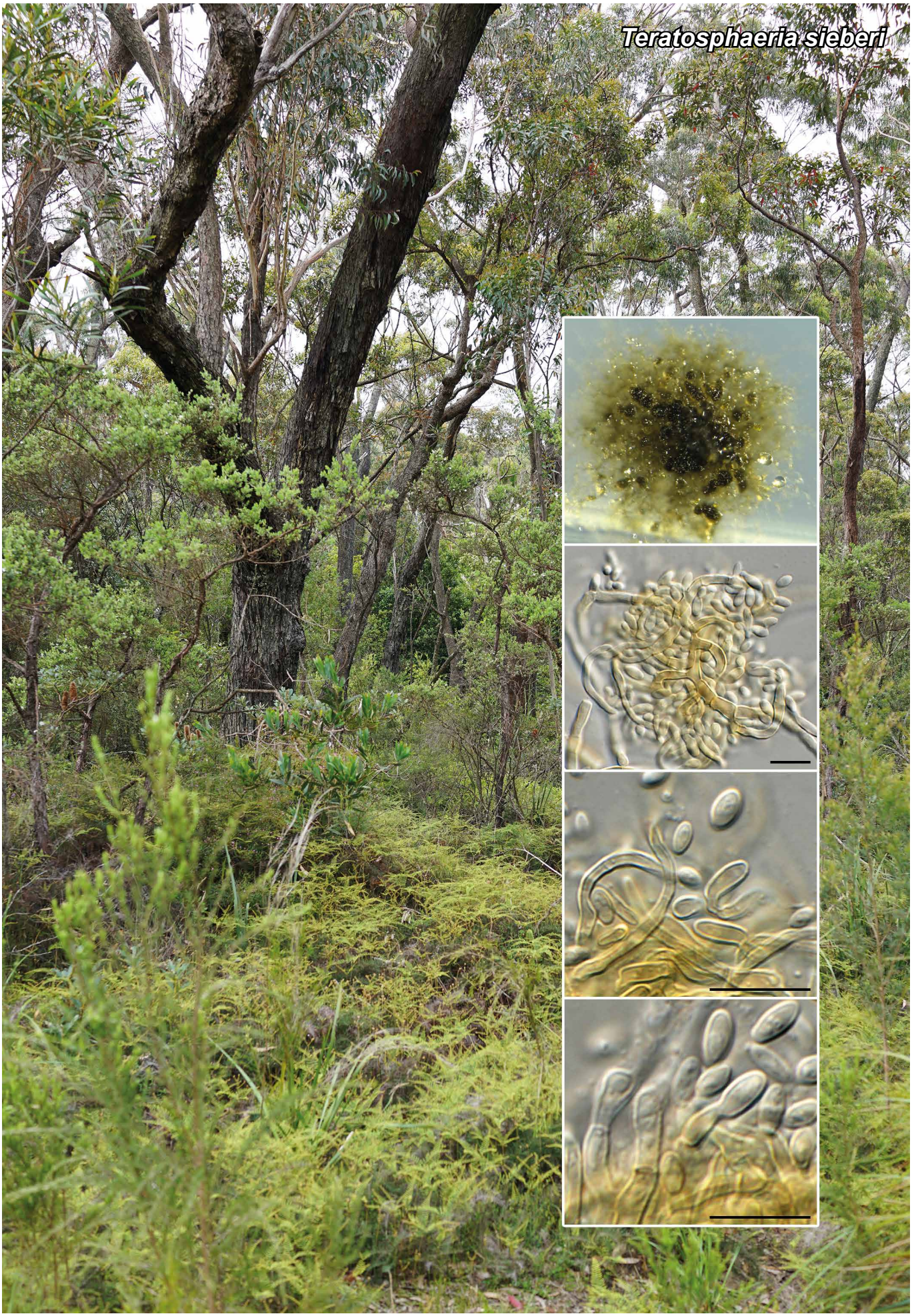
Teratosphaeria sieberi

Fungal Planet 777 – 13 July 2018

Teratosphaeria sieberi Crous, *sp. nov.*

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

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

Mycelium consisting of pale to medium brown, septate, branched, 3–5 µm diam hyphae. Hyphal aggregates forming stromata which resembles brown sporodochia, up to 100 µm diam, with conidiophores reduced to conidiogenous loci direct on hyphae, 1–1.5 µm diam. *Conidia* solitary, ellipsoid, apex subobtuse, base truncate, aseptate, hyaline to pale brown, smooth, (4–)6–7 × (2.5–)3 µm; aggregating in brown, slimy masses.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobed margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA surface smoke grey, reverse ochreous to umber. On PDA surface smoke grey, reverse scarlet with diffuse pigment. On OA surface olivaceous grey, with diffuse scarlet pigment.

Typus. Australia, New South Wales, Barron Ground Nature Reserve, on leaves of *Eucalyptus sieberi* (*Myrtaceae*), 26 Nov. 2016, *P.W. Crous* (holotype CBS 144443, culture ex-type CPC 32099 = CBS 144443, ITS, LSU and *rpb2* sequences GenBank MH327816.1, MH327852.1 and MH327872.1, MycoBank MB825432).

Notes — The *Teratosphaeriaceae*, which was recently revised by Quaedvlieg et al. (2014), includes numerous foliar pathogens of eucalypts (Hunter et al. 2011). *Teratosphaeria sieberi* is phylogenetically related to *T. mareebensis* (on leaves of *Eucalyptus alba*, Queensland), which is morphologically similar, but distinct from that species in having larger conidia (5–9 × 2–4 µm; Crous et al. 2011a).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Pleuropassalora armatae* (GenBank GU214640.1; Identities = 523/530 (99 %), 1 gap (0 %)), *Teratosphaeria considenianae* (GenBank GQ852792.1; Identities = 522/530 (98 %), 1 gap (0 %)) and *Teratosphaeria miniata* (GenBank GQ852803.1; Identities = 518/529 (98 %), no gaps). Closest hits using the LSU sequence are *Teratosphaeria mareebensis* (GenBank JF951169.1; Identities = 864/866 (99 %), no gaps), *Teratosphaeria complicata* (GenBank GQ852714.1; Identities = 840/843 (99 %), no gaps) and *Teratosphaeria hortaea* (GenBank FJ790299.1; Identities = 847/852 (99 %), no gaps). Closest hits using the *rpb2* sequence had highest similarity to *Teratosphaeria molleriana* (GenBank KX348104.1; Identities = 778/880 (88 %), no gaps), *Teratosphaeria stellenboschiana* (GenBank MF951743.1; Identities = 817/929 (88 %), no gaps) and *Teratosphaeria gauchensis* (GenBank KX348103.1; Identities = 789/900 (88 %), no gaps).

Colour illustrations. *Eucalyptus* trees at Barron Ground Nature Reserve; conidiomata sporulating on SNA, conidiogenous cells and conidia. Scale bars = 10 µm.

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Sporidesmium melaleucae

Fungal Planet 778 – 13 July 2018

Sporidesmiales Crous, *ord. nov.*

Classification — *Sporidesmiaceae*, *Sporidesmiales, Sordariomycetes.*

Mycelium consisting of hyaline, smooth, branched, septate hyphae, immersed or superficial. *Conidiophores* solitary or in clusters, erect, subcylindrical, unbranched, dark brown, septate. *Conidiogenous cells* terminal, medium brown, smooth, subcylindrical, holoblastic. *Conidia* dry, solitary, medium brown, smooth, obclavate to cylindrical or fusoid, straight to flexuous, apex obtuse, base obconically truncate, distoseptate.

Type family. *Sporidesmiaceae* Fr.
Type genus. *Sporidesmium* Link.
MycoBank MB 825433.

Notes — The order *Sporidesmiales* presently only contains the genus *Sporidesmium*.

Sporidesmium melaleucae Crous, *sp. nov.*

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

Mycelium consisting of hyaline, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* solitary or in clusters, erect, subcylindrical, dark brown, 1–2-septate, 12–30 × 4–6 µm. *Conidiogenous cells* terminal, medium brown, smooth, subcylindrical, holoblastic, 5–20 × 4–5 µm. *Conidia* solitary, medium brown, smooth, obclavate, straight to flexuous, apex obtuse, base obconically truncate, 3.5–4 µm diam, 5–21-distoseptate, (45–)80–130(–170) × (8–)9–10(–11) µm.

Culture characteristics — Colonies erumpent, with sparse aerial mycelium and even lobate margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA and PDA surface pale luteous, reverse luteous. On OA surface umber.

Typus. Australia, New South Wales, Tulaswalla Creek, on *Melaleuca* sp. (*Myrtaceae*), 27 Nov. 2016, *P.W. Crous* (holotype CBS H-23567, culture ex-type CPC 32707 = CBS 144435, ITS and LSU sequences GenBank MH327817.1 and MH327853.1, MycoBank MB825434).

Additional material examined. Australia, New South Wales, Tulaswalla Creek, on *Melaleuca* sp. (*Myrtaceae*), 27 Nov. 2016, *P.W. Crous,* CPC 32936, ITS and LSU sequences GenBank MH327818.1 and MH327854.1.

Notes — The genera *Sporidesmium* and *Ellisembia* are morphologically similar (Réblová 1999), and we choose to use the older name, *Sporidesmium*. Phylogenetically, *S. melaleucae* is allied to *E. bambusicola*, which has obclavate to ellipsoid conidia, 9–11-distoseptate, 40–55 × 10–12 µm. Morphologically, *S. melaleucae* is also similar to *E. bambusicola*, although it has much longer conidiophores (2–4-septate, 50–100 × 4–7 µm), and smaller conidia (60–130 × 13–15 µm) (Wu & Zhuang 2005).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence of CPC 32707 had highest similarity to *Cataractispora appendiculata* (GenBank KU975063.1; Identities = 322/379 (85 %), 18 gaps (4 %)), *Submersisphaeria aquatica* (GenBank KU975067.1; Identities = 477/583 (82 %), 30 gaps (5 %)) and *Pseudoproboscispora caudae-suis* (GenBank KU975068.1; Identities = 481/589 (82 %), 37 gaps (6 %)). The ITS sequences of CPC 32707 and CPC 32936 differed with 1 nucleotide (564/565). Closest hits using the LSU sequence are *Ellisembia bambusicola* (GenBank DQ408562.1; Identities = 809/822 (98 %), no gaps), *Fluminicola thailandensis* (GenBank MF374368.1; Identities = 780/829 (94 %), 7 gaps (0 %)) and *Fluminicola saprotrophitica* (GenBank MF374367.1; Identities = 769/818 (94 %), 7 gaps (0 %)). The LSU sequences of CPC 32707 and CPC 32936 differed with 1 nucleotide (842/843).

Colour illustrations. Tulaswalla Creek; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Discosia macrozamiae

Fungal Planet 779 – 13 July 2018

Discosia macrozamiae Crous, *sp. nov.*

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

Classification — *Sporocadaceae*, *Amphisphaeriales*, *Sordariomycetes*.

Conidiomata pycnidial, erumpent, subglobose to lenticular, unilocular, dark brown, to 250 µm diam; wall of polyclonal brown cells. *Conidiophores* lining the inner cavity, hyaline, smooth, subcylindrical to ampulliform, 0–2-septate, rarely branched at base, 7–15 × 2.5–3 µm. *Conidiogenous cells* terminal, integrated, hyaline, smooth, subcylindrical, 5–7 × 2–2.5 µm; proliferating inconspicuously percurrently at apex. *Conidia* cylindrical, 3-septate, pale brown, smooth with appendage at both ends, (25–)30–32(–35) × (2.5–)3 µm; basal cell 6–7 µm long, obconic with truncate hilum; second cell from base (9–)10–11(–12) µm long; third cell 4–5 µm long, with obtusely rounded apex. *Appendages* cellular, unbranched, filiform, excentric; apical appendage 7–11 µm long; basal appendage 10–16 µm long.

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

Typus. Australia, New South Wales, Australian Botanical Garden Mount Annan, on leaves of *Macrozamia miquelii* (*Zamiaceae*), 25 Nov. 2016, *P.W. Crous* (holotype CBS H-23593, culture ex-type CPC 32113 = CBS 144436, ITS, LSU, *tef1* and *tub2* sequences GenBank MH327819.1, MH327855.1, MH327883.1 and MH327894.1, MycoBank MB825435).

Additional material examined. Australia, New South Wales, Australian Botanical Garden Mount Annan, on leaves of *Macrozamia miquelii*, CPC 32109 = CBS 144437, ITS, LSU, *tef1* and *tub2* sequences GenBank MH327820.1, MH327856.1, MH327884.1 and MH327895.1.

Colour illustrations. *Macrozamia miquelii* at Australian Botanical Garden Mount Annan; conidiomata sporulating on PNA (scale bar = 250 µm), conidiogenous cells and conidia (scale bars = 10 µm).

Notes — In a phylogenetic treatment of *Discosia*, Tanaka et al. (2011) established genera for former 'sections' of the genus, recognizing *Adisciso* (*Discosia* spp. with a sexual morph), and *Immersidiscosia* (species occurring on *Eucalyptus*). Following the 'one fungus one name' approach, it is preferable to treat *Adisciso* under the older name, *Discosia*. The present collection is allied to, but distinct from, species presently recognized in this subclade, and a new species is introduced to accommodate this taxon.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence of CPC 32109 had highest similarity to *Discosia* cf. *pleurochaeta* (GenBank AB594777.1; Identities = 546/546 (100 %), no gaps), *Discosia italica* (GenBank KM678041.1; Identities = 552/556 (99 %), 1 gap (0 %)) and *Discosia pseudoartocreas* (GenBank NR_132068.1; Identities = 550/556 (99 %), 1 gap (0 %)). The ITS sequences of CPC 32109 and 32113 are identical (556/556). Closest hits using the LSU sequence of CPC 32109 are *Adisciso yakushimense* (GenBank AB593721.1; Identities = 802/803 (99 %), no gaps), *Discosia fagi* (GenBank KM678048.1; Identities = 871/873 (99 %), no gaps) and *Adisciso tricellulare* (GenBank NG_042334.1; Identities = 800/803 (99 %), no gaps). The LSU sequences of CPC 32109 and 32113 are identical (873/873). Closest hits using the *tef1* sequence of CPC 32109 had highest similarity to *Discosia brasiliensis* (GenBank KF827465.1; Identities = 363/399 (91 %), 12 gaps (3 %)), *Pestalotiopsis diversiseta* (GenBank JX399073.1; Identities = 224/249 (90 %), 12 gaps (4 %)) and *Pestalotiopsis yanglingensis* (GenBank KX895197.1; Identities = 221/246 (90 %), 6 gaps (2 %)). The *tef1* sequences of CPC 32109 and 32113 are identical (529/529). Closest hits using the *tub2* sequence of CPC 32109 had highest similarity to *Discosia brasiliensis* (GenBank KF827469.1; Identities = 805/832 (97 %), no gaps), *Pestalotiopsis microspora* (GenBank AF115396.1; Identities = 782/826 (95 %), no gaps) and *Pestalotiopsis paeoniicola* (GenBank KY930635.1; Identities = 781/826 (95 %), no gaps). The *tub2* sequences of CPC 32109 and 32113 are identical (874/874).

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Didymocyrtis brachylaenae

Fungal Planet 780 – 13 July 2018

Didymocyrtis brachylaenae Crous, *sp. nov.*

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

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

Conidiomata pycnidial, globose, brown, 200–350 µm diam, with central ostiole; wall of 3–6 layers of medium brown *textura angularis*. *Conidiophores* mostly reduced to conidiogenous cells lining the inner cavity, ampulliform to doliiform, 5–7 × 2.5–3.5 µm, proliferating percurrently at apex; a few conidiophores observed that are subcylindrical, branched, 1–2-septate, with terminal and intercalary conidiogenous cells. *Conidia* fusoid-ellipsoid to subcylindrical, widest in middle, 1(–3)-septate, apex subobtuse, base truncate, medium brown, smooth, granular, (8–)9–10(–13) × (2–)3 µm. *Spermatia* observed in same conidiomata as conidia, hyaline, smooth, aseptate, ellipsoid, 3–4.5 × 2 µm.

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

Typus. South Africa, Eastern Cape Province, Haga Haga, on leaves of *Brachylaena discolor* (*Asteraceae*), 24 Dec. 2010, *M.J. Wingfield* (holotype CBS H-23565, culture ex-type CPC 32651 = CBS 144438, ITS, LSU, *rpb2* and *tub2* sequences GenBank MH327821.1, MH327857.1, MH327873.1 and MH327896.1, MycoBank MB825436).

Colour illustrations. Brachylaena discolor at Haga Haga; symptomatic leaf, conidiogenous cells and conidia, spermatia, and 1-septate conidia. Scale bars = 10 µm.

Notes — The genus *Diederichomyces* was established by Trakunyingcharoen et al. (2014) for several phoma-like lichenicolous species. *Diederichomyces* was, however, reduced to synonymy under *Didymocyrtis* by Ertz et al. (2015), which is an older name, and has priority. Although phylogenetically related to *D. cladoniicola*, *D. brachylaenae* is distinct in having conidia that are 1(–3)-septate. Furthermore, although they were neither described nor illustrated, original isolations of *D. brachylaenae* were from a phaeosphaeria-like sexual morph, which is also consistent with its phylogenetic position in the *Phaeosphaeriaceae*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Phaeosphaeria poagena* (GenBank KJ869114.1; Identities = 461/476 (97 %), 3 gaps (0 %)), *Phaeosphaeria podocarpi* (GenBank NR_137933.1; Identities = 454/476 (95 %), 2 gaps (0 %)) and *Parastagonospora nodorum* (GenBank KM056326.1; Identities = 453/476 (95 %), 11 gaps (2 %)). Closest hits using the LSU sequence are *Didymocyrtis cladoniicola* (GenBank LN907456.1; Identities = 865/868 (99 %), no gaps), *Neosulcatispora agaves* (GenBank KT950867.1; Identities = 860/866 (99 %), no gaps) and *Phaeosphaeriopsis musae* (GenBank DQ885894.1; Identities = 864/872 (99 %), no gaps). Closest hits using the *rpb2* sequence had highest similarity to *Phaeosphaeria chiangraina* (GenBank KM434307.1; Identities = 511/597 (86 %), 2 gaps (0 %)), *Phaeosphaeria oryzae* (GenBank KM434306.1; Identities = 511/597 (86 %), 2 gaps (0 %)) and *Phaeosphaeria musae* (GenBank KM434304.1; Identities = 511/597 (86 %), 2 gaps (0 %)). Closest hits using the *tub2* sequence had highest similarity to *Stagonospora avenaria* f. sp. *avenaria* (GenBank AY870402.1; Identities = 902/968 (93 %), 12 gaps (1 %)), *Stagonospora avenae* f. sp. *triticea* (GenBank AY786330.1; Identities = 898/964 (93 %), 4 gaps (0 %)) and *Parastagonospora nodorum* (GenBank CP022806.1; Identities = 898/964 (93 %), 4 gaps (0 %)).

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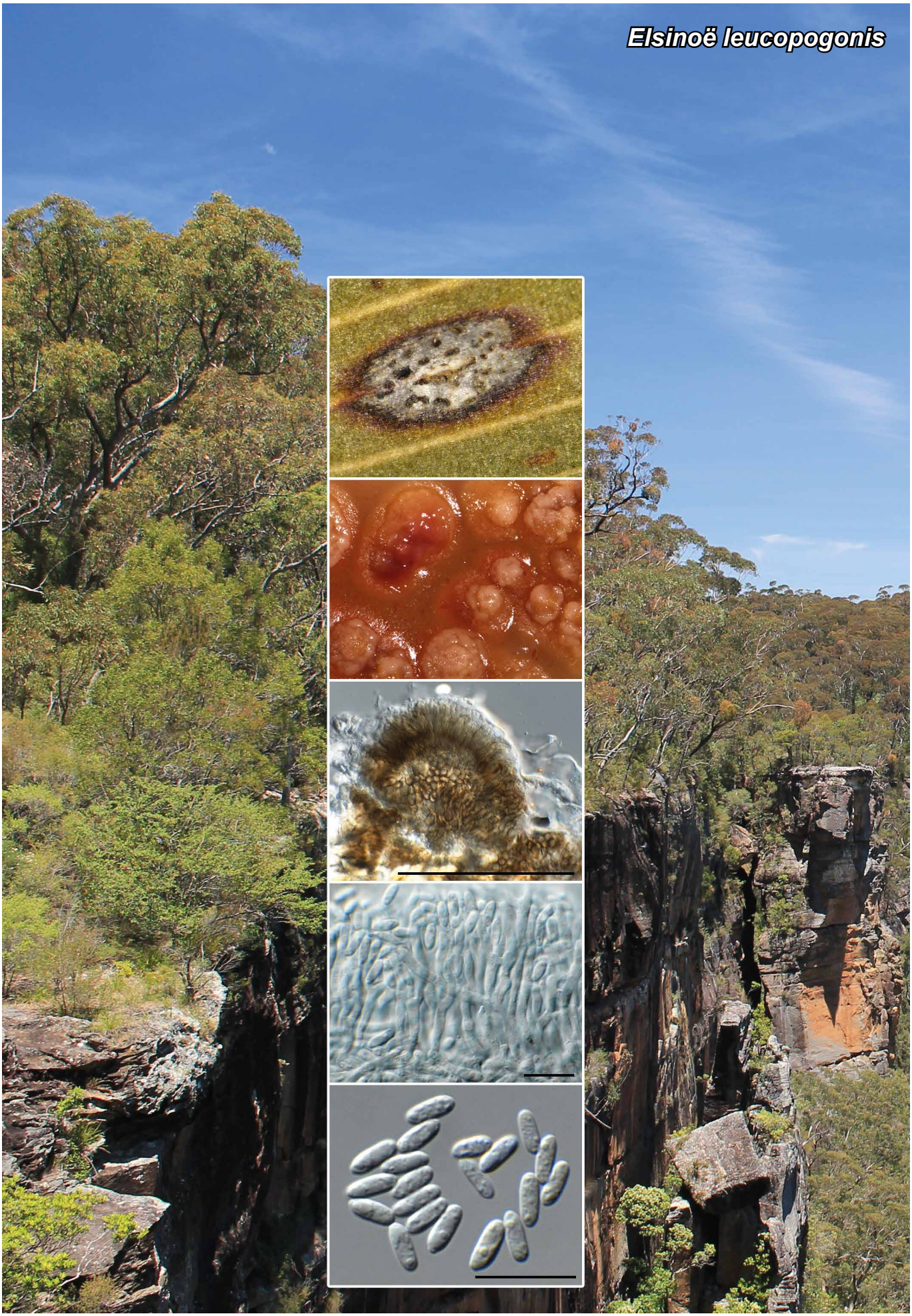
Elsinoë leucopogonis

Fungal Planet 781 – 13 July 2018

Elsinoë leucopogonis Crous, *sp. nov.*

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

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

Leaf spots amphigenous, but chiefly epiphyllous, ellipsoid, solitary, grey-brown, 1–3 µm diam, surrounded by a red-brown border. *Conidiomata* acervular, brown, 70–150 µm diam, coalescing with maturity, composed of *textura angularis. Conidiophores* subcylindrical, brown, smooth, 1–2-septate, 15–25 × 3–4 µm. *Conidiogenous cells* polyphialidic, with 1–2 integrated loci, pale brown, smooth, subcylindrical, 5–15 × 3–4 µm. *Conidia* hyaline, smooth, aseptate, guttulate, ellipsoid to subcylindrical, with obtuse apex and truncate hilum, 1 µm diam, (5–)6(–6.5) × (2–)2.5 µm *in vitro*.

Culture characteristics — Colonies erumpent, with sparse aerial mycelium, surface folded, with even, lobed margin, reaching 7 mm diam after 2 wk at 25 °C. On MEA and PDA surface saffron, reverse ochreous. On OA surface peach with diffuse scarlet pigment.

Typus. Australia, New South Wales, Barron Ground Nature Reserve, on leaves of *Leucopogon* sp. (*Epicridaceae*), 26 Nov. 2016, *P.W. Crous* (holotype CBS H-23564, culture ex-type CPC 32097 = CBS 144439, ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MH327822.1, MH327858.1, MH327874.1, MH327885.1 and MH327897.1, MycoBank MB825437).

Notes — A phylogenetic analysis of the genus *Elsinoë* was recently published by Fan et al. (2017), showing that most species are highly host specific. None of the species of *Elsinoë* are presently known from *Leucopogon*, and *E. leucopogonis* is also phylogenetically distinct from the taxa presently known based on their DNA sequence data (see Fungal Planet 782).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Elsinoë hederae* (GenBank NR_148146.1; Identities = 502/522 (96 %), 13 gaps (2 %)), *Elsinoë proteae* (GenBank NR_132796.1; Identities = 546/591 (92 %), 22 gaps (3 %)) and *Elsinoë theae* (GenBank NR_148174.1; Identities = 496/520 (95 %), 13 gaps (2 %)). Closest hits using the LSU sequence are *Elsinoë lepagei* (GenBank KX887004.1; Identities = 731/736 (99 %), no gaps), *Elsinoë hederae* (GenBank KX886994.1; Identities = 730/736 (99 %), no gaps) and *Elsinoë tectificae* (GenBank KX887055.1; Identities = 729/736 (99 %), no gaps). Closest hits using the *rpb2* sequence had highest similarity to *Elsinoë hederae* (GenBank KX887113.1; Identities = 640/744 (86 %), no gaps), *Elsinoë theae* (GenBank KX887175.1; Identities = 618/741 (83 %), 2 gaps (0 %)) and *Elsinoë eelemani* (GenBank KX398204.1; Identities = 648/812 (80 %), 10 gaps (1 %)). No significant hits were obtained when the *tef1* sequence was used in BLASTn and megablast searches, while the *tub2* sequence resulted in *Cyphellophora reptans* (GenBank KC455233.1; Identities = 261/332 (79 %), 22 gaps (6 %)) as best hit.

Colour illustrations. Forest trees close to collection site; leaf spot on *Leucopogon* sp., conidioma *in vivo* (scale bar = 150 µm), colony on MEA, conidiogenous cells and conidia (scale bars = 10 µm).

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Elsinoë banksiigena

Fungal Planet 782 – 13 July 2018

Elsinoë banksiigena Crous, *sp. nov.*

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

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

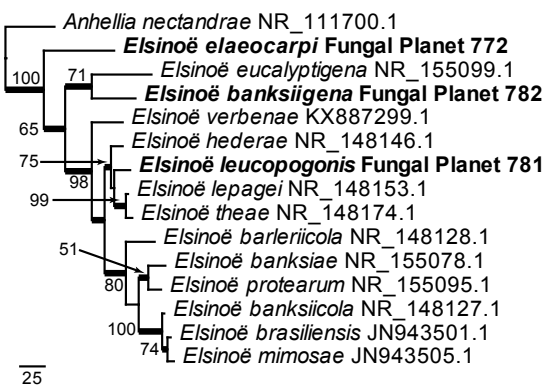
Leaf spots epiphyllous, subcircular to irregular, medium brown, somewhat raised, 1–5 µm diam, surrounded by a diffuse chlorotic border. *Conidiomata* acervular, brown, 30–50 µm diam, prominently breaking through epidermis on leaf surface. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, smooth, ampulliform to doliiform, 3–5 × 3–4 µm. *Conidia* hyaline, smooth, aseptate, guttulate, subcylindrical with obtuse ends, 2–4 × 1.5–2 µm *in vitro* and *in vivo*.

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

Typus. Australia, New South Wales, Seven Mile Beach, on leaves of *Banksia marginata* (*Proteaceae*), 26 Nov. 2016, *P.W. Crous* (holotype CBS H-23563, culture ex-type CPC 32402 = CBS 144440, ITS, LSU, *rpb2* and *tef1* sequences GenBank MH327823.1, MH327859.1, MH327875.1 and MH327886.1, MycoBank MB825438).

Notes — Two species of *Elsinoë* are known from *Banksia*, namely *E. banksiae* (on *B. serrata*) and *E. banksiicola* (on *B. prionotes*). A key to the species occurring on *Proteaceae* was provided by Fan et al. (2017). Phylogenetically, *E. banksiigena* is distinct from all taxa known from *Proteaceae*, being allied to *E. eliocarpiae* (see ITS phylogeny). Although it has been assumed that there was one dominant species of *Elsinoë* infecting various species of *Banksia*, the present study suggests that many more distinct *Elsinoë* spp. could await description.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Elsinoë eucalyptigena* (GenBank NR_155099.1; Identities = 503/591 (85 %), 29 gaps (4 %)), *Elsinoë fawcettii* (GenBank FJ010362.1; Identities = 441/527 (84 %), 30 gaps (5 %)) and *Sphaceloma bidentis* (GenBank KF421115.1; Identities = 516/615 (84 %), 43 gaps (6 %)). Closest hits using the LSU sequence are *Elsinoë quercus-ilicis* (GenBank KX887040.1; Identities = 720/740 (97 %), 4 gaps (0 %)), *Elsinoë eucalyptorum* (GenBank DQ923530.1; Identities = 859/885 (97 %), 4 gaps (0 %)) and *Sphaceloma erythrinae* (GenBank JN940392.1; Identities = 833/861 (97 %), 3 gaps (0 %)). Closest hits using the *rpb2* sequence had highest similarity to *Zalaria obscura* (GenBank KX579108.1; Identities = 492/661 (74 %), 5 gaps (0 %)), *Sarcinomyces crustaceus* (GenBank GU250948.1; Identities = 489/664 (74 %), 3 gaps (0 %)) and *Elsinoë pitangae* (GenBank KX887150.1; Identities = 541/746 (73 %), 11 gaps (1 %)). No significant hits were obtained when the *tef1* sequence was used in BLASTn and megablast searches.



The first of two equally most parsimonious trees obtained from the ITS alignment using PAUP v. 4.0b10 (Swofford 2003; 15 sequences including the ingroup, 522 included characters of which 141 were parsimony-informative). The tree was rooted with *Anhellia nectandrae* (GenBank NR_111700.1). Novel *Elsinoë* species described here are indicated in ***bold italic*** text and their corresponding Fungal Planet numbers are indicated. The scale bar represents the number of changes and parsimony bootstrap support values > 50 % from 1 000 replicates are indicated at the nodes (thickened lines are present in the strict consensus tree).

Colour illustrations. *Banksia marginata* at Seven Mile Beach; leaf spots, colony on MEA, conidioma (*in vivo*) (scale bar = 50 µm), conidiogenous cells and conidia (scale bars = 10 µm).

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Ochroconis musicola

Fungal Planet 783 – 13 July 2018

Ochroconis musicola Crous, *sp. nov.*

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

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

On OA. *Ascomata* occurring in clusters, globose, 50–100 µm diam, brown, surface smooth, lacking appendages; wall of 4–8 layers of brown *textura angularis. Asci* bitunicate, obovoid, 8-spored, with well-defined apical chamber, 2–3 µm diam, 25–40 × 15–18 µm. *Ascospores* fusoid-ellipsoid, guttulate, initially hyaline, but becoming pale brown with age, straight to slightly curved, initially medianly septate, prominently constricted at septum, later developing a septum in each of the two cells, widest just above median septum, encased in a mucoid sheath, up to 3.5 µm diam, (15–)19–22(–26) × (4–)5(–6) µm. Isolates only formed the sexual morph in culture.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium on OA and PDA (abundant on MEA), and even, smooth margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA and PDA surface isabelline, reverse brown vinaceous. On OA surface brown vinaceous.

Typus. Malaysia, on leaves of *Musa* sp. (*Musaceae*), 2010, *P.W. Crous* (holotype CBS H-23562, culture ex-type CPC 32927 = CBS 144441, ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MH327824.1, MH327860.1, MH327876.1, MH327887.1 and MH327898.1, MycoBank MB825439).

Notes — The genus *Ochroconis* was recently revised by Samerpitak et al. (2013), who also linked the first sexual morph to the genus, namely *O. sexualis*. Morphologically, *O. musicola* is quite distinct from *O. sexualis*, as the latter species has ascomata with appendages, and smaller ascospores (8–10 × 2.5–3.5 µm) that lack a mucoid sheath. *Ochroconis musicola* is also phylogenetically distinct and related to *O. constricta*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Ochroconis constricta* (GenBank KX610329.1; Identities = 429/514 (83 %), 39 gaps (7 %)), *Scolecobasidium dendroides* (GenBank FJ914704.1; Identities = 425/512 (83 %), 36 gaps (7 %)) and *Ochroconis dracaenae* (GenBank NR_145404.1; Identities = 422/512 (82 %), 33 gaps (6 %)). Closest hits using the LSU sequence are *Ochroconis podocarpi* (Gen-Bank MG386085.1; Identities = 786/835 (94 %), 6 gaps (0 %)), *Ochroconis macrozamiae* (GenBank KJ869180.1; Identities = 814/866 (94 %), 13 gaps (1 %)) and *Ochroconis musae* (GenBank KT272083.1; Identities = 817/872 (94 %), 8 gaps (0 %)). Closest hits using the *rpb2* sequence had highest similarity to *Ochroconis lascauxensis* (GenBank HE575203.1; Identities = 752/899 (84 %), no gaps), *Scolecobasidium terreum* (GenBank FR832487.1; Identities = 737/887 (83 %), 1 gap (0 %)) and *Mycosisymbrium cirrhosum* (GenBank KR349124.1; Identities = 732/908 (81 %), 2 gaps (0 %)). No significant hits were obtained when the *tef1* and *tub2* sequences were used in BLASTn and megablast searches.

Colour illustrations. Symptomatic leaves of *Musa* sp. in Malaysia; ascomata sporulating on OA (scale bars = 100 µm), asci and ascospores with sheaths (scale bars = 10 µm).

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Didymella cari

Fungal Planet 784 – 13 July 2018

Didymella cari Armstrong-Cho, Banniza & Crous, *sp. nov.*

Etymology. Name refers to *Carum*, one of the host genera from which this fungus was collected.

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

On PDA. *Conidiomata* separate, globose, brown, pycnidial, 200–350 µm diam, with central ostiole; wall of 3–6 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, ampulliform to globose, holoblastic, (9–)12–16 × (9–)12–13 µm. *Conidia* solitary, hyaline, smooth, guttulate, subcylindrical, straight to curved, apex obtuse, base truncate, 2.5–4 µm diam, (0–)1(–2)-septate, (1-septate conidia with septum above median), (8–)21–26(–31) × (4–)6(–7) µm.

Culture characteristics — Colonies covering dish in 2 wk with fluffy to moderate aerial mycelium. On MEA surface sienna, reverse fulvous. On PDA surface pale olivaceous grey to olivaceous grey, reverse iron-grey. On OA surface pale luteous to buff.

Typus. Canada, Saskatchewan, Choiceland, on living flower of *Carum carvi* (*Apiaceae*), 2015, *C. Armstrong-Cho* (holotype CBS H-23594, cultures ex-types CPC 33112 = CBS 144497 = A27, ITS, LSU, *actA* and *tub2* sequences GenBank MH327825.1, MH327861.1, MH327865.1 and MH327899.1, MycoBank MB825440).

Additional material examined. Canada, Saskatchewan, Choiceland, on living flower of *Coriandrum sativum* (*Apiaceae*), 2015, *C. Armstrong-Cho*, CPC 33113 = CBS 144498 = A74, ITS, LSU, *actA* and *tub2* sequences GenBank MH327826.1, MH327862.1, MH327866.1 and MH327900.1; Lemberg, on living flower of *Carum carvi*, 2015, *C. Armstrong-Cho*, CPC 33114 = CBS 144499 = A122F, ITS, LSU and *tub2* sequences GenBank MH327827.1, MH327863.1 and MH327901.1; Lorlie, on living stem of *Carum carvi*, 2016, *C. Armstrong-Cho*, CPC 33115 = CBS 144500 = A355, ITS sequence GenBank MH327828.1.

Colour illustrations. Coriander blossom blight; sporulation on caraway blossom (scale bar = 1 mm), conidia, and conidiogenous cells (right) (scale bars = 10 µm).

Notes — *Didymella cari* was isolated from blossom blight symptoms on coriander and caraway in Western Canada. Pathogenicity trials on coriander and caraway flowers showed that the isolates were pathogenic on both substrates. Phoma-like species reported from these hosts in the past include *Subplenodomus apiicola* from Brazil, *Phoma exigua* var. *exigua* from Poland and *Phoma multirostrata* from Australia (Mendes et al. 1998, Machowicz-Stefaniak et al. 2008, Golzar et al. 2015), which are clearly distinct based on their morphology (Boerema et al. 2004). Another taxon to consider is *Ascochyta carvi* (on leaves, stems and seeds of *Carum carvi* occurring in the former Czechoslovakia), although conidia of the latter species are significantly smaller, 0–1(–2)-septate, (6–)8–12(–14) × 2.5–4.5 µm (Ondrej 1983).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence of CPC 33112 had highest similarity to *Didymella macrostoma* (GenBank KY367515.2; Identities = 478/485 (99 %), no gaps) and *D. glomerata* (GenBank KT223334.1; Identities = 478/485 (99 %), no gaps), from which *D. cari* can easily be distinguished based on its conidial dimensions (Chen et al. 2015, 2017). The ITS sequences of CPC 33112–33115 were identical, but that of CPC 33114 differed with one nucleotide from the rest. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence of CPC 33112 had highest similarity to *D. macrostoma* (GenBank GU238096.1; Identities = 1 226/1 230 (99 %), 2 gaps (0 %)) and *D. tanaceti* (GenBank KT287040.1; Identities = 1 225/1 230 (99 %), 2 gaps (0 %)), *D. rosea* (GenBank KT287017.1; Identities = 1 225/1 230 (99 %), 2 gaps (0 %)). Except for two nucleotide changes, the LSU sequences of CPC 33112–33114 were identical. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the *actA* sequence of CPC 33112 had highest similarity to *D. macrostoma* (GenBank KT309303.2; Identities = 210/238 (88 %), 2 gaps (0 %)), *D. tanaceti* (GenBank KT286999.1; Identities = 206/237 (87 %), no gaps) and *D. pedeiae* (GenBank KT309272.2; Identities = 206/237 (87 %), no gaps). The *actA* sequences of CPC 33112 and CPC 33113 were identical. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the *tub2* sequence of CPC 33112 had highest similarity to *D. negriana* (GenBank KY632664.1; Identities = 279/300 (93 %), no gaps), *Stagonosporopsis heliopsidis* (GenBank KX928776.1; Identities = 277/298 (93 %), no gaps) and *Phoma adonidicola* (GenBank JQ934842.1; Identities = 275/296 (93 %), no gaps). The *tub2* sequences of CPC 33112–33114 were identical.

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