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RESEARCH ARTICLE

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Key words

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Abstract Novel species of fungi described in this study include those from various countries as follows: **Angola**, *Gnomoniopsis angolensis* and *Pseudopithomyces angolensis* on unknown host plants. **Australia**, *Dothiora corymbiae* on *Corymbia citriodora, Neoeucasphaeria eucalypti* (incl. *Neoeucasphaeria* gen. nov.) on *Eucalyptus* sp., *Fumagopsis stellae* on *Eucalyptus* sp., *Fusculina eucalyptorum* (incl. *Fusculinaceae* fam. nov.) on *Eucalyptus socialis, Harknessia corymbiicola* on *Corymbia maculata, Neocelosporium eucalypti* (incl. *Neocelosporium* gen. nov., *Neocelosporiaceae* fam. nov. and *Neocelosporiales* ord. nov.) on *Eucalyptus cyanophylla, Neophaeomoniella corymbiae* on *Corymbia citriodora*, *Neophaeomoniella eucalyptigena* on *Eucalyptus pilularis, Pseudoplagiostoma corymbiicola* on *Corymbia citriodora, Teratosphaeria gracilis* on *Eucalyptus gracilis, Zasmidium corymbiae* on *Corymbia citriodora.* **Brazil**, *Calonectria hemileiae* on pustules of *Hemileia vastatrix* formed on leaves of *Coffea arabica*, *Calvatia caatinguensis* on soil, *Cercospora solani-betacei* on *Solanum betaceum*, *Clathrus natalensis* on soil, *Diaporthe poincianellae* on *Poincianella pyramidalis*, *Geastrum piquiriunense* on soil, *Geosmithia carolliae* on wing of *Carollia perspicillata*, *Henningsia resupinata* on wood, *Penicillium guaibinense* from soil, *Periconia caespitosa* from leaf litter, *Pseudocercospora styracina* on *Styrax* sp., *Simplicillium filiforme* as endophyte from *Citrullus lanatus*, *Thozetella pindobacuensis* on leaf litter, *Xenosonderhenia coussapoae* on *Coussapoa floccosa.* **Canary Islands (Spain)**, *Orbilia amarilla* on *Euphorbia canariensis.* **Cape Verde Islands**, *Xylodon jacobaeus* on *Eucalyptus camaldulensis.* **Chile**, *Colletotrichum arboricola* on *Fuchsia magellanica.* **Costa Rica**, *Lasiosphaeria miniovina* on tree branch. **Ecuador**, *Ganoderma chocoense* on tree trunk. **France**, *Neofitzroyomyces nerii* (incl. *Neofitzroyomyces* gen. nov.) on *Nerium oleander.* **Ghana**, *Castanediella tereticornis* on *Eucalyptus tereticornis*, *Falcocladium africanum* on *Eucalyptus brassiana*, *Rachicladosporium corymbiae* on *Corymbia citriodora.* **Hungary**, *Entoloma silvae-frondosae* in *Carpinus betulus-Pinus sylvestris* mixed forest. **Iran**, *Pseudopyricularia persiana* on *Cyperus* sp. **Italy**, *Inocybe roseascens* on soil in mixed forest. **Laos**, *Ophiocordyceps houaynhangensis* on *Coleoptera* larva. **Malaysia**, *Monilochaetes melastomae* on *Melastoma* sp. **Mexico**, *Absidia terrestris* from soil. **Netherlands**, *Acaulium pannemaniae*, *Conioscypha boutwelliae*, *Fusicolla septimanifiniscientiae*, *Gibellulopsis simonii*, *Lasionectria hilhorstii*, *Lectera nordwiniana, Leptodiscella rintelii, Parasarocladium debruynii* and *Sarocladium dejongiae* (incl. *Sarocladiaceae* fam. nov.) from soil. **New Zealand**, *Gnomoniopsis rosae* on *Rosa* sp. and *Neodevriesia metrosideri* on *Metrosideros* sp. **Puerto Rico**, *Neodevriesia coccolobae* on *Coccoloba uvifera*, *Neodevriesia tabebuiae* and *Alfaria tabebuiae* on *Tabebuia chrysantha*. **Russia**, *Amanita paludosa* on bogged soil in mixed deciduous forest, *Entoloma tiliae* in forest of *Tilia* × *europaea*, *Kwoniella endophytica* on *Pyrus communis.* **South Africa**, *Coniella diospyri* on *Diospyros mespiliformis, Neomelanconiella combreti* (incl. *Neomelanconiellaceae*

Abstract (cont.)

fam. nov. and *Neomelanconiella* gen. nov.) on *Combretum* sp., *Polyphialoseptoria natalensis* on unidentified plant host, *Pseudorobillarda bolusanthi* on *Bolusanthus speciosus*, *Thelonectria pelargonii* on *Pelargonium* sp. **Spain**, *Vermiculariopsiella lauracearum* and *Anungitopsis lauri* on *Laurus novocanariensis*, *Geosmithia xerotolerans* from a darkened wall of a house, *Pseudopenidiella gallaica* on leaf litter. **Thailand**, *Corynespora thailandica* on wood, *Lareunionomyces loeiensis* on leaf litter, *Neocochlearomyces chromolaenae* (incl. *Neocochlearomyces* gen. nov.) on *Chromolaena odorata, Neomyrmecridium septatum* (incl. *Neomyrmecridium* gen. nov.), *Pararamichloridium caricicola* on *Carex* sp., *Xenodactylaria thailandica* (incl. *Xenodactylariaceae* fam. nov. and *Xenodactylaria* gen. nov.), *Neomyrmecridium asiaticum* and *Cymostachys thailandica* from unidentified vine. **USA**, *Carolinigaster bonitoi* (incl. *Carolinigaster* gen. nov.) from soil, *Penicillium fortuitum* from house dust, *Phaeotheca shathenatiana* (incl. *Phaeothecaceae* fam. nov.) from twig and cone litter, *Pythium wohlseniorum* from stream water, *Superstratomyces tardicrescens* from human eye, *Talaromyces iowaense* from office air. **Vietnam**, *Fistulinella olivaceoalba* on soil. Morphological and culture characteristics along with DNA barcodes are provided.

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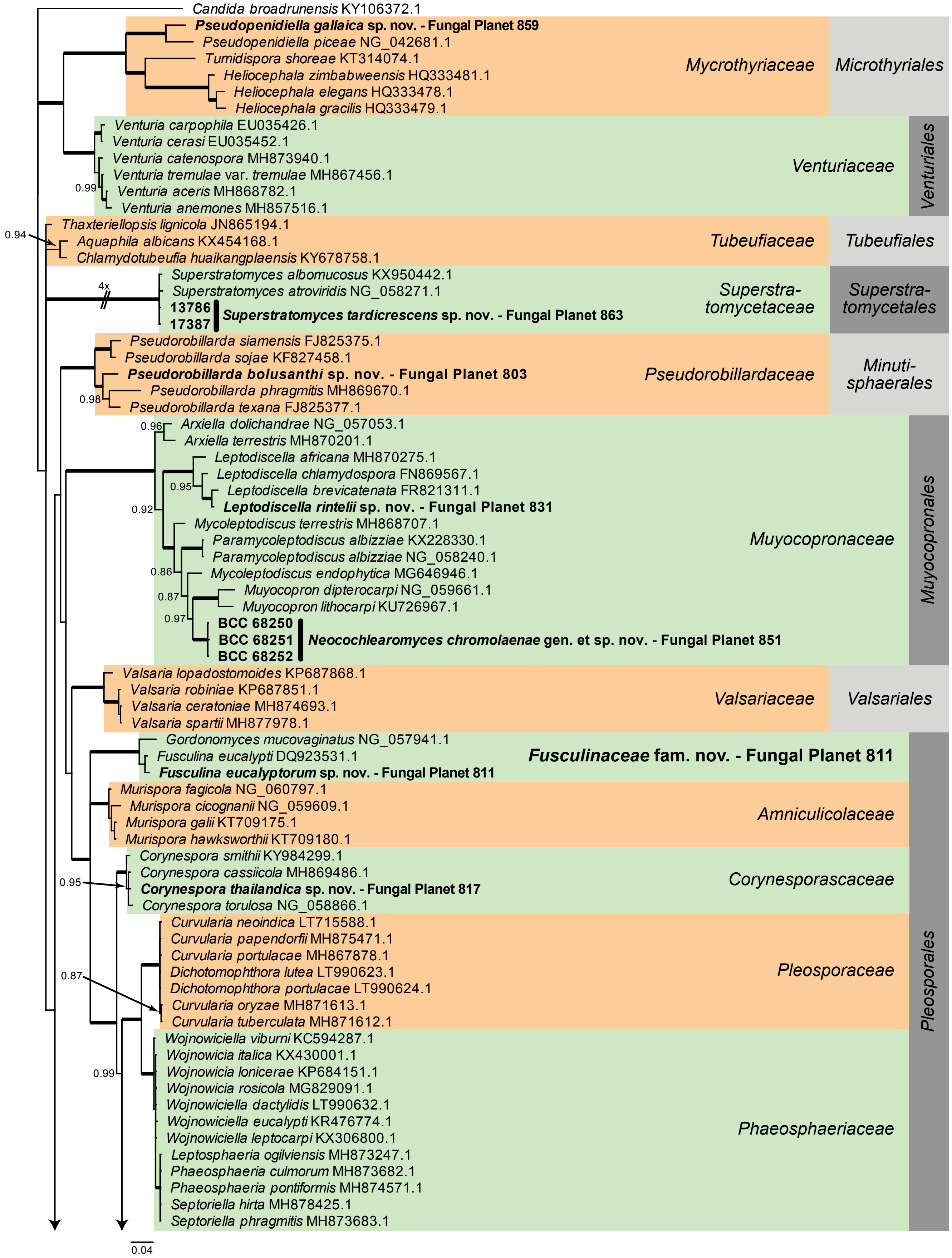
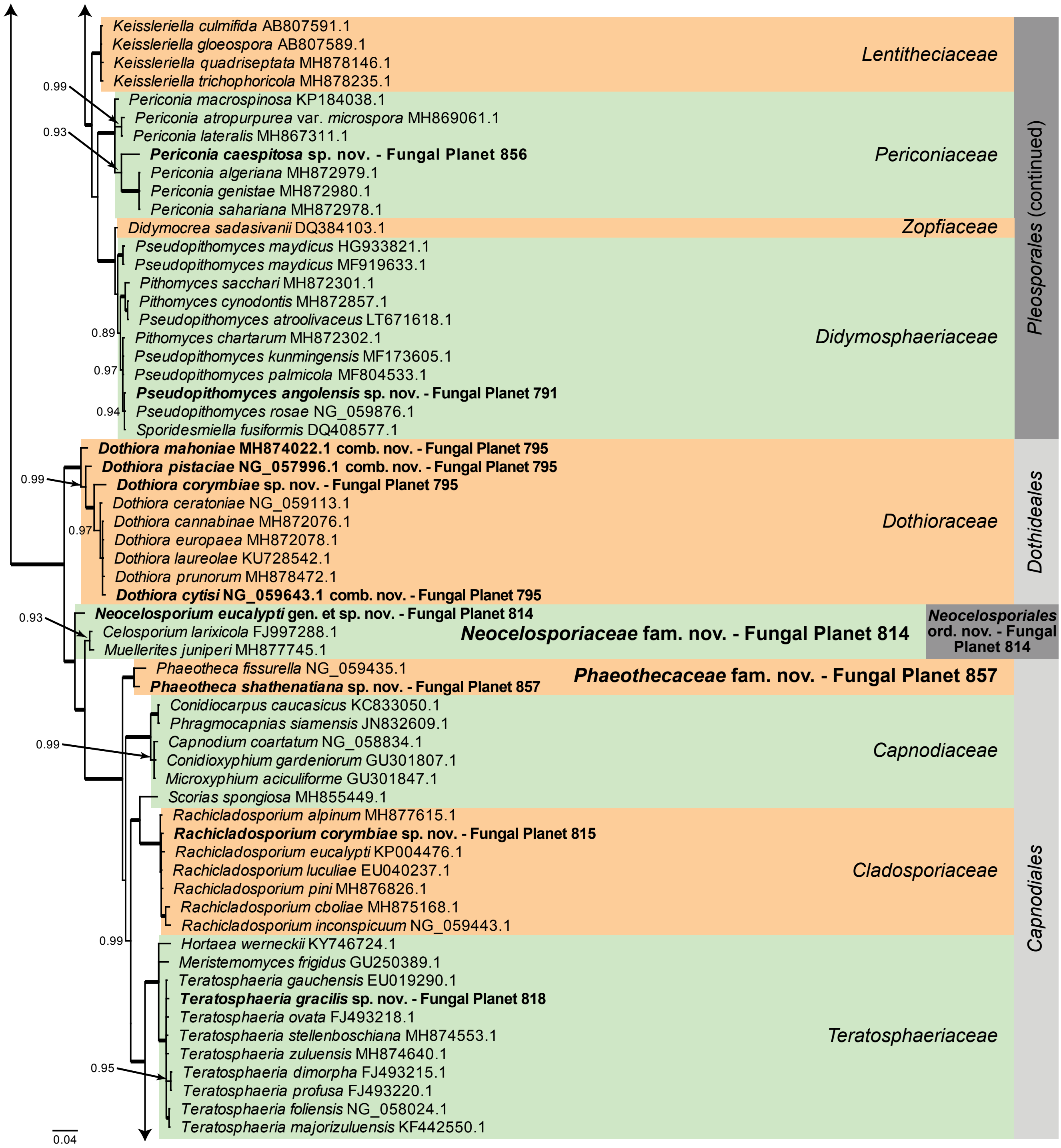
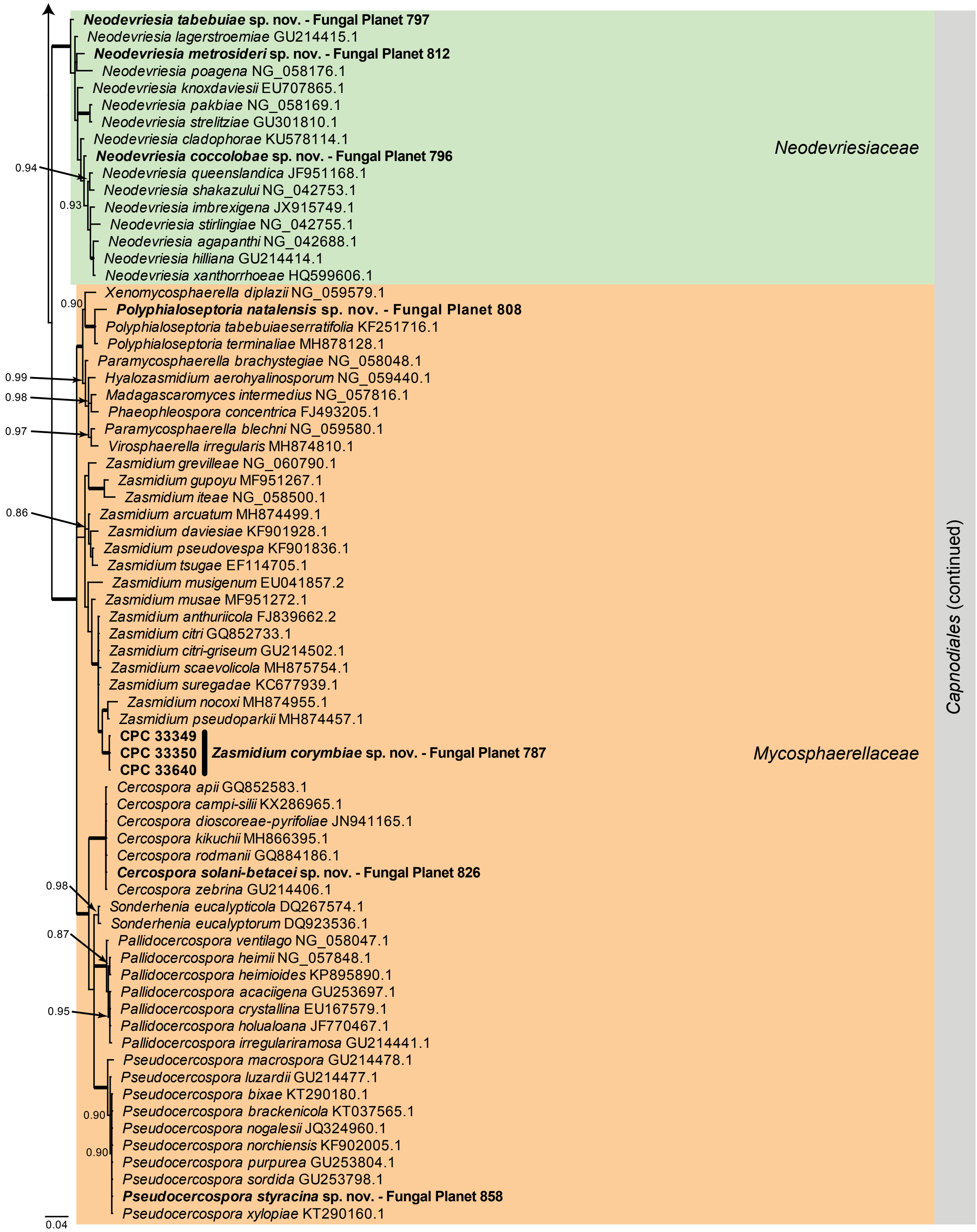


Overview *Dothideomycetes* phylogeny – part 1

Consensus phylogram (50 % majority rule) of 2478 trees resulting from a Bayesian analysis of the LSU sequence alignment (206 taxa including outgroup; 801 aligned positions; 464 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 S23436).



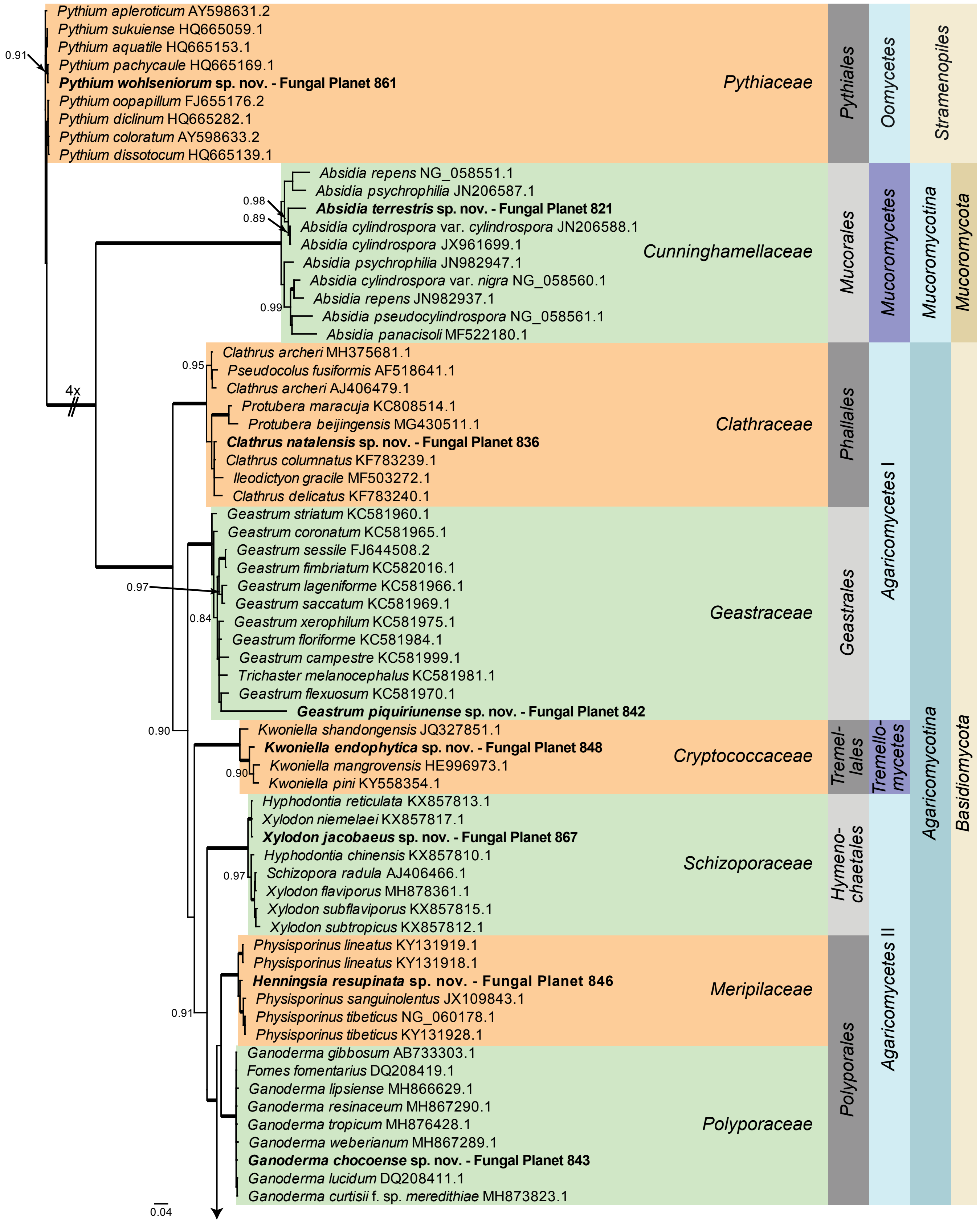
Overview *Dothideomycetes* phylogeny (cont.) – part 2



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

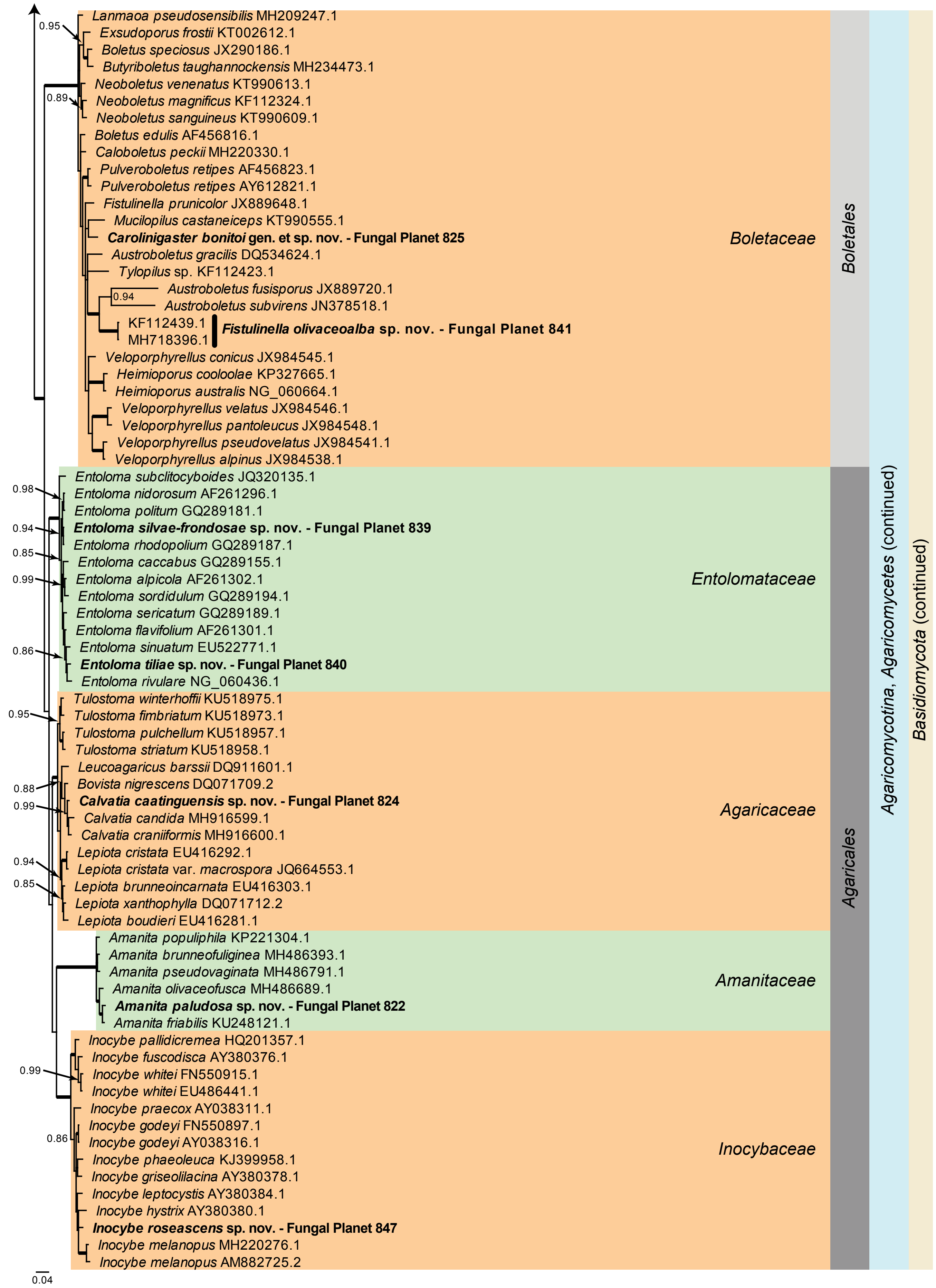
Overview *Orbiliomycetes*, *Leotiomycetes*, *Lecanoromycetes* and *Eurotiomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 12 452 trees resulting from a Bayesian analysis of the LSU sequence alignment (78 taxa including outgroup; 829 aligned positions; 360 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 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 S23436).

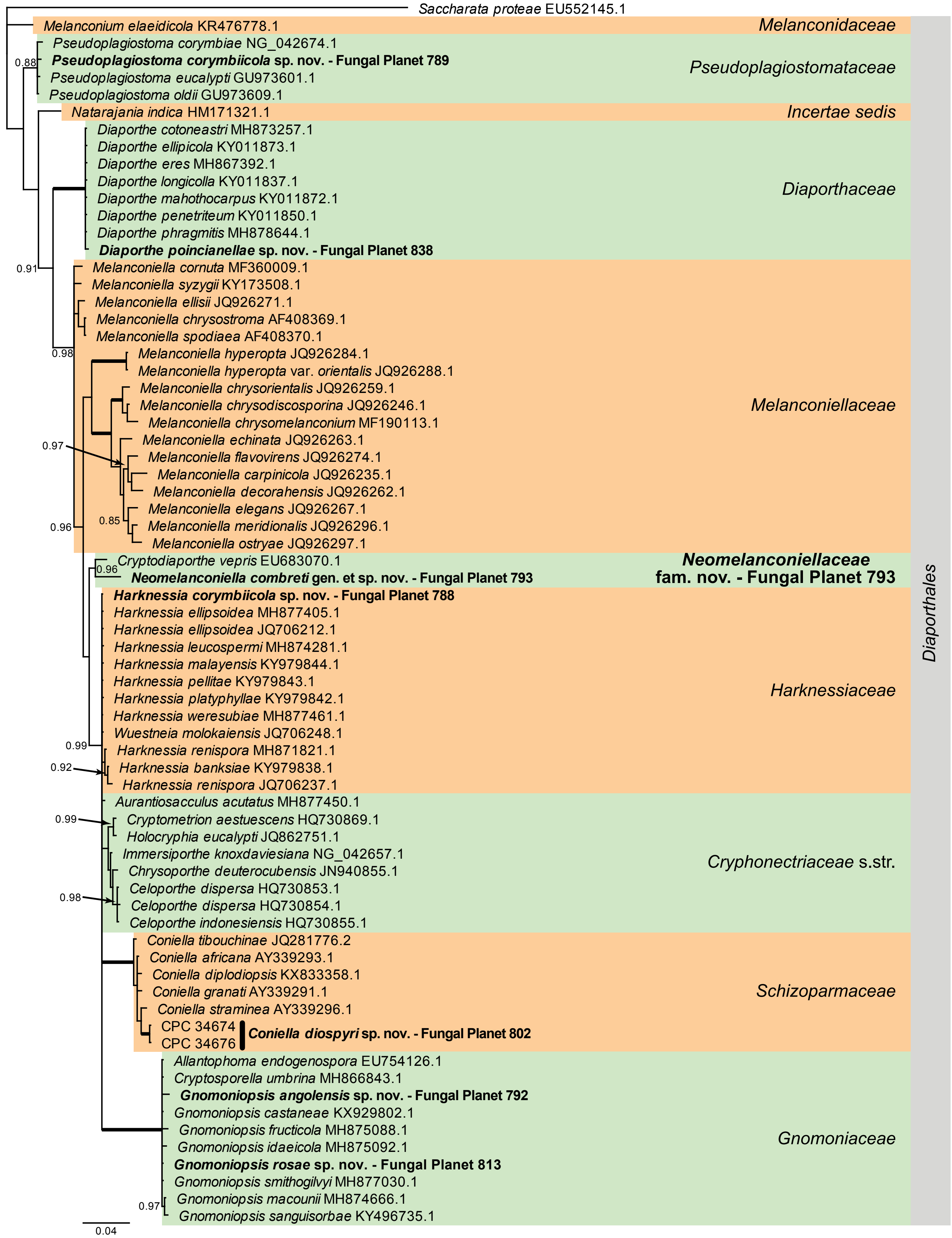


Overview *Stramenopiles*, *Mucoromycota* and *Basidiomycota* phylogeny – part 1

Consensus phylogram (50 % majority rule) of 113 852 trees resulting from a Bayesian analysis of the LSU sequence alignment (141 taxa including outgroup; 980 aligned positions; 654 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 the *Stramenopiles* clade 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 S23436).

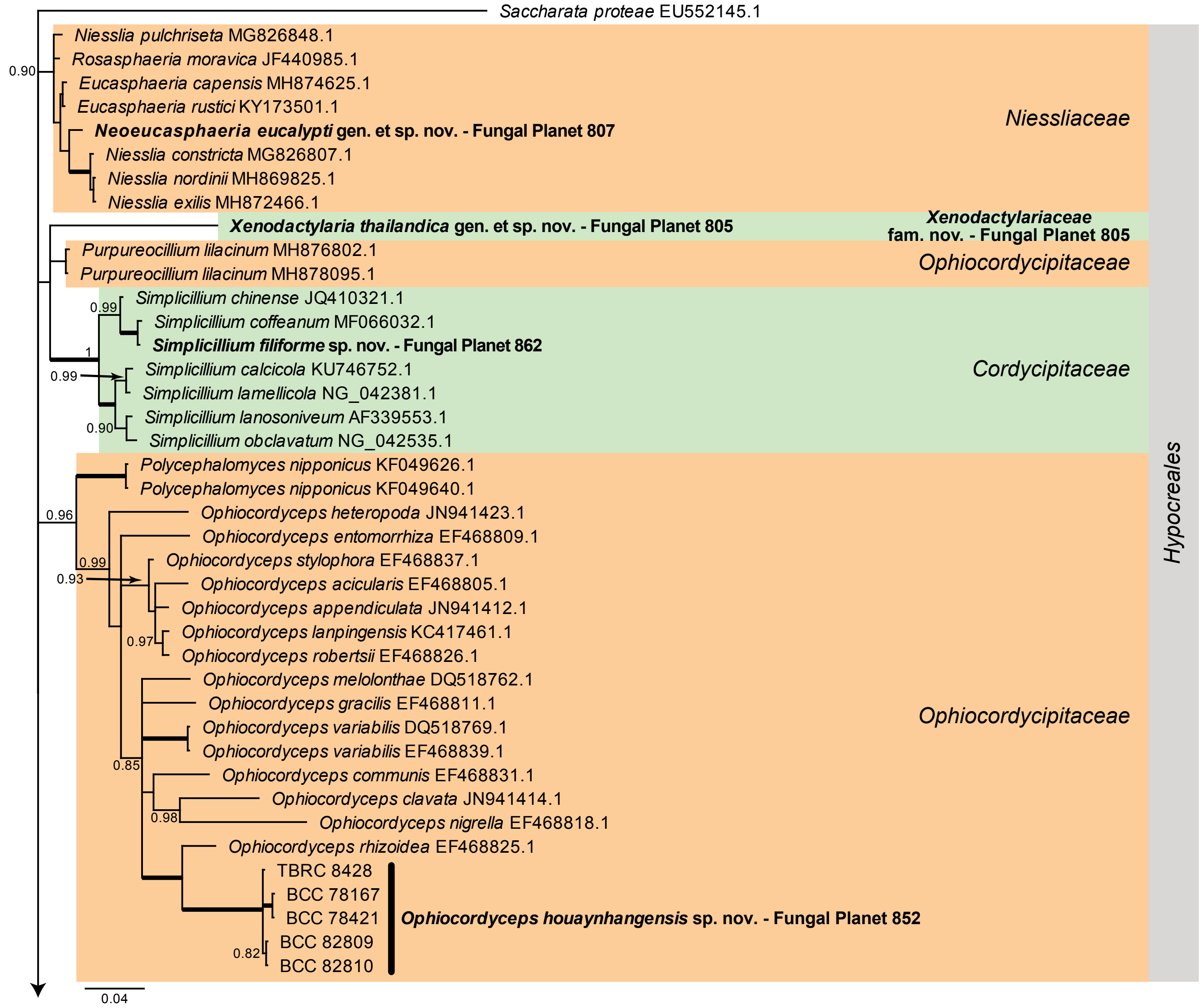


Overview *Stramenopiles*, *Mucoromycota* and *Basidiomycota* phylogeny (cont.) – part 2



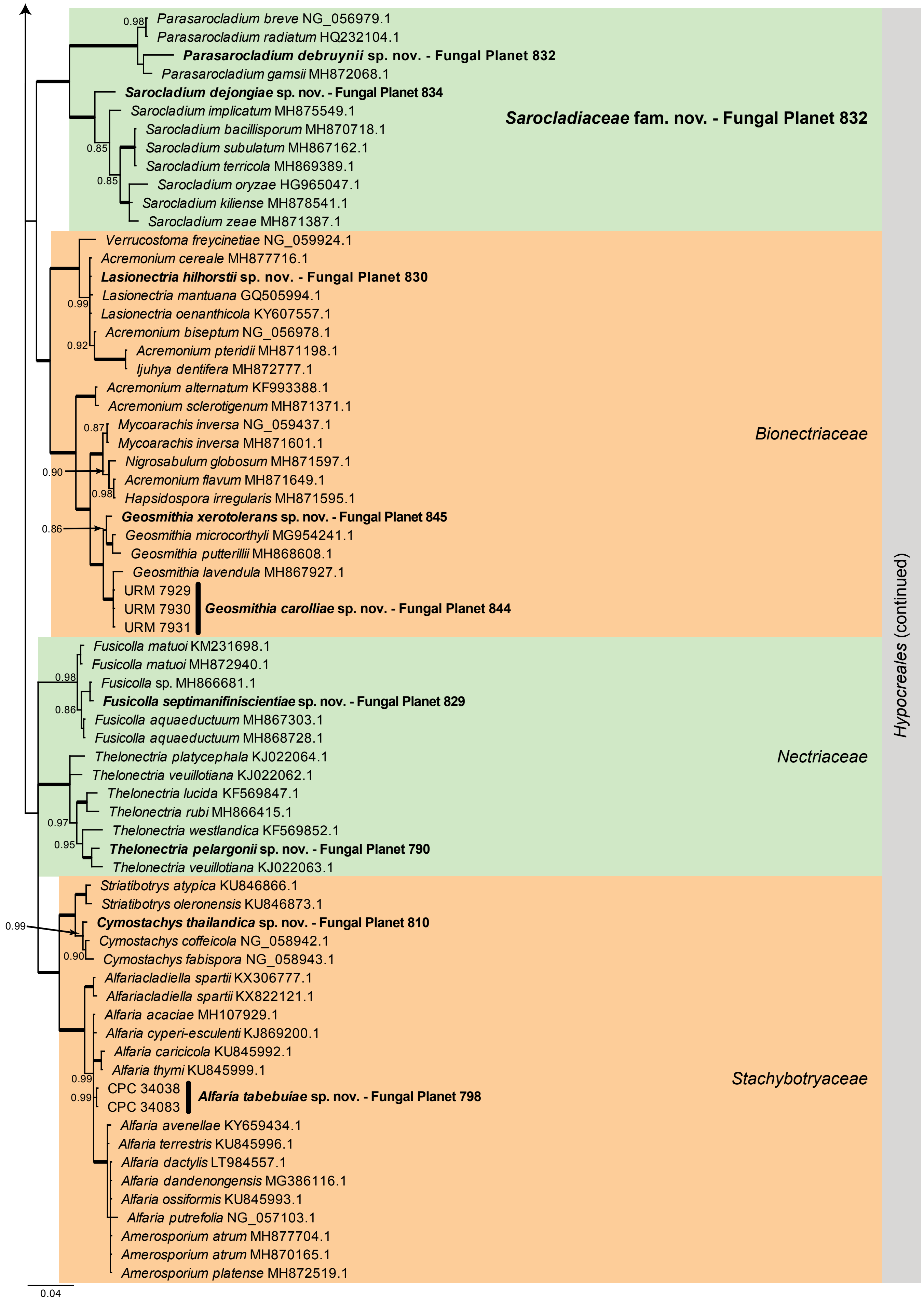
Overview *Diaporthales* (*Sordariomycetes*) phylogeny

Consensus phylogram (50 % majority rule) of 1052 trees resulting from a Bayesian analysis of the LSU sequence alignment (71 taxa including outgroup; 768 aligned positions; 176 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 S23436).

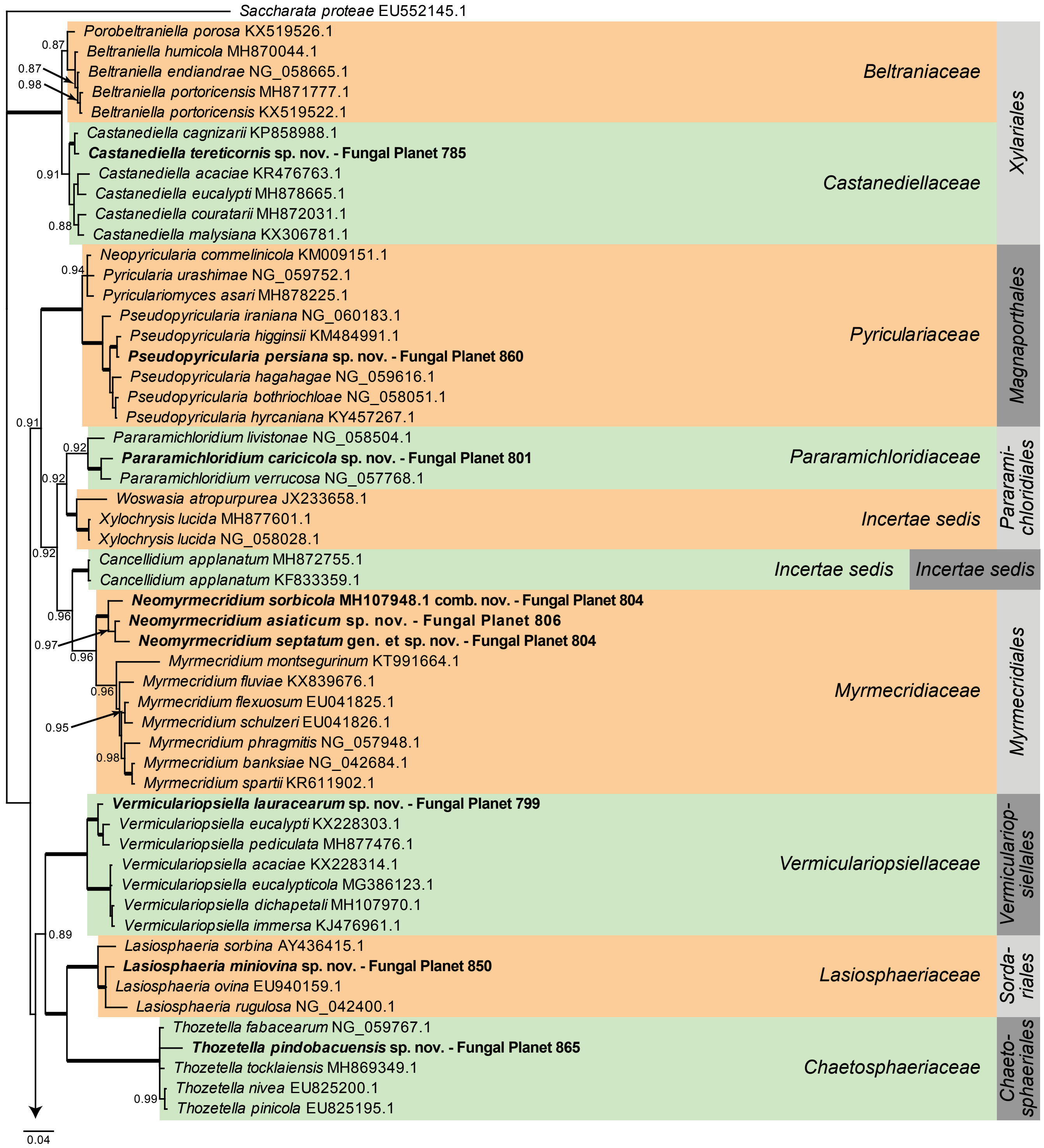


Overview *Hypocreales* (*Sordariomycetes*) phylogeny – part 1

Consensus phylogram (50 % majority rule) of 3078 trees resulting from a Bayesian analysis of the LSU sequence alignment (110 taxa including outgroup; 820 aligned positions; 339 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 S23436).

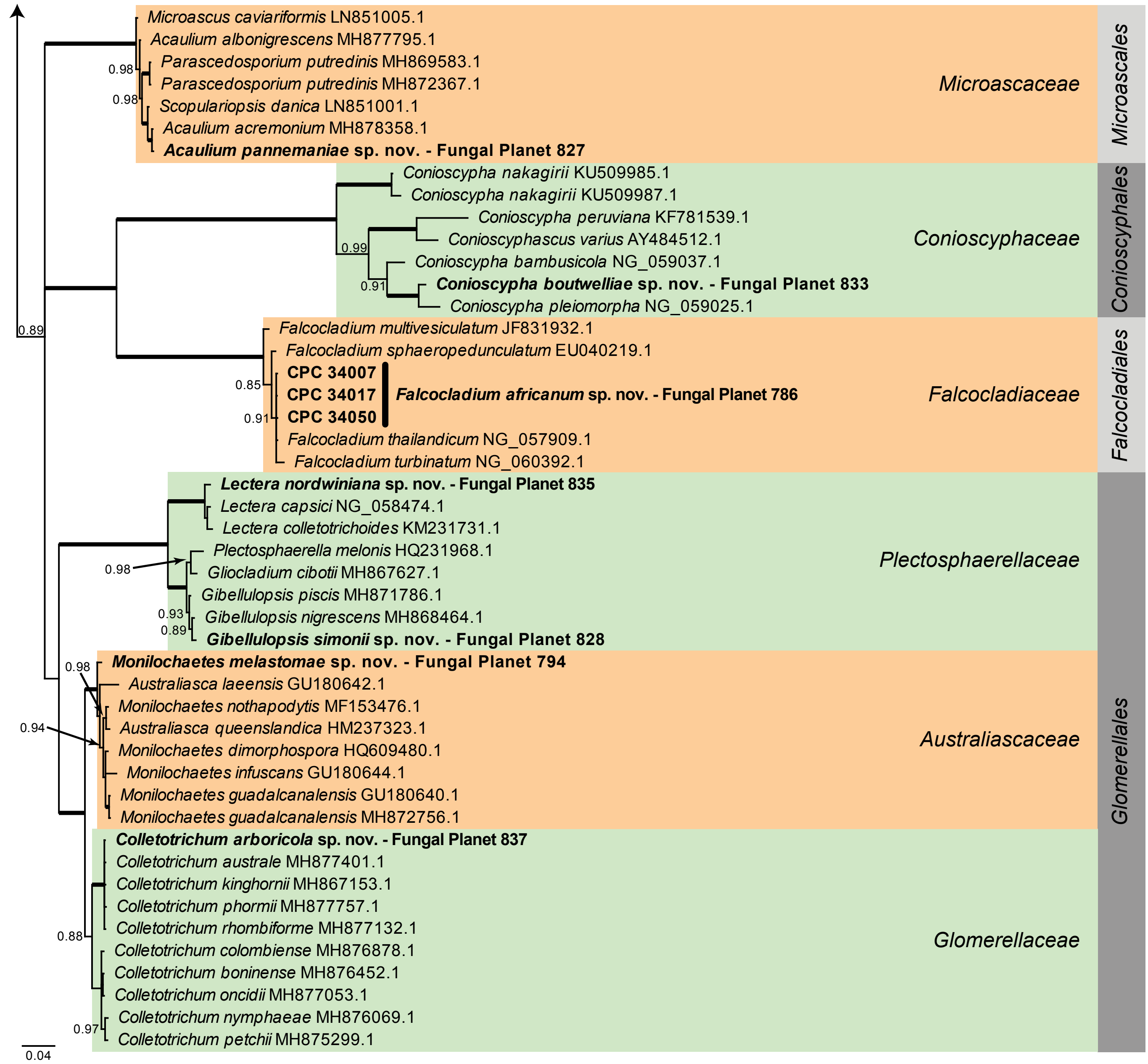


Overview *Hypocreales* (*Sordariomycetes*) phylogeny (cont.) – part 2

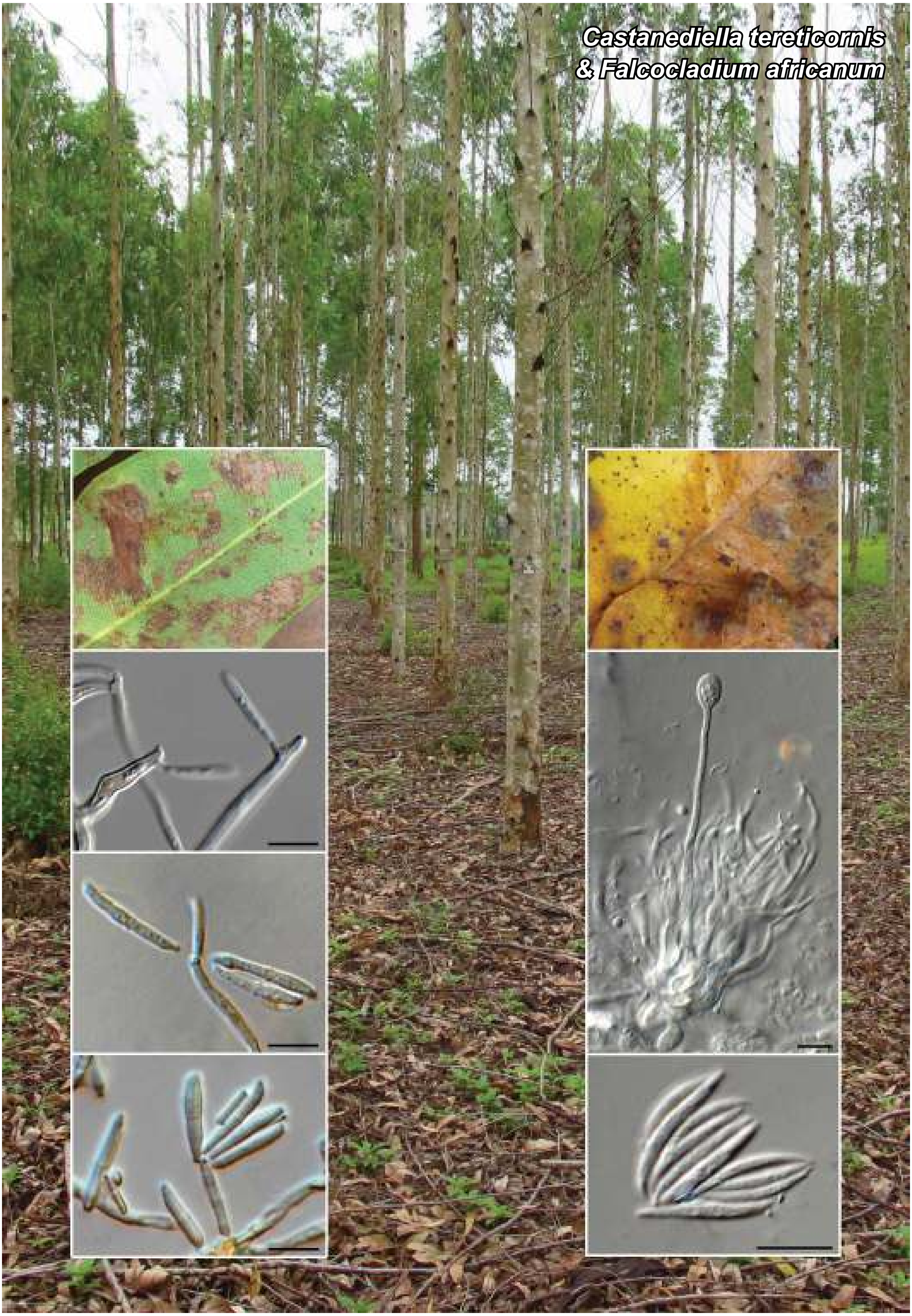


Overview other orders (*Sordariomycetes*) phylogeny – part 1

Consensus phylogram (50 % majority rule) of 452 trees resulting from a Bayesian analysis of the LSU sequence alignment (102 taxa including outgroup; 782 aligned positions; 396 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 S23436).



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


Castanediella tereticornis
& Falcocladium africanum

Fungal Planet 785 & 786 – 14 December 2018

Castanediella tereticornis Crous, *sp. nov.*

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

Classification — *Castanediellaceae*, *Xylariales*, *Sordariomycetes.*

Mycelium consisting of olivaceous, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* solitary, erect, pale brown, smooth, subcylindrical, unbranched, 0–2-septate, 5–30 × 2–3 µm. *Conidiogenous cells* integrated, terminal, subcylindrical, pale brown, smooth, 5–20 × 2–3 µm, apex at times slightly swollen, with several denticulate loci, 0.5–2 × 1–1.5 µm, unthickened, not darkened. *Conidia* solitary, aggregating in slimy mass, hyaline, smooth, 1-septate, subcylindrical, straight, inner plane flat, outer plane convex, apex acutely rounded, tapering to flat inner plane, base truncate, 0.5–1 µm diam, tapering toward inner flat plane, (16–)17–20(–22) × 2(–2.5) µm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface isabelline with diffuse red pigment, reverse dark brick; on PDA surface and reverse isabelline; on OA surface sepia.

Typus. Ghana, on leaves of *Eucalyptus tereticornis* (*Myrtaceae*), 21 June 2010, *M.J. Wingfield*, HPC 2175 (holotype CBS H-23765, culture ex-type CPC 34027 = CBS 145068, ITS and LSU sequences GenBank MK047417.1 and MK047468.1, MycoBank MB828165).

Notes — *Castanediella* was introduced for idriella-like fungi, distinguished by having branched conidiophores giving rise to straight or slightly curved conidia (Crous et al. 2015b, 2017b, Hernández-Restrepo et al. 2016, 2017). *Castanediella tereticornis* is phylogenetically distinct from the 12 species presently accepted in the genus, all of which are known from DNA sequence data.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Castanediella cagnizarii* (GenBank NR_156294.1; Identities = 543/555 (98 %), 6 gaps (1 %)), *Castanediella hyalopenicillata* (GenBank NR_156309.1; Identities = 491/504 (97 %), 5 gaps (0 %)) and *Pidoplitchkoviella terricola* (GenBank MH861046.1; Identities = 457/498 (92 %), 8 gaps (1 %)).

Falcocladium africanum Crous, *sp. nov.*

Etymology. Name refers to Africa, the continent where this fungus was collected.

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

Conidiophores penicillate, mostly synnematal, becoming sporodochial in older cultures, arising from superficial mycelium; stipe extensions hyaline, numerous per conidiophore, aseptate, thick-walled, 25–50 × 1.5–2.5 µm, arising from various positions in the conidiophore, terminating in vesicles that are sphaeropedunculate, to having lateral walls slightly flattened or even constricted, 4(–6) µm diam. *Conidiophore branches* primary branches hyaline, smooth, subcylindrical, 0–1-septate, 5–10 × 2–3 µm; secondary and tertiary branches hyaline, aseptate, 7–10 × 2–3 µm. *Conidiogenous cells* phialidic, in whorls of 2–6, ampulliform with elongated necks and periclinal thickening and minute collarettes, 7–11 × 2–3 µm. *Conidia* hyaline, smooth, 0–1-septate, falcate with a short, acute, thick-walled apical beak, and a basal appendage, (12–)15–18(–20) × 2(–2.5) µm; basal appendages exogenous on inner, shorter curve, 1.5–2 µm long, terminating in a rounded end; apical beak continuous with conidium body, 1.5–2 µm long.

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

Colour illustrations. *Eucalyptus tereticornis* plantation; Left column, *Castanediella tereticornis*, symptomatic leaf, conidiogenous cells and conidia. Right column, *Falcocladium africanum*, symptomatic leaf, conidiophore with stipe extension, vesicle and conidiogenous cells, and conidia. Scale bars = 10 µm.

Typus. Ghana, on leaves of *Eucalyptus brassiana* (*Myrtaceae*), June 2010, *M.J. Wingfield*, HPC 2177 (holotype CBS H-23787, culture ex-type CPC 34050 = CBS 145045, ITS, LSU, *actA* and *rpb2* sequences GenBank MK047418.1, MK047469.1, MK047518.1 and MK047532.1, MycoBank MB828166).

Additional materials examined. Sierra Leone, on leaves of *Eucalyptus tereticornis*, June 2010, *M.J. Wingfield*, HPC 2169, CPC 34017 = CBS 145046, ITS, LSU, *actA* and *rpb2* sequences GenBank MK047419.1, MK047470.1, MK047519.1 and MK047533.1; on leaves of *Eucalyptus brassiana* (*Myrtaceae*), June 2010, *M.J. Wingfield*, HPC 2166, CPC 34007, ITS and LSU sequences GenBank MK047420.1 and MK047471.1.

Notes — *Falcocladium* represents a genus of hyphomycetes associated with leaf litter, or considered to be weak foliar pathogens of *Eucalyptus* (Crous et al. 1994, 1997). Four species are presently known in the genus, having been collected on eucalypt leaves in Asia, Australia and South America. *Falcocladium africanum* represents the first species described from Africa, and differs from *F. thailandicum* (sphaeropedunculate vesicles, 6–7 µm diam, aseptate conidia, (19–)20–23(–24) × 1.5(–2) µm; Crous et al. 2007b) in vesicle shape, and having smaller, 0–1-septate conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 34050 had highest similarity to *Falcocladium thailandicum* (GenBank NR_156241.1; Identities = 638/656 (97 %), 6 gaps (0 %)), *Falcocladium sphaeropedunculatum* (GenBank EU040220.1; Identities = 567/661 (86 %), 43 gaps (6 %)) and *Falcocladium multivesiculatum* (GenBank JF831936.1; Identities = 420/466 (90 %), 15 gaps (3 %)). The ITS sequences of CPC 34007, 34017 and 34050 are identical. Closest hits using the ***rpb2*** sequence of CPC 34050 had only distant hits with *Fusarium* species (less than 80 % sequence similarity). The *rpb2* sequences of CPC 34017 and 34050 are identical as no other *rpb2* sequences are available for *Falcocladium* species.

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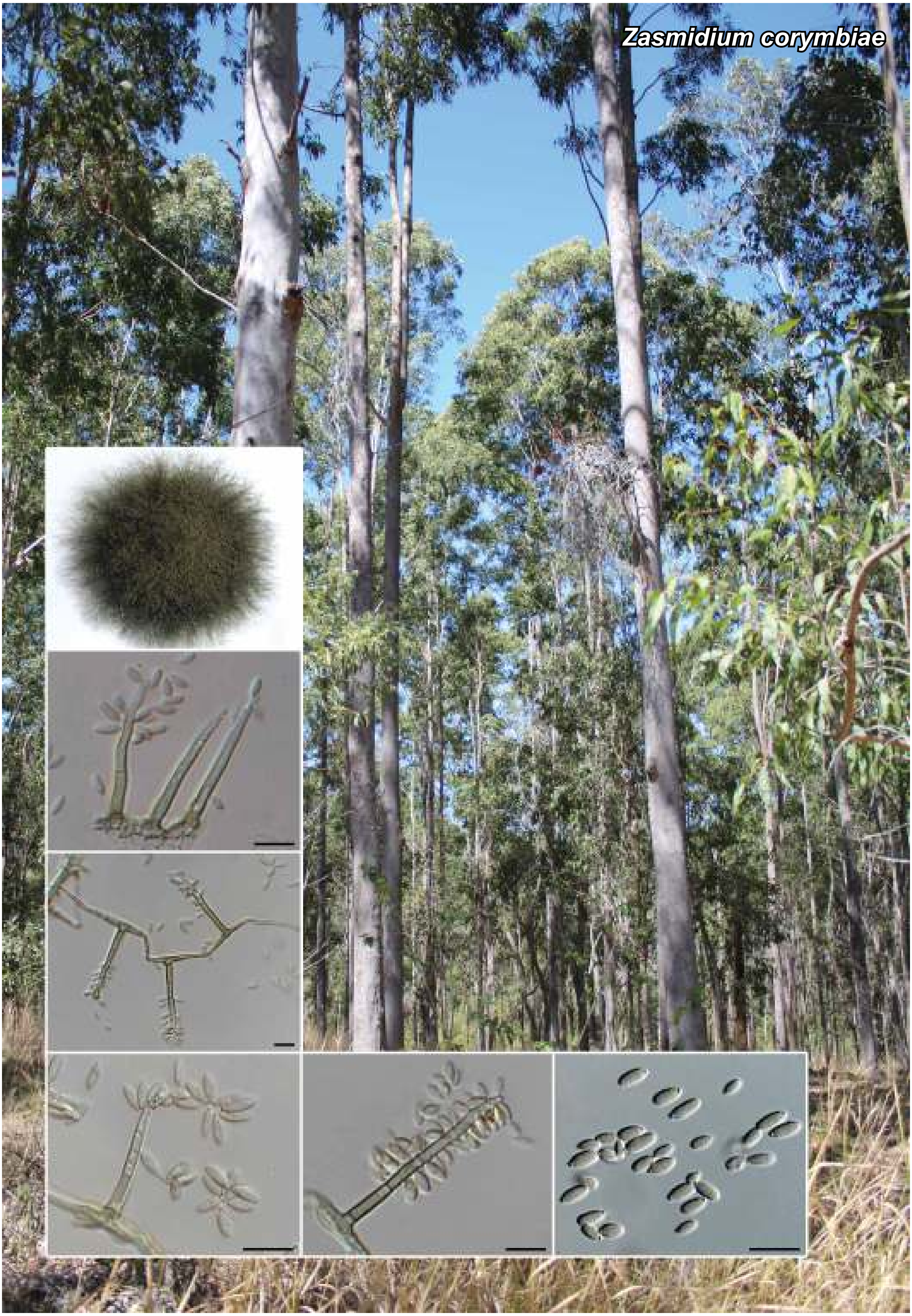
Zasmidium corymbiae

Fungal Planet 787 – 14 December 2018

Zasmidium corymbiae Crous, *sp. nov.*

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

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

Submerged hyphae smooth, hyaline, thin-walled, 2.5–3 µm wide; *aerial hyphae* pale brown, verrucose, 3–4 µm diam, encased in mucoid layer. *Conidiophores* arising vertically from creeping aerial hyphae, brown, verruculose, thick-walled, 1–4-septate, 30–60 × 3–4 µm. *Conidiogenous cells* integrated, terminal, cylindrical, with slight apical taper, 10–20 × 0.5–2 µm long, pale brown, proliferating sympodially, forming a rachis with slightly thickened and darkened, circular, somewhat protruding scars, c. 0.5 µm diam. *Conidia* solitary, aseptate, finely roughened, pale brown, oblong to ellipsoidal, (4–)5–6(–7) × (2–)2.5(–3) µm, with obtuse apex and truncate unthickened, non-pigmented base.

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

Typus. Australia, New South Wales, Jackadgery, Inglebar Plantation, on leaves of *Corymbia citriodora* (*Myrtaceae*), 18 Mar. 2015, *A.J. Carnegie*, HPC 2031 (holotype CBS H-23751, culture ex-type CPC 33349 = CBS 145047, ITS, LSU, *actA*, *cmdA*, *rpb2* and *tef1* sequences GenBank MK047421.1, MK047472.1, MK047520.1, MK047524.1, MK047534.1 and MK047555.1, MycoBank MB828167).

Additional material examined. Australia, New South Wales, Jackadgery, Inglebar Plantation, on leaves of *C. citriodora*, 18 Mar. 2015, *A.J. Carnegie*, CPC 33350 = CBS 145048, ITS, LSU, *actA*, *cmdA*, *rpb2* and *tef1* sequences GenBank MK047422.1, MK047473.1, MK047521.1, MK047525.1, MK047535.1 and MK047556.1; ibid., CPC 33640 = CBS 145049, ITS, LSU, *actA*, *cmdA*, *rpb2* and *tef1* sequences GenBank MK047423.1, MK047474.1, MK047522.1, MK047526.1, MK047536.1 and MK047557.1.

Colour illustrations. *Corymbia citriodora* plantation in Australia; colony on potato dextrose agar, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — *Zasmidium* and allied genera (*Periconiella*, ramichloridium-like, rasutoria-like, stenella-like, *Verrucisporota*) were recently revised by Videira et al. (2017), who presented an emended, wider circumscription of *Zasmidium* than that previously accepted by Braun et al. (2013). Several species are known to be associated with leaf spots on *Eucalyptus*, which are allied, but phylogenetically distinct from *Z. corymbiae*, which is more ramichloridium-like in morphology, having a terminal rachis on its conidiogenous cells, and aseptate conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 33349 had highest similarity to *Zasmidium strelitziae* (GenBank NR_156514.1; Identities = 509/543 (94 %), 13 gaps (2 %)), *Zasmidium commune* (GenBank KY979762.1; Identities = 503/542 (93 %), 10 gaps (1 %)) and *Zasmidium pseudovespa* (GenBank NR_137548.1; Identities = 473/513 (92 %), 10 gaps (1 %)). The ITS sequences of CPC 33349, 33350 and 33640 are identical. Closest hits using the **LSU** sequence of CPC 33349 are *Zasmidium anthuriicola* (GenBank FJ839662.2; Identities = 831/846 (98 %), 2 gaps (0 %)), *Zasmidium citri* (GenBank GQ852733.1; Identities = 830/845 (98 %), 2 gaps (0 %)) and *Zasmidium citri-griseum* (GenBank KP895903.1; Identities = 823/838 (98 %), 2 gaps (0 %)). The LSU sequences of CPC 33349, 33350 and 33640 are identical. Closest hits using the ***actA*** sequence of CPC 33349 had highest similarity to *Zasmidium commune* (GenBank KY979857.1; Identities = 555/585 (95 %), 9 gaps (1 %)), *Zasmidium podocarpi* (GenBank KY979861.1; Identities = 548/600 (91 %), 14 gaps (2 %)) and *Zasmidium musae* (as *Stenella musae*, GenBank EU514347.1; Identities = 494/540 (91 %), 6 gaps (1 %)). The *actA* sequences of CPC 33349, 33350 and 33640 are identical. Closest hits using the ***cmdA*** sequence of CPC 33349 had highest similarity to *Zasmidium cellare* (GenBank MH591756.1; Identities = 281/306 (92 %), no gaps), *Acrodontium crateriforme* (GenBank KX289012.1; Identities = 280/305 (92 %), no gaps) and *Zasmidium pseudovespa* (as *Mycosphaerella pseudovespa*, GenBank KF902548.1; Identities = 269/290 (93 %), no gaps). The *cmdA* sequences of CPC 33349, 33350 and 33640 are identical. Closest hits using the ***rpb2*** sequence of CPC 33349 had highest similarity to *Zasmidium citri-griseum* (GenBank MF951696.1; Identities = 765/916 (84 %), 8 gaps (0 %)), *Zasmidium indonesianum* (GenBank MF951710.1; Identities = 758/915 (83 %), 6 gaps (0 %)) and *Zasmidium cerophillum* (GenBank MF951694.1; Identities = 756/913 (83 %), 4 gaps (0 %)). The *rpb2* sequences of CPC 33349, 33350 and 33640 are identical. Only distant hits with *Pseudocercospora* species were obtained when the ***tef1*** sequence was used in blast searches. The *tef1* sequences of CPC 33350 and 33640 are identical, while CPC 33349 differs from them at 1 nt.

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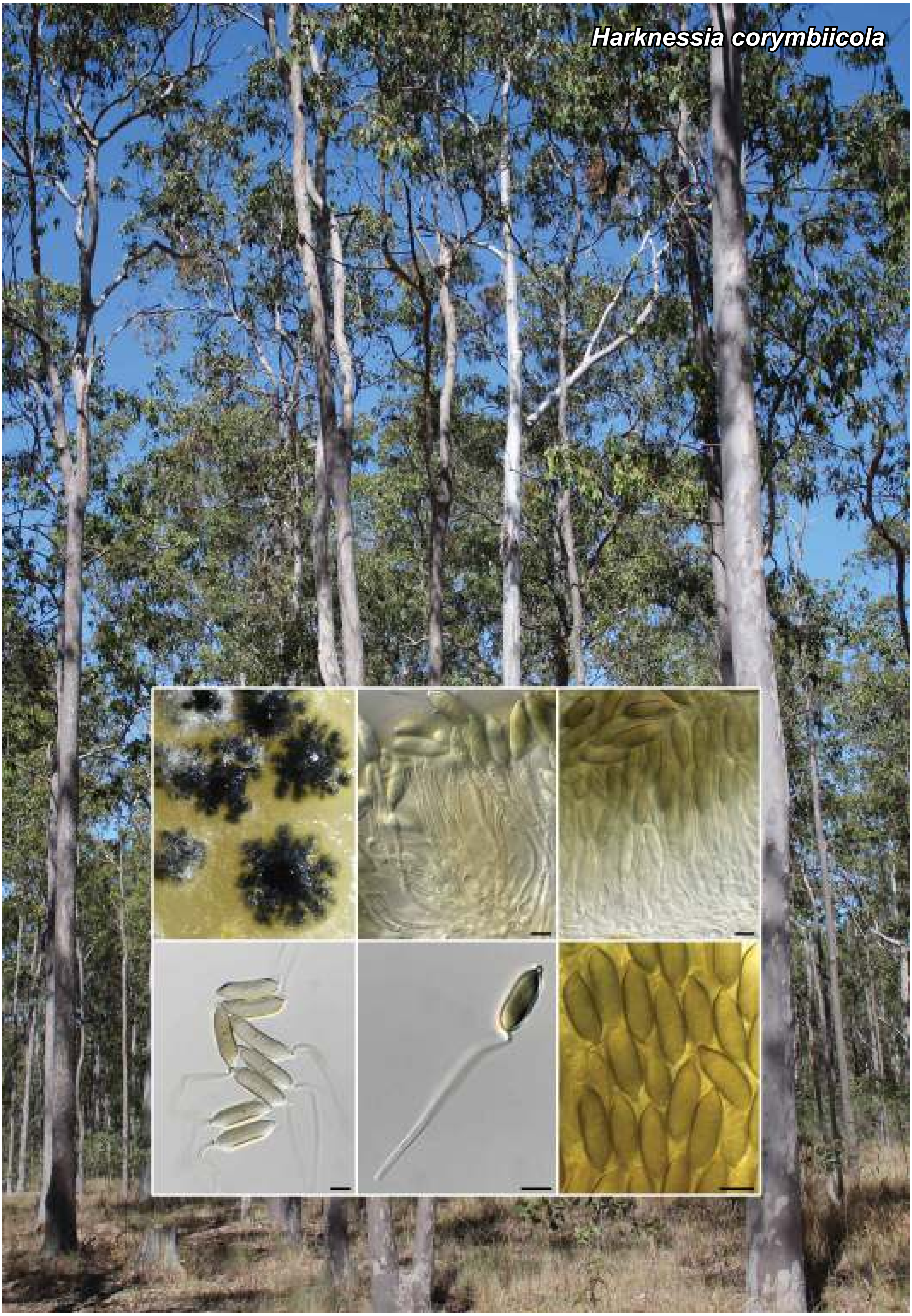
Harknessia corymbiicola

Fungal Planet 788 – 14 December 2018

Harknessia corymbiicola Crous, *sp. nov.*

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

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

Foliicolous. *Conidiomata* pycnidioid, separate to gregarious, subepidermal, becoming erumpent, stromatic, multilocular, up to 2 mm diam, individual locules 100–300 µm diam; with irregular opening and border of yellowish, furfuraceous cells; *conidiomatal wall* of *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner conidiomatal cavity. *Conidiogenous cells* 6–12 × 5–6 µm, ampulliform to subcylindrical, hyaline, smooth, invested in mucilage, percurrently proliferating once or twice near apex. *Conidia* (26–)28–32(–35) × (7–)8(–9) µm *in vitro*, fusoid with apiculus, aseptate, non-striate, medium brown, thick-walled, smooth-walled, granular to finely guttulate. *Basal appendage* (50–)65–80(–90) × 3(–4) µm *in vitro*, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm. *Microconidia* not seen.

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

Typus. AUSTRALIA, New South Wales, Grafton, Bom Bom State Forest, leaf litter of *Corymbia maculata* (*Myrtaceae*), 13 Mar. 2015, *A.J. Carnegie*, HPC 2034 (holotype CBS H-23752, culture ex-type CPC 33289 = CBS 145051, ITS, LSU and *tub2* sequences GenBank MK047424.1, MK047475.1 and MK047576.1, MycoBank MB828168).

Notes — *Harknessia* (*Harknessiaceae*; Crous et al. 2012a) is a genus of appendaged coelomycetous fungi that is commonly isolated from *Myrtaceae* and *Proteaceae. Harknessia* was treated by Marin-Felix et al. (2019), who accepted 38 species, recognising the majority as either endophytes, saprobes or foliar pathogens of minor importance. *Harknessia corymbiicola* represents a phylogenetically distinct species in the *H. weresubiae* species complex, being characterised by fusoid, apiculate conidia that lack striations, and have (50–)65–80(–90) µm long basal appendages.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Harknessia platyphyllae* (GenBank NR_155191.1; Identities = 625/640 (98 %), 11 gaps (1 %)), *Harknessia banksiae* (GenBank NR_155188.1; Identities = 625/641 (98 %), 5 gaps (0 %)) and *Harknessia banksiigena* (GenBank NR_155189.1; Identities = 614/630 (97 %), 7 gaps (1 %)). Closest hits using the **LSU** sequence are *Aurantiosacculus acutatus* (GenBank NG_042618.1; Identities = 840/843 (99 %), no gaps), *Harknessia ellipsoidea* (GenBank MH877405.1; Identities = 839/843 (99 %), no gaps) and *Harknessia pellitae* (GenBank KY979843.1; Identities = 839/843 (99 %), no gaps). Closest hits using the ***tub2*** sequence had highest similarity to *Harknessia eucalyptorum* (GenBank JQ706136.1; Identities = 615/651 (94 %), 11 gaps (1 %)), *Harknessia fusiformis* (GenBank JQ706139.1; Identities = 614/655 (94 %), 12 gaps (1 %)) and *Harknessia renispora* (GenBank AY720769.1; Identities = 609/652 (93 %), 9 gaps (1 %)).

Colour illustrations. *Corymbia maculata*, Bom Bom State Forest, Australia; Colony on oatmeal agar, conidiogenous cells and conidia with long basal appendages. Scale bars = 10 µm.

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Pseudoplagiostoma corymbiicola

Fungal Planet 789 – 14 December 2018

Pseudoplagiostoma corymbiicola Crous, *sp. nov.*

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

Classification — *Pseudoplagiostomataceae*, *Diaporthales*, *Sordariomycetes*.

Conidiomata amphigenous on leaves, acervular, subcuticular to subepidermal, brown, separate; wall consisting of 2–3 layers of brown *textura angularis*, up to 300 µm diam; dehiscence by means of irregular slits; exuding white to cream conidial masses. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, discrete, cylindrical to ampulliform with long cylindrical neck, hyaline, smooth, straight to curved, proliferating several times percurrently near apex, 15–30 × 3–5 µm. *Conidia* aseptate, hyaline, smooth, thick-walled, (1–2 µm diam), guttulate, elongate ellipsoidal, straight, apex broadly obtuse, tapering at base to a truncate hilum (1 µm diam), with minute marginal frill, (15–)16–17(–20) × (6–)7(–8) µm; encased in mucoid sheath (visible in Shear's mountant, less so in lactic acid).

Culture characteristics — Colonies flat, spreading, with fluffy, moderate aerial mycelium and feathery, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface olivaceous grey with dirty white margin, reverse umber in centre, luteous in outer region. On PDA surface dirty white to buff, reverse pale olivaceous. On OA surface dirty white to buff.

Typus. Australia, New South Wales, Dyraaba, Dyraaba plantation, on leaves of *Corymbia citriodora*, 14 Mar. 2015, *A.J. Carnegie*, HPC 2027 (holotype CBS H-23753, culture ex-type CPC 33275= CBS 145052, ITS, LSU, *tef1* and *tub2* sequences GenBank MK047425.1, MK047476.1, MK047558.1 and MK047577.1, MycoBank MB828169).

Notes — The genus *Pseudoplagiostoma* (*Pseudoplagiostomaceae*; *Diaporthales*) presently contains five species, all of which are considered to be foliar pathogens (Cheewangkoon et al. 2010). *Pseudoplagiostoma corymbiicola* (conidia (15–)16–17(–20) × (6–)7(–8) µm) is morphologically closest to *P. corymbiae* (conidia (14–)16–18(–19) × (7–)8–9(–10) µm; Crous et al. 2012b), although conidia of the latter species are slightly wider, and the two species are also phylogenetically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pseudoplagiostoma eucalypti* (GenBank GU973508.1; Identities = 561/569 (99 %), 3 gaps (0 %)), *Pseudoplagiostoma oldii* (GenBank GU973534.1; Identities = 560/569 (98 %), 4 gaps (0 %)) and *Pseudoplagiostoma variabile* (GenBank GU973536.1; Identities = 559/569 (98 %), 3 gaps (0 %)). Closest hits using the **LSU** sequence are *Pseudoplagiostoma corymbiae* (GenBank NG_042674.1; Identities = 834/840 (99 %), no gaps), *Juglanconis appendiculata* (GenBank KY427140.1; Identities = 812/841 (97 %), 2 gaps (0 %)), and *Pseudovalsa modonia* (GenBank MH875180.1; Identities = 811/840 (97 %), 1 gap (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Pseudoplagiostoma variabile* (GenBank GU973566.1; Identities = 311/332 (94 %), 3 gaps (0 %)), *Pseudoplagiostoma eucalypti* (GenBank GU973540.1; Identities = 303/332 (91 %), 4 gaps (1 %)) and *Pseudoplagiostoma oldii* (GenBank GU973564.1; Identities = 301/333 (90 %), 5 gaps (1 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Pseudoplagiostoma variabile* (as *Diaporthales* sp. CR-2010b, GenBank GU993863.1; Identities = 461/470 (98 %), no gaps), *Pseudoplagiostoma oldii* (as *Diaporthales* sp. CR-2010a, GenBank GU993862.1; Identities = 451/469 (96 %), no gaps) and *Pseudoplagiostoma eucalypti* (GenBank AB978372.1; Identities = 446/470 (95 %), no gaps).

Colour illustrations. Corymbia citriodora, Dyraaba plantation, Australia; conidiomata sporulating on pine needle agar, conidiogenous cells and conidia. Scale bars = 10 µm.

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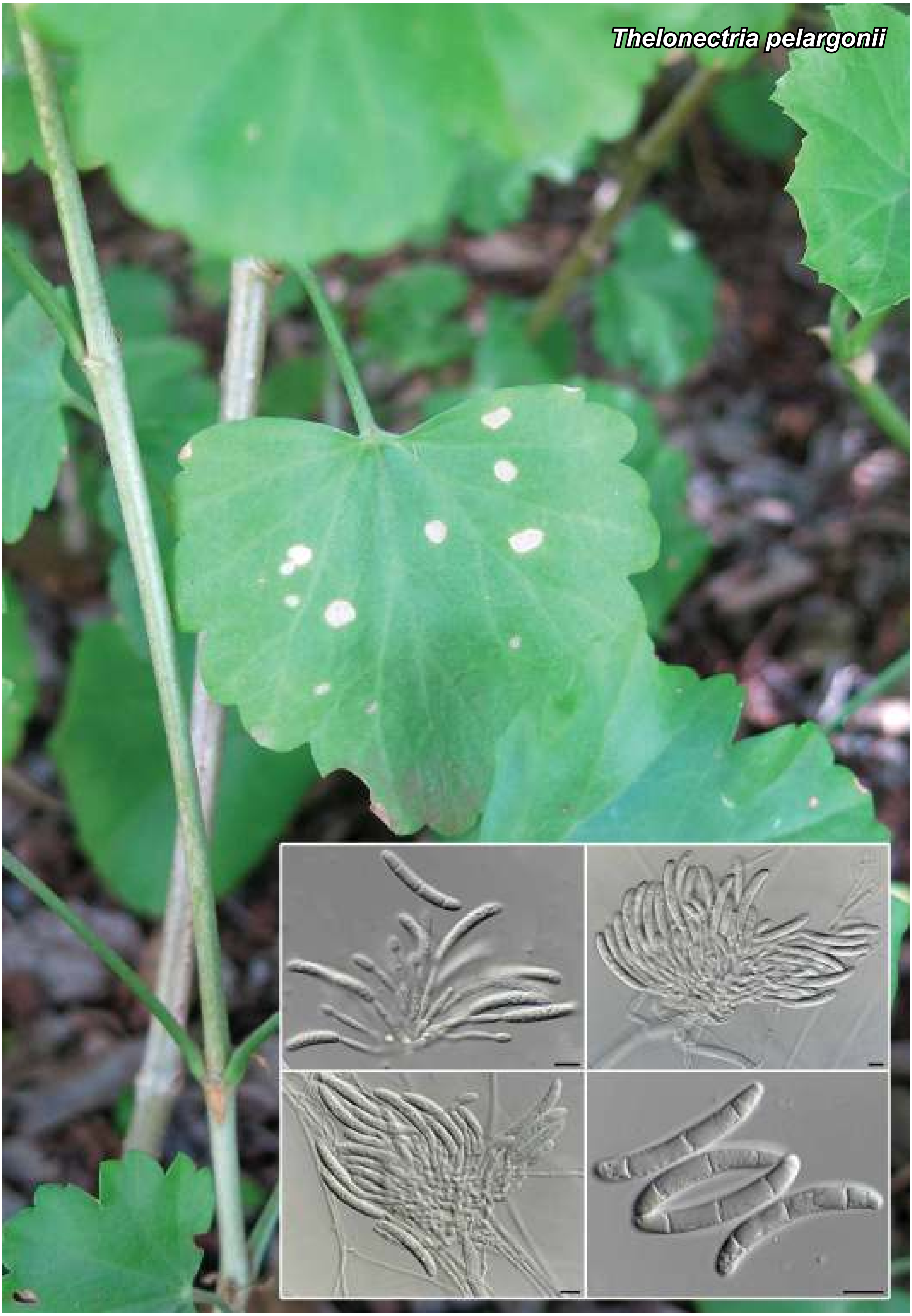
Thelonectria pelargonii

Fungal Planet 790 – 14 December 2018

Thelonectria pelargonii Crous, *sp. nov.*

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

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

Mycelium consisting of hyaline, smooth, branched, septate, 2.5–3.5 µm diam hyphae. *Conidiomata* sporodochial, sessile on agar, 50–200 µm diam, basal stroma of cells arising from wide hyphae, 8–15 µm diam, giving rise to tightly aggregated cluster of primary branches, aseptate, 10–20 × 4–7 µm, forming several secondary branches, 10–15 × 4–5 µm, giving rise to erect, tertiary and quarterly branches, 10–17 × 3–4 µm, forming 1–3 cymbiform to subcylindrical phialides with periclinal thickening, 12–25 × 3.5–4 µm. *Conidia* solitary, curved, subcylindrical with obtuse ends, hyaline, smooth, guttulate, 3–4-septate, (41–) 43–45(–47) × (6–)6.5(–7) µm. *Chlamydospores* and *ascomata* not seen.

Culture characteristics — Colonies spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface buff, reverse sienna to saffron. On PDA surface umber with diffuse sienna pigment, reverse umber. On OA surface sienna in centre, amber in outer region.

Typus. South Africa, Western Cape Province, Stellenbosch, *Pelargonium* sp. (*Geraniaceae*), 1 Feb. 2010, *P.W. Crous* (holotype CBS H-23754, culture ex-type CBS 145054, ITS, LSU, *his3*, *rpb2* and *tub2* sequences GenBank MK047426.1, MK047477.1, MK047530.1, MK047537.1 and MK047578.1, MycoBank MB828170).

Colour illustrations. *Pelargonium* sp. growing in South Africa; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — The genus *Thelonectria* was established for a genus of *Nectriaceae* with cylindrocarpon-like asexual morphs (Chaverri et al. 2011) and presently includes approximately 40 species that are known to be saprobes or pathogens of hardwood trees and shrubs. *Thelonectria pelargonii*, which is phylogenetically distinct from other species in the genus, was associated with roots of a *Pelargonium* sp. in South Africa, but presently nothing is known about its ecology.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Thelonectria veuillotiana* (GenBank KJ022014.1; Identities = 462/493 (94 %), 14 gaps (2 %)), *Thelonectria westlandica* (GenBank JQ403327.1; Identities = 480/515 (93 %), 11 gaps (2 %)) and *Cylindrocarpon olidum* (GenBank KC427020.1; Identities = 515/566 (91 %), 29 gaps (5 %)). Closest hits using the **LSU** sequence are *Thelonectria veuillotiana* (GenBank KJ022063.1; Identities = 818/829 (99 %), 1 gap (0 %)), *Thelonectria westlandica* (GenBank JQ403366.1; Identities = 807/824 (98 %), 1 gap (0 %)) and *Pleiocarpon strelitziae* (GenBank KY304672.1; Identities = 803/821 (98 %), 1 gap (0 %)). Closest hits using the ***his3*** sequence had highest similarity to *Thelonectria olida* (GenBank KM231487.1; Identities = 345/379 (91 %), 9 gaps (2 %)), *Penicillifer pulcher* (GenBank KM231456.1; Identities = 412/487 (85 %), 28 gaps (5 %)) and *Thelonectria discophora* (GenBank KM231489.1; Identities = 413/490 (84 %), 25 gaps (5 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Thelonectria lucida* (GenBank HQ897734.1; Identities = 798/870 (92 %), no gaps), *Thelonectria trachosa* (GenBank KM232343.1; Identities = 775/861 (90 %), no gaps) and *Acremonium macroclavatum* (GenBank HQ897740.1; Identities = 772/870 (92 %), no gaps). Closest hits using the ***tub2*** sequence had highest similarity to *Thelonectria westlandica* (GenBank HM352868.1; Identities = 564/612 (92 %), 6 gaps (0 %)), *Thelonectria lucida* (GenBank KJ022321.1; Identities = 473/515 (92 %), 7 gaps (1 %)) and *Coccinonectria pachysandricola* (GenBank KM232033.1; Identities = 549/626 (88 %), 21 gaps (3 %)).

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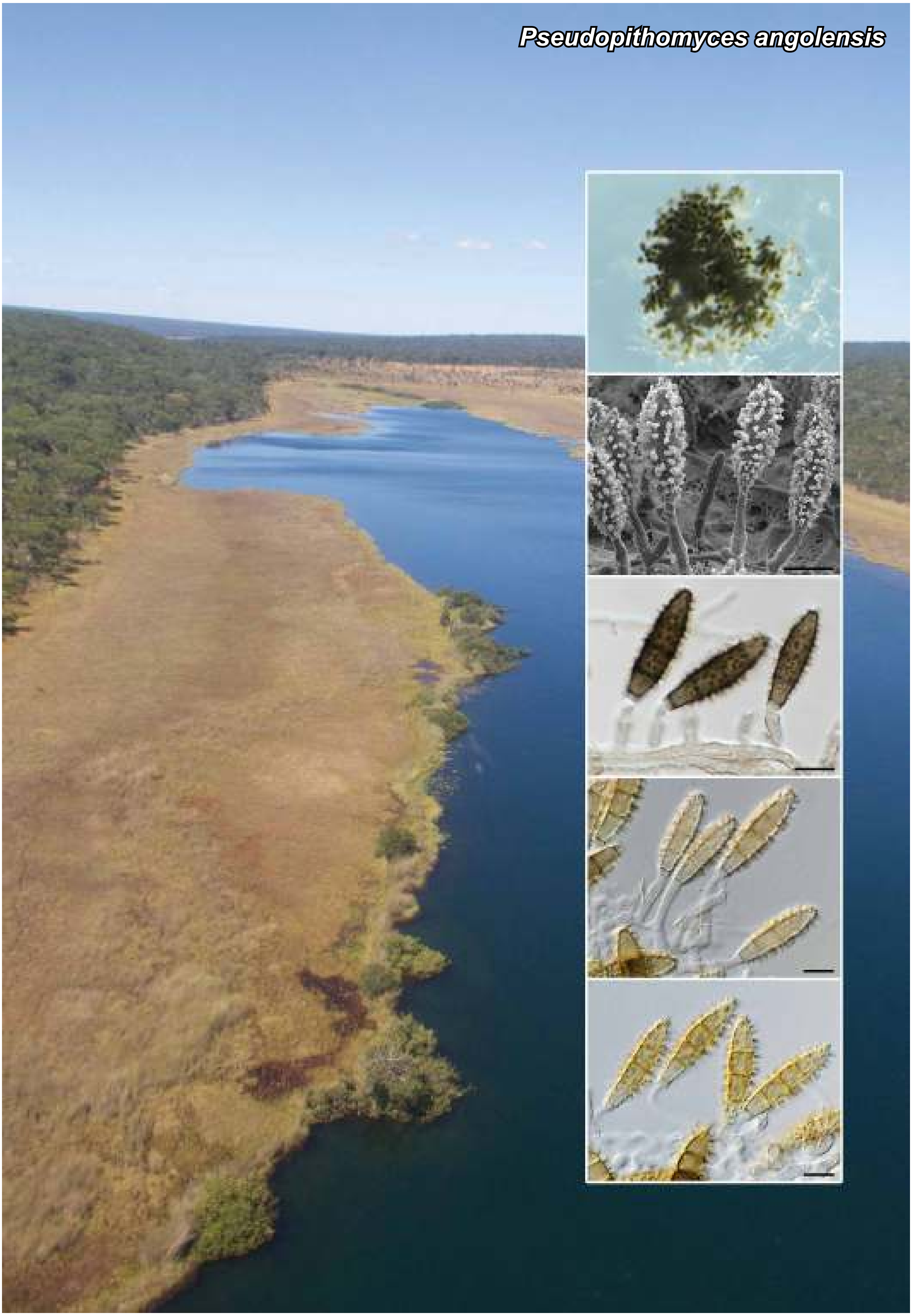

Pseudopithomyces angolensis

Fungal Planet 791 – 14 December 2018

Pseudopithomyces angolensis Crous, *sp. nov.*

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

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

Mycelium consisting of hyaline, septate, branched, 2–3.5 µm diam hyphae. *Conidiophores* solitary on aerial mycelium, but also becoming aggregated on agar surface, giving rise to sporodochia, up to 250 µm diam; conidiophores subcylindrical, branched or not, 1–3-septate, 10–25 × 2–3.5 µm, pale brown, smooth to verruculose. *Conidiogenous cells* smooth, pale brown, subcylindrical, proliferating percurrently, 7–15 × 2–3.5 µm; conidiogenesis peculiar in that the tip of the conidiogenesis cell is covered by the basal cap attached to conidia, and this is free from the conidiogenous cell itself. In young conidiogenous cells the conidiogenous cell is swollen at the apex, and the basal conidial cap appears to be attached to the tip, but later it is clearly a cap covering the apex of the conidiogenous cell. *Conidia* solitary, medium to dark brown, narrowly fusoid, apex obtuse, base with basal cup-shaped brown appendage; 3-septate, with two central cells somewhat darker than the apical and basal cell, (28–)30–34(–37) × (7–)8(–9) µm; wall covered in tubular warts, 1–3 × 1–1.5 µm (tubes open once mature); basal cap-like appendage brown, 2–3 × 3–4 µm.

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

Typus. Angola, Cuito Source Lake, leaf spot of unknown host plant, 13 Mar. 2014, *J. Roux*, HPC 2084 = NGA 242 (holotype CBS H-23756, culture ex-type CPC 33597 = CBS 145056, ITS, LSU and *rpb2* sequences GenBank MK047427.1, MK047478.1 and MK047538.1, MycoBank MB828171).

Notes — *Pseudopithomyces* contains around 10 species, distinguished from *Pithomyces* s.str. by having fusoid, echinulate to verruculose conidia that are visible as brown to black colonies on the host. In contrast, *Pithomyces* produces obovate to ovoid, verruculose, pale brown conidia that form whitish to yellowish colonies on the host (Ellis 1971). Colonies of *Pseudopithomyces angolensis* were small, black and shiny on leaves, and were initially assumed to represent packets of insect eggs. Morphologically, it is distinct from *P. chartarum* (conidia with 3 transverse and 1–2 vertical septa, 18–29 × 10–17 µm; Ellis 1971) in having longer, narrower conidia that lack vertical septa.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the **ITS** sequence had highest similarity to *Pithomyces chartarum* (strain CBS 485.71, GenBank MH860227.1; Identities = 596/601 (99 %), 1 gap (0 %)) and several other sequences labelled as *Pithomyces chartarum* or *Pseudopithomyces chartarum*; however, several other cultures of this species are more distant (e.g., CBS 805.72, CBS 679.71 and CBS 712.70, GenBank MH860611.1, MH860299.1 and MH859914.1; Identities = 588/607 (97 %), 7 gaps (1 %)). Closest hits using the **LSU** sequence are *Pseudopithomyces rosae* (GenBank NG_059876.1; Identities = 842/842 (100 %), no gaps), *Pseudopithomyces palmicola* (GenBank KU554628.1; Identities = 847/848 (99 %), no gaps) and *Pithomyces chartarum* (as *Leptosphaerulina chartarum*, GenBank LK936376.1; Identities = 847/848 (99 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Pithomyces chartarum* (as *Leptosphaerulina chartarum*, GenBank LK936415.1; Identities = 895/935 (96 %), 2 gaps (0 %)), *Sporidesmiella fusiformis* (GenBank DQ435079.1; Identities = 681/729 (93 %), 2 gaps (0 %)) and *Pseudopithomyces maydicus* (as *Pithomyces maydicus*, GenBank LK936419.1; Identities = 832/926 (90 %), 3 gaps (0 %)).

Colour illustrations. Cuito Source Lake, Angola; colony on synthetic nutrient poor agar, Scanning Electron Micrograph of conidia (photo: Jan Dijksterhuis), conidiogenous cells and conidia. Scale bars = 10 µm.

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Gnomoniopsis angolensis

Fungal Planet 792 – 14 December 2018

Gnomoniopsis angolensis Crous, *sp. nov.*

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

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

Conidiomata solitary, eustromatic, mono- to multilocular, with central ostiole, pycnidial, exuding a creamy conidial mass; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* lining the inner cavity, hyaline to subhyaline at base, subcylindrical with prominent apical taper, 0–2-septate, branched at base, 15–25 × 2.5–3.5 µm. *Conidiogenous cells* hyaline, smooth, ampulliform to cymbiform, terminal and intercalary, 10–15 × 2–3 µm, phialidic. *Conidia* solitary, hyaline, smooth, guttulate, subcylindrical, apex obtuse, tapering at base to truncate hilum, 0.5 µm diam, straight to slightly curved, aseptate, (8–)9–10(–11) × 2(–2.5) µm.

Culture characteristics — Colonies spreading, with sparse to moderate aerial mycelium and even, lobate margin, covering dish after 2 wk at 25 °C. On MEA surface sienna with zones of dirty white, reverse sienna with zones of luteous. On PDA surface greyish sepia, reverse pale mouse grey. On OA surface pale mouse grey.

Typus. ANGOLA, Cuanavale Source Lake, 1354 m, leaf spot of unknown host plant, 16 Mar. 2010, *J. Roux*, HPC 2080, NGA 315, WP1397 (holotype CBS H-23757, culture ex-type CPC 33595 = CBS 145057, ITS, LSU and *rpb2* sequences GenBank MK047428.1, MK047479.1 and MK047539.1, MycoBank MB828172).

Colour illustrations. Cuanavale Source Lake in Angola; symptomatic leaf, colony sporulating on oatmeal agar, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — *Gnomoniopsis* contains c. 15 species, most of which are endophytic or pathogenic to species of *Fagaceae*, *Onagraceae* and *Rosaceae* (Crous et al. 2012b). *Gnomoniopsis angolensis* is phylogenetically distinct from known species (Walker et al. 2010).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Gnomoniopsis smithogilvyi* (GenBank KC145878.1; Identities = 576/600 (96 %), 10 gaps (1 %)), *Discula quercina* (GenBank GQ452265.1; Identities = 571/597 (96 %), 6 gaps (1 %)) and *Gnomoniopsis castaneae* (GenBank MH384925.1; Identities = 564/590 (96 %), 10 gaps (1 %)). Closest hits using the **LSU** sequence are *Gnomoniopsis smithogilvyi* (GenBank MH877030.1; Identities = 837/841 (99 %), no gaps), *Allantophoma endogenospora* (GenBank EU754126.1; Identities = 835/839 (99 %), no gaps) and *Gnomoniopsis castaneae* (GenBank KX929802.1; Identities = 828/832 (99 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Gnomoniopsis clavulata* (GenBank EU219242.1; Identities = 809/869 (93 %), no gaps), *Gnomoniopsis paraclavulata* (GenBank EU219248.1; Identities = 793/870 (91 %), no gaps) and *Discula campestris* (GenBank EU199143.1; Identities = 792/869 (91 %), no gaps).

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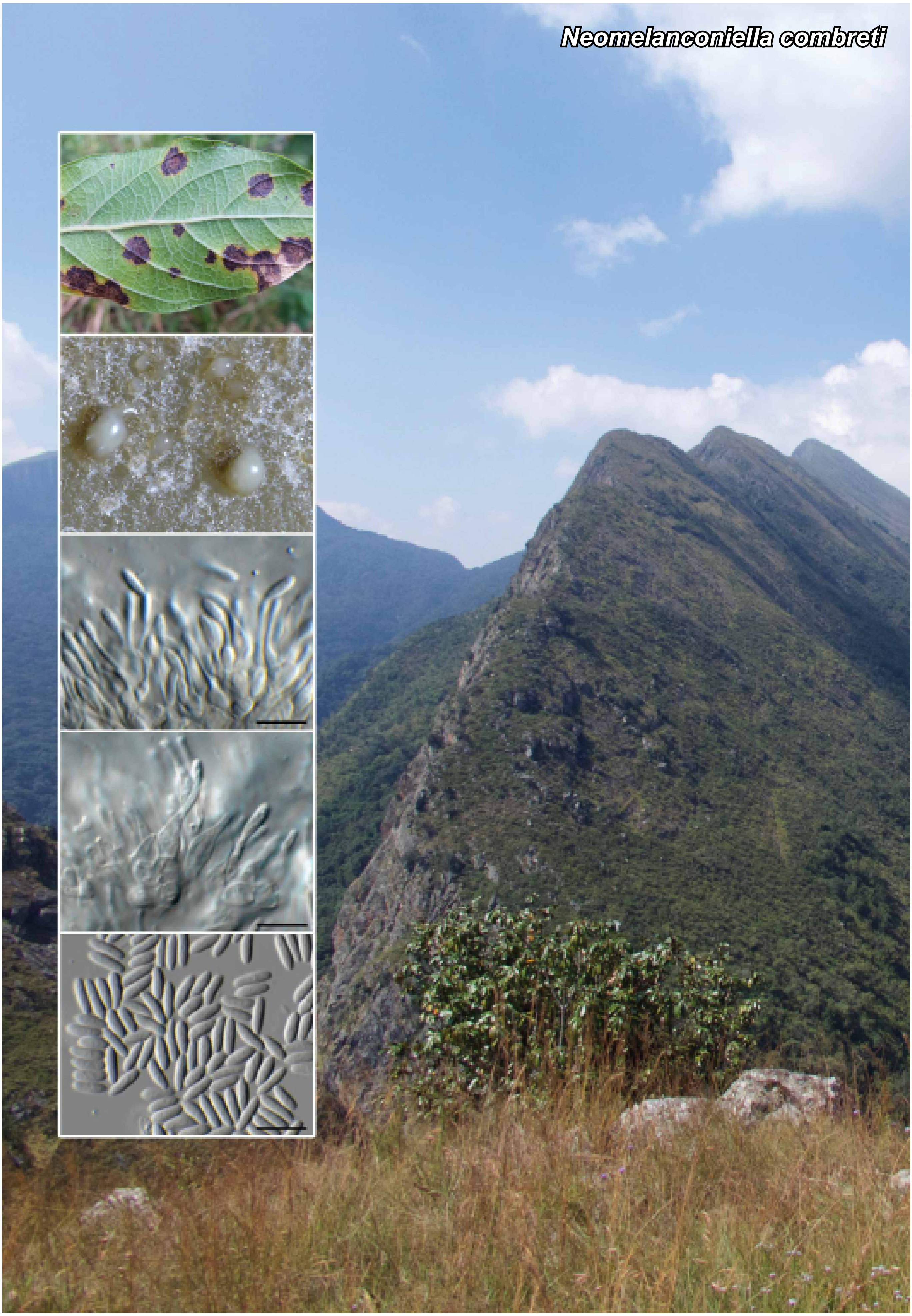
Neomelanconiella combreti

Fungal Planet 793 – 14 December 2018

Neomelanconiellaceae Crous, *fam. nov.*

MycoBank MB828247.

Neomelanconiella Crous, *gen. nov.*

Etymology. Name refers to *Melanconiella*, a genus which is morphologically similar.

Classification — *Neomelanconiellaceae*, *Diaporthales*, *Sordariomycetes*.

Conidiomata solitary to aggregated, pycnidial, brown with central ostiole; wall of 3–6 layers of medium brown *textura angularis. Conidiophores* lining the inner cavity, septate, hyaline, smooth, subcylindrical with slight apical taper, branched or not. *Conidiogenous cells* hyaline, smooth, ampulliform, terminal and intercalary, phialidic. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, subcylindrical to narrowly ellipsoid, apex obtuse, tapering to truncate hilum.

Type species. Neomelanconiella combreti Crous.
MycoBank MB828246.

Notes — The family *Neomelanconiellaceae* presently only includes *Neomelanconiella*, and clusters between *Melanconiellaceae* and *Harknessiaceae*.

Neomelanconiella combreti Crous, *sp. nov.*

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

Conidiomata solitary to aggregated, pycnidial, 200–250 µm diam, brown with central ostiole; wall of 3–6 layers of medium brown *textura angularis. Conidiophores* lining the inner cavity, 1–2-septate, hyaline, smooth, subcylindrical with slight apical taper, branched or not, 10–20 × 2.5–3.5 µm. *Conidiogenous cells* hyaline, smooth, ampulliform, terminal and intercalary, 7–12 × 2.5–3 µm, phialidic. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, subcylindrical to narrowly ellipsoid, apex obtuse, tapering to truncate hilum, 1 µm diam, (6–)7–8 × (1.5–)2(–2.5) µm.

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

Typus. South Africa, Limpopo Province, Haenertsburg, Wolkberg, Klipdraai Camp, leaf spot on *Combretum* sp. (*Combretaceae*), 30 Mar. 2010, *J. Roux*, HPC 2089 (holotype CBS H-23758, culture ex-type CPC 33664 = CBS 145058, ITS, LSU, *rpb2* and *tef1* sequences GenBank MK047429.1, MK047480.1, MK047540.1 and MK047559.1, MycoBank MB828173).

Colour illustrations. Wolkberg, South Africa; symptomatic leaf, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — *Melanconiella* presently includes approximately 20 species (Voglmayr et al. 2012), most of which occur on recently dead twigs and branches of *Betulaceae*, occurring in the north temperate zone. Asexual morphs of *Melanconiella* have in the past been described in *Melanconium*, although the latter genus is in need of revision (Sutton 1980). Morphologically, there is little to choose between *Melanconiella* and *Neomelanconiella*, although *N. combreti* occurs on leaves of *Combretaceae*, and in the Southern Hemisphere. *Neomelanconiella combreti* clusters with an isolate identified as *Cryptodiaporthe vepris* (AR 3559, on *Rubus idaeus* (*Rosaceae*), Austria), although the latter genus is now a synonym of *Plagiostoma* (Mejía et al. 2011).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Melanconiella ellisii* (GenBank JQ926269.1; Identities = 404/449 (90 %), 22 gaps (5 %)), *Sphaeronaemella fragariae* (GenBank AY271808.1; Identities = 394/440 (90 %), 16 gaps (4 %)) and *Melanconiella spodiaea* (GenBank JQ926299.1; Identities = 400/448 (89 %), 20 gaps (4 %)). Closest hits using the **LSU** sequence are *Sphaeronaemella fragariae* (GenBank MH866172.1; Identities = 817/845 (97 %), 9 gaps (1 %)), *Cryptodiaporthe vepris* (GenBank EU683070.1; Identities = 816/844 (97 %), 8 gaps (0 %)) and *Harknessia fusiformis* (GenBank JQ706220.1; Identities = 815/843 (97 %), 6 gaps (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Melanconiella hyperopta* var. *orientalis* (GenBank JQ926352.1; Identities = 743/925 (80 %), 9 gaps (0 %)), *Cryphonectria parasitica* (GenBank DQ862017.1; Identities = 722/934 (77 %), 19 gaps (2 %)) and *Synnemasporella toxicodendri* (GenBank MG682049.1; Identities = 716/924 (77 %), 21 gaps (2 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Melanconiella ellisii* (GenBank JQ926406.1; Identities = 239/282 (85 %), 18 gaps (6 %)), *Tubakia suttoniana* (GenBank MG592106.1; Identities = 228/274 (83 %), 16 gaps (5 %)) and *Tubakia oblongispora* (GenBank MG592084.1; Identities = 231/279 (83 %), 24 gaps (8 %)).

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Monilochaetes melastomae

Fungal Planet 794 – 14 December 2018

Monilochaetes melastomae Crous, *sp. nov.*

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

Classification — *Australiascaceae*, *Chaetosphaeriales*, *Sordariomycetes*.

Mycelium consisting of pale brown, smooth to finely roughened, branched, septate, 2.5–4 µm diam hyphae. *Conidiophores* solitary, erect, subcylindrical, brown, smooth, rarely branched at base, becoming paler brown toward apex, straight, 2–3(–8)-septate, 90–250 × 6–10 µm. *Conidiogenous cells* terminal, pale brown, smooth, subcylindrical with apical taper to truncate apex, 40–55 × 6–7 µm, phialidic with prominent periclinal thickening at apex, 3–4 µm diam. *Conidia* aseptate, occurring in unbranched chains (–30), ellipsoid to narrowly obovoid, hyaline, smooth, guttulate, apex obtuse, tapering at base to truncate hilum, 2 µm diam, (17–)18–19(–20) × (7.5–)8 µm.

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

Typus. Malaysia, leaf spots of *Melastoma* sp. (*Melastomataceae*), 25 July 2017, *M.J. Wingfield*, HPC 2199 (holotype CBS H-23759, culture ex-type CPC 34181 = CBS 145059, ITS and LSU sequences GenBank MK047430.1 and MK047481.1, MycoBank MB828174).

Colour illustrations. Symptomatic leaves of *Melastoma* sp. growing in Malaysia; conidial chains, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — *Monilochaetes* (sexual morph *Australiasca*) is a hyphomycetous genus with solitary, erect, sometimes curved or geniculate, dark brown conidiophores with prominently darkened septa, terminal, wide monophialides with a shallow collarette, and aseptate, rarely septate, hyaline conidia adhering in basipetal chains or heads (Réblová et al. 2011). Using the key of Réblová et al. (2011), *M. melastomae* is similar to *M. guadalcanalensis* (conidia 18–21 × 6–9 µm), although the former differs by forming shorter conidiophores and extremely long conidial chains, and is also phylogenetically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Australiasca queenslandica* (GenBank KP204397.1; Identities = 463/472 (98 %), no gaps), *Monilochaetes nothapodytis* (GenBank MF153475.1; Identities = 476/499 (95 %), 9 gaps (1 %)) and *Australiasca laeensis* (GenBank EF029187.1; Identities = 506/547 (93 %), 19 gaps (3 %)). Closest hits using the **LSU** sequence are *Monilochaetes dimorphospora* (GenBank HQ609480.1; Identities = 899/907 (99 %), no gaps), *Monilochaetes guadalcanalensis* (GenBank MH872756.1; Identities = 887/895 (99 %), no gaps) and *Australiasca queenslandica* (GenBank HM237323.1; Identities = 898/907 (99 %), no gaps).

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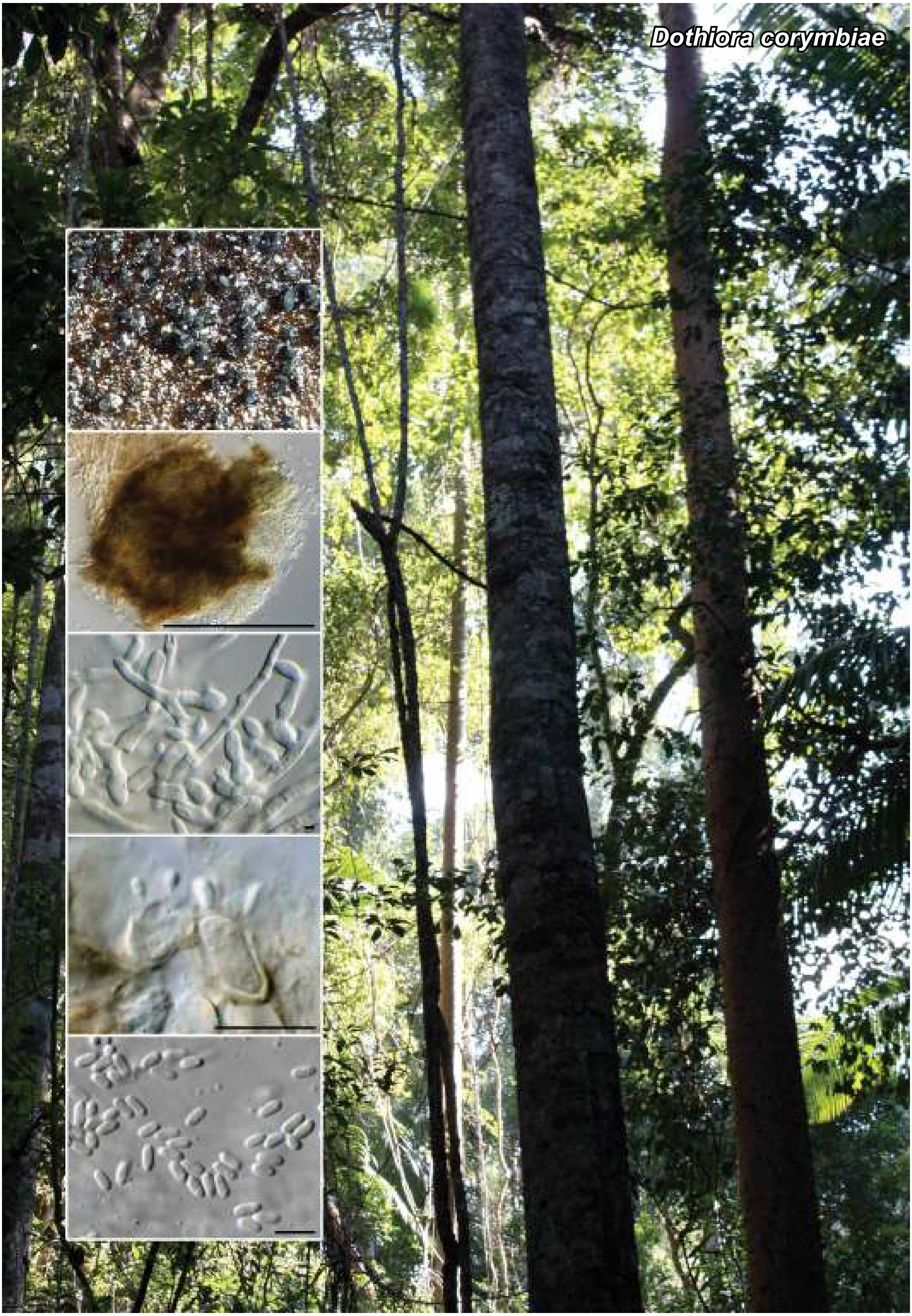
Dothiora corymbiae

Fungal Planet 795 – 14 December 2018

Dothiora corymbiae Crous, *sp. nov.*

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

Classification — *Dothideaceae*, *Dothideales*, *Dothideomycetes.*

Conidiomata pycnidial, separate, obovoid, papillate, brown, with central ostiole, 100–150 µm diam; wall of 4–8 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity, ellipsoid, hyaline, polyphialidic, with 1–3 loci per conidiogenous cell, 5–10 × 4–5 µm. *Conidia* solitary, hyaline, smooth, guttulate, subcylindrical with obtuse ends, straight, 4–5 × 2 µm; once discharged onto the agar surface, conidia turn brown, and become swollen, thick-walled, ellipsoid, 5–6 × 3–4 µm.

Culture characteristics — Colonies slimy, yeast-like, spreading, with sparse aerial mycelium and feathery, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface sepia, reverse hazel. On PDA surface and reverse sepia. On OA surface hazel to fawn.

Typus. AUSTRALIA, Queensland, Minden, on leaves of *Corymbia citriodora* (*Myrtaceae*), 1 Feb. 2010, *J. Roux*, CJA010 (holotype CBS H-23760, isotype BRIP 58843a, culture ex-type CPC 33719 = CBS 145060, ITS and LSU sequences GenBank MK047431.1 and MK047482.1, MycoBank MB828175).

Colour illustrations. Indigenous forest in Queensland, Australia; colony sporulating on malt extract agar, conidioma, hyphae, conidiogenous cells and conidia. Scale bars: conidioma = 150 µm, all others = 10 µm.

Notes — *Dothiora* was recently treated by Crous & Groenewald (2016, 2017). *Ascostromata* were shown to lack pseudoparaphyses, have bitunicate asci with hyaline, transversely septate ascospores (rarely with vertical septa). Conidiomata are pycnidial, conidiophores reduced to hyaline, phialidic conidiogenous cells, and *conidia* aseptate, hyaline, smooth, subcylindrical to ovoid or oblong, forming a hormonema-like synasexual morph. The present collection is thus best accommodated in *Dothiora.*

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neocylindroseptoria pistaciae* (GenBank KF251152.1; Identities = 512/577 (89 %), 37 gaps (6 %)), *Dothiora sorbi* (GenBank MH860401.1; Identities = 509/590 (86 %), 42 gaps (7 %)) and *Kabatina thujae* (GenBank MH858858.1; Identities = 484/555 (87 %), 38 gaps (6 %)). Closest hits using the **LSU** sequence are *Dothiora ceratoniae* (GenBank MH872233.1; Identities = 818/839 (97 %), 3 gaps (0 %)), *Dothiora schizospora* (GenBank MH868980.1; Identities = 817/839 (97 %), 2 gaps (0 %)) and *Dothiora cactacearum* (GenBank KY929177.1; Identities = 817/839 (97 %), 2 gaps (0 %)).

Dothiora Fr., Summa Veg. Scand., Sectio Post. (Stockholm): 418. 1849

Synonyms. *Cylindroseptoria* Thambug. & K.D. Hyde, Fung. Diversity 68: 125. 2014.

Neophaeocryptopus Wanas. et al., Fung. Diversity 78: 21. 2016.

For additional synonyms see Crous & Groenewald (2017).

Dothiora pistaciae (Quaedvlieg et al.) Crous, *comb. nov.*

MycoBank MB828176.

Basionym. *Cylindroseptoria pistaciae* Quaedvlieg et al., Stud. Mycol. 75: 359. 2013.

Synonym. *Neocylindroseptoria pistaciae* (Quaedvlieg et al.) Thambug. et al., Fung. Diversity 68: 125. 2014.

Dothiora mahoniae (A.W. Ramaley) Crous, *comb. nov.*

MycoBank MB828177.

Basionym. *Kabatina mahoniae* A.W. Ramaley, Mycotaxon 43: 443. 1992.

Dothiora cytisi (Wanas. et al.) Crous, *comb. nov.*

MycoBank MB828178.

Basionym. *Neophaeocryptopus cytisi* Wanas. et al., Fung. Diversity 78: 22. 2016.

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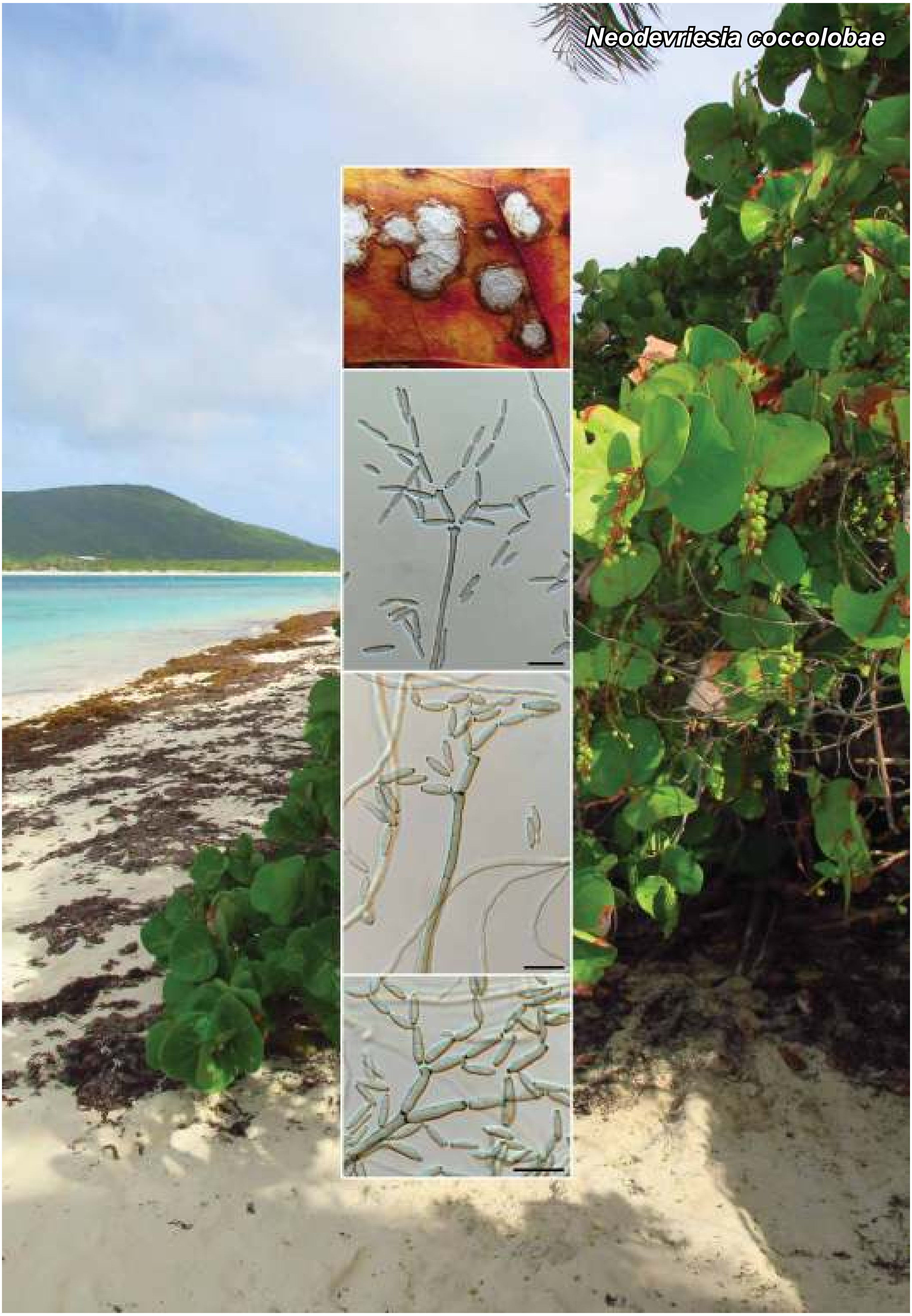
Neodevriesia coccolobae

Fungal Planet 796 – 14 December 2018

Neodevriesia coccolobae Crous, *sp. nov.*

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

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

Mycelium consisting of olivaceous, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* erect, mononematous, 1–5-septate, brown, smooth, subcylindrical, straight to flexuous, unbranched, 12–100 × 2.5–3.5 µm. *Conidiogenous cells* terminal, subcylindrical, brown, smooth, (7–)10–15 × (2–)2.5 µm, polyblastic, loci 1.5–2 µm diam, darkened. *Ramoconidia* 0(–1)-septate, subcylindrical, pale brown, smooth, 10–17 × 2.5–3.5 µm. *Conidia* in branched chains, 0(–1)-septate, pale brown, smooth, subcylindrical to narrowly fusoid, tapering at ends to truncate hila, 0.5–1 µm diam, (6–)7–8(–10) × (2–)2.5(–3) µm.

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

Typus. Puerto Rico, on leaves of *Coccoloba uvifera* (*Polygonaceae*), May 2017, *M.J. Wingfield*, HPC 2164 (holotype CBS H-23761, culture ex-type CPC 34073 = CBS 145064, ITS and LSU sequences GenBank MK047432.1 and MK047483.1, MycoBank MB828179).

Notes — Quaedvlieg et al. (2014) established *Neodevriesia* for a group of hyphomycetes with medium brown, unbranched conidiophores, thick-walled, medium brown, rarely septate conidia, occurring in short and mostly unbranched conidial chains, and lacking chlamydospores. *Neodevriesia* is generally plant-associated, and distinct from the mainly soil-inhabiting *Devriesia* s.str. *Neodevriesia coccolobae* is phylogenetically distinct from the approximately 20 species that are presently attributed to the genus.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neodevriesia imbrexigena* (as *Devriesia imbrexigena*, GenBank JX915745.1; Identities = 419/455 (92 %), 15 gaps (3 %)), *Scytalidium infestans* (GenBank MH873928.1; Identities = 481/526 (91 %), 9 gaps (1 %)) and *Neodevriesia cladophorae* (as *Devriesia* sp. MW-2016a, GenBank KU578112.1; Identities = 480/525 (91 %), 8 gaps (1 %)). Closest hits using the **LSU** sequence are *Neodevriesia cladophorae* (GenBank KU578114.1; Identities = 855/862 (99 %), no gaps), *Neodevriesia queenslandica* (as *Devriesia queenslandica*, GenBank JF951168.1; Identities = 889/899 (99 %), 4 gaps (0 %)) and *Neodevriesia imbrexigena* (as *Devriesia imbrexigena*, GenBank JX915749.1; Identities = 880/890 (99 %), 4 gaps (0 %)).

Colour illustrations. Beach at Puerto Rico; symptomatic leaf, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Neodevriesia tabebuiae

Fungal Planet 797 – 14 December 2018

Neodevriesia tabebuiae Crous, *sp. nov.*

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

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

Mycelium consisting of brown, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* erect, mononematous, 0–2-septate, brown, smooth, subcylindrical to geniculous-sinuous, unbranched, frequently reduced to conidiogenous loci on hyphae, 3–50 × 2–3 µm. *Conidiogenous cells* terminal, subcylindrical, pale brown, smooth, 3–15 × 2–3 µm, polyblastic, loci 1–1.5 µm diam, somewhat darkened and thickened. *Ramoconidia* 0–1-septate, subcylindrical, pale brown, smooth, 7–15 × 2–3 µm. *Conidia* in branched chains, 0–1-septate, pale brown, smooth to finely roughened, subcylindrical, tapering at ends to truncate hila, somewhat darkened, 1 µm diam, (6–)7–8(–10) × (2–)2.5(–3) µm.

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

Typus. Puerto Rico, on leaves of *Tabebuia chrysantha* (*Bignoniaceae*), May 2017, *M.J. Wingfield*, HPC 2178 (holotype CBS H-23762, culture ex-type CPC 34081 = CBS 145065, ITS and LSU sequences GenBank MK047433.1 and MK047484.1, MycoBank MB828180).

Colour illustrations. Forest in Puerto Rico; conidiophores, conidiogenous cells and conidial chains. Scale bars = 10 µm.

Notes — *Neodevriesia tabebuiae* and *N. coccolobae* were both collected from leaves of different plant species growing in Puerto Rico; however, their ITS sequences are only 94 % (498/532, including 2 gaps) similar. Phylogenetically, *N. tabebuiae* is distinct from the approximately 20 species that are presently attributed to *Neodevriesia*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neodevriesia lagerstroemiae* (GenBank GU214634.1; Identities = 519/572 (91 %), 21 gaps (3 %)), *Scytalidium infestans* (GenBank MH873928.1; Identities = 517/571 (91 %), 16 gaps (2 %)) and *Neodevriesia cladophorae* (as *Devriesia* sp. MW-2016a, GenBank KU578112.1; Identities = 507/561 (90 %), 15 gaps (2 %)). Closest hits using the **LSU** sequence are *Neodevriesia hilliana* (GenBank GU214414.1; Identities = 879/897 (98 %), 4 gaps (0 %)), *Neodevriesia shakazului* (GenBank NG_042753.1; Identities = 873/890 (98 %), 4 gaps (0 %)) and *Neodevriesia queenslandica* (as *Devriesia queenslandica*, GenBank JF951168.1; Identities = 879/899 (98 %), 4 gaps (0 %)).

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Alfaria tabebuiae

Fungal Planet 798 – 14 December 2018

Alfaria tabebuiae Crous, *sp. nov.*

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

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

Conidiomata sporodochial, superficial, cupulate, scattered to gregarious, oval in outline, 100–300 µm diam, with slimy, olivaceous brown conidial masses. *Setae* flexuous, unbranched, thick-walled, apex subobtuse, dark brown, verruculose, 6–8-septate, 130–200 × 6–7 µm. *Conidiophores* arising from the basal stroma, densely aggregated, subcylindrical, 3–5-septate, branched, becoming pigmented and verruculose toward apex, 30–50 × 2–3 µm. *Conidiogenous cells* integrated, terminal and intercalary, subcylindrical, becoming pigmented and verruculose in upper region, phialidic with periclinal thickening and flared collarette, 10–15 × 2–2.5 µm. *Conidia* aseptate, solitary, fusoid-ellipsoid, straight, apex subobtuse, base truncate, 1.5–2 µm diam, guttulate, granular, olivaceous brown, smooth, (6–)7(–7.5) × (2.5–)3 µm.

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

Typus. Puerto Rico, on leaves of *Tabebuia chrysantha* (*Bignoniaceae*), May 2017, *M.J. Wingfield*, HPC 2178 (holotype CBS H-23763, culture ex-type CPC 34038 = CBS 145066, ITS, LSU, *cmdA*, *rpb2*, *tef1* and *tub2* sequences GenBank MK047434.1, MK047485.1, MK047527.1, MK047541.1, MK047560.1 and MK047579.1, MycoBank MB828181).

Additional material examined. Puerto Rico, on leaves of *T. chrysantha*, May 2017, *M.J. Wingfield*, HPC 2178, CPC 34083 = CBS 145063, ITS, LSU, *cmdA*, *rpb2*, *tef1* and *tub2* sequences GenBank MK047435.1, MK047486.1, MK047528.1, MK047542.1, MK047561.1 and MK047580.1.

Notes — *Alfaria* was established for a fungus causing a disease on *Cyperus esculentus* in Spain, and presently contains close to 20 species (Crous et al. 2014a, 2018a, Lombard et al. 2016). *Alfaria tabebuiae* is phylogenetically closely related to *A. acaciae* (conidia (6–)8–10(–12) × (2.5–)3 µm; Crous et al. 2018a), although it has shorter conidia, and longer setae. Several isolates identified as *Amerosporium* spp. cluster in the *Alfaria* clade. However, *Amerosporium* has unilocular, spherical conidiomata, and is distinct from the sporodochial conidiomata of *Alfaria*. Synapomorphies between the genera are pigmented setae, phialidic conidiogenous cells and pigmented, aseptate conidia. The morphology of these '*Amerosporium'* isolates will be resolved in a later study.

Colour illustrations. Forest in Puerto Rico; colony sporulating on oatmeal agar, sporodochia with setae, conidiogenous cells and conidia. Scale bars = 10 µm.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 34038 had highest similarity to *Alfaria acaciae* (GenBank NR_158363.1; Identities = 572/582 (98 %), 5 gaps (0 %)), *Alfaria cyperi-esculenti* (GenBank KJ869143.1; Identities = 575/591 (97 %), 10 gaps (1 %)) and *Alfaria thymi* (GenBank NR_154714.1; Identities = 568/587 (97 %), 13 gaps (2 %)). The ITS sequences of CPC 34038 and 34083 differ with 1 nt. Closest hits using the **LSU** sequence of CPC 34038 are *Alfaria acaciae* (GenBank MH107930.1; Identities = 857/859 (99 %), no gaps), *Alfaria cyperi-esculenti* (GenBank KJ869200.1; Identities = 801/804 (99 %), no gaps) and *Alfaria thymi* (GenBank KU845999.1; Identities = 822/828 (99 %), 1 gap (0 %)). The LSU sequences of CPC 34038 and 34083 are identical. Closest hits using the ***cmdA*** sequence of CPC 34038 had highest similarity to *Alfaria terrestris* (GenBank KU845979.1; Identities = 486/542 (90 %), 4 gaps (0 %)), *Alfaria acaciae* (GenBank MH107991.1; Identities = 530/611 (87 %), 7 gaps (1 %)) and *Gregatothecium humicola* (GenBank KU846285.1; Identities = 482/542 (89 %), 4 gaps (0 %)). The *cmdA* sequences of CPC 34038 and 34083 are identical. Closest hits using the ***rpb2*** sequence of CPC 34038 had highest similarity to *Alfaria acaciae* (GenBank MH108001.1; Identities = 653/702 (93 %), no gaps), *Alfaria thymi* (GenBank KU846006.1; Identities = 508/578 (88 %), no gaps) and *Alfaria caricicola* (GenBank KU846001.1; Identities = 521/597 (87 %), no gaps). The *rpb2* sequences of CPC 34038 and 34083 are identical. Closest hits using the ***tef1*** sequence of CPC 34038 had highest similarity to *Alfaria acaciae* (GenBank MH108013.1; Identities = 378/437 (86 %), 22 gaps (5 %)), *Alfaria caricicola* (GenBank KU846008.1; Identities = 324/403 (80 %), 16 gaps (3 %)) and *Alfaria terrestris* (GenBank KU846010.1; Identities = 309/378 (82 %), 28 gaps (7 %)). The *tef1* sequences of CPC 34038 and 34083 differ with 1 nt. Closest hits using the ***tub2*** sequence of CPC 34038 had highest similarity to *Alfaria acaciae* (GenBank MH108035.1; Identities = 400/425 (94 %), 4 gaps (0 %)), *Alfaria terrestris* (GenBank KU846019.1; Identities = 327/350 (93 %), 3 gaps (0 %)) and *Alfaria putrefolia* (GenBank KU846017.1; Identities = 325/349 (93 %), 1 gap (0 %)). The *tub2* sequences of CPC 34038 and 34083 differ with 2 nt.

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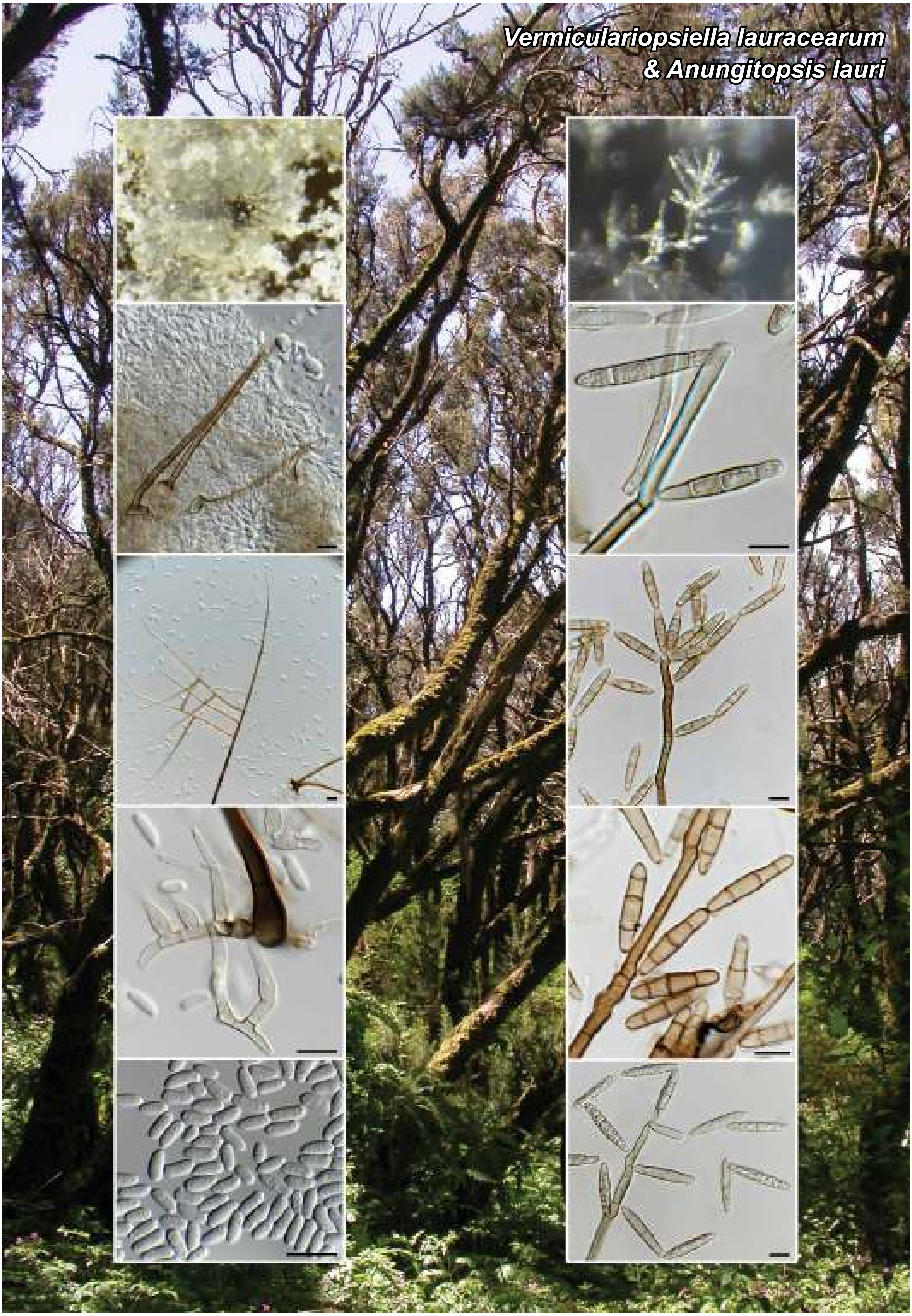
Vermiculariopsiella lauracearum
& Anungitopsis lauri

Fungal Planet 799 & 800 – 14 December 2018

Vermiculariopsiella lauracearum Crous, *sp. nov.*

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

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

Sporodochia developing on OA and PDA, erumpent, crystalline, up to 450 µm diam, with brown, erect setae dispersed throughout sporodochium, thick-walled, smooth-walled, straight to flexuous, 100–300 × 4–5 µm, 8–20-septate, tapering to an obtuse apex and with bulbous base, 7–9 µm diam, forming a series of lateral branches (up to 100 µm long) that again branch once with tertiary branch (up to 120 µm long). *Conidiogenous cells* phialidic, developing in a cluster around the base of setae, pale brown, smooth, subcylindrical with apical taper with periclinal thickening and minute collarette, 1–2 µm long, 20–25 × 3–3.5 µm. *Conidia* aseptate, solitary, hyaline, guttulate, straight to slightly curved, inequilateral with inner plane straight and outer plane convex, apex subobtusely rounded; base truncate but with excentric hilum, 0.5 µm diam, on inner straight plane, (9–)10(–11) × (3–)3.5(–4) µm.

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

Typus. Spain, La Gomera, leaf litter of *Laurus novocanariensis* (*Lauraceae*), 30 Mar. 2017, *A.L. van Iperen*, HPC 2058 (holotype CBS H-23755, culture ex-type CPC 33591 = CBS 145055, ITS and LSU sequences GenBank MK047436.1 and MK047487.1, MycoBank MB828182).

Notes — Species of *Vermiculariopsiella* produce sporodochia with brown, erect setae, stromatic, sub-hyaline conidiophores, phialidic conidiogenous cells, and hyaline, aseptate conidia (Crous et al. 2014a). There are presently more than 16 species known in the genus. *Vermiculariopsiella lauracearum* is morphologically distinct from known species based on its long, branched setae, and small conidia. *Vermiculariopsis circinotricha*, an apparent coelomycete (*Chaetomella* complex), was described from leaves of *Laurus* '*canariensis*' collected in Madeira (branched setae, conidia cylindrical, 14–19 × 1–1.5 µm). However, Sutton & Sarbhoy (1976) could not locate any type material, and hence the taxonomy of the genus has remained unresolved. Based on the original description and current information about the sexual morph of *Vermiculariopsiella*, it could well be that the illustrated black, ellipsoid sporocarp was of an ascoma (e.g., see *V. dichapetali*), in which case *Vermiculariopsis* would represent an older name for the genus *Vermiculariopsiella*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Vermiculariopsiella microsperma* (GenBank KY853478.1; Identities = 530/546 (97 %), 7 gaps (1 %)), *Vermiculariopsiella pediculata* (GenBank MH866028.1; Identities = 530/556 (95 %), 11 gaps (1 %)) and *Vermiculariopsiella eucalypti* (GenBank NR_154637.1; Identities = 514/540 (95 %), 5 gaps (0 %)). Closest hits using the **LSU** sequence are *Vermiculariopsiella eucalypti* (GenBank KX228303.1; Identities = 815/827 (99 %), no gaps), *Vermiculariopsiella pediculata* (GenBank MH877476.1; Identities = 829/843 (98 %), 3 gaps (0 %)) and *Vermiculariopsiella dichapetali* (GenBank MH107970.1; Identities = 811/839 (97 %), 4 gaps (0 %)).

Anungitopsis lauri Crous, *sp. nov.*

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

Classification — *Venturiaceae*, *Venturiales*, *Dothideomycetes*.

Mycelium consisting of branched, septate, pale olivaceous, smooth, 2–3 µm diam hyphae. *Conidiophores* solitary, erect, medium brown, smooth-walled, flexuous, arising from superficial hyphae, subcylindrical, rarely branched, multiseptate, 200–500 × 5–6 µm, with basal cell extending from hyphae or globose, up to 8 µm diam, lacking rhizoids. *Conidiogenous cells* integrated, subcylindrical, medium brown, smooth-walled, terminal and intercalary, 20–40 × 4–5 µm, polyblastic, with flat-tipped loci, 2–2.5 µm diam, not thickened nor darkened. *Conidia* in branched chains, subcylindrical to narrowly fusoid with obtusely rounded ends, hila truncate, 1–1.5 µm diam, unthickened, nor darkened, 3(–7)-septate, finely roughened, medina cells medium brown, end cells pale brown, (23–)30–35(–47) × (4–)5 µm.

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

Typus. Spain, La Gomera, leaf litter of *Laurus novocanariensis* (*Lauraceae*), 1300 m altitude, 30 Mar. 2017, *A.L. van Iperen*, HPC 2058 (holotype CBS H-23764, culture ex-type CPC 33999 = CBS 145067, ITS sequence GenBank MK047437.1, MycoBank MB828183).

Notes — *Anungitea* is a genus of hyphomycetes defined as having dark, solitary conidiophores, with a denticulate head with flattened conidiogenous scars that are unthickened and not darkened, and chains of cylindrical, 1-septate subhyaline conidia (Sutton 1973). *Anungitopsis* includes taxa with indistinguishable scars arranged in a rachis, and *Neoanungitea* is intermediate between these two genera, having a rachis, but with flat-tipped loci (Crous et al. 2017b). Crous et al. (2018a) introduced the genus *Pseudoanungitea* for species phylogenetically distinct from *Anungitea* s.str., having terminal and intercalary conidiogenous cells, and refractive, thickened scars that give rise to short conidial chains with somewhat darkened and refractive hila. *Anungitopsis lauri* is phylogenetically distinct from those species presently known from their DNA sequence data.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Anungitopsis speciosa* (GenBank EU035401.1; Identities = 601/614 (98 %) and *Neoanungitea eucalypti* (GenBank NR_156383.1; Identities = 495/607 (82 %), 41 gaps (6 %)).

Colour illustrations. *Laurus novocanariensis* growing in Spain. Left column, *Vermiculariopsiella lauracearum*, colony on malt extract agar, branched setae, conidiogenous cells and conidia. Right column, *Anungitopsis lauri*, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Pararamichloridium caricicola

Fungal Planet 801 – 14 December 2018

Pararamichloridium caricicola Crous, *sp. nov.*

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

Classification — *Pararamichloridiaceae*, *Pararamichloridiales*, *Sordariomycetes.*

Mycelium consisting of brown, smooth, branched, 1.5–2 µm diam hyphae. *Conidiophores* arising from superficial hyphae, subcylindrical, erect, flexuous, unbranched, brown, smooth, 1–6-septate, 35–100 × 2.5–3 µm. *Conidiogenous cells* integrated, terminal, subcylindrical with slight apical taper, brown, smooth, 10–25 × 2.5–3 µm; forming a rachis with numerous pimple-like denticles, 0.5 µm diam, inconspicuous, not darkened nor thickened. *Conidia* solitary, aseptate, pale brown, guttulate, covered in a sheath, which gives the surface a wrinkled appearance in lactic acid, ellipsoid, apex obtuse, base truncate, 1.5–2 µm diam, somewhat darkened, (4–)6–7(–8) × 3(–3.5) µm.

Culture characteristics — Colonies flat, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface ochreous, reverse salmon. On PDA surface and reverse greyish with patches of yellow-green. On OA surface buff with patches of ochreous.

Typus. THAILAND, Ratchaburi Province, on leaf of *Carex* sp. (*Cyperaceae*), 2008, *P.W. Crous*, HPC 2251 (holotype CBS H-23766, culture ex-type CPC 34533 = CBS 145069, ITS and LSU sequences GenBank MK047438.1 and MK047488.1, MycoBank MB828187).

Notes — *Pararamichloridium* has a ramichloridium-like morphology (Arzanlou et al. 2007), although it clusters distant from *Ramichloridium* s.str. (Videira et al. 2017). The genus presently includes two species (Crous et al. 2017b), that cluster phylogenetically distinct from *P. caricicola.*

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Pararamichloridium verrucosa* (GenBank NR_156653.1; Identities = 502/576 (87 %), 43 gaps (7 %)) and *Pararamichloridium livistonae* (GenBank NR_156652.1; Identities = 533/656 (81 %), 68 gaps (10 %)). Closest hits using the **LSU** sequence are *Pararamichloridium verrucosa* (GenBank MH873621.1; Identities = 882/897 (98 %), no gaps), *Pararamichloridium livistonae* (GenBank NG_058504.1; Identities = 801/836 (96 %), 3 gaps (0 %)) and *Paracapsulospora metroxyli* (as *Sordariomycetidae* sp. SK-2016a, GenBank KX646364.1; Identities = 849/894 (95 %), 5 gaps (0 %)).

Colour illustrations. Indigenous forest in Thailand; colony sporulating on synthetic nutrient poor agar, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Coniella diospyri

Fungal Planet 802 – 14 December 2018

Coniella diospyri Crous, *sp. nov.*

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

Classification — *Schizoparmaceae*, *Diaporthales*, *Sordariomycetes.*

Conidiomata separate, immersed to superficial, hyaline, becoming black, up to 300 µm diam; ostiole central, 20–25 µm diam; conidiomatal wall of 2–6 layers of medium *brown textura angularis*. *Conidiophores* densely aggregated, subulate, frequently branched below, 1–2-septate, 15–25 × 3–4 µm. *Conidiogenous cells* hyaline, smooth, subcylindrical, with apical taper, 6–8 × 2.5–3.5 µm, covered in a mucoid sheath, apex with visible periclinal thickening. *Conidia* solitary, aseptate, olivaceous brown, cylindrical, straight, smooth-walled, apex subobtuse, base truncate, multi-guttulate, germ slit absent, (19–)21–23(–25) × 3(–3.5) µm.

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

Typus. South Africa, Limpopo Province, Kruger National Park, on leaves of *Diospyros mespiliformis* (*Ebenaceae*), 19 Nov. 2010, *P.W. Crous* HPC 2259 (holotype CBS H-23767, culture ex-type CPC 34674 = CBS 145071, ITS, LSU, *rpb2* and *tef1* sequences GenBank MK047439.1, MK047489.1, MK047543.1 and MK047562.1, MycoBank MB828188).

Additional material examined. South Africa, Limpopo Province, Kruger National Park, on leaves of *Trichilia emetica* (*Meliaceae*), 19 Nov. 2010, *P.W. Crous*, HPC 2260, specimen CBS H-23786, culture CPC 34676 = CBS 145070, ITS, LSU and *tef1* sequences GenBank MK047440.1, MK047490.1 and MK047563.1.

Colour illustrations. *Diospyros mespiliformis* in Kruger National Park; colony sporulating on oatmeal agar, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — The genus *Coniella* was revised by Alvarez et al. (2016), and approximate 30 species are currently accepted in the genus (Marin-Felix et al. 2017, Raudabaugh et al. 2017). *Coniella diospyri* adds an additional species to the genus, being morphologically similar to the *C. castaneicola* complex, although it is phylogenetically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 34674 had highest similarity to *Coniella duckerae* (GenBank NR_154851.1; Identities = 600/611 (98 %), 2 gaps (0 %)), *Coniella quercicola* (GenBank AY339345.1; Identities = 562/577 (97 %), 6 gaps (1 %)) and *Coniella limoniformis* (GenBank NR_154819.1; Identities = 549/564 (97 %), 6 gaps (1 %)). The ITS sequences of CPC 34674 and 34676 are identical. Closest hits using the **LSU** sequence of CPC 34674 are *Coniella tibouchinae* (GenBank JQ281776.2; Identities = 900/911 (99 %), 3 gaps (0 %)), *Coniella granati* (GenBank MH869130.1; Identities = 892/901 (99 %), no gaps) and *Coniella straminea* (GenBank MH866234.1; Identities = 890/898 (99 %), 1 gap (0 %)). The LSU sequences of CPC 34674 and 34676 are identical. Closest hits using the ***rpb2*** sequence of CPC 34674 had highest similarity to *Coniella tibouchinae* (GenBank KX833507.1; Identities = 703/767 (92 %), no gaps), *Coniella limoniformis* (GenBank KX833492.1; Identities = 699/767 (91 %), no gaps) and *Coniella africana* (GenBank KX833421.1; Identities = 689/767 (90 %), no gaps). Closest hits using the ***tef1*** sequence of CPC 34674 had highest similarity to *Coniella tibouchinae* (GenBank JQ281778.1; Identities = 348/412 (84 %), 21 gaps (5 %)), *Coniella eucalyptorum* (GenBank KX833634.1; Identities = 292/337 (87 %), 14 gaps (4 %)) and *Coniella africana* (GenBank KX833600.1; Identities = 371/456 (81 %), 28 gaps (6 %)). The *tef1* sequences of CPC 34674 and 34676 are only 93 % (522/564, including 20 gaps) similar.

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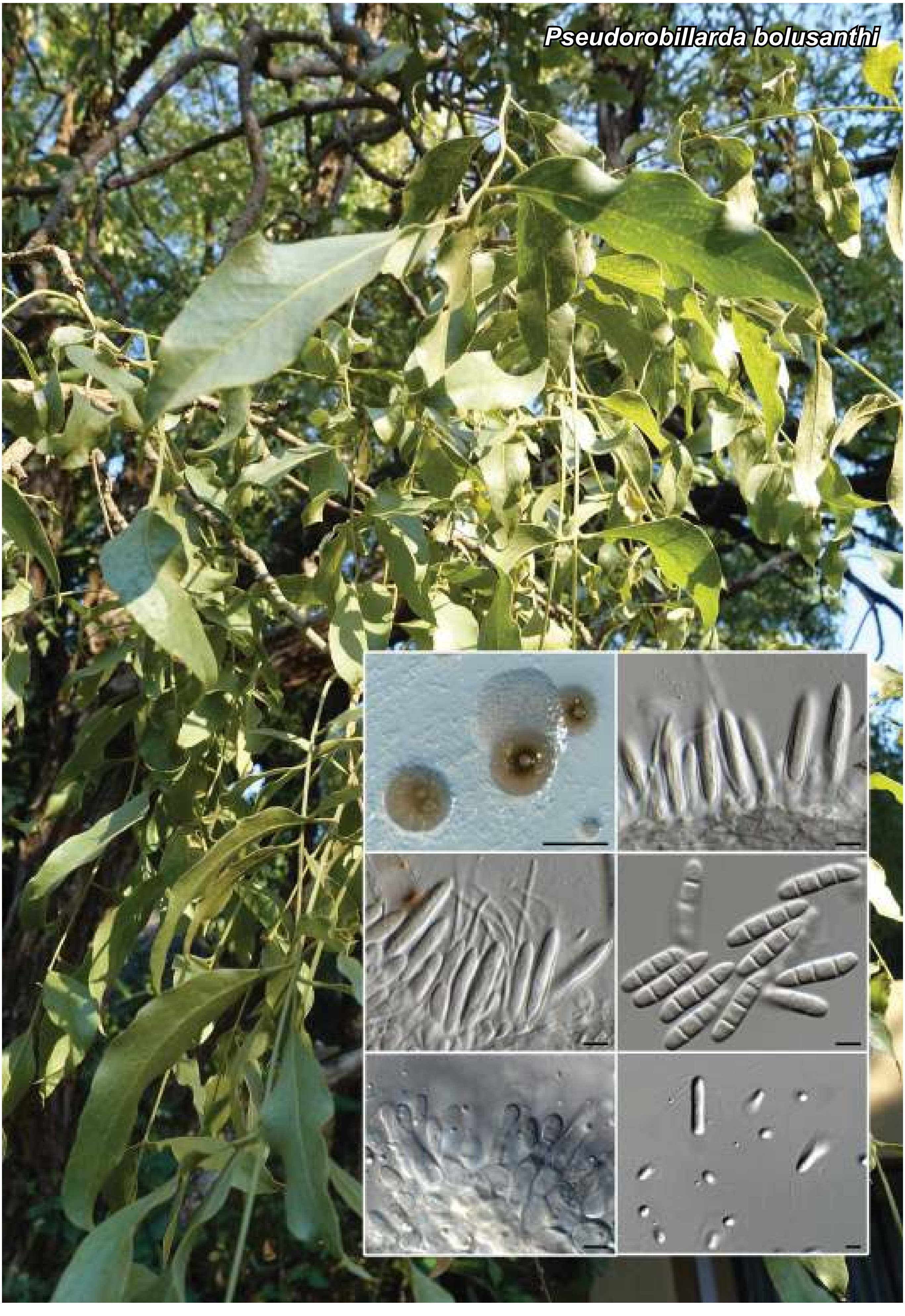
Pseudorobillarda bolusanthi

Fungal Planet 803 – 14 December 2018

Pseudorobillarda bolusanthi Crous, *sp. nov.*

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

Classification — *Pseudorobillardaceae*, *Pleosporales*, *Dothideomycetes.*

Conidiomata immersed, globose, 200–250 µm diam, with central ostiole 50–70 µm diam, surrounded by darker cells than conidiomatal body which is transparent; wall of 3–6 layers of thin-walled, flattened *textura angularis*; conidiomata giving rise to both micro- and macroconidia. *Macroconidiophores* lining the inner cavity, reduced to conidiogenous cells, hyaline, smooth, doliiform, phialidic with periclinal thickening and flared collarette, or proliferating percurrently when older, 4–7(–15) × 3–4 µm. *Paraphyses* numerous, hyphae-like, intermingled among conidiophores, aseptate, flexuous, extending above conidiophores, 50–70 × 1.5–2 µm. *Macroconidia* solitary, (1–)3-septate, guttulate, hyaline, smooth, septa thick and prominent with a central pore linking each cell, apex subobtuse, tapering to a truncate base, 3 µm diam, (21–)26–28(–30) × 6(–7) µm; apical appendages arising from splitting of the conidial sheath, hair-like, flexuous, unbranched, 3–5, up to 30 µm long, fragile, flexuous, unbranched, mostly absent. *Microconidiogenous cells* hyaline, smooth, subcylindrical to ampulliform, proliferating percurrently, 10–15 × 4–5 µm. *Microconidia* solitary, aseptate, hyaline, smooth, guttulate, subcylindrical, apex obtuse, base truncate, 4–8 × 2–4 µm; apical appendages hair-like, flexuous, unbranched, 3–5, up to 10 µm long, fragile, flexuous, unbranched.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface saffron, reverse ochreous. On PDA surface saffron, reverse umber. On OA surface saffron.

Typus. South Africa, Limpopo Province, Kruger National Park, on leaves of *Bolusanthus speciosus* (*Fabaceae*), 19 Nov. 2010, *P.W. Crous*, HPC 2263 (holotype CBS H-23782, culture ex-type CPC 34670 = CBS 145072, ITS and LSU sequences GenBank MK047441.1 and MK047491.1, MycoBank MB828189).

Colour illustrations. *Bolusanthus speciosus* in Kruger National Park; conidiomata on synthetic nutrient poor agar, conidiogenous cells, paraphyses and conidia. Scale bars: conidiomata = 200 µm, all others = 10 µm.

Notes — *Pseudorobillarda* was treated by Nag Raj (1993), and presently contains 15 species. Species of *Pseudorobillarda* have been recorded as saprobes, plant pathogens, and endophytes (Vujanovic & St-Arnaud 2003), but have also been isolated from soil (Kadowaki et al. 2014). *Pseudorobillarda bolusanthi* has paraphyses and 3-septate conidia, being most similar to *P. indica* (conidia 14.5–21.5 × 3.5–5.5 µm; Nag Raj 1993), but is distinct in having larger conidia with thick septa, and characteristic microconidia that also bear apical appendages.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pseudorobillarda siamensis* (GenBank FJ825370.1; Identities = 725/912 (79 %), 56 gaps (6 %)), *Acrocalymma aquatica* (GenBank JX276951.1; Identities = 562/642 (88 %), 20 gaps (3 %)) and *Rhizopycnis vagum* (GenBank HE585021.1; Identities = 558/637 (88 %), 19 gaps (3 %)). Closest hits using the **LSU** sequence are *Pseudorobillarda texana* (GenBank FJ825377.1; Identities = 815/854 (95 %), 4 gaps (0 %)), *Pseudorobillarda sojae* (GenBank KF827458.1; Identities = 814/861 (95 %), 6 gaps (0 %)) and *Pseudorobillarda phragmitis* (GenBank MH869670.1; Identities = 805/859 (94 %), 4 gaps (0 %)).

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Neomyrmecridium septatum

Fungal Planet 804 – 14 December 2018

Neomyrmecridium Crous, *gen. nov.*

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

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

Mycelium consisting of septate, branched hyphae, hyaline, smooth. *Conidiophores* solitary, erect, straight, unbranched, medium brown, smooth, subcylindrical, septate. *Conidiogenous cells* terminal, integrated, subcylindrical, medium brown, smooth, with several denticles at apex; not thickened nor darkened. *Conidia* solitary, hyaline, smooth, guttulate, becoming pale brown with age, upper two thirds encased in mucoid sheath, fusoid-ellipsoid, septate.

Type species. *Neomyrmecridium septatum* Crous.
MycoBank MB828190.

Neomyrmecridium septatum Crous, *sp. nov.*

Etymology. Name refers to its septate conidia.

Mycelium consisting of septate, branched hyphae, hyaline, smooth, 2–3 µm diam. *Conidiophores* solitary, erect, straight, unbranched, medium brown, smooth, subcylindrical, 1–4-septate, 40–70 × 4–5 µm. *Conidiogenous cells* terminal, integrated, subcylindrical, medium brown, smooth, 30–40 × 4–5 µm, with several denticles at apex, 1–1.5 × 1 µm; not thickened nor darkened. *Conidia* solitary, hyaline, smooth, guttulate, becoming pale brown with age, upper two thirds encased in mucoid sheath, 1–2 µm diam, fusoid-ellipsoid, apex obtuse, tapering in lower third to a truncate hilum, 0.5–1 µm diam, (1–)3-septate, (12–)14–16(–20) × (3.5–)4(–5) µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and even, smooth, lobate margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface and reverse apricot. On PDA surface apricot, reverse luteous. On OA surface pale luteous.

Typus. Thailand, Ratchaburi Province, on leaves of unidentified vine, 2008, *P.W. Crous*, HPC 2252 (holotype CBS H-23768, culture ex-type CPC 34585 = CBS 145073, ITS, LSU, *rpb1*, *rpb2* and *tef1* sequences GenBank MK047442.1, MK047492.1, MK047531.1, MK047544.1 and MK047564.1, MycoBank MB828191).

Colour illustrations. Indigenous forest in Thailand; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — *Myrmecridium* is a ramichloridium-like genus with hyaline mycelium, and relatively unpigmented, pimple-like denticles (Arzanlou et al. 2007). The genus presently contains 12 species, all of which are known from their DNA. Species are distinguished based on conidium and conidiophore morphology, as well as DNA phylogeny (Crous et al. 2015a, 2016a).

Myrmecridium sorbicola was recently introduced by Crous et al. (2018a), who commented on the fact that it was distinct from known species of *Myrmecridium* in having septate conidia. In the present additional species are added (also with septate conidia), resolving this clade to represent a new genus, clustering sister to *Myrmecridium* s.str.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Myrmecridium sorbicola* (GenBank MH107901.1; Identities = 502/564 (89 %), 19 gaps (3 %)), *Myrmecridium banksiae* (GenBank NR_111762.1; Identities = 480/553 (87 %), 15 gaps (2 %)) and *Myrmecridium spartii* (GenBank KX306762.1; Identities = 483/558 (87 %), 17 gaps (3 %)). Closest hits using the **LSU** sequence are *Myrmecridium sorbicola* (GenBank MH107948.1; Identities = 815/842 (97 %), 2 gaps (0 %)), *Myrmecridium schulzeri* (GenBank MH473005.1; Identities = 857/898 (95 %), 2 gaps (0 %)) and *Pleurophragmium acutum* (GenBank MH876650.1; Identities = 853/894 (95 %), no gaps). No significant hits were obtained when the ***rpb1***, ***rpb2*** and ***tef1*** sequences were used in blastn and megablast searches.

Neomyrmecridium sorbicola (Crous & R.K. Schumach.) Crous, *comb. nov.*

MycoBank MB828192.

Basionym. *Myrmecridium sorbicola* Crous & R.K. Schumach., Fungal Syst. Evol. 1: 191. 2018.

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Xenodactylaria thailandica

Fungal Planet 805 – 14 December 2018

Xenodactylariaceae Crous, *fam. nov.*

MycoBank MB828248.

Xenodactylaria Crous, *gen. nov.*

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

Classification — *Xenodactylariaceae*, *Myrmecridiales*, *Sordariomycetes.*

Mycelium consisting of smooth, hyaline, branched, septate, hyphae. *Conidiophores* reduced to conidiogenous cells on hyphae, erect to flexuous, hyaline, smooth, with 1 to several denticulate apical loci. *Conidia* occurring in branched chains, hyaline, smooth, subcylindrical, septate.

Type species. Xenodactylaria thailandica Crous.
MycoBank MB828193.

Xenodactylaria thailandica Crous, *sp. nov.*

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

Mycelium consisting of smooth, hyaline, branched, septate, 2–2.5 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells on hyphae, erect to flexuous, 5–20 × 2–3.5 µm, hyaline, smooth, with 1 to several denticulate apical loci, 1–2 × 1.5–2 µm. *Conidia* occurring in branched chains (mostly unbranched), hyaline, smooth, guttulate, subcylindrical, straight, apex obtuse, base truncate, 1.5–2 µm diam, 3(–5)-septate, (20–)24–27(–32) × (3–)4 µm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 22 mm diam after 2 wk at 25 °C. On MEA surface pale mouse grey, reverse olivaceous grey in centre, buff in outer region. On PDA surface and reverse buff. On OA surface olivaceous grey.

Typus. THAILAND, Ratchaburi Province, on leaves of unidentified vine, 2008, *P.W. Crous*, HPC 2252 (holotype CBS H-23769, culture ex-type CPC 34588 = CBS 145074, ITS and LSU sequences GenBank MK047443.1 and MK047493.1, MycoBank MB828194).

Notes — *Dactylaria* (De Hoog 1985) is heterogeneous (Crous et al. 2016a, 2017b), with its type species, *D. purpurella*, clustering in *Magnaporthales* (Klaubauf et al. 2014). *Xenodactylaria* is reminiscent of *Dactylaria* and *Cylindrosympodium*, but distinct in that all structures are hyaline, and conidia occur in short chains. Phylogenetically, it also clusters on its own, and a new genus and family is introduced to accommodate it.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Fusarium robustum* (GenBank MH861018.1; Identities = 454/548 (83 %), 37 gaps (6 %)), *Fusarium venenatum* (GenBank NR_156290.1; Identities = 454/550 (83 %), 38 gaps (6 %)) and *Fusarium sambucinum* (GenBank KM231813.1; Identities = 451/547 (82 %), 37 gaps (6 %)). Closest hits using the **LSU** sequence are *Acremonium pteridii* (GenBank MH871174.1; Identities = 827/896 (92 %), 9 gaps (1 %)), *Ijuhya dentifera* (GenBank MH872777.1; Identities = 822/892 (92 %), 9 gaps (1 %)) and *Purpureocillium lilacinum* (GenBank MH876802.1; Identities = 826/897 (92 %), 8 gaps (0 %)).

Colour illustrations. Indigenous forest in Thailand; conidiogenous cells and conidia. Scale bars = 10 µm.

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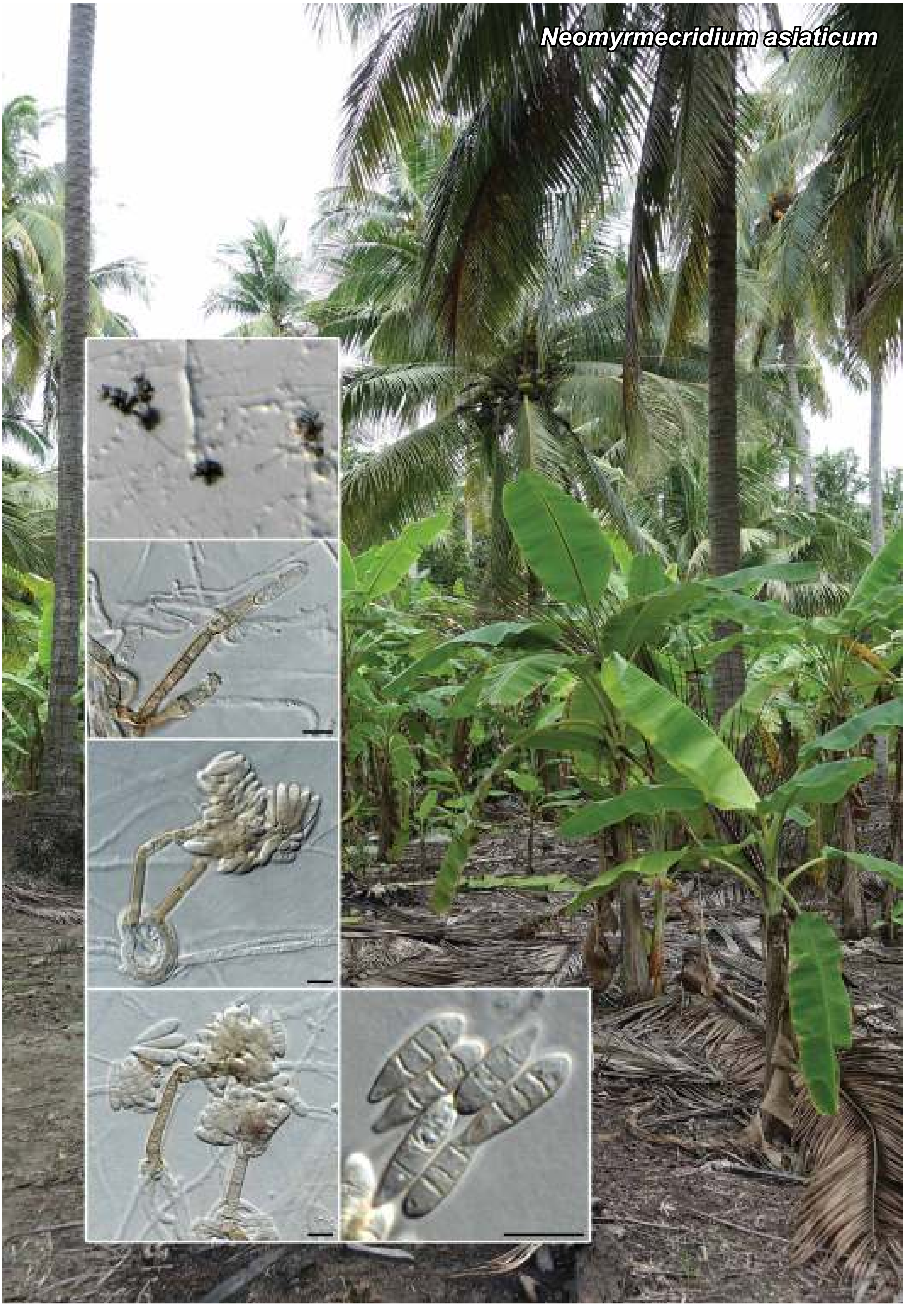
Neomyrmecridium asiaticum

Fungal Planet 806 – 14 December 2018

Neomyrmecridium asiaticum Crous, *sp. nov.*

Etymology. Name refers to Asia, the continent where this fungus was collected.

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

On SNA: *Mycelium* consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* arising from hyphal coils on creeping hyphae, solitary or in groups of up to three, medium brown, smooth- and thick-walled, mostly unbranched, 2–5-septate, 50–100 × 3–5 µm. *Conidiogenous cells* integrated, terminal, 5–35 × 4–7 µm, subcylindrical, apex obtuse, covered in protruding denticles, 0.5–1 × 1 µm, slightly darkened. *Conidia* solitary, (2–)3-septate, pale brown, thin- and smooth-walled, guttulate, surrounded by a wing-like gelatinous sheath c. 0.5 µm thick, ellipsoid to obovoid, (13–)15–16(–17) × (4–)4.5(–5) µm, tapering in lower conical cell to truncate hilum, 1–1.5 µm diam, not thickened nor darkened.

Culture characteristics — Colonies flat, spreading, with folded surface, sparse aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface and reverse saffron. On PDA surface luteous with patches of orange, reverse amber. On OA surface luteous with diffuse amber pigment.

Typus. Thailand, Ratchaburi Province, on leaves of unidentified vine, 2008, *P.W. Crous*, HPC 2252 (holotype CBS H-23774, culture ex-type CPC 34535 = CBS 145080, ITS and LSU sequences GenBank MK047444.1 and MK047494.1, MycoBank MB828195).

Colour illustrations. Agricultural farm in Thailand; colony sporulating on nutrient poor agar, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — *Neomyrmecridium asiaticum* represents a new species isolated from dead vines in Thailand, where it co-occurred with another new species, *N. septatum*. *Neomyrmecridium septatum* (conidia (1–)3-septate, (12–)14–16(–20) × (3.5–)4(–5) µm) is similar to *N. asiaticum* based on its conidium morphology, but the two species are phylogenetically distinct. The ITS sequences of *N. septatum* and *N. asiaticum* are 89 % (501/560 including 14 gaps) similar.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neomyrmecridium sorbicola* (GenBank MH107901.1; Identities = 510/562 (91 %), 11 gaps (1 %)), *Myrmecridium phragmitis* (GenBank NR_137782.1; Identities = 489/558 (88 %), 13 gaps (2 %)) and *Ramichloridium schulzeri* (GenBank MH859088.1; Identities = 481/552 (87 %), 13 gaps (2 %)). Closest hits using the **LSU** sequence are *Myrmecridium sorbicola* (GenBank MH107948.1; Identities = 826/842 (98 %), 2 gaps (0 %)), *Myrmecridium schulzeri* (GenBank MH473005.1; Identities = 856/887 (97 %), 2 gaps (0 %)) and *Pleurophragmium acutum* (GenBank MH876650.1; Identities = 853/886 (96 %), no gaps).

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Neoeucasphaeria eucalypti

Fungal Planet 807 – 14 December 2018

Neoeucasphaeria Crous, *gen. nov.*

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

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

Mycelium consisting of hyaline, smooth, thick-walled, branched, septate, hyphae, frequently encased in mucoid sheath. *Conidiomata* sporodochial, becoming aggregated with age, consisting of a dense series of branches that each give rise to conidiogenous cells. *Conidiogenous cells* hyaline, smooth, subcylindrical, phialidic, flexuous, with visible periclinal thickening. *Conidia* aggregating in an orange mass, individually hyaline, smooth, guttulate, ellipsoid, aseptate, straight, apex subobtuse, base truncate.

Type species. *Neoeucasphaeria eucalypti* Crous.
MycoBank MB828249.

Neoeucasphaeria eucalypti Crous, *sp. nov.*

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

Mycelium consisting of hyaline, smooth, thick-walled, branched, septate, 2–4 µm diam hyphae, frequently encased in mucoid sheath. *Conidiomata* sporodochial, 30–100 µm diam, becoming aggregated with age, consisting of a dense series of branches that each give rise to 1–6 conidiogenous cells. *Conidiogenous cells* hyaline, smooth, subcylindrical, phialidic, flexuous, 8–15 × 2–2.5 µm, with visible periclinal thickening. *Conidia* aggregating in an orange mass, individually hyaline, smooth, guttulate, ellipsoid, aseptate, straight, apex subobtuse, base truncate, (3–)4(–5) × (2–)2.5 µm.

Culture characteristics — Colonies flat, spreading, lacking aerial mycelium and smooth (MEA, OA), to feathery (PDA) margin, reaching 25 mm diam after 2 wk at 25 °C. On MEA, PDA and OA, surface and reverse orange.

Typus. AUSTRALIA, Victoria, Arthurs Seat, on *Eucalyptus* sp. (*Myrtaceae*), 23 Dec. 2016, *A.J. Carnegie*, HPC 1938 (holotype CBS H-23770, culture ex-type CPC 33366 = CBS 145075, ITS and LSU sequences GenBank MK047445.1 and MK047495.1, MycoBank MB828196).

Colour illustrations. *Eucalyptus* forest in Australia; colony sporulating on synthetic nutrient poor agar, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — *Neoeucasphaeria eucalypti* clusters basal to *Eucasphaeria* s.str., and is also distinct in having aseptate, ellipsoid conidia. *Eucasphaeria* contains two species, characterised by producing sporodochial conidiomata, hyaline, branched conidiophores, phialidic conidiogenous cells, and hyaline, 0–2-septate, falcate conidia (Crous et al. 2016a).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Eucasphaeria rustici* (GenBank KY173410.1; Identities = 534/542 (99 %), 2 gaps (0 %)), *Eucasphaeria capensis* (GenBank NR_156204.1; Identities = 556/565 (98 %), 5 gaps (0 %)) and *Rosasphaeria moravica* (GenBank NR_138377.1; Identities = 545/566 (96 %), 9 gaps (1 %)). Closest hits using the **LSU** sequence are *Eucasphaeria rustici* (GenBank KY173501.1; Identities = 812/819 (99 %), 2 gaps (0 %)), *Eucasphaeria capensis* (GenBank MH874625.1; Identities = 835/844 (99 %), 2 gaps (0 %)) and *Rosasphaeria moravica* (GenBank JF440985.1; Identities = 832/844 (99 %), 2 gaps (0 %)).

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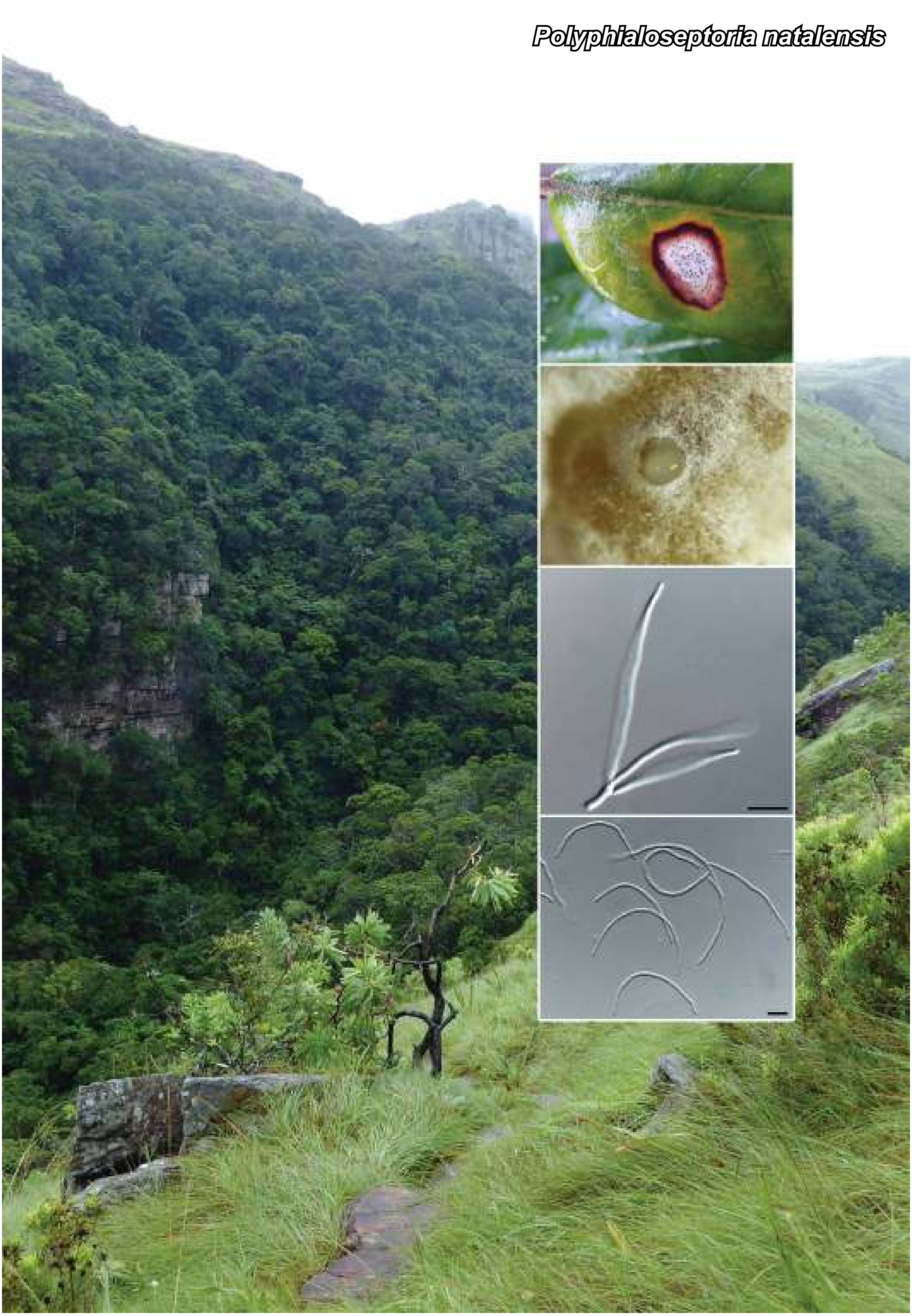
Polyphialoseptoria natalensis



Fungal Planet 808 – 14 December 2018

Polyphialoseptoria natalensis Crous, *sp. nov.*

Etymology. Name refers to the KwaZulu-Natal Province in South Africa, where this fungus was collected.

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

Conidiomata brown, erumpent, acervular on OA, globose, 200–350 µm diam; wall of several layers of pale *textura angularis. Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, smooth, subcylindrical, proliferating sympodially at apex, 10–15 × 2.5–3.5 µm, polyphialidic. *Conidia* hyaline, smooth, guttulate, solitary, scolecosporous, irregularly curved, apex subobtuse, base truncate, 3–8-septate, (40–)65–70(–80) × 2(–3) µm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with sparse aerial mycelium and smooth, lobate margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA surface saffron, reverse luteous. On PDA surface dirty white, reverse umber. On OA surface saffron.

Typus. South Africa, KwaZulu-Natal, Port Edward, Umtamuma N.R., on leaves of unidentified plant host, Feb. 2010, *J. Roux*, HPC 1702 (holotype CBS H-23771, culture ex-type CPC 33214 = CBS 145076, ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MK047446.1, MK047496.1, MK047545.1, MK047565.1 and MK047581.1, MycoBank MB828197).

Notes — *Polyphialoseptoria* was established by Quaedvlieg et al. (2013) to accommodate septoria-like species with pycnidial conidiomata, and conidiogenous cells with sympodial, and polyphialidic proliferation. *Polyphialoseptoria natalensis* adds a third species to the genus, which is phylogenetically distinct from the other known taxa.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Polyphialoseptoria terminaliae* (GenBank NR_156559.1; Identities = 509/532 (96 %), 9 gaps (1 %)), *Polyphialoseptoria tabebuiae-serratifoliae* (GenBank NR_156558.1; Identities = 490/518 (95 %), 9 gaps (1 %)) and *Xenomycosphaerella diplazii* (GenBank NR_154505.1; Identities = 476/538 (88 %), 29 gaps (5 %)). Closest hits using the **LSU** sequence are *Polyphialoseptoria tabebuiae-serratifoliae* (GenBank KF251716.1; Identities = 810/821 (99 %), no gaps), *Polyphialoseptoria terminaliae* (GenBank MH878128.1; Identities = 820/838 (98 %), 5 gaps (0 %)) and *Hyalozasmidium aerohyalinosporum* (GenBank NG_059440.1; Identities = 811/836 (97 %), 2 gaps (0 %)). Closest hits using the ***rpb2*** sequence are *Polyphialoseptoria terminaliae* (GenBank MF951615.1; Identities = 664/736 (90 %), no gaps), *Polyphialoseptoria tabebuiae-serratifoliae* (GenBank MF951613.1; Identities = 593/666 (89 %), no gaps) and *Deightonomyces daleae* (GenBank MF951485.1; Identities = 520/686 (76 %), 22 gaps (3 %)). No significant hits were obtained when the ***tef1*** sequence was used in blastn and megablast searches. Only distant hits with species of *Mycosphaerellaceae* were obtained when the ***tub2*** sequence was used in blastn and megablast searches.

Colour illustrations. Forest in Port Edward, Umtamuma, South Africa; symptomatic leaf, colony sporulating on oatmeal agar, conidiogenous cell and conidia. Scale bars = 10 µm.

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Fumagopsis stellae

Fungal Planet 809 – 14 December 2018

Fumagopsis stellae Crous & Carnegie, *sp. nov.*

Etymology. A fungus with star-shaped conidia, named for Stella Carnegie, the star of the Carnegie family.

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

Conidiomata sporodochial, slimy, solitary, erumpent, 100–200 µm diam, with dark brown, erect, flexuous, aseptate setae that are thick-walled, up to 90 µm long, 3–5 µm diam. *Mycelium* consisting of pale brown, smooth, septate, branched hyphae, prominently constricted at septa, 2–3.5 µm diam, with several cells becoming swollen and ellipsoid, 4–7 µm diam. *Conidiogenous cells* integrated on hyphae, terminal and lateral, subcylindrical, hyaline, smooth, 8–20 × 3–3.5 µm, mono- to polyblastic. *Conidia* variable, solitary, hyaline, smooth-walled, star-shaped, with 3–4 upright arms and one basal arm attached to the conidiogenous cell; lateral arms 1–3-septate, constricted at septa, ends obtusely rounded, arms 20–40 × 3–5 µm; basal arm 0(–1)-septate, subcylindrical, 10–30 × 3–5 µm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and feathery, lobate margin, reaching 7 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse fuscous black.

Typus. Australia, New South Wales, Kangaroo River State Forest, on leaves of *Eucalyptus* sp. (*Myrtaceae*), 23 Jan. 2010, *A.J. Carnegie*, HPC 1941 (holotype CBS H-23772, culture ex-type CPC 33216 = CBS 145078, ITS and LSU sequences GenBank MK047447.1 and MK047497.1, MycoBank MB828198).

Colour illustrations. *Eucalyptus* forest in Australia; star-shaped conidia, and brown, unbranched seta. Scale bars = 10 µm.

Notes — When this fungus was initially observed on host material, it had sporodochia with brown setae, giving rise to star-shaped conidia. In culture, it formed sporodochia, but very few brown setae were observed. Morphologically, it is reminiscent of *Vonarxia*, having sporodochia with dispersed brown setae, and star-shaped conidia (Crous et al. 2009), but it is phylogenetically distinct, and based on its aseptate setae, we choose to place it in *Fumagopsis*, a genus presently known from two species, *F. complexa* (on *Eugenia jambolana*, India; conidial lateral arms 55–70 × 2–2.8 µm; Wu & Sutton 1995) and *F. triglifioides* (on *Lucuma neriifolia*, Argentina; conidial lateral arms (12–)20–24 × 2–2.5 µm; Van der Aa & Van Oorschot 1985). Although the three species are distinct based on their conidium morphology, there are presently no molecular data to compare them with *F. stellatae*.

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 = 523/575 (91 %), 28 gaps (4 %)), *Exophiala eucalyptorum* (GenBank MH863133.1; Identities = 508/573 (89 %), 22 gaps (3 %)) and *Cladophialophora modesta* (GenBank MG757349.1; Identities = 343/388 (88 %), 12 gaps (3 %)). Closest hits using the **LSU** sequence are *Exophiala eucalyptorum* (GenBank KC455258.1; Identities = 821/862 (95 %), 4 gaps (0 %)), *Aphanophora eugeniae* (GenBank NG_056965.1; Identities = 819/862 (95 %), 2 gaps (0 %)) and *Ceramothyrium linnaeae* (GenBank MH874144.1; Identities = 816/861 (95 %), 1 gap (0 %)).

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Cymostachys thailandica

Fungal Planet 810 – 14 December 2018

Cymostachys thailandica Crous, *sp. nov.*

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

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

Conidiophores macronematous, mononematous, mostly in clusters, thin-walled, cymosely branched, erect, straight to flexuous, hyaline, 1–2-septate, smooth to slightly verruculose, 50–120 × 4–5 µm, bearing a whorl of 3–6 conidiogenous cells. *Conidiogenous cells* phialidic, clavate, olivaceous brown to dark brown at the apex, paler towards the base, smooth to slightly verruculose, 8–12 × 4–6 µm, with conspicuous collarette. *Conidia* acrogenous, aseptate, fabiform, dark brown, smooth to verruculose, (8–)9(–11) × (4–)5(–6) µm, rounded at ends, aggregating in mucoid mass.

Culture characteristics — Colonies spreading, with folded surface (MEA), sparse aerial mycelium and smooth, lobate margin, reaching 37 mm diam after 2 wk at 25 °C. On MEA surface pale olivaceous grey, reverse sienna. On PDA surface and reverse olivaceous grey. On OA surface isabelline.

Typus. Thailand, Ratchaburi Province, on leaves of unidentified vine, 2008, *P.W. Crous*, HPC 2252 (holotype CBS H-23773, culture ex-type CPC 34505 = CBS 145079, ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MK047448.1, MK047498.1, MK047546.1, MK047566.1 and MK047582.1, MycoBank MB 828199).

Colour illustrations. Indigenous forest in Thailand; colony sporulating on oatmeal agar, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — *Cymostachys* was established for stachybotrys-like fungi characterised by irregularly cymosely, branched conidiophores and olivaceous brown to dark brown, fabiform conidia. *Cymostachys thailandica* is phylogenetically distinct, but related to *C. coffeicola*, which is known from leaves of *Coffea arabica* (Cuba), and *Poinsettia* sp. (Thailand) (Lombard et al. 2016). The genus presently includes four species.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cymostachys coffeicola* (GenBank KU846052.1; Identities = 562/569 (99 %), 5 gaps (0 %)), *Cymostachys fabispora* (GenBank KU846054.1; Identities = 541/548 (99 %), 5 gaps (0 %)) and *Stachybotrys renispora* (GenBank KU144929.1; Identities = 543/551 (99 %), 6 gaps (1 %)). Closest hits using the **LSU** sequence are *Cymostachys coffeicola* (GenBank MH872746.1; Identities = 889/895 (99 %), 2 gaps (0 %)), *Stachybotrys nephrospora* (GenBank KP893314.1; Identities = 887/892 (99 %), 1 gap (0 %)) and *Memnoniella echinata* (GenBank MH866746.1; Identities = 877/895 (98 %), 3 gaps (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Cymostachys coffeicola* (GenBank KU846081.1; Identities = 712/721 (99 %), no gaps), *Cymostachys fabispora* (GenBank KU846082.1; Identities = 695/721 (96 %), no gaps) and *Striatibotrys eucylindrospora* (GenBank KU846975.1; Identities = 650/750 (89 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Cymostachys coffeicola* (GenBank KU846097.1; Identities = 455/476 (96 %), 2 gaps (0 %)), *Cymostachys fabispora* (GenBank KU846098.1; Identities = 418/478 (87 %), 11 gaps (2 %)) and *Striatibotrys rhabdospora* (GenBank KU847089.1; Identities = 232/263 (88 %), 5 gaps (1 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Cymostachys coffeicola* (GenBank KU846113.1; Identities = 336/343 (98 %), no gaps), *Cymostachys fabispora* (GenBank KU846114.1; Identities = 330/343 (96 %), 3 gaps (0 %)) and *Cymostachys garethjonesii* (GenBank KY124126.1; Identities = 274/286 (96 %), 3 gaps (1 %)).

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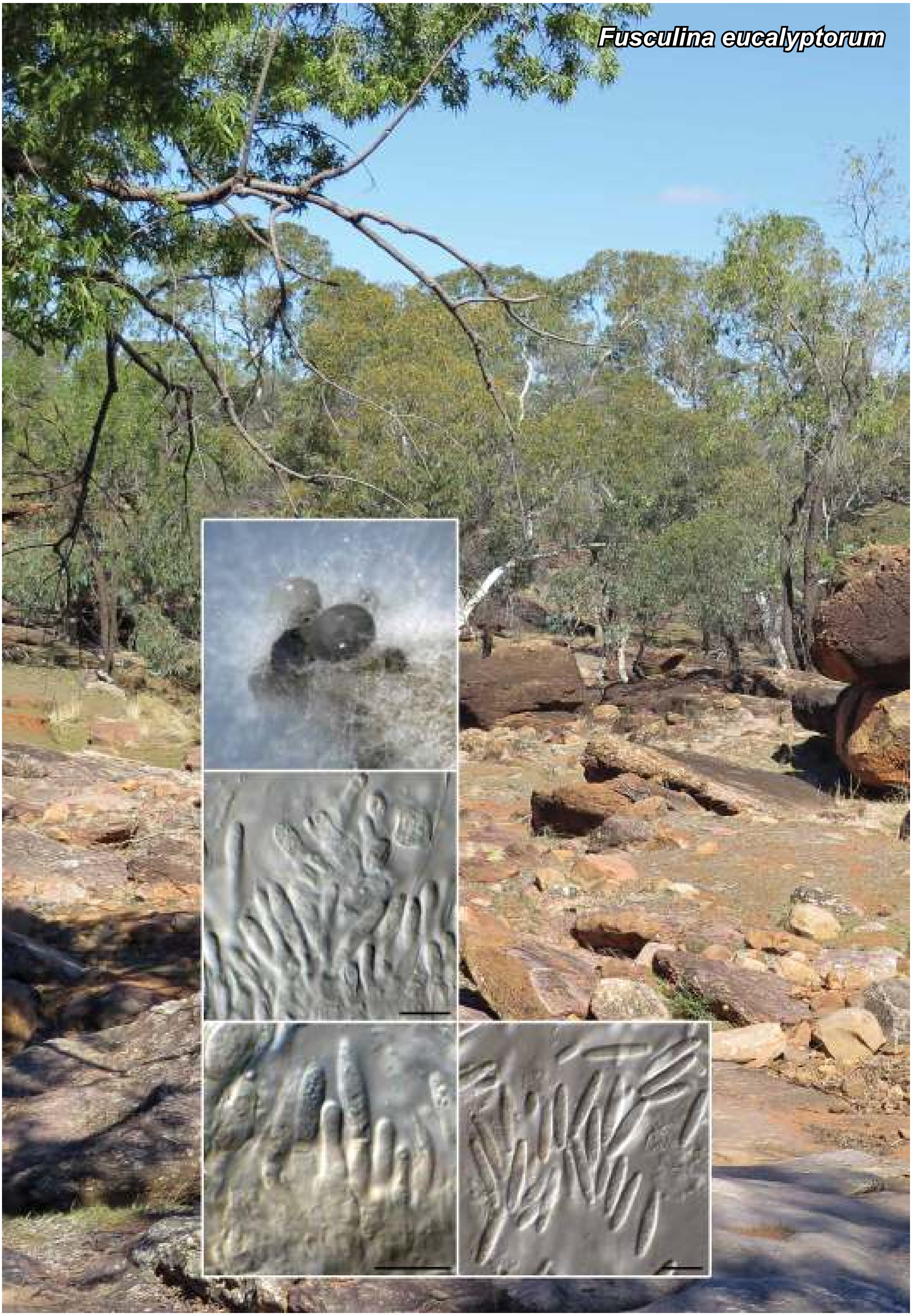
Fusculina eucalyptorum

Fungal Planet 811 – 14 December 2018

Fusculinaceae Crous, *fam. nov.*

Classification — *Fusculinaceae*, *Pleosporales*, *Dothideomycetes.*

Mycelium predominantly internal, but external hyphae brown, thick-walled, giving rise to chlamydospore-like cells. *Conidiomata* pycnidial, immersed, becoming slightly erumpent, brown, opening by irregular rupture; wall consisting of several layers of brown cells of *textura angularis*. *Paraphyses* intermingled among conidiogenous cells, cylindrical, branched below, septate; at times becoming fertile. *Conidiophores* reduced to dimorphic conidiogenous cells. *Primary conidiogenous cells* hyaline, smooth, ampulliform to subcylindrical, proliferating several times percurrently near apex, giving rise to *primary conidia*, hyaline to brown, smooth to verruculose, subcylindrical, obovoid to semiclavate, aseptate or 1-septate, with or without mucoid sheath. *Secondary conidiogenous cells* integrated among primary conidiogenous cells, hyaline, smooth, proliferating sympodially. *Secondary conidia* hyaline, smooth, granular, ellipsoid with rounded ends, or subcylindrical with obtuse apex and truncate base.

Type genus. *Fusculina* Crous & Summerell.
MycoBank MB828200.

Note — The family *Fusculinaceae* presently includes *Fusculina* and *Gordonomyces*. Both genera are associated with leaf spots, occurring on respectively *Myrtaceae* and *Proteaceae*.

Fusculina eucalyptorum Crous, *sp. nov.*

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

Conidiomata solitary, erumpent, pycnidial, globose, brown, 200–250 µm diam, exuding a creamy conidial mass; wall of 6–8 layers of brown *textura angularis*. On OA paraphyses observed among conidiophores, hyaline, smooth, septate, hyphae-like, 2–3 µm diam. On OA conidiomata are surrounded by chains of chlamydospore-like cells, prominently constricted at septa, hyaline to brown, 0–1-septate, up to 8 µm diam. *Conidiophores* lining the inner cavity, subcylindrical, 15–25 × 4–5 µm, smooth, hyaline, giving rise to 1–2 conidiogenous cells. *Conidiogenous cells* hyaline, smooth, terminal and intercalary, 7–15 × 3–4 µm, proliferating percurrently. *Conidia* solitary, hyaline, smooth, guttulate, aseptate, fusoid, apex subobtuse, base truncate, 2–2.5 µm diam, (10–)13–15(–17) × (3.5–)4 µm.

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

Typus. Australia, New South Wales, Mount Grenfell Historic Site, on leaves of *Eucalyptus socialis* (*Myrtaceae*), 24 Aug. 2015, *B.A. Summerell*, HPC 2221 (holotype CBS H-23775, culture ex-type CPC 34407 = CBS 145083, ITS and LSU sequences GenBank MK047449.1 and MK047499.1, MycoBank MB828201).

Colour illustrations. Mount Grenfell, Australia; colony sporulating on synthetic nutrient poor agar, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — The monotypic genus *Fusculina* was established for a fusicoccum-like genus occurring on leaf spots of *Eucalyptus* (Summerell et al. 2006). *Fusculina eucalyptorum* is distinct from *F. eucalypti* (conidia 16–22 × 3–4 µm) by having smaller conidia, and lacking secondary conidia and chlamydospores.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Fusculina eucalypti* (GenBank NR_132812.1; Identities = 653/712 (92 %), 9 gaps (1 %)), *Gordonomyces mucovaginatus* (GenBank NR_157428.1; Identities = 447/501 (89 %), 22 gaps (4 %)) and *Preussia minima* (GenBank JX427054.1; Identities = 380/471 (81 %), 21 gaps (4 %)). Closest hits using the **LSU** sequence are *Fusculina eucalypti* (GenBank DQ923531.1; Identities = 880/888 (99 %), no gaps), *Gordonomyces mucovaginatus* (GenBank NG_057941.1; Identities = 836/863 (97 %), 5 gaps (0 %)) and *Murispora fagicola* (GenBank NG_060797.1; Identities = 824/895 (92 %), 12 gaps (1 %)).

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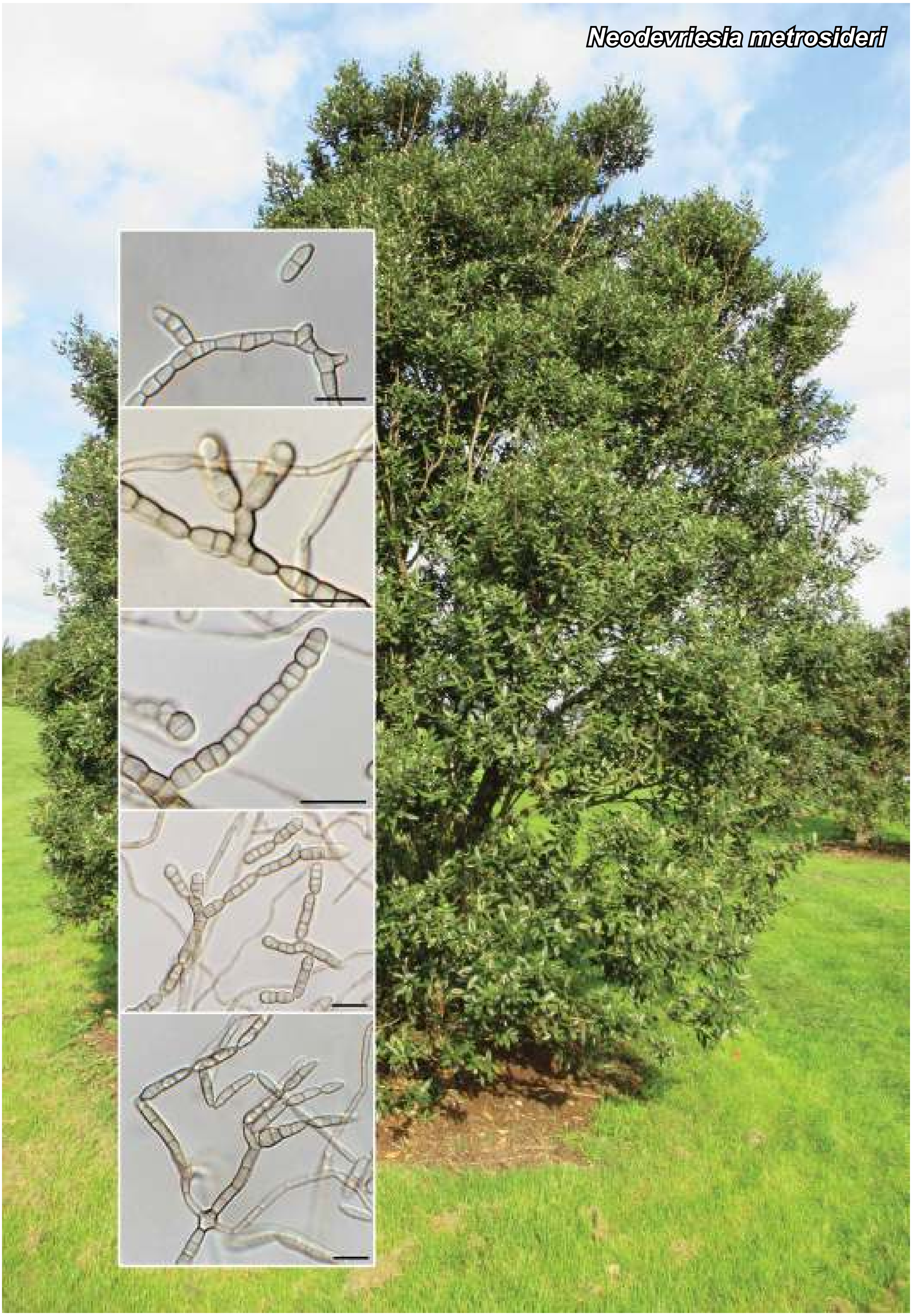
Neodevriesia metrosideri

Fungal Planet 812 – 14 December 2018

Neodevriesia metrosideri Crous, *sp. nov.*

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

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

Mycelium consisting of pale brown, smooth, septate, branched, 2–3 µm diam hyphae. *Conidiophores* solitary, erect, arising from superficial hyphae, subcylindrical, pale brown, smooth-walled, 1–4-septate, 8–30 × 2.5–3 µm. *Conidiogenous cells* terminal, integrated, subcylindrical, pale brown, smooth, 5–8 × 2.5–3 µm; loci inconspicuous, truncate, sympodial, 1–1.5 µm diam, not thickened nor darkened. *Conidia* occurring in branched chains, pale to medium brown, smooth-walled, guttulate, subcylindrical, 1–4-septate; ramoconidia 10–15 × 2–3 µm; conidia (10–)12–15(–17) × 2–3 µm.

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

Typus. New Zealand, Great Barrier Island, on *Metrosideros* sp. (*Myrtaceae*), 31 Aug. 2017, *R. Thangavel*, T17_03062B (holotype CBS H-23776, culture ex-type CPC 34458 = CBS 145084, ITS and LSU sequences GenBank MK047450.1 and MK047500.1, MycoBank MB828202).

Notes — The genus *Neodevriesia* (Quaedvlieg et al. 2014) which presently includes approximately 20 species, is discussed elsewhere in this paper. *Neodevriesia metrosideri* is phylogenetically distinct from all species in the genus. An interesting aspect of this species is the prominent difference between young and mature conidia, where young conidial chains are slender and pale olivaceous, and older chains are wider, prominently constricted at septa, and darker brown.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neodevriesia lagerstroemiae* (GenBank GU214634.1; Identities = 544/558 (97 %), 4 gaps (0 %)), *Devriesia fraserae* (as *Devriesia fraseriae*, GenBank NR_144961.1; Identities = 533/559 (95 %), 9 gaps (1 %)) and *Devriesia sardiniae* (GenBank KP791766.1; Identities = 529/555 (95 %), 4 gaps (1 %)). Closest hits using the **LSU** sequence are *Neodevriesia lagerstroemiae* (GenBank KF902149.1; Identities = 738/746 (99 %), no gaps), *Neodevriesia knoxdaviesii* (as *Teratosphaeria knoxdaviesii*, GenBank EU707865.1; Identities = 831/843 (99 %), 2 gaps (0 %)) and *Neodevriesia cladophorae* (as *Devriesia* sp. MW-2016a, GenBank KU578114.1; Identities = 825/839 (98 %), no gaps).

Colour illustrations. *Metrosideros* sp. growing in New Zealand; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Gnomoniopsis rosae

Fungal Planet 813 – 14 December 2018

Gnomoniopsis rosae Crous, *sp. nov.*

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

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

Conidiomata erumpent, globose, brown, 200–400 µm diam, acervular, opening by irregular rupture, exuding a creamy conidial mass; wall of 6–8 layers of brown *textura angularis*. *Conidiophores* lining the inner cavity, hyaline, smooth, 0–2-septate, subcylindrical, branched at base or not, 10–20 × 3–4 µm. *Conidiogenous cells* integrated, terminal and intercalary, hyaline, smooth, subcylindrical with apical taper, 6–13 × 2.5–3.5 µm; phialidic with prominent periclinal thickening. *Conidia* solitary, aseptate, fusoid, straight, hyaline, smooth-walled, guttulate, apex subobtuse, base truncate, 1 µm diam, (9–)10–12(–13) × (3–)3.5(–4) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and feathery, lobate margin, covering dish after 2 wk at 25 °C. On MEA and PDA surface greyish sepia, reverse umber. On OA surface ochreous centre, greyish sepia in outer region.

Typus. New Zealand, Auckland, Auckland Botanical Garden, on *Rosa* sp. (*Rosaceae*), 30 Aug. 2017, *R. Thangavel*, T17-03040A (holotype CBS H-23777, culture ex-type CPC 34440 = CBS 145085, ITS, LSU and *rpb2* sequences GenBank MK047451.1, MK047501.1 and MK047547.1, MycoBank MB828203).

Notes — *Gnomoniopsis* represents a genus of mostly host-specific fungi (Sogonov et al. 2008, Walker et al. 2010). *Gnomoniopsis rosae* is phylogenetically distinct from the species presently known from DNA. Unfortunately, only the asexual morph was found, making comparisons with older literature difficult.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cryptosporella umbrina* (GenBank MH855393.1; Identities = 618/620 (99 %), no gaps), *Discula quercina* (GenBank GQ452265.1; Identities = 574/623 (92 %), 30 gaps (4 %)) and *Gnomoniopsis smithogilvyi* (GenBank KY930638.1; Identities = 572/623 (92 %), 32 gaps (5 %)). Closest hits using the **LSU** sequence are *Gnomoniopsis smithogilvyi* (GenBank MH877030.1; Identities = 898/898 (100 %), no gaps), *Cryptosporella umbrina* (GenBank MH866843.1; Identities = 895/896 (99 %), 1 gap (0 %)) and *Gnomoniopsis idaeicola* (GenBank MH875092.1; Identities = 893/895 (99 %), no gaps). Closest hits using the ***rpb2*** sequence are *Gnomoniopsis paraclavulata* (GenBank EU219248.1; Identities = 692/758 (91 %), no gaps), *Discula campestris* (GenBank EU199143.1; Identities = 692/758 (91 %), no gaps) and *Gnomoniopsis clavulata* (GenBank EU219251.1; Identities = 689/758 (91 %), no gaps).

Colour illustrations. *Rosa* sp. growing in New Zealand; colony sporulating on oatmeal agar, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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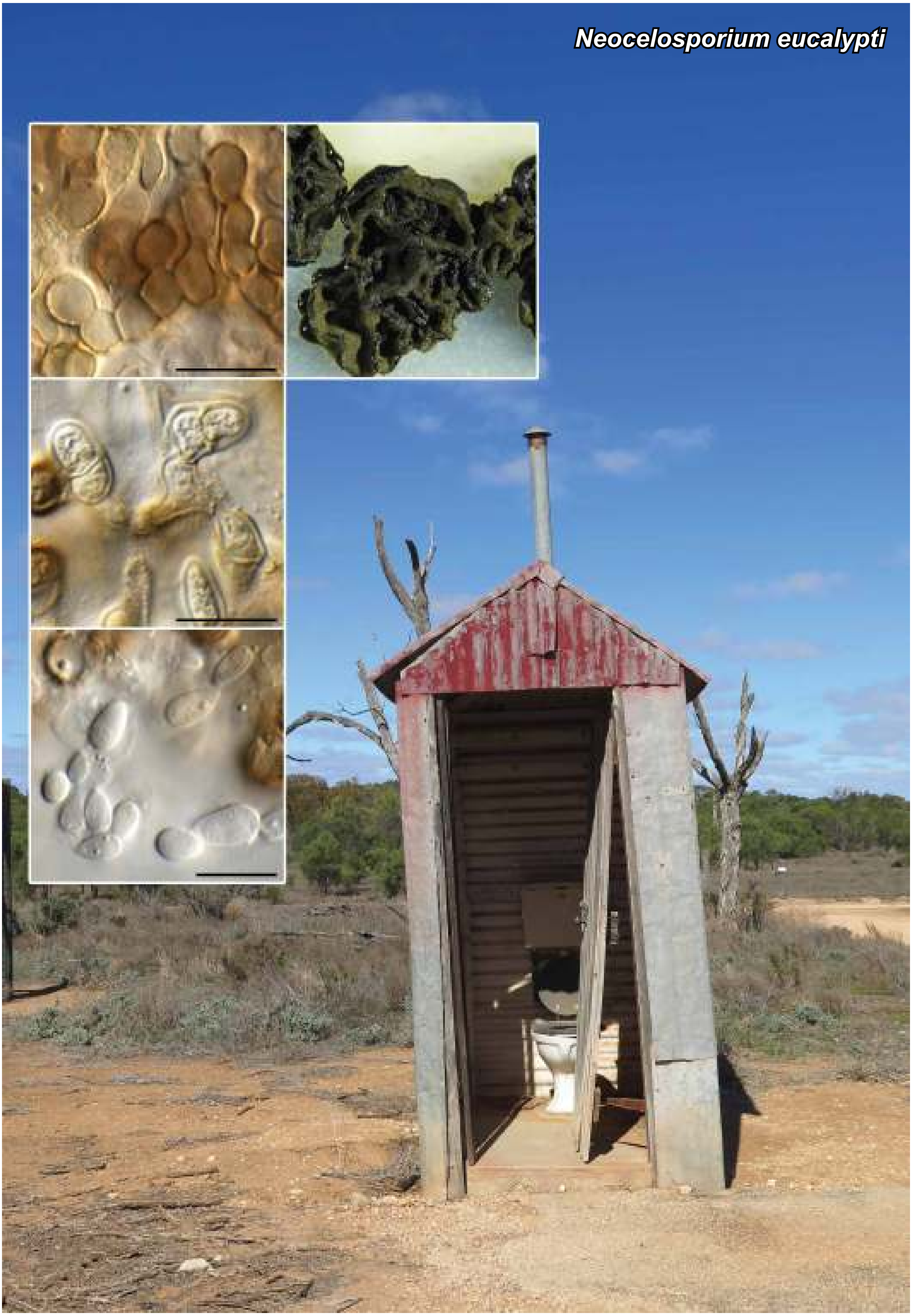
Neocelosporium eucalypti

Fungal Planet 814 – 14 December 2018

Neocelosporiales Crous, *ord. nov.*

MycoBank MB828204.

Neocelosporiaceae Crous, *fam. nov.*

Classification — *Neocelosporiaceae*, *Neocelosporiales*, *Dothideomycetes.*

Mycelium spreading, enclosed in mucus, consisting of medium to dark brown, verruculose hyphae; cells become constricted at septa, swollen, disarticulating, forming conidial propagules, 0–1-septate, ellipsoid, or hyphae forming cellular clumps with endoconidia. *Primary conidia* hyaline to brown, thin- to thick-walled, 0–3-septate, giving rise to *secondary conidia* via microcyclic conidiation. *Ascomata* globose, solitary to gregarious; wall of several layers of brown, thick-walled *textura angularis. Asci* 8-spored, bitunicate, fissitunicate, subcylindrical to clavate with ocular chamber. *Pseudoparaphyses* hyphae-like, anastomosting, branched, septate. *Ascospores* biseriate, ellipsoid to fusoid, brown, 3–4-septate, constricted at septa, smooth-walled, with mucilaginous sheath.

Type genus. Neocelosporium Crous.
MycoBank MB828205.

Note — The order *Neocelosporiales* presently includes three genera, *Neocelosporium*, *Celosporium* and *Muellerites*.

Neocelosporium Crous, *gen. nov.*

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

Mycelium spreading, enclosed in mucus, consisting of medium to dark brown, verruculose, hyphae; cells become constricted at septa, swollen, disarticulating, forming conidial propagules, 0–1-septate, ellipsoid. *Primary conidia* brown, thick-walled, giving rise to *secondary conidia* via microcyclic conidiation, ellipsoid, hyaline, smooth-walled, aseptate, apex obtuse, base truncate, forming on primary conidia or hyphal cells, becoming brown and thick-walled and swollen with age.

Type species. Neocelosporium eucalypti Crous.
MycoBank MB828206.

Neocelosporium eucalypti Crous, *sp. nov.*

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

Mycelium spreading, enclosed in mucus, medium to dark brown, verruculose, consisting of 4–5 µm diam hyphae; cells become constricted at septa, swollen, disarticulating, forming conidial propagules, 0–1-septate, ellipsoid, 5–10 µm diam. *Primary conidia* brown, thick-walled, giving rise to *secondary conidia* via microcyclic conidiation, ellipsoid, hyaline, smooth-walled, aseptate, apex obtuse, base truncate, forming on primary conidia or hyphal cells, 5–12 × 3–5 µm, becoming brown and thick-walled and swollen with age.

Culture characteristics — Colonies erumpent, spreading, with folded surface, sparse aerial mycelium and feathery, lobate margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse leaden black.

Typus. Australia, New South Wales, Mildura, Mungo National Park, on *Eucalyptus cyanophylla* (*Myrtaceae*), 27 Aug. 2015, *B.A. Summerell*, HPC 2224 (holotype CBS H-23778, culture ex-type CPC 34468 = CBS 145086, ITS and LSU sequences GenBank MK047452.1 and MK047502.1, MycoBank MB828207).

Notes — *Neocelosporium eucalypti* clusters with *Muellerites juniperi* (CBS 339.73) and *Celosporium laricicola* (Tsuneda et al. 2010). *Neocelosporium* is morphologically distinct, in that it has hyaline conidia that primarily arise on the surface of hyphae (clumps with a limited number of large, brown endoconidia are observed), whereas *Celosporium* is characterised by dematiaceous hyphae forming clumps with numerous hyaline to brown endoconidia.

Based on a megablast search of NCBIs GenBank nucleotide database, only distant hits were obtained using the **ITS** sequence, including *Celosporium larixicola* (GenBank FJ997287.1; Identities = 498/544 (92 %), 11 gaps (2 %)), *Gonatobotryum apiculatum* (GenBank MH859103.1; Identities = 531/597 (89 %), 21 gaps (3 %)) and *Scleroconidioma sphagnicola* (GenBank DQ182416.1; Identities = 511/578 (88 %), 19 gaps (3 %)). Closest hits using the **LSU** sequence are *Celosporium larixicola* (GenBank FJ997288.1; Identities = 789/816 (97 %), 2 gaps (0 %)), *Muellerites juniperi* (GenBank MH877745.1; Identities = 817/846 (97 %), 4 gaps (0 %)) and *Dothiora europaea* (GenBank MH872143.1; Identities = 843/883 (95 %), 2 gaps (0 %)).

Colour illustrations. Mildura, Mungo National Park, Australia; brown hyhae constricted at septa, colony on potato dextrose agar, and conidia. Scale bars = 10 µm.

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Rachicladosporium corymbiae

Fungal Planet 815 – 14 December 2018

Rachicladosporium corymbiae Crous, *sp. nov.*

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

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

Ascomata formed on PNA *in vitro*. *Ascomata* brown, globose, 70–90 µm diam, with central ostiole; wall of 3–4 layers of brown, flattened *textura angularis. Asci* bitunicate, sessile, fasciculate, obovoid with minute ocular chamber, 1–2 µm diam, 20–25 × 7–10 µm. *Pseudoparaphyses* absent. *Ascospores* multiseriate, hyaline, smooth, fusoid-ellipsoid, widest in middle of apical cell, constricted at septum, guttulate, 9–10 × 3 µm. *Mycelium* consisting of pale brown, smooth, septate, branched, 2–3 µm diam hyphae. *Conidiophores* solitary, erect, subcylindrical, medium brown, unbranched, smooth to verruculose, 10–30 × 3–4 µm. *Conidiogenous cells* terminal, integrated, brown, finely verruculose, subcylindrical, 10–20 × 3–4 µm; proliferating sympodially with 1–3 apical loci, darkened, thickened, 1.5–2 µm diam. *Conidia* occurring in branched chains, subcylindrical, tapering at both ends, 0–1-septate, verruculose to warty, brown; ramoconidia (9–)10–15 × 2.5–3.5 µm; conidia (8–)9–10(–12) × 2(–2.5) µm.

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

Typus. GHANA, on leaf spots of *Corymbia citriodora* (*Myrtaceae*), 21 June 2010, *M.J. Wingfield*, HPC 2172 (holotype CBS H-23779, culture ex-type CPC 34021 = CBS 145087, ITS and LSU sequences GenBank MK047453.1 and MK047503.1, MycoBank MB828208).

Colour illustrations. Mixed forest in Ghana; symptomatic leaf, ascomata forming on pine needle agar, pseudothecium, asci, conidiophores, conidiogenous cells and conidia. Scale bars: ascoma = 100 µm, all others = 10 µm.

Notes — Isolations were made from single germinating ascospores with an irregular mode of germination. Both the sexual and asexual morph formed in culture. *In vivo* ascomata were associated with *Teratosphaeria* spp., co-occurring on leaf spots. *Rachicladosporium* includes species associated with leaf spots that have a cladosporium-like morphology, but distinct in that conidiophores have an apical rachis, and conidia have slightly thickened hila (Crous et al. 2007a). *Rachicladosporium eucalypti* has a sexual mycosphaerella-like morph (Crous et al. 2014b), similar to that of *R. corymbiae*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Rachicladosporium eucalypti* (GenBank NR_155718.1; Identities = 544/574 (95 %), 6 gaps (1 %)), *Rachicladosporium pini* (GenBank JF951145.1; Identities = 544/574 (95 %), 5 gaps (0 %)) and *Rachicladosporium luculiae* (GenBank MH863123.1; Identities = 539/576 (94 %), 7 gaps (1 %)). Closest hits using the **LSU** sequence are *Rachicladosporium luculiae* (GenBank EU040237.1; Identities = 844/847 (99 %), 2 gaps (0 %)), *Rachicladosporium pini* (GenBank MH876826.1; Identities = 843/847 (99 %), 2 gaps (0 %)) and *Rachicladosporium paucitum* (GenBank KF309988.1; Identities = 759/763 (99 %), 2 gaps (0 %)).

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Neofitzroyomyces nerii

Fungal Planet 816 – 14 December 2018

Neofitzroyomyces Crous, *gen. nov.*

Etymology. Name relfects its morphological similarity to the genus *Fitzroyomyces*.

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

Conidiomata solitary, becoming aggregated, globose, hyaline to subhyaline, eustromatic, pycnidial; ostiole central; wall of several layers of hyaline to subhyaline *textura angularis. Conidiophores* hyaline, lining the inner cavity, subcylindrical, unbranched, septate, each giving rise to a cluster of up to 6 conidiogenous cells. *Conidiogenous cells* subcylindrical, terminal, hyaline, smooth, proliferating sympodially with several flat-tipped apical loci, not thickened nor darkened. *Conidia* solitary, aggregating in mucoid droplet, hyaline, smooth, flexuous, acicular, apex subobtuse, base truncate, septate, septoria-like in appearance.

Type species. *Neofitzroyomyces nerii* Crous.
MycoBank MB828209.

Neofitzroyomyces nerii Crous, *sp. nov.*

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

Conidiomata solitary, becoming aggregated, globose, hyaline to subhyaline, eustromatic, pycnidial, 80–150 µm diam; ostiole 20–30 µm diam; wall of 5–8 layers of hyaline to subhyaline *textura angularis. Conidiophores* hyaline, lining the inner cavity, subcylindrical, unbranched, 0–1-septate, 5–7 × 2–3 µm, each giving rise to a cluster of up to 6 conidiogenous cells. *Conidiogenous cells* subcylindrical, terminal, hyaline, smooth, 5–10 × 2–3 µm, proliferating sympodially with several flat-tipped apical loci, 0.5–1 µm diam, not thickened nor darkened. *Conidia* solitary, aggregating in mucoid droplet, hyaline, smooth, flexuous, acicular, apex subobtuse, base truncate, 3–6-septate, septoria-like in appearance, (25–)40–65(–80) × (1.5–)2 µm.

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

Typus. FRANCE, Mazan, associated with leaf spots on *Nerium oleander* (*Apocynaceae*), 20 July 2017, *P.W. Crous*, HPC 2191 (holotype CBS H-23780, culture ex-type CPC 33883 = CBS 145088, ITS and LSU sequences GenBank MK047454.1 and MK047504.1, MycoBank MB828210).

Notes — *Neofitzroyomyces* is phylogenetically closely related to the monotypic genus *Fitzroyomyces*, which was established for a septoria-like fungus occurring on leaves of *Cyperaceae* in Australia (Crous et al. 2017b). *Neofitzroyomyces* differs from *Fitzroyomyces* in that it has well-defined conidiophores, and conidiogenous cells that proliferate sympodially, with several flat-tipped apical loci.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Fitzroyomyces cyperi* (GenBank NR_156387.1; Identities = 419/466 (90 %), 13 gaps (3 %)), *Carestiella socia* (GenBank AY661682.1; Identities = 381/437 (87 %), 22 gaps (5 %)) and *Phacidiella eucalypti* (GenBank MH863073.1; Identities = 465/544 (85 %), 24 gaps (4 %)). Closest hits using the **LSU** sequence are *Phacidiella podocarpi* (GenBank NG_058118.1; Identities = 761/803 (95 %), 5 gaps (0 %)), *Conotrema populorum* (GenBank AY340542.1; Identities = 785/831 (94 %), 7 gaps (0 %)) and *Phacidiella eucalypti* (GenBank EF110617.1; Identities = 781/829 (94 %), 4 gaps (0 %)).

Colour illustrations. *Nerium oleander* with leaf spots in Mazan, France; conidiomata sporulating on potato dextrose agar, section through ascoma showing pale brown wall, conidiogenous cells and conidia. Scale bars: conidioma = 150 µm, all others = 10 µm.

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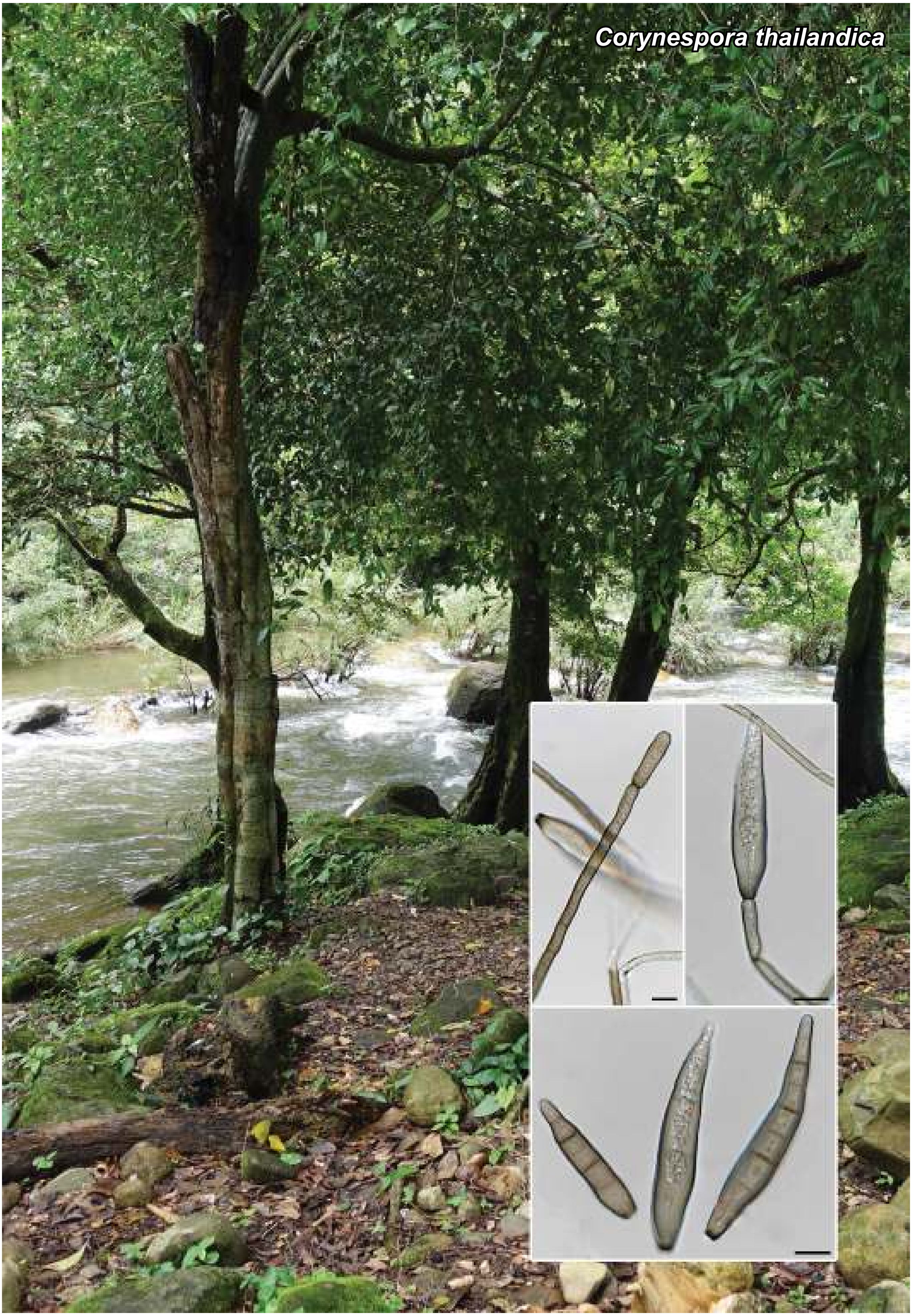
Corynespora thailandica

Fungal Planet 817 – 14 December 2018

Corynespora thailandica Crous, *sp. nov.*

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

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

Mycelium consisting of brown, finely roughened, branched, septate, 3–4 µm diam hyphae. *Conidiophores* solitary, erect, flexuous, subcylindrical, unbranched, brown, thick-walled, finely roughened, base swollen, up to 12 µm diam, conidiophores extremely long in culture, 5–6 µm diam, multi-septate. *Conidiogenous cells* integrated, terminal, monotretic, subcylindrical, brown, finely roughened, slightly darkened at apex, 3–4 µm diam, 25–30(–60) × 5–6 µm. *Conidia* obclavate, mostly solitary, thick-walled, brown, finely roughened, 4–8-distoseptate, (50–) 80–110(–200) × (9–)10–12(–13) µm; hila darkened, thickened, 3–4 µm diam.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and feathery, lobate margin, reaching 10 mm diam on PDA, 60 mm diam on OA and MEA after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, reverse iron-grey.

Typus. THAILAND, Nakhon Nayok Province, Wang Takhrai, on wood in forest, 2008, *P.W. Crous*, HPC 2143 (holotype CBS H-23781, culture ex-type CPC 33935 = CBS 145089, ITS, LSU and *tef1* sequences GenBank MK047455.1, MK047505.1 and MK047567.1, MycoBank MB828211).

Notes — The genus *Corynespora* is polyphyletic (Voglmayr & Jaklitsch 2017). Species occur on a range of substrates, varying from leaves to twigs, with several being regarded as serious plant pathogens. Based on the species treated by Ellis (1971, 1976), and those known from DNA sequence data, the present collection appears to represent a new taxon, described here as *Corynespora thailandica*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Corynespora cassiicola* (GenBank FJ852592.1; Identities = 537/557 (96 %), 6 gaps (1 %)), *Corynespora smithii* (GenBank KY984300.1; Identities = 536/558 (96 %), 9 gaps (1 %)) and *Corynespora torulosa* (GenBank NR_145181.1; Identities = 530/556 (95 %), 6 gaps (1 %)). Closest hits using the **LSU** sequence are *Corynespora cassiicola* (GenBank MH869486.1; Identities = 840/847 (99 %), 2 gaps (0 %)), *Corynespora torulosa* (GenBank NG_058866.1; Identities = 839/847 (99 %), 2 gaps (0 %)) and *Corynespora smithii* (GenBank KY984299.1; Identities = 839/847 (99 %), 2 gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Corynespora smithii* (GenBank KY984436.1; Identities = 396/464 (85 %), 19 gaps (4 %)), *Pyrenochaeta nobilis* (GenBank MF795880.1; Identities = 289/348 (83 %), 27 gaps (7 %)) and *Neocucurbitaria acerina* (GenBank MF795856.1; Identities = 286/347 (82 %), 17 gaps (4 %)).

Colour illustrations. Indigenous forest in Thailand; conidiogenous cells and conidia. Scale bars = 10 µm.

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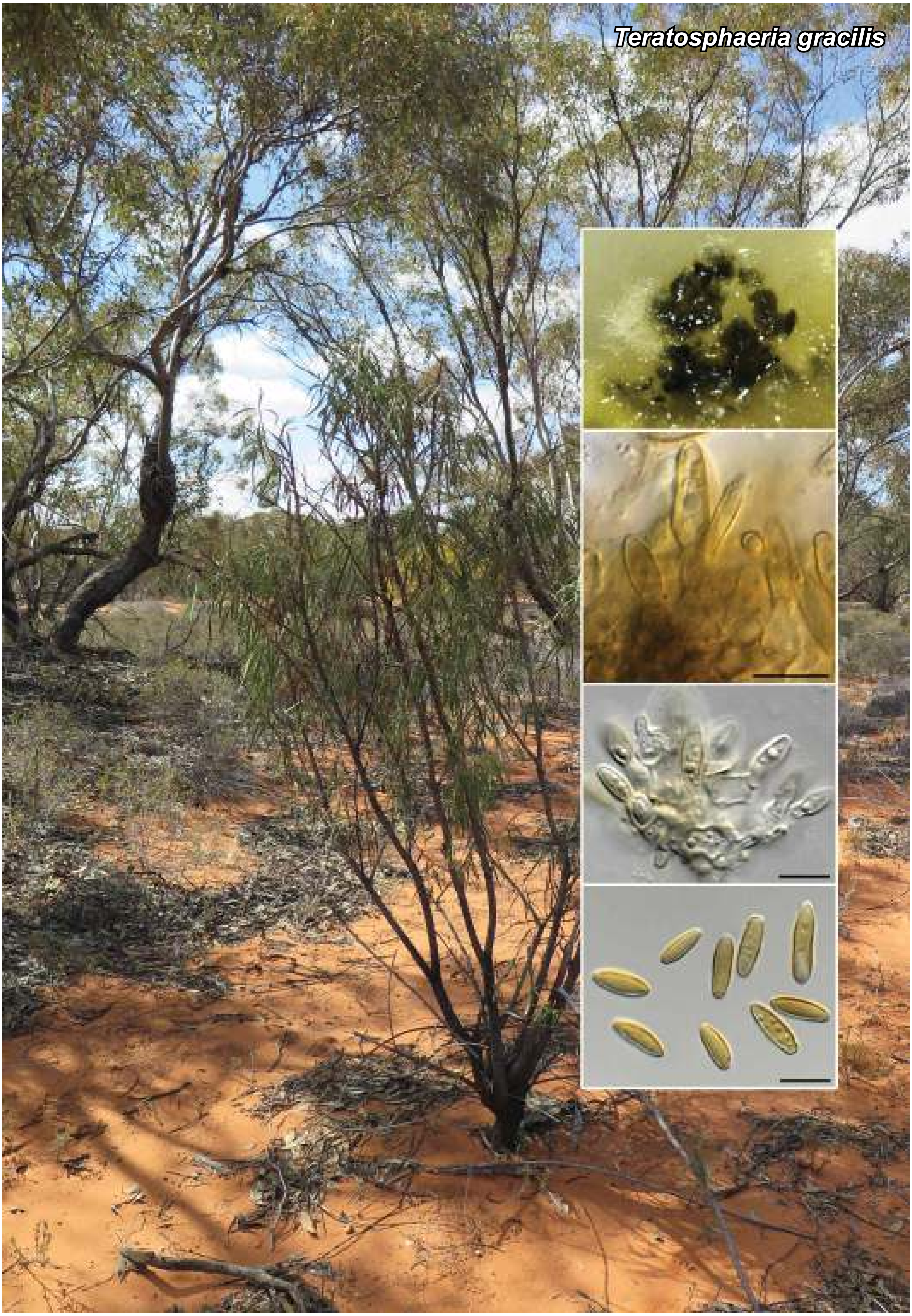
Teratosphaeria gracilis

Fungal Planet 818 – 14 December 2018

Teratosphaeria gracilis Crous, *sp. nov.*

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

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

Associated with insect damage on leaves. *Conidiomata* immersed, globose, dark brown, pycnidial, 90–120 µm diam, with central ostiole; wall of 6–8 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* brown, finely roughened, doliiform, 5–9 × 5–7 µm, proliferating percurrently at apex. *Conidia* solitary, fusoid to subcylindrical, apex subobtuse, base truncate, 2–4 µm diam, with minute marginal frill, 0(–1)-septate, guttulate, brown, finely roughened, (12–)15–20(–25) × (3.5–)4–5(–6) µm.

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

Typus. AUSTRALIA, New South Wales, Mildura, Mungo National Park, on *Eucalyptus gracilis* (*Myrtaceae*), 27 Aug. 2015, *B.A. Summerell*, HPC 2225 (holotype CBS H-23783, culture ex-type CPC 34393 = CBS 145090, ITS, LSU, *actA*, *cmdA*, *rpb2*, *tef1* and *tub2* sequences GenBank MK047456.1, MK047506.1, MK047523.1, MK047529.1, MK047548.1, MK047568.1 and MK047583.1, MycoBank MB828212).

Colour illustrations. Mungo National Park, Australia; colony sporulating on oatmeal agar, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — Numerous species of *Teratosphaeria* are associated with *Teratosphaeria* leaf disease (TLD) of *Eucalyptus* and the closely related genus *Corymbia* (Hunter et al. 2011). *Teratosphaeria* was recently treated by Quaedvlieg et al. (2014), resulting in the majority of the species occurring on eucalypts now being known from their DNA data. *Teratosphaeria gracilis* appears to represent yet another phylogenetically distinct species in the complex.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Teratosphaeria miniata* (GenBank MH863451.1; Identities = 485/501 (97 %), 2 gaps (0 %)), *Teratosphaeria biformis* (GenBank MH863387.1; Identities = 485/501 (97 %), 2 gaps (0 %)) and *Teratosphaeria molleriana* (GenBank MH862864.1; Identities = 485/501 (97 %), 2 gaps (0 %)). Closest hits using the **LSU** sequence are *Teratosphaeria stellenboschiana* (GenBank MH874553.1; Identities = 879/882 (99 %), no gaps), *Teratosphaeria gauchensis* (GenBank EU019290.1; Identities = 871/874 (99 %), 1 gap (0 %)) and *Teratosphaeria zuluensis* (GenBank MH874640.1; Identities = 878/882 (99 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Teratosphaeria destructans* (GenBank KF903447.1; Identities = 506/539 (94 %), 2 gaps (0 %)), *Teratosphaeria viscida* (GenBank KF903563.1; Identities = 505/539 (94 %), 2 gaps (0 %)) and *Teratosphaeria eucalypti* (GenBank KF903452.1; Identities = 505/540 (94 %), 3 gaps (0 %)). Closest hits using the ***cmdA*** sequence had highest similarity to *Teratosphaeria blakelyi* (GenBank KF902704.1; Identities = 371/411 (90 %), 10 gaps (2 %)), *Teratosphaeria majorizuluensis* (GenBank KF902733.1; Identities = 363/402 (90 %), 8 gaps (1 %)) and *Teratosphaeria gauchensis* (GenBank KF902727.1; Identities = 394/446 (88 %), 18 gaps (4 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Teratosphaeria molleriana* (GenBank KX348104.1; Identities = 775/868 (89 %), 2 gaps (0 %)), *Teratosphaeria stellenboschiana* (GenBank MF951743.1; Identities = 783/883 (89 %), no gaps) and *Teratosphaeria gauchensis* (GenBank KX348103.1; Identities = 783/883 (89 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Teratosphaeria miniata* (GenBank KF903323.1; Identities = 305/357 (85 %), 15 gaps (4 %)), *Teratosphaeria juvenalis* (GenBank KF903318.1; Identities = 307/361 (85 %), 22 gaps (6 %)) and *Teratosphaeria mareebensis* (GenBank KF903320.1; Identities = 302/359 (84 %), 13 gaps (3 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Teratosphaeria destructans* (GenBank KT343568.1; Identities = 517/603 (86 %), 19 gaps (3 %)), *Teratosphaeria nubilosa* (GenBank AY725599.1; Identities = 517/604 (86 %), 24 gaps (3 %)) and *Teratosphaeria zuluensis* (as *Coniothyrium zuluense*, GenBank AY244389.1; Identities = 362/403 (90 %), 12 gaps (2 %)).

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