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RESEARCH ARTICLE

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Key words

ITS DNA barcodes
LSU
novel fungal genera
novel fungal species
systematics

Abstract Novel species of microfungi described in the present study include the following from South Africa: *Cercosporella dolichandrae* from *Dolichandra unguiscati*, *Seiridium podocarpi* from *Podocarpus latifolius*, *Pseudocercospora parapseudarthriae* from *Pseudarthria hookeri*, *Neodevriesia coryneliae* from *Corynelia uberata* on leaves of *Afrocarpus falcatus*, *Ramichloridium eucleae* from *Euclea undulata* and *Stachybotrys aloeticola* from *Aloe* sp. (South Africa), as novel member of the *Stachybotriaceae* fam. nov. Several species were also described from Zambia, and these include *Chaetomella zambiensis* on unknown *Fabaceae*, *Schizoparme pseudogranati* from *Terminalia stuhlmannii*, *Diaporthe isoberliniae* from *Isoberlinia angolensis*, *Peyronellaea combreti* from *Combretum mossambiciensis*, *Zasmidium rothmanniae* and *Phaeococcomyces rothmanniae* from *Rothmannia engleriana*, *Diaporthe vangueriae* from *Vangueria infausta* and *Diaporthe parapterocarpi* from *Pterocarpus brenanii*. Novel species from the Netherlands include: *Stagonospora trichophoricola*, *Keissleriella trichophoricola* and *Dinemasporium trichophoricola* from *Trichophorum cespitosum*, *Phaeosphaeria poae*, *Keissleriella poagena*, *Phaeosphaeria poagena*, *Parastagonospora poagena* and *Pyrenochaetopsis poae* from *Poa* sp., *Septoriella oudemansii* from *Phragmites australis* and *Dendryphion europaeum* from *Hedera helix* (Germany) and *Heracleum sphondylium* (the Netherlands). Novel species from Australia include: *Anungitea eucalyptorum* from *Eucalyptus* leaf litter, *Beltraniopsis neolitseae* and *Acrodontium neolitseae* from *Neolitsea australiensis*, *Beltraniella endiandrae* from *Endiandra introrsa*, *Phaeophleospora parsoniae* from *Parsonia straminea*, *Penicillifer martinii* from *Cynodon dactylon*, *Ochroconis macrozamiae* from *Macrozamia* leaf litter, *Triposporium cycadicola*, *Circinotrichum cycadis*, *Cladosporium cycadicola* and *Acrocalymma cycadis* from *Cycas* spp. Furthermore, *Vermiculariopsiella dichapetali* is described from *Dichapetalum rhodesicum* (Botswana), *Ophiognomonia acadiensis* from *Picea rubens* (Canada), *Setophoma vernoniae* from *Vernonia polyanthes* and *Penicillium restingae* from soil (Brazil), *Pseudolachnella guaviyunis* from *Myrcianthes pungens* (Uruguay) and *Pseudocercospora neriicola* from *Nerium oleander* (Italy). Novelties from Spain include: *Dendryphiella eucalyptorum* from *Eucalyptus globulus*, *Conioscypha minutispora* from dead wood, *Diplogelasinospora moalensis* and *Pseudoneurospora canariensis* from soil and *Inocybe lanatopurpurea* from reforested woodland of *Pinus* spp. Novelties from France include: *Kellermania triseptata* from *Agave angustifolia*, *Zetiasplozna acaciae* from *Acacia melanoxylon*, *Pyrenochaeta pinicola* from *Pinus* sp. and *Pseudonectria rusci* from *Ruscus aculeatus.* New species from China include: *Dematiocladium celtidicola* from *Celtis bungeana*, *Beltrania pseudorhombica*, *Chaetopsina beijingensis* and *Toxicocladosporium pini* from *Pinus* spp. and *Setophaeosphaeria badalingensis* from *Hemerocallis fulva.* Novel genera of *Ascomycetes* include *Alfaria* from *Cyperus esculentus* (Spain), *Rinaldiella* from a contaminated human lesion (Georgia), *Hyalocladosporiella* from *Tectona grandis* (Brazil), *Pseudoacremonium* from *Saccharum spontaneum* and *Melnikomyces* from leaf litter (Vietnam), *Annellosympodiella* from *Juniperus procera* (Ethiopia), *Neoceratosperma* from *Eucalyptus* leaves (Thailand), *Ramopenidiella* from *Cycas calcicola* (Australia), *Cephalotrichiella* from air in the Netherlands, *Neocamarosporium* from *Mesembryanthemum* sp. and *Acervuloseptoria* from *Ziziphus mucronata* (South Africa) and *Setophaeosphaeria* from *Hemerocallis fulva* (China). Several novel combinations are also introduced, namely for *Phaeosphaeria setosa* as *Setophaeosphaeria setosa*, *Phoma heteroderae* as *Peyronellaea heteroderae* and *Phyllosticta maydis* as *Peyronellaea maydis.* Morphological and culture characteristics along with ITS DNA barcodes are provided for all taxa.

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HIGHER ORDER CLASSIFICATION OF TAXONOMIC NOVELTIES

ASCOMYCOTA

Arthoniomycetes
- ***Lichenostigmatales, Phaeococcomycetaceae***
  - *Phaeococcomyces rothmanniae*

Dothideomycetes
- ***Botryosphaeriales, Planistromellaceae***
  - *Kellermania triseptata*
- ***Capnodiales, Cladosporiaceae***
  - *Cladosporium cycadicola*
  - *Toxicocladosporium pini*
- ***Capnodiales, Dissoconiaceae***
  - *Ramichloridium eucleae*
- ***Capnodiales, Mycosphaerellaceae***
  - *Acervuloseptoria ziziphicola*
  - *Acrodontium neolitseae*
  - *Annellosympodiella juniperi*
  - *Cercosporella dolichandrae*
  - *Neoceratosperma eucalypti*
  - *Phaeophleospora parsoniae*
  - *Pseudocercospora neriicola*
  - *Pseudocercospora parapseudarthriae*
  - *Zasmidium rothmanniae*
- ***Capnodiales, Teratosphaeriaceae***
  - *Neodevriesia coryneliae*
  - *Ramopenidiella cycadicola*
- ***Pleosporomycetidae, Pleosporales, Incertae sedis, Cucurbitariaceae***
  - *Pyrenochaetopsis poae*
- ***Pleosporomycetidae, Pleosporales, Massarineae, Lentitheciaceae***
  - *Keissleriella poagena*
  - *Keissleriella trichophoricola*
- ***Pleosporomycetidae, Pleosporales, Massarineae, Massarinaceae***
  - *Stagonospora trichophoricola*
- ***Pleosporomycetidae, Pleosporales, Massarineae, Morosphaeriaceae***
  - *Acrocalymma cycadis*
- ***Pleosporomycetidae, Pleosporales, Pleosporineae, Didymellaceae***
  - *Peyronellaea combreti*
  - *Peyronellaea heteroderae*
  - *Peyronellaea maydis*
- ***Pleosporomycetidae, Pleosporales, Pleosporineae, Phaeosphaeriaceae***
  - *Parastagonospora poagena*
  - *Phaeosphaeria poae*
  - *Phaeosphaeria poagena*
  - *Septoriella oudemansii*
  - *Setophaeosphaeria badalingensis*
  - *Setophaeosphaeria hemerocallidis*
  - *Setophoma vernoniae*
- ***Pleosporomycetidae, Pleosporales, Pleosporineae, Pleosporaceae***
  - *Dendryphiella eucalyptorum*
  - *Dendryphion europaeum*
  - *Neocamarosporium goegapense*
  - *Pyrenochaeta pinicola*
- ***Pleosporomycetidae, Venturiales, Sympoventuriaceae***
  - *Ochroconis macrozamiae*
- ***Pleosporomycetidae, Venturiales, Venturiaceae***
  - *Anungitea eucalyptorum*

Eurotiomycetes
- ***Chaetothyriomycetidae, Chaetothyriales, Incertae sedis***
  - *Hyalocladosporiella tectonae*
  - *Melnikomyces vietnamensis*
- ***Eurotiomycetidae, Eurotiales, Trichocomaceae***
  - *Penicillium restingae*

Leotiomycetes
- ***Helotiales, Incertae sedis***
  - *Chaetomella zambiensis*
  - *Triposporium cycadicola*

Sordariomycetes
- ***Hypocreomycetidae, Hypocreales, Incertae sedis***
  - *Alfaria cyperi-esculenti*
  - *Chaetopsina beijingensis*
  - *Pseudoacremonium sacchari*
- ***Hypocreomycetidae, Hypocreales, Nectriaceae***
  - *Dematiocladium celtidicola*
  - *Penicillifer martinii*
  - *Pseudonectria rusci*
- ***Hypocreomycetidae, Hypocreales, Stachybotriaceae***
  - *Stachybotrys aloeticola*
- ***Hypocreomycetidae, Microascales, Incertae sedis***
  - *Cephalotrichiella penicillata*
  - *Conioscypha minutispora*
  - *Vermiculariopsiella dichapetali*
- ***Sordariomycetidae, Chaetosphaeriales, Chaetosphaeriaceae***
  - *Dinemasporium trichophoricola*
  - *Pseudolachnella guaviyunis*
- ***Sordariomycetidae, Diaporthales, Diaporthaceae***
  - *Diaporthe isoberliniae*
  - *Diaporthe parapterocarpi*
  - *Diaporthe vangueriae*
- ***Sordariomycetidae, Diaporthales, Gnomoniaceae***
  - *Ophiognomonia acadiensis*
- ***Sordariomycetidae, Diaporthales, Schizoparmaceae***
  - *Schizoparme pseudogranati*
- ***Sordariomycetidae, Sordariales, Lasiosphaeriaceae***
  - *Diplogelasinospora moalensis*
  - *Rinaldiella pentagonospora*
- ***Sordariomycetidae, Sordariales, Sordariaceae***
  - *Pseudoneurospora canariensis*
- ***Xylariomycetidae, Xylariales, Amphisphaeriaceae***
  - *Seiridium podocarpi*
  - *Zetiasplozna acaciae*
- ***Xylariomycetidae, Xylariales, Hyphonectriaceae***
  - *Beltraniella endiandrae*
- ***Xylariomycetidae, Xylariales, Incertae sedis***
  - *Beltrania pseudorhombica*
  - *Beltraniopsis neolitseae*
- ***Xylariomycetidae, Xylariales, Xylariaceae***
  - *Circinotrichum cycadis*

BASIDIOMYCOTA

- ***Agaricomycetes, Agaricomycetidae, Agaricales, Inocybaceae***
  - *Inocybe lanatopurpurea*

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Stagonospora trichophoricola

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Stagonospora trichophoricola Crous & Quaedvlieg, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Trichophorum.*

Conidiomata erumpent, globose, up to 300 µm diam, dark brown, glabrous, with central ostiole, up to 15 µm diam, separate on PNA but in clusters on OA. *Conidiophores* reduced to conidiogenous cells, hyaline, smooth, ampulliform, proliferating percurrently, 5–10 × 3–5 µm. *Conidia* hyaline, smooth, guttulate, fusoid-ellipsoidal with obtuse ends, 1–3(–4)-septate, constricted at septa, (12–)18–22(–25) × 4(–5) µm.

Culture characteristics — On SNA forming clusters of globose, dark brown chlamydospores, thick-walled, verruculose, up to 30 µm diam after 2 wk at 22 °C. Colonies spreading, flat with moderate aerial mycelium. Surface smoke-grey on OA and MEA, reverse iron-grey.

Typus. Netherlands, Rozendaal, on *Trichophorum cespitosum* (*Cyperaceae*), 2013, *W. Quaedvlieg* (holotype CBS H-21670, culture ex-type D652 = CBS 136764; ITS sequence GenBank KJ869110, LSU sequence GenBank KJ869168, RPB2 sequence GenBank KJ869232, MycoBank MB808885).

Colour illustrations. Landscape in Rozendaal, The Netherlands; conidiomata and conidia in culture. Scale bars = 10 µm.

Notes — The genus *Saccharicola* (*Massarinaceae*) was established by Eriksson & Hawksworth (2003) to accommodate *Leptosphaeria bicolor* and *L. taiwanensis*, with a note that they have stagonospora-like asexual morphs. The present collection from *Trichophorum cespitosum* is a typical *Stagonospora*, and appears to be phylogenetically closely related to *Saccharicola*, which probably is the sexual morph of *Stagonospora* s.str. (*Massarinaceae*; Quaedvlieg et al. 2013). We have not managed to find species of *Stagonospora* spp. described from *Trichophorum*, and *S. trichophoricola* is morphologically and phylogenetically distinct from the species treated by Quaedvlieg et al. (2013).

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Saccharicola bicolor* (GenBank AF455415; Identities = 481/485 (99 %), Gaps = 1/485 (0 %)), *Saccharicola taiwanensis* (GenBank AF439462; Identities = 456/471 (97 %), Gaps = 1/471 (0 %)) and *Stagonospora perfecta* (GenBank KF251258; Identities = 468/485 (96 %), Gaps = 2/485 (0 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Neottiosporina paspali* (GenBank EU754172; Identities = 833/838 (99 %), no gaps), *Stagonospora pseudovitensis* (GenBank KF251765; Identities = 829/835 (99 %), no gaps) and *Stagonospora* cf. *paludosa* (GenBank KF251757; Identities = 829/835 (99 %), no gaps).

RPB2. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the RPB2 sequence are *Neottiosporina paspali* (GenBank GU371779; Identities = 205/219 (94 %), no gaps), *Stagonospora duoseptata* (GenBank KF252260; Identities = 225/243 (93 %), no gaps) and *Stagonospora pseudocaricis* (GenBank KF302395; Identities = 224/250 (90 %), no gaps).

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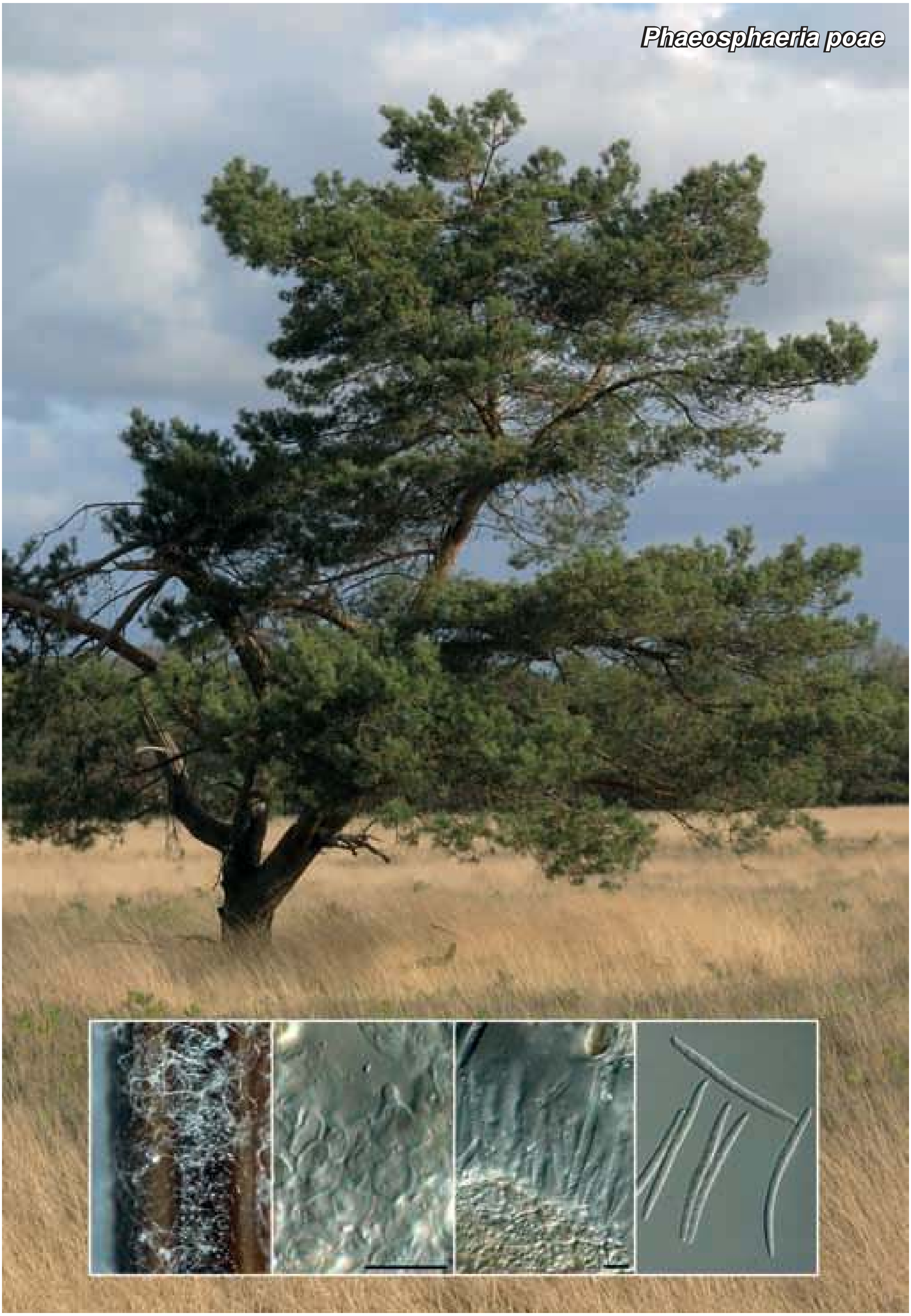
Phaeosphaeria poae

Fungal Planet 215 – 10 June 2014

Phaeosphaeria poae Crous & Quaedvlieg, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Poa*.

Conidiomata pycnidial, immersed, pale brown, globose, up to 200 µm diam with central ostiole; wall of 2–3 layers of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* ampulliform, hyaline, smooth, 5–7 × 4–5 µm, proliferating inconspicuously percurrently near the apex. *Conidia* solitary, pale brown, smooth, guttulate, narrowly obclavate to subcylindrical, tapering in upper third to a subobtuse apex, base truncate, 2–3 µm diam, straight to flexuous, (4–)6–8-septate, (38–)43–55(–65) × (3–)3.5–4(–5) µm.

Culture characteristics — Colonies flat, spreading, reaching 60 mm diam after 2 wk at 26 °C, with moderate aerial mycelium and even, lobate margins. On MEA surface dirty white to smoke-grey, reverse umber. On OA surface smoke-grey. On PDA surface smoke-grey, reverse olivaceous-grey.

Typus. Netherlands, Elspeet, on *Poa* sp. (*Poaceae*), 2013, *W. Quaedvlieg* (holotype CBS H-21671, culture ex-type D762 = CBS 136766; ITS sequence GenBank KJ869111, LSU sequence GenBank KJ869169, MycoBank MB808886).

Notes — The genus *Phaeosphaeria* has recently been characterised by Quaedvlieg et al. (2013) as having *Phaeoseptoria* asexual morphs. Several species of *Phaeosphaeria* were reported from *Poaceae* by Shoemaker & Babcock (1989). Although asexual morphs were not treated, references were made to 'pigmented *Stagonospora*', which is now confirmed as *Phaeoseptoria*. Most of the species treated by Shoemaker & Babcock (1989) have no known asexual morph, and those treated by Leuchtmann (1984) on *Poaceae* differ in conidial size to that of *Phaeosphaeria poae*.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Phaeosphaeria vagans* (GenBank KF251193; Identities = 517/530 (98 %), Gaps = 1/530 (0 %)), *Phaeosphaeria insignis* (GenBank AF439485; Identities = 490/504 (97 %), Gaps = 1/504 (0 %)) and *Phaeosphaeria culmorum* (GenBank JX981464; Identities = 515/530 (97 %), Gaps = 1/530 (0 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Phaeosphaeria ammophilae* (GenBank KF766314; Identities = 828/830 (99 %), Gaps = 1/830 (0 %)), *Wojnowicia hirta* (GenBank EU754223; Identities = 827/830 (99 %), Gaps = 1/830 (0 %)) and *Phaeosphaeria nigrans* (GenBank GU456331; Identities = 826/829 (99 %), no gaps).

Colour illustrations. Landscape at Elspeet, The Netherlands; conidiomata, conidiophores and conidia in culture. Scale bars = 10 µm.

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Keissleriella poagena

Fungal Planet 216 – 10 June 2014

Keissleriella poagena Crous & Quaedvlieg, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Poa*.

Ascomata pseudothecial, brown, erumpent to superficial, solitary, globose, up to 250 µm diam, with central ostiole; ostiole surrounded by aseptate, subcylindrical, thick-walled, dark brown setae that taper slightly to a subobtuse apex, up to 60 µm long with bulbous base, 5–8 µm diam; ascomatal wall of 3–6 layers of medium brown *textura angularis* to *globulosa*. *Asci* 8-spored, 70–140 × 10–12 µm, cylindro-clavate, stipitate, bitunicate, fissitunicate, apex obtuse, with well-defined apical chamber. *Pseudoparaphyses* cellular, filamentous, septate, anastomosing, embedded in mucilage, 2–3 µm diam, extending above the asci. *Ascospores* biseriate in asci, fusoid-ellipsoidal, 3-septate, constricted at septa, hyaline with subacute ends, surrounded by a mucilaginous sheath, 2–5 µm diam, (20–)21–23(–25) × (4–)4.5–5 µm.

Culture characteristics — Colonies erumpent, spreading, reaching 15 mm diam after 2 wk at 25 °C, with moderate aerial mycelium and lobate, smooth to feathery margins. On MEA surface pale olivaceous-grey, reverse umber. On OA surface dirty white with patches of pale olivaceous-grey. On PDA surface smoke-grey, reverse buff.

Typus. Netherlands, Raalte, on *Poa* sp. (*Poaceae*), 2013, *W. Quaedvlieg* (holotype CBS H-21672, culture ex-type D775 = CBS 136767; ITS sequence GenBank KJ869112, LSU sequence GenBank KJ869170, MycoBank MB808887).

Notes — *Keissleriella poagena* is phylogenetically closely allied to the genus *Keissleriella*, but morphologically different (Zhang et al. 2012b), in that we did not observe a papilla (then again, we studied it in culture not on host material) and ascospores were 3-septate. In agreement with *Keissleriella* are the brown setae surrounding the ostiole and the ascospores surrounded by a sheath. Presently, it seems best to place this species in *Keissleriella*, until more collections have been added to the *Lentitheciaceae*, which is a rather poorly known family.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Coniothyrium fuckelii* (GenBank HQ832837; Identities = 330/362 (91 %), Gaps = 9/362 (2 %)), *Paraphaeosphaeria sporulosa* (GenBank JX496227; Identities = 329/362 (91 %), Gaps = 9/362 (2 %)) and *Coniothyrium nitidae* (GenBank GU355659; Identities = 335/369 (91 %), Gaps = 16/369 (4 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Pleurophoma pleurospora* (GenBank JF740327; Identities = 678/687 (99 %), Gaps = 2/687 (0 %)), *Keissleriella cladophila* (GenBank JX681090; Identities = 676/686 (99 %), no gaps) and *Keissleriella genistae* (GenBank GU205222; Identities = 676/686 (99 %), no gaps).

Colour illustrations. Raalte, The Netherlands; ascomata, setae, asci and ascospores in culture. Scale bars = 10 µm.

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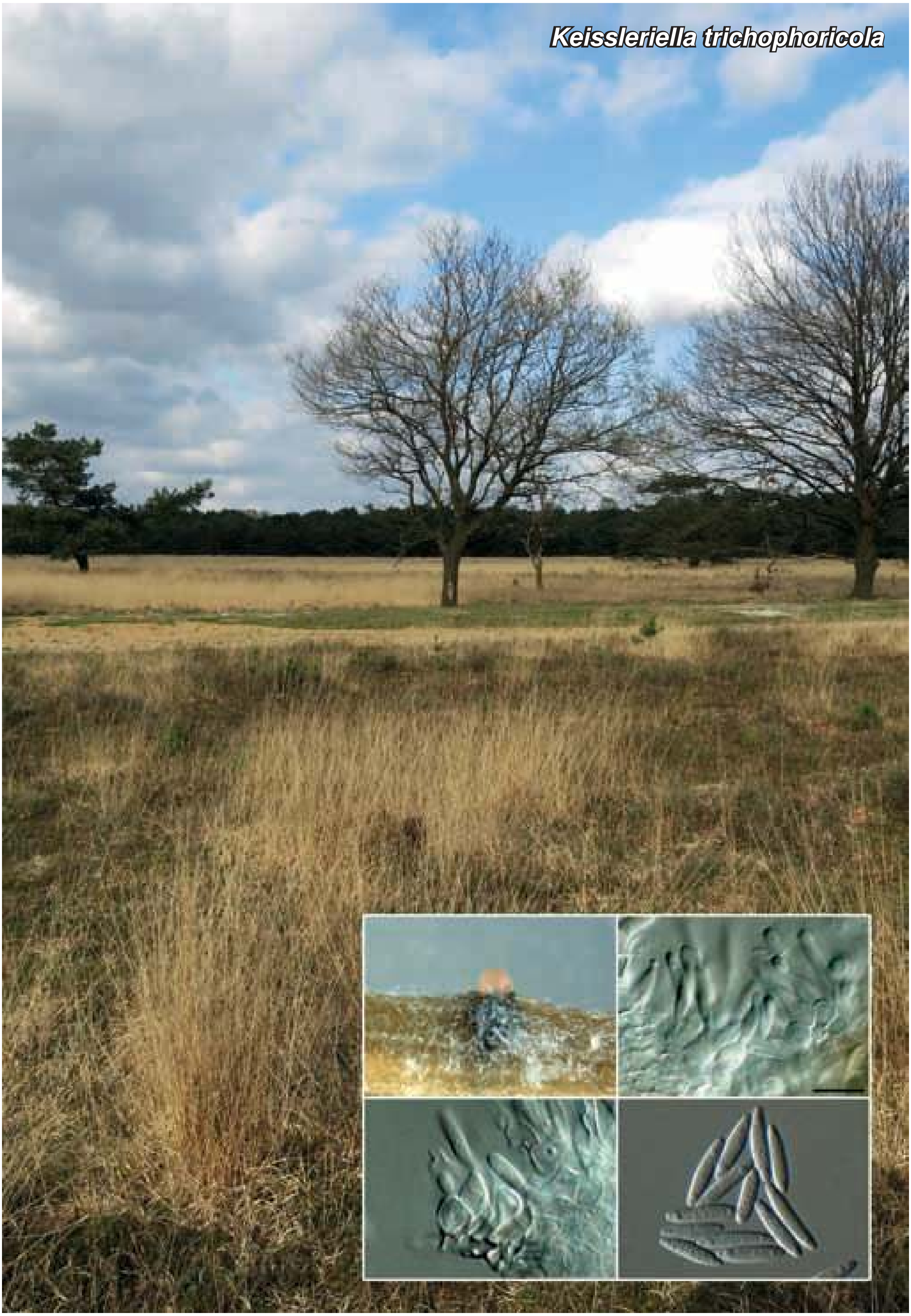
Keissleriella trichophoricola

Fungal Planet 217 – 10 June 2014

Keissleriella trichophoricola Crous & Quaedvlieg, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Trichophorum*.

Conidiomata solitary to aggregated, pycnidial, up to 200 µm diam; outer surface with brown setae; ostiolar region darker brown than rest of conidioma; wall of 4–6 layers of brown *textura angularis*, giving rise to 6–10 layers of hyaline cells of *textura globulosa*, that form conidiogenous cells and paraphyses. *Conidiogenous cells* hyaline, smooth, at times with a supporting cell, ampulliform to subcylindrical, 5–12 × 3–4 µm, proliferating via periclinal thickening at apex. *Paraphyses* intermingled among conidiogenous cells, hyaline, smooth, subcylindrical, branched below, septate with obtuse ends, up to 70 µm long, 2.5–3.5 µm diam. *Conidia* solitary, hyaline, smooth, fusoid-ellipsoidal, guttulate, widest in middle, apex subobtuse, base truncate, 1–1.5 µm diam, aseptate, (8–)11–13(–16) × 3(–3.5) µm.

Culture characteristics — Colonies erumpent, spreading, with sparse to moderate aerial mycelium, and lobate, even margins, reaching 20 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse ochreous. On OA surface umber in centre, rosy buff in outer zone. On PDA surface and reverse dirty white.

Typus. Netherlands, Elspeet, on *Trichophorum cespitosum* (*Cyperaceae*), 2013, *W. Quaedvlieg* (holotype CBS H-21673, culture ex-type D790 = CBS 136770; ITS sequence GenBank KJ869113, LSU sequence GenBank KJ869171, MycoBank MB808888).

Notes — Although the genus *Keissleriella* is poorly known (Zhang et al. 2012b), it has previously been linked to *Dendrophoma* asexual morphs (Bose 1961). The present collection is phoma-like in morphology and lacks a sexual morph. It is thus placed in *Keissleriella* primarily based on its phoma-like morphology and close phylogenetic affinity to species of *Keissleriella.*

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Coniothyrium fuckelii* (GenBank HQ832837; Identities = 330/362 (91 %), Gaps = 10/362 (2 %)), *Paraphaeosphaeria sporulosa* (GenBank JX496227; Identities = 329/362 (91 %), Gaps = 10/362 (2 %)) and *Paraphaeosphaeria neglecta* (GenBank JX496204; Identities = 329/362 (91 %), Gaps = 10/362 (2 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Pleurophoma pleurospora* (GenBank JF740327; Identities = 625/633 (99 %), no gaps), *Keissleriella genistae* (GenBank GU205222; Identities = 625/634 (99 %), Gaps = 2/634 (0 %)) and *Keissleriella cladophila* (GenBank JX681090; Identities = 625/634 (99 %), Gaps = 2/634 (0 %)).

Colour illustrations. Elspeet, The Netherlands; conidiomata, conidiogenous cells and conidia in culture. Scale bar = 10 µm.

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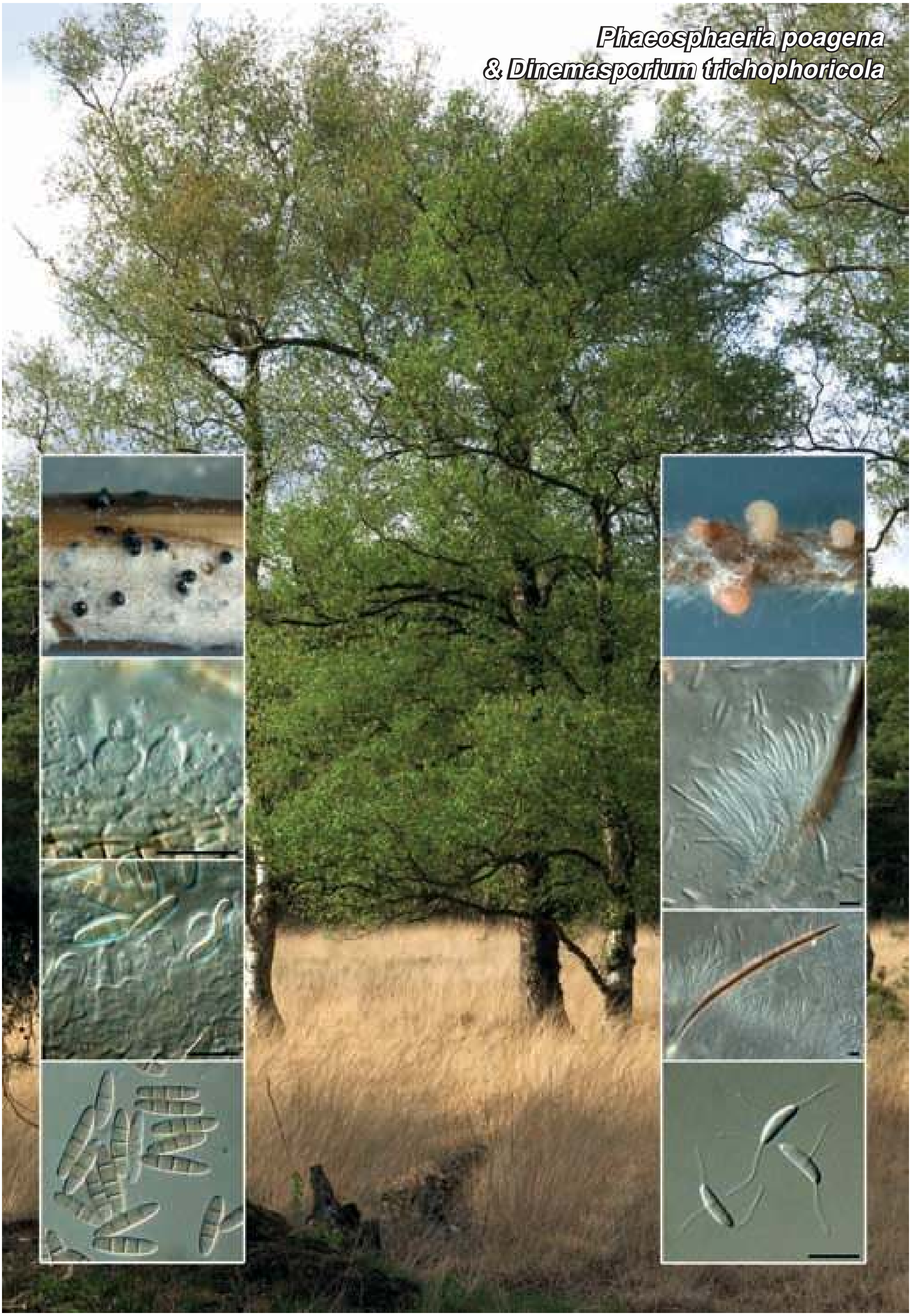
Phaeosphaeria poagena
& Dinemasporium trichophoricola

Fungal Planet 218 & 219 – 10 June 2014

Phaeosphaeria poagena Crous & Quaedvlieg, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Poa*.

Conidiomata pycnidial, globose, black, erumpent, up to 250 µm diam, with central ostiole; wall of 2–3 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells, hyaline, smooth, doliiform, 7–10 × 4–5 µm, with prominent periclinal thickening, or tightly aggregated percurrent proliferations. *Conidia* solitary, brown, smooth, fusoid-ellipsoidal to subcylindrical, (1–)3-septate, becoming slightly constricted at septa, apex subobtuse, base truncate, (8–)12–14(–16) × (2.5–)3(–3.5) µm.

Culture characteristics — Colonies flat, spreading, erumpent in centre, with moderate aerial mycelium and even, smooth margins, reaching 40 mm diam after 2 wk at 25 °C. On OA and PDA surface pale olivaceous-grey, with luteous zones.

Typus. Netherlands, Raalte, on *Poa* sp. (*Poaceae*), 2013, *W. Quaedvlieg* (holotype CBS H-21674, culture ex-type D791 = CBS 136771; ITS sequence GenBank KJ869114, LSU sequence GenBank KJ869172, TUB sequence GenBank KJ869242, MycoBank MB808889).

Notes — The present collection represents yet another novel *Phaeosphaeria* sp. from *Poa*, which is only known from its *Phaeoseptoria* morph. The asexual morph *Phaeoseptoria* is now treated as synonym of *Phaeosphaeria* (see Quaedvlieg et al. 2013). *Phaeosphaeria poagena* is described as new as its small conidial dimensions do not correspond with any of the asexual morphs recorded on *Poa* (Leuchtmann 1984, Shoemaker & Babcock 1989, Quaedvlieg et al. 2013).

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Ascochyta manawaorae* (GenBank GU230751; Identities = 458/478 (96 %), Gaps = 4/478 (0 %)), *Parastagonospora nodorum* (GenBank KF512822; Identities = 475/499 (95 %), Gaps = 8/499 (1 %)) and *Phaeosphaeria oryzae* (GenBank KF251186; Identities = 483/521 (93 %), Gaps = 10/521 (1 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Phaeosphaeria oryzae* (GenBank GQ387591; Identities = 823/830 (99 %), Gaps = 2/830 (0 %)), *Phaeosphaeriopsis musae* (GenBank DQ885894; Identities = 823/830 (99 %), Gaps = 2/830 (0 %)) and *Vrystaatia aloeicola* (GenBank KF251781; Identities = 815/822 (99 %), Gaps = 2/822 (0 %)).

TUB. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the TUB sequence are *Ophiostoma sparsiannulatum* (GenBank FJ907177; Identities = 183/217 (84 %), Gaps = 5/217 (2 %)), *Fusarium longipes* (GenBank GQ915443; Identities = 187/222 (84 %), Gaps = 7/222 (3 %)) and *Nectria antarctica* (GenBank HM484601; Identities = 187/224 (83 %), Gaps = 9/224 (4 %)).

Dinemasporium trichophoricola Crous & Quaedvlieg, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Trichophorum*.

On autoclaved *Trichophorum* leaves on SNA. *Conidiomata* sporodochial, up to 350 µm diam; basal layer up to 35 µm thick. *Setae* brown, simple, septate, subulate with acute apex (obtuse when young), unbranched, thick-walled, 1–9-septate, 70–250 × 4–8 µm. *Conidiophores* up to 65 µm long, invested in mucus. *Conidiogenous cells* determinate, proliferating percurrently near apex, hyaline, smooth, subcylindrical to lageniform, 7–22 × 2–2.5 µm. *Conidia* hyaline, aseptate, thin-walled, smooth, granular, naviculate to fusiform or ellipsoid, gently curved or straight, apex obtuse to subobtusely rounded, base truncate, (8–)9–11(–13) × 2.5(–3) µm, with a single unbranched, flexuous, tubular appendage at each end; basal appendage excentric, apical and basal appendages 9–13 µm long; lateral appendages (2), inserted 4–6 µm below apex, 8–11 µm long.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and even, smooth margins, reaching 55 mm diam after 2 wk at 25 °C. On OA surface buff with patches of saffron. On PDA surface and reverse dirty white.

Typus. Netherlands, Raalte, on *Trichophorum cespitosum* (*Cyperaceae*), 2013, *W. Quaedvlieg* (holotype CBS H-21675, culture ex-type D792 = CBS 136772; ITS sequence GenBank KJ869115, LSU sequence GenBank KJ869173, MycoBank MB808890).

Colour illustrations. Raalte, The Netherlands; conidiomata, conidiogenous cells and conidia of *Phaeosphaeria poagena* (left column); conidiomata, conidiophores, setae and conidia of *Dinemasporium trichophoricola* (right column). Scale bars = 10 µm.

Notes — Based on DNA phylogenetic data, Crous et al. (2012b) concluded that conidial appendages as sole taxonomic character were of insufficient value to determine generic boundaries in these coelomycetous fungi, and subsequently reduced *Stauronema* to synonymy with *Dinemasporium*. *Dinemasporium trichophoricola* is comparable with two species, namely *D. indicum* (conidia 7–13 × 2–3 µm, terminal appendages 6.5–17 µm, lateral appendages 8–20 µm long, but 3–4 µm below apex) and *D. pseudoindicum* (conidia 9–13 × 3–4 µm, terminal appendages 9–22 µm, lateral appendages 10–17 µm long, but 4–6 µm below apex). *Dinemasporium trichophoricola* can be distinguished from both species based on its shorter appendages. Of interest is that conidiomatal setae were observed to form on OA, but not on *Trichophorum* leaves on SNA, while conidia again developed lateral appendages on *Trichophorum* leaves, but not on OA.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Dinemasporium pseudoindicum* (GenBank JQ889277; Identities = 510/523 (98 %), Gaps = 9/523 (1 %)), *Dinemasporium strigosum* (GenBank JQ889286; Identities = 491/521 (94 %), Gaps = 17/521 (3 %)) and *Dinemasporium americana* (GenBank JQ889274; Identities = 470/499 (94 %), Gaps = 24/499 (4 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Dinemasporium pseudoindicum* (GenBank JQ889293; Identities = 670/674 (99 %), Gaps = 1/674 (0 %)), *Dinemasporium strigosum* (GenBank JQ889300; Identities = 669/674 (99 %), 1/674 (0 %)) and *Dinemasporium americana* (GenBank JQ889290; Identities = 669/674 (99 %), Gaps = 1/674 (0 %)).

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Parastagonospora poagena
& Pyrenochaetopsis poae

Fungal Planet 220 & 221 – 10 June 2014

Parastagonospora poagena Crous & Quaedvlieg, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Poa*.

Conidiomata erumpent, globose, brown, up to 350 µm diam with central ostiole, exuding a pinkish conidial mass; wall of 2–3 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells, hyaline, smooth, ampulliform to subcylindrical, proliferating inconspicuously percurrently near apex, 4–6 × 3–6 µm. *Conidia* solitary, subhyaline, smooth, granular, subcylindrical with taper in apical third to subobtuse apex, straight to gently curved, sigmoid, base truncate, 2.5–3 µm diam, 3–9-septate, (30–)40–55(–60) × (3–)3.5(–4) µm.

Culture characteristics — On OA flat, spreading with sparse aerial mycelium and even, smooth margins; surface dirty white with patches of pale olivaceous-grey, similar in reverse.

Typus. Netherlands, Raalte, on *Poa* sp. (*Poaceae*), 2013, *W. Quaedvlieg* (holotype CBS H-21676, culture ex-type D800 = CBS 136776; ITS sequence GenBank KJ869116, LSU sequence GenBank KJ869174, MycoBank MB808891).

Notes — The genus *Parastagonospora* was recently introduced to accommodate several cereal pathogens that could not be placed in *Stagonospora* or *Phaeosphaeria* (Quaedvlieg et al. 2013). Phylogenetically, *P. poasensis* is closely related to *P. avenae* (conidia (1–)3(–7)-septate, (17–)33(–46) × (2.5–)3.5(–4.5 µm); Bissett 1982), though it is distinct in its conidial morphology. Conidia of *P. poagena* are much larger than that of *P. poae* (1-septate, 20–32 × 2–2.5 µm; Quaedvlieg et al. 2013).

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Phaeosphaeria avenaria* f. sp. *triticae* (GenBank EF452729; Identities = 553/561 (99 %), Gaps = 1/561 (0 %)), *Phaeosphaeria avenaria* (GenBank U77358; Identities = 552/560 (99 %), no gaps) and *Parastagonospora avenae* (GenBank KF251174; Identities = 536/544 (99 %), no gaps).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Parastagonospora nodorum* (GenBank EU754175; Identities = 848/848 (100 %), no gaps), *Phaeosphaeria avenaria* f. sp. *triticae* (GenBank EF590322; Identities = 848/848 (100 %), no gaps) and *Phaeosphaeria nigrans* (GenBank KF251687; Identities = 828/828 (100 %), no gaps).

Pyrenochaetopsis poae Crous & Quaedvlieg, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Poa*.

Conidiomata globose, erumpent, up to 250 µm diam with central ostiole, up to 35 µm diam; outer surface covered with brown, erect setate, smooth, septate, with apical taper towards obtuse ends, 1.5–3 µm diam; wall of 2–3 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells, or with a single supporting cell, subcylindrical to ampulliform, hyaline, smooth, with periclinal thickening, 4–5 × 3–4 µm. *Conidia* solitary, hyaline, smooth, cylindrical with obtuse ends, eguttulate or with 1–2 small guttules, (3–)4–5(–7) × 1.5(–2) µm.

Culture characteristics — Colonies flat, spreading with sparse aerial mycelium and even, smooth margins. On OA surface olivaceous-grey. On MEA surface pale olivaceous-grey to olivaceous-grey, iron-grey in reverse.

Typus. Netherlands, Raalte, on *Poa* sp. (*Poaceae*), 2013, *W. Quaedvlieg* (holotype CBS H-21677, culture ex-type CBS 136769 = D779; ITS sequence GenBank KJ869117, LSU sequence GenBank KJ869175, ACT sequence GenBank KJ869226, TUB sequence GenBank KJ869243, MycoBank MB808892).

Notes — The genus *Pyrenochaetopsis* (based on *P. leptospora*) was introduced to accommodate phoma-like species with setose pycnidia (de Gruyter et al. 2010). Within *Pyrenochaetopsis*, *P. poae* is closely allied to *P. leptospora* (conidia 4.5–7 × 1–2 µm; Boerema et al. 2004) and is best distinguished based on phylogenetic data.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Pyrenochaetopsis leptospora* (GenBank JF740262; Identities = 477/478 (99 %), no gaps), *Dokmaia monthadangii* (GenBank JN559405; Identities = 491/498 (99 %), no gaps) and *Perisporiopsis* aff. *melioloides* (GenBank FJ884130; Identities = 476/486 (98 %), Gaps = 1/486 (0 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Didymosphaeria futilis* (GenBank GU205219; Identities = 851/851 (100 %), no gaps), *Pyrenochaetopsis microspora* (GenBank GQ387631; Identities = 851/851 (100 %), no gaps) and *Pyrenochaetopsis leptospora* (GenBank GQ387628; Identities = 851/851 (100 %), no gaps).

ACT. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ACT sequence are *Phaeosphaeria nodorum* (GenBank XM_001791742; Identities = 388/409 (95 %), no gaps), *Alternaria chlamydospora* (GenBank JQ671621; Identities = 466/512 (91 %), Gaps = 6/512 (1 %)) and *Embellisia eureka* (GenBank JQ671596; Identities = 454/500 (91 %), Gaps = 6/500 (1 %)). A blast2 comparison between the actin sequence of *Pyrenochaetopsis leptospora* strain CBS 101635 in Q-bank and our sequence revealed Identities = 252/265 (95 %), Gaps = 1/265 (0 %).

TUB. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the TUB sequence are *Ulocladium multiforme* (GenBank JQ672002; Identities = 252/293 (86 %), Gaps = 12/293 (4 %)), *Ulocladium atrum* (GenBank JQ671998; Identities = 252/293 (86 %), Gaps = 12/293 (4 %)) and *Embellisia planifunda* (GenBank JQ671950; Identities = 252/295 (85 %), Gaps = 15/295 (5 %)). A similar search in the Q-bank fungal nucleotide database (www.q-bank.eu) revealed highest similarity with *Pyrenochaetopsis leptospora* (CBS 536.66; Identities = 322/327 (98 %), no gaps), *Pyrenochaetopsis microspora* (CBS 102876; Identities = 322/327 (98 %), no gaps) and *Pyrenochaetopsis decipiens* (CBS 343.85; Identities = 287/331 (87 %), Gaps = 4/331 (1 %)).

Colour illustrations. Raalte, The Netherlands; conidiomata, conidiogenous cell and conidia of *Parastagonospora poae* (left column); conidiomata, conidiogenous cells and conidia of *Pyrenochaetopsis poae* (right column). Scale bars = 10 µm.

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Anungitea eucalyptorum

Fungal Planet 222 – 10 June 2014

Anungitea eucalyptorum Crous & R.G. Shivas, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Eucalyptus*.

Mycelium consisting of pale brown, smooth, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* dimorphic, erect, brown, mostly unbranched. *Microconidiophores* reduced to conidiogenous cells, subcylindrical, 1–3-septate, pale brown, 20–50 × 2–3 µm. *Conidiogenous cells* terminal, clavate, 15–25 × 4–6 µm, with several sympodial, flat-tipped apical loci, 1.5–2 µm diam, not thickened. *Macroconidiophores* erect, flexuous, dark brown, thick-walled, up to 180 µm tall, 2–4 µm diam. *Ramoconidia* giving rise to branched chains of cylindrical conidia, pale brown, smooth, subcylindrical, 0–1-septate, 12–17 × 2–3 µm, with 1–4 apical, flat-tipped scars, 1.5–2 µm diam. *Conidia* hyaline to very pale olivaceous, cylindrical, 0–1-septate, often with bluntly rounded ends, guttulate, (13–)14–15(–17) × 2.5(–3) µm.

Culture characteristics — Colonies reaching 20 mm diam after 2 wk at 22 °C, flat, spreading, with moderate aerial mycelium and feathery margins. On PDA surface and reverse olivaceous-grey. On OA surface iron-grey with diffuse apricot pigment. On MEA surface smoke-grey with olivaceous-grey outer region, iron-grey in reverse.

Typus. Australia, Queensland, Dave's Creek, S28°12'13.7" E153°12'9.5", on *Eucalyptus* (*Myrtaceae*) leaf litter, 11 July 2009, *P.W. Crous & R.G. Shivas* (holotype CBS H-21678, culture ex-type CPC 17207 = CBS 137967; ITS sequence GenBank KJ869118, LSU sequence GenBank KJ869176, TEF sequence GenBank KJ869234, MycoBank MB808893).

Notes — The genus *Anungitea* (*Venturiaceae*, see Crous et al. 2007c) was established for taxa with dark, solitary conidiophores, bearing a head with denticles with flattened conidiogenous scars that are unthickened nor darkened, and chains of cylindrical, 1-septate subhyaline conidia (Sutton 1973). *Phlogicylindrium* was established for species with aggregated, subhyaline, subcylindrical conidiophores that proliferate percurrently, giving rise to chains of hyaline, 1-septate, subcylindrical conidia (Summerell et al. 2006). The present collection fits well within the generic concept of *Angungitea*, and can be distinguished from *A. globosa* (conidia 9–14 × 2 µm, occurring on *Eucalyptus* in Hawaii, New Zealand and South Africa; Sutton & Hodges 1978, Crous & van der Linde 1993) by having larger conidia.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Phlogicylindrium eucalyptorum* (GenBank EU040223; Identities = 615/658 (93 %), Gaps = 19/658 (2 %)), *Phlogicylindrium uniforme* (GenBank JQ044426; Identities = 535/578 (93 %), Gaps = 19/578 (3 %)) and *Pestalotiopsis pauciseta* (GenBank GQ891045; Identities = 451/488 (92 %), Gaps = 11/488 (2 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Phlogicylindrium uniforme* (GenBank JQ044445; Identities = 872/885 (99 %), Gaps = 1/885 (0 %)), *Phlogicylindrium eucalypti* (GenBank DQ923534; Identities = 873/887 (98 %), Gaps = 1/887 (0 %)) and *Phlogicylindrium eucalyptorum* (GenBank EU040223; Identities = 864/879 (98 %), Gaps = 1/879 (0 %)).

TEF. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the TEF sequence are *Hypocrea crassa* (GenBank JN133572; Identities = 215/253 (85 %), Gaps = 9/253 (3 %)), *Trichoderma strigosellum* (GenBank JQ425702; Identities = 214/252 (85 %), Gaps = 6/252 (2 %)) and *Hypocrea virens* (GenBank FJ463363; Identities = 216/255 (85 %), Gaps = 13/255 (5 %)).

Colour illustrations. Dave's Creek, Queensland, Australia; conidiophores, conidiogenous cells and conidia in culture. Scale bars = 10 µm.

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Triposporium cycadicola
& Circinotrichum cycadis

Fungal Planet 223 & 224 – 10 June 2014

Triposporium cycadicola Crous & R.G. Shivas, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Cycas*.

Mycelium consisting of branched, septate, pale brown, 2–3 µm diam hyphae. *Conidiophores* dimorphic. *Macroconidiophores* erect, subcylindrical, flexuous, unbranched, 4–9-septate, 50–220 × 4–5 µm. *Conidiogenous cells* terminal, subcylindrical, brown, smooth, tapering towards a truncate holoblastic locus, 2–2.5 µm diam, 15–25 × 4–5 µm. *Conidia* solitary, brown, verruculose, thick-walled, guttulate, basal cell with truncate hilum, 2–2.5 µm diam, bearing 2–3 lateral arms, extending outwards; arms subcylindrical, tapering towards obtuse ends, 3–7-septate, (30–)55–65(–70) × (7–)8(–9) µm (including basal cell). *Synasexual morph* similar in morphology to macroconidiophores, but shorter, only up to 40 µm long, with terminal cell forming chalara-like conidiogenous cell, giving rise to chains of hyaline, aseptate, smooth microconidia, 3–6 × 2–3 µm.

Culture characteristics — Colonies reaching 20 mm diam after 2 wk at 22 °C, spreading with sparse aerial mycelium and even, smooth margins. On PDA surface umber, reverse grey-olivaceous. On OA surface umber. On MEA surface umber, reverse grey-olivaceous.

Typus. AUSTRALIA, Queensland, Brisbane Forest Park, S27°17'36.2" E152°44'42.0", on *Cycas* sp. (*Cycadaceae*) leaves, 15 July 2009, *P.W. Crous & R.G. Shivas* (holotype CBS H-21679, culture ex-type CPC 17215 = CBS 137968; ITS sequence GenBank KJ869119, LSU sequence GenBank KJ869177, TEF sequence GenBank KJ869235, MycoBank MB808894); CPC 17217, ITS sequence GenBank KJ869120.

Notes — The genus *Triposporium* differs from the morphologically similar *Actinocladium* and *Ceratosporella* by having stauriform conidia composited of a short basal cylindrical stalk, and 3–4-septate arms. However, the branches of the type species of *Triposporium*, *T. elegans*, morphologically differ from that of *T. cycadicola* in that they are more conical and have swollen apical cells (Seifert et al. 2011). The chalara-like synanamorph produced here in culture, also appears to be a unique record for the genus. Further collections are required, however, to resolve the phylogeny of *Triposporium* s.str.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Phialea strobilina* (GenBank EF596821; Identities = 630/692 (91 %), Gaps = 12/692 (1 %)), *Scleropezicula alnicola* (GenBank AF141168; Identities = 630/694 (91 %), Gaps = 17/694 (2 %)) and *Xenopolyscytalum pinea* (GenBank HQ599581; Identities = 573/653 (88 %), Gaps = 21/653 (3 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Phialea strobilina* (GenBank EF596821; Identities = 886/903 (98 %), Gaps = 1/903 (0 %)), *Rhytisma acerinum* (GenBank AF356696; Identities = 826/845 (98 %), Gaps = 2/845 (0 %)) and *Chalara acuaria* (GenBank FJ176248; Identities = 831/853 (97 %), Gaps = 6/853 (0 %)).

Circinotrichum cycadis Crous & R.G. Shivas, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Cycas*.

Mycelium consisting of brown, septate, smooth, 1.5–2.5 µm diam hyphae. *Setae* erect, dark brown, 4–7-septate, stalk dark brown, thick-walled, upper curled part medium brown, thin-walled, warty, tapering to obtusely rounded apex, foot cell arising from hyphae, lacking rhizoids, stalk 25–40 × 2–3 µm, apical curled part with 1–2 loops. *Conidiophores* reduced to conidiogenous cells, arranged in clusters around setae, pale olivaceous, smooth, ampulliform, 8–20 × 3–4 µm, proliferating inconspicuously percurrently at apex. *Conidia* hyaline, smooth, fusoid-ellipsoid, straight, apex obtuse, base truncate, (8–)9–11(–13) × 2(–2.5) µm; hilum truncate, not thickened nor darkened, 0.5 µm diam.

Culture characteristics — Colonies reaching up to 5 mm diam after 2 wk at 22 °C, spreading, erumpent, with sparse aerial mycelium and feathery margins. On PDA surface and reverse olivaceous-grey. On OA surface iron-grey. On MEA dirty white, with sienna margin, reverse umber.

Typus. AUSTRALIA, Queensland, Brisbane Forest Park, S27°17'36.2" E152°44'42.0", on *Cycas* sp. (*Cycadaceae*) leaves, 15 July 2009, *P.W. Crous & R.G. Shivas* (holotype CBS H-21680, culture ex-type CPC 17285 = CBS 137969; ITS sequence GenBank KJ869121, LSU sequence GenBank KJ869178, MycoBank MB808895).

Notes — The genus *Circinotrichum* is characterised by having unbranched, brown, solitary, sterile setae, surrounded at the base by clusters of aseptate, hyaline conidiogenous cells. It is distinguished from *Gyrothrix* in that the latter has branched setae (Seifert et al. 2011). The conidiogenesis is obscure in both genera due to the minute dimensions of the conidiogenous cell apices, and more studies are required to resolve this aspect. *Circinotrichum cycadis* is presently the only species known from *Cycas*.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Gibberella moniliformis* (GenBank JN232129; Identities = 430/496 (87 %), Gaps = 20/496 (4 %)), *Fusarium oxysporum* (GenBank JN232179; Identities = 424/488 (87 %), Gaps = 20/488 (4 %)) and *Calceomyces lacunosus* (GenBank JX658530; Identities = 413/464 (89 %), Gaps = 26/464 (5 %)). An identification using MycoID on MycoBank yielded a similarity of 549/586 (94 %) and Gaps = 6/586 (1 %) with *Circinotrichum olivaceum* strain CBS 101185.

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Anthostomella conorum* (GenBank EU552099; Identities = 865/897 (96 %), Gaps = 2/897 (0 %)) and *Barrmaelia macrospora* (GenBank KC774566; Identities = 856/897 (95 %), Gaps = 4/897 (0 %)).

Colour illustrations. Brisbane Forest Park, Queensland, Australia; conidiophores and conidia of *Triposporium cycadicola* in culture (left column); setae, conidiogenous cells and conidia of *Circinotrichum cycadis* in culture (right column). Scale bars = 10 µm.

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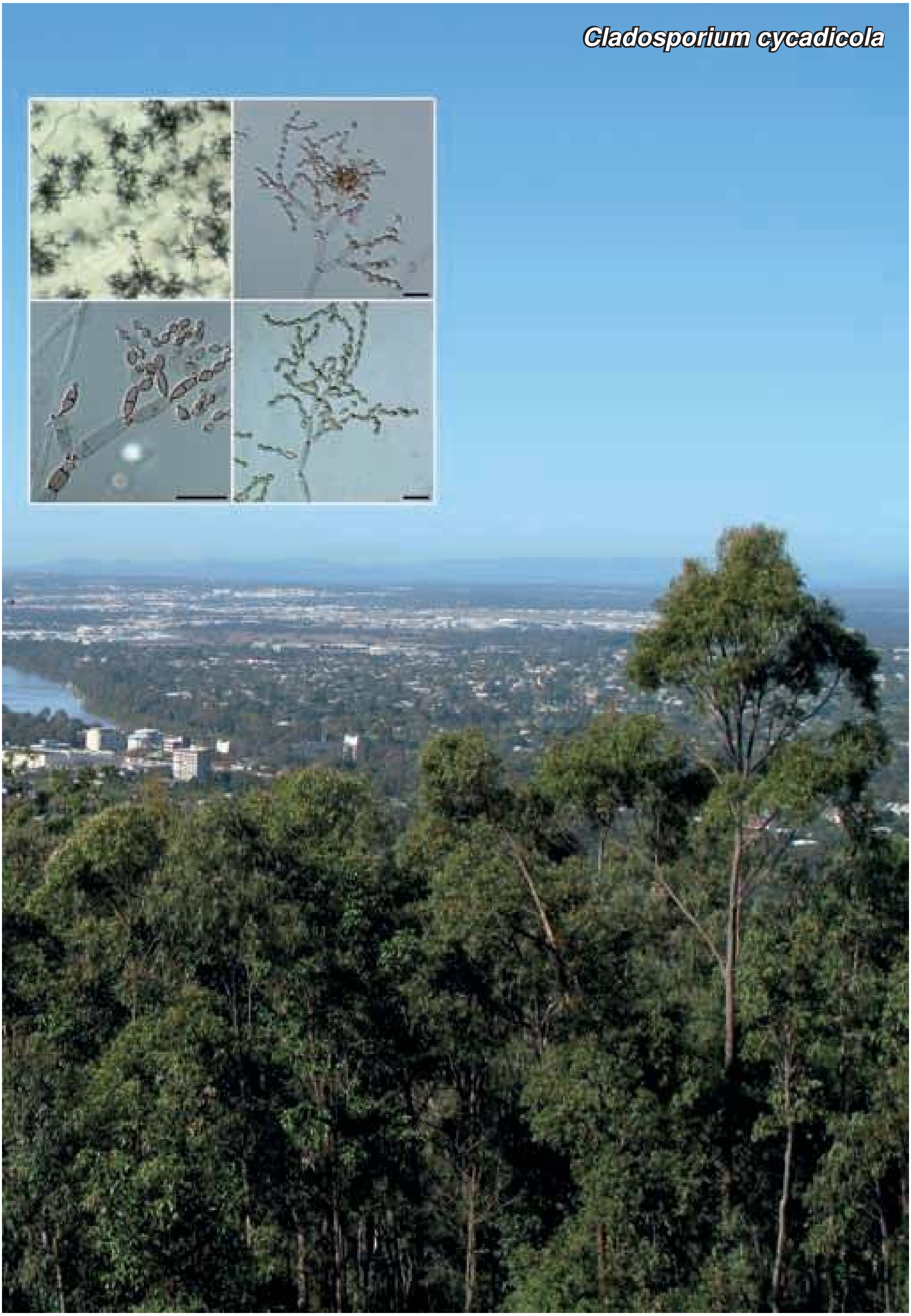
Cladosporium cycadicola

Fungal Planet 225 – 10 June 2014

Cladosporium cycadicola Crous & R.G. Shivas, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Cycas*.

Mycelium consisting of branched, septate, smooth, brown, 2–3 µm diam hyphae. *Conidiophores* erect, flexuous, subcylindrical, unbranched, 30–70 × 3–4 µm, 2–5-septate, giving rise to a conidiogenous apparatus with chains of branched conidia. *Primary ramoconidia* subcylindrical, pale brown, smooth, 0–1-septate, 17–27 × 2.5–3 µm; hila thickened, darkened and refractive, 0.5–1.5 µm diam. *Secondary ramoconidia* subcylindrical to fusoid-ellipsoidal, 7–14 × 1.5–3 µm. *Intercalary* and small *terminal conidia* in branched chains (–15), brown, smooth, ellipsoid, pale brown, guttulate, (4–)5(–6) × 2.5(–3) µm; hila thickened, darkened, refractive, 0.5 µm diam.

Culture characteristics — Colonies reaching 30 mm diam after 2 wk at 22 °C, spreading, folded, with sparse aerial mycelium and smooth, even margins. On PDA olivaceous-grey, reverse iron-grey. On OA surface iron-grey. On MEA surface and reverse olivaceous-grey.

Typus. AUSTRALIA, Queensland, Cairns Botanical Garden, S16°53'57.1" E145°44'48.7", on *Cycas media* (*Cycadaceae*) leaves, 12 Aug. 2009, *P.W. Crous & R.G. Shivas* (holotype CBS H-21681, culture ex-type CPC 17251 = CBS 137970; ITS sequence GenBank KJ869122, LSU sequence GenBank KJ869179, ACT sequence GenBank KJ869227, TEF sequence GenBank KJ869236, MycoBank MB808896).

Colour illustrations. Brisbane, Australia; conidiophores and conidia in culture. Scale bars = 10 µm.

Notes — Two species of *Cladosporium* have been described from *Cycas*, namely *C. apicale* and *C. cycadis* (Bensch et al. 2012). *Cladosporium cycadicola* can be distinguished from both species by being more allied to the *C. sphaerospermum* species complex (Zalar et al. 2007), having ramoconidia that are subcylindrical to fusoid-ellipsoid, 0–1-septate and intercalary and terminal conidia in long chains that are smaller than those in *C. apicale* and *C. cycadis*.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Cladosporium sphaerospermum* (GenBank EU570256; Identities = 635/647 (98 %), Gaps = 5/647 (0 %)), *Cladosporium cucumerinum* (GenBank HM148071; Identities = 632/644 (98 %), Gaps = 5/644 (0 %)) and *Cladosporium lignicola* (GenBank AF393709; Identities = 607/619 (98 %), Gaps = 5/619 (0 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Cladosporium sphaerospermum* (GenBank JN938884; Identities = 867/875 (99 %), Gaps = 1/875 (0 %)), *Cladosporium langeronii* (GenBank DQ780380; Identities = 863/876 (99 %), Gaps = 1/876 (0 %)) and *Cladosporium perangustum* (GenBank JF499856; Identities = 894/910 (98 %), Gaps = 1/910 (0 %)).

ACT. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ACT sequence are *Cladosporium dominicanum* (GenBank EF101368; Identities = 171/190 (90 %), no gaps), *Cladosporium exile* (GenBank HM148580; Identities = 200/235 (85 %), Gaps = 15/235 (6 %)) and *Cladosporium psychrotolerans* (GenBank EF101366; Identities = 162/191 (85 %), Gaps = 9/191 (4 %)).

TEF. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the complete TEF sequence is *Cladosporium dominicanum* (GenBank JN906986; Identities = 361/421 (86 %), Gaps = 19/421 (4 %)) with partial hits of the last exon with *Cladosporium angustisporum* (GenBank HM148236; Identities = 184/190 (97 %), no gaps) and *Cladosporium cladosporioides* (GenBank HM148267; Identities = 186/194 (96 %), no gaps).

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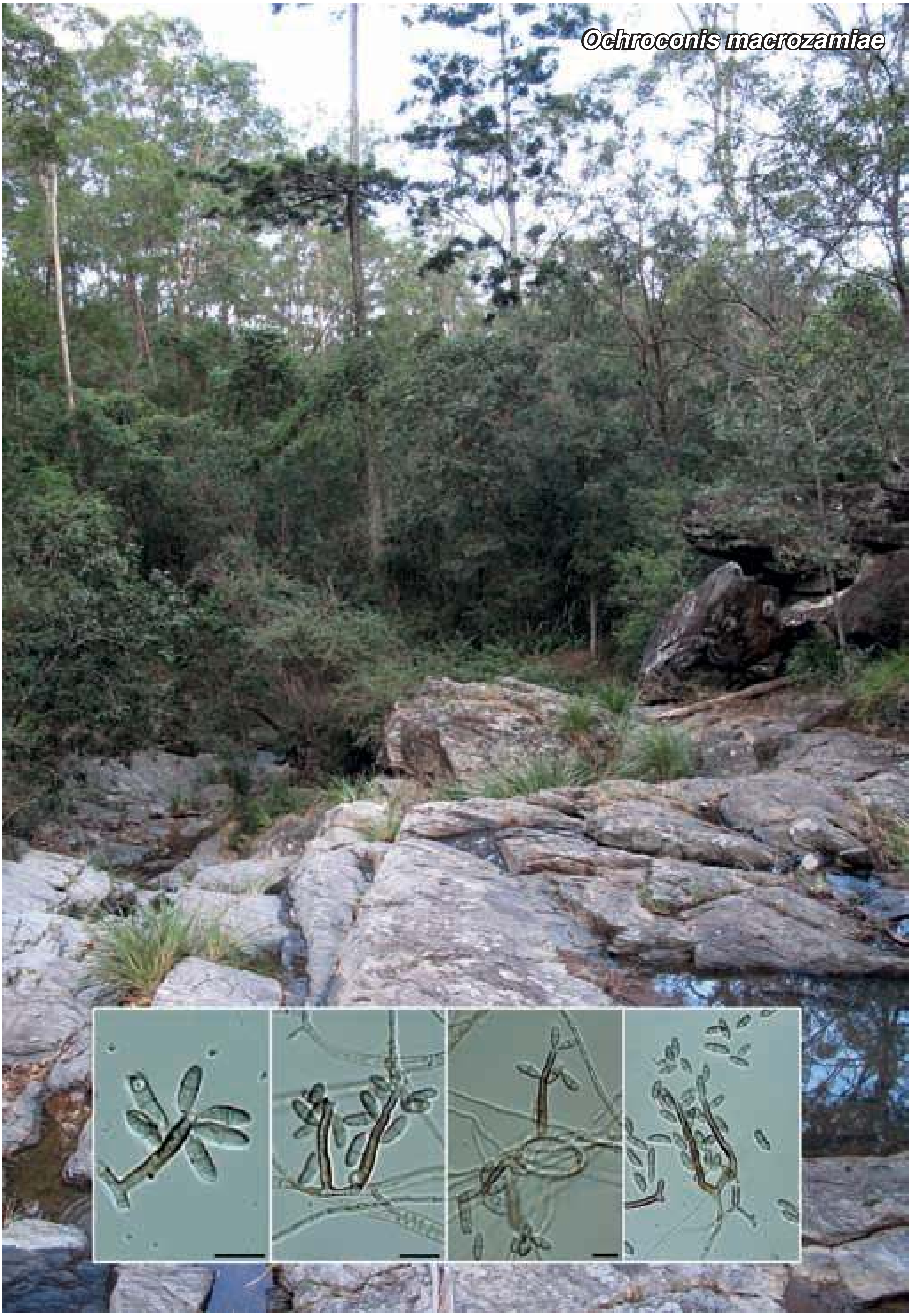
Ochroconis macrozamiae

Fungal Planet 226 – 10 June 2014

Ochroconis macrozamiae Crous & R.G. Shivas, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Macrozamia*.

Mycelium consisting of septate, branched, red-brown, smooth, 1.5–2 µm diam hyphae. *Conidiophores* erect, thick-walled, red-brown, straight to geniculous-sinuous, subcylindrical, 1–2-septate, 20–30 × 2.5–3 µm, solitary, tapering towards bluntly rounded conidiogenous cell, 10–12 × 2.5–3 µm, forming a rachis with minute denticles, 0.5 µm diam. *Conidia* red-brown, verruculose, constricted at median septum, broadly fusiform, mostly straight, with rounded apex and truncate, darkened base, 1 µm diam, (5–)8–10(–12) × (3–)3.5(–4) µm.

Culture characteristics — Colonies reaching 8 mm diam after 2 wk at 22 °C, erumpent, spreading, with moderate aerial mycelium and smooth, catenate margins. On PDA surface and reverse isabelline. On OA surface isabelline to sepia. On MEA surface isabelline with sepia margins, reverse dark brick.

Typus. Australia, Queensland, Brisbane, Slaughter Falls, on *Macrozamia* (*Zamiaceae*) leaf litter, 16 July 2009, *P.W. Crous & R.G. Shivas* (holotype CBS H-21682, culture ex-type CPC 17262 = CBS 137971; ITS sequence GenBank KJ869123, LSU sequence GenBank KJ869180, MycoBank MB808897).

Notes — Although commonly isolated from litter, species of *Ochroconis* are frequently associated with disease in cold-blooded animals. The genus *Ochroconis* was recently revised by Samerpitak et al. (2014) and shown to belong to the *Sympoventuriaceae*. Of the species presently known in the genus, *O. macrozamia* is phylogenetically related to *O. gamsii* (conidia 6–9 × 2.4–2.8 µm; de Hoog 1985), but can be distinguished based on its larger conidia.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Ochroconis gamsii* (GenBank HQ667520; Identities = 535/560 (96 %), Gaps = 15/560 (2 %)), *Ochroconis constricta* (GenBank AB161063; Identities = 432/446 (97 %), Gaps = 4/446 (1 %)) and *Ochroconis tshawytschae* (GenBank AB161066; Identities = 438/471 (93 %), Gaps = 10/471 (2 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Ochroconis gamsii* (GenBank AB161064; Identities = 592/611 (97 %), Gaps = 2/611 (0 %)), *Ochroconis humicola* (GenBank AB564618; Identities = 854/896 (95 %), Gaps = 6/896 (0 %)) and *Ochroconis tshawytschae* (GenBank KF282665; Identities = 816/859 (95 %), Gaps = 8/859 (0 %)).

Colour illustrations. Slaughter Falls, Brisbane, Australia; conidiophores and conidia in culture. Scale bars = 10 µm.

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Acrocalymma cycadis
& Ramopenidiella cycadicola

Fungal Planet 227 & 228 – 10 June 2014

Acrocalymma cycadis Crous & R.G. Shivas, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Cycas*.

Conidiomata brown, erumpent, globose, up to 300 µm diam, with central ostiole; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells or with a single supporting cell. *Conidiogenous cells* lining the inner cavity, subcylindrical, hyaline, smooth, 10–20 × 4–5 µm, proliferating percurrently at apex, or with prominent periclinal thickening at apex, 3–4 µm diam. *Conidia* hyaline, smooth, guttulate, solitary, subcylindrical, straight, apex obtusely rounded, hilum truncate, 1.5–2 µm diam, 0(–1)-septate, guttulate, (25–)28–32(–35) × (4–)5 µm, conidia at times becoming 1-septate and pale brown with age.

Culture characteristics — Colonies reaching up to 20 mm diam after 2 wk at 22 °C, spreading with sparse aerial mycelium and feathery margin. On PDA surface and reverse dirty white, olivaceous grey in centre. On OA surface olivaceous-grey, white in outer region. On MEA surface white, reverse ochreous.

Typus. Australia, Queensland, Cairns, S16°02'19.8" E145°27'39.1", on *Cycas calcicola* (*Cycadaceae*) leaf litter, 8 Aug. 2009, *P.W. Crous & R.G. Shivas* (holotype CBS H-21683, culture ex-type CPC 17345 = CBS 137972; ITS sequence GenBank KJ869124, LSU sequence GenBank KJ869181, MycoBank MB808898).

Notes — Alcorn & Irvin (1987) established the genus *Acrocalymma* for *A. medicaginis*, a species associated with a root and crown rot disease of *Medicago sativa*. A second species was recently described by Zhang et al. (2012a) from submerged wood in Thailand. *Acrocalymma cycadis* closely matches the generic description, forming pycnidial conidiomata that give rise to 0(–1)-septate, hyaline conidia with mucoid caps. All three species can be distinguished based on their conidial dimensions, those of *A. medicaginis* (11–21 × 3–5 µm) and *A. aquatic* (12–17 × 3–4 µm) being smaller than that of *A. cycadis*.

Ramopenidiella Crous & R.G. Shivas, *gen. nov.*

Etymology. Named after its conspicuous ramoconidia and morphological similarity to *Penidiella*.

Mycelium consisting of branched, septate, smooth, pale brown hyphae. *Conidiophores* dimorphic. *Microconidiophores* erect, brown, smooth, subcylindrical, reduced to conidiogenous cells. *Macroconidiophores* erect, brown, smooth, thick-walled, flexuous, unbranched, subcylindrical, septate; base arising from hyphae, lacking rhizoids. *Conidiogenous cells* integrated, terminal, brown, smooth, subcylindrical, containing several truncate, apical loci that are subdenticulate, and give rise to several ramoconidia. *Primary ramoconidia* brown, smooth, fusoid-ellipsoid, aseptate, constricted at base. *Secondary ramoconidia* pale brown, smooth, fusoid-ellipsoid, aseptate. *Intercalary* and *terminal conidia* pale brown, smooth, fusoid, ellipsoid, aseptate; hila somewhat thickened and darkened.

Type species. *Ramopenidiella cycadicola*.
MycoBank MB808899.

Ramopenidiella cycadicola Crous & R.G. Shivas, *sp. nov.*

Etymology. Named after the host genus from which it was isolated, *Cycas*.

Mycelium consisting of branched, septate, smooth, pale brown, 1.5–2 µm diam hyphae. *Conidiophores* dimorphic. *Microconidiophores* erect, brown, smooth, subcylindrical, reduced to conidiogenous cells, up to 15 µm long, 3–4 µm diam. *Macroconidiophores* erect, brown, smooth, thick-walled, flexuous, unbranched, subcylindrical, 3–8-septate, 40–130 × 3–4 µm; base arising from hyphae, lacking rhizoids. *Conidiogenous cells* integrated, terminal, brown, smooth, subcylindrical, 8–17 × 3–5 µm, containing several truncate, apical loci that are subdenticulate, 1 µm diam, and give rise to several ramoconidia. *Primary ramoconidia* brown, smooth, fusoid-ellipsoid, aseptate, 8–10 × 3–4 µm. *Secondary ramoconidia* pale brown, smooth, fusoid-ellipsoid, aseptate, 8–14 × 2.5–3 µm. *Intercalary* and *terminal conidia* pale brown, smooth, fusoid, ellipsoid, aseptate, (5–)8–9(–10) × 2(–2.5) µm; hila somewhat thickened and darkened, 0.5 µm diam.

Colour illustrations. *Cycas calcicola* in Queensland, Australia; conidiomata, conidiogenous cells and conidia (with mucoid appendages) of *Acrocalymma cycadis* in culture (left column); conidiophores and conidia of *Ramopenidiella cycadicola* in culture (right column). Scale bars = 10 µm.

Culture characteristics — Colonies reaching up to 8 mm diam after 2 wk at 22 °C, spreading, with sparse aerial mycelium and feathery, uneven margins. On PDA surface and reverse olivaceous-grey. On OA surface olivaceous-grey. On MEA surface olivaceous-grey, reverse iron-grey.

Typus. Australia, Queensland, Cairns, S16°02'19.8" E145°27'39.1", on *Cycas calcicola* (*Cycadaceae*) leaf litter, 8 Aug. 2009, *P.W. Crous & R.G. Shivas* (holotype CBS H-21684, culture ex-type CPC 17291 = CBS 137973; ITS sequence GenBank KJ869125, LSU sequence GenBank KJ869182, TEF sequence GenBank KJ869237, MycoBank MB808900).

Notes — The genus *Penidiella* was established by Crous et al. (2007a) to accommodate dematiaceous hyphomycetes with solitary, brown conidiophores, an apical set of branches and conidiogenous cells, and branched chains of 0(–1)-septate brown conidia with slightly thickened and darkened hila. The genus was too broadly defined however, and recently Quaedvlieg et al. (2014) showed that it was paraphyletic. The genus *Ramopenidiella* is distinguished from *Penidiella* in that the first whorl of primary ramoconidia appear as conidiophore branches qua pigmentation (darker than that of other conidia), but they are ramoconidia though not primary ramoconidia (sensu Bensch et al. 2012), as they are constricted at the base and very distinct in morphology from the secondary ramoconidia.

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Beltraniopsis neolitseae
& *Acrodontium neolitseae*

Fungal Planet 229 & 230 – 10 June 2014

Beltraniopsis neolitseae Crous & Summerell, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Neolitsea*.

Setae erect, dark brown, straight to somewhat flexuous, tapering to obtuse apex, 8–20-septate, 300–500 × 6–8 µm, with basal cell arising from superficial hyphae. *Conidiophores* arranged around base of setae, or occurring laterally on setae, pale brown to brown, smooth, flexuous when arising from hyphae, up to 80 µm tall, 3–5 µm diam, 3–5-septate. *Separating cells* ellipsoid to clavate, pale brown, smooth, 7–10 × 4–6 µm, with 1–3 terminal subdenticulate loci. On conidiophores separating cells usually originating from 1–2 supporting cells, medium to brown, 10–15 × 6–9 µm, with 1–4 terminal loci giving rise to separating cells. *Conidia* solitary, biconic, rostrate with short beak, aseptate, pale olivaceous-brown, smooth, with hyaline transverse band, usually only visible in older conidia, (27–)30–33(–35) × (6–)7–8(–9) µm.

Culture characteristics — Colonies covering dish within 2 wk at 22 °C, spreading, with sparse aerial mycelium and feathery margins. On PDA surface and reverse olivaceous-grey. On OA surface iron-grey. On MEA surface and reverse olivaceous-grey.

Typus. AUSTRALIA, New South Wales, Nightcap National Park, S28°38'41.3" E153°20'17.9", on *Neolitsea australiensis* (*Lauraceae*) leaves, 9 Mar. 2013, *B.A. Summerell* (holotype CBS H-21686, culture ex-type CPC 22168 = CBS 137974; ITS sequence GenBank KJ869126, LSU sequence GenBank KJ869183, MycoBank MB808901).

Notes — The genus *Beltraniopsis* is characterised by solitary, brown conidiophores with lobed foot cells that are fertile, with sympodial conidiogenesis, denticulate conidiogenous cells, separating cells, and brown, biconic conidia with an equatorial band of lighter pigment (Seifert et al. 2011). Using the key of Gusmão et al. (2000), *B. neolitsea* is most similar to *B. fabularis* (conidia 30–37 × 9 µm) but can be distinguished by having smaller conidia, separating cells and longer setae.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Beltrania querna* (GenBank EF029240; Identities = 533/568 (94 %), Gaps = 12/568 (2 %)), *Menisporopsis theobromae* (GenBank GU905996; Identities = 451/484 (93 %), Gaps = 15/484 (3 %)) and *Beltraniella portoricensis* (GenBank GU905993; Identities = 448/482 (93 %), Gaps = 9/482 (1 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Subramaniomyces fusisaprophyticus* (GenBank EU040241; Identities = 763/780 (98 %), Gaps = 3/780 (0 %)), *Pseudomassaria carolinensis* (GenBank DQ810233; Identities = 761/779 (98 %), Gaps = 3/779 (0 %)) and *Parapleurotheciopsis inaequiseptata* (GenBank EU040235; Identities = 752/781 (96 %), Gaps = 4/781 (0 %)).

Acrodontium neolitseae Crous & Summerell, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Neolitsea*.

Mycelium consisting of brown, septate, branched, smooth, 1.5–2 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* pale brown, smooth, elongate ampulliform, slightly constricted at base, straight to flexuous, tapering towards subacutely rounded apex, proliferating sympodially, forming a rachis in upper two thirds of conidiogenous cell, 30–60 × 2–2.5 µm, loci inconspicuous warts, slightly thickened, 0.3 µm diam. *Conidia* solitary, pale brown, smooth, ellipsoid with obtuse apex, tapering in lower part to truncate hilum, 0.3–0.5 µm diam, slightly darkened, (2–)2.5–3(–3.5) × (1.5–)2(–2.5) µm.

Culture characteristics — Colonies reaching up to 15 mm diam after 2 wk at 22 °C, spreading, erumpent, folded, with moderate aerial mycelium, and even, lobate margins. On PDA surface pale olivaceous-grey in centre, olivaceous-grey in outer region, reverse olivaceous-grey. On OA and MEA pale olivaceous-grey in centre, olivaceous-grey in outer region and underneath.

Colour illustrations. Nightcap National Park, New South Wales, Australia; conidiophores and conidia of *Beltraniopsis neolitseae* in culture (left column); conidiophores and conidia of *Acrodontium neolitseae* (right column) in culture. Scale bars = 10 µm.

Typus. AUSTRALIA, New South Wales, Nightcap National Park, S28°38'41.3" E153°20'17.9", on *Neolitsea australiensis* (*Lauraceae*) leaves, 9 Mar. 2013, *B.A. Summerell* (holotype CBS H-21687, culture ex-type CPC 22172 = CBS 137975; ITS sequence GenBank KJ869127, LSU sequence GenBank KJ869184, MycoBank MB808902).

Notes — The genus *Acrodontium* was established by de Hoog (1972) and accommodates around 10 species being saprobic on wood, bark or leaves, or even being fungicolous (Seifert et al. 2011). Using the key of de Hoog (1972), *A. neolitsea* is most similar to *A. hydnicola*, except that conidiophores are not branched but reduced to solitary conidiogenous cells. *Acrodontium* represents yet another genus newly shown to belong to the *Mycosphaerellaceae*.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Pseudocercosporella fraxini* (GenBank GU214682; Identities = 547/550 (99 %), no gaps), *Acrodontium crateriforme* (GenBank FN666566; Identities = 481/484 (99 %), no gaps) and *Pseudotaeniolina globosa* (GenBank KC311489; Identities = 505/560 (90 %), Gaps = 15/560 (2 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Pseudocercosporella fraxini* (GenBank GU214682; Identities = 843/843 (100 %), no gaps), *Phaeothecoidea melaleuca* (GenBank HQ599595; Identities = 814/842 (97 %), Gaps = 2/842 (0 %)) and *Phacellium paspali* (GenBank GU214669; Identities = 815/847 (96 %), Gaps = 6/847 (0 %)).

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Beltraniella endiandrae

Fungal Planet 231 – 10 June 2014

Beltraniella endiandrae Crous & Summerell, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Endiandra.*

Setae erect, dark brown, straight to flexuous, arising from superficial hyphae, frequently branched at base, subcylindrical, tapering to obtuse apices, 3–7-septate, 60–140 × 3–4 µm, basal cell sometimes slightly swollen. *Conidiophores* subcylindrical, pale brown, smooth, arising from superficial mycelium, straight to flexuous, 1–10-septate, 15–100 × 4–5 µm. *Conidiogenous cells* terminal or lateral, subcylindrical to somewhat clavate, pale brown, smooth, 15–30 × 4–6 µm; with 1–4 denticulate loci, 0.5–1 × 0.5 µm. *Supporting cells* pale brown, smooth, ellipsoid, aseptate, 8–10 × 4–5 µm. *Conidia* solitary, turbinate, pale brown, smooth, guttulate, aseptate, with hyaline band of pigment visible in older conidia, (22–)24–26(–27) × 6(–7) µm.

Culture characteristics — Colonies reaching 70 mm diam after 2 wk at 22 °C, flat, spreading, with moderate aerial mycelium and smooth, even margins. On PDA surface and reverse iron-grey. On OA iron-grey with patches of pale olivaceous-grey. On MEA surface pale olivaceous-grey, reverse umber.

Typus. Australia, New South Wales, Nightcap National Park, S28°33'91.8" E153°20'22.8", on *Endiandra introrsa* (*Lauraceae*) leaves, 9 Mar. 2013, *B.A. Summerell* (holotype CBS H-21688, culture ex-type CPC 22193 = CBS 137976; ITS sequence GenBank KJ869128, LSU sequence GenBank KJ869185, MycoBank MB808903).

Notes — The genus *Beltraniella* (*Hyphonectriaceae*, *Xylariales*; Shirouzu et al. 2010) was established for species with brown, unbranched, fertile setae and sympodially proliferating, denticulate conidiogenous cells, separating cells and biconic, brown conidia with a hyaline equatorial band (Seifert et al. 2011). Of the species presently known (Shirouzu et al. 2010), *B. endiandra* is most similar to *B. lyrata* (conidia 20–29 × 9–11 µm) in conidium length but differs in having narrower, non-clavate conidia.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Beltraniella portoricensis* (GenBank GU905993; Identities = 478/486 (98 %), Gaps = 1/486 (0 %)), *Menisporopsis theobromae* (GenBank GU905996; Identities = 473/488 (97 %), Gaps = 4/488 (0 %)) and *Beltrania rhombica* (GenBank GU797390; Identities = 494/514 (96 %), Gaps = 7/514 (1 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Pseudomassaria carolinensis* (GenBank DQ810233; Identities = 814/820 (99 %), Gaps = 1/820 (0 %)), *Subramaniomyces fusisaprophyticus* (GenBank EU040241; Identities = 818/833 (98 %), Gaps = 1/833 (0 %)) and *Parapleurotheciopsis inaequiseptata* (GenBank EU040235; Identities = 807/834 (97 %), Gaps = 2/834 (0 %)).

Colour illustrations. Nightcap National Park, New South Wales, Australia; setae, conidiophores and conidia in culture. Scale bars = 10 µm.

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Vermiculariopsiella dichapetali

Fungal Planet 232 – 10 June 2014

Vermiculariopsiella dichapetali Crous, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Dichapetalum*.

Ascomata black, globose, superficial, up to 600 µm diam, developing on OA but remaining sterile, covered in brown, erect setae, similar to that observed in sporodochia. *Sporodochia* developing on SNA, erumpent, crystalline, up to 500 µm diam, with brown, erect setae dispersed throughout sporodochium, thick-walled, roughened, straight to flexuous, 100–300 × 6–10 µm, 6–12-septate, tapering to an obtuse apex that is medium brown, and thinner walled than the stipe. *Conidiophores* tightly aggregated in a brown stroma, subcylindrical, 1–4-septate, brown and verruculose at base, becoming pale brown in upper region, 60–80 × 2.5–3.5 µm. *Conidiogenous cells* terminal, subcylindrical, pale brown to subhyaline, verruculose to smooth, frequently curved in upper part, apex 1–1.5 µm diam, with prominent cylindrical collarette, 1–2 µm long, 20–40 × 2.5–3 µm. *Conidia* solitary, hyaline, guttulate, straight to slightly curved, inequilateral with inner plane straight and outer plane convex, apex subobtusely rounded, but frequently somewhat constricted and curved towards inner plane; base truncate but with excentric hilum, 0.5 µm diam, on inner straight plane, (10–)17–22(–24) × 2.5(–3) µm.

Culture characteristics — Colonies reaching 50 mm diam after 2 wk at 22 °C, flat, spreading, with sparse aerial mycelium and smooth, even margins. On PDA surface and reverse buff with patches of hazel. On OA and MEA surface ochreous.

Typus. Botswana, B&B13358, on *Dichapetalum rhodesicum* (*Dichapetalaceae*), 17 Feb. 2013, *M. van der Bank* (holotype CBS H-21689, culture ex-type CPC 22463 = CBS 137977; ITS sequence GenBank KJ869129, LSU sequence GenBank KJ869186, MycoBank MB808904).

Notes — *Vermiculariopsiella* is characterised by having sporodochia with brown, erect setae dispersed throughout, stromatic, subhyaline conidiophores that give rise to phialidic conidiogenous cells with prominently curved apices, and hyaline, aseptate conidia (Seifert et al. 2011). The connection between *Vermiculariopsiella* and *Echinosphaeria* (sensu Puja et al. 2006) is obviously incorrect, as the asexual morph is an undescribed genus, and not *Vermiculariopsiella*. Presently there are around 16 species described in *Vermiculariopsiella*, and using the key of Marques et al. (2008), *V. dichapetali* is most similar to *V. elegans* (20–25 × 6–8 µm) and *V. indica* (22–30 × 8–11 µm) but distinguishable by its narrower conidia.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Apodus oryzae* (GenBank AY681200; Identities = 359/402 (89 %), Gaps = 10/402 (2 %)), *Cordana solitaria* (GenBank HE672150; Identities = 353/394 (90 %), Gaps = 9/394 (2 %)) and *Cercophora grandiuscula* (GenBank GQ922544; Identities = 378/430 (88 %), Gaps = 10/430 (2 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Dictyochaeta cylindrospora* (GenBank EF063575; Identities = 789/828 (95 %), Gaps = 6/828 (0 %)), *Dactylaria parvispora* (GenBank EU107296; Identities = 781/830 (94 %), Gaps = 6/830 (0 %)) and *Cryptadelphia groenendalensis* (GenBank EU528007; Identities = 777/829 (94 %), Gaps = 5/829 (0 %)).

Colour illustrations. *Dichapetalum rhodesicum* in Botswana (photo: John Burrows); sterile black ascomata, white conidiomata, setae, conidiogenous cells and conidia in culture. Scale bars = 10 µm.

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Chaetomella zambiensis

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Chaetomella zambiensis Crous, *sp. nov.*

Etymology. Named after the country where it was collected, Zambia.

On SNA. *Conidiomata* sporodochial, superficial, stipitate, separate, up to 250 µm diam, creamy in colour, globose, becoming cupulate; basal wall of brown *textura angularis*, which becomes hyaline towards apex, separating into paraphyses; conidioma surrounded by a brown outer layer of cylindrical cells with obtuse apices that give rise to brown, club-shaped setae, thick-walled, smooth to verruculose, 3–8-septate, basal cell swollen, apical cell clavate to ellipsoid, 50–90 × 4–6 µm. *Conidiophores* hyaline, smooth, branched, septate, filiform, giving rise to conidiogenous cells and paraphyses, up to 100 µm long, 1.5–2 µm diam. *Conidiogenous cells* terminal and lateral, monophialidic, subcylindrical, straight to curved, smooth, hyaline, with periclinal thickening and minute collarette, 3–20 × 1.5–2 µm. *Conidia* hyaline, smooth, aseptate, cymbiform, guttulate, apex acutely rounded, base with truncate hilum, 0.5 µm diam, (7–)8(–9) × (1.5–)2 µm.

Culture characteristics — Colonies reaching 70 mm diam after 2 wk at 22 °C, spreading, with moderate aerial mycelium and feathery margins. On PDA and OA surface and reverse dirty white. On MEA surface dirty white, reverse luteous.

Typus. Zambia, B&B13448, Unknown host (*Fabaceae*), 21 Feb. 2013, *M. van der Bank* (holotype CBS H-21690, culture ex-type CPC 22465 = CBS 137978; ITS sequence GenBank KJ869130, LSU sequence GenBank KJ869187, MycoBank MB808905).

Notes — The genus *Chaetomella* (*Leotiomycetes*) was treated by Rossman et al. (2004). Although there are more than 50 names in the genus, most taxa are poorly known, and the genus is in need of revision. Sutton (1980) included four species and one variety in *Chaetomella*, and reduced *Volutellospora* and *Harikrishnaella* to synonymy. Phylogenetically, *C. zambiensis* is best accommodated in *Chaetomella*, where it presents a novel lineage.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Chaetomella raphigera* (GenBank KF193635; Identities = 448/472 (95 %), Gaps = 6/472 (1 %)), *Zoellneria rosarum* (GenBank KF661532; Identities = 468/508 (92 %), Gaps = 5/508 (0 %)) and *Chaetomella oblonga* (GenBank AY487079; Identities = 446/486 (92 %), Gaps = 8/486 (1 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Chaetomella raphigera* (GenBank AY487086; Identities = 789/804 (98 %), no gaps), *Chaetomella acutiseta* (GenBank AY544679; Identities = 801/817 (98 %), no gaps) and *Chaetomella oblonga* (GenBank AY487080; Identities = 801/817 (98 %), no gaps).

Colour illustrations. Unknown *Fabaceae* in Zambia (photo: John Burrows); conidiomata, setae, conidiophores and conidia in culture. Scale bars = 10 µm.

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Phaeophleospora parsoniae

Fungal Planet 234 – 10 June 2014

Phaeophleospora parsoniae Crous & Summerell, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Parsonia.*

Leaf spots amphigenous, grey-brown in middle, brown in outer region, angular, confined by leaf veins, 2–6 mm diam. *Conidiomata* up to 150 µm diam, pycnidial, epiphyllous, immersed, black, with central ostiole. In culture conidiomata are more acervular, up to 350 µm diam, convulated, stromatic, irregular; outer layer with irregular, brown, verruculose hyphae; basal stroma brown, verruculose, giving rise to conidiophores; basal cells brown, verruculose, upper cells hyaline, smooth, 1–4-septate, subcylindrical, 10–25 × 2–3 µm, branched below. *Conidiogenous cells* hyaline, smooth, subcylindrical, terminal and lateral, 5–15 × 2–2.5 µm, proliferating percurrently at apex, or with periclinal thickening, intermixed among paraphyses, that are branched, similar in length and at times become fertile. *Conidia* solitary, straight to slightly curved, hyaline, smooth, guttulate, subcylindrical to narrowly fusoid-ellipsoidal, widest in the middle, tapering to subobtuse apex and truncate hilum, 0.5 µm diam, (5–)6–7(–7.5) × 2(–2.5) µm.

Culture characteristics — Colonies reaching 15 mm diam after 2 wk at 22 °C, erumpent, folded, spreading, with even, lobed margins. On PDA surface pale olivaceous-grey, reverse smoke-grey. On OA surface olivaceous-grey with vinaceous margin. On MEA surface pale olivaceous-grey, reverse iron-grey.

Typus. Australia, New South Wales, Brunswick Heads Nature Reserve, S28°31'90.8" E153°32'57.0", on *Parsonia straminea* (*Apocynaceae*) leaves, 9 Mar. 2013, *B.A. Summerell* (holotype CBS H-21691, culture ex-type CPC 22537 = CBS 137979; ITS sequence GenBank KJ869131, LSU sequence GenBank KJ869188, MycoBank MB808906).

Notes — The genus *Phaeophleospora* (based on *P. eugeniae*; Crous et al. 1997) is an asexual genus in the *Mycosphaerellaceae*, which is distinct from *Teratosphaeria* (= *Kirramyces*) and *Readeriella* (Crous et al. 2009a, b). *Phaeophleospora parsoniae* was isolated from oozing white conidial cirrhi associated with leaf spots on *Parsonia straminea.* We assume that it represents a microconidial state of a *Phaeophleospora* sp. In culture and on host material, however, no macroconidia were formed, and it is allocated to *Phaeophleospora* based on phylogenetic inference.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Septoria albopunctata* (GenBank JQ732933; Identities = 395/421 (94 %), Gaps = 6/421 (1 %)), *Mycosphaerella stromatosa* (GenBank EU167598; Identities = 446/479 (93 %), Gaps = 11/479 (2 %)) and *Mycosphaerella pseudoellipsoidea* (GenBank EU167585; Identities = 443/478 (93 %), Gaps = 8/478 (1 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Phaeophleospora eugeniae* (GenBank FJ493206; Identities = 818/821 (99 %), no gaps), *Phaeophleospora eugeniicola* (GenBank FJ493209; Identities = 814/821 (99 %), no gaps) and *Septoria albopunctata* (GenBank JQ732982; Identities = 813/820 (99 %), no gaps).

Colour illustrations. Brunswick Heads Nature Reserve, New South Wales, Australia; leaf spot, ascomata, conidiophores and conidia in culture. Scale bars = 10 µm.

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Schizoparme pseudogranati

Fungal Planet 235 – 10 June 2014

Schizoparme pseudogranati Crous, *sp. nov.*

Etymology. Named after its morphological similarity to *Pilidiella granati*.

Conidiomata pycnidial, erumpent, globose, up to 200 µm diam, unilocular with central ostiole; wall dark brown of *textura angularis*, becoming hyaline towards inner layers, with central cushion, convex, pulvinate, hyaline *textura angularis*, giving rise to conidiogenous cells. *Conidiophores* septate, branched, hyaline, smooth, 15–20 × 4–6 µm. *Conidiogenous cells* subcylindrical to obclavate, hyaline, smooth, 8–12 × 3–4 µm, with long, visible apical collarettes, invested in mucus; apex with visible periclinal thickening, rarely with percurrent proliferation. *Conidia* hyaline, smooth, guttulate, fusoid to naviculate, apex subobtuse, base truncate, thin-walled with mucoid appendage along the side of conidium, straight to curved, frequently inequalateral, (19–)21–24(–25) × (3–)4 µm.

Culture characteristics — Colonies covering the dish within 2 wk at 22 °C, with clear growth zones in concentric circles and sparse aerial mycelium. On PDA, OA and MEA surface buff, reverse buff to honey.

Typus. Zambia, OM4168, on *Terminalia stuhlmannii* (*Combretaceae*), 28 Feb. 2013, *M. van der Bank* (holotype CBS H-21692, culture ex-type CPC 22545 = CBS 137980; ITS sequence GenBank KJ869132, LSU sequence GenBank KJ869189, TUB sequence GenBank KJ869244, MycoBank MB808908).

Notes — The genus *Pilidiella* (1927) is linked to *Schizoparme* (1923) (*Schizoparmaceae*; Rossman et al. 2007) sexual morphs, suggesting that the better known *Schizoparme* would have preference for the holomorph, as Nag Raj (1993) regarded *Pilidiella* as synonym of *Coniella*, until van Niekerk et al. (2004) showed them to be two distinct genera. *Schizoparme pseudogranati* is a species intermediate between *Pilidiella granati* (conidia 9–16 × 3–4.5 µm) and *Schizoparme straminea* (= *P. castaneicola*; conidia 13–29 × 2.5–4 µm; Nag Raj 1993).

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Pilidiella granati* (GenBank JN815312; Identities = 611/617 (99 %), Gaps = 2/617 (0 %)), *Pilidiella diplodiella* (GenBank KC771899; Identities = 583/590 (99 %), Gaps = 2/590 (0 %)) and *Pilidiella diplodiopsis* (GenBank AY339334; Identities = 577/584 (99 %), Gaps = 2/584 (0 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Coniella musaiaensis* (GenBank AF408337; Identities = 855/857 (99 %), no gaps), *Schizoparme straminea* (GenBank AF362569; Identities = 852/857 (99 %), no gaps) and *Pilidiella tibouchinae* (GenBank JQ281777; Identities = 840/845 (99 %), no gaps).

TUB. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the TUB sequence are *Colletotrichum yunnanense* (GenBank JX519248; Identities = 205/248 (83 %), Gaps = 21/248 (8 %)), *Geosmithia langdonii* (GenBank HG799887; Identities = 201/245 (82 %), Gaps = 7/245 (2 %)) and *Colletotrichum crassipes* (GenBank FN599817; Identities = 271/361 (75 %), Gaps = 27/361 (7 %)).

Colour illustrations. Terminalia stuhlmannii in Zambia (photo: Olivier Maurin); conidiomata, conidiophores and conidia in culture. Scale bars = 10 µm.

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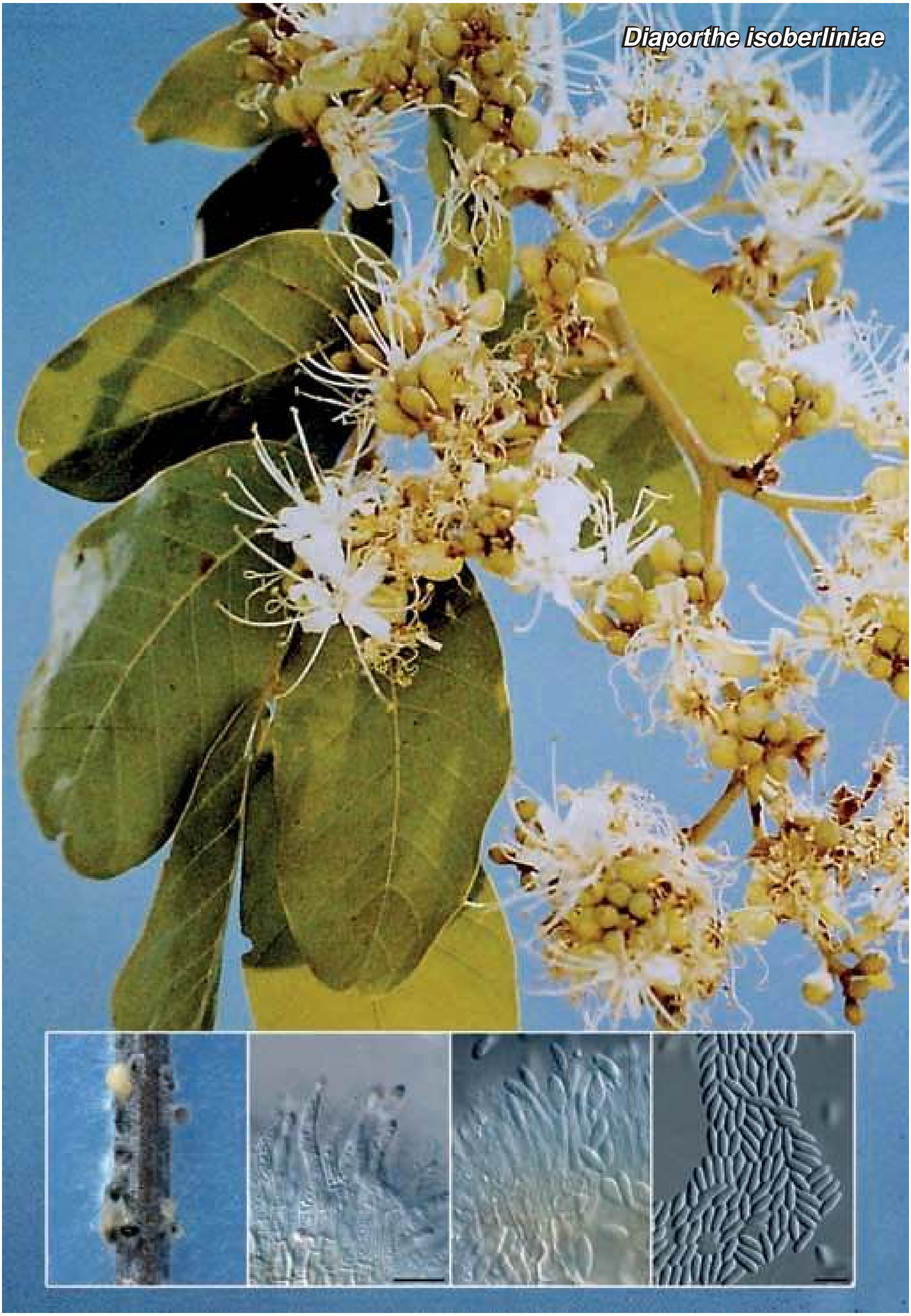
Diaporthe isoberliniae

Fungal Planet 236 – 10 June 2014

Diaporthe isoberliniae Crous, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Isoberlinia.*

On PNA. *Conidiomata* pycnidial, globose, up to 300 µm diam, black, erumpent, exuding creamy conidial droplets from central ostioles; walls of 3–6 layers of medium brown *textura angularis*. *Conidiophores* hyaline, smooth, 2–3-septate, branched, densely aggregated, cylindrical, straight to sinuous, 15–40 × 3–4 µm. *Conidiogenous cells* 10–14 × 2.5–3 µm, phialidic, cylindrical, terminal and lateral, with slight taper towards apex, 1 µm diam, with visible periclinal thickening; collarette flared, up to 4 µm long. *Paraphyses* not observed. *Alpha conidia* aseptate, hyaline, smooth, guttulate, fusoid-ellipsoid, tapering towards both ends, straight, apex subobtuse, base subtruncate, (6.5–)8–9(–10) × (2.5–)3(–3.5) µm. *Gamma conidia* not observed. *Beta conidia* not observed.

Culture characteristics — Colonies covering the dish within 2 wk at 22 °C, spreading, with moderate aerial mycelium. On PDA surface smoke-grey, with patches of dirty white, reverse olivaceous-grey. On OA surface dirty white. On MEA surface dirty white, reverse olivaceous-grey.

Typus. ZAMBIA, B&B13467, on *Isoberlinia angolensis* (*Fabaceae*), 23 Feb. 2013, *M. van der Bank* (holotype CBS H-21693, culture ex-type CPC 22549 = CBS 137981; ITS sequence GenBank KJ869133, LSU sequence GenBank KJ869190, TUB sequence GenBank KJ869245, MycoBank MB808909).

Notes — Presently there are no known species of *Diaporthe* (incl. *Phomopsis*) that have been described from *Isoberlinia.* Furthermore, *D. isoberliniae* also appears to be phylogenetically distinct from the species presently accommodated in GenBank, being most similar to sequences of *D. foeniculacea*, *P. theicola* and *D. neotheicola*.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Diaporthe foeniculacea* (GenBank KC343103; Identities = 541/558 (97 %), Gaps = 6/558 (1 %)), *Phomopsis theicola* (GenBank HE774477; Identities = 534/551 (97 %), Gaps = 6/551 (1 %)) and *Diaporthe neotheicola* (GenBank KC145914; Identities = 561/579 (97 %), Gaps = 6/579 (1 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Phomopsis columnaris* (GenBank AF439627; Identities = 826/836 (99 %), no gaps), *Diaporthe eres* (GenBank AF362565; Identities = 826/836 (99 %), no gaps) and *Phomopsis vaccinii* (GenBank AF439630; Identities = 825/836 (99 %), no gaps).

TUB. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the TUB sequence are *Diaporthe maytenicola* (GenBank KF777250; Identities = 693/739 (94 %), Gaps = 9/739 (1 %)), *Diaporthe hickoriae* (GenBank KC344086; Identities = 649/693 (94 %), Gaps = 1/693 (0 %)) and *Diaporthe stictica* (GenBank KC344180; Identities = 650/695 (94 %), Gaps = 6/695 (0 %)).

Colour illustrations. *Isoberlinia angolensis* in Zambia (photo: Mike Bingham); conidiomata, conidiophores and conidia in culture. Scale bars = 10 µm.

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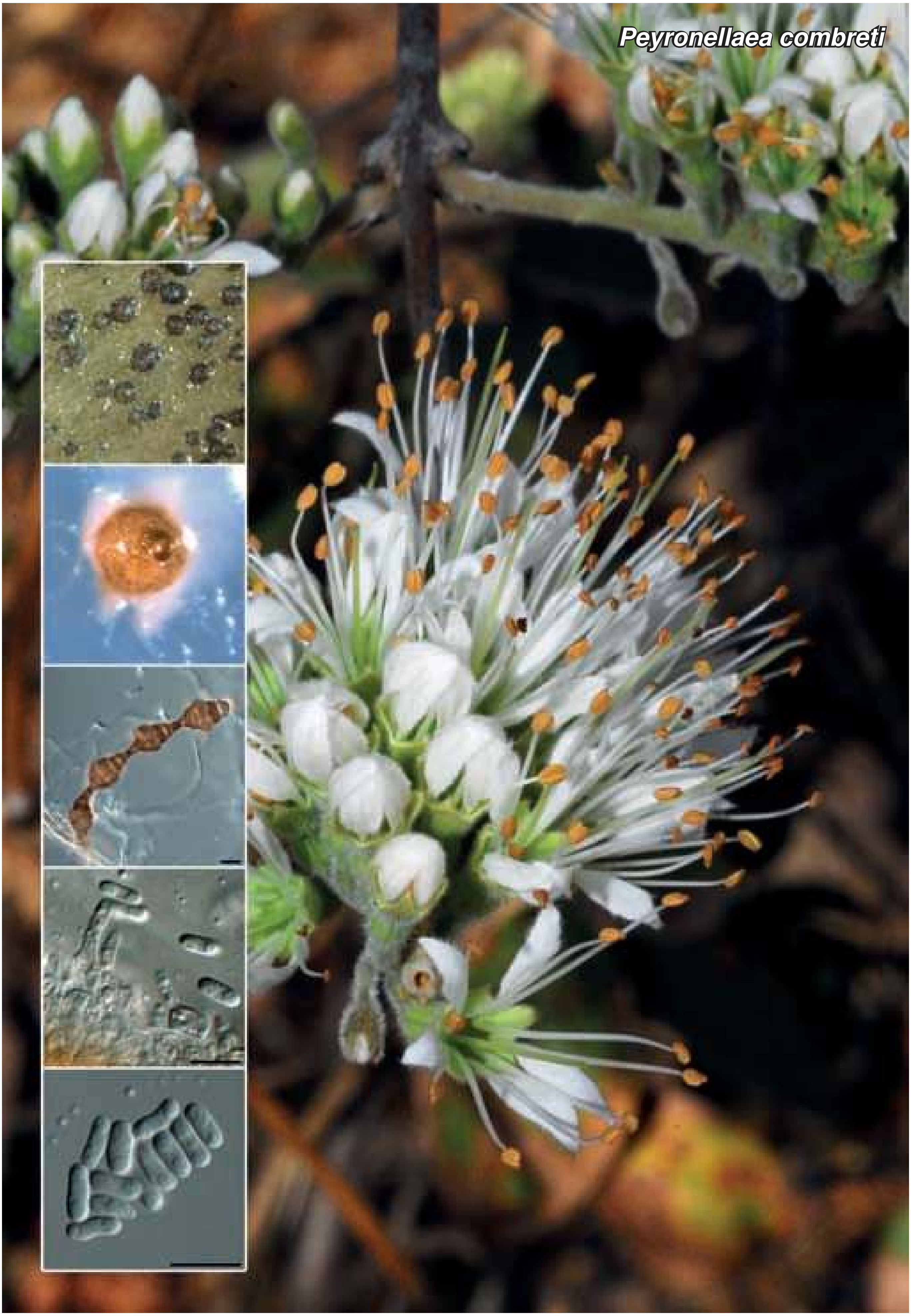
Peyronellaea combreti

Fungal Planet 237 – 10 June 2014

Peyronellaea combreti Crous, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Combretum*.

Conidiomata erumpent to superficial, medium brown, globose, up to 250 µm diam, becoming papillate with central ostiole, up to 25 µm diam; wall of 3–4 layers of pale brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, doliiform to ampulliform, 5–7 × 4–5 µm, with visible periclinal thickening and collarette. *Conidia* solitary, hyaline, smooth, guttulate, ellipsoid to subcylindrical with obtuse ends, straight to gently curved, (5–)8–10(–12) × 3.5(–4) µm. *Chlamydospores* arranged in alternarioid chains, muriformly septate, brown, smooth, up to 15 µm diam.

Culture characteristics — Colonies covering the dish within 2 wk at 22 °C, with sparse aerial mycelium and even, smooth margins. On PDA surface iron-grey with patches of dirty white, reverse iron-grey. On OA surface iron-grey. On MEA surface and reverse iron-grey.

Typus. Zambia, S16°55.766' E27°75.914', on *Combretum mossambicensis* (*Combretaceae*), 28 Feb. 2013, *M. van der Bank* (holotype CBS H-21694, culture ex-type CPC 22587 = CBS 137982; ITS sequence GenBank KJ869134, LSU sequence GenBank KJ869191, ACT sequence GenBank KJ869228, TUB sequence GenBank KJ869246, MycoBank MB808910).

Notes — Within *Phoma* section *Peyronellaea* species were formerly characterised by having dictyochlamydospores and in some cases epicoccum-like synasexual morphs (Boerema et al. 2004). In a subsequent phylogenetic study, Aveskamp et al. (2009) showed that chlamydospore formation evolved several times within the *Phoma* complex. Aveskamp et al. (2010) established *Peyronellaea* as a separate genus characterised by having multicellular chlamydospores. Within *Peyronellaea*, *P. combreti* appears distinct from the taxa currently known based on their DNA sequence data, and represents a novel taxon on *Combretum*.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Scytalidium acidophilum* (GenBank HQ213804; Identities = 525/529 (99 %), Gaps = 1/529 (0 %)), *Didymella fabae* (GenBank GQ305306; Identities = 531/536 (99 %), Gaps = 1/536 (0 %)) and *Peyronellaea pinodella* (GenBank EU167565; Identities = 531/536 (99 %), Gaps = 1/536 (0 %)). A similar search in the Q-bank fungal nucleotide database (www.q-bank.eu) revealed highest similarity with *Peyronellaea curtisii* (GenBank FJ427041; Identities = 483/486 (99 %), Gaps = 1/486 (0 %)), *Peyronellaea musae* (GenBank FJ427027; Identities = 483/486 (99 %), Gaps = 1/486 (0 %)) and *Peyronellaea curtisii* (GenBank FJ427039; Identities = 482/486 (99 %), Gaps = 1/486 (0 %)).

Colour illustrations. Combretum mossambiciensis in Zambia (photo: Olivier Maurin); conidiomata, chlamydospores, conidiogenous cells and conidia in culture. Scale bars = 10 µm.

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Peyronellaea prosopidis* (GenBank KF777232; Identities = 910/910 (100 %), no gaps), *Phoma pedeiae* (GenBank GU238126; Identities = 881/881 (100 %), no gaps) and *Phoma dimorpha* (GenBank GU238068; Identities = 881/881 (100 %), no gaps).

ACT. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ACT sequence are *Phaeosphaeria nodorum* (GenBank XM_001791742; Identities = 386/409 (94 %), no gaps), *Alternaria smyrnii* (GenBank JQ671675; Identities = 386/411 (94 %), no gaps) and *Chalastospora cetera* (GenBank JQ671626; Identities = 395/423 (93 %), Gaps = 1/423 (0 %)).

TUB. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the TUB sequence are *Phoma narcissi* (GenBank FJ427149; Identities = 334/343 (97 %), no gaps), *Phoma sancta* (GenBank FJ427171; Identities = 332/343 (97 %), no gaps) and *Phoma jolyana* (GenBank FJ427136; Identities = 332/343 (97 %), no gaps).

In a recent treatment of the genus *Peyronellaea* (Aveskamp et al. 2010) two combinations were incorrectly introduced, which are corrected herewith:

Peyronellaea heteroderae (Sen Y. Chen, D.W. Dicks. & Kimbr.) Crous, *comb. nov.* — MycoBank MB808912

Basionym. *Phoma heteroderae* Sen Y. Chen, D.W. Dicks. & Kimbr., Mycologia 88: 885. 1996 (1997).

= *Phoma pomorum* var. *calorpreferens* Boerema, Gruyter & Noordel. apud Boerema, Persoonia 15: 207. 1993.

≡ *Phoma calorpreferens* (Boerema, Gruyter & Noordel.) Aveskamp, Gruyter & Verkley, Mycologia 101: 370. 2009.

≡ *Peyronellaea calorpreferens* (Boerema, Gruyter & Noordel.) Aveskamp, Gruyter & Verkley, Stud. Mycol. 65: 31. 2010.

Notes — *Peyronellaea calorpreferens* is a nom. illeg., since *Phoma heteroderae*, which was cited as synonym, has priority at the species rank.

Peyronellaea maydis (Arny & R.R. Nelson) Crous, *comb. nov.* — MycoBank MB808913

Basionym. *Phyllosticta maydis* Arny & R.R. Nelson, Phytopathology 61: 1171. 1971.

≡ *Phoma zeae-maydis* Punith., Mycopathologia 112, 1: 50. 1990 (nom. nov. for *Phyllosticta maydis* in *Phoma*).

= *Mycosphaerella zeae-maydis* Mukunya & Boothr., Phytopathology 63: 530. 1973.

≡ *Didymella zeae-maydis* (Mukunya & Boothr.) Arx, Beih. Nova Hedwigia 87: 288. 1987.

≡ *Peyronellaea zeae-maydis* (Mukunya & Boothr.) Aveskamp, Gruyter & Verkley, Stud. Mycol. 65: 33. 2010.

Notes — *Phyllosticta maydis* represents the name with the oldest epithet for this species.

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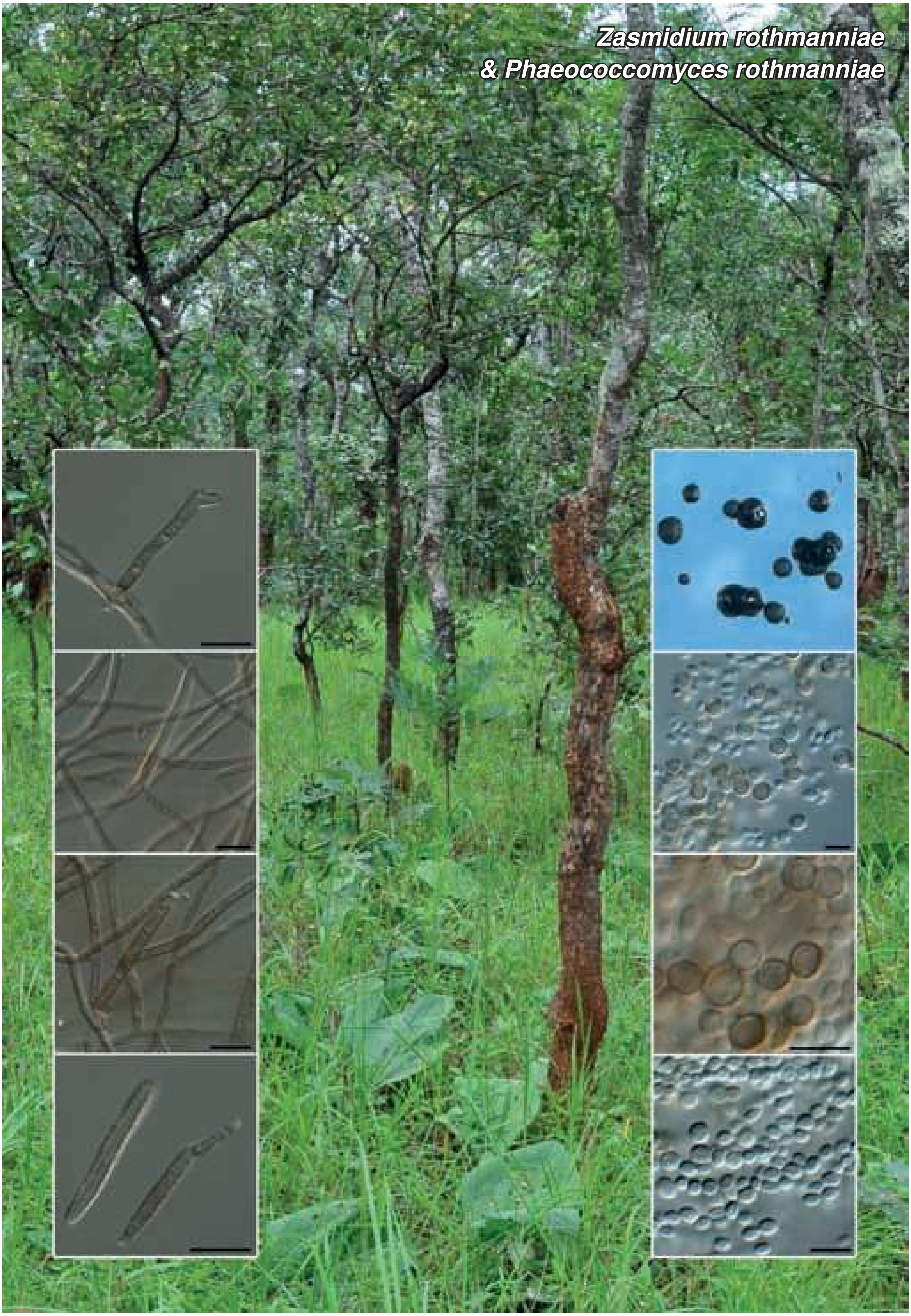
Zasmidium rothmanniae
& Phaeococcomyces rothmanniae

Fungal Planet 238 & 239 – 10 June 2014

Zasmidium rothmanniae Crous, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Rothmannia.*

Leaf spots brown, circular, amphigenous, up to 7 mm diam. On SNA. *Mycelium* consisting of septate, branched, brown, verruculose to warty, 3–4 µm diam hyphae. *Conidiophores* solitary on superficial mycelium, erect, medium brown, finely verruculose to smooth, subcylindrical, straight to once geniculate, 1–3-septate, 17–70 × 3–4 µm. *Conidiogenous cells* integrated, terminal, subcylindrical, medium brown, finely verruculose to smooth, proliferating sympodially, 10–20 × 3–3.5 µm; loci darkened, thickened and refractive, 2 µm diam. *Conidia* in branched chains, medium brown, verruculose, narrowly obclavate (subcylindrical in small conidia), apex subobtuse, base truncate, straight to curved, 1–6-septate, (25–)40–100(–150) × 2.5–3(–4) µm; loci thickened, darkened and refractive, 2 µm diam.

Culture characteristics — Colonies reaching 20 mm diam after 2 wk at 22 °C, erumpent, folded, with sparse to moderate aerial mycelium and even margin. On PDA surface olivaceous-grey, reverse iron-grey; on OA olivaceous-grey. On MEA surface and reverse iron-grey.

Typus. Zambia, OM4106, on *Rothmannia engleriana* (*Rubiaceae*), 21 Feb. 2013, *M. van der Bank* (holotype CBS H-21695, culture ex-type CPC 22656 = CBS 137983; ITS sequence GenBank KJ869135, LSU sequence GenBank KJ869192, MycoBank MB808914).

Notes — The genus *Zasmidium* is characterised by having pigmented, verruculose mycelium and conidiophores, and chains of verruculose conidia with darkened, thickened and refractive scars (Crous et al. 2007a, Braun et al. 2013). This morphology has, however, evolved several times within the *Mycosphaerellaceae*, rendering *Zasmidium* paraphyletic (Crous et al. 2009a). As far as we could establish, no cercosporoid fungi have thus far been described from *Rothmannia* and hence *Z. rothmanniae* is introduced as a new taxon.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Ramichloridium strelitziae* (GenBank EU041803; Identities = 518/557 (93 %), Gaps = 10/557 (1 %)), *Mycosphaerella pseudovespa* (GenBank DQ530216; Identities = 478/514 (93 %), Gaps = 11/514 (2 %)) and *Stenella queenslandica* (GenBank EU514295; Identities = 484/521 (93 %), Gaps = 14/521 (2 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Zasmidium anthuriicola* (GenBank KF251785; Identities = 594/604 (98 %), no gaps), *Zasmidium suregadae* (GenBank KC677939; Identities = 594/604 (98 %), no gaps) and *Zasmidium anthuriicola* (GenBank FJ839662; Identities = 594/604 (98 %), no gaps).

Phaeococcomyces rothmanniae Crous, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Rothmannia.*

Colonies lacking mycelium but consisting of a globular mass of chlamydospore-like cells; cells aseptate, brown (hyaline when young), 4–6 µm diam, covered in mucus, globose, thin-walled, verruculose, remaining attached to one another, giving rise to younger conidia via budding, ellipsoid to globose, hyaline, thin-walled, covered in mucus, smooth, 3–5 × 2–3 µm.

Culture characteristics — Colonies reaching 10 mm diam after 2 wk at 22 °C, surface folded, spreading, lacking aerial mycelium, with even, smooth margins. On PDA, OA and MEA black.

Typus. Zambia, OM4106, on *Rothmannia engleriana* (*Rubiaceae*), 21 Feb. 2013, *M. van der Bank* (holotype CBS H-21696, culture ex-type CPC 22668 = CBS 137984; ITS sequence GenBank KJ869136, LSU sequence GenBank KJ869193, MycoBank MB808915).

Notes — The genus *Phaeococcomyces* represents a genus of black yeasts with slimy, folded, slow-growing colonies that lack aerial mycelium. The genus *Phaeococcomyces* presently contains eight species (Crous et al. 2013b, Moreno-Rico et al. 2014). Compared to the presently known species, *P. rothmanniae* is phylogenetically closely allied to *P. nigricans* (conidia globose to broadly ellipsoidal, 4–6.5 × 4–5 µm; de Hoog 1979), though it has somewhat smaller conidia.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Phaeococcomyces nigricans* (GenBank AF050278; Identities = 508/541 (94 %), Gaps = 4/541 (0 %)) and *Phaeococcomyces* aff. *nigricans* (GenBank JX188194; Identities = 362/397 (91 %), Gaps = 13/397 (3 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Phaeococcomyces nigricans* (GenBank AF050278; Identities = 807/815 (99 %), no gaps), *Phaeococcomyces eucalypti* (GenBank KC005791; Identities = 791/816 (97 %), Gaps = 2/816 (0 %)) and *Phaeococcomyces mexicanus* (GenBank KJ152786; Identities = 791/816 (97 %), Gaps = 4/816 (0 %)).

Colour illustrations. *Rothmannia engleriana* in Zambia (photo: John Burrows); conidiophores and conidia of *Zasmidium rothmanniae* (left column) in culture; colonies and conidia of *Phaeococcomyces rothmanniae* (right column) in culture. Scale bars = 10 µm.

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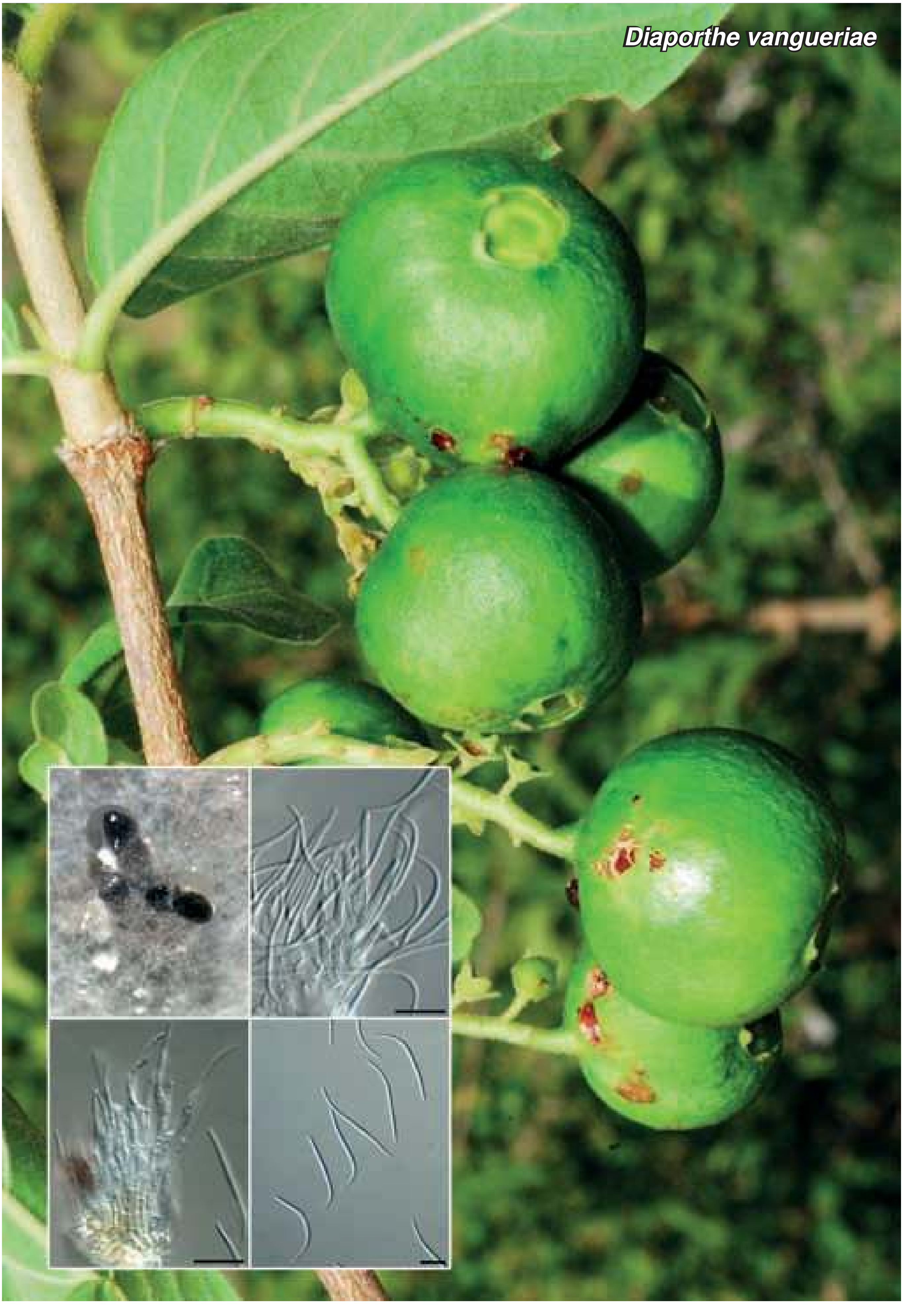
Diaporthe vangueriae

Fungal Planet 240 – 10 June 2014

Diaporthe vangueriae Crous, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Vangueria*.

On OA, sporulating poorly. *Conidiomata* pycnidial, globose, up to 350 µm diam, black, erumpent, exuding creamy conidial droplets from central ostioles; walls of 3–6 layers of medium brown *textura angularis*. *Conidiophores* hyaline, smooth, 2–3-septate, branched, densely aggregated, cylindrical, straight to sinuous, 20–30 × 2.5–4 µm. *Conidiogenous cells* 15–20 × 2–3 µm, phialidic, cylindrical, terminal and lateral, with slight taper towards apex, 1–1.5 µm diam, with visible periclinal thickening; collarette not flared, up to 2 µm long. *Paraphyses* subcylindrical, septate, dispersed among conidiophores, up to 50 µm long, 2–3 µm diam. *Alpha conidia* not observed. *Gamma conidia* not observed. *Beta conidia* spindle-shaped, aseptate, smooth, hyaline, apex acutely rounded, base truncate, tapering from the lower third towards the apex, (20–)28–35(–40) × 1.5(–2) µm.

Culture characteristics — Colonies covering the dish in 2 wk at 22 °C, with moderate aerial mycelium. On PDA surface honey, reverse honey with border of isabelline. On OA surface buff, with olivaceous-grey conidiomata. On MEA surface buff, reverse brick, with patches of isabelline.

Typus. Zambia, S16°27.627' E27°31.775', on twigs of *Vangueria infausta* (*Rubiaceae*), 20 Feb. 2012, *M. van der Bank* (holotype CBS H-21697, culture ex-type CPC 22703 = CBS 137985; ITS sequence GenBank KJ869137, LSU sequence GenBank KJ869194, TUB sequence GenBank KJ869247, MycoBank MB808916).

Notes — As far as we could establish, no species of *Diaporthe* (incl. *Phomopsis*) are presently known from *Vangueria*. Furthermore, *D. vangueriae* appears to be phylogenetically distinct from the taxa presently accommodated in GenBank, and is therefore introduced as a novel species, being closely related to *D. inconspicua*, *D. anacardii and D. neotheicola*.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Diaporthe inconspicua* (GenBank KC343125; Identities = 558/569 (98 %), Gaps = 3/569 (0 %)), *Diaporthe anacardii* (GenBank KC343024; Identities = 557/569 (98 %), Gaps = 3/569 (0 %)) and *Diaporthe neotheicola* (GenBank KC145897; Identities = 571/585 (98 %), Gaps = 4/585 (0 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Diaporthe maytenicola* (GenBank KF777210; Identities = 821/822 (99 %), no gaps), *Diaporthe canthii* (GenBank JX069848; Identities = 821/822 (99 %), no gaps) and *Diaporthe diospyricola* (GenBank KF777209; Identities = 820/822 (99 %), no gaps).

TUB. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the TUB sequence are *Diaporthe maytenicola* (GenBank KF777250; Identities = 716/731 (98 %), no gaps), *Diaporthe oncostoma* (GenBank KC344129; Identities = 659/691 (95 %), Gaps = 7/691 (1 %)) and *Diaporthe foeniculacea* (GenBank KC344070; Identities = 655/688 (95 %), Gaps = 3/688 (0 %)).

Colour illustrations. *Vangueria infausta* in Zambia (photo: Olivier Maurin); conidiomata, conidiophores and beta conidia in culture. Scale bars = 10 µm.

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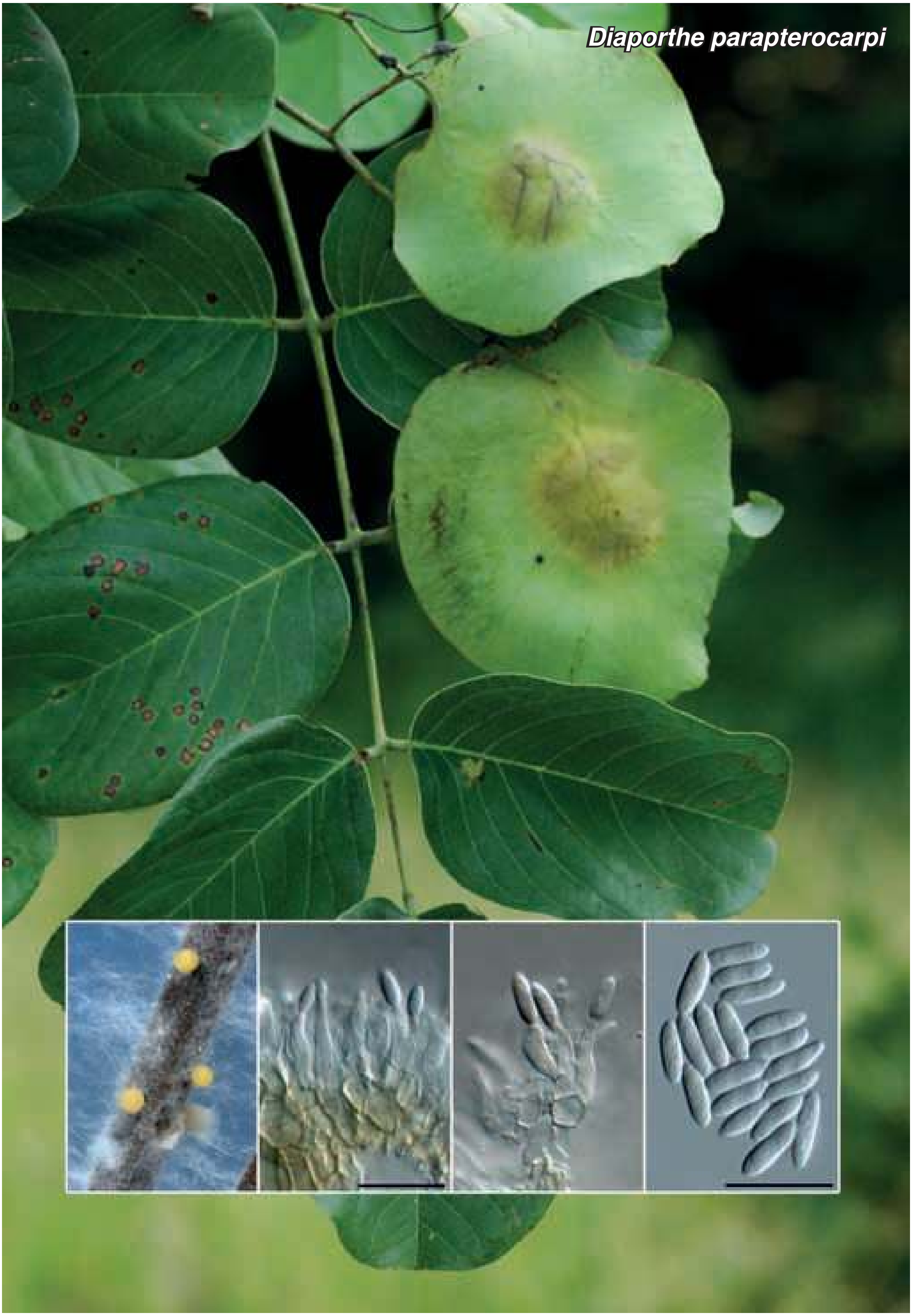
Diaporthe parapterocarpi

Fungal Planet 241 – 10 June 2014

Diaporthe parapterocarpi Crous, *sp. nov.*

Etymology. Named after its morphological similarity to *Diaporthe pterocarpi.*

On PNA. *Conidiomata* pycnidial, globose, up to 200 µm diam, black, erumpent, exuding yellow conidial droplets from central ostioles; walls of 3–6 layers of medium brown *textura angularis*. *Conidiophores* hyaline, smooth, 1–2-septate, branched, densely aggregated, cylindrical, straight to sinuous, 10–20 × 3–4 µm. *Conidiogenous cells* 9–12 × 2.5–3 µm, phialidic, cylindrical, terminal and lateral, with slight taper towards apex, 1–1.5 µm diam, with visible periclinal thickening; collarette absent, or 1 µm long, slightly flared. *Paraphyses* not observed. *Alpha conidia* aseptate, hyaline, smooth, guttulate, fusoid-ellipsoid, tapering towards both ends, straight, apex subobtuse, base subtruncate, (7.5–)8–10(–12) × 2.5(–3) µm. *Gamma conidia* not observed. *Beta conidia* not observed.

Culture characteristics — Colonies covering the dish in 2 wk at 22 °C, with moderate aerial mycelium; surface on MEA, OA and PDA dirty white with black conidiomata; reverse cinnamon with patches of isabelline.

Typus. ZAMBIA, OM4178, on *Pterocarpus brenanii* (*Fabaceae*), 1 Mar. 2013, *M. van der Bank* (holotype CBS H-21698, culture ex-type CPC 22729 = CBS 137986; ITS sequence GenBank KJ869138, LSU sequence GenBank KJ869195, TUB sequence GenBank KJ869248, MycoBank MB808917).

Notes — Two species of *Diaporthe* have been described from *Pterocarpus*, namely *D. pterocarpi* (alpha conidia 5–9 × 2–3 µm) and *D. pterocarpicola* (alpha conidia 5–8 × 2–3.5 µm) (Udayanga et al. 2012), both differing from *D. parapterocarpi* by their larger conidia. Our ITS sequence is different from those of both *D. pterocarpi* (GenBank JQ619901; Identities = 456/486 (94 %), Gaps = 7/486 (1 %)) and *D. pterocarpicola* (GenBank JQ619887; Identities = 461/492 (94 %), Gaps = 8/492 (1 %)).

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Diaporthe maytenicola* (GenBank KF777157; Identities = 557/572 (97 %), Gaps = 1/572 (0 %)), *Diaporthe neotheicola* (GenBank KC145902; Identities = 585/601 (97 %), Gaps = 4/601 (0 %)) and *Diaporthe rhusicola* (GenBank JF951146; Identities = 560/576 (97 %), Gaps = 4/576 (0 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Diaporthe maytenicola* (GenBank KF777210; Identities = 819/820 (99 %), no gaps), *Diaporthe canthii* (GenBank JX069848; Identities = 819/820 (99 %), no gaps) and *Diaporthe diospyricola* (GenBank KF777209; Identities = 818/820 (99 %), no gaps).

TUB. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the TUB sequence are *Diaporthe maytenicola* (GenBank KF777250; Identities = 712/732 (97 %), Gaps = 1/732 (0 %)), *Diaporthe foeniculacea* (GenBank KC344070; Identities = 650/688 (94 %), Gaps = 3/688 (0 %)) and *Diaporthe chamaeropis* (GenBank KC344017; Identities = 650/688 (94 %), Gaps = 3/688 (0 %)).

Colour illustrations. Pterocarpus brenanii in Zambia (photo: John Burrows); conidiomata, conidiophores and conidia in culture. Scale bars = 10 µm.

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Dendryphiella eucalyptorum

Fungal Planet 242 – 10 June 2014

Dendryphiella eucalyptorum Crous & E. Rubio, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Eucalyptus*.

Mycelium consisting of smooth, hyaline, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* erect, arising from hyphae, dark brown, subcylindrical, verruculose, branched above and below, up to 500 µm long, 3–5 µm diam, 7–12-septate. *Conidiogenous cells* integrated, terminal and intercalary, clavate, with 1–4 loci arranged at the apex, 20–40 × 6–10 µm; loci thickened, darkened and refractive, 1–2 µm diam. *Conidia* subcylindrical, apex obtuse, base bluntly rounded, medium brown, verruculose, (1–)3(–5)-septate, occurring in short chains, (19–)20–23(–25) × 5(–7) µm; hila thickened, darkened and refractive, 1 µm diam.

Culture characteristics — Colonies reaching 40 mm diam after 2 wk at 22 °C, spreading, with sparse aerial mycelium and even, smooth margins. On PDA surface hazel with patches of luteous, reverse olivaceous-grey with patches of luteous; on OA surface luteous with patches of isabelline; on MEA surface buff, reverse buff with patches of isabelline.

Typus. Spain, La Granda (Asturias), on small branches of *Eucalyptus globulus* (*Myrtaceae*), 10 May 2013, *E. Rubio* (holotype CBS H-21699, culture ex-type CPC 22927 = CBS 137987; ITS sequence GenBank KJ869139, LSU sequence GenBank KJ869196, MycoBank MB808918).

Notes — The genus *Dendryphiella* occurs commonly on herbaceous stems, and presently has around 10 species, characterised by branched to unbranched conidiophores, with polytretic conidiogenous cells, darkened, thickened scars, and brown, septate, catenulate conidia. Conidia of *D. eucalyptorum* are smaller than that of the type species, *D. vinosa* (13–39 × 4–8 µm; Ellis 1971, described from Congo bean in Cuba). Phylogenetically, *D. eucalypti* also appears distinct from *D. vinosa*, which probably represents a species complex. Matsushima (1983) described *D. eucalypti* from *Eucalyptus* leaf litter in Taiwan, having shorter conidiophores (150–400 µm), but conidia of overlapping dimensions, (1–)3(–4)-septate, (15–)17.5–25(–30) × (4–)4.5–6 µm. He distinguished *D. eucalypti* from *D. vinosa*, and by default also *D. eucalyptorum*, in that *D. eucalypti* has smooth conidia.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Dendryphiella vinosa* (GenBank DQ307316; Identities = 457/468 (98 %), no gaps), *Dictyosporium toruloides* (GenBank DQ018093; Identities = 418/489 (85 %), Gaps = 34/489 (6 %)) and *Dictyosporium heptasporum* (GenBank GU361946; Identities = 346/391 (88 %), Gaps = 16/391 (4 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Dendryphiella vinosa* (GenBank EU848590; Identities = 821/821 (100 %), no gaps), *Cheiromyces inflatus* (GenBank JQ267363; Identities = 798/821 (97 %), no gaps) and *Dictyosporium stellatum* (GenBank JF951177; Identities = 794/821 (97 %), Gaps = 5/821 (0 %)).

Colour illustrations. *Eucalyptus* tree in Spain; conidiophores and conidia in culture. Scale bars = 10 µm.

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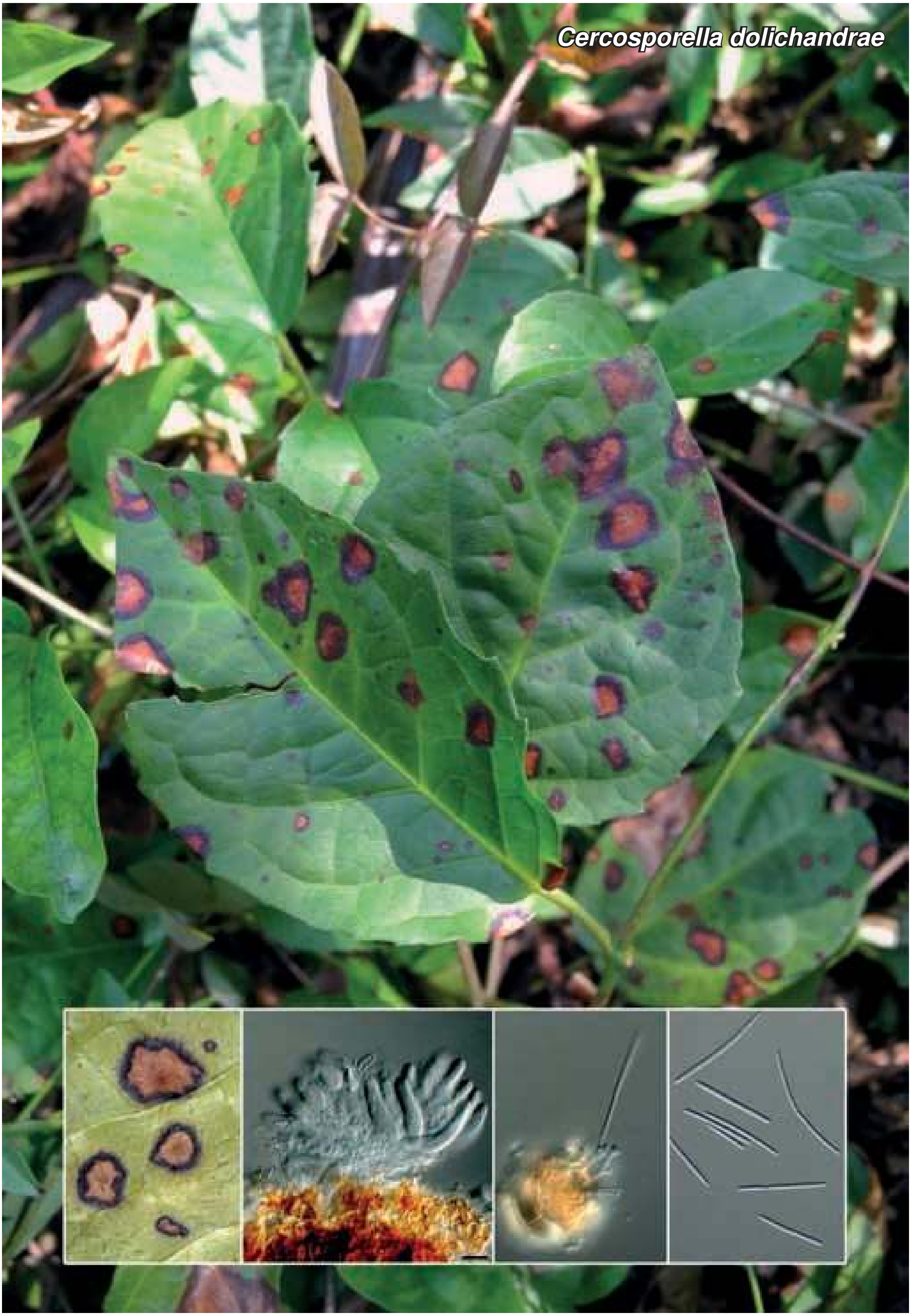
Cercosporella dolichandrae

Fungal Planet 243 – 10 June 2014

Cercosporella dolichandrae Crous & den Breeÿen, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Dolichandra.*

Leaf spots amphigenous, subcircular, ranging from small specks (1 mm diam) to larger spots (6 mm diam), medium brown, with a raised dark brown border, and diffuse dark brown margin. *Stromata* up to 40 µm diam, immersed, becoming erumpent, substromatal, consisting of brown, pseudoparenchymatal cells that develop into ascomata, up to 70 µm diam, with central ostiole, 10–15 µm diam; wall of 2–3 layers of brown *textura angularis*. *Asci* bitunicate, 8-spored, hyaline, smooth, obovoid, stipitate, with minute apical chamber, 25–30 × 7–9 µm. *Ascospores* multiseriate in asci, guttulate, medianly 1-septate, fusoid-ellipsoidal, widest in middle of apical cell, tapering towards both ends, constricted at septum, 10–12(–13) × (2.5–)3 µm. *Conidiophores* fasciculate (arising from stromata that become ascomatal initials and later fertile ascomata), hyaline, smooth, subcylindrical, rarely branched, 1–2-septate, 20–40 × 3–5 µm. *Conidiogenous cells* terminal, subcylindrical, clavate, hyaline, smooth, 10–20 × 3–4 µm, terminating in several prominent denticles, 1–2 × 1.5 µm; loci truncate, not thickened nor darkened, or very slightly darkened. *Conidia* occurring in branched chains, subcylindrical, 0–1(–3)-septate, (15–)22–45(–70) × 1.5(–2) µm.

Culture characteristics — Colonies reaching 5 mm diam after 2 wk at 22 °C, erumpent with moderate aerial mycelium and even, smooth margins. On PDA, OA and MEA surface pale olivaceous-grey with patches of smoke-grey; reverse olivaceous-grey.

Typus. South Africa, KwaZulu-Natal, Pietermaritzburg, S29°37'50.95" E30°25'51.67", on leaves of *Dolichandra unguiscati* (*Bignoniaceae*), 15 Nov. 2011, *A. King* (holotype CBS H-21700, culture ex-type CPC 22948 = CBS 138101; ITS sequence GenBank KJ869140, LSU sequence GenBank KJ869197, MycoBank MB808919).

Notes — Although *C. dolichandrae* has a typical mycosphaerella-like sexual morph, the genus *Mycosphaerella* is restricted to taxa with *Ramularia* asexual morphs, and will in future be regarded as synonym of the latter (Verkley et al. 2004, 2013, Crous et al. 2013a, Hyde et al. 2013, Kirk et al. 2013). *Cercosporella* on the other hand, is a separate genus in its own right, with appressoria attached to the mesophyll cells of the host plant, subhyaline fascicles of conidiophores giving rise to conidial chains of hyaline conidia with thickened conidial loci that are planate, while those in *Ramularia* are cladosporium-like (Kirschner 2009, Braun et al. 2013). Presently, no *Cercosporella* or *Ramularia* spp. are known from *Dolichandra unguiscati*, and hence *C. dolichandra* is introduced to accommodate this taxon. Cultures established from single ascospores and single conidia were identical based on their DNA sequence data, but only produced the asexual morph in culture.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Cercosporella virgaureae* (GenBank GU214658; Identities = 617/639 (97 %), Gaps = 4/639 (0 %)), *Mycosphaerella areola* (GenBank DQ459084; Identities = 510/537 (95 %), Gaps = 2/537 (0 %)) and *Passalora graminis* (GenBank GU214666; Identities = 605/645 (94 %), Gaps = 13/645 (2 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Cercosporella virgaureae* (GenBank GU214658; Identities = 835/843 (99 %), no gaps), *Cercosporella pfaffiae* (GenBank JQ990330; Identities = 812/826 (98 %), no gaps) and *Septoria obesa* (GenBank GU214493; Identities = 824/843 (98 %), no gaps).

Colour illustrations. Symptomatic leaves of *Dolichandra unguiscati*; leaf spots, ascoma with asci, conidiophores and conidia. Scale bar = 10 µm.

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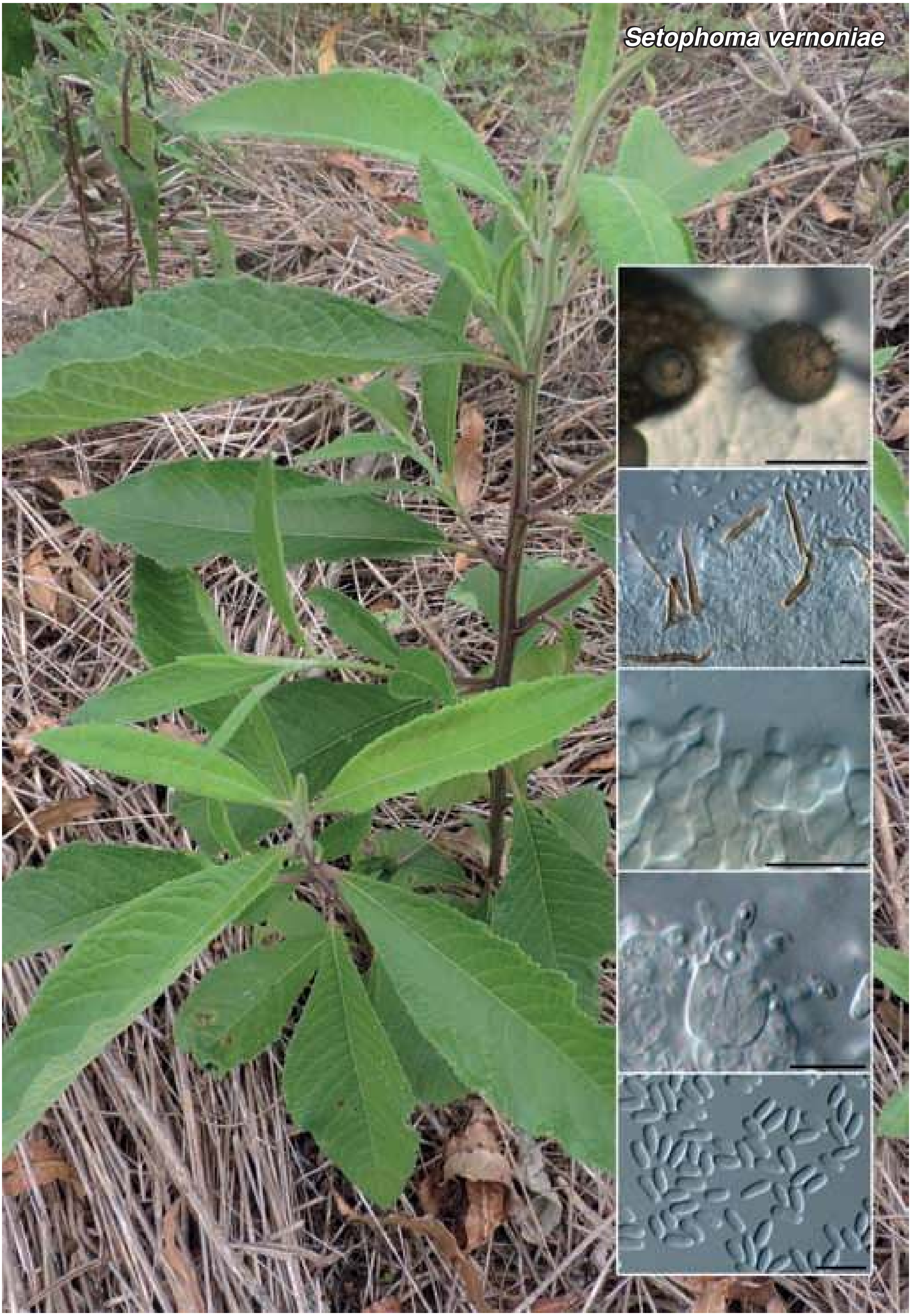
Setophoma vernoniae

Fungal Planet 244 – 10 June 2014

Setophoma vernoniae Crous & Alfenas, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Vernonia*.

Leaf spots amphigenous, angular, confined by leaf veins, 1–6 mm diam, brown to grey, at times surrounded by a broad dark purple margin. *Conidiomata* pycnidial, globose, superficial on SNA, pale brown, exuding a crystalline conidial mass, up to 300 µm diam, unilocular, with a central ostiole; conidiomatal wall of 3–4 layers of subhyaline *textura angularis*; outer wall with brown, unbranched setae, more prominent around upper part of conidioma, subcylindrical, flexuous to straight, base somewhat swollen, verruculose, apex obtusely rounded, smooth, thick-walled, 30–60 × 3–4 µm. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, smooth, ampulliform, proliferating with aggregated percurrent proliferations at apex, or at same level, with periclinal thickening visible at apex, ovoid, 4–10 × 3–4 µm. *Conidia* solitary, hyaline, smooth, aseptate, granular, subcylindrical to narrowly fusoid-ellipsoid with obtuse ends, straight, (5–)6(–8) × 2.5(–3) µm.

Culture characteristics — Colonies reaching 40 mm diam after 2 wk at 22 °C, spreading with moderate aerial mycelium and smooth, even margins. On PDA surface grey-olivaceous, outer region iron-grey, reverse iron-grey. On OA surface isabelline. On MEA surface olivaceous-grey, reverse cinnamon with patches of olivaceous-grey.

Typus. Brazil, Minas Gerais, Árvore de Natal, Viçosa, Viçosa - MG, on leaves of *Vernonia polyanthes* (*Compositae*), May 2013, *A.C. Alfenas* (holotype CBS H-21701, culture ex-type CPC 23123 = CBS 137988; ITS sequence GenBank KJ869141, LSU sequence GenBank KJ869198, MycoBank MB808920).

Notes — The genus *Setophoma* was introduced by de Gruyter et al. (2010) to accommodate phoma-like coelomycetes with setose pycnidia, phialidic conidiogenous cells, and hyaline, aseptate conidia. The present collection closely matches other species of *Setophoma* and represents a new taxon on *Vernonia polyanthes* from Brazil.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Setophoma chromolaena* (GenBank KF251244; Identities = 552/566 (98 %), Gaps = 2/566 (0 %)), *Coniothyrina agaves* (GenBank JX681075; Identities = 491/543 (90 %), Gaps = 10/543 (1 %)) and *Shiraia bambusicola* (GenBank AB105798; Identities = 497/552 (90 %), Gaps = 12/552 (2 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Setophoma chromolaena* (GenBank KF251747; Identities = 834/834 (100 %), no gaps), *Setophoma sacchari* (GenBank GQ387586; Identities = 871/876 (99 %), no gaps) and *Phaeosphaeriopsis musae* (GenBank DQ885894; Identities = 895/907 (99 %), Gaps = 1/907 (0 %)).

Colour illustrations. *Vernonia polyanthes* in Brazil; conidiomata, setae, conidiogenous cells and conidia in culture. Scale bars = 10 µm.

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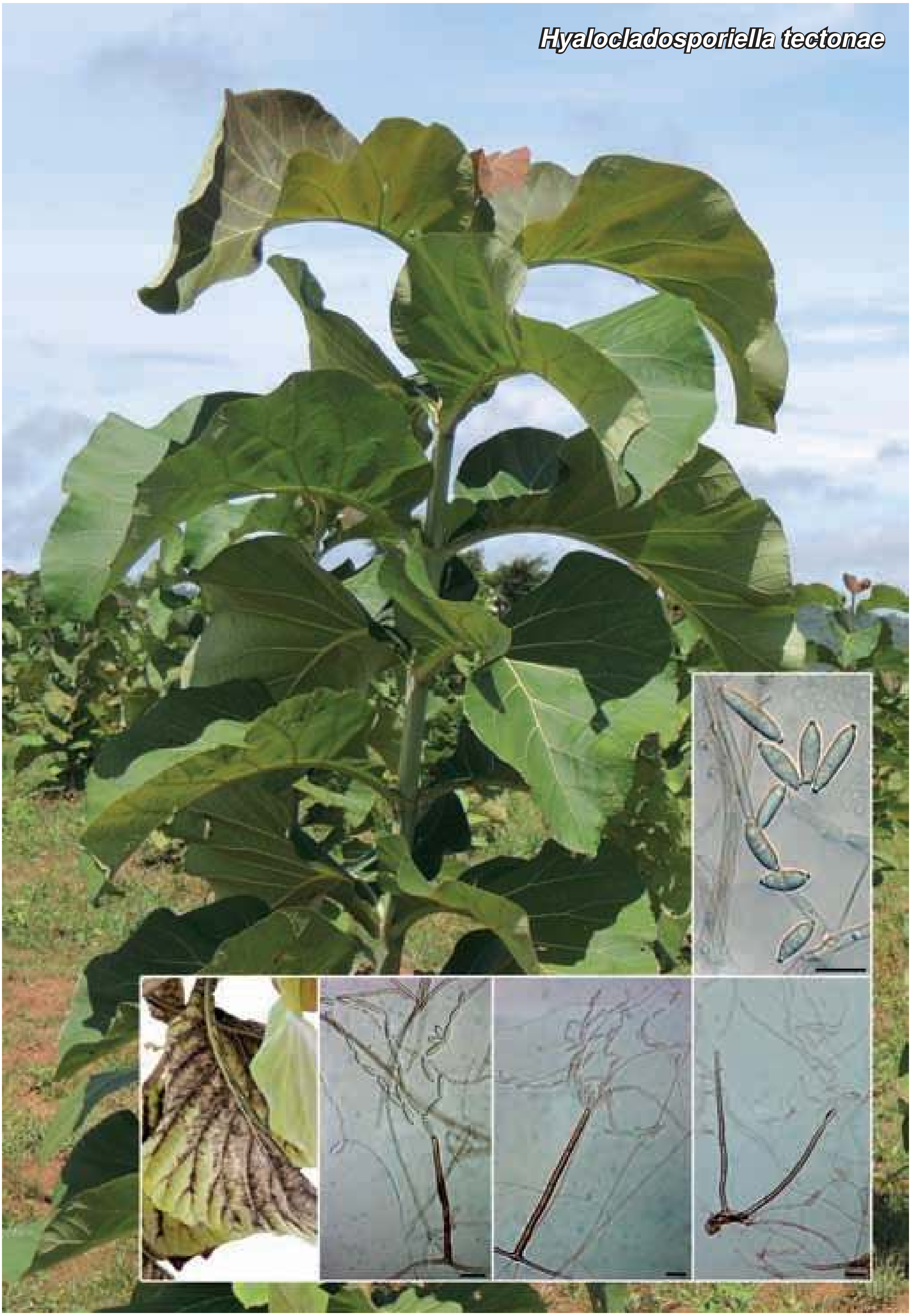

Hyalocladosporiella tectonae

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Hyalocladosporiella Crous & Alfenas, *gen. nov.*

Etymology. Named after its hyaline conidia and cladosporium-like morphology.

Mycelium consisting of hyaline, smooth, branched, septate hyphae. *Conidiophores* dimorphic. *Microconidiophores* erect, subcylindrical, straight to geniculate-sinuous, septate, brown, smooth. *Macroconidiophores* erect, brown, smooth, cylindrical, flexuous, unbranched, lacking rhizoids, septate. *Conidiogenous cells* integrated, terminal, subcylindrical, smooth, brown; loci sympodially arranged, subdenticulate, slightly thickened and darkened. *Primary ramoconidia* fusoid-ellipsoidal to subcylindrical, hyaline to pale olivaceous, smooth, guttulate, septate; hila thickened and darkened. *Secondary ramoconidia* in branched chains, fusoid-ellipsoidal, hyaline, smooth, guttulate, with 1–3 apical loci that are thickened and darkened. *Intermediary conidia* hyaline, guttulate, fusoid-ellipsoid. *Terminal conidia* hyaline, smooth, guttulate, fusoid-ellipsoid, loci thickened and darkened.

Type species. Hyalocladosporiella tectonae.
MycoBank MB808921.

Hyalocladosporiella tectonae Crous & Alfenas, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Tectona*.

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* dimorphic. *Microconidiophores* erect, subcylindrical, straight to geniculate-sinuous, 1–2-septate, brown, smooth, 20–30 × 3–3.5 µm. *Macroconidiophores* erect, brown, smooth, cylindrical, flexuous, unbranched, lacking rhizoids, 60–200 × 3 µm, 5–15-septate. *Conidiogenous cells* integrated, terminal, subcylindrical, smooth, brown, 15–30 × 3 µm; loci sympodially arranged, subdenticulate, 0.5–1 × 1–1.5 µm, slightly thickened and darkened. *Primary ramoconidia* fusoid-ellipsoidal to subcylindrical, hyaline to pale olivaceous, smooth, guttulate, 1–3-septate, 30–35 × 3–3.5 µm; hila thickened and darkened, 1 µm diam. *Secondary ramoconidia* in branched chains, fusoid-ellipsoidal, hyaline, smooth, guttulate, with 1–3 apical loci that are thickened and darkened, 1 µm diam. *Intermediary conidia* hyaline, guttulate, fusoid-ellipsoid, 10–15 × 3 µm. *Terminal conidia* hyaline, smooth, guttulate, fusoid-ellipsoid, (7–)8–9(–10) × 2.5(–3) µm, loci thickened and darkened, 0.5 µm diam.

Culture characteristics — Colonies reaching 30 mm diam after 2 wk at 22 °C, erumpent, folded, with moderate aerial mycelium and even, smooth margins. On PDA surface smoke-grey in the middle, becoming olivaceous-grey toward the margin, reverse olivaceous-grey. On OA surface olivaceous-grey. On MEA surface smoke-grey, margins olivaceous-grey, reverse iron-grey.

Typus. Brazil, Minas Gerais, Verde Novo, Colider-MT, on leaves of *Tectona grandis* (*Lamiaceae*), Apr. 2013, *A.C. Alfenas* (holotype CBS H-21702, culture ex-type CPC 23133 = CBS 137989; ITS sequence GenBank KJ869142, LSU sequence GenBank KJ869199, MycoBank MB808922).

Notes — Based on phylogenetic and morphological data, the genus *Cladosporium* (type is *C. herbarum*) was separated into several allied genera within the *Cladosporiaceae* (Arzanlou et al. 2007, Crous et al. 2007a, b, Bensch et al. 2012). *Hyalocladosporiella* represents yet another genus in this complex, that is phylogenetically allied to *Metulocladosporiella* (*Chaetothyriales*). *Metulocladosporiella* has dimorphic, solitary, pigmented conidiophores with an apical conidiogenous apparatus consisting of conidiogenous cells that give rise to ramoconidia and branched conidial chains that are fusoid-ellipsoid, pale brown, smooth, and have slightly darkened, thickened scars. *Hyalocladosporiella* is morphologically different from *Metulocladosporiella* in that it has septate ramoconidia and lacks the apical conidiophore branches observed in macroconidiophores of *Metulocladosporiella*.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Phaeococcomyces chersonesos* (GenBank AJ507323; Identities = 632/713 (89 %), Gaps = 30/713 (4 %)), *Knufia perforans* (GenBank JN040506; Identities = 595/674 (88 %), Gaps = 32/674 (4 %)) and *Knufia petricola* (GenBank KC978734; Identities = 584/666 (88 %), Gaps = 31/666 (4 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Metulocladosporiella musae* (GenBank DQ008162; Identities = 819/841 (97 %), Gaps = 6/841 (0 %)), *Metulocladosporiella musicola* (GenBank DQ008159; Identities = 814/838 (97 %), Gaps = 2/838 (0 %)) and *Coniosporium perforans* (GenBank FJ358237; Identities = 809/840 (96 %), Gaps = 2/840 (0 %)).

Colour illustrations. Tectona grandis in Brazil; diseased leaf, conidiophores and conidia in culture. Scale bars = 10 µm.

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Alfaria cyperi-esculenti

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Alfaria Crous, N.J. Montaño-Mata & García-Jim., *gen. nov.*

Etymology. Named in honour of Prof. dr Agustín Alfaro, Spanish plant pathologist and founder of the Plant Pathology Laboratory of the Universitat Politècnica de València (Spain).

Plant pathogenic, associated with leaf tip dieback and tuber rot. *Ascomata* black, hypophyllous on leaves, globose, immersed, subepidermal with central ostiole; wall of 6–10 layers of thin-walled brown *textura angularis*, upper region of perithecium somewhat darker brown than base or sides; ostiolar area containing several additional layers, thus thicker than base or sides. *Paraphyses* intermingled among asci, hyaline, smooth, subcylindrical, hyphal-like, with obtuse apices, septate, at times constricted at septa. *Asci* fasciculate, hyaline, short stipitate, subcylindrical with obtuse apices, unitunicate, with apical mechanism, not staining in Meltzer's reagent, containing 2–8 ascospores that are bi- to tri-seriate in ascus. *Ascospores* hyaline, smooth, granular, fusoid-ellipsoid, widest in middle with obtuse ends, 0–3-septate, at times with mucoid sheath or mucoid caps.

Type species. Alfaria cyperi-esculenti.
MycoBank MB808923.

Alfaria cyperi-esculenti Crous, N.J. Montaño-Mata & García-Jim., *sp. nov.*

Etymology. Named after the host from which it was isolated, *Cyperus esculentus.*

Associated with leaf tip dieback and tuber rot. *Ascomata* black, hypophyllous on leaves, globose, up to 300 µm diam, immersed, subepidermal with central ostiole, up to 20 µm diam; wall of 6–10 layers (10–20 µm diam) of thin-walled brown *textura angularis*, upper region of perithecium somewhat darker brown than base or sides; ostiolar area containing several additional layers, thus thicker than base or sides, up to 35 µm diam. *Paraphyses* intermingled among asci, hyaline, smooth, subcylindrical, hyphal-like, up to 90 µm long, 4–8 µm diam with obtuse apices, 1–4-septate, at times constricted at septa. *Asci* fasciculate, hyaline, short stipitate, subcylindrical with obtuse apices, 65–130 × 9–12 µm, unitunicate, with apical mechanism, not staining in Meltzer's reagent, containing 2–8 ascospores that are bi- to tri-seriate in ascus. *Ascospores* hyaline, smooth, granular, fusoid-ellipsoid, widest in middle with obtuse ends, 0–3-septate, at times with mucoid sheath or mucoid caps, (19–)24–28(–30) × (4–)5(–6) µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and even, lobate margins, reaching 15 mm diam after 2 wk at 25 °C. The optimum growth temperature was between 25–28 °C, with no growth at 31 °C. Colonies on PDA vary in growth rate at 25 °C from 1.5–2 mm/d. Sporulation was achieved on an artificial medium consisting of cornmeal agar supplemented with autoclaved *Cyperus esculentus* leaves. On MEA surface ochreous, reverse apricot. On OA surface saffron. On PDA surface and reverse pale luteous.

Typus. Spain, Valencia, on leaves of *Cyperus esculentus* (*Cyperaceae*), 14 June 2013, *A.M. Pérez Sierra* (holotype CBS H-21703, culture ex-type CPC 23153–23154; ITS sequence GenBank KJ869143, LSU sequence GenBank KJ869200, MycoBank MB808924).

Notes — Tiger nut (*Cyperus esculentus*) has been used as food for over 3000 yr, but also represents a major weed worldwide (Pascual et al. 1997). Its origin is in Africa and southern Europe, and its most common habitats are tropical and subtropical areas. In some countries tiger nuts are used as feed for livestock, fisheries and have been cited as a potential food for some birds. It is used in the manufacturing of emulsions for medical treatment for digestive dysfunctions. Its oil and fats are used to make soaps. With regard to human consumption the tubers can be consumed in different ways: fresh, roasted, malted or squeezed in refreshing drinks. In Spain, tiger nut is cultivated in Valencia province, eastern Spain, for the production of tiger nut milk ('horchata'). This beverage is one of the traditional drinks in this region.

Since 2002 a new fungal disease affecting this crop was detected in almost all tiger nut cultivated areas in Valencia. The symptoms appeared in plants randomly distributed in the field and consisted of leaf apical necrosis in the early stages of plant development (approximately the first 30–45 d). The symptoms could be detected as early as 15–20 d after plant emergence and the fruit bodies of the fungus could be observed on the affected leaves 7–10 d later. In parallel, a reddish orange discolouration could be observed on the tubers, which also extended to the inside of the tuber and subsequently resulted in tuber rot. The necrosis can also affect the inflorescences, where the fruiting bodies can be detected on the bracts, on the umbel peduncle and the pedicel of the spikes. However, the disease cannot be observed on leaves and stems that develop in later stages of development and therefore, the disease can be overlooked. *Alfaria cyperi-esculenti* was consistently isolated from affected plant material and its presence was confirmed in inflorescences, leaves and tubers. Since this species could not be accommodated elsewhere, the hypocrealean genus *Alfaria* is introduced to accommodate it.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Myrothecium leucotrichum* (GenBank AJ301992; Identities = 578/585 (99 %), Gaps = 2/585 (0 %)), *Myrothecium gramineum* (GenBank AY254151; Identities = 548/572 (96 %), Gaps = 9/572 (1 %)) and *Stachybotrys chartarum* (GenBank KC787692; Identities = 540/591 (91 %), Gaps = 21/591 (3 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Stachybotrys microspora* (GenBank KC305349; Identities = 784/801 (98 %), Gaps = 3/801 (0 %)), *Stachybotrys chlorohalonata* (GenBank JN938870; Identities = 780/804 (97 %), Gaps = 1/804 (0 %)) and *Stachybotrys chartarum* (GenBank JF746157; Identities = 780/804 (97 %), Gaps = 1/804 (0 %)).

Colour illustrations. Cyperus esculentus with leaf dieback symptoms; infected tuber; ascomata on leaf tissue; vertical section through ascoma, paraphyses, asci and ascospores. Scale bars: ascoma = 250 µm, all others = 10 µm.

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Pseudoacremonium sacchari

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Pseudoacremonium Crous, *gen. nov.*

Etymology. Name derived from pseudo- (false-, in Greek) and the genus name *Acremonium*.

Mycelium consisting of hyaline, septate, branched hyphae, developing brown zones with solitary brown, globose chlamydospores. *Conidiophores* erect, subcylindrical, rarely branched, 1–3-septate, smooth, but with age brown, verruculose and warty. *Conidiogenous cells* terminal, integrated (Type III phialides sensu Mostert et al. 2006), either elongate-ampulliform or navicular, tapering towards apex, with prominent periclinal thickening and inconspicuous collarette, hyaline, smooth, becoming brown and verruculose to warty. *Conidia* in unbranched chains, ellipsoid, aseptate, smooth, hyaline, thin-walled, becoming brown, verruculose, guttulate, with scar at each end, somewhat darkened and refractive; older conidia brown and verruculose, appearing flaky when mounted in lactic acid or water.

Type species. Pseudoacremonium sacchari.
MycoBank MB808925.

Pseudoacremonium sacchari Crous, *sp. nov.*

Etymology. Named after the host genus from which it was isolated, *Saccharum*.

Mycelium consisting of hyaline, septate, branched, 2–3 µm diam hyphae, developing brown zones with solitary brown, globose, 5–7 µm diam chlamydospores. *Conidiophores* erect, subcylindrical, rarely branched, 1–3-septate, up to 80 µm tall, 3–3.5 µm diam, hyaline, smooth, but with age brown, verruculose and warty. *Conidiogenous cells* terminal, integrated (Type III phialides sensu Mostert et al. 2006), either elongate-ampulliform or navicular, tapering towards apex, 25–30 × 2.5–4 µm, apex 1–1.5 µm diam, with prominent periclinal thickening and inconspicuous collarette, hyaline, smooth, becoming brown and verruculose to warty. *Conidia* in unbranched chains, ellipsoid, aseptate, smooth, hyaline, thin-walled, becoming brown, verruculose, guttulate, with scar at each end, 0.5–1 µm diam, somewhat darkened, and refractive, (6–)7–8(–9) × 2.5(–3) µm; older conidia brown and verruculose, appearing flaky when mounted in lactic acid or water.

Culture characteristics — Colonies reaching 7 mm diam after 2 wk at 22 °C, with sparse aerial mycelium and even, smooth margins. On PDA surface and reverse dirty white. On OA surface pale olivaceous-grey. On MEA surface cinnamon, reverse cinnamon with patches of vinaceous, with a diffuse brick pigment in agar.

Typus. VIETNAM, Dong Nai Province, Cat Tien National Park, Nam Cat Tien Sector, on leaves of *Saccharum spontaneum* (*Poaceae*), in association with *Pyricularia contorta*, 5 Mar. 2013, *A. Alexandrova & O. Deshcherevskaya* (holotype CBS H-21704, culture ex-type CPC 23155 = CBS 137990; ITS sequence GenBank KJ869144, LSU sequence GenBank KJ869201, MycoBank MB808926).

Notes — The acremonium-like morphology and pigmented conidia are reminiscent of the genus *Pseudogliomastix*, which clusters outside the *Hypocreales* (Rehner & Samuels 1995), and is thus unavailable to accommodate this taxon, for which the new genus *Pseudoacremonium* is established. *Pseudoacremonium* is characterised by forming chlamydospore, and having mycelium that turns brown with age, and unbranched conidial chains that become brown (encrusted, flaky) with slightly darkened scars at each end of the conidia.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Acremonium cerealis* (GenBank AB540571; Identities = 560/633 (88 %), Gaps = 31/633 (4 %)), *Acremonium persicinum* (GenBank AB540575; Identities = 555/634 (88 %), Gaps = 30/634 (4 %)) and *Stromatonectria caraganae* (GenBank HQ112288; Identities = 694/799 (87 %), Gaps = 41/799 (5 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Lasionectria mantuana* (GenBank GQ505994; Identities = 826/843 (98 %), no gaps), *Acremonium cerealis* (GenBank HQ232014; Identities = 815/832 (98 %), Gaps = 1/832 (0 %)) and *Hydropisphaera erubescens* (GenBank AY545726; Identities = 841/859 (98 %), Gaps = 2/859 (0 %)).

Colour illustrations. Cat Tien National Park, Vietnam; conidiophores and conidia in culture. Scale bars = 10 µm.

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Dendryphion europaeum

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Dendryphion europaeum Crous & R.K. Schumacher, *sp. nov.*

Etymology. Named after the fact that it occurs on diverse host substrates in Europe.

Mycelium consisting of branched, septate, hyaline to pale brown, 2.5–3 µm diam hyphae. *Conidiophores* erect, branched in upper part, forming a distinct stipe and conidiogenous apparatus; stipe 180–250 × 8–10 µm, 6–10-septate, dark brown, thick-walled, finely roughened, foot cell 10–17 µm diam, with prominent rhizoids. *Conidiophores* solitary, branches medium brown, verruculose, with 1–3 primary branches, subcylindrical, 10–15 × 5–7 µm; additional branches (–2), 8–10 × 5–6 µm. *Conidiogenous cells* subcylindrical to clavate, medium brown, verruculose, 6–10 × 5–7 µm, with rounded apex bearing a thickened, darkened, refractive, cicatrized scar, 1–2 µm diam. *Conidia* (15–)20–28(–33) × (6–)7 µm, (2–)3(–5)-septate, dry, catenate, in simple or branched chains, mostly subcylindrical, but also cheiroid, apical cell rounded, constricted at septa, medium brown, verruculose, basal cell rounded, with central hilum, darkened, thickened and refractive, 1–2 µm diam.

Culture characteristics — Colonies reaching 45 mm diam after 2 wk at 22 °C, spreading with moderate aerial mycelium and even, smooth margins. On PDA surface and reverse pale olivaceous-grey. On OA surface smoke-grey. On MEA surface dirty white, reverse buff with patches of isabelline.

Typus. GERMANY, from a garden, on twig of *Hedera helix* (*Araliaceae*), 26 Mar. 2013, *R. Jarling* (holotype CBS H-21705, culture ex-type CPC 23231 = CBS 137991; ITS sequence GenBank KJ869145, LSU sequence GenBank KJ869202, MycoBank MB808927). – NETHERLANDS, Huissen, on *Heracleum sphondylium* (*Apiaceae*), May 2013, *W. Quaedvlieg* (CPC 22943 = CBS 137991; ITS sequence GenBank KJ869146, LSU sequence GenBank KJ869203).

Notes — The genus *Dendryphion* is characterised by having apically branched conidiophores with polytretic dark scars, and chains of brown, septate (didymo or cheiro) conidia. Although there are more than 80 names, Seifert et al. (2011) recognise around six species. Inderbitzin et al. (2006) showed that *Dendryphion* was polyphyletic and erected *Brachycladium* and *Crivellea* to accommodate species allied to *Alternaria* (but see Woudenberg et al. 2013). Based on the morphological key provided by Siboe et al. (1999), *D. europaeum* appears distinct from currently recognised species based on its conidial morphology.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Dendryphion nanum* (GenBank KC989061; Identities = 554/583 (95 %), Gaps = 8/583 (1 %)), *Torula caligans* (GenBank JX156379; Identities = 375/426 (88 %), Gaps = 18/426 (4 %)) and *Massarina albocarnis* (GenBank EU552142; Identities = 566/675 (84 %), Gaps = 38/675 (5 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Arthopyrenia* sp. (GenBank GU385149; Identities = 856/877 (98 %), Gaps = 1/877 (0 %)), *Corynespora smithii* (GenBank GU323201; Identities = 831/877 (95 %), Gaps = 3/877 (0 %)) and *Roussoella hysterioides* (GenBank AB524622; Identities = 824/872 (94 %), Gaps = 2/872 (0 %)).

Colour illustrations. *Heracleum sphondylium* plants growing in Huissen, The Netherlands; conidiophores and conidia in culture. Scale bars = 10 µm.

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Annellosympodiella juniperi

Fungal Planet 249 – 10 June 2014

Annellosympodiella Crous & Assefa, *gen. nov.*

Etymology. Named after its morphological similarity to the genus *Annellosympodia*.

Conidiomata sporodochial on leaflets, arising from an erumpent brown stroma, consisting of brown, subcylindrical cells. *Conidiophores* densely aggregated, subcylindrical, brown, verruculose to warty, rejuvenating percurrently, septate. *Conidiogenous cells* integrated, terminal, brown, verruculose, proliferating percurrently with irregular annellations, and long, brown, tubular collarettes. Sympodial scars are also visible on the tubular collarette, circular, thickened, darkened and refractive, suggestive of sympodial proliferation. *Conidia* solitary, brown, verruculose to warty, guttulate, subcylindrical to narrowly obclavate, straight to curved, euseptate; hilum truncate, thickened and slightly darkened.

Type species. Annellosympodiella juniperi.
MycoBank MB808928.

Annellosympodiella juniperi Crous & Assefa, *sp. nov.*

Etymology. Named after the host genus from which it was isolated, *Juniperus*.

Conidiomata sporodochial on leaflets, arising from an erumpent brown stroma, 50–100 µm diam, 30–50 µm high, consisting of brown, subcylindrical, 5–15 × 3–4 µm cells. *Conidiophores* densely aggregated, subcylindrical, brown, verruculose to warty, rejuvenating percurrently, 1–4-septate, 25–50 × 4–7 µm. *Conidiogenous cells* 10–30 × 4–5 µm, integrated, terminal, brown, verruculose, proliferating percurrently with irregular annellations, and long, brown, tubular collarettes. Sympodial scars are also visible on the tubular collarette, circular, thickened, darkened and refractive, suggestive of sympodial proliferation. *Conidia* solitary, brown, verruculose to warty, guttulate, subcylindrical to narrowly obclavate, straight to curved, 4–9-euseptate, (30–)40–55(–70) × (5–)6(–7) µm; hilum truncate, thickened and slightly darkened, 4–5 µm diam.

Culture characteristics — Colonies reaching 7 mm diam after 2 wk at 22 °C, surface folded, erumpent, with even, smooth margins and sparse aerial mycelium. On PDA surface olivaceous-grey, reverse iron-grey. On OA surface olivaceous-grey. On MEA surface and reverse olivaceous-grey. Cultures were sterile.

Typus. ETHIOPIA, Addis Ababa, Mangadishu Forest, N8°58'01.8" E38°32' 56.4", on needles of *Juniperus procera* (*Cupressaceae*), 25 June 2013, *P.W. Crous & A. Assefa* (holotype CBS H-21706, culture ex-type CPC 23276 = CBS 137992; ITS sequence GenBank KJ869147, LSU sequence GenBank KJ869204, MycoBank MB808929).

Colour illustrations. Juniperus stand in Mangadishu Forest, Ethiopia; conidioma, conidiophores and conidia in vivo. Scale bars = 10 µm.

Notes — Two genera have thus far exhibited this strange mode of percurrent and sympodial proliferation (with darkened, thickened scars), namely *Annellophragmia* (Ellis 1971) and *Annellosympodia* (McTaggert et al. 2007). *Annellophragmia* has erect, brown synnemata, and is clearly distinct. *Annellosympodia* has superficial fascicles, no sporodochia, lacks a stroma, does not have long, prominent collarettes, and has 0–1-septate conidia. *Annellosympodiella* is thus introduced as a third genus in this complex, to accommodate the fungus occurring on *Juniperus* in Ethiopia. Two species with similar conidial morphology are known from *Jupinerus*, namely *Passalora juniper* and *P. sequoia*, but they have a distinct conidiogenesis (Braun et al. 2013). Phylogenetically, *Annellosympodiella* is a sister genus to *Ramichloridium*, though it is phylogenetically distinct (Arzanlou et al. 2007).

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Ramichloridium strelitziae* (GenBank EU041803; Identities = 557/624 (89 %), Gaps = 26/624 (4 %)), *Pallidocercospora ventilago* (GenBank KF777177; Identities = 538/603 (89 %), Gaps = 26/603 (4 %)) and *Mycosphaerella crystallina* (GenBank JQ732911; Identities = 554/621 (89 %), Gaps = 27/621 (4 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Ramichloridium biverticillatum* (GenBank EU041853; Identities = 834/853 (98 %), no gaps), *Periconiella velutina* (GenBank EU041838; Identities = 820/842 (97 %), no gaps) and *Penidiella nectandrae* (GenBank EU019275; Identities = 825/848 (97 %), no gaps).

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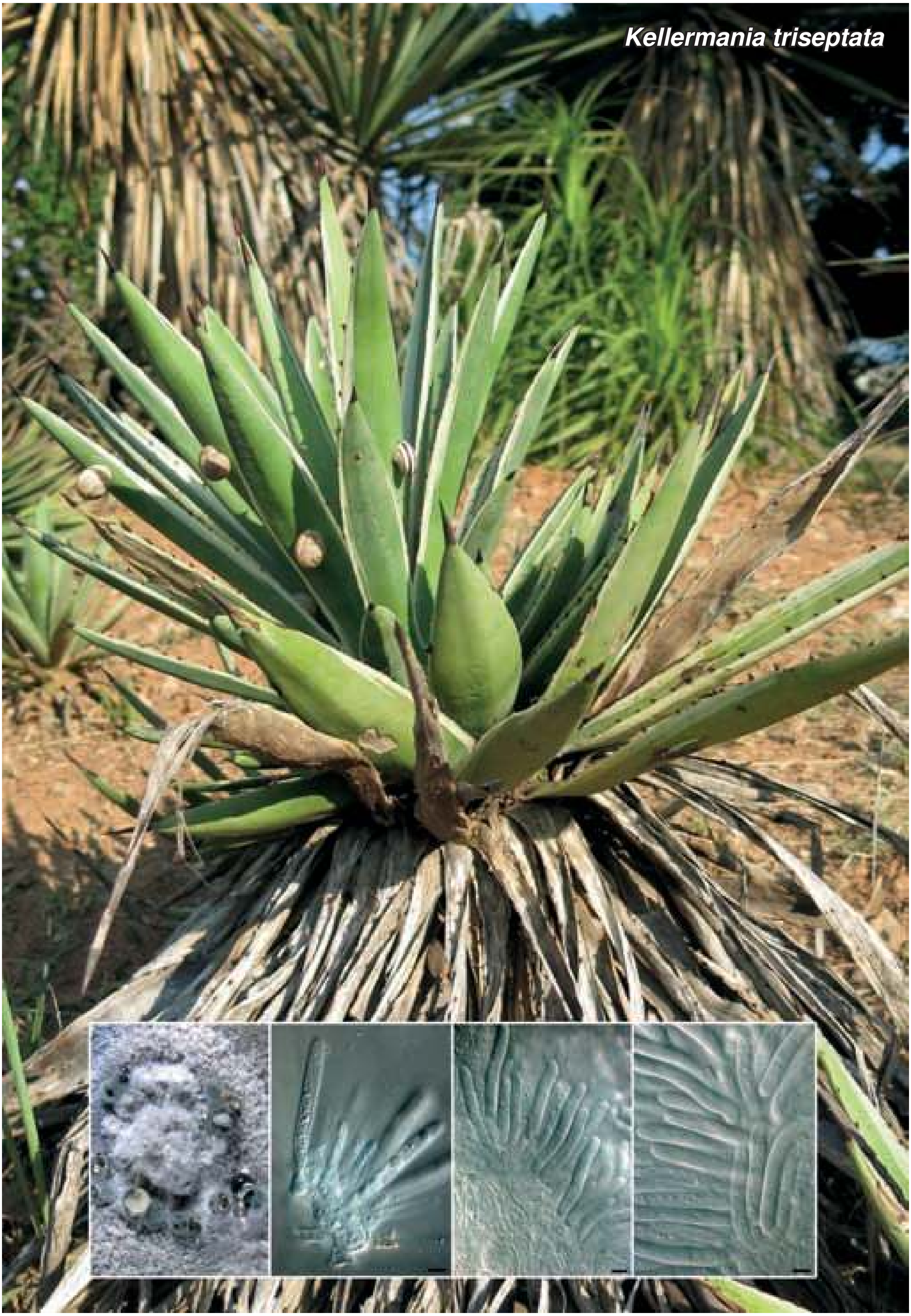
Kellermania triseptata

Fungal Planet 250 – 10 June 2014

Kellermania triseptata Crous, *sp. nov.*

Etymology. Named after its conidia that are 3-septate.

Foliicolous. *Conidiomata* pycnidial, black, solitary, immersed, globose, unilocular, up to 550 µm diam; wall of 8–10 cells of brown *textura angularis*; ostiole central, non-papillate, up to 20 µm diam, exuding a hyaline conidial cirrhus. *Conidiophores* lining the inner cavity, reduced to conidiogenous cells, hyaline, smooth, subcylindrical to ampulliform, 10–25 × 5–10 µm, proliferating percurrently at apex, invested in mucus. *Conidia* hyaline, straight or curved, smooth, guttulate, cylindrical to obclavate, 3-septate, (45–)52–60(–65) × (6–)7–9(–12) µm; frequently encased in a non-persistent 2 µm thick mucoid sheath; apex acutely rounded; conidial base truncate, with a minute, flaring marginal frill, 2–3 µm long.

Culture characteristics — Colonies reaching 40 mm diam after 2 wk at 22 °C. On MEA spreading, with sparse to moderate aerial mycelium, and lobed, even margins; surface smoke-grey, reverse olivaceous-grey with patches of dirty white. On OA surface dirty white. On PDA surface grey-olivaceous, outer region dirty white, reverse grey-olivaceous.

Typus. FRANCE, Nice, Nice Botanical Garden, N43°41'08.2" E007°12'34.4", on leaves of *Agave angustifolia* (*Agavaceae*), 24 July 2013, *P.W. Crous* (holotype CBS H-21707, culture ex-type CPC 23407 = CBS 137993; ITS sequence GenBank KJ869148, LSU sequence GenBank KJ869205, MycoBank MB808930).

Notes — The genus *Kellermania* (*Planistromellaceae*, *Botryosphaeriales*; Slippers et al. 2013), was recently revised by Minnis et al. (2012), who reduced several genera to synonymy under *Kellermania*, namely *Alpakesa*, *Piptarthron*, *Planistroma* and *Planistromella*. *Kellermania triseptata* is most similar to *K. macrospora*, which has conidia that are (3–)4(–5)-septate, (67–)85–97(–105) × (8–)9–10(–12) µm (Crous et al. 2013b), and thus somewhat larger than those of *K. triseptata*.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Kellermania macrospora* (GenBank KF766178; Identities = 879/885 (99 %), Gaps = 4/885 (0 %)), *Kellermania agaves* (GenBank KF777164; Identities = 830/925 (90 %), Gaps = 29/925 (3 %)) and *Kellermania micranthae* (GenBank KF766179; Identities = 810/898 (90 %), Gaps = 27/898 (3 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Kellermania confusa* (GenBank JX444870; Identities = 863/863 (100 %), no gaps), *Kellermania macrospora* (GenBank JX444874; Identities = 861/863 (99 %), no gaps) and *Kellermania dasylirionicola* (GenBank JX444872; Identities = 858/863 (99 %), no gaps).

Colour illustrations. *Agave angustifolia* in Nice Botanical Garden, France; conidiomata, conidiogenous cells and conidia in culture. Scale bars = 10 µm.

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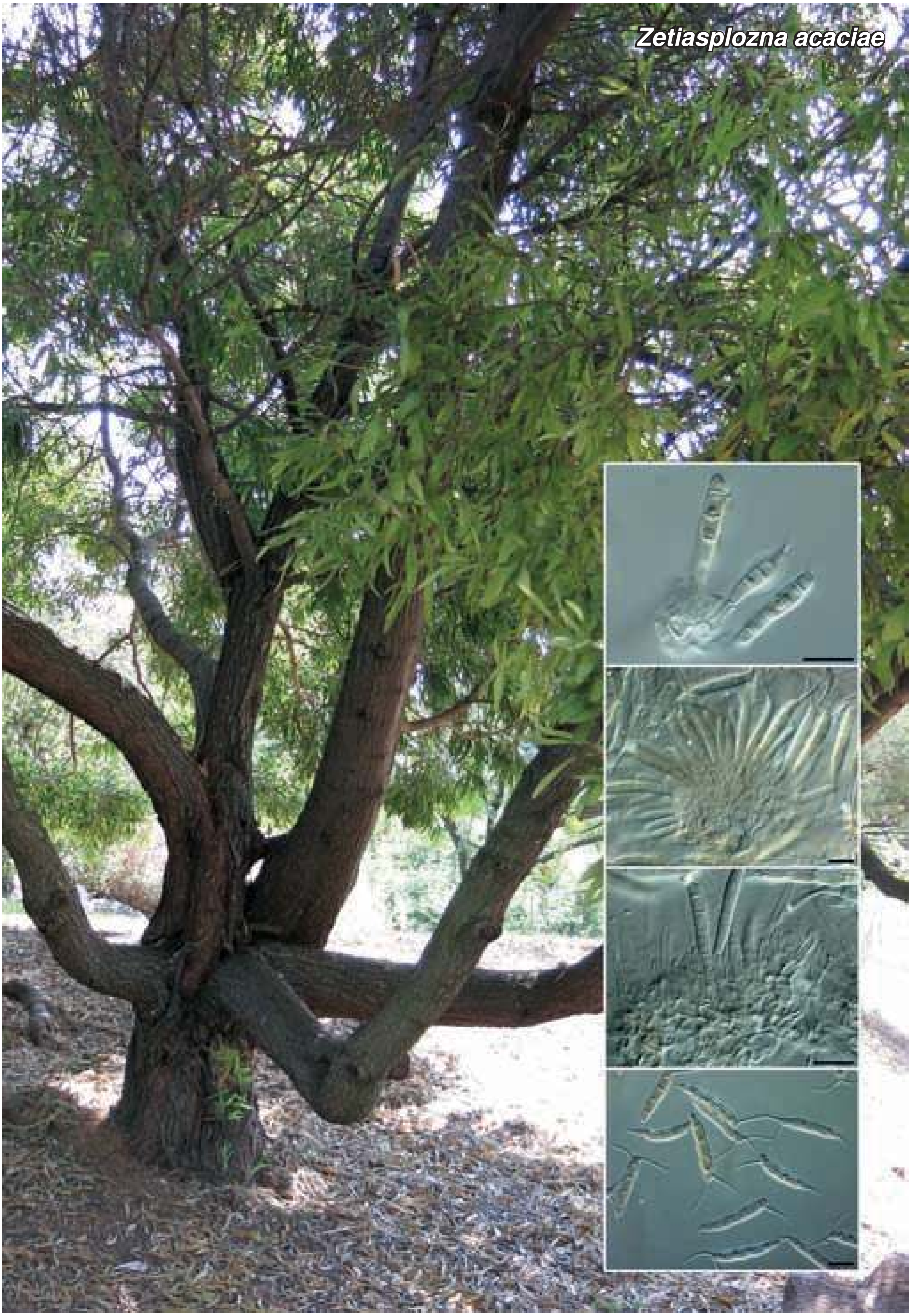
Zetiasplozna acaciae

Fungal Planet 251 – 10 June 2014

Zetiasplozna acaciae Crous, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Acacia*.

Foliicolous. *Conidiomata* stromatic, pycnidioid to indeterminate or variable, amphigenous, erumpent, globose or depressed globose, up to 200 µm diam, unilocular, glabrous brown, lacking an ostiole; wall of brown *textura angularis*, cells thick-walled and brown in the outer layers, becoming thin-walled and paler toward the conidial hymenium. *Conidiophores* arising all around the cavity of the conidioma from the innermost wall layer, reduced to conidiogenous cells or with a supporting cell, invested in mucus. *Conidiogenous cells* ampulliform, hyaline, thin-walled, smooth, 7–12 × 3–5 µm; proliferating percurrently near apex. *Conidia* subcylindrical, widest in upper region, 4-septate, smooth (warty with age), slightly constricted at the septa, (31–)33–37(–41) × (3.5–)4(–4.5) µm, bearing appendages; basal cell obconic with a truncate base, hyaline; apical cell conical, subhyaline, guttulate, devoid of contents, forming a tubular, unbranched central appendage; apical cell subhyaline, smooth with apical excentric appendage and lateral appendage in middle of apical cell; apical appendages unbranched, flexuous, cellular, not separated by a septum, 12–17 × 1 µm. Basal appendage single, unbranched, filiform, central, flexuous, 2–8 × 1 µm.

Culture characteristics — Colonies reaching 30 mm diam after 2 wk at 22 °C. On MEA spreading, with moderate to sparse aerial mycelium and even, smooth margins; surface grey-olivaceous in centre, dirty white in outer margin, reverse olivaceous-grey in middle, dirty white in outer region. On OA grey-olivaceous. On PDA grey-olivaceous, reverse also grey-olivaceous.

Typus. France, Nice, Nice Botanical Garden, N43°41'08.2" E007°12'34.4", on leaves of *Acacia melanoxylon* (*Leguminosae*), 20 July 2013, *P.W. Crous* (holotype CBS H-21708, culture ex-type CPC 23421 = CBS 137994; ITS sequence GenBank KJ869149, LSU sequence GenBank KJ869206, MycoBank MB808931).

Colour illustrations. *Acacia melanoxylon* in Nice Botanical Garden, France; conidiophores and conidia in culture. Scale bars = 10 µm.

Notes — The genus *Zetiasplozna* was established by Nag Raj (1993) for species that are bartalinia-like in general morphology, but have a centric basal appendage (excentric in *Bartalinia*), and apical appendages are apical and lateral on the apical cell (with central attachment point in *Bartalinia*). *Zetiasplozna acaciae* closely resembles *Z. thuemenii* (on leaves and fruit of diverse hosts, conidia 20–32 × 4–5 µm; Nag Raj 1993), except that it has much longer conidia.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Morinia pestalozzioides* (GenBank AY929325; Identities = 489/500 (98 %), Gaps = 1/500 (0 %)), *Morinia longiappendiculata* (GenBank AY929323; Identities = 485/500 (97 %), Gaps = 2/500 (0 %)) and *Bartalinia pondoensis* (GenBank JX854540; Identities = 644/676 (95 %), Gaps = 8/676 (1 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Bartalinia robillardoides* (GenBank EU552102; Identities = 836/850 (98 %), Gaps = 3/850 (0 %)), *Bartalinia pondoensis* (GenBank GU291796; Identities = 833/847 (98 %), Gaps = 3/847 (0 %)) and *Bartalinia laurina* (GenBank AF382369; Identities = 808/823 (98 %), Gaps = 2/823 (0 %)).

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Seiridium podocarpi

Fungal Planet 252 – 10 June 2014

Seiridium podocarpi Crous & A.R. Wood, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Podocarpus.*

Conidiomata stromatic, separate, globose, immersed to erumpent, black, up to 300 µm diam, unilocular; walls of 3–6 layers of brown *textura angularis*. *Conidiophores* lining the inner cavity, subcylindrical, unbranched or branched below, hyaline, 2–3-septate, smooth, up to 70 µm long. *Conidiogenous cells* discrete, integrated, subcylindrical, 10–20 × 2 µm, with several percurrent proliferations near apex. *Conidia* fusoid, wall smooth, not constricted at septa, 5-septate with central pore, guttulate, (23–)25–28(–30) × (8–)9–10 µm, wall 1.5 µm thick, with appendages; basal cell obconic, subhyaline to pale brown with a single, unbranched central appendage, 1–3 µm; apical cell broadly conical to bluntly rounded, subhyaline to pale brown with central appendage, unbranched, 1–3 µm.

Culture characteristics — Colonies reaching up to 20 mm diam after 2 wk at 22 °C. On MEA erumpent, spreading, with moderate aerial mycelium and even lobate margins; surface dirty white, reverse umber. On OA dirty white. On PDA surface dirty white with black sporulation, reverse pale olivaceous-grey in centre, dirty white in outer region.

Typus. South Africa, Western Cape Province, Knysna, Garden Route National Park, Velbroeksdraai picnic site, Diepwalle Forest, S33°56' E23°09', on leaves of *Podocarpus latifolius* (*Podocarpaceae*), 1 July 2013, *A.R. Wood* (holotype CBS H-21709, culture ex-type CPC 23429 = CBS 137995; ITS sequence GenBank KJ869150, LSU sequence GenBank KJ869207, MycoBank MB808932).

Colour illustrations. *Podocarpus latifolius* in South Africa; conidiomata, conidiophores and conidia in culture. Scale bars = 10 µm.

Notes — Morphologically *S. podocarpi* is comparable to *S. anceps*, *S. ceratosporum*, *S. cupressi* and *S. intermedium* (Nag Raj 1993). However, conidia of *S. anceps* (19–27 × 6.5–9 µm) are narrower and those of *S. ceratosporum* (29–35 × 10–12 µm) somewhat longer and wider. Although conidia of *C. intermedium* (22–33 × 9–11 µm) are similar in size, they differ in being more doliiform, being longitudinally striate and having shorter appendages. Conidia of *S. cupressi* (23–30 × 7–10 µm) are also similar in size but differ in having longer appendages (Nag Raj 1993).

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Seiridium phylicae* (GenBank KF574903; Identities = 450/465 (97 %), Gaps = 6/465 (1 %)), *Seiridium cardinale* (GenBank AF409995; Identities = 542/571 (95 %), Gaps = 9/571 (1 %)) and *Seiridium cupressi* (GenBank FJ430600; Identities = 545/575 (95 %), Gaps = 9/575 (1 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Seiridium phylicae* (GenBank KC005807; Identities = 827/829 (99 %), no gaps), *Seiridium unicorne* (GenBank DQ414532; Identities = 822/824 (99 %), no gaps) and *Seiridium eucalypti* (GenBank DQ414533; Identities = 822/824 (99 %), no gaps).

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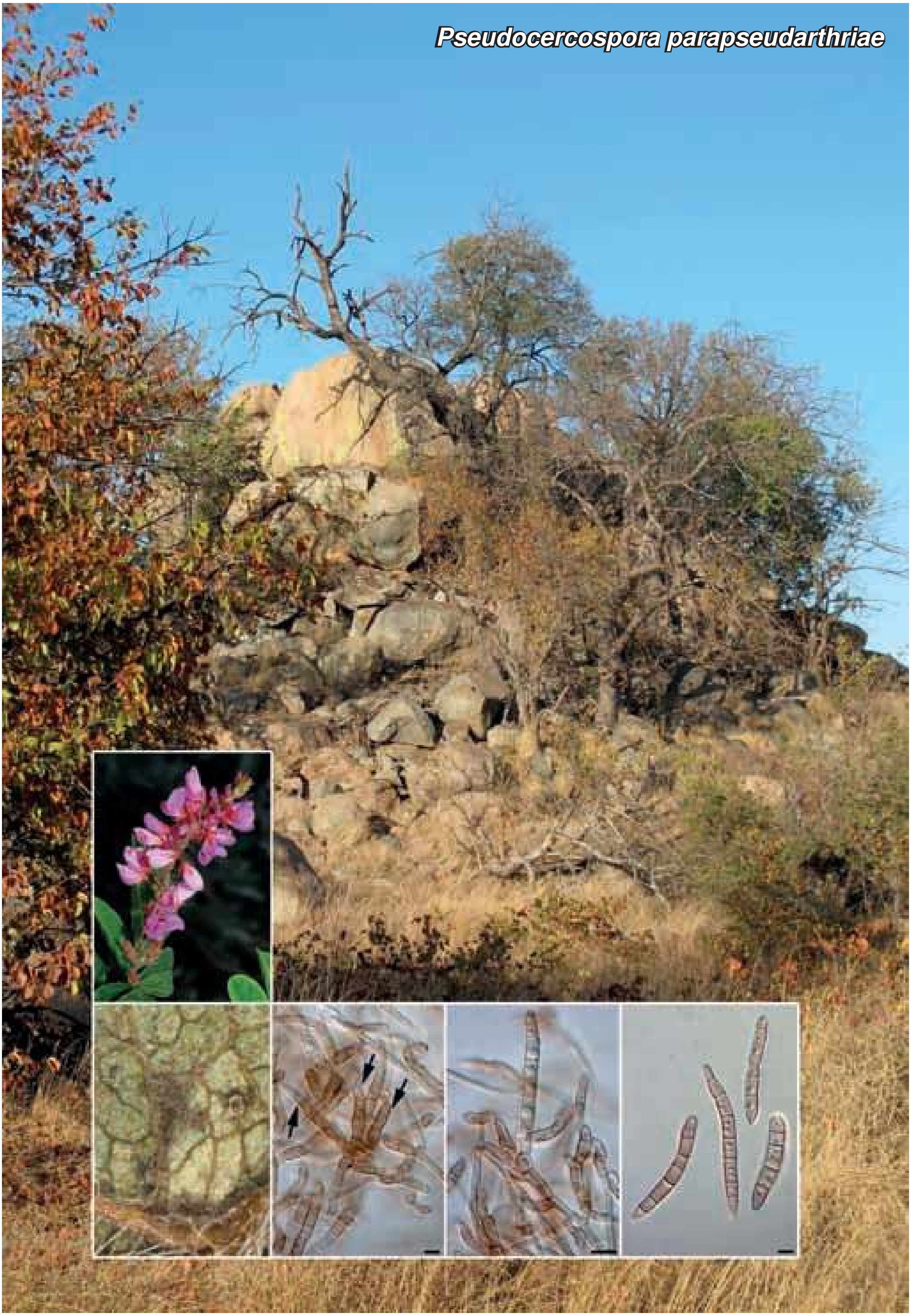
Pseudocercospora parapseudarthriae

Fungal Planet 253 – 10 June 2014

Pseudocercospora parapseudarthriae Crous & A.R. Wood, *sp. nov.*

Etymology. Named for its morphological similarity to *Pseudocercospora pseudarthria.*

Leaf spots amphigenous, chlorotic yellow, becoming pale brown, subcircular to irregular, 1–10 mm diam with diffuse margins. Sporulation hypophyllous, frequently associated with raised leaf veins. *Mycelium* consisting of smooth, septate, branched, pale brown, 3–4 µm diam hyphae, giving rise to conidiophores. *Conidiophores* creeping, branching, up to 100 µm long, 4–5 µm diam. *Conidiogenous cells* terminal and lateral, subcylindrical to clavate, pale brown, smooth, guttulate, 10–20 × 4–5 µm, proliferating sympodially and percurrently near apex. *Conidia* pale to medium brown, guttulate, finely roughened, subcylindrical, apex bluntly rounded, basal cell tapering abruptly to a truncate base, 2 µm diam, not thickened nor darkened, 3–6-septate, (27–)40–60(–75) × (5–)6(–7) µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margins, reaching 20 mm diam after 2 wk at 22 °C. On PDA, OA and MEA surface olivaceous-grey in middle, iron-grey in outer region, and in reverse.

Typus. South Africa, KwaZulu-Natal, Hilton, Doreen Clarke Nature Reserve, S29°34' E30°17', on leaves of *Pseudarthria hookeri* (*Leguminosae*), 5 Mar. 2013, *A.R. Wood* (holotype of *P. parapseudarthriae* CBS H-21710, culture ex-type CPC 23449 = CBS 137996; ITS sequence GenBank KJ869151, LSU sequence GenBank KJ869208, ACT sequence GenBank KJ869229, TEF sequence GenBank KJ869238, MycoBank MB808933).

Other specimens examined. South Africa, Mpumalanga, Nelspruit, Schagen, on leaves of *Pseudarthria hookeri*, L.C.C. Liebenberg, 13 July 1936, *PREM 32886*. – Sri Lanka (Ceylon), Peradeniya, on *Pseudarthria vicida*, 20 Dec. 1913, *T. Petch No. 4096*, holotype of *P. pseudarthria* K (M).

Colour illustrations. Scenic outcrop in Mpumalanga, South Africa; plant host, conidiophore fascicles on leaves, conidiophores and conidia in vivo. Scale bars = 10 µm.

Notes — Crous & Braun (1996) provided a description based on the type specimen of *P. pseudarthria* (on *Pseudarthria vicida*, Sri Lanka) and concluded that it was the same fungus as observed in South Africa on *Pseudarthria hookeri*. The fresh collection obtained here allowed us to again re-examine these collections, and led to the conclusion that although similar, the collections on *P. hookeri* represent a different taxon with longer conidiophores and conidia.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Pseudocercospora schizolobii* (GenBank DQ885903; Identities = 535/537 (99 %), no gaps), *Pseudocercospora cydoniae* (GenBank EF535716; Identities = 503/505 (99 %), Gaps = 1/505 (0 %)) and *Pseudocercospora flavomarginata* (GenBank GU269799; Identities = 498/500 (99 %), no gaps).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Pseudocercospora timorensis* (GenBank KC677937; Identities = 811/811 (100 %), no gaps), *Pseudocercospora mombin* (GenBank KC677935; Identities = 811/811 (100 %), no gaps) and *Pseudocercospora jahnii* (GenBank KC677933; Identities = 811/811 (100 %), no gaps).

ACT. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ACT sequence are *Pseudocercospora madagascariensis* (GenBank JX902140; Identities = 531/537 (99 %), no gaps), *Pseudocercospora cruenta* (GenBank JQ325012; Identities = 580/588 (99 %), no gaps) and *Pseudocercospora cercidis-chinensis* (GenBank JX902131; Identities = 529/537 (98 %), no gaps).

TEF. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the TEF sequence are *Pseudocercospora variicolor* (GenBank GU384538; Identities = 299/313 (96 %), no gaps), *Pseudocercospora ravenalicola* (GenBank GU384521; Identities = 295/314 (94 %), no gaps) and *Pseudocercospora lonicericola* (GenBank JQ324999; Identities = 476/508 (94 %), Gaps = 3/508 (0 %)).

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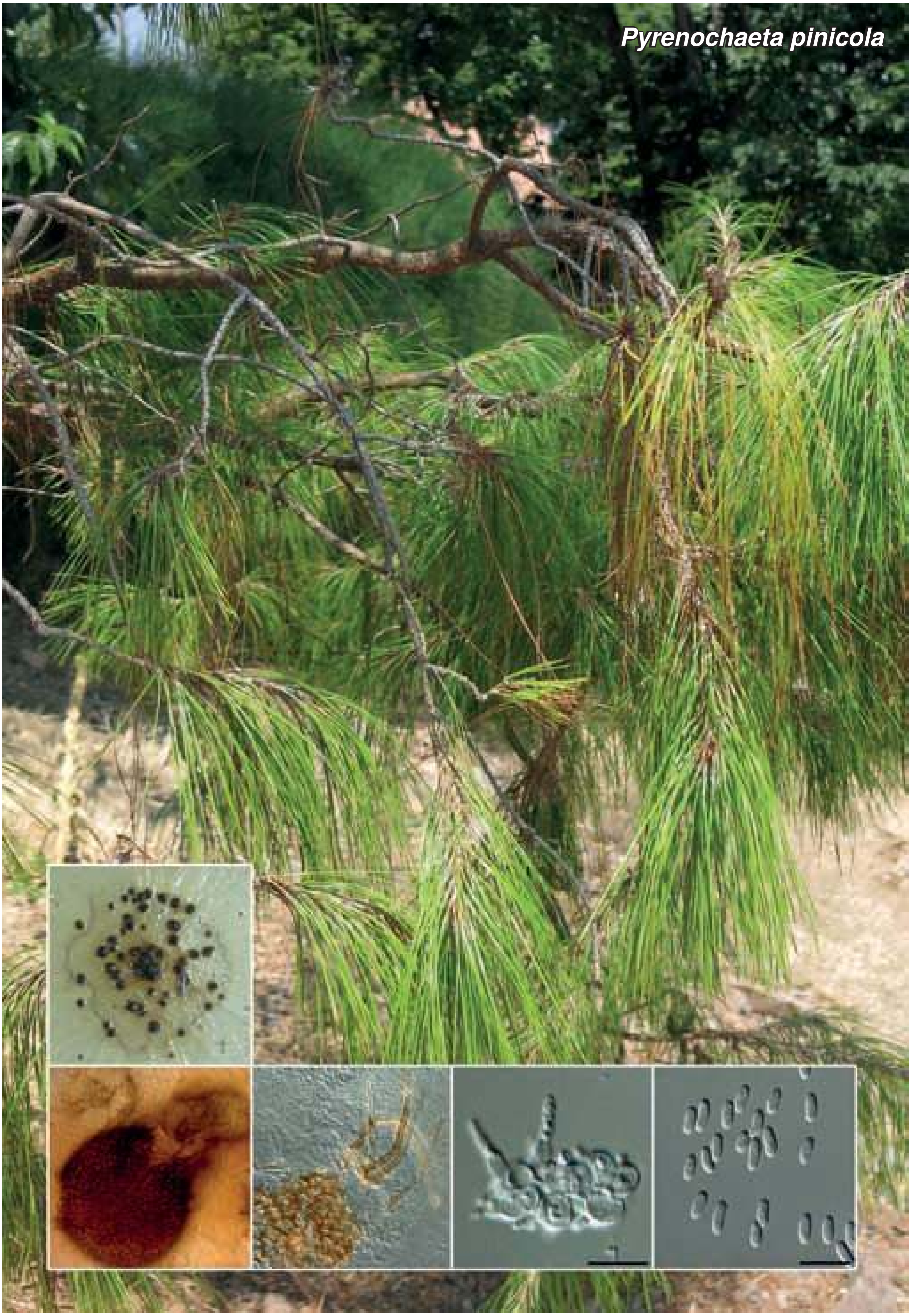
Pyrenochaeta pinicola

Fungal Planet 254 – 10 June 2014

Pyrenochaeta pinicola Crous, *sp. nov.*

Etymology. Named after the host genus from which it was isolated, *Pinus*.

Conidiomata immersed but becoming erumpent to superficial, brown, globose, up to 200 µm diam with prominent wide central ostiole, 40–60 µm diam, surrounded by a crest of brown setae, straight, flexuous, unbranched, septate with obtusely rounded ends, 50–150 µm long, 3–5 µm wide; conidiomatal wall of 3–4 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, smooth, ampulliform, lining the inner cavity, 4–6 × 3–4 µm, with prominent periclinal thickening. *Conidia* solitary, hyaline, smooth, thin-walled, guttulate, subcylindrical with obtuse ends, straight to slightly curved, allantoid, (4–)4.5–5.5(–6) × 2(–2.5) µm.

Culture characteristics — Colonies reaching 15 mm diam after 2 wk at 22 °C. On MEA erumpent, surface folded, with moderate aerial mycelium, and smooth, lobed margin. Surface dirty white, reverse salmon. On OA surface grey-olivaceous. On PDA surface and reverse dirty white with patches of smoke-grey.

Typus. FRANCE, Nice, L'aire d'Esterel petrol filling station, on needles of *Pinus* sp. (*Pinaceae*), 20 July 2013, *P.W. Crous* (holotype CBS H-21711, culture ex-type CPC 23455 = CBS 137997; ITS sequence GenBank KJ869152, LSU sequence GenBank KJ869209, ACT sequence GenBank KJ869230, TUB sequence GenBank KJ869249, MycoBank MB808934).

Notes — The genus *Pyrenochaeta* is characterised by having species with distinct, elongated, septate, acropleurogenous conidiophores produced in pycnidial conidiomata usually covered by long, brown setae (de Gruyter et al. 2010). Phylogenetically, *P. pinicola* is closely allied to *P. protearum* (Crous et al. 2011). Both species have brown, elongated setae and conidiophores reduced to conidiogenous cells. They differ in that *P. protearum* has smaller conidia, (3–)4–5(–6) × (2–)2.5(–3) µm (Crous et al. 2011) and colonies that tend to be more smoke-grey to olivaceous-grey on MEA and PDA in culture.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Pyrenochaeta protearum* (GenBank JQ044434; Identities = 791/794 (99 %), Gaps = 1/794 (0 %)), *Pyrenochaeta unguis-hominis* (GenBank JX966641; Identities = 318/334 (95 %), Gaps = 4/334 (1 %)) and *Ochrocladosporium frigidarii* (GenBank FJ755255; Identities = 318/335 (95 %), Gaps = 8/335 (2 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Pyrenochaeta protearum* (GenBank JQ044453; Identities = 859/860 (99 %), no gaps), *Pyrenochaeta nobilis* (GenBank DQ678096; Identities = 834/845 (99 %), no gaps) and *Paraleptosphaeria orobanches* (GenBank JF740299; Identities = 855/868 (99 %), no gaps).

ACT. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ACT sequence are *Chalastospora gossypii* (GenBank JQ671625; Identities = 428/471 (91 %), Gaps = 9/471 (1 %)), *Embellisia phragmospora* (GenBank JQ671623; Identities = 428/471 (91 %), Gaps = 9/471 (1 %)) and *Macrospora scirpicola* (GenBank JQ671613; Identities = 428/471 (91 %), Gaps = 9/471 (1 %)).

TUB. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the TUB sequence are *Phoma nigrificans* (GenBank AY749030; Identities = 265/302 (88 %), Gaps = 3/302 (0 %)), *Coniothyrium clematidis-rectae* (GenBank FJ515624; Identities = 249/284 (88 %), Gaps = 3/284 (1 %)) and *Phoma nebulosa* (GenBank GU237633; Identities = 257/294 (87 %), Gaps = 3/294 (1 %)).

Colour illustrations. *Pinus* sp. next to the roadside in France; conidiomata, setae, conidiogenous cells and conidia in culture. Scale bars = 10 µm.

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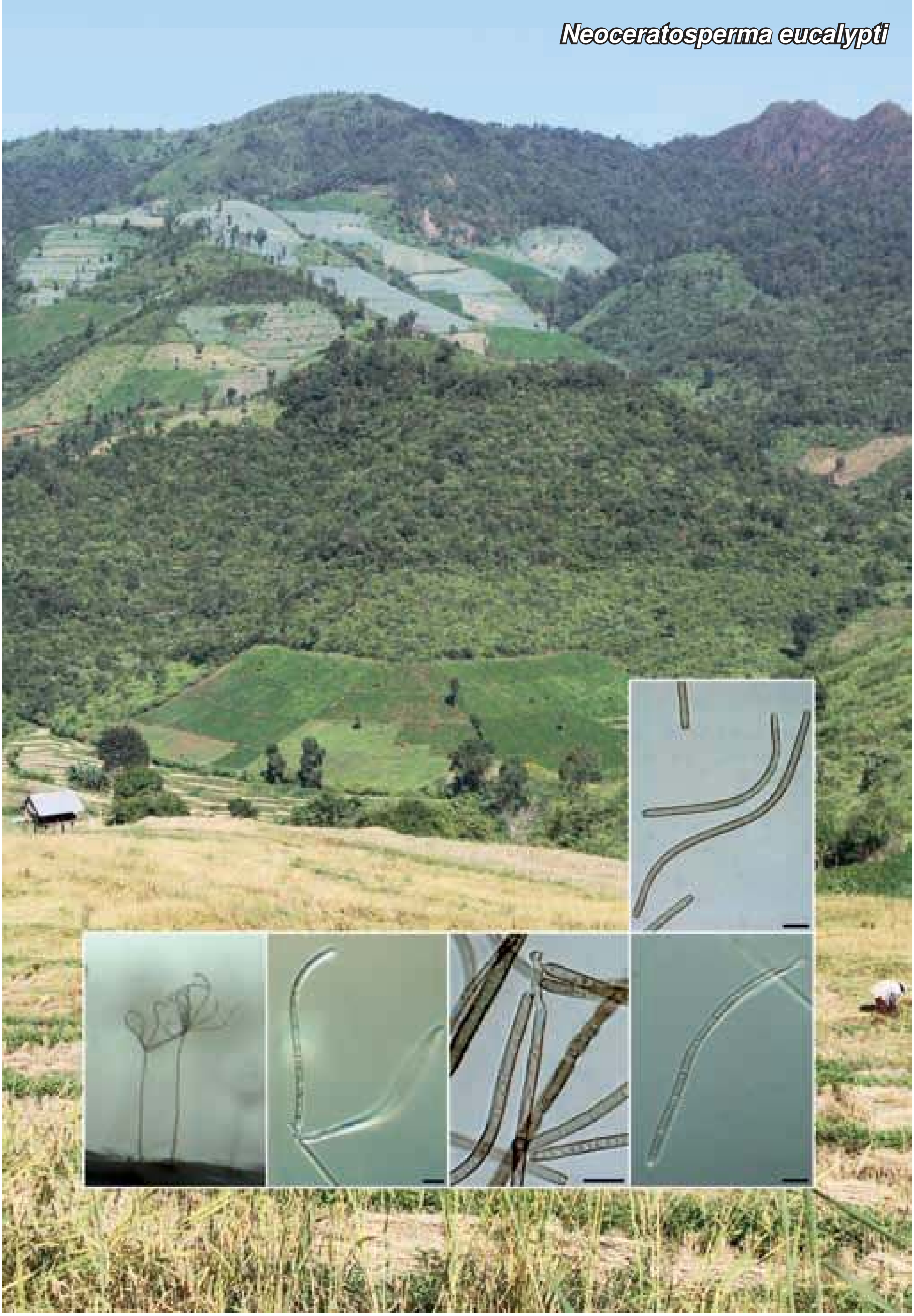
Neoceratosperma eucalypti

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Neoceratosperma Crous & Cheew., *gen. nov.*

Etymology. Named after its morphological similarity to the genus *Ceratosperma*.

Mycelium consisting of branched, septate, brown, verruculose hyphae that turn warty with age. *Conidiophores* reduced to conidiogenous cells, or septate, erect, brown, verruculose, unbranched, subcylindrical, dark brown and smooth at the base. *Conidiogenous cells* subcylindrical, brown, verruculose, but conidiogenous apical area smooth, forming a short rachis that proliferates sympodially; loci somewhat thickened and darkened. *Conidia* solitary, rarely in unbranched chains, subcylindrical, medium brown, becoming dark brown, verruculose, becoming warty, distoseptate, less obvious when older (dark brown, warty), straight to irregularly curved; apex obtuse, base truncate, but scars somewhat thickened and darkened.

Type species. Neoceratosperma eucalypti.
MycoBank MB808935.

Neoceratosperma eucalypti Crous & Cheew., *sp. nov.*

Etymology. Named after the genus from which it was collected, *Eucalyptus*.

Mycelium consisting of branched, septate, brown, verruculose 2–3 µm diam (warty with age, warts 1 µm diam) hyphae. *Conidiophores* reduced to conidiogenous cells, or 1–15-septate, erect, brown, verruculose, unbranched, subcylindrical, up to 100 µm long, 3–4 µm diam, dark brown and smooth at the base. *Conidiogenous cells* subcylindrical, brown, verruculose, but conidiogenous apical area smooth, 2–27 × 2–4 µm, forming a short rachis that proliferates sympodially; loci somewhat thickened and darkened, 1–1.5 µm diam. *Conidia* solitary, rarely in unbranched chains, subcylindrical, medium brown, becoming dark brown, verruculose, becoming warty, 1–7-distoseptate, less obvious when older (dark brown, warty), straight to irregularly curved, 40–150(–200) × 3–4 µm; apex obtuse, base truncate, but scars somewhat thickened and darkened, 1–1.5 µm diam.

Culture characteristics — Colonies reaching 10 mm diam after 2 wk at 22 °C. On MEA surface erumpent with moderate aerial mycelium, margins uneven. Surface olivaceous-grey, reverse iron-grey, similar on OA and PDA.

Typus. Thailand, Chiang Mai, on living *Eucalyptus* (*Myrtaceae*) leaves, Sept. 2013, *R. Cheewangkoon* (holotype CBS H-21712, culture ex-type CPC 23465 = CBS 137998; ITS sequence GenBank KJ869153, LSU sequence GenBank KJ869210, MycoBank MB808936).

Colour illustrations. Countryside in Chiang Mai, Thailand; conidiophores and conidia (note sympodial proliferation, and conidia with distoseptation) in culture. Scale bars = 10 µm.

Notes — The genus *Ceratosperma* was established by Sutton & Hodges (1981) for a fungus occurring on *Eucalyptus* leaves in Brazil, characterised by superficial mycelium, holoblastic conidiogenous cells, and solitary, pigmented, smooth, distoseptate conidia. It is distinguished from *Neoceratosperma* in that the latter has flexuous conidiophores that give rise to several conidia in a short sympodial rachis, conidia are solitary, but can also occur in unbranched chains, and all structures are prominently verruculose and have slightly thickened, darkened hila and scars. Morphologically, *Neoceratosperma* therefore resembles the *Stenella-Zasmidium* generic complex, though it is distinct in that conidia are distoseptate (lumina reduced, clearly visible when immature). The introduction of *Neoceratosperma* adds yet another genus to the *Mycosphaerellaceae* (Crous et al. 2009a–c).

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Mycosphaerella crystallina* (GenBank EU167579; Identities = 656/708 (93 %), Gaps = 16/708 (2 %)), *Pallidocercospora acaciigena* (GenBank GU214661; Identities = 655/708 (93 %), Gaps = 16/708 (2 %)) and *Passalora brachycarpa* (GenBank GU214664; Identities = 653/707 (92 %), Gaps = 11/707 (1 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Passalora haldinae* (GenBank KC677925; Identities = 842/859 (98 %), no gaps), *Mycosphaerella elaeocarpi* (GenBank EU040212; Identities = 851/872 (98 %), no gaps) and *Xenosonderhenia syzygii* (GenBank JX069856; Identities = 862/885 (97 %), no gaps).

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Neodevriesia coryneliae

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Neodevriesia coryneliae Crous & A.R. Wood, *sp. nov.*

Etymology. Named after the fungal genus from which it was isolated, *Corynelia.*

Restricted to ascomata of *Corynelia uberata* on *Afrocarpus* leaves. Description on SNA: *mycelium* consisting of branched, septate, brown, 2–3 µm diam hyphae. *Conidiophores* arising from hyphae, erect, long, flexuous, unbranched, 100–400 × 6–10 µm, 6–25-septate, brown, verruculose, thick-walled, bearing an apical conidiogenous apparatus; conidiophore base lacking rhizoids. *Ramoconidia* fusoid-ellipsoidal, brown, 8–10 × 3–4 µm, brown, finely roughened, hila truncate, 1–1.5 µm diam, not thickened nor darkened; 1–3 apical loci giving rise to short, branched chains (–7) of conidia that have 1–3 apical loci; intermediate conidia brown, finely roughened, fusoid-ellipsoidal, 8–10 × 3–4 µm; apical conidia ellipsoid, brown, finely roughened, 6–8 × 3–4 µm, hila 1 µm diam, not thickened, nor refractive. *Conidia* ellipsoid, brown, finely roughened, 6–8 × 2–3 µm, remaining attached in chains and appearing red-brown when mounted in lactic acid.

Culture characteristics — Colonies reaching 5 mm diam after 2 wk at 22 °C. On MEA surface erumpent with sparse aerial mycelium and uneven margin; olivaceous-grey, also in reverse. On OA olivaceous-grey. On PDA pale olivaceous-grey, reverse olivaceous-grey.

Typus. South Africa, Western Cape Province, Knysna, Garden Route National Park, Velbroeksdraai picnic site, Diepwalle Forest, S33°56' E23°09', on *Corynelia uberata* on leaves of *Afrocarpus falcatus* (*Podocarpaceae*), 1 July 2013, *A.R. Wood* (holotype CBS H-21713, culture ex-type CPC 23534 = CBS 137999; ITS sequence GenBank KJ869154, LSU sequence GenBank KJ869211, TEF sequence GenBank KJ869239, TUB sequence GenBank KJ869250, MycoBank MB808937).

Notes — The genus *Neodevriesia* was introduced by Quaedvlieg et al. (2014) to accommodate several foliicolous, saprobic or plant pathogenic taxa, now representing the *Neodevriesiaceae*, which Ruibal et al. (2009, 2011) referred to as '*Teratosphaeriaceae* 2'. *Neodevriesia corynelia* is the first member of the genus known to be mycophylic. In culture it proved to be extremely slow-growing, which is possibly indicative of its unique ecology.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Teratosphaeria knoxdaviesii* (GenBank EU707865; Identities = 535/573 (93 %), Gaps = 11/573 (1 %)), *Devriesia lagerstroemiae* (GenBank GU214634; Identities = 525/565 (93 %), Gaps = 11/565 (1 %)) and *Devriesia fraseriae* (GenBank HQ599602; Identities = 525/571 (92 %), Gaps = 14/571 (2 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Devriesia xanthorrhoeae* (GenBank HQ599606; Identities = 759/773 (98 %), no gaps), *Devriesia shakazului* (GenBank KC005797; Identities = 758/773 (98 %), no gaps) and *Devriesia hilliana* (GenBank GU214414; Identities = 758/773 (98 %), no gaps).

TEF. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the TEF sequence is *Devriesia pseudoamericana* (GenBank HM177416; Identities = 119/128 (93 %), no gaps).

TUB. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the TUB sequence are *Coniothyrium zuluense* (GenBank AY244392; Identities = 282/348 (81 %), Gaps = 18/348 (5 %)), *Teratosphaeria tinara* (GenBank FJ532027; Identities = 280/347 (81 %), Gaps = 20/347 (5 %)) and *Teratosphaeria foliensis* (GenBank FJ532015; Identities = 279/348 (80 %), Gaps = 22/348 (6 %)).

Colour illustrations. Afrocarpus falcatus tree in South Africa; conidiophore with swollen basal cell, conidiophores and conidia in culture (note diffuse reddish pigment around conidia when mounted in lactic acid). Scale bars = 10 µm.

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Ramichloridium eucleae

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Ramichloridium eucleae Crous & van der Linde, *sp. nov.*

Etymology. Named after the host genus from which it was isolated, *Euclea*.

Mycelium consisting of branched, septate, smooth, pale brown, 1.5–2 µm diam hyphae. *Conidiophores* dimorphic, arising from hyphae. *Microconidiophores* reduced to conidiogenous cells, erect, pale to medium brown, 7–20 × 3–4 µm. *Macroconidiophores* erect, straight to flexuous, 1–4-septate, 40–90 × 2.5–3 µm, unbranched, medium brown, smooth, basal cell lacking rhizoids, 4–7 µm diam. *Conidiogenous cells* terminal, integrated, pale to medium brown, smooth, containing whorls of denticle-like loci in swollen regions of the conidiogenous cell, denticles 0.5 µm long, 1 µm diam, darkened and somewhat refractive, 20–40 × 2–3 µm. *Conidia* solitary, fusoid-ellipsoid, medianly 1-septate, guttulate, pale to medium brown, covered in muricate ornamentation, (9–)13–14(–15) × (4–)5 µm; basal hilum darkened, refractive and thickened.

Culture characteristics — Colonies reaching 7 mm diam after 2 wk at 22 °C. On MEA surface erumpent, with sparse aerial mycelium, lobed margins; surface olivaceous-grey, reverse iron-grey. On OA pale olivaceous-grey with diffuse red zone. On PDA pale olivaceous-grey.

Typus. South Africa, North West Province, Magaliesberg/Hekpoort District, Shelter Rock hiking trial, off R560, S25°50'16.2" E27°39'16.0", on leaves of *Euclea undulata* (*Ebenaceae*), 27 July 2013, *E.J. van der Linde* (holotype CBS H-21714, culture ex-type CPC 23551 = CBS 138000; ITS sequence GenBank KJ869155, LSU sequence GenBank KJ869212, MycoBank MB808938).

Notes — The genus *Ramichloridium*, together with species of *Dissoconium* represent the *Dissoconiaceae* (*Capnodiales*; Crous et al. 2009a, Li et al. 2012), to which *R. eucleae* is allied. *Ramichloridium apiculatum* (3–7.5 × 2–4 µm) and *R. indicum* (5–10 × 4–9 µm) are distinct from *R. eucleae* in that they have much smaller conidia (Arzanlou et al. 2007).

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Ramichloridium apiculatum* (GenBank JN850989; Identities = 490/532 (92 %), Gaps = 15/532 (2 %)), *Dissoconium proteae* (GenBank EU707897; Identities = 553/604 (92 %), Gaps = 19/604 (3 %)) and *Ramichloridium indicum* (GenBank EU041799; Identities = 477/523 (91 %), Gaps = 13/523 (2 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Ramichloridium luteum* (GenBank JQ622099; Identities = 825/835 (99 %), no gaps), *Ramichloridium apiculatum* (GenBank GU214687; Identities = 868/880 (99 %), no gaps) and *Ramichloridium indicum* (GenBank EU041856; Identities = 836/848 (99 %), no gaps).

Colour illustrations. *Euclea undulata* habitat in South Africa; conidiophores and conidia in culture. Scale bars = 10 µm.

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Melnikomyces vietnamensis

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Melnikomyces Crous & U. Braun, *gen. nov.*

Etymology. Named in honour of Dr Vadim Mel'nik, in recognition of his contribution to the systematics of ascomycetous fungi.

Mycelium consisting of brown, septate, branched, smooth, thick-walled hyphae. *Conidiophores* dimorphic. Type A conidiophores reduced to conidiogenous cells, terminal and intercalary; loci inconspicuous, truncate. *Conidia* globose to subglobose, occurring in short, branched chains, brown, smooth, guttulate, chlamydospore-like in appearance, disarticulating into solitary conidial propagules. Type B conidiophores subcylindrical, brown, smooth, erect, straight or once geniculate, reduced to conidiogenous cells, or long flexuous, multiseptate. *Conidiogenous cells* subcylindrical to subclavate, mostly terminal but also intercalary, brown, smooth, developing a rachis with numerous denticle-like loci, conidiogenesis holoblastic. *Conidia* solitary, brown, verruculose, fusoid-ellipsoidal, medianly 1-septate, ends subobtuse, young conidia with visible basal marginal frill, secession rhexolytic.

Type species. Melnikomyces vietnamensis.
MycoBank MB808939.

Melnikomyces vietnamensis Crous & U. Braun, *sp. nov.*

Etymology. Named after the country from where it was collected, Vietnam.

Mycelium consisting of brown, septate, branched, smooth, thick-walled, 2–2.5 µm diam hyphae. *Conidiophores* dimorphic. Type A conidiophores reduced to conidiogenous cells, terminal and intercalary; loci inconspicuous, truncate, 1.5–2 µm diam. *Conidia* globose to subglobose, occurring in short, branched chains, brown, smooth, guttulate, chlamydospore-like in appearance, 5–10 µm diam, disarticulating into solitary conidial propagules. Type B conidiophores subcylindrical, brown, smooth, erect, straight or once geniculate, reduced to conidiogenous cells, or long flexuous, multiseptate, 10–60 × 2.5–4 µm. *Conidiogenous cells* 5–15 × 2.5–4 µm, subcylindrical to subclavate, mostly terminal but also intercalary, brown, smooth, developing a rachis with numerous denticle-like loci, 1 µm long. *Conidia* solitary, brown, verruculose, fusoid-ellipsoidal, medianly 1-septate, ends subobtuse, young conidia with visible basal marginal frill, 0.5 µm long, (7–)9–10(–11) × (2.5–)3(–3.5) µm.

Culture characteristics — Colonies spreading, erumpent, with sparse to moderate aerial mycelium; surface folded with lobate, smooth margins. On MEA surface olivaceous-grey, reverse blood colour with diffuse blood pigment spreading into agar; reaching 22 mm diam after 2 wk at 22 °C. On PDA surface olivaceous-grey with wide brown border; reverse umber. On OA surface bay with copious amounts of mucus.

Typus. Vietnam, Dong Nai Province, Cat Tien National Park, Nam Cat Tien Sector, polydominant monsoon tropical forest, on dry leaves of an unidentified broadleaved tree, in association with *Braunomyces dictyosporus*, 16 Nov. 2011, coll. *Yu. Novozhilov*, isol. *D. Shabunin* (holotype CBS H-21715, culture ex-type CPC 23554 = CBS 136209; ITS sequence GenBank KJ869156, LSU sequence GenBank KJ869213, MycoBank MB808940).

Notes — The *Scolecobasidium* complex represents several genera. Seifert et al. (2011) commented on a humicola-like synasexual morph linked to some species, which would suggest that our taxon, with its dimorphic conidiophores, could be accommodated here. Unfortunately, *Scolecobasidium terreum* (type of *Scolecobasidium*) clusters distant to our fungus. Samerpitak et al. (2014) recently reviewed this complex, and introduced the genus *Verruconis* for thermophilic species (brain infections), while *Ochroconis* was seen as mesophilic, linked to infections in cold-blooded animals. Phylogenetically, *M. vietnamensis* is allied to *Scolecobasidium cateniphorum* (*Chaetothyriales*, *incertae sedis*), *Verruconis verruculosa* and *Scolecobasidiella avellanea* (type of *Scolecobasidiella*).

Two species are presently known in *Scolecobasidiella*, namely *S. avellanea* and *S. tropicalis*. However, the phylogenetic relationship of *Scolecobasidiella* to *Melnikomyces* is still somewhat distant. Morphologically, *Melnikomyces* fits the general characteristics of the genus, except that has a synasexual morph forming globose conidia, which has not been observed in any of the other two species.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Dactylaria purpurella* (GenBank AY265335; Identities = 538/624 (86 %), Gaps = 34/624 (5 %)), *Ochroconis humicola* (GenBank AY265334; Identities = 525/629 (83 %), Gaps = 41/629 (6 %)) and *Scolecobasidium terreum* (GenBank FR832480; Identities = 294/330 (89 %), Gaps = 13/330 (3 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Scolecobasidiella avellanea* (GenBank EF204505; Identities = 796/830 (96 %), Gaps = 1/830 (0 %)), *Verruconis verruculosa* (GenBank KF282668; Identities = 819/869 (94 %), Gaps = 5/869 (0 %)) and *Scolecobasidium cateniphorum* (GenBank EU107309; Identities = 786/834 (94 %), Gaps = 8/834 (0 %)).

Colour illustrations. Cat Tien National Park, Vietnam; conidiophores and two conidial types formed in culture. Scale bars = 10 µm.

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Dematiocladium celtidicola

Fungal Planet 259 – 10 June 2014

Dematiocladium celtidicola Crous, M.J. Wingf. & Y. Zhang ter, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Celtis*.

Setae unbranched, flexuous, 200–400 × 12–20 µm, arising from pseudoparenchymatous cells in a basal stroma or microsclerotia (ascomatal initials?), adjacent to cells that give rise to conidiophore stipes; setae yellow-brown, smooth to finely roughened, thick-walled, basal cell rounded and well-defined; stipe becoming thinner walled towards the acute apex; apical cell sometimes becoming fertile, setae extending beyond the conidiophores. *Conidiophores* consisting of a stipe, a penicillate arrangement of fertile branches, and rarely, an extension of the stipe, signifying continued growth and eventual branching of the stipe and secondary penicillate conidiophores. *Stipe* septate, hyaline, smooth, arising from tightly arranged pale to medium brown pseudoparenchymatous cells in a basal stroma, 40–150 × 4–5 µm. *Conidiogenous apparatus* 30–40 µm long, 40–50 µm wide; branches hyaline, smooth, 1–2-septate; primary branches subcylindrical to more swollen and doliiform to ellipsoid, 10–15 × 5–10 µm; additional branches (up to 2), 10–15 × 5–7 µm; terminal branches producing 1–6 phialides. *Phialides* elongate doliiform to reniform or subcylindrical, straight to slightly curved, aseptate, 10–20 × 3–4 µm; apex with minute periclinal thickening and inconspicuous collarette. *Conidia* cylindrical, rounded at both ends, straight, hyaline, (31–)35–38(–43) × 3(–3.5) µm, 1-septate, lacking a visible abscission scar, held in parallel clusters by colourless slime. *Chlamydospores* globose, 15–25 µm wide, thick-walled, red-brown, forming microsclerotia.

Culture characteristics — Colonies reaching 50 mm diam after 2 wk at 22 °C. On MEA spreading, with sparse aerial mycelium and smooth, even margins; surface with concentric circles of orange and ochreous, reverse apricot. On OA orange. On PDA surface and reverse orange, outer region amber.

Typus. CHINA, Beijing, Great Wall of China, N40°21'36.8" E116°00'52.2", on leaves of *Celtis bungeana* (*Ulmaceae*), 1 Sept. 2013, *P.W. Crous*, *M.J. Wingfield* & *Y. Zhang* (holotype CBS H-21716, culture ex-type CPC 23617 = CBS 138002; ITS sequence GenBank KJ869157, LSU sequence GenBank KJ869214, MycoBank MB808941).

Notes — The genus *Dematiocladium* was introduced to accommodate a cylindrocladium-like fungus growing on *Celtis tala* in Argentina, characterised by having pigmented setae (Crous et al. 2005). Due to its penicillate conidiophores and cylindrical, hyaline conidia, the genus *Dematiocladium* resembles *Calonectria* (= *Cylindrocladium*) (Lombard et al. 2010) and genera in the *Cylindrocarpon* complex (Chaverri et al. 2011, Cabral et al. 2012), but is distinct in that it has dematiaceous stipes dispersed among its conidiophores.

Although *D. celtidis* was collected from leaf litter of *Celtis tala* in Argentina, *D. celtidicola* was associated with leaf spots on living leaves of *Celtis bungeana* in China, suggesting that it could be a potential plant pathogen. Inoculation studies would be required, however, to prove this assumption.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Heliscus submersus* (GenBank HQ897796; Identities = 524/559 (94 %), Gaps = 13/559 (2 %)), *Glionectria tenuis* (GenBank EF495240; Identities = 519/556 (93 %), Gaps = 21/556 (3 %)) and *Gliocladiopsis sagariensis* (GenBank JQ666063; Identities = 505/541 (93 %), Gaps = 21/541 (3 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Dematiocladium celtidis* (GenBank AY793438; Identities = 869/876 (99 %), no gaps), *Gliocephalotrichum bulbilium* (GenBank JQ666076; Identities = 891/903 (99 %), no gaps) and *Neonectria ramulariae* (GenBank HM042435; Identities = 878/890 (99 %), no gaps).

Colour illustrations. Symptomatic *Celtis bungeana* next to the Great Wall, China; conidiophores, setae and conidia in culture. Scale bars = 10 µm.

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Beltrania pseudorhombica
& Chaetopsina beijingensis

Fungal Planet 260 & 261 – 10 June 2014

Beltrania pseudorhombica Crous & Y. Zhang ter, *sp. nov.*

Etymology. Named after this morphological similarity to *Beltrania rhombica.*

Setae erect, dark brown, thick-walled, indistinctly septate, straight to somewhat flexuous, tapering to an acute apex, up to 5-septate, 130–220 × 4–5 µm, with lobed basal cell, 10–12 µm diam. *Conidiophores* erect, unbranched, medium brown, smooth, 2–3-septate, 30–50 × 4–5 µm. *Conidiogenous cells* terminal, pale brown, smooth, polyblastic with several flat-tipped denticles, 1.5–2 µm. *Separating cells* pale brown, finely roughened, 7–12 × 5–6 µm, with several apical, flat-tipped denticles, 1 µm diam. *Conidia* solitary, biconic, pale brown, aseptate, with a distinct median transverse band of lighter pigment, (20–)22–25(–26) × (7–)8(–9) µm, apical appendage 7–11 × 1 µm, tapering to an acutely rounded tip.

Culture characteristics — Colonies reaching 70 mm diam after 2 wk at 22 °C. On MEA spreading, with fluffy aerial mycelium and lobate margins; surface and reverse dirty white. On OA surface iron-grey, outer region dirty white. On PDA surface and reverse dirty white.

Typus. China, Beijing, Fragrant Hill, N39°59'18.4" E116°11'25", on needles of *Pinus tabulaeformis* (*Pinaceae*), 1 Sept. 2013, *P.W. Crous & Y. Zhang* (holotype CBS H-21717, culture ex-type CPC 23656 = CBS 138003; ITS sequence GenBank KJ869158, LSU sequence GenBank KJ869215, MycoBank MB808942).

Notes — The genus *Beltrania* is characterised by having pigmented, unbranched setae, and basal conidiophores that give rise to conidiogenous cells that proliferate sympodially by means of short protruding denticles, giving rise to separating cells and conidia that are brown, biconic, with an equatorial band of lighter pigment, and a single apical appendage (Seifert et al. 2011). *Beltrania pseudorhombica* differs from *B. rhombica* in having longer setae and shorter, narrower conidia (setae 200–300 µm long, conidia 15–30 × 7–14 µm; Ellis 1971).

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Beltrania rhombica* (GenBank GU797390; Identities = 502/508 (99 %), Gaps = 3/508 (0 %)), *Beltrania querna* (GenBank GU905994; Identities = 487/494 (99 %), Gaps = 1/494 (0 %)) and *Menisporopsis theobromae* (GenBank GU905996; Identities = 471/488 (97 %), Gaps = 4/488 (0 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Parapleurotheciopsis inaequiseptata* (GenBank EU040235; Identities = 794/814 (98 %), Gaps = 2/814 (0 %)), *Pseudomassaria carolinensis* (GenBank DQ810233; Identities = 792/812 (98 %), Gaps = 1/812 (0 %)) and *Subramaniomyces fusisaprophyticus* (GenBank EU040241; Identities = 791/813 (97 %), Gaps = 1/813 (0 %)).

Chaetopsina beijingensis Crous & Y. Zhang ter, *sp. nov.*

Etymology. Named after the location where it was collected in China, Beijing.

Conidiophores erect, setiform, tapering towards acutely rounded apex, mostly flexuous, yellow-brown, turning red-brown in 3 % KOH, fertile in mid region, unbranched, verruculose, 200–350 × 8–13 µm, 12–16-septate, thick-walled (2 µm diam), base bulbous, up to 15 µm diam; fertile region consisting of irregularly branched, dense aggregated conidiogenous cells. *Conidiogenous cells* ampulliform to lageniform, hyaline, smooth, mono- to polyphialidic, 6–12(–20) × 3.5–5 µm. *Conidia* hyaline, smooth, guttulate, subcylindrical, aseptate, apex and base bluntly rounded, base rarely with flattened hilum, (11–)12–13(–14) × 2(–2.5) µm.

Culture characteristics — Colonies reaching 15 mm diam after 2 wk at 22 °C. On MEA spreading with sparse aerial mycelium; surface folded, margins smooth, even, umber. On OA salmon. On PDA umber in centre, dirty white in outer region.

Typus. China, Beijing, Fragrant Hill, N39°59'18.4" E116°11'25", on needles of *Pinus tabulaeformis* (*Pinaceae*), 1 Sept. 2013, *P.W. Crous & Y. Zhang* (holotype CBS H-21718, culture ex-type CPC 23629 = CBS 138004; ITS sequence GenBank KJ869159, LSU sequence GenBank KJ869216, MycoBank MB808943).

Notes — The genus *Chaetopsina* has nectria-like sexual morphs that are accommodated in *Chaetopsinectria* (Luo & Zhuang 2010). Several species have been reported from *Pinus* needles, the most common being *C. fulva* (conidia cylindrical, 8–12 × 1.5 µm; Kirk & Sutton 1985), while Crous et al. (2013b) also introduced *C. pini* (conidia (13–)15–16(–18) × 2(–2.5) µm) and *C. pinicola* (conidia (11–)13–15(–17) × 2(–2.5) µm) from Thailand. *Chaetopsina beijingensis* is similar to the two species described from Thailand, though it is distinguishable by having smaller conidia.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Chaetopsina fulva* (GenBank GU075861; Identities = 499/510 (98 %), no gaps), *Chaetopsina pinicola* (GenBank KF777145; Identities = 573/597 (96 %), Gaps = 8/597 (1 %)) and *Cosmospora chaetopsinae* (GenBank GU075858; Identities = 470/510 (92 %), Gaps = 16/510 (3 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Chaetopsina fulva* (GenBank GU075867; Identities = 786/786 (100 %), no gaps), *Chaetopsina pinicola* (GenBank KF777201; Identities = 775/786 (99 %), no gaps) and *Chaetopsina pini* (GenBank KF777200; Identities = 772/786 (98 %), no gaps).

Colour illustrations. *Pinus tabulaeformis* in China; setae, conidiophores and conidia of *Beltrania pseudorhombica* in culture (left column); conidiophores, setae and conidia of *Chaetopsina beijingensis* in culture (right column). Scale bars = 10 µm.

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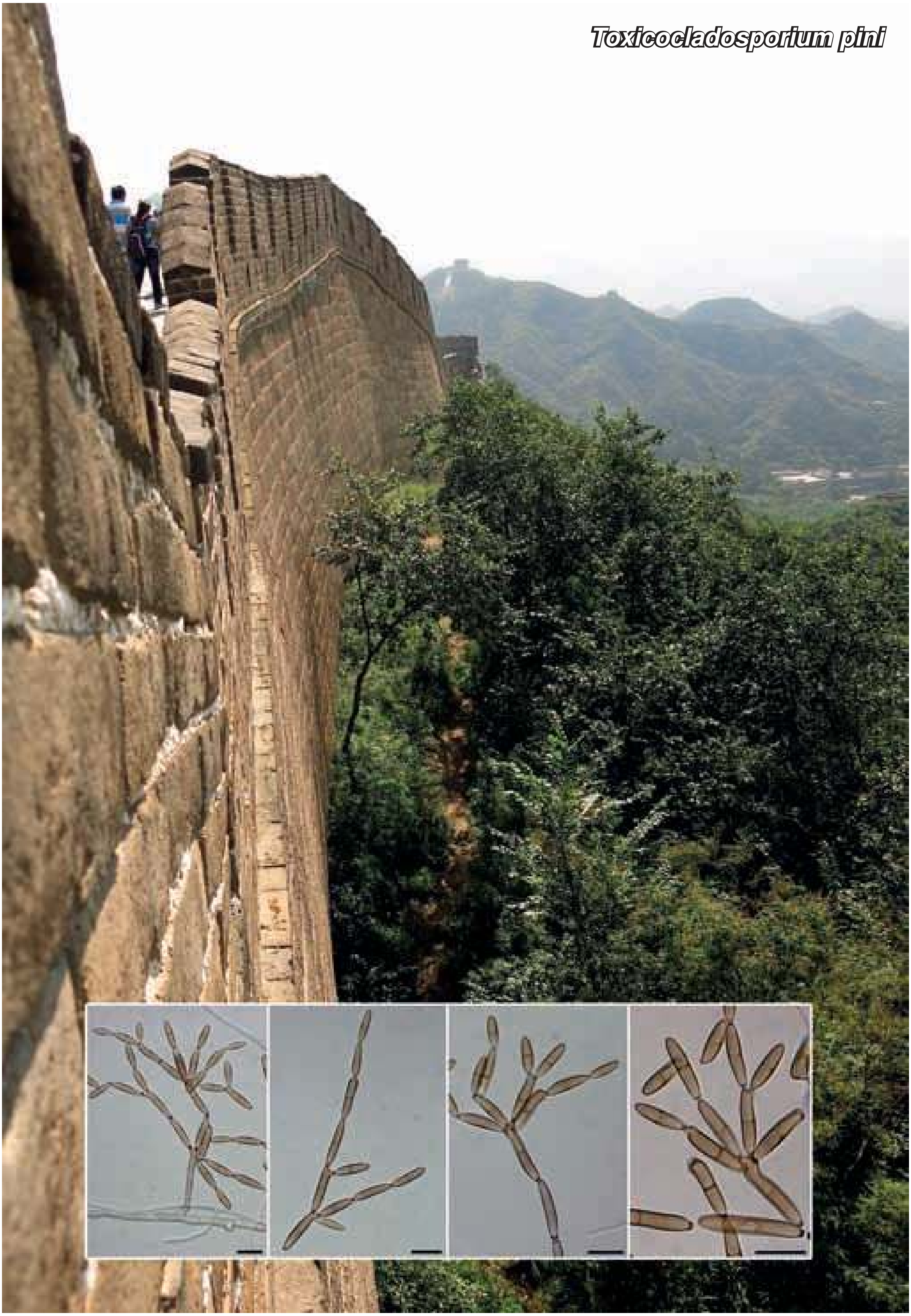
Toxicocladosporium pini



Fungal Planet 262 – 10 June 2014

Toxicocladosporium pini Crous & Y. Zhang ter, *sp. nov.*

Etymology. Named after the host from which it was collected, *Pinus*.

Mycelium consisting of smooth, hyaline, branched, septate, 1.5–2.5 µm diam hyphae. *Conidiophores* dimorphic. *Microconidiophores* erect, subcylindrical, straight to geniculate-sinuous, 10–17 × 3–4 µm. *Macroconidiophores* brown, erect, finely verruculose, straight to geniculate-sinuous, 2–8-septate, 30–90 × 3–4 µm. *Conidiogenous cells* integrated, terminal and lateral, 5–20 × 3–3.5 µm, subcylindrical, brown, finely verruculose; loci thickened and darkened, 1 µm diam. *Ramoconidia* subcylindrical, brown, finely verruculose, 0–1-septate, 12–17 × 3(–3.5) µm. *Intercalary conidia* brown, finely verruculose, 0–1-septate, fusoid-ellipsoid, 12–14 × 3 µm. *Terminal conidia* brown, finely verruculose, 0–1-septate, fusoid-ellipsoidal, 8–10(–11) × 2.5(–3) µm; loci thickened and darkened, 1 µm diam.

Culture characteristics — Colonies reaching 10 mm diam after 2 wk at 22 °C. On MEA surface erumpent, with sparse aerial mycelium and even, lobed margins. Surface and reverse olivaceous-grey, similar on OA and PDA.

Typus. China, Beijing, Badaling, N40°20'45.1" E116°00'48.3", on needles of *Pinus* sp. (*Pinaceae*), 1 Sept. 2013, *P.W. Crous & Y. Zhang* (holotype CBS H-21719, culture ex-type CPC 23639 = CBS 138005; ITS sequence GenBank KJ869160, LSU sequence GenBank KJ869217, MycoBank MB808944).

Colour illustrations. Scenic view from next to the Great Wall in China; conidiophores and conidia in culture. Scale bars = 10 µm.

Notes — The genus *Toxicocladosporium* was introduced for a cladosporium-like genus with dimorphic conidiophores, and conidia having hila that are slightly darkened, thickened and refractive (Crous et al. 2007b, Bensch et al. 2012). Phylogenetically, *T. pini* is most similar to *T. pseudoveloxum* (ramoconidia 0–1-septate, broadly ellipsoid to subcylindrical, 8–15 × 2.5–4 µm; intermediate and terminal conidia ellipsoid, (6–)7–10(–11) × (2–)2.5(–3) µm; Crous et al. 2011) and *T. protearum* (ramoconidia 0–1-septate, subcylindrical, 15–20 × 2.5–3.5 µm; intermediate and terminal conidia subcylindrical to narrowly fusoid-ellipsoidal, (9–)11–13(–16) × (2–)2.5(–3) µm; Crous et al. 2010). Although *T. pini* can be distinguished from *T. protearum* based on conidial dimensions, it is very similar to *T. pseudoveloxum* and can only be distinguished based on DNA data.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Toxicocladosporium pseudoveloxum* (GenBank JF499847; Identities = 572/580 (99 %), Gaps = 3/580 (0 %)), *Toxicocladosporium protearum* (GenBank HQ599586; Identities = 539/547 (99 %), Gaps = 2/547 (0 %)) and *Toxicocladosporium veloxum* (GenBank FJ790288; Identities = 516/524 (98 %), Gaps = 1/524 (0 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Toxicocladosporium pseudoveloxum* (GenBank JF499868; Identities = 878/878 (100 %), no gaps), *Toxicocladosporium chlamydosporum* (GenBank FJ790302; Identities = 875/875 (100 %), no gaps) and *Toxicocladosporium veloxum* (GenBank FJ790306; Identities = 874/875 (99 %), no gaps).

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Setophaeosphaeria hemerocallidis
& Setophaeosphaeria badalingensis

Fungal Planet 263 & 264 – 10 June 2014

Setophaeosphaeria Crous & Y. Zhang ter, *gen. nov.*

Etymology. Named after the presence of setae and its morphological similarity to the genus *Phaeosphaeria*.

Ascomata pseudothecial, immersed on leaves and stems, subepidermal with central ostiole, somewhat papillate, globose, somewhat dispersed, up to 200 µm diam; wall of 2–3 layers of brown *textura angularis*. *Asci* narrowly ellipsoid, bitunicate, 8-spored, 2–3-seriate, rostrate, short stipitate, apical chamber inconspicuous, straight to curved; intermingled among hyaline hyphal pseudoparaphyses. *Ascospores* pale brown, fusoid-ellipsoid, with mucoid caps at each end, guttulate, smooth, 5-septate, second cell from apex somewhat swollen. *Conidiomata* developing in culture, pycnidial, brown, globose, erumpent, with central, round to ellipsoid ostiole; wall of 2–3 layers of pale brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* ampulliform, hyaline, smooth; proliferating several times percurrently at apex. *Conidia* hyaline, smooth, subcylindrical, guttulate, aseptate, apex bluntly rounded, base truncate with marginal frill.

Type species. Setophaeosphaeria hemerocallidis.
MycoBank MB808945.

Setophaeosphaeria hemerocallidis Crous & Y. Zhang ter, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Hemerocallis*.

Ascomata pseudothecial, immersed on leaves and stems, subepidermal with central ostiole (20–30 µm diam), somewhat papillate, globose, somewhat dispersed, up to 200 µm diam; wall of 2–3 layers of brown *textura angularis*. *Asci* narrowly ellipsoid, bitunicate, 8-spored, 2–3-seriate, rostrate, short stipitate, apical chamber inconspicuous, straight to curved, 40–50 × 8–10 µm; intermingled among hyaline hyphal pseudoparaphyses, 1.5–2.5 µm diam. *Ascospores* pale brown, fusoid-ellipsoid, with mucoid caps (3 µm long) at each end, guttulate, smooth, 5-septate, second cell from apex somewhat swollen, (23–)24–25(–27) × 4(–4.5) µm. *Conidiomata* developing in culture, pycnidial, brown, globose, erumpent, up to 400 µm diam, with central, round to ellipsoid ostiole, 20–40 µm diam; wall of 2–3 layers of pale brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* ampulliform, hyaline, smooth, 8–15 × 3–5.5 µm; proliferating several times percurrently at apex. *Conidia* hyaline, smooth, subcylindrical, guttulate, aseptate, apex bluntly rounded, base truncate with marginal frill, (11–)13–16(–19) × (3–)3.5(–4) µm.

Culture characteristics — Colonies reaching 20 mm diam after 2 wk at 22 °C. On MEA colonies folded, with sparse aerial mycelium and smooth, even margin; surface pale olivaceous-grey, reverse olivaceous-grey. On OA olivaceous-grey. On PDA surface pale olivaceous-grey, with patches of olivaceous-grey, reverse olivaceous-grey.

Typus. CHINA, Beijing, Badaling, N40°20'45.1" E116°00'48.3", on leaf dieback of *Hemerocallis fulva* (*Hemerocallidaceae*), 1 Sept. 2013, *P.W. Crous & Y. Zhang* (holotype CBS H-21720, culture ex-type CPC 23645 = CBS 138006; ITS sequence GenBank KJ869161, LSU sequence GenBank KJ869218, MycoBank MB808946).

Notes — The genus *Phaeosphaeria* (typified by *P. oryzae*) was recently epitypified by Quaedvlieg et al. (2013), and shown to be the sexual morph of the genus *Phaeoseptoria* (based on *P. papaya*). *Setophaeosphaeria* is distinguished from *Phaeosphaeria* in that the latter lacks ascomatal setae and phoma-like asexual morphs. Phylogenetically, *S. hemerocallidis* is closely related to *Phaeosphaeria setosa*, which has a phoma-like asexual morph. The two species can be distinguished based on dimensions of their ascospores, those of *P. setosa* being smaller (4–5-septate, 18–22 × 5–5.5 µm; Leuchtmann 1984). A new combination is herewith also introduced in *Setophaeosphaeria* to accommodate *P. setosa*.

Setophaeosphaeria setosa (Leuchtm.) Crous, *comb. nov.*

Basionym. *Phaeosphaeria setosa* Leuchtm., Sydowia 37: 159. 1984.
MycoBank MB808947.

Setophaeosphaeria badalingensis Crous & Y. Zhang ter, *sp. nov.*

Etymology. Named after the location from where this species was collected, Beijing, Badaling.

Conidiomata immersed (on OA) to erumpent (on PNA), brown in surface view, but at higher magnification (1 000×) body pale brown, apex brown, globose, up to 250 µm diam with central ostiole and papillate neck; wall of 6–8 layers of *textura angularis*, pale brown on outside, becoming hyaline inwards. *Setae* brown, unbranched, flexuous, septate, covering conidioma, flexuous, smooth, with obtuse ends, up to 200 µm long, 2–2.5 µm wide. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, ampulliform, 4–7 × 3–4 µm; apex with prominent periclinal thickening. *Conidia* solitary, hyaline, smooth, guttulate, subcylindrical with obtuse ends, straight or gently curved, (5–)6(–7) × (2.5–)3 µm.

Culture characteristics — Colonies reaching 25 mm diam after 2 wk at 22 °C. On MEA spreading, with sparse aerial mycelium, surface folded, margins even, lobed, surface smoke-grey, reverse olivaceous-grey. On OA surface olivaceous-grey. On PDA surface and reverse olivaceous-grey.

Typus. CHINA, Beijing, Badaling, N40°20'45.1" E116°00'48.3", on leaf dieback of *Hemerocallis fulva* (*Hemerocallidaceae*), 1 Sept. 2013, *P.W. Crous & Y. Zhang* (holotype CBS H-21721, culture ex-type CPC 23643 = CBS 138007; ITS sequence GenBank KJ869162, LSU sequence GenBank KJ869219, MycoBank MB808948).

Notes — *Setophaeosphaeria badalingensis* is phylogenetically distinct from *S. setosa* and *S. hemerocallidis*, and also has smaller conidia than those observed in *S. hemerocallidis*, (11–)13–16(–19) × (3–)3.5(–4) µm.

Colour illustrations. *Hemerocallis fulva* at Badaling, China; ascomata, asci and ascospores of *Setophaeosphaeria hemerocallidis* in culture (left column); conidiomata, setae, conidiogenous cells and conidia of *S. badalingensis* in culture (right column). Scale bars = 10 µm.

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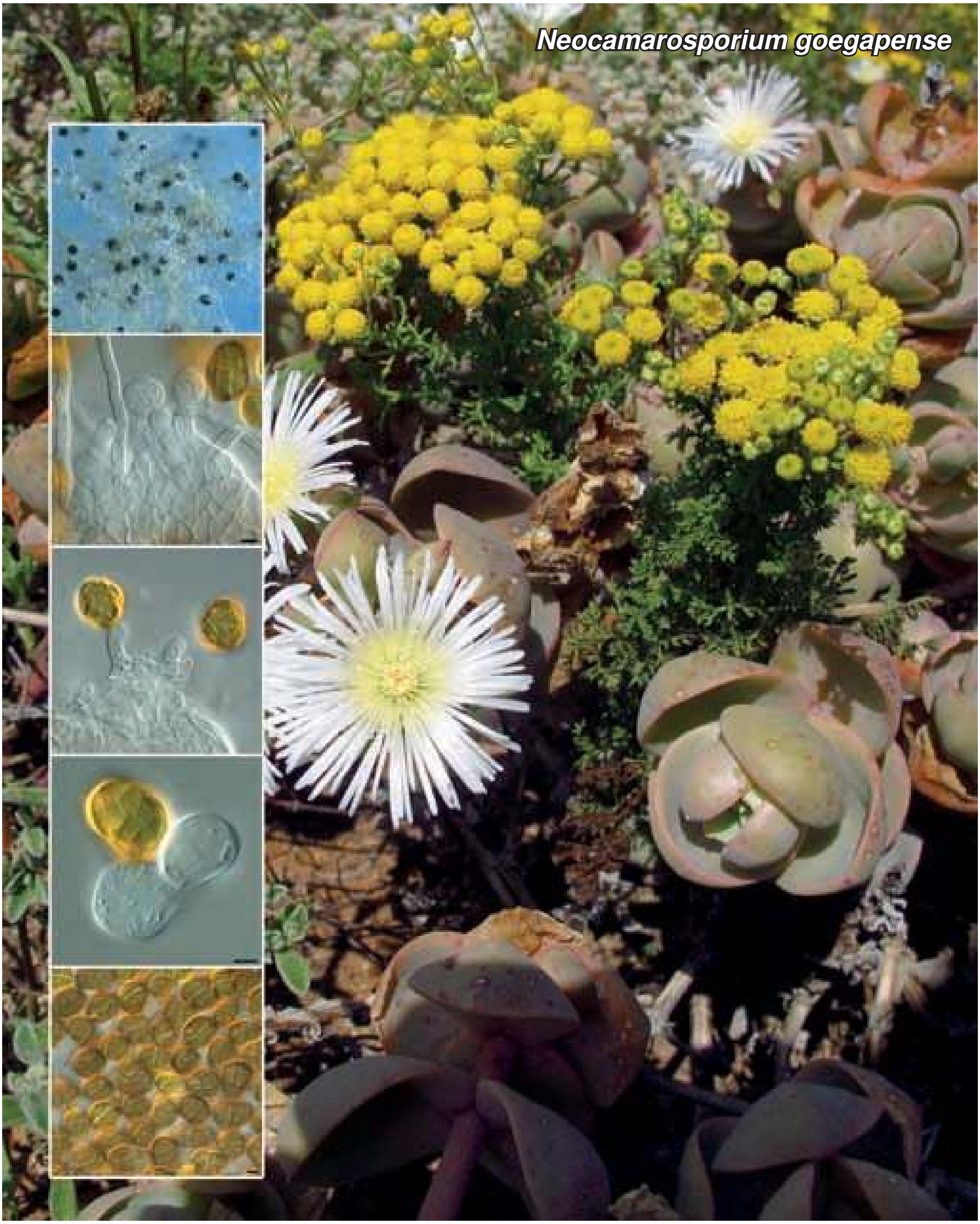
Neocamarosporium goegapense

Fungal Planet 265 – 10 June 2014

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

Etymology. Named after its morphological similarity to the genus *Camarosporium*.

Conidiomata brown to black, immersed, becoming erumpent, globose with papillate apex and central ostiole; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner layer of conidioma, separate, hyaline, smooth, ampulliform; proliferating several times percurrently near apex, or at the same level, giving rise to prominent periclinal thickening. *Conidia* solitary, initially hyaline, aseptate, thick-walled, developing a central septum and then becoming muriformly septate, shape variable from globose to obovoid to ellipsoid, golden brown, finely roughened, thick-walled.

Type species. Neocamarosporium goegapense.
MycoBank MB808949.

Neocamarosporium goegapense Crous & M.J. Wingf., *sp. nov.*

Etymology. Named after the Goegap Nature Reserve, where this fungus was collected.

Conidiomata brown to black, immersed, becoming erumpent, globose with papillate apex and central ostiole, up to 300 µm diam; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner layer of conidioma, separate, hyaline, smooth, ampulliform, 7–9 × 5–6 µm; proliferating several times percurrently near apex, or at the same level, giving rise to prominent periclinal thickening. *Conidia* solitary, initially hyaline, aseptate, thick-walled, developing a central septum and then becoming muriformly septate, shape variable from globose to obovoid to ellipsoid, golden brown, finely roughened, thick-walled, (15–)20–22(–24) × 15–17(–19) µm.

Culture characteristics — Colonies reaching 55 mm diam after 2 wk at 22 °C. On MEA flat, spreading, with sparse aerial mycelium and feathery margins. On MEA surface grey-olivaceous, reverse umber. On OA grey-olivaceous. On PDA grey-olivaceous with patches of citrine, reverse greenish black in middle, citrine in outer region.

Typus. South Africa, Northern Cape Province, Springbok, Goegap Nature Reserve, on dying leaves of *Mesembryanthemum* sp. (*Aizoaceae*), Sept. 2013, *M.J. Wingfield* (holotype CBS H-21722, culture ex-type CPC 23676 = CBS 138008; ITS sequence GenBank KJ869163, LSU sequence GenBank KJ869220, MycoBank MB808950).

Notes — The genus *Camarosporium* (based on *C. quaternatum*) presently contains several hundred species, and is accepted as in urgent need of revision. *Camarosporium* is characterised by having pycnidial conidiomata, conidiophores reduced to conidiogenous cells that are hyaline, and line the inner cavity, proliferating percurrently, giving rise to brown, smooth, muriformly septate conidia (Sutton 1980, Crous et al. 2006). A morphologically similar genus is *Camarosporellum*, though the latter appears to have holoblastic conidiogenesis. Phylogenetically, *Neocamarosporium* is allied to a clade containing taxa accommodated in *Phoma*, *Chaetosphaeronema* and *Pleospora*, and is thus morphologically quite distinct.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Phoma betae* (GenBank KC460811; Identities = 464/486 (95 %), Gaps = 2/486 (0 %)), *Ascochyta obiones* (GenBank GU230752; Identities = 471/496 (95 %), Gaps = 3/496 (0 %)) and *Phoma schachtii* (GenBank FJ427066; Identities = 419/447 (94 %), Gaps = 7/447 (1 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Phoma betae* (GenBank EU754179; Identities = 846/848 (99 %), Gaps = 1/848 (0 %)), *Chaetosphaeronema hispidulum* (GenBank EU754145; Identities = 845/847 (99 %), no gaps) and *Pleospora bjoerlingii* (GenBank AY849954; Identities = 805/807 (99 %), Gaps = 1/807 (0 %)).

Colour illustrations. Mesembryanthemum sp. growing in Goegap Nature Reserve, South Africa; conidiomata, conidiophores and conidia in culture. Scale bars = 10 µm.

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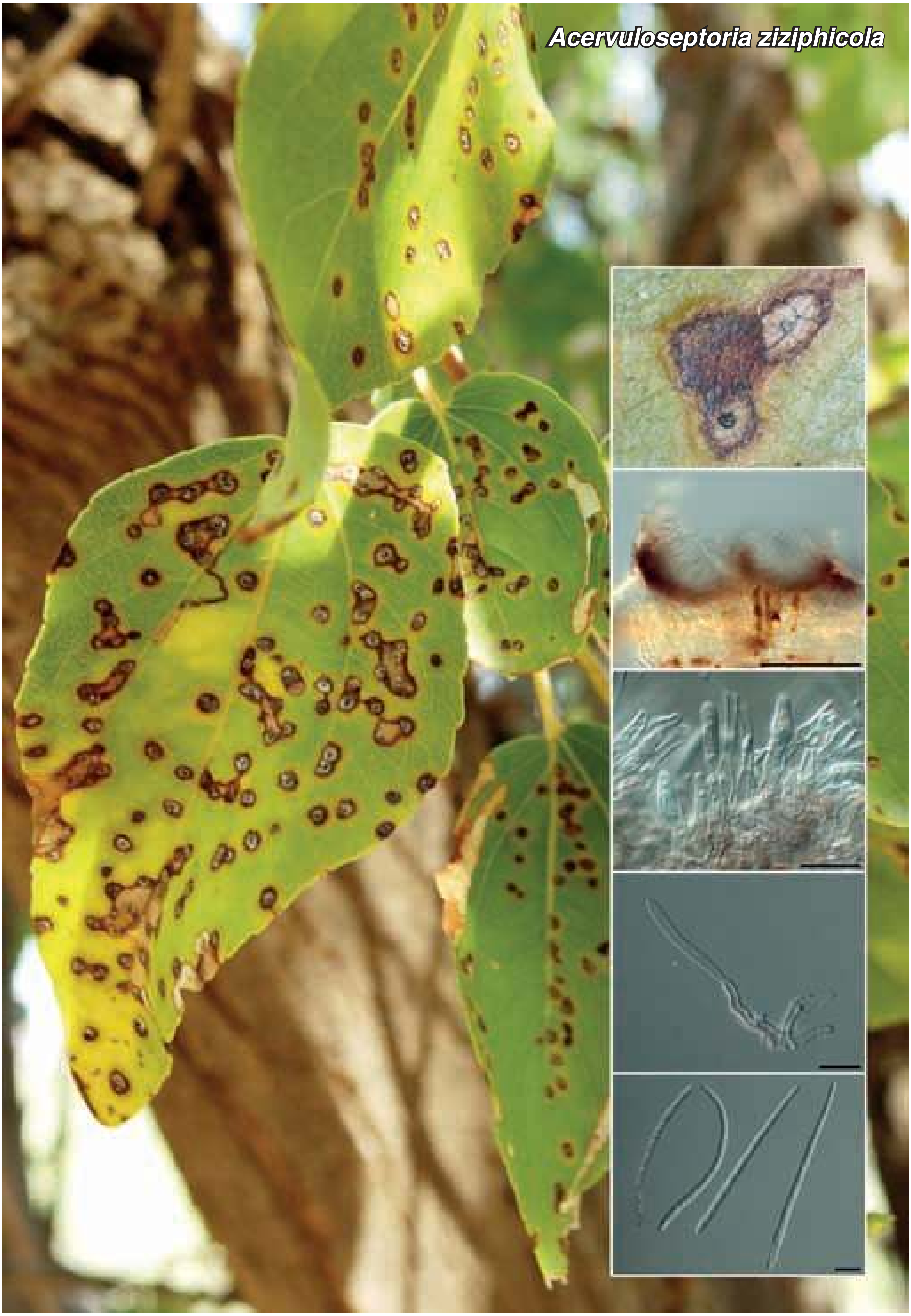
Acervuloseptoria ziziphicola

Fungal Planet 266 – 10 June 2014

Acervuloseptoria Crous & Jol. Roux, *gen. nov.*

Etymology. Named after its acervular-like conidiomata and its morphological similarity to the genus *Septoria*.

Plant pathogenic, foliicolous. *Conidiomata* black, amphigenous, exuding a creamy-white conidial cirrhus, subepidermal, erumpent, multilocular, with upper layer breaking open irregularly and leaving conidioma to have acervular appearance; wall of 3–6 layers of brown *textura angularis* to *textura intricata*, basal layers pale brown, roof of conidioma dark brown; in culture conidiomata acervular with elements of conidiomatal roof remaining like brown strands along the sides of conidioma. *Conidiophores* subcylindrical, straight to once geniculate, pale brown, verruculose, septate, branched or not. *Conidiogenous cells* terminal and lateral, subcylindrical, pale brown to subhyaline, verruculose to smooth, proliferating sympodially and percurrently. *Conidia* narrowly obclavate to subcylindrical, flexuous, guttulate, smooth, hyaline, apex subacutely rounded, base obconically truncate, septate.

Type species. Acervuloseptoria ziziphicola.
MycoBank MB808951.

Acervuloseptoria ziziphicola Crous & Jol. Roux, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Ziziphus*.

Leaf spots amphigenous, subcircular, 2 mm diam, grey-brown in middle with raised red-brown border and diffuse chlarotic margin. *Conidiomata* black, amphigenous, exuding a creamy-white conidial cirrhus, subepidermal, erumpent, up to 500 µm diam, up to 100 µm high, multilocular, with upper layer breaking open irregularly and leaving conidioma to have acervular appearance; wall of 3–6 layers of brown *textura angularis* to *textura intricata*, basal layers pale brown, roof of conidioma dark brown; in culture conidiomata acervular with elements of conidiomatal roof remaining like brown strands along the sides of conidioma. *Conidiophores* subcylindrical, straight to once geniculate, pale brown, verruculose, 1–3-septate, branched or not, 15–40 × 3–4 µm. *Conidiogenous cells* terminal and lateral, subcylindrical, pale brown to subhyaline, verruculose to smooth, proliferating sympodially and percurrently, 8–12 × 3–4 µm. *Conidia* narrowly obclavate (frequently subcylindrical in culture), flexuous, guttulate, smooth, hyaline, apex subacutely rounded, base obconically truncate, (40–)55–75(–80) × 3(–4) µm, 3(–5)-septate.

Culture characteristics — Colonies reaching 5 mm diam after 2 wk at 22 °C. On MEA surface flat, spreading with even margins, lacking aerial mycelium; surface salmon, reverse umber. On OA surface umber. On PDA surface salmon with patches of umber, reverse similar.

Typus. South Africa, Northern Cape Province, Richtersveld, Potjiespram, associated with leaf spots of *Ziziphus mucronata* (*Rhamnaceae*), Sept. 2013, *J. Roux* (holotype CBS H-21723, culture ex-type CPC 23707 = CBS 138009; ITS sequence GenBank KJ869164, LSU sequence GenBank KJ869221, MycoBank MB808952).

Colour illustrations. Ziziphus mucronata in South Africa; leaf spot, conidiomata, conidiophores and conidia in culture. Scale bars = 10 µm.

Notes — Two species of *Septoria* have been described from *Zizyphus*, namely *S. zyzyphi* (conidia 15 × 1 µm, Michelia 1: 173. 1878) and *S. capensis* (conidia 30–50 × 2–2.5 µm, Hedwigia 24: 33. 1885). Both species differ from the present collection, however, in their conidium dimensions.

The genus *Septoria* and allied genera were recently treated by Quaedvlieg et al. (2013). *Acervuloseptoria* differs from these genera in that it has peculiar conidiomatal morphology, with black, erumpent conidiomata, from which the top layer disintegrates, leaving a conidiomatal body that appears acervular. The conidiophores are also somewhat different in that they are slightly pigmented and verruculose in their lower part. Phylogenetically, *Acervuloseptoria* also appears distinct from those genera presently known in this generic complex (Quaedvlieg et al. 2013, Verkley et al. 2013).

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Cercosporella virgaureae* (GenBank GU214658; Identities = 506/537 (94 %), Gaps = 11/537 (2 %)), *Mycosphaerella areola* (GenBank DQ459084; Identities = 501/532 (94 %), Gaps = 9/532 (1 %)) and *Septoria protearum* (GenBank KF251235; Identities = 484/525 (92 %), Gaps = 20/525 (3 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Cercosporella virgaureae* (GenBank GU214658; Identities = 844/855 (99 %), no gaps), *Caryophylloseptoria lychnidis* (GenBank KF251791; Identities = 800/812 (99 %), no gaps) and *Septoria dysentericae* (GenBank GU253866; Identities = 840/855 (98 %), no gaps).

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Pseudocercospora neriicola

Fungal Planet 267 – 10 June 2014

Pseudocercospora neriicola Crous, Frisullo & Camele, *sp. nov.*

Etymology. Named after the host genus on which it was collected from, *Nerium.*

Leaf spots amphigenous, subcircular, coalescing, medium brown, frequently with grey-brown central zone associated with sporulating fascicles, 5–25 mm diam, or associated with tip blight. *Conidiomata* sporodochial, amphigenous, olivaceous-grey on leaves, up to 200 µm diam, with a well-developed brown stroma up to 180 µm diam. *Conidiophores* brown, finely verruculose, subcylindrical, erect to gently curved, reduced to conidiogenous cells, or 1-septate, 10–30 × 4–7 µm. *Conidiogenous cells* terminal, brown, smooth to finely verruculose at base, 10–20 × 4–5 µm, proliferating sympodially at apex; scars truncate, not thickening nor darkened. *Conidia* solitary, medium brown, guttulate, smooth, subcylindrical to narrowly obclavate, apex obtuse, base obconically truncate, not thickened, nor darkened, straight to curved, undergoing microcyclic conidiation, (25–)50–60(–80) × 3(–3.5) µm, (3–)5–7(–10)-septate. *Spermatogonia* intermingled among conidiomata. Spermatia hyaline, smooth, rod-shaped, 4–5 × 1 µm.

Culture characteristics — Colonies reaching 10 mm diam after 2 wk at 22 °C. On MEA surface erumpent, folded, margins lobed, smooth, with moderate aerial mycelium, pale olivaceous-grey, reverse iron-grey. On OA surface pale olivaceous-grey. On PDA surface pale olivaceous-grey, reverse iron-grey.

Typus. ITALY, Lecce, on leaves of *Nerium oleander* (*Apocynaceae*), 16 Oct. 2013, *I. Camele* (holotype CBS H-21724, culture ex-type CPC 23765 = CBS 138010; ITS sequence GenBank KJ869165, LSU sequence GenBank KJ869222, ACT sequence GenBank KJ869231, TEF sequence GenBank KJ869240, MycoBank MB808953).

Notes — Of the *Pseudocercospora* species known to occur on *Nerium*, conidia of *P. neriicola* are larger and have more septa than that of *P. neriella* (conidia subcylindrical, 15–50 × 3–5(–6) µm, 0–4(–5)-septate) but smaller than conidia of *P. kurimensis* (conidia narrowly obclavate, 20–115 × 2–5 µm, 3–11-septate). *Pseudocercospora kurimensis* also has superficial mycelium and hypophyllous fascicles (Braun 1996).

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Pseudocercospora abelmoschi* (GenBank EF535719; Identities = 504/504 (100 %), no gaps), *Pseudocercospora eriobotryae* (GenBank JN662323; Identities = 507/508 (99 %), Gaps = 1/508 (0 %)) and *Pseudocercospora cruenta* (GenBank GU269689; Identities = 499/500 (99 %), Gaps = 1/500 (0 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Pseudocercospora timorensis* (GenBank KC677937; Identities = 841/841 (100 %), no gaps), *Pseudocercospora eupatorii-formosanae* (GenBank KC677930; Identities = 841/841 (100 %), no gaps) and *Pseudocercospora oenotherae* (GenBank JQ 324961; Identities = 841/841 (100 %), no gaps).

ACT. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ACT sequence are *Pseudocercospora madagascariensis* (GenBank JX902140; Identities = 532/537 (99 %), no gaps), *Pseudocercospora cercidis-chinensis* (GenBank JX902131; Identities = 530/537 (99 %), no gaps) and *Pseudocercospora cruenta* (GenBank JQ325012; Identities = 589/597 (99 %), no gaps).

TEF. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the TEF sequence are *Pseudocercospora prunicola* (GenBank GU384393; Identities = 297/305 (97 %), no gaps), *Pseudocercospora corylopsidis* (GenBank GU384437; Identities = 296/305 (97 %), no gaps) and *Pseudocercospora guianensis* (GenBank GU384436; Identities = 295/305 (97 %), no gaps).

Colour illustrations. Symptomatic *Nerium oleander* in Italy; leaf spot, fascicles, conidiophores and conidia in vivo. Scale bar = 10 µm.

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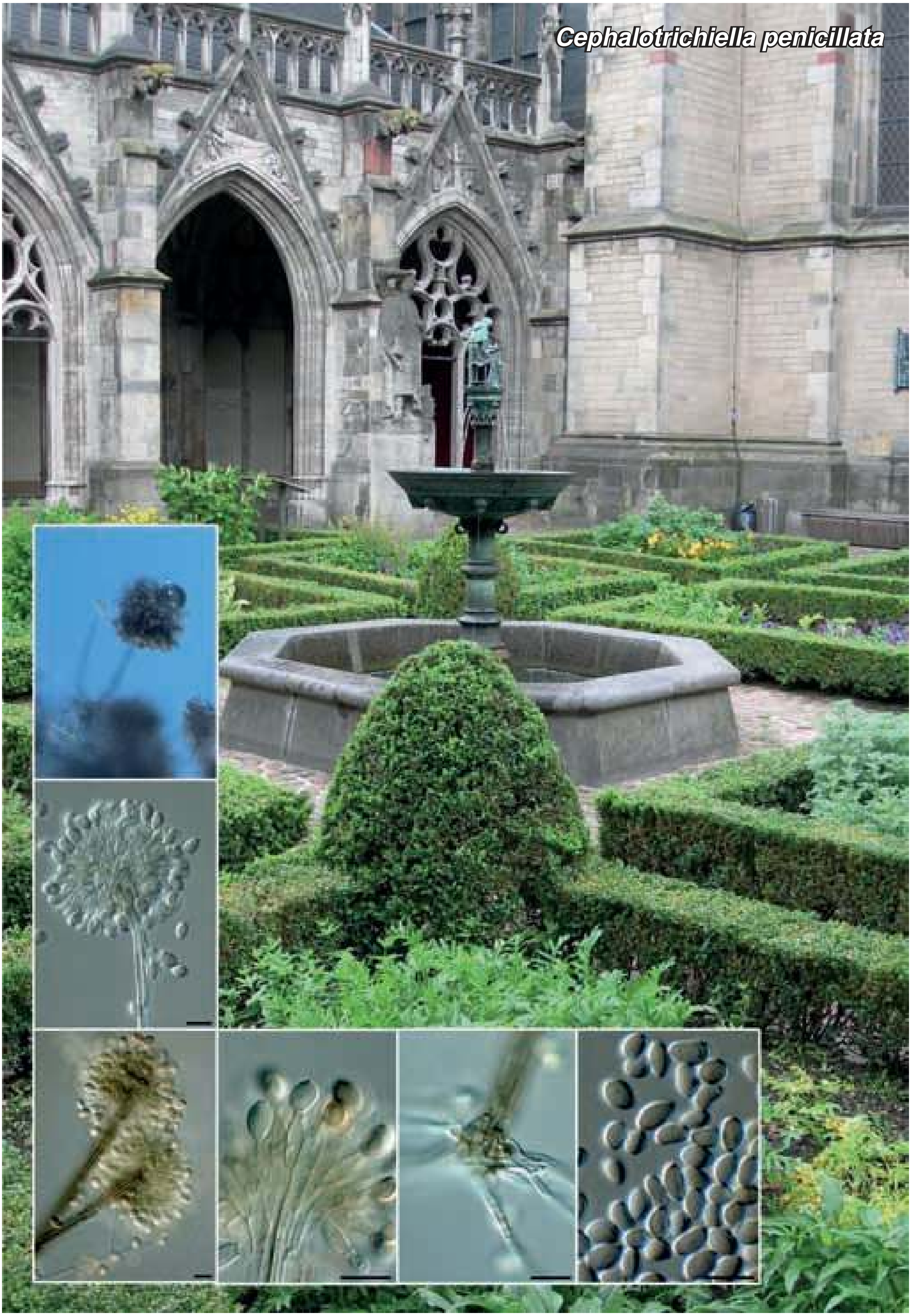
Cephalotrichiella penicillata

Fungal Planet 268 – 10 June 2014

Cephalotrichiella Crous, *gen. nov.*

Etymology. Named after its morphological similarity to the genus *Cephalotrichum*.

Mycelium consisting of pale brown, smooth, branched, septate hyphae. *Conidiophores* erect, olivaceous-brown, synnematous, consisting of up to 20 hyphae, olivaceous-brown, smooth; conidiophore base with rhizoids, stem straight, erect to flexuous, with penicillate conidiogenous apparatus. Primary branches olivaceous-brown, smooth, subcylindrical, giving rise to secondary and tertiary branches. *Conidiogenous cells* ampulliform, smooth, pale olivaceous, with inconspicuous percurrent proliferation at the apex. *Conidia* in a dry mass, solitary, olivaceous-brown, smooth to verruculose, guttulate, ellipsoid but with inequilateral sides, subacute apex, truncate base, not thickened nor darkened, with minute marginal frill.

Type species. Cephalotrichiella penicillata.
MycoBank MB808954.

Cephalotrichiella penicillata Crous, *sp. nov.*

Etymology. Named after its penicillate conidiophores.

Mycelium consisting of pale brown, smooth, branched, septate, 2–2.5 µm diam hyphae. *Conidiophores* erect, olivaceous-brown, synnematous, consisting of up to 20 hyphae, 2–2.5 µm diam, olivaceous-brown, smooth, septa 25–35 µm apart; conidiophore base with rhizoids, stem straight, erect to flexuous, 150–400 × 7–15 µm with penicillate conidiogenous apparatus. Primary branches olivaceous-brown, smooth, subcylindrical, 12–15 × 2.5–3.5 µm, giving rise to 1–2 secondary and tertiary branches, 5–7 × 3–4 µm; tertiary branches give rise to 2–4 conidiogenous cells. *Conidiogenous cells* ampulliform, smooth, pale olivaceous, 6–8 × 2.5–3.5 µm, with inconspicuous percurrent proliferation at the apex. *Conidia* in a dry mass, solitary, olivaceous-brown, smooth to verruculose, guttulate, ellipsoid but with inequilateral sides, subacute apex, truncate base, 1.5–2 µm diam, with minute marginal frill, (5–)6–7(–8) × (3.5–)4(–4.5) µm.

Culture characteristics — Colonies reaching 12 mm diam after 2 wk at 22 °C, spreading with sparse aerial mycelium and lobed, feathery margins. On MEA surface pale olivaceous-grey, reverse olivaceous-grey. On OA and PDA surface olivaceous-grey.

Typus. Netherlands, Utrecht, isolated from air, Dec. 2013, *P.W. Crous* (holotype CBS H-21725, culture ex-type CPC 23865 = CBS 138011; ITS sequence GenBank KJ869166, LSU sequence GenBank KJ869223, MycoBank MB808955).

Notes — Morphologically, *Cephalotrichiella* resembles the genus *Graphium* in having pigmented, synnematous conidiophores and pigmented conidia. It is somewhat different in that the conidiophores are much taller, more similar to *Leptographium*, and conidia are inequilateral. The conidiophores of *Ceratocladiella* have dry conidial masses, resembling those of *Cephalotrichum* (incl. *Doratomyces*) (Seifert et al. 2011). It is distinct from *Cephalotrichum*, however, in that it has a well-defined penicillate head of conidiogenous cells, in contrast to *Cephalotrichum*, which also has lateral conidiogenous cells. Phylogenetically, *Cephalotrichiella* is allied to the genera in the *Microascales*, but still clusters distant, hence we introduce a new genus to accommodate it.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Scedosporium prolificans* (GenBank AY228124; Identities = 370/418 (89 %), Gaps = 15/418 (3 %)), *Kernia pachypleura* (GenBank DQ318208; Identities = 580/694 (84 %), Gaps = 52/694 (7 %)) and *Pseudallescheria boydii* (GenBank GU566282; Identities = 544/653 (83 %), Gaps = 45/653 (6 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Graphium eumorphum* (GenBank JF746156; Identities = 843/873 (97 %), Gaps = 5/873 (0 %)), *Pseudallescheria boydii* (GenBank AY882372; Identities = 836/866 (97 %), Gaps = 5/866 (0 %)) and *Scedosporium apiospermum* (GenBank FJ345358; Identities = 848/879 (96 %), Gaps = 5/879 (0 %)).

Colour illustrations. Inner garden next to the Dom tower in Utrecht, The Netherlands; synnematous conidiophores, conidiogenous cells, conidiophores with rhizoids and conidia in culture. Scale bars = 10 µm.

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Septoriella oudemansii

Fungal Planet 269 – 10 June 2014

Septoriella oudemansii Crous & Quaedvlieg, *sp. nov.*

Etymology. Named after Cornelius Anton Jan Abraham Oudemans, who established the genus *Septoriella* in 1889, based on a specimen collected from *Phragmites*.

Conidiomata up to 250 µm diam, separate, immersed, globose, brown, with central ostiole, oozing a brown conidial cirrhus; wall of 3–4 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, ampulliform, 5–11 × 4–5 µm; apex with minute periclinal thickening or percurrent proliferation. *Conidia* solitary, subcylindrical, yellow-brown with obtuse ends, becoming slightly constricted at septa with age, and then slightly wider in the middle, smooth, 3(–5)-septate, guttulate, with flared mucoid appendages at ends (best visible in water mounts), up to 3 µm long, (17–)23–32(–35) × (3.5–)4(–6) µm.

Culture characteristics — Colonies reaching 40 mm diam after 2 wk at 22 °C. On MEA erumpent, spreading, with moderate aerial mycelium and lobate, feathery margins. On MEA surface dirty white, reverse umber. On OA surface pale olivaceous-grey in centre, dirty white in outer region. On PDA surface pale olivaceous grey, reverse olivaceous-grey.

Typus. Netherlands, Veenendaal, leaves of *Phragmites australis* (*Poaceae*), 24 Jan. 2014, *W. Quaedvlieg* (holotype CBS H-21726, culture ex-type CPC 24116 = CBS 138012; LSU sequence GenBank KJ869224, MycoBank MB808956).

Notes — The genus *Septoriella* is based on *S. phragmitis*, collected from *Phragmites* in the Netherlands. It is characterised by having immersed, brown pycnidial conidiomata, hyaline, percurrently proliferating conidiogenous cells, and filiform, fusiform to subcylindrical, brown, septate conidia with mucoid caps (Nag Raj 1993). Two species are known from *Phragmites*, namely *S. phragmitis* (conidia (3–)5(–7)-septate, 49–90 × 2–3 µm) and *S. phragmiticola* (nom. nud., from *Phragmites* in Taiwan; Nag Raj 1993). *Septoriella oudemansii* is distinguished from *S. phragmitis* by having shorter, wider, subcylindrical, 3-septate conidia.

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Phaeosphaeria caricis* (GenBank GU301860; Identities = 822/823 (99 %), no gaps), *Phaeosphaeria ammophilae* (GenBank KF766314; Identities = 845/847 (99 %), no gaps) and *Ophiosphaerella herpotricha* (GenBank DQ767656; Identities = 845/847 (99 %), no gaps).

Colour illustrations. Phragmites australis in Veenendaal, The Netherlands; conidiomata, conidiogenous cells and conidia in culture. Scale bars = 10 µm.

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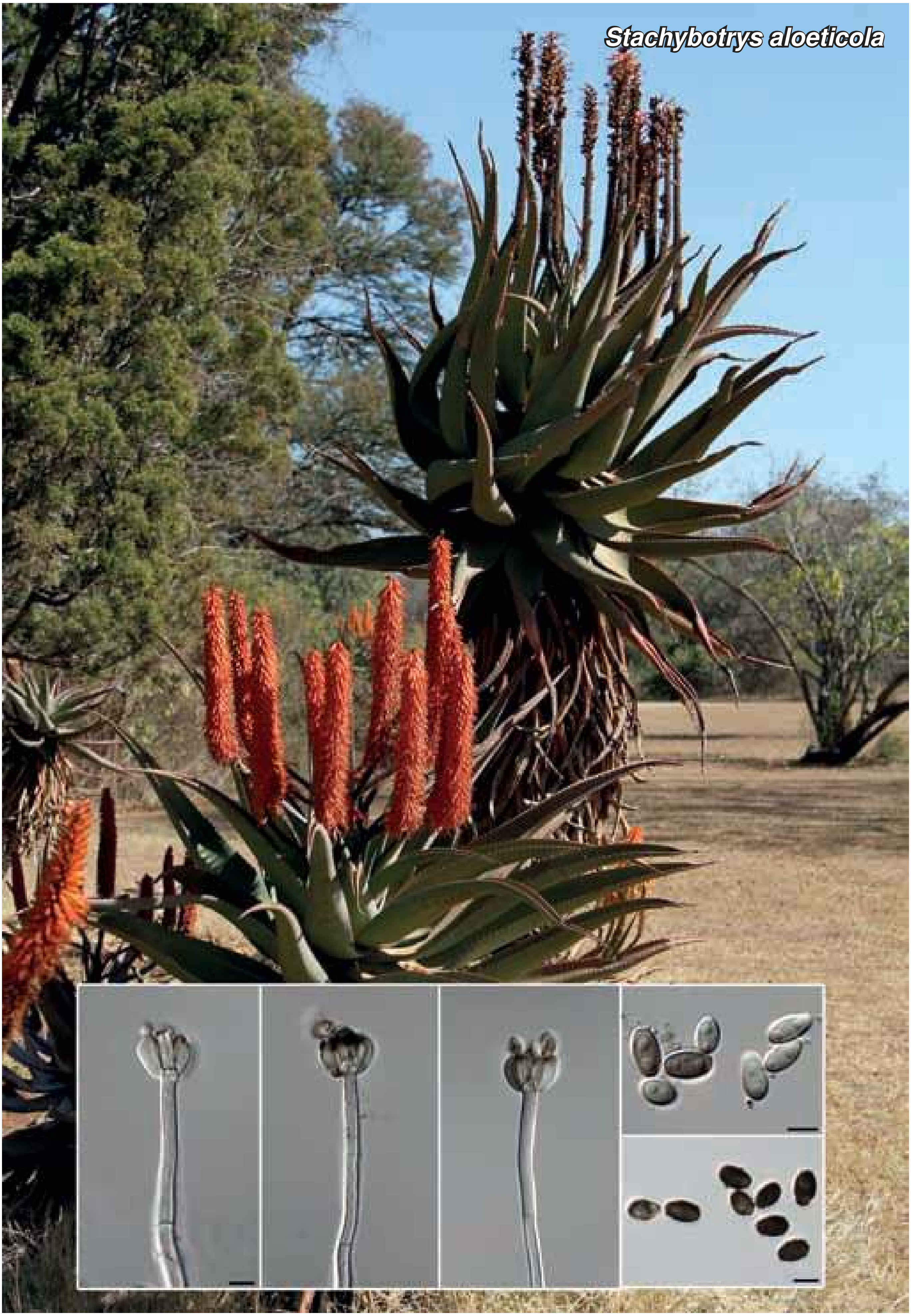
Stachybotrys aloeticola

Fungal Planet 270 – 10 June 2014

Stachybotriaceae L. Lombard & Crous, *fam. nov.*

MycoBank MB808764.

Saprobic or pathogenic on plant material, commonly isolated from soil. *Ascomata* solitary, scattered or aggregated in small groups, superficial or totally immersed in host tissue, bright to dark yellow to orange, not changing colour in KOH, globose to subglobose to obpyriform, ostiolate. *Ascomatal wall* thick, consisting of 1–2 layers, sometimes covered with intertwined hyphae. *Asci* clavate to cylindrical, containing 4–8 biseriate ascospores, apex rounded to nearly truncate with a refractive apical ring. *Ascospores* ellipsoidal to fusiform to broadly reniform, 1–3-septate sometimes constricted at septum, hyaline. *Conidiophores* simple, sporodochial or synnematous. Simple conidiophore macronematous, mononematous, solitary or in groups, erect, slightly curved, simple or irregularly branched, 1–4-septate, smooth, hyaline, bearing 2–8, slightly curved or erect, clavate to broadly reniform phialides with conspicuous collarettes. Sporodochial and synnematous conidiophores scattered, amphigenous, pulvinate, gelatinous, hyaline to dark green, with or without marginal hyphae, with or without hyaline setae, containing irregularly penicillate, bi- or terverticillately branched conidiogenous apparatus. *Conidiogenous cells* cylindrical, proliferating percurrently. *Conidia* 0–1-septate, elongated, cylindrical, subcylindrical, fusiform or ellipsoid, hyaline becoming darker with age, smooth, striate or roughened, aggregated in a slimy, dark green to black mass.

Type genus. *Stachybotrys* Corda, Icon. Fung. 1: 21. 1837. MycoBank MB10052.

Type species. *Stachybotrys chartarum* (Ehrenb.) S. Hughes, Canad. J. Bot. 36: 812. 1958. MycoBank MB306362.

Other genera included

Myrothecium Tode, Fung. Meckl. Sel. 1: 25. 1790 — MycoBank MB9049

Type species. *Myrothecium inundatum* Tode, Fung. Meckl. Sel. 1: 25. 1790. MycoBank MB234957.

Peethamabra Subram. & Bhat, Rev. Mycol. 42: 52. 1978. — MycoBank MB3786

Type species. *Peethambara sundara* Subram. & Bhat, Rev. Mycol. 42: 49. 1978. MycoBank MB319247.

Notes — The family *Stachybotriaceae* is established to accommodate the genera *Myrothecium*, *Peethambara* and *Stachybotrys*. These three genera were earlier classified as *incertae sedis* in the order *Hypocreales*, although phylogenetic studies have shown that these genera form a monophyletic lineage distinct from other families in the *Hypocreales* (Castlebury et al. 2004, Summerbell et al. 2011). Castlebury et al. (2004) refrained from introducing this new family, arguing that more sexual morphs in these genera were required to justify a formal description. Since the abolishment of dual nomenclature for fungi (Hawksworth et al. 2011), the asexual and sexual morphs are regarded as equal, with priority given to the older name (Rossman et al. 2013), and therefore we introduce *Stachybotriaceae* as a new family in the order *Hypocreales*.

Stachybotrys aloeticola L. Lombard & Crous, *sp. nov.*

Etymology. Named after the host genus from which it was isolated, *Aloe*.

Conidiophores simple, macronematous, mononematous, single or in groups, mostly unbranched, erect, straight to slightly flexuous, 1–3-septate, smooth, hyaline, 72–143 × 3–5 µm, bearing a whorl of 3–5 phialides. *Phialides* terminal, clavate to broadly reniform, hyaline becoming pale brown, 8–11 × 4–6 µm, smooth with conspicuous collarettes. *Conidia* acrogenous, aggregated in slimy masses, aseptate, allantoid to fusiform, 7–9 × 3–5 µm (av. 8 × 4 µm), containing 1–2 oil droplets.

Culture characteristics — Colonies reached 30 mm diam after 7 d at 22 °C. On PDA superficial, partly immersed, white becoming granulate and dark in the centre as conidia are formed.

Typus. South Africa, Eastern Cape Province, Grahamstown, on *Aloe* sp. (*Aloaceae*), 26 July 2011, *P.W. Crous* (holotype CBS H-21727, culture ex-type CBS 137940 = CPC 19705; ITS sequence GenBank KJ817888, LSU sequence GenBank KJ817890, BTUB = KJ817886, MycoBank MB808881); CPC 19706 = CBS 137941, ITS = KJ817889, LSU = KJ817891, BTUB = KJ817887.

Notes — *Stachybotrys* species are saprobes, commonly isolated from soil and decaying plant material, and are also associated with health risks in buildings with long-term water damage (Castlebury et al. 2004). *Stachybotrys aloeticola* is commonly isolated from dying leaves of *Aloe* spp. in South Africa (unpubl. data) and is thus far only known to occur on this host genus. Morphologically, it is similar to *S. nephrospora* (Hansford 1943) but can be distinguished from this species by having longer conidiophores (up to 143 µm) compared to *S. nephrospora* (up to 130 µm). Furthermore, *S. aloeticola* produces smaller conidia (7–9 × 3–5 µm (av. 8 × 4 µm)) than reported for *S. nephrospora* (8–11 × 4.5–6 µm; Hansford 1943).

Based on megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS (GenBank KJ817888) sequence are *S. nephrospora* (GenBank AF081476; Identities = 633/642 (99 %), Gaps = 4/642 (0 %)) and *S. microspora* (GenBank AF081475; Identities = 591/646 (91 %), Gaps = 10/646 (1 %)). Closest hits using LSU (GenBank KJ817890) sequences are *Didymostilbe matsushimae* (GenBank AY283545; Identities = 810/836 (97 %), Gaps = 6/836 (0 %)), *Melanopsamma pomiformis* (GenBank AY489709; Identities = 810/836 (97 %), Gaps = 7/836 (0 %)) and *Stachybotrys echinata* (GenBank AY489736; Identities = 806/834 (97 %), Gaps = 5/834 (0 %)). Closest hit using β-tubulin (GenBank KJ817886) sequences are *Cylindrocladiella infestans* (GenBank JN098762; Identities = 319/367 (87 %), Gaps = 14/367 (3 %)) and *Cylindrocladiella variabilis* (GenBank JN098722; Identities = 319/367 (87 %), Gaps = 16/367 (3 %)).

Colour illustrations. *Aloe* sp., South Africa; conidiophores and conidia in culture. Scale bars = 10 µm.

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Conioscypha minutispora
a
b
a'
b'
c'

Fungal Planet 271 – 10 June 2014

Conioscypha minutispora Hern.-Restr., Gené & Guarro, *sp. nov.*

Etymology. Name refers to the conidia that are smaller than those of the other species presently known.

Description based on substratum in vivo. *Colonies* effuse, black. *Mycelium* immersed, composed of branched, septate, smooth, hyaline, 1–2 µm wide hypha. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* cuneiform, percurrent, smooth, hyaline, 7–10 × 4–5 µm, with a cup-like collarette up to 4 µm wide at the apex. *Conidia* unicellular, ellipsoidal, obovoid or subglobose, 6–9 × 5–6 µm, apex rounded, base truncate with a central pore of 1 µm diam, dark brown and smooth.

Culture characteristics — Colonies on potato carrot agar reaching 15 mm diam after 4 wk at 25 °C, powdery, olive-brown (4F8) with zones of white mycelium; reverse sallow (4D3) (Kornerup & Wanscher 1984). Sporulation abundant. Conidiogenous apparatus and conidia very similar to those observed on the natural substratum. *Conidia* 7–8 × 5–6 µm.

Typus. Spain, Cantabria, Ucieda, Saja-Besaya Natural Park, on unidentified dead wood, 27 Sept. 2010, coll. *M. Hernández-Restrepo*, *J. Mena & J. Guarro*, isol. M. Hernández-Restrepo (holotype CBS H-21464, cultures ex-type FMR 11245 = CBS 137253; ITS sequence GenBank KF924559, SSU sequence GenBank HF937347, LSU sequence GenBank KF924559, MycoBank MB807097).

Notes — The genus *Conioscypha* (*Sordariomycetes*) has a particularly mode of conidiogenesis characterised by the production of blastic conidia at inconspicuous loci along the hypha. After repeated basipetal succession, the remains of the outer wall of conidia accumulate to form collarettes (Shearer 1973, Goh & Hyde 1998, Réblová & Seifert 2004). Currently, the genus has eight species, which can be found on dead wood, bamboo and leaves (Shearer 1973, Chen & Tzean 2000, Réblová & Seifert 2004). *Conioscypha minutispora* differs from other members of the genus in that it has smaller and concolorous conidia. Based on its conidial shape, *C. minutispora* resembles *C. japonica*; however, in the latter species conidia have the pigment deposited irregularly at the periphery of the wall, giving the appearance of roughness (Udagawa & Toyazaki 1983).

A BLAST search based on the D1/D2 sequence of the isolate FMR 11245 showed that the closest species were *C. lignicola* (GenBank AY484513) with a similarity of 95 % and *C. varia* (GenBank AY484512) with a similarity of 89 %. However, both species can be easily differentiated from *C. minutispora* based on their conidial morphology. The conidia of *C. lignicola* are globose, oviform or pyriform and measure 15–17 × 12 µm, while those of *C. varia* differ in shape (ovoid, flammiform, naviculiform, subellipsoidal) and measure 8.4–15 × 5.6–8.5 µm (Shearer 1973).

Colour illustrations. Forest in the Saja-Besaya Natural Park where the sample was collected. Photo plate: a. Conidiogenous cells with conidia; b. conidia. Scale bars a, b = 5 µm. Line drawing: a’. Habit; b’. conidiogenous cell with dark conidia; c’. conidia. Scale bar b’–c’ = 5 µm.

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Diplogelasinospora moalensis

Fungal Planet 272 – 10 June 2014

Diplogelasinospora moalensis Dania García, Y. Marín & Cano, *sp. nov.*

Etymology. Named after woodland Moal, surrounding the village where the soil samples were collected.

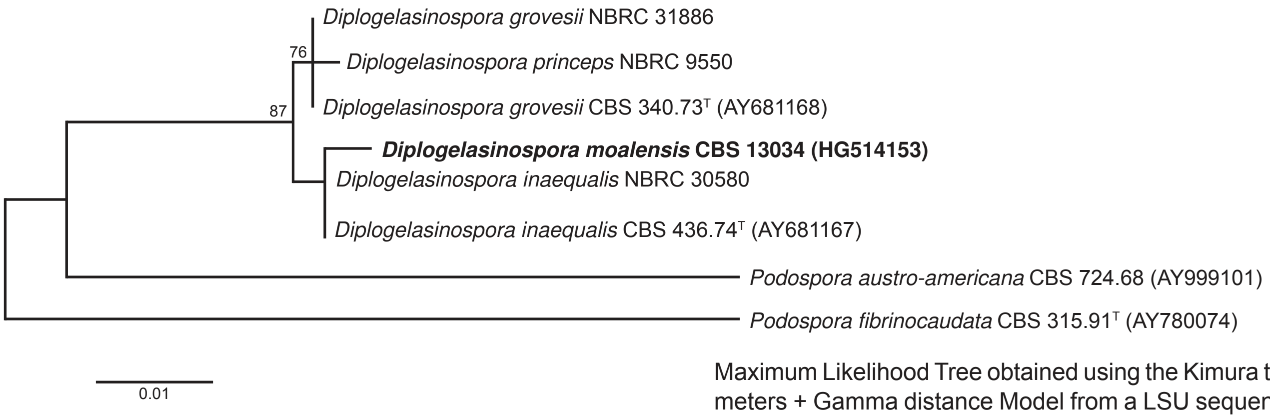
Mycelium consisting of branched, septate, smooth, 2–5 µm diam hyphae. *Ascomata* cleistothecial, superficial to immersed, scattered to grouped, at first yellowish brown, becoming black at maturity, 170–310 µm diam, hairy, covered by hyphae-like, setae. *Setae* flexuous, slightly rugose- and thick-walled, and yellowish brown to brown, up to 500 µm long, measuring 2–7 µm at base. *Peridium* membranaceous to slightly carbonaceous, brown to black and opaque, 3–4-layered, 2–5 µm thick, outer layer *textura intricata* composed of brown, thick-walled hypha-like cells which cover a second layer with *textura cephalothecoid* cells; inner layers hyaline, cells of *textura angularis*. *Asci* 8-spored, soon evanescent, lacking a distinct apical ring, at first cylindrical, becoming cylindrical-clavate, short stipitate, 150–180 × 14–22 µm. *Paraphyses* abundant, cylindrical to moniliform, septate and sometimes constricted at the septa, 3–13 µm diam. *Ascospores* at first aseptate and hyaline, irregularly uniseriate, ellipsoidal, becoming transversely septate without constriction at the septum, which is near the upper third of the ascospore; one cell becoming dark brown to black, whereas the other remaining hyaline or less frequently pale yellowish brown and usually collapsing at maturity. Ascospores (18–)20–27 µm in length, dark cell 16–19 × 15–18 µm; both cells showing ornamented walls with circular inwardly projecting pits showing an endodentate endosporium; germ pore inconspicuous, subapical to laterally disposed at dark cell, 1–2 µm diam.

Culture characteristics — Colonies on Czapek agar and oatmeal agar attaining 80 mm diam after 14 d at 25 °C; velvety to cottony olive-brown (4E8); reverse dark brown (8F4) (Kornerup & Wanscher 1984). Minimum and maximum temperature of growth: 10 and 45 °C, respectively. Production of initial ascomata were detected at 25, 30 and 35 °C after 14 d, mature ascomata were observed after 21 d at the same temperatures.

Typus. SPAIN, Principado de Asturia, Cangas del Narcea, Veiga de Rengos, Moal, 14 Aug. 2012, *G. Sisó-Boix & D. García* (holotype CBS H-21382, cultures ex-type FMR 13034 = CBS 136018; ITS sequence GenBank HG514152, LSU sequence GenBank HG514153, MycoBank MB804992).

Notes — The genus *Diplogelasinospora* was erected to accommodate *D. princeps* characterised by non-ostiolate ascomata and 2-cell ascospores with pitted walls (Udawaga & Horie 1972). Although the ex-type strain of *D. princeps* was isolated from flax seed, the other strains of this species had been isolated from soil, the same source where the other species of the genus were collected. Currently, the genus includes two other species, namely *D. grovesii* and *D. inaequalis* (Udagawa et al. 1973). The morphological characters used for species delimitation are the total length of the ascospores, the septum position and the ornamentation of the ascospore wall (Udawaga & Horie 1972, Udagawa et al. 1973). *Diplogelasinospora moalensis* has a septum in the upper third of the ascospores, as observed in *D. inaequalis*; however, the latter has smaller ascospores (up to 22 µm) and the ornamentation pattern is similar to *D. princeps* and *D. grovesii*, i.e. reticulated wall formed by circular to elongate pits (up to 3 µm in *D. princeps*). On the other hand, *D. moalensis* has finely ornamented ascospores showing small, inward pits. Both ornamentation patterns are similar to those found in *Gelasinospora* (syn. *Neurospora*); however, Cai et al. (2006) confirmed that *Diplogelasinospora* is phylogenetically unrelated to *Gelasinospora* and showed that *Diplogelasinospora* is more related to *Lasiosphaeriaceae* than *Sordariaceae*.

A Blast search using the ITS sequence of our isolate showed a 98 % and 96 % similarity with those of *D. inaequalis* (AY681201) and *D. grovesii* (NR_077164), respectively. The LSU tree corroborated that *D. moalensis* is a new taxon in the genus, more closely related to *D. inaequalis* (NBRC 30580 and CBS 436.74) (TreeBASE ID 14810). The two branches formed suggest that the septal position is an informative character in this group, since the species with a median septum, such as *D. princeps* (NBRC 9550) and *D. grovesii* (CBS 340.73 and NBRC 31886) form a separate lineage, whereas those species with the septum displaced in the upper third generate another group. Although only a tentative hypothesis should currently be suggested, the inclusion of more isolates and new taxa may possibly help to solve the phylogenetic position of the genus and elucidate the real value of these morphological characters.



Colour illustrations. Moal forest, Asturias, Spain; *Diplogelasinospora moalensis* growing on Czapeck and OAT, asci and ascospores. Scale bars = 10 µm

Maximum Likelihood Tree obtained using the Kimura two Parameters + Gamma distance Model from a LSU sequence alignment generated with MUSCLE in MEGA v. 5.2 (Tamura et al. 2011). The bootstrap support values above 70 % from 1 000 replicates are shown at the nodes. Bar represents number of substitutions per site. The species described here is printed in **bold** face. *Podospora austro-americana* and *Podospora fibrinocaudata* were used as outgroup. ^{T} = Ex-type strain.

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Inocybe lanatopurpurea

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Inocybe lanatopurpurea Esteve-Rav. & G. Moreno, *sp. nov.*

Etymology. From Latin *lanatus* and *purpureus*, referring to the lanose veil and purple colour of the basidiomata.

Basidiomata agaricoid and stipitate. *Pileus* 10–25 mm, hemispherical convex to convex, broadly umbonate or not, slightly hygrophanous, not translucently striate, margin deflexed to straight, purple-brown to dark purple-grey (Mu 2.5YR 4/1-3) when moist, slightly pallescent on drying, then grey lilaceous at the margin (Mu 10R 4/1-3) and paler to greyish buff at the centre on drying (Mu 10R 6/1-2; 7.5YR 7/1-3); surface fibrillose to flocculose, with age often breaking into adpressed scales at the centre, in some cases squamulose to subsquarrose towards the disc, when young covered by abundant whitish fibrillose veil, breaking into individual lanose to fibrillose scales (*Cortinarius paleaceus*-like). *Lamellae* rather crowded, adnexed, broad, ventricose, pale pink lilaceous at first, then cream to brown or yellowish brown, with whitish crenulate edge. *Stipe* 10–35 × 3–5 mm, cylindrical, with rounded to slightly attenuated base, purplish to grey lilaceous to purplish red ('red wine-like'), paler or whitish towards the base, covered when young by abundant fibrillose to floccose whitish veil, apex fibrillose. *Context* whitish in the pileus, sometimes yellowish at the centre, purplish red to concolorous in the stipe (Mu 10R 5/1-3), fibrose. *Smell* slightly spermatic when cut, *taste* not recorded. *Spores* 8.5–*10*–11.3(–11.5) × 5.1–*5.6*–6 µm, Qm: 1.5–*1.75*–1.95 (n = 30), smooth, amygdaliform with oval to subpapillate apex, yellow in 5 % NH$_4$OH, thin-walled. *Basidia* 28–33 × 8.5–11 µm, 4-spored, clavate. *Lamella edge* sterile, composed by cheilocystidia and numerous hyaline, clavate paracystidia. *Cheilocystidia* numerous, 50–60(–65) × 10–13.5(–15) µm, fusiform to sublageniform, rather crystalliferous, sometimes filled with intracellular diffuse yellowish pigment, walls 1–2 µm thick, distinctly pale yellow to yellow (but neither bright or intense as in *Inocybe cincinnata*, i.e.) in NH$_4$OH. *Pleurocystidia* similar to cheilocystidia, somewhat longer, 55–65(–80) × 10–15(–18) µm. *Hymenophoral trama* regular, made up of cylindrical cells, 5–13 µm, with diffuse yellowish intracellular. *Stipitipellis* a cutis bearing numerous hyaline caulocystidioid hairs at the upper third, 5–8 µm wide, often sinuate in outline; caulocystidia absent or sparse at the extreme apex (insertion zone), similar to hymenial cystidia and hardly crystalliferous. *Clamp-connections* abundant in all tissues.

Habitat & Distribution — Known from humus of conifer forests (*Pinus pinaster*, *P. radiata*, *P. sylvestris*) in Spain, and also isolated from a *Populus tremula* ectomycorrhiza (ITS sequence GenBank FN669213) in Estonia (Bahram et al. 2011, as *Inocybe* sp. P156).

Typus. Spain, Andalucía, Jaén province, Santa Elena, road to Miranda del Rey km 4, Llano de las Américas, path to Barranco del Lobo, N38°21'8" W3°33'44", 760 m, in humus of re-forested woodland of *Pinus pinaster* and *P. radiata*, in acid soil, 30 Dec. 2013, *F. Esteve-Raventós*, *G. Moreno & J.D. Reyes* (holotype AH 40445, ITS sequence GenBank KJ432290, MycoBank MB 807747).

Colour illustrations. Llano de las Américas, Santa Elena, Jaén province, reforested forest with *Pinus pinaster* and *P. radiata*, where the holotype was collected (J.D. Reyes); basidiomata, cheilocystidia, basidia and pleurocystidium, pleurocystidium, terminal hairs at the stipe apex, spores (all from holotype). Scale bars = 1 cm (basidiomata), 10 µm (microscopic elements).

Additional specimens examined. Spain, Castilla-La Mancha, Guadalajara province, Aldeanueva de Atienza, river Pelagallinas, N41°11'34" W3°5'58", 1380 m, in humus of *Pinus sylvestris* and *P. pinaster* forest, in acid soil, 12 Oct. 2006, *F. Esteve-Raventós*, *G. Moreno*, *F. Prieto*, *F.D. Calonge*, *M.A. González & M. Heykoop*, AH 34456, ITS sequence GenBank KJ432289; Andalucía, Jaén province, Santa Elena, road to Miranda del Rey Km 4, Llano de las Américas, path to Barranco del Lobo, N38°21'8" W3°33'44", 760 m, in humus of re-forested woodland of *Pinus pinaster* and *P. radiata*, 28 Nov. 2009, *F. Esteve-Raventós & J.D. Reyes*, AH 36498, ITS sequence GenBank KJ432291.

Notes — Colour codes are taken from Munsell (1994), spore measurements are according to Heinemann & Rammeloo (1985) and terminology follows Vellinga (1988) and Kuyper (1986).

Morphologically, *I. lanatopurpurea* can be distinguished by the abundant lanose whitish veil, rather persistent upon development and forming small woolly scales on the pileus; another characteristic feature is the distinct colour, purple-brown to grey purplish or lilaceous, also present clearly in the stipe context; microscopically it shows rather narrow and fusiform cystidia, with (pale) yellow, not very thick (1–2 µm) walls. Among *Inocybe* representatives showing violet, lilac or purplish colours (section *Lilacinae*, see Heim (1931) and Bon (1997)), *I. cincinnata* differs by the brown tinged paracystidia at the lamella edge and brighter yellow cystidia wall in ammonia solutions; *I. griseolilacina* shows smaller, wider and often subcapitate cystidia and a pelargonium-like smell; *I. amethystina* is, apparently, very similar (Kuyper 1986), but the flocculose-subsquamose pileus is devoid of woolly traces of veil and the cystidia are broader (15–20 µm). In the phylogenetic tree presented here, *I. amethystina* clusters in a very different clade, as is the case of *I. griseolilacina* and *I. cincinnata* s.l. All these species do not present caulocystidia, or these are found sparsely at the extreme apex or insertion area of the stipe.

Inocybe lanatopurpurea is phylogenetically close to *I. lavandulochlora* (92 %), which exhibits lilac-violet colours in the stipe (Esteve-Raventós & Villarreal 2001) and 91 % similar to *I. chondroderma* (Matheny et al. 2013) both showing yellow colours in the basidiomata, never brown, greyish or purplish. The European *I. subnudipes* is probably related phylogenetically with these taxa, but the original description does not mention any violet, lilac or similar colour in primordial or young specimens, and type material has not been sequenced yet. At least two closely related sister lineages (98–97 % similar) can be detected, both composed of unpublished sequences produced by Berbee et al. (unpubl.). Provisional identifications in public databases were not displayed in the tree until these have been confirmed by their authors. Whether these sister lineages can be considered conspecific with that of *I. lanatopurpurea*, should be addressed through the study of these specimens. However, molecular differences seem comparable to those found between, e.g., *I. chondroderma* and *I. lavandulochlora*/*I. subnudipes*, so we choose here a conservative approach for *I. lanatopurpurea*, comprising exclusively of the type lineage. Collections studied by the authors are indicated in **bold** in the phylogenetic tree (see figure in MycoBank) for ITS sequences.

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Ophiognomonia acadiensis

Fungal Planet 274 – 10 June 2014

Ophiognomonia acadiensis A.K. Walker, Hirooka, D.M. Walker, *sp. nov.*

Etymology. Named after the region where it was collected, the Acadian forest of coastal New Brunswick, Canada.

Perithecia known only from culture, black, globose to subglobose, 1–4 necks per base, (240–)257–326(–372) µm high × (190–)198–324(–390) µm diam (av. = 294 × 263, S.D. 31, 49, n1 = 30, n2 = 30). *Necks* central, curved to sinuous, 532–996(–1170) µm long × 52–105 µm wide (av. = 690 × 66, S.D. 150, 14, n1 = 40, n2 = 35). *Asci* fusiform, apex rounded, stipe long tapering, apical ring conspicuous, (17–)21–32 × (6.5–)7–10 µm (av. = 26 × 8, S.D. 4.6, 1.1, n1 = 42, n2 = 42), ascospores arranged parallel. *Ascospores* hyaline, fusiform, ends bluntly rounded, straight to slightly curved, 1-septate, slight constriction at septum, 10–13 × 1.5–3 µm (av. = 11 × 2, S.D. 0.7, 0.5, n1 = 50, n2 = 50) whip-like ephemeral polar appendages, 16–29 × 0.5–1 µm.

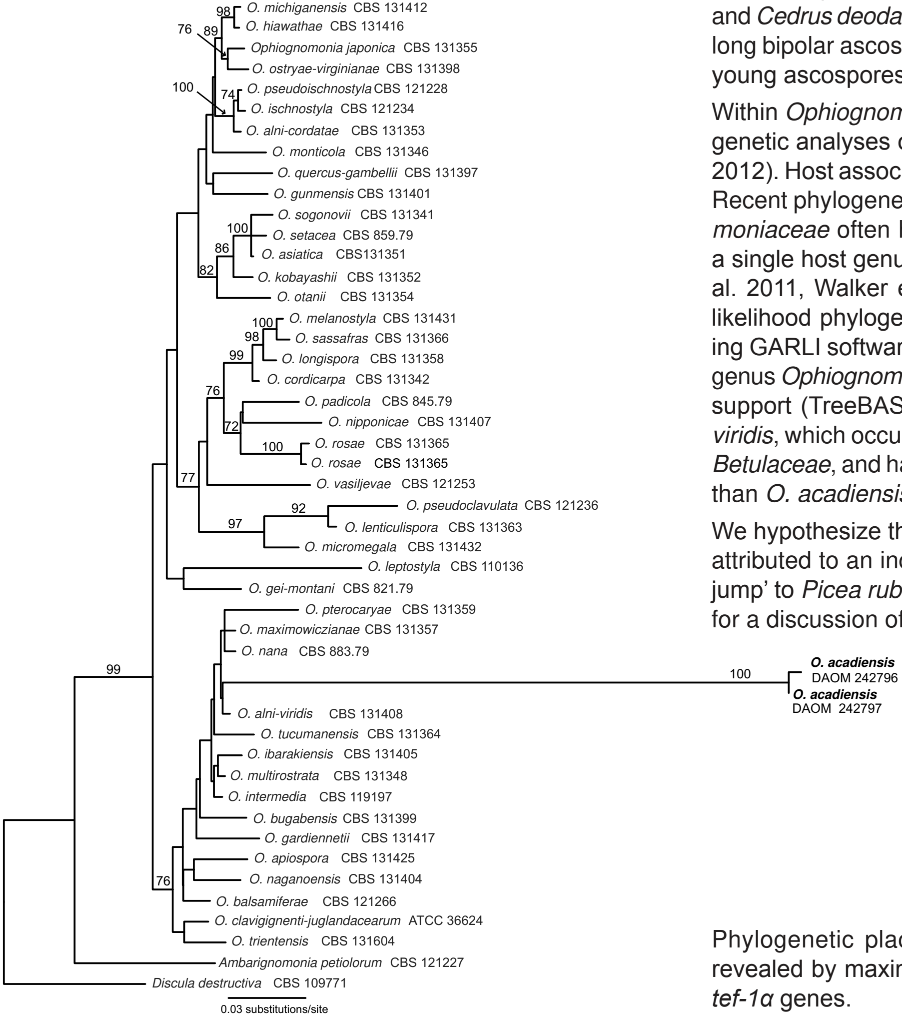
Culture characteristics — Colonies reaching 25 mm diam on 2 % malt extract agar (Difco) after 1 wk at 17 °C in the dark; margins regular; colonies hyaline, producing immature perithecia after 1 wk and mature perithecia after 1 mo incubation at 17 °C in the dark.

Typus. Canada, New Brunswick, Charlotte County, Lepreau, Basin Road, N45°8'15.576" W66°27'2.052". Dried perithecia from culture obtained from surface sterilised green needles collected from living branches of *Picea rubens*, 6 Aug. 2013, *A.K. Walker & J. Walker* (holotype DAOM 242791, ex-type culture AW 548 = DAOM 242797; ITS, LSU, *tef-1α* and MS204 sequences GenBank KJ412998–KJ413001, MycoBank MB807724).

Notes — Nine species of *Ophiognomonia* have been reported from Canada, all from angiosperm hosts (Walker et al. 2012). This is the first record of a species of *Ophiognomonia* isolated from a conifer; however the asexual species *Sirococcus conigenus*, *S. piceicola* and *S. tsugae* in the related genus *Gnomoniopsis* occur as pathogens and saprobes of *Picea* spp. and *Cedrus deodara.* The combination of long perithecial necks, long bipolar ascospore appendages and gelatinous sheaths in young ascospores is unique to this species.

Within *Ophiognomonia* species are delimited based on phylogenetic analyses of variable molecular markers (Walker et al. 2012). Host association is also useful for species identification. Recent phylogenetic studies have shown that species of *Gnomoniaceae* often have a narrow host range, associating with a single host genus or species (Sogonov et al. 2008, Mejía et al. 2011, Walker et al. 2010, 2012). A three-gene maximum likelihood phylogenetic analysis (ITS, MS204 and *tef-1α*) using GARLI software revealed *O. acadiensis* belongs within the genus *Ophiognomonia* with 99 % maximum likelihood bootstrap support (TreeBASE ID 15333) with its closest sister *O. alni-viridis*, which occurs on *Alnus* spp. and *Betula papyrifera* in the *Betulaceae*, and has larger asci and more elongate ascospores than *O. acadiensis*.

We hypothesize that the long branch of *O. acadiensis* may be attributed to an increase in evolutionary rate following a 'host jump' to *Picea rubens* in the *Pinaceae* (see Walker et al. 2014 for a discussion of this topic in *Ophiognomonia*).



Phylogenetic placement of *Ophiognomonia acadiensis* as revealed by maximum likelihood analysis of ITS, MS204 and *tef-1α* genes.

Colour illustrations. Background photo of coastal *Picea rubens* forest near the collection site courtesy David Malloch. Morphological photos by Y. Hirooka & A.K. Walker. Scale bars of perithecia = 300 µm. Scale bar of perithecium in median cross section = 100 µm. Scale bars of asci and ascospores = 10 µm.

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Penicillium restingae
CYA 25°C
CYA 37°C
MEA 25°C
G25N 25°C

Fungal Planet 275 – 10 June 2014

Penicillium restingae J.P. Andrade, P.A.S. Marbach, C.M.S. Motta & J.T. De Souza, *sp. nov.*

Etymology. Referring to the sandbanks ecosystem, known as restinga in Brazil, where this species was isolated from.

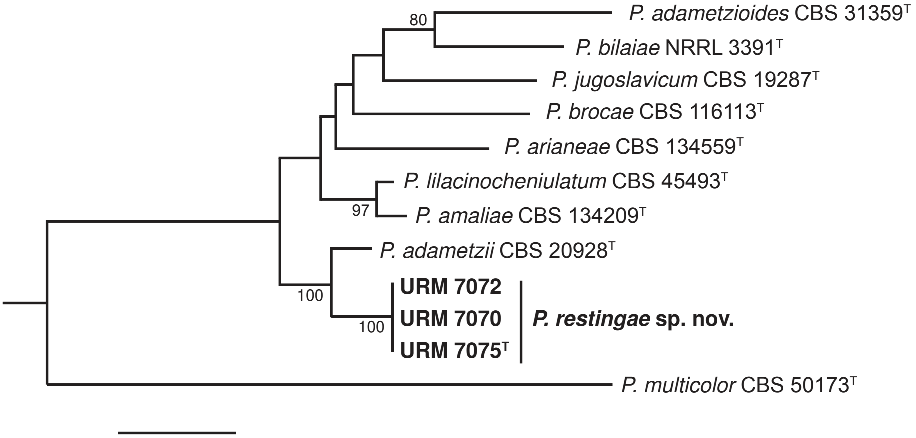
Conidiophores strictly monoverticillate. *Stipes* smooth-walled, short, 10–22(–40) × 1–2(–3) µm. *Conidiophores vesiculate* 2–9(–12) × 2–6 µm. *Phialides* ampulliform, 4–6 × 1.2–2(–4) µm. *Conidia* with walls finely roughened, spheroidal, 1.5–2 (–2.5) µm. *Sclerotia* not observed.

Culture characteristics — (in the dark, colony diam after 7 d): Colonies on Czapek yeast extract agar (CYA) 25 °C 18–27 mm, plane or umbonate, radially and concentrically sulcate or wrinkled, low to moderately deep, mycelium white, texture velutinous to slightly floccose, sporulation light to moderate, conidial colour *en masse* pale grey to green-grey (1B1–1D2; Kornerup & Wanscher 1984), exudate clear to yellow-brown, red-brown soluble pigment occasionally produced, reverse typically pale to pale grey, less commonly light yellow or red-brown (2A2–1B1–4A4–8D8). CYA 37 °C 23–33 mm, colony diameter was the only difference observed between these two temperatures. CYA 5 °C no growth. Colonies on malt extract agar (MEA) 25 °C 16–23 mm, usually umbonate, in some isolates plane, mycelium white, texture floccose, sporulation light to moderate, conidial colour *en masse* white to light grey (1A1–1C1), exudate absent, soluble pigment absent, reverse pale yellow to pale grey (1A3–1B1). Colonies on 25 % glycerol nitrate agar (G25N) 25 °C 9–18 mm, plane, mycelium white, texture floccose or less commonly velutinous, reverse pale (2A2).

Typus. Brazil, Bahia, in soil from the Guaibim sandbank, S13°18' W38°57', 20 Jan. 2011, *J.P. Andrade* (holotype CMR H-12 (dried culture on MEA), culture ex-type URM 7075; ITS sequence GenBank KF803355, BenA sequence GenBank KF803349, Cmd sequence GenBank KF803352, MycoBank MB807051).

Additional specimens examined. URM 7070 and URM 7072, both from soil, Brazil, Bahia, *J.P. Andrade*. The former strain was isolated on 13 Mar. 2011, the latter on 22 May 2011. Sequence GenBank accession numbers: ITS KF803354, KF803353; BenA KF803348, KF803347; Cmd KF803351, KF803350.

Notes — Comparison of ITS, BenA and Cmd sequences to the ones available in public databases and subsequent phylogenetic analyses show that *P. restingae* is most closely related to *P. adametzii* in the section *Sclerotiora* (Visagie et al. 2013). It differs from *P. adametzii* by several insertions, deletions and substitutions in ITS, BenA and Cmd sequences (TreeBASE ID 15230). The morphology of *P. restingae* resembles that of *P. restrictum* (Pitt 1988). *Penicillium restingae* differs from *P. adametzii* in colony diameter on MEA 25 °C, CYA 37 °C and stipe length and from *P. restrictum* in having a vesiculate conidiophores, smaller conidia and showing faster growth rate on CYA 37 °C.



Maximum likelihood tree of *Penicillium* strains belonging to section *Sclerotiora* based on 1 090 aligned nucleotides (combined ITS, BenA and Cmd data). Analysis performed using MEGA v. 5.1 with the Tamura 3-parameter substitution model. Bootstrap analysis employed 1 000 re-samplings; only bootstrap support values above 80 % presented at the nodes. *Penicillium multicolor* was used as outgroup. The scale indicates the number of substitutions per site. The new species is presented in **bold** font (T = ex-type).

Colour illustrations. Brazil, Bahia, Guaibim sandbank; colonies growing on CYA, MEA and G25N; conidiophores with conidia. Scale bar = 10 µm.

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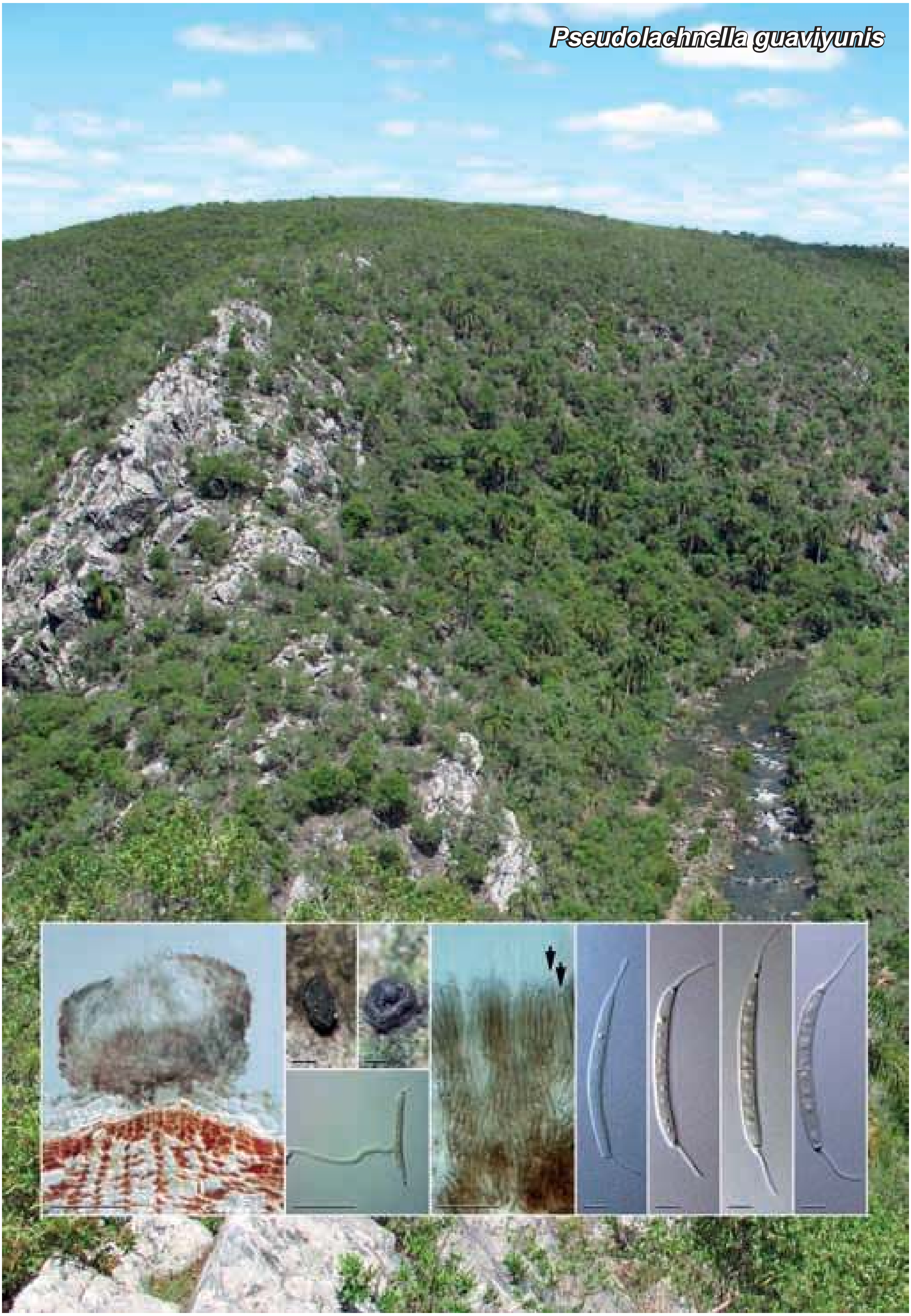
Pseudolachnella guaviyunis

Fungal Planet 276 – 10 June 2014

Pseudolachnella guaviyunis Marinc., T.A. Duong, M.J. Wingf. & C.A. Perez, *sp. nov.*

Etymology. A common name of the host plant in Uruguay, Guaviyú.

Conidiomata scattered, oval to rounded in outline, up to 688 µm long, up to 416 µm wide, up to 199 µm deep, cupulate with the edge slightly curved-in in sectional view, filled with agglutinated conidial mass, olivaceous-black; basal stroma well-developed, subepidermal, up to 85 µm thick, of *textura angularis* or *epidermoidea*, cells thick-walled, subhyaline when intercellular to pale brown, cells bordering the lateral wall becoming darker and thicker; lateral walls consisting of cells of *textura porrecta* in a few strata, cells thin-walled, pale brown to brown, marginal cells of each strata becoming darker. *Conidiomatal setae* absent. *Conidiophores* arising in the concavity of the conidioma, septate and branched at the base, pale brown, smooth. *Conidiogenous cells* phialidic, discrete, subhyaline to pale brown, cylindrical, with conspicuous collarette, often showing percurrent proliferation, 15–26 × 2–3 µm. *Conidia* hyaline when young and becoming pale brown with age, fusiform, straight or slightly curved, gradually tapering towards the apex, with an obtuse, truncate base, smooth or verruculous with age, bearing cellular appendages at both ends, (26.5–)33–36(–43.5) × (2–)2.5–3(–3.5) µm, aseptate when young, developing 3 septa with age, germinating from any of 4 cells; *apical appendages* 5.5–14 µm long, centric; *basal appendages* 4.5–13 µm long, excentric, both appendages 0.5–1 µm wide at the base and tapering towards the apex.

Culture characteristics — The cultures on 2 % malt extract agar showing optimum growth at 25 °C in the dark, reaching 22 mm after 22 d, sterile, above iron-grey, reverse fuscous-black (Rayner 1970), growing circular, radially striated with lobate edge, mycelia flat, velvety, medium dense, exuding dark brown pigmentation around the colony in 2 mm width.

Typus. Uruguay, Quebrada de los Cuervos, on *Myrcianthes pungens*, Oct. 2012, *M.J. Wingfield & C. Perez* (holotype PREM 60964, culture ex-holotype CBS 134695 = CMW 39055, ex-isotypes CMW 39018–39020; ITS sequence of CBS 134695 GenBank KJ834524, LSU sequence of CBS 134695 GenBank KJ834525, MycoBank MB808837).

Colour illustrations. *Myrcianthes pungens* trees growing at the 'Quebrada de los Cuervos' in Uruguay; conidioma in sectional view (bar = 100 µm) and on the host substrate (350 µm), germinating conidium (25 µm), branched conidiophores and phialidic conidiogenous cells with conspicuous collarette (arrows) (20 µm); conidia from young to mature (5 µm).

Notes — Cupulate fruiting structures were found on the bark of *Myrcianthes pungens* in Uruguay. The morphological features of this isolate best match those of the genus *Pseudolachnella*, other than the absence of noticeable conidiomatal setae. Currently there are eight *Pseudolachnella* species recognised worldwide from herbaceous stems or leaves of monocotyledonous host plants, mostly palm trees in Asia (Nag Raj 1993, Zhao et al. 2004, Sato et al. 2008). The Uruguayan collection introduced as the new species *P. guaviyunis*, is recognised here primarily based on conidial morphology and DNA sequence data.

Both *Pseudolachnella* and *Pseudolachnea* are closely related to *Dinemasporium*. When Sutton (1980) limited *Dinemasporium* to the species with aseptate conidia, he restricted the species with septate conidia to *Pseudolachnea*. Nag Raj (1993) further limited *Pseudolachnea* to the species with 1-septate conidia and *Pseudolachnella* to those with multiseptate conidia. No sexual state is known for *Pseudolachnella* and *Pseudolachnea*, whereas one species of *Dinemasporium* is known based on its sexual state, *Phomatospora dinemasporium* (*Xylariales*). However, the identity of the sexual state in this case is considered to be doubtful (Duan et al. 2007).

A recent study applying ribosomal DNA sequence data revealed the phylogenetic placement of *Pseudolachnea* and *Dinemasporium* within the chaetosphaerialean clade. However, the phylogenetic position of *Pseudolachnella* could not be determined due to the lack of cultures (Crous et al. 2012b). The present study suggests that *Pseudolachnella* resides in the *Chaetosphaeriales* but that it is distantly related to *Pseudolachnea*, thus consistent with the views of Nag Raj (1993).

A case study of *Dinemasporium* and related genera by Crous et al. (2012b) suggested that the appendage morphology could be a useful characteristic in species delimitation but not in generic separation. *Pseudolachnella* species are heterogeneous in terms of appendage morphology: short (to 4 µm) or long (to 47 µm) in length, simple or branched, single or multiple in number. *Pseudolachnella guaviyunis* can be distinguished by its simple appendages at both ends of the conidia, measuring up to 14 µm in length.

A megablast search of the NCBIs GenBank nucleotide sequence database using the ITS sequence of *Pseudolachnella guaviyunis* showed that its closest relatives are *Pseudolachnea fraxini* (GenBank JQ 889287; Identities = 464/533 (87 %), Gaps = 23/533 (4 %)) and *Dinemasporium strigosum* (GenBank JQ889283; Identities = 495/579 (85 %); Gaps = 34/579 (5 %)). A megablast search using the LSU sequence of *Pseudolachnella guaviyunis* showed that it was most similar to *Pseudolachnea fraxini* (GenBank JQ889301; Identities = 810/839 (97 %); Gaps = 1/839 (0 %)) and *Dinemasporium strigosum* (GenBank JQ 889299; Identities = 807/841 (96 %); Gaps = 3/841 (0 %)).

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Pseudonectria rusci

Fungal Planet 277 – 10 June 2014

Pseudonectria rusci Lechat, Gardiennet & J. Fourn., *sp. nov.*

Etymology. The epithet is derived from the host *Ruscus aculeatus*.

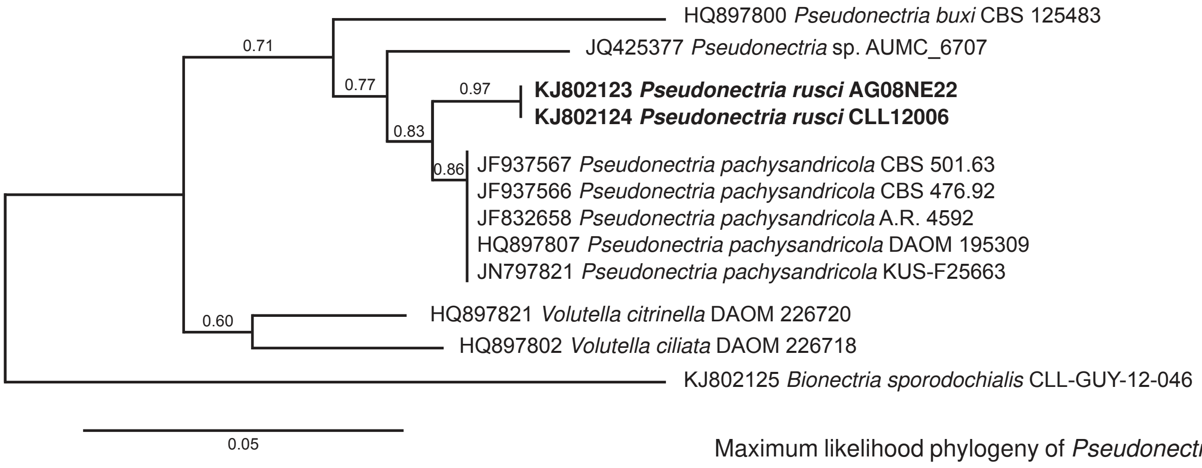
Ascomata superficial, scattered on cladodes and stems of dying *Ruscus aculeatus*, not obviously stromatic but seated on old volutella-like sporodochia, globose with a pointed apex, 180–200 µm diam, smooth, orange, turning pale pink to pale purple in 3 % KOH, yellow in lactic acid, collapsing laterally upon drying, setose. *Ascomatal* wall 20–25 µm thick, made of two regions: outer region 15–20 µm thick, composed of thick-walled ellipsoid to elongate cells with wall 1.5–2 µm thick; inner region 5–10 µm thick composed of thin-walled, flattened, hyaline cells; apex made of tightly aggregated cylindrical cells 8–12 × 2–2.5 µm. *Cells* at the surface of the perithecial wall angular, 10–15 µm diam. *Setae* scattered on surface of ascomata except on ostiolar region, 60–135 µm long, 6–11 µm wide at base, simple, hyaline, stiff, straight to slightly curved upwards, with acute apices, thick-walled, wall refractive, 2.5–3 µm wide at base, becoming thinner toward the apex, aseptate. *Asci* unitunicate, narrowly clavate, stipitate, 60–70 × 8–10 µm, with eight ascospores that are irregularly biseriate in upper part and uniseriate below, apex simple, truncate, with hyaline, thin-walled moniliform paraphyses inserted between the asci, up to 10 µm wide toward base. *Ascospores* 12–15 × 3–3.5 µm, ellipsoid to fusiform, medianly septate, with two droplets in each cell, slightly constricted at the septum, pale brownish yellow when mature, finely verrucose.

Culture characteristics — After 2 wk on 2 % potato-dextrose-agar (PDA) with 5 mg/L streptomycin: colonies 6–7 cm diam, pale salmon, sporodochia orange-yellow, setae 170–230 µm long, 5–7 µm wide at base, tapering with acute tip, aseptate, hyaline. Conidiophores 25–40 × 3–4 µm, branched, ultimate branches bearing 2–4 phialides. Phialides cylindrical, 10–15 × 1.5–2 µm with a flared collarette. Conidia fusiform, 8–10 × 2.5–4 µm, aseptate containing many minute droplets, smooth, hyaline. Asexual state in culture identical to volutella-like asexual morph occurring on natural substratum.

Typus. France, Côte d'Or, Corcelles-Les-Monts, Bois de La Combe au Pré, 25 Nov. 2008, on dead stem and cladodes of *Ruscus aculeatus*, *A. Gardiennet* (holotype deposited at Faculté de Pharmacie de Lille, France (LIP) AG08NE22, culture ex-type CBS126108; ITS GenBank sequence KJ802123 & KJ802124, MycoBank MB808720).

Additional specimens examined. France, Côte d'Or, Messigny-et-Vantoux, bois de la Combe, 26 Nov. 2009, *A. Gardiennet*, AG09321; Deux-Sèvres, Villiers-en-Bois, forêt de Chizé, 25 Feb. 2012, *C. Lechat*, CLL12006; Ariège, Rimont, Las Muros, 470 m, 29 Dec. 2012, *J. Fournier*, JF 12124.

Notes — The present new taxon fits well within the genus *Pseudonectria* as defined by Rossman et al. (1999), in having minute superficial setose ascomata occurring on dying or recently dead plant material, and being associated with a volutella-like sexual state. Its close affinities with other members of the genus and the asexual-sexual state connection are confirmed by DNA sequence data. However, it deviates from typical *Pseudonectria* spp. by its ascomatal wall changing colour in KOH and 1-septate ascospores.



Maximum likelihood phylogeny of *Pseudonectria* inferred from ITS1-5.8S-ITS2 sequences, rooted on *Bionectria sporodochialis*. Analysis performed online at www.phylogeny.fr (alignments edited with GBlock 0.91b), run in PhyML 3.0aLRT using the GRT+I+Γ model. Branch supports assessed by the SH-aLRT statistical test.

Colour illustrations. Ruscus aculeatus on which the sample was collected, ascomata on host substratum, vertical section through ascomatal wall, asci and ascospores. Scale bars = 100, 10 and 10 µm.

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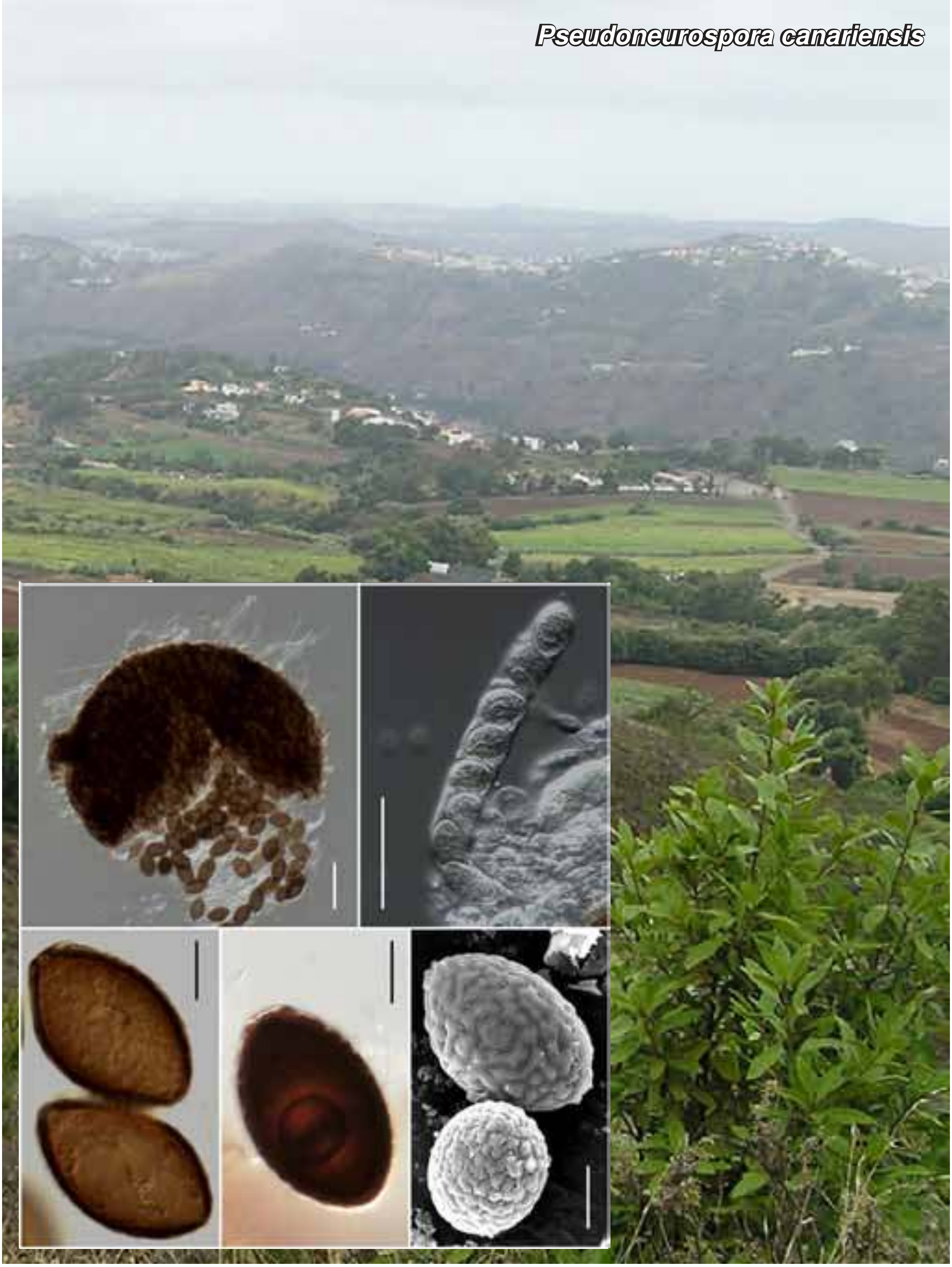

Pseudoneurospora canariensis

Fungal Planet 278 – 10 June 2014

Pseudoneurospora canariensis Y. Marín, Stchigel, Dania García, Guarro & Cano, *sp. nov.*

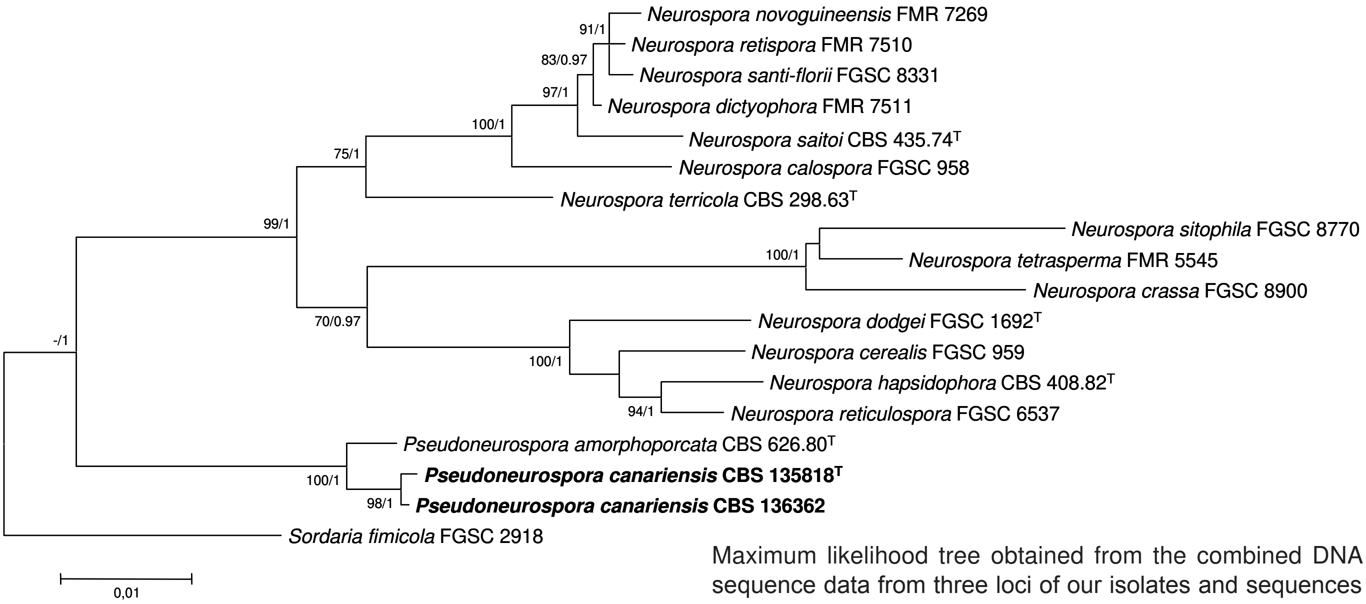
Etymology. *Canariensis* = from Canary Islands, Spain; referring to the geographical origin of the fungus.

Mycelium composed of subhyaline to brown, branched, septate, smooth-walled, thin- to thick-walled hyphae, 1.5–9 µm wide. *Ascomata* non-ostiolate, superficial to immersed, scattered to grouped, at first yellowish brown and translucent, becoming dark yellowish brown to black at maturity, 120–220 µm diam, covered by moniliform hyphae, up to 17 µm wide; setae scarce, sinuose, smooth- and thick-walled, septate, brown, up to 150 µm long, 3–8 µm at the base, apex rounded; peridium 3–4-layered, 5–15 µm thick, brown, of *textura angularis* to *globulosa*, composed of brown, thick-walled, flattened cells, measuring 13–35 × 12–23 µm; ascomatal initials arising as side branches from mycelium, involving neighbouring hyphae, coiled and contorted. *Paraphyses* absent. *Asci* 8-spored, clavate, short-stipitate, 200–300 × 20–25 µm, without apical structures, soon evanescent. *Ascospores* uniseriate, aseptate, ellipsoidal, (30–)33–36 × (18–)22–25 µm, at first with a hyaline, smooth-walled exosporium and a pigmented, echinulate endosporium, becoming dark brown to black at maturity, opaque, strongly verrucose to tuberculate, with a slightly protruding apical germ pore, 1.5–2.5 µm diam.

Culture characteristics — Colonies on potato carrot agar attaining a diameter of more than 80 mm in 14 d at 25 °C, velvety to powdery, brown (5E5–5F5) (Kornerup & Wanscher 1984); reverse dark brown (8F4), black at the margins. Colonies on oatmeal agar attaining 52–61 mm diam in 14 d at 25 °C, velvety to granular, brown (5E5–5F5); reverse of the same colour than the surface. The fungus does not grow below 5 °C nor above 40 °C. Optimal ascomatal production occurred between 15 °C and 25 °C.

Typus. Spain, Gran Canaria, Pico de Osorio, from forest soil, 10 Aug. 2009, coll. *M. Calduch & A.M. Stchigel*, isol. *Y. Marín* (holotype CBS H-21353, cultures ex-type CBS 135818 = FMR 12156; other strain CBS 136362 = FMR 12323; LSU sequences of CBS 135818 and CBS 136362 GenBank HG326871 and HG326872, respectively; Tub sequences of CBS 135818 and CBS 136362 GenBank HG423208 and HG423209, respectively; and tef-1 sequences of CBS 135818 and CBS 136362 GenBank HG326875 and HG326876, respectively; MycoBank MB804881).

Notes — Hitherto, *Pseudoneurospora* has been a monotypic genus (García et al. 2004). The molecular analyses carried out by Nygren et al. (2011), based on seven gene regions including fragments of the β-tubulin (Tub), translation elongation factor 1-α (tef-1), protein kinase C (pkc), 28S rDNA, mitogen-activated protein kinase-2 (mak-2), nonidentical kinase-1 (nik-1) and hypothetical protein-coding (NCU02332) genes, corroborated *Pseudoneurospora* as a different genus to *Neurospora*. Our phylogenetic tree obtained by sequencing of 28S rDNA, Tub and tef-1 loci corroborated our fungus as representing a new species of *Pseudoneurospora*. *Pseudoneurospora canariensis* can be distinguished from *Pseudoneurospora amorphoporcata*, the type species of the genus, by the production of small, non-ostiolate ascomata (pyriform and ostiolate in *P. amorphoporcata*), the absence of an apical ring in the asci (present in those of *P. amorphoporcata*) and by the presence of a single apical germ pore on the ascospores (one at each end in *P. amorphoporcata*).



Maximum likelihood tree obtained from the combined DNA sequence data from three loci of our isolates and sequences retrieved from the GenBank (Nygren et al. 2011) (TreeBASE ID 14380). In the tree, branch lengths are proportional to distance. Bootstrap support values ≥ 70 / Bayesian posterior probability scores ≥ 0.95 are indicated on the nodes. *Sordaria fimicola* (FGSC2918) was used as outgroup. Ex-type strains of the different species are indicated with ^{T}. Strains of the new species proposed in this study are indicated in **bold**.

Colour illustrations. Pico de Osorio, Gran Canaria, Spain. Ascomata, ascus and ascospores. Scale bars (top) = 50 µm, (bottom) = 10 µm.

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Rinaldiella pentagonospora

Fungal Planet 279 – 10 June 2014

Rinaldiella D.A. Sutton, Y. Marín, Guarro & E.H. Thomps., *gen. nov.*

Etymology. Named in honour of the eminent medical mycologist Michael G. Rinaldi.

Ascomata immersed, ostiolate, pyriform to subglobose, dark brown to black, covered with hyphal-like hairs, with a conspicuous conical neck. *Peridium* membranaceous, translucent, brown to yellowish brown, *textura epidermoidea*. *Asci* 8-spored, fasciculate, clavate to cylindrical, without apical ring, short stipitate, early evanescent. *Paraphyses* and periphyses hyaline, filiform, septate. *Ascospores* biseriate to uniseriate, clavate, hyaline, and aseptate when young, finally becoming transversely 1-septate; upper cell polygonal, 5-angled in side view, truncate at the base and with a slightly acuminate apex, brown, thick-walled, warted, with an apical germ pore; lower cell subhyaline, conical and slightly warted.

Type species. *Rinaldiella pentagonospora*.
MycoBank MB807137.

Rinaldiella pentagonospora D.A. Sutton, Y. Marín, Guarro *&* E.H. Thomps., *sp. nov.*

Etymology. Named after the shape of the upper cell of the ascospore.

Mycelium composed of brown to pale olive brown, septate, branched, smooth-walled hyphae, 1–6 µm diam. *Ascomata* immersed, ostiolate, pyriform to subglobose, dark brown to black, 180–300 × 160–230 µm, covered with long, yellowish brown, septate hypha-like hairs, 2–3 µm diam, with a conspicuous conical neck; neck 20–40 µm long, 50–90 µm wide at the base, with brown, papillate cells around the ostiole. *Peridium* membranaceous, translucent, 4–6-layered, 7–11 µm thick, brown to yellowish brown *textura epidermoidea. Asci* 8-spored, fasciculate, clavate to cylindrical, 50–71 × 6–12 µm, without apical ring, short stipitate, early evanescent. *Paraphyses* and *periphyses* hyaline, filiform, septate, 0.5–2 µm wide. *Ascospores* biseriate to uniseriate, clavate, hyaline, and aseptate when young, finally becoming transversely 1-septate; upper cell polygonal, 5-angled in side view, truncate at the base and with a slightly acuminate apex, brown, thick-walled, 9–10 × 7–8 µm, ornamented with rounded warts of 0.5–1 µm diam, with an apical germ pore, 0.5–1 µm diam; lower cell subhyaline, conical and slightly warted, 3–5 µm long.

Culture characteristics — Colonies on PDA growing slowly, reaching 5–8 mm diam after 30 d at 22–25 °C, velutinose, elevated, folded, zonate and slightly radiate, dark green; ascomata produced after 2 mo; reverse dark green.

Typus. USA, Georgia, Dahlonega, from a contaminated human lesion, May 2011, *J.L. Robertson & D.R. Hospenthal* (holotype CBS H-20903, cultures ex-type UTHSC 11-1352 = FMR 12018; LSU sequence GenBank KC702790, ITS sequence GenBank KC702789, MycoBank MB564228).

Colour illustrations. Dahlonega, Georgia (Photo credit: Jack Anthony); ascomata, ascus and ascospores. Scale bars = 50 µm, 10 µm, 2.5 µm.

Notes — This fungus was found contaminating a lesion in a man probably acquired when he struck his hand against a tree. Morphologically, *Rinaldiella* resembles *Apiosordaria* (*Sordariales*, *Ascomycota*). However, the genetic distances between the present species and the members of that genus, in our unpublished DNA sequence database, are too long to be considered the same genus, and are closer to other genera of the same order. Currently, *Apiosordaria* comprises 24 saprobic species (Guarro et al. 2012) usually isolated from soil or herbivore dung. The similarity of D1/D2 and ITS sequences of our fungus with the type species of *Apiosordaria*, *A. verruculosa* and the ex-type strains of *A. striatispora* and *A. yaeyamensis*, which are the most closely related species morphologically, is 92.69, 90.92 and 92.09 %; and 80.11, 78.11 and 80.28 %, respectively. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the D1/D2 sequence is *Immersiella immersa* (GenBank AY436409 and AY436408; Identities = 583/604 (97 %), Gaps 2/604 (0 %)); and using ITS, no sequences with significant identities were found. *Rinaldiella* is very different morphologically from *Immersiella*, the latter producing cylindrical, sigmoid or geniculate and 1-celled ascospores (Miller & Huhndorf 2004).

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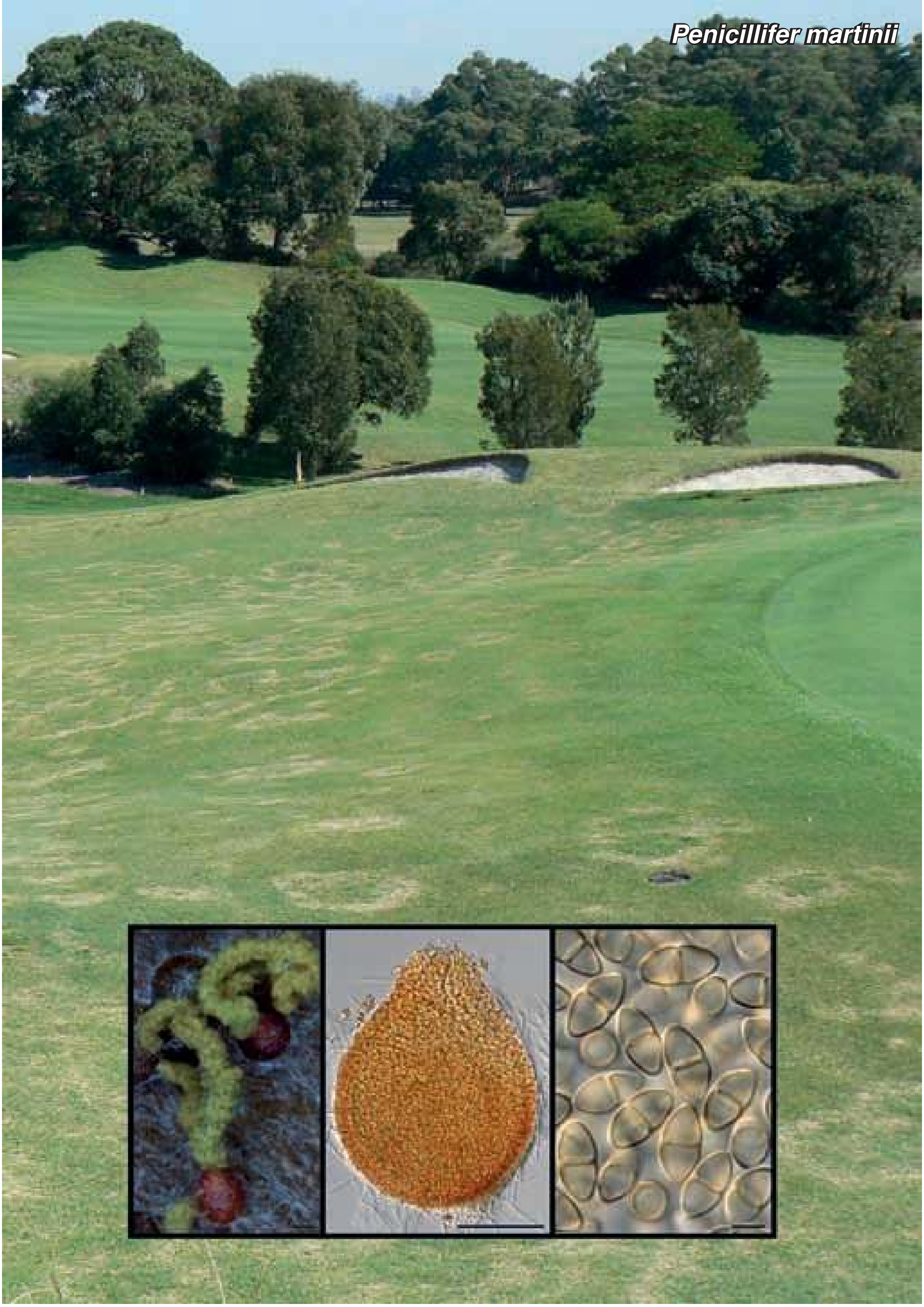
Penicillifer martinii

Fungal Planet 280 – 10 June 2014

Penicillifer martinii P. Wong, Y.P. Tan & R.G. Shivas, *sp. nov.*

Etymology. Named in honour of Dr P.M. Martin, University of Sydney, for his significant contribution to turf research and education.

On potato dextrose agar after 2 wk in the dark. *Colonies* 4–5 cm diam, mostly adpressed with sparse to moderately abundant hazel aerial mycelium towards the centre, becoming dark vinaceous between the centre and the margin, vinaceous buff at the margins; reverse brown vinaceous, paler at the margin. *Mycelium* consists of septate, yellow to pale brown, branched, smooth hyphae, 2–6(–10) µm. *Ascomata* superficial, non-stromatic, solitary, abundant near the colony margin, globose to ovoidal, 250–400 µm high × 250–300 µm diam, luteus to cinnamon coloured, KOH-, yellow in lactic acid, glabrous, with numerous dense cylindrical, clavate to capitate hyaline cells lining and protruding from the ostiole. *Ascomatal surface* of broadly ellipsoidal to subployhedrally irregular cells, 7–27 µm diam, with 1–3 µm thick walls. *Asci* broadly clavate, 53–70 × 24–36 µm. *Ascospores* bi- to multiseriate, ellipsoidal, 20–27 × 11–14 µm, pale yellow, with a median septum, constricted at the septum, ends rounded; wall even, 1 µm thick, smooth in profile to faintly punctate in surface view, exuded *en masse* in green cirri, which become yellowish green to cinnamon with age.

Typus. Australia, New South Wales, Sydney, Rose Bay, Royal Sydney Golf Club, from rotted roots of *Cynodon dactylon*, 1 Mar. 2012, *P.T.W. Wong* (holotype BRIP 59225, includes ex-type culture; ITS sequence GenBank KJ869167, LSU sequence GenBank KJ869225, TEF sequence GenBank KJ869241, MycoBank MB808332).

Additional material examined. Australia, Sydney, Pagewood, Bonnie Doon Golf Club, from rotted roots of *C. dactylon*, Feb. 2013, *P.T.W. Wong PW13001* (BRIP 59296); Pymble, Avondale Golf Club, from rotted roots of *C. dactylon*, Feb. 2013, *P.T.W. Wong PW13002* (BRIP 59297, includes culture); Little Bay, St Michael's Golf Club, from rotted roots of *C. dactylon*, Feb. 2013, *P.T.W. Wong PW13005* (BRIP 59298, includes culture); Little Bay, New South Wales Golf Club, from rotted roots of *C. dactylon*, May 2013, *P.T.W. Wong PW13018* (BRIP 59308, includes culture).

Colour illustrations. Patch disease at Bonnie Doon Golf Club, New South Wales; ascomata with cirri, ascomatum, ascospores. Scale bars (from left to right) = 100 µm, 100 µm, 10 µm.

Notes — *Penicillifer martinii* was isolated from diseased roots and stolons of *Cynodon dactylon* and *Pennisetum clandestinum* from fairways with a patch disease at a number of golf clubs in Sydney, New South Wales, Australia. Pathogenicity tests with *P. martinii* have shown that it is only slightly pathogenic to *C. dactylon*, causing some brown lesions on the roots. Perithecia of *P. martinii* have been also observed on diseased roots and stolons of *C. dactylon* incubated in humid chambers at room temperature (20–30 °C) for several months. Nine species of *Penicillifer* Emden (1968) have been described (Matsushima 1971, 1975, Samuels 1989, Watanabe 1990, Polishook & Bills 1991), four of which have sexual morphs described in *Viridispora* (Rossman et al. 1999). The combination of the comparatively large and septate ascospores separates *P. martinii* from the other species that produce viridispora-like morphs. An asexual morph was not observed in cultures of *P. martinii*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Viridispora diparietispora* (GenBank JN049838; Identities 464/483 (96 %), Gaps = 7/483 (1 %)), *Viridispora* sp. (GenBank JQ863229; Identities = 514/552 (93 %), Gaps = 11/552 (1 %)), and *V. alata* (GenBank EU860055; Identities = 485/532 (91 %), Gaps 12/532 (2 %)). Closest hits using TEF sequence are *V. alata* (GenBank JF832592; Identities = 337/367 (92 %), Gaps 13/367 (3 %)), *Gliocladiopsis irregularis* (GenBank JQ666104; Identities = 352/422 (83 %), Gaps 30/422 (7 %)) and *G. mexicana* (GenBank JQ666103; Identities = 352/422 (83 %), Gaps 30/422 (7 %)).

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