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RESEARCH ARTICLE

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Key words

ITS DNA barcodes
LSU
novel fungal species
systematics

Abstract Novel species of microfungi described in the present study include the following from South Africa: *Camarosporium aloes*, *Phaeococcomyces aloes* and *Phoma aloes* from *Aloe*, *C. psoraleae*, *Diaporthe psoraleae* and *D. psoraleae-pinnatae* from *Psoralea*, *Colletotrichum euphorbiae* from *Euphorbia*, *Coniothyrium prosopidis* and *Peyronellaea prosopidis* from *Prosopis*, *Diaporthe cassines* from *Cassine*, *D. diospyricola* from *Diospyros*, *Diaporthe maytenicola* from *Maytenus*, *Harknessia proteae* from *Protea*, *Neofusicoccum ursorum* and *N. cryptoaustrale* from *Eucalyptus*, *Ochrocladosporium adansoniae* from *Adansonia*, *Pilidium pseudoconcavum* from *Greyia radlkoferi*, *Stagonospora pseudopaludosa* from *Phragmites* and *Toxicocladosporium ficiniae* from *Ficinia*. Several species were also described from Thailand, namely: *Chaetopsina pini* and *C. pinicola* from *Pinus* spp., *Myrmecridium thailandicum* from reed litter, *Passalora pseudotithoniae* from *Tithonia*, *Pallidocercospora ventilago* from *Ventilago*, *Pyricularia bothriochloae* from *Bothriochloa* and *Sphaerulina rhododendricola* from *Rhododendron*. Novelties from Spain include *Cladophialophora multiseptata*, *Knufia tsunedae* and *Pleuroascus rectipilus* from soil and *Cyphellophora catalaunica* from river sediments. Species from the USA include *Bipolaris drechsleri* from *Microstegium*, *Calonectria blephiliae* from *Blephilia*, *Kellermania macrospora* (epitype) and *K. pseudoyuccigena* from *Yucca*. Three new species are described from Mexico, namely *Neophaeosphaeria agaves* and *K. agaves* from *Agave* and *Phytophthora ipomoeae* from *Ipomoea*. Other African species include *Calonectria mossambicensis* from *Eucalyptus* (Mozambique), *Harzia cameroonensis* from an unknown creeper (Cameroon), *Mastigosporella anisophylleae* from *Anisophyllea* (Zambia) and *Teratosphaeria terminaliae* from *Terminalia* (Zimbabwe). Species from Europe include *Auxarthron longisporum* from forest soil (Portugal), *Discosia pseudoartocreas* from *Tilia* (Austria), *Paraconiothyrium polonense* and *P. lycopodinum* from *Lycopodium* (Poland) and *Stachybotrys oleronensis* from *Iris* (France). Two species of *Chrysosporium* are described from Antarctica, namely *C. magnasporum* and *C. oceanitesii*. Finally, *Licea xanthospora* is described from Australia, *Hypochnicium huinayensis* from Chile and *Custingophora blanchettei* from Uruguay. Novel genera of *Ascomycetes* include *Neomycosphaerella* from *Pseudopentameris macrantha* (South Africa), and *Paramycosphaerella* from *Brachystegia* sp. (Zimbabwe). Novel hyphomycete genera include *Pseudocatenomycopsis* from *Rothmannia* (Zambia), *Neopseudocercospora* from *Terminalia* (Zambia) and *Neodeightoniella* from *Phragmites* (South Africa), while *Dimorphiopsis* from *Brachystegia* (Zambia) represents a novel coelomycetous genus. Furthermore, *Alanphillipsia* is introduced as a new genus in the *Botryosphaeriaceae* with four species, *A. aloes*, *A. aloeigena* and *A. aloetica* from *Aloe* spp. and *A. euphorbiae* from *Euphorbia* sp. (South Africa). A new combination is also proposed for *Brachysporium torulosum* (Deightoniella black tip of banana) as *Corynespora torulosa*. 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

Dothideomycetes

Botryosphaeriales, Botryosphaeriaceae
Alanphillipsia aloeigena
Alanphillipsia aloes
Alanphillipsia aloetica
Alanphillipsia euphorbiae
Neofusicoccum cryptoaustrale
Neofusicoccum ursorum

Botryosphaeriales, Planistromellaceae
Kellermania agaves
Kellermania pseudoyuccigena

Capnodiales, Cladosporiaceae
Toxicocladosporium ficiniae

Capnodiales, Mycosphaerellaceae
Neodeightoniella phragmiticola
Neomycosphaerella pseudopentameridis
Neopseudocercospora terminaliae
Pallidocercospora ventilago
Paramycosphaerella brachystegia
Passalora pseudotithoniae
Sphaerulina rhododendricola

Capnodiales, Teratosphaeriaceae
Teratosphaeria terminaliae

Pleosporomycetidae, Pleosporales, Corynesporascaceae
Corynespora torulosa

Pleosporomycetidae, Pleosporales, incertae sedis
Ochrocladosporium adansoniae

Pleosporales, Massarineae, Massarinaceae
Stagonospora pseudopaludosa

Pleosporomycetidae, Pleosporales, Lophiostomataceae
Dimorphiopsis brachystegiae

Pleosporomycetidae, Pleosporales, Pleosporineae, Didymellaceae
Coniothyrium prosopidis
Peyronellaea prosopidis
Phoma aloes

Pleosporomycetidae, Pleosporales, Pleosporineae, Phaeosphaeriaceae
Camarosporium aloes
Camarosporium psoraleae
Neophaeosphaeria agaves
Paraconiothyrium lycopodinum
Paraconiothyrium polonense

Pleosporomycetidae, Pleosporales, Pleosporineae, Pleosporaceae
Bipolaris drechsleri

Eurotiomycetes

Chaetothyriomycetidae, Chaetothyriales, Chaetothyriaceae
Knufia tsunedae

Herpotrichiellaceae
Cladophialophora multiseptata
Phaeococcomyces aloes

Cyphellophoraceae
Cyphellophora catalaunica

Eurotiomycetidae, Onygenales, Onygenaceae
Auxarthron longisporum
Chrysosporium magnasporum
Chrysosporium oceanitesii

Leotiomycetes

Helotiales
Pilidium pseudoconcavum

Pseudeurotiaceae
Pleuroascus rectipilus

Sordariomycetes

Hypocreomycetidae, Coronophorales, Scortechiniaceae
Pseudocatenomycopsis rothmanniae

Hypocreomycetidae, Glomerellales, Glomerellaceae
Colletotrichum euphorbiae

Hypocreomycetidae, Hypocreales, incertae sedis
Harzia cameroonensis
Stachybotrys oleronensis

Hypocreomycetidae, Hypocreales, Nectriaceae
Calonectria blephiliae
Calonectria mossambicensis
Chaetopsina pini
Chaetopsina pinicola

Hypocreomycetidae, Microascales, Gondwanamycetaceae
Custingophora blanchettei

Incertae sedis
Myrmecridium thailandicum

Sordariomycetidae, Diaporthales, Diaporthaceae
Diaporthe cassines
Diaporthe diospyricola
Diaporthe maytenicola
Diaporthe psoraleae
Diaporthe psoraleae-pinnatae

Sordariomycetidae, Diaporthales, Cryphonectriaceae
Mastigosporella anisophylleae

Sordariomycetidae, Diaporthales, Harknessiaceae
Harknessia proteae

Sordariomycetidae, Magnaporthales, Magnaporthaceae
Pyricularia bothriochloae

Xylariomycetidae, Xylariales, Amphisphaeriaceae
Discosia pseudoartocreas

BASIDIOMYCOTA

Agaricomycetes, Polyporales, Meruliaceae
Hypochnicium huinayensis

CHROMISTA

Oomycota, Oomycetes, Pythiales, Pythiaceae
Phytophthora ipomoeae

MYXOMYCOTA

Myxomycetes, Liceales, Liceaceae
Licea xanthospora

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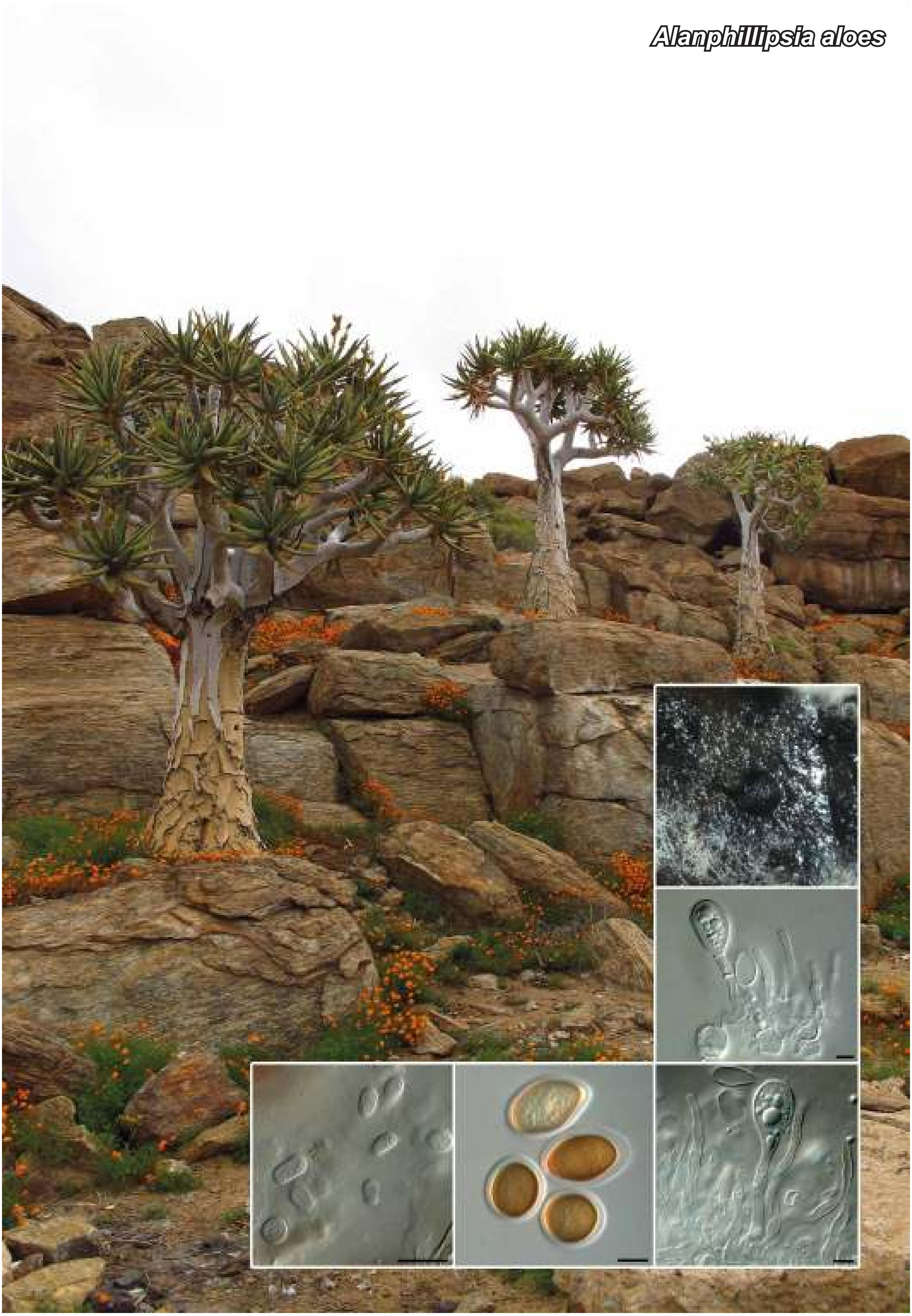
Alanphillipsia aloes

Fungal Planet 158 – 26 November 2013

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

Etymology. Named after Dr Alan J.L. Phillips, in acknowledgement for the tremendous contribution that he has made to elucidate the taxonomy of members of the *Botryosphaeriaceae*.

Conidiomata immersed, globose with central ostiole, dark brown; wall of several layers of brown *textura angularis*. *Paraphyses* intermingled among conidiophores, lining the inner cavity, hyaline, smooth, subcylindrical, branched at base or not, aseptate or transversely septate, with obtuse to subobtuse apices. *Conidiophores* hyaline, smooth, subcylindrical, flexuous or straight, septate. *Macroconidiogenous cells* terminal, integrated, hyaline, smooth, subcylindrical to lageniform, proliferating percurrently near apex. *Macroconidia* solitary, hyaline when young, becoming golden-brown to medium brown, verruculose, granular to guttulate, surrounded by a persistent, hyaline outer layer (absent in some species, or reduced to a basal frill or basal and apical appendage), ellipsoid to obclavate or subcylindrical with truncate scar on hyaline layer. *Microconidiogenous cells* in the same conidioma, hyaline, smooth, subcylindrical, proliferating inconspicuous percurrently at apex. *Microconidia* hyaline, smooth, granular, subcylindrical to ellipsoid, apex obtuse, base truncate, with minute marginal frill.

Type species. Alanphillipsia aloes.
MycoBank MB805816.

Alanphillipsia aloes Crous & M.J. Wingf., *sp. nov.*

Etymology. Named after the host genus on which it occurs, *Aloe*.

Colonies sporulating on MEA: *Conidiomata* immersed, globose with central ostiole, dark brown, up to 300 µm diam; wall of several layers of brown *textura angularis*. *Paraphyses* intermingled among conidiophores, lining the inner cavity, hyaline, smooth, subcylindrical, branched at base or not, up to 80 µm long, 2–4 µm wide at base, transversely septate, with obtuse to subobtuse apices. *Conidiophores* hyaline, smooth, subcylindrical, flexuous or straight, 1–3-septate, 20–40 × 3–7 µm. *Macroconidiogenous cells* terminal, integrated, hyaline, smooth, subcylindrical to lageniform, 10–20 × 3–4 µm; proliferating inconspicuously 1–3 times percurrently near apex. *Macroconidia* solitary, hyaline when young, becoming golden-brown to medium brown, verruculose, granular to guttulate, surrounded by a persistent, hyaline outer layer up to 5 µm diam, ellipsoid to obclavate or at times subcylindrical with truncate scar on hyaline layer, 3–4 µm diam (with minute marginal frill), not thickened, but somewhat refractive, (26–)30–38(–50) × (15–)18–22(–23) µm. *Microconidiogenous cells* in the same conidioma, hyaline, smooth, subcylindrical, 7–18 × 3–5 µm, proliferating inconspicuous percurrently at apex. *Microconidia* hyaline, smooth, granular, subcylindrical to ellipsoid, apex obtuse, base truncate (3–4 µm diam), with minute marginal frill, 6–12 × 3.5–4.5 µm.

Culture characteristics — Colonies on MEA, PDA and OA covering the dish within 2 wk, surface olivaceous-grey, reverse iron-grey, with moderate pale olivaceous-grey aerial mycelium.

Typus. South Africa, Western Cape Province, Clanwilliam, on dark lesions of dying *Aloe dichotoma* (*Xanthorrhoeaceae*), Sept. 2012, *M.J. Wingfield* (holotype CBS H-21418, cultures ex-type CPC 21298 = CBS 136410, ITS sequence GenBank KF777138, LSU sequence GenBank KF777194, MycoBank MB805817).

Colour illustrations. Aloe dichotoma in Clanwilliam, South Africa. Colony on MEA, conidiogenous cells, paraphyses, macro- and microconidia. Scale bars = 10 µm.

Notes — *Allanphillipsia* is reminiscent of *Aplosporella* (verruculose conidia, presence of paraphyses) (Damm et al. 2007, Slippers et al. 2013), but distinct in that it has a hyaline outer layer. In this regard it also resembles *Cytosphaera*, though the latter has eustromatic, irregularly pulvinate, erumpent to superficial conidiomata, phialides with periclinal thickening, and hyaline conidia (Sutton 1980).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Botryosphaeria sumachi* (GenBank DQ377865; Identities = 919/926 (99 %), no gaps), *Diplodia corticola* (GenBank DQ377848; Identities = 921/929 (99 %), no gaps) and *Phaeobotryosphaeria porosa* (GenBank DQ377895; Identities = 918/926 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *Diplodia pseudoseriata* (GenBank EU860383; Identities = 522/558 (94 %), Gaps = 11/558 (1 %)), *Phaeobotryosphaeria eucalypti* (GenBank JX646803; Identities = 511/532 (96 %), Gaps = 6/532 (1 %)) and *P. citrigena* (GenBank EU673329; Identities = 524/546 (96 %), Gaps = 5/546 (0 %)).

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Alanphillipsia aloeigena

Fungal Planet 159 – 26 November 2013

Alanphillipsia aloeigena Crous & M.J. Wingf., *sp. nov.*

Etymology. Named after the host genus on which it occurs, *Aloe*.

Conidiomata black, pycnidial, up to 500 µm diam, erect with elongated neck and central ostiole, surface covered with mycelial hairs, forming individually on WA, OA and PNA; wall of 6–10 layers of brown, thick-walled *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* hyaline, smooth, subcylindrical to ampulliform, 3–5 × 10–25 µm, proliferating percurrently at apex. *Conidia* smooth, hyaline, becoming pale brown with age, guttulate to granular, thick-walled, subcylindrical, straight to irregularly curved, apex obtuse, becoming clavate with age; base truncate, but with prominent basal frill which appears as flared appendage, 1–2 µm long, but in exceptional cases up to 5 µm long, (25–)28–38(–50) × (6–)7–8(–10) µm; the basal frill can be seen on immature conidia to extend up to 5 µm along the side of the tapered conidium, suggesting that this is a true appendage, and not a mere marginal frill that results from rhexolytic conidiation; on some conidia this is visible as an outer layer that completely encloses the conidium as additional layer, not as mucoid sheath. A few microconidia were observed in culture, which were hyaline, smooth, subcylindrical with obtuse ends, 5–10 × 3–4 µm.

Culture characteristics — Colonies covering the dish within 2 wk, with moderate aerial mycelium and even, smooth margins. On MEA surface pale olivaceous-grey in centre, olivaceous-grey in outer zone, sepia in reverse. On PDA surface and reverse olivaceous-grey with patches of iron-grey. On OA iron-grey with patches of olivaceous-grey and dirty white.

Typus. South Africa, Namakwaland, Goegap Nature Reserve, on leaves of *Aloe melanocantha* (*Xanthorrhoeaceae*), 26 Sept. 2012, *M.J. Wingfield* (holotype CBS H-21419, culture ex-type CPC 21286 = CBS 136408, ITS sequence GenBank KF777137, LSU sequence GenBank KF777193, MycoBank MB805818).

Colour illustrations. *Aloe melanocantha* in Goegap Nature Reserve, South Africa. Colony on PNA, conidiogenous cells and conidia. Scale bar = 10 µm.

Notes — *Alanphillipsia aloeigena* is morphologically interesting in that its conidia, which eventually turn brown with age, are formed inside a thin-walled sheath that can extend at either end into appendages.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Phaeobotryosphaeria visci* (GenBank DQ377869; Identities = 799/805 (99 %), no gaps), *Botryosphaeria sumachi* (GenBank DQ377865; Identities = 799/805 (99 %), no gaps) and *Sphaeropsis sapinea* (GenBank EU754157; Identities = 798/805 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *P. citrigena* (GenBank EU673329; Identities = 540/560 (96 %), Gaps = 6/560 (1 %)), *Diplodia pseudoseriata* (GenBank EU860383; Identities = 538/574 (94 %), Gaps = 16/574 (2 %)) and *P. eucalypti* (GenBank JX646803; Identities = 511/531 (96 %), Gaps = 7/531 (1 %)).

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Colletotrichum euphorbiae
& Alanphillipsia euphorbiae

Fungal Planet 161 & 162 – 26 November 2013

Colletotrichum euphorbiae Damm & Crous, *sp. nov.*

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

Sexual morph not observed. *Asexual morph on SNA. Conidiomata* poorly developed and conidiophores formed directly on hyphae or globose, closed conidiomata, apparently opening by rupture, wall cells medium brown, angular. *Setae* not observed. *Conidiophores* pale brown, smooth-walled, septate, branched, to 50 µm long. *Conidiogenous cells* pale brown, smooth-walled, cylindrical, percurrent proliferation often observed, 13.5–23 × 5.5–7 µm, opening 1.5–2.5 µm diam, collarette 0.5 µm long, periclinal thickening sometimes observed. *Conidia* hyaline to pale orange, smooth-walled, aseptate, straight, sometimes slightly curved, cylindrical to clavate, with one end round and one end truncate, guttulate (17–)23–28(–28.5) × (6–)6.5–7 µm, mean ± SD = 25.6 ± 2.6 × 6.7 ± 0.2 µm, L/W ratio = 3.8. *Appressoria* formed in SNA slide culture after 20 d, single, medium to dark brown, smooth-walled, roundish to clavate, the edge lobate to undulate, (6.5–)8.5–14.5(–20.5) × (5.5–)6–10.5(–16) µm, mean ± SD = 11.5 ± 3.4 × 8.2 ± 2.2 µm, L/W ratio = 1.4. For description on *Anthriscus* stem and OA, see MycoBank.

Culture characteristics (near UV light with a 12 h photoperiod, 20 °C after 10 d) — Colonies on SNA flat, with undulate to lobate margin, hyaline, covered by thin, felty, white, aerial mycelium, the *Anthriscus* stem, filter paper and medium partly covered by orange conidiomata, reverse similar colours; growth 16–19 mm in 7 d (22.5–26.5 mm in 10 d). Conidia in mass orange.

Typus. South Africa, Western Cape Province, Kirstenbosch Botanical Garden, on leaves of *Euphorbia* sp. (*Euphorbiaceae*), Sept. 2012, *M.J. Wingfield* (holotype CBS H-21409, culture ex-type CBS 134725 = CPC 21823, ITS sequence GenBank KF777146, GAPDH sequence GenBank KF777131, TUB2 sequence GenBank KF777247, ACT sequence GenBank KF777125, CHS-1 sequence GenBank KF777128, HIS3 sequence GenBank KF777134, LSU sequence GenBank KF777202, MycoBank MB805820). For additional specimens, see MycoBank.

Notes — The genus *Colletotrichum* is currently under review; major species complexes such as *C. acutatum*, *C. boninense* and *C. gloeosporioides* were treated recently (Damm et al. 2012a, b, Weir et al. 2012). *Colletotrichum euphorbiae* forms cylindrical to clavate conidia with one end round and one end truncate, often in closed fruit bodies. Conidia with similar shapes were formed by other *Colletotrichum* species as well, especially by *C. sansevieriae* (Nakamura et al. 2006) and the species of the *C. orbiculare* complex (Damm et al. 2013). However, only conidia of *C. euphorbiae* exceed 20 µm on average in length. Closest matches in blastn searches with the ITS sequence were *C. sansevieriae* strains from *Sansevieria* spp. in Korea, Florida and Australia (KC847065, Park et al. 2013; JF911349, JF911350, Palmateer et al. 2012 and HQ433226, Aldoud et al. 2011), with 96–97 % identity. The ITS sequence of the ex-holotype strain of *C. sansevieriae* in GenBank (AB212991, Nakamura et al. 2006) only comprised 159 bp (ITS2) and was therefore not included in the ITS phylogeny of Cannon et al. (2012).

Reports of *Colletotrichum* species on *Euphorbia* include *C. capsici*, *C. dematium*, *C. euchroum* (conidia 12–20 × 4–5 µm; Sydow & Sydow 1913), *C. lineola* and *C. gloeosporioides* (Damm et al. 2009, Farr & Rossman 2013). Only *C. gloeosporioides* (s.lat.) was previously reported from *Euphorbia* in Africa (Doidge 1950, Crous et al. 2000). All these taxa form either shorter or curved conidia or are not closely related to *C. euphorbiae*.

Alanphillipsia euphorbiae Crous & M.J. Wingf., *sp. nov.*

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

Conidiomata erumpent, pycnidial, globose with central ostiole up to 300 µm diam; wall of 3–6 layers of dark brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, subcylindrical to ampulliform, 10–15 × 4–6 µm; proliferating several times percurrently near apex. *Paraphyses* intermingled among conidiogenous cells, hyaline, smooth, 0–2-septate, subcylindrical, 35–50 × 3–5 µm. *Conidia* solitary, brown, guttulate, finely roughened, ellipsoid to somewhat clavate, aseptate, apex obtuse, base truncate, 3–5 µm diam, (18–)20–23(–26) × (12–)13–14(–16) µm.

Colour illustrations. Kirstenbosch Botanical Garden, South Africa. Left column *Colletotrichum euphorbiae*: conidiomata SNA; conidiogenous cells and conidia. Scale bars = 100, 10 and 10 µm. Right column *Alanphillipsia euphorbiae*: conidiomata on PDA and on PNA; paraphyses and conidiogenous cells; conidia. Scale bar = 10 µm.

Culture characteristics — Colonies covering dish in 2 wk, with abundant, fluffy aerial mycelium. On PDA surface and reverse iron-grey. On MEA surface olivaceous-grey, reverse iron-grey. On OA surface iron-grey with patches of dirty white.

Typus. South Africa, Western Cape Province, Kirstenbosch Botanical Garden, on leaves of *Euphorbia* sp. (*Euphorbiaceae*), Sept. 2012, *M.J. Wingfield* (holotype CBS H-21421, culture ex-type CPC 21629, 21628 = CBS 136411, ITS sequence GenBank KF777140, LSU sequence GenBank KF777196, MycoBank MB805821).

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Diplodia corticola* (GenBank DQ377848; Identities = 870/875 (99 %), no gaps), *Botryosphaeria sumachi* (GenBank DQ377865; Identities = 888/894 (99 %), no gaps) and *Phaeobotryosphaeria porosa* (GenBank DQ377895; Identities = 887/894 (99 %), no gaps).

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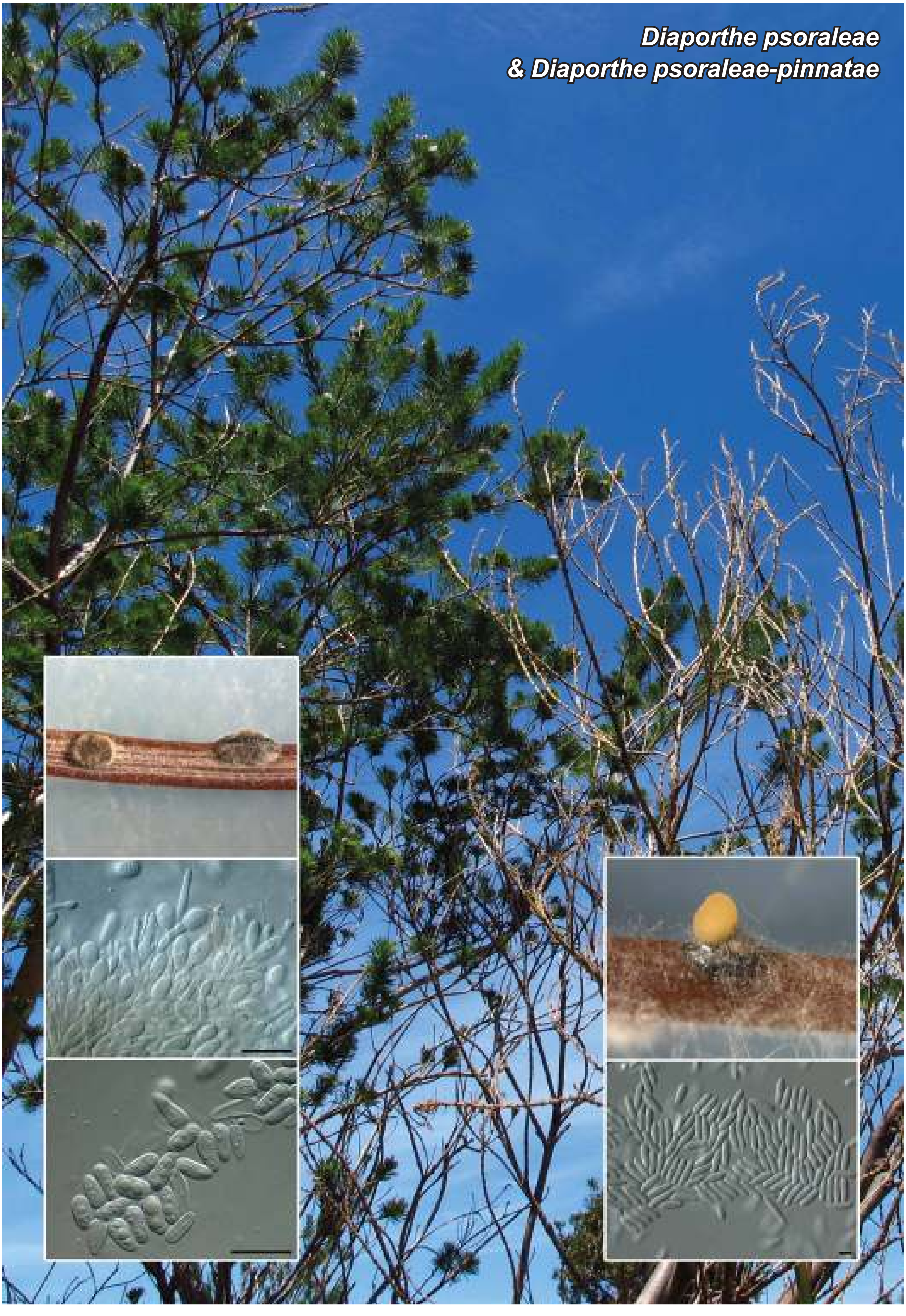

Diaporthe psoraleae
& Diaporthe psoraleae-pinnatae

Fungal Planet 163 & 164 – 26 November 2013

Diaporthe psoraleae Crous & M.J. Wingf., *sp. nov.*

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

On PNA. *Conidiomata* pycnidial, globose, aggregated in a large stroma up to 600 µm diam, black, erumpent, exuding creamy conidial droplets from central ostioles; walls of 3–6 layers of medium brown *textura angularis*. *Conidiophores* hyaline, smooth, 1–2-septate, unbranched, densely aggregated, cylindrical, straight to sinuous, 25–40 × 4–6 µm. *Conidiogenous cells* 10–25 × 2.5–3.5 µm, phialidic, cylindrical, terminal, with slight taper towards apex, 1–2 µm diam, with visible periclinal thickening; collarette not observed. *Paraphyses* cylindrical, hyaline, smooth, 1–2-septate, up to 40 µm long, 1.5–2 µm diam. *Alpha conidia* aseptate, hyaline, smooth, guttulate, obovoid to fusoid-ellipsoid, tapering towards both ends, straight, widest just below apex, in upper third of conidium, apex obtuse, base rounded to obconically truncate, (11–)13–15(–16) × (4–)6–7(–8) µm. *Gamma conidia* not observed. *Beta conidia* not observed.

Culture characteristics — Colonies covering MEA and OA dishes after 2 wk, but only reaching 55 mm diam on PDA, margins feathery, uneven, with sparse aerial mycelium. On PDA surface and reverse umber; on MEA surface hazel in centre, sepia in outer region, brown-vinaceous underneath; on OA surface vinaceous-buff to isabelline.

Typus. South Africa, Western Cape Province, Betty's Bay, Harold Porter National Botanical Garden, on stems of *Psoralea pinnata* (*Fabaceae*), 28 Oct. 2012, *M.J. Wingfield* (holotype CBS H-21422, culture ex-type CPC 21634, 21635 = CBS 136412, ITS sequence GenBank KF777158, LSU sequence GenBank KF777211, TEF sequence GenBank KF777245, TUB sequence GenBank KF777251, MycoBank MB805822).

Notes — No species of *Diaporthe* are presently known to occur on *Psoralea* in South Africa (Crous et al. 2000, Gomes et al. 2013). Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Diaporthe eres* (GenBank AF362565; Identities = 873/875 (99 %), no gaps), *D. eucalyptorum* (GenBank JX069846; Identities = 878/881 (99 %), no gaps) and *D. musigena* (GenBank JF951158; Identities = 878/881 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *D. cinerascens* (GenBank KC343050; Identities = 552/572 (97 %), Gaps = 3/572 (0 %)), *D. neotheicola* (GenBank KC145902; Identities = 575/598 (96 %), Gaps = 4/598 (0 %)) and *D. rhusicola* (GenBank JF951146; Identities = 553/576 (96 %), Gaps = 4/576 (0 %)). Closest hits using the TEF sequence had highest similarity to *D. neotheicola* (GenBank JQ809273; Identities = 390/460 (85 %), Gaps = 28/460 (6 %)), *D. oncostoma* (GenBank KC343888; Identities = 410/495 (83 %), Gaps = 22/495 (4 %)) and *D. vaccinii* (GenBank KC343954; Identities = 413/499 (83 %), Gaps = 23/499 (4 %)). Closest hits using the TUB sequence had highest similarity to *D. hickoriae* (GenBank KC344086; Identities = 645/690 (93 %), Gaps = 2/690 (0 %)), *D. stictica* (GenBank KC344180; Identities = 645/690 (93 %), Gaps = 3/690 (0 %)) and *D. foeniculacea* (GenBank KC344069; Identities = 640/691 (93 %), Gaps = 10/691 (1 %)).

Diaporthe psoraleae-pinnatae Crous & M.J. Wingf., *sp. nov.*

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

On PNA. *Conidiomata* pycnidial, globose, up to 250 µm diam, black, erumpent, exuding creamy conidial droplets from central ostioles; walls of 3–6 layers of medium brown *textura angularis*. *Conidiophores* hyaline, smooth, 0–1-septate, unbranched, densely aggregated, cylindrical, straight to sinuous, 15–25 × 2.5–3.5 µm. *Conidiogenous cells* 8–15 × 2–3 µm, phialidic, cylindrical, terminal, with slight taper towards apex, 1–1.5 µm diam, with visible periclinal thickening; collarette slightly flared, up to 1 µm long when present. *Paraphyses* not observed. *Alpha conidia* aseptate, hyaline, smooth, guttulate, subcylindrical to fusoid-ellipsoid, tapering towards both ends, straight, apex obtuse, base subtruncate, (7–)9–10(–12) × (2–)2.5–3 µm. *Gamma conidia* not observed. *Beta conidia* not observed.

Culture characteristics — Colonies covering plates within 2 wk, spreading with sparse aerial mycelium. On MEA surface honey to buff, reverse honey with patches of cinnamon; on OA surface olivaceous-grey in centre, pale olivaceous-grey in outer region; on PDA honey on surface and reverse.

Colour illustrations. *Psoralea pinnata* dieback at Harold Porter National Botanical Garden, Betty's Bay, South Africa. Left column *Diaporthe psoraleae*: conidiomata on PNA; conidiogenous cells and alpha conidia. Right column *Diaporthe psoraleae-pinnatae*: conidioma on PNA; alpha conidia. Scale bars = 10 µm.

Typus. South Africa, Western Cape Province, Betty's Bay, Harold Porter National Botanical Garden, on stems of *Psoralea pinnata* (*Fabaceae*), 28 Oct. 2012, *M.J. Wingfield* (holotype CBS H-21423, culture ex-type CPC 21638, 21639 = CBS 136413, ITS sequence GenBank KF777159, LSU sequence GenBank KF777212, TUB sequence GenBank KF777252, MycoBank MB805823).

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Phaeocytostroma plurivorum* (GenBank FR748104; Identities = 880/884 (99 %), no gaps), *Diaporthe decedens* (GenBank AF408348; Identities = 874/878 (99 %), no gaps) and *Phomopsis viticola* (GenBank AF439635; Identities = 857/862 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *D. helianthi* (GenBank AJ312349; Identities = 552/584 (95 %), Gaps = 13/584 (2 %)), *D. ambigua* (GenBank KC343010; Identities = 543/575 (94 %), Gaps = 11/575 (1 %)) and *Phomopsis limonii* (GenBank KC145856; Identities = 553/588 (94 %), Gaps = 11/588 (1 %)). Closest hits using the TUB sequence had highest similarity to *D. rhoina* (GenBank KC344157; Identities = 663/692 (96 %), Gaps = 2/692 (0 %)), *D. acerina* (GenBank KC343974; Identities = 639/706 (91 %), Gaps = 21/706 (2 %)) and *Diaporthe* cf. *nobilis* (GenBank KC344116; Identities = 636/703 (90 %), Gaps = 14/703 (1 %)).

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Harzia cameroonensis

Fungal Planet 169 – 26 November 2013

Harzia cameroonensis Crous & Jol. Roux, *sp. nov.*

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

Foliicolous. *Mycelium* consisting of hyaline, smooth, branched, septate hyphae, 3–4 µm diam. *Conidiophores* dimorphic. *Microconidiophores* erect, cylindrical, straight or curved, mostly unbranched, hyaline, smooth, 3–8-septate, 30–200 × 3–4 µm. *Microconidiogenous cells* terminal or lateral, having swollen vesicles that are aspergillus-like, globose to somewhat clavate, elongated, hyaline, smooth, 6–8 µm diam, covered in ampulliform, hyaline phialides, 7–10 × 2.5–3.5 µm; apex 1.5 µm diam, with minute, non-flared collarettes. *Microconidia* hyaline, smooth, aseptate, ellipsoid to clavate, apex obtuse, tapering to truncate base, 2–5 × 1.5–2 µm. *Macroconidiophores* terminal or lateral on hyphae, 1–4-septate, branched or not, frequently aggregated, giving rise to clusters of conidia, subcylindrical, hyaline, smooth, 10–50 × 5–7 µm. *Macroconidiogenous cells* hyaline, smooth, terminal and lateral, subcylindrical to ampulliform, 7–15 × 5–8 µm, with a terminal separating cell, 3–10 × 3–5 µm; with rhexolytic separation, leaving a non-flared collarette on the conidiogenous cell. *Macroconidia* solitary, globose to obovoid, guttulate, hyaline and smooth when young, becoming brown, thick-walled (2 µm diam), warty and ridged with age, developing a basal transverse septum, (18–)26–36(–40) × (15–)25–32(–36) µm; basal marginal frill hyaline, not flared, cylindrical, 3–10 µm long; basal hilum truncate, 4–6 µm diam; conidia 1-septate, with transverse septum (2–3 µm thick) developing 3–10 µm from hilum, with visible central pore in septum.

Culture characteristics — Colonies covering the dish within 2 wk, with moderate aerial mycelium; on MEA surface and reserve cinnamon; on PDA surface and reverse buff; on OA surface buff to honey.

Typus. Cameroon, Mount Cameroon campsite, unknown creeper plant host, 24 Oct. 2012, *J. Roux* (holotype CBS H-21428, culture ex-type CPC 22065, 22066 = CBS 136420, ITS sequence GenBank KF777163, LSU sequence GenBank KF777216, MycoBank MB805830).

Colour illustrations. Mount Cameroon campsite; mycelium giving rise to macroconidiophores with macroconidia of *H. cameroonensis*, and microconidiophores and microconidia of a *Proteophiala* synasexual morph. Scale bars = 10 µm.

Notes — *Harzia cameroonensis* is a typical species of *Harzia*, with sympodially branched, hyaline superficial mycelium, brown conidia and a *Proteophiala* synasexual morph. *Harzia* is distinguished from *Olpitrichum* (which also has a *Proteophiala* synasexual morph), by having conidia separated by means of a separating cell. Of the three species of *Harzia* presently known, *H. cameroonensis* is distinct based on its larger, 1-septate conidia (Domsch et al. 2007). Although *Harzia* has been linked to *Melanconium* sexual morphs (Goh et al. 1998), the genus may well be polyphyletic, and more collections are required to resolve its phylogeny.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Sphaerodes fimicola* (GenBank AY015628; Identities = 820/843 (97 %), Gaps = 1/843 (0 %)), *Melanospora brevirostris* (GenBank AY015627; Identities = 820/843 (97 %), Gaps = 1/843 (0 %)) and *Sphaerodes quadrangularis* (GenBank GQ354530; Identities = 825/853 (97 %), Gaps = 1/853 (0 %)). Closest hits using the ITS sequence had highest similarity to *Harzia acremonioides* (GenBank HQ698593; Identities = 579/618 (94 %), Gaps = 20/618 (3 %)) and *Sphaerodes fimicola* (GenBank JQ034510; Identities = 441/494 (89 %), Gaps = 31/494 (6 %)). The GenBank sequence of *Harzia acremonioides* (GenBank HQ698593) also contained 491 nucleotides of LSU sequence; a similarity of 99 % (502/505 nucleotides) was observed between our sequence and this combined ITS/LSU sequence. Unfortunately, it was not possible to compare the complete length of our LSU sequence (853 nucleotides) with the corresponding complete LSU sequence of *Harzia acremonioides*.

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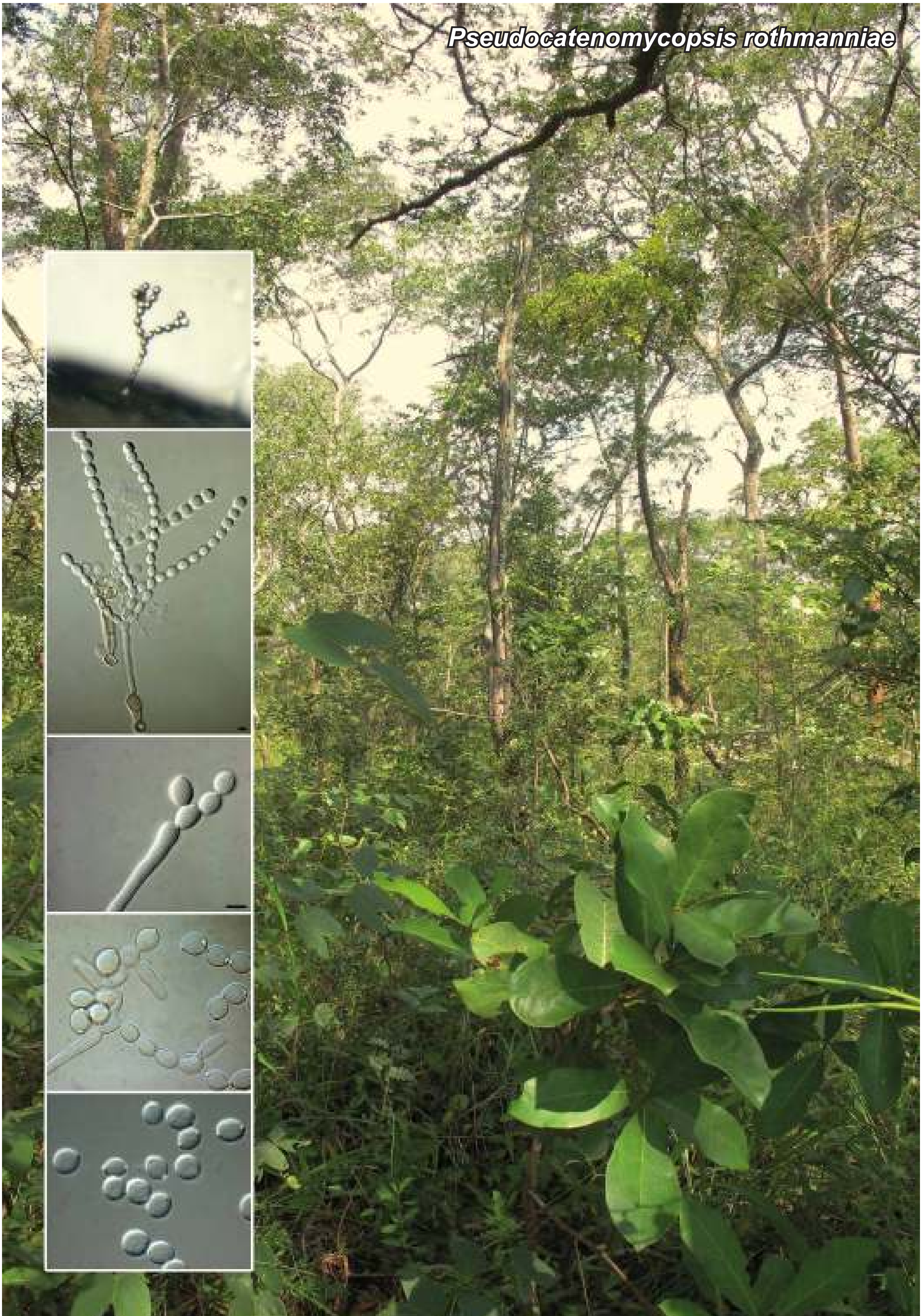
Pseudocatenomycopsis rothmanniae

Fungal Planet 173 – 26 November 2013

Pseudocatenomycopsis Crous & L.A. Shuttlew., *gen. nov*.

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

Mycelium consisting of hyaline, smooth, branched, septate hyphae. *Conidiophores* erect, solitary, smooth, straight to flexuous, initially hyaline and smooth, becoming brown; base lacking rhizoids, not swollen, forming a T-cell, multiseptate, generally not constricted at septa. *Conidiogenous apparatus* apical, consisting of a conidiogenous cell giving rise to chains of branched conidia, or a ramoconidium giving rise to conidial chains. *Conidiogenous cells* hyaline, smooth (becoming brown with age), subcylindrical, with flattened, unthickened scars; in some cases hila have convex thickening, extending into the conidiogenous cell, slightly reflective. *Ramoconidia* 0–1-septate fusoid-ellipsoid to doliiform or subcylindrical, hyaline, smooth, but turning brown with age, with 1–3 flattened scars that can be thickened, giving rise to conidial chains or a few cylindrical hyphal-like cells that again become fertile, forming conidial chains, but chains can also again form ramoconidia higher up, giving rise to newly branched conidial chains. *Conidia* aseptate, hyaline, smooth, ellipsoid to ovoid, granular, ends with truncate, flattened scars that can have a convex thickening extending into the conidium, and that are somewhat refractive.

Type species. Pseudocatenomycopsis rothmanniae.
MycoBank MB805836.

Pseudocatenomycopsis rothmanniae Crous & L.A. Shuttlew., *sp. nov*.

Etymology. Named after the host genus on which it occurs, *Rothmannia*.

Colonies growing well on OA. *Mycelium* consisting of hyaline, smooth, branched, septate, 3–4 µm diam hyphae. *Conidiophores* erect, solitary, smooth, straight to flexuous, up to 300 µm tall, 5–8 µm diam, initially hyaline and smooth, becoming brown; base lacking rhizoids, not swollen, forming a T-cell, 3–10-septate, generally not constricted at septa. *Conidiogenous apparatus* apical, consisting of a conidiogenous cell giving rise to chains of branched conidia, or a ramoconidium giving rise to conidial chains. *Conidiogenous cells* hyaline, smooth (becoming brown with age), subcylindrical, 10–30 × 10–12 µm, with 1–3 flattened, unthickened scars, 2–3 µm diam; in some cases hila have convex thickening, extending into the conidiogenous cell, slightly reflective. *Ramoconidia* 0–1-septate when present, fusoid-ellipsoid to doliiform or subcylindrical, 10–20 × 8–12 µm, hyaline, smooth, but turning brown with age, with 1–3 flattened scars, 2–3 µm diam, that can be thickened, giving rise to conidial chains or a few cylindrical hyphal-like cells that again become fertile, forming conidial chains, but chains can also again form ramoconidia higher up, giving rise to newly branched conidial chains. *Conidia* (10–)13–16(–18) × (10–)11–13(–14) µm, aseptate, hyaline, smooth, ellipsoid to ovoid, granular, ends with truncate, flattened scars, 3–4 µm diam, that can have a convex thickening extending into the conidium, and that are somewhat refractive.

Culture characteristics — Colonies not growing on MEA, PDA and SNA. Colonies grow well on OA, surface white due to sporulation, but medium turns pale olivaceous-grey; colonies reaching 20 mm diam after 1 mo.

Typus. Zambia, S14°48.514' E24°7.959' on stem of *Rothmannia engleriana* (*Rubiaceae*), Jan. 2013, *L.A. Shuttleworth* (holotype CBS H-21432, culture ex-type CPC 22733, 22734 = CBS 136445, ITS sequence GenBank KF777185, LSU sequence GenBank KF777237, MycoBank MB805837).

Colour illustrations. *Rothmannia engleriana* in Zambia. Conidiophores giving rise to branched chains of conidia. Scale bars = 10 µm.

Notes — *Pseudocatenomycopsis* resembles the genus *Catenomycopsis* (based on *C. rosea*; sexual morph *Chaenothecopsis haematopus*). Although the genus *Catenomycopsis* is monotypic, more than 80 taxa have been described in *Chaenothecopsis*, with asexual morphs ranging from phialophora-like hyphomycetes to coelomycetes (Tibell & Constantinescu 1991), suggesting that *Chaenothecopsis* is polyphyletic.

Catenomycopsis is characterised by having hyaline, penicillate conidiophores giving rise to branched conidial chains (Tibell & Constantinescu 1991). However, *Pseudocatenomycopsis* can be distinguished by having conidiophores that eventually turn brown, and conidiogenous loci and conidial hila have a prominent convex, reflective thickening, which is absent in *Catenomycopsis.*

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Neofracchiaea callista* (GenBank AY695269; Identities = 853/903 (94 %), Gaps = 6/903 (0 %)), *Cryptosphaerella cylindriformis* (GenBank FJ968973; Identities = 856/907 (94 %), Gaps = 1/907 (0 %)) and *Scortechiniellopsis leonensis* (GenBank FJ968993; Identities = 852/903 (94 %), Gaps = 1/903 (0 %)). Closest hits using the ITS sequence had highest similarity to *Parasympodiella elongata* (GenBank GQ303280; Identities = 539/658 (82 %), Gaps = 28/658 (4 %)), *Parasympodiella laxa* (GenBank GQ303285; Identities = 508/619 (82 %), Gaps = 36/619 (5 %)) and *Parasympodiella eucalypti* (GenBank GQ303284; Identities = 525/648 (81 %), Gaps = 34/648 (5 %)).

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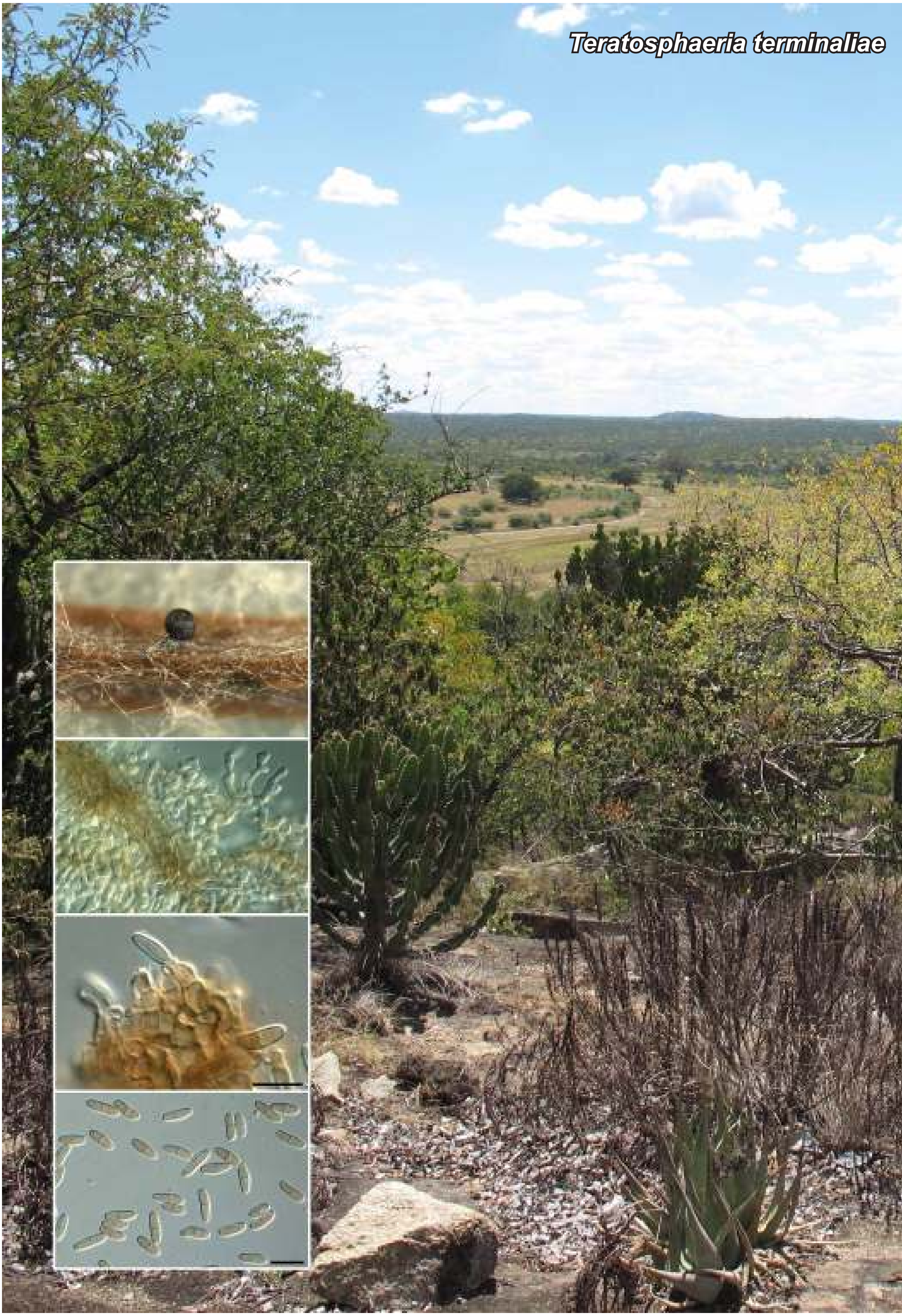
Teratosphaeria terminaliae

Fungal Planet 178 – 26 November 2013

Teratosphaeria terminaliae Crous & Jol. Roux, *sp. nov.*

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

On PNA. *Conidiomata* uniloculate, pycnidial, immersed, globose, dark brown to black, up to 200 µm diam with central ostiole; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, brown, verruculose, ampulliform to doliiform, proliferating several times percurrently near apex, 4–8 × 3–5 µm. *Conidia* (8–)10–14(–22) × (2.5–)3(–4) µm, brown, smooth, guttulate, subcylindrical to obclavate, apex obtuse to subobtuse, widest in middle in small conidia, or in middle of basal cell in larger conidia, (0–)1–2(–4)-septate; base truncate, 1.5 µm diam with minute marginal frill when present.

Culture characteristics — Colonies reaching 60 mm diam after 2 wk with sparse to moderate aerial mycelium and even, lobed margins. On PDA surface and reverse iron-grey; on MEA surface olivaceous-grey, reverse iron-grey; on OA surface olivaceous-grey with patches of dirty white.

Typus. Zimbabwe, 60 km from Zwivashane, Filabussi village, on leaves of *Terminalia cericea* (*Combretaceae*), 27 Mar. 2012, *J. Roux & L. Jimu* (holotype CBS H-21437, culture ex-type CPC 21175, 21176 = CBS 136428, ITS sequence GenBank KF777189, LSU sequence GenBank KF777240, MycoBank MB805842).

Notes — Presently no species of *Teratosphaeria* are known from *Terminalia*. Based on DNA sequence data it shares 98 % similarity (ITS) with *T. macowanii*. *Teratosphaeria macowanii* is a pathogen that attacks *Protea* spp. in South Africa and Malawi (Crous et al. 2013b), and is distinct in its superficial conidiomata, and sooty appearance on infected leaves.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Teratosphaeria macowanii* (GenBank EU019254; Identities = 873/878 (99 %), no gaps), *T. maxii* (GenBank DQ885898; Identities = 873/878 (99 %), no gaps) and *Colletogloeopsis dimorpha* (GenBank DQ923528; Identities = 869/878 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *T. macowanii* (GenBank EU707894; Identities = 631/647 (98 %), Gaps = 3/647 (0 %)), *T. wingfieldii* (GenBank EU707896; Identities = 628/646 (97 %), Gaps = 2/646 (0 %)) and *T. maxii* (GenBank EU707869; Identities = 628/646 (97 %), Gaps = 2/646 (0 %)).

Colour illustrations. Filabussi village, Zimbabwe; conidioma on PNA; mycelium; conidiogenous cells and conidia. Scale bars = 10 µm.

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Camarosporium psoraleae

Fungal Planet 181 – 26 November 2013

Camarosporium psoraleae Crous & M.J. Wingf., *sp. nov.*

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

Conidiomata immersed to erumpent, solitary with central ostiole, globose, up to 400 µm diam; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, phialidic with prominent periclinal thickening and thick channel (at times also with percurrent proliferation), globose to doliiform, 7–12 × 6–9 µm. *Conidia* brown, finely roughened, ellipsoid to ovoid, with obtuse ends, 1–3 transversely septate, developing 1–6 oblique to transverse septa, at times becoming constricted at primary septa, (12–)14–16(–18) × (8–)10(–11) µm. *Paraphyses* hyaline, hyphal-like, smooth, intermingled among conidiogenous cells, subcylindrical, base bulbous, tapering to obtuse apex, 1–4-septate, 5–7 µm diam at base, 2–3 µm diam at apex, 30–100 µm long, unbranched or branched at base, and anastomosing. *Microconidiogenous cells* intermingled among macroconidiogenous cells, hyaline, smooth, ampulliform to doliiform to irregular, mono- to polyphialidic, proliferating percurrently, or with periclinal thickening, 5–8 × 4–6 µm. *Microconidia* hyaline, smooth, guttulate, bacilliform to subcylindrical, apex obtuse, base truncate, 4–6 × 2–3 µm.

Culture characteristics — Colonies covering the dish in 2 wk, with sparse aerial mycelium. On MEA surface dirty white with cinnamon, reverse cinnamon. On OA surface cinnamon. On PDA surface cinnamon to buff, reverse buff.

Typus. South Africa, Western Cape Province, Betty's Bay, Harold Porter National Botanical Garden, on stems of *Psoralea pinnata* (*Fabaceae*), 28 Oct. 2012, *M.J. Wingfield* (holotype CBS H-21440, culture ex-type CPC 21632 = CBS 136628, ITS sequence GenBank KF777143, LSU sequence GenBank KF777199, MycoBank MB805845).

Colour illustrations. *Psoralea* dieback in Harold Porter National Botanical Garden, South Africa; conidiomata on PNA; paraphyses; macroconidia; conidiogenous cells and microconidia. Scale bars = 10 µm.

Notes — Although the mode of conidiogenesis and the presence of paraphyses is different from that observed in the type species of *Camarosporium*, *C. propinquum* (Sutton 1980), the present taxon is best accommodated in this genus. Phylogenetically *C. phragmites* is closely related to *C. leucadendri*, though conidia of the latter are larger, (15–)16–19(–21) × (8–)9.5–11(–12) µm (Marincowitz et al. 2008a).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Microdiplodia hawaiiensis* (GenBank DQ885897; Identities = 896/897 (99 %), Gaps = 1/897 (0 %)), *Camarosporium leucadendri* (GenBank EU552106; Identities = 876/877 (99 %), no gaps) and *C. brabeji* (GenBank EU552105; Identities = 871/872 (99 %), Gaps = 1/872 (0 %)). Closest hits using the ITS sequence had highest similarity to *C. leucadendri* (GenBank EU552106; Identities = 559/561 (99 %), Gaps = 1/561 (0 %)), *C. mamanes* (GenBank DQ885900; Identities = 557/561 (99 %), no gaps) and *Myrothecium verrucaria* (GenBank AB693919; Identities = 470/483 (97 %), Gaps = 2/483 (0 %)).

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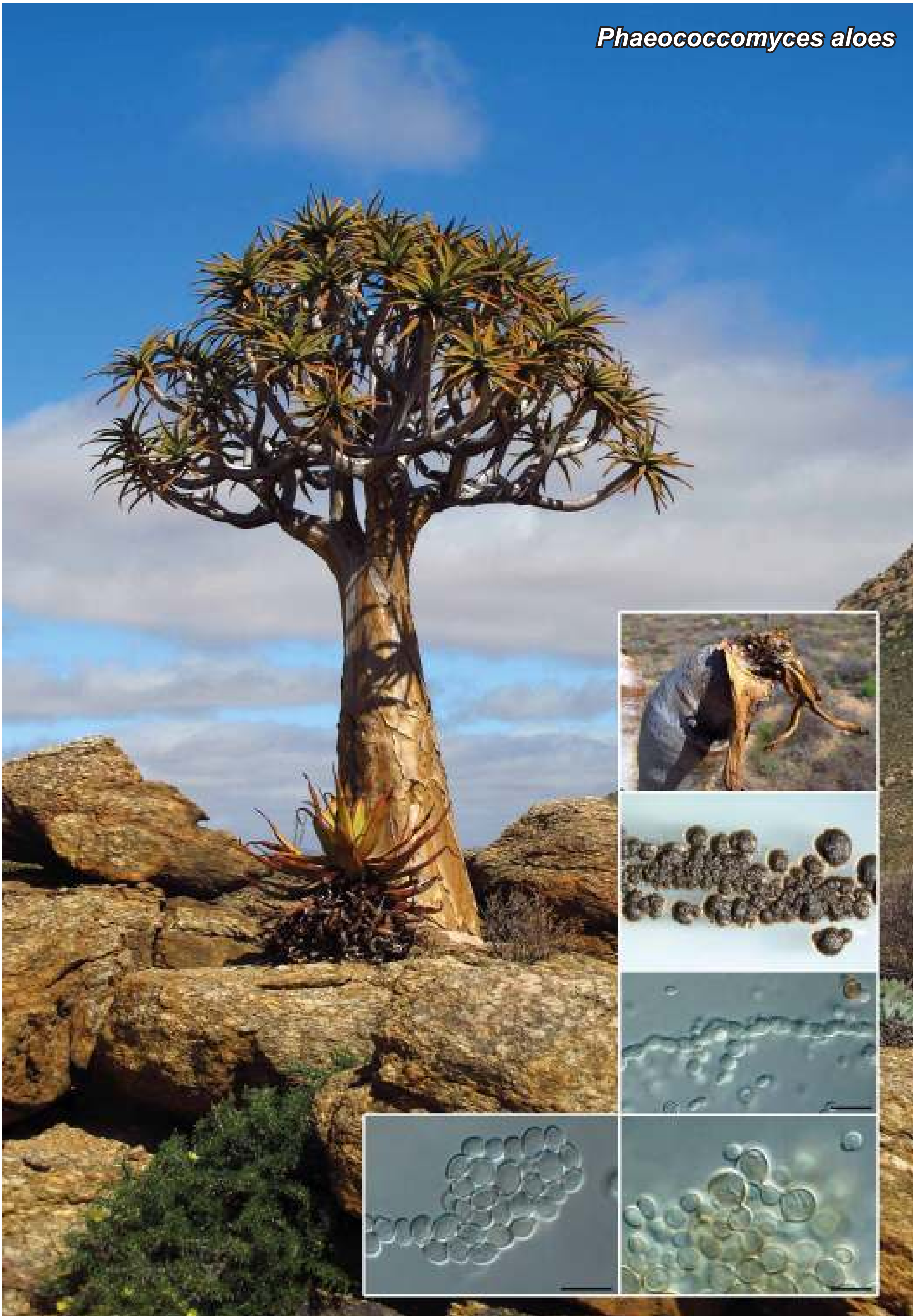
Phaeococcomyces aloes

Fungal Planet 182 – 26 November 2013

Phaeococcomyces aloes Crous & M.J. Wingf., *sp. nov.*

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

Colonies lacking mycelium but consisting of a globular mass of chlamydospore-like cells; cells aseptate, brown (hyaline when young), 3–7 µm diam, covered in mucus, globose, thin-walled, remaining attached to one another through younger end cells at colony margin, which detach during slide preparation; ellipsoid to globose, hyaline, thin-walled, covered in mucus, smooth, 4–7 × 3.5–6.5 µm.

Culture characteristics — Colonies reaching 7 mm diam after 2 wk, lacking aerial mycelium, erumpent with smooth, lobate margins; surface and reverse on OA, MEA and PDA iron-grey.

Typus. South Africa, Western Cape Province, Clanwilliam, on dark lesions on dead bark of *Aloe dichotoma* (*Xanthorrhoeaceae*), Sept. 2012, *M.J. Wingfield* (holotype CBS H-21441, culture ex-type CPC 21873 = CBS 136431, ITS sequence GenBank KF777182, LSU sequence GenBank KF777234, MycoBank MB805846).

Notes — Although traditionally regarded as a genus associated with phaeohyphomycosis of humans, species of *Phaeococcomyces* are commonly isolated from a range of substrates including leaves, twigs and even rocks. The genus *Phaeococcomyces* presently contains six species. When compared to these taxa, conidia of *Phaeococcomyces aloes* are larger than those of *P. eucalypti* (conidia 3–5 × 2.5–5 µm; Crous et al. 2012a), but more similar to that of *P. nigricans* (conidia globose to broadly ellipsoidal, 4–6.5 × 4–5 µm; de Hoog 1979).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Phaeococcomyces catenatus* (GenBank AF050277; Identities = 884/886 (99 %), no gaps), *Exophiala placitae* (GenBank EU040215; Identities = 880/882 (99 %), no gaps) and *Sarcinomyces petricola* (GenBank FJ358249; Identities = 871/873 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *E. placitae* (GenBank EU040215; Identities = 631/653 (97 %), Gaps = 7/653 (1 %)), *P. catenatus* (GenBank AF050277; Identities = 569/584 (97 %), Gaps = 5/584 (0 %)) and *Cladophialophora proteae* (GenBank FJ372388; Identities = 487/591 (82 %), Gaps = 40/591 (6 %)).

Colour illustrations. Aloe dichotoma in Clanwilliam, South Africa; colonies on SNA; ellipsoid to globose conidia remaining attached to one another. Scale bars = 10 µm.

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Phoma aloes

Fungal Planet 183 – 26 November 2013

Phoma aloes Crous & M.J. Wingf., *sp. nov.*

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

Conidiomata pycnidial, erumpent, globose, up to 180 µm diam, brown, with central ostiole; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, smooth, ampulliform to doliiform, 5–7 × 3–4 µm; apex with minute periclinal thickening. *Conidia* dimorphic. *Macroconidia* ellipsoid, medium brown, smooth, medianly (0–)1-septate, widest at septum, apex subobtuse, tapering towards truncate base, (7–)8(–9) × (3–)4 µm. *Microconidia* subcylindrical, straight to slightly curved, ends obtuse, aseptate, hyaline, becoming pale brown, 4–7 × 2–2.5 µm.

Culture characteristics — Colonies reaching 50–60 mm diam after 2 wk on MEA and OA, with moderate aerial mycelium and even, smooth margins; on PDA only reaching 20 mm diam after 2 wk, and margins feathery. On MEA surface pale olivaceous-grey, reverse iron-grey; on PDA surface umber, reverse chestnut; on OA surface olivaceous-grey.

Typus. South Africa, Western Cape Province, Clanwilliam, on dark lesions on dead bark of *Aloe dichotoma* (*Xanthorrhoeaceae*), Sept. 2012, *M.J. Wingfield* (holotype CBS H-21442, cultures ex-type CPC 21549 = CBS 136432, ITS sequence GenBank KF777183, LSU sequence GenBank KF777235, MycoBank MB805847).

Colour illustrations. *Aloe dichotoma* in Clanwilliam, South Africa; conidiomata on PDA; conidiogenous cells, young and mature conidia. Scale bars = 10 µm.

Notes — *Phoma aloes* can be distinguished from two other similar taxa that have been described from this host based on the size of its conidia. Conidia of *Macrophoma aloes* are larger, 14.8 × 6.4 µm, while those of *Phoma aloicola* are again somewhat smaller, 4.5–7 × 2–4.5 µm.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Phoma cladoniicola* (GenBank JQ238625; Identities = 910/914 (99 %), no gaps), *Phaeosphaeria avenaria* f. sp. *avenaria* (GenBank EU223257; Identities = 908/914 (99 %), Gaps = 1/914 (0 %)) and *Phaeosphaeriopsis musae* (GenBank DQ885894; Identities = 907/914 (99 %), no gaps). Closest hits using the ITS sequence are *Phoma foliaceiphila* (GenBank JQ318008; Identities = 559/587 (95 %), Gaps = 3/587 (0 %)), *Sclerococcum parmeliae* (GenBank JQ342180; Identities = 556/584 (95 %), Gaps = 3/584 (0 %)) and *Phoma cladoniicola* (GenBank JQ238629; Identities = 561/591 (95 %), Gaps = 4/591 (0 %)).

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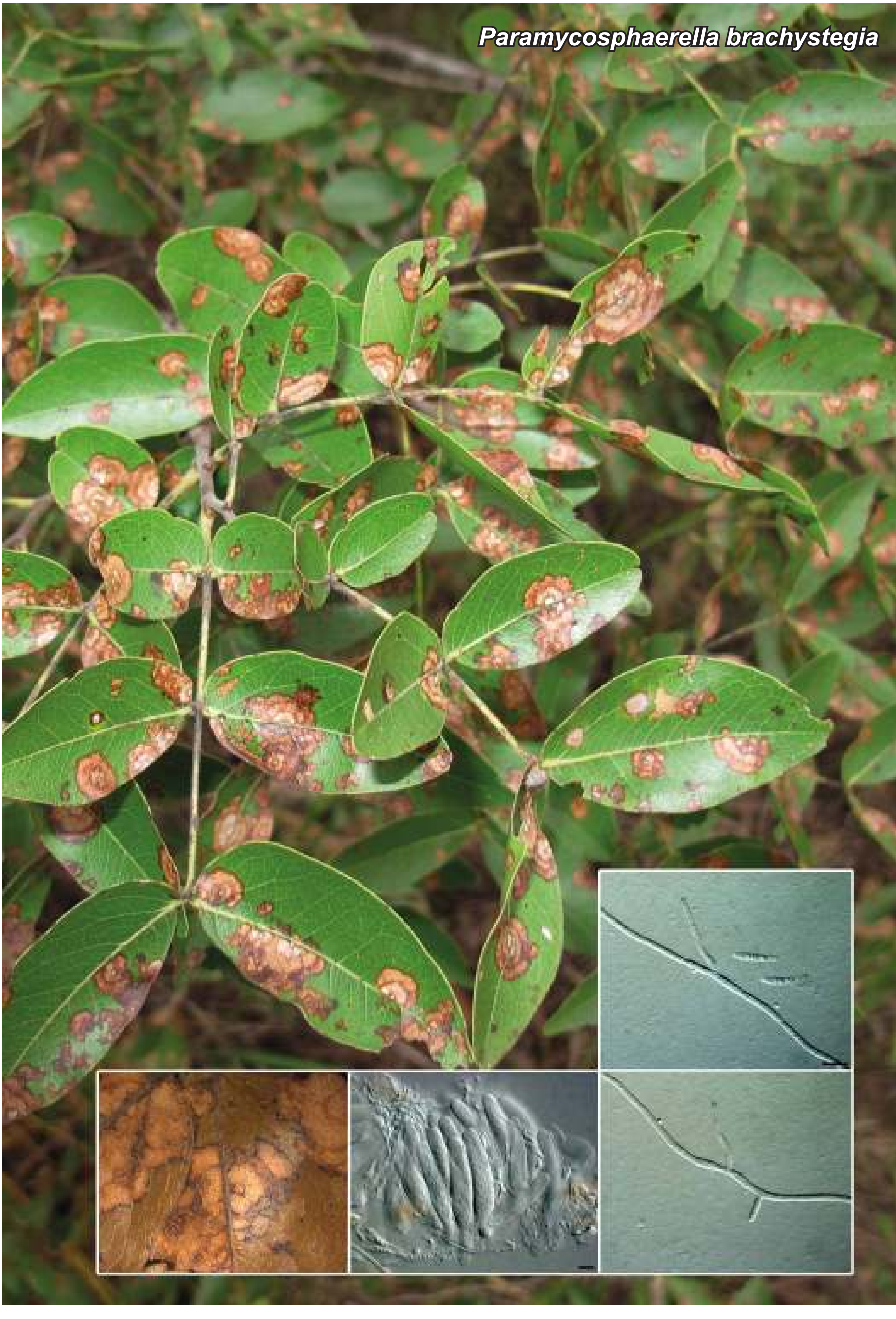
Paramycosphaerella brachystegia

Fungal Planet 186 – 26 November 2013

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

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

Follicolous, plant pathogenic. *Ascomata* erumpent, amphigenous, brown, globose, with central ostiole; wall of 2–3 layers of brown *textura angularis*. *Asci* fasciculate, bitunicate with apical chamber, 8-spored, subcylindrical to narrowly ellipsoid. *Ascospores* tri- to multiseriate, thin-walled, guttulate, not to very slightly constricted at septum, obovoid, remaining hyaline.

Type species. Paramycosphaerella brachystegia.
MycoBank MB805850.

Paramycosphaerella brachystegia Crous & Jol. Roux, *sp. nov.*

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

Leaf spots amphigenous, subcircular to somewhat angular, confined by leaf veins, 5–15 mm diam, pale brown with raised, dark brown border. *Ascomata* intermingled among spermatogonia, erumpent, amphigenous, up to 120 µm diam, brown, globose, with central ostiole, 15 µm diam; wall of 2–3 layers of brown *textura angularis*. *Asci* fasciculate, bitunicate with apical chamber, 8-spored, subcylindrical to narrowly ellipsoid, 40–55 × 10–12 µm. *Ascospores* tri- to multiseriate, thin-walled, guttulate, obovoid, widest in middle of apical cell, not to very slightly constricted at septum, apex subobtuse, base subobtuse, 18–20(–23) × 3(–3.5) µm; ascospores germinating with germ tubes parallel to the long axis, developing lateral branches, remaining hyaline, becoming slightly constricted at septum, 3–4 µm diam.

Culture characteristics — Colonies reaching 25 mm diam after 2 wk, erumpent with moderate aerial mycelium, and water droplets; margin smooth, lobate. On PDA surface pale olivaceous-grey with patches of iron-grey, reverse iron-grey; on OA pale olivaceous-grey with red diffuse zone surrounding colony; on MEA surface pale olivaceous-grey, with patches of olivaceous-grey; reverse iron-grey, surrounded by a diffuse red pigment.

Typus. Zimbabwe, Mtau forest reserve, near Mvuma, on leaves of *Brachystegia* sp. (*Fabaceae*), 2 Apr. 2012, *J. Roux* (holotype CBS H-21445, culture ex-type CPC 21136, 21137 = CBS 136436, ITS sequence GenBank KF777178, LSU sequence GenBank KF777230, MycoBank MB805851).

Notes — Although a *Mycosphaerella* sp. has been reported from *Brachystegia* in Malawi, no species has been formally named on this host (Peregrine & Siddiqi 1972) and thus it is described here as new. *Paramycosphaerella* is morphologically a typical '*Mycosphaerella*', although it lacks a *Ramularia* asexual state and is phylogenetically distinct and can thus no longer be accommodated in the latter genus (Crous et al. 2009a). *Paramycosphaerella brachystegia* clusters with species such as '*M.*' *intermedia* and '*M.*' *marksii* (clade 8 sensu Crous et al. 2013a) which will also have to be relocated to *Paramycosphaerella*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Mycosphaerella marksii* (GenBank GU214447; Identities = 871/877 (99 %), no gaps), *M. intermedia* (GenBank DQ246247; Identities = 870/877 (99 %), no gaps) and *M. wachendorfiae* (GenBank JF951163; Identities = 867/876 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *M. marksii* (GenBank GQ852747; Identities = 602/648 (93 %), Gaps = 14/648 (2 %)), *Microcyclosporella mali* (GenBank JQ358791; Identities = 629/680 (93 %), Gaps = 14/680 (2 %)) and *Mycosphaerella rosigena* (GenBank EU167587; Identities = 623/678 (92 %), Gaps = 13/678 (1 %)).

Colour illustrations. Leaves of *Brachystegia* sp., Zimbabwe; close-up of leaf spots; asci and ascospores; germinating ascospores. Scale bars = 10 µm.

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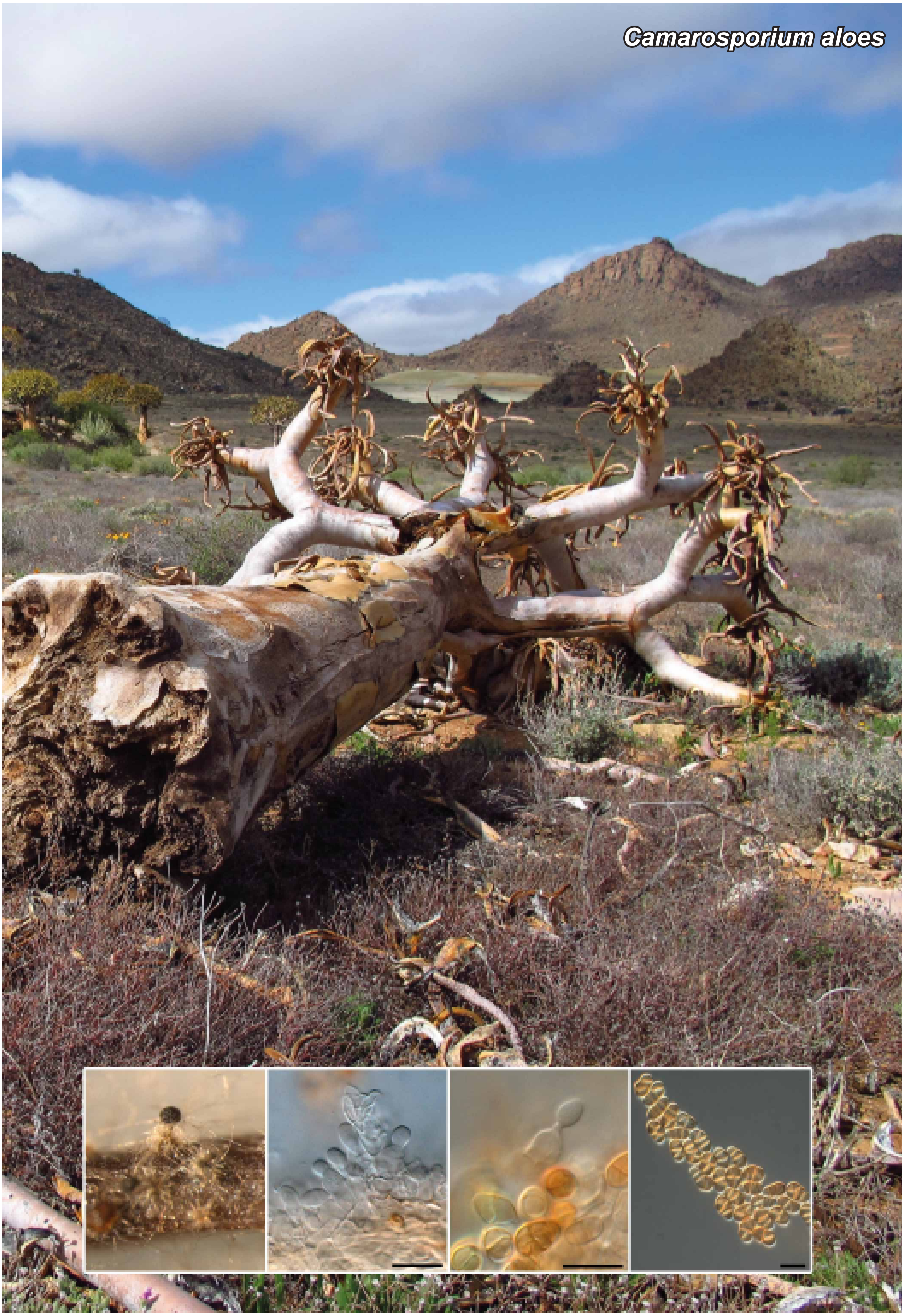
Camarosporium aloes

Fungal Planet 187 – 26 November 2013

Camarosporium aloes Crous & M.J. Wingf., *sp. nov.*

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

Conidiomata erumpent, brown, globose, pycnidial with central ostiole, up to 250 µm diam; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, ampulliform to doliiform, 5–10 × 4–5 µm; apex with several inconspicuous percurrent proliferations. *Conidia* solitary, initially hyaline, smooth, aseptate, ellipsoid, becoming subcylindrical to clavate or obovoid with 3 transverse eusepta, developing vertical and oblique septa, constricted at median septum or not, apex obtuse, base bluntly rounded to truncate, (9–)11–13(–14) × (4–)6–7(–8) µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and smooth, even margins, reaching 50 mm diam after 2 wk. On MEA surface olivaceous-grey with patches of iron-grey, reverse iron-grey; on OA surface isabelline with patches of cinnamon.

Typus. South Africa, Western Cape Province, Clanwilliam, on dark lesions on dead bark of *Aloe dichotoma* (*Xanthorrhoeaceae*), Sept. 2012, *M.J. Wingfield* (holotype CBS H-21446, culture ex-type CPC 21572 = CBS 136437, ITS sequence GenBank KF777142, LSU sequence GenBank KF777198, MycoBank MB805852).

Notes — As far as we could determine, no species of *Camarosporium* have been named on *Aloe*. Ramaley & Barr (1995) described several species from '*Agavaceae*' (= *Asparagaceae*). None of these taxa, however, have conidia small enough to compare with those of *C. aloes*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Camarosporium quaternatum* (GenBank DQ377884; Identities = 859/863 (99 %), Gaps = 1/863 (0 %)), *Herpotrichia parasitica* (GenBank GQ387617; Identities = 846/853 (99 %), no gaps) and *Coniothyrium telephii* (GenBank GQ387599; Identities = 846/853 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *Trametes ochracea* (GenBank KC292372; Identities = 470/494 (95 %), Gaps = 4/494 (0 %)), *Ochrocladosporium frigidarii* (GenBank EU040234; Identities = 469/494 (95 %), Gaps = 4/494 (0 %)) and *Coniothyrium carteri* (GenBank KF251209; Identities = 534/563 (95 %), Gaps = 4/563 (0 %)).

Colour illustrations. Dead *Aloe dichotoma*, Clanwilliam, South Africa. Conidioma on PNA; conidiogenous cells; conidia. Scale bars = 10 µm.

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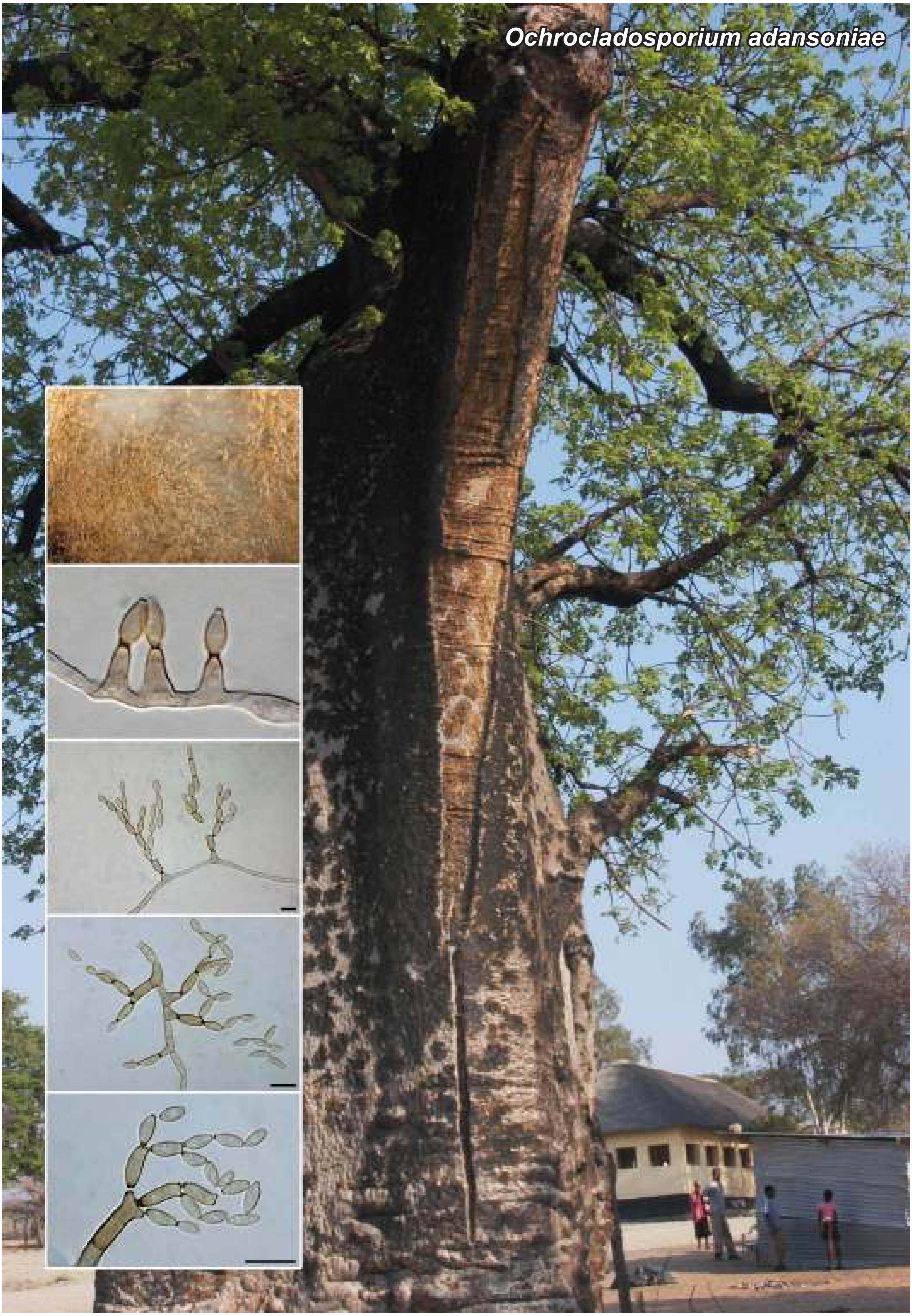
Ochrocladosporium adansoniae

Fungal Planet 190 – 26 November 2013

Ochrocladosporium adansoniae Crous & Cruywagen, *sp. nov.*

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

Mycelium consisting of branched, septate, 2–3 µm wide hyphae, occasionally constricted at septa, subhyaline to pale brown, smooth, thin-walled, giving rise to two types of conidiophores. *Macronematous conidiophores* solitary, erect, arising from superficial hyphae, 20–50 × 4–6 µm, 1–3(–4)-septate, without a swollen or lobed base or rhizoids, but with a T-shaped foot cell, wall ≤ 1 µm wide, guttulate, with thick septa, dark brown, finely verruculose. *Conidiogenous cells* integrated, terminal, subcylindrical to doliiform, pale brown, finely verruculose, 5–15 × 4–5.5 µm, loci somewhat protruding 1.5–2 µm wide, thickened and somewhat darkened. *Micronematous conidiophores* representing solitary conidiogenous loci on hyphae, or erect, medium brown, finely verruculose, doliiform to subcylindrical, 5–10 × 3–4 µm, mostly unbranched, rarely branched below, proliferating sympodially via 1(–3) loci, 1.5–2 µm wide, denticle-like, somewhat thickened and darkened. Ramoconidia 0–1-septate, (7–)9–12(–13) × (3.5–)4(–5) µm, medium brown, guttulate, finely verruculose, ellipsoid to ovoid. *Conidia* ellipsoid to ovoid, aseptate, medium brown, thin-walled, finely verruculose, occurring in branched chains, (7–)8–9(–11) × (3–)3.5–4 µm; hila 1 µm wide, somewhat darkened and thickened.

Culture characteristics — Colonies flat, spreading, reaching 35 mm diam after 2 wk, with sparse aerial mycelium, and smooth, even margins. On OA surface olivaceous-grey in centre, iron-grey in outer region; on MEA surface olivaceous-grey, reverse iron-grey.

Typus. South Africa, Limpopo Province, Muswodi village, Venda, S22°34'36.0" E30°31'18.9", on stems of *Adansonia digitata* (*Malvaceae*), July 2012, *E. Cruywagen* (holotype CBS H-21449, culture ex-type CPC 21227, 21228 = CBS 136439, ITS sequence GenBank KF777176, MycoBank MB805855).

Colour illustrations. Stem of *Adansonia digitata*, Muswodi village, Venda, South Africa; colony on PDA; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — The genus *Ochrocladosporium* was established by Crous et al. (2007a) to accommodate two species, *O. elatum* and *O. frigidarii*. The genus is distinguished from *Cladosporium* by commonly having dimorphic conidiophores, and conidiogenous loci and conidial scars that are neither thickened nor darkened. With regards to the latter feature, *O. adansonia* is somewhat deviant from the established concept of *Ochrocladosporium*.

Closest hits using the ITS sequence had highest similarity to *Ochrocladosporium elatum* (GenBank EU040233; Identities = 475/494 (96 %), Gaps = 5/494 (1 %)), *Trametes ochracea* (GenBank EU661884; Identities = 482/502 (96 %), Gaps = 6/502 (1 %)) and *Coniothyrium carteri* (GenBank KF251209; Identities = 543/561 (97 %), Gaps = 2/561 (0 %)).

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Neofusicoccum ursorum
& Neofusicoccum cryptoaustrale

Fungal Planet 201 & 202 – 26 November 2013

Neofusicoccum ursorum Pavlic, Maleme, Slippers & M.J. Wingf., *sp. nov.*

Etymology. Name refers to the Koala 'bears' that feed on the *Eucalyptus* trees that were sampled in this study.

Colonies initially white with fluffy aerial mycelium changing after 3–4 d to pale olivaceous grey from the middle of the colony (both sides); margins regular. Optimum temperature for growth 30 °C, colonies grown on malt extract agar covering a 90 mm diam plate after 7 d of incubation in the dark. *Conidiomata* pycnidial (produced in vitro on pine needles on water agar within 14 d), solitary, semi-immersed, papillate, covered by hyphal hairs, black, up to 645 μm diam. *Conidiogenous cells* hyaline, holoblastic, cylindrical to subcylindrical (9–)10–14(–15.5) × (2–)2.5–3(–3.5) μm (av. of 50 conidiogenous cells 12 × 2.8 μm). *Conidia* hyaline, smooth with contents having fine granular appearance, aseptate, fusiform to ellipsoid, (20.8–)22–26(–28.5) × (5.5–)6.5–8 μm (av. of 50 conidia, 24 × 7 μm).

Typus. South Africa, Gauteng Province, Pretoria, from branches and leaves of living *Eucalyptus* trees, May 2005, *H.M. Maleme* (holotype PREM 59815, culture ex-type CMW 24480 = CBS 122811); Gauteng Province, *Eucalyptus* trees, *H.M. Maleme* (paratype PREM 59816, culture ex-paratype CMW 23790, MycoBank MB512478).

Neofusicoccum cryptoaustrale Pavlic, Maleme, Slippers & M.J. Wingf., *sp. nov.*

Etymology. Referring to a cryptic species closely related to *N. australe*.

Colonies initially white with fluffy aerial mycelium, changing to straw-yellow after 3 d of incubation. After 4–7 d the colour changed to pale olivaceous-grey from the middle of the colony to the irregular margin. Optimum temperature for growth at 25 °C, covering a 90 mm diam malt extract agar plate after 3 d of incubation in the dark. *Conidiomata* pycnidial (produced in vitro on pine needles on water agar within 14 d), solitary, semi-immersed, papillate, covered by hyphal hairs, black, up to 575 μm diam. *Conidiogenous cells* hyaline, holoblastic, cylindrical to subcylindrical (11–)11.5–12.5(–13) × (2–)2.5(–3) μm (av. of 50 conidiogenous cells 12 × 2.5 μm). *Conidia* hyaline, smooth with granular contents, aseptate, fusiform, apices rounded, (18–)20.5–21(–26.5) × 5–6(–6.5) μm (av. of 50 conidia 19 × 5.5 μm), becoming brown and 1–2-septate with age.

Typus. South Africa, Gauteng Province, Pretoria, from branches and leaves of living *Eucalyptus* trees, May 2005, *H.M. Maleme* (holotype PREM 59817, culture ex-type CMW 23785 = CBS 1122813); Gauteng Province, *Eucalyptus* trees, *H.M. Maleme* (paratype PREM 59818, culture ex-paratype CMW 20738, MycoBank MB512477).

Additional specimens examined: South Africa, Gauteng Province, Pretoria, from branches and leaves of living *Eucalyptus* trees, May 2005, *H.M. Maleme* (PREM 60063, culture CMW 23787, PREM 60064, culture CMW 23784, PREM 60065, culture CMW 23786).

Notes — *Neofusicoccum* species are common endophytes and plant pathogens on a variety of forest trees (Slippers & Wingfield 2007, Slippers et al. 2009). In this study *N. parvum*, *N. ursorum* and *N. cryptoaustrale* were the dominant endophytes in leaves on variety of *Eucalyptus* species planted in a Pretoria arboretum and its surroundings. Concordance between sequence polymorphisms of the ITS rDNA (GenBank FJ752741–FJ752745), EF-1α (FJ752710–FJ752714) and β-tubulin (FJ752753–FJ752757) loci confirmed the distinction of *N. cryptoaustrale* from *N. australe*, and the closely related *N. luteum.* The fungi in this latter complex are widespread in various parts of the world. They are especially common in Australia, South Africa and Mediterranean parts of Europe where they are important as pathogens of native and non-native hosts (Slippers et al. 2004, Pavlic et al. 2007, Marincowitz et al. 2008b, Taylor et al. 2009). It is thus important to monitor the future impact and spread of *N. cryptoaustrale*. *Neofusicoccum ursorum* is clearly distinguished from sister taxa such as *N. vitifusiforme* by ITS rDNA (GenBank FJ752745, FJ752746) and EF-1α sequence data (GenBank FJ752708, FJ752709).

Colour illustrations. *Eucalyptus* plantation, South Africa. Left column *N. ursorum*: pycnidia on PNA; conidia; conidiogenous cells. Scale bars = 500 μm, 10 μm. Right column *N. cryptoaustrale*: pycnidium on PNA; 2-septate dark conidia; 2-septate and aseptate conidia; conidiogenous cells. Scale bars = 500 μm, 10 μm.

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Custingophora blanchettei

Fungal Planet 205 – 26 November 2013

Custingophora blanchettei Marinc., Z.W. de Beer, M.J. Wingf., C.A. Perez, *sp. nov.*

Etymology. Named for Prof. Robert A. Blanchette, recognising his important contributions to the study of wood inhabiting fungi.

Conidiophores abundant on MEA, macronematous, mononematous, upright, mostly intercalary, single or infrequently in small groups, arising from rhizoid foot cells, 67–310 µm tall. *Stipes* straight, single, mostly unbranched or rarely branched by successive growing from the inflated apex measuring 32–250 µm in length, gradually tapering towards the top and becoming inflated at the extreme apex on which a cluster of 10–15 phialides are borne, becoming sinuous at the upper 1/3 to 1/2, evenly pigmented or becoming paler towards the apex when young, smooth, 2–19-septated, 55–297 µm tall, 4.5–8 µm wide at the base, 3.5–6 µm wide at the apex. *Conidiogenous cells* monophialidic, monoverticilliate, cylindrical to obovoid, aseptate, pigmented, with distinct collarettes, 10.5–18.5 µm long, 3–4.5 µm wide. *Conidia* hyaline, oblong, aseptate, straight or curved, one end often truncated or tapered, (8.5–)10–10.5(–12.5) × (2.5–)3(–3.5) µm, produced in slimy droplets. *Ascomata* abundant, mostly superficial or bases partly imbedded in host tissue; *bases* subglobose, 96–179 × 79–148 µm, black to dark brown, peridium of *textura angularis*; *ostiolar necks* straight or slightly curved, dark brown becoming paler at the tip, without distinct ostiolar hyphae, 294–544 µm long, 24–38 µm wide at the base, tapering towards the apex, 12–20 µm wide. *Asci* not observed. *Ascospores* hyaline, fusiform, aseptate, pointed at both ends, straight or curved, 7.5–11 × 2–2.5 µm (in 2 % KOH), with residues of gelatinous sheath visible.

Culture characteristics — Colonies on 2 % malt extract agar fertile, showing the best growth at 25 °C in the dark reaching 80 mm in 21 d, growing circular with entire edge, flat, with vegetative hyphae mostly submerged and a layer of upright conidiophores developing in a circle, resulting in the colony appearing olivaceous-brown.

Typus. Uruguay, near Maldonado, on soft wood of a *Phytolacca dioica* (*Phytolaccaceae*), Oct. 2012, *M.J. Wingfield & C.A. Perez* (holotype PREM 60874, culture ex-holotype CBS 134692 = CMW 39052, isotype PREM 60875, cultures ex-isotype CBS 134693 = CMW 39053, CMW 39000–39002, 39054, ITS sequence of CBS 134692, GenBank KF680045 and LSU sequence of CBS 134692, GenBank KF680046, MycoBank MB805540).

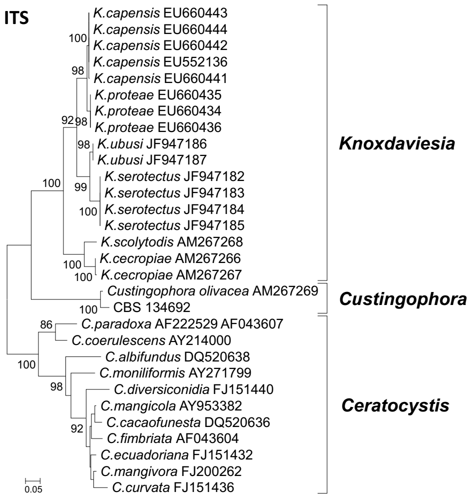
Notes — The genus *Custingophora* was erected for *Cus. olivacea*, known only from its original discovery on compost in Germany (Stolk & Hennebert 1968). Subsequently three additional species were described in the genus (Morgan-Jones & Sinclair 1980, Pinnoi et al. 2003, Kolařík & Hulcr 2009). Later, Kolařík & Hulcr (2009) treated the asexual states of two *Gondwanamyces* spp. in *Custingophora*. However, de Beer et al. (2013b) concurred with Viljoen et al. (1999) and van der Linde et al. (2012) and distinguished between *Custingophora* and *Knoxdaviesia*. De Beer et al. (2013b) also applied one fungus one name principles (Hawksworth 2011, Hawksworth et al. 2011) under which *Knoxdaviesia*, the oldest name, has priority over the sexual genus *Gondwanamyces*. *Knoxdaviesia* was thus redefined to accommodate species with known sexual states previously treated in *Gondwanamyces* (de Beer et al. 2013b). Phylogenetic analyses of the ribosomal DNA sequences in the present study (ITS tree) support the separate treatment of *Custingophora* and *Knoxdaviesia* (= *Gondwanamyces*) in the *Gondwanamycetaceae* and *Microascales* (Réblovà et al. 2011, de Beer et al. 2013a).

The sexual state for the type species of *Custingophora*, *Cus. olivacea* is not known. *Custingophora blanchettei* produced ascomata abundantly on the host tissue but they were overmature and no asci or fresh ascospores were collected. The dried ascomata were scraped from the substrate and mounted in 2 % KOH. A few ascospores were obtained, and although the presence of a gelatinous sheath was evident, its exact shape could not be determined. The ascomata of *Cus. blanchettei* resemble those of *K. capensis* and *K. scolytodis* that lack ostiolar hyphae, but differ from those of *K. proteae* and *K. wingfieldii*, which have divergent ostiolar hyphae (Wingfield et al. 1988, Wingfield & van Wyk 1993, Kolařík & Hulcr 2009, Crous et al. 2012c).

Based on the current classification, *Cus. blanchettei*, is the second species in the genus, and can be distinguished from *Cus. olivacea* by its larger conidia. The ITS sequence of *Cus. blanchettei* differs in 25 bp positions from that of *Cus. olivacea*, and the two species form a well-supported lineage distinct from *Knoxdaviesia* spp. (see ITS tree). The phylogenetic distance between the two *Custingophora* species is comparable to the distance between *Ceratocystis* spp. such as *C. mangivora* and *C. curvata*, or *C. mangicola* and *C. cacaofunesta*.

Colour illustrations. *Phytolacca dioica* growing near Maldonado in Uruguay; ascomata and conidiophores on the host tissue (200 µm); ascospores (5 µm); conidiophores on MEA (50 µm); conidiogenous cells (10 µm); rhizoid foot cell (20 µm); conidia (5 µm).

Maximum likelihood tree based on sequences of the ribosomal internal transcribed spacer (ITS) regions constructed in MEGA v. 5.05 (Tamura et al. 2011). The two species of *Custingophora* differed in 25 bp positions from each other. The sequences were aligned online in MAFFT v. 7 (http://mafft.cbrc.jp/alignment/server/index.html) and the dataset consisted of 707 characters. Support values at branches were obtained from 1 000 bootstrap replicates.



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Calonectria mossambicensis

Fungal Planet 212 – 26 November 2013

Calonectria mossambicensis S. Maússe-Sitoe, S.F. Chen & Jol. Roux, *sp. nov.*

Etymology. Name refers to Mozambique, the country where this fungus was first isolated.

On SNA. *Conidiophores* with a stipe bearing penicillate clusters of fertile branches, stipe extensions and terminal vesicles. *Stipes* septate, hyaline, smooth, 58–102 × 3–7 µm; stipe extensions septate, straight to flexuous, 91–203 µm long, 2–6 µm wide at the apical septum, terminating in an obpyriform to ellipsoid vesicle, 2–8 µm diam. *Conidiogenous apparatus* 37–87 × 19–59 µm; primary branches aseptate, 8–24 × 2–7 µm; secondary branches aseptate, 5–20 × 1–9 µm, tertiary branches aseptate, 4–15 × 1–6 µm, each terminal branch producing 2–6 phialides; phialides doliiform to reniform, hyaline, aseptate, 5–11 × 2–4 µm, apex with minute periclinal thickening and inconspicuous collarette. *Macroconidia* cylindrical, rounded at both ends, straight, (35–)38–46(–50) × 3–6 µm (av. = 42 × 4 µm), 1-septate, lacking a visible abscission scar, held in parallel cylindrical clusters by colourless slime. *Megaconidia*, *microconidia* and *sexual morph* not seen.

Culture characteristics — Colonies fast growing with optimal growth temperature at 25 °C covering the petri dish (90 mm) in 16 d (growth at 10–30 °C) on malt extract agar (Biolab, Midland, Johannesburg); abundant white aerial mycelium with sparse sporulation; chlamydospores arranged in chains, extensive throughout the medium, forming microsclerotia.

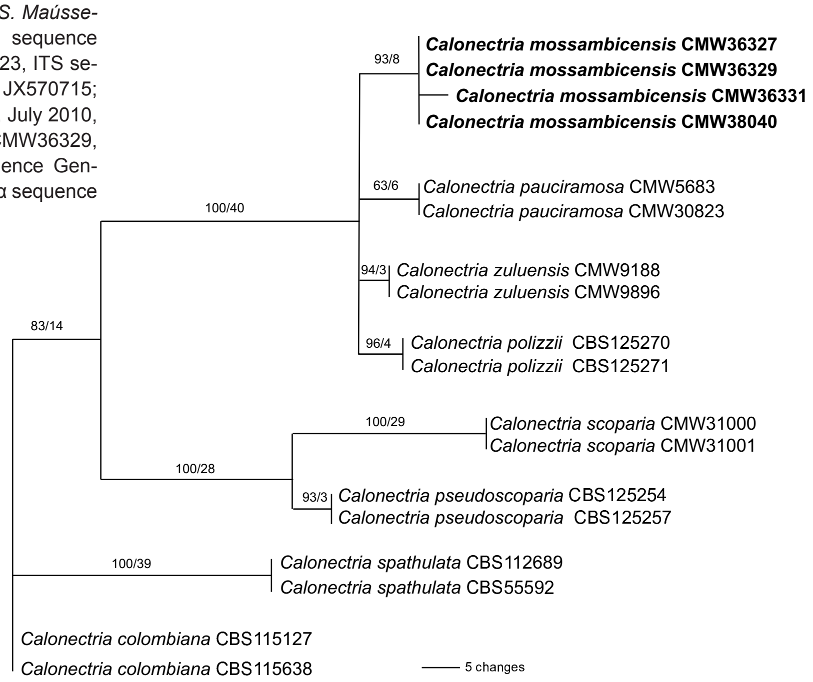
Typus. Mozambique, Manica, Bandula, cutting clones of *E. grandis* × *E. camaldulensis*, July 2010, *J. Roux & S. Maússe-Sitoe* (holotype PREM 60821, cultures ex-type CMW36327, Calmodulin sequence GenBank JX570722, Histone H3 sequence GenBank JX570726, ITS sequence GenBank JX570730, TEF-1α sequence GenBank JX570718, MycoBank MB801447).

Additional material examined. Mozambique, Manica, Bandula, cutting clones of *E. grandis* × *E. camaldulensis*, July 2010, *J. Roux & S. Maússe-Sitoe*, Herb. PREM 60869, culture CMW38040, Calmodulin sequence GenBank JX5707190, Histone H3 sequence GenBank JX570723, ITS sequence GenBank JX570727 and TEF-1α sequence GenBank JX570715; Zambézia, Gurué, cutting clones of *E. grandis* and *E. urophylla*, July 2010, *J. Roux & S. Maússe-Sitoe*, Herb. PREM 60867, culture CMW36329, Calmodulin sequence GenBank JX570721, Histone H3 sequence GenBank JX570725, ITS sequence GenBank JX570729 and TEF-1α sequence GenBank JX570717.

Colour illustrations. Symptomatic seedlings of clones of *E. grandis* × *E. camaldulensis* at Ifloma nursery in Manica Province, Mozambique. Culture morphology showing abundant white aerial mycelium with sparse sporulation; conidiogenous apparatus with a stipe extension; 1-septate macroconidia. Scale bars = 10 µm.

Notes — *Calonectria mossambicensis* (conidia av. = 42 × 4 µm) is morphologically most similar to *Ca. pauciramosa* (av. = 50 × 4.5 µm), *Ca. pollizzi* (av. = 37 × 4 µm) and *Ca. zuluensis* (av. = 36 × 4 µm), but can be distinguished based on the size of its macroconidia (Crous 2002, Lombard et al. 2010). Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the Calmodulin sequence is *Ca. pollizi* (GenBank GQ2674362; Identities = 475/476 (99 %), Gaps = 0/476 (0 %)), followed by *Ca. pauciramosa* and *Ca. zuluensis*. Closest hits using Histone H3 sequence is *Ca. pauciramosa* (GenBank HQ285798) and *Ca. polizzi* (GenBank JN607260), both with 100 % similarities. Closest hits using ITS sequence yielded highest similarity to *Ca. spathulata* (GenBank AF307350; Identities = 512/512 (100 %), Gaps = 0/512 (0 %)) and *Ca. pauciramosa* (GenBank GQ280608; Identities = 517/520 (99 %), Gaps = 1/520 (0 %)). Closest hits using TEF-1α sequence yielded 100 % similarity to *Ca. polizzi* (GenBank JN607260), *Ca. pauciramosa* (GenBank FJ972499) and *Ca. macroconidialis* (GenBank GQ267313).

One of 322 equally most parsimonious trees obtained from a heuristic search of the combined Calmodulin, Histone H3, ITS and TEF-1α regions (TL = 1 569, CI = 0.854, RI = 0.908, RC = 0.775, HI = 0.146). Bootstrap support values (%) from 1 000 replications followed by branch lengths are indicated above the branches. The tree is rooted to *Ca. colombiana*. Isolates collected from *Eucalyptus* in Mozambique in this study are in **bold**.



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