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RESEARCH ARTICLE

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Key words

ITS DNA barcodes
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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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Toxicocladosporium ficiniae

Fungal Planet 154 – 26 November 2013

Toxicocladosporium ficiniae Crous & A.R. Wood, *sp. nov.*

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

Leaf spots absent, sporulating on dead tissue. On SNA: *Mycelium* consisting of branched, septate, smooth, pale brown, 2–3 µm diam hyphae. *Conidiophores* solitary, arising from superficial mycelium, erect, brown, unbranched or branched above, subcylindrical, straight to flexuous, 10–40 × 3–5 µm, 1–15-septate, apical septum becoming dark brown and thickened. *Conidiogenous cells* integrated, polyblastic, terminal and lateral, smooth, brown, 5–15 × 2.5–4 µm; scars truncate, thickened and darkened, 1.5–2 µm wide. *Primary ramoconidia* medium brown, smooth to finely verruculose, aseptate, subcylindrical, 15–35 × 3–4 µm. *Secondary ramoconidia* giving rise to branched chains of conidia, subcylindrical, polyblastic, brown, smooth to finely verruculose, 0–1-septate, 12–20 × 2.5–3 µm; scars darkened, thickened, 1.5–2 µm diam. *Intercalary conidia* subcylindrical to fusoid-ellipsoidal, brown, smooth to finely verruculose, (9–)10–11 × (2.5–)3 µm. *Small terminal conidia* fusoid-ellipsoidal, brown, smooth to finely verruculose, (7–)8–9 × (2.5–)3 µm; hila thickened and darkened, 1–1.5 µm diam.

Culture characteristics — Colonies after 2 wk reaching 30 mm diam, erumpent, folded, with even, smooth margins, and moderate aerial mycelium. On MEA surface pale olivaceous-grey in centre, and olivaceous-grey in outer region, iron-grey underneath. On OA olivaceous-grey in centre, with pale olivaceous-grey aerial mycelium, surrounded by a prominent scarlet to red zone in agar; on PDA centre pale olivaceous-grey, outer region isabelline, with pale brown pigment diffusing into agar; reverse brown-vinaceous.

Typus. South Africa, Western Cape Province, Bracken Nature Reserve, on leaves of *Ficinia indica* (*Cyperaceae*), 18 Aug. 2012, *A. Wood* (holotype CBS H-21413, culture ex-type CPC 21283, 21282 = CBS 136406, ITS sequence GenBank KF777190, LSU sequence GenBank KF777241, MycoBank MB805812).

Colour illustrations. Bracken Nature Reserve; conidiophores and conidia in culture. Scale bars = 10 µm.

Notes — The genus *Toxicocladosporium* was established by Crous et al. (2007a) to accommodate cladosporium-like taxa with subdenticulate conidiogenous loci, and somewhat thickened, conspicuously darkened-refractive loci. Since the genus was established, several additional taxa have been added (Crous et al. 2009b, 2010a, b, 2012a, c, Crous & Groenewald 2011, Bensch et al. 2012).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Toxicocladosporium strelitziae* (GenBank JX069858; Identities = 877/885 (99 %), no gaps), *T. irritans* (GenBank EU040243; Identities = 877/885 (99 %), no gaps) and *T. posoqueriae* (GenBank KC005803; Identities = 875/885 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *T. veloxum* (GenBank FJ790288; Identities = 595/612 (97 %), Gaps = 4/612 (0 %)), *T. pseudoveloxum* (GenBank JF499849; Identities = 630/649 (97 %), Gaps = 2/649 (0 %)) and *T. banksiae* (GenBank HQ599598; Identities = 659/679 (97 %), Gaps = 3/679 (0 %)).

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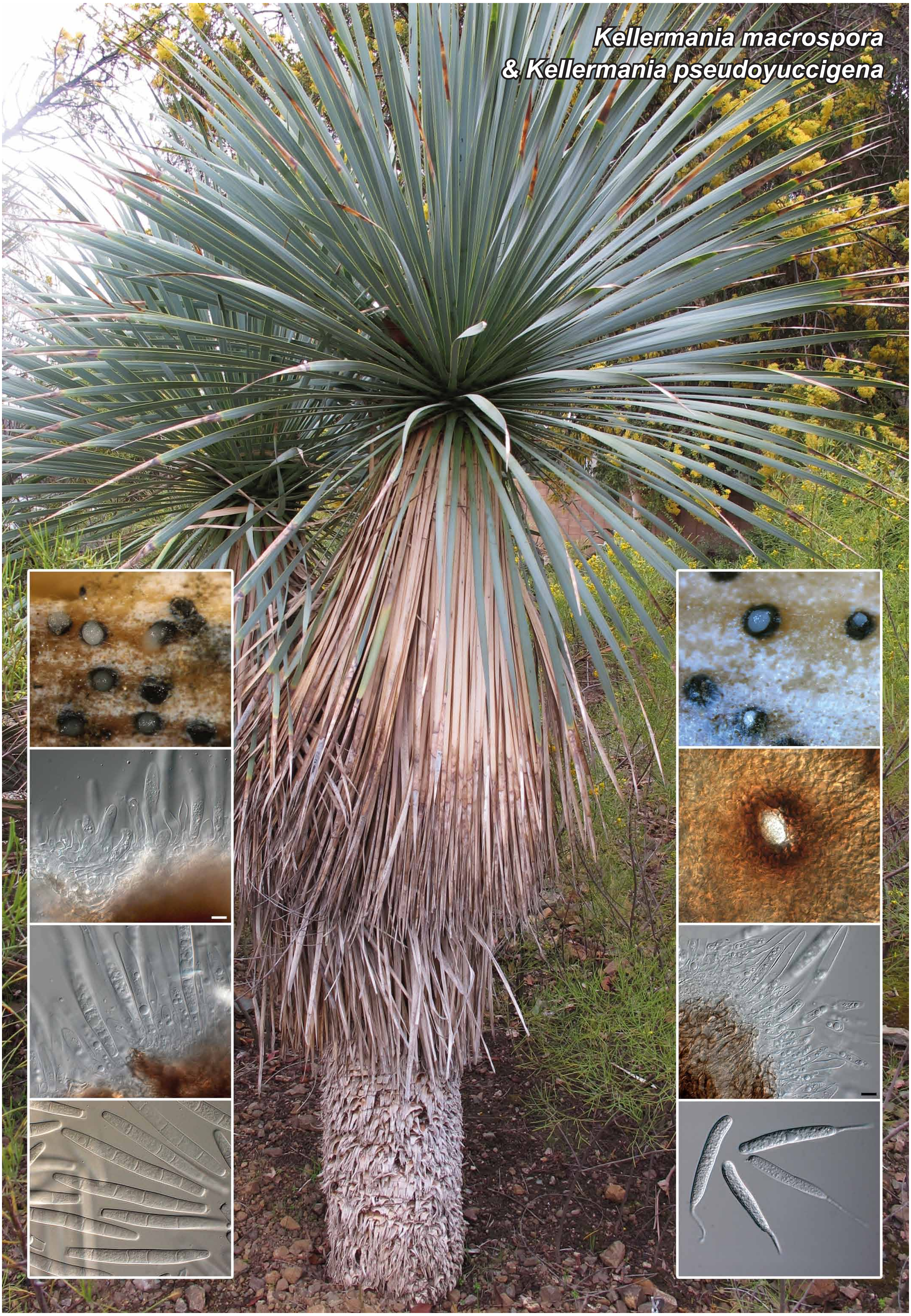
Kellermania macrospora
& Kellermania pseudoyuccigena

Fungal Planet 155 & 156 – 26 November 2013

Kellermania macrospora (Durieu & Mont.) Minnis & A.H. Kenn., Persoonia 29: 19. 2012

Basionym. *Septoria macrospora* Durieu & Mont., Exploration scientifique de l'Algérie 1: 589. 1849.

≡ *Hendersonia montagnei* Cooke, Nuovo Giorn. Bot. Ital. 10: 19. 1878. Note: This nom. nov. was established since the epithet '*macrospora*' was occupied by *H. macrospora* Berk. & Broome 1850.

≡ *Hendersonia piptarthra* Sacc., Michelia 2: 111. 1880. Note: This nom. nov. was established since the epithet '*macrospora*' is occupied by *H. macrospora* Berk. & Broome 1850. It is a nom. illeg. via superfluous, ICBN Art. 52, since *H. montagnei* was already published as a replacement name.

≡ *Stagonospora macrospora* (Durieu & Mont.) Sacc., Syll. Fung. 3: 450. 1883.

≡ *Piptarthron macrosporum* (Durieu & Mont.) Höhn., Hedwigia 60: 203. 1918.

Foliicolous. *Conidiomata* pycnidial, black, solitary, immersed, globose, unilocular, up to 600 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 × 5–8 µm, proliferating percurrently at apex, invested in mucus. *Conidia* hyaline, smooth, guttulate, cylindrical to obclavate, (3–)4(–5)-septate, (67–)85–97(–105) × (8–)9–10(–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 50 mm diam after 2 wk, with moderate aerial mycelium and feathery margins. On PDA surface pale mouse grey, reverse dark mouse grey; on OA surface fluffy, white to dirty white.

Typus. ALGERIA, on leaves of *Agave* sp., holotype PC 85781. – USA, California, Walnut Creek, Ruth Bancroft Garden, 1552 Bancroft Road, on leaves of *Yucca rostrata* (*Asparagaceae*), 20 Mar. 2012, *P.W. Crous* (epitype designated here CBS H-21414, culture ex-epitype CPC 20391, 20390 = CBS 136549, ITS sequence GenBank KF777165, LSU sequence GenBank KF777218, MycoBank MBT176315).

Notes — The genus *Kellermania* (= *Alpakesa*, *Piptarthron*, *Planistroma*, *Planistromella*, ?*Septoplaca*) belongs to the *Planistromellaceae*, which is a separate family in the *Botryosphaeriales* (Minnis et al. 2012, Slippers et al. 2013). *Kellermania macrospora* (holotype PC 85781; conidia 3–5-septate, (60–)65–70(–78) × (9–)10–11 µm) closely matched that morphology of the epitype, and the strain identified by Minnis et al. (2012) as *K. macrospora* (CBS 131716; conidia 54.5–93 × 6.5–11 µm, 3–5(–7)-septate, occurring on *Agave* sp.).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Kellermania yuccigena* (GenBank JX444883; Identities = 728/729 (99 %), Gaps = 1/729 (0 %)), *K. yuccifoliorum* (GenBank JX444882; Identities = 727/728 (99 %), no gaps) and *K. uniseptata* (GenBank JX444881; Identities = 726/728 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *K. macrospora* (GenBank JX444858; Identities = 403/403 (100 %), no gaps), *K. unilocularis* (GenBank JX444865; Identities = 355/370 (96 %), no gaps) and *K. yuccifoliorum* (GenBank JX444867; Identities = 342/358 (96 %), no gaps).

Kellermania pseudoyuccigena Crous, *sp. nov.*

Etymology. Named after its morphological similarity to *Kellermania yuccigena*.

Foliicolous. *Conidiomata* pycnidial, black, solitary, immersed, globose, unilocular, up to 300 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, 5–12 × 3–6 µm, proliferating percurrently at apex, invested in mucus. *Conidia* hyaline, smooth, guttulate, cylindrical, 1-septate (submedian), (40–)50–60 × (6–)8–9 µm; apex giving rise to a simple setulate, unbranched appendage, 18–32 µm long; conidial base truncate, with a minute marginal frill, 1 µm long.

Culture characteristics — Colonies reaching 45 mm diam after 2 wk, with moderate aerial mycelium and feathery, lobate margins. On PDA surface dirty white, reverse greyish sepia; on OA surface dirty white.

Typus. USA, California, Walnut Creek, Ruth Bancroft Garden, 1552 Bancroft Road, on leaves of *Yucca rostrata* (*Asparagaceae*), 20 Mar. 2012, *P.W. Crous* (holotype CBS H-21415, culture ex-type CPC 20418, 20388, 20386 = CBS 136446, ITS sequence GenBank KF777166–KF777168, LSU sequence of CPC 20388, 20418 GenBank KF777219–KF777220, MycoBank MB805813).

Colour illustrations. *Yucca rostrata* in the Ruth Bancroft Garden, California. Left column: conidiomata, conidiogenous cells and conidia of *K. macrospora*. Right column: conidiomata, ostiolar area, conidiogenous cells and conidia of *K. pseudoyuccigena*. Scale bars = 10 µm.

Notes — *Kellermania pseudoyuccigena* occurs on the same leaves in association with *K. pentaseptata*. Morphologically *K. pseudoyuccigena* (conidia (40–)50–60 × (6–)8–9 µm) closely resembles *K. yuccigena*, but can be distinguished in the conidia of the latter species are generally wider (50–61 × 9–10 µm) when studied in culture under standardised conditions.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Kellermania yuccigena* (GenBank JX444883; Identities = 874/875 (99 %), Gaps = 1/875 (0 %)), *K. yuccifoliorum* (GenBank JX444882; Identities = 873/874 (99 %), no gaps) and *K. uniseptata* (GenBank JX444881; Identities = 872/874 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *K. yuccigena* (GenBank JX444868; Identities = 460/461 (99 %), no gaps), *K. uniseptata* (GenBank JX444866; Identities = 453/461 (98 %), Gaps = 2/461 (0 %)) and *K. yuccifoliorum* (GenBank JX444867; Identities = 452/461 (98 %), Gaps = 3/461 (0 %)).

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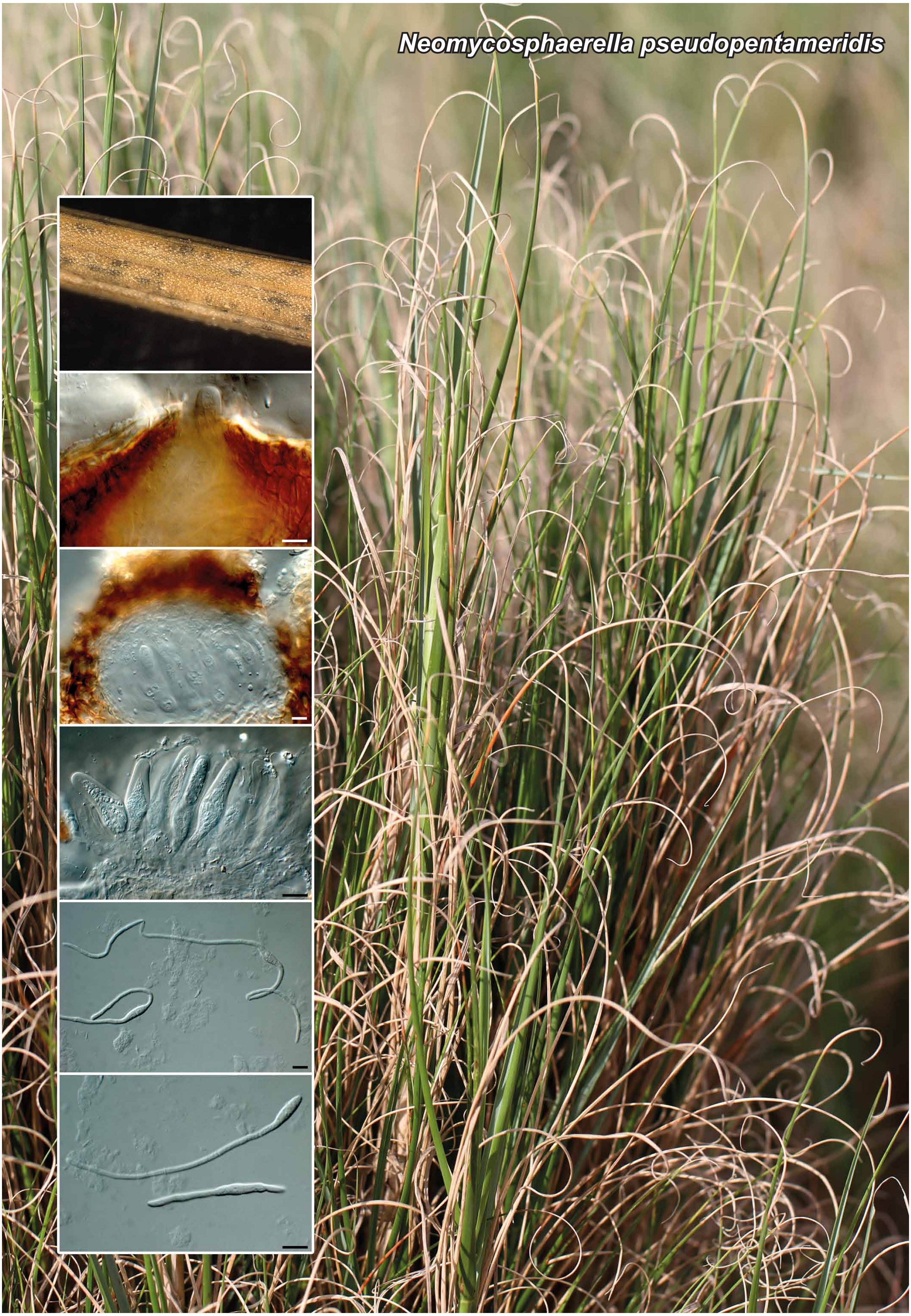
Neomycosphaerella pseudopentameridis

Fungal Planet 157 – 26 November 2013

Neomycosphaerella Crous, *gen. nov.*

Etymology. Resembling the genus *Mycosphaerella*.

Foliicolous, phytopathogenic. *Ascomata* immersed, subepidermal, frequently in a brown stroma, unilocular, in rows of 2–4, globose, with central ostiole; wall of 2–4 layers of brown *textura angularis*. *Asci* fasciculate, stipitate, 8-spored, with minute ocular chamber, obovoid, straight to slightly curved, hyaline. *Ascospores* tri- to multiseriate, hyaline, smooth, granular, medianly 1-septate; ascospores becoming brown and verruculose with age.

Type species. Neomycosphaerella pseudopentameridis.
MycoBank MB805814.

Neomycosphaerella pseudopentameridis Crous, *sp. nov.*

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

Foliicolous, associated with leaf tip blight. *Ascomata* immersed, subepidermal, frequently in a brown stroma, unilocular, in rows of 2–4, globose, up to 120 µm diam, with central ostiole, 10–15 µm diam; wall of 2–4 layers of brown *textura angularis*. *Asci* fasciculate, stipitate, 8-spored, with minute ocular chamber, obovoid, straight to slightly curved, hyaline, 35–55 × 10–12 µm. *Ascospores* tri- to multiseriate, hyaline, smooth, granular, medianly 1-septate, slightly constricted at septum, (15–)16–17(–18) × (3.5–)4(–5) µm; ascospores becoming brown and verruculose with age.

Culture characteristics — Colonies reaching 30 mm diam after 2 wk. On MEA surface folded, with sparse aerial mycelium and smooth, even margins. On MEA surface pale olivaceous-grey, reverse iron-grey. On OA surface pale olivaceous-grey with patches of grey-sepia. On PDA surface olivaceous-grey, reverse iron-grey.

Typus. South Africa, Western Cape Province, Cape Town, Green Point Park, on leaves of *Pseudopentameris macrantha* (*Poaceae*), 22 July 2012, *P.W. Crous* (holotype CBS H-21416, culture ex-type CPC 21127, 21126 = CBS 136407, ITS sequence GenBank KF777173, LSU sequence GenBank KF777226, MycoBank MB805815).

Notes — Morphologically *Neomycosphaerella* resembles the genus *Mycosphaerella*, though is not associated with a *Ramularia* asexual state (Crous et al. 2009a, Koike et al. 2011), and clusters apart from *Ramularia* s.str., being closer related to *Brunneosphaerella.* Three species of *Brunneosphaerella* are presently known, all of which are foliar pathogens of *Proteaceae* (Crous et al. 2011b). *Neomycosphaerella* is distinct from *Brunneosphaerella* in that the latter genus has ascospores that are pigmented, 3-septate, and frequently also have mucoid caps.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Passalora intermedia* (GenBank FJ790292; Identities = 856/873 (98 %), Gaps = 4/873 (0 %)), *Mycosphaerella parkii* (GenBank DQ246245; Identities = 854/873 (98 %), Gaps = 4/873 (0 %)) and *Brunneosphaerella protearum* (GenBank JN712512; Identities = 854/874 (98 %), Gaps = 6/874 (0 %)). Closest hits using the ITS sequence had highest similarity to *B. nitidae* (GenBank GU214625; Identities = 598/648 (92 %), Gaps = 17/648 (2 %)), *Passalora intermedia* (GenBank FJ790261; Identities = 572/621 (92 %), Gaps = 16/621 (2 %)) and *B. protearum* (GenBank JN712448; Identities = 585/636 (92 %), Gaps = 17/636 (2 %)).

Colour illustrations. Pseudopentameris macrantha growing at Green Point Park, South Africa. Immersed ascomata, section through ascomata showing wall structure and ostiole, asci, germinating ascospores. Scale bars = 10 µm.

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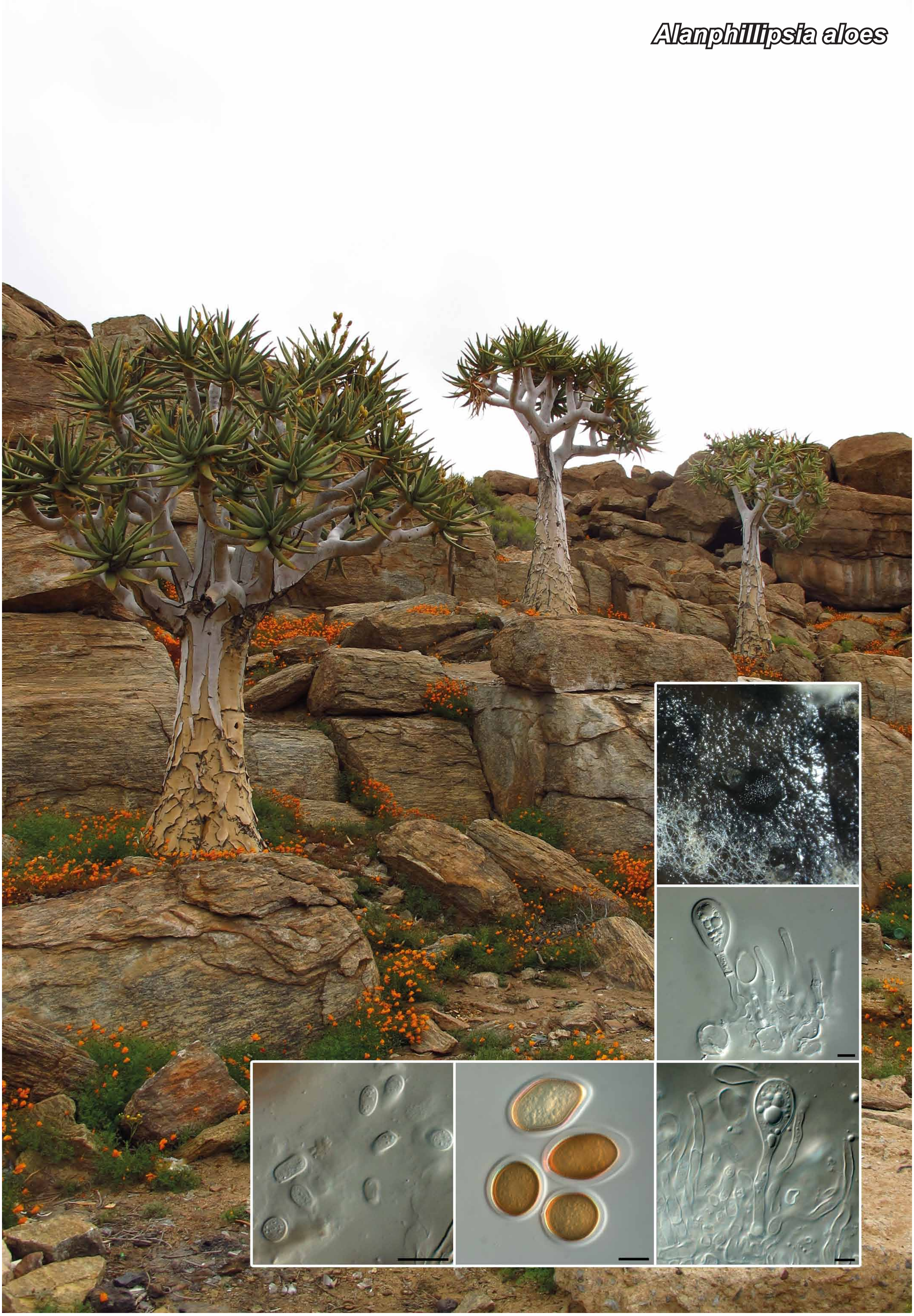
Alanphillipsia aloes

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

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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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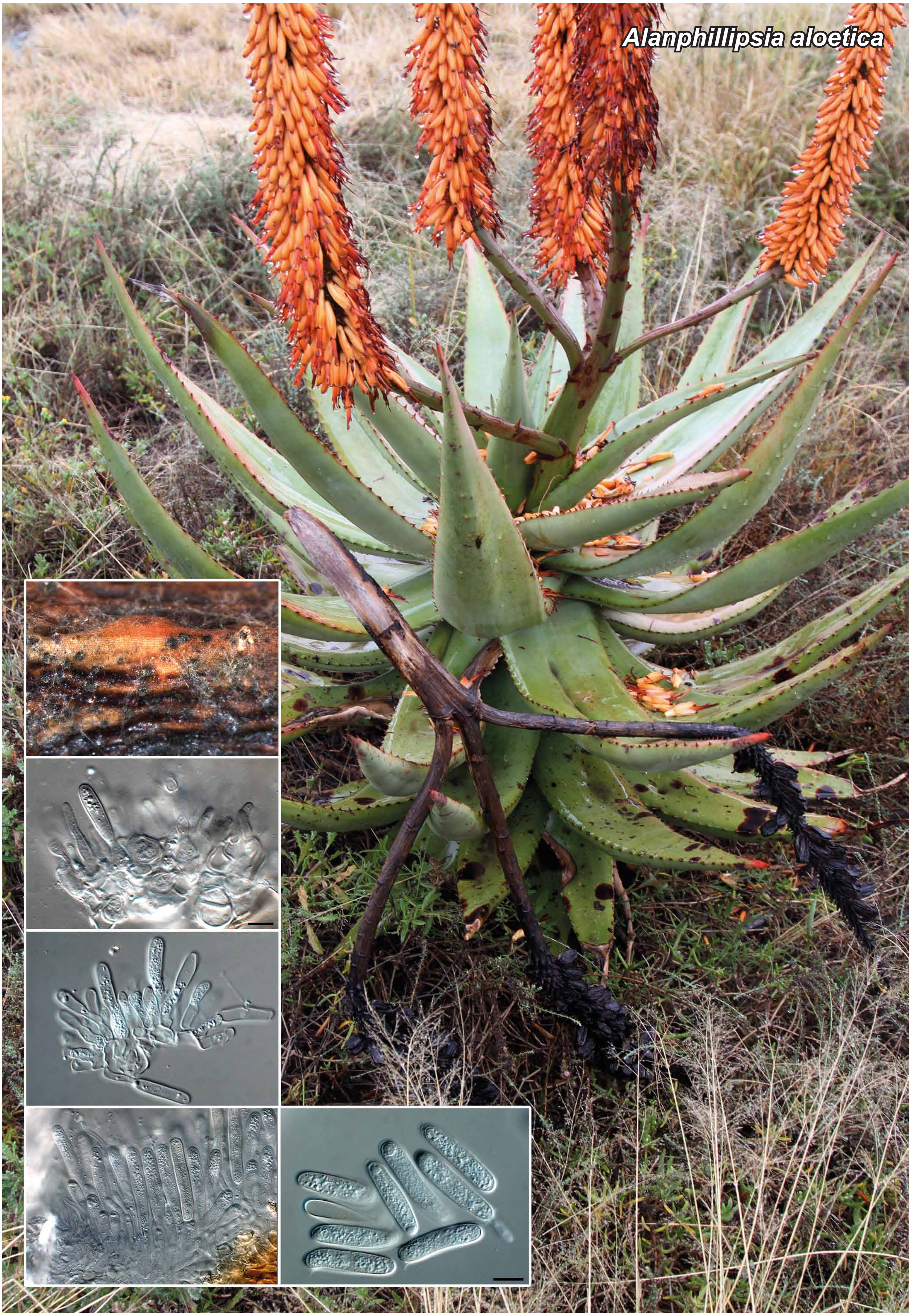
Alanphillipsia aloetica

Fungal Planet 160 – 26 November 2013

Alanphillipsia aloetica Crous, *sp. nov.*

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

Conidiomata erumpent in agar, globose, up to 400 µm diam, opening by means of a central ostiole, but appearing like a longitudinal rupture when mature, exuding a pale crystalline conidial mass; wall of 3–6 layers of *textura angularis*. *Conidiophores* reduced to conidiogenous cells, or a supporting cell. *Conidiogenous cells* lining the inner cavity, ampulliform to subcylindrical, hyaline, smooth, 10–20 × 4–5 µm, proliferating percurrently near apex. *Paraphyses* intermingled among conidiogenous cells, hyaline, smooth, subcylindrical, 30–60 × 3–5 µm, aseptate. *Conidia* hyaline, becoming pale brown at maturity, smooth, subcylindrical, granular, apex obtuse, base truncate, 3–4 µm diam, aseptate, (20–)30–33(–35) × (5–)6(–7) µm, encased in mucilaginous sheath, with long basal marginal flared appendage, 1–6 µm long.

Culture characteristics — Colonies after 2 wk on OA and PDA covering the dish, reaching 65 mm diam on MEA; aerial mycelium sparse, margins even, lobate. On MEA surface olivaceous-grey with iron-grey margins; reverse iron-grey. On PDA surface and reverse iron-grey. On OA surface iron-grey with pale olivaceous-grey aerial mycelium.

Typus. South Africa, Eastern Cape, Uitenhage, on *Aloe* sp. (*Xanthorrhoeaceae*), 14 July 2012, *P.W. Crous* (holotype CBS H-21420, culture ex-type CPC 21110, 21109 = CBS 136409, ITS sequence GenBank KF777139, LSU sequence GenBank KF777195, MycoBank MB805819).

Notes — *Alanphillipsia aloetica* is phylogenetically closely related to *A. aloeigena* (ITS: Identities = 689/693 (99 %), Gaps = 2/693 (0 %)), but morphologically distinct in that conidiomata frequently open by what appears to be a longitudinal slit, paraphyses can be present, and conidia are shorter and wider than those of *P. aloes*, (25–)28–38(–50) × (6–)7–8(–10) µm.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Diplodia corticola* (GenBank DQ377848; Identities = 852/ 859 (99 %), no gaps), *Botryosphaeria sumachi* (GenBank DQ377865; Identities = 870/878 (99 %), no gaps) and *Diplodia rosulata* (GenBank DQ377897; Identities = 869/878 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *Phaeobotryosphaeria eucalypti* (GenBank JX646803; Identities = 512/533 (96 %), Gaps = 9/533 (1 %)), *P. citrigena* (GenBank EU673329; Identities = 534/556 (96 %), Gaps = 8/556 (1 %)) and *P. porosa* (GenBank AY343378; Identities = 474/495 (96 %), Gaps = 10/495 (2 %)).

Colour illustrations. *Aloe* sp. growing in Uitenhage, South Africa. Conidiomata on leaf; conidiogenous cells and conidia. Scale bars = 10 µm.

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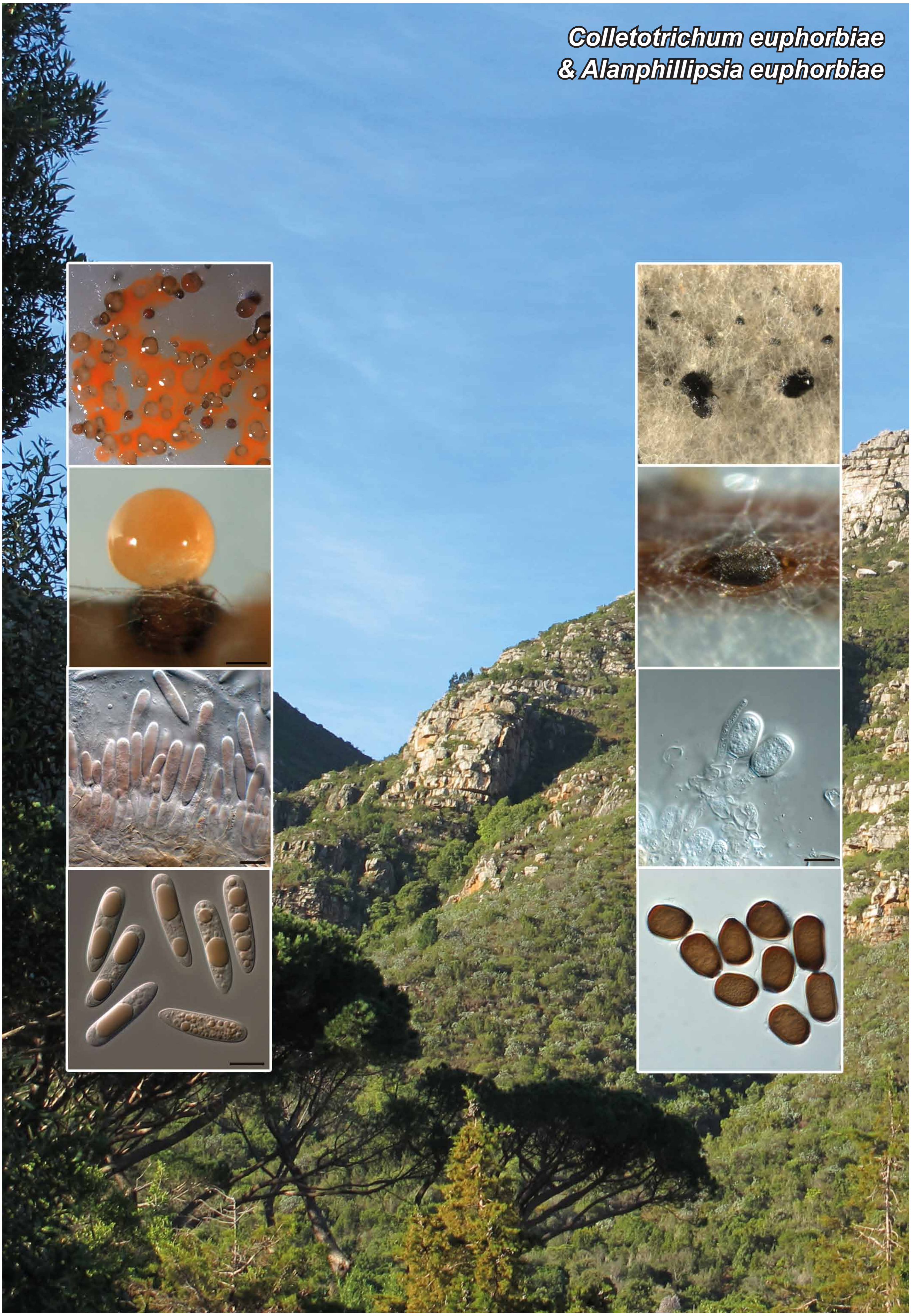
Colletotrichum euphorbiae
& Alanphillipsia euphorbiae

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.

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 %)).

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.

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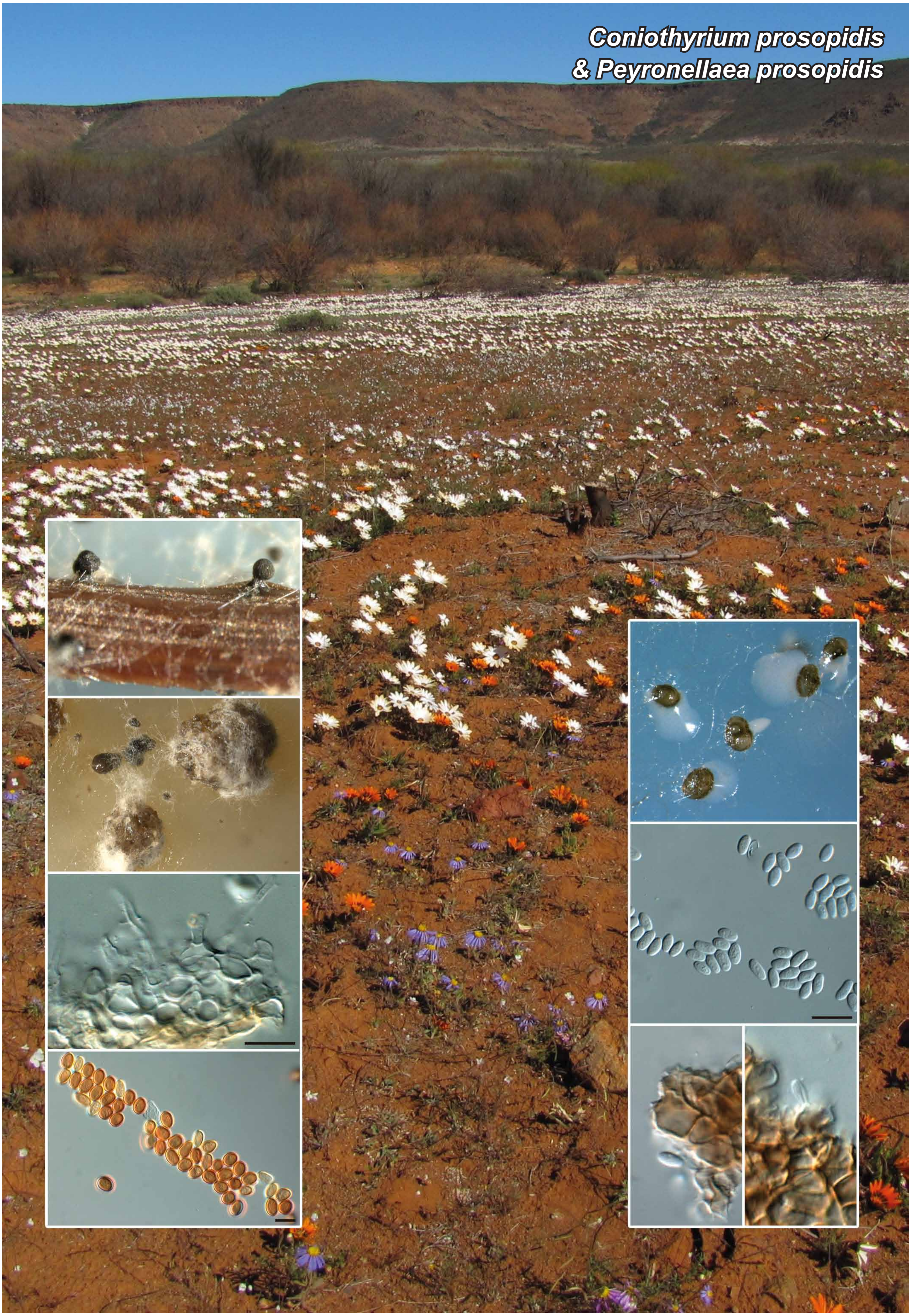
Coniothyrium prosopidis
& Peyronellaea prosopidis

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Coniothyrium prosopidis Crous & A.R. Wood, *sp. nov.*

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

Conidiomata immersed to erumpent, globose, up to 150 µm diam, brown with central ostiole, up to 80 µm diam; exuding a black conidial mass; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, ampulliform, hyaline, smooth, 5–8 × 4–5 µm; proliferating via periclinal thickening or with inconspicuous percurrent proliferation near apex. *Conidia* solitary, ellipsoid to globose, thin-walled but appearing thick-walled with age, brown, smooth, granular, (7–)8–9(–10) × (4–)5–6(–7) µm.

Culture characteristics — Colonies covering dish in 2 wk, with moderate to sparse aerial mycelium. On PDA surface and reverse olivaceous-grey; on OA surface iron-grey; on MEA surface olivaceous-grey, reverse iron-grey.

Typus. South Africa, Northern Cape Province, Calvinia, associated with a bark disease on *Prosopis* sp. (*Fabaceae*), Sept. 2012, *A. Wood* (holotype CBS H-21424, cultures ex-type CPC 21699 = CBS 136415; additional collections studied, CPC 21701, 21703, 21705, 21708; ITS sequence GenBank KF777149–KF777153, LSU sequence GenBank KF777204–KF777206, MycoBank MB805824).

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence of CPC 21699 are *Phoma aliena* (GenBank KC311486; Identities = 910/911 (99 %), no gaps), *Ascochyta pisi* (GenBank DQ678070; Identities = 910/911 (99 %), no gaps) and *Phoma negriana* (GenBank GU238117; Identities = 874/875 (99 %), no gaps). Closest hits using the ITS sequence of CPC 21699 had highest similarity to *Coniothyrium nitidae* (GenBank JN712453; Identities = 653/663 (98 %), Gaps = 1/663 (0 %)), *Microsphaeropsis proteae* (GenBank JN712497; Identities = 652/667 (98 %), Gaps = 6/667 (0 %)) and *Ascochyta pisi* var. *pisi* (GenBank EU167557; Identities = 657/677 (97 %), Gaps = 7/677 (1 %)). *Coniothyrium prosopidis* is allied to *C. nitidae*, but neither belong to *Coniothyrium* s.str. (Aveskamp et al. 2010).

Peyronellaea prosopidis Crous & A.R. Wood, *sp. nov.*

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

Conidiomata pycnidial, brown, immersed to superficial, globose, up to 200 µm diam, with 1–3 ostioles, 10–15 µm diam; wall of 3–5 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, ampulliform to doliiform, 4–8 × 5–6 µm; apex with minute periclinal thickening. *Conidia* hyaline, smooth, granular, ellipsoid, aseptate, thin-walled, ends obtusely rounded, (5–)5.5–6(–7) × (2.5–)3(–3.5) µm. *Chlamydospores* intercalary on hyphae, arranged in chains, globose, brown, 5–9 µm diam.

Culture characteristics — Colonies covering dish in 2 wk, with moderate to fluffy aerial mycelium. On PDA surface and reverse iron-grey; on OA surface iron-grey with patches of pale olivaceous-grey due to fluffy aerial mycelium; on MEA surface pale olivaceous-grey with patches of olivaceous-grey, reverse iron-grey.

Typus. South Africa, Western Cape Province, Calvinia, associated with a stem disease of *Prosopis* sp. (*Fabaceae*), Sept. 2012, *A. Wood* (holotype CBS H-21425, culture ex-type CPC 21698 = CBS 136414, ITS sequence GenBank KF777180, LSU sequence GenBank KF777232, MycoBank MB805825); CPC 21704 = CBS 136550, ITS sequence GenBank KF777181, LSU sequence GenBank KF777233.

Colour illustrations. *Prosopis* sp. dieback in Calvinia, South Africa. Left column *Coniothyrium prosopidis*: conidiomata on PNA and PDA; conidiogenous cells, conidia. Right column *Peyronellaea prosopis*: conidiomata on SNA; conidia and conidiogenous cells. Scale bars = 10 µm.

Notes — Several small-spored coelomycetes have in recent years been collected from *Prosopis*, some of which, like *Prosopidicola mexicana*, showed potential to be evaluated as biocontrol agent of this invasive weed (Lennox et al. 2004). Likewise *Peyronellaea prosopidis* was also isolated from stem lesions on *Prosopis*, although its potential as biocontrol agent has yet to be investigated.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequences are *Phoma pedeiae* (GenBank GU238127; Identities = 875/875 (100 %), no gaps), *Phoma dimorpha* (GenBank GU238068; Identities = 875/875 (100 %), no gaps) and *Peyronellaea coffeae-arabicae* (GenBank GU238006; Identities = 875/875 (100 %), no gaps). Closest hits using the ITS sequences had highest similarity to *Scytalidium acidophilum* (GenBank HQ213804; Identities = 500/500 (100 %), no gaps), *Phoma pomorum* (GenBank AY904062; Identities = 500/500 (100 %), no gaps) and *Phoma glomerata* (GenBank AY183371; Identities = 500/500 (100 %), no gaps). Based on a search with the ITS sequences in Q-Bank (www.q-bank.eu), the sequences were identical to diverse strains of *Peyronellaea pomorum* var. *pomorum* (Identities = 483/483 (100 %), no gaps).

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Pallidocercospora ventilago

Fungal Planet 167 – 26 November 2013

Pallidocercospora ventilago Crous & Cheew., *sp. nov.*

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

Conidiomata pycnidial, globose, erumpent, brown, with central ostiole, up to 150 µm diam, exuding a pale brown conidial mass; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* ampulliform, medium brown, smooth to finely verruculose with several prominent percurrent proliferations near apex, 7–15 × 3–6 µm. *Conidia* solitary, scolecosporous, curved, guttulate, pale brown, smooth, narrowly obclavate, apex subacutely rounded, base obconically rounded with truncate hilum, 1.5–2 µm diam, with minute marginal frill, 3–7-septate, (30–)50–57(–60) × (2–)2.5(–3) µm.

Culture characteristics — Colonies reaching 20 mm diam after 2 wk; surface folded, margin feathery, aerial mycelium sparse. On MEA surface and reverse iron-grey; on PDA centre pale olivaceous-grey, outer region iron-grey, reverse iron-grey; on OA surface olivaceous-grey.

Typus. Thailand, Chiang Mai, Chiang Mai Botanical Garden, on leaves of *Ventilago denticulata* (*Rhamnaceae*), 2 Nov. 2012, *P.W. Crous* (holotype CBS H-21426, culture ex-type CPC 21817, 21818 = CBS 136417, ITS sequence GenBank KF777177, LSU sequence GenBank KF777229, MycoBank MB805826).

Colour illustrations. Symptomatic leaves of *Ventilago denticulata* in Chiang Mai Botanical Garden; leaf spot, colony on OA, vertical section through conidioma, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — In resolving the *Septoria/Pseudocercospora* complex occurring on pistachio, Crous et al. (2013c) reported that contrary to the recent circumscription of *Pseudocercospora* s.str. (Crous et al. 2013a), a species with pycnidial conidiomata and pigmented conidia, *Septoria pistacina* (= *P. pistacina*), also proved to be a member of *Pseudocercospora*. In this study reference was also made to a member of *Pallidocercospora* that had pycnidial conidiomata, which is described here as *P. ventilago.* In both *Pseudocercospora* and *Pallidocercospora*, there thus appears to be a continuum of conidiomatal morphologies.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Mycosphaerella holualoana* (= *Pallidocercospora holualoana*; GenBank JF770467; Identities = 875/878 (99 %), no gaps), *M. heimioides* (= *P. heimioides*; GenBank GU214439; Identities = 875/878 (99 %), no gaps) and *M. heimii* (= *P. heimii*; GenBank GU214438; Identities = 875/878 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *M. heimii* (= *P. heimii*; GenBank EU882122; Identities = 612/619 (99 %), Gaps = 0/619 (0 %)), *M. crystallina* (= *P. crystallina*; GenBank JQ732911; Identities = 641/649 (99 %), Gaps = 1/649 (0 %)) and *M. acaciigena* (= *P. acaciigena*; GenBank EF394822; Identities = 589/598 (98 %), Gaps = 1/598 (0 %)).

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Neodeightoniella phragmiticola

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Neodeightoniella Crous & W.J. Swart, *gen. nov.*

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

Foliicolous, plant pathogenic. *Conidiophores* fasciculate, arising from stromata, amphigenous, associated with weakly developed brown stroma of a few brown cells; fascicles with 3–6 conidiophores. *Conidiophores* erect, brown, unbranched, finely roughened, straight to slightly flexuous, subcylindrical, septate. *Conidiogenous cells* terminal and integrated, subcylindrical, brown, finely roughened; scars terminal and lateral on conidiogenous cells, darkened, thickened, protruding, tretic with central pore. *Conidia* solitary, pale brown, surface finely roughened, fusoid-ellipsoid, straight or gently curved, 1-septate; apical cell globose, with prominent mucoid cap; basal cell funnel-shaped, widest two thirds from basal hilum, tapering prominently to truncate hilum, thickened, darkened, with central pore.

Type species. Neodeightoniella phragmiticola.
MycoBank MB805827.

Neodeightoniella phragmiticola Crous & W.J. Swart, *sp. nov.*

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

Foliicolous. *Leaf spots* amphigenous, brown to dark brown, ellipsoid, up to 5 µm diam. *Conidiophores* fasciculate, arising from stromata, amphigenous, associated with weakly developed brown stroma of a few brown cells; fascicles with 3–6 conidiophores. *Conidiophores* erect, brown, unbranched, finely roughened, straight to slightly flexuous, subcylindrical, 0–2-septate, 40–70 × 5–10 µm. *Conidiogenous cells* terminal and integrated, subcylindrical, brown, finely roughened, 15–60 × 5–10 µm; scars terminal and lateral on conidiogenous cells, darkened, thickened, protruding, tretic with central pore, 3–4 µm diam. *Conidia* solitary, pale brown, surface finely roughened, fusoid-ellipsoid, straight or gently curved, (33–)34–38(–40) × (15–)16–18(–20) µm, 1-septate; apical cell globose, 10–12 × 14–16 µm, with prominent mucoid cap, 8–15 × 20–25 µm; basal cell funnel-shaped, widest two thirds from basal hilum, 20–27 × 15–20 µm, tapering prominently to truncate hilum, thickened, darkened, 3–4 µm diam, with central pore.

Culture characteristics — After 2 wk at 25 °C reaching 30 mm diam; with moderate aerial mycelium and lobed, smooth margins. On OA and PDA surface dirty white with patches of rosy buff. On MEA surface rosy buff with patches of pale purplish grey, reverse fuscous black in centre, apricot in outer region.

Typus. South Africa, Free State, Bultfontein, on leaves of *Phragmites australis* (*Poaceae*), 31 Jan. 2013, *W.J. Swart*, holotype CBS H-21427, cultures ex-type CPC 22059, 22060 = CBS 136418. Additional collections at same venue but different plants: cultures CPC 22061, 22062; cultures CPC 22057, 22058; ITS sequence GenBank KF777170–KF777172, LSU sequence GenBank KF777223–KF777225, MycoBank MB805828).

Notes — *Neodeightoniella* resembles the genus *Deightoniella* (based on *D. africana*, on *Imperata* sp., West Africa), in having pale brown, fusoid-ellipsoid, unequally 1-septate conidia arising from brown conidiophores. It is distinct in that conidiophores do not undergo percurrent rejuvenation (seen as nodal swellings in the type of *Deightoniella*), have prominent apical and lateral conidiogenous loci on the conidiogenous cells, conidia have a prominent mucoid cap, and conidiophores are arranged in fascicles.

Colour illustrations. Symptomatic leaves of *Phragmites australis* in Bultfontein, South Africa; conidiophores, conidia with mucoid caps (arrows), and germinating conidia. Scale bars = 10 µm.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Septoria rumicum* (GenBank KF252034; Identities = 786/792 (99 %), no gaps) and *Passalora fusimaculans* (GenBank KF251817; Identities = 786/792 (99 %), no gaps).

The genus *Deightoniella* presently contains a heterogeneous assemblage of taxa. Crous et al. (2011a) described the genus *Utrechtiana* (based on *U. cibiessia*, pathogenic to *Phragmites australis* in The Netherlands). An earlier name exists for the taxon, namely *D. roumeguerei* (on *P. australis* in France) (Constantinescu 1983). This taxon fits *Deightoniella* (based on *D. africana*, occurring on leaves of *Imperata cylindrica* var. *africana*; *Poaceae*) rather well, as conidiophores are solitary, and a reexamination of the type material found the conidiogenous cells to rejuvenate percurrently as in *D. africana* (see Seifert & Gams 2011 for synonymy). Assuming that *D. africana* and *D. roumeguerei* are congeneric, *Deightoniella* belongs to the *Magnaporthaceae*.

Another species accommodated in *Deightoniella* is *D. torulosa*, which causes Deightoniella black tip, leaf spot and fruit speckle of banana (Ploetz 2003). This species was originally placed in *Deightoniella* as the conidiophores were also observed to rejuvenate internally and percurrently, creating the same nodose swellings as observed in the type, *D. africana*. Phylogenetically, however, *D. torulosa* clusters with isolates of *Corynespora cassicola*, the type species of the genus *Corynespora*. This finding suggests that the species of *Deightoniella* with distoseptate conidia belong elsewhere.

Corynespora torulosa (Syd.) Crous, *comb. nov.*

Basionym. Brachysporium torulosum Syd., Hedwigia 49: 83. 1909.
≡ *Deightoniella torulosa* (Syd.) M.B. Ellis, Mycol. Pap. 66: 7. 1957.
≡ *Helminthosporium torulosum* (Syd.) S.F. Ashby, Trop. Agric. (Trinidad) 10: 6. 1932.
= *Cercospora musarum* S.F. Ashby, Bull. Dept. Agric. (Kingston) 2: 109. 1913.

Specimens examined. Brazil, Pará, on *Musa cavendishii* (*Musaceae*), 24 Jan. 1908, *C.F. Baker*, ex Herb. Sydow, portion of holotype of *Brachysporium torulosum* (9810) in IMI. – Mexico, Colima, Tecomán, on *M. cavendishii*, *M. de Jesús Yáñez-Morales*, 17 Nov. 2008 (CBS H-21456 epitype designated here 'MBT176329', cultures ex-epitype CPC 15989, 15990 = CBS 136419, ITS sequence GenBank KF777154, LSU sequence GenBank KF777207, MycoBank MB805829).

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Corynespora smithii* (GenBank GU323201; Identities = 874/882 (99 %), no gaps) and *C. cassiicola* (GenBank GU301808; Identities = 811/820 (99 %), Gaps = 4/820 (0 %)).

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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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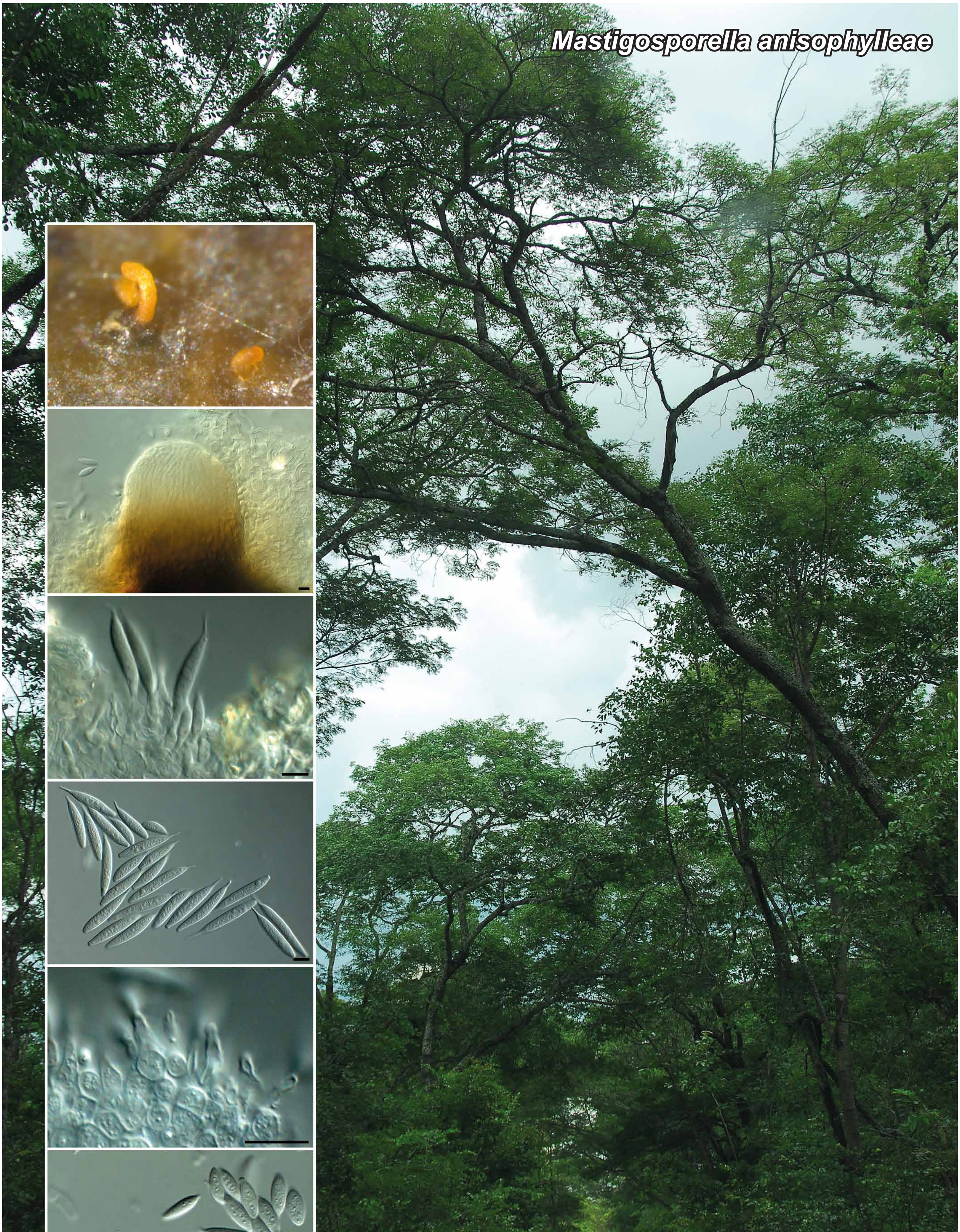
Mastigosporella anisophylleae

Fungal Planet 170 – 26 November 2013

Mastigosporella anisophylleae Crous, *sp. nov.*

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

Conidiomata immersed, pycnidial, up to 250 µm diam, yellowish on host tissue, with central ostiole which can become papillate (or not, in which case the conidioma can open by means of an irregular split), exuding a yellow conidial cirrhus; wall of 6–10 layers of hyaline to subhyaline *textura globulosa* to *angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, smooth, lining the inner cavity, subcylindrical to ampulliform or doliiform, 5–12 × 3–5 µm; proliferating several times inconspicuous percurrently near apex. *Conidia* solitary, aseptate, fusoid-ellipsoid, hyaline, smooth, thick-walled, granular, developing a solitary apical appendage (cellular, type A1 sensu Nag Raj 1993), which is part of the conidial body, which develops while still attached to the conidiogenous cell, attenuating into an acutely rounded tip; conidium body (21–)27–30(–32) × (4.5–)5–5.5(–6) µm (excluding appendage); basal hilum truncate, 1.5–2 µm diam, with minute marginal frill; apical appendage developing as continuation of conidium body, containing cytoplasm, (5–)6–7(–8) µm.

Culture characteristics — Colonies covering dish in 2 wk at 25 °C, flat, spreading, with sparse dirty white aerial mycelium and patches of orange due to copious sporulation. On PDA surface grey-olivaceous, reverse smoke-grey; on OA surface dirty white to apricot; on MEA surface ochreous, reverse umber.

Typus. Zambia, -14.90099 25.45409, on *Anisophyllea* sp. (*Anisophylleaceae*), 21 Feb. 2013, *M. van der Bank* (holotype CBS H-21429, culture ex-type CPC 22461, 22462 = CBS 136421, ITS sequence GenBank KF779492, LSU sequence GenBank KF777221, MycoBank MB805831).

Notes — The genus *Mastigosporella* (presumed sexual morph *Wuestneiopsis*) is characterised by yellowish pycnidial conidiomata, and hyaline conidiogenous cells that proliferate percurrently, giving rise to narrowly ellipsoid to fusoid conidia that form an appendage (type A1) while still attached to the conidiogenous cell, becoming a tubular extension of the conidium body (Nag Raj 1993). Presently the genus is known from two species, *M. hyalina* (on *Quercus coccinea*, USA; conidia 18–28 × 3.5–5 µm) and *M. nyssae* (on *Nyssa* spp., USA; conidia 16–25 × 5–7 µm), which are smaller than those of *M. anisophyllea.*

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Cryphonectria decipiens* (GenBank JQ862750; Identities = 817/828 (99 %), Gaps = 1/828 (0 %)), *Aurifilum marmelostoma* (GenBank HQ730874; Identities = 826/838 (99 %), Gaps = 1/838 (0 %)) and *Cryphonectria macrospora* (GenBank AF408340; Identities = 825/837 (99 %), Gaps = 1/837 (0 %)).

The *Cryphonectriaceae* represents a family of ascomycetous fungi characterised by erumpent conidiomata with bright yellow-brown furfuraceous margins (Rossman et al. 2007). Several foliicolous genera on diverse woody hosts have in recent years been added to this family, namely *Aurantiosacculus* and *Foliocryphia* on *Eucalyptus* (Cheewangkoon et al. 2009, Crous et al. 2012b), and *Chrysocrypta* on *Corymbia* (Crous et al. 2012c). The present study links yet another genus to the *Cryphonectriaceae*, namely *Mastigosporella.*

Colour illustrations. *Anisophyllea* sp. and undergrowth along country road in Zambia (photo credit: Olivier Maurin); oozing conidial mass, papillate conidioma, conidiogenous cells and conidia. Scale bars = 10 µm.

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Dimorphiopsis brachystegiae

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Dimorphiopsis Crous, *gen. nov.*

Etymology. Named after its dimorphic conidiomata.

Mycelium consisting of pale to brown, septate, branched, smooth, 2–3 µm diam hyphae, at times with intercalary chlamydospore-like cells. Conidiomata vary from immersed pycnidia to superficial sporodochia, opening by irregular rupture of wall, globose to irregular; conidiomatal wall not clearly distinguishable, consisting of globose, aseptate, medium brown cells that are densely aggregated but not clearly attached, forming conidia inwardly towards centrum of conidioma. *Conidiogenous cells* dissolving early, aggregated, hyaline to pale brown, smooth, ampulliform to globose, 4–6 × 4–5 µm, with inconspicuous terminal, phialidic openings. *Conidia* solitary, pale brown when immature, becoming dark brown, roughened to warty, golden to dark brown, medianly 1-distoseptate, thick-walled, ellipsoid, constricted at septum, with obtuse ends, and flattened basal scar.

Type species. Dimorphiopsis brachystegiae.
MycoBank MB805832.

Dimorphiopsis brachystegiae Crous, *sp. nov.*

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

Originally isolated as a coelomycetous fungus from leaves of *Brachystegia spiciformis*. *Mycelium* consisting of pale to brown, septate, branched, smooth, 2–3 µm diam hyphae, at times with intercalary chlamydospore-like cells. In culture conidiomata immersed in agar or superficial (sporodochial), opening by irregular rupture of wall, up to 400 µm diam, globose to irregular; conidiomatal wall not clearly distinguishable, consisting of globose, aseptate, medium brown cells that are densely aggregated but not clearly attached, forming conidia inwardly towards centrum of conidioma. *Conidiogenous cells* dissolving early, aggregated, hyaline to pale brown, smooth, ampulliform to globose, 4–6 × 4–5 µm, with inconspicuous terminal, phialidic openings. *Conidia* solitary, pale brown when immature, becoming dark brown, roughened to warty, golden to dark brown, medianly 1-distoseptate, thick-walled, ellipsoid, constricted at septum, with obtuse ends, and flattened basal scar, 1 µm diam, (8–)9–10(–11) × (6–)7(–8) µm.

Culture characteristics — Colonies spreading, erumpent, with no aerial mycelium, and smooth, lobate margins. On OA, PDA and MEA greenish black; colonies reaching 20 mm diam after 2 wk at 25 °C.

Typus. Zambia, -16.46045 27.52961, on leaves of *Brachystegia spiciformis* (*Fabaceae*), 28 Mar. 2013, *M. van der Bank* (holotype CBS H-21430, culture ex-type CPC 22679, 22680 = CBS 136422, ITS sequence GenBank KF777160, LSU sequence GenBank KF777213, MycoBank MB805833).

Colour illustrations. *Brachystegia spiciformis* in Zambia (photo credit: Olivier Maurin). Conidiomata on OA, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — It is debatable if this odd fungus is a coelomycete or hyphomycete. On PNA it is a hyphomycete with sporodochia on sterile pine needles, but a coelomycete with immersed conidiomata in the water agar. As we could not locate a description of any morphologically similar fungus, we describe it here as new.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Lophiostoma quadrisporum* (GenBank AB619011; Identities = 814/860 (95 %), Gaps = 3/860 (0 %)), *L. fuckelii* (GenBank GU385192; Identities = 851/900 (95 %), Gaps = 3/900 (0 %)) and *L. alpigenum* (GenBank GU385193; Identities = 850/901 (94 %), Gaps = 4/901 (0 %)). Only distant hits were obtained with species of *Lophiostoma* using the ITS sequence, e.g. *L. macrostomum* (GenBank EU552140; Identities = 511/635 (80 %), Gaps = 45/635 (7 %)), *L. fuckelii* (GenBank EU552139; Identities = 488/606 (81 %), Gaps = 46/606 (7 %)) and *L. arundinis* (GenBank AJ496633; Identities = 464/577 (80 %), Gaps = 31/577 (5 %)).

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Neopseudocercospora terminaliae

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Neopseudocercospora Crous, *gen. nov.*

Etymology. Named after its resemblance to the genus *Pseudocercospora*.

Foliicolous, plant pathogenic. *Mycelium* superficial, consisting of branched, septate, medium brown, hyphae, at times constricted at septa, lacking hyphopodia. *Conidiophores* solitary, erect, medium brown, subcylindrical, straight to once geniculate, septate. *Conidiogenous cells* integrated, terminal, medium brown, smooth, subcylindrical, proliferating several times percurrently near apex. *Conidia* solitary, medium brown, smooth, subcylindrical, straight to gently curved, apex obtuse, base truncate, rarely with minute marginal frill, not thickened nor darkened, transversely euseptate (with central pore), rarely with longitudinal septa, guttulate to finely granular, surface finely roughened.

Type species. Neopseudocercospora terminaliae.
MycoBank MB805834.

Neopseudocercospora terminaliae Crous, *sp. nov.*

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

Colonies occurring on the underside of leaves, associated with pale brown leaf spots, indistinct, confined by leaf veins, 1–5 mm diam, covering lesion with black conidial mass. *Mycelium* superficial, consisting of branched, septate, medium brown, 3–4 µm diam hyphae, at times constricted at septa, lacking hyphopodia. *Conidiophores* solitary, erect, medium brown, subcylindrical, straight to once geniculate, 0–3-septate, 15–40 × 4–6 µm. *Conidiogenous cells* integrated, terminal, medium brown, smooth, subcylindrical, 5–25 × 5–7 µm; proliferating several times percurrently near apex. *Conidia* solitary, medium brown, smooth, subcylindrical, straight to gently curved, apex obtuse, base truncate, 5–6 µm diam, rarely with minute marginal frill, not thickened nor darkened, transversely 7–11-euseptate (with central pore), rarely with longitudinal septa, guttulate to finely granular, surface finely roughened, (65–)70–75(–80) × (8–)10 µm.

Culture characteristics — Colonies erumpent, surface folded, with sparse aerial mycelium and lobate, feathery margins, reaching 10 mm diam after 2 wk. On MEA surface iron-grey with patches of olivaceous-grey, reverse iron-grey; on OA and PDA surface dirty white with patches of pale olivaceous-grey.

Typus. Zambia, -11.91237 25.30100, on *Terminalia* sp. (*Combretaceae*), 24 Feb. 2013, *M. van der Bank* (holotype CBS H-21431, culture ex-type CPC 22685, 22686 = CBS 136423, ITS sequence GenBank KF777175, LSU sequence GenBank KF777228, MycoBank MB805835).

Colour illustrations. *Terminalia* sp. in Zambia (photo credit: Olivier Maurin); conidiophores giving rise to conidia (note some conidia broken, not disarticulating). Scale bars = 10 µm.

Notes — *Neopseudocercospora* is reminiscent of the genera *Sporidesmium*, *Sporidesmajora* and *Phaeomycocentrospora* (Wu & Zhuang 2005, Yang et al. 2010, Crous et al. 2013a). *Sporidesmium*, however, belongs to the *Sordariomycetes*, and *Phaeomycocentrospora* to the *Pleosporales* (Crous et al. 2013a). *Sporidesmajora* has very long conidiophores, and obclavate conidia with darker basal cells, and belongs to the *Micropeltidaceae* (Yang et al. 2010). *Neopseudocercospora* belongs to the *Mycosphaerellaceae*, where it clusters with *Microcyclosporella* and zasmidium-like species (Clade 8 sensu Crous et. al 2013a). Within this family, it is reminiscent of some species of *Pseudocercospora* (Crous et al. 2013a). However, the combination of characters that include exclusively superficial hyphae, solitary conidiophores, conidiogenous cells that proliferate percurrently, and conidia that also have longitudinal septa, is not typical for *Pseudocercospora*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Mycosphaerella parkii* (GenBank DQ246245; Identities = 854/891 (96 %), Gaps = 7/891 (0 %)), *Mycosphaerella madeirae* (GenBank DQ204756; Identities = 851/890 (96 %), Gaps = 5/890 (0 %)) and *Phaeophleospora concentrica* (GenBank FJ493205; Identities = 851/892 (95 %), Gaps = 9/892 (1 %)). Closest hits using the ITS sequence had highest similarity to *Mycosphaerella milleri* (GenBank EU167577; Identities = 465/536 (87 %), Gaps = 16/536 (2 %)), *Phloeospora ulmi* (GenBank F251200; Identities = 455/527 (86 %), Gaps = 32/527 (6 %)) and *Pseudocercosporella capsellae* (GenBank U214662; Identities = 470/545 (86 %), Gaps = 26/545 (4 %)).

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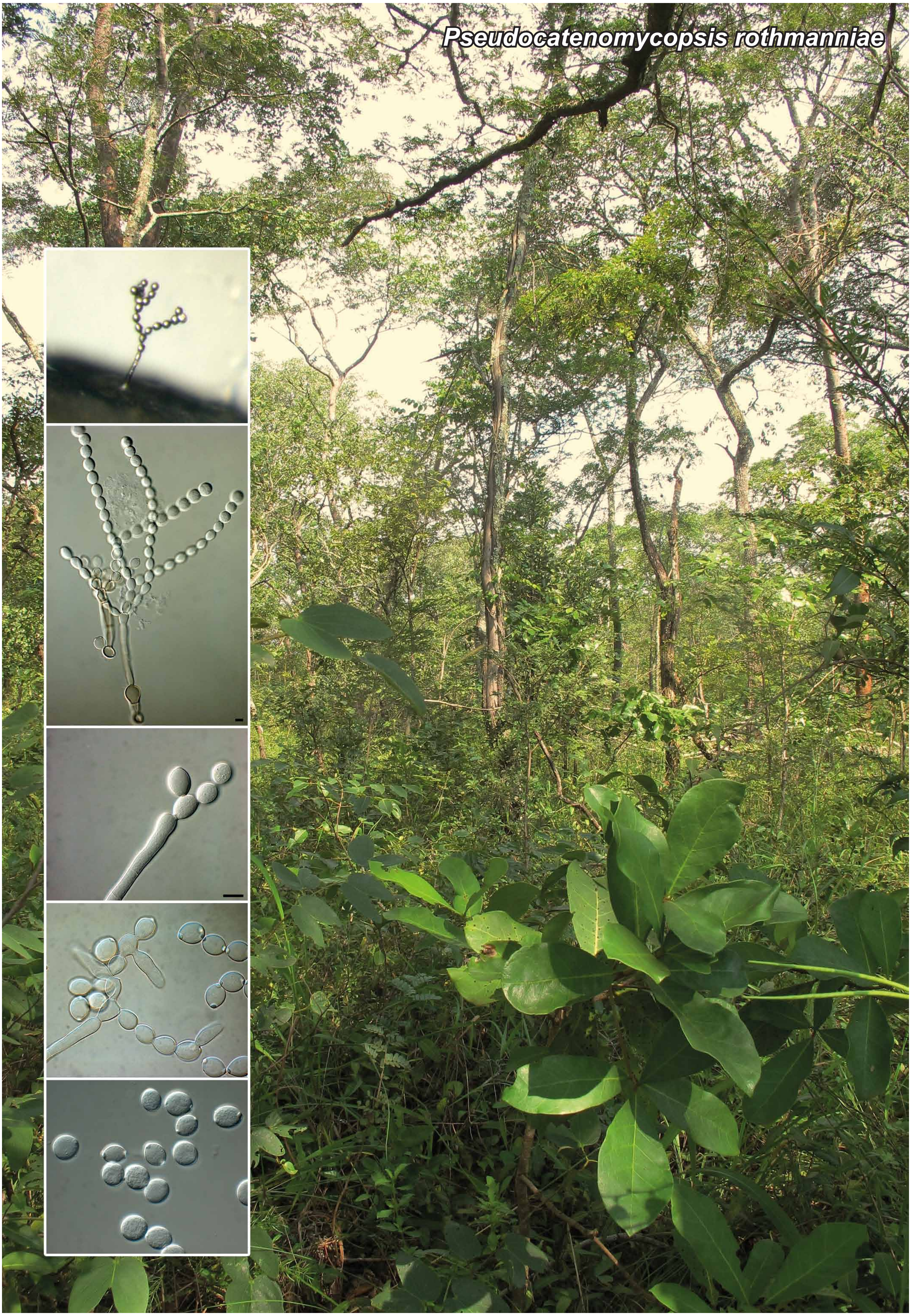
Pseudocatenomycopsis rothmanniae

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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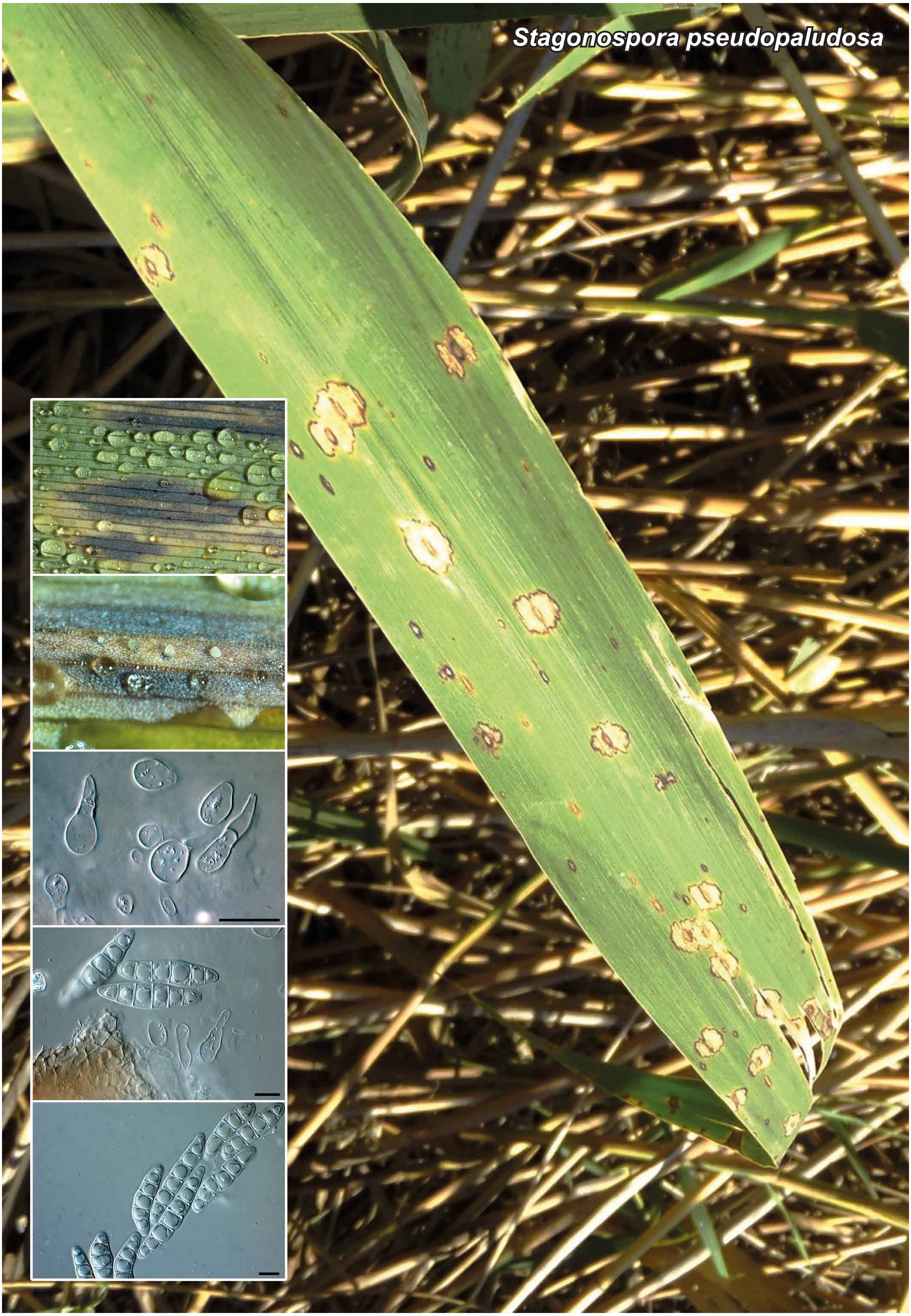
Stagonospora pseudopaludosa

Fungal Planet 174 – 26 November 2013

Stagonospora pseudopaludosa Crous & W.J. Swart, *sp. nov.*

Etymology. Named after its morphological similarity to *Stagonospora paludosa*.

Leaf spots angular, amphigenous, pale brown, up to 7 mm diam. *Conidiomata* immersed, globose, substomatal, black, up to 250 µm diam; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells or with 1 supporting cell. *Conidiogenous cells* hyaline, smooth, lining the inner cavity, ampulliform to subglobose, 10–20 × 5–12 µm; proliferating percurrently near apex. *Conidia* solitary, hyaline, smooth, fusoid-ellipsoid, straight to gently curved, widest in middle of conidium, apex subobtuse, base truncate (2–5 µm diam), with minute marginal frill, thick-walled, granular, with large central guttulate in each cell, (3–)5(–6)-septate, (43–)50–60(–70) × (9–)10–11(–13) µm.

Culture characteristics — Colonies covering the dish after 2 wk at 25 °C; colonies spreading, erumpent with abundant aerial mycelium and lobate margins. Surface pale olivaceous-grey with patches of olivaceous-grey on MEA, PDA and OA.

Typus. South Africa, Free State, Bultfontein, on leaves of *Phragmites australis* (*Poaceae*), 31 Jan. 2013, *W.J. Swart* (holotype CBS H-21433, cultures ex-type CPC 22654–22655 = CBS 136424, ITS sequence GenBank KF777188, LSU sequence GenBank KF777239, MycoBank MB805838).

Colour illustrations. Symptomatic leaves of *Phragmites australis* in Bultfontein, South Africa; close-up of lesions, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — Morphologically, *S. pseudopaludosa* resembles *S. paludosa* (Quaedvlieg et al. 2013). However, based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Stagonospora uniseptata* (GenBank KF251767; Identities = 821/832 (99 %), no gaps), *S. pseudovitensis* (GenBank KF251765; Identities = 820/832 (99 %), no gaps) and *Neottiosporina paspali* (GenBank EU754172; Identities = 822/835 (98 %), no gaps). Closest hits using the ITS sequence had highest similarity to *S. pseudovitensis* (GenBank KF251262; Identities = 446/469 (95 %), Gaps = 6/469 (1 %)), *S. perfecta* (GenBank KF251258; Identities = 445/468 (95 %), Gaps = 5/468 (1 %)) and *S.* cf. *paludosa* (GenBank KF251254; Identities = 433/456 (95 %), Gaps = 5/456 (1 %)).

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Calonectria blephiliae

Fungal Planet 175 – 26 November 2013

Calonectria blephiliae Crous & Hodges, *sp. nov.*

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

Conidiophores with a stipe bearing a suite of penicillate, fertile branches, a stipe extension, and a terminal vesicle; stipe septate, hyaline, smooth, 90–220 × 5–7 µm; stipe extensions septate, straight to flexuous, 200–280 µm long, 3.5–4.5 µm wide at apical septum, terminating in a clavate to ellipsoid vesicle, 7–10 µm diam. *Conidiogenous apparatus* 100–150 µm long and 90–110 µm wide; primary branches aseptate or 1-septate, 33–70 × 6–8 µm; secondary branches aseptate, 15–25 × 4–5 µm; tertiary and additional branches (–4), aseptate, 8–22 × 3–5 µm, each terminal branch producing 2–4 phialides; phialides doliiform to reniform, hyaline, aseptate, 7–12 × 3–4 µm; apex with minute periclinal thickening and inconspicuous collarette. *Macroconidia* cylindrical, rounded at both ends, straight, (42–)48–52(–55) × (4–)4.5(–5) µm, 1-septate, aggregated in parallel cylindrical clusters. *Megaconidia* and *microconidia* not seen.

Culture characteristics — Colonies with moderate aerial mycelium and feathery margin. On PDA surface and reverse chestnut; on MEA surface bay, reverse chestnut; on OA surface bay, reverse umber.

Typus. USA, North Carolina, Ellerbe, associated with dead lower stems of *Blephilia ciliata* (*Lamiaceae*), 18 Sept. 2012, *T. Sharp* (holotype CBS H-21434, culture ex-type CPC 21859 = CBS 136425, ITS sequence GenBank KF777141, LSU sequence GenBank KF777197, TEF sequence GenBank KF777243, TUB sequence GenBank KF777246, MycoBank MB805839).

Notes — Morphologically *Calonectria blephiliae* is part of the *C. morganii* species complex (Schoch et al. 1999, 2000).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Calonectria variabilis* (GenBank GQ280785; Identities = 874/874 (100 %), no gaps), *C. sulawesiensis* (GenBank GQ280760; Identities = 874/874 (100 %), no gaps) and *C. insularis* (GenBank GQ280710; Identities = 874/874 (100 %), no gaps). Closest hits using the ITS sequence had highest similarity to *C. sulawesiensis* (GenBank GQ280638; Identities = 569/571 (99 %), Gaps = 2/571 (0 %)), *C. cerciana* (GenBank GQ280560; Identities = 569/571 (99 %), Gaps = 1/571 (0 %)) and *C. morganii* (GenBank GQ280626; Identities = 568/571 (99 %), Gaps = 3/571 (0 %)). Closest hits using the TEF sequence had highest similarity to *C. morganii* (GenBank FJ918557; Identities = 483/488 (99 %), Gaps = 1/488 (0 %)), *C. sulawesiensis* (GenBank GQ267343; Identities = 483/490 (99 %), Gaps = 3/490 (0 %)) and *C. variabilis* (GenBank GQ267335; Identities = 486/494 (98 %), Gaps = 7/494 (1 %)). Closest hits using the TUB sequence had highest similarity to *C. morganii* (GenBank DQ521600; Identities = 536/537 (99 %), Gaps = 1/537 (0 %)), *C. pauciramosa* (GenBank FJ795548; Identities = 516/517 (99 %), Gaps = 1/517 (0 %)) and *C. pseudonaviculata* (GenBank GQ267214; Identities = 562/564 (99 %), Gaps = 1/564 (0 %)).

Colour illustrations. Symptomatic *Blephilia ciliata*; conidiophores sporulating on CLA; conidiogenous cells, cylindrical, 1-septate conidia and terminal vesicles. Scale bars = 10 µm.

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Harknessia proteae

Fungal Planet 176 – 26 November 2013

Harknessia proteae Crous, *sp. nov.*

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

Foliicolous. *Conidiomata* separate, immersed, globose to subglobose, unilocular, erumpent, punctiform, up to 400 µm diam; ostiole with pale brown furfuraceous margin; basal and lateral walls up to 7 layers thick, of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Macroconidiogenous cells* discrete, hyaline, smooth, lageniform to subcylindrical, 15–25 × 3–5 µm; proliferating enteroblastically near apex. *Macroconidia* fusoid-ellipsoid, with longitudinal striations along its length, at times apiculate, granular to guttulate, brown, with central guttule, base truncate, (30–)33–36(–40) × (14–)15–16(–17) µm. Basal appendage 12–30 × 2–4 µm, collapsing once released from conidiogenous cell; conidiogenous cells and appendages at times enclosed in mucilage. *Microconidiogenous cells* in same conidioma, subcylindrical to lageniform, hyaline, smooth, with periclinal thickening at apex, 6–10 × 3–4 µm. *Microconidia* holoblastic, apical and lateral, hyaline, aseptate, smooth, ellipsoid to fusiform, 4–6 × 2.5–3 µm.

Culture characteristics — Colonies spreading with moderate to abundant aerial mycelium; surface dirty white to cream or pale luteous; covering the dish in 1 mo; sporulating with black conidiomata, oozing black spore masses.

Typus. South Africa, Mpumalanga, Buffelskloof Private Nature Reserve, latitude -25.302596656391604, longitude: 30.504741668701172, on leaves of *Protea roupelliae* subsp. *roupelliae* (*Proteaceae*), Sept. 2012, *M. van der Bank* (holotype CBS H-21435, culture ex-type CPC 21835 = CBS 136426, ITS sequence GenBank KF777162, LSU sequence GenBank KF777215, MycoBank MB805840).

Notes — Two species of *Harknessia* are known from *Proteaceae*, namely *H. leucospermi* (conidia (23–)25–27(–30) µm) and *H. protearum* (conidia (21–)23–24(–26) µm (Lee et al. 2004, Crous et al. 2012d, 2013b). *Harknessia proteae* can be distinguished from these species by having larger, more fusoid-ellipsoid conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Wuestneia molokaiensis* (GenBank JQ706246; Identities = 884/884 (100 %), no gaps), *Harknessia gibbosa* (GenBank JQ706226; Identities = 884/884 (100 %), no gaps) and *H. eucalypti* (GenBank JQ706215; Identities = 883/883 (100 %), no gaps). Closest hits using the ITS sequence had highest similarity to *H. ravenstreetina* (GenBank JQ706113; Identities = 428/431 (99 %), no gaps), *H. eucalypti* (GenBank JQ706089; Identities = 733/739 (99 %), Gaps = 4/739 (0 %)) and *H. globispora* (GenBank JQ706105; Identities = 687/693 (99 %), Gaps = 2/693 (0 %)).

Colour illustrations. *Protea roupelliae* subsp. *roupelliae* in Buffelskloof Private Nature Reserve, South Africa (photo credit: Olivier Maurin); conidioma on OA; macro- and microconidia. Scale bars = 10 µm.

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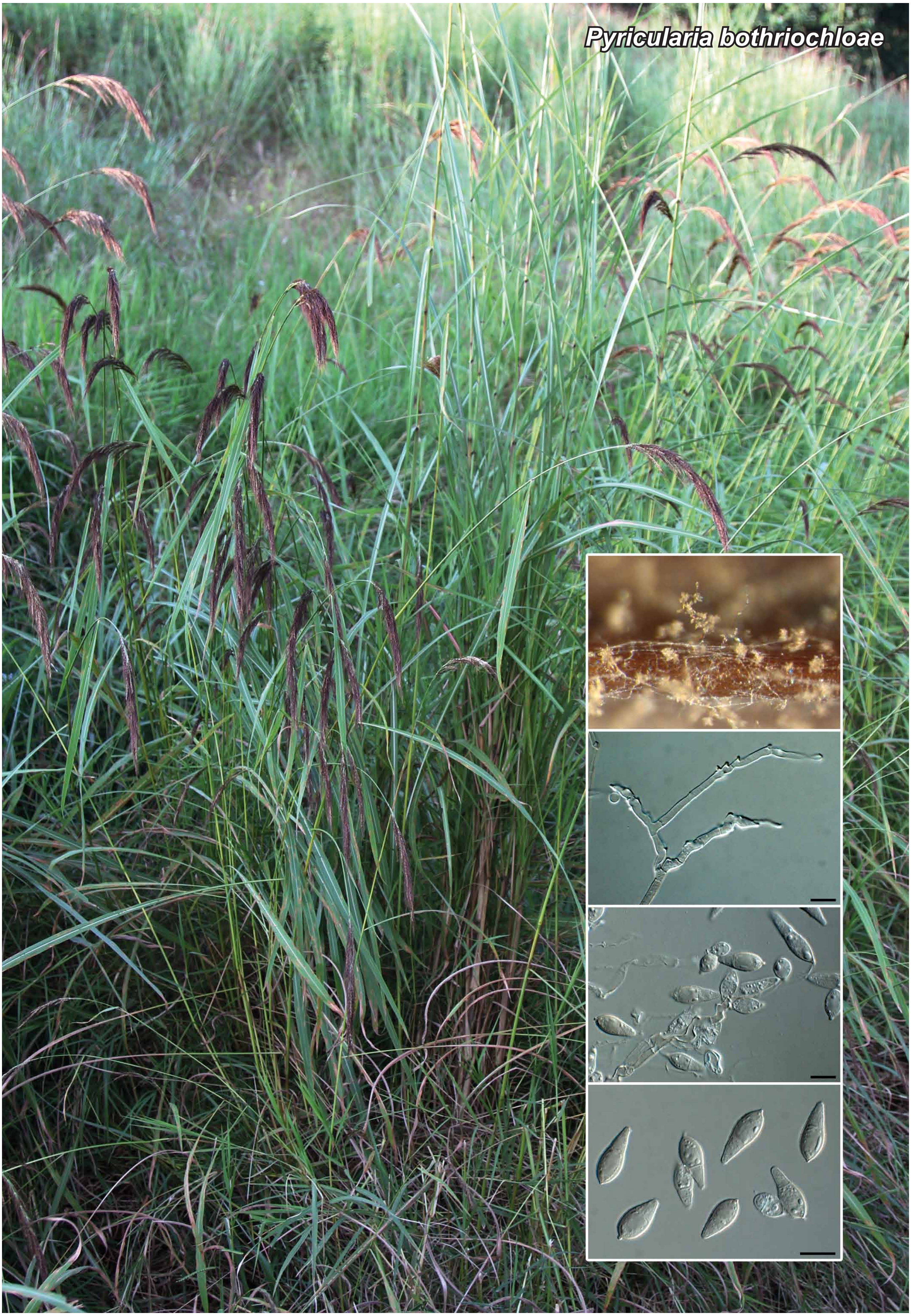
Pyricularia bothriochloae

Fungal Planet 177 – 26 November 2013

Pyricularia bothriochloae Crous & Cheew., *sp. nov.*

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

Leaf spots angular, pale to medium brown with red-purple margin, up to 4 mm diam. On SNA. *Mycelium* consisting of smooth, hyaline, branched, septate hyphae, 1.5–2 µm diam. *Conidiophores* solitary, erect, straight or curved, branched or not, medium brown, smooth, 90–180 × 3–6 µm, 5–8-septate. *Conidiogenous cells* 8–30 × 3–4 µm, integrated, terminal and lateral, pale brown, smooth, forming a rachis with several protruding denticles, phialidic with minute periclinal thickening, 1–1.5 µm long, 1–2 µm diam. *Conidia* solitary, obclavate, pale brown, smooth to finely roughened, guttulate, (18–)19–22(–23) × (6–)7–8(–9) µm; apical cell 6–8 µm long, basal cell 11–14 µm long.

Culture characteristics — Colonies covering plates in 2 wk, with moderate aerial mycelium. On OA surface with patches of olivaceous-grey, iron-grey and pale olivaceous-grey; on MEA surface and reverse honey to isabelline; on PDA surface and reverse olivaceous-black.

Typus. THAILAND, Royal Project, N18°09'24.8" E98°23'19.6", on leaves of *Bothriochloa bladhii* (*Poaceae*), 29 Oct. 2012, *P.W. Crous* (holotype CBS H-21436, culture ex-type CPC 21650, 21651 = CBS 136427, ITS sequence GenBank KF777186, LSU sequence GenBank KF777238, MycoBank MB805841).

Colour illustrations. *Bothriochloa bladhii* growing in Thailand; colony sporulating on PNA; conidiophores and conidia. Scale bars = 10 µm.

Notes — *Pyricularia bothriochloa* represents a novel species of *Pyricularia* on *Bothriochloa bladhii* from Thailand, which does not correspond to any species presently in GenBank, or in our own unpublished DNA sequence database.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Dactylaria higginsii* (GenBank DQ341512; Identities = 861/875 (98 %), Gaps = 1/875 (0 %)), *Utrechtiana cibiessia* (GenBank JF951176; Identities = 883/909 (97 %), no gaps) and *Pyricularia borealis* (GenBank DQ341511; Identities = 833/860 (97 %), no gaps). Closest hits using the ITS sequence had highest similarity to *Magnaporthe oryzae* (GenBank JQ747492; Identities = 641/703 (91 %), Gaps = 17/703 (2 %)), *Dactylaria junci* (GenBank AY265320; Identities = 496/546 (91 %), Gaps = 15/546 (2 %)) and *Dactylaria higginsii* (GenBank AB274438; Identities = 420/464 (91 %), Gaps = 15/464 (3 %)).

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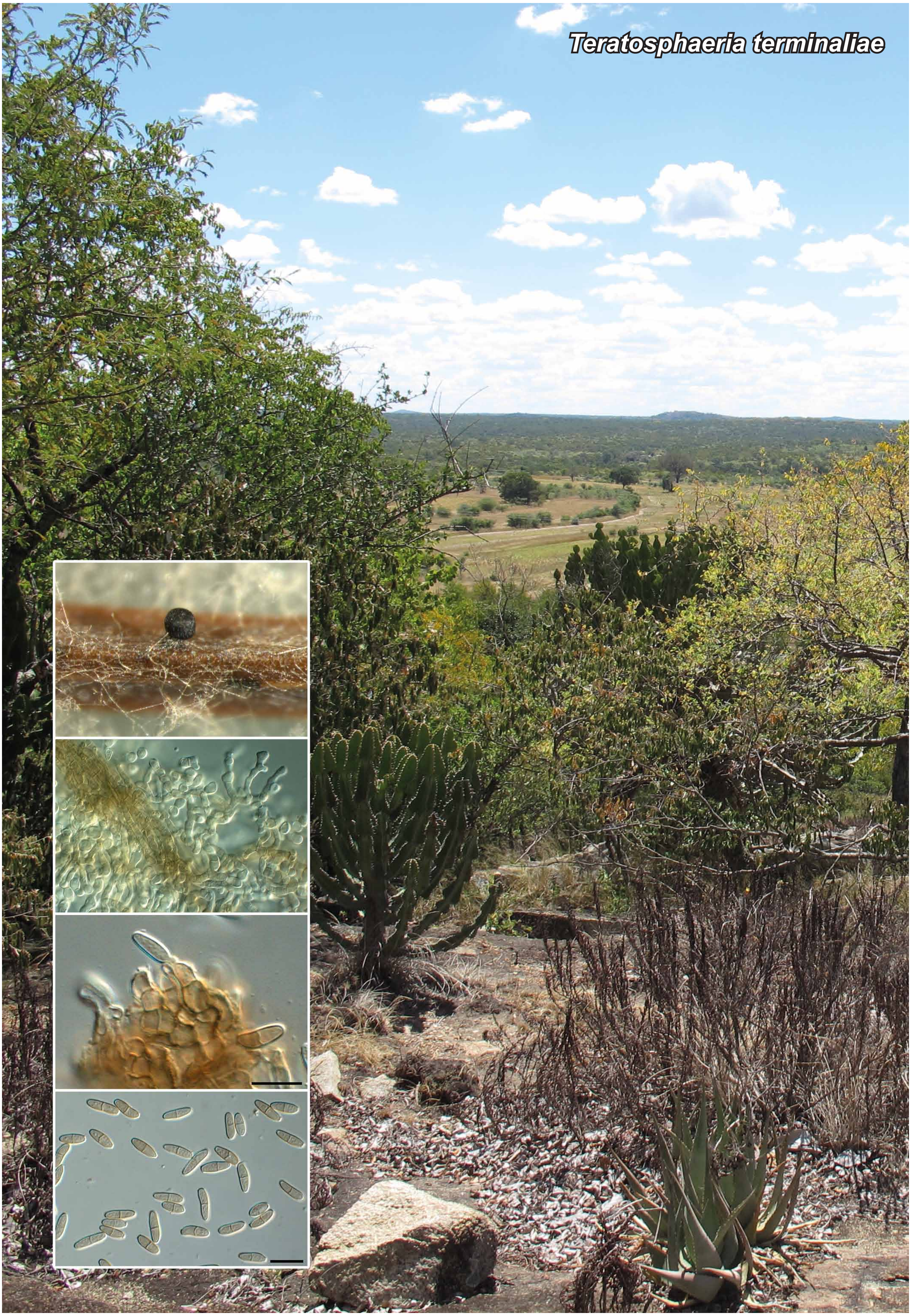
Teratosphaeria terminaliae

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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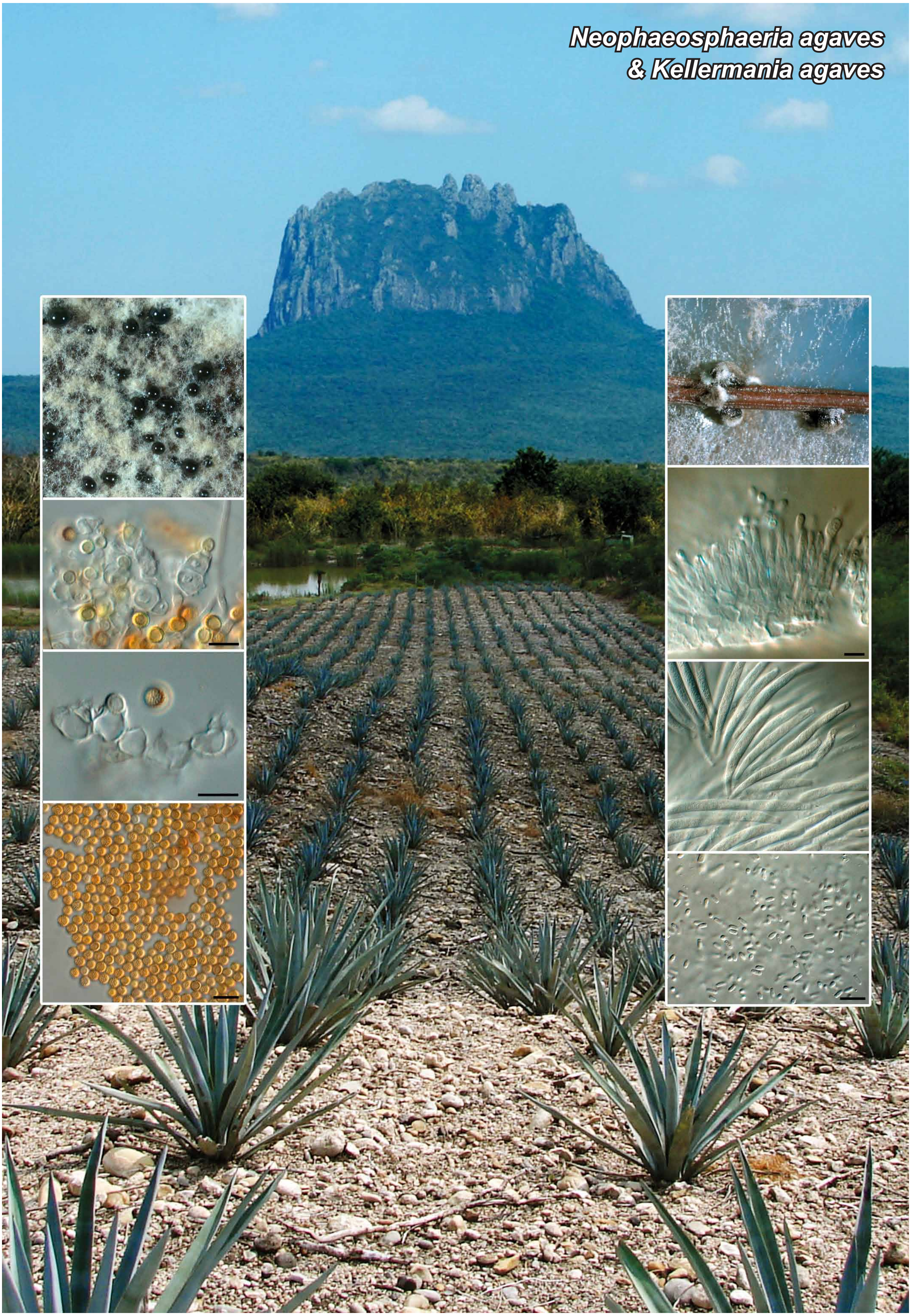
Neophaeosphaeria agaves
& Kellermania agaves

Fungal Planet 179 & 180 – 26 November 2013

Neophaeosphaeria agaves Crous & Yáñez-Moral., *sp. nov.*

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

Conidiomata immersed on PNA, superficial on PDA, globose, up to 300 µm diam, exuding a black, globoid conidial mass through central ostiole; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, smooth, ampulliform, lining the inner cavity, phialidic, with prominent periclinal thickening, 4–10 × 4–6 µm. *Conidia* solitary, globose to subglobose, thick-walled, spiny, golden-brown, (3–)4–5(–6) × (4–)5(–6) µm; lacking any visible abscission scar.

Culture characteristics — Colonies after 2 wk reaching 50 mm diam, with moderate aerial mycelium, and even, smooth, lobed margins. On MEA surface dirty white in middle, cinnamon in outer region; reverse dark brick in middle, cinnamon in outer region. On OA patches of dirty white, honey and dark brick. On PDA surface olivaceous-grey with patches of pale olivaceous-grey, reverse iron-grey to olivaceous-grey.

Typus. Mexico, southern region of Tamaulipas State, on leaves of *Agave tequilana* var. *azul* (*Asparagaceae*), 17 Aug. 2012, *M. de Jesús Yáñez-Morales & Lamberto Zúñiga-Estrada* (holotype CBS H-21438, culture ex-type CPC 21264, 21265 = CBS 136429, ITS sequence GenBank KF777174, LSU sequence GenBank KF777227, MycoBank MB805843).

Notes — *Neophaeosphaeria agaves* is phylogenetically closely related to other species of the genus *Neophaeosphaeria.* The genus *Neophaeosphaeria* has coniothyrium-like anamorphs (Câmara et al. 2003), which have thus far all been described from *Yucca* spp. (*Asparagaceae*). As *Agave* also occurs in the *Asparagaceae*, it is thus not surprising to find species of *Neophaeosphaeria* on this host. *Neophaeosphaeria agaves* is morphologically distinct from other species in the genus by having rather small, (3–)4–5(–6) × (4–)5(–6) µm, aseptate, spiny conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Neophaeosphaeria filamentosa* (GenBank GQ387577; Identities = 870/875 (99 %), no gaps), *Subplenodomus violicola* (GenBank GU238156; Identities = 861/876 (98 %), Gaps = 2/876 (0 %)) and *Leptosphaeria biglobosa* (GenBank GU237980; Identities = 860/875 (98 %), no gaps). Closest hits using the ITS sequence had highest similarity to *Neophaeosphaeria conglomerata* (GenBank AF250824; Identities = 682/695 (98 %), Gaps = 2/695 (0 %)), *N. filamentosa* (GenBank AF250825; Identities = 677/693 (98 %), Gaps = 1/693 (0 %)) and *N. quadriseptata* (GenBank AF250826; Identities = 666/695 (96 %), Gaps = 2/695 (0 %)).

Kellermania agaves Crous & Yáñez-Moral., *sp. nov.*

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

Conidiomata pycnidial, black, separate, globose, erumpent, up to 350 µm diam, unilocular with central ostiole; wall of several layers of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Macrocondiogenous cells* lining the inner cavity, hyaline, smooth, subcylindrical to ampulliform, 7–15 × 2–3.5 µm; proliferating several times percurrently near apex. *Macroconidia* (47–)53–58(–60) × (5–)5.5(–6) µm, solitary, hyaline, smooth, guttulate, aseptate, thin-walled, subcylindrical, widest in middle, tapering in upper third to subacute apex, base truncate with minute marginal frill, conidia surrounded by persistent mucoid sheath, 1 µm diam. *Microconidiogenous cells* hyaline, smooth, subcylindrical, frequently with a supporting cell giving rise to 1–2 conidiogenous cells, 4–10 × 2–3 µm; apex with periclinal thickening. *Microconidia* hyaline, smooth, granular, subcylindrical, straight, apex obtuse, base truncate, 3–5 × 2–2.5 µm.

Culture characteristics — Colonies after 2 wk covering the dish with sparse aerial mycelium; on MEA, OA and PDA surface and reverse iron-grey.

Colour illustrations. *Agave tequilana* var. *azul* plantation, Mexico. Left column *Neophaeosphaeria agaves*: conidiomata on PDA; conidiogenous cells and conidia. Right column *Kellermania agaves*: conidiomata on PNA; conidiogenous cells, macro- and microconidia. Scale bars = 10 µm.

Typus. Mexico, Edo. de Mexico, on grey leaf lesions of *Agave tequilana* var. *azul* (*Asparagaceae*), 28 Nov. 2012, *M. de Jesús Yáñez-Morales* (holotype CBS H-21439, culture ex-type CPC 21713 = CBS 136430, ITS sequence GenBank KF777164, LSU sequence GenBank KF777217, MycoBank MB805844).

Notes — *Kellermania agaves* is characterised by having cylindrical, aseptate conidia. It needs to be compared to other similar taxa in the genus, namely *K. attenuata* (on *Yucca* sp., Mexico; conidia 70–85 × 3–5 µm) and *K. crassispora* (on *Nolina* sp., USA; conidia 56.8–78.4 × 12.8–14.5 µm). It can easily be distinguished from both these taxa based on its conidial dimensions (Nag Raj 1993, Minnis et al. 2012).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Kellermania plurilocularis* (GenBank JX444878; Identities = 836/849 (98 %), Gaps = 1/849 (0 %)), *K. dasylirionis* (GenBank JX444873; Identities = 851/866 (98 %), Gaps = 1/866 (0 %)) and *K. micranthae* (GenBank JX444875; Identities = 853/870 (98 %), Gaps = 3/870 (0 %)). Closest hits using the ITS sequence had highest similarity to *K. plurilocularis* (GenBank JX444862; Identities = 394/400 (99 %), Gaps = 1/400 (0 %)), *K. dasylirionicola* (GenBank JX444856; Identities = 377/387 (97 %), Gaps = 0/387 (0 %)) and *K. micranthae* (GenBank JX444859; Identities = 376/390 (96 %), Gaps = 3/390 (0 %)).

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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).

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 %)).

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.

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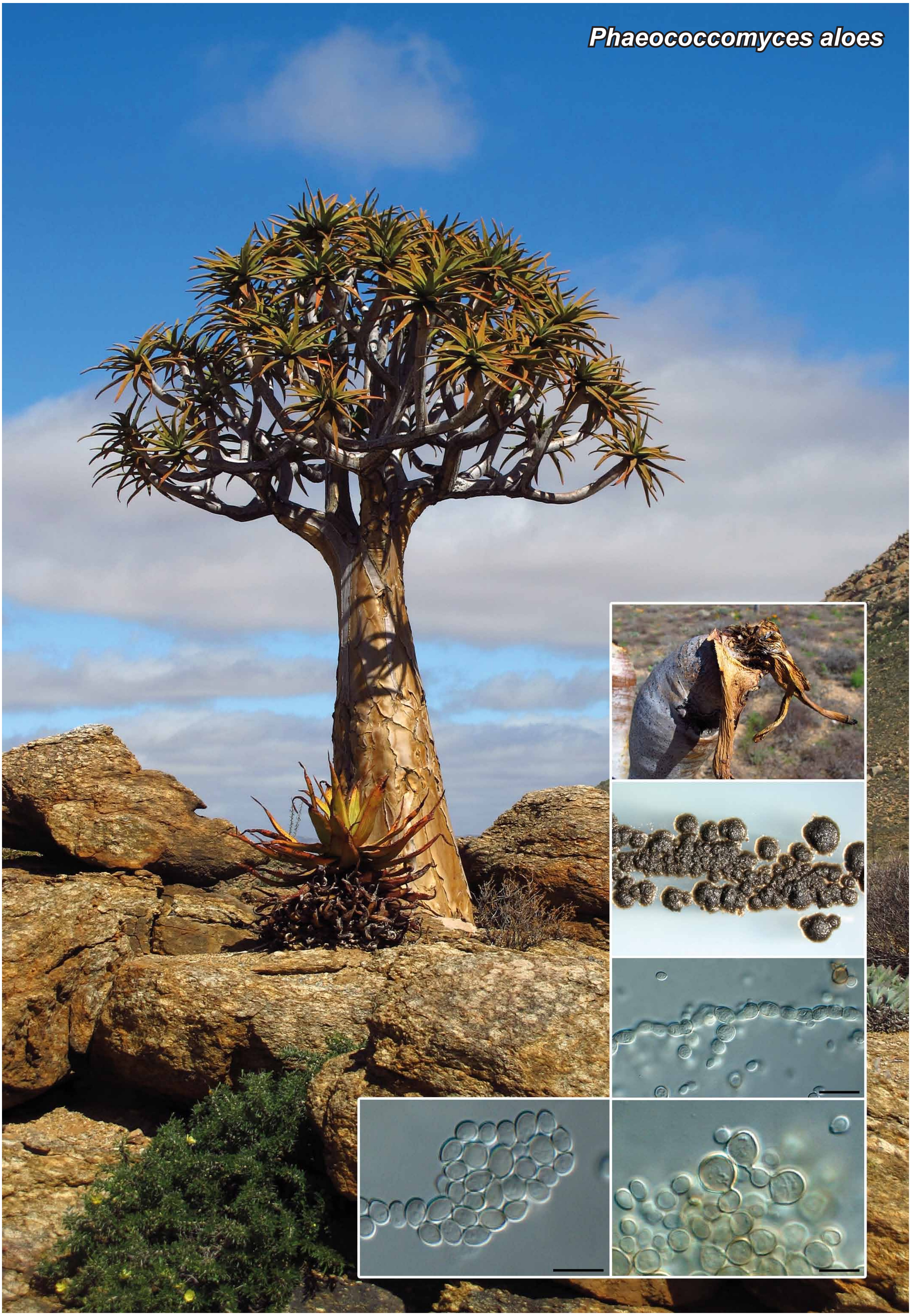
Phaeococcomyces aloes

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).

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

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 %)).

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Phoma aloes

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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).

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 %)).

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

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Pilidium pseudoconcavum

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Pilidium pseudoconcavum Crous, *sp. nov.*

Etymology. Named after its morphological similarity to *Pilidium concavum*.

On SNA. *Conidiomata* sporodochial, superficial, 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. *Conidiophores* hyaline, smooth, branched, septate, filiform, giving rise to conidiogenous cells and paraphyses, up to 100 μm long, 1.5–3 μm diam. *Conidiogenous cells* terminal and lateral, monophialidic, subcylindrical, straight to curved, smooth, hyaline, with periclinal thickening and minute collarette, 3–18 × 1.5–2 μm. *Conidia* hyaline, smooth, aseptate, cymbiform, guttulate, ends acute, (5–)7–8(–11) × (2–)2.5(–3) μm.

Culture characteristics — Colonies reaching 50 mm diam after 2 wk, surface slimy, folded, flat, lacking aerial mycelium, with smooth, lobate margin. On PDA surface and reverse buff to honey; on MEA surface and reverse cinnamon; on OA surface honey.

Typus. South Africa, Mpumalanga, Buffelskloof Private Nature Reserve, latitude -25.302596656391604, longitude: 30.504741668701172, on leaves of *Greyia radlkoferi* (*Melianthaceae*), Sept. 2012, *M. van der Bank* (holotype CBS H-21443, culture ex-type CPC 21642, 21643 = CBS 136433, ITS sequence GenBank KF777184, LSU sequence GenBank KF777236, MycoBank MB805848).

Notes — Species from the genus *Pilidium* are known to have *Hainesia* synasexual morphs (Rossman et al. 2004). *Pilidium concavum* (synasexual morph *Hainesia lythri*, sexual morph *Discohainesia oenotherae*) is commonly encountered as pathogen in eucalypt cutting nurseries, where it uses wounds on cuttings as infection loci (Crous et al. 1989). Morphologically *Pilidium pseudoconcavum* resembles *P. concavum* (conidia 5.5–8.2(–10.9) × 1.4–2(–2.7) μm; Rossman et al. 2004), though it is phylogenetically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Pilidium concavum* (GenBank AY487095; Identities = 853/866 (98 %), Gaps = 4/866 (0 %)), *Pilidium acerinum* (GenBank AY487092; Identities = 840/859 (98 %), no gaps) and *Chaetomella raphigera* (GenBank AY487077; Identities = 823/856 (96 %), no gaps). Closest hits using the ITS sequence had highest similarity to *Pilidium concavum* (GenBank JX047867; Identities = 487/505 (96 %), Gaps = 3/505 (0 %)) and numerous distant hits to uncultured fungal sequences and unrelated species.

Colour illustrations. Flower of *Greyia radlkoferi*, Buffelskloof Private Nature Reserve, South Africa (photo credit: Olivier Maurin); conidiomata on PNA; conidioma; paraphyses and conidiogenous cells; conidia. Scale bar = 10 μm.

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Sphaerulina rhododendricola

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Sphaerulina rhododendricola Crous & Cheew., *sp. nov.*

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

Conidiomata immersed, globose, brown with central ostiole, up to 150 µm diam, exuding a creamy-white conidial mass; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* subcylindrical, 0–1-septate, unbranched or branched at base, hyaline or pale brown, straight to geniculate-sinuous, smooth, 10–30 × 3–4 µm. *Conidiogenous cells* integrated, hyaline, smooth, subcylindrical, 10–30 × 2–2.5 µm; proliferating percurrently or sympodially near apex. *Conidia* solitary, hyaline, smooth, guttulate, subcylindrical to narrowly obclavate, apex obtuse, base obconically truncate, hilum 1.5 µm diam, (0–)3(–6)-septate, (17–)28–35(–55) × (2–)2.5(–3) µm.

Culture characteristics — Colonies reaching 30 mm diam after 2 wk, spreading, with moderate aerial mycelium and even, lobate margins. On MEA surface iron-grey with patches of dirty white; on PDA surface iron-grey with patches of pale olivaceous-grey, reverse iron-grey.

Typus. THAILAND, Chiang Mai, Chiang Mai Botanical Garden, on leaves of *Rhododendron* sp. (*Ericaceae*), 2 Nov. 2012, *P.W. Crous* (holotype CBS H-21444, culture ex-type CPC 21813, 21814 = CBS 136435, ITS sequence GenBank KF777187, LSU sequence GenBank KF779493, MycoBank MB805849).

Colour illustrations. *Rhododendron* sp. in Chiang Mai Botanical Garden; conidioma on PNA; colony sporulating on OA; conidiophores and conidia. Scale bars = 10 µm.

Notes — Species of *Sphaerulina* are morphologically very similar to those accommodated in the genus *Septoria* (Quaedvlieg et al. 2013, Verkley et al. 2013), but can be distinguished based on DNA sequence data. Several species of *Septoria* have been described from *Azalea* and *Rhododendron*, all of which can be distinguished from *S. rhododendricola* based on their conidial dimensions, namely *S. solitaris* (*Rhododendron* sp., USA, conidia 20 × 2 µm), *S. azaleae* (*Azalea indica*, Italy, conidia (12–)14–16(–18) × 1.5–2.5, 0–3-septate), *S. azaleae-indicae* (*Azalea indica*, Brazil, conidia 50–65 × 1.5 µm, indistinctly septate) and *S. rhododendri* (*Rhododendron* sp., USA, conidia 40 µm long, filiform) (Pirone et al. 1960).

Closest hits using the ITS sequence had highest similarity to *Pseudocercosporella chaenomelis* (GenBank JQ793663; Identities = 609/611 (99 %), no gaps), *Mycosphaerella berberidis* (GenBank EU167603; Identities = 659/663 (99 %), no gaps) and *Cercospora coniogrammes* (GenBank JX143583; Identities = 573/580 (99 %), no gaps).

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Paramycosphaerella brachystegia

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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).

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

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 %)).

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Camarosporium aloes

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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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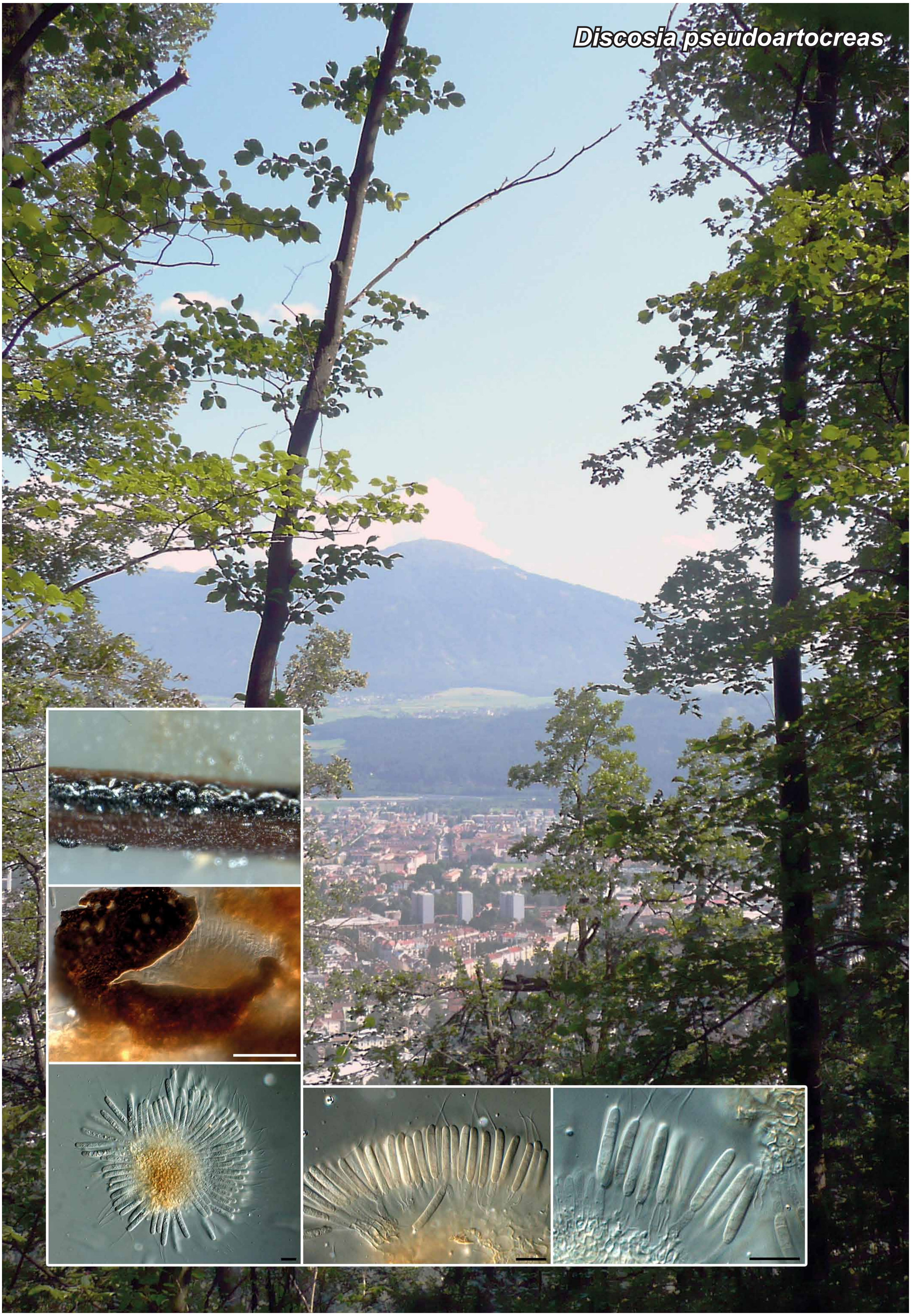
Discosia pseudoartocreas

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Discosia pseudoartocreas Crous & Damm, *sp. nov.*

Etymology. Named after its morphological similarity to *Discosia artocreas*.

On PNA. *Conidiomata* stromatic, pycnidial, erumpent to superficial, subglobose to lenticular, unilocular, dark brown, up to 150 µm diam; wall composed of polygonal brown cells. *Conidiophores* lining the inner cavity, hyaline to pale brown, subcylindrical, 0–1-septate, branched below or not, 7–15 × 2–3 µm. *Conidiogenous cells* integrated, terminal, hyaline to pale brown, subcylindrical, 5–8 × 1.5–2 µm. *Conidia* cylindrical, 3-septate, pale brown, with an appendage at both ends, (11–)14–16(–17) × 2.5(–3) µm; basal cell 2.5–3 µm long, obconic with truncate hilum, second cell from base 5–8 µm long, third cell 3–4 µm long and apical cell 2–3 µm long with obtusely rounded apex. *Appendages* cellular, unbranched, filiform, eccentric; apical appendage 10–13 µm long, basal appendage 7–11 µm long.

Culture characteristics — Colonies reaching 70 mm diam after 2 wk, spreading, flat, with sparse aerial mycelium; margins feathery on PDA, but smooth and even on MEA and OA. On PDA surface olivaceous-grey in centre, iron-grey in outer region, iron-grey underneath; on MEA olivaceous-grey with patches of iron-grey, reverse iron-grey; on OA surface mycelium growing in concentric zones, olivaceous grey with pale olivaceous grey zones.

Typus. Austria, Innsbruck, on leaves of *Tilia* sp. (*Tiliaceae*), 11 Aug. 2012, *U. Damm* (holotype CBS H-21447, culture ex-type CPC 21117, 21118 = CBS 136438, ITS GenBank sequence KF777161, LSU GenBank sequence KF777214, MycoBank MB805853).

Colour illustrations. Innsbruck, Austria; conidiomata on PNA; ruptured conidioma; conidiogenous cells giving rise to conidia. Scale bars = 10 µm.

Notes — Members of the genus *Discosia* are saprobes and plant pathogens of numerous vascular plants, and have a global distribution. *Discosia artocreas*, the type species of the genus, is cosmopolitan and characterised by having a wide host range (Vanev 1992). In his study of the genus, Vavev (1992) chose CBS 241.66 as representative of *D. artocreas*, as the original type had been lost. In a recent phylogenetic study on *Discosia* and related genera, Tanaka et al. (2011) showed isolates identified as *D. artocreas* to be paraphyletic. Morphologically *D. pseudoartocreas* closely resembles *D. artocreas* (conidia (16.3–)18(–20) × (1.8–)2.1(–2.5) µm; Vanev 1992), (conidia (12.5–)14–22 × 2–3 µm; Nag Raj 1993), though conidia are smaller.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Discosia artocreas* (GenBank AB593705; Identities = 786/786 (100 %), no gaps), *D.* aff. *brasiliensis* (GenBank AB593706; Identities = 786/786 (100 %), no gaps) and *D.* aff. *artocreas* (GenBank AB593704; Identities = 785/786 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to '*Discosia* sp. 1' (GenBank AB594778; Identities = 543/546 (99 %), Gaps = 1/546 (0 %)), *D.* aff. *artocreas* (GenBank AB594772; Identities = 543/546 (99 %), Gaps = 1/546 (0 %)) and '*Discosia* sp. 2' (GenBank AB594780; Identities = 542/546 (99 %), Gaps = 1/546 (0 %)).

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Myrmecridium thailandicum

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Myrmecridium thailandicum Crous & Cheew., *sp. nov.*

Etymology. Named after the country where this fungus was collected, Thailand.

On SNA *mycelium* consisting of hyaline, thin-walled, smooth, 2–3 µm diam hyphae. *Conidiophores* erect, unbranched, straight, medium brown, thick-walled, up to 300 µm tall, 3–4 µm wide, 3–15-septate, basal cell often inflated, 3–5 µm wide. *Conidiogenous cells* integrated, cylindrical, 12–30 µm long, medium brown, fertile region forming a rachis with pimple-like denticles arranged in whorls along the conidiogenous axis, less than 0.5 µm long, and 0.5 µm wide, unpigmented, slightly thickened scars. *Conidia* solitary, pale brown, thin-walled, finely verruculose, on MEA some conidia have a wing-like gelatinous sheath up to 0.5 µm thick, ellipsoid to obovoid or fusiform, (6–)7(–8) × (3–)3.5(–4) µm; tapering from obtuse apex to subtruncate base; hilum unthickened, 0.5 µm thick.

Culture characteristics — Colonies reaching 60 mm diam after 2 wk, flat, spreading, with sparse aerial mycelium and feathery margin. On MEA surface umber with patches of orange, in reverse orange; on PDA surface sienna, reverse umber; on OA centre umber, outer region luteous.

Typus. Thailand, Chiang Mai, Boa Keaw Silvicultural Research Station, on reed litter next to pond, 29 Oct. 2012, *P.W. Crous* (holotype CBS H-21448, culture ex-type CPC 21696, 21694 = CBS 136551, ITS sequence GenBank KF777169, LSU sequence GenBank KF777222, MycoBank MB805854).

Colour illustrations. Reed litter next to pond at Chiang Mai, Boa Keaw Silvicultural Research Station; colony on OA; conidiophores and conidia. Scale bars = 10 µm.

Notes — The genus *Myrmecridium* was established by Arzanlou et al. (2007) to accommodate taxa in the *Ramichloridium* complex that have hyaline to pale brown hyphae, relatively unpigmented pimple-like denticles and aseptate conidia with wing-like gelatinous sheaths. The genus is presently known from four species, including two varieties (Crous et al. 2011a, 2012c).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Myrmecridium banksiae* (GenBank JX069855; Identities = 865/885 (98 %), no gaps), *M. schulzeri* (GenBank EU041835; Identities = 866/887 (98 %), Gaps = 2/887 (0 %)) and *M. flexuosum* (GenBank EU041825; Identities = 865/887 (98 %), Gaps = 2/887 (0 %)). Closest hits using the ITS sequence had highest similarity to *M. flexuosum* (GenBank EU041768; Identities = 481/523 (92 %), Gaps = 7/523 (1 %)), *M. schulzeri* (GenBank EU041777; Identities = 514/560 (92 %), Gaps = 9/560 (1 %)) and *M. phragmitis* (GenBank JQ044425; Identities = 509/557 (91 %), Gaps = 6/557 (1 %)).

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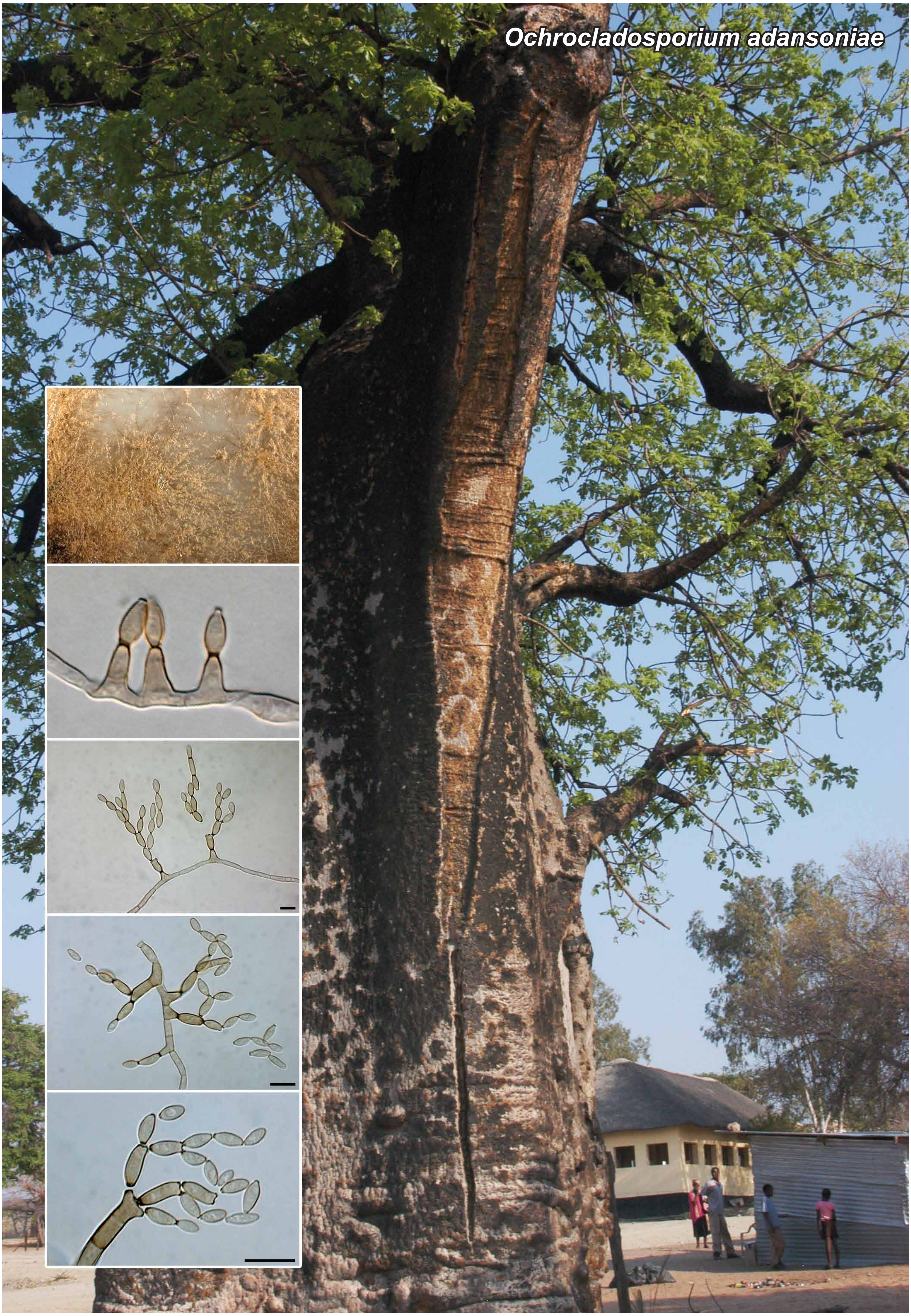
Ochrocladosporium adansoniae

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).

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 %)).

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

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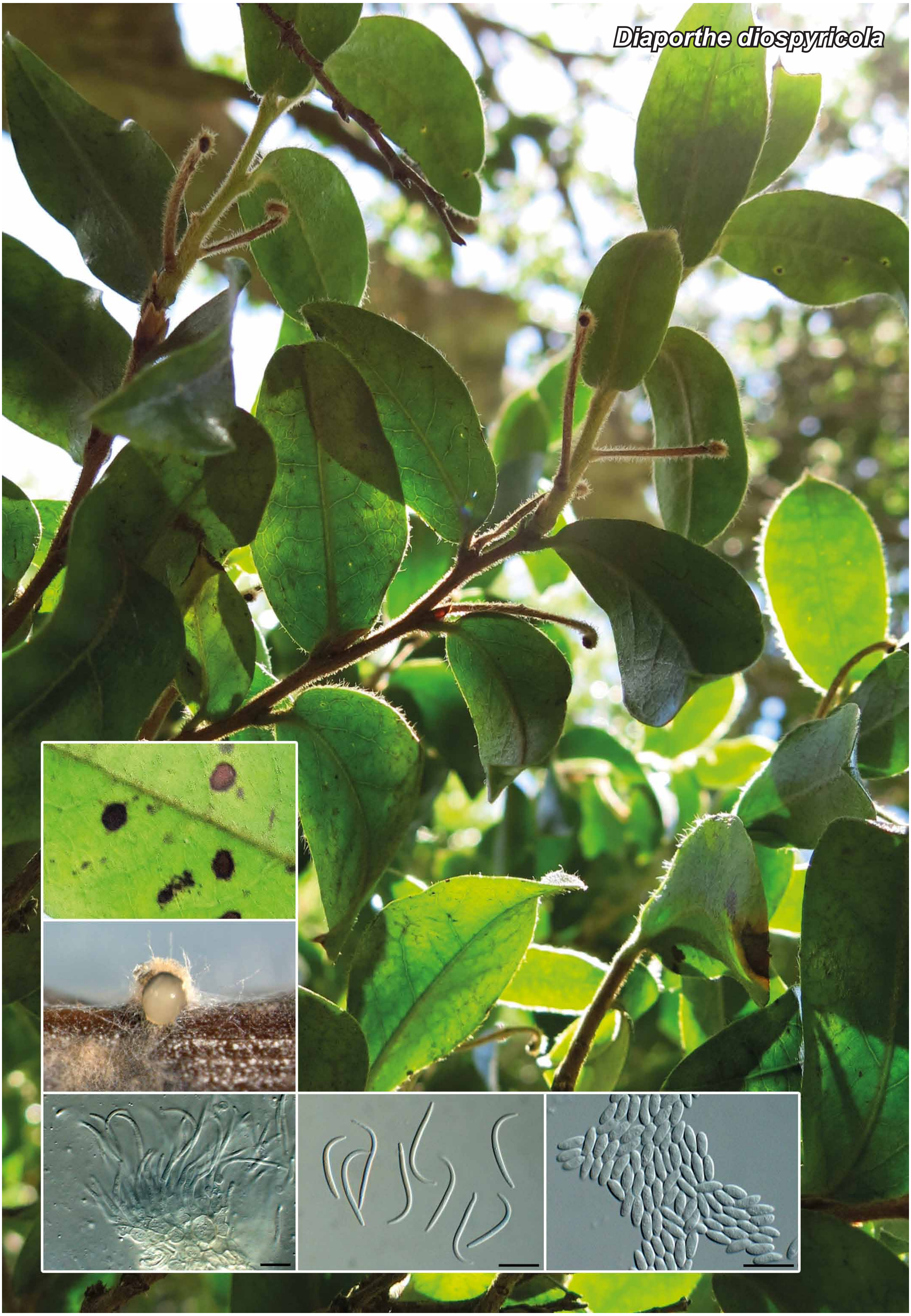
Diaporthe diospyricola

Fungal Planet 191 – 26 November 2013

Diaporthe diospyricola Crous, *sp. nov.*

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

On PNA. *Conidiomata* pycnidial, globose, up to 400 µm diam, black, erumpent, exuding creamy conidial droplets from central ostioles; walls of 3–6 layers of medium brown *textura angularis*. *Conidiophores* hyaline, smooth, 2–4-septate, branched, densely aggregated, cylindrical, straight to sinuous, 20–50 × 2.5–4 µm. *Conidiogenous cells* 7–15 × 1.5–2.5 µm, phialidic, cylindrical, terminal and lateral, with slight taper towards apex, 1–1.5 µm diam, with visible periclinal thickening; collarette not observed. *Paraphyses* not observed. *Alpha conidia* aseptate, hyaline, smooth, guttulate, fusoid-ellipsoid, tapering towards both ends, straight, apex subobtuse, base subtruncate, (5.5–) 6–7(–7.5) × (2–)2.5(–3) µm. *Gamma conidia* not observed. *Beta conidia* spindle-shaped, aseptate, smooth, hyaline, apex acutely rounded, base truncate, tapering from lower third towards apex, curved, (18–)25–27(–30) × 1.5(–2) µm.

Culture characteristics — Colonies covering dish in 2 wk with sparse aerial mycelium. On OA surface dirty white; on MEA centre iron-grey, outer region dirty white, reverse iron-grey in centre, outer region apricot; on PDA surface ochreous, reverse saffron.

Typus. South Africa, Western Cape Province, Kirstenbosch Botanical Garden, on leaves of *Diospyros whyteana* (*Ebenaceae*), 30 July 2012, *P.W. Crous* (holotype CBS H-21450, culture ex-type CPC 21170, 21169 = CBS 136552, ITS sequence GenBank KF777156, LSU sequence GenBank KF777209, MycoBank MB805856).

Notes — Morphologically *D. diospyricola* has shorter and wider conidia than *P. diospyri* (Sacc.) Traverso & Spessa (conidia 7–8 × 2 µm), and its homonyms, *P. diospyri* Zerova (conidia 7.2–9 × 2.1–2.9 µm), *P. diospyri* Grove (conidia 8–10 × 2 µm) and *P. diospyri* Bongini (conidia 6–7 × 3.5 µm) (Uecker 1988). *Diaporthe diospyricola* is also phylogenetically distinct from *D. foeniculaceae* (= *D. diospyri*, CBS 287.56; Gomes et al. 2013).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Diaporthe oncostoma* (GenBank AF408353; Identities = 852/853 (99 %), no gaps), *D. eres* (GenBank AF362565; Identities = 851/853 (99 %), no gaps) and *D. canthii* (GenBank JX069848; Identities = 844/845 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *Phomopsis sophorae* (GenBank JQ694110; Identities = 589/608 (97 %), Gaps = 6/608 (0 %)), *D. chamaeropis* (GenBank KC343049; Identities = 557/576 (97 %), Gaps = 5/576 (0 %)) and *D. neotheicola* (GenBank KC145902; Identities = 583/607 (96 %), Gaps = 9/607 (1 %)).

Colour illustrations. Leaves of *Diospyros whyteana* in Kirstenbosch Botanical Garden, South Africa; conidioma on PNA; beta and alpha conidia. Scale bars = 10 µm.

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Diaporthe cassines

Fungal Planet 192 – 26 November 2013

Diaporthe cassines Crous, *sp. nov.*

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

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, 0–1-septate, branched or not, densely aggregated, cylindrical, straight to sinuous, 10–20 × 2.5–4 µm. *Conidiogenous cells* 10–15 × 2–3 µm, phialidic, cylindrical, terminal and lateral, with slight taper towards apex, 1–1.5 µm diam, with visible periclinal thickening; collarette flared, up to 4 µm long. *Paraphyses* cylindrical, hyaline, smooth, branched, 1–3-septate, 20–50 × 2.5–3 µm diam. *Alpha conidia* aseptate, hyaline, smooth, guttulate, fusoid-ellipsoid, tapering towards both ends, straight, apex subobtuse, base subtruncate, (8–)9–11(–12) × (3–)3.5(–4) µm. *Gamma conidia* not observed. *Beta conidia* not observed.

Culture characteristics — Colonies reaching 60 mm diam after 2 wk, with sparse aerial mycelium and feathery, lobate margins. On PDA surface umber in centre, dirty white in outer region, similar in reverse; on OA surface dirty white; on MEA surface ochreous in centre, dirty white in outer region, umber in reverse.

Typus. South Africa, Western Cape Province, Kirstenbosch Botanical Garden, on leaves of *Cassine peragua* (*Celastraceae*), 29 Dec. 2012, *P.W. Crous* (holotype CBS H-21451, culture ex-type CPC 21916, 21917 = CBS 136440, ITS sequence GenBank KF777155, LSU sequence GenBank KF777208, TEF sequence GenBank KF777244, MycoBank MB805857).

Colour illustrations. Leaf spots on *Cassine peragua* at Kirstenbosch Botanical Garden, South Africa; conidiomata on PNA; conidiogenous cells giving rise to alpha conidia. Scale bars = 10 µm.

Notes — Presently no species of *Diaporthe* have been reported on *Cassine*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Diaporthe medusaea* (GenBank AF362560; Identities = 868/874 (99 %), no gaps), *D. cynaroidis* (GenBank EU552122; Identities = 861/867 (99 %), no gaps) and *D. pardalota* (GenBank AF408355; Identities = 855/861 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to '*Diaporthe* sp. 1' (GenBank JN225920; Identities = 568/586 (97 %), Gaps = 3/586 (0 %)), '*Diaporthe* sp. 2' (GenBank JN225919; Identities = 566/584 (97 %), Gaps = 3/584 (0 %)) and *D. beckhausii* (GenBank KC343041; Identities = 560/584 (96 %), Gaps = 3/584(0 %)). Closest hits using the TEF sequence had highest similarity to *Diaporthe* sp. (GenBank JX862536; Identities = 545/597 (91 %), Gaps = 5/597 (0 %)), *D. viticola* (GenBank KC343963; Identities = 544/604 (90 %), Gaps = 10/604 (1 %)) and *D. cynaroidis* (GenBank EU552093; Identities = 307/344 (89 %), Gaps = 4/344 (1 %)).

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Diaporthe maytenicola

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Diaporthe maytenicola Crous, *sp. nov.*

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

On PNA. *Conidiomata* pycnidial, globose, up to 250 µm diam, black, erumpent, exuding creamy-white conidial droplets from central ostioles; walls of 3–6 layers of medium brown *textura angularis*. *Conidiophores* hyaline, smooth, 1–3-septate, branched, densely aggregated, cylindrical, straight to sinuous, 20–40 × 2–3 µm. *Conidiogenous cells* 10–20 × 1.5–2 µm, phialidic, cylindrical, terminal and lateral, with slight taper towards apex, 1–1.5 µm diam, with visible periclinal thickening; collarette flared, up to 2 µm long when present. *Paraphyses* not observed. *Alpha conidia* aseptate, hyaline, smooth, guttulate, fusoid-ellipsoid, tapering towards both ends, straight, apex subobtuse, base subtruncate, (7–)9–10(–12) × (2.5–)3 µm. *Gamma conidia* not observed. *Beta conidia* spindle-shaped, aseptate, smooth, hyaline, apex acutely rounded, base truncate, tapering from lower third towards apex, curved, 17–25 × 1.5(–2) µm.

Culture characteristics — Colonies covering dish within 2 wk, with sparse aerial mycelium. On PDA surface amber, reverse ochreous; on OA surface dirty white; on MEA surface ochreous, reverse ochreous with patches of umber due to sporulation.

Typus. South Africa, Western Cape Province, Kirstenbosch Botanical Garden, on leaves of *Maytenus acuminata* var. *acuminata* (*Celastraceae*), 29 Dec. 2012, *P.W. Crous* (holotype CBS H-21452, culture ex-type CPC 21896, 21897 = CBS 136441, ITS sequence GenBank KF777157, LSU sequence GenBank KF777210, TUB sequence GenBank KF777250, MycoBank MB805858).

Colour illustrations. *Maytenus acuminata* var. *acuminata* in Kirstenbosch Botanical Garden, South Africa; conidiomata on PNA; conidiogenous cells and alpha conidia. Scale bars = 10 µm.

Notes — Alpha conidia of *D. maytenicola* are larger than those of *D. mayteni* (5–7 × 2–3 µm), which was also recently described from *Maytenus ilicifolia* collected in Brazil (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 = 853/854 (99 %), no gaps), *Phomopsis vaccinii* (GenBank AF439630; Identities = 852/854 (99 %), no gaps) and *D. oncostoma* (GenBank AF408353; Identities = 852/854 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *D. chamaeropis* (GenBank KC343049; Identities = 562/572 (98 %), Gaps = 1/572 (0 %)), *D. neotheicola* (GenBank KC143192; Identities = 516/528 (98 %), Gaps = 2/528 (0 %)) and *D. elaeagni* (GenBank KC343064; Identities = 559/574 (97 %), Gaps = 3/574 (0 %)). Closest hits using the TUB sequence had highest similarity to *D. foeniculacea* (GenBank KC344069; Identities = 656/687 (95 %), Gaps = 3/687 (0 %)), *D. chamaeropis* (GenBank KC344017; Identities = 656/687 (95 %), Gaps = 3/687 (0 %)) and *D. oncostoma* (GenBank KC344128; Identities = 654/690 (95 %), Gaps = 7/690 (1 %)).

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Passalora pseudotithoniae

Fungal Planet 194 – 26 November 2013

Passalora pseudotithoniae Crous & Cheew., *sp. nov.*

Etymology. Named after its morphological similarity to *Passalora tithoniae*.

Leaf spots amphigenous, brown, angular, confined by leaf veins, 2–5 mm diam. *Conidiophores* amphigenous, fasciculate, 40–100 µm tall, 3–4 µm wide, straight to geniculate-sinuous, mostly unbranched, subcylindrical, 1–3-septate, brown, smooth to finely verruculose, arising from a weakly developed brown stroma, up to 50 µm wide and 60 µm tall. *Conidiogenous cells* integrated, brown, smooth to finely verruculose, terminal, subcylindrical to once geniculate, 15–35 × 3–4.5 µm; loci thickened and darkened, 2 µm diam, mostly solitary and terminal, but also lateral on conidiogenous cells. *Conidia* occurring in long branched chains, brown, granular, smooth, subcylindrical to narrowly obclavate, apex obtuse to truncate, base obconically truncate, 1–6-septate, scars 2 µm diam, thickened and darkened, (30–)40–65(–130) × (4–)5(–5.5) µm.

Culture characteristics — Colonies reaching 25 mm diam after 2 wk, flat, spreading with sparse aerial mycelium and even, smooth margins. On PDA surface olivaceous-grey, reverse iron-grey; on MEA surface folded, olivaceous-grey with patches of pale olivaceous-grey, reverse olivaceous-grey.

Typus. THAILAND, Royal Project, N18°09'24.8" E98°23'19.6", on leaves of *Tithonia diversifolia* (*Asteraceae*), 5 Nov. 2012, *P.W. Crous* (holotype CBS H-21453, culture ex-type CPC 21688, 21689 = CBS 136442, ITS sequence GenBank KF777179, LSU sequence GenBank KF777231, MycoBank MB805859).

Notes — *Passalora pseudotithonia* is morphologically similar to *P. tithoniae* (on *Tithonia diversifolia*, Trinidad; conidia 1–5-septate, 20–65 × 3–5.5 µm) (Ellis 1976), but distinct in that it has much longer conidia. Another recently described species from this host is *P. stromatica* (on *Tithonia diversifolia*, Brazil) which has wider conidiophores (4–8 µm) and 0–2-septate, subcylindrical to obclavate, 15.5–61.5 × 2.5–6.5 µm conidia (Fernandes et al. 2013).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are '*Passalora* sp.' (GenBank GU214668; Identities = 879/880 (99 %), no gaps), *Passalora tithoniae* (GenBank KC677927; Identities = 854/855 (99 %), no gaps) and *P. ageratinae* (GenBank GU214453; Identities = 855/857 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to '*Passalora* sp.*'* (GenBank GU214668; Identities = 670/677 (99 %), Gaps = 1/677 (0 %)), *P. ageratinae* (GenBank GU214639; Identities = 630/638 (99 %), no gaps) and *Dothistroma septosporum* (GenBank GU256362; Identities = 538/552 (97 %), Gaps = 3/552 (0 %)). Our ITS sequence differs from the sequence of *P. tithoniae* on GenBank (KC677895) with the presence of an 8-bp indel (Identities = 459/467 (98 %), Gaps = 8/467 (1 %)).

Colour illustrations. *Tithonia diversifolia* in Thailand; symptomatic leaves; conidiophores and conidia. Scale bars = 10 µm.

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Chaetopsina pini
& Chaetopsina pinicola

Fungal Planet 195 & 196 – 26 November 2013

Chaetopsina pini Crous & Cheew., *sp. nov.*

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

Conidiophores erect, setiform, tapering towards acutely rounded apex, mostly flexuous, medium brown, turning red-brown in 3 % KOH, fertile in mid region, unbranched, verruculose, 130–180 × 6–8 µm, 7–10-septate, thick-walled (2 µm diam), base bulbous, up to 13 µm diam; fertile region consisting of irregularly branched, dense aggregated conidiogenous cells. *Conidiogenous cells* ampulliform to lageniform, hyaline, smooth, mono- to polyphialidic, 5–20 × 3–5 µm; apical collarette up to 2 µm long, not flared. *Conidia* hyaline, smooth, granular, cylindrical, aseptate, apex and base bluntly rounded, base rarely with flattened hilum, (13–)15–16(–18) × 2(–2.5) µm. Conidiophore base surrounded by cinnamon coloured ascomata, but these remained infertile.

Culture characteristics — Colonies reaching 50 mm diam after 2 wk, flat, spreading, with sparse aerial mycelium and even, lobate margins. On MEA surface and reverse cinnamon; on PDA surface and reverse brown-vinaceous; on OA surface vinaceous-buff.

Typus. Thailand, Chiang Mai, Boa Keaw Silvicultural Research Station, on needle litter of *Pinus caribaea* (*Pinaceae*), 29 Oct. 2012, *P.W. Crous* (holotype CBS H-21454, culture ex-type CPC 21622, 21623 = CBS 136443, ITS sequence GenBank KF777144, LSU sequence GenBank KF777200, MycoBank MB805860).

Notes — Although morphologically similar, the genera *Chaetopsina* and *Kionochaeta* are phylogenetically distinct (Okada et al. 1997). Both genera have mono- to polyphialides, and setose conidiophores. However, species of *Chaetopsina* have conidiophores that turn yellow in lactic acid, while those of *Kionochaeta* are brown, and tend to have verticillate to penicillate fertile nodes (Seifert et al. 2011). Furthermore, the genus *Chaetopsina* has nectria-like sexual morphs that are accommodated in *Chaetopsinectria* (Luo & Zhuang 2010). The common species of *Chaetopsina* reported from *Pinus* is *C. fulva*, which has cylindrical conidia, 8–12 × 1.5 µm (Kirk & Sutton 1985), thus smaller than those reported here for *C. pini*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Chaetopsinectria chaetopsinae* (GenBank DQ119553; Identities = 869/880 (99 %), no gaps), *Chaetopsina fulva* (GenBank GU075867; Identities = 865/879 (98 %), no gaps) and *Cosmospora chaetopsinae-penicillatae* (GenBank GU075865; Identities = 857/879 (97 %), no gaps). Closest hits using the ITS sequence had highest similarity to *Volutella ciliata* (GenBank AJ301966; Identities = 633/730 (87 %), Gaps = 37/730 (5 %)), *Stachybotrys bisbyi* (GenBank AF081480; Identities = 636/735 (87 %), Gaps = 36/735 (4 %)) and *Chaetopsina penicillata* (GenBank HQ897798; Identities = 528/611 (86 %), Gaps = 30/611 (4 %)).

Chaetopsina pinicola Crous & Cheew., *sp. nov.*

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

Conidiophores erect, setiform, tapering towards acutely rounded apex, mostly flexuous, medium brown, turning red-brown in 3 % KOH, fertile in mid region, unbranched, verruculose, 130–250 × 8–12 µm, 11–15-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, 5–12 × 3–4 µm. *Conidia* hyaline, smooth, guttulate, subcylindrical, aseptate, apex and base bluntly rounded, base rarely with flattened hilum, (11–)13–15(–17) × 2(–2.5) µm.

Culture characteristics — Colonies reaching 45 mm diam after 2 wk, with sparse aerial mycelium, and flattened, lobate margins. On PDA surface and reverse sepia; on OA surface sepia with patches of honey; on MEA surface and reverse honey.

Typus. Thailand, Chiang Mai, Chiang Mai Botanical Garden, pine arboretum, on needles of *Pinus* sp. (*Pinaceae*), 2 Nov. 2012, *P.W. Crous* (holotype CBS H-21455, culture ex-type CPC 21819, 21820 = CBS 136444, ITS sequence GenBank KF777145, LSU sequence GenBank KF777201, MycoBank MB805861).

Colour illustrations. Boa Keaw Silvicultural Research Station, Chiang Mai, Thailand; Left column *C. pini*: Conidiophores, conidiogenous cells and conidia. Right column *C. pinicola*: Conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — *Chaetopsina pinicola* differs from *C. pini* by having conidia with an average range shorter than those of *C. pini*, and having longer conidiophores and shorter conidiogenous cells. Conidiophores of *C. pini* were also surrounded by ascomatal initials, though these were never observed in cultures of *C. pinicola*, suggesting that the former may have a *Chaetopsinectria* state in vivo.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Chaetopsinectria chaetopsinae* (GenBank DQ119553; Identities = 881/889 (99 %), no gaps), *Chaetopsina fulva* (GenBank GU075867; Identities = 877/888 (99 %), no gaps) and *Volutella citrinella* (GenBank HQ843772; Identities = 859/876 (98 %), no gaps). Closest hits using the ITS sequence had highest similarity to *Chaetopsina fulva* (GenBank GU075861; Identities = 490/513 (96 %), Gaps = 8/513 (1 %)), *Cosmospora chaetopsinae* (GenBank GU075858; Identities = 472/505 (93 %), Gaps = 11/505 (2 %)) and *Chaetopsina penicillata* (GenBank HQ897798; Identities = 551/598 (92 %), Gaps = 10/598 (1 %)).

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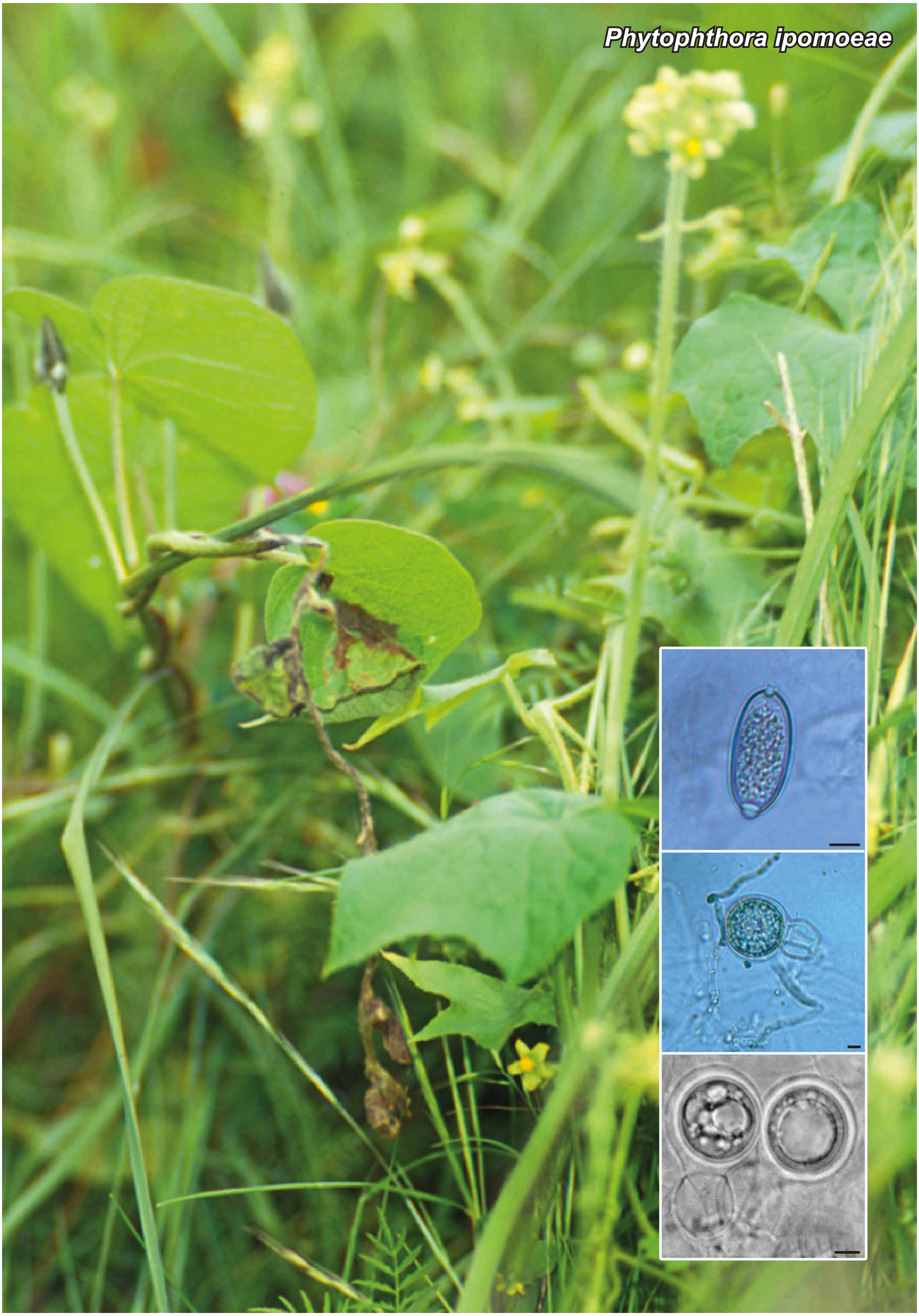
Phytophthora ipomoeae

Fungal Planet 197 – 26 November 2013

Phytophthora ipomoeae Flier & Grünwald, *sp. nov.*

Etymology. Named after its host plant, *Ipomoea longipedunculata*.

Mycelial colonies grow well on Rye A agar. Minimum growth at approximately 11 °C, optimum at 20 °C and maximum at 25 °C. *Hyphae* non-septate and freely branching, (4–)5.5 (–7.5) µm diam. *Sporangiophores* aerial, sparsely formed on rye agar with compound-sympodial and intermediate branches, with swellings where sporangia emerge. *Sporangia* semi-papillate, ellipsoid or obovoid, caducous with short pedicel, on average 39 µm long (range 35–47.5 µm), with a length/width ratio of 1.9, germinating directly with germ tubes or indirectly with 4–8 zoospores. *Antheridia* amphygynous, average length 19 µm, ratio of length/width 1.3. *Oogonia* smooth-walled, average diam 32.5 µm, with tapered base. *Oospores* smooth-walled, rarely tinted yellow, almost filling the oogonial cavity, average diam 28.8 µm. Isolates homothallic.

Typus. Mexico, Toluca, on leaves of *Ipomoea longipedunculata* (*Convolvulaceae*), 1999, *W.G. Flier & N.J. Grünwald* (holotype CBS H-21401, culture ex-type CBS 109229 = PIC 99169 = MUCL 30219, ITS sequence GenBank AY770742, MycoBank MB805536).

Colour illustrations. Symptoms of infection of *P. ipomoeae* on *Ipomoea longipedunculata* growing in a weed patch on a hill in Metepec, Mexico; sporangium and oospores of *P. ipomoeae* produced in culture. Scale bars = 10 µm.

Notes — The holotype description of this previously published species *P. ipomoeae* Flier & Grünwald was invalid and is corrected here (Flier et al. 2002). The species has more recently also been described on *Ipomoea purpurea* (Badillo-Ponce et al. 2004).

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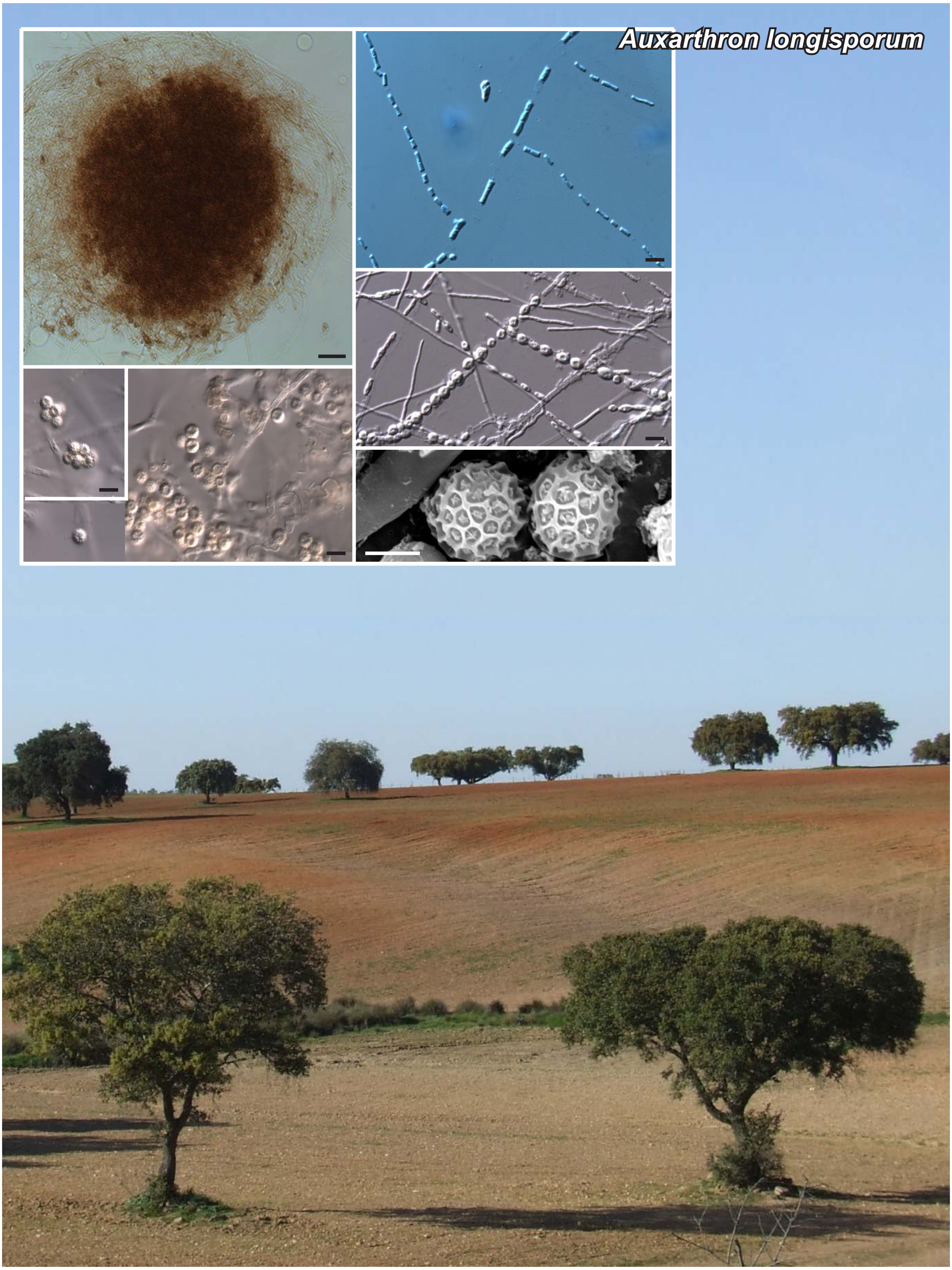
Auxarthron longisporum

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Auxarthron longisporum Stchigel, Y. Marín, Guarro & Cano, *sp. nov.*

Etymology. *longus*- and -*sporarum* (L.), referring to the long arthroconida.

Mycelium composed of hyaline, branched, septate, smooth- and thick-walled hyphae, 1–4 µm wide. *Ascomata* superficial, scattered or aggregated, globose, 170–450 µm diam, initially white, soon becoming orange-brown to reddish brown; peridial hyphae pale yellow to orange-brown, thick-walled, tuberculate, septate, 1.5–2.5 µm wide, branched and anastomosed to form a loosely reticulate network. *Asci* 8-spored, globose, 9–11 × 7.5–10 µm, evanescent. *Ascospores* subhyaline to golden-yellow or reddish brown, spherical, 3.5–4.5 µm, regularly reticulate, with small polygonal meshes, and narrow and conspicuous ridges. *Conidia* entero-arthric, aseptate, cylindrical, barrel-shaped or irregularly shaped, hyaline, 4–24 × 1–5.5 µm, formed from broad primary hyphae and from narrow, flexuose lateral branches, which sometimes are slightly curved. *Chlamydospores* present in mycelium, spherical to pyriform, 3.5–10 µm.

Culture characteristics — Colonies on oatmeal agar attaining 50–55 mm diam after 15 d at 25 °C, velvety and slightly cottony, margins arachnoid, yellowish white to light yellow (M. 3A3–3A5) (Kornerup & Wanscher 1984); reverse yellowish white to pale yellow (4A2–A3). Colonies on potato dextrose agar attaining 41–47 mm diam after 15 d at 25 °C, cottony to slightly granulate, white to pale yellow (3A1–3A3); reverse pale yellow to light yellow (4A3–4A5). Minimum and maximum temperature of growth: 5 and 30 °C, respectively. Ascomata are not produced at 30 °C. Optimal ascomatal production at 25 °C.

Typus. Portugal, Beja, Castro Verde, from forest soil, 28 Dec. 1996, coll. *A.M. Stchigel*, *J*, *Guarro & S.K. Abdullah*, isol. *A.M. Stchigel* (holotype CBS H-21352, cultures ex-type CBS 135817 = FMR 12768, ITS sequence GenBank HG326873, LSU sequence GenBank HG326874, MycoBank MB804882).

Notes — Hitherto, the genus *Auxarthron* encompassed 18 species. Some phylogenetic studies placed this genus into the family *Onygenaceae* (Sigler et al. 2002, Sugiyama et. al. 2002). To date, species of this genus has not been considered as human pathogens. However, Hubka et al. (2013) recently described *Auxarthron ostraviense* associated with a confirmed case of onychomycosis. A Blast search of the LSU sequence of our isolate showed a high degree of similarity (95 %) with those of *Auxarthron californiense* (AF038352), *Malbranchea gypsea* (AB359425) and *Malbranchea flocciformis* (AB359421). A Blast search using the ITS sequence of our isolate showed a 92 % similarity with those of *Auxarthron chlamydosporum* (AJ426458) and *A. concentricum* (AJ271428). Morphologically, the species most similar to *A. longisporum* are *A. chlamydosporum*, due to the production of chlamydospores and tuberculate peridial hyphae, and *A. concentricum*, with similar ascospore ornamentation (under the scanning microscope). However, *A. longisporum* can be distinguished from *A. concentricum* by the presence of ascospores with smaller polygonal meshes in the former, and from *A. chlamydosporum* because the arthroconidia are twice as long in *A. longisporum* than in *A. chlamydosporum*. On the other hand, *A. longisporum* is not able to grow above 30 °C, while *A. chlamydosporum* and *A. concentricum* grow at this temperature.

Colour illustrations. Castro Verde, Beja, Portugal; ascoma, arthroconidia, chlamydospores, asci and ascospores. Scale bars: ascoma = 50 µm; arthroconidia, chlamydospores, asci and ascospores = 5 µm; ascospore (SEM) = 2 µm.

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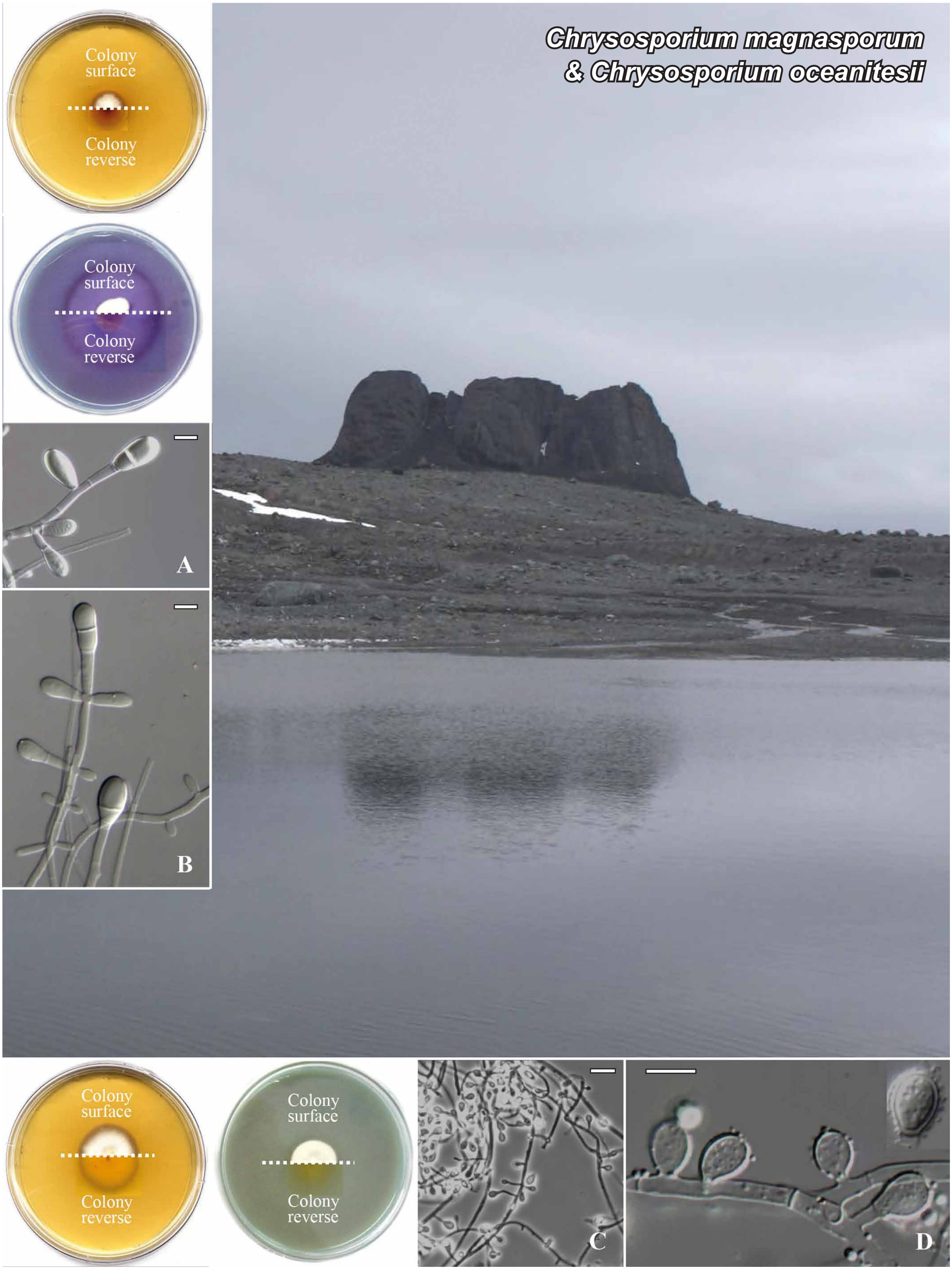
Chrysosporium magnasporum
& *Chrysosporium oceanitesii*
Colony surface
Colony reverse
Colony surface
Colony reverse
A
B
Colony surface
Colony reverse
Colony surface
Colony reverse
C
D

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Chrysosporium magnasporum Stchigel, Cano, Mac Cormack & Guarro, *sp. nov.*

Etymology. From the Latin *magna*-, big, and -*sporum*, spore, referring to the big size of the conidia.

Hyphae hyaline, septate, smooth-walled, 3–9 µm wide, straight, branched. *Conidia* hyaline, thin- and smooth-walled, terminal and lateral over the main hyphae or developing on right-angled side branches of variable length, sessile or on often swollen protrusions, solitary, obovate, clavate, nearly ellipsoid or obpyriform, commonly 1–2-celled, rarely 3-celled, 10–27 × 7–12 µm, with a broad basal scar measuring 3–9 µm. Intercalary conidia absent. *Chlamydospores* absent. *Sexual morph* not observed.

Culture characteristics — Colony on phytone yeast-extract agar (PYE) attaining 14–16 mm diam at 15 °C after 4 wk, white, downy, slightly raised, margins defined; reverse brownish orange (M. 5A7) (Kornerup & Wanscher 1984), producing a diffusible pigment of the same colour. On OMA, colony attaining 11–13 mm diam at 15 °C after 4 wk, similar as on PYE, but greyish yellow (4B4) at the centre and a reverse concolorous with agar medium. At 5 °C on PYE, colonies 8–10 mm diam after 4 wk, white, cottony, reverse light orange (5A4). Not growing above 20 °C.

Physiology — Keratinolytic. Sensitive to cycloheximide (0.1 %). The fungus grows on bromocresol purple-milk solids-glucose (BCP-MS-G) agar (Kane et al. 1997) alkalinising the medium, with hydrolysis of milk solids. Lipase activity not detected on Tween® 80 opacity test medium (TOTM) (Slifkin 2000).

Typus. ANTARCTICA, South Shetland Archipelago, King George Island, Potter Cave, from pellet of *Catharacta skua* Brunnich, 11 Nov. 1996, *W.P. Mac Cormack* (holotype CBS H-20944, culture ex-type FMR 11770 = CBS 132551, ITS sequence GenBank HG329727, LSU sequence GenBank HG329728, MycoBank MB804874).

Notes — *Chrysosporium* (*Onygenales*) is a large polyphyletic genus (Vidal et al. 2000) with more than 80 species. *Chrysosporium magnasporum* is only morphologically comparable to *C. keratinophylum* (sexual morph and current name *Aphanoascus keratinophilus*; Cano & Guarro 1990), because of its large (3.5–22 × 3–11 µm) and smooth-walled (or nearly so) conidia. However, *C. magnasporum* produces conidia with up to two septa (always aseptate in *C. keratinophylum*) and they are larger (10–27 × 7–12 µm) than in *C. keratinophylum*. Furthermore, whereas *C. keratinophylum* can grow above 30 °C, *C. magnasporum* is a psychrotrophic species, showing a maximum growth temperature of around 20 °C.

Chrysosporium oceanitesii Stchigel, Cano, Archuby & Guarro, *sp. nov.*

Etymology. From *Oceanites*, referring to substratum from which the fungus was isolated.

Hyphae hyaline, septate, smooth-walled, 1–5 µm wide, straight, branched. *Conidia* hyaline, yellowish in mass, thick-walled, asperulate to verrucose, terminal and lateral, borne over the main hyphae or developing on right-angled side branches of variable length, sessile or on often swollen protrusions, rarely intercalary, solitary, obovate, clavate, nearly ellipsoid or obpyriform, commonly aseptate, 7–17 × 4–10 µm, with a basal scar measuring 1–5 µm. *Chlamydospores* absent. *Sexual morph* not observed.

Culture characteristics — Colony on PYE attaining 30–35 mm diam at 15 °C after 4 wk, white but light yellow (4A4) at the centre, downy, raised, margins defined; reverse orange (5A7) without production of a diffusible pigment. On OMA, colony attaining 27–30 mm diam at 15 °C after 4 wk, hairy and powdery (by conidia production), margins not defined, pale yellow (3A3), reverse vivid yellow (3A8) due to the production of a diffusible pigment of the same colour. Colonies on PYE at 5 °C and 25 °C, white, cottony, reaching 23–26 mm and 10–13 mm diam after 4 wk, respectively. Not growing above 30 °C.

Colour illustrations. Potter Cave and Three Brothers Hill, King George Island, South Shetland Archipelago, Antarctica; *Chrysosporium magnasporum* (left column) and *C. oceanitesii* (row) colonies on PYE and BCP-MS-G agar, conidiophores and conidia. Scale bars: A, B, D = 10 µm; C = 25 µm.

Physiology — Keratinolytic. Sensitive to cycloheximide (0.1 %). The fungus grows on BCP-MS-G agar acidifying the medium, with no hydrolysis of milk solids. Lipase activity not detected on TOTM.

Typus. ANTARCTICA, South Shetland Archipelago, King George Island, Three Brothers Hill, from a dead juvenile of *Oceanites oceanicus*, 10 Jan. 2011, *A. Archuvy* (holotype CBS H-20945, culture ex-type FMR 11771 = CBS 132552, ITS sequence GenBank HG329729, LSU sequence GenBank HG329730, MycoBank MB804875).

Notes — The *Chrysosporium* asexual morph of *Renispora flavissima* shows morphological similarities with *C. oceanitesii*. However, *C. oceanitesii* produces slightly larger conidia, which are never globose (as in *R. flavissima*) and grow well at 5 °C (*R. flavissima* does not grow below 20 °C). *Chrysosporium* asexual morphs of *Arthroderma* spp. are easily distinguishable from *C. oceanitesii* because they produce smaller conidia (up to 7 × 3 µm). *Chrysosporium vallenarense* (van Oorschot & Piontelli 1985) bears some resemblance, because of the ellipsoid to ovoid, verrucose to tuberculate conidia. However, *C. vallenarense* is resistant to cycloheximide (*C. oceanitesii* is sensitive), produces colonies on PYE with a brown reverse due to the production of a diffusible pigment (absent in *C. oceanitesii*) and the conidia are smaller (5–10 × 4–6 µm) than those of *C. oceanitesii*.

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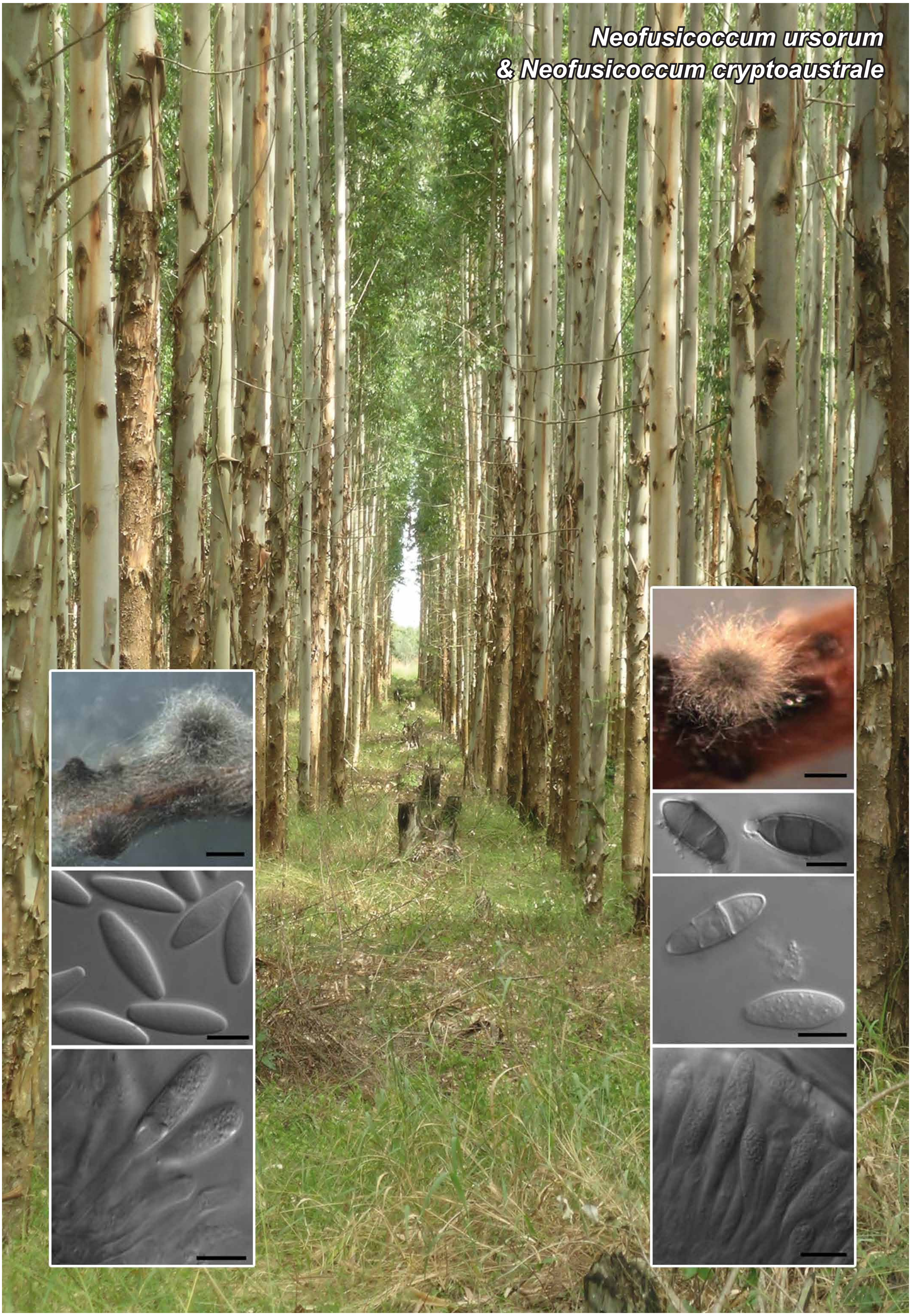
Neofusicoccum ursorum
& Neofusicoccum cryptoaustrale

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).

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.

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).

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Cyphellophora catalaunica

Fungal Planet 203 – 26 November 2013

Cyphellophora catalaunica Madrid, Gené, Guarro & Crous, *sp. nov.*

Etymology. The name refers to the Spanish autonomic community where the fungus was collected, Catalonia.

Vegetative *hyphae* septate, branched, pale olivaceous to pale brown, smooth- and thin-walled, 1–2.5 µm wide, often forming strands and coils. Distinct conidiophores absent. *Conidiogenous cells* intercalary, monophialidic, cylindrical, 2–3 µm wide, with a lateral neck, 1.5–4.5 × 1–2 µm, bearing a conspicuous collarette. *Conidia* acicular, straight to curved, 0–3-septate, subhyaline to pale olivaceous brown, smooth and thin-walled, (11–)15.5–26(–28) × 1.5–2 µm.

Culture characteristics — Colonies on OA attaining 12 mm after 14 d at 24 °C, creamy to mucoid, yeast-like, funiculose at the centre, dark olivaceous-grey with a pale grey, regular margin; reverse dark olivaceous-grey. Optimum growth temperature 24 °C, minimum below 6 °C, maximum between 27 and 30 °C.

Typus. Spain, Girona Province, sediments of Ter river, Pals beach, July 1991, *J. Gené* (holotype CBS H-21383, culture ex-type CPC 22929 = FMR 3992, MycoBank MB805277).

Notes — The genus *Cyphellophora* currently includes 17 species, eight of which are clinically-relevant and are mainly reported from mild skin and nail infections of humans (de Hoog et al. 2000, Feng et al. 2013a, Réblová et al. 2013). Some species of this genus seem to be widespread in nature and have been isolated from soil, plants, water and other substrates (Feng et al. 2013b). The genus traditionally encompassed black yeast-like phialidic asexual morphs with elongate, often curved, septate conidia, but recently has been recircumscribed to add some taxa with aseptate conidia previously placed in *Phialophora*. *Cyphellophora* species form a monophyletic group in the *Chaetothyriales* for which the family *Cyphellophoraceae* was erected (Réblová et al. 2013).

The closest BLAST hits for the ITS sequence of *C. catalaunica* (GenBank accession HG003670) were *C. laciniata* (JQ766423 and others, 97 % identical), *C. vermispora* (JQ766426 and others, 96–97 % identical), *C. fusarioides* (JQ766429 and others, 96 % identical) and *C. suttonii* (JQ766436 and others, 95 % identical). The former three species can be easily distinguished from *C. catalaunica* by conidial dimensions, i.e. wider in *C. laciniata* (11–25 × 2–5 µm) and shorter in *C. fusarioides* (3.5–8.5 × 1.0–1.5 µm) and *C. vermispora* (6.5–13 × 1–1.5 µm) (Feng et al. 2013b). The conidia of *C. suttonii* are (10–)15–20(–30) × 1.0–1.2 µm, near the size range of *C. catalaunica*, but in *C. suttonii* they have 3–8 septa (de Hoog et al. 2000, Feng et al. 2013b).

Colour illustrations. Catalan coast landscape near the sampling site. Colony on OA after 14 d at 24 °C, conidiogenous cells (arrows) and conidia, hyphal coil. Scale bars = 5 µm.

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Paraconiothyrium polonense

Fungal Planet 204 – 26 November 2013

Paraconiothyrium polonense J. Pawłowska, Wilk, Śliwińska-Wyrzychowska, Mętrak & Wrzosek, *sp. nov.*

Etymology. Named after Poland, the country where the fungus was collected.

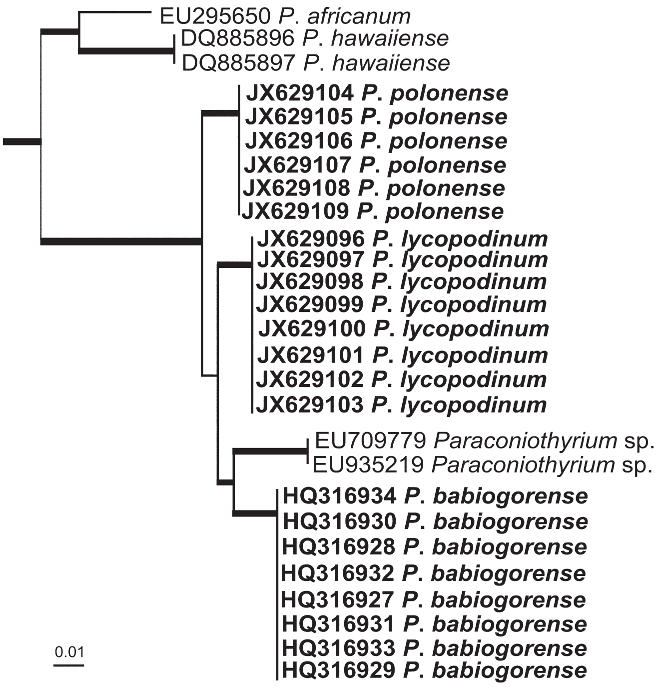
Conidiomata pycnidial, complex, mostly superficial, subglobose, black, uni-ostiolate, 0.1–0.2 mm diam. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* discrete, phialidic, ampulliform, hyaline to pale brown, 3–5 × 5–7 µm. *Conidia* hyaline to pale brown, cylindrical to short-cylindrical, rounded at both ends, aseptate, sometimes 1-septate, thin and smooth-walled, with 2–5 oil guttules, 1–2 × 8–9 µm.

Culture characteristics — Colonies on potato dextrose agar (PDA) reach 5 mm diam after 7 d and 25 mm diam after 28 d (~17 °C, in the dark). Colonies are colonial-buff to deep colonial-buff, and honey-yellow to isabella in reverse (Ridgway 1912).

Typus. POLAND, Hutki, Lesser Poland (50.33132N, 19.48460E) from healthy looking strobilus of *Lycopodium clavatum*, 17 July 2011, *A. Śliwińska-Wyrzychowska* (holotype WA0000019015, culture ex-type CBS 134153, ITS sequence GenBank JX629096, LSU sequence GenBank KF700360, MycoBank MB802724).

Notes — *Paraconiothyrium polonense* is the most similar to *P. babiogorense* (Budziszewska et al. 2011). However, *P. polonense* has pycnidial conidiomata that are smaller than the eustromatic ones of *P. babiogorense*. It was isolated from a different host and according to the ITS phylogeny, *P. polonense* is also different from *P. babiogorense.*

PhyML tree obtained from ITS nrDNA sequences data (GTR model, 522 sites, ln(L) = -1146.2, bootstrap = 100) of selected representatives of the genus *Paraconiothyrium*. Branches in **bold** indicate bootstrap support values higher than 80 %.



Paraconiothyrium lycopodinum (Sacc. & Paol.) J. Pawłowska, Wilk, Śliwińska-Wyrzychowska, Mętrak & Wrzosek, *comb. nov.*

Basionym. *Coniothyrium lycopodinum* Sacc. & Paol., Bull. Soc. Roy. Bot. Belgique 28: 98. 1889.

≡ *Clisosporium lycopodinum* (Sacc. & Paol.) Kuntze, Revis. Gen. Pl. 3: 458. 1898.

Conidiomata pycnidial, complex, mostly superficial, globose to subglobose, dark brown to black, ostiolate, 0.5–1.5 mm diam. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* discrete, phialidic, ampulliform, hyaline to pale brown, 3–4 × 5–7 µm. *Conidia* hyaline when liberated, later pale brown, ellipsoidal, rounded at both ends, aseptate, sometimes 1-septate, one or two polar guttules, 1–2 × 2–4 µm.

Culture characteristics — Colonies on PDA reach 5 mm after 7 d and 25 mm after 28 d (~17 °C, in the dark). Colonies are colonial-buff to deep colonial-buff and honey-yellow to isabella in reverse (Ridgway 1912).

Colour illustrations. *Lycopodium clavatum* from Puszcza Augustowska forest (Poland) and *Paraconiothyrium polonense*, culture on PDA, pycnidia and conidia. Scale bar = 10 µm.

Typus. POLAND, Lemańsk, Silesia (50.99046N, 19.09053E) from healthy looking strobilus of *Lycopodium annotinum*, 10 Aug. 2011, *A. Śliwińska-Wyrzychowska* (neotype designated here WA0000019023 'MBT176142', culture ex-neotype CBS 134705, ITS sequence GenBank JX629104, LSU sequence GenBank KF700359, MycoBank MB802730).

Notes — *Coniothyrium lycopodinum* was described in 1889 from leaves of *Lycopodium annotinum* from a mountain forest in Siberia (Saccardo 1889). Although its type material does not exist for comparison, our isolate compares well with the original diagnosis. However, Saccardo (1889) mentions 'perithecia' instead of 'pycnidia', yet it is clearly a question of terminology, as the same term is also used in his diagnosis for *Phoma veratrina* (Saccardo 1889: 96). Conidial dimensions given in the original description are also slightly different from those of our isolate (6 × 2 µm vs 2–4 × 1–2 µm), but this can be ascribed to the observations made directly on natural substrate vs isolates grown on synthetic media, as variability of conidial morphology on different media is a well-known phenomenon (Crous et al. 1992, Hambleton et al. 1998).

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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).

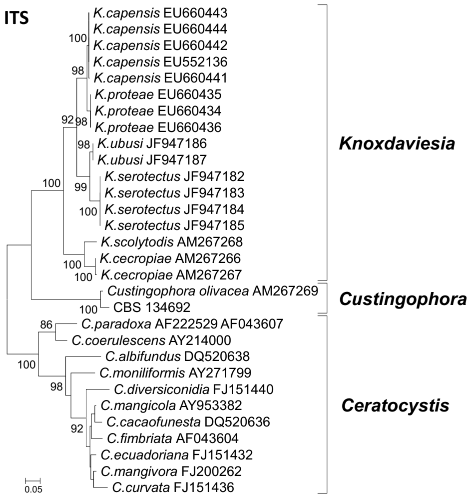
Notes — The genus *Custingophora* was erected for *Cus. olivacea*, known only from its original discovery on compost in Germany (Stolk & Hennebert 1968). Subsequently three additional species were described in the genus (Morgan-Jones & Sinclair 1980, Pinnoi et al. 2003, Kolařík & Hulcr 2009). Later, 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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Licea xanthospora
2 µm

Fungal Planet 206 – 26 November 2013

Licea xanthospora E.M. Davison, P.J.N. Davison, M.D. Barrett & R.L. Barrett, *sp. nov.*

Etymology. Derived from the Greek *xanthos* and *spora*, in reference to the yellow spores.

Sporangia single, gregarious, or plasmodiocarpous, sessile, without hypothallus, hemispheric to pulvinate, plasmodiocarps often reticulate; variable in size 0.1–2 × 0.1–1.8 mm, total height less than 0.25 mm; dark brick, rusty tawny occasionally purplish chestnut. *Peridium* thick, double, the two walls usually closely adhering, separating at maturity; outer wall thick with included debris, yellow brown in transmitted light, inner wall thin, iridescent, yellow in transmitted light, smooth; dehiscence along preformed lines into large plates, inner wall thickened at plate margin. *Columella* absent. *Spores* in mass sienna, yellow in transmitted light, globose, densely ornamented with capitate warts, 12–15.5 µm diam, no germ-pore seen. *Plasmodium* not seen.

Typus. Australia, Western Australia, Bachsten Camp, Regent River Reserve, S15°59'24" E125°18'50", 26 Jan. 2010, *M.D. & R. Barrett*, MB 27, developed in moist chamber on leaf litter of *Melaleuca* sp. and *Planchonia careya* (holotype PERTH 08481636, MycoBank MB804927); Western Australia, Charnley River Homestead, S16°42'36" E125°27'36", 28 Jan. 2010, *M.D. & R. Barrett*, RB 34, developed in moist chamber on leaf litter of *Melaleuca viridiflora*, paratype PERTH 08481628; Western Australia, Charnley River Homestead, S16°42'36" E125°27'36", 28 Jan. 2010, *M.D. & R. Barrett*, RB 36, developed in moist chamber on leaf litter of *Antidesma ghaesambilla*, paratype PERTH 08481601.

Colour illustrations. Charnley River, Kimberley area, Western Australia, paratype locality; mature sporangia on litter (from moist chamber) showing their range of form; plasmodiocarp on litter (from moist chamber); margin of peridium; spores; SEM spores. Scale bar = 10 µm (margin of peridium and spores); 2 µm (SEM).

Notes — *Licea* is a genus of small, usually inconspicuous myxomycetes. They are most frequently observed on bark that has been incubated for several weeks in moist chambers. *Licea xanthospora* is unusual because of its relatively large size and yellow, verruculose spores (as seen under the light microscope) that are capitate under the scanning electron microscope. It differs from other sessile species that dehisce along preformed lines, as described in Poulain et al. (2011), because the peridium is opaque, whereas the peridum of *L. sambucina* is translucent, and in the colour of the spore mass which is sienna, whereas it is fuscous red-brown in *L. minima*, and dark brown or black in *L. chelonoides*, *L. pusilla*, *L. pygmaea* and *L. testudinacea.* Also there are no tubercles at the plate margins as in *L. chelonoides*, *L. minima*, *L. pusilla* and *L. pygmaea*. On this basis it is described as a species new to science.

Licea xanthospora occurs in the Kimberley area of Western Australia, where it has been found in *Eucalyptus miniata* woodland over sand flats and *Melaleuca / Antidesma* thickets over swampy alluvial soils.

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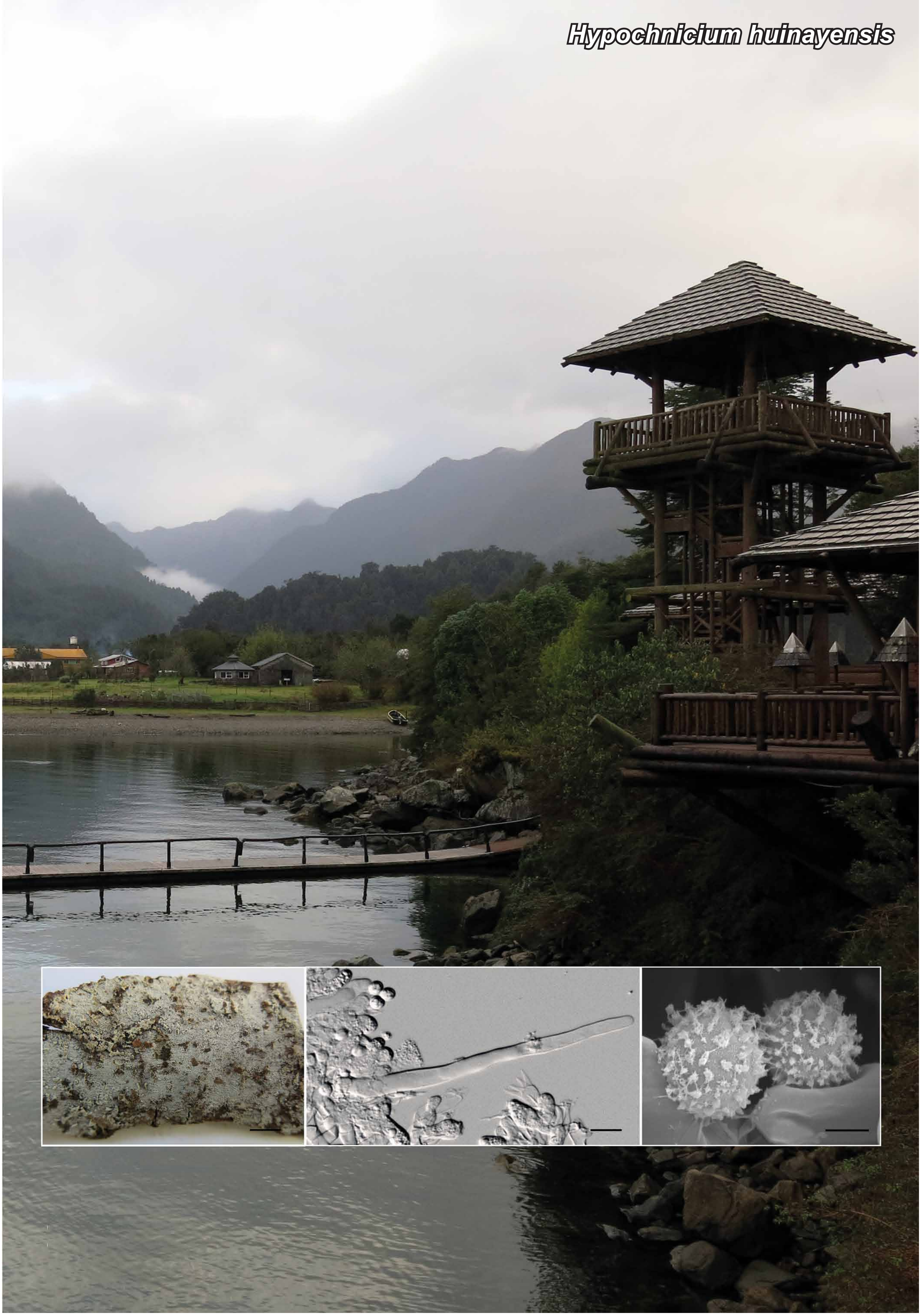

Hypochnicium huinayensis

Fungal Planet 207 – 26 November 2013

Hypochnicium huinayensis Tellería, M. Dueñas & M.P. Martín, *sp. nov.*

Etymology. Named in honour of the San Ignacio del Huinay Foundation, promoter of scientific research and sustainable development in Chilean fjord region.

Basidioma resupinate, effused, loosely adnate, thin, furfuraceous; hymenophore porose-reticulate, sometimes more or less tuberculate, greyish white to cream; margin not specially differentiated. *Hyphal system* monomitic; hyphae hyaline, thin-walled, ramified, with clamps, 4–5 µm wide; subicular texture open and subhymenial hyphae densely interwoven. *Cystidia* numerous, enclosed or projecting, thin-walled, somewhat thick-walled in the basal part, non encrusted, subcylindrical to fusiform, sometimes basely tapering to a stalk-like hyphal part, long, 110–240 × 9–12 µm. *Basidia* subclaviform to suburniform, 25–30 × 7–9 µm. *Spores* almost globose, 6.5–8(–9) × 6.5–8 µm, thick-walled, uniguttulate, ornamented in Melzer and cotton blue, smooth in 3 % KOH, cyanophilous.

Habitat — Decayed wood in Valdivian temperate rainforest from Chilean Northern Patagonian region.

Typus. Chile, Los Lagos (X Region), Palena, Comuna Hualaihué, Comau fjord, Huinay, path to Cerro del Tambor, S42°22'44.5" W72°24'25.8", on unidentified wood, 100 m, 26 Apr. 2012, *M. Dueñas*, *M.P. Martín* & *M.T. Telleria*, 19598Tell. (holotype MA-Fungi 86742, ITS sequence GenBank HG000303, MycoBank MB805569).

Additional specimens examined. Chile, Los Lagos (X Region), Palena, Comuna Hualaihué, Comau fjord, Huinay, path to Cerro del Tambor, S42°22'44.5" W72°24'25.8", on *Eucryphia cordifolia* (*Cunoniaceae*), 24 m, 25 Apr. 2012, *M. Dueñas*, *M.P. Martín* & *M.T. Telleria*, 13980MD (MA-Fungi 86743), ITS sequence GenBank HG326616.

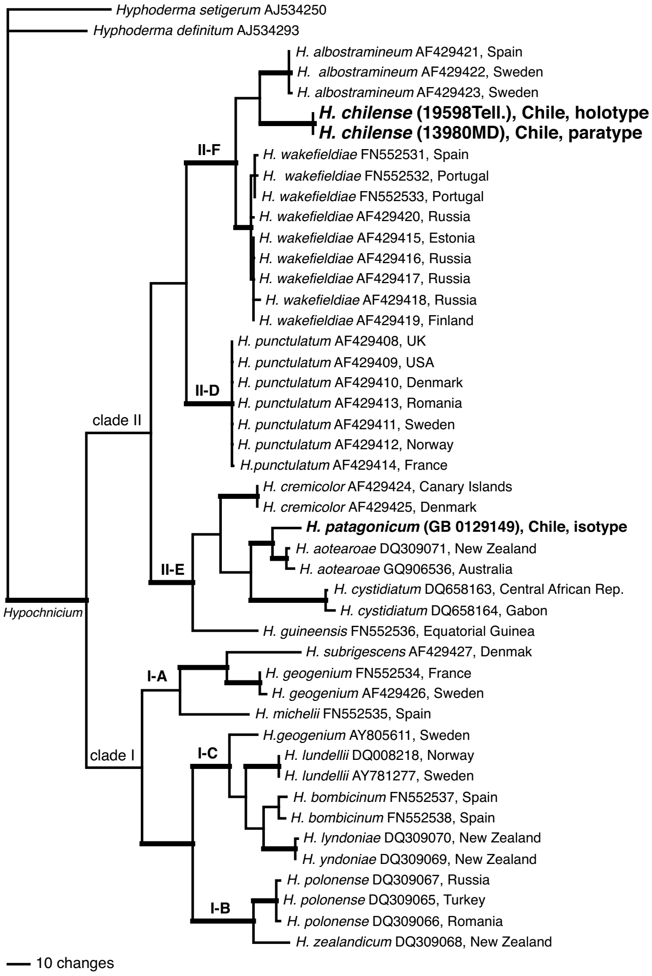
Notes — Phylogenetic analyses (parsimony and Bayesian), based on two specimens of *H. huinayensis*, and previously published data (Paulus et al. 2007, Tellería et al. 2010), clearly grouped *Hypochnicium* sequences in two main clades according to the spore morphology (clade I: smooth spores; clade II: ornamented spores); the six main subclades described in Tellería et al. (2010) were resolved. Specimens of *H. huinayensis* cluster together as a group of their own in the subclade II-F, as sister group of the three sequences of *H. albostramineum*, two from Sweden and one from Spain (intraspecific K2P *H. albostramineum* < 0.00370; interspecific K2P *H. huinayensis/H. albostramineum* > 0.0683).

The four species, *Hypochnicium bombycinum*, *H.* aff. *eriksonii*, *H. lundelii* and *H. polonense*, reported from the Argentinean Patagonia (Greslebin & Rajchenberg 2003) have smooth spores (clade I), while *H. patagonicum* and *H. huinayensis*, described from Chilean Patagonia (Gorjón & Hallenberg 2013), have ornamented spores (clade II). The ITS sequences for 19598Tell. (holotype) and 13980MD of *H. huinayensis* were identical (Kimura-2-Parameter pairwise distances, K2P, obtained using PAUP v. 4.0b10 was 0.0) and different to the ITS sequence (HG000304) of *H. patagonicum* (isotype, GB0129149) (interspecific K2P *H. chilense/H. patagonicum* > 0.14289).

Colour illustrations. San Ignacio del Huinay scientific field station, Chilean Patagonia, when the fungus was collected on decayed wood in Valdivian temperate rainforest (M.T. Tellería); basidioma (MA-Fungi 86743), scale bar = 50 mm; hymenium with cystidium, basidium and spores (MA-Fungi 86742), scale bar = 15 µm; spores by SEM (MA-Fungi 86742), scale bar = 2.5 µm.

From a morphological point of view, *H. huinayensis* is related to *H. albostramineum*, *H. punctulatum* and *H. patagonicum*. These species all share basal hyphae that are thin- to thick-walled in *H. patagonicum*, differing by the following combination of morphological characters: *H. patagonicum* has thick-walled and septate cystidia, whereas in *H. huinayensis*, *H. albostramineum* and *H. punctulatum* they are thin-walled and non-septate. *Hypochnicium albostramineum* has spores that are broadly ellipsoid to ellipsoid, 8–9.5(–12) × 6.5–7.5 µm, whereas in *H. huinayensis* and *H. punctulatum* they are almost globose or ellipsoid to globose, 6.5–8(–9) × 6.5–8 µm and 7.5–8 × 6.5–7 µm, respectively.

Maximum parsimony phylogram of ITS sequence analysis (one of the 100 most parsimonious trees), showing the clades and subclades; two *Hyphoderma* species as outgroup. The phylogenetic position of *Hypochicum chilense* and *H. patagonicum* are indicated in **bold**. Branches with bootstrap support (BS) ≥ 70 % (based on 10 000 replicates) are thickened. Country of origin for each included species is stated.



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Stachybotrys oleronensis

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Stachybotrys oleronensis Lechat, Hairaud & Lesage-Meessen, *sp. nov.*

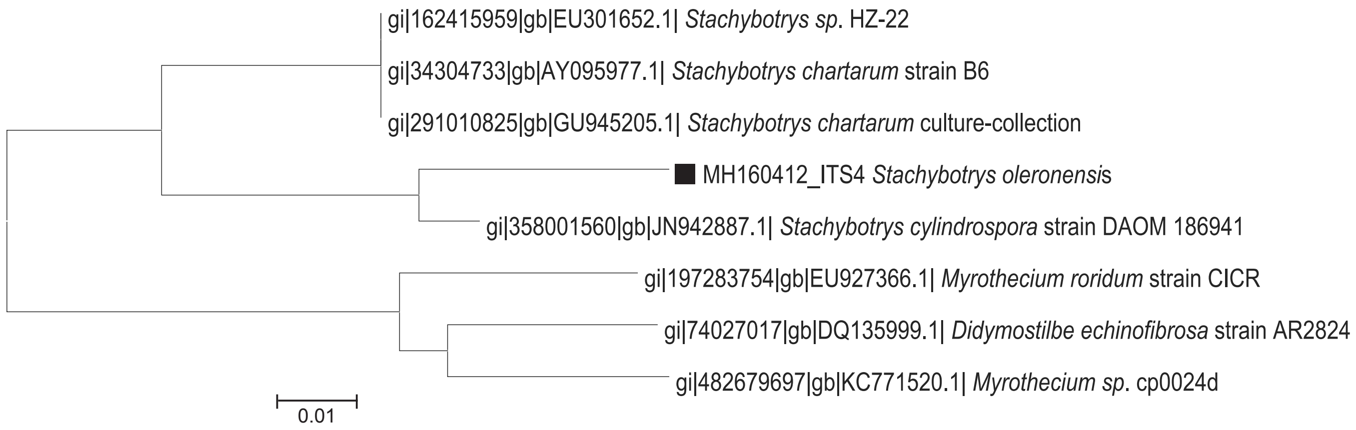
Etymology. The epithet is derived from Île d'Oléron, France, where this species was collected.

Ascomata scattered, subglobose to obpyriform, 275–290 µm high, 230–250 µm diam, non-stromatic, totally immersed in host tissues, with only rounded apex of papilla with erect hairs protruding at surface of periderm, orange, not changing colour in 3 % KOH or lactic acid, completely covered by thick-walled, intertwined hyphae, except in ostiolar region, 2.5–3.5 µm diam with wall 2 µm thick, hyaline. *Hairs* erect, hyaline, cylindrical, thick-walled (2–2.5 µm), 1–2-septate, rounded at tip, often broken, 50–80 µm long, 4.5–5 µm wide apically, 7–9.5 µm wide at base. *Apex* of papilla rounded, of thick-walled (2–3 µm), clavate cells 10–17 × 4–6 µm. *Ascomatal wall* covered with intertwined hyphae, 22–30 µm thick, of a single region composed of globose to ellipsoidal cells, 3–8 × 2–2.8, hyaline to pale yellowish, wall 1–1.5 µm thick, with abundant orange oily droplets, cells becoming narrower toward centre. *Asci* clavate, (65–)70–85(–90) × 10–12(–14) µm (av. = 80 × 11 µm, n = 20), containing 8 irregularly biseriate ascospores, completely filling each ascus, apex rounded to nearly truncate with a refractive apical ring. *Ascospores* ellipsoidal to fusiform with rounded ends, (14.5–)16–18.5(–19.5) × 4.5–5 µm (av. = 17.5 × 4.5 µm, n = 30), 1-septate, not constricted at septum, with 1–2 guttules in each cell, orange *en masse*, spinulose. Paraphyses branched containing numerous orange oily droplets.

Culture characteristics — Colony grown at 25 °C, on Difco potato dextrose agar with 5 mg/L streptomycin, yellowish white, reaching 4–5 cm diam after 2 wk, becoming pale yellow in centre, floccose aerial mycelium white to pale pink in median area, pinkish white at margin, producing a pale brown colouration. No conidia produced in culture after 3 wk, but the molecular data indicate that this species belongs in *Stachybotrys*.

Typus. France, Charente Maritime, Île d'Oléron, Saint Trojan, on leaf of *Iris pseudacorus*, 16 Apr. 2012, *M. Hairaud* (holotype deposited at LIP, France MH160412, culture ex-type CIRM BRFM MH160412, ITS sequence GenBank KF777192, MycoBank MB803657).

Notes — In springtime a search of dead leaves of *Iris pseudacorus* in a usually wet zone of the Ile d'Oléron revealed an interesting collection of a hypocrealean fungus appearing nectriella-like in having immersed ascomata. No species corresponding to our specimen was found in Rossman et al. (1999) or other literature. The ascospores were cultured. Surprisingly a sequence of this isolate placed this species in the genus *Stachybotrys*. At present no sexual states have been discovered for any species of *Stachybotrys* although *Peethambara* is closely related based on Castlebury et al. (2004). No species of *Nectriella* have been sequenced but *S. oleronensis* resembles *N. funicola* because of the intertwined hyphal wall and differs from it by smaller ascomata and smaller ascospores (14.5–)16–18(–19) × 4.5–5 µm vs (14–)16–26 × 4–8 µm. *Stachybotrys oleronensis* also resembles *N. paludosa* but differs from it by longer hairs 50–80 µm vs 8 × 2 µm and shorter ascospores (14.5–)16–18.5(–19.5) × 4.5–5 µm vs (12–)14–23 × 4–5 µm.



ITS tree placing *Stachybotrys oleronensis* in *Stachybotrys*.

Colour illustrations. Wet zone with *Iris pseudacorus*; ascoma on host substratum; ascus with ascospores. Scale bars = 100 and 10 µm.

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Knufia tsunedae

Fungal Planet 209 – 26 November 2013

Knufia tsunedae Madrid, Guarro & Crous, *sp. nov.*

Etymology. Dedicated to Dr Akihiko Tsuneda, in recognition of his contributions to the study of meristematic and endoconidial fungi.

Hyphae septate, branched, pale olivaceous to dark olivaceous-brown, smooth to asperulate, 1.5–5 µm wide. *Endoconidia* mostly broadly ellipsoidal to subglobose, aseptate to muriform, pale olivaceous to pale olivaceous-brown, smooth-walled, (7–)9.5–16(–20.5) × (6–)8–14(–17) µm, formed singly or in groups within cells of torulose hyphae and in intercalary and terminal, ellipsoidal to subglobose, pale olivaceous to dark brown, smooth-walled mother cells up to 21.5 µm wide.

Culture characteristics — Colonies on oatmeal agar attaining 42 mm after 21 d at 24 °C, olivaceous-black, umbonate and yeast-like at the centre, flat, with scarce tufts of aerial mycelium toward the periphery; reverse olivaceous-black, no exudates or soluble pigments observed. Growth positive between 6–33 °C, optimum between 24 and 27 °C. No growth observed at 36 °C.

Typus. Spain, León Province, near Besande, from soil, 12 May 2009, coll. *M. Hernández & J. Mena*, isol. *H. Madrid* (holotype CBS H-21340, cultures ex-type CPC 22931 = FMR 10621; ITS sequence GenBank HG003669, LSU sequence GenBank HG003672, MycoBank MB804798).

Notes — The genus *Knufia* currently includes six species. The generic type, *K. cryptophialidica*, was isolated from tumour-like stem and branch deformities of *Populus tremuloides* in Canada (Hutchison et al. 1995). Other species have been reported from bark of *Populus*, rocks and clinical samples (Tsuneda & Currah 2004, Tsuneda et al. 2011, Saunte et al. 2012). One species, *K. epidermidis*, causes opportunistic skin infections in humans (Li et al. 2008, Li & Chen 2010). The species described herein does not grow at body temperature and is not expected to pose a danger to humans.

Knufia tsunedae produced some smooth-walled arthroconidia in the primary culture, but they were not observed in subcultures, including the one used for the species description. After some transfers the ex-type isolate became sterile. Morphologically, *K. tsunedae* is similar to *K. endospora*, but the endoconidia in the latter species are much smaller (3–5 × 4.5–6 µm) and aseptate (Tsuneda & Currah 2004).

The closest BLAST hits for the ITS sequence of *K. tsunedae* were members of the *Chaetothyriales* (*Eurotiomycetes*) such as *Bahusakala australiensis* GQ272637 (identities 519/534, 97 %), *Knufia chersonesos* JN040514 (identities 515/551, 93 %) and *Knufia perforans* JN040506 (identities 510/553, 92 %). Though *B. australiensis* showed higher ITS identity than *Knufia* spp., the latter genus was considered more appropriate for the new species because the phylogenetic placement of type species of *Bahusakala*, *B. olivaceonigra* is unknown, and no strain of this species is available for DNA sequence studies. Furthermore, *B. olivaceonigra* does not produce endoconidia and has rugose and striate arthroconidia (Ellis 1971). According to Seifert et al. (2011 and references therein), the genus *Bahusakala* probably has sexual morphs in *Aulographina* (*Asterinaceae*, *Dothideomycetes*) or *Xylogone* (*Leotiomycetes*). Further studies are required to assess if *B. australiensis* needs to be transferred to *Knufia*.

Colour illustrations. Sample area near Besande; colony on oatmeal agar after 21 d at 24 °C; mother cells; broken mother cell and endoconidium (arrow); endoconidia (arrows). Scale bars = 10 µm.

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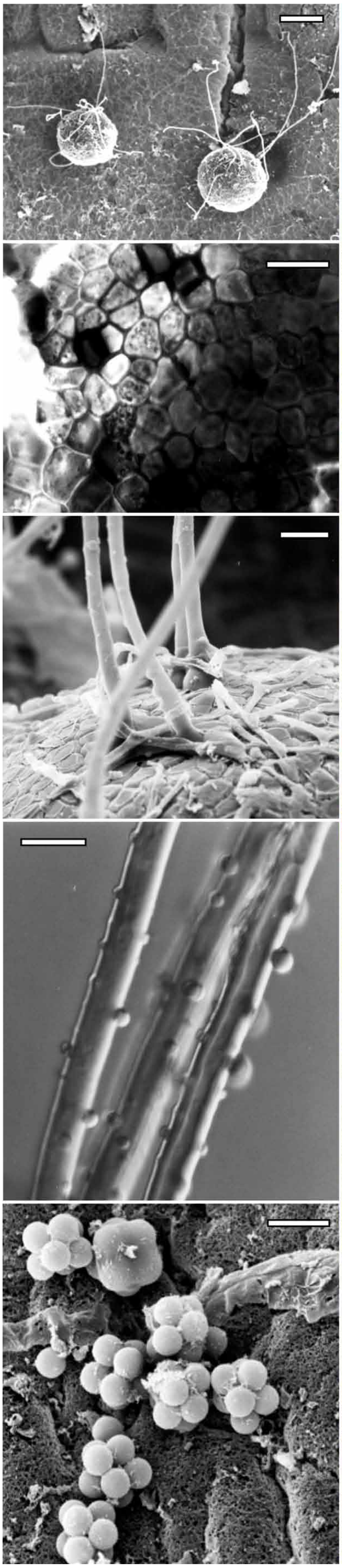

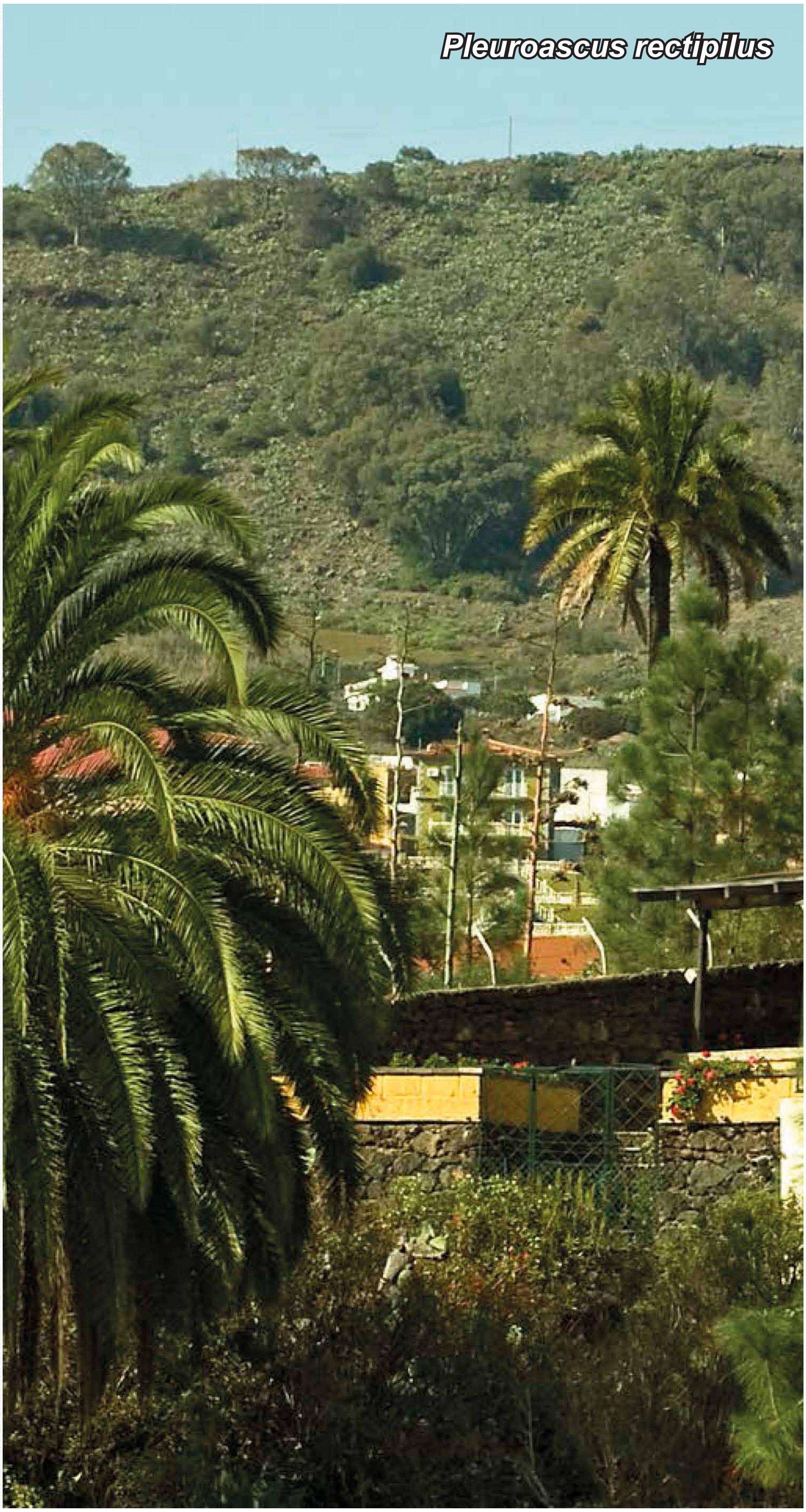
Pleuroascus rectipilus

Fungal Planet 210 – 26 November 2013

Pleuroascus rectipilus Stchigel, Guarro & Cano, *sp. nov.*

Etymology. From the Latin *rectus*- and -*pilus*, referring to the erect setae, in contrast to the extremely coiled hairs of the type species of the genus, *Pleuroascus nicholsonii*.

Mycelium composed of hyaline, branched, anastomosing, septate, smooth-walled hyphae, 1–5 µm wide. Ascomatal initials coiled. *Ascomata* superficial, non-ostiolate, spherical, pale brown at first, becoming dark brown to black with the age, purplish black under reflected light, opening when old by irregular breaking between adjacent cells, 150–250 µm diam, setose. *Setae*-like hairs 10–15 per ascoma, erect, sinuose, septate, echinulate to tuberculate, orange-brown, dark purple under reflected light, becoming subhyaline and occasionally contorted at the tip, 40–1000 µm long, 10–15 µm wide at the base, thick-walled. *Peridium* of *textura angularis* in surface view, brown to dark brown, 6–9-layered, 15–20 µm thick; outer-wall brown, 1–2-layered, 5 µm thick, cells prismatic, 3–9 µm diam; inner-wall subhyaline, 5–7-layered, 10–15 µm thick, composed of flattened cells. *Paraphyses* absent. *Asci* 8-spored, prototunicate, catenate, soon evanescent, irregularly disposed at the centrum of the ascoma, 5–7 µm diam. *Ascospores* 1-celled, hyaline to subhyaline, spherical, 2–3 µm diam, thick-walled, grouped in two tetrads inside the ascus and decussately arranged. *Asexual morph* not seen.

Culture characteristics — Colonies on OA attaining 42–45 mm diam in 30 d at 25 °C, flat, granulose due to the production of numerous ascomata, greyish brown, reverse orange-yellow to olive-brown, soluble pigment greyish orange, without exudates. Colonies on PDA attaining 14–17 mm diam in 4 wk, cottony, brownish grey, reverse brown; soluble pigment greyish orange; exudates absent. No growth on PCA at 5 °C, nor at 35 °C. At 15 °C, colonies are similar to those at 25 °C, but grow more slowly.

Typus. Spain, Canary Islands Archipelago, Gran Canaria Island, Santa Brígida, from soil, 22 Aug. 1998, *B. Acosta* (holotype CBS H-20169, culture ex-type FMR 8954 = CBS 120411 = MUCL 49873, LSU sequence GenBank HG329726, MycoBank MB512587).

Colour illustrations. Collection site on Canary Islands; *Pleuroascus rectipilus* (CBS 120411). Ascomata (SEM), peridial wall, basal region of setae (SEM), setae ornamentation, asci and ascospores (SEM). Scale bars: ascomata = 100 µm; peridial wall, basal region of setae and setae ornamentation = 10 µm; asci and ascospores = 5 µm.

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *P. nicholsonii* (CBS 345.73, AF096196) and *Connersia rilstonii* (CBS 537.74, AF096189), with a 97 % and 96 % identity, respectively. *Pleuroascus rectipilus* is characterised by its dark-coloured, stiff, sinuous, spinulose to tuberculate, broad setae-like hairs, while these are hyaline to subhyaline, coiled, smooth-walled, and considerably narrower in *P. nicholsonii*. *Connersia rilstonii* is superficially similar to *Pleuroascus* species, but lacks peridial hairs, and the ascospores are irregularly ellipsoidal to moon-shaped.

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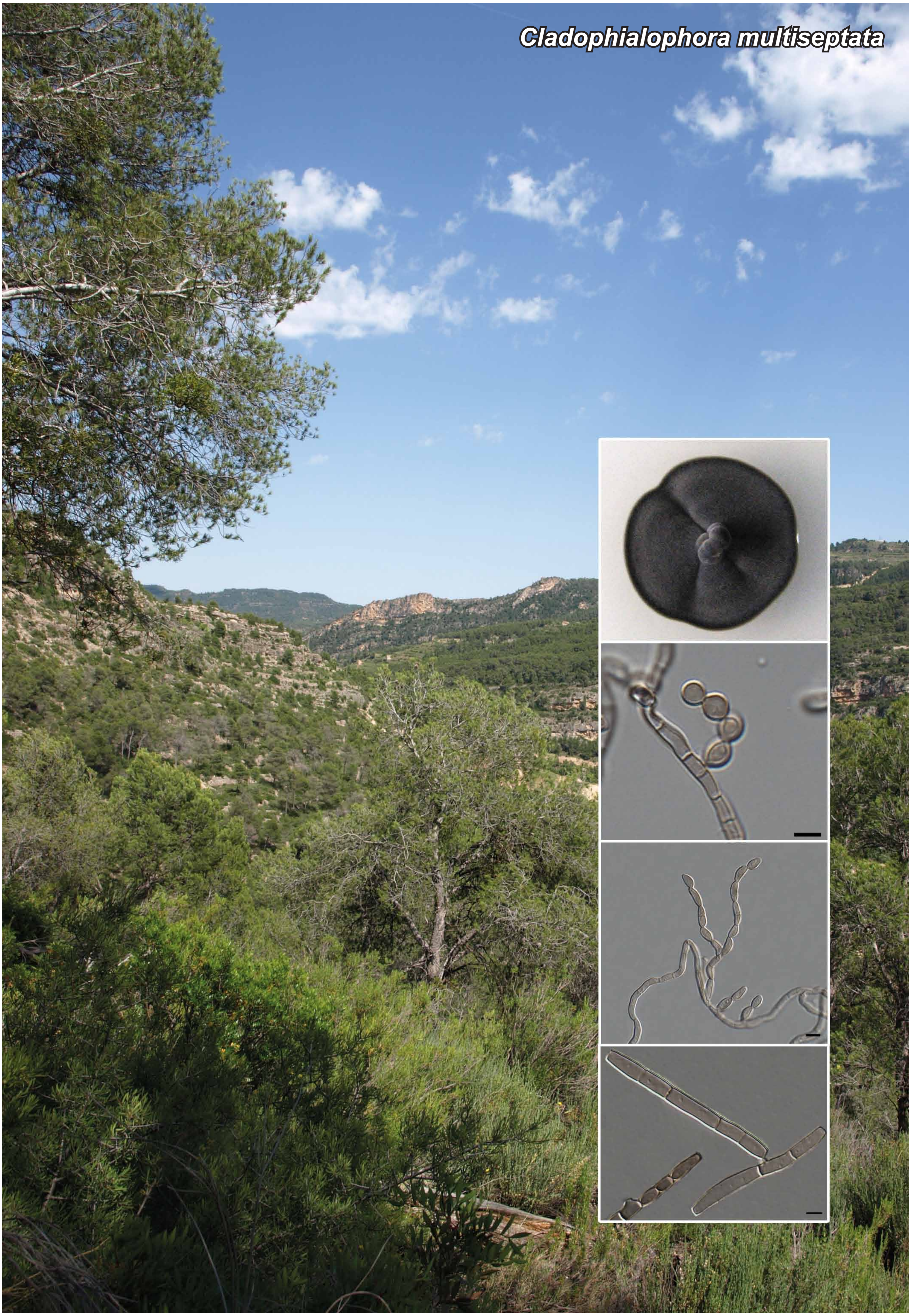
Cladophialophora multiseptata

Fungal Planet 211 – 26 November 2013

Cladophialophora multiseptata Madrid, Cano, Najafz., de Hoog, C. Silvera & Crous, *sp. nov.*

Etymology. Named after the often multiseptate arthroconidia produced by the fungus in culture.

Hyphae septate, branched, pale olivaceous to pale olivaceous-brown, smooth to asperulate, thin-walled, 2–4 µm wide, often constricted at the septa, with anastomoses. *Conidiophores* micronematous, mononematous, septate or aseptate, simple, mostly subcylindrical, pale brown to pale olivaceous-brown, thin-walled, smooth to asperulate, length indeterminate, 2–4 µm wide, releasing the conidia schizolytically. *Conidiogenous cells* intercalary, lateral or terminal, subcylindrical to fusiform, 6–13 × 3–5 µm. *Conidia* 0–1-septate, pale olivaceous to brown, smooth to asperulate, thin-walled, mostly ellipsoid to fusiform, rarely subglobose to globose, 4.5–18 × 3–5 µm, with non-thickened, non-darkened scars, forming coherent, simple or branched, terminal or lateral, acropetal chains. *Arthroconidia* intercalary, pale brown to brown, subcylindrical, mostly 1–11-septate, 18–149 × 3–4.5 µm. *Sexual morph* not observed.

Culture characteristics — Colonies on PDA after 21 d attaining 3 mm at 15 °C, 9 mm at 25 °C and 9–11 mm at 30 °C, not growing at 35 °C, velvety, strongly convoluted at the centre, radially folded, olive-grey with olivaceous-black, slightly lobate margin; reverse black, no exudates or soluble pigments observed.

Typus. Spain, Alicante Province, Carrascal de la Font Roja Natural Park, from soil, 23 Jan. 2007, coll. *R. Silvera & G. Etchart*, isol. *H. Madrid* (holotype IMI 397931, culture ex-type IMI 397931 = FMR 10591 = CPC 23682 = CBS 136675, ITS sequence GenBank HG003668, LSU sequence GenBank HG003671, MycoBank MB804080).

Colour illustrations. Sampling area in Carrascal de la Font Roja National Park; Colony on PDA after 21 d at 25 ºC, conidiogenous cells and chains of elongate conidia; conidiogenous cells and a chain of subglobose to globose conidia; arthroconidia. Scale bars = 5 µm.

Notes — *Cladophialophora* is a species-rich genus in the *Chaetothyriales*. It includes several clinically-relevant taxa which cause phaeohyphomycosis, chromoblastomycosis and mycetoma in vertebrates (de Hoog et al. 2000, Badali et al. 2008). *Cladophialophora* also includes saprobes occurring in soil and on plant debris, endophytes and some species associated with plant disease (Crous et al. 2007b, de Hoog et al. 2007). The genus is characterised by the production of acropetal chains of globose to elongate blastoconidia with scars which usually are neither thickened nor darkened. The type species, *C. carrionii* occasionally also produces phialides (de Hoog et al. 2000).

BLAST searches revealed that the ITS sequence of *C. multiseptata* (GenBank accession HG003668) shows relatively high percentage identities to those of *C. chaetospira* (EU035405 and others, 94–95 % identical), *C. boppii* (EU103997 and others, 91–92 % identical), *C. carrionii* (EU137266 and others, 89–90 % identical) and *C. yegresii* (EU137322 and others, 89 % identical). *Cladophialophora multiseptata* can be distinguished from its closest relatives by the abundant production of septate intercalary arthroconidia in culture.

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Calonectria mossambicensis

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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.

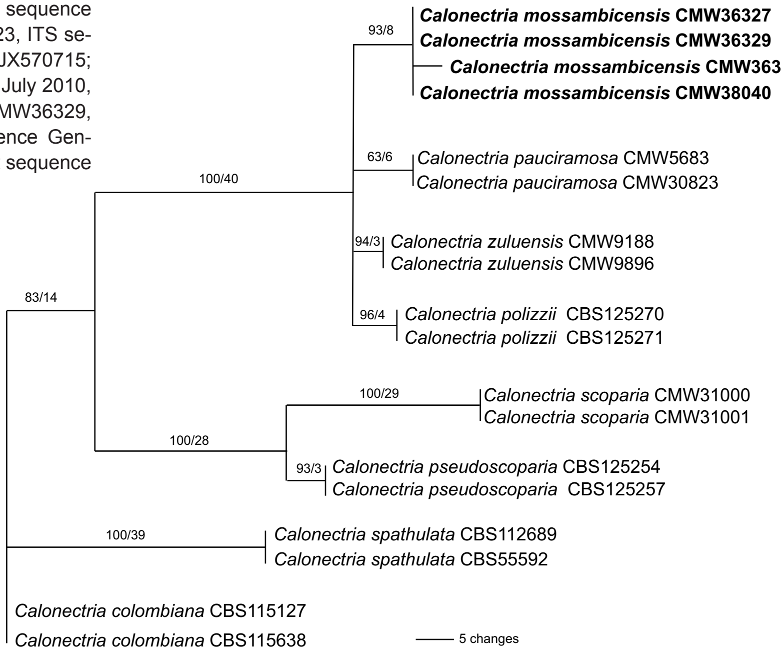
Typus. Mozambique, Manica, Bandula, cutting clones of *E. grandis* × *E. camaldulensis*, July 2010, *J. Roux & S. Maússe-Sitoe* (holotype PREM 60821, cultures ex-type CMW36327, Calmodulin sequence GenBank JX570722, Histone H3 sequence GenBank JX570726, ITS sequence GenBank JX570730, TEF-1α sequence GenBank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

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Bipolaris drechsleri Manamgoda & Minnis, *sp. nov.*

Etymology. Named in honour of Charles Drechsler (1892–1986), a USDA scientist who worked on this group of fungi.

Leaf spots irregular, small, distinct, purplish, with dark margin, surrounded by a chlorotic halo. *Conidiophores* macronematous, arising singly or in groups of two to three, straight to flexuous, cylindrical, geniculate in upper part, simple or with one dichotomous branch, pale brown, septate, smooth-walled, (74–)95–300(–602) × 4–6 µm (x̄ = 250, SD = 152, n = 35; x̄ = 5, SD = 1, n = 35). *Conidiogenous cells* integrated, intercalary, with sympodial proliferation, monotretic or polytretic, dark brown, with circular scars. *Conidia* solitary, curved or straight, ellipsoidal, obclavate, obclavate-ellipsoidal, rostrate, rarely obovoid, apex and base obtuse, smooth-walled, pale to dark golden-brown, sometimes paler in end cells, (39–)50–80(–102) × (10–)13–19(–20) µm (x̄ = 66, SD = 14, n = 125; x̄ = 16, SD = 3, n = 125), 3–10-distoseptate (x̄ = 7), septa accentuated; hilum inconspicuous or slightly protuberant, dark brown to black; germinating with a germ tube at each end of conidia.

Culture characteristics — Colonies (35–)45–60(–70) mm diam on PDA (Difco) after 5 d at 25 °C in dark, white when young, becoming whitish grey at maturity; margin irregular, effuse, velvety, concolorous; stromata not formed in culture. Reverse black, with white margin.

Habitat — On living leaves of *Microstegium vimineum* and other grasses as in Kleczewski et al. (2012).

Distribution — USA (Indiana, Maryland, West Virginia).

Typus. USA, Indiana, Big Oaks Wildlife Refuge, on living leaves of *Microstegium vimineum*, 2010, *N. Kleczewski* (holotype BPI 892682; ex-type culture AR4841 = CBS 136207, MycoBank MB 805272).

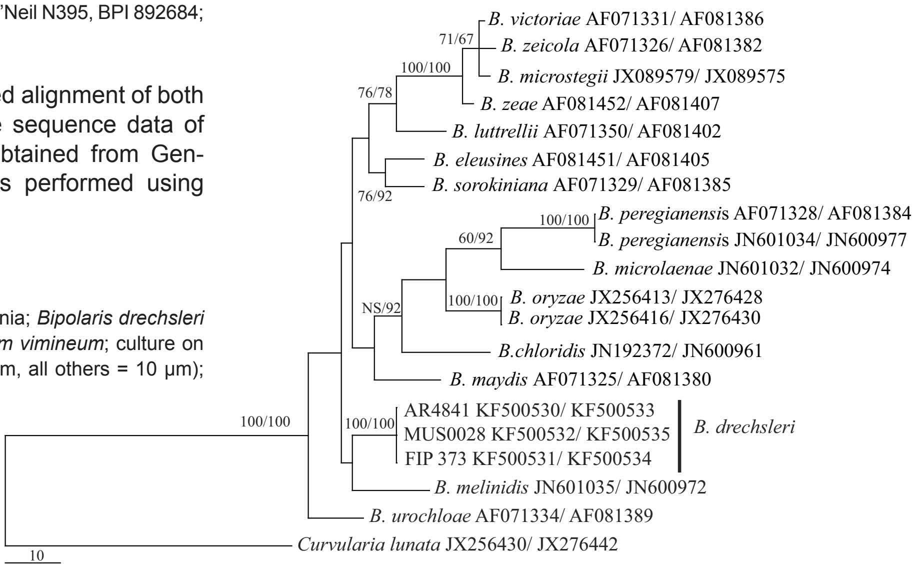
Additional material examined. USA, West Virginia, Arnoldsburg, on living leaves of *Microstegium vimineum*, *N. Kleczewski*, BPI 892683; culture MI036 = CBS 136208; Maryland, Montgomery Co., Wheaton, Brookside Garden, on an unidentified ornamental grass, Oct. 1995, N. O'Neil N395, BPI 892684; culture FIP 373= CBS 136245.

Phylogenetic analysis — A concatenated alignment of both ITS and GPDH loci was made using the sequence data of *B. drechsleri* and *Bipolaris* sequences obtained from GenBank. A maximum likelihood search was performed using the RAxML BlackBox v. 7.6.3 in CIPRES Science Gateway platform (Miller et al. 2010). Parsimony trees were inferred by PAUP v. 4.0b10 (Swofford 2003) using a heuristic search option with 1 000 random sequence additions. The alignment and tree were uploaded to TreeBASE (ID 14626).

Colour illustrations. Collection site in West Virginia; *Bipolaris drechsleri* (AR 4841). Symptom development on *Microstegium vimineum*; culture on PDA; conidiophores and conidia (scale bar = 50 µm, all others = 10 µm); conidiophores; conidia.

Notes — The host *Microstegium vimineum*, common name Japanese stilt grass, is an annual grass in the *Poaceae*, subfamily *Panicoideae*, tribe *Andropogoneae*. Currently, *M. vimineum* is one of a number of serious non-native invasive species in the eastern United States (Flory et al. 2011). The fungal genus *Bipolaris* includes a number of grass pathogens (Manamgoda et al. 2011). Recently a new species occurring on *Microstegium vinimeum* was described as *B. microstegii* (Crous et al. 2012a). *Bipolaris drechsleri* has conidial dimensions similar to *B. microstegii*, but *B. drechsleri* has shorter conidiophores and conidiophores with more proliferations than *B. microstegii*. Overlapping conidial dimensions between species is common in the genus *Bipolaris* (Sivanesan 1987) and a phylogenetic species recognition criterion is essential for defining species in this genus (Manamgoda et al. 2011). Comparing ITS and GPDH with the available data in GenBank revealed that the fungus belongs in *Bipolaris* sensu Manamgoda et al. (2012). *Bipolaris microstegii* is phylogenetically close to *B. victoriae* and *B. zeicola*, but the latter two species do not show a close phylogenetic relationship with *B. drechsleri*, which clusters with *B. melinidis*.

Phylogram generated from maximum parsimony analysis based on combined ITS and GPDH gene sequences. Parsimony bootstrap values/RAxML rapid bootstrapping estimations ≥ 60 % are shown above the branches. GenBank numbers of included sequences for each species are given as ITS/GPDH.



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