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RESEARCH ARTICLE

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**Key words**

ITS DNA barcodes
LSU
novel fungal species
systematics

**Abstract** Novel species of microfungi described in the present study include the following from Australia: *Bagadiella victoriae* and *Bagadiella koalae* on *Eucalyptus* spp., *Catenulostroma eucalyptorum* on *Eucalyptus laevopinea*, *Cercospora eremochloae* on *Eremochloa bimaculata*, *Devriesia queenslandica* on *Scaevola taccada, Diaporthe musigena* on *Musa* sp., *Diaporthe acaciigena* on *Acacia retinodes*, *Leptoxyphium kurandae* on *Eucalyptus* sp., *Neofusicoccum grevilleae* on *Grevillea aurea*, *Phytophthora fluvialis* from water in native bushland, *Pseudocercospora cyathicola* on *Cyathea australis*, and *Teratosphaeria mareebensis* on *Eucalyptus* sp. Other species include *Passalora leptophlebiae* on *Eucalyptus leptophlebia* (Brazil), *Exophiala tremulae* on *Populus tremuloides* and *Dictyosporium stellatum* from submerged wood (Canada), *Mycosphaerella valgourgensis* on *Yucca* sp. (France), *Sclerostagonospora cycadis* on *Cycas revoluta* (Japan), *Rachicladosporium pini* on *Pinus monophylla* (Netherlands), *Mycosphaerella wachendorfiae* on *Wachendorfia thyrsifolia* and *Diaporthe rhusicola* on *Rhus pendulina* (South Africa). Novel genera of hyphomycetes include *Noosia banksiae* on *Banksia aemula* (Australia), *Utrechtiana cibiessia* on *Phragmites australis* (Netherlands), and *Funbolia dimorpha* on blackened stem bark of an unidentified tree (USA). Morphological and culture characteristics along with ITS DNA barcodes are provided for all taxa.

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Neighbour-joining tree obtained using a distance analysis with a general time reversible (GTR) substitution model on the partial 28S nrRNA gene alignment (780 nucleotides including alignment gaps) as implemented in PAUP v4.0b10 (Swofford 2003). Novel species are indicated in a red font and the orders are indicated on the right-hand side of the figure. The scale bar indicates the number of substitutions per site and the bootstrap support values (based on 1 000 replicates) are shown by colour-coded dots for values >79 % (see legend on figure). The tree was rooted to species of the order *Peronosporales*.


Cercospora eremochloae

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# *Cercospora eremochloae* R.G. Shivas & A.J. Young, *sp. nov*.

Conidiophora 2–10, fasciculis laxis in stromatum pagina, erecta, geniculata-sinuata, paulum attenuata, ramosa vel inramosa, rubella-brunnea pallidiorescentia ad apicem, 100–275 × 4–6 µm, usque ad 20 septata, paries levis. Cellulae conidiogenae terminales, monoblasticae vel polyblasticae, sympodiales, geniculatae, brunneolae; cicatrices conidiales conspicuae, crassatae et refractivae, terminales et laterales. Conidia solitaria vel catenis brevibus ramosis et inramosis, cylindracea, ellipsoidea, obovoidea, obclavata, fusiformia, recta, hyalina ad subhyalina, 10–35 × 3.0–7.5 µm, (0–)1–4(–6)-septata, levia, extrema rotundata, basis obconice truncata, hila crassata et refractiva.

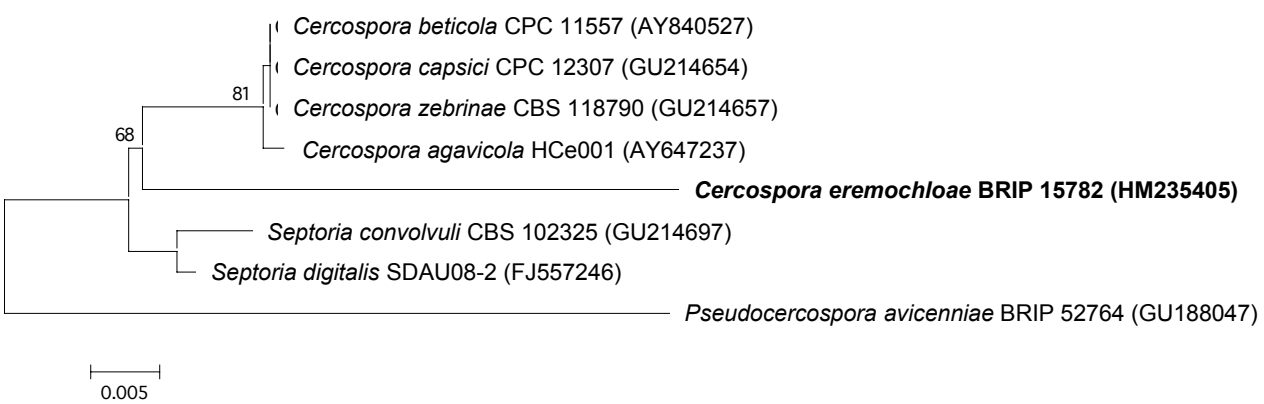
*Etymology*. Derived from the name host plant genus, *Eremochloa* (*Poaceae*).

*Leaf spots* amphigenous, narrow elliptical, often elongated, up to 7 cm long, 0.5–1.5 mm wide, smaller leaf spots bordered by veins, centres orange to pale brown with darker reddish to purplish brown diffuse margins. *Mycelium* internal. *Stromata* reddish brown, erumpent, usually filling stomatal opening; up to 40 µm diam. *Conidiophores* 2–10, in loose fascicles on the surface of the stromata, erect, geniculate-sinuous, slightly attenuated, branched or unbranched, reddish brown becoming paler towards the apex, 100–275 × 4–6 µm, up to 20-septate, wall smooth. *Conidiogenous cells* terminal, monoblastic or polyblastic, sympodial, geniculate, pale brown; conidial scars conspicuous, thickened and refractive, terminal and lateral. *Conidia* solitary or in short branched and unbranched chains, cylindrical, ellipsoid, obovoid, obclavate to fusiform, straight, hyaline to subhyaline, 10–35 × 3.0–7.5 µm, (0–)1–4(–6)-septate, smooth, ends rounded, base obconically truncate, hila thickened and refractive.

*Typus*. Australia, Queensland, Mareeba, *Eremochloa bimaculata*, 30 Apr. 1987, *J.L. Alcorn*, BRIP 15782, holotype; IMI 321201, isotype; ITS sequence GenBank HM235405, and LSU sequence GenBank HM235406, MycoBank MB560159.

Notes — Species of *Cercospora* s.str. have conspicuously thickened and darkened conidial scars and hyaline or subhyaline, solitary (rarely catenate) conidia formed on pigmented (rarely hyaline to subhyaline) conidiophores (Braun 1995, Crous & Braun 2003, Crous et al. 2009b, c). *Cercospora eremochloae* differs from *Cercospora* s.str. in having non-acicular, hyaline to faintly pigmented conidia that are either solitary or in short, branched to unbranched chains. DNA sequence data indicated, however, that *C. eremochloae* clusters with the *Cercospora* complex, which forms a well-defined clade in the *Mycosphaerellaceae* (Crous et al. 2009b, c). When this specimen was examined by B.C. Sutton in 1988, he reported that he would place it in *Phaeoramularia* as the conidia were catenate and that this specimen was unlike any of the graminicolous members of the '*Cercospora*' groups. However *Phaeoramularia* was reduced to synonymy with *Passalora* (Crous & Braun 2003), which currently represents an unresolved and inordinately wide complex of taxa (Crous et al. 2009b, c).

BLASTn results of the ITS sequence of *C. eremochloae* indicated similarity to sequences of *Mycosphaerella berberidis* (EU167603; Identities = 481/499 (96 %), Gaps = 6/499 (1 %)), and *Cercospora agavicola* (AY647237; Identities = 481/501 (96 %), Gaps = 10/501 (1 %)). The LSU sequence (HM235406) shared 877/885 sequence identities with *C. zebrinae* (GU214657), indicating it is phylogenetically distinct from *Cercospora* s.str. Genomic DNA of *C. eremochloae* (holotype) is stored in the Australian Biosecurity Bank (http://www.padil.gov.au/).




Maximum Likelihood Tree obtained using the General Time Reversible Model from an ITS sequence alignment generated with MUSCLE in MEGA4 (Tamura et al. 2007). The bootstrap support values from 1 000 replicates are shown at the nodes. Bar represents number of substitutions per site. The species described here is printed in **bold** face. The tree was rooted to *Pseudocercospora avicenniae* (GenBank GU188047).

*Colour illustrations*. Grasses with unknown beetle where *C. eremochloae* was collected; leaf spots; conidiophores and conidia. Scale bar top left = 5 mm, others = 10 µm.

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Exophiala tremulae
a
b
c
d
e

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# ***Exophiala tremulae*** W. Wang, *sp. nov*.

*Exophialae pisciphilae* similis, sed conidiis minoribus, 3–4 × 1–1.5 µm.

*Etymology*. Named after its host species, *Populus tremuloides*.

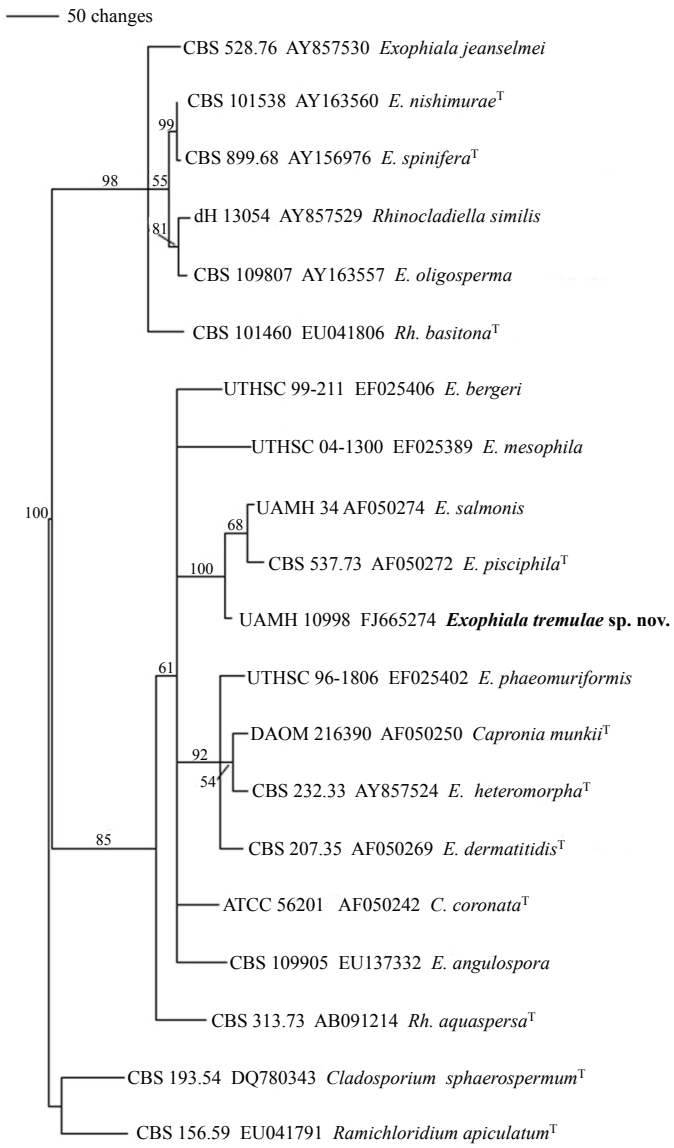
Hyphae smooth, straight to toruloid, up to 1.5 µm wide. *Conidiophores* monilioid, branched, smooth, up to 30 µm long (Fig. a, b). *Conidiogenous cells* annellidic (Fig. b–e), arising from conidiophores or directly from vegetative hyphae (Fig. a, b), ellipsoidal to ampulliform (Fig. b, d, e), 2.2–6 × 1.5–2 µm, annellides elongated (Fig. d, e), 8 × 1.3 µm. *Conidia* cylindrical, rounded at the apex, truncate at the base, hyaline, smooth, 0–1-septate (Fig. b–d), 3–4 × 1–1.5 µm. *Seta*-like hyphae and chlamydospores absent. *Teleomorph* unknown.

Culture characteristics — Colonies on 2 % potato-dextrose agar (PDA) at 22 °C after 14 d were 10–15 mm diam, velvety to floccose, olivaceous to greyish black, aerial hyphae humped, pale brown at the centre, reverse olivaceous to black. Colonies on 2 % malt extract agar (MEA) and cereal agar (25 g Pablum™ Mixed Cereal baby food (Mead Johnson & Co., Pittsburgh, PA, USA), 5 g select agar (Invitrogen, Carlsbad, CA, USA), 1 L $dH_2O$) grew faster (15–20 mm diam at 22 °C after 14 d) while growth was slower on Sabouraud's agar and V-8 juice agar (only 10 mm diam at 22 °C after 14 d). Sporulation occurred on MEA and oatmeal agar after about 1 mo of incubation. Yeast-like growth occurred on PDA after 7 d.

Known distribution — Only from the type locality.

*Typus*. Canada, Alberta, Edmonton, Lamont, alt. c. 664 m, from roots of apparently healthy 5–7-year-old *Populus tremuloides* sapling, 23 June 2004, W. Wang, holotype UAMH 10998, ITS sequence GenBank FJ665274 and LSU sequence GenBank JF951155, MycoBank MB519208.

Notes — *Exophiala tremulae* tested negatively for phenoloxidase and positively for gelatinase and cellulase. It was unable to break down casamino acids but acidified the media as indicated by the yellow colour formation in the agar. This suggests that *E. tremulae* could act as a saprobe of primary incidence (Munk 1957). The ecological role of *E. tremulae* is presently still unknown. BLASTn results of the ITS sequence showed that *E. tremulae* had a high similarity to *E. pisciphila* (94 % identical) and *E. salmonis* (96 % identical).




Single most parsimonious tree (TL = 880; CI = 0.651; RI = 0.568; HI = 0.349) obtained from a heuristic search with 1 000 random taxon additions of an ITS sequence alignment with PAUP v4.0b10 (Swofford 2003), showing the relationship between *Exophiala tremulae* sp. nov. and other related *Capronia* spp., *Exophiala* spp., and *Rhinodadiella* spp. The scale bar shows 50 changes, and bootstrap support values over 50 % from 1 000 replicates are shown at the nodes. The species described here is printed in **bold** face. Ex-types were flagged with 'T'. GenBank, ATCC, CBS, DAOM, dH, UAMH, and UTHSC accession numbers are also indicated. The tree was rooted to *Cadosporium sphaerospermum* and *Ramichloridium apiculatum*. The alignment and tree is available in MycoBank (Accession MB519208).

*Colour illustrations*. *Populus tremuloides* stand in Alberta, Canada. a. Toruloid hyphae and conidiophores; b. conidiogenous cells (arrows) and conidia (arrow head); c. annellide (arrow); d. annellations (arrow); e. an elongated annellide (arrow). — Scale bars: a = 20 µm; b = 1.5 µm; c, d = 2 µm; e = 1 µm.

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Funbolia dimorpha

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## ***Funbolia*** Crous & Seifert, *gen. nov.*

*Spadicoidis* morphologice similis, sed conidiis dimorphis, sine septis fuscatis.

*Etymology*. Named after the Fungal Barcode of Life group that convened at Front Royal, Virginia (USA) in 2007 to initiate the CBOL Fungal Working Group.

Associated with bark of a living tree. *Mycelium* of pale brown to hyaline, branched hyphae, giving rise to conidiophores. *Conidiophores* solitary, erect, straight to flexuous, cylindrical, unbranched, or branched below, brown, finely verruculose, multi-euseptate. *Conidiogenous cells* terminal and lateral, pale to medium brown, finely verruculose, subcylindrical to somewhat swollen, clavate to irregular; loci aggregated in a rachis, at times subdenticulate with minute collarette; scars thickened along the rim, erumpent, but not darkened nor refractive. *Conidia* dimorphic, medium brown, finely verruculose, ellipsoidal when 1-septate, becoming subcylindrical when multiseptate, apex obtusely rounded, tapering from basal septum to an obconically truncate hilum, not thickened, nor darkened (at times appearing to have a marginal frill); transversely euseptate.

*Type species*. *Funbolia dimorpha.*
MycoBank MB560161.

Notes — *Funbolia* resembles genera such as *Spadicoides* (but conidia lack the darkened septa), *Neta* (but lacks setae), *Thysanorea* (but has dimorphic conidia), and *Catenulisubulispora* (which lacks dimorphic conidia and has beaked conidia) (Seifert et al. 2011). Because it could not be accommodated in any of the genera listed here and its DNA sequences did not match any fungi currently deposited in GenBank, we introduce a new genus here to accommodate it.

## ***Funbolia dimorpha*** Crous & Seifert, *sp. nov.*

Conidiophora solitaria, erecta, ramosa vel non ramosa, subtiliter verruculosa, pluri-euseptata. Cellulae conidiogenae terminales et laterales, pallide vel medio-brunneae, subtiliter verruculosae, subcylindraceae vel leniter inflatae, clavatae vel irregulares; locis conidiogenis aggregatis in rache, interdum subdenticulatis. Conidia dimorpha, medio-brunnea, subtiliter verruculosa, conidiis 1-septatis, (6–)8–11(–20) × (4–)5 µm, et conidiis (2–)3(–7)-euseptatis, (15–)20–35(–45) × (4–)5 µm.

*Etymology*. Named after its dimorphic conidia.

*Mycelium* consisting of pale brown to hyaline, smooth, branched hyphae, 2–3 µm diam, becoming somewhat verruculose at fertile regions, giving rise to conidiophores. *Conidiophores* solitary, erect, straight to flexuous, cylindrical, unbranched, or branched below (branched conidiophores developing with age), 50–100 × 3–4 µm, brown, finely verruculose, multi-euseptate, septa 5–17 µm apart, becoming somewhat darkened, but not thickened. *Conidiogenous cells* terminal and lateral, pale to medium brown, finely verruculose, subcylindrical to somewhat swollen, clavate to irregular, 7–20 × 2.5–5 µm; conidiogenous loci dispersed on conidiogenous cells in young cultures, aggregated in a rachis on conidiogenous cells in older cultures, at times subdenticulate with minute collarette, up to 1 µm tall, and 1 µm diam; scars thickened along the rim, erumpent, but neither darkened nor refractive. *Conidia* dimorphic, medium brown, finely verruculose, ellipsoidal when 1-septate, (6–)8–11(–20) × (4–)5 µm, becoming subcylindrical when multiseptate, apex obtusely rounded, tapering from basal septum to an obconically truncate hilum, 1 µm diam, not thickened, nor darkened (at times appearing to have a marginal frill); (2–)3(–7)-euseptate, becoming darkened in older conidia, and also constricted at septa, (15–)20–35(–45) × (4–)5 µm; microcyclic conidiation observed in culture.

Culture characteristics — (in the dark, 25 °C, after 1 mo): Colonies flat, spreading, with sparse to moderate aerial mycelium and even, lobate margins, reaching 8–10 mm diam. On potato-dextrose agar surface isabelline, reverse olivaceous; on oatmeal agar surface isabelline; on malt extract agar margin somewhat feathery, surface umber, reverse chestnut, with diffuse isabelline pigment surrounding colony.

*Typus*. USA, Virginia, Front Royal, N 38°53'35" W 78°10'50", on blackened stem bark of unidentified tree, 14 May 2007, *P.W. Crous & K.A. Seifert*, holotype CBS H-20577, cultures ex-type CPC 14170 = CBS 126491, ITS sequence GenBank JF951136 and LSU sequence GenBank JF951156, MycoBank MB560158.

Notes — Based on a megablast search of NCBI's GenBank nucleotide database, the closest hit using the ITS sequence is *Didymosphaeria futilis* (GenBank EU552123; Identities = 471/552 (85 %), Gaps = 28/552 (5 %)) followed by species of *Cladonia* with shorter homology, e.g. *Cladonia subtenuis* (GenBank DQ482701; Identities = 242/271 (89 %), Gaps = 8/271 (3 %)). Closest hits using the LSU sequence yielded highest similarity to *Heleiosa barbatula* (GU479787; Identities = 834/891 (94 %), Gaps = 8/891 (1 %)), *Caloplaca sublobulata* (EF489950; Identities = 859/947 (91 %), Gaps = 24/947 (3 %)) and *Caloplaca regalis* (EU161240; Identities = 850/938 (91 %), Gaps = 24/938 (3 %).

*Colour illustrations*. Blackened bark of unidentified tree at Front Royal, Virginia; conidiophores giving rise to dimorphic conidia in culture. Scale bar = 10 µm.

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Neofusicoccum grevilleae

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# ***Neofusicoccum grevilleae*** Crous & R.G. Shivas, *sp. nov.*

*Neofusicocci parvi* simile, sed conidiis majoribus, (20–)25–28(–32) × (6–)7–8(–10) µm.

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

*Leaf spots* medium brown, situated along leaf margins, surrounded by a dark red-brown border; spots extending to the mid-rib, up to 7 mm diam, and up to 2 cm long. *Conidiomata* amphigenous, pycnidioid, stromatic, up to 200 µm diam (on sterilised pine needles); wall consisting of 3–5 layers of brown *textura angularis*. *Conidiophores* lining the inner layer of conidioma, hyaline, smooth, 0–1-septate, 15–30 × 3–5 µm. *Conidiogenous cells* phialidic, integrated, doliiform to subcylindrical, 15–25 × 3–4 µm, proliferating 2–3 times percurrently near apex. *Conidia* hyaline, smooth, thin-walled, with granular cytoplasm, fusoid-ellipsoidal, widest in middle or in upper third of conidium, apex subobtuse, base truncate, (20–)25–28(–32) × (6–)7–8(–10) µm (av. 25.7 × 7.5 µm; L : W = 3.4 : 1).

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies flat, spreading, with abundant, grey aerial mycelium, covering the dish after 7 d. On potato-dextrose agar, oatmeal agar and malt extract agar iron-grey; sporulating poorly on water agar supplemented with sterile pine needles; no *Dichomera* synanamorph observed.

*Typus*. Australia, Queensland, Brisbane, on leaves of *Grevillea aurea*, 14 July 2009, *P.W. Crous & R.G. Shivas*, holotype CBS H-20578, cultures ex-type CPC 16999 = CBS 129518, ITS sequence GenBank JF951137 and LSU sequence GenBank JF951157, MycoBank MB560162.

Notes — Based on a megablast search of NCBI's GenBank nucleotide database, the closest hit using the ITS sequence is representatives of the *Neofusicoccum ribis* complex, e.g. *Neofusicoccum ribis* (HQ392732; Identities = 548/561 (98 %), Gaps = 2/561 (0 %)) and *Neofusicoccum parvum* (EU080926; Identities = 561/575 (98 %), Gaps = 5/575 (0 %)). A similar search using the LSU sequence confirms this association with closest hits including *Neofusicoccum ribis* (DQ246263; Identities = 903/906 (99 %), Gaps = 0/906 (0 %)) and *Neofusicoccum mangiferae* (DQ377921; Identities = 908/912 (99 %), Gaps = 0/912 (0 %)). *Neofusicoccum grevilleae* is morphologically similar to *N. parvum* (conidia 12–25 × 5–7.5 µm; Crous et al. 2006) and *N. ribis* (conidia 16–24 × 5–7 µm; Slippers et al. 2004), but can be distinguished from it in having slightly larger conidia (20–32 × 6–10 µm).

*Colour illustrations*. *Grevillea aurea* in Brisbane Botanical Garden; symptomatic leaf; culture sporulating on sterile pine needle; conidiogenous cells and conidia. Scale bar = 10 µm.

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Diaporthe musigena

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# ***Diaporthe musigena*** Crous & R.G. Shivas, *sp. nov.*

*Phomopsis longicollae* similis, sed conidiis majoribus, (7–)8–10(–12) × (2–)2.5(–3) µm, discernitur.

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

*Pycnidia* associated with necrotic leaf tissue; pycnidia in culture on pine needle agar subglobose, up to 250 µm diam, somewhat erumpent, with elongated black necks, mostly submerged into tissue; yellow conidial droplets exuding from ostioles; walls consisting of 3–6 layers of medium brown *textura angularis*. *Conidiophores* hyaline, smooth, 1–3-septate, branched, densely aggregated, cylindrical, straight to sinuous, 15–40 × 1.5–2.5 µm. *Conidiogenous cells* phialidic, cylindrical, terminal and lateral, with slight taper towards apex, 0.5–1 µm, with visible periclinal thickening; collarette not flared, 2–5 µm long. *Paraphyses* hyaline, smooth, cylindrical, septate, extending above conidiophores, straight, flexuous, unbranched, or branched below, up to 80 µm long, 2–2.5 µm wide at base. *Alpha conidia* aseptate, hyaline, smooth, fusiform, tapering towards both ends, straight to slightly curved, acutely rounded, and base subtruncate, (7–)8–10(–12) × (2–)2.5(–3) µm. *Gamma conidia* aseptate, hyaline, smooth, ellipsoid-fusoid, apex acutely rounded, base subtruncate to acutely rounded, 7–9 × 4–5 µm. *Beta conidia* developing in older cultures, conidia aseptate, hyaline, smooth, spindle-shaped, apex acutely rounded, base truncate, tapering more prominently in upper third, straight to curved, (14–)19–22(–25) × (1.5–)2 µm.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies on potato-dextrose agar, oatmeal agar and malt extract agar fast growing, with abundant dirty white to cream, fluffy aerial mycelium, and small patches of grey olivaceous due to pycnidial formation.

*Typus*. Australia, Queensland, Brisbane, S 27°28'34.8" E 152°58'40.8" on leaves of *Musa* sp., 14 July 2009, *P.W. Crous & R.G. Shivas*, holotype CBS H-20579, cultures ex-type CPC 17026, 17025 = CBS 129519, ITS sequence GenBank JF951138 and LSU sequence GenBank JF951158, MycoBank MB560160.

Notes — Two *Phomopsis* (teleomorph: *Diaporthe*) species are known from *Musa*, but they have smaller conidia than *D. musigena*, namely *Phomopsis musae* (alpha conidia 5–9 × 1.5–2.5 µm, beta conidia 17–23 × 1 µm, on stems and fruits, France), and *P. musicola* (alpha conidia 5–9 × 2–2.5 µm, Honolulu, Hawaii). *Diaporthe musae*, described from *Musa* in Argentina (Uecker 1988), has no known *Phomopsis* state, and thus cannot be compared to the present collection. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence of *D. musigena* are *Phomopsis longicolla* (FJ755236; Identities = 519/525 (99 %), Gaps = 1/525 (0 %)) and *Diaporthe phaseolorum* (EF488422; Identities = 541/550 (98 %), Gaps = 1/550 (0 %)). The association with *Phomopsis*/*Diaporthe* was confirmed by the LSU sequence.

*Colour illustrations*. *Musa* sp. in Brisbane Botanical Garden; symptomatic leaf; sporulation on potato-dextrose agar; conidiophores giving rise to alpha and beta conidia. Scale bar = 10 µm.

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Pseudocercospora cyathicola

Fungal Planet 74 – 31 May 2011

# ***Pseudocercospora cyathicola*** Crous & R.G. Shivas, *sp. nov.*

*Pseudocercosporae macadamiae* similis, sed conidiis majoribus, (35–)60–80(–90) × (2–)3(–3.5) µm, discernitur.

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

Occurring on dead fronds, associated with a *Mycosphaerella*-like teleomorph. *Mycelium* internal, consisting of smooth, pale brown, septate, branched, 2.5–3 µm diam hyphae. *Stromata* amphigenous on fronds, brown, erumpent, up to 60 µm diam and 40 µm high, giving rise to fascicles of conidiophores. *Conidiophores* subcylindrical, pale to medium brown, smooth, straight to geniculate-sinuous, unbranched, 30–70 × 2–3 µm, 1–3-septate. *Conidiogenous cells* terminal, integrated, pale brown, smooth, proliferating percurrently, scars inconspicuous, on truncate ends, 1.5–2 µm wide. *Conidia* solitary, pale brown, smooth, guttulate, subcylindrical but irregular in width, straight to irregularly curved, hilum truncate, 2 µm wide, neither thickened nor darkened, tapering from the middle of the conidium to an acutely rounded apex, 3–9-septate, (35–)60–80(–90) × (2–)3(–3.5) µm.

Culture characteristics — (in the dark, 25 °C, after 1 mo): Colonies spreading, somewhat erumpent, with moderate aerial mycelium and smooth, lobate margins, reaching 35–45 mm diam. On malt extract agar surface olivaceous grey, with patches of smoke-grey; reverse iron-grey; on potato-dextrose agar surface pale olivaceous grey, margin olivaceous grey, reverse iron-grey; on oatmeal agar surface pale olivaceous grey, margin olivaceous grey.

*Typus*. Australia, Queensland, Brisbane, on fronds of *Cyathea australis*, 14 July 2009, *P.W. Crous & R.G. Shivas*, holotype CBS H-20580, cultures ex-type CPC 17047 = CBS 129520, CPC 17048, ITS sequence GenBank JF951139 and LSU sequence GenBank JF951159, MycoBank MB560163.

Notes — DNA sequence data of the ITS region of *P. cyathicola* is 100 % identical to sequences deposited as *P. macadamiae* in GenBank (EU541884; Identities = 473/473 (100 %), Gaps = 0/473 (0 %)). The LSU sequence confirms its association with *Pseudocercospora*. However, *P. cyathicola* is morphologically different from the latter by having unbranched conidiophores, and conidia that are longer than those of *P. macadamiae* (17–)45–69 × 2–2.5 µm (Beilharz et al. 2003). *Pseudocercospora cyathicola* is distinct from *P. cyatheae* (on *Cyathea* sp., Japan), which has conidiogenous cells with a rim-like thickening at the tip, and cylindrical to obclavate conidia, 30–50 × 3.7–5.5 µm (Nakashima et al. 2006).

*Colour illustrations*. *Cyathea australis* in Brisbane Botanical Garden; conidiophores giving rise to conidia. Scale bar = 10 µm.

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Diaporthe acaciigena

Fungal Planet 75 – 31 May 2011

# ***Diaporthe acaciigena*** Crous, Pascoe & Jacq. Edwards, *sp. nov.*

*Phomopsis amygdali* similis, sed conidiis majoribus, (9–)10–11(–12) × (4–)6–6.5(–7) µm, discernitur.

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

On potato-dextrose agar. *Conidiomata* associated with brown leaf spots, pycnidial, brown, superficial to embedded, solitary to aggregated, opening via a central ostiole, exuding a creamy conidial cirrhus; pycnidia up to 200 µm diam; wall 15–30 µm diam, consisting of several layers of brown *textura angularis*. *Conidiophores* lining the inner layer of the cavity, subcylindrical, hyaline, smooth, reduced to conidiogenous cells, or 1–3-septate, branched, with terminal and lateral conidiogenous cells, 10–30 × 2–3 µm. *Conidiogenous cells* phialidic, hyaline, smooth, subcylindrical, with slight taper towards apex, 10–20 × 1.5–2 µm; apex with visible periclinal thickening and minute, flaring collarette, 1 µm long. *Alpha conidia* hyaline, smooth, granular, aseptate, ellipsoid to subclavate, widest in middle or lower third, apex obtusely rounded, base also obtusely rounded, with visible flat hilum when young, (9–)10–11(–12) × (4–)6–6.5(–7) µm. *Beta conidia* hyaline, smooth, aseptate, guttulate, allantoid, mostly somewhat curved, apex obtuse, base also obtusely rounded to somewhat flattened, 7–8(–10) × (1.5–)2 µm.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies spreading with sparse aerial mycelium, covering the dish in 2 wk; on potato-dextrose agar, surface dirty white to cream, reverse ochreous; on oatmeal agar surface vinaceous-buff; on malt extract agar surface greyish sepia, reverse fuscous-black.

*Typus*. Australia, Victoria, Otway Ranges, Anglesea, S 38°23'21.7" E 144°11'12.7" on leaves of *Acacia retinodes*, 16 Oct. 2009, *P.W. Crous*, *I.G. Pascoe & J. Edwards*, holotype CBS H-20581, cultures ex-type CPC 17622 = CBS 129521, ITS sequence GenBank JF951140 and LSU sequence GenBank JF951160, MycoBank MB560164.

Notes — Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Phomopsis amygdali* (GU133064; Identities = 575/602 (96 %), Gaps = 12/602 (2 %)) and *Diaporthe phaseolorum* (AF001018; Identities = 574/611 (94 %), Gaps = 21/611 (3 %) van Rensburg et al. 2006), from which *P. acaciigena* is clearly distinct based on its larger conidial dimensions. The association with *Phomopsis*/*Diaporthe* was confirmed by the LSU sequence.

*Colour illustrations*. Mixed stand of *Eucalyptus* and *Acacia* in the Grampians; sporulation on sterile pine needle; conidiophores giving rise to alpha and beta conidia. Scale bar = 10 µm.

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Bagadiella victoriae

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# ***Bagadiella victoriae*** Crous, I.J. Porter & Jacq. Edwards, *sp. nov.*

*Bagadiellae lunatae* similis, sed conidiis majoribus, (15–)17–22(–25) × (1–)1.5 µm, discernitur.

*Etymology*. Named after the state of Victoria, Australia, where this fungus was collected.

On potato-dextrose agar. Conidiophores aggregated in brown fascicles on leaves. In culture on potato-dextrose agar, sporulating on conidiophores that occur solitary on hyphae. *Mycelium* consisting of medium brown, smooth, septate, 2–2.5 µm diam hyphae. *Conidiophores* subcylindrical, brown, smooth, straight to gently curved, 1–3-septate, 30–50 × 2–3 µm. *Conidiogenous cells* terminal, integrated, pale to medium brown, smooth, 10–15 × 1.5–2 µm; apex with flared collarette, 1–2 × 2–3 µm. *Conidia* hyaline, smooth, curved, with bluntly rounded apex and truncate base, (15–)17–22(–25) × (1–)1.5 µm.

Culture characteristics — (in the dark, 25 °C, after 1 mo): Colonies spreading, flat, with sparse aerial mycelium, and submerged, feathery margin, reaching 40–60 mm diam; on potato-dextrose agar, surface olivaceous grey with patches of pale olivaceous grey and smoke-grey, reverse iron-grey with patches of smoke-grey; on oatmeal agar surface umber in inner region, with patches of chestnut; on malt extract agar surface ochreous to dirty white, reverse umber.

*Typus*. Australia, Victoria, Main Ridge, 244 Shands Road, Sunny Ridge Strawberry Farm, S 38°24'3.1" E 144°59'36.9" on leaves of *Eucalyptus* sp., 12 Oct. 2009, *P.W. Crous*, *I.J. Porter & J. Edwards*, holotype CBS H-20582, cultures ex-type CPC 17688 = CBS 129522, ITS sequence GenBank JF951141 and LSU sequence GenBank JF951161, MycoBank MB560165.

Notes — Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Bagadiella* sp. CPC 16622 (GQ303270; Identities = 711/713 (99 %), Gaps = 0/713 (0 %)) and *Bagadiella lunata* (GQ303269; Identities = 702/714 (98 %), Gaps = 5/714 (1 %)) (Cheewangkoon et al. 2009). These associations were also supported by the LSU sequence.

*Colour illustrations*. *Eucalyptus* trees at Sunny Ridge Strawberry Farm, Melbourne; conidiogenous cells and conidia. Scale bar = 10 µm.

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Bagadiella koalae

Fungal Planet 77 – 31 May 2011

# ***Bagadiella koalae*** Crous, Pascoe, I.J. Porter & Jacq. Edwards, *sp. nov.*

*Bagadiellae lunatae* similis, sed conidiis majoribus, (15–)17–20 × 1.5–2 µm, discernitur.

*Etymology*. Named after the koala that was observed eating these *Eucalyptus globulus* leaves.

On potato-dextrose agar. Conidiophores aggregated in brown fascicles on leaves. In culture on potato-dextrose agar, sporulating on conidiophores that occur solitary on hyphae. *Mycelium* consisting of medium brown, smooth, septate, 2–2.5 µm diam hyphae. *Conidiophores* subcylindrical, brown, smooth, straight to gently curved, 1–3-septate, 15–30 × 3–4 µm. *Conidiogenous cells* terminal, integrated, pale to medium brown, smooth, 7–15 × 2–3 µm; apex with flared collarette, 1–2 × 2–3 µm. *Conidia* hyaline, smooth, curved, with bluntly rounded apex and truncate base, (15–)17–20 × 1.5–2 µm.

Culture characteristics — (in the dark, 25 °C, after 1 mo): Colonies spreading, flat, with sparse aerial mycelium, and submerged, feathery margin, reaching 35–60 mm diam; on potato-dextrose agar, surface grey olivaceous, reverse olivaceous grey; on oatmeal agar surface umber with patches of peach; on malt extract agar surface ochreous, reverse umber.

*Typus*. Australia, Victoria, Otway Ranges, Kennett River, Great Ocean Road, on leaves of *Eucalyptus globulus* eaten by koala, 18 Oct. 2009, *P.W. Crous*, *I.G. Pascoe, I.J. Porter & J. Edwards*, holotype CBS H-20583, cultures ex-type CPC 17682 = CBS 129523, ITS sequence GenBank JF951142 and LSU sequence GenBank JF951162, MycoBank MB560166.

Notes — Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Bagadiella* sp. CPC 16622 (GQ303270; Identities = 706/713 (99 %), Gaps = 4/713 (1 %)) and *Bagadiella lunata* (GQ303269; Identities = 702/707 (99 %), Gaps = 1/707 (0 %)) (Cheewangkoon et al. 2009). These associations were also supported by the LSU sequence. *Bagadiella victoriae* is distinct on its ITS sequence (Identities = 705/712 (99 %), Gaps = 4/712 (1 %)) and LSU sequence (Identities = 918/922 (99 %), Gaps = 0/922 (0 %)).

*Colour illustrations*. Koala at Kennett River, eating leaves of *Eucalyptus globulus* from which *B. koalae* was isolated; conidiogenous cells and conidia. Scale bar = 10 µm.

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Mycosphaerella wachendorfiae

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# *Mycosphaerella wachendorfiae* Crous, *sp. nov.*

Ascis fasciculatis, obovoidibus, bitunicatis, octosporis, 40–60 × 12–20 µm. Ascosporis hyalinis, levibus, fusoidibus-ellipsoideis, (15–)18–20(–22) × (4–)5(–6) µm.

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

*Leaf spots* dark brown, amphigenous, starting as specks or irregular spots with diffuse margins, developing into linear lesions that run along the side of the leaf, and cause tip die-back, with distinct brown margins. *Ascomata* up to 130 µm diam, amphigenous, brown, subepidermal, globose, with central ostiole, up to 30 µm wide. *Asci* fasciculate, obovoid, bitunicate, incurved, 8-spored, 40–60 × 12–20 µm, with apical chamber, 2 µm diam, and multi-layered endotunica; remnants of hamathecial tissue remaining among asci. *Ascospores* hyaline, smooth, fusoid-ellipsoidal, guttulate, tapering towards both ends, widest in middle of apical cell, constricted at septum, (15–)18–20(–22) × (4–)5(–6) µm; ascospores germinating from both ends, with germ tubes parallel to the long axis; spores prominently distorting, becoming up to 10 µm wide, but remaining hyaline, smooth. *Mycelium* consisting of smooth, septate, branched, 2–4 µm diam hyphae, frequently covered in a wide mucoid sheath, up to 5 µm diam. *Anamorph* only observed on malt extract agar. *Conidiophores* reduced to *conidiogenous cells* or a single supporting cell, subcylindrical, straight or flexuous, 2–20 × 3–5 µm, hyaline, but eventually becoming brown and somewhat warty, with several percurrent proliferations at the apex, solitary, though they appear to become aggregated in sporodochia as well. *Conidia* solitary, subcylindrical to fusoid-ellipsoidal, with obtusely rounded apex, and truncate base with marginal frill, guttulate, thick-walled, smooth, hyaline, straight to slightly curved, (12–)13–16(–20) × (3.5–)4(–4.5) µm.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies slow growing, erumpent, with sparse aerial mycelium, folded surface, and lobed, feathery margin, reaching 6 mm diam; on malt extract agar surface olivaceous grey with patches of dirty white, reverse sienna; on oatmeal agar surface sienna; on potato-dextrose agar surface olivaceous grey with patches of saffron and dirty white, reverse saffron with patches of smoke-grey.

*Typus*. South Africa, Western Cape Province, Hermanus, Fernkloof Nature Reserve, S 34°23'38" E 19°16'9.7", on leaves of *Wachendorfia thyrsifolia*, 2 May 2010, *K.L. Crous & P.W. Crous*, holotype CBS H-20584, cultures ex-type CPC 18338 = CBS 129579, ITS sequence GenBank JF951143 and LSU sequence GenBank JF951163, MycoBank MB560167.

Notes — The anamorph observed in culture is quite unique for *Mycosphaerella*, and appears to represent a hyaline form of the genus *Colletogloeopsis* (Crous & Wingfield 1997), which has since been reduced to synonymy with *Teratosphaeria* (Crous et al. 2007a, b, 2009b, c). The anamorph would be best placed in the genus *Ahmadia* (Sutton 1980), though no sequence data of any other members of *Ahmadia* are presently available for any possible comparisons.

*Mycosphaerella wachendorfiae* represents the first *Mycosphaerella*-like fungus known from this host, other than *Ramularia miae* (Crous & Groenewald 2006). Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Mycosphaerella rosigena* (GU214632; Identities = 489/529 (92 %), Gaps = 18/529 (3 %)) and *Mycosphaerella madeirae* (DQ302976; Identities = 458/496 (92 %), Gaps = 16/496 (3 %)). A similar search using the LSU sequence yields high similarity to *Pseudocercospora eispermogonia* (DQ204758; Identities = 869/879 (99 %), Gaps = 0/879 (0 %)), *Mycosphaerella marksii* (GU214447; Identities = 868/879 (99 %), Gaps = 0/879 (0 %)), *Mycosphaerella intermedia* (DQ246248; Identities = 867/879 (99 %), Gaps = 0/879 (0 %)) and *Mycosphaerella rosigena* (EU167587; Identities = 819/831 (99 %), Gaps = 2/831 (0 %)).

*Colour illustrations*. *Wachendorfia thyrsifolia* at Fernkloof Nature Reserve; symptomatic leaf; asci, germinating and ungerminated ascospores; mycelium with conidiogenous cells and conidia. Scale bars = 10 µm.

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Passalora leptophlebiae

Fungal Planet 79 – 31 May 2011

# ***Passalora leptophlebiae*** Crous, Alfenas, R. Alfenas & O.L. Pereira, *sp. nov.*

*Passalorae eucalypti* similis, sed conidiis minoribus, (15–)18–22(–27) × 3(–3.5) µm, discernitur.

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

*Leaf spots* amphigenous, subcircular to irregular or angular, 1–6 mm diam, confined by leaf veins, medium brown, with raised border and red-purple margin, becoming confluent; sporulation amphigenous. *Conidiophores* arising from stomata situated on brown stromata up to 100 µm diam, giving rise to densely aggregated, brown, finely verruculose conidiophores that are straight to geniculate-sinuous, 20–50 × 3–4.5 µm, 1–3-septate. *Conidiogenous cells* 15–30 × 3–3.5 µm, integrated, terminal, apex obtuse, brown to medium brown, finely verruculose, with many, densely aggregated, terminal and lateral loci; scars dark brown, thickened, refractive, 1 µm diam. *Conidia* solitary, rarely in branched chains, pale brown, smooth, guttulate, subcylindrical to narrowly obclavate, base obconically truncate, apex subobtuse, (15–)18–22(–27) × 3(–3.5) µm, 1–3-septate; hila thickened, darkened, refractive, 1 µm diam.

Culture characteristics — (in the dark, 25 °C, after 1 mo): On malt extract agar colonies erumpent, spreading, with moderate aerial mycelium; surface folded, with even, lobed margins, reaching 15 mm diam; surface smoke-grey in centre, with patches of pale olivaceous grey and olivaceous grey; iron-grey in reverse.

*Typus*. Brazil, Minas Gerais, Viçosa, University Forestry Nursery, on leaves of *Eucalyptus leptophlebia*, 23 Aug. 2010, *P.W. Crous, A.C. Alfenas, R. Alfenas & O.L. Pereira*, holotype CBS H-20585, cultures ex-type CPC 18480 = CBS 129524, ITS sequence GenBank JF951144 and LSU sequence GenBank JF951164, MycoBank MB560168.

Notes — Leaf spots associated with two cercosporoid species. A *Cercospora* sp. (not treated here) is distinguished from *Passalora leptophlebiae* by having less dense fascicles, wider and longer conidiophores, scars up to 2 µm wide, and hyaline conidia. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are '*Passalora*' *eucalypti* (AF309617; Identities = 503/507 (99 %), Gaps = 1/507 (0 %)), *Penidiella tasmaniensis* (AF173307; Identities = 503/507 (99 %), Gaps = 1/507 (0 %)), *Passalora saururi* (AF222836; Identities = 484/497 (97 %), Gaps = 5/497 (1 %)) and *Pseudocercospora humuli* (GU214676; Identities = 587/625 (94 %), Gaps = 21/625 (3 %)). The megablast search using the LSU sequence had as closest hits '*Passalora*' *eucalypti* (GU214458; Identities = 931/933 (99 %), Gaps = 0/933 (0 %)) and *Pseudocercospora* spp. (typically with Identities = 915/934 (98 %), Gaps = 2/934 (0 %)). Morphologically *Passalora leptophlebiae* is most similar to two other species occurring on *Eucalyptus*, namely *P. eucalypti* (conidia 14–40 × (1.5–)2–2.5 µm; Crous 1998), and *Penidiella tasmaniensis* (conidia 4–20 × 2–2.5 µm; Crous et al. 1998, 2009c), but is distinct based on its conidial dimensions (15–)18–22(–27) × 3(–3.5) µm.

*Colour illustrations*. *Eucalyptus leptophlebia* seedling at Viçosa University Forestry Nursery; leaf spots; fascicle of conidiophores and conidia. Scale bars = 10 µm.

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Rachicladosporium pini

Fungal Planet 80 – 31 May 2011

# ***Rachicladosporium pini*** Crous & Quaedvlieg, *sp. nov.*

*Rachicladosporii luculiae* simile, sed ramoconidiis majoribus, 15–22 × 3–4 µm, discernitur.

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

On oatmeal agar. *Mycelium* consisting of smooth, septate, branched, 2–3 µm wide hyphae. *Conidiophores* erect, brown, smooth, cylindrical, thick-walled, unbranched or branched once, 2- to multiseptate, 25–130 × 3–4 µm. *Conidiogenous cells* terminal, 5–12 × 3–4 µm, brown, smooth, proliferating sympodially, subcylindrical or clavate, with one to several aggregated, flattened, somewhat thickened and darkened scars, 1–2 µm diam. *Primary ramoconidia* brown, smooth, thick-walled, subcylindrical, 0–1-septate, 15–22 × 3–4 µm. *Secondary ramoconidia* fusoid-ellipsoidal, 9–15 × 2.5–3 µm, smooth, brown, with 1–3 terminal scars, 1 µm diam. *Intercalary conidia* in short, branched chains of up to 4, brown, smooth, fusoid-ellipsoidal, 8–11 × 2–2.5(–3) µm. *Terminal conidia* medium brown to brown, smooth, fusoid-ellipsoidal, (5–)6–7(–8) × 2–2.5(–3) µm; scars flattened, somewhat thickened and darkened, 0.5–1 µm diam.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies spreading, erumpent with sparse aerial mycelium, folded surface and lobed margin, reaching 15 mm diam. On oatmeal agar olivaceous grey; on potato-dextrose agar iron-grey with excessive slime production, iron-grey in reverse; on malt extract agar surface olivaceous grey, reverse iron-grey.

*Typus*. Netherlands, Hilversum, Pinetum Blijdenstein, on needles of *Pinus monophylla*, 19 June 2009, *W. Quaedvlieg*, holotype CBS H-20586, cultures ex-type CPC 16770 = CBS 129525, ITS sequence GenBank JF951145 and LSU sequence GenBank JF951165, MycoBank MB560169.

Notes — Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Rachicladosporium luculiae* (EU040237; Identities = 536/557 (96 %), Gaps = 12/557 (2 %)) and *Rachicladosporium cboliae* (GU214650; Identities = 627/657 (95 %), Gaps = 12/657 (2 %)). These associations were supported by the LSU sequence. Morphologically, *R. pini* is very similar to *R. luculiae* and *R. cboliae* (Crous et al. 2007b, 2009b), but can be distinguished based on its larger ramoconidia.

*Colour illustrations*. *Pinus monophylla* tree at the Pinetum Blijdenstein in Hilversum; conidiophores giving rise to chains of conidia. Scale bars = 10 µm.

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Diaporthe rhusicola

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# ***Diaporthe rhusicola*** Crous, *sp. nov.*

*Diaporthis neotheicolae* similis, sed conidiis majoribus, (7–)8–9(–10) × 3(–3.5) µm, discernitur.

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

*Leaf spots* brown, amphigenous, subcircular, up to 1 cm diam, similar to those associated with *Muribasidiospora indica* on this host (Crous et al. 2003), except that in the latter they tend to be red to red-purple in colour. *Pycnidia* formed readily on potato-dextrose agar (PDA), oatmeal agar (OA) and malt extract agar (MEA); erumpent, flattened, black, multilocular, up to 600 µm diam. *Conidiophores* on PDA lining the inner cavity, hyaline, smooth, 1–3-septate, subcylindrical, unbranched or branched (below or above), 20–40 × 2–3 µm. *Conidiogenous cells* terminal, hyaline, smooth, subcylindrical, 15–25 × 2–3 µm, tapering somewhat towards a truncate apex, 1–1.5 µm, with a flaring collarette, up to 5 µm wide and long. *Paraphyses* intermingled among conidiophores, hyaline, smooth, subcylindrical, branched or not, up to 80 µm long, 2–3 µm wide. *Conidia* (7–)8–9(–10) × 3(–3.5) µm, solitary, hyaline, smooth, guttulate, subcylindrical to fusoid-ellipsoidal, apex obtuse, widest in middle, tapering to a truncate base, 1 µm diam.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies spreading, with moderate to fluffy aerial mycelium and feathery margins, covering the dish in 2 wk; on MEA surface dirty white, reverse dirty white with patches of iron-grey; on OA iron-grey in centre, with patches of olivaceous grey and pale olivaceous grey; on PDA olivaceous grey in centre, with dirty white outer region, forming a diffuse yellow pigment in agar.

*Typus*. South Africa, Western Cape Province, Cape Town, Kirstenbosch Botanical Garden, on leaves of *Rhus pendulina* (White Karee), 8 May 2010, *P.W. Crous*, holotype CBS H-20589, cultures ex-type CPC 18191 = CBS 129528, ITS sequence GenBank JF951146 and LSU sequence GenBank JF951166, MycoBank MB560170.

Notes — Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Phomopsis* sp. BLE12 (FN868477; Identities = 574/574 (100 %), Gaps = 0/574 (0 %)), *Phomopsis* sp. FE 86 (FJ440699; Identities = 537/537 (100 %), Gaps = 0/537 (0 %)), *Phomopsis* sp. 1 (AY485723; Identities = 514/517 (99 %), Gaps = 1/517 (0 %)) and *Diaporthe neotheicola* (anamorph: *Phomopsis theicola*) (DQ286286; Identities = 519/523 (99 %), Gaps = 2/523 (0 %)) (Santos & Phillips 2009). As far as we could establish, this is the first association of *Diaporthe* with a leaf spot disease on *Rhus pendulina.*

*Colour illustrations*. Leaf symptoms on *Rhus pendulina* in Kirstenbosch Botanical Garden; conidiophores giving rise to conidia. Scale bars = 10 µm.

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Sclerostagonospora cycadis

Fungal Planet 82 – 31 May 2011

# ***Sclerostagonospora cycadis*** Crous & G. Okada, *sp. nov.*

*Sclerostagonosporae leucadendri* similis, sed conidiis minoribus, (6–)7–10(–13) × 3–4(–4.5) µm.

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

On oatmeal agar. *Conidiomata* pycnidial, globose, solitary, brown, 60–300 µm diam, opening mostly by means of a single, central ostiole, up to 30 µm diam, lined with hyaline, 0–1-septate periphyses, 2–2.5 µm wide; wall consisting of 2–3 layers of brown *textura angularis*. *Conidiophores* reduced to annellides. *Conidiogenous cells* ampulliform to subcylindrical, 3–6 × 3–5 µm, hyaline, smooth, becoming brown, with 1–3 apical, percurrent proliferations. *Paraphyses* interspersed among conidiogenous cells, 0–3-septate, simple or branched, hyaline, 10–30 × 2–2.5 µm. *Conidia* ellipsoid to subcylindrical (apex obtuse, base truncate), smooth, medium brown, (0–)1–3-septate, becoming constricted at septa with age, (6–)7–10(–13) × 3–4(–4.5) µm.

Culture characteristics — (in the dark, 25 °C, after 1 mo): *Colonies* on potato-dextrose agar and oatmeal agar spreading, reaching 40–50 mm diam, with sparse aerial mycelium, smooth, with catenulate margins; surface buff to honey with patches of mouse-grey; reverse honey with patches of mouse-grey.

*Typus*. Japan, Umihotaru Parking Area, Tokyo Bay Aqualine highway, on living leaves of *Cycas revoluta*, 22 Oct. 2005, *P.W. Crous & G. Okada,* holotype CBS H-20161, culture ex-type CPC 12388 = CBS 123538, ITS sequence GenBank FJ372393 and LSU sequence GenBank FJ372410, MycoBank MB560171.

Notes — The present fungus is placed in *Sclerostagonospora* due to the presence of pycnidia, conidiogenous cells with percurrent proliferations, and pigmented conidia. The anamorph genus *Sclerostagonospora* has been linked to *Leptosphaeria* (Crous & Palm 1999, Crous et al. 2004) and *Montagnula* (Huhndorf 1992), and is paraphyletic.

Presently nine species of *Sclerostagonospora* are listed in *Index Fungorum*, none of which occur on *Zamiaceae*, or resemble *S. cycadis* in morphology. BLASTn results of the ITS sequence revealed an identity of 99 % with *Sclerostagonospora* sp. (GenBank accession DQ286767; Identities = 532/538 (99 %), Gaps = 3/538 (1 %)) and *Sclerostagonospora opuntiae* (GenBank accession DQ286768; Identities = 531/538 (99 %), Gaps = 3/538 (1 %)). The LSU sequence has 99 % identity to the latter two GenBank sequences as well as sequences of *Phaeosphaeria* species. *Sclerostagonospora cycadis* is morphologically similar to *Hendersonia togniniana,* which was described from *Cycas revoluta* plants cultivated in a botanical garden in Italy. Conidia of the latter, however, are brown, oblong-ellipsoidal, 3-septate, 10–12 × 6–7 µm, thus being wider than that of the present species (Saccardo 1899).

*Colour illustrations*. *Cycas revoluta* growing at Sakae-cho, Asaka, Saitama; colony on oatmeal agar; conidiogenous cells and conidia. Scale bar = 10 µm.

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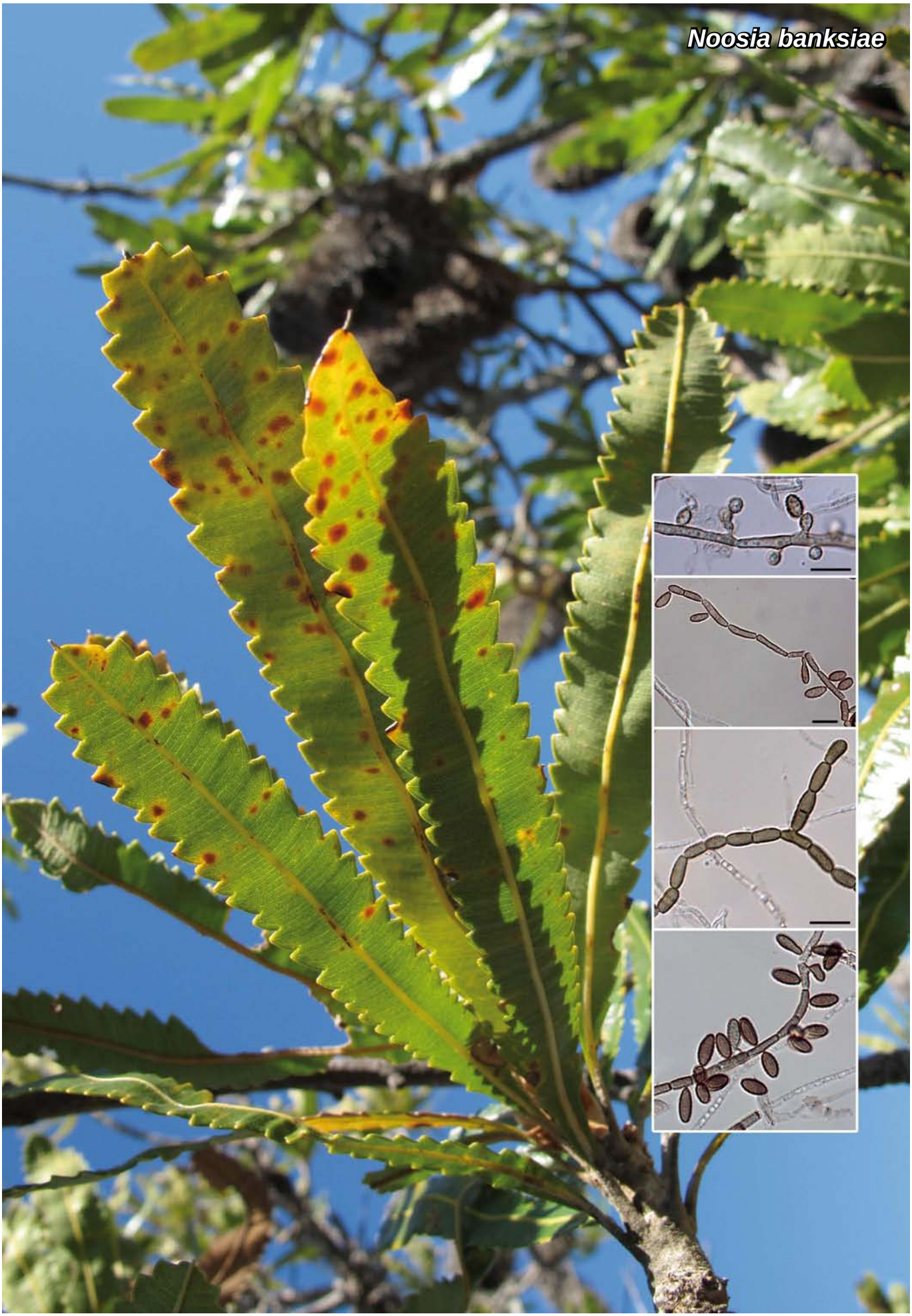
Noosia banksiae

Fungal Planet 83 – 31 May 2011

## ***Noosia*** Crous, R.G. Shivas & McTaggart, *gen. nov.*

Conidiophoris ad cellulas conidiogenas reductis, solitariis, lateralibus vel integratis, inconspicuis, lateralibus vel terminalibus, poris minutis, verruciformibus, 0.5 µm diam, conidiis solitariis vel in catenis brevibus efferentibus. Conidiis dimorphis; conidiis primariis aseptatis, primo globosis, subhyalinis, levibus, deinde fusoidibus-ellipsoideis, brunneis, verruculosis, solitariis vel in catenis brevibus; conidiis secundariis (phragmoconidiis) ex cellulis hypharum disarticulantium formantibus, brunnescentibus et verruculosis.

*Etymology*. Named after the town Noosa, in Queensland (Australia), where this fungus was collected.

Associated with leaf spots. *Mycelium* consisting of hyaline, smooth, branched, 2–5 µm diam hyphae, becoming brown and verruculose with age, frequently aggregating in hyphal strands of up to 20. *Conidiophores* reduced to conidiogenous cells that are solitary, lateral, or integrated, inconspicuous, lateral and terminal, with small, pimple-like pores of up to 0.5 µm diam, giving rise to conidia that can be solitary or in short chains of up to 5. *Conidia* dimorphic; primary conidia aseptate, initially globose, subhyaline, smooth, becoming fusoid-ellipsoidal, brown, verruculose, solitary or in short, branched chains; apex obtuse, base truncate with minute, unthickened pore; secondary conidia arising as phragmoconidia from disarticulating hyphal cells that become brown and verruculose.

*Type species*. *Noosia banksiae.*
MycoBank MB560172.

## ***Noosia banksiae*** Crous, R.G. Shivas & McTaggart, *sp. nov.*

Conidiophoris ad cellulas conidiogenas reductis, solitariis, lateralibus vel integratis, inconspicuis, lateralibus vel terminalibus, poris minutis, apiculatoidibus, 0.5 µm diam, conidiis solitariis vel in catenis brevibus (ad 5) efferentibus. Conidiis dimorphis; conidiis primariis aseptatis, primo globosis, subhyalinis, levibus, deinde fusoidibus-ellipsoideis, brunneis, verruculosis, solitariis vel in catenis brevibus, ramosis, (4–)7–10(–13) × (3.5–)4(–5) µm; conidiis secundariis (phragmoconidiis) ex cellulis hypharum disarticulantium formantibus, brunnescentibus et verruculosis, 5–15 × 4–5 µm.

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

Immersed *mycelium* on potato-dextrose agar consisting of hyaline, smooth, up to 5 µm diam hyphae; aerial mycelium consisting of hyphae that are smooth, branched, septate, hyaline, 2–3 µm diam; hyphae become brown and verruculose with age, frequently aggregating in hyphal strands of up to 20. *Conidiophores* reduced to conidiogenous cells that are solitary, lateral, or integrated, inconspicuous, lateral and terminal, with small, pimple-like pores of up to 0.5 µm diam, giving rise to conidia that can be solitary or in short chains of up to 5. *Conidia* dimorphic; primary conidia aseptate, initially globose, subhyaline, smooth, becoming fusoid-ellipsoidal, brown, verruculose, solitary or in short, branched chains, (4–)7–10(–13) × (3.5–)4(–5) µm; apex obtuse, base truncate with minute, unthickened pore; secondary conidia arising as phragmoconidia from disarticulating hyphal cells that become brown, verruculose, 5–15 × 4–5 µm; secondary conidia in short chains when young, but forming directly on conidiogenous cells that can be reduced to loci on hyphae when mature.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies spreading, erumpent, with sparse to moderate aerial mycelium and lobate margins, reaching 30 mm diam; on malt extract agar smoke-grey, reverse grey olivaceous with dirty white outer margin; on oatmeal agar olivaceous grey in centre, dirty white in outer region; on potato-dextrose agar isabelline on surface and reverse.

*Colour illustrations*. Leaf spots on *Banksia aemula* in Noosa National Park; hyphae giving rise to short chains of conidia, or breaking up into phragmospores. Scale bars = 10 µm.

*Typus*. Australia, Queensland, Noosa, S 26°34'14.0" E 153°4'21.6", on leaves of *Banksia aemula*, 13 July 2009, *P.W. Crous, R.G. Shivas & A.R. McTaggart*, holotype CBS H-20587, culture ex-type CPC 17282 = CBS 129526, ITS sequence GenBank JF951147 and LSU sequence GenBank JF951167, MycoBank MB560173.

Notes — Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are species of *Periconia*, albeit with poor coverage across the sequence length. A similar search using the LSU sequence gives as closest hits *Sporidesmium tengii* (DQ408559; Identities = 847/856 (99 %), Gaps = 1/856 (0 %)), *Massarina igniaria* (DQ810223; Identities = 825/845 (98 %), Gaps = 2/845 (0 %)), *Byssothecium circinans* (AY016357; Identities = 863/895 (96 %), Gaps = 12/895 (1 %)) and *Corynespora smithii* (GU323201; Identities = 856/890 (96 %), Gaps = 5/890 (1 %)). *Noosia* has some resemblance to the genera *Conioscypha* (it forms similar strange phialides in vitro, but never in vivo), *Trichobotrys* (but setae lacking, and supporting cells lacking at maturity), and *Periconiella* s.l., which is also a generic complex (Seifert et al. 2011). Based on the fact that the present fungus is distinct from those presently known, and that the DNA sequence could not be matched with any currently deposited in GenBank, a new genus is herewith introduced to accommodate it.

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Devriesia queenslandica

Fungal Planet 84 – 31 May 2011

# ***Devriesia queenslandica*** Crous, R.G. Shivas & McTaggart, *sp. nov.*

*Devriesiae lagerstroemiae* similis, sed ramoconidiis majoribus, 10–20 × 2–3 µm, discernitur.

*Etymology*. Named after the state of Queensland, Australia, where this fungus was collected.

*Mycelium* consisting of smooth, pale brown, septate, 2–3 µm diam hyphae. *Conidiophores* erect, subcylindrical, pale brown, smooth, straight to somewhat flexuous, unbranched, reduced to conidiogenous cells or up to 3-septate, 5–45 × 3–4 µm. *Conidiogenous cells* terminal, integrated, subcylindrical, smooth, pale brown, proliferating sympodially, 5–15 × 2.5–4 µm; scars flattened, thickened, somewhat darkened, 0.5–1.5 µm diam. *Primary ramoconidia* 0(–1)-septate, guttulate, subclindrical, smooth, pale brown, 10–20 × 2–3 µm. *Secondary ramoconidia* 0(–1)-septate, guttulate, subcylindrical, smooth, pale brown, 10–20 × 2–3 µm, frequently with lateral branch at apex, up to 10 µm long; hila somewhat thickened and darkened, 1–1.5 µm diam. *Intercalary conidia* subcylindrical to somewhat fusoid-ellipsoidal, pale brown, smooth, guttulate, 9–12 × 2–2.5 µm. *Terminal conidia* subcylindrical to fusoid-ellipsoidal, pale brown, smooth, guttulate, (5–)7–9(–11) × 2–2.5 µm; hila flattened, somewhat thickened and darkened, 0.5–1 µm diam. *Chlamydospores* thick-walled, brown, globose, in intercalary chains, up to 20 µm diam.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies spreading, erumpent, with even, lobate margins and moderate aerial mycelium, reaching 10 mm diam after 2 wk; on malt extract agar pale olivaceous grey in centre, olivaceous grey in outer region, iron-grey in reverse; on oatmeal agar olivaceous grey; on potato-dextrose agar olivaceous grey in centre, iron-grey in outer region and underneath.

*Typus*. Australia, Queensland, Daintree, S 16°02'19.8" E 145°27'39.1", on leaves of *Scaevola taccada*, 8 Aug. 2009, *P.W. Crous, R.G. Shivas & A.R. McTaggart*, holotype CBS H-20588, culture ex-type CPC 17306 = CBS 129527, ITS sequence GenBank JF951148 and LSU sequence GenBank JF951168, MycoBank MB560174.

Notes — *Devriesia queenslandica* was isolated from prominent leaf spots on *Scaevola taccada* caused by *Zasmidium scaevolicola* (Shivas et al. 2010), and appears to be a secondary coloniser of these leaf spots, though nothing is known about its potential status as a plant pathogen. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are cf. *Passalora* sp. CPC 11876 (GU214642; Identities = 579/589 (98 %), Gaps = 5/589 (1 %)), *Devriesia lagerstroemiae* (GU214634; Identities = 543/586 (93 %), Gaps = 22/586 (4 %)) and *Devriesia hilliana* (GU214633; Identities = 550/600 (92 %), Gaps = 27/600 (5 %)). Based on morphology, *D. queenslandica* can be distinguished from *D. lagerstroemiae* and *D. hilliana* by its conidial dimensions (Crous et al. 2009b).

*Colour illustrations*. *Scaevola taccada* at Cape Tribulation, northern Queensland, leaves with spots caused by *Zasmidium scaevolicola*; conidiophores with conidiogenous cells giving rise to chains of conidia. Scale bars = 10 µm.

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Teratosphaeria mareebensis

Fungal Planet 85 – 31 May 2011

# ***Teratosphaeria mareebensis*** Crous & R.G. Shivas, *sp. nov.*

*Teratosphaeriae considenianae* similis, sed conidiis minoribus, (5–)7–8(–9) × (2–)2.5–3(–4) µm, discernitur.

*Etymology*. Named after the town of Mareeba, where this fungus was collected.

*Mycelium* consisting of smooth, medium brown, septate, 2–3 µm diam hyphae; hyphal cells becoming shorter (4–7 µm long) in specific areas, becoming fertile and developing conidiogenous cells that form slimy conidial masses. *Conidiophores* reduced to conidiogenous cells that are integrated in hyphae as inconspicuous phialidic loci, 1–2 µm diam, with 1–2 loci per conidiogenous cell; collarette absent. *Conidia* medium brown, smooth, fusoid-ellipsoidal, widest in middle, apex obtuse, base somewhat flattened, (5–)7–8(–9) × (2–)2.5–3(–4) µm, on potato-dextrose agar conidial ends develop a darkened, thickened region, though this is not observed in sporulating colonies on oatmeal agar.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies spreading, erumpent; surface irregular with moderate aerial mycelium, and even, lobed margin, reaching 15 mm diam after 2 wk; on malt extract agar surface olivaceous grey, outer region iron-grey, and iron-grey in reverse; on oatmeal agar surface olivaceous grey; on potato-dextrose agar surface olivaceous grey, iron-grey in outer region and reverse.

*Typus*. Australia, Queensland, Cairns, Mareeba, S 16°58.755' E 145° 20.608', on leaves of *Eucalyptus alba*, 10 Aug. 2009, *P.W. Crous & R.G. Shivas*, holotype CBS H-20590, culture ex-type CPC 17272 = CBS 129529, ITS sequence GenBank JF951149 and LSU sequence GenBank JF951169, MycoBank MB560175.

Notes — Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Teratosphaeria considenianae* (GQ852791; Identities = 512/524 (98 %), Gaps = 2/524 (0 %)), and *T. miniata* (GQ852803; Identities = 507/520 (98 %), Gaps = 3/520 (1 %)). A similar search using the LSU sequences yielded high identity with *T. hortaea* (FJ790299; Identities = 851/854 (99 %), Gaps = 0/854 (0 %)), *T. complicata* (GQ852714; Identities = 842/845 (99 %), Gaps = 0/845 (0 %)) and *T. brunneotingens* (EU019286; Identities = 907/911 (99 %), Gaps = 0/911 (0 %)). Morphologically *T. mareebensis* can be distinguished from *T. considenianae* by its smaller conidia (Summerell et al. 2006, Crous et al. 2009b, c), and the fact that conidia of the latter do not have darkened, thickened ends as in *T. mareebensis*.

*Colour illustrations*. *Eucalyptus* sp. growing at the DPI research farm near Mareeba; hyphae with conidiogenous cells giving rise to conidia. Scale bars = 10 µm.

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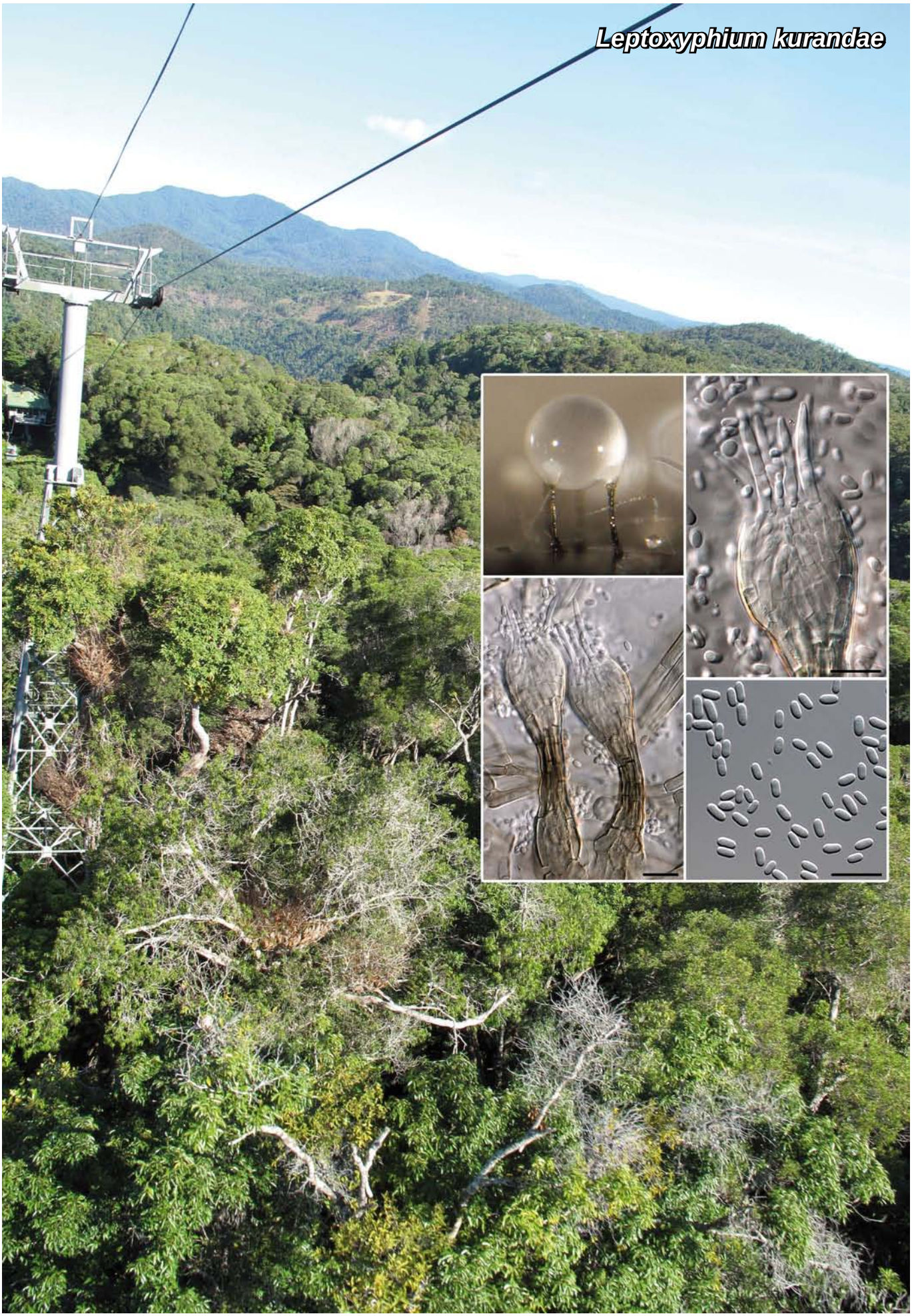
Leptoxyphium kurandae

Fungal Planet 86 – 31 May 2011

# ***Leptoxyphium kurandae*** Crous & R.G. Shivas, *sp. nov.*

*Leptoxyphii madagascariensis* simile, sed conidiis majoribus, (4–)6–7(–9) × 2–3 µm, discernitur.

*Etymology*. Named after the town of Kuranda, where this fungus was collected.

*Mycelium* consisting of medium, grey-brown hyphae, 5–9 µm diam, septate, branched, constricted at septa, forming hyphal ropes, thick-walled, finely verruculose, frequently encased in mucoid sheath. *Conidiomata* synnematous, separate or in clusters of 2–3, erect, straight to slightly flexuous; bulbous base brown, 30–50 × 25–35 µm; cylindrical part dark olivaceous-brown, 60–100 × 12–15 µm, hyphal apex 30–50 × 25–40 µm, loose apical hyphae flaring, 20–35 × 2.5–3 µm. *Conidiophores* subcylindrical to subulate, 0–2-septate, 15–25 × 2–3 µm, tightly aggregated in apical part of synnema, among synnematous hyphae that diverge close to apex. *Conidiogenous cells* integrated, terminal, phialidic, 7–10 × 2–2.5 µm, tapering to a truncate apex, with periclinal thickening and visible collarette. *Conidia* broadly ellipsoid with rounded ends, aseptate, eguttulate, hyaline, smooth, (4–)6–7(–9) × 2–3 µm, aggregating in hyaline, slimy masses at apex of synnemata.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies spreading, erumpent, with sparse to moderate aerial mycelium and even margins, reaching 30 mm diam after 2 wk; on malt extract agar surface olivaceous grey, outer region umber, and iron-grey in reverse; on oatmeal agar surface iron-grey; on potato-dextrose agar surface olivaceous grey, grey olivaceous in outer region and reverse.

*Typus*. Australia, Queensland, Cairns, Kuranda, S 16°49'24.6", E 145° 38'2.6", on leaves of *Eucalyptus* sp., 13 Aug. 2009, *P.W. Crous & R.G. Shivas*, holotype CBS H-20591, culture ex-type CPC 17274 = CBS 129530, ITS sequence GenBank JF951150 and LSU sequence GenBank JF951170, MycoBank MB560176.

Notes — Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Leptoxyphium* sp. TMS-2011 (HQ631026; Identities = 574/576 (99 %), Gaps = 0/576 (0 %)), *Leptoxyphium madagascariense* (GQ303277; Identities = 617/628 (98 %), Gaps = 2/628 (0 %)) and *Polychaeton citri* (GU214649; Identities = 656/704 (93 %), Gaps = 23/704 (3 %)). A similar search using the LSU sequence yielded the closest hits to be *Microxyphium citri* (AY004337; Identities = 914/914 (100 %), Gaps = 0/914 (0 %)) and *Leptoxyphium fumago* (GU214430; Identities = 878/882 (99 %), Gaps = 2/882 (0 %)). Morphologically *L. kurandae* can be distinguished from *L. madagascariense*, by its larger conidia (Cheewangkoon et al. 2009).

*Colour illustrations*. *Eucalyptus* and other rainforest trees viewed from the cable car at Kuranda; conidiophores sporulating on agar; synnematous conidiophores with hyphal apices and conidia. Scale bars = 10 µm.

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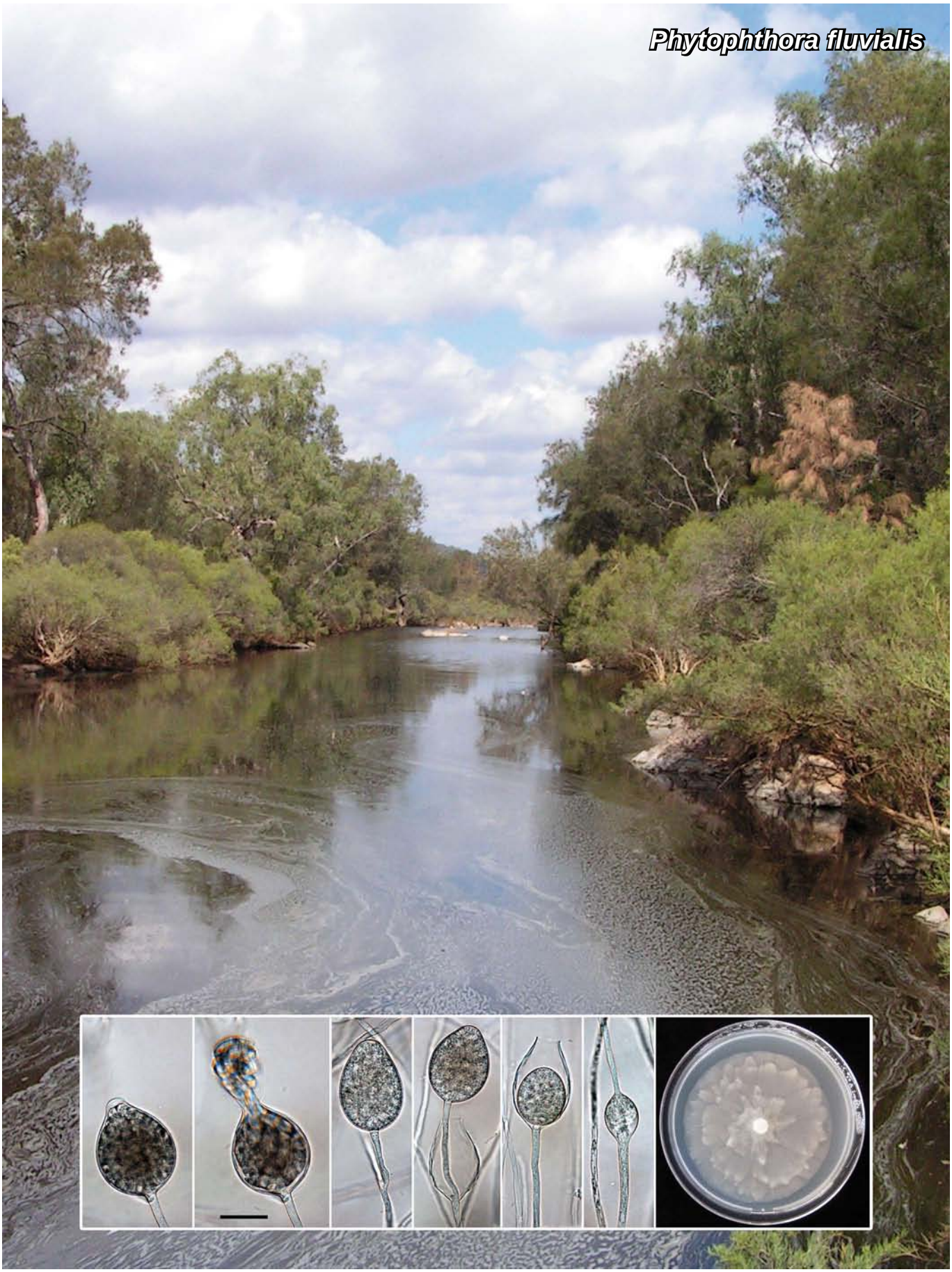

Phytophthora fluvialis

Fungal Planet 87 – 31 May 2011

# ***Phytophthora fluvialis*** T. Jung & T.I. Burgess, *sp. nov.*

*Phytophthorae litoralis* similis, sed inflationibus hypharum non catenulatis et sine hyphis radiatis, sporangiis in medio maioribus (53 × 36.4 µm), chlamydosporis nullis et caelis optimis (31.5 °C) et maximis (37.5 °C) altioribus. Regiones 'rDNA ITS', 'LSU', '*cox*1' et 'HSP' cum sequentibus unicis (GenBank JF701436, JF951171, JF701442, JF701439).

*Etymology.* Named for the riparian ecosystems from which all isolates were recovered.

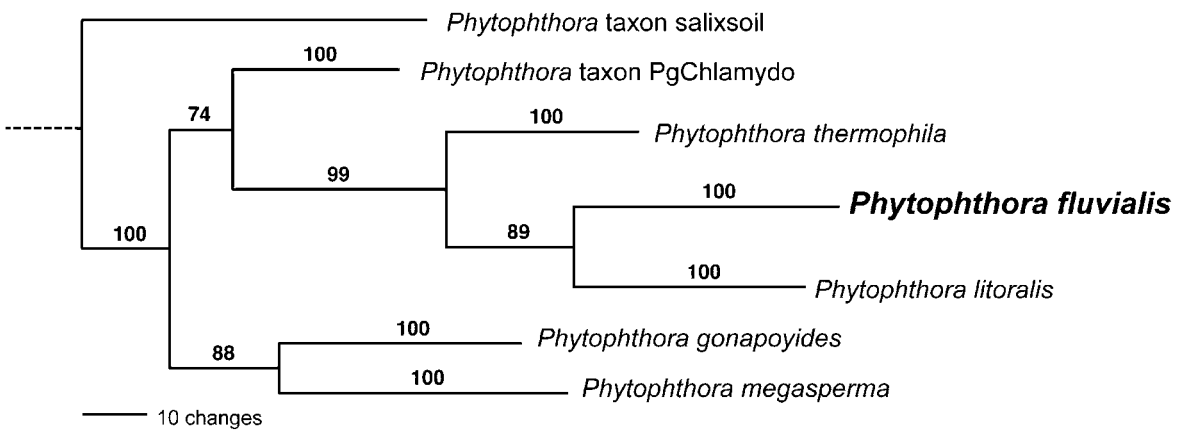
*Sporangia* produced abundantly in non-sterile soil extract, non-caducous, nonpapillate, broad-ovoid to elongated ovoid, limoniform or less frequently ellipsoid or obpyriform; 53 ± 7.6 × 36.4 ± 6.1 µm (overall range 37–72 × 21–54 µm), length/breadth ratio 1.5 ± 0.2. *Sporangial proliferation* external and in chains of internally proliferating sporangia in both a nested and extended way; secondary lateral sporangia regularly formed. Internally proliferating sporangiophores, sometimes branching inside or just outside of the empty sporangium. Diplanetism of zoospore cysts and the formation of microsporangia common in all isolates. Ellipsoid non-catenulate hyphal swellings (12.1 ± 4.7 µm) without radiating hyphae infrequently formed. *Chlamydospores* not observed. *Gametangia* not produced in single culture or when paired with A1 and A2 tester strains of *P. cinnamomi*. Radial growth rates on V8 agar at optimum (31.5 °C) and near the maximum (38 °C) temperature 5.9 ± 0.6 mm/d and 1.2 ± 0.2 mm/d, respectively.

Culture characteristics — Colonies on carrot agar (CA), V8A and potato-dextrose agar are stellate to rosaceous with limited aerial mycelium.

*Typus*. Western Australia, Moore River, baited from water in native bushland, Dec. 2009, *D. Hüberli*, holotype MURU 468; cultures ex-type CBS 129424 = MUCC 771, ITS sequence GenBank JF701436, *cox*1 sequence JF701442, HSP90 sequence JF701439 and LSU sequence GenBank JF951171, MycoBank MB561042.

*Additional specimens examined.* Western Australia, Moore River, baited from water in native bushland, Dec. 2009, *D. Hüberli,* MUCC 772; Badgingarra, baited from water in native bushland, 2007, collected by *Glevan Consulting,* VHS17350.

Notes — Phylogenetically, *P. fluvialis* shares a common ancestor with *P. litoralis* and resides in a strongly supported cluster along with *P. thermophila.* In a multigene phylogeny of the ITS, HSP90 and *cox*1 gene regions, *P. fluvialis* differs from *P. litoralis* by 77 steps (2.65 %), *P. thermophila* by 91 steps (3.13 %) and from the next closest relative, *P.* taxon PgChlamydo, by 116 steps (3.99 %). *Phytopthora fluvialis, P. litoralis and P. thermophila* have all been isolated from waterways north of Perth in Western Australia (Jung et al. 2011). *Phytophthora fluvialis* has a similar life strategy to *P. litoralis,* being sterile and having abundant and continuous asexual multiplication in watercourses via chains of nested and extended internally proliferating sporangia, external proliferation, the production of secondary lateral sporangia and the frequent germination of cysts by releasing secondary zoospores (diplanetism) or by forming microsporangia. These two species can be separated by the absence of catenulate hyphal swellings and chlamydospores in *P. fluvialis*, the higher maximum temperature for growth of *P. fluvialis* (38 °C) compared with *P. litoralis* (35 °C) and the production of smaller sporangia in *P. litoralis* (av. 43.6 ± 7.7 × 29.4 ± 5.4 µm).




One of three most parsimonious trees (TL = 371; CI = 0.78; RI = 0.89; RC = 0.70) obtained from a heuristic search with 100 random taxon additions of a combined ITS, *cox*1 and HSP90 sequence alignment using PAUP v4.0b10 (Swofford 2003). The scale bar shows 10 changes, and bootstrap support values from 1 000 replicates are shown at the nodes. Three isolates of each species were included in the analysis. The species described here is printed in **bold** face. The tree was rooted to *Phytophthora inundata* (not shown). The alignment and tree is available in TreeBASE (Accession SN11399).

*Colour illustrations.* A typical river in Western Australia (T. Jung); ovoid sporangium just before and during release of zoospores; ovoid, secondary lateral sporangium; extended proliferation of nonpapillate sporangium; nested proliferation; ellipsoid hyphal swelling (T. Jung). Scale bar = 25 µm. Rosaceous colony on carrot agar (T.I. Burgess).

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Catenulostroma eucalyptorum

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# ***Catenulostroma eucalyptorum*** Crous & Carnegie, *sp. nov.*

*Catenulostromatis excentrici* simile, sed conidiis minoribus; cellulis primariis 7–9 × 2–4 µm, cellulis secundariis 4–5 × 2–2.5 µm, discernitur.

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

*Leaf spots* amphigenous (intermingled among those of *Aulographina eucalypti*), subcircular with concentric rings, medium brown to somewhat reddish brown, with a raised margin, 5–10 mm diam. *Mycelium* internal and external; internal hyphae subcuticular, pale brown, branched, septate, 2–3.5 µm diam, emerging through stomata or cracks, anastomosing to form sporodochia that give rise to conidiophores forming chains of conidia. *Conidiomata* amphigenous, concentrically arranged, dark brown, dry and powdery, discrete, up to 300 µm diam. *Conidiophores* micronematous, branched, pale to medium brown, smooth, aggregated, 7–20 × 3–4 µm. *Conidiogenous cells* holothallic, integrated, terminal, subcylindrical to somewhat doliiform, conidial chains fragmenting into separate conidia, 6–8 × 2–3 µm. *Conidia* catenulate, smooth, pale brown, 4-celled, upper two primary cells 7–9 × 2–4 µm, with truncate ends where attached, 1.5–2 µm diam, cells separated from each other by a broad, dark brown area; each primary cell giving rise to a smaller basal cell that is globose, thin-walled, pale brown, 4–5 × 2–2.5 µm.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies slow growing, erumpent, with even margins, reaching 3 mm diam after 2 wk; on MEA surface olivaceous grey, and iron-grey in reverse; on OA surface olivaceous grey; on PDA surface grey olivaceous, reverse iron-grey.

*Typus*. Australia, New South Wales, Ebor, S 30°14'21" E 152°31'55", on leaves of *Eucalyptus laevopinea*, 28 July 2009, *A.J. Carnegie*, holotype CBS H-20592, culture ex-type CPC 17586 = CBS 129578, ITS sequence GenBank JF951151 and LSU sequence GenBank JF951174, MycoBank MB560177.

Notes — *Catenulostroma eucalyptorum* is most similar to *C. excentricum* (formerly *Trimmatostroma*, see Crous et al. 2007a), which has larger conidia (primary cells 9–11 × 3–4 µm, secondary cells 2.5–4.5 µm diam; Sutton & Ganapathi 1978). Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Teratosphaeria suberosa* (GQ852831; Identities = 625/648 (96 %), Gaps = 9/648 (1 %)), *Phaeothecoidea intermedia* (GQ852754; Identities = 616/639 (96 %), Gaps = 1/639 (0 %)) and *Phaeothecoidea eucalypti* (EF394857; Identities = 622/646 (96 %), Gaps = 5/646 (1 %)). The megablast search using the LSU sequence had as highest identity sequences of *Phaeothecoidea intermedia* (GQ852628; Identities = 864/871 (99 %), Gaps = 1/871 (0 %)) and *Phaeothecoidea eucalypti* (EU019280; Identities = 51/858 (99 %), Gaps = 0/858 (0 %)).

*Colour illustrations*. Mature *Eucalyptus grandis* plantation in northern NSW; leaf spot; aggregated conidiophores with conidiogenous cells giving rise to conidia. Scale bars = 10 µm.

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Mycosphaerella valgourgensis

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# ***Mycosphaerella valgourgensis*** Crous, *sp. nov.*

*Mycosphaerellae deightonii* similis, sed ascosporus majoribus, (13–)17–19(–22) × 3(–3.5) µm, discernitur.

*Etymology*. Named after the town where it was collected, Valgourge.

*Leaf spots* ellipsoid to subcircular, amphigenous, dark brown with a raised border, up to 3 cm long, and 1 cm diam. *Ascostromata* amphigenous, up to 500 µm diam, black, erumpent through epidermis, containing several ascomata up to 180 µm diam, thick-walled, of several layers of *textura angularis*; ostiole central, periphysate. *Asci* fasciculate, broadly ellipsoid, straight to incurved, bitunicate, 8-spored, with apical chamber, 40–50 × 8–10 µm. *Ascospores* hyaline, smooth, fusoid-ellipsoidal, medianly 1-septate, guttulate, slightly incurved, widest just above septum, tapering towards both acutely rounded ends, thick-walled, (13–)17–19(–22) × 3(–3.5) µm; ascospores germinate after 24 h on malt extract agar from both ends, with germ tubes parallel to the long axis of the spore, and lateral branches also developing, becoming constricted at median septum, but remaining hyaline, 5–6 µm diam. Hyphomycete anamorph formed in culture. *Mycelium* consisting of hyaline, smooth, septate, branched, 2–3 µm diam hyphae. *Conidiogenous cells* holoblastic, terminal on hyphae, hyaline, subcylindrical, smooth, 10–20 × 3–4 µm. *Conidia* solitary, subcylindrical to narrowly obclavate, straight to flexuous, apex obtuse, base truncate, multiseptate, 45–150 × 3–4 µm; hila truncate, not thickened nor darkened, with visible marginal frill; with age conidia tend to become pale olivaceous and finely verruculose.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies slow growing, erumpent, with folded surface and sparse aerial mycelium; margins even, lobate, reaching 4 mm diam after 2 wk; on malt extract agar surface pale olivaceous grey, reverse umber; on potato-dextrose agar surface olivaceous grey with patches of apricot to scarlet, reverse iron-grey with patches of scarlet due to diffuse red pigment and crystals in agar; on oatmeal agar surface smoke-grey with patches of olivaceous grey, with diffuse red pigment in agar.

*Typus*. France, Ardeche, Valgourge, Domaine Le Fraysse, N 44°35.469' E 004°07.710', on leaves of *Yucca* sp., 15 July 2010, *P.W. Crous*, holotype CBS H-20593, culture ex-type CPC 18385 = CBS 129531, ITS sequence GenBank JF951152 and LSU sequence GenBank JF951175, MycoBank MB560178.

Notes — Several species of *Mycosphaerella* are listed from *Yucca* by Aptroot (2006). *Mycosphaerella sphaerelloides* (type could not be located; Aptroot 2006), was seen as a synonym of *Mycosphaerella tassiana* (now *Davidiella*) by von Arx (1949). *Mycosphaerella yuccae* was shown to be a species of *Guignardia* (Aptroot 2006), while *M. yuccina* appeared to be a possible species of *Dothidea* (immature specimen) (Aptroot 2006). Two species relevant for comparison to *M. valgourgensis* are *M. acervata* (≡ *Planistromella acervata*), which has larger ascospores (24–29 × 3.5–5 µm; Aptroot 2006), and *M. deightonii* (anamorph *Pseudocercospora concentrica*), which again has smaller ascospores than *M. valgourgensis* (14.5–17 × 3.5–4 µm; Sivanesan 1984). Based on several collections made by Annette Ramaley, Barr (1996) concluded that *Planistromella acervata* represented a species complex (based on differences in ascospore sizes, and certain collections with different ascospores being able to form anamorphs in culture).

With the description of *M. valgourgensis,* we name a species presently intermediate between *M. acervata* and *M. deightonii*. Furthermore, the cercosporoid anamorph studied here is also, *Pseudocercospora*-like, clustering apart from *Pseudocercospora* s.str. Morphologically it is also rather different from *Pseudocercospora*, with conidia initially being hyaline, and later becoming pale brown and verruculose, with a basal marginal frill. Lastly, the newly introduced family, *Planistromellaceae* (Barr 1996) is clearly heterogeneous, and the type species, *P. yuccifoliorum* with its 3-septate ascospores and *Kellermania* anamorph would probably cluster apart from *M. valgourgensis*, but further collections are required to resolve this. Interestingly enough, *M. valgourgensis* (*Planistromella* sensu Barr, based on its erumpent, aggregated stromatic ascomata, and remnants of hamathecial tissue) clusters close to *Dothistroma* anamorphs, for which Barr (1996) established the genus *Eruptio*, based on their aggregated, stromatic, multiloculate ascomata. The latter feature may well end up being the only unifying character to separate taxa in this clade from *Mycosphaerella* s.str. However, the generic names *Eruptio* (based on *E. acicula* with *Lecanosticta* anamorph), *Mycosphaerella* (based on *M. punctiformis*, and having *Ramularia* anamorphs) and *Planistromella* (based on *P. yuccifoliorum* and having *Kellermania* anamorphs), are clearly not congeneric with *M. valgourgensis*. More taxa need to be added to the alignment to clarify the genera in this specific clade of the *Mycosphaerellaceae*. For the present, however, this species is best described in *Mycosphaerella* until the generic concepts of this clade are better resolved.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Mycosphaerella aurantia* (EU853471; Identities = 494/494 (100 %), Gaps = 0/494 (0 %)), *Mycosphaerella microsora* (EU167599; Identities = 645/647 (99 %), Gaps = 0/647 (0 %)) and *Mycosphaerella buckinghamiae* (EU707856; Identities = 603/605 (99 %), Gaps = 0/605 (0 %)). A similar search using the LSU sequence obtained as closest hits sequences of *Passalora bellynckii* (GU214454; Identities = 879/880 (99 %), Gaps = 0/880 (0 %)), *Passalora* sp. CBS 115525 (GU214460; Identities = 878/880 (99 %), Gaps = 0/880 (0 %)) and *Mycosphaerella keniensis* (DQ246259; Identities = 878/880 (99 %), Gaps = 0/880 (0 %)).

*Colour illustrations*. *Yucca* sp. growing at Domaine Le Fraysse, Valgourge; erumpent ascoma; asci and ascospores; germinating ascospore; conidia. Scale bars = 10 µm.

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Utrechtiana cibiessia

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## ***Utrechtiana*** Crous & Quaedvlieg, *gen. nov.*

Conidiophoris atrobrunneis, erectis, basi subglobosa, cellulis conidiogenis subcylindraceis, brunneis formantibus, apicibus clavatis, obtuse rotundatis, cum cicatricibus truncatis, interdum incrassatis, sed neque fuscatis neque refractis. Conidiis pallide brunneis, ellipsoideis, guttulatis et granulatis, delicate verruculosis, paulum supra medium 1-septatis, tenuitunicatis, apice obtuse vel acute rotundato, basi obtuse rotundata, cum hilo truncato, fuscato et incrassato et poro centrali.

*Etymology*. Named after the University of Utrecht, on which campus it was collected.

Hyphomycetous, associated with leaf spots. *Mycelium* internal, consisting of septate, smooth, hyaline, branched hyphae. *Conidiophores* solitary, erect, bursting through epidermis, with circular scar where base of conidiophore is attached to immersed hyphal network; conidiophores dark brown, erect, base subglobose, giving rise to a subcylindrical, brown conidiogenous cell that ends in a clavate, bluntly rounded apex, with truncate, flattened scar; sometimes thickened, not darkened, nor refractive. *Conidia* pale brown, ellipsoid, guttulate to granular, finely verruculose, 1-septate slightly above the conidial median, thin-walled, apex bluntly to acutely rounded, base obtusely rounded with a flattened, darkened and thickened hilum that has a central pore.

*Type species*. *Utrechtiana cibiessia.*
MycoBank MB560179.

## ***Utrechtiana cibiessia*** Crous & Quaedvlieg, *sp. nov.*

Conidiophoris 18–45 × 10–12 µm, atrobrunneis, erectis, basi subglobosa, 10–12 × 10–15 µm, cellulis conidiogenis subcylindraceis, subtile verruculosis, mediobrunneis, sed apicem versus pallide brunneis, 8–20 × 8–10 µm formantibus. Conidiis pallide brunneis, ellipsoideis, guttulatis vel granulatis, subtile verruculosis, paulum supra medium 1-septatis, corpis conidiorum (25–)26–28(–30) µm longis, cellulis basalibus (12–)15–17(–19) × (12–)13–15(–18) µm, cellulis apicalibus (8–)10–12(–15) × 14–15(–16) µm.

*Etymology*. Named after the Centraalbureau voor Schimmelcultures (CBS-KNAW) in front of which, on Utrecht Campus, the fungus was collected.

*Leaf spots* amphigenous, prominent, ellipsoid, centre pale brown, outer region dark brown, surrounded by chlorotic halo, varying from specks 1 mm diam to spots up to 10 mm diam. *Mycelium* internal, consisting of septate, smooth, hyaline, branched hyphae, 2–4 µm diam. *Conidiophores* amphigenous on leaf, solitary, though aggregated on leaf spots, erect, bursting through epidermis (not stomata) on surface, with circular scar where base of conidiophore is attached, 6–8 µm diam, with central point linked to immersed hyphal network; conidiophores 18–45 × 10–12 µm, dark brown, erect, base subglobose, 10–12 × 10–15 µm, giving rise to a subcylindrical, finely verruculose, medium brown conidiogenous cell that becomes pale brown at apex, 8–20 × 8–10 µm, that ends in a clavate, bluntly rounded apex, tapering near the apex to a truncate, flattened scar, 3–5 µm diam, sometimes thickened, not darkened, nor refractive. *Conidia* pale brown, ellipsoid, guttulate to granular, finely verruculose, 1-septate slightly above the conidial median, somewhat constricted at septum, thin-walled, apex bluntly to acutely rounded, base obtusely rounded with a flattened hilum, 3–4 µm diam, with a thickened rim if viewed directly from above (with central pore, but no pore visible on conidiogenous scar), darkened and thickened when viewed from the side, extending 1–1.5 µm into the conidial body; (25–)26–28(–30) µm long; basal cell (12–)15–17(–19) × (12–)13–15(–18) µm, apical cell (8–)10–12(–15) × 14–15(–16) µm.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies spreading, erumpent with moderate aerial mycelium and even margins, reaching 10 mm diam. On oatmeal agar dirty white; on potato-dextrose agar surface and reverse dirty white; on malt extract agar surface dirty white, turning grey olivaceous when fertile, reverse luteous.

*Typus*. Netherlands, Utrecht, De Uithof University Campus, intersection of Harvardlaan with Uppsalalaan, on leaves of *Phragmites australis* growing along water canals, 14 Dec. 2010, *W. Quaedvlieg,* holotype CBS H-20594, cultures ex-type CPC 18917, 18916 = CBS 128780, ITS sequence GenBank JF951153 and LSU sequence GenBank JF951176, MycoBank MB560180.

Notes — *Utrechtiana* should be compared to three other morphologically similar genera, namely *Polytrincium* (Simon et al. 2009), *Polythrinciopsis* (Walker 1966) and *Passalora* (Crous et al. 2009b). It is however morphologically distinct from all three genera by having solitary conidiophores with solitary, terminal conidiogenous loci, and the absence of any stroma. *Polythrinciopsis phragmites*, which also occurs on *Phragmites* in Australia (Walker 1966), is superficially similar in having 1-septate, obovate conidia, but distinct in having conidiophores in fascicles arising from a poorly developed stroma, superficial mycelium, and conidiogenous loci (thickened and darkened) arranged along the side of the conidiogenous cell. Further collections and cultures would be required, however, to determine if *Polythrinciopsis* is distinct from *Polythrincium* and *Passalora*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Magnaporthe grisea* (HQ020360; Identities = 441/474 (93 %), Gaps = 13/474 (3 %)), *Magnaporthe oryzae* (GU073121; Identities = 485/527 (92 %), Gaps = 20/527 (4 %)) and *Pyricularia commelinicola* (FJ850125; Identities = 408/445 (92 %), Gaps = 21/445 (5 %)). An identical search using the LSU sequence revealed a similar high similarity to *Pyricularia borealis* (DQ341511; Identities = 844/863 (98 %), Gaps = 5/863 (1 %)), *Magnaporthe grisea* (AF362554; Identities = 860/881 (98 %), Gaps = 6/881 (1 %)) and *Buergenerula spartinae* (DQ341492; Identities = 843/866 (97 %), Gaps = 5/866 (1 %)). As we are not currently aware of a genus of hyphomycetes with a similar morphology to this fungus occurring on *Phragmites* (Seifert et al. 2011), and the fact that the present fungus is distinct from those presently deposited in GenBank, a new genus is herewith introduced to accommodate it.

*Colour illustrations*. Symptomatic *Phragmites australis* growing next to a water channel on the Uithof, Utrecht campus; solitary conidiophores on leaf spot; conidiophores giving rise to conidia; germinating conidium. Scale bars = 10 µm.

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Dictyosporium stellatum

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# ***Dictyosporium stellatum*** G.P. White & Seifert, *sp. nov.*

Coloniae stellatae, sporidochia 200–500 µm lata. Cellulae conidiogenae 6.5–11 × 4.5–10 µm, globosae, ellispodeae vel clavatae. Conidia brunnea, complanata, (50–)95–140(–175) µm longa, (27.5–)30–40(–52.5) µm lata, 7.5–15 µm crassa, cellulae 3.5–6.5 µm longae, 4.5–6 µm latae, 6–12 µm crassae, diposita in 5–7 serietibus.

*Etymology*. From *stellata* (L.), referring to the star-like appearance of the colonies on the natural substrate.

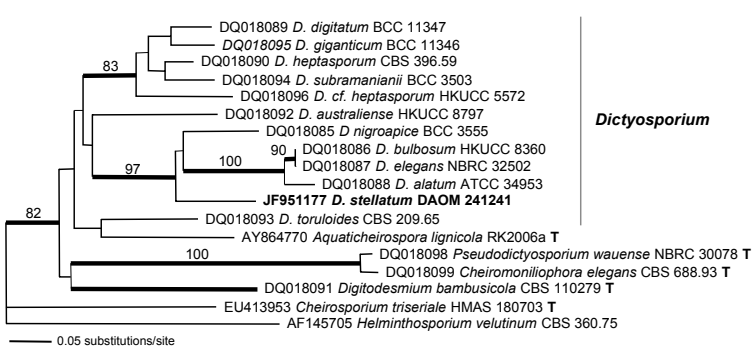
*Colonies* on the natural substratum conspicuous, black, scattered, up to c. 7 mm diam, irregular in outline, composed of stellate sporodochia c. 200–500 µm wide, comprised of conidia radiating from a central point, often coalescing into irregular masses; often associated with or growing on stromata of a *Hypoxylon*-like fungus. *Mycelium* immersed in the substrate, not seen. *Conidiophores* c. 2–5 µm wide, micronematous, inconspicuous, composed of hyaline, thin-walled, irregularly branched, frequently septate hyphae. *Conidiogenous cells* 6.5–11 × 4.5–10 µm, globose, ellipsoidal or clavate, often remaining attached to the base of the conidium, hyaline and thin-walled, often collapsing, hyaline and thin-walled, sometimes becoming brown and thicker walled and then not collapsing; clavate cells with cylindrical connections to the basal cells of conidia rarely observed, perhaps suggestive of sympodial proliferation of conidiogenous cells that do not detach with the conidia. *Conidia* (50–)95–140(–175) µm long, (27.5–)30–40(–52.5) µm wide, 7.5–15 µm thick, dark brown, paler in apical cells, planar, cheiroid in ventral view, cylindrical to acicular in lateral view, consisting of (59–)110–165(–180) cells; individual cells discoid or doliiform, more oblong in side view than in face view, 3.5–6.5 µm tall, 4.5–6 µm wide in face view, 6–12 µm deep; typically arranged in (5–)6(–7) columns, 14–33 cells per column, the inner columns nested within the outer columns, the outer columns derived from the basal cell of the conidium; the intermediate columns are derived from the first or second cell of the outer columns; the inner columns derived from the first or second cell of the intermediate columns; usually with 2–3 central columns longest and of equal length, 2–3 peripheral columns shorter and of equal length, and one of the outer columns shortest but with several variations observed, including additional branching of one or more of the columns resulting in conidia with up to 9 columns, or straight or curved extension of 1–2 adjacent columns far beyond than the rest of the columns. Conidial appendages absent. Conidia germinating by hyaline hyphae 2–3 µm wide from the terminal cells of each column.

Culture characteristics — Colonies on cornmeal agar at RT 8–15 mm radius after 15 d, planar, obverse and reverse hyaline, margin uneven, sporulating after about 10 d, and then colonies with a uneven, spotty ring of conidial clusters around the inoculum, surface otherwise smooth and overlaid with sparse, hyaline aerial hyphae.

*Typus*. Canada, Ontario, Renfrew Co., Blithfield Twp., Barry Lake, developed in moist chamber on previously submerged wood, collected 3 Sept. 2008, observed 26 Dec. 2008, *Nancy Hiscock*, holotype DAOM 241241; culture ex-type CCFC 241241, ITS sequence GenBank JF951154 and LSU sequence GenBank JF951177, MycoBank MB561250.

Notes — *Dictyosporium stellatum* produces the longest conidia of the approximately 34 species described (Goh et al. 1999, Cai et al. 2003, Crous et al. 2009a). Stellate sporodochia, which give the species its epithet, have not been reported in other species. Despite the many collections attributable to this genus deposited in DAOM by the senior author and his mentor Dr S.J. Hughes over several decades, no other specimens were found and thus *D. stellatum* may be a rare fungus. On the holotype, sporulation was often most prolific on stromata of a *Hypoxylon*-like fungus, and some parasitism may be involved.

The phylogenetic analysis below is based on recent internal transcribed spacer (ITS) analyses of *Dictyosporium* and related cheiroid genera (Tsui et al. 2006, Cai et al. 2008) with our own species added. Our species has distinct ITS sequences from those sequenced to date and sits in a well-supported clade that includes the type species, *D. elegans*. Although *Dictyosporium* appears monophyletic in this NJ tree, it is paraphyletic with the *Pseudodictyosporium/Cheiromoniliophora/Cheirosporium* clade in nine of ten MPTs in a heuristic parsimony analyses (not shown). No analyses have well-supported overall structure, perhaps reflecting the scant sampling of species in this group.




*Colour illustrations*. The shoreline of Barry Lake where the holotype was collected; stellate sporodochial on surface of wood through the dissecting microscope (taken with CombineZ) and through the compound microscope; a single conidium in lateral view showing three planes of focus and the different lengths of the arms; a single conidium in face view. Scale bar = 10 µm.

Neighbour-joining tree (TL = 448; CI = 0.538; RI = 0.596) of an ITS sequence alignment generated by MAFFT (Katoh et al. 2005) using PAUP v4.0b10 (Swofford 2003). Bootstrap support values above 70 % from 1 000 replicates are shown at the nodes and branches occurring in the strict consensus of 10 MPTs from a heuristic parsimony search of the same alignment are in **bold**; type strains are indicated with **T**. The species described here is printed in **bold** face. The tree was rooted with *Helminthosporium vellutinum*.

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