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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: *Diaporthe ceratozamiae* on *Ceratozamia robusta*, *Seiridium banksiae* on *Banksia marginata*, *Phyllosticta hymenocallidicola* on *Hymenocallis littoralis*, *Phlogicylindrium uniforme* on *Eucalyptus cypellocarpa*, *Exosporium livistonae* on *Livistona benthamii* and *Coleophoma eucalyptorum* on *Eucalyptus piperita*. Several species are also described from South Africa, namely: *Phoma proteae*, *Pyrenochaeta protearum* and *Leptosphaeria proteicola* on *Protea* spp., *Phaeomoniella niveniae* on *Nivenia stokoei*, *Toxicocladosporium leucadendri* on *Leucadendron* sp. and *Scorias leucadendri* on *Leucadendron muirii*. Other species include *Myrmecridium phragmitis* on *Phragmites australis* (Netherlands) and *Camarographium carpini* on *Carpinus betulus* (Russia). Furthermore, *Pseudoidriella syzygii* on *Syzygium* sp. represents a novel genus of hyphomycetes collected in Australia. Morphological and culture characteristics along with ITS DNA barcodes are provided for all taxa.

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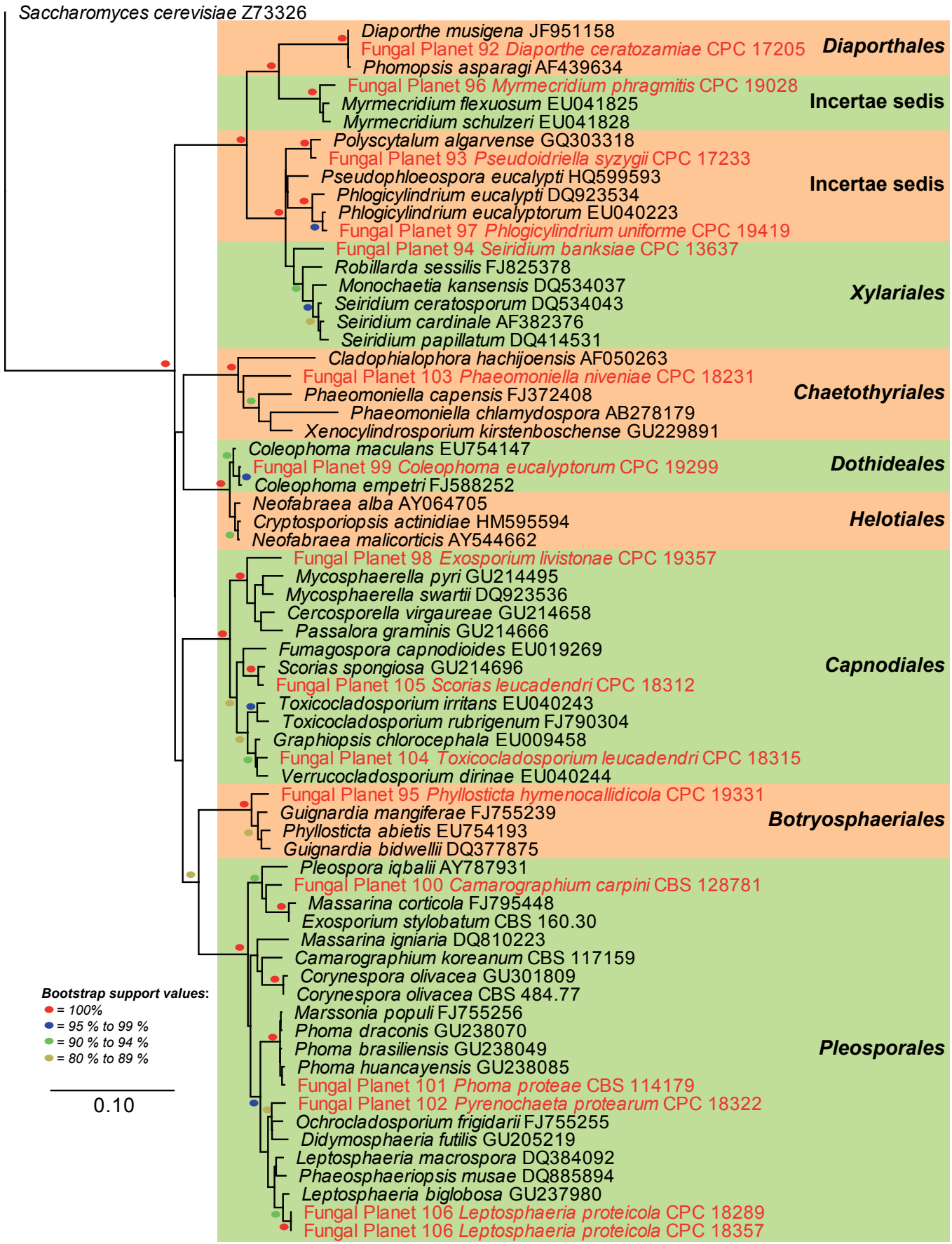

Neighbour-joining tree obtained using a distance analysis with the HKY85 substitution model on the partial 28S nrRNA gene alignment (851 nucleotides including alignment gaps) as implemented in PAUP v. 4.0b10 (Swofford 2003). Novel species are indicated in a red font and the orders are indicated on the 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 *Saccharomyces cerevisiae* (GenBank Z73326).

Diaporthe ceratozamiae

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Diaporthe ceratozamiae Crous & R.G. Shivas, *sp. nov*.

Phomopsis phyllanthicolae similis, sed conidiis majoribus, (6.5–)8–9(–10) × 2–2.5(–3) µm, discernitur.

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

Leaf spots medium brown, associated with leaf margins, thus of variable length, up to 15 mm diam. *Pycnidia* associated in necrotic leaf tissue; pycnidia in culture on pine needle agar subglobose, up to 300 µm diam, somewhat erumpent; 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, 15–30 × 3–4 µm. *Conidiogenous cells* phialidic, cylindrical, terminal and lateral, with slight taper towards apex, 1–1.5 µm, with visible periclinal thickening; collarette not flared, 1 µm long. *Paraphyses* hyaline, smooth, cylindrical, usually with 1–2 basal septa, wall thickened, extending above conidiophores, straight, flexuous, unbranched, or branched below, up to 60 µm long, 1.5–2.5 µm wide at base. *Alpha conidia* aseptate, hyaline, smooth, fusiform, tapering towards both ends, straight, acutely rounded at apex, base subtruncate, (6.5–)8–9(–10) × 2–2.5(–3) µm. *Beta* and *gamma conidia* not seen.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies spreading, covering the dish within 2 wk; on oatmeal agar surface dirty white, lacking aerial mycelium; on potato-dextrose agar and malt extract agar having moderate aerial mycelium, agar surface dirty white, with patches of grey olivaceous; reverse saffron to luteous.

Typus. Australia, Queensland, Brisbane, S 27°28'34.8" E 152°58'40.8" on leaves of *Ceratozamia robusta* (*Zamiaceae*), 14 July 2009, *P.W. Crous & R.G. Shivas*, holotype CBS H-20757, cultures ex-type CPC 17205 = CBS 131306, ITS sequence GenBank JQ044420 and LSU sequence GenBank JQ044440, MycoBank MB560695.

Notes — Phylogenetically *Diaporthe ceratozamiae* is closely related to *Phomopsis phyllanthicola* (on branches of *Phyllanthus emblica*, China; ITS: GenBank FJ441632; Identities = 530/537 (99 %), Gaps = 0/537 (0 %)) and *Phomopsis liquidambari* (on oak stems, China; ITS: GenBank FJ478124; Identities = 582/591 (98 %), Gaps = 1/591 (0 %)), but distinct in that *P. phyllanthicola* has smaller alpha conidia (6.6–8.2 × 1.5–1.8 µm) (Chang-Qing et al. 2005). We are not aware of any other species of *Diaporthe* (incl. *Phomopsis*) that has been described from *Ceratozamia*, and believe this to represent a novel taxon. A megablast search using its LSU sequence retrieves numerous sequences of species of *Diaporthe* and *Phomopsis*, confirming the placement of *D. ceratozamiae* in the *Diaporthaceae*.

Colour illustrations. *Ceratozamia robusta* in Brisbane; sporulation on pine needle agar; conidiophores giving rise to alpha conidia, intermingled among paraphyses. Scale bar = 10 µm.

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Pseudoidriella syzygii

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

Mycelium ex hyphis laevibus, hyalinis, ramosis, septatis compositum, sine chlamydosporis. Conidiomata sporodochialia, massis sporarum erectis, flammuliformibus, crystallinis. Conidiophora subcylindrica, laevia, hyalina, ramosa, transverse septata. Cellulae conidiogenae hyalinae, leaves, terminales vel laterales, sympodialiter proliferantes, cicatricibus conidialibus applanatis, neque incrassatis, neque fuscatis. Conidia hyalina, laevia, guttulata, recta vel curvata, falcata, in medio latissima, apicem versus attenuata, apice anguste obtuso, basi truncata, in medio 1-septata.

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

Hyphomycetous, associated with insect damage on leaves. *Mycelium* consisting of smooth, hyaline, branched, septate, hyphae, lacking chlamydospores. *Conidiomata* sporodochial, with spore masses erect like candle flames, crystalline. *Conidiophores* subcylindrical, smooth, hyaline, branched, transversely septate. *Conidiogenous cells* hyaline, smooth, terminal and lateral, with 2–3 at apex of conidiophore, proliferating sympodially, scars flattened, not thickened nor darkened. *Conidia* hyaline, smooth, guttulate, straight to curved, falcate, widest in the middle, tapering towards narrowly obtuse apex and truncate base, medianly 1-septate.

Type species. *Pseudoidriella syzygii*.
MycoBank MB560696.

Pseudoidriella syzygii Crous & R.G. Shivas, *sp. nov.*

Conidiomata sporodochialia, massis sporarum erectis, flammuliformibus. Conidiophora subcylindrica, laevia, hyalina, ramosa, 0–4-septata, 10–50 × 3–4 µm. Cellulae conidiogenae hyalinae, leaves, terminales vel laterales, 10–15 × 2–3 µm; sympodialiter proliferantes. Conidia hyalina, laevia, guttulata, recta vel curvata, falcata, in medio latissima, apicem versus attenuata, apice anguste obtuso, basi truncata, in medio 1-septata, (39–)45–50(–53) × (2.5–)3(–4) µm.

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

Associated with insect damage on leaves of *Syzygium* sp. *Mycelium* consisting of smooth, hyaline, branched, septate, 1.5–2.5 µm diam hyphae, lacking chlamydospores. *Conidiomata* sporodochial, with spore masses erect like candle flames, crystalline, up to 400 µm diam. *Conidiophores* subcylindrical, smooth, hyaline, branched, 0–4-septate, 10–50 × 3–4 µm. *Conidiogenous cells* hyaline, smooth, terminal and lateral, with 2–3 at apex of conidiophore, 10–15 × 2–3 µm; proliferating sympodially, scars flattened, not thickened nor darkened, 2 µm diam. *Conidia* hyaline, smooth, guttulate, straight to curved, falcate, widest in the middle, tapering towards narrowly obtuse apex and truncate base, medianly 1-septate, (39–)45–50(–53) × (2.5–)3(–4) µm.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies erumpent, slow growing, with sparse aerial mycelium and feathery, lobate margins, reaching 8 mm diam after 2 wk. On oatmeal agar, malt extract agar and potato-dextrose agar dirty white on surface, salmon in reverse.

Typus. Australia, Queensland, Mackay, Eungella National Park, on leaves of *Syzygium* sp. (*Myrtaceae*), 14 July 2009, *P.W. Crous & K.L. Crous*, holotype CBS H-20758, cultures ex-type CPC 17233 = CBS 131307, ITS sequence GenBank JQ044421 and LSU sequence GenBank JQ044441, MycoBank MB560697.

Notes — Morphologically *Pseudoidriella* resembles the genus *Idriella* (based on *I. lunata*, a soilborne fungus) (anamorphic *Helotiales*), which is characterised by smooth, pale brown conidiophores with sympodial proliferation, hyaline, smooth, aseptate, falcate conidia, and dark brown chlamydospores (Ellis 1971, Seifert et al. 2011). *Pseudoidriella* is distinct in having structures that are hyaline throughout, 1-septate conidia, and lacking chlamydospores, with similarities to *Microdochium* (a complex of which some taxa have *Monographella* teleomorphs, *Amphisphaeriaceae*) that has generic synonyms including *Lanosa*, *Gloeocercospora* and *Gerlachia* (Seifert et al. 2011). Of these, it is unlikely that *Gloeocercospora* is a synonym (based on *G. sorghi*), as the latter causes zonate leaf spot on sorghum, and has long, multiseptate conidia, and forms abundant, black sclerotia (Braun 1995), reminiscent of *Ramulispora sorghi* (Crous et al. 2003). *Pseudoidriella* resembles *Microdochium* by having short, 1-septate conidia, but is phylogenetically distinct. A detailed study is underway to resolve other genera within this complex. A megablast search of the NCBIs GenBank nucleotide sequence database using the ITS sequence of *Pseudoidriella syzygii* retrieves as closest hits *Cylindrium elongatum* (*Hypocreales*, *Nectriaceae*; GenBank AY853244; Identities = 422/445 (95 %), Gaps = 4/445 (1 %)) and *Polyscytalum algarvense* (incertae sedis; GenBank GQ303287; Identities = 490/545 (90 %), Gaps = 35/545 (6 %)), amongst others. It has very little similarity to the ITS sequence of *Microdochium phragmitis* strain CBS 285.71 (GenBank EU926218). A megablast search of the NCBIs GenBank nucleotide sequence database using the LSU sequence of *Pseudoidriella syzygii* retrieves as closest hits *Polyscytalum algarvense* (incertae sedis; GenBank GQ303318; Identities = 876/886 (99 %), Gaps = 0/886 (0 %)) and *Plectosphaera eucalypti* (incertae sedis; GenBank DQ923538; Identities = 857/893 (96 %), Gaps = 7/893 (1 %)), amongst others.

Colour illustrations. Eungella National Park; sporulation on pine needle agar; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

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Seiridium banksiae

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Seiridium banksiae Crous & Summerell, *sp. nov.*

Seiridii cardinalis simile, sed conidiis majoribus, (24–)27–30(–35) × (11–)12–13(–14) µm, discernitur.

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

Leaf spots amphigenous, circular to subcircular, medium brown on upper surface, with grey central region and black conidiomata; lower surface dirty white due to leaf hairs. *Conidiomata* stromatic, acervular, amphigenous, intraepidermal, oval to ellipsoid, up to 200 µm diam; wall of *textura angularis*. *Conidiophores* lining the basal cavity, hyaline, smooth, subcylindrical, 0–2-septate, unbranched, or branched below, 10–20 × 5–8 µm. *Conidiogenous cells* discrete, subcylindrical, hyaline, smooth, 10–15 × 3–4 µm, with minute apical periclinal thickening, proliferating 1–2 times percurrently. *Conidia* fusiform, straight to slightly curved, (24–)27–30(–35) × (11–)12–13(–14) µm, 3-distoseptate with visible septal pores, medium brown, verruculose, thick-walled; apical cell attenuated towards apex; basal cell lacking appendage, truncate, 3–4 µm diam, at times with minute marginal frill.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies flat, spreading, with sparse aerial mycelium and feathery, lobate margin; reaching 60 mm diam after 2 wk. On all media mouse-grey in centre, dirty white in outer region..

Typus. Australia, Tasmania, Crescent Bay, S 43°11'29.7" E 147°51'00.7" on leaves of *Banksia marginata* (*Proteaceae*), 14 Oct. 2006, *B.A. Summerell & P. Summerell*, holotype CBS H-20756, cultures ex-type CPC 13637 = CBS 131308, ITS sequence GenBank JQ044422 and LSU sequence GenBank JQ044442, MycoBank MB560698.

Notes — Although Crous et al. (2004) recorded some *Seiridium* spp. from *Proteaceae*, the first taxon described from this family was *S. proteae* (Marincowitz et al. 2008). *Seiridium banksiae* is rather distinct from *S. proteae* and the taxa treated by Sutton (1980) and Nag Raj (1993) based on its 3-septate conidia with attenuated apical cells, and conidial dimensions. A megablast search of the NCBIs GenBank nucleotide sequence database using the ITS sequence of *S. banksiae* retrieves as closest hits *Discostroma fuscellum* (*Xylariales*, *Amphisphaeriaceae*; GenBank JF320818; Identities = 538/569 (95 %), Gaps = 8/569 (1 %)) and *Seimatosporium parasiticum* (*Xylariales*, *Amphisphaeriaceae*; GenBank AB594808; Identities = 524/556 (94 %), Gaps = 8/556 (1 %)), amongst others. A megablast search of the NCBIs GenBank nucleotide sequence database using the LSU sequence of *S. banksiae* retrieves as closest hits *Seiridium ceratosporum* (*Xylariales*, *Amphisphaeriaceae*; GenBank DQ534043; Identities = 807/842 (96 %), Gaps = 6/842 (1 %)), *Robillarda sessilis* (incertae sedis; GenBank FJ825378; Identities = 785/821 (96 %), Gaps = 5/821 (1 %)) and *Monochaetia kansensis* (*Xylariales*, *Amphisphaeriaceae*; GenBank DQ534037; Identities = 802/841 (95 %), Gaps = 4/841 (0 %)), amongst others. *Seiridium banksiae* clusters somewhat apart from other species of *Seiridium*, and it is probably not congeneric with the type species (*S. marginatum*) of the genus. The latter, however, is presently not known from culture, and needs to be recollected.

Colour illustrations. Coastline of Tasmania; sporulation on oatmeal agar; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

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Phyllosticta hymenocallidicola

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Phyllosticta hymenocallidicola Crous, Summerell & Romberg, *sp. nov.*

Phyllostictae citricarpae similis, sed conidiis minoribus, (8–)9–10(–11) × (6–)6.5–7 µm, discernitur.

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

Associated with brown leaf spots and leaf tip blight. *Conidiomata* pycnidial, solitary, black, erumpent, globose, exuding colourless to opaque conidial masses; pycnidia up to 200 µm diam; pycnidial wall of several layers of brown *textura angularis*, up to 30 µm thick; inner layer of hyaline *textura angularis*. *Ostiole* central, up to 20 µm diam, rim lined with darker brown cells. *Conidiophores* subcylindrical to ampulliform, reduced to conidiogenous cells, or with 1–2 supporting cells, at times branched at base, 10–25 × 4–7 µm. *Conidiogenous cells* terminal, subcylindrical to doliiform, hyaline, smooth, coated with a mucoid layer, 7–15 × 3–4 µm; inconspicuously proliferating several times percurrently near apex. *Conidia* (8–)9–10(–11) × (6–)6.5–7 µm, solitary, hyaline, aseptate, thin and smooth walled, coarsely guttulate, or with large, single, central guttule, ellipsoid to obovoid, tapering towards a narrowly truncate base, 2–3 µm wide, enclosed in a thin (frequently not persistent) mucoid layer, 1 µm thick, and bearing a hyaline mucoid apical appendage, 3–5(–8) × 1.5(–2) µm, flexible, unbranched, tapering towards an acutely rounded tip.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies reaching 55 mm after 2 wk on oatmeal agar (OA) and potato-dextrose agar (PDA), but only 25 mm diam on malt extract agar (MEA). Colonies on PDA with smooth, lobate margins, sparse aerial mycelium, surface and reverse olivaceous grey; on MEA colonies folded, erumpent, irregular with feathery margin, and sparse aerial mycelium, olivaceous grey (surface), iron-grey (reverse). On OA with feathery, lobate margins and sparse aerial mycelium, olivaceous grey in centre, pale olivaceous grey in outer region.

Typus. Australia, Northern Territory, Darwin, Charles Darwin University, S 12°22'25.2" E 130°52'07.4" on leaves of *Hymenocallis littoralis* (*Amaryllidaceae*), 1 May 2011, *P.W. Crous & M. Romberg*, holotype CBS H-20759, cultures ex-type CPC 19332, 19331 = CBS 131309, ITS sequence GenBank JQ044423 and LSU sequence GenBank JQ044443, MycoBank MB560699; Darwin, in front of Vibe Hotel, Kitchener Drive, Darwin Conference Centre, on leaves of *Hymenocallis littoralis*, 27 Apr. 2011, *P.W. Crous & B.A. Summerell*, CBS H-20760, cultures CPC 19330, 19329 = CBS 131310, ITS sequence GenBank JQ044424.

Notes — During a meeting of the Australasian Society for Plant Pathology in Darwin (April 2011), a serious leaf spot and tip blight disease was noticed on the *Hymenocallis littoralis* plants growing in front of the conference centre. Furthermore, during a workshop on the taxonomy of plant pathogenic fungi at the Charles Darwin University, the same disease was spotted on these plants growing on campus. The fungus consistently associated with the dieback proved to be a species of *Phyllosticta*, described here as *P. hymenocallidicola*. *Phyllosticta hymenocallidis*, which was originally described from this host, was shown to be a synonym of *Phoma narcissi*, a common pathogen of *Narcissus*, *Hippeastrum* and other *Amaryllidaceae*, on which it causes a leaf scorch, neck rot and red leaf spot disease (Boerema 1993). No other species of *Phyllosticta* is presently known from this host, and this taxon also appeared to be phylogenetically distinct from those presently deposited in GenBank (Wulandari et al. 2009, Glienke et al. 2011). A megablast search of the NCBIs GenBank nucleotide sequence database using the ITS sequence of *P. hymenocallidis* retrieves as closest hits *Phyllosticta owaniana* strain KSJM1 (isolated as plant endophyte of *Guazuma ulmifolia* in India; GenBank HQ680382; Identities = 571/571 (100 %), Gaps = 0/571 (0 %)), *Phyllosticta* sp. strain KSJM2 (isolated as plant endophyte of *Cassia alata* in India; GenBank HQ680383; Identities = 531/531 (100 %), Gaps = 0/531 (0 %)) and *Guignardia citricarpa* isolate FLP-21 (from leaves of sweet orange in Brazil; GenBank FJ769643; Identities = 521/545 (96 %), Gaps = 8/545 (1 %)), amongst others. However, the retrieved sequence of *Phyllosticta owaniana* (GenBank HQ680382) does not match those for the same species of Wulandari et al. (2009) and Glienke et al. (2011). A megablast search of the NCBIs GenBank nucleotide sequence database using the LSU sequence of *P. hymenocallidis* confirms its placement in the genus; closest hits include *Guignardia vaccinii* (GenBank FJ588242; Identities = 917/923 (99 %), Gaps = 0/923 (0 %)), *Phyllosticta* sp. (GenBank DQ377929; Identities = 849/856 (99 %), Gaps = 0/856 (0 %)) and *Guignardia citricarpa* (GenBank EU754165; Identities = 861/877 (98 %), Gaps = 4/877 (0 %)), amongst others.

Colour illustrations. *Hymenocallis littoralis* growing on campus at Charles Darwin University; flower; sporulation on oatmeal agar; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

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Myrmecridium phragmitis

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Myrmecridium phragmitis Crous, *sp. nov.*

Myrmecridii schulzeri simile, sed conidiis minoribus, (6.5–)7–8(–9) × (2.5–)3(–3.5) µm, discernitur.

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

On synthetic nutrient poor agar: *Hyphae submerged* and creeping, hyaline, thin-walled, 1–2 µm diam. *Conidiophores* arising vertically from creeping aerial hyphae, unbranched, straight, medium brown to reddish brown, thick-walled, 1–4-septate, up to 100 µm tall, 3.5–4.5 µm diam; basal cell somewhat inflated, 3–4 µm diam. *Conidiogenous cells* integrated, cylindrical, 25–50 µm long, pale brown, forming a rachis with scattered pimple-shaped denticles less than 1 µm long and approx. 0.5 µm wide, apically pointed, pigmented, slightly thickened. *Conidia* solitary, 0–1-septate, subhyaline, thin-walled, smooth, guttulate, surrounded by a wing-like gelatinous sheath, approx. 0.5 µm thick, ellipsoid to obovoid or fusoid, (6.5–)7–8(–9) × (2.5–)3(–3.5) µm, tapering to a subtruncate hilum; hilum unpigmented, not darkened.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies reaching up to 20 mm diam after 2 wk. On malt extract agar surface erumpent, slimy with sparse aerial mycelium, ropy hyphal strands and feathery, lobate margin; surface and reverse orange. On potato-dextrose agar erumpent, margin feathery, lobate, lacking aerial mycelium; surface and reverse luteous to orange. On oatmeal agar spreading, slimy, lacking aerial mycelium, with smooth margins; centre pale orange, margin saffron.

Typus. Netherlands, Bilthoven, Evert Cornelislaan No 11, on stems of *Phragmites australis* (*Poaceae*), 1 June 2011, *P.W. Crous*, holotype CBS H-20761, culture ex-type CPC 19028 = CBS 131311, ITS sequence GenBank JQ044425 and LSU sequence GenBank JQ044444, MycoBank MB560700.

Notes — The *Ramichloridium* complex was recently revised by Arzanlou et al. (2007), leading to the recognition and subsequent description of several genera, including *Myrmecridium*. The latter genus is characterised by having hyaline mycelium, and relatively unpigmented, pimple-like denticles. Two species are presently known, namely *M. schulzeri* (var. *schulzeri* and var. *tritici*) and *M. flexuosum*. *Myrmecridium phragmitis* is easily distinguished from these species by having 1-septate conidia. A megablast search of the NCBIs GenBank nucleotide sequence database using the ITS sequence of *M. phragmitis* retrieves as closest hits *Myrmecridium schulzeri* (GenBank EU041770; Identities = 526/545 (97 %), Gaps = 6/545 (1 %)) and *Myrmecridium flexuosum* (GenBank EU041768; Identities = 499/524 (95 %), Gaps = 9/524 (2 %)), amongst others. A megablast search of the NCBIs GenBank nucleotide sequence database using the LSU sequence supports this placement.

Colour illustrations. Harvested *Phragmites* being transported on a barge in the Netherlands (photographed by U. Damm during the CBS outing to Giethoorn); conidiophores giving rise to conidia; conidia (note wing-like gelatinous sheath). Scale bars = 10 µm.

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Phlogicylindrium uniforme

Fungal Planet 97 – 6 December 2011

Phlogicylindrium uniforme Crous & Summerell, *sp. nov.*

Phlogicylindrii eucalypti simile, sed conidiis minoribus, (14–)16–20(–21) × (1.5–)2(–2.5) µm, discernitur.

Etymology. Named after its cylindrical, highly uniformly conidia.

Occurring on lesions of living leaves in association with *Mycosphaerella* spp., probably as secondary invader. On pine needle agar: *Conidiomata* visible as slimy, erect tufts of hyaline conidial masses, resembling candle flames, synnematous, indeterminate; conidiomata gradually turn brown with age due to the slime binding the conidial mass. *Conidiophores* consisting of an intricate network of brown, smooth, branched cells, 2.5–4 µm wide. *Conidiogenous cells* subhyaline, smooth, becoming pale brown with age, ampulliform with elongated necks on which percurrent proliferations are clearly visible; 15–35 × 2–3 µm. *Conidia* formed apically on conidiogenous cells, hyaline, cylindrical with obtusely rounded ends, 1-septate, uniform in width, guttulate, (14–)16–20(–21) × (1.5–)2(–2.5) µm; conidia anastomosing while still aggregated in mucus on the conidiophore.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies after 2 wk on all media reaching 25 mm diam. On oatmeal agar lacking aerial mycelium, margin smooth, lobate, surface blood colour, with bay pigment diffusing into agar. On malt extract agar erumpent, lacking aerial mycelium, centre vinaceous-buff, outer margin blood, reverse blood to chestnut. On potato-dextrose agar lacking aerial mycelium with feathery margin, surface and reverse umber.

Typus. Australia, New South Wales, Berambing, Bells Line of Road, S 33°32'5.8" E 150°26'39.9", alt. 794 m, on leaves of *Eucalyptus cypellocarpa* (*Myrtaceae*), 16 Nov. 2010, *B.A. Summerell*, holotype CBS H-20762, cultures ex-type CPC 19419 = CBS 131312, ITS sequence GenBank JQ044426 and LSU sequence GenBank JQ044445, MycoBank MB560701.

Notes — The genus *Phlogicylindrium* was introduced in 2006 for *P. eucalypti*, a species associated with *Eucalyptus* leaves (Summerell et al. 2006). A second species, *P. eucalyptorum*, was subsequently described (Crous et al. 2007c). *Phlogicylindrium uniforme* can easily be distinguished from these two species based on its smaller conidia (14–21 × 1.5–2.5 µm), that also tend to be uniformly cylindrical in shape. Thus far the genus has only been reported from leaves of *Eucalyptus*. A megablast search of the NCBIs GenBank nucleotide sequence database using the ITS sequence of *P. uniforme* retrieves as closest hits *Phlogicylindrium eucalyptorum* (GenBank EU040223; Identities = 571/578 (99 %), Gaps = 0/578 (0 %)) and *Phlogicylindrium eucalypti* (GenBank DQ923534; Identities = 552/562 (98 %), Gaps = 3/562 (1 %)), amongst others. A megablast search of the NCBIs GenBank nucleotide sequence database using the LSU sequence of *P. uniforme* confirms this placement.

Colour illustrations. *Eucalyptus cypellocarpa*; conidiophores giving rise to conidia on pine needle agar; cylindrical, 1-septate conidia. Scale bars = 10 µm.

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Exosporium livistonae

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Exosporium livistonae Crous & Summerell, *sp. nov.*

Exosporii tiliae simile, sed conidiis minoribus, (45–)60–70(–80) × (7–)8(–10) µm, discernitur.

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

Leaf spots subcircular, 5–10 mm diam, pale brown with dark brown border, but also covering the leaf surface as prominent leaf tip dieback, with epiphyllous sporulation. *Conidiomata* fasciculate, forming a prominent brown stroma of *textura globulosa*, giving rise to fascicles of 2–80 conidiophores that are loosely aggregated, cylindrical, unbranched, straight to flexuous, olivaceous brown, finely verruculose throughout, basal cell somewhat swollen, up to 10 µm diam, walls 0.5 µm thick, 5–12-euseptate, 100–200 × 4–6 µm. *Conidiogenous cells* terminal and lateral, finely verruculose, olivaceous brown, integrated, proliferating sympodially, 15–70 × 4–6 µm; loci prominent, extending up to 1 µm diam, thickened, darkened, circular, 3–4 µm diam, with central pore, 0.5 µm diam. *Conidia* solitary, uniformly olivaceous brown and finely verruculous, 5-distoseptate, wall 2–3 µm thick; widest at second septum from base, septa with visible pore, tapering to subobtusely rounded apex; basal cell truncate, tapered towards hilum, thickened, darkened, 3–3.5 µm diam, somewhat protruding from conidial body, (45–)60–70(–80) × (7–)8(–10) µm.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies after 2 wk on all media reaching 30 mm diam, with sparse aerial mycelium and feathery, lobate margins. On malt extract agar surface folded, erumpent, pale mouse-grey to olivaceous grey. On oatmeal agar olivaceous grey, and on potato-dextrose agar olivaceous grey with reddish pigment diffusing into the agar.

Typus. Australia, Northern Territory, Litchfield National Park, on leaves of *Livistona benthamii* (*Arecaceae*), 25 Apr. 2011, *P.W. Crous & B.A. Summerell*, holotype CBS H-20763, cultures ex-type CPC 19357 = CBS 131313, ITS sequence GenBank JQ044427 and LSU sequence GenBank JQ044446, MycoBank MB560702.

Notes — *Exosporium* is characterised by having a stroma that gives rise to fasciculate conidiophores with sympodial proliferation, and darkened scars, each with a visible central pore. Conidia are brown, distoseptate, and have a truncate, somewhat darkened base (Ellis 1971, Seifert et al. 2011). The genus is based on *E. tiliae* (from *Tilia* in Germany) (Ellis 1961). A strain lodged in CBS as *E. tiliae* (CBS 484.77, CBS H-713, Québec, Canada) clustered in *Pleosporales*, and was shown to be a *Corynespora* species in the *C. olivacea* complex occurring on *Tilia*. *Corynespora olivacea* is commonly confused with *E. tiliae*, but is distinct by having short, 0–2-septate conidiophores with a single apical pore (Ellis 1960).

Exosporium livistonae is the first species of *Exosporium* described from *Livistona* (Taylor & Hyde 2003), given the fact that *Exosporium palmivorum* is not a member of *Exosporium* s.str. A megablast search of the NCBIs GenBank nucleotide sequence database using the ITS sequence of *E. livistonae* retrieves as closest hits *Mycosphaerella brassicicola* (*Capnodiales*, *Mycosphaerellaceae*; GenBank EU167607; Identities = 457/528 (87 %), Gaps = 30/528 (6 %)) and *Pseudocercospora ocimicola* (*Capnodiales*, *Mycosphaerellaceae*; GenBank GU214678; Identities = 461/533 (86 %), Gaps = 35/533 (7 %)), amongst others. A megablast search of the NCBIs GenBank nucleotide sequence database using the LSU sequence of *E. livistonae* retrieves as closest hits *Mycosphaerella marksii* (*Capnodiales*, *Mycosphaerellaceae*; GenBank GU214447; Identities = 896/933 (96 %), Gaps = 6/933 (1 %)), *Mycosphaerella dearnessii* (*Capnodiales*, *Mycosphaerellaceae*; GenBank GU214663; Identities = 897/935 (96 %), Gaps = 6/935 (1 %)) and *Mycosphaerella elaeocarpi* (*Capnodiales*, *Mycosphaerellaceae*; GenBank EU040212; Identities = 876/914 (96 %), Gaps = 8/914 (1 %)), amongst others. However, nucleotide sequences representing *Exosporium stylobatum* (strain CBS 160.30; ITS sequence GenBank JQ044428, LSU sequence GenBank JQ044447) and *Corynespora olivacea* (as *Exosporium tiliae*) (strain CBS 484.77; ITS sequence GenBank JQ044429, LSU sequence GenBank JQ044448) blasted with genera in *Pleosporales* and predominantly those belonging to *Massarinaceae* (see phylogenetic tree). No taxa resembling *Exosporium* in morphology have thus far been reported from *Mycosphaerellaceae* (Crous 2009), and thus this taxon appears to represents a novel genus.

Colour illustrations. *Livistona benthamii* in Litchfield National Park; fascicle of conidiophores; conidiophores giving rise to conidia (note base and scars at apex); conidia. Scale bar = 10 µm.

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Coleophoma eucalyptorum

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Coleophoma eucalyptorum Crous & Summerell, *sp. nov.*

Coleophomae cylindrosporae similis, sed conidiis minoribus, (10–)11–12(–14) × (2–)2.5 µm, discernitur.

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

Leaf spots angular to subcircular, 2–4 mm diam, dark brown, amphigenous. On pine needle agar. *Conidiomata* pycnidial, dark brown to black, globose, outer wall brown with crusty dark brown residue on outer cells, up to 250 µm diam, opening by means of central ostiole. *Conidiophores* lining the inner cavity, intermingled among paraphyses, hyaline, smooth, subcylindrical, guttulate, branched at base or not, 0–3-septate, at times reduced to conidiogenous cells, 5–12 × 3–5 µm. *Paraphyses* intermingled among conidiophores, hyaline, smooth, cylindrical or elongated-clavate, transversely multiseptate or with basal septum only, 2–5 µm diam, up to 80 µm long, branched below or not; those paraphyses that become multiseptate, tend to become fertile, with each cell turning into a conidiogenous cell with single locus, resulting in branches of conidiogenous cells. *Conidiogenous cells* hyaline, smooth, guttulate (in lactic acid, not in Shear's solution), doliiform to ampulliform, with visible periclinal thickening, 5–9 × 3–4 µm; conidiogenous cells mostly solitary, but at times in chains on old paraphyses that become septate and fertile. *Conidia* hyaline, smooth, guttulate, cylindrical, apex obtuse, base with flattened, truncate locus, (10–)11–12(–14) × (2–)2.5 µm.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies after 2 wk reaching 40–50 mm on oatmeal agar (OA) and potato-dextrose agar (PDA), but only up to 12 mm diam on malt extract agar (MEA). On MEA colonies erumpent with moderate aerial mycelium, and lobate, smooth margins; surface pale olivaceous grey to olivaceous grey with patches of dirty white; reverse olivaceous grey. On OA olivaceous grey with patches of iron-grey due to wet mycelium. On PDA surface olivaceous grey, reverse iron-grey.

Typus. Australia, New South Wales, Blue Mountains, Kurrajong Heights, S 33°22'25.4" E 150°37'55.7", on leaves of *Eucalyptus piperita* (*Myrtaceae*), 16 Nov. 2010, *B.A. Summerell*, holotype CBS H-20770, cultures ex-type CPC 19299 = CBS 131314, ITS sequence GenBank JQ044430 and LSU sequence GenBank JQ044449, MycoBank MB560703.

Notes — The present collection closely matches other species in the genus *Coleophoma*, having pycnidia that give rise to phialidic conidiogenous cells intermingled among paraphyses, as well as cylindrical, aseptate, hyaline conidia. Sutton (1980) reported *C. empetri* to occur on *Eucalyptus* (conidia 12.5–18 × 2–3 µm), while Yuan (1996) described *C. eucalypti* from leaves of *E. pellita* collected on Melville Island, Australia (conidia 7–11 × 1.5–2 µm). *Coleophoma eucalyptorum* can easily be distinguished from these species in having conidia that are different in size (10–14 × 2–2.5 µm). Although Yuan (1996) reported *C. eucalypti* to be associated with defoliation of *E. pellita*, *C. eucalyptorum* has only been associated with leaf spots on *E. piperita*, and pathogenicity still remains to be proven. A megablast search of the NCBIs GenBank nucleotide sequence database using the ITS sequence of *C. eucalyptorum* retrieves as closest hits numerous sequences of *Coleophoma empetri* (GenBank FJ480134; Identities = 521/533 (98 %), Gaps = 1/533 (0 %)). A megablast search of the NCBIs GenBank nucleotide sequence database using the LSU sequence of *C. eucalyptorum* retrieves as closest hits *Coleophoma empetri* (GenBank FJ588252; Identities = 918/920 (99 %), Gaps = 0/920 (0 %)), *Coleophoma maculans* (GenBank EU754147; Identities = 870/875 (99 %), Gaps = 0/875 (0 %)) and *Cryptosporiopsis actinidiae* (GenBank HM595594; Identities = 933/944 (99 %), Gaps = 0/944 (0 %)), amongst others.

Colour illustrations. *Eucalyptus piperita*; conidiomata forming on synthetic-nutrient poor agar; conidiophores and conidiogenous cells intermingled among paraphyses, with cylindrical conidia. Scale bar = 10 µm.

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Camarographium carpini

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Camarographium carpini Melnik, Crous & Verkley, *sp. nov.*

Camarographii koreani simile, sed conidiis majoribus, (50–)54–58(–60) × (19–)20–22(–24) µm, discernitur.

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

Conidiomata pycnidial, numerous, separate, dispersed, single, subepidermal, (200–)450–700(–1000) µm diam, unilocular, completely immersed in the bark of the host, globose, rarely slightly depressed, with central, 50–80 µm wide ostiolum, which is almost inconspicuous and has an indistinct pore perforating the bark in a notably raised area; the location of mature pycnidia is not easy to note due to the slimy mass of extruded yellowish brown conidia. *Conidiomatal wall* up to 100 µm thick, composed at the outer layers of thick-walled, dark brown *textura angularis*, and at the inner layers of thin-walled, subhyaline *textura angularis*; the most inner layer gives rise to conidiogenous cells lining the internal chamber of the whole conidioma; mature conidiomata tend to have empty locules. *Paraphyses* intermingled among conidiogenous cells in some conidiomata, hyaline, smooth, subcylindrical with obtuse ends, 1–4-septate, up to 50 µm long, 2–3.5 µm diam, extending above the conidiogenous cells. *Conidiogenous cells* hyaline, discrete, holoblastic, annellidic, with 1–2 percurrent proliferations, broadly ampulliform or doliiform, 8–12 × 8–10 µm. *Conidia* abundant, initially subhyaline, but later becoming yellowish brown in pycnidia, extruding in a slimy mass; young, subhyaline conidia have 3–5 transversal distosepta, whereas in mature conidia the compartments between the septa develop bodies (endoconidia?) that are ellipsoid to subglobose, thick-walled, verruculose, (3–)5–8(–10) × (3–)5–7 µm, at times guttulate, and get released in clusters of 4, in sacks that appear to be the remnants of the conidial compartments. Outer conidial wall smooth, subhyaline, 1 µm thick; conidia oblong-ellipsoidal or slightly clavate, sometimes with light constriction in median point, (50–)54–58(–60) × (19–)20–22(–24) µm, with 3.5–4(–5) µm diam scar at the base.

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

Typus. Russia, St. Petersburg, Botanical Garden of the Komarov Botanical Institute, on thin, dried twigs of *Carpinus betulus* (*Betulaceae*), 27 Sept. 2010, *V. Mel'nik*, (holotype LE 226162; paratypes LE 261808, LE 261817; isotypes HAL 2424 F, CBS H-20506), cultures ex-isotype CPC 18919, 18918 = CBS 128781, ITS sequence GenBank JQ044431 and LSU sequence GenBank JQ044450, MycoBank MB560014.

Notes — In September 2010, V. Mel'nik collected an interesting coelomycete on dried twigs of *Carpinus betulus* in the Botanical Garden of the Komarov Botanical Institute (St. Petersburg, Russia). The pycnidial conidiomata, holoblastic annellidic conidiogenous cells and distoseptate, pale coloured conidia provided clues to the fact that this specimen could belong to the *Shearia-Camarosporium-Stegonsporiopsis-Camarographium* group. Verkley et al. (2005) published a detailed survey of these genera. Further investigations revealed this specimen to belong to *Camarographium*. A comparison of the fungus from *Carpinus betulus* with published descriptions revealed this collection to represent a new species of *Camarographium*, most similar to *C. koreanum. Camarographium carpini* can be distinguished from *C. koreanum* in that the conidial exudate of *C. koreanum* remains white (vs yellow-brown), and its conidia are narrower (52–62 × 17–19.5 µm) (Verkley et al. 2005). A megablast search of the NCBIs GenBank nucleotide sequence database using the ITS sequence of *C. carpini* retrieves as closest hits *Preussia africana* (GenBank EU551208; Identities = 435/484 (90 %), Gaps = 14/484 (3 %)) and *Preussia flanaganii* (GenBank AY943061; Identities = 453/506 (90 %), Gaps = 22/506 (4 %)), amongst others. However, the ITS sequence is distant to *Camarographium koreanum* strain CBS 117159 (ITS sequence GenBank JQ044432; Identities = 434/535 (81 %), Gaps = 46/535 (9 %)). A megablast search of the NCBIs GenBank nucleotide sequence database using the LSU sequence of *C. carpini* retrieves as closest hits *Preussia dubia* (GenBank GQ203736; Identities = 922/945 (98 %), Gaps = 6/945 (1 %)), *Sporormiella pulchella* (GenBank GQ203747; Identities = 921/944 (98 %), Gaps = 4/944 (0 %)) and *Sporormia fimetaria* (GenBank GQ203728; Identities = 920/944 (97 %), Gaps = 4/944 (0 %)), amongst others. Similar to the ITS sequence, the LSU sequence is distant to *Camarographium koreanum* strain CBS 117159 (LSU sequence GenBank JQ044451; Identities = 900/948 (95 %), Gaps = 10/948 (1 %)). *Camarographium carpini* is not congeneric with *C. koreanum*, and fresh collections of the type species, *C. stephensii*, would be required to resolve the generic phylogeny.

Key to Camarographium species (adapted from Verkley et al. 2005)

1. Conidiomata in linear stromata, on petioles of *Pteridium aquilinum*, conidia 22–28 µm wide . . . . . *C. stephensii*
1. Conidiomata pycnidial, on other substrata 2
2. Conidia up to 20 µm wide 3
2. Conidia smaller 4
3. Conidia 52–62 × 17–19.5 µm, extruding a white conidial mass, immersed in bark of *Cornus kousa*, microconidia present . . . . . *C. koreanum*
3. Conidia 50–60 × 19–24 µm, extruding a yellowish brown conidial mass, immersed in bark of *Carpinus betulus*, microconidia absent . . . . . *C. carpini*
4. Conidia hyaline, 14.5–16 × 4–7 µm, on leaves of *Atriplex moneta* . . . . . *C. atriplicis*
4. Conidia brown, on other substrata 5
5. Conidia 5.6–7.5 µm wide, on fruits of *Prunus domestica* . . . . . *C. fructicola*
5. Conidia 7–12 µm wide, on spines of *Acacia sphaerocephala* . . . . . *C. indicum*

Colour illustrations. Carpinus betulus growing in the Botanical Garden of the Komarov Botanical Institute, St. Petersburg; transverse section through conidiomata, revealing cavities; conidia, with young conidium attached to conidiogenous cell; broken conidium revealing endoconidia. Scale bars = 10 µm.

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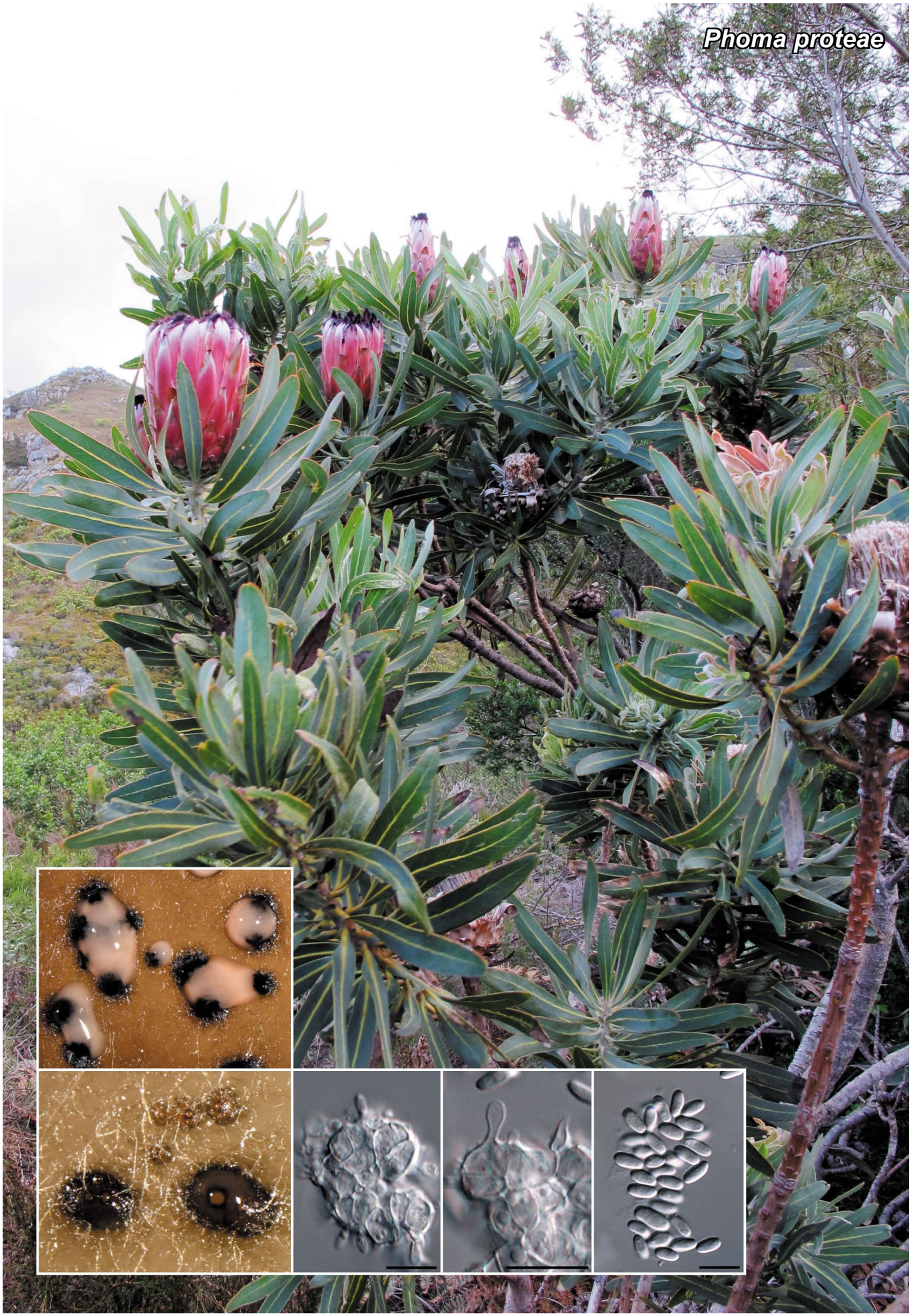
Phoma proteae

Fungal Planet 101 – 6 December 2011

Phoma proteae Crous, *sp. nov.*

Phomae huancayensis similis, sed conidiis minoribus, (4.5–)5–6.5(–7) × (2.5–)3(–3.5) µm, discernitur.

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

Leaf spots circular to subcircular, up to 2 cm diam, dark brown, amphigenous, or associated with leaf tip dieback. On pine needle agar. *Conidiomata* pycnidial, brown, globose, erumpent, solitary or aggregated, smooth, with central ostiole, up to 50 µm diam, darker brown at ostiolar area, with elongated, globoid cells extending into cavity, brown at base, hyaline at apex, up to 15 µm long and 4 µm wide; wall consisting of 2–3 layers of brown *textura angularis*. *Conidiogenous cells* phialidic, ampulliform to doliiform, lining the inner cavity, hyaline, smooth, with visible periclinal thickening, 5–7 × 5–7 µm. *Conidia* hyaline, smooth, broadly ellipsoid with obtuse ends, (4.5–)5–6.5(–7) × (2.5–)3(–3.5) µm. *Chlamydospores* not seen (also not on other agar media).

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies flat, spreading, with moderate aerial mycelium and regular, even margins, covering the dish in 2 wk. On oatmeal agar surface grey olivaceous, with salmon spore masses in centre. On malt extract agar olivaceous grey in centre, dirty white to smoke-grey in outer region; iron-grey on reverse, cinnamon in outer region. On potato-dextrose agar olivaceous grey on surface, and iron-grey on reverse.

Typus. South Africa, Western Cape Province, Somerset West, Karibia Farm, on leaves of *Protea* cv. Carnival (*P. compacta* × *P. neriifolia*) (*Proteaceae*), 21 July 1998, *J.E. Taylor & S. Denman*, holotype CBS H-20771, cultures ex-type CPC 1854 = CBS 114179, ITS sequence GenBank JQ044433 and LSU sequence GenBank JQ044452, MycoBank MB560705.

Notes — Crous et al. (2004) report *Phoma sorghina* to be associated with Phoma brown stem canker of *Leucospermum cordifolium* (*Proteaceae*), while Marincowitz et al. (2008) report several *Phoma* spp. as saprobes on *Proteaceae* leaf and twig litter. *Phoma proteae*, which is associated with leaf spots on *Protea* 'Carnival', appears to represent a novel species, not matching any of those recently circumscribed (Aveskamp et al. 2009, 2010, de Gruyter et al. 2009, 2010). A megablast search of the NCBIs GenBank nucleotide sequence database using the ITS sequence of *P. proteae* retrieves as closest hits *Coniothyrium fuckelii* (GenBank AB665314; Identities = 518/523 (99 %), Gaps = 2/523 (0 %)) and several *Phoma* species with identical similarities (Identities = 517/522 (99 %), Gaps = 1/522 (0 %)), e.g. *Phoma herbarum* (GenBank AB456575), *Phoma glomerata* (GenBank EU273521) and *Phoma pomorum* (GenBank AY904062), amongst others. Performing a similar search against the *Phoma* database present in Q-bank (www.q-bank.eu), retrieves high identity to *Phoma huancayensis* strain CBS 105.80 (conidia larger, 4–12 × 2.5–4.5 µm; Boerema et al. 2004) (Identities = 483/486 (99 %), Gaps = 0/486 (0 %)). A megablast search of the NCBIs GenBank nucleotide sequence database using the LSU sequence of *P. proteae* confirms the placement based on ITS.

Colour illustrations. *Protea neriifolia* growing on the mountain slopes; conidiomata sporulating on malt extract agar and oatmeal agar; conidiogenous cells, and conidia. Scale bars = 10 µm.

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Pyrenochaeta protearum

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Pyrenochaeta protearum Crous, *sp. nov.*

Pyrenochaetae nobilis similis, sed conidiis minoribus, (3–)4–5(–6) × 2–2.5(–3) µm, discernitur.

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

Leaf spots not seen, presumed endophyte sporulating under moist conditions. On pine needle agar. *Mycelium* consisting of hyaline to pale brown, smooth, to finely verruculose 2–3 µm hyphae, forming intercalary chains of brown, ellipsoid chlamydospores, 8–15 µm diam. *Conidiomata* solitary, up to 300 µm diam, globose, brown, with central ostiole, surrounded by dark brown setae that are septate, straight, thick-walled, with obtuse ends, up to 100 µm tall, 4–5 µm diam. *Conidiogenous cells* phialidic, lining the cavity, hyaline, smooth, subcylindrical to ampuliform, 5–7 × 3–5 µm; apex 1–1.5 µm diam. *Conidia* hyaline, smooth, aseptate, guttulate or not, ellipsoid with obtuse ends, (3–)4–5(–6) × (2–)2.5(–3) µm.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies flat, spreading, with sparse aerial mycelium and even, lobate margins, reaching 25 mm diam after 2 wk. On oatmeal agar surface grey olivaceous. On malt extract agar olivaceous grey in centre, with patches of smoke-grey, olivaceous grey in reverse. On potato-dextrose agar olivaceous grey on surface and reverse.

Typus. South Africa, Western Cape Province, Hermanus, Fernkloof Nature Reserve, on leaves of *Protea mundii* (*Proteaceae*), 4 May 2010, *P.W. Crous*, holotype CBS H-20772, cultures ex-type CPC 18322 = CBS 131315, ITS sequence GenBank JQ044434 and LSU sequence GenBank JQ044453, MycoBank MB560706.

Notes — *Pyrenochaeta protearum* was isolated from asymptomatic leaves and is assumed to be endophytic. Morphologically it can be distinguished from *Phoma proteae* (conidia 4.5–7 × 2.5–3.5 µm) by having smaller conidia, and conidiomata with setae. A megablast search of the NCBIs GenBank nucleotide sequence database using the ITS sequence of *P. protearum* retrieves as closest hits *Pyrenochaetopsis microspora* (GenBank HM751085; Identities = 371/393 (94 %), Gaps = 17/393 (4 %)) and *Monodictys arctica* (GenBank EU686521; Identities = 378/425 (89 %), Gaps = 26/425 (6 %)), amongst others. Performing a similar search against the *Phoma* database present in Q-bank (www.q-bank.eu), retrieves high identity to *Pyrenochaeta dolichi* strain CBS 124143 (Identities = 362/398 (91 %), Gaps = 22/398 (6 %)). A megablast search of the NCBIs GenBank nucleotide sequence database using the LSU sequence of *P. protearum* retrieves as closest hits *Leptosphaeria macrospora* (GenBank DQ384092; Identities = 924/944 (98 %), Gaps = 2/944 (0 %)), *Phaeosphaeriopsis musae* (GenBank DQ885894; Identities = 922/944 (98 %), Gaps = 3/944 (0 %)) and *Coniothyrium obiones* (GenBank DQ678054; Identities = 903/920 (98 %), Gaps = 0/920 (0 %)), amongst others.

Colour illustrations. *Protea mundii* in the Fernkloof Nature Reserve, Hermanus, South Africa; conidiomata forming on oatmeal agar and malt extract agar; conidiomatal wall that tends to develop setae; conidiogenous cells; conidia. Scale bars = 10 µm.

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Phaeomoniella niveniae

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Phaeomoniella niveniae Crous, *sp. nov.*

Phaeomoniellae prunicolae similis, sed conidiis majoribus, 3–4(–5) × 1.5(–2) µm, discernitur.

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

Leaf spots subcircular, brown, amphigenous, up to 6 mm diam, or associated with leaf tip blight. On pine needle agar. *Mycelium* thick-walled, hyaline, covered in mucoid sheath, septate, branched, 2–4 µm diam. *Conidiomata* pycnidial, up to 250 µm diam, green-brown, aggregated, opening by irregular rupture, wall of 2–3 layers of *textura angularis*. *Conidiophores* hyaline, smooth, subcylindrical, consisting of dense clusters of conidiogenous cells, 1–5-septate, 5–20 × 3–4 µm. *Conidiogenous cells* hyaline, smooth, subcylindrical to ampulliform, terminal and lateral, 4–7 × 2.5–3 µm, monophialidic, opening 1–1.5 µm diam with minute collarette. *Conidia* hyaline, smooth, baciliform to ellipsoid, with rounded ends, 3–4(–5) × 1.5(–2) µm. *Chlamydospores* not seen.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies erumpent, spreading, with folded surface and feathery, lobed margins, reaching 15 mm diam after 2 wk. On potato-dextrose agar primrose with patches of dark herbage green due to sporulation, reverse primrose. On malt extract agar surface honey with patches of isabelline due to sporulation, reverse honey. On oatmeal agar concolorous with medium, with isabelline patches due to sporulation; colonies with sweet fruity odour.

Typus. South Africa, Western Cape Province, Betties Bay, Harold Porter Botanical Garden, on leaves of *Nivenia stokoei*, 4 May 2010, *P.W. Crous*, holotype CBS H-20773, cultures ex-type CPC 18231 = CBS 131316, ITS sequence GenBank JQ044435 and LSU sequence GenBank JQ044454, MycoBank MB560707.

Notes — The genus *Phaeomoniella* was established for *P. chlamydospora*, a species commonly associated with Petri disease of grapevines (Crous & Gams 2000, Mostert et al. 2006). Subsequent to this, additional species have been recorded from hosts such as *Encephalartos* (Crous et al. 2008), pines (Lee et al. 2006), and fruit trees (Damm et al. 2010). *Phaeomoniella niveniae* can be distinguished from the taxa presently recognised based on its conidial dimensions, culture characteristics, and distinct DNA phylogeny. A megablast search of the NCBIs GenBank nucleotide sequence database using the ITS sequence of *P. niveniae* retrieves as closest hits *Phaeomoniella zymoides* (GenBank GQ154600; Identities = 537/552 (97 %), Gaps = 5/552 (1 %)), *Phaeomoniella capensis* (GenBank FJ372391; Identities = 573/652 (88 %), Gaps = 47/652 (7 %)) and numerous other sequences identified as *Phaeomoniella* sp. A megablast search of the NCBIs GenBank nucleotide sequence database using the LSU sequence of *P. niveniae* retrieves as closest hits *Xenocylindrosporium kirstenboschense* (GenBank GU229891; Identities = 811/874 (93 %), Gaps = 17/874 (2 %)), *Phaeomoniella capensis* (GenBank FJ372408; Identities = 802/875 (92 %), Gaps = 17/875 (2 %)) and *Capronia villosa* (GenBank AF050261; Identities = 836/918 (91 %), Gaps = 26/918 (3 %)), amongst others.

Colour illustrations. *Nivenia stokoei* growing at the Harold Porter Botanical Garden, Betties Bay, South Africa; colonies sporulating on potato-dextrose agar and oatmeal agar; conidiophores; conidia. Scale bars = 10 µm.

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Toxicocladosporium leucadendri

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Toxicocladosporium leucadendri Crous, *sp. nov.*

Toxicocladosporium rubrigenae similis, sed conidiis majoribus, (6–)7–8(–9) × (2.5–)3(–4) µm, discernitur.

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

Leaf spots absent, sporulating on dead tissue under moist conditions. On synthetic nutrient poor agar. *Mycelium* consisting of pale brown, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* solitary, erect, unbranched or branched above, subcylindrical, straight to flexuous, 50–150 × 3–5 µm, 6–15-septate, apical septum becoming dark brown and thickened. *Conidiogenous cells* integrated, polyblastic, terminal and lateral, subcylindrical, smooth, brown, 8–20 × 4–6 µm; scars truncate, thickened and darkened, 3–4 µm diam. *Primary ramoconidia* medium brown, verruculose to warty, 1–2-septate, 25–45 × 3–5 µm. *Secondary ramoconidia* giving rise to branched chains of conidia, subcylindrical, polyblastic, brown, verruculose to warty, 0–1-septate, 15–20 × 3–4 µm, frequently forking close to apex; scars darkened, thickened, 1.5–2.5 µm diam. *Intercalary conidia* subcylindrical to fusoid-ellipsoidal, brown, smooth to somewhat warty, 9–11(–15) × (2.5–)3(–4) µm. *Small terminal conidia* fusoid-ellipsoidal, brown, smooth, (6–)7–8(–9) × (2.5–)3(–4) µm; hila thickened and darkened, 0.5–1 µm diam.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies spreading, flat, with even, lobed margins, and irregular surface, reaching 30 mm diam after 2 wk. On potato-dextrose agar pale smoke-grey in centre, becoming olivaceous grey in outer region, and honey at margin. On malt extract agar surface with patches of smoke grey and iron-grey in middle, honey in outer region. On oatmeal agar iron-grey with patches of olivaceous grey and dirty white.

Typus. South Africa, Western Cape Province, Hermanus, Fernkloof Nature Reserve, on leaves of *Leucadendron* sp. (*Proteaceae*), 4 May 2010, *P.W. Crous*, holotype CBS H-20774, cultures ex-type CPC 18315 = CBS 131317, ITS sequence GenBank JQ044436 and LSU sequence GenBank JQ044455, MycoBank MB560708.

Notes — The genus *Toxicocladosporium* (*Davidiellaceae*) is somewhat reminiscent of *Penidiella* (*Teratosphaeriaceae*) (Crous et al. 2007a, b, Crous et al. 2011b). *Toxicocladosporium leucadendri* differs from known taxa, many of which also occur in the fynbos vegetation (Crous et al. 2011b), based on a combination of culture characteristics, conidiophore and conidial dimensions. A megablast search of the NCBIs GenBank nucleotide sequence database using the ITS sequence of *P. leucadendri* retrieves as closest hits *Graphiopsis chlorocephala* (GenBank EU009456; Identities = 595/712 (84 %), Gaps = 51/712 (7 %)) and *Verrucocladosporium dirinae* (GenBank EU040244; Identities = 470/516 (91 %), Gaps = 17/516 (3 %)), amongst others. A megablast search of the NCBIs GenBank nucleotide sequence database using the LSU sequence of *P. leucadendri* retrieves as closest hits *Graphiopsis chlorocephala* (GenBank EU009458; Identities = 922/935 (99 %), Gaps = 0/935 (0 %)), *Verrucocladosporium dirinae* (GenBank EU040244; Identities = 896/910 (98 %), Gaps = 0/910 (0 %)) and *Rachicladosporium cboliae* (GenBank GU214484; Identities = 846/866 (98 %), Gaps = 9/866 (1 %)), amongst others.

Colour illustrations. View from the mountain at Fernkloof Nature Reserve, Hermanus, South Africa; colonies sporulating on oatmeal agar; conidiophores with branched chains of conidia forming on synthetic nutrient-poor agar. Scale bars = 10 µm.

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Scorias leucadendri

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Scorias leucadendri Crous, *sp. nov.*

Scorias spongiosae simile, sed conidiis majoribus, 3–4(–5) × 1.5(–2) µm, discernitur.

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

Leaf spots absent, sporulating on dead tissue under moist conditions. On synthetic nutrient poor agar. *Mycelium* consisting of olivaceous green hyphae, 2–6 µm diam, septate, branched, constricted at septa, forming hyphal ropes, thick-walled, warty, frequently encased in mucoid sheath. *Conidiomata* pycnidial, stalked, flask-shaped, separate or in clusters of 2–4, erect, straight to slightly flexuous, base brown, 20–30 µm diam, widest in middle of subcylindrical part, dark olivaceous brown, swollen, 180–600 × 16–50 µm; body consisting of dark brown, spirally twisted hyphae along the length of conidiomata, 3–5 µm diam; apex 12–17 µm diam, loose apical hyphae flaring, subhyaline, septate, 35–100 × 2.5–3.5 µm. *Conidiogenous cells* lining the inner cavity, phialidic, 3–6 × 3–4 µm, tapering to a truncate apex, with periclinal thickening. *Conidia* broadly ellipsoid with rounded ends, aseptate, eguttulate, hyaline, smooth, 3–4(–5) × 1.5(–2) µm, aggregating in hyaline, slimy masses at apex of synnemata.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies spreading, flat, with sparse to moderate aerial mycelium, and even, lobate margins; reaching 20 mm diam after 2 wk. On potato-dextrose agar grey olivaceous on surface and underneath. On malt extract agar surface olivaceous black and slimy in centre, grey olivaceous in outer region, iron-grey underneath. On oatmeal agar olivaceous grey in centre, iron-grey in outer region.

Typus. South Africa, Western Cape Province, Hermanus, Fernkloof Nature Reserve, on leaves of *Leucadendron muirii* (*Proteaceae*), 4 May 2010, *P.W. Crous*, holotype CBS H-20775, cultures ex-type CPC 18312 = CBS 131318, ITS sequence GenBank JQ044437 and LSU sequence GenBank JQ044456, MycoBank MB560709.

Notes — *Scorias leucadendri* is a typical species of *Scorias* with its elongated, flask-shaped pycnidia, narrow neck and ostiolar hyphae, though it is reminiscent of *Leptoxyphium* (Cheewangkoon et al. 2009, Crous et al. 2011a). It is distinct from other species of *Scorias* based on it having a body consisting of dark brown, spirally twisted hyphae running along the length of its conidiophores, its conidial dimensions, and lacking a sponge-like subiculum. A megablast search of the NCBIs GenBank nucleotide sequence database using the ITS sequence of *L. leucadendri* retrieves as closest hits *Scorias spongiosa* (GenBank GU214696; Identities = 629/646 (97 %), Gaps = 4/646 (1 %)), *Antennariella placitae* (GenBank GQ303268; Identities = 455/495 (92 %), Gaps = 22/495 (4 %)) and *Leptoxyphium kurandae* (GenBank JF951150; Identities = 583/661 (88 %), Gaps = 44/661 (7 %)), amongst others. A megablast search of the NCBIs GenBank nucleotide sequence database using the LSU sequence of *L. leucadendri* retrieves as closest hits *Scorias spongiosa* (GenBank GU214696; Identities = 935/942 (99 %), Gaps = 4/942 (0 %)), *Fumagospora capnodioides* (GenBank EU019269; Identities = 844/872 (97 %), Gaps = 10/872 (1 %)) and *Graphiopsis chlorocephala* (GenBank EU009458; Identities = 912/945 (97 %), Gaps = 14/945 (1 %)), amongst others.

Colour illustrations. *Leucadendron muirii* growing in Fernkloof Nature Reserve, Hermanus, South Africa; colonies sporulating on malt extract agar; conidiomata with spirally twisted hyphae along the length of conidiophores, and loose apical hyphae; conidia. Scale bars = 10 µm.

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Leptosphaeria proteicola

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Leptosphaeria proteicola Crous, *sp. nov.*

Microsphaeropsis proteae similis, sed conidiis majoribus, (3.5–)4.5–5(–7) × (2.5–)3(–4) µm, discernitur.

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

Leaf spots absent, sporulating on dead tissue under moist conditions. On synthetic nutrient poor agar. *Conidiomata* pycnidial, dark brown to black, aggregated in clusters, pycnidia up to 400 µm diam, opening by means of central ostiole, up to 50 µm diam; wall of 2–3 layers of dark brown *textura angularis*. *Conidiophores* hyaline, smooth, subcylindrical, reduced to conidiogenous cells or 1–2-septate, 7–17 × 3–6 µm. *Conidiogenous cells* hyaline, smooth, ampulliform to subcylindrical, phialidic, 5–10 × 3–6 µm; locus 1.5–2 µm diam, with inconspicuous collarette. *Conidia* solitary, initially hyaline, smooth, aseptate, becoming red-brown, thin-walled, ellipsoid to obovoid, apex obtuse, base truncate, (3.5–)4.5–5(–7) × (2.5–)3(–4) µm; hilum truncate or bluntly rounded, unthickened, 2–3 µm diam.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies spreading, with fluffy aerial mycelium, and even, smooth margins; reaching 40 mm diam after 2 wk. On potato-dextrose agar surface olivaceous grey, reverse iron-grey with sectors of olivaceous grey. On malt extract agar surface olivaceous grey with patches of smoke-grey; margin honey, frequently sectored; iron-grey underneath, with patches of olivaceous grey and honey at margin. On oatmeal agar smoke-grey with margins concolorous with agar medium.

Typus. South Africa, Western Cape Province, Hermanus, Fernkloof Nature Reserve, on leaves of *Protea repens* (*Proteaceae*), 4 May 2010, *P.W. Crous*, holotype CBS H-20776, cultures ex-type CPC 18357 = CBS 131319, ITS sequence GenBank JQ044438 and LSU sequence GenBank JQ044457, MycoBank MB560710; Western Cape Province, Hermanus, Fernkloof Nature Reserve, on leaves of *P. mundii*, 4 May 2010, *P.W. Crous*, cultures CPC 18290, 18289, ITS sequence GenBank JQ044439 and LSU sequence GenBank JQ044458.

Notes — *Leptosphaeria proteicola* was initially considered to represent a species of *Coniothyrium* or *Microsphaeropsis*, similar to *M. proteae* (Swart et al. 1998), based on the fact that conidia become brown at maturity. Phylogenetically, however, it clusters with species of *Leptosphaeria*, and is thus described in this genus. A megablast search of the NCBIs GenBank nucleotide sequence database using the ITS sequence of *P. proteicola* retrieves little hits with high similarity to identified sequences. A megablast search of the NCBIs GenBank nucleotide sequence database using the LSU sequence of *L. proteicola* retrieves as closest hits *Leptosphaeria biglobosa* (GenBank GU237980; Identities = 869/878 (99 %), Gaps = 0/878 (0 %)), *Phoma violicola* (GenBank GU238156; Identities = 869/879 (99 %), Gaps = 2/879 (0 %)) and *Phoma dimorphospora* (GenBank GU238069; Identities = 869/880 (99 %), Gaps = 3/880 (0 %)), amongst others. Comparing the ITS and LSU sequences of *L. proteicola* with that of *M. proteae* strain CPC 1423 yielded an identity value of 88 % (GenBank JN712495; Identities = 422/479 (88 %), Gaps = 18/479 (4 %)) and 97 % (GenBank JN712561; Identities = 830/855 (97 %), Gaps = 6/855 (1 %)) for ITS and LSU respectively.

Colour illustrations. *Protea repens* growing in the Fernkloof Nature Reserve, Hermanus, South Africa; colonies sporulating on oatmeal agar; conidiogenous cells; conidia. Scale bars = 10 µm.

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