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*, *Phlegicylindrium uniforme* on *Eucalyptus cypellocarpa*, *Exosporium livistoneae* 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 *Nivienia stokoei*, *Toxicocephalosporium leucadendri* on *Leucadendron* sp. and *Scorias leucadendri* on *Leucadendron munii*. 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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**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*, *Phlegicylindrium uniforme* on *Eucalyptus cypellocarpa*, *Exosporium livistoneae* 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 *Nivienia stokoei*, *Toxicocephalosporium leucadendri* on *Leucadendron* sp. and *Scorias leucadendri* on *Leucadendron munii*. 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 rRNA 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
Fungal Planet 92 – 6 December 2011

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

*Phomopsis phyllanthicola* similis, sed conidios 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. *Conidigenous 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 potatosaccharose 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.
Pseudoidriella Crous & R.G. Shivas, gen. nov.


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, transverse 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 MB560896.

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

Conidiomata sporodochialia, massis sporarum erectis, fimmuliformibus. Conidiophora subcylindrica, laevia, hyalina, ramosa, 0–4-septata, 10–50 × 3–4 µm. Cellulæ conidiogenæ hyalinae, leaves, terminales vel laterales, 10–15 × 2–3 µm; symposium septata. 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-septated, 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, guttulata, 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, apices obtusae, basi truncatae, in medio 1-septata, (39–)45–50(–53) × (2.5–)3(–4) µm.


Notes — Morphologically Pseudoidriella resembles the genus Idriella (based on I. lunata, a soilborne fungus) (anamorphic Helotiaceae), which is characterised by smooth, pale brown conidiophores with sympodial proliferation, hyaline, smooth, aseptate, falcate conidia, and dark brown chlamydospores (Ellis 1971, Sefert 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 (Sefert 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 = 7/445 (2 %)), 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 NCBI 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.
Seiridium banksiae Crous & Summerell, sp. nov.


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

*Phyllostictae citricarpeae similis, sed conidiis minoribus, (8–)9–10(–11) × (6–)6.5–7 µm, discemittur.*

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

Associated with brown leaf spots and leaf tip blight. *Conidia*-mata 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 conidigenous cells, or with 1–2 supporting cells, at times branched at base, 10–25 × 4–7 µm. *Conidiogenous cells* terminal, subcylindrical to doliform, 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, asceptate, thin and smooth walled, coarsely guttulate, or with large, single, central guttule, ellipsoid to obvoid, 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 olivaceousgrey; 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.

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

**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, F.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, F.W. Crous & B.A. Summerell, CBS H-20760, cultures CPC 19330, 19329 = CBS 131310, ITS sequence GenBank JQ044442.

*Notes.* — During a meeting of the Australasian Society for Plant Pathology in Darwin (April 2011), a serious leaf spot and 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 hymenocallidicola*, 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 NCBI's GenBank nucleotide sequence database using the ITS sequence of *P. hymenocallidicola* 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 NCBI's GenBank nucleotide sequence database using the LSU sequence of *P. hymenocallidicola* 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.

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**Myrmecridium phragmitis** Crous, *sp. nov.*

*Myrmecridium* 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 un-pigmented, 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 surface 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.

**Typos.** 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 NCBI’s 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 NCBI’s GenBank nucleotide sequence database using the LSU sequence supports this placement.
Phlogicylindrium uniforme
**Phlogicylindrium uniforme** Crous & Summerell, *sp. nov.*

*Phlogicylindrium 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. *Conidigenous 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 conidigenous 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 NCBI’s 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 NCBI’s 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.*
Exosporium livstonae Crous & Summerell, sp. nov.

Exosporium tiliae simile, sed conidii minoribus. (45–)60–70–(80) 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 verruculose, 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 agar, mycelium darkened, 100–200 µm, discernitur. Exosporium palmivorum is not a member of Exosporium s.str. A megablack search of the NCBI GenBank nucleotide sequence database using the ITS sequence of E. livstonae retrieves as closest hits Mycosphaerella brassicicola (Capnodiales, Mycosphaerellaceae; GenBank EU167607; Identities = 457/528 (87 %), Gaps = 30/528 (6 %)) and Pseudocercospora oicinica (Capnodiales, Mycosphaerellaceae; GenBank GU214678; Identities = 461/533 (86 %), Gaps = 35/533 (7 %)), amongst others. A megablack search of the NCBI GenBank nucleotide sequence database using the LSU sequence of E. livstonae retrieves as closest hits Mycosphaerella markii (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 elaecarpi (Capnodiales, Mycosphaerellaceae; GenBank EU040212; Identities = 876/914 (96 %), Gaps = 8/914 (1 %)), amongst others. However, nucleotide sequences representing Exosporium stylbatum (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 Mycosphaerellaceae (as closest hits Mycosphaerella brassicicola (Capnodiales, Mycosphaerellaceae; GenBank EU167607; Identities = 457/528 (87 %), Gaps = 30/528 (6 %)) and Pseudocercospora oicinica (Capnodiales, Mycosphaerellaceae; GenBank GU214678; Identities = 461/533 (86 %), Gaps = 35/533 (7 %)), amongst others. However, nucleotide sequences representing Exosporium stylbatum (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 Mycosphaerellaceae and predomi

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) clusterd 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 livstonae 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 megablack search of the NCBI GenBank nucleotide sequence database using the ITS sequence of E. livstonae retrieves as closest hits Mycosphaerella brassicicola (Capnodiales, Mycosphaerellaceae; GenBank EU167607; Identities = 457/528 (87 %), Gaps = 30/528 (6 %)) and Pseudocercospora oicinica (Capnodiales, Mycosphaerellaceae; GenBank GU214678; Identities = 461/533 (86 %), Gaps = 35/533 (7 %)), amongst others. However, nucleotide sequences representing Exosporium stylbatum (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
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, cylindrical or elongated-clavate, transversely multisepitate or with basal septum only, 2–5 µm diam, up to 80 µm long, branched below or not; those paraphyses that become multisepitate, 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.

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, aspitate, 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. pellita, 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.

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.

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Fungal Planet description sheets

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

Camarographium koreani simile, sed conidiosi 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 conidium. 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 conidigenous cells lining the internal chamber of the whole conidioma; mature conidiomata tend to have empty locules. Paraphyses intermingled among conidigenous 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 conidigenous cells. Conidigenous cells hyaline, discrete, holoblastic, annellidic, with 1–2 percurrent proliferations, broadly ampulliform or doliform, 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 mature conidia are 3.5–4(–5) µm diam scar at the base.

Culture characteristics — Colonies erumpent, spreading, with sparse to moderate aerial mycelium, and even, lobate margins; reaching 30 mm diam after (in the dark, 25 °C, after 2 wk): Conidia 14.5–16 × 4–7 µm, at 3.5–4(–5) µm diam scar at the base.

Typus. RussiA, St. Petersburg, Botanical Garden of the Komarov Botanical Institute, on thin, dried twigs of Carpinus betulus (Betulaceae), 27 Sept. 2010, V. Mel’nık (holotype LE 226162; paratypes LE 261808, LE 261817; isotypes HAL 2424 F, CBS H-20506), cultures ex-isotype CPC 18919, 18918 = CBS LE 261817; 3.5–4(–5) µm diam scar at the base.

Notes — In September 2010, V. Mel’nık collected an interesting coelomycete on dried twigs of Carpinus betulus in the Botanical Garden of the Komarov Botanical Institute (St. Petersburg, Russia). The pycnidial conidomata, holoblastic annellidic conidigenous cells and distoseptate, pale coloured conidia provided clues to the fact that this specimen could belong to the Shearia-Camarosporium-Stegosporiopsis-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 megablaster search of the NCBI 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 megablaster search of the NCBI GenBank nucleotide sequence database using the LSU sequence of C. carpini retrieves as closest hits Preussia dubia (GenBank HQ203736; Identities = 922/945 (96 %), Gaps = 6/945 (1 %), Sporormia 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 JQ444451; 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
2. Conidiomata pycnidial, on other substrata ....... 3
3. Conidia up to 20 µm wide ............. 3
4. Conidia smaller .................................. 4
5. Conidia 52–62 × 17–19.5 µm, extruding a white conidial mass, immersed in bark of Cornus kousa, microconidia present .................................................. C. koreanum
6. Conidia 50–60 × 19–24 µm, extruding a yellowish brown conidial mass, immersed in bark of Carpinus betulus, microconidia absent ........................................... C. carpinii
7. Conidia hyaline, 14.5–16 × 4–7 µm, on leaves of Atriplex moneta ..................... C. atripilicis
8. Conidia brown, on other substrata ............... 5
9. Conidia 5.6–7.5 µm wide, on fruits of Prunus domestica .................. C. fructicola
10. Conidia 7–12 µm wide, on spines of Acacia sphaerocephala .......................... C. indicum
Phoma proteae
Phoma proteae Crous, sp. nov.

Phoma huancayensis similis, sed conidii minoribus, (4.5–)5–6.5(–7) × (2.5–)3(–3.5) µm, discimtur.

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, globose 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 olive-grey in centre, dirty white to smoke-grey in outer region; iron-grey on reverse. On potato-dextrose agar olivaceous grey on surface, and iron-grey on reverse.

Typus. SOUTH AFRICA, Western Cape Province, Somerset West, Kariba 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 AY904602), 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.
Pyrenochaeta protearum
**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 ampulliform, 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.


**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 NCBI’s 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.

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Phaeomoniella niveniae
**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 conidigenous cells, 4–7×2.5–3 µm, monophialidic, opening 1–1.5 µm diam with minute collarette. *Conidia* hyaline, smooth, bacilliform 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.

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 NCBI’s 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 NCBI’s GenBank nucleotide sequence database using the LSU sequence of *P. niveniae* retrieves as closest hits *Xenocylindrosporum 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.
Toxicocladosporium leucadendri
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. *Intercalar 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, 0.5–1.5 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 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 NCBI’s 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 NCBI’s 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 ciboliae* (GenBank GU214484; Identities = 846/866 (98 %), Gaps = 9/866 (1 %)), amongst others.
Scorias leucadendri
Scorias leucadendri Crous, sp. nov.

Scorias spongiae 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 running 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.


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 Leptothyphium (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 NCBI 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 GU030268; Identities = 455/495 (92 %), Gaps = 22/495 (4 %)) and Leptothyphium kurandae (GenBank JF951150; Identities = 583/661 (88 %), Gaps = 44/661 (7 %)), amongst others. A megablast search of the NCBI 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.
Leptosphaeria proteicola
Leptosphaeria proteicola Crous, sp. nov.

Microsphaeropsis proteae similis, sed conidiis majoribus, (3.5–)4.5–5(–7) \times (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) \times (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.

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 NCBI’s GenBank nucleotide sequence database using the ITS sequence of L. proteicola retrieves little hits with high similarity to identified sequences. A megablast search of the NCBI’s GenBank nucleotide sequence database using the LSU sequence of L. proteicola retrieves L. 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 = 0/479 (0 %)) and 97 % (GenBank JN712561; Identities = 830/855 (97 %), Gaps = 6/855 (1 %)) for ITS and LSU respectively.