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RESEARCH ARTICLE

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P.W. Crous[1], B.A. Summerell[2], R.G. Shivas[3], T.I. Burgess[4], C.A. Decock[5], L.L. Dreyer[6], L.L. Granke[7], D.I. Guest[8], G.E.St.J. Hardy[4], M.K. Hausbeck[7], D. Hüberli[4], T. Jung[9], O. Koukol[10], C.L. Lennox[11], E.C.Y. Liew[2], L. Lombard[1], A.R. McTaggart[3], J.S. Pryke[12], F. Roets[13], C. Saude[14], L.A. Shuttleworth[8], M.J.C. Stukely[15], K. Vánky[16], B.J. Webster[17], S.T. Windstam[18], J.Z. Groenewald[1]

Key words

ITS DNA barcodes
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Abstract Novel species of microfungi described in the present study include the following from Australia: *Phytophthora amnicola* from still water, *Gnomoniopsis smithogilvyi* from *Castanea* sp., *Pseudoplagiostoma corymbiae* from *Corymbia* sp., *Diaporthe eucalyptorum* from *Eucalyptus* sp., *Sporisorium andrewmitchellii* from *Enneapogon* aff. *lindleyanus, Myrmecridium banksiae* from *Banksia,* and *Pilidiella wangiensis* from *Eucalyptus* sp. Several species are also described from South Africa, namely: *Gondwanamyces wingfieldii* from *Protea caffra*, *Montagnula aloes* from *Aloe* sp., *Diaporthe canthii* from *Canthium inerne, Phyllosticta ericarum* from *Erica gracilis, Coleophoma proteae* from *Protea caffra, Toxicocladosporium strelitziae* from *Strelitzia reginae,* and *Devriesia agapanthi* from *Agapanthus africanus*. Other species include *Phytophthora asparagi* from *Asparagus officinalis* (USA), and *Diaporthe passiflorae* from *Passiflora edulis* (South America). Furthermore, novel genera of coelomycetes include *Chrysocrypta corymbiae* from *Corymbia* sp. (Australia), *Trinosporium guianense*, isolated as a contaminant (French Guiana), and *Xenosonderhenia syzygii*, from *Syzygium cordatum* (South Africa). *Pseudopenidiella piceae* from *Picea abies* (Czech Republic), and *Phaeocercospora colophospermi* from *Colophospermum mopane* (South Africa) represent novel genera of hyphomycetes. Morphological and culture characteristics along with ITS DNA barcodes are provided for all taxa.

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[1] CBS-KNAW Fungal Biodiversity Centre, Uppsalalaan 8, 3584 CT Utrecht, The Netherlands; corresponding author e-mail: p.crous@cbs.knaw.nl.
[2] Royal Botanic Gardens and Domain Trust, Mrs Macquaries Rd, Sydney, NSW 2000, Australia.
[3] Plant Biosecurity Science, Department of Agriculture, Fisheries and Forestry, Ecosciences Precinct, Dutton Park 4102, Queensland, Australia.
[4] Centre for Phytophthora Science and Management, Murdoch University, 90 South Street, Murdoch, WA 6150, Australia
[5] Mycothèque de l'Université catholique de Louvain (MUCL, BCCM™), Earth and Life Institute – ELIM – Mycology, Université catholique de Louvain, Croix du Sud 2 bte L7.05.25, B-1348 Louvain-la-Neuve, Belgium
[6] Department of Botany and Zoology and DST/NRF Centre of Excellence in Tree Health Biotechnology, Stellenbosch University, Stellenbosch, South Africa.
[7] Department of Plant Pathology, Michigan State University, East Lansing, USA.
[8] Faculty of Agriculture, and Environment, University of Sydney, Australian Technology Park, Eveleigh, NSW 2015, Australia.
[9] Phytophthora Research and Consultancy, Thomastr. 75, D-83098 Brannenburg, Germany.
[10] Department of Botany, Faculty of Science, Charles University in Prague, Benátská 2, CZ-128 01, Praha 2, Czech Republic.
[11] Department of Plant Pathology, Stellenbosch University, Stellenbosch 7600, South Africa.
[12] Department of Conservation Ecology and Entomology, Stellenbosch University, Stellenbosch, South Africa.
[13] Department of Conservation Ecology and Entomology and DST/NRF Centre of Excellence in Tree Health Biotechnology, Stellenbosch University, Stellenbosch, South Africa.
[14] Department of Plant Agriculture, University of Guelph, Guelph, Canada.
[15] Science Division, Department of Environment and Conservation, Locked Bag 104, Bentley Delivery Centre, WA 6983, Australia.
[16] Herbarium Ustilaginales Vánky (HUV), Gabriel-Biel-Str. 5, D-72076 Tübingen, Germany.
[17] Department of Plant Pathology, University of Wisconsin, Madison, USA.
[18] Department of Biological Sciences, State University of New York, Oswego, USA.

Neighbour-joining tree obtained using a distance analysis with a general time reversible (GTR) substitution model on the partial 28S nrRNA gene alignment (812 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 to species of the order *Peronosporales*.


Phytophthora amnicola

Fungal Planet 107 – 4 June 2012

Phytophthora amnicola T.I. Burgess & T. Jung, *sp. nov.*

Etymology. Named for the riverside habitat of this species.

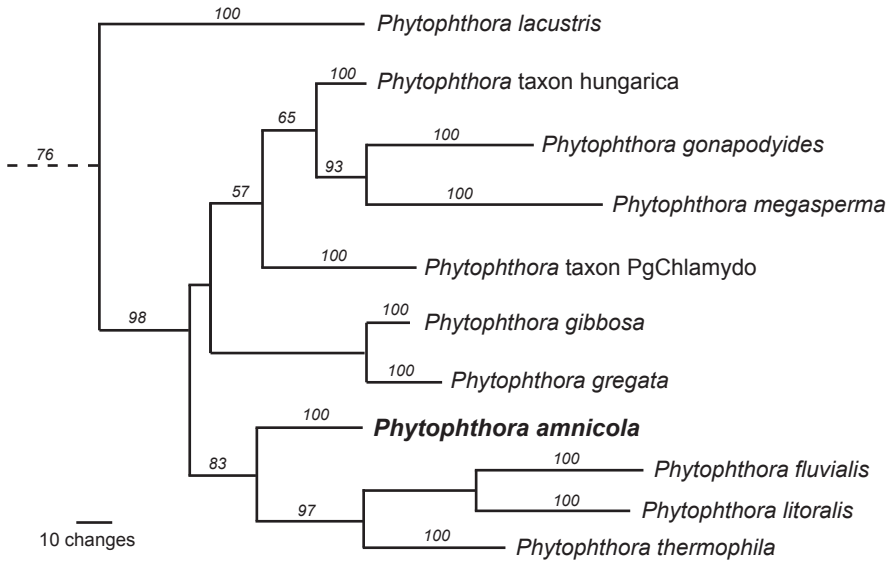
Sporangia produced abundantly in non-sterile soil extract, non-caducous, non-papillate, frequently ovoid to limoniform or rarely ellipsoid, obpyriform or pyriform, often with a long tapering base; 62 ± 9.0 × 35.3 ± 5.6 µm (overall range 39–78 × 17–43 µm), length/breadth ratio 1.8 ± 0.2. *Sporangial proliferation* in chains of internally proliferating sporangia in both a nested and extended way. Internally proliferating sporangiophores, sometimes branching inside or just outside the empty sporangium. Ellipsoid to irregular, catenulate hyphal swellings in clusters (14.2 ± 4.0 µm). Club-shaped, knotty lateral hyphae formed in water. *Chlamydospores* not observed. *Gametangia* not produced in single culture or when paired with A1 and A2 tester strains of *P. cinnamomi*. Radial growth rates on V8 agar at optimum temperature (25–32.5 °C) and near the maximum temperature (37.5 °C) 6.4 ± 0.4 mm/d and 0.3 ± 0.07 mm/d, respectively.

Culture characteristics — Colonies are rosaceous on carrot agar and stellate with limited aerial mycelium on V8 agar; growth on potato-dextrose agar is very slow.

Typus. Western Australia, Perth, Poison Gully Creek, baited from still water, Dec. 2009, *D. Hüberli*, holotype MURU 471; cultures ex-type CBS 131652 = DH228, ITS, ß-tubulin, HSP90, *cox*1, NADH, and LSU sequence GenBank JQ029956, JQ029952, JQ029944, JQ029948, JQ029940, and JX069838 respectively, MycoBank MB563849.

Additional specimens examined. Western Australia, Pemberton, baited from soil beneath dying *Patersonia* spp., Dec. 2009, *Department of Environment and Conservation*, VHS19503; Perth, Lake Jualbup, baited from still water, DH013; Perth, Canning River, baited from still water, DH237.

Notes — Phylogenetically, *P. amnicola* resides in a strongly supported terminal clade and shares a common ancestor with *P. fluvialis, P. litoralis*, and *P. thermophila* (Crous et al. 2011a, Jung et al. 2011). In a multigene phylogeny of the ITS, HSP90, BT, NADH, and *cox*1 gene regions, *P. amnicola* differs from *P. fluvialis* by 144 steps (3.1 %), *P. litoralis* by 158 steps (3.4 %), and *P. thermophila* by 121 steps (2.6 %). These four species have all been isolated from waterways in the south-west of Western Australia. *Phytophthora amnicola* has a life strategy similar to *P. litoralis* and *P. fluvialis,* being sterile and having abundant and continuous asexual multiplication in watercourses via chains of nested and extended proliferating sporangia, external proliferation, and the production of secondary lateral sporangia. The species can be separated by its overall larger sporangia and its broad optimum for growth (25–32.5 °C) as opposed to a peak at 32.5 °C for the other species. As with *P. thermophila* and *P. litoralis, P. amnicola* grows very slowly on PDA, but unlike these species it produces rosaceous colonies on carrot agar.



The most parsimonious tree (TL = 965; CI = 0 64; RI = 0.78) obtained from a heuristic search with 100 random taxon additions of a combined ITS, BT, HSP90, *cox*1, and NADH sequence alignment using PAUP v. 4.0b10. The scale bar shows 10 changes, and bootstrap support values from 1 000 replicates are shown at the nodes. Two isolates of each known species and four isolates of *P. amnicola* were included in the analysis. The species described here is printed in **bold** face. The tree was rooted to *P. inundata, P. humicola,* and *P. asparagi* (not shown). The alignment and tree are available in TreeBASE (www.treebase.org).

Colour illustrations. Typical niche for recovery of *P. amnicola* (T.I. Burgess); mature sporangia: limoniform; limoniform with widening of sporangiophore toward the base; ovoid sporangia; internal nested proliferation; internal nested and extended proliferation; catenulate hyphal swellings; club-shaped knotty lateral hyphae (T. Jung). Scale bar = 25 µm. Stellate colony on V8 agar (T.I. Burgess).

Treena I. Burgess, Daniel Hüberli & Giles E.St.J. Hardy, Centre for Phytophthora Science and Management, Murdoch University, 90 South Street, Murdoch, WA 6150, Australia; e-mail: tburgess@murdoch.edu.au, daniel.huberli@agric.wa.gov.au & g-hardy@murdoch.edu.au
Michael J.C. Stukely, Science Division, Department of Environment and Conservation, Locked Bag 104, Bentley Delivery Centre, WA 6983, Australia; e-mail: mike.stukely@dec.wa.gov.au
Thomas Jung, Phytophthora Research and Consultancy, Thomastr. 75, D-83098 Brannenburg, Germany; e-mail: dr.t.jung@t-online-de


Gnomoniopsis smithogilvyi

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Gnomoniopsis smithogilvyi L.A. Shuttleworth, E.C.Y. Liew & D.I. Guest, *sp. nov.*

Etymology. Named after New Zealand Plant Pathologist, Dr Harvey Smith, and the Australian chestnut grower, David Ogilvy, for their contribution to our understanding of the pathogen, and its epidemiology (Ogilvy 1998, Smith & Ogilvy 2008).

Diseased kernels with pale, medium and dark brown lesions occurring on endosperm and embryo of the chestnut. Lesions occur as spotting, or with a clear margin at the stylar end, hilum end, sides of the kernel, or a combination of these. Perithecia in Australia occur on overwintered dead burrs and branches of *Castanea sativa* and *C. crenata* × *C. sativa* hybrids. They are observed on chestnut varieties Decoppi Marone, Purton's Pride and Red Spanish. *Perithecia* abundant, without stroma, semi or fully immersed in host tissue, solitary or in groups up to 25, black, globose to subglobose, mostly convex when dry, sometimes concave at sides or apex, (101.5–)238.7(–409.5) µm high (SD = 55, n = 60), (96.5–)242(–410.5) µm diam (SD = 60, n = 68); solitary neck, central, straight or curved, sometimes flexuous, shorter or longer than perithecial diameter, apex sometimes translucent, necks sometimes absent, (113–)223(–399) µm long (SD = 70.5, n = 69), (18.5–)38.5(–55) µm diam at base (SD = 6.5, n = 62), (19.5–)30.5(–56.5) µm diam at apex (SD = 5.2, n = 101). *Asci* hyaline, unitunicate, inoperculate, obovoid to cylindrical, (20.5–)31(–37.5) µm long (SD = 3.5, n = 79), (4–)5(–6.5) µm diam (SD = 0.5, n = 79), with visible apical ring 1–2 µm wide, containing eight, biseriate ascospores. *Ascospores* hyaline, 1-septate, pyriform, straight or slightly curved, ends rounded, broader at distal end, (4–)7(–12) µm long (SD = 1.5, n = 101), (1–)2(–3) µm diam (SD = 0.5, n = 101), length-to-width ratio (l : w) = 3.5, medianly 1-septate, constricted at septum; distal cell with 2–multiple guttules, and basal cell with 1–multiple guttules, appendages absent. Germinating ascospores produced the anamorph in culture.

Anamorph culture characters fast growing, attaining 85 mm after 8–13 d at 25 °C (mean 11 d, n = 3). *Mycelia* flat and transparent on malt extract agar (MEA), woolly to felty and dense on malt yeast agar (MYA) and potato-dextrose agar (PDA), margins diffuse to irregular on MEA, regular on MYA and PDA, developing in concentric circles particularly on MYA and PDA, colour on MEA bronze (5E5) (Kornerup & Wanscher 1978), on MYA grey (5B1) and beaver (5F4), on PDA grey (5B1) and hair brown (5E4). Reverse colours similar to surface. *Conidiomata* produced in all cultures, abundant, black to brownish grey (7F2), globose to subglobose, both erumpent and immersed in media oozing conidia of varying colours. On MEA (69–)245.5(–449.5) µm high (SD = 99, n = 30), (67.5–)255(–477.5) µm wide (SD = 105, n = 30), height-to-width ratio (h : w) = 1, with greyish orange (5B3) conidia. On MYA conidiomata (102–)288.5 (–535.5) µm high (SD = 124.5, n = 30), (108.5–)305.5(–616.5) µm wide (SD = 152, n = 30), h : w = 1, with light orange (6A4) conidia. On PDA conidiomata (84.5–)203.5(–488.5) µm high (SD = 90.5, n = 30), (69.5–)217.5(–471) µm wide (SD = 93.5, n = 30), h : w = 1, with pale orange (6A3) conidia. *Conidia* hyaline, oval, obovoid, fusoid, pyriform, straight or curved, allantoid, multi-guttulate, without appendages, on MEA (6–)8(–9.5) µm long (SD = 0.5, n = 76), (2–)2.5(–4) µm wide (SD = 0.4, n = 76), l : w = 3, on MYA (5.5–)6.5(–7.5) µm long (SD = 0.5, n = 76), (2–)3(–3.5) µm wide (SD = 0.5, n = 76), l : w = 2.5, on PDA (6.5–)7.5(–9.5) µm long (SD = 0.5, n = 76), (2–)3(–4) µm wide (SD = 0.5, n = 76), l : w = 2.5.

Typus. Australia, New South Wales, Mullion Creek, 'Brittle Jacks' chestnut orchard, as a saprobe on dead burrs of *Castanea* sp., Dec. 2009, *L.A. Shuttleworth*, holotype CBS H-20623, isotype RBG 5586; ex-type culture CBS 130190 = RBG 5585, β-tubulin sequence GenBank JQ910639, ITS sequence GenBank JQ910642, LSU sequence GenBank JX069842, rpb2 sequence GenBank JQ910648, and tef1-α sequence GenBank JQ910645, MycoBank MB800259.

Notes — *Gnomoniopsis smithogilvyi* overwinters in its teleomorph form as a saprobe on dead burrs and branches of *Castanea* sp. (*Fagaceae*), and is isolated from rotten chestnut kernels, or as an endophyte from asymptomatic flowers, leaves and stems (Shuttleworth 2012). Species of *Gnomoniopsis* on *Castanea* are documented as endophytes and associated with rotten chestnuts and chestnut galls in Italy (Gentile et al. 2009, Tamietti et al. 2009, Magro et al. 2010, Vettraino et al. 2011), are documented in New Zealand (Sogonov et al. 2008), and have been isolated from chestnut blight cankers in India (Dar & Rai 2011). Multi-gene phylogenetic analyses using β-tubulin, ITS, rpb2 and tef1-α genes showed *G. smithogilvyi* is most closely related to *G. clavulata* (CBS 121255) and *G. paraclavulata* (CBS 123202) (Shuttleworth 2012). Key morphological differences between *G. smithogilvyi* and the other two species include the aggregation of perithecia in host tissue (*G. smithogilvyi* are single or in groups up to 25, *G. clavulata* and *G. paraclavulata* are recorded as single (Sogonov et al. 2008)), perithecia of *G. smithogilvyi* are larger (mean) height and width than the other two species and perithecia of *G. smithogilvyi* have longer necks, ascospores of *G. smithogilvyi* are smaller than the other two species and the position of the septum in the ascospores is different (*G. smithogilvyi* has a median septum, *G. clavulata* has a submedian septum (36 % of ascospore length), *G. paraclavulata* has a submedian septum (40 % of ascospore length); Walker et al. 2010). The three species share the same host range, occurring on members of *Fagaceae*. To date *G. clavulata* has been recorded on *Fagus sylvatica*, *Quercus* spp. (*Q. ilicifolia, Q. falcata, Q. marilandica, Q. nigra, Q. prinus, Q. rubra*) (Sogonov et al. 2008, Walker et al. 2010), *G. paraclavulata* has been recorded on *Q. alba* (Sogonov et al. 2008), and *G. smithogilvyi* has been recorded on *Castanea* sp., *C. sativa,* and *Q. ilex* (Sogonov et al. 2008, Shuttleworth 2012). Phylogenetic analysis of the ITS region grouped Australian ascospore isolates, chestnut rot isolates, and endophyte isolates in the same node as isolates from India, Italy, and New Zealand with 100 % maximum parsimony bootstrap and 1.00 Bayesian posterior probability. This indicates that species of *Gnomoniopsis* are present in these countries, and that *G. smithogilvyi* is likely one of them.

Colour illustrations. Chestnut orchard photo, Australia, Victoria, Benambra. Micrographs (top to bottom), dead burr; chestnut kernel with chestnut rot symptoms, perithecia immersed and erumpent in burr tissue; asci containing ascospores; anamorph culture isolate on PDA. Scale bars: 200, 10, 500 µm. All images L.A. Shuttleworth.

Lucas A. Shuttleworth & David I. Guest, Faculty of Agriculture, and Environment, University of Sydney, Australian Technology Park, Eveleigh, NSW 2015, Australia;
e-mail: lucas.shuttleworth@sydney.edu.au & david.guest@sydney.edu.au
Edward C.Y. Liew, Royal Botanic Gardens and Domain Trust, Mrs Macquaries Rd, Sydney, NSW 2000, Australia;
e-mail: edward.liew@rbgsyd.nsw.gov.au


Gondwanamyces wingfieldii

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Gondwanamyces wingfieldii Roets & Dreyer, *sp. nov.*

Etymology. Named after Professor M.J. Wingfield, who spearheaded research on *Gondwanamyces* from *Proteaceae*.

Ascomata produced superficially on host tissue; bases black, globose, ornamented, (71.5–)88.6–120.8(–172.4) µm diam, necks black, smooth-walled, (58.4–)89.7–132.1(–191.5) µm long, (17.1–)18.3–31.3(–32.2) µm wide at the base, (9.5–)11.0–12.3(–13.1) µm wide at the apex, with ornamental hyphae. *Asci* evanescent. *Ascospores* 1-celled, hyaline, fusiform with a hyaline gelatinous sheath giving a falcate appearance, accumulating in a hyaline droplet at the neck apex, (9.4–)10.2–11.4(–12.9) × (1.5–)1.8–2.2(–2.4) µm. *Conidiophores* macronematous, mononematous, brown, septate, arising from well-developed rhizoids; stipe erect, simple, inflated at the apex, (49.8–)58.8–90.9(–108.2) × (3.85–)4.4–5.5(–6.2) µm. *Conidiogenous cells* (phialides) produced terminally on conidiophores, discrete, ovoid, brown, producing conidia at the apex, (4.7–)5.1–6.3(–7.0) × (2.3–)2.6–3.8(–4.7) µm. *Conidia* holoblastic, hyaline, aseptate, smooth-walled, cylindrical to allantoid, rounded at the apex and truncate at the base, produced in mucoid masses at the apex of conidiophores, (3.2–)3.37–4.4(–5.7) × (2.0–)2.2–2.7(–3.2) µm.

Culture characteristics — Colonies reach c. 40 mm diam on 2 % malt extract agar (MEA, Biolab, Midrand, South Africa) after 8 d at 25 °C; aerial mycelium sparse, hyaline at first, becoming olivaceous buff with age; margins regular; colonies fertile.

Typus. South Africa, KwaZulu-Natal Province, Boston, Good Hope Farm (29°40S, 29°58E), within infructescences of *Protea caffra*, Jan. 2011, *F. Roets*, holotype PREM 60728; cultures ex-type CFR 150 = CBS 132470; paratypes PREM 60729–60730; cultures CFR 151–152; ITS sequence of CFR 150 GenBank JQ844903 and LSU sequence of CFR 150 GenBank JQ844902, MycoBank MB800003.

Notes — *Gondwanamyces wingfieldii* is the first species of the genus collected from the infructescences of a species of *Protea* from outside the boundaries of the Cape Floral Kingdom of South Africa. Its host plant species has one of the widest distributions of all *Protea* spp. and extends from the KwaZulu-Natal Drakensberg in South Africa northwards into tropical Africa. It is possible that the distribution range of *G. wingfieldii* follows that of its host.

The ascomata of *G. wingfieldii* are morphologically similar to those of *G. capensis*, *G. proteae,* and *G. scolytodis* except that the perithecial bases are always strongly ornamented. Ascospores of *G. wingfieldii* are similar to those of *G. proteae* and *G. scolytodis* in that they are covered by a lunate sheath (Kolarik & Hulcr 2009). This character differentiates these species from *G. capensis* (Wingfield & van Wyk 1993). *Gondwanamyces proteae* has divergent ostiolar hyphae at the tip of the ascomatal neck unlike *G. capensis*, *G. scolytodis,* and *G. wingfieldii*. *Gondwanamyces wingfieldii* and *G. scolytodis* can be distinguished by the much larger ascospores produced by the latter (11–20 µm) and different anamorphic stages. The anamorph produced by *G. wingfieldii* is *Custingophora*-like, similar to the other *Protea*-associated species, *G. capensis* and *G. proteae*, whilst the conidiophores of *G. scolytodis* are hyaline with an indeterminate origin (Kolarik & Hulcr 2009). The teleomorphs of two non-*Protea* associated species from South Africa, *G. serotecta* and *G. ubusi*, are unknown, but these share anamorph characteristics with *G. wingfieldii* (van der Linde et al. 2011). The conidia of the former two are, however, more than double the length of those produced by *G. wingfieldii*.

A megablast search in GenBank using ITS sequence data retrieved *G. capensis* (GenBank EU552135.1; Identities = 623/629 (99 %), Gaps = 3/629 (0 %)) as closest sister. *Gondwanamyces proteae* (GenBank AY372072.1; Identities = 610/630 (97 %), Gaps = 10/630 (2 %)) was retrieved as sister to *G. capensis* and *G. wingfieldii*. The ITS sequences of the *Euphorbia*-associated *G. serotecta* (GenBank JF947182.1; Identities = 529/608 (87 %), Gaps = 39/608 (6 %)) and *G. ubusi* (GenBank JF947186.1; Identities = 532/612 (87 %), Gaps = 43/612 (7 %)) were retrieved as sister to all *Protea*-associated species. *Gondwanamyces scolytodis* (GenBank AM267268.1) was retrieved with Identities = 486/581 (84 %) and Gaps = 44/581 (8 %).

Colour illustrations. Protea sp. from the KwaZulu-Natal Province highlands; ascomata; ascomatal tip with oozing ascospores; ascospores; anamorph with conidiogenous cells; conidia. Scale bars = 10 µm.

Francois Roets, Department of Conservation Ecology and Entomology and DST/NRF Centre of Excellence in Tree Health Biotechnology, Stellenbosch University, Stellenbosch, South Africa;
e-mail: fr@sun.ac.za
James S. Pryke, Department of Conservation Ecology and Entomology, Stellenbosch University, Stellenbosch, South Africa;
e-mail: jpryke@sun.ac.za
Léanne L. Dreyer, Department of Botany and Zoology and DST/NRF Centre of Excellence in Tree Health Biotechnology, Stellenbosch University, Stellenbosch, South Africa;
e-mail: ld@sun.ac.za


Phytophthora asparagi

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Phytophthora asparagi Saude & Hausbeck*, sp. nov.*

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

Water-soaked lesions on shoots slightly above or below the soil line, which may elongate and result in curved growth of the spear (Shephard's crook) under conditions favourable for the pathogen. Water-soaked lesions on the storage roots cause roots to shrivel as lesions expand. Yellow to brown discolouration of the internal tissue of the storage roots may occur. *Oospores* abundantly produced on V8 agar, oogonia 25–45 µm diam, antheridia amphigynous, homothallic. *Sporangia* sparsely produced on V8 agar and abundantly produced on dilute V8 agar, non-caducous, non-papillate, ovoid or obpyriform; 20–60 µm long × 10–35 µm wide. *Sporangial proliferation* external and internal. *Chlamydospores* not observed. *Hyphae* coenocytic, hyaline, 1.25–1.5 µm diam. Radial growth rate on V8 agar in the dark at optimum (25 °C) was ~11 mm/d, no growth at 5 and 30 °C (Saude et al. 2008).

Culture characteristics — (in light, 25 °C, after 7 d): Colony morphology on V8 agar stellate to rosaceous, white mycelia appressed to medium with aerial hyphae.

Typus. USA, Southwest Michigan, *Asparagus officinalis*, Spring 2006, *C. Saude & M.K. Hausbeck*, holotype SP326 (Cornell herbarium), culture ex-type SP326 = ATCC MYA-4826 = CBS 132095, ITS sequence GenBank EF185089 and LSU sequence GenBank JX069843, MycoBank MB511931.

Additional specimens examined. USA, Northwest and Central Michigan, *Asparagus officinalis*, Spring 2004 and 2005, *C. Saude*, 48 isolates (Saude et al. 2008).

Notes — *Phytophthora asparagi* causes spear and root rot of asparagus. The pathogen may be readily isolated from diseased spears and isolated with more difficulty from diseased crowns and storage roots (Saude et al. 2008).

Colour illustrations. Diseased asparagus spear in a commercial grower's field in Michigan; dark lesions on storage root tissue; sporangia; oogonium with oospore and amphigynous antheridium. Scale bars = 10 µm.

Leah L. Granke, Department of Plant Pathology, Michigan State University, East Lansing, USA;
e-mail: grankele@msu.edu
Catarina Saude, Department of Plant Agriculture, University of Guelph, Guelph, Canada;
e-mail: csaude@uoguelph.ca
Sofia T. Windstam, Department of Biological Sciences, State University of New York, Oswego, USA;
e-mail: sofia.windstam@oswego.edu
Bryan J. Webster, Department of Plant Pathology, University of Wisconsin, Madison, USA;
e-mail: bjwebster2@wisc.edu
Mary K. Hausbeck, Department of Plant Pathology, Michigan State University, East Lansing, USA;
e-mail: hausbec1@msu.edu


Diaporthe passiflorae

Fungal Planet 111 – 4 June 2012

Diaporthe passiflorae Crous & L. Lombard, *sp. nov.*

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

Sporulating on the surface of an old granadilla fruit (endophyte?). *Pycnidia* in culture on oatmeal agar sporulating poorly, globose, up to 300 µm diam, black, erumpent; cream conidial droplets exuding from central ostioles; walls consisting of 3–6 layers of medium brown *textura angularis*. *Conidiophores* hyaline, smooth, 2–3-septate, branched, densely aggregated, cylindrical, straight to sinuous, 20–30 × 2.5–4 µm. *Conidiogenous cells* 7–15 × 1.5–2.5 µm, phialidic, cylindrical, terminal and lateral, with slight taper towards apex, 1–1.5 µm diam, with visible periclinal thickening; collarette not flared, up to 2 µm long when present. *Paraphyses* not observed. *Alpha conidia* aseptate, hyaline, smooth, guttulate, fusoid to ellipsoid, tapering towards both ends, straight, apex subobtuse, base subtruncate, (5.5–)6–7(–8) × (2–)2.5–3(–3.5) µm. *Gamma conidia* aseptate, hyaline, smooth, ellipsoid-fusoid, apex acutely rounded, base subtruncate, 10–12 × 2–2.5 µm. *Beta conidia* spindle-shaped, aseptate, smooth, hyaline, apex acutely rounded, base truncate, tapering from lower third towards apex, curved, (14–)16–18(–20) × 1.5(–2) µm.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies fluffy, with abundant aerial mycelium, covering the dish within 2 wk; on oatmeal agar, malt extract agar, and potato-dextrose agar, surface dirty white, with patches of pale olivaceous grey.

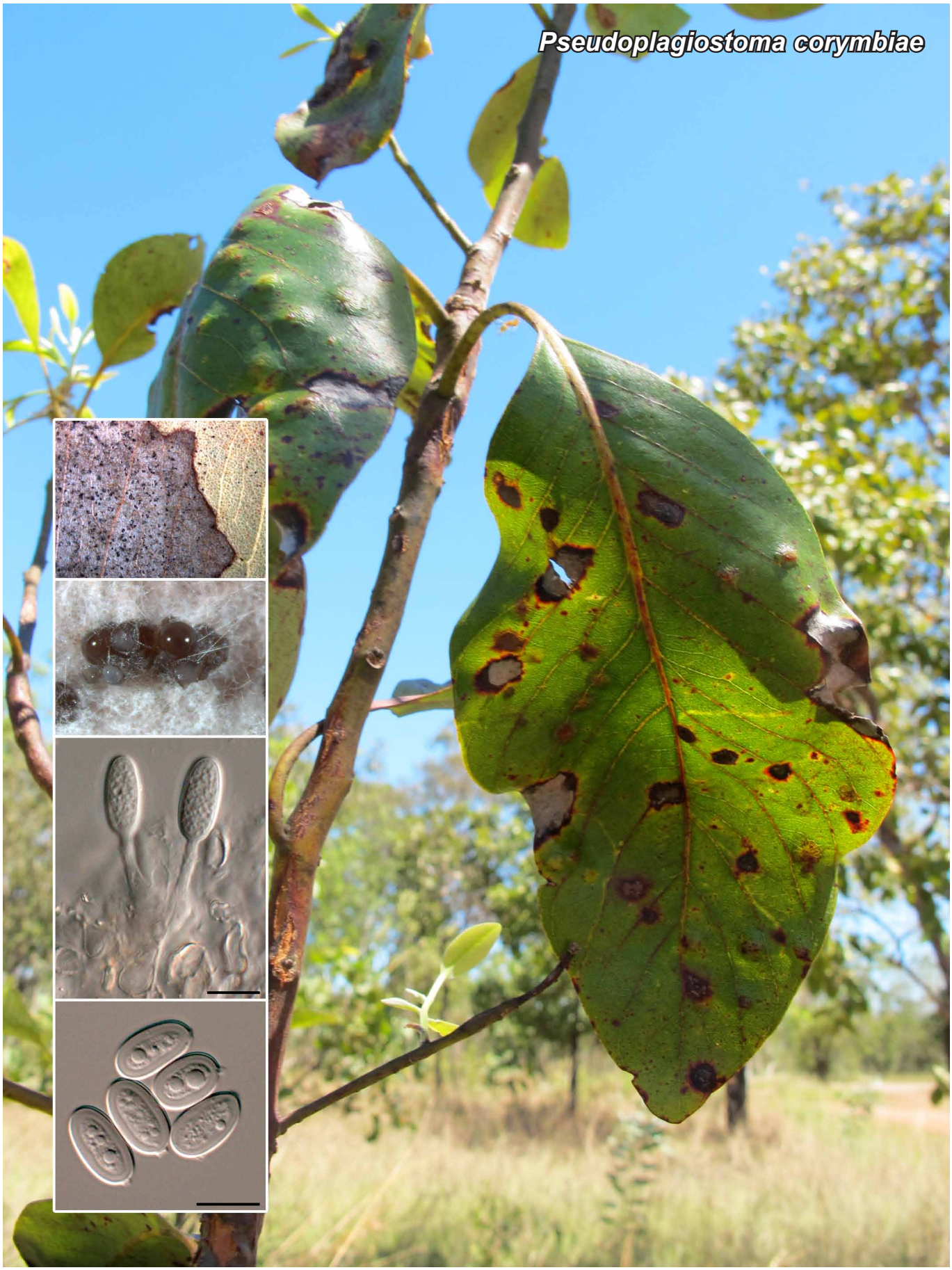
Typus. South America, imported into the Netherlands, on fruit of *Passiflora edulis* (*Passifloraceae*), Apr. 2011, *P.W. Crous*, holotype CBS H-20956, cultures ex-type CPC 19184, 19183 = CBS 132527, ITS sequence GenBank JX069860 and LSU sequence GenBank JX069844, MycoBank MB800372.

Notes — Phomopsis rot of *Passiflora edulis* (granadilla) has traditionally been linked to infections of *P. tersa*, which damages the leaves, fruit and twigs, causing losses of up to 40 % (Lutchmeah 1992). *Phomopsis tersa* has been confirmed from countries such as Portugal, Malta, Mauritius, Sarawak, Sri Lanka, and Fiji (Sutton 1980, Lutchmeah 1992). Two to three days following harvest, the stalk collapses, and turns brown. Within 10 d, the whole fruit is affected, and black conidiomata are observed on the fruit surface (Lutchmeah 1992). Conidia of *D. passiflorae* are much larger (14–20 × 1.5–2 µm) than those of *P. tersa* (6.5–7.5 × 2.5 µm) (Sutton 1980).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the ITS sequence is *Diaporthe phaseolorum* (GenBank EU272513; Identities = 597/612 (98 %), Gaps = 7/612 (1 %)), followed by *Phaeocytostroma ambiguum* (GenBank FR748042; Identities = 597/634 (94 %), Gaps = 18/634 (3 %)), and *Diaporthe phaseolorum* var. *caulivora* (GenBank AF000567; Identities = 579/609 (95 %), Gaps = 12/609 (2 %)). Closest hits using the LSU sequence yielded highest similarity to *Diaporthe leucospermi* (GenBank JN712524; Identities = 920/928 (99 %), Gaps = 0/928 (0 %)), followed by *Diaporthe cynaroidis* (GenBank EU552122; Identities = 910/921 (99 %), Gaps = 2/921 (0 %)), and *Diaporthe rhusicola* (GenBank JF951166; Identities = 915/932 (98 %), Gaps = 2/932 (0 %)).

Colour illustrations. *Passiflora edulis* in Brazil (Photo by A.C. Alfenas); diseased granadilla with pycnidia; pycnidium sporulating in culture; conidiogenous cells, beta and alpha conidia. Scale bar = 10 µm.

Pedro W. Crous, Lorenzo Lombard & Johannes Z. Groenewald, CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@cbs.knaw.nl, l.lombard@cbs.knaw.nl & e.groenewald@cbs.knaw.nl


Pseudoplagiostoma corymbiae

Fungal Planet 112 – 4 June 2012

Pseudoplagiostoma corymbiae Crous & Summerell, *sp. nov.*

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

Leaf spots large, up to 3 cm diam, subcircular to somewhat irregular, medium brown with thin red-brown border. *Conidiomata* amphigenous on leaves, acervular, subcuticular to subepidermal, brown, separate; wall consisting of 2–3 layers of brown *textura angularis*, up to 300 µm diam; dehiscence by means of irregular slits; exuding white to cream conidial masses. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, discrete, cylindrical to ampulliform with long cylindrical neck, hyaline, smooth, straight to curved, proliferating several times percurrently near apex, 10–20 × 4–7 µm. *Conidia* aseptate, hyaline, smooth, thick-walled, (1–2 µm diam), guttulate, elongate ellipsoidal, straight, apex broadly obtuse, tapering at base to a truncate hilum (1 µm diam), with minute marginal frill, (14–)16–18(–19) × (7–)8–9(–10) µm.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies reaching 60 mm diam. On malt extract agar with smooth, lobate margins and sparse aerial mycelium; surface smoke-grey, reverse ochreous with patches of grey; on PDA and OA smoke-grey on surface and reverse.

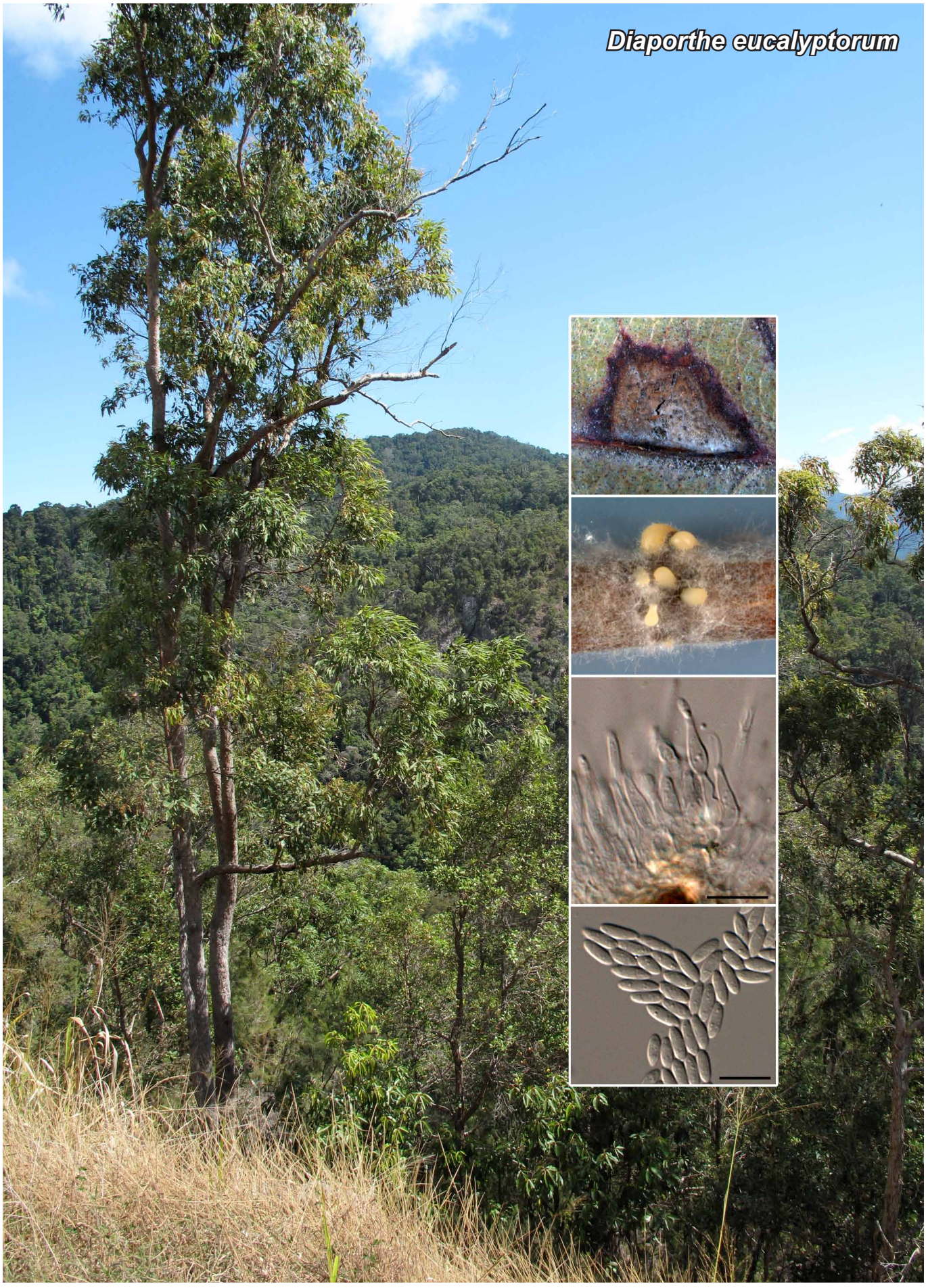
Typus. Australia, Northern Territory, Harrison Dam Conservation Area, S12°41.953' E131°24.008', on leaves of *Corymbia* sp. (*Myrtaceae*), 25 Apr. 2011, *P.W. Crous & B.A. Summerell*, holotype CBS H-20957, cultures extype CPC 19287 = CBS 132529, ITS sequence GenBank JX069861 and LSU sequence GenBank JX069845, MycoBank MB800373.

Notes — The genus *Pseudoplagiostoma* (*Pseudoplagiostomaceae*; *Diaporthales*) contains three species associated with leaf spots on *Eucalyptus*, viz. *P. eucalypti*, *P. oldii,* and *P. variabile* (Cheewangkoon et al. 2010). Using the key provided by Cheewangkoon et al. (2010), *P. corymbiae* is distinct from *P. oldii* (pigmented at maturity), and is most similar to *P. eucalypti* in conidial shape (ellipsoid), and dimensions (14–)16–19 (–22) × (6–)7–9(–11) µm. However, conidia of *P. corymbiae* tend to be somewhat longer and narrower, and it has longer conidiogenous cells (10–20 × 4–7 µm) than those of *P. eucalypti* (6–15 × 2–6 µm).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the ITS sequence is *Pseudoplagiostoma variabile* (GenBank GU973536; Identities = 565/573 (99 %), Gaps = 3/573 (1 %)), followed by *Pseudoplagiostoma eucalypti* (GenBank GU973526; Identities = 563/573 (98 %), Gaps = 2/573 (0 %)), and *Pseudoplagiostoma oldii* (GenBank GU973535; Identities = 562/573 (98 %), Gaps = 4/573 (1 %)). Closest hits using the LSU sequence yielded highest similarity to *Cytospora* cf. *austromontana* (GenBank EU552118; Identities = 870/907 (96 %), Gaps = 7/907 (1 %)), *Diaporthe acaciigena* (GenBank JF951160; Identities = 870/907 (96 %), Gaps = 9/907 (1 %)), and *Harknessia gibbosa* (GenBank JQ706226; Identities = 869/907 (96 %), Gaps = 7/907 (1 %)).

Colour illustrations. *Corymbia* sp. with leaf spots at the Harrison Dam Conservation Area; close-up of leaf spot; conidiomata sporulating in culture; conidiogenous cells and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@cbs.knaw.nl & e.groenewald@cbs.knaw.nl
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs Macquaries Rd, Sydney, NSW 2000, Australia;
e-mail: Brett.Summerell@rbgsyd.nsw.gov.au


Diaporthe eucalyptorum

Fungal Planet 113 – 4 June 2012

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

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

Leaf spots amphigenous, irregular, 2–7 mm diam, medium brown, with raised margin and red-purple border. *Pycnidia* in culture on pine needle agar, subglobose, up to 350 µm diam, black, erumpent; white to cream conidial droplets exuding from central ostioles; walls consisting of 3–6 layers of medium brown *textura angularis*. *Conidiophores* hyaline, smooth, reduced to conidiogenous cells or up to 4-septate, densely aggregated, straight to sinuous, unbranched or branched below, 15–60 × 3–4 µm. *Conidiogenous cells* 10–30 × 2–3 µm, phialidic, cylindrical, terminal and lateral, with slight taper towards apex, 1–1.5 µm diam, with visible periclinal thickening and flared collarette up to 2 µm long, surrounded by a prominent flaring mucoid sheath. *Paraphyses* hyaline, smooth, cylindrical, 1–3-septate, flexuous, unbranched or branched below, up to 70 µm long, 2–3 µm wide at base. *Alpha conidia* aseptate, hyaline, smooth, guttulate, fusoid, tapering towards both ends, straight, apex subobtuse, base subtruncate, (5.5–)6.5–7(–8) × (2–)2.5(–3) µm. *Beta* and *gamma conidia* not seen.

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

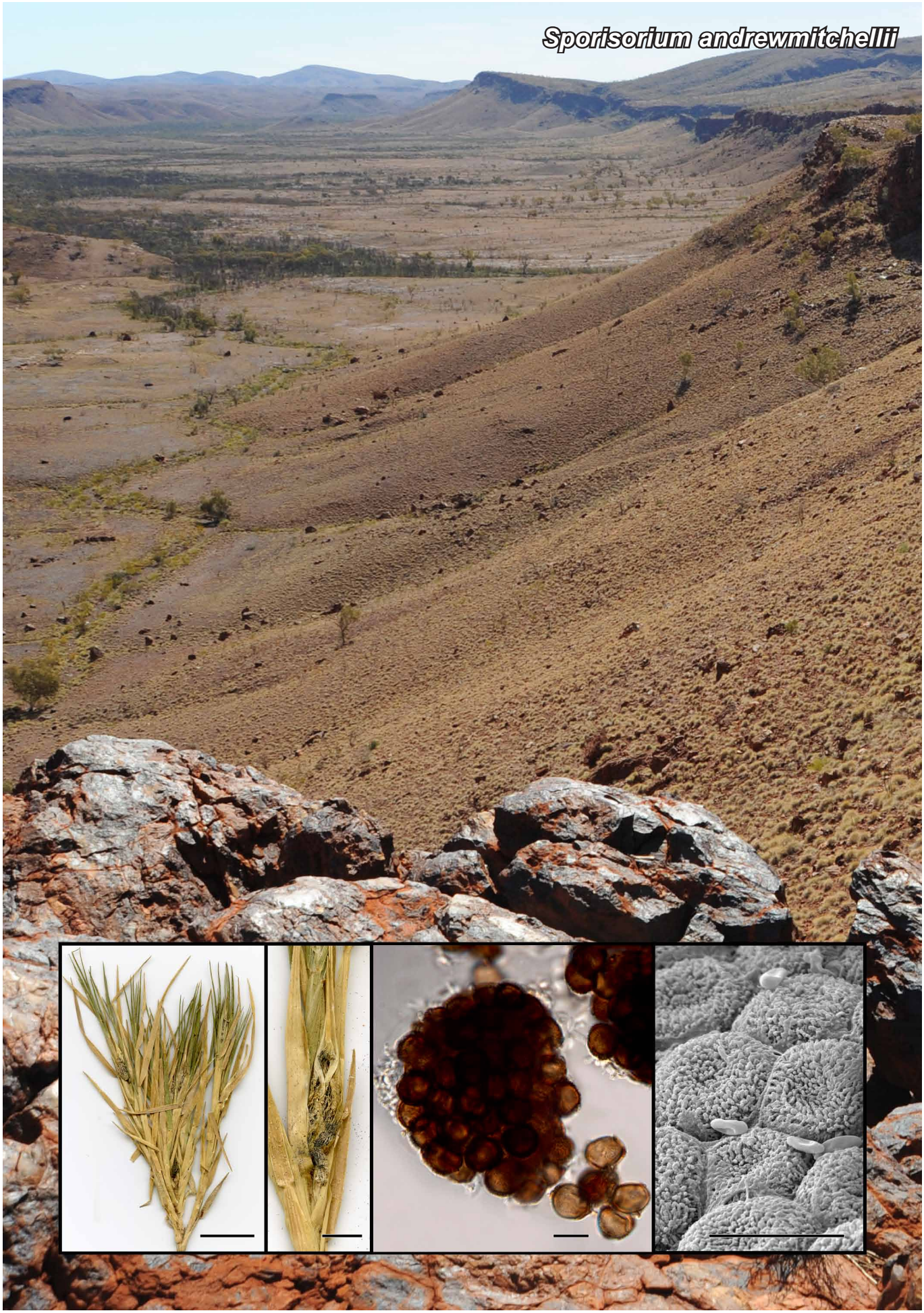
Typus. Australia, Queensland, Cairns Road to Atherton Giles Highway, on leaves of *Eucalyptus* sp., 16 Aug. 2009, *P.W. Crous*, holotype CBS H-20958, cultures ex-type CPC 17203 = CBS 132525, ITS sequence GenBank JX069862 and LSU sequence GenBank JX069846, MycoBank MB800374.

Notes — *Phomopsis eucalypti* has been reported from living and dead leaves of *Eucalyptus* in Russia (Uecker 1988), and has also been recorded as a pathogen of *Eucalyptus* in India (Mohanan & Sharma 1987). *Diaporthe eucalyptorum* is distinguished by having shorter conidia ((5.5–)6.5–7(–8) × (2–)2.5(–3) µm than those of *P. eucalypti* 6.9–9.2(–12) × 2–2.5 µm (Uecker 1988)).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the ITS sequence is *Diaporthe ceratozamiae* (GenBank JQ044420; Identities = 657/675 (97 %), Gaps = 6/675 (1 %)), followed by *Phaeocytostroma plurivorum* (GenBank FR748046; Identities = 650/674 (96 %), Gaps = 1/674 (0 %)) and *Stenocarpella maydis* (GenBank FR748052; Identities = 653/680 (96 %), Gaps = 10/680 (1 %)). Closest hits using the LSU sequence yielded highest similarity to *Diaporthe ceratozamiae* (GenBank JQ044440; Identities = 852/856 (99 %), Gaps = 3/856 (0 %)), *Diaporthe musigena* (GenBank JF951158; Identities = 852/856 (99 %), Gaps = 3/856 (0 %)), and *Phomopsis longicolla* (GenBank FJ755236; Identities = 851/855 (99 %), Gaps = 4/855 (0 %)).

Colour illustrations. *Eucalyptus* growing along highway in northern Queensland; close-up of leaf spot; pycnidia sporulating in culture; conidiogenous cells and alpha conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@cbs.knaw.nl & e.groenewald@cbs.knaw.nl
Roger G. Shivas, Plant Biosecurity Science, Ecosciences Precinct, Dutton Park 4102, Queensland, Australia;
e-mail: roger.shivas@deedi.qld.gov.au


Sporisorium andrewmitchellii

Fungal Planet 114 – 4 June 2012

Sporisorium andrewmitchellii R.G. Shivas, McTaggart & Vánky, *sp. nov*.

Etymology. Named after Andrew Arthur Mitchell (1949–), a botanist and friend, who has collected many rare and unusual smut fungi on grasses and sedges in Australia.

Sori on the top of sterile shoots destroying the basal part of the uppermost, congested leaves, swollen, narrow ovoid or fusiform, 10–20 × 2–6 mm, partly hidden by intact leaf sheaths, covered by a yellowish peridium of host and fungal origin, at maturity revealing numerous (20 or more) filiform columellae intermixed with black spore balls. Infection systemic, all shoots on an infected plant affected. *Spore balls* variable in shape and size, subglobose, ovoid, ellipsoidal or irregular, 40–210 × 30–140 µm, opaque, composed of tens or hundreds of agglutinated spores which separate only by hard pressure. *Spores* subglobose, ellipsoidal to subpolyhedrally irregular, 9–13.5 × 8–12 µm, yellowish brown; wall slightly uneven, 0.5–1(–1.5) µm thick, finely and densely verruculose, spore profile of the outermost spores finely, densely subechinulate; inner spores lighter, wall thinner, densely punctate, profile smooth. *Sterile cells* of the peridium in chains, single cells variable, globoid, elongated, subpolyangularly irregular, 6–16 µm long, hyaline; wall even, thin, c. 0.5 µm thick, smooth.

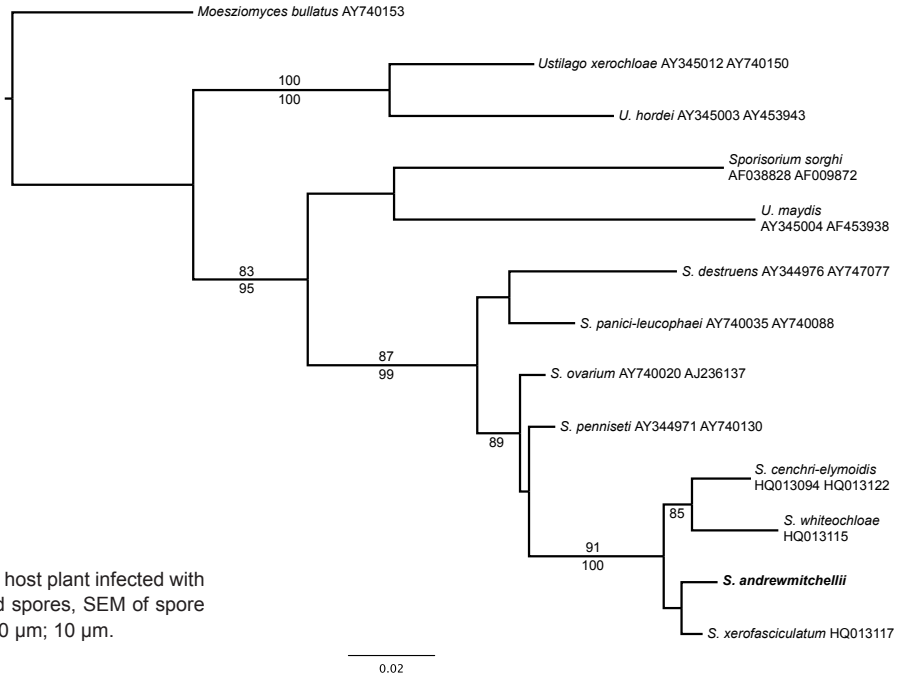
On *Poaceae*: *Enneapogon* aff. *lindleyanus*. Known only from the type collection.

Typus. Australia, Western Australia, Central Hamersley Ranges, S22°43' 20.0", E119°19'37.0", on *Enneapogon* aff. *lindleyanus*, 1 July 2011, *A.A. Mitchell & B. Matthews*, holotype BRIP 54879, isotype PERTH, HUV 21.982, ITS sequence GenBank JQ995369 and LSU sequence GenBank JQ995370, MycoBank MB800262.

Notes — Six smut fungi are known on grasses in the tribe *Pappophoreae* of the subfam. *Chloridoideae*, i.e. on *Enneapogon*, *Pappophorum,* and *Schmidtia*. These are, *Sporisorium modestum*, *Ustilago austroafricana*, *U. enneapogonis*, *U. pappophori*, *U. schlechteri*, and *U. schmidtiae* (Vánky 2012). A key to the smut fungi of the tribe *Pappophoreae* follows.

1. Sori in basal part of the uppermost, congested, swollen leaf sheaths and leaves 2
1. Sori in the flowers, ovaries or in the whole inflorescence 3
2. Spores single, sparsely echinulate; columellae absent . . . . . *U. schlechteri*
2. Spores in balls, densely verruculose; columellae present . . . . . *S. andrewmitchellii*
3. Sori in whole inflorescence 4
3. Sori in the flowers or ovaries of an inflorescence 5
4. Sori only in the inflorescence; spores 10.5–13.5(–14.5) µm long . . . . . *U. enneapogonis*
4. Sori also in the basal part of the uppermost leaves; spores 9.5–12 µm long . . . . . *U. pappophori*
5. Sori in flowers 6
5. Sori in some ovaries; spores 9–12 µm long *U. schmidtiae*
6. Sori in all flowers; columellae and sterile cells present; spores 11–14 µm long . . . . . *S. modestum*
6. Sori in some flowers; columellae and sterile cells absent; spores 6.5–9(–10) µm long . . . . . *U. austroafricana*

A BLASTn search of the ITS region of *Sporisorium andrewmitchellii* had high identity to species of *Sporisorium* with filiform columellae, spore balls, a host derived peridium and with hosts in the tribe *Paniceae*; namely *S. xerofasciculatum* (GenBank HQ013117; 97 % identical over 99 % query coverage), *S. cenchri-elymoidis* (GenBank HQ013094; 95 % identical over 98 % query coverage), and *S. whiteochloae* (GenBank HQ013115; 94 % identical over 100 % query coverage). A combined maximum likelihood analysis of the ITS and LSU regions of *S. andrewmitchellii* and closely related taxa from GenBank recovered identical topologies in RAxML v. 7.2.8 and PhyML 3.0. Bootstrap values from a ML search in RAxML are shown above the nodes and aRLT values from a search in PhyML are shown below the nodes.



Colour illustrations. Central Hamserley Ranges; host plant infected with *Sporisorium andrewmitchellii*; sorus, spore ball and spores, SEM of spore surface. Scale bars (left to right) = 2 cm; 0.5 mm; 10 µm; 10 µm.

Roger G. Shivas & Alistair R. McTaggart, Plant Biosecurity Science, Ecosciences Precinct, Dutton Park 4102, Queensland, Australia;
e-mail: roger.shivas@deedi.qld.gov.au & Alistair.Mctaggart@deedi.qld.gov.au
Kálmán Vánky, Herbarium Ustilaginales Vánky (HUV), Gabriel-Biel-Str. 5, D-72076 Tübingen, Germany;
e-mail: VANKY.K@cityinfonetz.de


Montagnula aloes

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Montagnula aloes Crous, *sp. nov.*

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

Ascomata separate, globose, imbedded in host tissue, subepidermal, becoming erumpent, up to 450 µm diam, papillate with central ostiole, up to 60 µm diam, exuding masses of brown spores; wall of 6–12 layers of olivaceous brown *textura angularis*; sporulating in culture, forming brown ascomata in aerial mycelium and in agar on PNA, OA, and MEA. *Pseudoparaphyses* cylindrical, hyaline, cellular, 3–5 µm diam, anastomosing between and above asci, branched, septate. *Asci* bitunicate, 8-spored, clavate, fissitunicate, with low ocular chamber, 5 µm diam, 1 µm high (visible only in young asci), with a long furcate pedicel (up to 100 µm long), 110–250 × 20–30 µm. *Ascospores* (32–)33–36(–38) × (10–)13–14(–16) µm, biseriate, ovoid to ellipsoid, medium brown, finely verruculose, 3-euseptate, prominently constricted at septa, somewhat more so at primary septum, widest in middle of second cell from apex, ends acutely rounded, becoming obtusely rounded at maturity.

Culture characteristics — (in the dark, 25 °C): Colonies erumpent, spreading with moderate aerial mycelium; on MEA surface rosy buff, reverse cinnamon, covering dish in 3 wk; on PDA slow growing, reaching only 25 mm diam after 3 wk, with sparse aerial mycelium and feathery margins, surface cinnamon, reverse cinnamon with patches of isabelline; on OA covering dish in 3 wk, surface and reverse rosy buff.

Typus. South Africa, Kwazulu-Natal, Durban, Salt Rock, on the beach, on dead leaf tips of *Aloe* sp. (*Xanthorrhoeaceae*), 16 July 2011, *P.W. Crous*, holotype CBS H-20959, cultures ex-type CPC 19672, 19671 = CBS 132531, ITS sequence GenBank JX069863 and LSU sequence GenBank JX069847, MycoBank MB800375.

Notes — The present collection matches species of *Chaetoplea* in having immersed ascomata, pseudoparaphyses, clavate, furcate asci, and ovoid to ellipsoid, medium brown ascospores that are transversely septate. *Chaetoplea* is distinguished from *Montagnula* by lacking muriformly septate ascospores, and from *Kalmusia* by lacking distoseptate ascospores (Zhang et al. 2009, 2012). Furthermore, *Montagnula aloes* is homothallic, sporulates well in culture, and does not form any anamorph. Although it seems to suit the morphological concept of *Chaetoplea*, it clusters with *Montagnula opulenta*, a didymosporous species, suggesting that muriformly septate ascospores may not be significant at generic level. For this reason, we choose to name it in *Montagnula* (1896), which is older than *Chaetoplea* (1931).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the ITS sequence is *Munkovalsaria appendiculata* (GenBank DQ435529; Identities = 498/526 (95 %), Gaps = 10/526 (2 %)), followed by *Aporospora terricola* (GenBank DQ865097; Identities = 472/506 (93 %), Gaps = 18/506 (4 %)), and *Microdiplodia miyakei* (GenBank HQ248187; Identities = 492/540 (91 %), Gaps = 23/540 (4 %)). Closest hits using the LSU sequence yielded highest similarity to *Montagnula opulenta* (GenBank DQ678086; Identities = 847/856 (99 %), Gaps = 4/856 (0 %)), *Coniothyrium nitidae* (GenBank EU552112; Identities = 880/905 (97 %), Gaps = 7/905 (1 %)), and *Microdiplodia hawaiiensis* (GenBank DQ885897; Identities = 880/907 (97 %), Gaps = 7/907 (1 %)).

Colour illustrations. Sugarbird playing on *Aloe* sp. in the rain; sporulation on pine needle agar; immersed ascomata on leaf tissue; vertical section through ascoma; ascomatal wall; asci and ascospores. Scale bars: 100, 10, 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@cbs.knaw.nl & e.groenewald@cbs.knaw.nl


Diaporthe canthii

Fungal Planet 116 – 4 June 2012

Diaporthe canthii Crous, *sp. nov.*

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

Leaf spots brown, amphigenous, circular, 2–8 mm diam, with raised border. *Pycnidia* amphigenous, associated with necrotic tissue; pycnidia in culture on PNA subglobose, up to 400 µm diam, erumpent; cream conidial masses exuding from ostioles; walls consisting of 3–6 layers of medium brown *textura angularis*. *Conidiophores* hyaline, smooth, 1–3-septate, branched, densely aggregated, cylindrical, straight to sinuous, 15–40 × 2–4 µm. *Conidiogenous cells* phialidic, cylindrical, terminal and lateral, with slight taper towards apex, 1.5–2 µm, with visible periclinal thickening; collarette not flared, 1–2 µm long. *Paraphyses* not seen. *Alpha conidia* aseptate, hyaline, smooth, fusiform, tapering towards both ends, straight, acutely rounded at apex, base subtruncate, (11–)12–14(–15) × (2.5–)3(–3.5) µm. *Gamma conidia* elongated, fusoid, wider in upper third, apex acutely rounded, with taper towards truncate hilum, 15–18 × 2.5(–3) µm. *Beta conidia* spindle-shaped, curved, 25–18 × 1.5 µm (rarely observed).

Culture characteristics — (in the dark, 25 °C): Colonies spreading, erumpent, covering the dish in 3 wk at 25 °C, with sparse aerial mycelium. On MEA and PDA dirty white with black conidiomata, oozing creamy spore masses; on OA dirty white with patches of orange and black sporulation.

Typus. South Africa, Western Cape Province, Kirstenbosch Botanical Garden, on leaves of *Canthium inerne* ('Gewone bokdrol' in Afrikaans) (*Rubiaceae*), 30 July 2011, *P.W. Crous*, holotype CBS H-20960, cultures ex-type CPC 19741, 19740 = CBS 132533, ITS sequence GenBank JX069864 and LSU sequence GenBank JX069848, MycoBank MB800376.

Notes — Presently there are no records of *Diaporthe* or *Phomopsis* species associated with *Canthium inerne* in South Africa (Crous et al. 2000). *Diaporthe canthii* is associated with prominent leaf spots on this host, and older infections result in leaves with a shot-hole appearance, as diseased tissue frequently drops out leaving holes in the leaves.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the ITS sequence is *Diaporthe rhusicola* (GenBank JF951146; Identities = 554/571 (97 %), Gaps = 7/571 (1 %)), followed by *Diaporthe phaseolorum* (GenBank AF001014; Identities = 554/574 (97 %), Gaps = 11/574 (2 %)), and *Phomopsis theicola* (GenBank GQ281809; Identities = 546/566 (96 %), Gaps = 11/566 (2 %)). Closest hits using the LSU sequence yielded highest similarity to *Diaporthe oncostoma* (GenBank AF408353; Identities = 864/866 (99 %), Gaps = 0/866 (0 %)), *Diaporthe rhusicola* (GenBank JF951166; Identities = 872/878 (99 %), Gaps = 2/878 (0 %)), and *Diaporthe musigena* (GenBank JF951158; Identities = 869/875 (99 %), Gaps = 0/875 (0 %)).

Colour illustrations. Symptomatic leaves of *Canthium inerne*; close-up of leaf spot, with pycnidia in the central region; conidiomata sporulating on pine needle agar; conidiogenous cells and alpha conidia. Scale bar = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@cbs.knaw.nl & e.groenewald@cbs.knaw.nl


Phyllosticta ericarum

Fungal Planet 117 – 4 June 2012

Phyllosticta ericarum Crous, *sp. nov.*

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

Disease symptoms associated with leaf tip blight. *Conidiomata* pycnidial, solitary, black, erumpent, globose, exuding colourless to opaque conidial masses; *pycnidia* up to 180 µm diam; pycnidial wall of several layers of *textura angularis*, up to 30 µm thick; inner wall of hyaline *textura angularis*. *Ostiole* central, up to 20 µm diam. *Conidiophores* subcylindrical to ampulliform, reduced to conidiogenous cells, or with 1–2 supporting cells, at times branches at base, 20–40 × 4–6 µm. *Conidiogenous cells* terminal, subcylindrical, hyaline, smooth, coated in a mucoid layer, 12–20 × 3–4 µm; proliferating several times percurrently near apex. *Conidia* (8–)9–10(–12) × (6–)7 µm, solitary, hyaline, aseptate, thin and smooth walled, coarsely guttulate, or with a single large central guttule, ellipsoid or obovoid, tapering towards a narrow truncate base, 2–3 µm diam, enclosed in a thin, persistent mucoid sheath, 3–4 µm thick, and bearing a hyaline, apical mucoid appendage, (5–)8–10(–12) × 1.5(–2) µm, flexible, unbranched, tapering towards an acutely rounded tip.

Culture characteristics — (in the dark, 25 °C after 3 wk): Colonies erumpent, spreading, with moderate aerial mycelium and feathery margins, reaching 60 mm diam. On MEA surface olivaceous grey, reverse iron-grey; on OA iron-grey; on PDA iron-grey on surface and reverse.

Typus. South Africa, Western Cape Province, Stellenbosch, Stellenbosch Botanical Garden, on leaves of *Erica gracilis* (*Ericaceae*), 18 Aug. 2011, *P.W. Crous & C.L. Lennox*, holotype CBS H-20961, cultures ex-type CPC 19745, 19744 = CBS 132534, ITS sequence GenBank JX069865 and LSU sequence GenBank JX069849, MycoBank MB800377.

Notes — Van der Aa (1973) regarded *Phyllosticta ericae* (on dead leaves *of Erica carnea*, Germany) as identical to *P. pyrolae* (conidia 4.5–7.5 × 4–9 µm; on *Pyrola rotunifolia*, USA). Phylogenetically*, P. pyrolae* is distinct from *P. ericarum*. Okane et al. (2001) compared *Phyllosticta* isolates occurring on *Ericaceae*, and concluded that *P. pyrolae* is distinct from *P. capitalensis*, which proved to be a dominant endophyte associated with *Ericaceae*. *Phyllosticta capitalensis* was recently shown to have an extremely wide host range, occurring on numerous economically important crops, on which it is commonly incorrectly identified (Glienke et al. 2011).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the ITS sequence is *Guignardia philoprina* (GenBank AF312008; Identities = 622/626 (99 %), Gaps = 1/626 (0 %)), followed by *Phyllosticta citribraziliensis* (GenBank FJ538352; Identities = 605/606 (99 %), Gaps = 1/606 (0 %)), and *Phyllosticta citrichinaensis* (GenBank JN791665; Identities = 627/639 (98 %), Gaps = 6/639 (1 %)). Closest hits using the LSU sequence yielded highest similarity to *Phyllosticta hymenocallidicola* (GenBank JQ044443; Identities = 908/914 (99 %), Gaps = 0/914 (0 %)), *Guignardia vaccinii* (GenBank FJ588242; Identities = 907/915 (99 %), Gaps = 0/915 (0 %)), and *Guignardia philoprina* (GenBank DQ377878; Identities = 898/915 (98 %), Gaps = 2/915 (0 %)).

Colour illustrations. Leaves and flowers of *Erica gracilis*; conidiogenous cells and conidia with mucoid sheaths. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@cbs.knaw.nl & e.groenewald@cbs.knaw.nl
Cheryl L. Lennox, Department of Plant Pathology, Stellenbosch University, Stellenbosch 7600, South Africa;
e-mail: clennox@sun.ac.za


Coleophoma proteae

Fungal Planet 118 – 4 June 2012

Coleophoma proteae Crous, *sp. nov.*

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

Leaf spots amphigenous, subcircular, up to 30 mm diam, brown, with concentric circles. *Conidiomata* immersed, subepidermal, amphigenous, globose, sporulating profusely on leaves (and in culture), with conidiomata arranged in concentric circles; up to 250 µm diam; wall of 2–6 layers of dark brown *textura angularis*. *Paraphyses* intermingled among conidiophores, hyaline, subcylindrical, 0–2-septate, up to 40 µm long, 2–3 µm diam, tapering towards obtusely rounded apex. *Conidiophores* hyaline, smooth, subcylindrical, 1–3-septate, 15–40 × 3–4 µm. *Conidiogenous cells* hyaline, smooth, subcylindrical, apical or lateral on conidiophores, 10–17 × 2.5–3.5 µm; tapering towards a truncate apex, 2–2.5 µm diam, with minute periclinal thickening. *Conidia* solitary, guttulate, hyaline, smooth, subcylindrical, apex obtuse, base tapered towards flattened scar, 1.5–2 µm diam, (11–)12–14(–17) × (3–)4(–5) µm.

Culture characteristics — (in the dark, 25 °C after 3 wk): Colonies erumpent, spreading with sparse aerial mycelium and feathery margins, reaching 25 mm diam. On MEA surface iron-grey, with patches of olivaceous grey, reverse iron-grey; on OA olivaceous grey; on PDA smoke grey, with patches of honey.

Typus. South Africa, Gauteng, Walter Sisulu National Botanical Gardens, on leaves of *Protea caffra* (*Proteaceae*), 5 July 2011, *P.W. Crous, M.K. Crous & M. Crous*, holotype CBS H-20962, cultures ex-type CPC 19715, 19714 = CBS 132532, ITS sequence GenBank JX069866 and LSU sequence GenBank JX069850, MycoBank MB800378.

Notes — The genus *Coleophoma* has pycnidial conidiomata with central ostioles, persistent, hyaline paraphyses, phialidic conidiogenous cells with periclinal thickening, and hyaline, cylindrical conidia. Although the genus *Coleophoma* was recently treated (Nag Raj 1978, Sutton 1980), no phylogenetic overview is presently available. Wu et al. (1996) provided a treatment of 22 taxa, accepting six species, a key to which is presented in Duan et al. (2007). Based on this key, *C. proteae* is most similar to *C. prunicola* (pathogenic to *Prunus*) and *C. fusiformis* (pathogenic to *Rhododendron*) (conidia 20–28 × 4.5–5.5 µm), but distinct in having somewhat smaller conidia. *Coleophoma proteae* was associated with serious leaf blight disease on *Protea caffra*. This is the first record of Coleophoma leaf disease on *Proteaceae*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the ITS sequence is *Coleophoma eucalyptorum* (GenBank JQ044430; Identities = 524/550 (95 %), Gaps = 6/550 (1 %)), followed by *Coleophoma empetri* (GenBank FJ480134; Identities = 511/533 (96 %), Gaps = 5/533 (1 %)), and *Neofabraea eucalypti* (GenBank GQ303279; Identities = 518/555 (93 %), Gaps = 12/555 (2 %)). Closest hits using the LSU sequence yielded highest similarity to *Coleophoma eucalyptorum* (GenBank JQ044449; Identities = 892/901 (99 %), Gaps = 2/901 (0 %)), *Coleophoma empetri* (GenBank FJ588252; Identities = 890/901 (99 %), Gaps = 2/901 (0 %)), and *Cryptosporiopsis actinidiae* (GenBank HM595594; Identities = 886/902 (98 %), Gaps = 4/902 (0 %)).

Colour illustrations. Symptomatic leaves of *Protea caffra* in Walter Sisulu National Botanical Gardens; conidiomata sporulating on oatmeal agar; conidiogenous cells, paraphyses and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@cbs.knaw.nl & e.groenewald@cbs.knaw.nl


Chrysocrypta corymbiae

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Chrysocrypta Crous & Summerell, *gen. nov.*

Etymology. *Chryso* (Greek) = orange, and cryptos (Greek) = hidden.

Conidiomata characteristic yellow-orange structures on leaf spots, eustromatic, separate, subepidermal, subglobose, opening by means of irregular rupture; wall of 3–6 layers of orange-brown *textura angularis*; conidiomata exuding slimy orange masses of conidia. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity of conidioma, hyaline, smooth, ampulliform, apex truncate, with minute periclinal thickening, at times apical part elongated into a long neck. *Conidia* dimorphic, intermixed in same conidiomata. *Macroconidia* broadly ellipsoid to obovoid, hyaline, smooth, granular to guttulate, thick-walled, apex obtuse, base flattened. *Microconidia* hyaline, smooth, guttulate, fusoid-ellipsoid, apex acutely rounded, base truncate.

Type species. *Chrysocrypta corymbiae*.
MycoBank MB800379.

Chrysocrypta corymbiae Crous & Summerell, *sp. nov.*

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

Leaf spots amphigenous, subcircular, 5–15 µm diam, grey-brown with raised, dark brown border. *Conidiomata* visible as characteristic yellow-orange structures on leaf spots, eustromatic, separate, subepidermal, subglobose, opening by means of irregular rupture; up to 400 µm diam in culture (on PNA); wall of 3–6 layers of orange-brown *textura angularis*; conidiomata exuding slimy orange masses of conidia. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity of conidioma, hyaline, smooth, ampulliform, 4–6 × 5–10 µm; apex truncate, 1.5 µm diam, with minute periclinal thickening, at times apical part elongated into a long neck, up to 15 µm long, 2–3 µm diam. *Conidia* dimorphic, intermixed in same conidiomata. *Macroconidia* broadly ellipsoid to obovoid, hyaline, smooth, granular to guttulate, thick-walled, apex obtuse, base flattened, 1–1.5 µm diam, (7–)8–9(–11) × (4–)5(–6) µm. *Microconidia* hyaline, smooth, guttulate, fusoid-ellipsoid, apex acutely rounded, base truncate, 1–1.5 µm diam, 5–7 × 2.5–3 µm.

Culture characteristics — (in the dark, 25 °C after 3 wk): Colonies spreading, flat, covering surface of dish, with sparse aerial mycelium. On MEA bright orange, reverse cinnamon; on OA cinnamon; on PDA surface dirty white with orange sporulation.

Typus. Australia, Northern Territory, Mary River National Park, Mary River Conservation Reserve, S12°54.130' E131°37.594', leaves of *Corymbia* sp., 24 Apr. 2011, *P.W. Crous & B.A. Summerell*, holotype CBS H-20963, cultures ex-type CPC 19279 = CBS 132528, ITS sequence GenBank JX069867 and LSU sequence GenBank JX069851, MycoBank MB 800380.

Notes — The *Cryphonectriaceae* was recently introduced as family for the *Cryphonectria-Endothia* stem canker pathogens occurring on woody hosts (Gryzenhout et al. 2006). In a recent paper by Vermeulen et al. (2011), reference is made to the fact that the family now includes 13 genera. However, this assumes that *Cryphonectriaceae* only occurs on stems of woody hosts, which is incorrect, as several genera are also well-established foliar pathogens of these hosts, e.g. *Foliocryphia* on *Eucalyptus coccifera* in Tasmania (Cheewangkoon et al. 2009), and *Aurantiosacculus* on various eucalypt species in Australia (Crous et al. 2012). *Chrysocrypta* is similar to *Foliocryphia*, but distinct in forming dimorphic conidia. The introduction of *Chrysocrypta* adds yet another genus to this family, which is associated with leaf spots on *Corymbia*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the ITS sequence is *Amphiporthe leiphaemia* (GenBank AJ293882; Identities = 523/614 (85 %), Gaps = 44/614 (7 %)), followed by *Amphilogia gyrosa* (GenBank EF026147; Identities = 533/630 (85 %), Gaps = 49/630 (8 %)), and *Cryphonectria nitschkei* (GenBank GQ290656; Identities = 421/473 (89 %), Gaps = 27/473 (6 %)). Closest hits using the LSU sequence yielded highest similarity to species of *Harknessia*, e.g. *Harknessia renispora* (GenBank JQ706237; Identities = 851/875 (97 %), Gaps = 6/875 (1 %)), *Foliocryphia eucalypti* (GenBank GQ303307; Identities = 847/875 (97 %), Gaps = 6/875 (1 %)), and *Endothia gyrosa* (GenBank DQ470972; Identities = 847/877 (97 %), Gaps = 10/877 (1 %)).

Colour illustrations. Termite mount and vegetation at Mary River Conservation Reserve; conidiomata sporulating on malt extract agar; conidiogenous cells and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@cbs.knaw.nl & e.groenewald@cbs.knaw.nl
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs Macquaries Rd, Sydney, NSW 2000, Australia;
e-mail: Brett.Summerell@rbgsyd.nsw.gov.au


Pseudopenidiella piceae

Fungal Planet 120 – 4 June 2012

Pseudopenidiella Crous & Koukol, *gen. nov.*

Etymology. Named after its morphological resemblance to the genus *Penidiella*.

Mycelium consisting of pale brown, finely verruculose, branched, septate hyphae. *Conidiophores* dimorphic: *microconidiophores* reduced to conidiogenous cells on hyphae, visible as slight thickenings on hyphal cells, somewhat erumpent, pale brown, apex truncate. *Macroconidiophores* subcylindrical with slight apical taper, pale brown to brown, erect, solitary on hyphae, unbranched, with one basal septum, or multi-septate, base somewhat swollen, lacking rhizoids, smooth, but becoming verruculose towards apical conidiogenous cell. *Conidiogenous cells* terminal, obtusely rounded to clavate, finely verruculose, pale brown; loci apical, 1–3 per conidiogenous cell, inconspicuous, somewhat flattened, truncate. *Ramoconidia* pale brown, finely verruculose, subcylindrical to fusoid-ellipsoid, aseptate, giving rise to branched chains of conidia. *Conidia* finely verruculose, pale brown, subcylindrical to ellipsoid, aseptate; hila inconspicuous, truncate, not thickened nor darkened.

Type species. *Pseudopenidiella piceae*.
MycoBank MB800382.

Pseudopenidiella piceae Crous & Koukol, *sp. nov.*

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

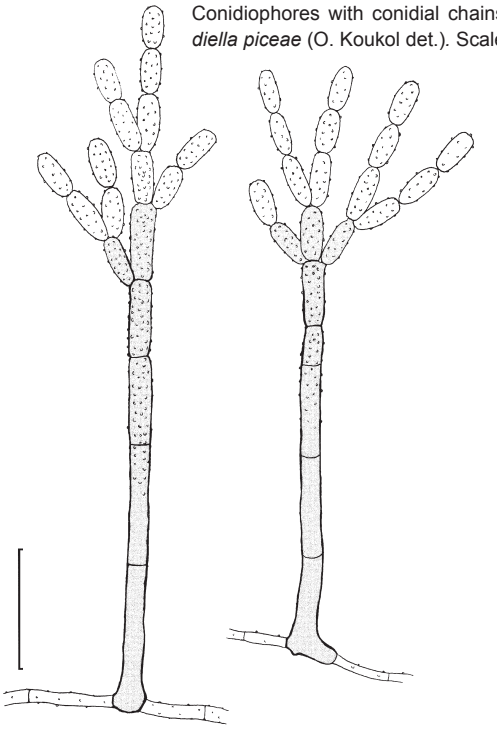
On synthetic nutrient-poor agar. *Mycelium* consisting of pale brown, finely verruculose, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* dimorphic: *microconidiophores* reduced to conidiogenous cells on hyphae, visible as slight thickenings on hyphal cells, somewhat erumpent, pale brown, up to 3 µm high, apex truncate 1 µm diam. *Macroconidiophores* subcylindrical with slight apical taper, pale brown to brown, erect, solitary on hyphae, unbranched, with one basal septum, or up to 8-septate, base somewhat swollen, up to 5 µm diam, lacking rhizoids, smooth, but becoming verruculose towards apical conidiogenous cell, up to 150 µm tall, 3–4 µm wide. *Conidiogenous cells* terminal, obtusely rounded to clavate, finely verruculose, pale brown, 9–12 × 3–4 µm; loci apical, 1–3 per conidiogenous cell, inconspicuous, somewhat flattened, truncate, 0.5–1 µm diam. *Ramoconidia* pale brown, finely verruculose, subcylindrical to fusoid-ellipsoid, aseptate, 8–12 × 2–3 µm giving rise to branched chains of conidia (–7). *Conidia* finely verruculose, pale brown, subcylindrical to ellipsoid, aseptate, (6–)7–9(–10) × (2.5–)3 µm; hila inconspicuous, truncate, not thickened nor darkened, 0.5–1 µm diam.

Culture characteristics — (in the dark, 25 °C after 3 wk): Colonies erumpent, spreading, with moderate aerial mycelium, and feathery margins, reaching 25 mm diam. On MEA surface greyish sepia, reverse fuscous black; on OA greyish sepia; On PDA greyish sepia, margin fuscous black, reverse fuscous-black.

Typus. Czech Republic, Šumava National Park, Forest under Kostelní vrch Hill near Srní, N49°3'57.088" E°1327'33.881", needle litter of *Picea abies*, 11 Nov. 2007, leg. *P. Baldrian,* isol. *O. Koukol*, holotype CBS H-20964, cultures ex-type CPC 19969 = CBS 131453 = CCF 4180, ITS sequence GenBank JX069868 and LSU sequence GenBank JX069852, MycoBank MB800383.

Notes — *Pseudopenidiella* is distinct from *Cladosporium* in not having the coronate-type scars on its conidial hila or conidiogenous cells. It is reminiscent of *Digitopodium*, but distinct in that it lacks rhizoids, has ramoconidia, and has aseptate conidia. In having penicillate conidiophores *Pseudopenidiella* is similar to *Penidiella*, but again distinct in having aseptate conidia, and lacking darkened, somewhat thickened scars on its conidial scars and hila (Crous et al. 2007b, Bensch et al. 2012).

A megablast search of NCBIs GenBank nucleotide database using the ITS sequence did not reveal any close hits; the only hit with some degree of coverage and identity was with '*Cladosporium* sp. EXP0486F' (GenBank DQ914668; Identities = 425/480 (89 %), Gaps = 27/480 (6 %)), which was obtained from *Elaeocarpus dentatus* litter in New Zealand (Collado et al. 2007) using a dilution-to-extinction technique, but is unrelated to the true *Cladosporium* spp. (*Cladosporiaceae*). Closest hits using the LSU sequence yielded highest similarity to species of *Heliocephala*, e.g. *Heliocephala zimbabweensis* (GenBank HQ333481; Identities = 817/914 (89 %), Gaps = 24/914 (3 %)) and species of *Fusicladium*, e.g. *Fusicladium carpophilum* (GenBank EU035426; Identities = 812/917 (89 %), Gaps = 34/917 (4 %)) and *Metacoleroa dickiei* (GenBank DQ384100; Identities = 814/923 (88 %), Gaps = 38/923 (4 %)).



Conidiophores with conidial chains of *Pseudopenidiella piceae* (O. Koukol det.). Scale bar = 20 µm.

Colour illustrations. *Picea abies* at Šumava National Park; conidiophores sporulating on synthetic nutrient-poor agar; conidiophores giving rise to conidial chains. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@cbs.knaw.nl & e.groenewald@cbs.knaw.nl
Ondřej Koukol, Department of Botany, Faculty of Science, Charles University in Prague, Benátská 2, CZ-128 01, Praha 2, Czech Republic;
e-mail: ondrej.koukol@natur.cuni.cz


Trinosporium guianense

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Trinosporium Crous & Decock, *gen. nov.*

Etymology. Named after its trigonous conidia.

Mycelium consisting of septate, branched, hyaline, smooth, hyphae, encased in a mucoid sheath. *Conidiomata* pycnidial, separate, globose, with a central ostiole, lined with periphyses; wall of 2–3 layers of brown *textura angularis*. *Conidiophores* lining the inner cavity, subcylindrical, hyaline, smooth, reduced to conidiogenous cells or branched, 1–3-septate with conidiogenous cells terminal and lateral. *Conidiogenous cells* hyaline to pale brown, smooth, thin-walled, ampulliform to subcylindrical; apex with periclinal thickening, but at times also with 1–2 percurrent proliferations. *Conidia* brown, smooth, widest at apex, with three lateral, rounded lobes, tapering towards a truncate base.

Type species. *Trinosporium guianense*.
MycoBank MB800384.

Trinosporium guianense Crous & Decock, *sp. nov.*

Etymology. Named after the locality from where it was collected, French Guiana.

Mycelium consisting of septate, branched, hyaline, smooth, 3–8 µm diam hyphae, encased in a mucoid sheath, up to 6 µm thick. *Conidiomata* 30–150 µm diam, separate, globose, with a central ostiole, up to 25 µm diam, lined with periphyses; wall of 2–3 layers of brown *textura angularis*. *Conidiophores* lining the inner cavity, subcylindrical, hyaline, smooth, reduced to conidiogenous cells or branched, 1–3-septate with conidiogenous cells terminal and lateral, 8–16 × 3–4 µm. *Conidiogenous cells* hyaline to pale brown, smooth, thin-walled, ampulliform to subcylindrical, 4–8 × 3–4 µm; apex with periclinal thickening, but at times also with 1–2 percurrent proliferations. *Conidia* brown, smooth, widest at apex, with three lateral, rounded lobes, tapering towards a truncate base, 1 µm diam; conidia 3–4 µm wide at apex, 3–4 µm tall.

Culture characteristics — (in the dark, 25 °C after 3 wk): Colonies semi-erumpent, flat, spreading, lacking aerial mycelium; surface slimy, with irregular, feathery margins, reaching 35 mm diam; on MEA, OA, and PDA fuscous-black.

Typus. French Guiana, Municipality of Regina, Nouragues Nature Reserve, CNRS 'Inselberg' research forest plot, approx. N04°05.5', W52°40.6', elev. approx. 120 m, isolated as a contaminant when trying to isolate a specimen of *Amauroderma* sp. (*Basidiomycota, Ganodermataceae*), coll. number ex-FG-11-486, July 2011, *C. Decock*, holotype CBS H-20965, culture ex-type MUCL 53977 = CBS 132537 = CPC 19878, ITS sequence GenBank JX069869 and LSU sequence GenBank JX069853, MycoBank MB800385.

Notes — The genus *Trinosporium* is characteristic in that it has ostiolate, pycnidial conidiomata, and brown, trigonous conidia. *Trinosporium* is reminiscent of *Readeriella*, which however, clusters in *Teratosphaeriaceae* (Crous et al. 2007a, 2009a, b). It is similar to *Tribolospora*, but the latter has hyaline conidia, with up to six protuberances (Sutton 1980). One possible earlier name for *Trinosporium* is *Trigonosporium,* known from two species, *T. australiense* and *T. cochinchinense*. However, conidia of the type (*T. australiense*) are hyaline, and Sutton (1971) was unable to resolve details related to its conidiogenesis, meaning that the genus remains obscure, pending fresh collections from *Cupaniopsis serrata* (= *Cupania serrata*) in Australia.

Based on a megablast search of NCBIs GenBank nucleotide database, only distant hits were obtained using the ITS sequence, e.g. *Sarea difformis* (GenBank JF440614; Identities = 468/554 (84 %), Gaps = 54/554 (10 %)), followed by *Sarea resinae* (GenBank JF440615; Identities = 483/583 (83 %), Gaps = 61/583 (10 %)), and *Umbilicaria esculenta* (GenBank EU534208; Identities = 479/586 (82 %), Gaps = 52/586 (9 %)). Closest hits using the LSU sequence yielded highest similarity to *Amorphotheca resinae* (GenBank EU040230; Identities = 819/863 (95 %), Gaps = 8/863 (1 %)), *Tricladium angulatum* (GenBank GQ477311; Identities = 810/856 (95 %), Gaps = 2/856 (0 %)), and *Potebniamyces pyri* (GenBank DQ470949; Identities = 821/871 (94 %), Gaps = 14/871 (2 %)).

Colour illustrations. Rain forest at Nouragues Nature Reserve; conidiomata sporulating on malt extract agar; hyphae with mucoid sheath, conidiogenous cells and conidia. Scale bar = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@cbs.knaw.nl & e.groenewald@cbs.knaw.nl
Cony A. Decock, Mycothèque de l'Université catholique de Louvain (MUCL, BCCM™), Earth and Life Institute – ELIM – Mycology,
Université catholique de Louvain, Croix du Sud 2 bte L7.05.25, B-1348 Louvain-la-Neuve, Belgium;
e-mail: cony.decock@uclouvain.be


Phaeocercospora colophospermi

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Phaeocercospora Crous, *gen. nov.*

Etymology. *Phaeo* (= pigmented) and its morphological similarity to *Cercospora*.

Foliicolous, associated with leaf spots. *Caespituli* amphigenous, subepidermal, arising from subepidermal, globular fruiting bodies (immature structures with undefined white contents); wall of 2–3 layers of *textura angularis*, bursting through epidermis, forming grey sporodochia with densely aggregated conidiophores. *Conidiophores* subcylindrical to ampulliform, brown, finely verruculose, aggregated, 0–2-septate. *Conidiogenous cells* terminal, brown, finely verruculose, ampulliform, tapering to a truncate apex, proliferating several times percurrently at apex (proliferations irregular, rough). *Conidia* solitary, brown, finely verruculose, guttulate, subcylindrical to narrowly obclavate, straight to mildly curved, apex subobtuse, base truncate with marginal frill, transversely septate; hila and scars not thickened, nor darkened or refractive.

Type species. *Phaeocercospora colophospermi*.
MycoBank MB800386.

Phaeocercospora colophospermi Crous, *sp. nov.*

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

Leaf spots amphigenous, brown, angular, vein-limited, 1–4 mm diam, with raised border. *Caespituli* amphigenous, subepidermal, arising from subepidermal, globular fruiting bodies up to 150 µm diam (immature structures with undefined white contents); wall of 2–3 layers of *textura angularis*, bursting through epidermis, forming grey sporodochia with densely aggregated conidiophores. *Conidiophores* subcylindrical to ampulliform, brown, finely verruculose, aggregated, 0–2-septate, 15–25 × 5–7 µm. *Conidiogenous cells* terminal, brown, finely verruculose, ampulliform, tapering to a truncate apex, 2.5–3.5 µm diam, proliferating several times percurrently at apex (proliferations irregular, rough), 12–20 × 5–7 µm. *Conidia* solitary, brown, finely verruculose, guttulate, subcylindrical to narrowly obclavate, straight to mildly curved, apex subobtuse, base truncate with marginal frill, 1–3-septate, (25–)45–55(–65) × (4.5–)5–6(–7) µm, up to 85 µm long in culture, and 3–5-septate; hila and scars not thickened, nor darkened or refractive.

Culture characteristics — (in the dark, 25 °C after 3 wk): Colonies erumpent, but not spreading, slow-growing, reaching 5 mm diam, lacking aerial mycelium, and with smooth, irregular margins. On MEA iron-grey on surface and in reverse; on OA iron-grey with diffuse red-brown pigment in agar; on PDA olivaceous grey with patches of pale olivaceous grey due to profuse sporulation.

Typus. South Africa, Mpumalanga, Kruger Game Reserve, Satara Rest Camp, on leaves of *Colophospermum mopane* (*Fabaceae*), 11 July 2011, *P.W. Crous & K.L. Crous*, holotype CBS H-20966, cultures ex-type CPC 19813, 19812 = CBS 132687, ITS sequence GenBank JX069870 and LSU sequence GenBank JX069854, MycoBank MB800387.

Notes — *Phaeocercospora* is reminiscent of the genera *Pseudocercospora*, *Scolecostigmina,* and *Cercostigmina*. However, *Scolecostigmina* (based on *S. mangiferae*) (Braun et al. 1999) clusters in a clade sister to *Pseudocercospora* s.str., and distant from *Phaeocercospora*. Although *Cercostigmina concentrica* (the type species of *Cercostigmina*) (Braun & Hill 2002) is not known from culture, other taxa with a similar morphology cluster in *Pseudocercospora* s.str., suggesting that *Cercostigmina* should be treated as synonym of *Pseudocercospora* (Crous et al. 2001, 2006). The *Dothistroma* clade is not well resolved, and other than *Dothistroma* and *Phaeocercospora*, also includes taxa with a *Passalora*-like morphology (scars and hila thickened, darkened and refractive).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the ITS sequence is *Mycosphaerella laricina* (GenBank EU167595; Identities = 519/562 (92 %), Gaps = 13/562 (2 %)), followed by *Passalora sequoiae* (GenBank GU214667; Identities = 519/563 (92 %), Gaps = 16/563 (3 %)), and *Passalora loranthi* (GenBank EU853479; Identities = 504/548 (92 %), Gaps = 16/548 (3 %)). Closest hits using the LSU sequence yielded highest similarity to *Passalora perplexa* (GenBank GU214459; Identities = 873/876 (99 %), Gaps = 0/876 (0 %)), *Mycosphaerella pini* (= *Dothistroma septosporum*, GenBank GU214427; Identities = 871/876 (99 %), Gaps = 0/876 (0 %)), and *Dothistroma pini* (GenBank GU214426; Identities = 870/876 (99 %), Gaps = 0/876 (0 %)).

Colour illustrations. *Colophospermum mopane* tree at Satara Rest Camp; symptomatic leaf; close-up of leaf spot; colony sporulating in culture; conidia and conidiogenous cells. Scale bar = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@cbs.knaw.nl & e.groenewald@cbs.knaw.nl


Myrmecridium banksiae

Fungal Planet 123 – 4 June 2012

Myrmecridium banksiae Crous, *sp. nov.*

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

Colonies on synthetic nutrient-poor agar. *Hyphae submerged* and creeping, hyaline, thin-walled, 2–4 µm diam. *Conidiophores* arising vertically from creeping aerial hyphae, unbranched, straight, to geniculate-sinuous, medium brown, not thick-walled, 1–5-septate, 15–90 µm tall, 3–5 µm diam. *Conidiogenous cells* integrated, cylindrical, 10–50 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, aseptate, pale brown, thin-walled, smooth to verruculose in middle, granular to guttulate, surrounded by a wing-like gelatinous sheath in the middle, approx. 0.5 µm thick, ellipsoid to obovoid or fusoid, (9–)10–12(–14) × (2.5–)3–3.5 µm, tapering to a subtruncate hilum; hilum unpigmented, not darkened.

Culture characteristics — (in the dark, 25 °C after 3 wk): Colonies flat to erumpent, spreading, lacking aerial mycelium on PDA and OA, with moderate aerial mycelium on MEA, reaching 50 mm diam. On MEA surface grey olivaceous, outer region greyish sepia and cinnamon; on OA grey olivaceous with patches of cinnamon; on PDA cinnamon.

Typus. Australia, Victoria, Melbourne, *Banksia* leaf litter (*Proteaceae*), 1 Aug. 2011, *P.W. Crous*, holotype CBS H-20967, cultures ex-type CPC 19853, 19852 = CBS 132537, ITS sequence GenBank JX069871 and LSU sequence GenBank JX069855, MycoBank MB800388.

Notes — The genus *Myrmecridium* was established by Arzanlou et al. (2007) on the basis of its hyaline mycelium, and pale to unpigmented, pimple-like denticles. Three species are presently known, namely *M. schulzeri* (var. *schulzeri* and var. *tritici*) (conidia 6–12 × 3–4 µm), *M. flexuosum* (conidia 5–9 × 3–4 µm), and *M. phragmitis* (conidia 6.5–9 × 2.5–3.5 µm; Crous et al. 2011b). *Myrmecridium banksiae* is easily distinguishable from known species by having larger conidia (9–14 × 2.5–3.5 µm).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the ITS sequence is *Myrmecridium schulzeri* (GenBank EU041778; Identities = 514/530 (97 %), Gaps = 5/530 (1 %)), followed by *Myrmecridium phragmitis* (GenBank JQ044425; Identities = 521/547 (95 %), Gaps = 6/547 (1 %)). Closest hits using the LSU sequence yielded highest similarity to *Myrmecridium schulzeri* (GenBank EU041835; Identities = 864/865 (99 %), Gaps = 0/865 (0 %)), *Myrmecridium phragmitis* (GenBank JQ044444; Identities = 869/884 (98 %), Gaps = 0/884 (0 %)) and *Myrmecridium flexuosum* (GenBank EU041825; Identities = 855/865 (99 %), Gaps = 0/865 (0 %)).

Colour illustrations. Coastal region along Great Ocean Road; colony sporulating on synthetic nutrient-poor agar; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@cbs.knaw.nl & e.groenewald@cbs.knaw.nl


Xenosonderhenia syzygii

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Xenosonderhenia Crous, *gen. nov.*

Etymology. Similar to *Sonderhenia*, but distinct in lacking distoseptate conidia.

Foliicolous, associated with leaf spots. *Conidiomata* pycnidial, black, globose, substomatal, erumpent, predominantly epiphyllous, with central ostiole, lined with periphyses; wall of 2–3 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, subcylindrical to doliiform; finely verruculose, pale brown, proliferating apically with several percurrent proliferations. *Conidia* subcylindrical, brown, finely verruculose, apex obtuse, base truncate with visible scar, (1–)3-euseptate, but septa with visible central pore. *Conidia* of synanamorph intermingled in same conidioma, but conidiogenous cells proliferating percurrently or sympodially; conidia hyaline to subhyaline, narrowly obclavate, apex subobtuse, base truncate, straight to curved, transversely multi-septate. Synanamorph also hyphomycetous, developing in aerial mycelium; conidiophores subcylindrical, straight to curved, 0–2-septate, hyaline to subhyaline, proliferating sympodially at apex. *Conidiophores* solitary or fasciculate or forming on a reduced stroma.

Type species. *Xenosonderhenia syzygii.*
MycoBank MB800389.

Xenosonderhenia syzygii Crous, *sp. nov.*

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

Leaf spots amphigenous, irregular, 2–10 mm diam, medium brown with irregular white patches due to raised epidermis, surrounded by a wide, red-purple border with visible black conidiomata aggregated around the outer zones of lesions. *Conidiomata* pycnidial, black, globose, substomatal, erumpent, predominantly epiphyllous, up to 120 µm diam, with central ostiole, 10 µm diam, lined with periphyses; wall of 2–3 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, subcylindrical to doliiform, 4–6 × 3–4 µm; finely verruculose, pale brown, proliferating apically with several percurrent proliferations. *Conidia* subcylindrical, brown, finely verruculose, apex obtuse, base truncate with visible scar (2.5–3 µm diam), (1–)3-euseptate, but septa with visible central pore, (12–)13–15 × (4.5–)5–6 µm.

In culture on synthetic nutrient-poor agar — Dimorphic, forming a synanamorph. *Conidiomata* pycnidial, exuding masses of brown conidia. *Conidiophores* reduced to conidiogenous cells, or one supporting cell, proliferating percurrently. *Conidia* cylindrical, brown, finely verruculose, apex obtuse, base truncate, 3–5-euseptate, 15–23 × 4–5 µm. *Conidia* of synanamorph intermingled in same conidioma, but conidiogenous cells proliferating percurrently or sympodially; conidia hyaline to subhyaline, narrowly obclavate, apex subobtuse, base truncate, straight to curved, 25–80 × 2.5–3 µm, up to 11-septate. Synanamorph also developing in aerial mycelium (on PNA); conidiophores subcylindrical, straight to curved, 0–2-septate, hyaline to subhyaline, 8–15 × 2–3 µm, proliferating sympodially at apex. *Conidiophores* solitary or fasciculate or on a reduced stroma.

Culture characteristics — (in the dark, 25 °C after 3 wk): Colonies erumpent, spreading, moderate to woolly aerial mycelium, feathery margins, reaching 10 mm diam. On MEA surface dirty white, reverse iron-grey with patches of orange; on OA olivaceous grey with patches of orange; on PDA dirty white, reverse olivaceous grey.

Colour illustrations. Waterfall at Lowveld Botanical Garden, Nelspruit; symptomatic leaf; close-up of leaf spots; conidiomata sporulating on potato-dextrose agar; conidiogenous cells giving rise to dimorphic conidia. Scale bars = 10 µm.

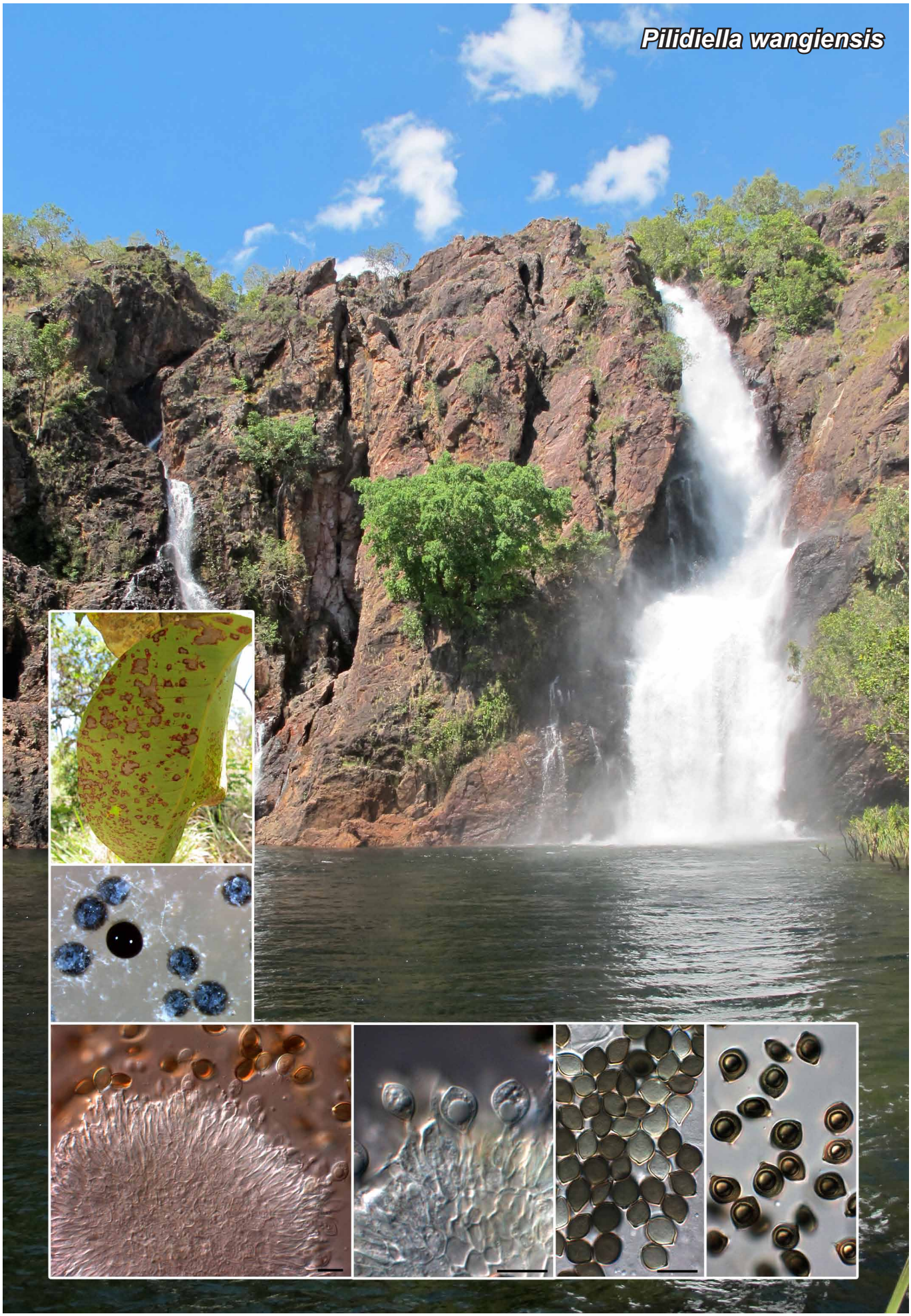
Typus. South Africa, Mpumalanga, Nelspruit, Lowveld Botanical Garden, on leaves of *Syzygium cordatum* (*Myrtaceae*), 17 Aug. 2011, *P.W. Crous*, *M.K. Crous, M. Crous & K.L. Crous*, holotype CBS H-20968, cultures ex-type CPC 19790 = CBS 132688, ITS sequence GenBank JX069872 and LSU sequence GenBank JX069856, MycoBank MB800390.

Notes — In the past *Hendersonia* was mainly seen as a genus to accommodate pigmented counterparts of *Stagonospora*, though the genus has since been rejected in favour of the latter (Sutton 1977). Taxa occurring on *Eucalyptus* were subsequently placed in the genus *Sonderhenia* (Swart & Walker 1988), which appears to represent a distinct phylogenetic lineage in the *Mycosphaerellaceae* (Crous et al. 2009a, b). *Sonderhenia* is characterised by having pigmented, percurrently proliferating conidiogenous cells, and brown, distoseptate, oval to subcylindrical conidia, and *Mycosphaerella*-like teleomorphs. Based on its distoseptate conidia, *Sonderhenia* is clearly distinct from *Xenosonderhenia*.

Two other genera of pycnidial coelomycetous fungi with brown, percurrently proliferating conidiogenous cells occur in the *Mycosphaerellaceae*, namely *Readeriella* and *Phaeophleospora*. *Phaeophleospora* has brown, scolecosporous conidia, is paraphyletic (Crous et al. 2009a, b), but clusters apart from *Xenosonderhenia*. *Readeriella* has conidia with subtruncate bases, *Cibiessiae* synanamorphs, and also clusters apart from *Xenosonderhenia*. Morphologically *Xenosonderhenia* is unique in being dimorphic, and forming hyaline to subhyaline, narrowly obclavate conidia of a synanamorph on culture, which occur separately, or in the same conidiomata with *Xenosonderhenia* conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the ITS sequence is *Mycosphaerella elaeocarpi* (GenBank EU040212; Identities = 500/535 (93 %), Gaps = 14/535 (3 %)), followed by *Mycosphaerella elongata* (GenBank EF394833; Identities = 478/504 (95 %), Gaps = 7/504 (1 %)), and *Mycosphaerella coacervata* (GenBank EU167596; Identities = 490/533 (92 %), Gaps = 16/533 (3 %)). Closest hits using the LSU sequence yielded highest similarity to *Mycosphaerella elaeocarpi* (GenBank EU040212; Identities = 859/864 (99 %), Gaps = 0/864 (0 %)), *Mycosphaerella marasasii* (GenBank GU214445; Identities = 855/879 (97 %), Gaps = 10/879 (1 %)), and *Mycosphaerella stromatosa* (GenBank EU167598; Identities = 848/877 (97 %), Gaps = 4/877 (0 %)).

Pedro W. Crous & Johannes Z. Groenewald, CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@cbs.knaw.nl & e.groenewald@cbs.knaw.nl


Pilidiella wangiensis

Fungal Planet 125 – 4 June 2012

Pilidiella wangiensis Crous & Summerell, *sp. nov.*

Etymology. Named after Wangi Falls in Australia, where this fungus was collected.

Leaf spots large, circular, brown, up to 20 mm diam, with red-brown margins. *Colonies* on OA. *Conidiomata* pycnidial, amphigenous, solitary, globose, up to 200 µm diam; wall composed on dark brown *textura angularis*, of 2–4 layers, 7–10 µm thick, pale to dark brown; ostiole central. *Conidiophores* formed on a central cushion of hyaline cells, mostly reduced to conidiogenous cells, subcylindrical, branched below, 15–30 × 3–5 µm, smooth, hyaline, 1–2-septate. *Conidiogenous cells* phialidic with apical periclinal thickening, or percurrent proliferation, 15–20 × 3–4 µm, smooth, hyaline, with minute collarette, and invested in mucilage. *Conidia* (9–)10–11(–13) × (7–)8–9(–10) µm, broadly ellipsoidal to globose, apiculate, granular with central guttule, hyaline, becoming medium brown, frequently with minute basal cellular appendage, hyaline, cylindrical, 1–2 µm long; conidia at times flattened along one side, or collapsing with age; apex tapering to an apiculus, 1–2 µm diam, base tapering to a truncate hilum, 1–1.5 µm diam.

Culture characteristics — (in the dark, 25 °C, after 3 wk): Colonies flat, spreading, with moderate aerial mycelium, covering dish. Surface on MEA, OA, and PDA dirty white with patches of black sporulation; reverse dirty white with iron-grey zones due to sporulation, but on MEA bright orange with patches of olivaceous grey.

Typus. Australia, Northern Territory, Litchfield National Park, Wangi Falls, on leaves of *Eucalyptus* sp. (*Myrtaceae*), 24 Apr. 2011, *P.W. Crous & B.A. Summerell*, holotype CBS H-20969, cultures ex-type CPC 19398, 19397 = CBS 132530, ITS sequence GenBank JX069873 and LSU sequence GenBank JX069857, MycoBank MB800391.

Notes — The first phylogenetic overview of the genera *Coniella* and *Pilidiella* was published by van Niekerk et al. (2004). Since then, several additional species have been added to this complex (Rajeshkumar et al. 2011, Miranda et al. 2012). Morphologically *P. wangiensis* is most similar to *Coniella australiensis* (conidia 10–14 × 7–11 µm; *Pelargonium australe*, Australia) (Sutton 1980), but differs in having somewhat smaller conidia (9–13 × 7–10 µm), and having an apical apiculus, which is lacking in *C. australiensis*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the ITS sequence is *Coniella granati* (GenBank HQ166057; Identities = 582/629 (93 %), Gaps = 31/629 (5 %)), followed by *Pilidiella eucalyptorum* (GenBank EU301050; Identities = 556/600 (93 %), Gaps = 21/600 (4 %)), and *Pilidiella quercicola* (GenBank AY339345; Identities = 545/586 (93 %), Gaps = 28/586 (5 %)). Closest hits using the LSU sequence yielded highest similarity with species of *Harknessia*, e.g. *Harknessia fusiformis* (GenBank JQ706221; Identities = 877/890 (99 %), Gaps = 4/890 (0 %)), *Pilidiella eucalyptorum* (GenBank AF408391; Identities = 860/876 (98 %), Gaps = 0/876 (0 %)), and *Pilidiella granati* (GenBank AF408380; Identities = 861/877 (98 %), Gaps = 1/877 (0 %)).

Colour illustrations. Wangi Falls, Litchfield National Park, Northern Territory; symptomatic *Eucalyptus* leaf; conidiomata forming on oatmeal agar; cushion of conidiogenous cells; conidiogenous cells and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@cbs.knaw.nl & e.groenewald@cbs.knaw.nl
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs Macquaries Rd, Sydney, NSW 2000, Australia;
e-mail: Brett.Summerell@rbgsyd.nsw.gov.au


Toxicocladosporium strelitziae

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Toxicocladosporium strelitziae Crous, *sp. nov.*

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

Colonies sporulating on synthetic nutrient-poor agar. *Mycelium* consisting of branched, septate, smooth, pale brown, 1.5–2.5 µm wide hyphae. *Conidiophores* dimorphic. *Macroconidiophores* solitary, arising from superficial mycelium, erect, brown, unbranched or branched above, verruculose, subcylindrical, straight to flexuous, 40–70 × 2–3.5 µm, 2–5-septate. *Microconidiophores* reduced to conidiogenous cells on hyphae, pale brown, smooth, erect, subcylindrical, 3–7 × 2.5–3.5 µm. *Conidiogenous cells* integrated, polyblastic, terminal and lateral, smooth, brown, 10–15 × 2.5–3.5 µm; scars truncate, thickened and darkened, 1.5–2 µm wide. *Primary ramoconidia* medium brown, smooth to finely verruculose, aseptate, subcylindrical, 12–20 × 2–3.5 µm. *Secondary ramoconidia* giving rise to branched chains of conidia, subcylindrical, polyblastic, brown, finely verruculose, aseptate, 10–17 × 2–3.5 µm; scars darkened, thickened, 0.5–1 µm diam. *Intercalary conidia* subcylindrical to fusoid-ellipsoidal, brown, finely verruculose, 10–12 × 2–2.5 µm. *Small terminal conidia* fusoid-ellipsoidal, brown, finely verruculose, (5–)7–8(–9) × 2(–2.5) µm; hila thickened and darkened, 0.5–1 µm diam.

Culture characteristics — (in the dark, 25 °C after 3 wk): Colonies flat to semi erumpent, spreading, with sparse to moderate aerial mycelium, and smooth, even margins, reaching 35 mm diam. On MEA surface folded, olivaceous grey, reverse iron-grey; on OA iron-grey; on PDA surface and reverse iron-grey.

Typus. South Africa, Mpumalanga, Kruger Game Reserve, Satara Rest Camp, on leaves of *Strelitzia reginae* (*Strelitziaceae*), 11 July 2011, *P.W. Crous*, holotype CBS H-20970, cultures ex-type CPC 19763, 19762 = CBS 132535, ITS sequence GenBank JX069874 and LSU sequence GenBank JX069858, MycoBank MB800392.

Notes — The genus *Toxicocladosporium* was established for *T. irritans*, a species with dimorphic conidiophores, and dark, thick-walled conidial and conidiophore septa, lacking coronate scars as observed in *Cladosporium* s.str. (Crous et al. 2007b). Since it was initially described, a further six species have been added to the genus (Crous & Groenewald 2011). *Toxicocladosporium* is phylogenetically closely related to *T. pseudoveloxum*, but is distinct in having longer, narrower conidiophores (20–50 × 3–4 µm in *T. pseudoveloxum*), and larger, aseptate ramoconidia (0–1-septate, 8–15 × 2.5–4 µm in *T. pseudoveloxum*) (Crous & Groenewald 2011).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the ITS sequence is *Toxicocladosporium pseudoveloxum* (GenBank JF499849; Identities = 540/557 (97 %), Gaps = 7/557 (1 %)), followed by *Toxicocladosporium irritans* (GenBank EU040243; Identities = 527/539 (98 %), Gaps = 2/539 (0 %)), and *Toxicocladosporium banksiae* (GenBank HQ599598; Identities = 538/557 (97 %), Gaps = 10/557 (2 %)). Closest hits using the LSU sequence yielded highest similarity to *Toxicocladosporium irritans* (GenBank EU040243; Identities = 939/939 (100 %), Gaps = 0/939 (0 %)), *Toxicocladosporium pseudoveloxum* (GenBank JF499868; Identities = 927/940 (99 %), Gaps = 4/940 (0 %)), and *Graphiopsis chlorocephala* (GenBank EU009458; Identities = 918/940 (98 %), Gaps = 3/940 (0 %)).

Colour illustrations. Strelitzia reginae flower with minute brown lesions; sporulation on synthetic nutrient-poor agar; conidiophores giving rise to conidial chains. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@cbs.knaw.nl & e.groenewald@cbs.knaw.nl


Devriesia agapanthi

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Devriesia agapanthi Crous, *sp. nov.*

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

Ascomata amphigenous on dead leaf tissue at soil level, immersed, substomatal, solitary, brown, subglobose, up to 100 µm diam, ostiole central, 10 µm diam; wall of 2–3 layers of brown *textura angularis*. *Asci* fasciculate, subsessile, obclavate, bitunicate, hyaline, 30–40 × 8–12 µm, with visible ocular chamber. *Ascospores* hyaline, smooth (becoming brown and verruculose in older asci), multiseriate, guttulate, medianly septate, with minute constriction at septum, straight to slightly curved, fusoid-ellipsoidal, widest in middle of apical cell, tapering to obtusely rounded ends, (10–)12–13(–14) × 3(–3.5) µm. *Colonies* homothallic, sporulating in culture.

Culture characteristics — (in the dark, 25 °C after 3 wk): Colonies variable on agar media, hardly growing on PDA and SNA, erumpent, lacking aerial mycelium, iron-grey, reaching 2–4 mm diam. On MEA and OA spreading, with sparse aerial mycelium, and smooth, lobate margins; reaching 20 mm diam. On MEA olivaceous grey, iron-grey at margin, and in reverse; on OA iron-grey. Chlamydospore-like structures not observed in culture.

Typus. South Africa, Western Cape Province, Knysna, Pledge Nature Reserve, leaves of *Agapanthus africanus* (*Amaryllidaceae*), 28 July 2011, *P.W. Crous*, holotype CBS H-20971, cultures ex-type CPC 19834, 19833 = CBS 132689, ITS sequence GenBank JX069875 and LSU sequence GenBank JX069859, MycoBank MB800393.

Notes — Seifert et al. (2004) introduced the genus *Devriesia* to accommodate five *Cladosporium*-like fungi that were heat resistant, produced chlamydospore-like structures, and occurred in soil. Since its initial description an additional 10 species have been described (Crous & Groenewald 2011), which considerably broadened the generic circumscription. The present collection represents the first potential teleomorph linked to this complex, suggesting that when found, teleomorphs of *Devriesia* would be *Teratosphaeria*-like in morphology (Crous et al. 2007a, 2009a, b). No anamorph was found on the host, nor observed to form in culture.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the ITS sequence is *Devriesia hilliana* (GenBank GU214633; Identities = 532/551 (97 %), Gaps = 7/551 (1 %)), followed by *Devriesia xanthorrhoeae* (GenBank HQ599605; Identities = 514/530 (97 %), Gaps = 9/530 (2 %)), and *Devriesia lagerstroemiae* (GenBank GU214634; Identities = 509/558 (91 %), Gaps = 34/558 (6 %)). Closest hits using the LSU sequence yielded highest similarity to *Devriesia hilliana* (GenBank GU214414; Identities = 889/894 (99 %), Gaps = 0/894 (0 %)), *Devriesia xanthorrhoeae* (GenBank HQ599606; Identities = 887/894 (99 %), Gaps = 0/894 (0 %)), and *Devriesia queenslandica* (GenBank JF951168; Identities = 882/894 (99 %), Gaps = 0/894 (0 %)).

Colour illustrations. Fallen tree along path at Pledge Nature Reserve, with *Agapanthus africanus* growing among other bulb plants; conidiomata on dead leaf tissue; asci; germinating ascospores on malt extract agar; ascospores. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@cbs.knaw.nl & e.groenewald@cbs.knaw.nl

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