



## Fungal Planet description sheets: 214–280

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### Key words

ITS DNA barcodes

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**Abstract** Novel species of microfungi described in the present study include the following from South Africa: *Cercospora dolichandrae* from *Dolichandra unguis-cati*, *Seiridium podocarpi* from *Podocarpus latifolius*, *Pseudocercospora parapseudarthriae* from *Pseudarthria hookeri*, *Neodevriesia coryneliae* from *Corynelia uberata* on leaves of *Afrocarpus falcatus*, *Ramichloridium eucaleae* from *Euclea undulata* and *Stachybotrys aloeticola* from *Aloe* sp. (South Africa), as novel member of the *Stachybotriaceae* fam. nov. Several species were also described from Zambia, and these include *Chaetomella zambiensis* on unknown Fabaceae, *Schizoparme pseudogranati* from *Terminalia stuhlmannii*, *Diaporthe isoferliniae* from *Isoferlinia angolensis*, *Peyronellaea combreti* from *Combretum mossambicense*, *Zasmidium rothmanniae* and *Phaeococcomyces rothmanniae* from *Rothmannia engleriana*, *Diaporthe vangueriae* from *Vangueria infausta* and *Diaporthe parapterocarpi* from *Pterocarpus brenanii*. Novel species from the Netherlands include: *Stagonospora trichophoricola*, *Keissleriella trichophoricola* and *Dinemasporium trichophoricola* from *Trichophorum cespitosum*, *Phaeosphaeria poae*, *Keissleriella poagena*, *Phaeosphaeria poagena*, *Parastagonospora poagena* and *Pyrenopeziza poae* from *Poa* sp., *Septoriella oudemansii* from *Phragmites australis* and *Dendryphion europaeum* from *Hedera helix* (Germany) and *Heracleum sphondylium* (the Netherlands). Novel species from Australia include: *Anungitea eucalyptorum* from *Eucalyptus* leaf litter, *Beltraniopsis neolitseaee* and *Acrodontium neolitseaee* from *Neolitsea australiensis*, *Beltraniella endiandrae* from *Endiandra introrsa*, *Phaeophleospora parsoniae* from *Parsonia straminea*, *Penicillifer martinii* from *Cynodon dactylon*, *Ochroconis macrozamiae* from *Macrozamia* leaf litter, *Triplosporium cycadicola*, *Circinotrichum cycadis*, *Cladosporium cycadicola* and *Acrocalymma cycadis* from *Cycas* spp. Furthermore, *Vermiculariopsiella dichapetalii* is described from *Dichapetalum rhodesicum* (Botswana), *Marasmius vladimirii* from leaf litter (India), *Ophiognomonia acadiensis* from *Picea rubens* (Canada), *Setophoma vernoniae* from *Vernonia polyanthes* and *Penicillium restingae* from soil (Brazil), *Pseudolachnella guaviyunis* from *Myrcianthes pungens* (Uruguay) and *Pseudocercospora nericae* from *Nerium oleander* (Italy). Novelties from Spain include: *Dendryphiella eucalyptorum* from *Eucalyptus globulus*, *Conioscypha minutispora* from dead wood, *Diplogelasinopora moalensis* and *Pseudoneurospora canariensis* from soil and *Inocybe lanatopurpurea* from reforested woodland of *Pinus* spp. Novelties from France include: *Kellermania trizeptata* from *Agave angustifolia*, *Zetiasplozna acaciae* from *Acacia melanoxylon*, *Pyrenopeziza pinicola* from *Pinus* sp. and *Pseudonectria ruscicola* from *Ruscus aculeatus*. New species from China include: *Dematiocladium celtidicola* from *Celtis bungeana*, *Beltrania pseudorhombica*, *Chaetopsis beijingensis* and *Toxicocladosporium pini* from *Pinus* spp. and *Setophaeosphaeria badalingensis* from *Hemerocallis fulva*. Novel genera of *Ascomycetes* include *Alfaria* from *Cyperus esculentus* (Spain), *Rinaldiella* from a contaminated human lesion (Georgia), *Hyalocladosporiella* from *Tectona grandis* (Brazil), *Pseudoacremonium* from *Saccharum spontaneum* and *Melnikomyces* from leaf litter (Vietnam), *Annellosympodiella* from *Juniperus procera* (Ethiopia), *Neoceratosperma* from *Eucalyptus* leaves (Thailand), *Ramopenidiella* from *Cycas calcicola* (Australia), *Cephalotrichiella* from air in the Netherlands, *Neocamarosporium* from *Mesembryanthemum* sp. and *Acervuloseptoria* from *Ziziphus mucronata* (South Africa) and *Setophaeosphaeria* from *Hemerocallis fulva* (China). Several novel combinations are also introduced, namely for *Phaeosphaeria setosa* as *Setophaeosphaeria setosa*, *Phoma heteroderae* as *Peyronellaea heteroderae* and *Phyllosticta maydis* as *Peyronellaea maydis*. Morphological and culture characteristics along with ITS DNA barcodes are provided for all taxa.

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## HIGHER ORDER CLASSIFICATION OF TAXONOMIC NOVELTIES

### ASCOMYCOTA

#### Arthoniomycetes

*Lichenostigmatales, Phaeococomycetaceae*

*Phaeococomyces rothmanniae*

#### Dothideomycetes

*Botryosphaerales, Planistromellaceae*

*Kellermania triseptata*

*Capnodiales, Cladosporiaceae*

*Gladosporium cycadicola*

*Toxicocladosporium pini*

*Capnodiales, Dissosconiacae*

*Ramichloridium eucleae*

*Capnodiales, Mycosphaerellaceae*

*Acervuloseptoria ziziphicola*

*Acrodontium neolitsea*

*Annellosympodiella juniperi*

*Cercospora dolichandrae*

*Neoceratosperma eucalypti*

*Phaeophleospora parsoniae*

*Pseudocercospora neriicola*

*Pseudocercospora parapseudarthriae*

*Zasmidium rothmanniae*

*Capnodiales, Teratosphaeriaceae*

*Neodevriesia coryneliae*

*Ramopenidiella cycadicola*

*Pleosporomycetidae, Pleosporales, Incertae sedis, Cucurbitariaceae*

*Pyrenopeziza poae*

*Pleosporomycetidae, Pleosporales, Massarinaeae, Lentitheciaceae*

*Keisslerella poagena*

*Keisslerella trichophoricola*

*Pleosporomycetidae, Pleosporales, Massarinaeae*

*Stagonospora trichophoricola*

*Pleosporomycetidae, Pleosporales, Massarinaeae*

*Acrocalymma cycadis*

*Pleosporomycetidae, Pleosporales, Pleosporineae, Didymellaceae*

*Peyronellaea combreti*

*Peyronellaea heteroderae*

*Peyronellaea maydis*

#### Pleosporomycetidae, Pleosporales, Pleosporineae, Phaeosphaeriaceae

*Parastagonospora poagena*

*Phaeosphaeria poae*

*Phaeosphaeria poagena*

*Septoriella oudemansi*

*Setophaeosphaeria badalingensis*

*Setophaeosphaeria hemerocalcidis*

*Setopoma vernoniae*

#### Pleosporomycetidae, Pleosporales, Pleosporineae, Pleosporaceae

*Dendryphiella eucalyptorum*

*Dendryphion europaeum*

*Neocamarosporum goegapense*

*Pyrenochaeta pinicola*

#### Pleosporomycetidae, Venturiiales, Sympoventuriaceae

*Ochroconis macrozamiae*

#### Pleosporomycetidae, Venturiiales, Venturiaceae

*Anungitea eucalyptorum*

#### Eurotiomycetes

##### Chaetothyriomycetidae, Chaetothyriales, Incertae sedis

*Hyalocladosporiella tectonae*

*Melnikomyces vietnamensis*

##### Eurotiomycetidae, Eurotiales, Trichocomaceae

*Penicillium restingae*

#### Leotiomycetes

##### Helotiales, Incertae sedis

*Chaetomella zambiensis*

*Triposporium cycadicola*

#### Sordariomycetes

##### Hypocreomycetidae, Hypocreales, Incertae sedis

*Alfaria cyperi-esculentii*

*Chaetopsina beijingensis*

*Pseudoacremonium sacchari*

##### Hypocreomycetidae, Hypocreales, Nectriaceae

*Dematiocladium celtidicola*

*Penicillifer martinii*

*Pseudonectria risci*

##### Hypocreomycetidae, Hypocreales, Stachybotriaceae

*Stachybotrys aloeticola*

#### Hypocreomycetidae, Microascales, Incertae sedis

*Cephalotrichiella penicillata*

*Conioscypha minutispora*

*Vermiculariopsis dichapetali*

#### Sordariomycetidae, Chaetosphaeriales, Chaetosphaeraceae

*Dinemasperium trichophoricola*

*Pseudolachnella guaviyunis*

#### Sordariomycetidae, Diaporthales, Diaporthaceae

*Diaporthe isoberliniae*

*Diaporthe parapterocarpi*

*Diaporthe vangueriae*

#### Sordariomycetidae, Diaporthales, Gnomoniaceae

*Ophiognomonia acadiensis*

#### Sordariomycetidae, Diaporthales, Schizopharmaceae

*Schizopharne pseudogranati*

#### Sordariomycetidae, Sordariales, Lasiosphaeriaceae

*Diplogelasinospora moalensis*

*Rinaldiella pentagonospora*

#### Sordariomycetidae, Sordariales, Sordariaceae

*Pseudoneurospora canariensis*

#### Xylariomycetidae, Xylariales, Xylariaceae

*Seiridium podocarpi*

*Zefiasploza acaciae*

#### Xylariomycetidae, Xylariales, Hyphonectriaceae

*Beltraniella endiandrae*

#### Xylariomycetidae, Xylariales, Incertae sedis

*Beltrania pseudorhombica*

*Beltraniopsis neolitsea*

#### Xylariomycetidae, Xylariales, Xylariaceae

*Circinotrichum cycadis*

### BASIDIOMYCOTA

#### Agaricomycetes, Agaricomycetidae, Agaricales, Inocybaceae

*Inocybe lanatopurpurea*

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## ***Dematiocladium celtidicola* Crous, M.J. Wingf. & Y. Zhang ter, sp. nov.**

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

Setae unbranched, flexuous, 200–400 × 12–20 µm, arising from pseudoparenchymatous cells in a basal stroma or micro-sclerotia (ascomatal initials?), adjacent to cells that give rise to conidiophore stipes; setae yellow-brown, smooth to finely roughened, thick-walled, basal cell rounded and well-defined; stipe becoming thinner walled towards the acute apex; apical cell sometimes becoming fertile, setae extending beyond the conidiophores. Conidiophores consisting of a stipe, a penicillate arrangement of fertile branches, and rarely, an extension of the stipe, signifying continued growth and eventual branching of the stipe and secondary penicillate conidiophores. Stipe septate, hyaline, smooth, arising from tightly arranged pale to medium brown pseudoparenchymatous cells in a basal stroma, 40–150 × 4–5 µm. Conidiogenous apparatus 30–40 µm long, 40–50 µm wide; branches hyaline, smooth, 1–2-septate; primary branches subcylindrical to more swollen and doliiform to ellipsoid, 10–15 × 5–10 µm; additional branches (up to 2), 10–15 × 5–7 µm; terminal branches producing 1–6 phialides. Phialides elongate doliiform to reniform or subcylindrical, straight to slightly curved, aseptate, 10–20 × 3–4 µm; apex with minute periclinal thickening and inconspicuous collarette. Conidia cylindrical, rounded at both ends, straight, hyaline, (31)–35–38(–43) × 3(–3.5) µm, 1-septate, lacking a visible abscission scar, held in parallel clusters by colourless slime. Chlamydospores globose, 15–25 µm wide, thick-walled, red-brown, forming microsclerotia.

Culture characteristics — Colonies reaching 50 mm diam after 2 wk at 22 °C. On MEA spreading, with sparse aerial mycelium and smooth, even margins; surface with concentric circles of orange and ochreous, reverse apricot. On OA orange. On PDA surface and reverse orange, outer region amber.

**Typus.** CHINA, Beijing, Great Wall of China, N40°21'36.8" E116°00'52.2", on leaves of *Celtis bungeana* (*Ulmaceae*), 1 Sept. 2013, P.W. Crous, M.J. Wingfield & Y. Zhang (holotype CBS H-21716, culture ex-type CPC 23617 = CBS 138002; ITS sequence GenBank KJ869157, LSU sequence GenBank KJ869214, MycoBank MB808941).

**Notes** — The genus *Dematiocladium* was introduced to accommodate a cylindrocladium-like fungus growing on *Celtis tala* in Argentina, characterised by having pigmented setae (Crous et al. 2005). Due to its penicillate conidiophores and cylindrical, hyaline conidia, the genus *Dematiocladium* resembles *Calonectria* (= *Cylindrocladium*) (Lombard et al. 2010) and genera in the *Cylindrocarpon* complex (Chaverri et al. 2011, Cabral et al. 2012), but is distinct in that it has dematiaceous stipes dispersed among its conidiophores.

Although *D. celtidis* was collected from leaf litter of *Celtis tala* in Argentina, *D. celtidicola* was associated with leaf spots on living leaves of *Celtis bungeana* in China, suggesting that it could be a potential plant pathogen. Inoculation studies would be required, however, to prove this assumption.

**ITS.** Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Heliscus submersus* (GenBank HQ897796; Identities = 524/559 (94 %), Gaps = 13/559 (2 %)), *Glionectria tenuis* (GenBank EF495240; Identities = 519/556 (93 %), Gaps = 21/556 (3 %)) and *Gliocladiopsis sagariensis* (GenBank JQ666063; Identities = 505/541 (93 %), Gaps = 21/541 (3 %)).

**LSU.** Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Dematiocladium celtidis* (GenBank AY793438; Identities = 869/876 (99 %), no gaps), *Gliocephalotrichum bulbilium* (GenBank JQ666076; Identities = 891/903 (99 %), no gaps) and *Neonectria ramulariae* (GenBank HM042435; Identities = 878/890 (99 %), no gaps).

**Colour illustrations.** Symptomatic *Celtis bungeana* next to the Great Wall, China; conidiophores, setae and conidia in culture. Scale bars = 10 µm.

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## ***Neocamarosporium* Crous & M.J. Wingf., gen. nov.**

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

**Conidiomata** brown to black, immersed, becoming erumpent, globose with papillate apex and central ostiole; wall of 3–6 layers of brown *textura angularis*. **Conidiophores** reduced to conidiogenous cells. **Conidiogenous cells** lining the inner layer of conidioma, separate, hyaline, smooth, ampulliform; proliferating several times percurrently near apex, or at the same level,

giving rise to prominent periclinal thickening. **Conidia** solitary, initially hyaline, aseptate, thick-walled, developing a central septum and then becoming muriformly septate, shape variable from globose to obovoid to ellipsoid, golden brown, finely roughened, thick-walled.

**Type species.** *Neocamarosporium goegapense*.  
Mycobank MB808949.

## ***Neocamarosporium goegapense* Crous & M.J. Wingf., sp. nov.**

**Etymology.** Named after the Goegap Nature Reserve, where this fungus was collected.

**Conidiomata** brown to black, immersed, becoming erumpent, globose with papillate apex and central ostiole, up to 300 µm diam; wall of 3–6 layers of brown *textura angularis*. **Conidiophores** reduced to conidiogenous cells. **Conidiogenous cells** lining the inner layer of conidioma, separate, hyaline, smooth, ampulliform, 7–9 × 5–6 µm; proliferating several times percurrently near apex, or at the same level, giving rise to prominent periclinal thickening. **Conidia** solitary, initially hyaline, aseptate, thick-walled, developing a central septum and then becoming muriformly septate, shape variable from globose to obovoid to ellipsoid, golden brown, finely roughened, thick-walled, (15–20–22(–24) × 15–17(–19) µm.

**Culture characteristics** — Colonies reaching 55 mm diam after 2 wk at 22 °C. On MEA flat, spreading, with sparse aerial mycelium and feathery margins. On MEA surface grey-olivaceous, reverse umber. On OA grey-olivaceous. On PDA grey-olivaceous with patches of citrine, reverse greenish black in middle, citrine in outer region.

**Typus.** SOUTH AFRICA, Northern Cape Province, Springbok, Goegap Nature Reserve, on dying leaves of *Mesembryanthemum* sp. (Aizoaceae), Sept. 2013, M.J. Wingfield (holotype CBS H-21722, culture ex-type CPC 23676 = CBS 138008; ITS sequence GenBank KJ869163, LSU sequence GenBank KJ869220, MycoBank MB808950).

**Notes** — The genus *Camarosporium* (based on *C. quaternatum*) presently contains several hundred species, and is accepted as in urgent need of revision. *Camarosporium* is characterised by having pycnidial conidiomata, conidiophores reduced to conidiogenous cells that are hyaline, and line the inner cavity, proliferating percurrently, giving rise to brown, smooth, muriformly septate conidia (Sutton 1980, Crous et al. 2006). A morphologically similar genus is *Camarosporellum*, though the latter appears to have holoblastic conidiogenesis. Phylogenetically, *Neocamarosporium* is allied to a clade containing taxa accommodated in *Phoma*, *Chaetosphaeronema* and *Pleospora*, and is thus morphologically quite distinct.

**ITS.** Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Phoma betae* (GenBank KC460811; Identities = 464/486 (95 %), Gaps = 2/486 (0 %)), *Ascochyta obiones* (GenBank GU230752; Identities = 471/496 (95 %), Gaps = 3/496 (0 %)) and *Phoma schachtii* (GenBank FJ427066; Identities = 419/447 (94 %), Gaps = 7/447 (1 %)).

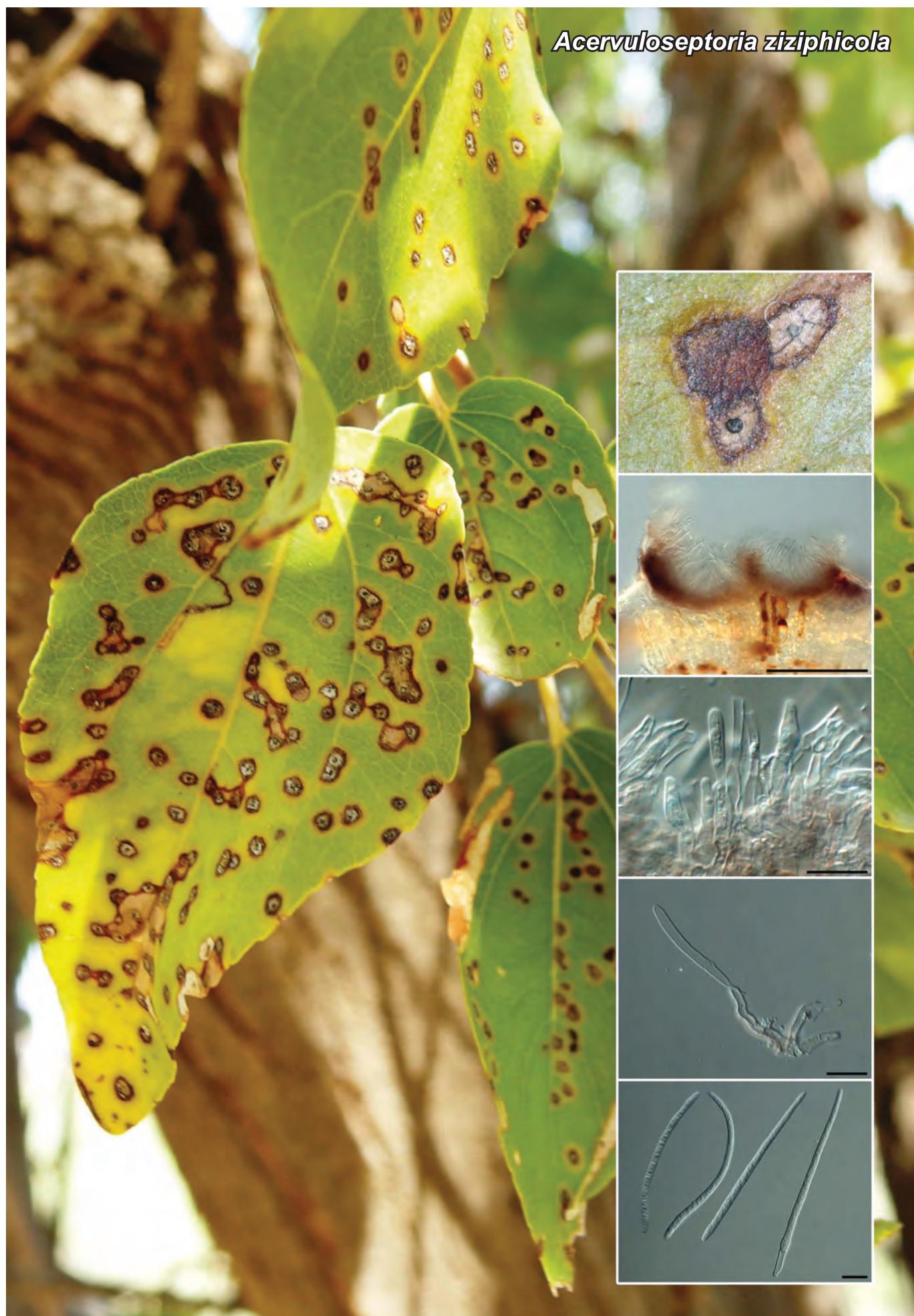
**LSU.** Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Phoma betae* (GenBank EU754179; Identities = 846/848 (99 %), Gaps = 1/848 (0 %)), *Chaetosphaeronema hispidulum* (GenBank EU754145; Identities = 845/847 (99 %), no gaps) and *Pleospora bjoerlingii* (GenBank AY849954; Identities = 805/807 (99 %), Gaps = 1/807 (0 %)).

**Colour illustrations.** *Mesembryanthemum* sp. growing in Goegap Nature Reserve, South Africa; conidiomata, conidiophores and conidia in culture. Scale bars = 10 µm.

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## ***Acervuloseptoria* Crous & Jol. Roux, gen. nov.**

**Etymology.** Named after its acervular-like conidiomata and its morphological similarity to the genus *Septoria*.

Plant pathogenic, foliicolous. *Conidiomata* black, amphigenous, exuding a creamy-white conidial cirrus, subepidermal, erumpent, multilocular, with upper layer breaking open irregularly and leaving conidioma to have acervular appearance; wall of 3–6 layers of brown *textura angularis* to *textura intricata*, basal layers pale brown, roof of conidioma dark brown; in culture conidiomata acervular with elements of conidiomatal roof remaining like brown strands along the sides of conidioma.

*Conidiophores* subcylindrical, straight to once geniculate, pale brown, verruculose, septate, branched or not. *Conidiogenous cells* terminal and lateral, subcylindrical, pale brown to subhyaline, verruculose to smooth, proliferating sympodially and percurrently. *Conidia* narrowly obclavate to subcylindrical, flexuous, guttulate, smooth, hyaline, apex subacutely rounded, base obconically truncate, septate.

*Type species.* *Acervuloseptoria ziziphicola*.

MycoBank MB808951.

## ***Acervuloseptoria ziziphicola* Crous & Jol. Roux, sp. nov.**

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

*Leaf spots* amphigenous, subcircular, 2 mm diam, grey-brown in middle with raised red-brown border and diffuse chlorotic margin. *Conidiomata* black, amphigenous, exuding a creamy-white conidial cirrus, subepidermal, erumpent, up to 500 µm diam, up to 100 µm high, multilocular, with upper layer breaking open irregularly and leaving conidioma to have acervular appearance; wall of 3–6 layers of brown *textura angularis* to *textura intricata*, basal layers pale brown, roof of conidioma dark brown; in culture conidiomata acervular with elements of conidiomatal roof remaining like brown strands along the sides of conidioma. *Conidiophores* subcylindrical, straight to once geniculate, pale brown, verruculose, 1–3-septate, branched or not, 15–40 × 3–4 µm. *Conidiogenous cells* terminal and lateral, subcylindrical, pale brown to subhyaline, verruculose to smooth, proliferating sympodially and percurrently, 8–12 × 3–4 µm. *Conidia* narrowly obclavate (frequently subcylindrical in culture), flexuous, guttulate, smooth, hyaline, apex subacutely rounded, base obconically truncate, (40–)55–75(–80) × 3(–4) µm, 3(–5)-septate.

**Culture characteristics** — Colonies reaching 5 mm diam after 2 wk at 22 °C. On MEA surface flat, spreading with even margins, lacking aerial mycelium; surface salmon, reverse umber. On OA surface umber. On PDA surface salmon with patches of umber, reverse similar.

**Typus.** SOUTH AFRICA, Northern Cape Province, Richtersveld, Potjiespram, associated with leaf spots of *Ziziphus mucronata* (Rhamnaceae), Sept. 2013, J. Roux (holotype CBS H-21723, culture ex-type CPC 23707 = CBS 138009; ITS sequence GenBank KJ869164, LSU sequence GenBank KJ869221, MycoBank MB808952).

**Notes** — Two species of *Septoria* have been described from *Ziziphus*, namely *S. zizyphi* (conidia 15 × 1 µm, *Michelia* 1: 173. 1878) and *S. capensis* (conidia 30–50 × 2–2.5 µm, *Hedwigia* 24: 33. 1885). Both species differ from the present collection, however, in their conidium dimensions.

The genus *Septoria* and allied genera were recently treated by Quaedvlieg et al. (2013). *Acervuloseptoria* differs from these genera in that it has peculiar conidiomatal morphology, with black, erumpent conidiomata, from which the top layer disintegrates, leaving a conidiomatal body that appears acervular. The conidiophores are also somewhat different in that they are slightly pigmented and verruculose in their lower part. Phylogenetically, *Acervuloseptoria* also appears distinct from those genera presently known in this generic complex (Quaedvlieg et al. 2013, Verkley et al. 2013).

**ITS.** Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Cercosporaella virgaureae* (GenBank GU214658; Identities = 506/537 (94 %), Gaps = 11/537 (2 %)), *Mycosphaerella areola* (GenBank DQ459084; Identities = 501/532 (94 %), Gaps = 9/532 (1 %)) and *Septoria protearum* (GenBank KF251235; Identities = 484/525 (92 %), Gaps = 20/525 (3 %)).

**LSU.** Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Cercosporaella virgaureae* (GenBank GU214658; Identities = 844/855 (99 %), no gaps), *Caryophylloseptoria lychnidis* (GenBank KF251791; Identities = 800/812 (99 %), no gaps) and *Septoria dysentericae* (GenBank GU253866; Identities = 840/855 (98 %), no gaps).

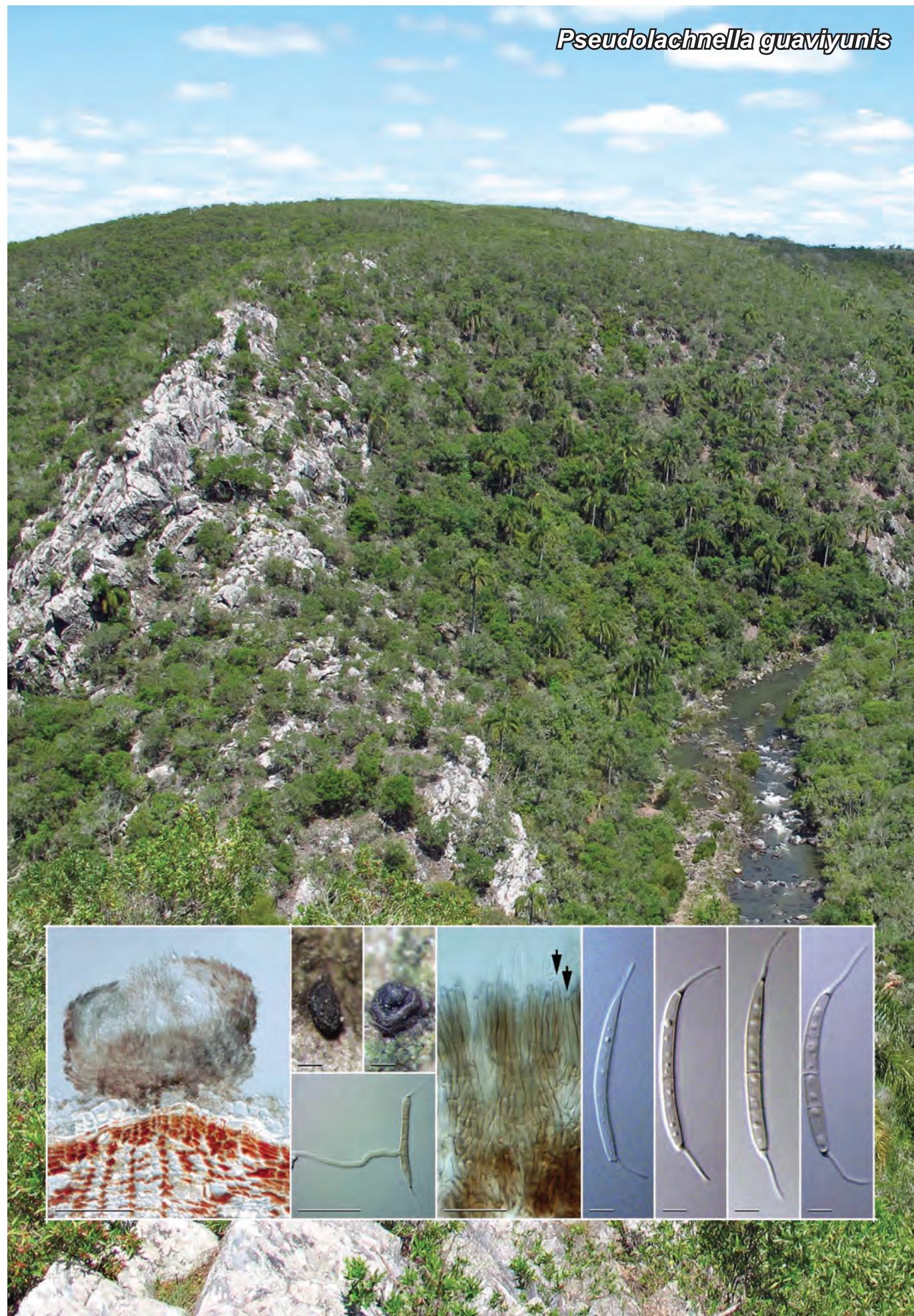
**Colour illustrations.** *Ziziphus mucronata* in South Africa; leaf spot, conidiomata, conidiophores and conidia in culture. Scale bars = 10 µm.

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*Pseudolachnella guaviyunis*

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## **Pseudolachnella guaviyunis** Marinc., T.A. Duong, M.J. Wingf. & C.A. Perez, sp. nov.

**Etymology.** A common name of the host plant in Uruguay, Guaviyú.

**Conidiomata** scattered, oval to rounded in outline, up to 688 µm long, up to 416 µm wide, up to 199 µm deep, cupulate with the edge slightly curved-in in sectional view, filled with agglutinated conidial mass, olivaceous-black; basal stroma well-developed, subepidermal, up to 85 µm thick, of *textura angularis* or *epidermoidea*, cells thick-walled, subhyaline when intercellular to pale brown, cells bordering the lateral wall becoming darker and thicker; lateral walls consisting of cells of *textura porrecta* in a few strata, cells thin-walled, pale brown to brown, marginal cells of each strata becoming darker. **Conidiomatal setae** absent. **Conidiophores** arising in the concavity of the conidio-*ma*, septate and branched at the base, pale brown, smooth. **Conidiogenous cells** phialidic, discrete, subhyaline to pale brown, cylindrical, with conspicuous collarette, often showing percurrent proliferation, 15–26 × 2–3 µm. **Conidia** hyaline when young and becoming pale brown with age, fusiform, straight or slightly curved, gradually tapering towards the apex, with an obtuse, truncate base, smooth or verruculous with age, bearing cellular appendages at both ends, (26.5–)33–36(–43.5) × (2–)2.5–3(–3.5) µm, aseptate when young, developing 3 septa with age, germinating from any of 4 cells; **apical appendages** 5.5–14 µm long, centric; **basal appendages** 4.5–13 µm long, excentric, both appendages 0.5–1 µm wide at the base and tapering towards the apex.

**Culture characteristics** — The cultures on 2 % malt extract agar showing optimum growth at 25 °C in the dark, reaching 22 mm after 22 d, sterile, above iron-grey, reverse fuscous-black (Rayner 1970), growing circular, radially striated with lobate edge, mycelia flat, velvety, medium dense, exuding dark brown pigmentation around the colony in 2 mm width.

**Typus.** URUGUAY, Quebrada de los Cuervos, on *Myrcianthes pungens*, Oct. 2012, M.J. Wingfield & C. Perez (holotype PREM 60964, culture ex-holotype CBS 134695 = CMW 39055, ex-isotypes CMW 39018–39020; ITS sequence of CBS 134695 GenBank KJ834524, LSU sequence of CBS 134695 GenBank KJ834525, MycoBank MB808837).

**Colour illustrations.** *Myrcianthes pungens* trees growing at the 'Quebrada de los Cuervos' in Uruguay; conidio-*ma* in sectional view (bar = 100 µm) and on the host substrate (350 µm), germinating conidium (25 µm), branched conidiophores and phialidic conidiogenous cells with conspicuous collarette (arrows) (20 µm); conidia from young to mature (5 µm).

**Notes** — Cupulate fruiting structures were found on the bark of *Myrcianthes pungens* in Uruguay. The morphological features of this isolate best match those of the genus *Pseudolachnella*, other than the absence of noticeable conidiomatal setae. Currently there are eight *Pseudolachnella* species recognised worldwide from herbaceous stems or leaves of monocotyledonous host plants, mostly palm trees in Asia (Nag Raj 1993, Zhao et al. 2004, Sato et al. 2008). The Uruguayan collection introduced as the new species *P. guaviyunis*, is recognised here primarily based on conidial morphology and DNA sequence data.

Both *Pseudolachnella* and *Pseudolachnea* are closely related to *Dinemasporium*. When Sutton (1980) limited *Dinemasporium* to the species with aseptate conidia, he restricted the species with septate conidia to *Pseudolachnea*. Nag Raj (1993) further limited *Pseudolachnea* to the species with 1-septate conidia and *Pseudolachnella* to those with multiseptate conidia. No sexual state is known for *Pseudolachnella* and *Pseudolachnea*, whereas one species of *Dinemasporium* is known based on its sexual state, *Phomatospora dinemasporium* (Xylariales). However, the identity of the sexual state in this case is considered to be doubtful (Duan et al. 2007).

A recent study applying ribosomal DNA sequence data revealed the phylogenetic placement of *Pseudolachnea* and *Dinemasporium* within the chaetosphaerialean clade. However, the phylogenetic position of *Pseudolachnella* could not be determined due to the lack of cultures (Crous et al. 2012b). The present study suggests that *Pseudolachnella* resides in the *Chaetosphaeriales* but that it is distantly related to *Pseudolachnea*, thus consistent with the views of Nag Raj (1993).

A case study of *Dinemasporium* and related genera by Crous et al. (2012b) suggested that the appendage morphology could be a useful characteristic in species delimitation but not in generic separation. *Pseudolachnella* species are heterogeneous in terms of appendage morphology: short (to 4 µm) or long (to 47 µm) in length, simple or branched, single or multiple in number. *Pseudolachnella guaviyunis* can be distinguished by its simple appendages at both ends of the conidia, measuring up to 14 µm in length.

A megablast search of the NCBI's GenBank nucleotide sequence database using the ITS sequence of *Pseudolachnella guaviyunis* showed that its closest relatives are *Pseudolachnea fraxini* (GenBank JQ 889287; Identities = 464/533 (87 %), Gaps = 23/533 (4 %)) and *Dinemasporium strigosum* (GenBank JQ889283; Identities = 495/579 (85 %); Gaps = 34/579 (5 %)). A megablast search using the LSU sequence of *Pseudolachnella guaviyunis* showed that it was most similar to *Pseudolachnea fraxini* (GenBank JQ889301; Identities = 810/839 (97 %); Gaps = 1/839 (0 %)) and *Dinemasporium strigosum* (GenBank JQ 889299; Identities = 807/841 (96 %); Gaps = 3/841 (0 %)).

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