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Key words
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Abstract Novel species of fungi described in the present study include the following from Australia: Vermici spatulae, Malundomyces natalis (incl. Malundomyces gen. nov.), Fusciadium paraeumonaum, Neotrichinotrysma paraeuxcentricum, and Pseudophloeospora eucalyptorum on leaves of Eucalyptus spp., Anungitea grevilleae (on leaves Grevillea spp.), Pyrenochaeta acaciae (on leaves of Acacia sp.), and Brunnecarpos bankiae (incl. Brunneocarpos gen. nov.) on cones of Banksia attenuata. Novel foliicolous taxa from South Africa include Neosulcata sp., streitziatae (on Streitziia nicolai), Colletotrichum lobeae (on Lobeola floridana), Cylindrosynymyceodes brabei (incl. Cylindrosynymyceodes gen. nov.) on Brabeiella stellatifoliolium, Sclerotocassonospora ericae (on Erica sp.), Spathomanomyces cypri (on Cyprea phaeocephala), and Phaeosphaeria breonadii (on Breonadia microcephala). Novelities described from Robben Island (South Africa) include Woenwicciella cephali and Diaportio cissampeli (both on Cissampelos capensis), Phaeotheca sallicolae (on Salicornia meyeriana), Paracylindrocarpon alocoloida (incl. Paracylindrocarpon gen. nov.) on Aloe sp., and Libertosomyces myopori (incl. Libertosomyces gen. nov.) on Myoporum serratum. Several novelties are recorded from La Réunion (France), namely Phaeosphaeriopsis aganathi (on Agapanthus sp.), Roussoeilla solani (on Solanum mauritianum), Vermici spatulae acaciae (on Acacia heterophylla), Bothriocercis acacia (on Acacia meermansii), Chalara clemidia (on Chalara clemidia), Cystospora tibouchiae (on Tibouchina semidecandra), Diaportio oceae (on Oceae obtusata), Castanediella eucalyptolica, Phaeosphaeria eucalyptica and Fuscidium eucalyptolica (on Eucalyptus robusta), Larenunomyces syzygii (incl. Larenunomyces gen. nov.) and Parawiesiensomyces syzygii (incl. Parawiesiensomyces gen. nov.) on leaves of Syzygium jambos. Novel taxa from the USA include Meristentomyces arctostaphylos (on Arctostaphylos patula), Orocnochon dracaea (on Dracaena reflexa), Rasasmonia columbienis (air of a hotel conference room), Paeclomyces tabacinus (on Nicotiana tabacum), Toxicocladopus hominis (from human broncalveolar lavage fluid), Naphthoformacrospora (from respiratory secretion of a patient with pneumonia), and Penidiellopsis radularis (incl. Penidiellopsis gen. nov.) from a human nail. Novel taxa described from Malaysia include Prosopidicola albiziae (on Albizia falcata), Proxipryculcaria asari (on Asarum sp.), Diaportio passiflorica (on Passiflora foetida), Paramycoleptidiscus albiziae (incl. Paramycoleptidiscus gen. nov.) on Albizia falcata, and Malaysianca phaii (incl. Malaysianca gen. nov.) on Phaius reflexipetatus. Two species are newly described from human patients in the Czech Republic, namely Microascus longicornis (from toenails of patient with suspected onychomyiasis), and Chinomyces ochrus (from sole skin of patient). Furthermore, Alternaria querciicola is described on leaves of Quercus brantii (Iran), Stemphylium beticola on leaves of Beta vulgaris (The Netherlands), Scleroderma caverdeanum on soil (Cape Verde Islands), Scleroderma denusium on soil, and Blastostyledes meliponea (from bee honey (Brazil), Ganderoma mbreoboenum on angiosperms (Ghana), Geoglossum raitviirii and Entoloma krutianicum on soil (Russia), Priceomyces vitoshaensis on Pterostichus melas (Carabidae) (Bulgaria) is the only one for which the family is listed, Ganderoma edoendense on decaying wood (Eucalyptus cordata) in Korea), Cercophora vinosa on decorticated branch of Saxa sp. (France), Coprinus pinetorum, Coprinus littoralis and Xerocomellus poederi on soil (Spain). Two genera from Colombia include Helminthosporiella and Uwemyces on leaves of Elaeis oleifera. Two species are described from India, namely Russula intervenosa (ectomycorrhizal with Shorea robusta), and Crinipellis odorata (on bark of Mytragyna paviflor). Novelities from Thailand include Cyphellaphora gamssii (on leaf litter), Pisolithus aureosertic and Corynascus citrinus (on soil). Two species are newly described from Cuba in Cuba, namely Dendrophycella paravivex (on Citrus sinensis), and Ramularia citriola on Citrus floridana. Morphological and cultural characteristics along with ITS rDNA barcodes are provided for all taxa.

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Overview Dothideomycetes phylogeny

Consensus phylogram (50% majority rule) of 42,902 trees resulting from a Bayesian analysis of the LSU sequence alignment (173 taxa including outgroup; 743 aligned positions; 375 unique site patterns) using MrBayes v. 3.2.5 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families, orders and classes are indicated with bold face. The alignment and tree were deposited in TreeBASE (Submission ID 19280).
Overview Dothideomycetes phylogeny (cont.)
Overview Eurotiomycetes, Geoglossomycetes, Lecanoromycetes and Leotiomycetes phylogeny

Consensus phylogram (50 % majority rule) of 9 452 trees resulting from a Bayesian analysis of the LSU sequence alignment (46 taxa including out-group; 769 aligned positions; 421 unique site patterns) using MrBayes v. 3.2.5 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families, orders and classes are indicated in bold face. The alignment and tree were deposited in TreeBASE (Submission ID 19280).

Overview Saccharomycotina and Agaricomycotina phylogeny

Consensus phylogram (50 % majority rule) of 3 352 trees resulting from a Bayesian analysis of the LSU sequence alignment (46 taxa including out-group; 769 aligned positions; 421 unique site patterns) using MrBayes v. 3.2.5 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families, orders and classes are indicated in bold face. The alignment and tree were deposited in TreeBASE (Submission ID 19280).
Overview Sordariomycetes phylogeny

Consensus phylogram (50% majority rule) of 21 302 trees resulting from a Bayesian analysis of the LSU sequence alignment (88 taxa including outgroup; 740 aligned positions; 299 unique site patterns) using MrBayes v. 3.2.5 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families, orders and classes are indicated with coloured blocks to the right of the tree. GenBank accession numbers are indicated in front of the species names. The tree was rooted to Saccharomyces cerevisiae (GenBank J01355.1) and the novel species described in this study for which LSU sequence data were available are indicated in bold face. The alignment and tree were deposited in TreeBASE (Submission ID 19280).
Thyrostroma cornicola
Fungal Planet 400 – 4 July 2016

**Thyrostroma cornicola** Crous & H.D. Shin, *sp. nov.*

*Etymology.* Name refers to *Cornus,* the plant genus from which this fungus was collected.

*Classification — Incertae sedis, Pleosporales, Dothideomycetes.*

*Sporodochia* dark brown, punctiform, to 300 µm diam. *Stromata* immersed to superficial, brown, 100–150 µm diam. *Conidiophores* brown, finely roughened, subcylindrical, 1–3-septate, 10–50 × 7–10 µm. *Conidiogenous cells* brown, subcylindrical, finely roughened, 7–20 × 7–10 µm, proliferating percurrently at apex. *Conidia* clavate, ellipsoid to fusoid, medium brown, with (1–)3 transverse septa, and 0–3 oblique or longitudinal septa, apex broadly obtuse, base truncate, 5–6 µm diam, (25–)30–36(–40) × (12–)14–17(–26) µm.

*Culture characteristics —* Colonies covering dish after 2 wk at 25 °C, with fluffy aerial mycelium. On MEA surface pale mouse-grey to mouse-grey, reverse dark mouse-grey. On PDA and OA surface mouse-grey, reverse dark mouse-grey.

*Typus. KOREA,* Incheon, Namdong-gu, Incheon Arboretum, N37°27'37.1" E126°45'22.6", on leaves of *Cornus officinalis* (Cornaceae), 28 Oct. 2014, P.W. Crous & H.D. Shin (holotype CBS H-22589, culture ex-type CPC 25427 = CBS 141280; ITS sequence GenBank KX228250.1, LSU sequence GenBank KX228302.1, tef1 sequence GenBank KX228372.1, MycoBank MB816999).

*Notes —* The genus *Thyrostroma* is based on the description of *T. compactum* (CBS 700.70, ITS, LSU sequences GenBank KX228250.1, KX228302.1), the ITS of which is 99 % (539/542) similar to the present collection. However, *T. compactum* is associated with *Thyrostroma* canker of *Ulmus* spp. in Europe and the USA (Ellis 1971), while the present collection is associated with leaf spots on *Cornus officinalis* in Korea. Conidia of *T. compactum* are 28–64 × 18–25 µm, with 2–4 transverse, and 1 to several, longitudinal or oblique septa (Ellis 1971), thus with conidia appearing somewhat larger than those observed in the present collection.

Although *Thyrostroma* was linked to *Dothidotthia* by Phillips et al. (2008), this treatment shows that the type of the genus clusters in the *Pleosporales,* suggesting that the asexual morph of *Dothidotthia* is thyrostroma-like, but that the two genera are not congeneric.

*Colour illustrations.* Symptomatic leaves of *Cornus officinalis*; sporodochia on PNA, sporulation on PNA, conidiophores and conidia. Scale bars = 10 µm.
Vermiculariopsiella eucalypti
Vermiculariopsiella eucalypti Crous, Jacq. Edwards & P.W.J. Taylor, sp. nov.

Etymology. Name refers to Eucalyptus, the plant genus from which this fungus was collected.

Classification — Chaetosphaeriaceae, Chaetosphaeriales, Sordariomycetes.

Colonies sporulating profusely throughout on SNA. Setae erect, brown, cylindrical, straight to flexuous, 120–220 × 4–5 µm, thick-walled, finely roughened, 8–15-septate, tapering towards apex, developing a head of lateral coiled to whip-like branches (constricted at base where attached to setae), that are brown, septate, tapering, containing coiled, septate lateral branches that could again contain coiled, lateral, branched, mostly aseptate branches. Conidiophores arranged in a whorl around base of setae, pale brown, smooth, subcylindrical, branched or not, 0–6-septate, containing conidiogenous cells that are arranged laterally along its length or at times reduced to conidiogenous cells, 20–50 × 3–5 µm. Conidiogenous cells solitary, monophialidic, discrete, ampulliform to subulate, pale brown, 15–25 × 3–5 µm, apex 1–1.5 µm diam, with minute collarette (1–2 µm long), at times with percurrent proliferation at apex. Conidia asymmetrical, fusoid to subfusoid or oblong, base bluntly rounded to somewhat inflated, aseptate, smooth, finely granular, (5–)7–9(–10) × (2–)2.5(–3) µm.

Culture characteristics — Colonies spreading, with sparse aerial mycelium, and even, lobate margins, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface pale mouse-grey, reverse dark mouse-grey. On PDA surface and reverse pale mouse-grey. On OA surface mouse-grey.

Typus. AUSTRALIA, Victoria, Toolangi State Forest, S37°33'25.3" E145°31'55.9", on leaves of Eucalyptus regnans (Myrtaceae), 9 Nov. 2014, P.W. Crous, J. Edwards & P.W.J. Taylor (holotype CBS H-22590, culture ex-type CPC 25525 = CBS 141281; ITS sequence GenBank KX228251.1, LSU sequence GenBank KX228303.1, MycoBank MB817000).

Notes — The setose conidiomata with brown, branched setae and basally arranged phialides with periclinal thickening are typical characteristics of the genus Vermiculariopsiella. On ITS V. eucalypti is 95 % (487/511) similar to V. pediculata (FMR 12187; GenBank HF678527.1), followed by V. dichapetali (Crous et al. 2014a; CPC 22463; GenBank KJ869129.1; 488/555 (88 %)). Vermiculariopsiella pediculata has smaller conidiogenous cells (14–15 × 3–4 µm), and narrower conidia (5–9 × 2 µm) (Hérandez-Restrepo et al. 2012). The closest hits using a megablast search of the LSU sequence were 96 % (792/827) similar to Dictyochaeta cylindrospora (GenBank EF063575.1; Chaetosphaeriaceae, Chaetosphaeriales), 96 % (777/813) to Vermiculariopsiella dichапetali (GenBank KJ869186.1; incertae sedis, Microascales), 94 % (780/827) to Pseudobotryis terrestris (GenBank KF771875.1; incertae sedis) and 94 % (781/830) to Barbatosphaeria fimbriata (GenBank KM492867.1; incertae sedis).

Colour illustrations. Toolangi State Forest; conidiophores with setae on PNA, conidiogenous cells and conidia. Scale bars = 10 µm.
Anungitea grevilleae
**Fungal Planet 402 – 4 July 2016**

**Anungitea grevilleae** Crous & Jacq. Edwards, *sp. nov.*

*Etymology.* Name refers to Grevillea, the plant genus from which this fungus was collected.

*Classification.* — *Incertae sedis,* **Xylariales,** Sordariomycetes.

*Mycelium* of pale brown, smooth, septate, branched, 1.5–2.5 µm hyphae. *Setae* intermingled among conidiophores, flexuous, subcylindrical with taper to acutely rounded apices, multisep-tate, brown, smooth, base bulbous, 4–5 µm diam, up to 500 µm tall, 2.5–3.5 µm wide. *Conidiophores* erect, flexuous, dark brown, thick-walled, 1–4-septate, 15–70 × 2.5–3.5 µm, with several sympodial, flat-tipped apical loci, 1–1.5 µm diam, not thickened. *Ramoconidia* giving rise to branched chains of cylindrical conidia, hyaline to pale brown, smooth, subcylindrical, 0–1-septate, 15–20 × 2–3 µm, with 1–3 flat-tipped apical scars, 1.5–2 µm diam. *Conidia* hyaline, rarely pale olivaceous, cylindrical, 0–1-septate, guttulate, ends truncate, (10–)13–16(–22) × (2–)2.5–3 µm.

*Culture characteristics.* — Colonies reaching up to 40 mm diam after 2 wk at 25 °C, with spreading, flat surface; margins smooth, even, and sparse to moderate aerial mycelium. On MEA surface umber with patches of ochreous, reverse chestnut. On OA surface umber with patches of honey. On PDA surface and reverse umber.

*Typus.* **AUSTRALIA,** Victoria, Royal Botanic Gardens Cranbourne, S38°7′49.6″E145°16′9″, on leaves of Grevillea sp. (*Proteaceae*), 7 Nov. 2014, P.W. Crous & J. Edwards (holotype CBS H-22591, culture ex-type CPC 25576 = CBS 141282; ITS sequence GenBank KX228252.1, LSU sequence GenBank KX228304.1, MycoBank MB817001).

Notes — On ITS *Anungitea grevilleae* is 98 % (553/566) similar to *A. eucalyptorum* (CPC 17207 = CBS 137967; Gen-Bank KJ691118.1). Morphologically, the two species are distinct in that *A. eucalyptorum* has shorter ramoconidia (12–17 × 2–3 µm), and somewhat larger conidia (10(–)13–16(–22) × (2–)2.5–3 µm). The most obvious difference lies in the dimorphic conidiophores observed in *A. eucalyptorum,* where microconidiophores can be reduced to conidiogenous cells, and macroconidiophores are up to 180 µm tall (Crous et al. 2014a).

*Colour illustrations.* Leaves of Grevillea sp.; conidiophores sporulating on PNA, seta, conidiophores and conidia. Scale bars = 10 µm.

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Neosulcatispora strelitziae
Neosulcatispora strelitziae Crous & M.J. Wingf., *sp. nov.*

**Etymology.** Name refers to *Strelitzia*, the plant genus from which this fungus was collected.

**Classification.** *Phaeosphaeriaceae, Pleosporales, Dothideomycetes.*

*Leaf spots* amphigenous, subcircular to irregular, grey-brown with dark brown margin, 3–8 mm diam. *Conidiomata* erumpent, globose, dark brown to black, to 350 μm diam with central ostiole (to 40 μm diam), exuding a pale olivaceous conidial mass; wall of 3–4 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells, or with a supporting cell, lining the inner cavity, hyaline, smooth, ampulliform, 4–6 × 3–4 μm, phialidic, with periclinal thickening or tightly aggregated percurrent proliferations. *Conidia* solitary, golden-brown, smooth, ellipsoid, 0–1-septate, (4–)5–7(–8) × (2.5–)3 μm.

**Culture characteristics.** Colonies flat, spreading, with moderate aerial mycelium, and smooth lobate margins, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface mouse-grey, reverse greyish sepia. On OA surface honey with black conidiomata. On PDA surface and reverse pale mouse-grey.

**Typus.** **SOUTH AFRICA,** Eastern Cape Province, Haga Haga, on leaves of *Strelitzia nicolai* (Strelitziaceae), Dec. 2014, M.J. Wingfield (holotype CBS H-22592, culture ex-type CPC 25657 = CBS 141283; ITS sequence GenBank KX228253.1, LSU sequence GenBank KX228305.1, tub2 sequence GenBank KX228380.1, MycoBank MB817002).

**Notes.** The ITS, LSU and *tub2* sequences of the present collection are 410/470 (87 %), 835/837 (99 %) and 440/533 (83 %) similar to *Neosulcatispora agaves* (CBS 140661; KT-950853.1, KT950867.1, KT950883.1, respectively), which was recently described from leaves of *Agave vera-cruz* growing in La Réunion (Crous et al. 2015b). Morphologically, *N. strelitziae* differs from *N. agaves* in that its conidiophores are reduced to conidiogenous cells, and its conidia are smooth, whereas they are larger ((7–)9–11(–12) × (3.5–)4(–4.5) μm), and prominently striate in *N. agaves* (Crous et al. 2015b).

*Colour illustrations.* *Strelitzia nicolai* plants; conidiomata sporulating on PNA, conidiogenous cells and conidia. Scale bars = 10 μm.
Colletotrichum ledabouriae
Fungal Planet 404 – 4 July 2016

**Colletotrichum ledebouriae** Crous & M.J. Wingf., sp. nov.

*Etymology.* Name refers to *Ledebouria*, the plant genus from which this fungus was collected.

*Classification.* *Glomerellaceae*, *Glomerellales*, *Sordariomycetes*.

*Leaf spots* circular, amphigenous, pale brown with raised dark brown border, 10–20 mm diam. *Conidiomata* (on pine needle agar; PNA) acervular, to 350 µm diam, conidiophores and setae on a cushion of pale brown stroma. *Setae* dark brown, smooth-walled, 2–4-septate, 80–120 × 5–7 µm, tapering to subacute apex. *Conidiophores* hyaline to pale brown, smooth-walled, septate, branched, to 50 µm tall, 4–5 µm wide. *Conidiogenous cells* hyaline to pale brown, smooth-walled, 15–23 × 3.5–4.5 µm. *Conidia* hyaline, smooth-walled, guttulate, aseptate, straight, subcylindrical, apex obtuse, base truncate with hilum 1–1.5 µm diam, (15–)17–21(–22) × (5–)6 µm.

Culture characteristics — Colonies covering dish after 1 mo at 25 °C, with moderate to woolly aerial mycelium. On MEA surface grey olivaceous, reverse dark brick. On OA surface smoke grey. On PDA surface and reverse grey olivaceous.

*Typus.* **SOUTH AFRICA**, Eastern Cape Province, Haga Haga, on leaves of *Ledebouria floridunda* (Hyacinthaceae), Dec. 2014, M.J. Wingfield (holotype CBS H-22593, culture ex-type CPC 25671 = CBS 141284; ITS sequence GenBank XK228254.1, LSU sequence GenBank XK228306.1, actA sequence GenBank XK228357.1, his3 sequence GenBank XK228365.1, MycoBank MB817003).

Notes — *Ledebouria* is a genus of deciduous or weakly evergreen bulb plants that occur in Sub-Saharan Africa, but almost nothing is known regarding fungal diseases of these plants (Crous et al. 2000). As far as we could establish, this is the first record of anthracnose disease on *Ledebouria*. On ITS *C. ledebouriae* is 98 % (563/572) similar to *C. sansevieriae* (MAFF239721; GenBank KC790947.1). The most similar sequences based on actA and his3 are 94 % (242/257) and 93 % (346/372) to *C. neosansevieriae* (GenBank KR476790.1 and KR476792.1), and 90 % (230/255) and 92 % (343/371) to *C. euphorbiae* (GenBank KF777125.1 and KF777134.1). Conidia of *C. sansevieriae* are larger (12.5–(18.4)–32.5 × 2.8–(6.4)–8.8 µm; Nakamura et al. 2006) than those of *C. ledebouriae*, but overlap with those of *C. neosansevieriae* ((16–)18–22(–25) × (4–)5–6 µm; Crous et al. 2015a).

Colour illustrations. Coastline at Haga Haga in the Eastern Cape Province; conidiomata sporulating on OA and PNA, setae and conidia. Scale bars = 10 µm.
Cyphellophora gamsii
Cyphellophora gamsii Crous, sp. nov.

Etymology. Named for Walter Gams, who collected and isolated this fungus.

Classification — Cyphellophoraceae, Chaetothyriales, Eurotiomycetes.

Mycelium consisting of smooth, pale brown, branched, septate, 1.5–2 µm diam hyphae. Conidiophores reduced to conidiogenous cells on hyphae, erect, straight, cylindrical, 2–6 x 1.5–2 µm; apex with flared collarette, 1–2 µm long. Conidia solitary, granular, hyaline, smooth, curved, falcate to flexuous, tapering from middle to subacutely rounded apex with mucoid cap, and towards truncate hilum, 0.5 µm diam, (0–)3-septate, (22–)30–40(–50) x (1.5–)2 µm; microcyclic conidiation observed in culture.

Culture characteristics — Colonies reaching up to 20 mm diam after 2 wk at 25 °C, with spreading, flat surface; margins smooth, lobate, and moderate aerial mycelium. On MEA and PDA surface mouse-grey, reverse dark mouse-grey. On OA surface dark mouse-grey.

Typus. THAILAND, Chiang Mai, Mushroom Research Centre, on leaf litter, Aug. 2014, W. Gams (holotype MFLU 16-1139, culture ex-type CPC 25967; ITS sequence GenBank KX228255.1, LSU sequence GenBank KX228307.1, tub2 sequence GenBank KX228381.1, MycoBank MB817005).

Notes — The genus Cyphellophora includes species that are associated with plant litter, as well as human and animal skin and nails (Gao et al. 2015). Cyphellophora gamsii is a typical species in the genus, being 99 % (812/821) similar on LSU to other known species. On ITS C. gamsii is 99 % (531/537) similar to Cyphellophora sp. (CBS 112.94; GenBank JQ766437.1) and 95 % (582/615) to C. laciniata (CBS 190.61; GenBank EU035416.1). No highly similar tub2 sequences were found. Morphologically, C. gamsii is quite distinct from other species in the genus by having large, 3-septate conidia (Decock et al. 2003, Gao et al. 2015).

Colour illustrations. Mountain stream at Chiang Mai; hyphae with fertile conidiogenous loci and conidia on PNA. Scale bars = 10 µm.
Cylindrosympodioides brabejum
Cylindrosympodioides Crous & M.J. Wingf., gen. nov.

Etymology. Name refers to the morphological similarity with the genus Cylindrosympodium.

Classification — Incertae sedis, Venturiales, Dothideomycetes.

Mycelium consisting of smooth, pale brown, branched, septate, hyphae. Conidiophores erect, medium brown, cylindrical, septate. Conidiogenous cells terminal, subcylindrical, pale brown, proliferating sympodially, scars unthickened, slightly darkened, flat. Conidia solitary, hyaline, acicular, straight to slightly curved, guttulate, multisepate, apex subobtusely rounded, base prominently truncate, unthickened but slightly darkened. Fusicladium-like synasexual morph developing on SNA, intermixed on hyphae with Cylindrosympodioides morph. Conidiophores reduced to conidiogenous cells, brown, am朴iform to fusoid-ellipsoid, proliferating sympodially, scars somewhat darkened. Conidia solitary, brown, verruculose, guttulate, thick-walled, fusoid-ellipsoid, sepatate, widest at median septum, apex subobtusely rounded, base truncate.

Type species. Cylindrosympodioides brabejum Crous & M.J. Wingf. MycoBank MB817076.

Cylindrosympodioides brabejum Crous & M.J. Wingf., sp. nov.

Etymology. Name refers to Brabejum, the plant genus from which this fungus was collected.

Mycelium consisting of smooth, pale brown, branched, septate, 1.5–2 µm diam hyphae. Conidiophores erect, medium brown, cylindrical, 0–2-septate, 10–25 × 2.5–3.5 µm. Conidiogenous cells terminal, subcylindrical, pale brown, 7–15 × 2.5–3 µm, proliferating sympodially, scars unthickened, slightly darkened, flat, 1.5–2 µm diam. Conidia solitary, hyaline, acicular, straight to slightly curved, guttulate, multisepate, apex subobtusely rounded, base prominently truncate, 2 µm diam, unthickened but slightly darkened, (55–)100–110(–120) × (1.5–)2(–2.5) µm. Fusicladium-like synasexual morph developing on SNA, intermixed on hyphae with Cylindrosympodioides morph. Conidiophores reduced to conidiogenous cells, brown, am朴iform to fusoid-ellipsoid, 5–7 × 3–4 µm, proliferating sympodially, scars somewhat darkened, 0.5 µm diam. Conidia solitary, brown, verruculose, guttulate, thick-walled, fusoid-ellipsoid, (1–)3-septate, widest at median septum, apex subobtusely rounded, base truncate, 1 µm diam, (12–)15–17(–20) × (2.5–)3(–3.5) µm.

Culture characteristics — Colonies reaching up to 15 mm diam after 2 wk at 25 °C, with spreading, flat surface; margins smooth, lobate, and moderate aerial mycelium. On MEA surface isabelline, reverse sepia. On OA surface dark brick. On PDA surface isabelline, reverse sepia.

Typus. SOUTH AFRICA, Western Cape Province, Franschhoek, on leaves of Brabejum stellatifolium (Proteaceae), 17 Jan. 2015, P.W. Crous & M.J. Wingfield (holotype CBS H-22594, culture ex-type CPC 25934 = CBS 141285; ITS sequence GenBank KX228256.1, LSU sequence GenBank KX228308.1, MycoBank MB817008).

Notes — The genus Cylindrosympodium (based on C. varibale) is characterised by its solitary, sepatate, cylindrical to subacicular, hyaline conidia with truncate bases, somewhat darkened hila, and brown conidiogenous structures with sympodial proliferation (Crous et al. 2007d). Cylindrosympodioides, which shares a similar morphology with species of Cylindrosympodium, is distinct in that it has acicular conidia with slightly thickened hila, and a fusicladium-like synasexual morph, which has conidiophores that are reduced to conidiogenous cells. Cylindrosympodioides is phylogenetically also closer to Venturia, whereas Cylindrosympodium forms a distinct sister lineage basal in the Venturiaeae.

Colour illustrations. Symptomatic leaves of Brabejum stellatifolium; conidiogenous cells with Fusicladium conidia, colony on SNA, conidiophores and conidia of Cylindrosympodioides morph. Scale bars = 10 µm.
Dendryphiella paravinosa
**Dendryphiella paravinosa** Crous & Guarnaccia, *sp. nov.*

**Etymology.** Name reflects the morphological similarity to *Dendryphiella vinosa*.

**Classification —** Dictyosporiaceae, Pleosporales, Dothideomycetes.

*Mycelium* consisting of hyaline to pale brown, smooth to verruculose 2–3 µm diam hyphae. *Conidiophores* solitary, erect, dark brown, subcylindrical, verruculose, branched above and below, to 150 µm long, 10–20 × 6–7 µm, 5–7-septate. *Conidiogenous cells* integrated, terminal and intercalary, clavate, with several loci arranged at the apex, 2–3 µm diam; loci thickened, darkened, refractive, 2–3 µm diam, with central pore. *Conidia* subcylindrical, apex obtuse, base bluntly rounded, medium brown, verruculose, (1–)3-septate, occurring in short chains (10–)24–27(–33) × (6–)7(–7.5) µm; hila thickened, darkened, refractive, 2–3 µm diam.

Culture characteristics — Colonies reaching up to 40 mm diam after 2 wk at 25 °C, with spreading, flat surface; margins smooth, lobate, and moderate aerial mycelium. On MEA surface honey to ochreous, reverse umber. On OA surface chestnut. On PDA surface umber to ochreous, reverse umber.

**Typus.** Italy, Sicily, Scordia (CT), on leaves of *Citrus sinensis* (Rutaceae), Mar. 2015, V. Guarnaccia (holotype CBS H-22595, culture ex-type CPC 26176 = CBS 141286; ITS sequence GenBank KX228257.1, LSU sequence GenBank KX228309.1, MycoBank MB817009); Sicily, Scordia (CT), on leaves of *Citrus limon*, Mar. 2015, V. Guarnaccia, CPC 26182 (ITS sequence GenBank KX228258.1).

**Notes** — The genus *Dendryphiella* is characterised by branched to unbranched conidiophores, with polytretic conidiogenous cells, darkened, thickened scars, and brown, septate, catenulate conidia (Crous et al. 2014a). Conidia of *D. paravinosa* resemble those of *D. vinosa* (13–39 × 4–8 µm; Ellis 1971, described from Congo bean in Cuba), but are smaller. *Dendryphiella paravinosa* CPC 26176 = CBS 141286 is identical to CPC 26182, and they are 90 % (424/472) related to *D. vinosa* (NBRC 32669; GenBank DQ307316.1), 88 % (374/427) to *Dictyosporium toruloides* (FMR 11942; GenBank HF677181.1) and 90 % (526/582) to *Dendryphiella eucalyptorum* (CPC 22927 = CBS 137987; GenBank KJ869139.1).
Phaeosphaeriopsis agapanthi
**Phaeosphaeriopsis agapanthi** Crous & M.J. Wingf., *sp. nov.*

*Etymology.* Name refers to *Agapanthus*, the host plant from which this fungus was collected.

*Classification.* *Phaeosphaeriaceae*, *Pleosporales*, *Dothideomycetes*.

**Conidiomata** erumpent, globose, black, to 250 µm diam with central ostiole; wall of 2–3 layers of black *textura angularis*. **Conidiophores** reduced to conidiogenous cells lining the inner cavity, ampulliform to doliiform, hyaline, phialidic, with periclinal thickening, or percurrent proliferation, 5–7 × 5–6 µm. **Conidia** solitary, aseptate, golden-brown, verruculose, subcylindrical, apex obtuse, base bluntly rounded to truncate, (6–)7–8(–9) × 3(–3.5) µm.

**Culture characteristics.** Colonies reaching up to 40 mm diam after 2 wk at 25 °C, with spreading, flat surface; margins smooth, lobate (feathery on PDA), and sparse to moderate aerial mycelium. On MEA surface pale luteous, reverse luteous. On OA and PDA surface and reverse pale luteous.

*Typus.* France, La Réunion, S21°3’39.5” E55°32’10.6”, on leaves of *Agapanthus precox* (Amaryllidaceae), 8 Mar. 2015, P.W. Crous & M.J. Wingfield (holotype CBS H-22596, culture ex-type CPC 26303 = CBS 141287; ITS sequence GenBank KX228260.1, LSU sequence GenBank KX228311.1, MycoBank MB817012); ibid., CPC 26301 = CBS 141316 (ITS sequence GenBank KX228259.1, LSU sequence GenBank KX228310.1).

Notes — The genus *Phaeosphaeriopsis* (based on *P. glaucopunctata*) is characterised by immersed, globose to subglobose to pyriform ascomata, cylindrical asci and septate, verrucose ascospores with coniothyrium-like or *Phaeostagonospora* asexual morphs (Câmara et al. 2003). The genus was recently revised by Thambugala et al. (2014), who accepted seven species. The aseptate conidia of *P. agapanthi* suggest that it should be compared to *P. obtusispora*, but, based on ITS, phylogenetically it is closest 98 % (558/568) to *P. triseptata* (MFLUCC 13-0347; GenBank KJ522476.1), and only 93 % (525/563) to *P. obtusispora* (GenBank AF250822). Of the two isolates studied, CPC 26301 is identical on its DNA sequence (ITS) to CPC 26303.

Colour illustrations. Symptomatic leaves of *Agapanthus precox*; conidiomata sporulating on PNA and OA, conidiogenous cells and conidia. Scale bars = 10 µm.
Roussoella solani
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**Roussoella solani** Crous & M.J. Wingf., sp. nov.

*Etymology.* Name refers to *Solanum*, the plant genus from which this fungus was collected.

*Classification.* - *Roussoellaceae*, *Pleosporales*, *Dothideomycetes*.

*Conidiomata* immersed to erumpent, solitary, globose, brown, to 150 μm diam with central ostiole, exuding a grey-brown conidial mass; wall of 3–4 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, ampulliform to doliform, 4–6 × 3–4 μm, phialides with visible periclinal thickening. *Conidia* solitary, aseptate, smooth, pale brown, subcylindrical, apex obtuse, base bluntly rounded to truncate, (4–)5.5–6.5(–7) × 2(–3) μm.

*Culture characteristics.* - Colonies reaching up to 40 mm diam after 2 wk at 25 °C, with spreading, erumpent surface; margins smooth to feathery, lobate, and moderate aerial mycelium. On MEA surface pale luteous with patches of scarlet, reverse luteous with patches ofumber. On OA surface sienna with patches ofumber and scarlet. On PDA surface pale vinaceous with diffuse scarlet pigment in agar, reverse isabelline in centre, scarlet at margin.

*Typus.* FRANCE, La Réunion, on stems of *Solanum mauritianum* (*Solanaceae*), 13 Mar. 2015, P.W. Crous & M.J. Wingfield (holotype CBS H-22597, culture ex-type CPC 26331 = CBS 141288; ITS sequence GenBank KX228261.1, LSU sequence GenBank KX228312.1, MycoBank MB817016).

*Notes.* - Based on the LSU sequence, *Roussoella solani* is accommodated in the *Roussoellaceae* (e.g. 98 % (787/803) similarity to *R. thailandica* GenBank KJ474846.1), but on ITS data it is phylogenetically distinct from other known taxa within the genus, showing less than 90 % similarity. Unfortunately, *R. solani* is known only from its asexual morph and hence a full morphological comparison with other species known in the genus is presently not possible. Recent studies have shown that several species of *Roussoella* occur on woody plants (Crous et al. 2014b, 2015b), and are not only restricted to monocotyledons.

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*Colour illustrations.* Valley in La Réunion; conidiomata sporulating on PNA, conidiogenous cells and conidia. Scale bars = 10 μm.
Ramularia citricola Crous & Guarnaccia, sp. nov.

Etymology. Name refers to Citrus, the plant genus from which this fungus was collected.

Classification — Mycosphaerellaceae, Capnodiales, Dothideomycetes.

Mycelium consisting of septate, branched, hyaline, smooth, 2–2.5 µm diam hyphae. Conidiophores solitary, arising from hyphae as lateral branches, or terminal in loose fascicles, straight to geniculate-sinuous, erect, hyaline, smooth, subcylindrical, reduced to conidiogenous loci on hyphae, or 0–1-septate, erect, 2–20 × 2–2.5 µm. Conidiogenous cells hyaline, smooth, subcylindrical, 2–16 × 2–2.5 µm; loci terminal, thickened, darkened and refractive, 1 µm diam. Primary ramoconidia hyaline, smooth to finely roughened, subcylindrical, 0–1-septate, 22–33 × 2.5–3 µm. Secondary ramoconidia subcylindrical, 0–1-septate, finely roughened, guttulate, 8–22 × 2–2.5 µm. Intermediary conidia subcylindrical-fusiform, 0(–1)-septate, 7–9 × 2 µm. Conidia in branched chains, ellipsoid-fusoid, smooth to finely roughened, (3–)6–8(–9) × 2 µm; loci thickened, darkened and refractive, 0.5 µm diam.

Culture characteristics — Colonies reaching up to 15 mm diam after 2 wk at 25 °C, with spreading, erumpent, folded surface; margins smooth, lobate, and sparse aerial mycelium. On MEA surface luteous, reverse ochreous. On OA surface mouse-grey. On PDA surface pale mouse-grey to mouse-grey, reverse mouse-grey.

Typus. Italy, Sicily, Messina, on twigs of Citrus floridana (Rutaceae), Mar. 2015, V. Guarnaccia (holotype CBS H-22598, culture ex-type CPC 26192 = CBS 141449; ITS sequence GenBank KX228262.1, LSU sequence GenBank KX228313.1, actA sequence GenBank KX228358.1, rpb2 sequence GenBank KX228369.1, tef1 sequence GenBank KX228373.1, MycoBank MB817020).

Notes — On ITS Ramularia citricola is 99 % (524/531) similar to R. grevilleana (CPC 4903; GenBank GU214691.1) and 98 % (523/531) R. grevilleana (isolate s208; GenBank GU939181.1). None of the sequences from the protein coding genes resulted in similarities higher than 92 %. Ramularia grevilleana can be distinguished from R. citricola by having larger conidia that are ellipsoid-ovoid, subcylindrical-fusoid, (8–)15–45(–55) × (1.5–)2.5–4.5(–5) µm, 0–2(–3)-septate (Braun 1998). Two species of Ramularia have been described from Citrus, namely R. citri and R. citrifolia. Ramularia citri (on Citrus aurantium, Italy) was described from fallen, dry leaves (asymptomatic), with catenate conidia, oblong, 8–14 × 3.5–4 µm, 0–2-septate. Type material of the latter species could not be traced, and its generic affinity remains unclear (Braun 1998). Ramularia citrifolia (hyperparasitic on Meliola butleri on Citrus tankan, Taiwan) was allocated to Eriomycopsis by Braun (1993).
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**Vermiculariopsiella acaciae** Crous, M.J. Wingf., sp. nov.

**Etymology.** Name refers to Acacia, the plant genus from which this fungus was collected.

**Classification.** Chaetosphaeriaceae, Chaetosphaeriales, Sordariomycetes.

Sporodochia on SNA and OA erumpent, crystalline, to 450 µm diam, with brown, erect setae distributed throughout conidia, thick-walled, roughened, flexuous, 180–250 × 4–5 µm, 5–7-septate, tapering to an obtuse apex. Conidiophores aggregated in stroma, subcylindrical, 1–2-septate, branched or not, 25–40 × 3–4 µm. Conidiogenous cells terminal, subcylindrical, pale brown to hyaline, smooth to verruculose, at times curved at the apex, 15–27 × 2.5–3 µm, apex 1.5 µm diam, collarette flaring, 1–2 µm long. Conidia dimorphic. On OA solitary, hyaline, guttulate, aseptate, straight to slightly curved, inequilateral with inner plane straight, outer plane convex, apex subobtusely rounded, base truncate with excentric hilum, 0.5–1 µm diam, (14–)18–22(–25) × 3(–3.5) µm. On SNA forming ellipsoid, straight, hyaline, smooth, guttulate conidia, apex subobtusely rounded, base truncate, 4–7 × 2–2.5 µm.

Culture characteristics. Colonies reaching up to 40 mm diam after 2 wk at 25 °C, with spreading, flat surface; margins smooth, lobate, and sparse aerial mycelium. On MEA surface pale luteous, reverse luteous. On OA surface dirty white to pale luteous. On PDA surface and reverse dirty white.

**Type.** France, La Réunion, S21°5’45.7” E55°33’3.6”, on leaves of Acacia heterophylla (Fabaceae), 7 Mar. 2015, P.W. Crous & M.J. Wingfield (holotype CBS H-22599, culture ex-type CPC 26291 = CBS 141289; ITS sequence GenBank KX228263.1, LSU sequence GenBank KX228314.1, MycoBank MB817023).

Notes. Based on ITS DNA sequence data Vermiculariopsiella acaciae is 97 % (539/557) similar to V. dichapetali (CPC 22463; GenBank KJ869129.1; from leaves of Dichapetalum rhodesicum, Botswana) and 89 % (489/548) similar to V. eucalypti described elsewhere in the present study. Morphologically, the latter two species can be distinguished from V. dichapetali in having much larger conidiogenous cells (20–40 × 2.5–3 µm), setae (100–300 × 6–10 µm, 6–12-septate), and lacking dimorphic conidia (Crous et al. 2014a). The closest hits using a megablast search of the LSU DNA sequence data are 99 % (816/819) similar to Vermiculariopsiella dichapetali (GenBank KJ869186.1; incertae sedis, Microascales), 96 % (820/857) to Dictyochaeta cylindrospora (GenBank EF063575.1; Chaetosphaeriales, Chaetosphaeriales), 94 % (793/841) to Dactylaria parvispora (GenBank EU107296.1; Orbilaceae, Orbiliales) and 94 % (808/858) to Cryptadelphia groenendalensis (GenBank EU528007.1; incertae sedis).

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Meristemomyces arctostaphylos
**Fungal Planet 412 – 4 July 2016**

**Meristemomyces arctostaphylos** Crous & M.J. Wingf., *sp. nov.*

**Etymology.** Name refers to *Arctostaphylos*, the plant genus from which this fungus was collected.

**Classification.** *Meristemomyces* belongs to the taxonomic family *Teratosphaeriaceae*, order *Capnodiales*, class *Dothideomycetes*.

*Mycelium.* Mycelium consisting of brown, thick-walled, verruculose, branched, septate, 2.5–4 µm hyphae, frequently encased in a mucoid sheath. Conidiophores solitary, brown, verruculose, terminal or lateral on hyphae, multisepctate, flexuous, subcylindrical, up to 150 µm long, 3–5 µm diam, or reduced to conidigenous loci on hyphae. *Conidiogenous cells* brown, verruculose, thick-walled, subcylindrical to irregular, 3–10 × 3–6 µm, with 1–3 terminal flat-tipped loci, 1.5–2 µm diam. *Conidia* in branched chains, brown, thick-walled, verruculose. Secondary ramoconidia fusoid-ellipsoid to subcylindrical, 1–3-septate, 15–20 × 5–9 µm, with 1–3 flat-tipped unthickened, not darkened loci, 1.5–2 µm diam. *Conidium* brown, verruculose, thick-walled, 1(–3)-septate, fusoid-ellipsoid, (9–)10–12(–13) × (4–)5(–6) µm; loci not thickened nor darkened, 1.5–2 µm diam, frequently with minute marginal frill.

**Culture characteristics.** Colonies reaching up to 15 mm diam after 2 wk at 25 °C, with spreading, erumpent, folded surface; margins smooth, lobate, and sparse aerial mycelium. On MEA surface iron-grey, reverse olivaceous grey. On OA, PDA and MEA surface dark-mouse-grey to greenish black, reverse greenish black.

**Notes.** The genus *Meristemomyces* is monotypic, based on *M. frigidus*, isolated from rocks in the Himalayas (Egidi et al. 2014). Based on ITS sequence data, *M. arctostaphylos* is 91 % (404/443) similar to the type culture of *M. frigidus* (CBS 136109 = COFEE 5508; GenBank KF309961.1) and 99 % (458/460) to *Xenomeris raetica* (CBS 485.61; GenBank EF114690.1). Morphologically, *M. arctostaphylos* is quite distinct from *M. frigidus*, as the latter species produces arthoconidia by disarticulation, while *M. arctostaphylos* has well-defined conidiophores giving rise to a series of secondary ramoconidia, and septate conidia.

*Xenomeris raetica* was described on leaf litter of *Arctostaphylos uva-ursi* in Switzerland. The fungus is known only by its sexual morph. The present collection was obtained on the same host genus, but from the USA. Although only the asexual morph was found, based on DNA data, it appears to be 99 % similar to a strain identified as *Xenomeris raetica* (CBS 485.61), suggesting that this could be the same fungus. However, CBS 485.61 is not an ex-type strain, and *M. arctostaphylos* is a common hyphomycete on leaves of *Arctostaphylos*. Furthermore, the genus *Xenomeris* is regarded as a member of *Venturiaceae*, not *Teratosphaeriaceae*, thus the possible synonymy of *Meristemomyces* under the older *Xenomeris* can only be resolved once fresh collections of *Xenomeris raetica* have been obtained.

**Typus.** USA, Utah, near Long Valley, on leaves of *Arctostaphylos patula* (Ericaceae), Oct. 2014, M.J. Wingfield (holotype CBS H-22600, culture ex-type CPC 25574 = CBS 141290; ITS sequence GenBank KX228264.1, LSU sequence GenBank KX228315.1, MycoBank MB817026).

Colour illustrations. *Arctostaphylos patula* plants in the USA; colonies sporulating on PDA, conidiophores and chains of conidia. Scale bars = 10 µm.
Pyrenochaeta acaciae
Pyrenochaeta acaciae Crous, Jacq. Edwards & Pascoe, sp. nov.

**Etymology.** Name refers to Acacia, the plant genus from which this fungus was collected.

**Classification — Cucurbitariaceae, Pleosporales, Dothideomycetes.**

**Conidiomata** immersed to erumpent, solitary, globose, brown, to 150 µm diam, with central ostiole to 35 µm diam, exuding a caramel coloured conidial mass; wall of 2–3 layers of brown textura angularis; ostiolar area with several cylindrical, brown, thick-walled, septate setae, with obtuse ends to 70 µm long. **Conidiophores** 0–3-septate, but mostly reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, ampulliform to subcylindrical, 4–8 × 2.5–3.5 µm, phialidic with periclinal thickening. **Conidia** solitary, hyaline (pale olivaceous in mass), smooth, aseptate, allantoid with obtuse ends, (3–)4–4.5(–5) × (1.5–)2 µm.

**Culture characteristics —** Colonies reaching up to 40 mm diam after 2 wk at 25 °C, with spreading, flat surface; margins smooth, lobate, and sparse aerial mycelium. On MEA surface folded, sepia with patches of isabelline and buff, reverse isabelline. On OA surface isabelline. On PDA surface and reverse isabelline.

**Typus.** **AUSTRALIA,** Victoria, roadside bushland opposite 125 Gurdies-St. Helier road, The Gurdies, S38°22’49” E145°34’14”, on leaves of Acacia sp. (Fabaceae), 7 Nov. 2014, P.W. Crous, J. Edwards & I.G. Pascoe (holotype CBS H-22601, culture ex-type CPC 25527 = CBS 141291; ITS sequence GenBank KX228265.1, LSU sequence GenBank KX228316.1, MycoBank MB817028).

Notes — Based on ITS *Pyrenochaeta acaciae* is 98 % (409/416) similar to *P. protearum* (CBS 131315; GenBank JQ044434.1) and 98 % (425/433) to *P. pinicola* (CPC 23455; GenBank KJ869152.1). *Pyrenochaeta protearum* can be distinguished from *P. acaciae* by having setae surrounding its conidiomatal ostiole that are longer (up to 100 µm tall), and conidia that are wider ((3–)4–5(–6) × (2–)2.5(–3) µm) (Crous et al. 2011). *Pyrenochaeta pinicola* is distinct by having larger conidia, (4–)4.5–5.5(–6) × 2(–2.5) µm, and longer setae (up to 150 µm tall) (Crous et al. 2014a).

**Colour illustrations.** Symptomatic leaves of *Acacia* sp.; conidiomata sporulating on PDA, conidiogenous cells and conidia. Scale bars: conidioma = 100 µm, others = 10 µm.
Castanediella eucalypticola
& Phaeophleospora eucalypticola
Castanediella eucalypticola Crous & M.J. Wingf., sp. nov.

*Etymology.* Name refers to *Eucalyptus*, the plant genus from which this fungus was collected.

*Classification.* — *Incertae sedis, Xylariales, Sordariomycetes.*

*Mycelium* consisting of pale brown, branched, septate hyphae, 2–5 µm diam, frequently in hyphal strands, and forming hyphal coils. *Conidiophores* erect, solitary, unbranched, 0–2-septate, subcylindrical, medium brown, smooth, 5–30 × 3–5 µm. *Conidigenous cells* terminal and intercalary, subcylindrical to ampulliform or lanceolate, pale brown, smooth, polyblastic, terminating in a swollen apex, 1.5–3 µm diam, with several scars, 5–20 × 3–3.5 µm. *Conidia* solitary, hyaline, smooth, falcate, straight to curved, widest in the middle, apex subobtusely rounded, base truncate, 0.5 µm diam, (15–)20–26 (30) × (2.5–)3 µm.

*Culture characteristics.* — Colonies reaching up to 30 mm diam after 2 wk at 25 °C, with spreading, erumpent surface; margins smooth, lobate, and sparse aerial mycelium. On *MEA* surface seipa, reverse isabelline. On *OA* surface cinnamon. On *PDA* surface honey, reverse isabelline.

Phaeophleospora eucalypticola Crous & M.J. Wingf., sp. nov.

*Etymology.* Name refers to *Eucalyptus*, the plant genus from which this fungus was collected.

*Classification.* — *Mycosphaerellaceae, Capnodiales, Dothideomycetes.*

*Conidiomata* (on pine needle agar; PNA) pycnidal, erumpent, solitary, brown, globose, to 300 µm diam, with central ostiole, to 20 µm diam; wall of 2–3 layers of brown *textura angularis*. *Conidiophores* lining the inner cavity, hyaline, smooth, reduced to conidigenous cells, or with a supporting cell, branched at base or not, ampulliform to subcylindrical, 5–10 × 2.5–3.5 µm, proliferating inconspicuously percurrently at apex, 1 µm diam. *Conidia* hyaline, smooth, solitary, asceptate, gutulate, ellipsoid to obovoid, base truncate, 0.5 µm diam, (3.5–)4.5–6 (7) × (1.5–)2 (2.5) µm.

*Culture characteristics.* — Colonies reaching up to 15 mm diam after 2 wk at 25 °C, with spreading, erumpent surface; margins smooth, lobate, and moderate aerial mycelium. On *MEA, PDA* and *OA*, surface and reverse mouse-grey.
Sclerostagonospora ericae
Fungal Planet 416 – 4 July 2016

Sclerostagonospora ericae Crous & M.J. Wingf., sp. nov.

Etymology. Name refers to Erica, the plant genus from which this fungus was collected.

Classification — Phaeosphaeriaceae, Pleosporales, Dothideomycetes.

Conidiomata (on pine needle agar; PNA) pycnidial, solitary or in small clusters, immersed or semi-erumpent, to 200 µm diam, globose, pale brown, with 1–3 dark brown, semi-papillate osti- oles, to 40 µm diam; wall of 3–4 layers of pale brown textura angularis. Conidiophores reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, ampulliform to doliform, 4–5 × 3–5 µm, proliferating inconspicuously percurrently at apex. Conidia solitary, pale brown, smooth, subcylindrical, guttulate, 1(–3)-septate, constricted at median septum, (7–)8–10(–11) × (2.5–)3 µm.

Culture characteristics — Colonies reaching up to 60 mm diam after 2 wk at 25 °C, with spreading, flat surface; margins smooth, lobate, and moderate aerial mycelium. On MEA surface dirty white to buff, reverse sepia. On OA surface buff. On PDA surface buff, reverse cinnamon.

Typus. SOUTH AFRICA, Western Cape Province, Franschhoek, on leaves of Erica sp. (Ericaceae), Nov. 2014, M.J. Wingfield (holotype CBS H-22606, culture ex-type CPC 25927 = CBS 141318; ITS sequence GenBank KX228268.1, LSU sequence GenBank KX228319.1, tef1 sequence GenBank KX228375.1, tub2 sequence GenBank KX228383.1, MycoBank MB817031).

Notes — Based on LSU sequences, Sclerostagonospora ericae is identical (813/813) to S. opuntiae (GenBank DQ-286772.1; Huhndorf 1992). However, the genus Sclerostagonospora is based on S. heraclei, and the latter is presently not known from DNA or culture, hence the concept of Sclero- stagonospora remains unsettled. On ITS S. ericae is 98 % (550/560) similar to S. opuntiae (GenBank DQ286768.1) and 94 % (541/574) similar to Stagonospora foliicola (GenBank KF251256.1).

Colour illustrations. Erica sp. in Franschhoek; conidiomata sporulating on OA, conidiogenous cells, ostiolar region and conidia. Scale bars: conidiomata and ostioles = 200 µm, all others = 10 µm.
Dothiorella acaecicola
**Dothiorella acacicola** Crous & M.J. Wingf., *sp. nov.*

**Etymology.** Name refers to *Acacia*, the plant genus from which this fungus was collected.

**Classification.** *Botryosphaeriaceae, Botryosphaeriales, Dothideomycetes.*

**Conidiomata** (on pine needle agar; PNA) pycnidial, solitary, black, erumpent, globose, to 400 µm diam, with central ostiole; wall of 2–3 layers of brown *textura angularis*. Conidiophores reduced to conidiogenous cells, or with a supporting cell, lining the inner cavity, hyaline, smooth, subcylindrical to doliform, straight to geniculose-sinuous, 7–20 × 5–11 µm; proliferating percurrently at apex. Conidia solitary, initially hyaline, becoming pigmented while attached to conidiogenous cells, golden-brown to brown, granular to guttulate, surface roughened (at times with hyaline outer sheath), obvoid, medially 1-septate, slightly constricted at septum, apex obtuse, base truncate, 3–5 µm diam, (22–)24–27(–32) × (9–)10(–11) µm.

**Culture characteristics.** Colonies covering dish after 2 wk at 25 °C, with spreading, flat surface; margins smooth, lobate, and moderate aerial mycelium. On MEA, PDA and OA surface and reverse dark mouse-grey.

**Typus.** FRANCE, La Réunion, S21°12'47.6" E55°36'48.7", on leaves of *Acacia mearnsii* (Fabaceae), 8 Mar. 2015, P.W. Crous & M.J. Wingfield (holotype CBS H-22607, culture ex-type CPC 26349 = CBS 141295; ITS sequence GenBank KX228269.1, LSU sequence GenBank KX228320.1, tef1 sequence GenBank KX228376.1, MycoBank MB817032).

**Notes.** Based on LSU sequence data *Dothiorella acacicola* is 99 % similar to several *Dothiorella* spp. (e.g. 791/801 with *D. ulmicola* GenBank KR611900.1). Based on ITS sequence data *Dothiorella acacicola* is 97 % (523/538) similar to *D. longicollis* (CBS 122068; GenBank KF766162.1). The two species can be distinguished from each other by the fact that conidia of *D. longicollis* are smaller, (17–)19–22(–23) × (7–)8.5–9.5(–10) µm (Phillips et al. 2013).

**Colour illustrations.** *Acacia mearnsii* trees growing in La Réunion; conidiomata sporulating on PNA, conidiogenous cells and conidia. Scale bars = 10 µm.

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Chalara clidemiae
Fungal Planet 418 – 4 July 2016

**Chalara clidemiae** Crous & M.J. Wingf., sp. nov.

**Etymology.** Name refers to Clidemia, the plant genus from which this fungus was collected.

**Classification —** *Incertae sedis, Helotiales, Leotiomycetes.*

*Mycelium* consisting of hyaline, smooth, branched, septate, 1.5–2.5 μm diam hyphae. *Conidiophores* arranged in terminal clusters on hyphae, 25–30 × 3–4 μm, 1–5-septate, subcylindrical, smooth, hyaline in bottom half, but upper two cells medium brown. *Conidiogenous cells* terminal, swollen in bottom third, venter cylindrical, brown, smooth, phialidic, 15–25 × 3.5–4 μm. *Conidia* hyaline, smooth, guttulate, subcylindrical, apex obtuse, base truncate, (3–)4(–)5 × (2–)2.5 μm, forming long, curvy chains or slimy masses on older phialides.

**Culture characteristics —** Colonies reaching up to 30 mm diam after 2 wk at 25 °C, with spreading, flat surface; margins smooth, lobate, and sparse to moderate aerial mycelium. On MEA surface dirty white, reverse buff. On OA surface ochreous. On PDA surface luteous, reverse ochreous.

**Typus.** FRANCE, La Réunion, on twigs of *Clidemia hirta* (Melastomataceae), 6 Mar. 2015, P.W. Crous & M.J. Wingfield (holotype CBS H-22608, culture ex-type CPC 28423 = CBS 141319; ITS sequence GenBank KX228270.1, LSU sequence GenBank KX228321.1, MycoBank MB817033).

Notes — The genus *Chalara* is paraphyletic, with species occupying different positions within *Helotiales* (Cai et al. 2009). Based on ITS sequence data *Chalara clidemiae* is 91 % (492/538) similar to *Chalara pseudoaffinis* (CCF 3979; GenBank FR667224.1). On LSU it is 98 % (841/855) similar to *Chalara africana* (OC0018; GenBank FJ176249.1) and 96 % (821/854) to *Chalara parvispora* (CBS 385.94; GenBank FJ176253.1).

*Colour illustrations. Clidemia hirta* on La Réunion; conidiophores spore-lating on PNA, phialides and conidia. Scale bars = 10 μm.
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**Mulderomyces** Crous, Jacq. Edwards & P.W.J. Taylor, *gen. nov.*

*Etymology.* Named after Prof. dr. Theo W. Mulder, the scientific director of the institutes of the Royal Dutch Academy of Arts and Sciences (KNAW), on the occasion of his farewell symposium, 20 June 2016.

*Classification.* *Incertae sedis,* Ostropales, Lecanoromycetes.

**Conidiomata** pycnidial, solitary, pale brown, erumpent, globose, with central ostiole; wall of 6–8 layers of subhyaline to pale brown *textura angularis.* **Conidiophores** lining the inner cavity, hyaline, smooth, subcylindrical, septate, branched. **Conidigenous cells** hyaline, smooth, subcylindrical, terminal and lateral; proliferating sympodially, scars inconspicuous. **Conidia** cylindrical, hyaline, smooth, guttulate, straight with subobtuse ends, 2–6-septate, prominently constricted at septa (cells linked by a narrow isthmus), with mature conidia breaking into phragmospores.

*Type species.* *Mulderomyces natalis* Crous, Jacq. Edwards & P.W.J. Taylor. MycoBank MB817034.

**Mulderomyces natalis** Crous, Jacq. Edwards & P.W.J. Taylor, *sp. nov.*

*Etymology.* *Natalis* (Latin genitive noun), refers to the birth date of the first author, on which day this fungus was collected.

**Conidiomata** (on pine needle agar; PNA) pycnidial, solitary, pale brown, erumpent, globose, to 200 µm diam, with central ostiole; wall of 6–8 layers of subhyaline to pale brown *textura angularis.* **Conidiophores** lining the inner cavity, hyaline, smooth, subcylindrical, 1–4-septate, branched, 10–30 × 3–5 µm. **Conidigenous cells** hyaline, smooth, subcylindrical, terminal and lateral, 8–15 × 3–5 µm; proliferating sympodially, scars inconspicuous. **Conidia** cylindrical, hyaline, smooth, guttulate, straight with subobtuse ends, 2–6-septate, prominently constricted at septa (cells linked by a narrow isthmus), with mature conidia breaking into phragmospores, (22–)50–75(–90) × (2–)3 µm.

*Culture characteristics.* — Colonies reaching up to 20 mm diam after 2 wk at 25 °C, with spreading, flat surface; margins smooth, lobate, and sparse aerial mycelium. On MEA surface cinnamon, reverse brick. On OA surface rosy buff. On PDA surface rosy buff, reverse cinnamon.

*Typus.* AUSTRALIA, Victoria, Melbourne, Moonee Ponds Creek, on leaves of *Eucalyptus* sp. (Myrtaceae), 2 Nov. 2014, P.W. Crous, J. Edwards & P.W.J. Taylor (holotype CBS H-22609, culture ex-type CPC 25519 = CBS 141286; ITS sequence GenBank KX228271.1, LSU sequence GenBank KX228322.1, MycoBank MB817035).

*Notes.* — The LSU sequence of *Mulderomyces natalis* is 91 % similar to species of *Xylographa* (lichenised ascomycetes; e.g. 738/810 to *X. opegraphella* GenBank KJ462366.1) and 92 % (746/812) similar to *Furcaspora eucalypti* (GenBank EF110613; Crous et al. 2007c). Phylogenetically, it appears quite distinct from all taxa presently available in GenBank, both on LSU and ITS. Morphologically, *Mulderomyces* resembles species of *Phacidella*, except that the nature of its conidia is different with cells not linked by a narrow isthmus, and its conidiomata become cupulate with age (Sutton 1980).

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Wojnowiciella cissampeli & Diaporthe cissampeli
**Wojnowiciella cissampeli** Crous & Roets, *sp. nov.*

**Etymology.** Name refers to Cissampelos, the plant genus from which this fungus was collected.

**Classification.** *Phaeosphaeriaceae, Pleosporales, Dothideomycetes.*

Conidiomata (on pine needle agar; PNA) pycnidial, solitary, black, erumpent, or immersed in agar, globose, to 300 µm diam, non-papillate, with a central ostiole; pycnidial wall of 3–6 layers of brown *textura angularis*. Conidiophores reduced to conidigenous cells. Conidiogenous cells lining the inner cavity, hyaline, smooth, ampulliform to doliiform, phialidic, 3–6 × 4–5 µm. *Conidia* subcylindrical, straight to curved, apex subobtuse, base truncate, widest in middle, (0–)3–7-septate, rarely with 1–2 oblique septa, thick-walled, verruculose, guttulate, golden-brown, (20–)22–25(–27) × (4.5–)5(–6) µm.

Culture characteristics — Colonies reaching up to 20 mm diam after 2 wk at 25 °C, with spreading, flat surface; margins smooth, lobate, and moderate aerial mycelium. On MEA surface mouse-grey to greyish sepia, reverse greyish sepia. On OA surface pale mouse-grey in centre, sienna in outer region. On PDA surface pale mouse-grey, reverse greyish sepia.

**Diaporthe cissampeli** Crous & Roets, *sp. nov.*

**Etymology.** Name refers to Cissampelos, the plant genus from which this fungus was collected.

**Classification.** *Diaporthaceae, Diaporthales, Sordariomycetes.*

Conidiomata (on pine needle agar; PNA) pycnidial, solitary, black, erumpent, globose, to 200 µm diam, exuding creamy droplets from central ostioles; walls consisting of 3–6 layers of medium brown *textura angularis*. Conidiophores hyaline, smooth, 1–2-septate, branched, densely aggregated, subcylindrical, straight to sinuous, 12–20 × 3–5 µm. Conidiogenous cells 7–10 × 2–3 µm, phialidic, cylindrical, terminal and lateral with slight taper towards apex, 1–1.5 µm diam, with visible periclinal thickening; collarette not observed. Paraphyses not observed. Alpha conidia aseptate, hyaline, smooth, guttulate, subcylindrical, tapering towards both ends, apex subobtuse, base subtruncate, (7.5–)9–11(–12) × (2–)2.5(–3) µm. Gamma conidia not observed. Beta conidia not observed.

Culture characteristics — Colonies covering dish after 2 wk at 25 °C, with smooth, even margins, and moderate aerial mycelium. On MEA surface dirty white with patches of pale mouse-grey, reverse luteous. On OA and PDA surface and reverse dirty white.

**Notes.** Based on ITS *Diaporthe cissampeli* is 98 % (561/577) similar to *D. neotheicola* (ICMP 10076; GenBank KF145914.1; Gomes et al. 2013). No high similarity (> 99 %) hits were obtained when the protein coding sequences were blasted against NCBI's GenBank nucleotide database. No other species of *Diaporthaceae* are known from *Cissampelos* (Crous et al. 2000) and hence *D. cissampeli* is herewith introduced as new.

**Diaporthe cissampeli** (holotype CBS H-22610, culture ex-type CPC 27455 = CBS 141297; ITS sequence GenBank KX228324.1, LSU sequence GenBank KX228323.1, MycoBank MB817036).

**Notes.** On ITS *Wojnowiciella cissampeli* is 98 % (565/577) similar to *W. eucalypti* (CPC 25024; GenBank KP744471.1), and 99 % (546/552) to *Wojnowicia lonicerae* (MFLUCC 13-0737; GenBank KP744471.1). Morphologically, conidia of *W. cissampeli* are smaller than those of *W. eucalypti*, (10–)28–30(–33) × (4–)6–7 µm (Crous et al. 2015a), and *Wojnowicia lonicerae* (38–42 × 5–5.5–6 µm) (Liu et al. 2015).

**Colour illustrations.** *Cissampelos capensis* growing on Robben Island; *Wojnowiciella cissampeli* (left column): conidiomata sporulating on OA (scale bar = 300 µm), conidiogenous cells and conidia; *Diaporthe cissampeli* (right column): conidiomata sporulating on PNA (scale bar = 200 µm), conidiogenous cells and conidia. Scale bars = 10 µm.
**Prosopidicola albizziae** Crous & M.J. Wingf., sp. nov.

**Etymology.** Name refers to Albizzia, the host genus from which this fungus was collected.

**Classification.** *Incertae sedis, Diaporthales, Sordariomycetes.*

*Conidiomata* (on pine needle agar; PNA) pycnidial, separate or aggregated in an eustromatic stroma with one to several ostioles, mouse-grey, erumpent, to 300 µm diam; wall up to 10 layers of grey-brown *textura angularis*. Conidiophores reduced to conidiogenous cells. Conidiogenous cells tightly aggregated, hyaline, smooth, ampulliform, 5–12 × 3–4 µm, mono- to polyphialidic, with 1–2 apical loci with visible periclinal thickening, at times with percurrent proliferation. Conidia solitary, subhyaline to grey-brown, smooth, guttulate, straight to variously curved, ellipsoid to fusoid-ellipsoid, apex obtuse, base truncate to bluntly rounded, 1–1.5 µm diam, (5–)7–9(–11) × (2.5–)3–3.5(–4) µm.

**Culture characteristics.** Colonies reaching up to 20–30 mm diam after 2 wk at 25 °C, with spreading, flat surface; margins uneven, feathery, and sparse to moderate aerial mycelium. On MEA, PDA and OA surface and reverse pale mouse-grey.

**Typus.** MAIEYS, Sabah, Tawau, on leaves of Albizzia falcataria (Fabaceae), May 2015, M.J. Wingfield (holotype CBS H-22611, culture ex-type CPC 27478 = CBS 141298; ITS sequence GenBank KX228274.1, LSU sequence GenBank KX228325.1, MycoBank MB817037); ibid., associated with stem cankers on *Albizzia falcataria*, CPC 27484 (ITS sequence GenBank KX228275.1, LSU sequence GenBank KX228326.1, tub2 sequence GenBank KX228385.1).

Notes — Phylogenetically, CPC 27478 is identical to CPC 27484. Based on LSU sequence data, *Prosopidicola albizziae* is 99 % (807/815) similar to *P. mexicana*, which was regarded as a potential biocontrol agent of *Prosopis glandulosa*, causing a pod disease of this host in Mexico and the USA (Texas) (Lennox et al. 2004). However, on ITS the two species are only 84 % (512/607) similar. Morphologically, *P. albizziae* has smaller conidia than those of *P. mexicana*, (8–)10–13(–20) × (3.5–)4.5–5.5(–6) µm. *Prosopidicola* was noted to have conidiogenous cells that vary from being phialidic with periclinal thickening, or with prominent percurrent proliferation, becoming darkened at the apex (Lennox et al. 2004).

**Colour illustrations.** Albizzia falcataria trees; conidiomata sporulating on PNA, conidiogenous cells and conidia. Scale bars = 10 µm.
Phaeotheca salicorniae
**Phaeotheca salicorniae** Crous & Roets, *sp. nov.*

**Etymology.** Name refers to *Salicornia*, the plant genus from which this fungus was collected.

**Classification.** *Incertae sedis, Capnodiales, Dothideomycetes.*

**Mycelium.** Consisting of hyaline, smooth, septate, branched, 3–5 µm diam hyphae, that swell in areas up to 20 µm diam, terminal or intercalary, and develop numerous endoconidia, brown, verruculose, globose to obovoid, muriformly septate, 5–8 µm diam, bursting open to release several endoconidia that are red-brown, verruculose, aseptate, ellipsoid to subglobose or irregularly, 3–6 × 3–5 µm.

**Culture characteristics.** Colonies reaching up to 10 mm diam after 2 wk at 25 °C, with spreading, flat surface; margins smooth, lobate, and lacking aerial mycelium. On MEA, PDA and OA surface and reverse black.

**Typus.** **South Africa,** Western Cape Province, Robben Island, on leaves and twigs of *Salicornia meyeriana* (*Amaranthaceae*), May 2015, P.W. Crous & F. Roets (holotype CBS H-22612, culture ex-type CPC 27406 = CBS 141299; ITS sequence GenBank KX228276.1, LSU sequence GenBank KX228327.1, MycoBank MB817038).

**Notes.** Based on the LSU sequence data, *Phaeotheca salicorniae* is 99 % (828/834) similar to *Phaeotheca triangularis* (CBS 471.90; GenBank EU019279.1). On ITS the two species are 99 % (828/834) similar. The genus *Phaeotheca* presently includes three species, with *P. triangularis* (isolated from an air-conditioning system in Belgium) being characterised by ellipsoid to subglobose to triangular endoconidia. In *P. salicorniae* the endoconidia differ in shape and are slightly larger, 5.5–7 × 4.5–5.5 µm (De Hoog et al. 1997), and hyphal swellings up are to 70 µm diam. The genus *Phaeotheca* is polyphylectic, and its taxonomy will be revised in a separate study (J. Bezerra et al. in prep.).

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**Colour illustrations.** Salicornia sp.; hyphae with endoconidia on PNA. Scale bars = 10 µm.
Paracylindrocarpon aloicola
Fungal Planet 424 – 4 July 2016

**Paracylindrocarpon** Crous, Roets & L. Lombard, *gen. nov.*

*Etymology.* Name reflects a morphological similarity to the genus *Cylindrocarpon.*

*Classification.*— *Bionectriaceae, Hypocreales, Sordariomycetes.*

*Mycelium* consisting of hyaline, smooth, branched, septate hyphae, forming hyphal coils. *Conidiophores* solitary, hyaline, smooth, erect, straight to geniculate-sinuous, arising from superficial hyphae, unbranched or branched, septate. *Conidigenous cells* hyaline, smooth, subcylindrical with slight apical taper, straight to slightly irregularly curved, terminal or lateral on conidiophores, apex with minute periclinal thickening. *Conidia* hyaline, smooth, granular, cylindrical, apex obtuse, base truncate, (0–)3-septate.

*Type species.* Paracylindrocarpon aloicola Crous, Roets & L. Lombard. MycoBank MB817039.

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**Paracylindrocarpon aloicola** Crous, Roets & L. Lombard, *sp. nov.*

*Etymology.* Name refers to *Aloe*, the plant genus from which this fungus was collected.

*Mycelium* consisting of hyaline, smooth, branched, septate, 3–4 µm diam hyphae, forming hyphal coils. *Conidiophores* solitary, hyaline, smooth, erect, straight to geniculate-sinuous, arising from superficial hyphae, unbranched or branched, 1–4-septate, 20–50 × 3–4 µm. *Conidigenous cells* hyaline, smooth, subcylindrical with slight apical taper, straight to slightly irregularly curved, terminal or lateral on conidiophores, 20–30 × 2.5–3 µm, apex with minute periclinal thickening, 1.5–2 µm diam. *Conidia* hyaline, smooth, granular, cylindrical, apex obtuse, base truncate, 1 µm diam, (0–)3-septate, (17–)20–24(–27) × (2.5–)3 µm.

*Culture characteristics.*— Colonies reaching up to 30 mm diam on PDA and OA, 15 mm diam on MEA after 2 wk at 25 °C, with spreading, flat surface; margins smooth, lobate, and sparse to moderate aerial mycelium. On MEA surface pale luteous with patches of saffron, and diffuse scarlet pigment in agar, reverse amber. On PDA and OA surface and reverse pale luteous.

*Typus. South Africa,* Western Cape Province, Robben Island, on leaves and twigs of *Aloe* sp. (*Xanthorrhoeaceae*), May 2015, P.W. Crous & F. Roets (holotype CBS H-22613, culture ex-type CPC 27362 = CBS 141300; ITS sequence GenBank KX228277.1, LSU sequence GenBank KX228328.1, tub2 sequence GenBank KX228386.1, MycoBank MB817040).

*Notes.*— Based on LSU *Paracylindrocarpon aloicola* has 99 % (791/794) similarity to *Hydropisphaera erubescens* (ATCC 36093; GenBank AF193230.1). Likewise, ITS is 99 % (559/567) similar to *Hydropisphaera erubescens* (GenBank FJ969800.1) and 94 % (536/572) to *Fusariella sinensis* (OUCMB110131; GenBank KP269041.1). The genus *Hydropisphaera* is based on *H. peziza*, which has an *Acremonium* asexual morph (Samuels 1976). *Hydropisphaera erubescens* has a cylindrocarpon-like asexual morph with 1–3-septate conidia (Samuels 1978), showing some resemblance to the present collection, suggesting that some members of *Hydropisphaera* would be better accommodated in *Paracylindrocarpon* once the genus has been revised. The genus *Cylindrocarpon* (*Nectriaceae*) has recently been revised, and shown to be polyphyletic (Halleen et al. 2004, Chaverri et al. 2011, Lombard et al. 2014), with *Paracylindrocarpon* (*Bionectriaceae*) representing yet another additional genus in this complex.

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**Colour illustrations.** Symptomatic leaves of *Aloe* sp. growing on top of old gun turret on Robben Island; colony sporulating on PNA, conidiophores and conidia. Scale bars = 10 µm.
Fusicladium eucalypticola
Fungal Planet description sheets

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**Fusicladium eucalypticola** Crous & M.J. Wingf., *sp. nov.*

**Etymology.** Name refers to *Eucalyptus*, the plant genus from which this fungus was collected.

**Classification —** *Sympoventuriaceae*, *Venturiales*, *Dothideomycetes*.

*Mycelium* consisting of pale brown, smooth, branched, septate, 1.5–3 µm diam hyphae. *Conidiophores* reduced to conidigenous cells, or with basal supporting cell. *Conidiogenous cells* erect, brown, smooth, subcylindrical, straight, 5–20 × 2.5–3 µm, with a single terminal locus, thickened and darkened, 1–2 µm diam. *Primary ramoconidia* brown, smooth, subcylindrical, 0–2-septate, 15–25 × 3 µm, with 1–2 apical loci. *Secondary ramoconidia* brown, smooth, subcylindrical to fusoid-ellipsoid, 15–20 × 3–5 µm, 1–3-septate; loci thickened, darkened, 0.5–1 µm diam. *Conidia* occurring in branched chains of up to 15 conidia, fusoid-ellipsoid, pale brown, smooth, guttulate, aseptate, (5–)7–10(–12) × (2.5–)3(–4) µm; hila thickened, darkened, 0.5 µm diam.

**Culture characteristics —** Colonies reaching up to 15 mm diam after 2 wk at 25 °C, with spreading, flat surface; margins smooth, lobate, and moderate aerial mycelium. On MEA, PDA and OA surface and reverse sienna.

**Typus.** **FRANCE**, La Réunion, on leaves of *Eucalyptus robusta* (Myrtaceae), 8 Mar. 2015, **P.W. Crous & M.J. Wingfield** (holotype CBS H-22614, culture ex-type CPC 27238 = CBS 141301; ITS sequence GenBank KX228278.1, LSU sequence GenBank KX228278.1, MycoBank MB817041).

Notes — The LSU sequence of *Fusicladium eucalypticola* is 99 % (868/871) similar to *F. eucalypti* (CBS 128216; GenBank HQ599601.1) and 94 % (824/872) to *F. africanaum* (CPC 12829; GenBank EU035424.1). Based on ITS DNA sequence data *F. eucalypticola* is 99 % (532/539) similar to *F. eucalypti* (CBS 128216; GenBank HQ599600.1) and 86 % (319/371) to *F. convolvularum* (CPC 3884; GenBank AY251082.1). *Fusicladium eucalypti* (on *Eucalyptus* sp., Queensland, Australia) has smaller secondary ramoconidia, being 0–1-septate, (10–)12–13(–15) × (2–)2.5–3 µm, and narrower conidia, (7–)8–9(–10) × (2–)2.5(–3) µm (Crous et al. 2010a).

*Notes —* The LSU sequence of *Fusicladium eucalypticola* is 99 % (868/871) similar to *F. eucalypti* (CBS 128216; GenBank HQ599601.1) and 94 % (824/872) to *F. africanaum* (CPC 12829; GenBank EU035424.1). Based on ITS DNA sequence data *F. eucalypticola* is 99 % (532/539) similar to *F. eucalypti* (CBS 128216; GenBank HQ599600.1) and 86 % (319/371) to *F. convolvularum* (CPC 3884; GenBank AY251082.1). *Fusicladium eucalypti* (on *Eucalyptus* sp., Queensland, Australia) has smaller secondary ramoconidia, being 0–1-septate, (10–)12–13(–15) × (2–)2.5–3 µm, and narrower conidia, (7–)8–9(–10) × (2–)2.5(–3) µm (Crous et al. 2010a).

Colour illustrations. Forest undergrowth on La Réunion Island; conidiophores and conidia on PNA. Scale bars = 10 µm.
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**Paramycoleptodiscus** Crous & M.J. Wingf., *gen. nov.*

*Etymology.* Name reflects a morphological similarity with the genus *Mycoleptodiscus*.

*Classification.* — *Incertae sedis*, Acrospermales, Dothideomycetes.

*Mycelium* consisting of hyaline, branched, septate hyphae that become brown, constricted at septa, forming a cluster of globose, brown, chlamydospore-like cells that form a stroma; stroma brown, solitary, globose, but with age joining along the length of hyphae to become strands of radiating stromata; stroma forming a sporodochium of densely aggregated, dark brown, finely roughened conidigenous cells, subglobose to slightly ampulliform, containing a single, central phialidic locus, slightly papillate, with cylindrical collarette. *Conidia* solitary, aseptate, hyaline, smooth, granular, falcate, slightly curved, widest in middle, apex subobtusely rounded, base with well-defined fusarium-like foot cell.

*Type species.* *Paramycoleptodiscus albizziae* Crous & M.J. Wingf. MycoBank MB817042.

**Paramycoleptodiscus albizziae** Crous & M.J. Wingf., *sp. nov.*

*Etymology.* Name refers to *Albizzia*, the plant genus from which this fungus was collected.

*Mycelium* consisting of hyaline, branched, septate, 2–3 µm diam hyphae that become brown, constricted at septa, up to 6 µm diam, forming a cluster of globose, brown, chlamydospore-like cells up to 8 µm diam, that form a stroma; stroma brown, up to 100 µm diam, solitary, globose, but with age joining along the length of hyphae to become strands of radiating stromata; stroma forming a sporodochium of densely aggregated, dark brown, finely roughened conidigenous cells, subglobose to slightly ampulliform, 7–12 × 5–12 µm, containing a single, central phialidic locus, slightly papillate, 2–3.5 µm diam, with cylindrical collarette, 2–3 µm long. *Conidia* solitary, aseptate, hyaline, smooth, granular, falcate, slightly curved, widest in middle, apex subobtusely rounded, base with well-defined fusarium-like foot cell, (23–)26–32(–37) × (3–)4 µm (including foot cell), 1–3 × 1–1.5 µm.

Culture characteristics — Colonies reaching up to 15 mm diam after 2 wk at 25 °C, with spreading, erumpent surface; margins smooth, lobate, and sparse to moderate aerial mycelium. On MEA surface and reverse mouse-grey. On OA surface mouse-grey. On PDA surface mouse-grey, reverse dark mouse-grey.

*Typus.* MALAYSIA, Sabah, Tawau, on leaves of *Albizzia falcata* (Fabaceae), May 2015, M.J. Wingfield (holotype CBS H-22615, culture ex-type CPC 27552 = CBS 141320; ITS sequence GenBank KX228279.1, LSU sequence GenBank KX228330.1, MycoBank MB817043).

Notes — The LSU sequence of *Paramycoleptodiscus albizziae* is 95 % (544/572) similar to *Mycoleptodiscus terrestris* (type of *Mycoleptodiscus*; CBS 231.53; GenBank JN711859) and 94 % (754/800) to *Arxiella dolichandrae* (CBS 138853; GenBank KP004477.1). No highly similar sequences were obtained with the ITS sequence. *Paramycoleptodiscus* is distinct from *Mycoleptodiscus* (Sutton 1973) in that the latter has septate conidia with apical appendages, whereas in *Paramycoleptodiscus* the conidia are aseptate, and have a basal appendage in the form of a foot cell.

*Colour illustrations.* Stand of Albizzia falcata trees; conidiomata sporulating on OA, sporodochia, conidigenous cells and conidia. Scale bar = 10 µm.
Malaysiasca phaii
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**Malaysiasca** Crous & M.J. Wingf., *gen. nov.*

*Etymology.* Name refers to Malaysia, the country where it was collected.

*Classification.* — *Incertae sedis, Glomerellales, Sordariomycetes.*

*Stroma.* brown, globose, erumpent, giving rise to a fascicle of conidiophores. *Conidiophores* subcylindrical, unbranched, erect, flexuous, basal cell slightly swollen; thick-walled, finely roughened, granular to slightly guttulate, septate, grey-brown, becoming somewhat pale brown towards slightly tapered apex, rejuvenating percurrenty, with apical conidiogenous cells. *Conidiogenous cells* integrated, pale brown, subcylindrical, phialidic, with periclinal thickening and minute collarette. *Conidia* solitary, aggregating in a slimy mass, ellipsoidal to cylindrical-ellipsoid to somewhat clavate, prominently guttulate, frequently with large central guttule, apex obtuse, base truncate, scar slightly thickened and darkened, frequently excentric. Ascoma perithecial, base immersed in substrate, obpyriform, papillate, dark brown with setae around base of perithecium, pale brown; wall of 3–5 layers of pale brown *textura prismatica*. *Paraphyses* persistent, hyaline, branched, septate, longer than asci. *Asci* uniloculate, cylindrical-clavate, short-stipitate, apex truncate with shallow annulus, 8-spored. *Ascospores* biseriate in ascus, ellipsoid to oblong, apiculate at ends, with one end having minute mucoid cap, hyaline, smooth, frequently with large central guttule, becoming 1-septate and pale brown after discharge.

*Type species.* *Malaysiasca phaii* Crous & M.J. Wingf. MycoBank MB817044.

**Malaysiasca phaii** Crous & M.J. Wingf., *sp. nov.*

*Etymology.* Name refers to Phaius, the plant genus from which this fungus was collected.

*Stroma.* brown, globose, erumpent, to 150 µm diam, giving rise to a fascicle of 2–10 conidiophores. *Conidiophores* subcylindrical, unbranched, erect, flexuous, basal cell slightly swollen, 7–12 µm diam; thick-walled, finely roughened, granular to slightly guttulate, 5–8-septate, grey-brown, becoming somewhat pale brown towards slightly tapered apex, rejuvenating percurrenty, 150–220 × 5–7 µm, with apical conidiogenous cell. *Conidiogenous cells* integrated, pale brown, subcylindrical and phialidic, with periclinal thickening and minute collarette. *Conidia* solitary, aggregating in a slimy mass, ellipsoidal to cylindrical-ellipsoid to somewhat clavate, prominently guttulate, frequently with large central guttule, apex obtuse, base truncate, scar slightly thickened and darkened, frequently excentric, 3–4 µm diam, (16–)18–20–24) × (8–)9–10(–11) µm. On PNA developing a sexual morph after 4 wk, and essentially dissolving the cellolytic tissue of the pine needle in the process. *Ascomata* perithecial, base immersed in pine needles, to 250 µm wide, 400 µm tall, obpyriform, papillate, dark brown with setae around base of perithecium, pale brown; wall of 3–5 layers of pale brown *textura prismatica*. *Paraphyses* persistent, hyaline, branched, septate, longer than asci, 2.5–4 µm diam. *Asci* 55–80 × 9–12 µm, unitunicate, cylindrical-clavate, short-stipitate, apex truncate with shallow annulus, 8-spored. *Ascospores* biseriate in ascus, ellipsoid to oblong, apiculate at ends, with one end having minute mucoid cap, hyaline, smooth, frequently with large central guttule, becoming 1-septate and pale brown after discharge, (22–)24–27(–30) × (6–)7(–8) µm.

*Culture characteristics.* — Colonies reaching up to 25 mm diam after 2 wk at 25 °C, with spreading, flat surface; margins feathery, lobate, and sparse aerial mycelium. On MEA surface and reverse pale luteous. On OA surface dark mouse-grey. On PDA surface and reverse mouse-grey.

*Type.* MALAYSIA, Sabah, Tawau, on leaves of *Phaius reflexipetalus* (Orchidaceae), 30 May 2015, M.J. Wingfield (holotype CBS H-22616, culture ex-type CPC 27548 = CBS 141321; ITS sequence GenBank KX222828.1, LSU sequence GenBank KX228331.1, actA sequence GenBank KX228359.1, MycoBank MB817045).

*Notes.* — The LSU sequence of *Malaysiasca phaii* is 98 % (784/797) similar to that of *Monilochaetes dimorphospora* (MUCJ 40959, GenBank HQ609480.1), 98 % (783/797) to *Monilochaetes guadalcanalensis* (CBS 346.76; GenBank GU180640.1) and 98 % (782/797) to *Australiasca queenslandica* (BRIP 24334c; GenBank HM237323.1). Morphologically, *Malaysiasca* resembles the genus *Australiasca* (Rélová et al. 2011), but is distinct in that it forms a stroma that gives rise to fascicles of conidiophores, whereas stromata are absent in *Australiasca*. In general the asexual morph is similar to species of *Monilochaetes*, and would be difficult to distinguish without the aid of molecular data.

*Colour illustrations.* Forest undergrowth in Malaysia; ascomata, ascospores and asci; stroma giving rise to conidiophores, conidiogenous cells and conidia. Scale bars: ascomata = 250 µm, all others = 10 µm.

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Libertasomyces myoporii
**Libertasomyces** Crous & Roets, gen. nov.

**Etymology.** This fungus was collected on Robben Island off the west coast of Cape Town, South Africa. The word robben is Dutch for ‘seal’, and thus ‘seal island’ is where Nelson Mandela, the first democratically elected President of South Africa, was imprisoned for 18 of the 27 years he served behind bars before the fall of apartheid. *Libertas* (Latin) for freedom.

**Classification — Incertae sedis, Pleosporales, Dothideomycetes.**

**Conidiomata** pycnidial, solitary, dark brown, erumpent, globose, with central ostiole; wall of 3–6 layers of brown textura angularis. **Conidiophores** reduced to conidiogenous cells. **Conidiogenous cells** lining the inner cavity, hyaline, smooth, ampulliform to doliiform, phialidic with prominent periclinal thickening. **Conidia** solitary, hyaline, smooth, granular, thin-walled, ellipsoid, widest in middle, apex obtuse, base truncate to bluntedly rounded, aseptate.

**Type species.** *Libertasomyces myopori* Crous & Roets. MycoBank MB817046.

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**Libertasomyces myopori** Crous & Roets, sp. nov.

**Etymology.** Name refers to *Myoporum*, the plant genus from which this fungus was collected.

**Conidiomata** (on pine needle agar; PNA) pycnidial, solitary, dark brown, erumpent, globose, to 300 µm diam, with central ostiole; wall of 3–6 layers of brown textura angularis. **Conidiophores** reduced to conidiogenous cells. **Conidiogenous cells** lining the inner cavity, hyaline, smooth, ampulliform to doliiform, phialidic with prominent periclinal thickening, 3–6 × 3–4 µm. **Conidia** solitary, hyaline, smooth, granular, thin-walled, ellipsoid, widest in middle, apex obtuse, base truncate to bluntedly rounded, aseptate, (4–)4.5–5(–6) × (2–)2.5–3(–3.5) µm.

**Culture characteristics —** Colonies reaching up to 30 mm diam after 2 wk at 25 °C, with spreading, erumpent surface; margins smooth, lobate, and moderate aerial mycelium. On MEA surface dirty white, reverse luteous. On OA surface honey. On PDA surface buff with patches of isabelline, reverse isabelline to buff.

**Typus.** SOUTH AFRICA, Western Cape Province, Robben Island, on twigs of *Myoporum serratum* (Myoporaceae), May 2015, P.W. Crous & F. Roets (holotype CBS H-22617, culture ex-type CPC 27354 = CBS 141302; ITS sequence GenBank XX226261.1, LSU sequence GenBank XX228332.1, MycoBank MB817047).

**Notes —** On LSU *Libertasomyces myopori* is 98 % (792/808) similar to *Camarosporium quaternatum* (CBS 134.97; GenBank DQ377883.1), 98 % (791/808) to *Leptosphaeria rubefaciens* (CBS 387.80; GenBank JF740311.1), 97 % (787/809) to *Plenodomus visci* (CBS 122783; GenBank EU754195.1) and 97 % (786/808) to *Neoplatysporoides aloicola* (CPC 24435; GenBank KR476754.1), and represents another genus being phoma-like in morphology. *Neoplatysporoides aloicola* (CPC 24435; GenBank KR476719.1) also represents the most similar ITS sequence at 92 % (534/580). *Libertasomyces* is morphologically quite distinct from *Neoplatysporoides* in that conidia remain hyaline and aseptate, in contrast to those of *Neoplatysporoides* that are 0–1-septate, golden brown, and with longitudinal striations (Crous et al. 2015a).

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*Colour illustrations. Myoporum serratum growing on Robben Island; conidiomata sporulating on OA, conidiogenous cells and conidia. Scale bars = 10 µm.*
Fusicladium paraamoenum
Fungal Planet description sheets

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Fusicladium paraamoenum Crous, Jacq. Edwards & P.W.J. Taylor, sp. nov.

Etymology. Name reflects morphological similarity to Fusicladium amoenum.

Classification — Sympoventuriaceae, Venturiales, Dothideomycetes.

Mycelium consisting of pale brown, smooth, branched, septate, 2.5–3.5 μm diam hyphae. Conidiophores erect, solitary, subcylindrical, dark brown, thick-walled, smooth, rarely branched below, 25–120 × 3–4 μm, 1–7-septate. Conidiogenous cells integrated, terminal, rarely lateral, 10–30 × 3–4 μm, brown, smooth, with several sympodial denticle-like loci, 1–1.5 μm diam, thickened and darkened. Conidia occurring in short chains, subcylindrical, pale brown, smooth, guttulate, (0–)1(–3)-septate, ends obtusely rounded, hila thickened and darkened, 1.5–2 μm diam, (13–)15–20(–28) × (3–)3.5(–4) μm.

Culture characteristics — Colonies reaching up to 10 mm diam after 2 wk at 25°C, with spreading, erumpent surface; margins smooth, lobate, and moderate aerial mycelium. On MEA and PDA surface umber, reverse chestnut. On OA surface umber with chestnut outer margin.

Typus. AUSTRALIA, Victoria, Toolangi State Forest, S37°33′25.3″ E145°31′55.9″, on leaves of Eucalyptus regnans (Myrtaceae), 9 Nov. 2014, P.W. Crous, J. Edwards & P.W.J. Taylor (holotype CBS H-22618, culture ex-type CPC 25596 = CBS 141322; ITS sequence GenBank KX228282.1, LSU sequence GenBank KX228333.1, MycoBank MB817046).

Notes — On ITS Fusicladium paraamoenum is 98 % (560/574) similar to F. amoenum (CBS 254.95; GenBank EU035425.1) and 97 % (527/545) to F. intermedium (CBS 110746; GenBank EU035432.1). The LSU sequence is 99 % (907/909) similar to F. amoenum (CBS 254.95; GenBank EU035425.1) and 99 % (897/909) to F. intermedium (CBS 110746; GenBank EU035432.1). Conidia of F. paraamoenum are larger than those of F. amoenum (6–)10.5–12.8(–17.3) × (1.5–)2.4–3(–3.8) μm (Ho et al. 1999).

Colour illustrations. Eucalyptus regnans trees at Toolangi State Forest; conidiophores and conidia on SNA. Scale bars = 10 μm.
Ochroconis dracaenae
**Fungal Planet 430 – 4 July 2016**

**Ochroconis dracaenae** Crous, *sp. nov.*

**Etymology.** Name refers to *Dracaena*, the plant genus from which this fungus was collected.

**Classification.** — *Sympoventuriaceae, Venturiales, Dothideomycetes.*

*Mycelium* consisting of smooth, pale brown, septate, branched, 1.5–3 µm diam hyphae. *Conidiophores* solitary, erect, brown, smooth, arising from superficial hyphae, subcylindrical, straight to geniculate-sinuous, branched below or not, 1–6-septate, 10–30 × 2–3 µm. *Conidiogenous cells* brown, smooth, terminal and lateral on conidiophores, 5–15 × 2.5–3 µm, containing several apical, cylindrical denticles, 1–1.5 × 1 µm. *Conidia* solitary, subcylindrical, ends obtuse, pale brown, verruculose, medianly 1-septate, hilum thickened and darkened, 1 µm diam, (6.5–7–9(–10) × (3–)3.5(–5) µm.

**Culture characteristics.** — Colonies reaching up to 20 mm diam after 2 wk at 25 °C, with spreading erumpent surface; margins smooth, lobate, and moderate aerial mycelium. On MEA surface isabelline, reverse brown-vinaceous. On OA surface brown-vinaceous. On PDA surface and reverse isabelline.

**Typus.** USA, Texas, Austin, on leaf spots of *Dracaena reflexa* (Asparagaceae), Aug. 2013, P.W. Crous (holotype CBS H-22619, culture ex-type CPC 26115 = CBS 141323; ITS sequence GenBank KX228283.1, LSU sequence GenBank KX228334.1, rpb2 sequence GenBank KX228370.1, tef1 sequence GenBank KX228377.1, MycoBank MB817049).

**Notes.** — On ITS *Ochroconis dracaenae* is 96 % (691/719) similar to *O. humicola* (UZ1582_14; GenBank KP326578.1) and 97 % (626/647) to *O. musae* (CBS 121963; GenBank HQ-667535.1). No better matches were obtained with the protein coding sequences. *Ochroconis dracaenae* has smaller conidia than *O. humicola* (8–20 × 3–5 µm) and *O. musae* (9.0–13.5 × 4.8–6.7 µm) (Crous et al. 2014a, Samerpitak et al. 2015).

**Colour illustrations.** Forest path along walkway in Austin, Texas; conidiogenous cells and conidia on SNA. Scale bars = 10 µm.
Cytospora tibouchinae
**Cytospora tibouchinae** Crous & M.J. Wingf., *sp. nov.*

**Etymology.** Name refers to Tibouchina, the plant genus from which this fungus was collected.

**Classification.** *Valsaceae, Diaporthales, Sordariomycetes.*

Conidiomatal (on pine needle agar; PNA) stromata up to 500 µm diam, rosette cytosporoid, subdivided by invaginations, up to six radially arranged. *Conidiophores* hyaline, smooth, branched, 0–3-septate, 15–25 × 2–3 µm, embedded in a gelatinous layer. *Conidiogenous cells* phialidic, with periclinal thickening, tapering towards apices, collarettes minute, 8–14 × 1.5–2 µm. *Conidia* hyaline, smooth, guttulate, allantoid, aseptate, (3–) 3.5(–4) × 1(–1.5) µm.

**Culture characteristics.** Colonies covering dish after 2 wk at 25 °C, with spreading, flat surface; margins smooth, and with moderate aerial mycelium. On MEA surface grey-olivaceous, reverse greyish sepia. On OA surface olivaceous grey. On PDA surface smoke grey with patches of honey, reverse grey olivaceous.

**Typus.** France, La Réunion, on stems of *Tibouchina semidecandra* (Melastomataceae), 12 Mar. 2015, P.W. Crous & M.J. Wingfield (holotype CBS H-22620, culture ex-type CPC 26333 = CBS 141324; ITS sequence GenBank KX228284.1, LSU sequence GenBank KX228335.1, MycoBank MB817050).

**Notes.** Based on ITS sequence data *Cytospora tibouchinae* is 98% (561/575) similar to *Cytospora myrtagena* (CMW4046; GenBank AY347380.1) (Adams et al. 2005, Rossman et al. 2015). Morphologically, *Cytospora tibouchinae* has conidia of similar dimensions, 3–3.5(–4) × 1 µm, but the two species can be distinguished in that *C. myrtagena* has unbranched conidiophores, and shorter conidiogenous cells, 5–7 × 1 µm (Adams et al. 2005).

**Colour illustrations.** *Tibouchina semidecandra* on La Réunion Island; conidiomata sporulating on PNA, conidiophores and conidia. Scale bars = 10 µm.
Neotrimmatostroma paraexcenticum
**Fungal Planet 432 – 4 July 2016**

**Neotrimmatostroma paraexcentricum** Crous, Jacq. Edwards & Pascoe, *sp. nov.*

*Etymology.* Name reflects a morphological similarity to *Neotrimmatostroma excentricum*.

*Classification.* — Teratosphaeriaceae, Capnodiales, Dothideomycetes.

*Leaf spots.* Separate, coalescing with age, medium brown, subcircular with indistinct margins, 2–7 mm diam, amphigenous, but more prominent on epiphyllous surface. *Mycelium* immersed, consisting of pale brown, septate, branched, 2–3 µm diam hyphae. *Conidiomata* sporodochial, chiefly epiphyllous, concentrically arranged, dark brown, dry powdery, discrete, to 400 µm diam. *Conidiophores* micronematous, branched, septate, medium brown, smooth, densely aggregated, with differential thickening of periclinal wall, one side thinner than the other, to 30 µm tall, 3–4 µm diam. *Conidiogenous cells* holothallic, integrated, terminal, doliform to subcylindrical, 7–10 × 3–4 µm. *Conidia* in sparsely branched chains, smooth, pale brown, 4-celled, consisting of upper and lower cells with truncate ends, separated by a thick, dark brown transverse septum, each primary cell with a smaller, lateral, globose secondary cell on either side of the primary septum. The two primary cells together are 9–11 µm diam, the secondary cells 4–5 µm diam.

*Culture characteristics.* — Colonies reaching up to 7 mm diam after 2 wk at 25 °C, with margins smooth, lobate, and sparse aerial mycelium. On MEA, PDA and OA surface and reverse iron-grey.

*Typus.* AUSTRALIA, Victoria, Phillip Island, Oswin Roberts Reserve, on leaves of *Eucalyptus* sp. (Myrtaceae), 8 Nov. 2014, P.W. Crous, J. Edwards & I.G. Pascoe (holotype CBS H-22621, culture ex-type CPC 25594 = CBS 141325; ITS sequence GenBank KX228265.1, LSU sequence GenBank KX228336.1, tef1 sequence GenBank KX228378.1, MycoBank MB817051).

*Notes.* — On ITS *Neotrimmatostroma paraexcentricum* is 98% (467/476) similar to *N. excentricum* (CBS 121102; GenBank KF901518.1) and on tef1 it is 89% (331/372) similar to the same isolate (GenBank KF903123.1). Although morphologically similar, the two species can be distinguished in that the secondary conidium cells of *N. excentricum* are 2.5–4.5 µm diam, thus smaller than those of *N. paraexcentricum* (Sutton & Ganapathi 1978, Quaedvlieg et al. 2014).

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**Colour illustrations.** Symptomatic leaves of *Eucalyptus* sp.; conidiomata sporulating on leaf spot, colony on OA, conidiophores and conidia. Scale bars = 10 µm.
Setophoma cyperi
Setophoma cyperi Crous & M.J. Wingf., sp. nov.

Etymology. Name refers to Cyperus, the plant genus from which this fungus was collected.

Classification — Phaeosphaeriaceae, Pleosporales, Dothideomycetes.

Associated with leaf scorch symptoms on Cyperus. Ascomata immersed on host, erumpent in culture, black, globose, to 200 µm diam., with central ostiole; wall of 3–4 layers of dark brown textura angularis. Pseudoparaphyses intermingled among asci, hyaline, septate, branched prominently, constricted at septa, 2–4 µm diam. Asci bitunicate with apical chamber, subcylindrical, hyaline, smooth, fasciculate, stipitate, 8-spored, 65–80 × 11–13 µm. Ascospores tri- to multiseriate, fusoid with subobtusely rounded ends, finely verruculose, red-brown, guttate, 2-septate, slightly constricted at septa, with central cell somewhat swollen, (26–)27–29(–31) x (3.5–)4(–4.5) µm.

Culture characteristics — Colonies reaching up to 30 mm diam on MEA and OA, 10 mm diam on PDA, after 2 wk at 25 °C, with spreading, erumpent surface; margins feathery, and moderate aerial mycelium. On MEA, PDA and OA surface dirty white, reverse dirty white to luteous.

Typus. SOUTH AFRICA, Eastern Cape Province, Haga Haga, on leaves of Cyperus sphaerocephala (Cyperaceae), Dec. 2014, M.J. Wingfield (holotype CBS H-22622, culture ex-type CPC 25702 = CBS 141450; ITS sequence GenBank KX228286.1, LSU sequence GenBank KX228337.1, MycoBank MB817052).

Notes — On LSU Setophoma cyperi is 98 % similar to several genera in Phaeosphaeriaceae, including Setophoma (e.g. 825/844 to S. sacchari CBS 333.39, GenBank GQ387586.1). De Gruyter et al. (2010) introduced the genus Setophoma to accommodate Pyrenochaeta sacchari, and Phookamsak et al. (2014) recently reported a sexual morph for the genus in Phaeosphaeriaceae.
Lareunionomyces syzygii
Fungal Planet 434 – 4 July 2016

**Lareunionomyces** Crous & M.J. Wingf., *gen. nov.*

*Etymology.* Named after the island where this fungus was collected, La Réunion.

*Classification.* — *Incertae sedis, Helotiales, Leotiomyces.*

*Mycelium* consisting of hyaline, smooth, branched hyphae. *Conidiophores* solitary, erect, unbranched, subcylindrical, dark brown, smooth, 3–7-septate, 50–100 × 5–8 μm, thick-walled, basal cell slightly swollen, to 10 μm diam, lacking rhizoids. *Penicillate conidiogenous apparatus* pale brown, smooth; primary branches brown, smooth, subcylindrical to clavate, giving rise to up to several secondary branches, pale brown, subcylindrical to clavate; tertiary branches pale brown, giving rise to several phialides. *Phialides* subulate, pale brown, flexuous, venter cylindrical, with prominent collarette. *Conidia* hyaline, smooth, guttulate, subcylindrical, aseptate, apex bluntly rounded, base truncate, in short chains that form slimy spore masses.

*Type species.* Lareunionomyces syzygii Crous & M.J. Wingf. MycoBank MB817053.

**Lareunionomyces syzygii** Crous & M.J. Wingf., *sp. nov.*

*Etymology.* Name refers to *Syzygium*, the plant genus from which this fungus was collected.

*Mycelium* consisting of hyaline, smooth, branched, 2–3 μm diam hyphae. *Conidiophores* solitary, erect, unbranched, subcylindrical, dark brown, smooth, 3–7–septate, 50–100 × 5–8 μm, thick-walled, basal cell slightly swollen, to 10 μm diam, lacking rhizoids. *Penicillate conidiogenous apparatus* pale brown, smooth; primary branches brown, smooth, subcylindrical to clavate, 8–15 × 4–6 μm, giving rise to up to 8 secondary branches, pale brown, subcylindrical to clavate, 4–10 × 4–5 μm; tertiary branches pale brown, 4–7 × 3–4 μm, giving rise to several phialides. *Phialides* subulate, pale brown, flexuous, 9–12 × 2–2.5 μm, venter cylindrical, with prominent collarette, 4–6 μm long, apex 1.5–2 μm diam. *Conidia* hyaline, smooth, guttulate, subcylindrical, aseptate, apex bluntly rounded, base truncate, (3.5–)4(–5) × (1.5–)2 μm, in short chains that form slimy spore masses.

*Culture characteristics.* — Colonies reaching up to 8 mm diam after 2 wk at 25 °C, with spreading, erumpent surface; margins smooth, lobate, and sparse aerial mycelium. On MEA surface pale luteous, reverse umber. On PDA and OA surface and reverse umber.

**Typus. France,** La Réunion, on leaves of *Syzygium jambos* (Myrtaceae), 12 Mar. 2015, P.W. Crous & M.J. Wingfield (holotype CBS H-22623, culture ex-type CPC 26531 = CBS 141326; ITS sequence GenBank KX228287.1, LSU sequence GenBank KX228338.1, MycoBank MB817054).

*Colour illustrations.* Branch of *Syzygium jambos*; colony on OA, conidiophores and conidia. Scale bars = 10 μm.

Notes — Based on its mode of conidiogenesis, Wingfield et al. (1987) regarded *Sporendocladia* as separate from *Phialocephala* and Jacobs et al. (2003) showed that this complex is paraphyletic. Based on identification in the MycoBank nucleotide database the LSU sequence of the present collection is 98.4 % similar to an isolate identified as *Sporendocladia foliicola* (CBS 201.95) and it is possible that these two species could be congeneric. The type of *Sporendocladia* (S. castanea) is regarded as synonym of *S. fumosa* (Wingfield et al. 1987, Crous & Wingfield 1994) but the culture, CBS 518.93, is not congeneric with the present collection, and hence a new genus is introduced here to accommodate the present collection. Morphologically, *Sporendocladia* is similar to *Lareunionomyces*, except that the latter genus has a more intricate conidiogenous apparatus, with numerous tightly aggregated branches and phialides.
Parawiesneriomyces Crous & M.J. Wingf., gen. nov.

**Etymology.** Name reflects a morphological similarity to the genus *Wiesneriomyces*.

**Classification** — *Wiesneriomyctaceae, Tubeufiales, Dothideomycetes*.

**Mycelium** consisting of brown, finely verrucose, branched, septate hyphae, giving rise to hyphopodia-like structures, with several lateral branches, creating a cauliflower-like appearance. Setae loosely associated with sporodochia, erect, flexuous, base bulbous, lacking rhizoids, apex acute, thick-walled, smooth, granular, dark brown, septate. *Conidiomata* sporodochial, solitary, becoming somewhat gregarious in older cultures, hyaline, becoming pale luteous with age; arising from a basal stroma of loosely aggregated brown hyphae that give rise to densely aggregated, hyaline, penicillate conidiophores. *Conidiophores* hyaline, smooth, penicillate, septate (constricted at septa), branched, with several series of branches. Conidigenous cells terminal, clavate, hyaline, smooth, straight to gently curved, polyblastic, with several flat-tipped apical loci. *Conidia* solitary, aggregated in mucoid mass, hyaline, smooth, granular, prominently guttulate, subcyllindrical, widest in middle with taper towards both ends that are obtusely rounded, septate, prominently constricted at septa, joined by a narrow isthmus.

*Type species.* *Parawiesneriomyces syzygii* Crous & M.J. Wingf. MycoBank MB817060.

Parawiesneriomyces syzygii Crous & M.J. Wingf., sp. nov.

**Etymology.** Name refers to *Syzygium*, the plant genus from which this fungus was collected.

**Mycelium** (on SNA, OA and PNA) consisting of brown, finely verrucose, branched, septate 3–5 µm diam hyphae, giving rise to hyphopodia-like structures, up to 25 µm tall, with several lateral branches (5–15 µm diam), creating a cauliflower-like appearance. Setae loosely associated with sporodochia, erect, flexuous, base bulbous (7–15 µm diam), lacking rhizoids, apex acute, thick-walled, smooth, granular, dark brown, 8–12-septate (at times minutely constricted at some septa), 180–300 µm tall. *Conidiomata* sporodochial, 80–300 µm diam, solitary, becoming somewhat gregarious in older cultures, hyaline, becoming pale luteous with age; arising from a basal stroma of loosely aggregated brown hyphae that give rise to densely aggregated, hyaline, penicillate conidiophores. *Conidiophores* hyaline, smooth, penicillate, septate (constricted at septa), branched, 40–80 × 3–4 µm, with up to three series of branches. *Conidigenous cells* terminal, clavate, hyaline, smooth, straight to gently curved, 5–8 × 3–4 µm, polyblastic, with several flat-tipped apical loci, 0.5–1.5 µm diam. *Conidia* solitary, aggregated in mucoid mass, hyaline, smooth, granular, prominently guttulate, subcyllindrical, widest in middle with taper towards both ends that are obtusely rounded, 4–6–7-septate, prominently constricted at septa, joined by a narrow isthmus, (41–)65–75(–80) × 2(–3.5) µm, median cells 9–12 µm long, terminal cells 8–10 × 2–3 µm.

**Culture characteristics** — Colonies reaching up to 60 mm diam after 3 wk at 25 °C, with spreading, flat surface; margins smooth, even, and moderate aerial mycelium. On MEA, OA and PDA surface and reverse mouse-grey with patches of dark mouse-grey.

**Colour illustrations.** Conidiomata sporulating on PNA, seta, cauliflower-like lateral branch, conidigenous apparatus and conidia. Scale bars: seta = 300 µm, all others = 10 µm.

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Pseudophloeospora eucalyptorum
Pseudophloeospora eucalyptorum Crous, Jacq. Edwards & Pascoe, sp. nov.

Etymology. Name refers to Eucalyptus, the plant genus from which this fungus was collected.

Classification — Incertae sedis, Xylariales, Sordariomycetes.

Leaf spots amphigenous, angular to irregular, medium to dark brown, 2–7 µm diam with raised border. Conidiomata pycnidal on host, in culture appearing more acervular to even sporodochial, brown, to 250 µm diam; wall of 3–6 layers of pale brown textura angularis. Conidiophores lining inner cavity, hyaline, smooth, subcylindrical, branched, 1–5-septate, 15–60 × 2.5–3.5 µm. Conidiogenous cells terminal and lateral, hyaline, smooth, tapering towards truncate apex, proliferating sympodially as well as inconspicuously percurrently at apex, 5–15 × 2–2.5 µm. Conidia hyaline, smooth, filiform, guttulate, flexuous, subcylindrical, widest in lower third, tapering to an acutely rounded apex, and truncate base, 1.5 µm diam, 3-septate, (30–)50–67(–75) × 2.5(–3) µm.

Culture characteristics — Colonies reaching up to 30 mm diam after 2 wk at 25 °C, with spreading, erumpent, folded surface; margins feathery, lobate, and moderate aerial mycelium. On MEA surface dirty white, with patches of pale mouse grey, reverse sienna with patches of luteous. On OA surface dirty white. On PDA surface sienna to luteous, reverse ochreous.

Type. AUSTRALIA, Victoria, near Gurdies Winery, Gurdies-St. Heller Road, The Gurdies, S38°22'49.8" E145°34'23.4", on leaves of Eucalyptus sp. (Myrtaceae), 7 Nov. 2014, P.W. Crous, J. Edwards & I.G. Pascoe (holotype CBS H-22624, culture ex-type CPC 25600 = CBS 141327; ITS sequence GenBank KX228289.1, LSU sequence GenBank KX228340.1, MycoBank MB817055).

Notes — On ITS Pseudophloeospora eucalyptorum is 98 % (612/625) similar to Pseudophloeospora eucalypti (CBS 128212; GenBank HQ599592). Morphologically, the two species can be distinguished in that on average the conidia of P. eucalypti are larger, (60–)65–75(–80) × (1.5–)2(–2.5) µm (Crous et al. 2010b).
Proxipyricularia asari
**Proxipyricularia asari** Crous & M.J. Wingf., sp. nov.

**Etymology.** Name refers to *Asarum*, the plant genus from which this fungus was collected.

**Classification — Pyriculariaceae, Magnaporthales, Sordariomyces.**

Ascomata separate, immersed, globose, brown, to 200 µm diam, with central papillate ostiole; wall of 2–4 layers of brown *textura angularis*. *Hamathecium* dissolving upon maturity, with some cells remaining among asci. *Asci* unitunicate, hyaline, smooth, 8-spored, subcylindrical, stipitate, apical mechanism refractive, but not straining in Meltzer’s, 50–75 × 10–12 µm. *Ascospores* biseriate, fusoid-ellipsoid, widest in middle, with taper towards subobtusely rounded ends, slightly curved to straight, 3-septate, pale brown, guttulate, (16–)18–20(–22) × (4–)5 µm. *Conidiophores* solitary, erect, straight to flexuous, unbranched, subcylindrical, brown, smooth, 1–8-septate, 55–200 × 3.5–5 µm. *Conidiogenous cells* integrated, terminal, apex somewhat swollen with numerous denticle-like loci, 1–1.5 µm tall and in diam, slightly thickened and darkened, 25–60 × 3.5–5 µm. *Conidia* solitary, pyriform, brown, finely verruculose, guttulate, granular, apex subobtusely rounded, with or without mucoid cap, base truncate, hilum 1.5 µm diam, darkened, thickened, 2-septate, (20–)22–24(–26) × (6.5–)7–8 µm.

**Culture characteristics — Colonies covering dish after 2 wk at 25 °C, with moderate aerial mycelium and smooth, even margins.** On MEA surface pale mouse-grey with patches of dirty white, reverse isabelline with patches of pale fuscous. On OA surface honey with patches of pale mouse grey. On PDA surface honey, reverse isabelline to honey.

**Typus.** **MALAYSIA**, Sabah, on leaves and stems of *Asarum* sp. (*Aristolochiaceae*), May 2015, M.J. Wingfield (holotype CBS H-22625, culture ex-type CPC 27444 = CBS 141328; ITS sequence GenBank KX228291.1, LSU sequence GenBank KX228361.1, *rpb1* sequence GenBank KX228368.1, *actA* sequence GenBank MB817056; ibid., CPC 27442 (ITS sequence GenBank KX228290.1, LSU sequence GenBank KX228341.1, *actA* sequence GenBank KX228360.1)).

**Notes —** On LSU *Proxipyricularia asari* is 99 % (736/740) similar to species of *Proxipyricularia*, *Neopyricularia* and *Pyricularia*. *rpb1* sequence is 92 % (900/978) similar to *Pyricularia ctenantheicola* (GR0001; GenBank KM485098.1) and 89 % (868/957) to *Proxipyricularia zingiberis* (HYZM201-0-1; GenBank KM485091.1), suggesting that this may even represent yet another genus in this complex (Klaubauf et al. 2014).
Diaporthe passifloricola
Diaporthe passifloricola Crous & M.J. Wingf., sp. nov.

Etymology. Name refers to Passiflora, the plant genus from which this fungus was collected.

Classification — Diaporthaceae, Diaporthales, Sordariomycetes.

Conidiomata (on pine needle agar; PNA) pycnidial, solitary, black, erumpent, globose, to 250 µm diam, with short black neck, exuding creamy droplets 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, 20–50 × 3–4 µm. Conidiogenous cells 7–20 × 1.5–2.5 µm, phialidic, cylindrical, terminal and lateral with slight taper towards apex, 1–1.5 µm diam, with visible pericentral thickening; collarette not observed. Paraphyses not observed. Alpha conidia aseptate, hyaline, smooth, guttulate, fusoid-ellipsoid, tapering towards both ends, apex subobtuse, base truncate, 1–1.5 µm diam, with visible periclinal thickening; collarette not observed. Beta conidia spindle-shaped, aseptate, smooth, hyaline, apex acutely rounded, base truncate, tapering from lower third towards apex, curved, (20–)22–25(–27) × 1.5(–2) µm.

Culture characteristics — Colonies covering dish after 2 wk at 25 °C, with even, smooth margins, and fluffy aerial mycelium. On MEA surface dirty white, reverse luteous to ochreous. On OA surface dirty white. On PDA surface dirty white, reverse saffron.

Typus. MALAYSIA, Kota Kinabalu, on leaf spots of Passiflora foetida (Passi- floraceae), May 2015, M.J. Wingfield (holotype CBS H-22626, culture ex-type CPC 27480 = CBS 141329; ITS sequence GenBank KJ197284.1, LSU sequence GenBank KX228343.1, his3 sequence GenBank KX228367.1, tub2 sequence GenBank KX228387.1, MycoBank MB817057).

Notes — On ITS Diaporthe passifloricola is 98 % (556/567) similar to D. miriciae (BRIP 56918a; GenBank KJ197284.1) and 90% (466/519)–93 % (402/430) similar to five sequences of ‘Phomopsis’ tersa deposited on GenBank (e.g. KF516000.1 and JQ585648.1). The his3 sequence is 100 % (380/380) identical to D. absenteum (LC3564; GenBank KP293559.1) and 99% (378/380) to the sterile Diaporthe ‘sp. 1 RG-2013’ (LGMF947; GenBank KC343687.1), whereas the tub2 sequence is 99 % (513/517) to the sterile Diaporthe ‘sp. 1 RG-2013’ (LGMF947; GenBank KC344171.1) and 99% (589/595) to D. miriciae (BRIP 56918a; GenBank KJ197264.1). Although alpha conidia of D. miriciae are similar in size ((6–)7.5(–9) × 2–2.5(–3) µm), beta conidia are larger (20–35 × 1.0–1.5 µm) and conidiophores are shorter (10–20 × 1.5–3 µm) (Thompson et al. 2015). Other species previously reported from Passiflora include D. passiflorae (conidia 14–20 × 1.5–2 µm; Crous et al. 2012a) and ‘Phomopsis’ tersa (conidia 6.5–7.5 × 2.5 µm) (Sutton 1980). ‘Phomopsis’ tersa has alpha conidia of similar dimensions, but has much larger conidiomata (to 650 µm diam), shorter conidiophores (to 15 µm long) and lacks beta conidia (Sutton 1980).

Colour illustrations. Flower of Passiflora foetida; conidiomata sporulating on PNA, conidiophores, beta and alpha conidia. Scale bars: conidiomata = 250 µm, all others = 10 µm.
Diaporthe ocoteae
Fungal Planet description sheets

Diaporthe ocoteae Crous & M.J. Wingf., sp. nov.

Etymology. Name refers to Ocotea, the plant genus from which this fungus was collected.

Classification — Diaporthaceae, Diaporthales, Sordariomycetes.

Conidiomata (on pine needle agar; PNA) pycnidial, solitary, black, erumpent, globose, to 300 µm diam, exuding creamy droplets 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, 15–35 × 2.5–4 µm. Conidiogenous cells 7–15 × 2–3 µm, phialidic, cylindrical, terminal and lateral with slight taper towards apex, 1.5 µm diam, with visible periclinal thickening; collarette not flared, up to 1 µm long when present. Paraphyses cylindrical, hyaline, smooth, 1–6-septate, 30–80 × 2–3 µm. Alpha conidia aseptate, hyaline, smooth, guttulate, fusoid, tapering towards both ends, apex subobtuse, base subtruncate, (8–)9–10(–13) × (2–)2.5–3 µm. Gamma conidia not observed. Beta conidia not observed.

Culture characteristics — Colonies covering dish after 2 wk at 25 °C, with sparse to moderate aerial mycelium. On MEA surface dirty white with patches of pale mouse grey, reverse umber with patches of luteous. On OA surface pale luteous with patches of umber. On PDA surface and reverse pale luteous with patches of pale mouse-grey.

Typus. FRANCE, La Réunion, on leaves of Ocotea obtusata (Lauraceae), 6 Mar. 2015, P.W. Crous & M.J. Wingfield (holotype CBS H-22627, culture ex-type CPC 26217 = CBS 141130; ITS sequence GenBank KX228293.1, LSU sequence GenBank KX228344.1, tub2 sequence GenBank KX228388.1, MycoBank MB817058).

Notes — Based on LSU sequence data Diaporthe ocoteae is 99 % similar to species of Diaporthe and Phaeocytostroma (Lamprecht et al. 2011, Rossman et al. 2015) and based on ITS < 95 % and tub2 < 90 % similar to presently known species of Diaporthe. As far as we could establish, no Diaporthe sp. has thus far been described from Ocotea and hence Diaporthe ocoteae is introduced as a new species.

Colour illustrations. Forest on La Réunion; conidiomata sporulating on PNA, conidiophores and conidia. Scale bar = 10 µm.
Phaeosphaeria breonadiae
Fungal Planet 440 – 4 July 2016

**Phaeosphaeria breonardiae** Crous & Jol. Roux, *sp. nov.*

**Etymology.** Name refers to *Breonadia*, the plant genus from which this fungus was collected.

**Classification.** *Phaeosphaeriaceae, Pleosporales, Dothideomycetes.*

Leaf spots prominent on hypophyllous leaf surface, subcircular, medium brown, erumpent, with raised margin, 3–7 mm diam, with immersed black pseudothecia; upper leaf surface with pale green spot, lacking any ascomata. *Ascomata* globose to papillate, dark brown with central darker brown ostiole, up to 30 µm diam, solitary, but commonly aggregated in a cluster, joined by stromatic tissue, up to 250 µm diam; wall of several layers of brown *textura angularis*. *Asci* short stipitate, bitunicate, cylindrical-ellipsoid, with obtuse apex and small apical chamber, 35–60 × 8–11 µm, 8-spored, straight to irregularly curved. *Pseudoparaphyses* intermingled among asci, hyaline, septate, anastomosing, hyphae-like, 2.5–3.5 µm diam. *Ascospores* bi- to triseriate in asci, fusoid-ellipsoidal with obtuse ends, 3-septate, constricted at median septum, second cell from apex swollen, medium brown, smooth, guttulate to granular, (16–)18–20(–21) × (3.5–)4–5 µm; ascospores are homothallic and produce the sexual morph in culture; ascospores deforming somewhat at germination, brown, finely roughened, with germ tubes growing parallel to the long axis of the spore.

Culture characteristics — Colonies reaching up to 40 mm diam after 2 wk at 25 °C, with spreading, flat surface; margins uneven, feathery; aerial mycelium absent to sparse. On MEA surface dirty white to pale luteous, reverse luteous. On OA surface luteous. On PDA surface luteous, reverse saffron.

**Typus.** **SOUTH AFRICA.** Limpopo Province, Wolkberg, on leaves of *Breonadia microcephala* (Rubiaceae), Jan. 2015, J. Roux (holotype CBS H-22631, culture ex-type CPC 25944 = CBS 141334; ITS sequence GenBank KX228294.1, LSU sequence GenBank KX228345.1, tef1 sequence GenBank KX228379.1, MycoBank MB817062).

Notes — At least three species are present on these lesions. One of these resembled *Teratosphaeria*, another having aseptate ascospores and the third being the *Phaeosphaeria* ascomycete described here. LSU sequence data places *Phaeosphaeria breonardiae* with 98 % identity in *Phaeosphaeria*. Based on ITS, it is 99 % (564/566) similar to ‘*Phoma sp. 2’ TMS-2011 voucher SC12d10p12-12 (GenBank HQ631048.1), an isolate obtained from decaying sugarcane in the USA (Shrestha et al. 2011). The isolate did not produce the asexual morph in culture, but based on its DNA sequence, it appears to be the same, or closely related species to the USA isolate (Shrestha et al. 2011). The tef1 sequence did not yield results showing high similarity to other fungi.

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Alternaria quercicola
Alternaria quercicola Woudenb. & Mirab., sp. nov.

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

**Classification.** Pleosporaceae, Pleosporales, Dothideomycetes

Associated with shothole disease symptoms on leaves. Infected tissues die and cannot expand as the leaf continues to grow, eventually tearing out, creating the typical disease symptoms. Primary conidiophores solitary, smooth, straight to slightly curved, septate, pale brown with a hyaline tip, (16–)21–37–(48) × 3–4(–5) µm, bearing 0–1 geniculate conidiogenous extensions with darkened conidiogenous loci. Conidia solitary or in short chains, simple or branched, pale olive-brown, (narrowly) ovoid to obpyriform, primary conidia (25–)31–51–(57) × (6–)8–11(–12) µm, with 3–8 transverse septa and occasionally 1 oblique or longitudinal septa, rough walled at the lower sections and smooth walled at the top sections. The conidial body sometimes constricted near thickened and darkened transverse septa. Conidia can form an apical secondary conidiophore, which can again form a geniculate conidiogenous extension. Sexual morph not observed.

Culture characteristics — After 7 d cultures on SNA flat, fimbriate, colourless, aerial mycelium sparse, colonies reaching 50 mm diam; cultures on PCA flat, entire, colourless, aerial mycelium sparse, colonies reaching 60 mm diam.

**Typus.** Iran, Fars province, on leaves of Quercus brantii (Fagaceae), 3 May 2013, M. Mirabolfathy (holotype CBS H-22640, culture ex-type CPC 26163 = CBS 141466; ITS sequence GenBank KX228295.1, LSU sequence GenBank KX228346.1, gapdh sequence GenBank KX228362.1, MycoBank MB817068); ibid., CPC 26164, CPC 26165 (ITS, LSU, gapdh sequences GenBank KX228296.1–KX228297.1, KX228347.1–KX228348.1, KX228363.1–KX228364.1).

Notes — Species of Alternaria are commonly associated with leaf spot, postharvest and other diseases of various crops. Recent molecular studies have revealed that species of the genus cluster in several distinct species clades, now referred to as sections, which places A. quercicola within section Infectoria (Woudenberg et al. 2013, 2014, 2015). Based on the gene loci sequenced, A. quercicola is clearly distinct from other taxa in the Infectoria complex. Alternaria querci represents a potentially similar species occurring on Fagaceae in China (Zhang et al. 1999). Unfortunately, no culture was available for study, and the description was insufficient to make a good comparison.

Colour illustrations. Iran, Quercus brantii (Persian oak) tree; conidiophores, with conidiogenous cells and conidia. Scale bars = 10 µm.
Stemphylium beticola
**Stemphylium beticola** Woudenb. & Hanse, *sp. nov.*

*Etymology.* Named after the plant genus from which it was collected, *Beta*.

*Classification.* *Pleosporaceae, Pleosporales, Dothideomycetes.*

**Conidiophores** solitary, straight to flexuous, occasionally branched, septate, smooth, pale brown, (41–)45–72(–88) × 4–5 μm, bearing 1–3 darkened percurrent rejuvenation sites. **Conidigenous cells** swollen at the apex, darkened, 5–6 μm wide. **Conidia** solitary, conidium body pale olive-brown, verrucose, ellipsoid to cylindrical, (21–)22–26(–30) × (13–)14–16(–18) μm, L/W = 1.6, with 2–4 *transverse septa* and 1–3 *longitudinal* and 0–2 *oblique septa* per transverse sector. Constricted at 1–2 darkened transverse septa. Occasionally with an apical **secondary conidiophore** observed on agar, pseudothecia globose, ellipsoid or irregular, single or aggregated, ranging from 100–300 μm tall.

**Culture characteristics.** — After 7 d cultures on SNA flat, fimbriate, colourless with abundant black ascomatal initials in the agar, aerial mycelium sparse, white, colonies reaching 45–55 mm diam; cultures on PCA flat, entire to undulate, colourless with abundant black ascomata in the agar, aerial mycelium sparse, floccose, (greenish) olivaceous; colonies reaching 50–60 mm diam.

**Typos. Netherlands.** Noord-Brabant, Langenboom, on leaves of *Beta vulgaris* (Amaranthaceae), 17 Aug. 2011, P. Wilting (holotype CBS H-22486, culture ex-type GV11-265a = CBS 141024; ITS sequence GenBank KU850520, LSU sequence GenBank KX228349.1, gapdh sequence GenBank KU850667, MycoBank MB815876).

Additional specimens examined. **Netherlands,** Drenthe, Eerste Exloërmond, on leaves of *Beta vulgaris*, 11 Sept. 2012, B. Hanse, GV12-474a1 = CBS 141026; ITS sequence GenBank KU850522, gapdh sequence GenBank KU850669; Groningen, Nieuwe Pekela, on leaves of *Beta vulgaris*, 17 July 2012, J. Lingbeek, GV12-288-2 = CBS 141025; ITS sequence GenBank KU850521.1, gapdh sequence GenBank KU850668.1.

**Notes.** — In 2007 a new leaf spot disease was first discovered on sugar beet (*Beta vulgaris*) in the Netherlands, which spread rapidly throughout the country in the following years (Hanse 2013). Currently, the disease has been detected in Belgium, Denmark, Germany, Poland, Slovakia, Sweden and the UK (unpubl. data). The disease manifests in June–August and starts with small, irregular, yellow spots on the leaves of sugar beet. The yellow spots become necrotic from the centre of the lesion outwards with tissue turning brown. The spots spread over all the leaves of the plant, and in case of severe infestation, heavily infected leaves will die. Due to this loss of leaves the canopy, and thus sugar yield, declines. A *Stemphylium* sp. was detected as the causative agent and additional field trials showed that the fungus is hard to control with the current registered fungicides in the Netherlands (Hanse et al. 2015). Host range tests under climate room conditions showed that the fungus was not restricted to sugar beet, but could also infect potato (*Solanum tuberosum*), white mustard (*Sinapis alba*), red beet (*Beta vulgaris*), spinach (*Spinacia oleracea*) and fat hen (*Chenopodium album*) (Hanse et al. 2015). Blast searches of the ITS and gapdh gene sequences give high similarity hits with isolates CBS 116599 (P107), CBS 135690 (P212) and CBS 133892 (P221), which were regarded a new *Stemphylium* species by Inderbitzin et al. (2009). Here we describe the species as *Stemphylium beticola*.

**Colour illustrations.** The Netherlands, *Beta vulgaris* field; yellow leaf spots on *Beta vulgaris*; ascomata; conidiophores with conidigenous cells and conidia. Scale bars: ascomata = 100 μm, others = 10 μm.

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**Maximum likelihood tree based on a multiple sequence alignment of the ITS and gapdh sequences containing 1 083 characters in total.** The analysis was run with RAxML v. 7.2.6 (Stamatakis & Alachiotis 2010) using the GTR+CAT model and included 500 bootstrap replicates. The tree was rooted to *S. xanthosomatis*. Bootstrap support values are indicated at the nodes.

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Rasamsonia columbiensis Jurjević, Hubka & S.W. Peterson, sp. nov.

Etymology: The species is named for the type locality, District of Columbia, USA.

Classification — Trichocomaceae, Eurotiales, Eurotomyces.

On MEA: Stipes predominantly arising from aerial hyphae, verru- cose, (50–)100–250–(300) × 2.5–4 μm, terminating in ap- precised biverticillate structures, occasionally monoverticillate or terticellate, branches on substratal and intercalary posi- tions, appearing as separate stipes, short 5–50–(75) × 2.5–4 μm; metulae in terminal whorls of 2–5, verrucose, 8–12–(17) × 2.5–4.5 μm; phialides with long tapering collula, acerose, occasionally rough (8–)9–12–(16) × 2.5–3.5–(5) μm; conidia smooth walled, cylindrical to ovoid, (2.5–)3–4–(7) × 2.5–4.5 μm diam.

Culture characteristics — (in darkness, 25 °C after 7 d): Colonies on malt extract agar (MEA) 30–31 mm diam, colony texture velutinous to slightly floccose, mycelium white, sporulation abundant, cream-buff to chamois (R30), exudate absent, soluble pigments absent, reverse cream-buff to chamois (R30). Colonies on Czapek yeast autolysate agar (CZA) 14–15 mm diam, colony texture slightly floccose, mycelium white, at margins c. 2–3 mm broad zone of submerged growth, sporulation abundant, conidia en masse cream-buff to chamois (R30), exudate absent, soluble pigments absent, reverse cream-buff to chamois (R30). Colonies on creatine sucrose agar (CREA) 19–20 mm diam, colony texture velutinous to slightly floccose, mycelium white, at margins c. 4–5 mm broad zone of submerged growth, sporulation abundant, cream-buff to chamois centrally (R30). Colonies on Czapek yeast autolysate agar with 5 % NaCl 2–3 mm diam, sporulation absent.

Colonies on Czapek yeast autolysate agar (CZA) 14–15 mm diam, moderate to good growth, no acid production, mycelium white, predominantly submerged, sporulation good at the centre of the colony. Growth rates at different temperatures: colonies on CZA/MEA (in mm) 20 °C 9–10/19–20; 30 °C 16–17/43–45; 35 °C 15–17/38–39; 37 °C 15–16/30–31; 41 °C 9–10/19–20; 45 °C no growth. Colonies on MEA at 41 °C radially moderate deep sulphate, no exudate, reverse chamois to Isabella colour (R30); on CZA at 41 °C, very poor sporulation, mycelium white, colony texture fungicolous to lightly floccose, exudate absent, soluble pigments absent.

Notes — BLAST analysis of the ITS and β-tubulin sequences of Rasamsonia columbiensis with reference sequences (Hou- braken et al. 2013, Tanney & Seifert 2013) gave the closest match with the ex-type strain of R. brevistipitata CBS 128785T: ITS 96 %, β-tubulin 87 %. Rasamsonia columbiensis fails to grow at 45 °C, while closely related R. brevistipitata grows. Also R. columbiensis has larger spores ((2.5–)3–4–(7) × 2.5–4.5 μm) than R. brevistipitata ((2–)2.5–3–(3.5) × 1.7–2.1 μm).

Best scoring maximum likelihood tree (T92+G substitution model) based on sequences of the ITS rDNA showing relationships of Rasamsonia columbiensis to other Rasamsonia species. The tree was constructed with the IQ-TREE v. 1.4.0 (Nguyen et al. 2015). Dataset contained 21 taxa and a total of 697 characters with 169 characters variable and 125 parsimony-informative. Support values at branches were obtained from 1 000 bootstrap replicates. Only bootstrap support ≥ 70 % are shown on the branches; ex-type strains are designated by a superscript 1.
Microascus longicollis
Microascus longicollis was associated with a case of suspected onychomycosis of the great toenail of a 48-yr-old female living in the Czech Republic. The fungus was isolated in pure culture from the nail scrapings collected during the first visit and the direct microscopic examination was positive for hyphae. The etiological significance of the isolate could not be confirmed because the second mycological examination (negative) was performed several months after initiation of the treatment at the time of significant clinical improvement (naftifine hydrochloride: 2 mo, without effect; changed to ciclopirox olamine: effective). Repeated isolation of the same non-dermatophyte fungus in pure culture is required for confirmation of its etiological role (Summerbell et al. 2005).

**Microascus longicollis** Hubka, Lysková, Cmokova & M. Kolařík, *sp. nov.*

**Etymology.** Refers to the long annellate zone.

**Classification.** *Microascaeae, Microascales, Sordariomycetes.*

Ascomata immersed, less commonly superficial, predominantly formed in the colony centre, globose or subglobose, (60–)80–230 μm diam, without ostiolar neck, black, glabrous, ripening after 2–3 weeks of cultivation on OA, ascomata are absent or develop tardily on other media (3–6 weeks on MEA and PDA), peridium with a *textura angularis*. Ascii globose, subglobose, ellipsoidal or pyriform, 10–15(–17.5) × 9–13.5 μm. Ascospores lemon-shaped, pale brown, 4.5–5.5 × 3–4 μm. *Conidiophores* represented by individual conidiogenous cells (annellides) on the hyphae, sometimes supported by a basal cell of 3.5–5 × 2–3 μm, bearing 1–4 annellides. *Anellides* with a swollen base, 4.5–7(–9) × 2.5–3.5(–4.5) μm, tapering to a cylindrical annellated zone, up to 30 μm long and 1.5–2.5 μm wide. The celled, thick-walled, hyaline to pale brown, brown in mass, ovate, pyriform or ellipsoidal, with a rounded or pointed apex and truncate base, smooth, 3.5–5(–6) × 2.5–3.5 μm. *Chlamydospores* globose to ellipsoidal, 5–10 × 6–6.5 μm.

**Culture characteristics.** — (in the dark, 25 °C after 14 d): Colonies on OA attained 25–27 mm diam, flat, predominantly submerged, greyish brown in the centre (ISC-NBS No. 61) due to production of black ascomata, reverse greyish brown (No. 61) in the colony centre. Colonies on PCA attained 24–28 mm diam, flat, predominantly submerged except of granular central part, dark greyish yellow (No. 91) to pale yellowish green (No. 121), reverse pale yellowish green (No. 121), centrally raised, slightly radially furrowed, surrounded by 5 mm broad submerged zone, light greyish olive (No. 109) to greyish yellowish green (No. 122), reverse greyish olive. Colonies on MEA attained 23–27 mm diam, downy, centrally raised, slightly radially furrowed, surrounded by 5 mm broad submerged zone, light greyish olive (No. 109) to greyish yellowish green (No. 122), surrounded by 5 mm broad submerged zone, reverse dark greyish yellow (No. 91) to greyish brown (No. 61). Colonies on MEA after 7 d at 37 °C and 40 °C attained 12–15 and 4–6 mm diam, respectively.

**Type.** CZECH REPUBLIC, Prague, ex toenails of 48-yr-old female with suspected onychomycosis, 20 Dec. 2013, P. Lysková (holotype PRM 935209, isotype PRM 935210, culture ex-type CCF 5317 = CBS 141177; ITS and LSU sequence GenBank LT548275, β-tubulin sequence GenBank LT548282, TEF-1a sequence GenBank LT548287, MycoBank MB816867).

**Notes.** — The ability of this species to grow at 40 °C, ascomata without ostiolar neck, lemon-shaped ascospores and annellides with annellate zone up to 30 μm long make *M. longicollis* well distinguishable from all species accepted to date (Sandoval-Denis et al. 2016, Jagielski et al. 2016).

**Colour illustrations.** Czech Republic, toenail with suspected onychomycosis; Colonies, top to bottom: 21-d-old colonies of Microascus longicollis growing on OA, MEA and PDA at 25 °C; micromorphology, left to right: annellides, conidia (top row), ascospores (bottom row), ascomata, asc. Scale bars = 10 μm, scale bar of the subfigure with ascomata = 100 μm.

**Best scoring maximum likelihood tree (GTR+G+I substitution model) based on sequences of the TEF-1 a showing the relationship of M. longicollis to other Microascus species.** The tree was constructed with IQ-TREE v. 1.4.0 (Nguyen et al. 2015). Dataset contained 30 taxa and a total of 812 characters of which 226 were variable and 166 parsimony-informative. Support values at branches were obtained from 1 000 bootstrap replicates. Only bootstrap support ≥ 70 % are shown on the branches; ex-type strains are designated by a superscript 7. **

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Paecilomyces tabacinus
**Paecilomyces tabacinus** Jurjević, Hubka & S.W. Peterson, sp. nov.

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

**Classification.** Named after the host from which it was isolated, Tobacco.

**Colour illustrations.** Tobacco plant; 7-d-old cultures of *Paecilomyces tabacinus* on MEA (25 °C - top, 37 °C - middle, 41 °C - bottom), chlamydospores, conidia and conidiophores on MEA. Scale bars = 10 µm.

**Culture characteristics.** (in darkness, 25 °C after 7 d): Colonies on malt extract agar (MEA) 74–88 mm diam, colony texture floccose, mycelium white to sayal-brown (R29), sporulation very good, conidia *en masse* light-buff to warm-buff (R15), exudate absent, soluble pigments absent, reverse Isabella colour to brownish olive (R30). Colonies on Czapek yeast agar with 20 % sucrose (CY20S) 9–11 mm diam, sporulation very poor, mycelium white, submerged, reverse uncoloured. Colonies on Dichloran glycerol agar (DG18) 8–10 mm diam, sporulation very poor, mycelium white, submerged, reverse uncoloured. No growth on CYA with 5 % NaCl. Colonies on Oatmeal agar (OA) 37–39 mm diam, colony texture floccose, mycelium white, sporulation very good, conidia *en masse* light-buff to warm-buff (R15), exudate absent, soluble pigments absent. Colonies on creatine sucrose agar (CREA) 40–42 mm diam, poor to moderate growth, no acid production, mycelium white, colony texture floccose to submerged into the agar, sporulation poor to good. On MEA (colony diam in mm) at 30 °C > 90; 35 °C > 90; 37 °C 68–71; 41 °C 18–19; no growth at 45 °C.

**Typus.** USA, North Carolina, Durham, tobacco leaves, greenhouse, 5 June 2015, Z. Jurjević (holotype BP1 910044, cultures ex-type CBS 141098 = CCF 5290, ITS and LSU sequence GenBank LT548280, β-tubulin sequence GenBank LT548286, calmodulin sequence GenBank LT548288, MycoBank MB816870).

Notes — BLAST searches of the sequences of *P. tabacinus* showed highest degree of similarity with *Byssochlamys zollerniae* CBS 374.70 %; ITS 97 %, β-tubulin 94 %, calmodulin 95 %. Another strain with an identical ITS sequence (GenBank GU-934506) originated from roots of *Salix*, Canada (Corredor et al. 2012).

*Paecilomyces tabacinus* is distinguished by production of elipsoidal or fusiform conidia and numerous coarsely roughened chlamydospores (smooth, finely roughened or absent in the majority of species). Closely related *B. zollerniae* also produces warted chlamydospores but can be differentiated by the production of sexual state in culture and by having smaller conidia.

Best scoring maximum likelihood tree (T92+G substitution model) based on sequences of the ITS rDNA region showing relationship of *P. tabacinus* to *Paecilomyces* and *Byssochlamys* species belonging to Eurotioidae (Samson et al. 2009). The tree was constructed with IQ-TREE v. 1.4.0 (Nguyen et al. 2015). Dataset contained 19 taxa and a total of 588 characters with 138 characters variable and 79 parsimony-informative. Support values at branches were obtained from 1 000 bootstrap replicates. Only bootstrap support ≥ 70 % are shown on the branches; ex-type strains are designated by a superscript 1.
Chrysosporium echinulatum
**Chrysosporium echinulatum** Hubka, Mallátová, Cmokova & M. Kolařík, sp. nov.

**Etymology.** Refers to the surface ornamentation of conidia.

**Classification —** Onygenaceae, Onygenales, Eurotiomycetes.

Hyphae hyaline, septate, smooth-walled, 1.5–5 µm wide, straight, sparsely branched. Conidia hyaline, yellowish in mass, terminal and lateral conidia sessile or on short right-angled side protrusions (occasionally swollen) of variable length, solitary or in chains, initially smooth-walled, nearly all becoming echinulate at maturity, obovoid to clavate, 1-celled, 4.5–7 × 2.5–4 µm. Intercalary conidia solitary or in short chains, smooth-walled, barrel-shaped to ellipsoid. Chlamydospores absent. Racquet hyphae present. Sexual morph not observed.

**Culture characteristics —** (in the dark, 25 °C after 14 d): Colonies on potato dextrose agar (PDA) attained 28–45 mm diam, floccose, flat or with slightly elevated centre, white with light yellow (NBS-ISCC No. 86) to pale orange yellow (No. 71) colony centre, reverse moderate orange yellow (No. 71). Colonies on malt extract agar (MEA) attained 33–36 mm diam, morphology similar to PDA with more pronounced submerged growth at the colony margins. Colonies on phytone yeast extract agar (PYE) attained 28–37 mm diam, morphology similar to PDA. Colonies on oatmeal agar (OA) attained 35–45 mm diam, flat, downy, pale yellowish pink (No. 31), reverse uncoloured. No growth at 35 °C.

**Typus.** CZECH REPUBLIC, České Budějovice, ex skin scales from the sole of a 35-yr-old woman, 21 Aug. 2012, N. Mallátová (holotype PRM 935095, isotype PRM 935096, culture ex-type CCF 4652 = UAMH 11824 = CBS 141178; ITS and LSU sequence GenBank LT548276, MycoBank MB816868).

Notes — BLAST analysis with the ITS rDNA region sequence gave closest hits to *C. pannicola* CBS 116.63 (98 %, 526/539 bp, GenBank AJ005368), *C. fluviale* IMI 378764 (92 %, 498/540 bp, GenBank AJ005367) and *C. minutisporosum* CBS 101577 (91 %. 468/515 bp, GenBank AJ131689). LSU rDNA showed 99 % similarity (548/555 bp) to *Aphanoascus durus* CBS 118.85 (GenBank AB075345) and *A. terreus* CBS 342.64 (556/564 bp, GenBank KC989709); other species showed 95 % or lower similarity.

*Chrysosporium echinulatum* resembles *C. pannicola* (= *C. evolocanii*) and can be distinguished by the inability to grow at 35 °C and smaller conidia. *Chrysosporium echinulatum* was associated with a case of suspected tinea pedis in a 35-yr-old woman living in the Czech Republic. The fungus was isolated in pure culture from the skin scales collected during the first visit and the direct microscopic examination was positive for hyphae. The mycological examination was not repeated and the etiological significance of the fungus is unclear. We believe that the infection was in fact caused by a dermatophyte, which was not isolated or overgrown by the *Chrysosporium* isolate.
**Fungal Planet 447 – 4 July 2016**

*Scleroderma capeverdeanum* M.P. Martín, M. Dueñas & Telleria, *sp. nov.*

**Etymology.** The name refers to the country where the holotype was collected.

**Classification.** *Sclerodermataceae, Boletales, Agaricomycetes.*

Macroscopic characteristics — *Basidiomes* epigeanous, depressed globose to subglobose, 0.8–20 mm diam., sessile (all the sizes from dry specimens); the base attached to the substrate by a tuft of mycelium and rhizomorphs. *Peridium* thin (up to 1 mm thick), 2-layered: external layer pale yellowish to yellowish brown (colour 250; Séguy 1936) covered by dark brown scales (colour 701), very thin in young specimens, leaving the surface finely areolated; internal layer whitish. *Dehiscence* by an irregular and lacerate apical pore. *Gleba* compact when young, becoming powdery when old, blue greyish (colour 493) to grey-violet (colour 660).

Microscopic characteristics — *Basidiospores* globose, 8.5–9.5 (–10.5) µm diam., including ornamentation, densely echinulate (ornamentation 0.5–1 µm high), dark brown in 5% KOH. Outer layer of *peridium* composed of interwoven hyphae, hyaline to yellowish, 3.5–4 µm diam.; the inner layer composed of interwoven hyphae, hyaline, 3–5 µm diam., with clamp-connections.

**Typus.** CAPE VERDE, Santiago Island, Parque Natural Serra de Malagueta, Concejo Sta. Catarina, alt. 907 m, N15°10'28" W28°40'37", on a slope under *Furcraea foetida* and *Lantana camara*, 20 Sept. 2010, M.P. Martín MPM3238 (holotype MA-Fungi 87406, ITS sequence GenBank KU747111, LSU sequence GenBank KU747110, MycoBank MB816518).

Additional material examined of *Scleroderma bovista.* CAPE VERDE, Santiago Island, Parque Natural Serra de Malagueta, Concejo Sta. Catarina, alt. 914 m, N15°10'28" W28°40'37", on a slope, 20 Sept. 2010, M.P. Martín MPM3241 (MA-Fungi 87407, ITS sequence GenBank KX017590).

Notes — Mature basidiomes of *Scleroderma capeverdeanum* show a peridium with brown squamules, similar to *Scleroderma verrucosum*, a species widely distributed in Azores, Canaria Islands, Madeira and Morocco (Kreisel 2001), also with echinulate spores; however, in young specimens, the *peridium* is finely areolated as in *Scleroderma bovista*, but this species has reticulate spores. Specimens of *S. capeverdeanum* were found in the same locality as collection MA-Fungi 87407 of *Scleroderma bovista*, as indicated in the additional material examined. Based on a megalast search of NCBI GenBank nucleotide database, the closest hits using ITS sequences of *S. capeverdeanum* were two sequences of Chinese specimens collected under *Eucalyptus grandis* (GenBank HM237117 and HM237114), and misidentified as *S. polyrhizum* and *S. aurantium*, respectively. In the ITS analyses *S. capeverdeanum* cluster with these two sequences from China, as a sister group of *S. dunensis*, a new species described from Brazil (this issue). Until now, no species of *Scleroderma* were reported from Cape Verde.

Strict consensus tree of 100 equally most parsimonious trees was obtained after heuristic search (PAUP v. 4.0a147) of ITS nrDNA sequences. The two new *Scleroderma* species described in this issue are marked with rectangles: *S. capeverdeanum* and *S. dunensis* (see Fungal Planet 448). New sequences of *S. bovista* from Cape Verde, and *S. nitidum* from Brazil are marked in bold. The accession number from EMBL/GenBank or UNITE databases are indicated. Bootstrap values greater than 50% are indicated on the branches. As in our preliminary studies (Phosri et al. 2009, Rusevska et al. 2014), *Pisolithus arhizus* was included as outgroup.

**Colour illustrations.** Cape Verde, Parque Natural Serra de Malagueta, where the species was collected (M.T. Telleria); basidiome (holotype MA-Fungi 87406), echinulate spores (holotype MA-Fungi 87406). Scale bars: basidiomata = 0.5 cm; spores = 1 µm.

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**Scleroderma dunensis** B.D.B. Silva, Sulzbacher, Grebenc, Baseia & M.P. Martin, sp. nov.

**Etymology.** The name refers to the type locality, Parque Estadual Dunas do Natal.

**Classification — Sclerodermataceae, Boletales, Agaricomycetes.**

Macroscopic characteristics — **Basidiomes** epigeous, depressed subglobose to subglobose, 12–17 mm diam, sessile or shortly pseudopodiate, up to 2 mm (all the sizes from dry specimens), the base attached to the substrate by a tuft of mycelium and rhizomorphs. **Peridium** composed of two layers, thin, up to 2 mm thick, pale yellowish to yellowish brown (colour 4A2, 4B4; Kornerup & Wanscher 1978), surface smooth towards the base and covered by small and thin scales on top, dark brown (colour 5D4, 5E4). **Dehiscence** by an irregular and lacerate apical pore. **Gleba** compact when young, becoming powdery when old, greyish (colour 5E4) brownish (colour KWS54).

Microscopic characteristics — **Basidiospores** globose to subglobose, 8.3–10.7 × 8.0–10.8 μm diam, including ornamentation, echinulate, composed of dense narrow pyramidal warts, 0.9–1.3 μm high, dark brown in 5% KOH. Outer layer of peridium composed of interwoven hyphae, hyaline to yellowish, 2.5–4.0(–5.0) μm diam; the inner layer composed of interwoven hyphae, hyaline, 3.0–5.5 μm diam, with clamp-connections.

**Typus.** Brasil, Rio Grande do Norte, Natal, Parque Estadual Dunas do Natal, alt. 73 m, S06°22′47″ W35°01′40″, on soil close to Coccoloba sp., 14 May 2010, B.D.B. Silva & A.G. Leite (holotype UFRN-Fungos 2033, isotype MA-Fungi 47736, ITS sequence GenBank KU747112, LSU sequence GenBank KU747105, MycoBank MB614792).

Additional material examined. Brasil, Rio Grande do Norte, Baía Formosa, Reserva Particular do Patrimônio Natural Mata Estrela, alt. 52 m, S06°22′79″ W35°01′23″ on soil close to Coccoloba sp., 12 June 2010, B.D.B. Silva et al. (UFRN-Fungos 1359, ITS sequence GenBank KU747113, LSU sequence GenBank KU747106); ibid., (UFRN-Fungos 1361, ITS sequence GenBank KU747114, LSU sequence GenBank KU7471107); ibid., 19 June 2010, B.D.B. Silva et al. (UFRN-Fungos 2035, ITS sequence GenBank KU747117); ibid., (UFRN-Fungos 2549, ITS sequence GenBank KU747115, LSU sequence GenBank KU747108); ibid., 14 July 2010, B.D.B. Silva et al. (UFRN-Fungos 2553, ITS sequence GenBank KU747118); Natal, Parque Estadual Dunas do Natal, alt. 73 m, S06°22′47″ W35°01′40″ on soil close to Coccoloba sp., 9 July 2013, M.A. Sulzbacher, T. Grebenc (UFRN-Fungos 2501, ITS sequence GenBank KU747119); ibid., (UFRN-Fungos 2499, ITS sequence GenBank KU747120); Paraíba, Reserva Biológica Guaribas, alt. 198 m, S06°44′50″ W35°08′40″ on soil close to Coccoloba sp., 27 July 2012, B.D.B. Silva et al. (UFRN-Fungos 2551, ITS sequence GenBank KU747116, LSU sequence GenBank KU747109); ibid., 30 June 2013, M.A. Sulzbacher (UFRN-Fungos 2206, ITS sequence GenBank KU747121).

**Notes — Scleroderma dunensis** is one of the most common species occurring on sand dunes from the Parque Estadual Dunas do Natal, growing usually close to Coccoloba spp. Several previous reports for this locality consider this species to be **S. nitidum** (Gurgel et al. 2008, Sulzbacher et al. 2013). **Scleroderma dunensis** resembles **S. areolatum**, **S. nitidum** and **S. verrucosum**, mainly by echinulate basidiospores and peridium opening by irregular dehiscence, differing fundamentally by larger basidiomes and spores in **S. areolatum** (15–30 mm diam; 10–15 μm), **S. nitidum** (20–25 mm diam; 7–11 μm) and **S. verrucosum** (25–30 mm diam; 9–12 μm) (Guzmán et al. 2013). However, the ITS nrDNA and LSU sequences of **S. dunensis** show greater similarity with a species from Cape Verde (see tree figure in **Fungal Planet 447**)) instead of **S. areolatum**, **S. nitidum** or **S. verrucosum**.

Colour illustrations. Brazil, Parque Estadual Dunas do Natal, Coccoloba sp. growing next to the locality where the type species was collected; a. peridium (holotype UFRN-Fungos 2033), details of the scales on top; b. basidiome (UFRN-Fungos 2033); c. cross section showing gleba (UFRN-Fungos 2033); d. echinulate spores (UFRN-Fungos 2035). Scale bars: a = 1 mm; b–c = 2 mm; d = 2 μm.

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Ganoderma mbrekobenum
**Ganoderma mbrekobenum** E.C. Otto, Blanchette, Held, C.W. Barnes & Obodai, sp. nov.

*Etymology.* Named after the Ghanaian Twi word ‘mbrekoben’, which translates to reddish brown mushroom.

*Classification.* Ganodermataceae, Polyporales, Agaricomycetes.

**Description.** Mature *basidiomata* annual, pileate, stipitate, dimitic, applanate, woody to corky when dried, homogenous context structure, pileus maroon to liver brown when dry, surface hard and glabrous, margin rounded, thickened, maroon to liver brown when dry. *Stipe* subcylindrical (> 5 cm), lateral, columnar, with one solitary column, maroon; borders with hymenophore thickened. *Pore surface* smooth, creamy to snuff brown when dry, pores 4–6 mm per mm, round to somewhat irregular and slightly elongated, 105–247 × 76–207 µm (av. 167.2 × 123.8 µm; SD 32, 26; n = 100), dissepiments 44–152 µm (av. 83.6 µm; SD 23; n = 100); tubes 0.1–0.7 mm long, dark brown. *Hyphal system* dimitic; generative hyphae slightly inconspicuous, branched, thin-walled and hyaline; skeletal hyphae most prevalent in the basidiocarp, occasionally branched, pale to dark brown, 2.5–7 µm thick, tapering towards the end. *Basidia* not observed. *Basidiospores* brown, ovoid to broadly ellipsoid with a truncate base, bitunicate, verruculose, 8–11.5 × 6–8 µm (av. 10.4 × 7.1 µm; SD 0.7, 0.4; n = 100), perispore thin; exospore with intermediate thick inter-walled pillars; endospore thick, dark brown. *Chlamydospores* not observed.

*Culture characteristics.* — No live culture obtained.

**Typus.** GHANA, Brong Ahafo and Greater Accra Regions, on angiosperms, June 2015, M. Obodai (holotype MIN 850481, paratype MIN 850482, holotype ITS sequence GenBank KX000896, LSU sequence GenBank KX000897, paratype ITS sequence GenBank KX000898, LSU sequence GenBank KX000899, holotype MycoBank MB816172).

The phylogenetic tree with *G. mbrekobenum* was constructed using the Maximum Likelihood plugin PHYML in Geneious R9 (http://www.geneious.com, Kearse et al., 2012), and the substitution model determined by jModelTest (Posada, 2008) according to Corrected Akaike Information Criterion (AICc). *Ganoderma enigmatica* (GenBank KR183855 and KR150678) is the outgroup. Bootstrap support values ≥ 50 % are given above branches. The phylogenetic position of *G. mbrekobenum* is indicated in bold. The *Ganoderma* species is followed by the sample ID and the three letter United Nations country code, in order of appearance ZAF: South Africa, GHA: Ghana, EGY: Egypt, IND: India, MYS: Malaysia, CHN: China, USA: United States.

**Notes.** *Ganoderma mbrekobenum* causes decay in the roots and trunks of angiosperm trees in the southern regions of Ghana. Sequences were downloaded from GenBank for phylogenetic analysis with *G. mbrekobenum* sequences using the program Geneious R9 (http://www.geneious.com, Kearse et al., 2012). The complete ITS sequence of the *G. mbrekobenum* holotype was used for the Blastn search. The results gave the highest score to an isolate *Ganoderma* sp. (EGDA, GenBank LN774971) from Egypt, with a single nucleotide difference. The next 14 Blastn hits were to *Ganoderma* sp. sequences from a single institution in India. The analysis included only the top three of these sequences, having four to six differences from the *G. mbrekobenum* holotype. A few isolated sequences with various *Ganoderma* species names had relatively high Blastn scores, but were excluded from the analysis because they did not align with their respective species and are likely *G. mbrekobenum*, or closely related. The closest legitimate *Ganoderma* species were *G. applanatum* and *G. fornicatum*, both with 94 % identity. Additional sequences of other recently described *Ganoderma* species from Africa (Coetzee et al., 2015, Crous et al. 2015b) were included in the analysis. The final alignment was edited by hand for alignment errors.

**Colour illustrations.** Ghana, Brong Ahafo Region, native tree species along the road of the Ayum forest (background); basidiocarp in the field with basidiocarps covering the pileus, basidiocarp in lab with basidiocarps cleaned off; skeletal hyphae, basidiospores by light microscopy and SEM. Scale bars = 3 cm (basidiocarps), 10 µm (microscopic structures).

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Geoglossum raitviiirii
**Geoglossum raitviirii** Fedosova & E.S. Popov, sp. nov.

**Etymology.** Named after the Estonian mycologist Ain Raitviir, in recognition of his contribution to the study of the Geoglossaceae from the Russian Far East.

**Classification — Geoglossaceae, Geoglossales, Geoglossomycetes.**

Ascocarps scattered to gregarious, clavate, stipitate, 2.2–4.5 cm tall, dark brown. **Ascigerous part** clavate, broadly clavate, 1/4–1/2 of the total ascocarp length, 0.5–1.8 cm long, black to dark brown, darker than the stipe, compressed, dumbbell-shaped or oval in cross section, sharply delimited from the stipe in fresh condition, in herbarium material smooth, ceraceous-pubescent due to prominent paraphyses tips extending from the hymenium. **Stipe** terete, compressed, brown, in fresh conditions lighter than the ascigerous part, dark brown and concolorous in herbarium material, rough, squamous. **Asci** clavate to broadly clavate, (161.5–)172.5–176.5(–191.5) × (21–)24.5–26.5–(31) μm (measured in KOH), Q = (5.5–)6.5–7.5(–8), 8-spored, with euamyploid apical ring and inamylloid wall in MLZ and IKI. **Ascos-** spores elongate-clavate, sub fusiform to fusiform, narrowed to apical cells of paraphyses, euamyloid apical ring and inamyloid wall in MLZ and IKI, Stipes pubescent due to prominent paraphyses tips extending from the stipe. **Hyphae of the stipe surface** straight, moderately septate, formed by chains of several pale brown cells, apical cells clavate.

**Habit, Habitat & Distribution —** In small groups on soil in broadleaf forests. The species is known only from two localities in Primorye, Russia.

*Typus.** Primorsky Kray, Terneysky District, Sikhote-Alin Nature Reserve, right side of the Pobednyaya River, the road from Marya ranger station to Ust-Shanduy ranger station, N45°14'19” E136°30'40”, 18 Aug 2013, A. Fedosova (holotype LE303983, ITS sequence GenBank KT936308, LSU sequence GenBank KU988891, MycoBank MB814883).

*Additional specimen examined.** Primorsky Kray, Khansky District, Kedrovaya Pad Nature Reserve, valley of the Kedrovaya River, vicinity of the main reserve station, broadleaf forest, on soil along a brook, 18 Aug 2005, E. Popov (LE291814, ITS sequence GenBank KT936309).

*Notes — Geoglossum raitviirii* is characterised by medium sized brown ascocarps with squamous or granulose stipes, which are normally lighter than the ascigerous part, relatively short and broad, 8-spored ascii, predominantly 7-septate ascospores, and long, swollen apical cells of the paraphyses. Among other species of Geoglossum with 7-septate ascospores it is most similar to *G. chamaecyparinum*, *G. variabilisporum*, and *G. lineare*. Geoglossum chamaecyparinum (Araujo & Iglesias 2014) shares similar morphology with *G. raitviirii*, but differs in more narrow and long ascii ((164.5–)181.5–196(–217) × (16–)19.5–23(–25.5) μm) and more narrow ascospores ((50–)72–82(–90) × (5–)6–(6.5) μm). Geoglossum variabilisporum can be recognised by smaller ascocarps (0.6–1.9 cm), narrower and shorter ascii ((124–)145.5–169(–187) × (15.5–)18.5–21(–24) μm) and by presence of the considerable number of ascospores with more than 7 septa (Araujo & Iglesias 2014). Geoglossum chamaecyparinum and *G. variabilisporum* are known from Spain, where they were found on sandy soil under Chamaecyparis lawsoniana. *Geoglossum lineare* described from pasture land in Sweden can be separated from *G. raitviirii* by the smooth viscid stipe of ascocarps, stout straight paraphyses, smaller ascii (140–155 × 13–16 μm) and 3–7-septate ascospores (45–65 × 4.5–5.5 μm) (Hakelie 1967).

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**Colour illustrations.** Primorsky Kray, Terneysky District, Sikhote-Alin Nature Reserve; spores, apical cells of paraphyses, amyloid reaction of the ascal apical ring, ascii, hyphae of the stipe surface, ascocarps (all from holotype), type locality. Scale bars = 1 cm (ascocarps), 10 μm (microscopic structures).

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Toxicocladosporium hominis
**Toxicocladosporium hominis** Sandoval-Denis, Gené & Deanna A. Sutton, *sp. nov.*

**Etymology.** Referring to the isolation source of the ex-type strain.

**Classification.** *Cladosporiaceae, Capnodiales, Dothideomycetes.*

Colonies sporulating on synthetic nutrient-poor agar. *Mycelium* branched, septate, smooth, subhyaline to pale brown, hyphae 1.5–3 μm wide. *Conidiophores* simple or branched, subcylindrical, erect, thickening toward the apex, dark brown, smooth and thick-walled, 70–113 × 3–3.5 μm. *Conidiogenous cells* integrated, polyblastic, terminal, geniculate, dark brown, 13–30 × 3–4 μm; scars truncate, thickened and darkened, 1.5–2 μm wide. *Primary ramoconidia* cylindrical, dark brown, smooth and thick-walled, 15–32 × 2–4 μm, 0–2-septate. *Secondary ramoconidia* subcylindrical to cylindrical, pale to dark brown, smooth- and thick-walled, 11–15 × 2.5–4 μm, 0–1-septate, sometimes constricted at the septum, giving rise to branched conidial chains; scars thickened, 0.5–1.5 μm diam. *Intercalary conidia* subcylindrical, brown, smooth- and thick-walled, 9–16 × 3–4 μm, 0–1-septate, usually constricted at the septum. *Small terminal conidia* ellipsoidal to clavate, brown, smooth-walled, 5.5–8 × 2.5–3.5 μm.

Culture characteristics — Colonies on PDA at 25 °C attaining 13–18 mm diam after 14 d, deep green to dark green (3D3/F8) (Kornerup & Wanscher 1978), erumpent and folded, velvety; reverse olive-brown (4D4/4D6). On SNA at 25 °C attaining 8–10 mm diam after 14 d, olive-brown (4E5/E8), flat to slightly unobunate, velvety to dusty; reverse olive-brown (4F6). On OA at 25 °C attaining 9–12 mm diam after 14 d, olive-brown (4E4/4D3), flat, velvety to dusty; reverse olive-brown (4E4/4D3).

Typus. USA, Florida, Daytona Beach, from human bronchoalveolar lavage fluid, D.A. Sutton (holotype FMR H-13297, isotype deposited at CBS, cultures ex-type FMR 13297 = UTHSCSA DI-13-172 = CBS 140694, ITS sequence GenBank LN834444, LSU sequence GenBank LN834448, MycoBank MB614942).

Notes — The genus *Toxicocladosporium*, typified by *T. irritans*, currently includes 12 species. Segregated from *Cladosporium, Toxicocladosporium* differs in the presence of conspicuous, dark septa in the conidiophores and conidia, and by having flat, thickened and refractive conidigenous scars in contrast to the coronate scars of *Cladosporium* (Crous et al. 2007b). *Toxicocladosporium hominis* is phylogenetically related and morphologically similar to *T. strelitziae* (Crous et al. 2012b), from which it differs in the production of larger conidiogenous cells (13–30 × 3–4 μm) and intercalary conidia (9–16 × 3–4 μm) vs 10–15 × 2.5–3.5 μm and 10–12 × 2–2.5 μm, respectively, in *T. strelitziae*. In addition, the latter species has smooth to verruculose ramoconidia, secondary ramoconidia and intercalary conidia, without constrictions in the medial portion or at the septum.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hit using the ITS sequence is *T. strelitziae* CBS 132535 (GenBank KM8116684; Identities = 513/522 (98 %), Gaps = 2/522 (0 %)), followed by *T. irritans* CBS 185.58 (GenBank EU040243; Identities = 510/526 (97 %), Gaps = 4/526 (0 %)) and *T. pini* CPC 23639 (GenBank KJ869160; Identities = 505/527 (96 %), Gaps = 6/527 (1 %)). Closest hits using the LSU sequence were to *T. strelitziae* CBS 132535 (GenBank NG042687; Identities = 542/547 (99 %), Gaps = 2/547 (0 %)), *T. irritans* CBS 185.58 (GenBank EU040243; Identities = 542/547 (99 %), Gaps = 2/547 (0 %)) and *Cladosporium* sp. ATCC 28310 (GenBank KP780464; Identities = 539/547 (99 %), Gaps = 2/547 (0 %)).
Pisolithus aureosericus
Pisolithus aureosericeus M.P. Martín, Kaewgrajang, Phosri & Watling, sp. nov.

Etymology. From Latin aureus and aereus, referring to the colour and texture of the peridium.

Classification — Sclerodermataceae, Boletales, Agaricomycetes.

Macroscopic characteristics — Basidiomes subglobose to broadly ellipsoidal, gasterocarp, 10–50 mm, sessile. Peridium surface slightly velvety, golden yellow at first, later buff to snuff brown. Rhizomorphs at the base, small, 0.8–1.3 mm high × 0.3–0.5 diam. Gleba orange-brown becomes ferruginous powdery mass at maturity by the breakdown of the peridioles. Peridioles subglobose to broadly ellipsoidal, 0.2–0.8 × 1.0–1.2 mm diam, thin-walled, surface smooth, bright yellow or greenish yellow, later a snuff-brown powdery mass when they mature.

Microscopic characteristics — Constituent hypheae intertwined, cream to ochraceous, thin-walled, 2–3.5 mm broad, septate without encrustation, clamp-connections present. Basidia not seen. Spores globose to subglobose, 8.5–10 × 8–11 µm excluding ornamentation, pale brown, densely ornamented with pyramidal spines (0.5–0.8 µm long).

TyDUS THAILAND, Nakhon Ratchasima, alt. 470 m, N14°29'59"E101°56'22", on clay loam soil, under Hopea odorata trees, 8 Aug. 2012, T. Kaewgrajang KUFF001 (holotype Herbarium Kasetsart University, ITS sequence GenBank KU351837, MycoBank MB851695).

Additional materials examined. THAILAND, Nakhon Ratchasima, alt. 470 m, N14°29'59"E101°56'22", on clay loam soil, under Hopea odorata trees, 8 Aug. 2012, T. Kaewgrajang KUFF002 (Herbarium Kasetsart University, ITS sequence GenBank KU351835, KU351836); ibid., T. Kaewgrajang KUFF003 (Herbarium Kasetsart University, ITS sequences GenBank KU351838, KU351839, KU351840).

Notes — The genus Pisolithus has for a long time been considered a genus of species with mainly a xerophytic life-strategy, being found in shrub-land, woodland-clearings, even wasteland, and all generally on highly mineral soils (Pilát 1958). For many years the dark coloured, elongated, narrow stemmed Pisolithus kissingii was perhaps the only species linked to tropical areas being described from the rain forest in Sumatra (Fischer 1906); although, specimens of this genus had been located amongst the dried collections of the late John H. Corner now housed in the herbarium of the Royal Botanic Garden, Edinburgh. However, after intensive work in the last few years in more tropical plant-communities has demonstrated a wealth of species of Pisolithus present certainly in South-East Asia. The present study delimited a further species, similar in colour to P. aurantioscabrosus, but differing markedly in the smoother and slightly velvety outer surface of the exoperidium in contrast to the erect squamules of the former. Phylogenetic analyses (parsimony), based on three collections (six specimens/six sequences) of P. aureosericeus, and previously published data, mainly from Martín et al. (2002), Phosri et al. (2012), Martín et al. (2013) clearly grouped the new sequences with species of P. aurantioscabrosus from Malaysia collected under Shorea macropera. However, the specimens of P. aureosericeus form a cluster together as a group of their own, and were collected under Hopea odorata. Moreover, the peridium surface is slightly velvety and golden yellow, and the basidiospores are strongly ornamented with wedge-shaped extensions giving a very rough appearance; although Pisolithus spores are ornamented this present feature is rather uncommon in the genus and helps to delimit this new taxon under the microscope.

One of the 100 equally most parsimony trees obtained after a heuristic search of the ITS sequence alignment (PAUP v. 4.0b10). Following Phosri et al. (2012) and Martin et al. (2013), sequences of Suillus luteus and Scleroderma citrinum were included as outgroup. Pisolithus sequences were distributed in 15 main clades, clade number after Martin et al. (2002); percentage of bootstrap values (> 50 %) are indicated on the branches. The P. aureosericeus clade is marked with a grey square (H: Holotype; P: Paratypes); the accession number from EMBL/GenBank or UNITE databases are indicated to the rest of terminals.

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Coprinus littoralis
Coprinus littoralis G. Moreno, Carlavilla, Heykoop, Manjón, A. Sánchez, sp. nov.

Etymology. Name reflects the habitat, littoral dunes, from which this fungus was collected.

Classification — Agaricaeae, Agaricales, Agaricomycetes.

Cap up to 45 × 25 mm (measured on dried herbarium specimens), ovoid to broadly ellipsoid, becoming revolute at margin when mature and strongly deliquescent, first whitish, later with pinkish tinges, veil thick, ochraceous, persistent at centre, star-shaped, not deliquescent, recalling that of Coprinus vosoustii. Gills crowded, first white, then pinkish, later black, strongly deliquescent; gill-edge could not be observed due to deliquescence. Stem 55–65 × 3–6 mm, whitish, with whitish ephemerale ring; base up to 13 mm wide and bulbous to napiiform, strongly rooting, 20–35 mm in length; hollow, with central strand. Spores 13–20 × 8–12 µm av. 15.5–17.5 × 9.5–10.6 µm (3 collections), Qp = 1.60–1.72, ellipsoid, smooth, sometimes slightly broadened base, dark black, gill pore central to slightly eccentric toward the abaxial spore side, up to 2.5–3 µm diam. Basidia and pseudoparaphyses could not be observed due to deliquescence. Pleurocystidia not observed. Cheilocystidia probably present in young specimens but the material studied was always very mature, with the gill-edge completely deliquesced. Clamp-connections absent, only pseudoclamps present. Elements of veil 45–200 × 5–30 µm, consisting of cylindrical septate hyphae, rarely branched, densely packed, very variable in size and shape.

Habit, Habitat & Distribution — Growing solitary on sand in littoral dunes with psammophilous vegetation. Very rare in the studied area.

Typus. **Spain**, Huelva, Playa Coto de Doñana, National Park of Doñana, psammophilous in dunes, 5 Apr. 2013, A. Sánchez (holotype at AGH 45819, ITS sequence GenBank KU686920, LSU sequence GenBank KU686903, MycoBank MB18523).

Additional specimens examined. **Coprinus littoralis**. **Spain**, Huelva, Playa de Doñana, National Park of Doñana, psammophilous in dunes, 6 Apr. 2013, A. Sánchez, paratype AGH 45860 (ITS, LSU sequences GenBank, KU686921, KU686904), idem, 7 Apr. 2013, AH 45859 (ITS, LSU sequences GenBank, KU686922, KU686905). **Coprinus comatus**. **Spain**, Alcalá de Henares, Campus universitario, Facultad de Biología, in a garden, 15 Nov. 2008, J. Rejos & G. Moreno, AH 44095 (ITS, LSU sequences GenBank, KU686915, KU686898); Madrid, Valdemorillo, in open area in a forest of Quercus ilex subspp. ballota, 10 Apr. 2010, M. Hinojosa & J.C. Campos, AH 45823 (ITS, LSU sequences GenBank, KU686913, KU686898); Madrid, Canillejas, in parking of the Capricho Park, 23 Mar. 2014, J.L. Domingo, AH 44089 (ITS, LSU sequences GenBank, KU686914, KU686897); Madrid, Las Matas, on side of a path, 8 May 2014, I. Morales, AH 45796 (ITS, LSU sequences GenBank, KU686896, KU686899); Guadalajara, in a garden, 6 Dec. 2014, J.R. Carlavilla, AH 45795 (ITS, LSU sequences GenBank, KU686911, KU686894); Alcalá de Henares, Campus universitario, Residencia Crusa, in a garden, 29 Oct. 2015, P. Rosario, AH 45832 (ITS, LSU sequences GenBank, KU686912, KU686895); Madrid, Alcalá de Henares, Campus universitario, Escuela Politécnica, in a garden, 6 Nov. 2015, A. López-Villalba, J.R. Carlavilla & G. Moreno, AH 45830 (ITS, LSU sequences GenBank, KU686917, KU686900).

Notes — **Coprinus littoralis** is characterised by its medium size sporocarp (as compared with **Coprinus comatus**), its large spores (13–20 × 8–12 µm) with slightly eccentric germ pore and by growing in littoral dunes.

In our ITS phylogeny (MycoBank supplementary data) **Coprinus littoralis** is significantly related to **C. comatus**, **C. sterquilinus**, **C. vosoustii** and **C. pinetorum**. They all belong to subsect. **Coprinus** s. Ujlé (the **C. comatus** group). **Coprinus comatus** differs from **C. littoralis** by its more robust habit, smaller spores (9–12.5 × 7–9 µm) and by fruiting on strongly nitrified sites (gardens, roadsides and paths or on lawns). **Coprinus sterquilinus** differs from **C. littoralis** by its larger spores (17–26 × 10–15 µm) and the habitat on dung. **Coprinus vosoustii**, considered by Moreno & Heykoop (1998) as a synonym of **C. calyptratus**, resembles **C. littoralis** because of the thick and persistent star-shaped ochraceous veil on the cap as well as by the large spores. Nevertheless, **Coprinus littoralis** differs from **C. vosoustii** by the strict psammophilous habitat and the absence of a napiform rooting stipe. **Coprinus pinetorum** differs from **C. littoralis** by its fibrillose flocculose veil, smaller spores (8–11 × 5.5–8 µm) and by fruiting among needles of **Pinus halepensis**.

Macroscopically, **Coprinus spadiceisporus**, a very rare species described from the State of Washington by Van de Bogart (1976), is also a **C. comatus**-like fungus. Nevertheless, it differs from **C. littoralis** by fruiting on dung and by its veil with somewhat appressed scales (Van de Bogart 1976). Ujlé et al. (1998) revised the type of **C. spadiceisporus** and synonymised it with **C. roseistipitatus**, which also was described fruiting on dung of rabbit and deer. **Coprinus spadiceisporus** has been collected in Spain (Lleida) by Tabarés & Rocabruna (2002) fruiting on dung of rabbit. Another **C. comatus**-like fungus which resembles **Coprinus littoralis** is **C. levisticolens**. However, **Coprinus levisticolens** differs from **C. pinetorum** by its scaly cap, smaller spores (11–14 × 7–8 µm) and by fruiting on sandy soil under **Populus alba** and **Crataegus** spp. (Ludwig & Roux 1995).
Coprinus pinetorum
Coprinus pinetorum G. Moreno, Carlavilla, Heykoop & Manjón, sp. nov.

Etymology. Name reflects the habitat, humus of Pinus halepensis, from which this fungus was collected.

Classification — Agaricaeae, Agaricales, Agaricomycetes.

Cap 35–45 × 25–35 mm when still closed, ellipsoid to subcylindrical, becoming revolute at margin when mature, first whitish, later with pinkish tinges, veil first fibrillose to flocculose, then breaking up into small and fragile whitish upturned scales, except at centre, that stays smooth and becomes creamy to strawish creamy. Gillis crowded, first white, and then pinkish to black, the gill-edge whitish, probably due to the presence of numerous cheliocystidia, strongly deliquescent when mature. Stem 60–120 × 10–17 mm, whitish, with movable fragile ring on lower part, upperside strawish whitish, underside greyish flesh coloured, with up to 22 mm wide bulbous to subbulbous base, hollow, with central strand. Spores 8–11 × (5–)5.5–8 µm av. 8.1–10.6 × 5.9–6.9 µm (4 collections), Qav = 1.38–1.62, smooth, ellipsoid, sometimes slightly broomed base, dark black, germ pore central, up to 1–1.5 µm diam. Basidia 14–35 × 10–13 µm (excl. sterigmata), sterigmata up to 4 µm in length, 4-spored, hyaline, sometimes with brownish vacuolar pigment toward the base, surrounded by 6–8 pseudoparaphyses. Cheliocystidia probably present in young specimens but the material studied was always very mature, with the gill-edge completely deliquesced. Pleurocystidia not observed. Clamp-connections absent, only pseudoclamps present. Elements of veil 35–220 × 9–35 µm, consisting of cylindrical branched hyphae, septate, densely packed and very variable in size and shape.

Habit, Habitat & Distribution — Growing gregarious on basic soil under Pinus halepensis. Rare in the studied area.

Typus. Span., Madrid, Rivas Vaciamadrid, in humus of Pinus halepensis, 18 Nov. 2011, M. Martin, L. Rubio-Casas, L. Rubio-Roldán & G. Moreno (holotype AH 44094, ITS sequence GenBank KU686924, LSU sequence GenBank KU686907, MycoBank MB815824).

Additional specimens examined. Coprinus pinetorum: Span., Madrid, Rivas Vaciamadrid, in humus of Pinus halepensis, 18 Nov. 2011, M. Martin, L. Rubio-Casas, L. Rubio-Roldán & G. Moreno, paratype AH 45797 (ITS, LSU sequences GenBank, KU686925, KU686908); idem, 22 Nov. 2014, M. Martin, paratype AH 45798 (ITS, LSU sequences GenBank, KU686926, KU686909); Almería, Sierra de los Filabres, in humus of Pinus halepensis, 30 Nov. 2002, G. Moreno & R. Galán, paratype AH 45815 (ITS, LSU sequences GenBank, KU686927, KU686910). Coprinus comatus: Span., Alcalá de Henares, Campus universitario, Facultad de Biología, in a garden, 15 Nov. 2008, J. Rejas & G. Moreno, AH 44095 (ITS, LSU sequences GenBank, KU686915, KU686898); Madrid, Valdemorillo, in open area in a forest of Quercus ilex subs. ballotà, 10 Apr. 2010, M. Hinojosa & J.C. Campos, AH 45823 (ITS, LSU sequences GenBank, KU686913, KU686896); Madrid, Canillejas, in parking of the Capricho Park, 23 Mar. 2014, J.L. Domingo, AH 44089 (ITS, LSU sequences GenBank, KU686914, KU686897); Madrid, Las Matas, on side of a path, 8 May 2014, I. Morales, AH 45796 (ITS, LSU sequences GenBank, KU686916, KU686899); Guadalajara, in a garden, 6 Dec. 2014, J.R. Carlavilla, AH 45795 (ITS, LSU sequences GenBank, KU686911, KU686894); Alcalá de Henares, Campus universitario, Residencia Crusa, in a garden, 28 Oct. 2015, P. Rosario, AH 45832 (ITS, LSU sequences GenBank, KU686912, KU686895); idem, 4 Nov. 2015, AH 45831 (ITS, LSU sequences GenBank, KU686918, KU686901); Alcalá de Henares, Campus universitario, Escuelas Politécnicas, in a garden, 6 Nov. 2015, A. López-Villaiba, J.R. Carlavilla & G. Moreno, AH 45830 (ITS, LSU sequences GenBank, KU686917, KU686900). Coprinus littoralis: Span., Huelva, Playa Coto de Doñana, National Park of Doñana, psammophilous in dunes, 5 Apr. 2013, A. Sánchez, holotype AH 45819 (ITS, LSU sequences GenBank, KU686920, KU686903); Huelva, Playa de Doñana, National Park of Doñana, psammophilous in dunes, 6 Apr. 2013, A. Sánchez, AH 45860 (ITS, LSU sequences GenBank, KU686921, KU686904); idem, 7 Apr. 2013, AH 45859 (ITS, LSU sequences GenBank, KU686922, KU686905). Coprinus vosoustii: Span., Madrid, Ciudad Universitaria, Facultad de Farmacia y Medicina, in a garden, 13 May 1976, K. Tabba, AH 1284 (ITS, LSU sequences GenBank, KU686919, KU686902); idem, 8 May 1977, G. Moreno, AH 556 (ITS, LSU sequences GenBank, KU686923, KU686906).

Notes — Coprinus pinetorum is characterised by its small size (as compared with C. comatus), its spores with slightly broadened base (8–11 × 5.5–8 µm) and by fruiting among needles of Pinus halepensis.

In our ITS phylogeny (MycoBank supplementary data) Coprinus pinetorum is significantly related to C. comatus, C. sterquilinus, C. vosoustii and C. littoralis. They all belong to subsect. Coprinus s. Ujlé (the C. comatus group). Coprinus comatus differs from C. pinetorum by its more robust habit and by fruiting on strongly nitrified sites (gardens, roadsides and paths or on lawns). Coprinus sterquilinus differs from C. pinetorum by its solitary basidiocarps, very large spores (17–26 × 10–15 µm) and the habitat on dung. Coprinus vosoustii differs from C. pinetorum by its ovoid cap, thick ochraceous and persistent veil forming a star-shaped layer at centre, and much larger spores (17–20 × 10–12 µm). Coprinus littoralis differs from C. pinetorum by its larger basidiocarps, larger spores (13–20 × 8–12 µm) with slightly eccentric germ pore and the psammophilous habitat in littoral dunes.

Macroscopically, C. spadiceisporus, a very rare species described from the State of Washington by Van de Bogart (1976), is also a C. comatus-like fungus. Nevertheless, it differs from C. pinetorum by fruiting on dung and by its spores with eccentric germ pore (Van de Bogart 1976). Another C. comatus-like fungus which resembles Coprinus pinetorum is C. levisicolens. However, C. levisicolens differs from C. pinetorum by its scaly cap, larger spores (11–14.5 × 7–8 µm) with eccentric germ pore and by fruiting on sandy soil under Populus alba and Crataegus spp. (Ludwig & Roux 1995).

Colour illustrations. Spain, Rivas Vaciamadrid, humus of Pinus halepensis, where the holotype was collected; basidiomata and fruit body section, cylindrical hyphae of veil, 4-spored basidia, spores under LM, smooth spores with central germ pore under SEM (from the holotype). Scale bars = 1 cm (basidiomata), 10 µm (veil, basidia, spores under LM), 2 µm (spores under SEM).
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*Priceomyces vitoshaensis* Gouliamova, Dimitrov, M.T. Sm., M.M. Stoilova-Disheva & M. Groenew., *sp. nov.*

**Etymology.** The specific epithet ‘vitoshaensis’ was derived from the locality Vitosha Nature Park where insect hosts of the ex-type strain were collected.

**Classification.** — *Debaryomycetaceae, Saccharomycetales, Saccharomyces.*

After 7 d growth at 25 °C on 5 % glucose broth, cells are globose, ovoid, oblong, 2–5 × 3–7 μm, occurring singly, in pairs, in small clusters or in small chains, and proliferating by multilateral budding. Dalmatia plate culture after 10 d on morphology (*Wickerham 1951*) and potato-dextrose agar (PDA) at 20–25 °C did not show pseudohyphae. After 3 d of incubation on yeast extract, malt extract, pepton, glucose agar (YM), the single strains formed asci after conjugation of independent cells. The asci were lytic, releasing 1–2 round and smooth ascospores. For physiological characteristics see MycoBank MB802453.

**Typus.** *Bulgaria*, Sofia, Nature Park Vitosha, in birch forest, above village Bistritsa, N42°35'10" E23°21'36", from Vitosha Nature Park where insect hosts of the ex-type strain were collected.

— Notes. — The most similar sequence in GenBank is *C. northwykensis* (98 % identity in both LSU and ITS sequences). Phylogenetic analyses, using an alignment of concatenated LSU and ITS sequences of known species present in the *Priceomyces* clade and the new yeast strains, placed the latter with *C. northwykensis* in a separate subclade (100 % support). Pairwise comparison of sequences from multiple alignment data showed that the new strains have 97 % identity with *C. northwykensis* (1 121 identical nt., 14 subst. in ITS and 11 subst., 1 gap in LSU), 93 % with *C. fermenticarens* (1 080 identical nt., 44 subst. in ITS and 23 subst., 3 gaps in LSU) and 91 % identity with *P. melissophilus* (1 054 nt., 47 subst., 10 gaps in ITS and 24 subst., 2 gaps in LSU). Nine physiological characteristics distinguish the new strains from *C. northwykensis*. They can assimilate celllobiose, salicin, ribitol, succinate, methyl-α-gluco-side and nitrite. They cannot assimilate ethanol and they do not grow in 0.01 % cycloheximide and at 35 °C. Thus, we assign these strains to the newly proposed species, *Priceomyces vitoshaensis*.

**New combinations in the genus Priceomyces.**

Based on the results of phylogenetic analysis of combined LSU and ITS rDNA we propose new combinations in the genus *Priceomyces* for the following species that previously belonged to the genus *Candida*.

**Priceomyces fermenticarens** (Van der Walt & Baker) Gouliamova, Dimitrov, M.T. Sm., M.M. Stoilova-Disheva & M. Groenew., *comb. nov.* — MycoBank MB310255

**Basionym.** *Candida fermenticarens*, Van der Walt & Baker, Bothalia 12: 561. 1978.

**Priceomyces northwykensis** (Ravella et al.) Gouliamova, Dimitrov, M.T. Sm., M.M. Stoilova-Disheva & M. Groenew., *comb. nov.* — MycoBank MB560189

**Basionym.** *Candida northwykensis*, Ravella et al., *Curr. Microbiol.* 63: 115. 2011.

**Colour illustrations.** Bulgaria, Vitosha Mountain, large stone river Zlatnite Mostove (Golden Bridges) (Photo: Alexandra Toneva); *a.* *Pterostichus melas* (Carabidae, www.zin.ru/Animalia/Coleoptera); b. morphology of cells of *Priceomyces vitoshaensis* 3′ in 5 % glucose broth; c. arrows indicating the conjugated asci with ascospores. Scale bars = 10 μm (cells), 5 μm (asci with ascospores).

**Notes.** — Colour illustrations. Bulgaria, Vitosha Mountain, large stone river Zlatnite Mostove (Golden Bridges) (Photo: Alexandra Toneva); *a.* *Pterostichus melas* (Carabidae, www.zin.ru/Animalia/Coleoptera); b. morphology of cells of *Priceomyces vitoshaensis* 3′ in 5 % glucose broth; c. arrows indicating the conjugated asci with ascospores. Scale bars = 10 μm (cells), 5 μm (asci with ascospores).

Phylogenetic analysis of the alignment of the ITS1+2 region, and the LSU (D1/D2 domains) rRNA gene using a maximum likelihood analysis (MEGA v. 6) for *Priceomyces vitoshaensis* 3′ and related species.

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Nothophoma macrospora Valenzuela-Lopez, Stchigel, Cano & Deanna A. Sutton, sp. nov.

Etymology. G. μακρό-, large, and -spora, spore, referring to the big size of the conidia.

Classification — Didymellaceae, Pleosporales, Dothideomycetes.

Hyphae pale to dark brown, 3–10 µm wide, thin- to thick-walled, smooth to granulose due to production of dark granules, septate, anastomosing. Conidiomata pycnidial dark brown, pyriform to heart-shaped by the occasional production of 2–3(–4) necks, rarely globose, 100–300 × 100–300 µm; peridium 3–5-layered, 15–25 µm thick, peridial cells globose to polygonal, pale to dark brown, 5–10 µm diam, thick-walled; neck usually present, pale to the peridial wall, cylindrical to conical, (50–)190–150 × (50–)180–110 µm, papillate, ornamented with a crown of short, subhyaline, conical to digitiform projections around the ostiolum, ostiolum of late opening; exuded conidial masses not observed; conidiogenous cells enteroblastic, phialidic, globose to flask-shaped, hyaline, thin-walled, 5–10 µm diam; conidia (9–)10–15 × 2.5–3(–3.5) µm, hyaline, cylindrical to slightly clavate at one or both ends, (0–)2-septate, narrowing slightly at the septa, guttulate, sometimes producing a similar conidia on a lateral bulge, then forming irregular. Chlamydospores absent, but some hyphae cells become darker, thicker and barrel-shaped.

Culture characteristics — Colonies on OA reaching 30 mm diam in 7 d at 25 °C, olive brown (M.4F3), flattened, granulose due to the production of numerous pycnidia; reverse concolorous. Colonies on MEA attaining 37–41 mm in 7 d at 25 °C, yellowish white (M.4A2) to light brown (M.6D8), flattened, compact, reverse concolorous. OA pH spot test: negative. Crystals absent.

Typus. USA, Arizona, Phoenix, from respiratory secretion of a patient with pneumonia, 1 Apr. 2009, D.A. Sutton (holotype CBS H-22377, cultures ex-type UTHSC Di09-853 = FMR 13767 = CBS 140674, ITS sequence GenBank LN880536, LSU sequence GenBank LN880537, actA sequence GenBank LN880539, tub2 sequence GenBank LN880538, MycoBank MB815051).

Notes. — This fungus was isolated from a human clinical specimen. Morphologically, Nothophoma macrospora resembles the species previously classified into Phoma section Macrospora (Boerema et al. 2004), i.e. Phoma andropogonivora, P. boeremae, P. chenopodi, P. commelinicola, P. gossypiiocola, P. necator, P. rabei, P. xanthina and P. zeae-maydis. These species produce the largest conidia of the genus. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are Leptosphaerula australis (GenBank:KF293970; Identities = 493/497 (99 %), gaps 1/497 (0 %)); Didymella glemorae (GenBank:AB369471; Identities = 493/497 (99 %), gaps 1/497 (0 %)) and Peyronellaea prosopidis (GenBank:KF777232; Identities = 887/889 (99 %), no gaps). Closest hits using ITS sequence are Leptosphaerula australis (GenBank:KF293970; Identities = 493/497 (99 %), gaps 1/497 (0 %)); Didymella glemorae (GenBank:AB369471; Identities = 493/497 (99 %), gaps 1/497 (0 %)) and Peyronellaea prosopidis (GenBank:KF777232; Identities = 887/889 (99 %), no gaps). Closest hits using ITS and LSU sequence are Leptosphaerula australis (GenBank:KF293970; Identities = 493/497 (99 %), gaps 1/497 (0 %)); Didymella glemorae (GenBank:AB369471; Identities = 493/497 (99 %), gaps 1/497 (0 %)). In a similar search in the Q-Bank fungal nucleotide database (www.q-bank.eu), the closest hit is Nothophoma anigozanthi CBS 381.91 (Identities = 468/473 (99 %), gaps = 1/473 (0 %)). The closest hit using the beta-tubulin (tub2) sequence is Nothophoma gossypiiocola (GenBank:GU237611; Identities = 323/335 (99 %), no gaps), as well as was using the actin (actA) sequence against Q-Bank (Nothophoma gossypiiocola CBS 377.67; Identities = 214/224 (96 %), no gaps). Our phylogenetic tree, built by using the ITS, LSU, tub2 and actA sequences, corroborated that our fungus represents a new species of the genus Nothophoma, N. gossypiiocola being the most phylogenetically and morphologically related species. Nothophoma macrospora differs from N. gossypiiocola by its lower growing rate on OA, the shape (pyriform to heart-shaped vs globose), the number of necks (up to 4 vs 0–1) and the ornamentation (papillate vs non-papillate) of the pycnidia, and the presence of conidial septa (up to 2 vs non-septate).

Maximum likelihood tree obtained from the combined DNA sequences dataset from four loci of our isolate and sequences retrieved from the GenBank and the Q-Bank databases (TreeBASE ID 18137). Above the nodes are presented the bootstrap support values ≥ 70 %, and the Bayesian posterior probability scores ≥ 0.95 are indicated below. Neosaccycha pascalii (CBS 560.81 & CBS 561.81) was used as outgroup. Ex-type strains of the different species are indicated with 1. The new species proposed in this study is indicated in bold. The alignment was performed by MEGA v. 6.06 (Tamura et al. 2013), and the tree building by MEGA v. 6.06 and by MrBayes v. 3.2.4 (Huelsenbeck & Ronquist 2001).

Nomenclature. — Nicomedes Valenzuela-Lopez, Mycology Unit, Medical School and IISPV, Universitat Rovira i Virgili (URV), Sant Llorenç 21, 43201 Reus, Tarragona, Spain; Microbiology Unit, Medical Technology Department, Faculty of Health Science, University of Antofagasta, Av. Universidad de Antofagasta s/n, 02800 Antofagasta, Chile; e-mail: nicomedes.vl@gmail.com

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Entoloma kruticianum
Entoloma kruticiuanum O.V. Morozova, M.Yu. Dyakov, E.S. Popov & A.V. Alexandrova, sp. nov.

Etymology. The epithet refers to the type locality – Krutitsy Village in the Tver Region of Russia.

Classification — Entolomataceae, Agaricales, Agaricomycetes.

Basidiomata small-sized, mycenoid. Pileus 5–12 mm diam, hemispherical to convex, not hygrophanous, not translucently striate, with appendiculate margin, radially fibrillose to slightly squamulose in the centre, deep violet (15E7–8; Komerup & Wanscher 1978), darker in the centre (15F6–8). Lamellae moderately distant, adnate-empirginate or almost free, ventricose, reddish lilac (14C3–4, 14D3–4), becoming greyish pink, with paler entire edge. Stipe 20–70 × 1–2 mm, cylindrical, longitudinally fibrillose-striate, deep blue to deep violet (19D8–E8), clearly different from the pileus, white tomentose tuudinally fibrillose-striate, deep blue to deep violet (19D8–E8, 19D7–E8), narrower than the pileus, with clavate, clamped, cuticularised cheilocystidia (if present). The ITS1-5.8S-ITS2 region of the newly described species has been compared with those of the other species (mostly derived from the type material, data from Morozova et al. 2014). Molecular data support their differences (p-distance from the closest species E. lepidissimum – 8 %). The similar dark blue species distinguish (except for the colour of the pileus): E. coelestinum – by the white lamellae, smaller spores and more conical pileus, E. chytrophilum possesses white lamellae, nodulose spores and more applanate pileus. Both varieties of E. callichroum are characterized by the similar coloration of the basidiomata, but their spores are larger and cheilocystidia (if present) are broadly clavate, never lageniform. One more species with coloured lamellae – E. euchroum – usually is more robust and possesses larger spores with rather blunt angles.

Phylogenetic tree derived from Bayesian analysis, based on nrITS1-5.8S-ITS2 data. Analysis was performed under GTR model, for 3 M generations, using MrBayes v. 3.2.1 (Ronquist et al. 2012). The ML analysis was run in the RAxML server (http://phylobench.vital-it.ch/raxml-bb/index.php (Stamatakis et al. 2008)). Posterior probability (PP > 0.95) values from the Bayesian analysis followed by bootstrap values from the Maximum Likelihood (BS > 70 %) analysis are added to the left of a node (PP/BS).

Notes — Entoloma kruticiuanum represents a species of the subgenus Leptonia due to the presence of clamp-connections, absence of brilliant granules and plagiotrichoderm to trichoderm pileipellis. It resembles E. lepidissimum by its small-sized mycenoid basidiomata with deep blue and violet colours, including coloured lamellae. Microscopically, the scattered cheilocystidia also make them similar. However, E. kruticiuanum can be recognized by the colour of the pileus, which is clearly different from the stipe, the presence of the reddish lilac tint in the lamellae, as well as smaller spores with pronounced angles and attenuate hilum. The ITS1-5.8S-ITS2 region of the newly described species has been compared with those of the other Leptonia species (mostly derived from the type material, data from Morozova et al. 2014). Molecular data support their differences (p-distance from the closest species E. lepidissimum – 8 %). The similar dark blue species distinguish (except for the colour of the pileus): E. coelestinum — by the white lamellae, smaller

Colour illustrations. Russia, Tver’ Region, Staritsa District, vicinities of the Krutitsy Village, type locality; pileipellis, spores, cheilocystidia, basidiomata (all from holotype). Scale bars = 1 cm (basidiomata), 10 μm (spores, cheilocystidia and pileipellis).

Typus. Russia, Tver Region, Staritsa District, vicinities of the Krutitsy Village, N56°18'35.2" E34°52'07.7", 13 Sept. 2015, E. Popov & A. Alexandrova (holotype LE 311767, ITS sequence GenBank KU666558, LSU sequence GenBank KU710222, MycoBank MB815745).

Phylogenetic tree derived from Bayesian analysis, based on nrITS1-5.8S-ITS2 data. Analysis was performed under GTR model, for 3 M generations, using MrBayes v. 3.2.1 (Ronquist et al. 2012). The ML analysis was run in the RAxML server (http://phylobench.vital-it.ch/raxml-bb/index.php (Stamatakis et al. 2008)). Posterior probability (PP > 0.95) values from the Bayesian analysis followed by bootstrap values from the Maximum Likelihood (BS > 70 %) analysis are added to the left of a node (PP/BS).

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Xerocomellus poederi
Xerocomellus poederi G. Moreno, Heykoop,Esteve-Rav., P. Alvarado & Traba, sp. nov.

Etymology: Named after Reinhold Pöder, Austrian mycologist and specialist in Boletales, who passed away in August 2015.

Classification — Boletaceae, Boletales, Agaricomycetes.

Cap 1.2–5.5 cm broad, convex becoming plane convex, sometimes depressed at centre, pale brown (Mu 7.5YR 6/3, 6/4), brown pinkish (Mu 5YR 6/3, 6/4) to dark brown when mature (Mu 5YR 3/1, 3/2, 3/3), becoming darker in herbarium specimen; surface dry, smooth, the epicutis cracking in age with reddish tinges in the cracks on the upper part (Mu 10R 4/6, 4/8); context in cap whitish, reddish under the epicutis, staining slightly bluish when bruised or cut. Margin irregular, concolorous to slightly paler, not hygrophanous nor striate. Tubes up to 0.8 mm in length, depressed around the stipe, ventricose, narrower towards the margin, whitish to pale yellowish when young (Mu 2.5Y 8/3, 8/4) then yellowish (Mu 2.5Y 7/4, 7/6), turning slightly bluish when bruised or cut. Stem 2.5–6 × 0.3–0.6 cm, cylindrical, solid, tapered downward, often curved, fragile, dark reddish (Mu 10R 3/4, 3/6), yellowish at the apex (Mu 2.5Y 8/4, 8/6), surface slightly granulose; context in stem whitish at the apex, dark red in the lower half or lower two thirds, turning slightly bluish when bruised or cut. Odour and taste not distinctive. Spore-print olive brown (Mu 2.5Y 5/3, 5/4). Spores (10.5–)11–16 (–17) × 3–4.5 (–5) µm, av. 11.9–14.6 × 4.4–5 µm (8 collections), Qav. = 2.56–3.17, fusiform, smooth with obtuse apex, with a distinct suprahilar depression, not amyloid or nectarious, containing 1–3 lipidic globose drops or one ellipsoid drop filling almost the entire spore volume; under the SEM spores lack any ornamentation. Basidia 4-spored, 33–45 × 9–13 µm, sterigmatum up to 5 µm in height, clavate, hyaline. Pleurocystidia numerous, fusiform, with obtuse apex, 33–55 × 8–12 µm, hyaline, sometimes with yellowish content. Cheilocystidia similar to pleurocystidia. Caulocystidium throughout the stem consisting of basidia, basidioles and cystidia similar to those present in the hymenium. Pileipellis a trichodermium consisting of septate hyphae, the cylindrical cells of the hyphae with thick walls, terminal cells very variable in shape, cylindrical (narrower than lower cells) to lageniform, 30–40 × 9–11 µm, with abundant yellowish pigment forming patches or strips. Clamp-connections not seen.

Habit, Habitat & Distribution — Growing solitary to gregarious on acid soil under Quercus robur. Very abundant in the studied area.

Typus. SPAN, Lugo, Parque Río Rato, Concello de Lugo, in humus of Quercus robur, 1 Nov. 2013, G. Moreno & J.M. Traba (holotype AH 44050, ITS sequence GenBank KU355475, LSU sequence GenBank KU355488, MycoBank MB815475).

Additional specimens examined. Xerocomellus poederi: SPAN, Lugo, Parque Río Rato, Concello de Lugo, in humus of Quercus robur, 1 Nov. 2013, G. Moreno & J.M. Traba, paratype AH 44051 (ITS, LSU sequences GenBank, KU355476, KU355489); idem, paratype AH 45804 (ITS, LSU sequences GenBank, KU355478, KU355491); Lugo, Concello de O Corgo, Finca O Fia, in humus of Quercus robur, 2 Nov. 2013, G. Moreno, J.M. Traba & J.M. Castro-Marcote, paratype AH 45855; A Coruña, Vimianzo, in humus of Quercus robur, Corylus avellana and Laurus nobilis, 29 Aug. 2015, J.M. Castro-Marcote, paratype AH 45803 (ITS, LSU sequences GenBank, KU355480, KU355491); Orense, Leiro, in humus of Quercus robur, 23 Nov. 2013, J.M. Castro-Marcote, paratype AH 45805 (ITS, LSU sequences GenBank, KU355479, KU355492). Xerocomellus chrysenteron: SPAN, Madrid, La Barranca, Navacerrada, in humus of Pinus sylvestris, 29 Oct. 2013, V. Córdoba, AH 44023 (ITS, LSU sequences GenBank, KU355474, KU355485); Segovia, Ermita de Montaneses, Riaza, in humus of Quercus pyrenaica, 20 June 2010, D. Saavedra, Y. Fernández & L. Rubio-Casas, AH5968 (ITS, LSU sequences GenBank, KU355473, KU355486). Xerocomellus porosporus: SPAN, Segovia, Ermita de Montaneses, Riaza, in humus of Quercus pyrenaica, 12 June 2010, L. Rubio-Roldán & L. Rubio-Casas, AH 38964 (ITS, LSU sequences GenBank, KU355481, KU355493). Xerocomellus riparillus: SPAN, Madrid, Villa de San Antonio, in humus of Populus alba, 3 July 2010, M. Martín, AH56971 (ITS, LSU sequences GenBank, KU355482, KU355494). Xerocomus submentosus: SPAN, Avilá, El Tiemblo, in humus of Castanea sativa and Quercus pyrenaica, 27 June 2010, J.A. Rodea, AH38974 (ITS sequence GenBank, KU355483); Toledo, Real de San Vicente, in humus of Quercus ilex ssp. ballota, 23 Nov. 2013, R. Loaiza, AH 44076 (ITS, LSU sequences GenBank, KU355484, KU355495); Segovia, Fresno de Cantespino, in humus of Quercus pyrenaica and Q. ilex ssp. ballota, 8 Sept. 2013, J.M. Barrasa, AH45790 (ITS, LSU sequences GenBank, KU355485, KU355496).

Notes — Xerocomellus poederi is morphologically characterised by its small size, the reddish cylindrical fusiform long stem in relation to the cap diameter, the dark reddish context in the lower part of the stipe and by fruiting isolated to gregarious on acid soil under Quercus robur.

In our ITS phylogeny (MycoBank supplementary data) Xerocomellus poederi is closely related to X. chrysenteron, X. porosporus and X. sarnarii, and to a lesser degree to X. dryophilus, all of them belonging to the difficult X. chrysenteron complex (Peintner et al. 2003). The whole genus is strikingly different from Xerocomus and other taxa. Xerocomellus chrysenteron differs from X. poederi because of its more robust habit and its differently coloured stem context, with greenish to yellowish green tinges in the base, never dark reddish, and also because of its association with conifers or Fagus in Southern Europe. Xerocomellus porosporus differs from X. poederi because of the dark brownish colours lacking dark reddish tinges in the context at the base of the stem, as well as its apically truncate spores with a distinct germ pore. Xerocomellus dryophilus, a species described by Thiers (1975) from California, resembles X. poederi because of the dark reddish context at the base of the stem, a feature which led many authors to confuse both taxa (Simionini 1994, Pérez de Gregorio 1995, Ladurner & Simionini 2003); however, it differs from X. poederi because of its larger habit, the short stem in relation with the cap diameter, and a strict association to Quercus agrifolia (coast Live Oak) (Bessette et al. 2000, Desjardin et al. 2015). Xerocomellus sarnarii, a species described recently by Ariyawansa et al. (2015) from Italy, is macroscopically similar to X. poederi; however, it differs from X. poederi because of its spores which have a small truncate at the apex and a strict association with Mediterranean sclerophyllous forests of Quercus ilex and Q. suber.

For the description of the colours the Munsell soil colour charts were used (Munsell 1994).
Helminthosporiella stilbacea
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**Helminthosporiella** Hern.-Restr., G.A. Sarria & Crous, *gen. nov.*

_Etymology._ Similar to the genus _Helminthosporium._

_Classification._ — *Massarinaceae, Pleosporales, Dothideomycetes._

_Mycelium._ Superficial and immersed, hyphae hyaline to pale brown, smooth, branched, septate. Conidiophores erect, brown to red-brown, synnematous, septate, compacted. _Conidiogenous cells_ polytretic, sympodial, integrated, determinate, terminal, cylindrical. _Conidia_ catenate in easily disarticulating chains, obclavate, subcylindrical, occasionally bifurcate, brown, distoseptate, hilum darkened, thickened and refractive. Sexual morph unknown.

_Type species._ *Helminthosporiella stilbacea* (Moreau) Hern.-Restr., G.A. Sarria & Crous. MycoBank MB816988.

**Helminthosporiella stilbacea** (Moreau) Hern.-Restr., G.A. Sarria & Crous, *comb. & stat. nov._

_Basionym._ Cercospora palmicola f. stilbacea Moreau, Rev. Mycol. 12: 38. 1947.
  - *Helminthosporium stilbaceum* (Moreau) S. Hughes, Mycol. Pap. 48: 38. 1952.
  - *Exosporium stilbaceum* var. _stilbaceum* (Moreau) M.B. Ellis, Mycol. Pap. 82: 38. 1961.
  - *Exosporium stilbaceum* var. _macrosporum_ Subramon. & V.G. Rao, Journal of the Annamalai University, part B, Sciences 29: 404. 1971.

_Mycelium._ Superficial and immersed, hyphae hyaline to pale brown, smooth, branched, septate. Conidiophores erect, brown to red-brown, synnematous, septate, compacted, 620–1400 × 19–54 μm, individual hyphae 3–4 μm wide. _Conidiogenous cells_ mono- or polytretic, integrated, determinate, terminal, cylindrical, 31–67 × 4.5–7 μm, straight or curved at the apex. _Conidia_ catenate in easily disarticulating chains, obclavate, subcylindrical, occasionally bifurcate, medium brown, 26–83 × 7–10 μm, (1–)3–5(–6)-distoseptate, striate-wall, hilum darkened, thickened and refractive.

_Character culture characteristics._ — Colonies on OA, reaching 9–12 mm diam after 1 wk at 25 °C in the dark. Velvety, with concentric rings and some black spots in the agar, olivaceous to green, margin entire, white; reverse grey olivaceous. Colonies on MEA, reaching 20–27 mm diam after 1 wk at 25 °C in the dark. Velvety, elevate, dark brick, margin irregular, reverse vinaceous buff.

_Specimen examined._ COLOMBIA, Barrancabermeja, CENIPALMA, on leaves of *Elaeis oleifera*, May 2013, G. Andrea Sarria (culture CPHMZC-01, ITS sequence GenBank KX228298.1, LSU sequence GenBank KX228355.1, MycoBank MB816989).

_Notes._ — This species was initially introduced as _Cercospora palmicola f. stilbacea_ by Moreau (1947) as a ‘form’, different from _C. palmicola_ due to the presence of a ‘coremium’. Later it was transferred to _Exosporium_ (Ellis 1961). Nevertheless, the generic placement of this species is doubtful in _Cercospora_ or _Exosporium_ and was tentatively accepted in _Helminthosporium_ (Braun et al. 2014). _Helminthosporium_ as well as _Helminthosporiella_ are asexual genera in _Massarinaceae_ with polytretic conidiogenous cells and distoseptate conidia. However, they are molecular and morphologically different. _Helminthosporiella_ shows terminal conidiogenous cells and catenate conidia and species of _Helminthosporium_ have both terminal and intercalary conidiogenous cells and solitary conidia. Another genus morphologically similar is _Corynespora_. But _Helminthosporiella_ differs from _Corynespora_ in having polytretic and sympodial, instead of monotretic and percurrent conidiogenous cells. Unfortunately, it was not possible to propose a formal epi- or neotypification, since the geographical origin of the specimen examined was not the same as described in the protologue (Democratic Republic of the Congo).

**ITS.** Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequences are _Helminthosporium velutinum_ (GenBank JN198435; Identities = 446/480 (93 %), Gaps = 5/480 (1 %)), _Helminthosporium sp._ (GenBank KJ877647; Identities = 447/480 (93 %), Gaps = 9/480 (1 %)) and _Helminthosporium sp._ (GenBank JN662484, Identities = 496/552 (90 %), Gaps = 16/552 (2 %)).

**LSU.** Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequences are _Corynespora leucadendri_ (GenBank KF251654, Identities = 820/840 (98 %), Gaps = 7/840 (0 %)), _Corynespora olivacea_ (GenBank JQ044448, Identities = 831/858 (97 %), Gaps = 6/858 (0 %)) and _Byssothecium circinans_ (GenBank AY016357; Identities = 830/858 (97 %), Gaps = 7/858 (0 %)) (MycoBank supplementary data).

 Colour illustrations. Nursery of _Elaeis oleifera_ in CENIPALMA, Colombia; _Helminthosporiella stilbacea:_ synnemata, conidiogenous cells and conidia. Scale bars = 10 μm.

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Penidiellopsis radicularis
Fungal Planet 460 – 4 July 2016

Penidiellopsis Sandoval-Denis, Gené, Deanna A. Sutton & Guarro, gen. nov.

Etymology. Named after its morphological resemblance to the genus Peniella.

Classification — Teratosphaeriaceae, Capnodiales, Dothideomycetes.

Conidiophores differentiated, solitary, erect, straight to geniculate-sinuous, rarely branched, pale to medium brown, smooth- and thick-walled. Conidiogenous cells integrated, terminal or intercalary, pale to medium brown, smooth, mono- and polyblastic, giving rise to one or more sets of ramoconidia, scars truncate, slightly darkened, unthickened and not refractive. Ramoconidia 0–1-septate, obovoid, ellipsoid or slightly clavate, pale to medium brown, smooth- and thick-walled, apical part with denticle-like loci, basal scar flattened, slightly darkened, unthickened and not refractive. Conidia in acropetal chains, 0-septate, obovoid, ellipsoid or limoniform, pale to medium brown, smooth, thick-walled, with conidial scars truncate or protuberant, somewhat darkened, unthickened and not refractive.

Type species. Penidiellopsis radicularis Sandoval-Denis, Gené, Deanna A. Sutton & Guarro.

MycoBank MB815361.

Penidiellopsis radicularis Sandoval-Denis, Gené, Deanna A. Sutton & Guarro, sp. nov.

Etymology. Named after its root-like growth pattern in culture media.

Mycelium superficial and immersed, composed of septate, branched, pale brown, smooth to finely verruculose and thin-walled hyphae, 1.5–4.5 μm wide. Conidiophores straight or geniculate, septate, slightly constricted at the septum, 40–150 × 3.5–5 μm, pale to medium-brown, usually darkening at the medial portion, smooth-, thick-walled. Conidiogenous cells terminal or intercalary, 12–18 × 4–5 μm, with one or several conidiogenous loci, 1–2.5 μm wide. Ramoconidia 0–1-septate, ellipsoid, obovoid or somewhat clavate, 7–11 × 3–4 μm, pale to medium brown, smooth and thick-walled. Conidia 0-septate, obovoid or limoniform, 5–9 × 3–4 μm, pale brown, smooth and thick-walled, with protuberant conidial scars.

Culture characteristics — (in the dark, 25 °C after 14 d), colonies on PDA attaining 6–7 mm diam, dark green (30F3/F8) (Kornerup & Wanscher 1978), erumpent and folded, velvety; reverse dark green (30F3) to black. On SNA attaining 4–8 mm diam, dark green (30F8) to black, flat, velvety; reverse dark green (30F8).

Typus. USA, South Carolina, West Columbia, from human nail, date unknown, D.A. Sutton (holotype CBS H-22389, culture ex-type CBS 140695 = UTHSC Di-13-256 = FMR 13369; ITS sequence GenBank LN834441, LSU sequence GenBank LN834445, MycoBank MB815362).

Notes — The genus Penidiellopsis (Ps.) is similar to Peniella (Pa.), however, both genera are clearly differentiated genetically and morphologically. While Penidiellopsis produces pennisate branched conidiophores, those of Penidiellopsis are mostly unbranched, although its conidial chains exhibit a continuous bi- or trifurcating elongation pattern (Crous et al. 2007a). The monotypic genus Xenopenidiella exhibits also similar morphological features, however, is genetically distinct and produces dimorphic conidiophores with loosely branched apices (Quaedvlieg et al. 2014).

Our phylogenetic results showed that Pa. radicularis is closely related to Pa. aggregata and Pa. drakensbergensis, two species not included in Peniella s.str. (sensu Quaedvlieg et al. 2014) (for phylogenetic tree, see MycoBank). However, the new genus Penidiellopsis is genetically well-delimited, and also differs from the latter two species by its shorter ramoconidia (vs 6–15 μm and 10–15 μm long in Pa. aggregata and Pa. drakensbergensis, respectively) and its wider, aseptate intermediate and terminal conidia.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hit using the ITS sequence is Pa. aggregata CBS 128772 (GenBank JF499842; Identities = 466/508 (92 %), Gaps = 11/508 (2 %)), followed by Pa. drakensbergensis CPC 19778 (GenBank NR_111821; Identities = 469/519 (90 %), Gaps = 23/519 (4 %)) and Teratosphaeria agapanthi CBS 129664 (GenBank JF770456; Identities = 435/509 (89 %), Gaps= 18/509 (3 %)). Closest hits using the LSU sequence were to Pa. aggregata CBS 128772 (GenBank JF499862; Identities = 539/551 (98 %), Gaps = 0/551 (0 %)), Pa. drakensbergensis CPC 19778 (GenBank KC005792; Identities = 536/551 (97 %), Gaps = 0/551 (0 %)) and Teratosphaeria macowanii CPC 1872 (GenBank EU019254; Identities = 534/551 (97 %), Gaps = 0/551 (0 %)).

Colour illustrations. USA, South Carolina, view of the Gervais Street Bridge (image credit: Wikimedia commons); conidiophores, conidiogenous cell bearing conidia in branched chains. Scale bars = 5 μm.

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Ganoderma ecuadoriense
**Ganoderma ecuadoriense** W.A. Salazar, C.W. Barnes & Ordóñez, *sp. nov.*

*Etymology.* Name reflects the geographical origin from which the fungus was collected.

*Classification* — *Ganodermataceae, Polyporales, Agaricomycetes.*

*Basidiomata* annual, flabelliform, pileate, pileus 21.6 × 21.8 mm, surface glabrous, woody, reddish brown, laccate, upper surface covered by cinnamon coloured powder of deposited basidiospores. *Basidiospore* surface smooth, white when fresh and dark brown when dry, pores 5–7 per mm, round, thick walls. *Stipe* missing from sample, but lateral. *Hyphal system* dimitic, skeletal hyphae yellow to pale brown, 3.5–5.5 μm wide, end in ramifications, generative hyphae thin-walled, hyaline to pale yellow, 1–2.5 μm wide. *Hyphae* faintly amyloid when dispersed and slightly dextrinoid when in masses with Melzer. *Cuticule cells* club-like, slight amyloid reaction to 5 % KOH and Melzer. Resin deposits between the trama and cuticle. *Basidia* not observed. *Basidiospores* hyaline to pale yellow, truncated, 8–10.5 × 4.5–7 μm, no reaction to 5 % KOH or Melzer.

Typus. ECUADOR. Orellana Province, Yasuní Research Station, on decaying wood, Mar. 2013, A. Salazar (holotype QCAM3430, ITS sequence GenBank KU128524, LSU sequence GenBank KX228350, TreeBASE Submission ID 18454, MycoBank MB816866).

Notes — Morphological identification using the Neotropical *Polyporaceae* key (Ryvarden 2004), revealed *G. ecuadoriense* to be very similar to *G. perzonatum*. However, based on a Blastn ITS sequence comparison, after trimming the 18S and 28S sequences (Schoch et al. 2014), the highest similarities were obtained with *G. orbiforme* from Brazil, and *G. cupreum*, *G. mastoporum* and *G. fornicatum* from China. The sequence of *Ganoderma* sp. VPB202 from Brazil is actually identical, but has a low query score due to the discrepancy in sequence length, missing roughly 25 bases at the 3’ end of ITS2. There were seven consistent differences, three in ITS1 and four in ITS2, between *G. ecuadoriense*, collected in the North-western Amazon basin in Ecuador, and *G. orbiforme*, collected in the South-eastern Amazon in Brazil. Twenty sequences, 16 for *G. ecuadoriense* and four for *G. orbiforme* were used in the DNA alignment analysis. The *Ganoderma* sp. VPB202 sequence suggests *G. ecuadoriense* occurs throughout the Amazon basin, but due to the missing bases of the ITS2 sequence, this is somewhat speculative.

Phylogenetic analysis was done using the Maximum Likelihood plugin PHYML in Geneious v. 7.1 (http://www.geneious.com, Kearse et al. 2012), and the substitution model HKY85 determined by jModelTest (Posada 2008) according to Corrected Akaikie Information Criterion (AICc). One hundred bootstrap replicates were used. Included in the analysis were representative species found in the Blastn search, plus *G. perzonatum* sequences because of its morphological similarity. Sample nomenclature: species name, isolate number, three letter United Nations country code: AUS = Australia, BRA = Brazil, CHN = China, CMR = Camaroon, ECU = Ecuador and MYS = Malaysia.

Colour illustrations. Ecuador, Yasuni National Park rain forest; basidiocarps, skeletal and generative hyphae, basidiospores. Scale bars = 10 μm.
Blastobotrys meliponae
Blastobotrys meliponae  R.N. Barbosa, Boekhout, G.A. Silva, Souza-Motta & N. Oliveira, sp. nov.

Etymology. me.li.po’nae. N.L. gen. n. meliponae, of the bee genus Melipona.

Classification — Trichonomascaceae, Saccharomycetales, Saccharomycetes.

Hyphae thin, 1–1.5 μm wide, septate, branched, hyaline. Chlamydospores globose or subglobose, terminal or intercalary, up to 5.5 μm diam. Conidiophores erect, sympodially branched, 130–260 μm long or more, 2.0–2.6 μm wide, simple or branched, tapering upwards, producing 1–2 joint conidiogenous cells. Conidiogenous cells are discrete, shortly pedicellate, globose to subglobose, (1.6–)2.5–3(–4) μm, with one seta. The conidiogenous cells separate easily from the conidiophores and are densely covered with conidia (up to 15 conidia, but mostly 6–13). Setae straight, sometimes slightly curved, narrowing towards the apex, 1-septate, not deciduous, 55–124 μm long or more (260 μm after 18 d of growth). Conidia holoblastic, globose, smooth, sessile, 1–1.5 (can be up to 2) μm diam; may form directly on 1–2 μm diam hyphae and below the tip of conidiophores. In yeast-like colonies, growth with budding observed on hyphae. Glucose, galactose and sucrose are fermented, and maltose, raffinose and xylose are not fermented. L-Arabinose, D-xylose, acetate, glucuronate, erythritol, D-galactose, D-glucose, lactose, D-maltose, L-sorbose and L-rhamnose are assimilated. D-glucosamine, glycerol, raffinose, and mellibiose are not assimilated. Nitrate and citrate are not assimilated. Does not hydrolyse urea.

Culture characteristics — Colonies on 5 % malt extract agar (5 % ME) at 25 °C grow slowly, white with irregular margins, delicately downy, cerebriform, opaque, with light brownish reverse; 8 mm after 7 d. Colonies on yeast malt agar (YM) similar to those on 5 % ME but with light yellowish reverse; 11 mm in 7 d. Colonies on restricted growth agar (RG) similar to those on 5 % ME, but differ by plane colonies, and a colourless reverse; 5 mm in 7 d. Colonies at 27 °C, 28 °C, 30 °C and 37 °C were similar to colonies at 25 °C. At 10 °C no growth was observed.

Typus. BRAZIL, Recife, Pernambuco, isolated from honey of the bee Melipona scutellaris collected in Atlantic Forest (S8°7’30” W34°52’30”), metabolically inactive culture, holotype URM 7224, isotype CBS 14100, ITS sequences GenBank KT448719, KT448720, KT448721, LSU sequences GenBank KR779215, KR779216, KR779217, MycoBank MB812601).

Notes — Based on phylogenetic analyses using only sequences of the D1/D2 domains, the three isolates formed a clade with B. proliferans, but the sequences showed only 91 % identity with the LSU sequences of that species in a BLASTn analysis, indicating that these isolates represented a new yeast species of Blastobotrys. Members of Blastobotrys with a high similarity of the LSU rDNA D1/D2 domains to the new species were: B. attinorum (GenBank GU373758; 92 %), B. proliferans (GenBank EF584541; 91 %) and B. nivea (GenBank DQ442690; 90 %). Blastobotrys meliponae differs from B. nivea in having sympodially branched conidiophores, lacking budding cells and chlamydospores, but with lateral conidia forming directly on the hyphae. The species can be distinguished from B. aristata by the size of the conidiogenous cells (3–8 × 4.5–9 μm), conidiophore branching, number and size (100 μm) of setae, absence of lateral conidia formed directly on the hyphae, absence of chlamydospores and growth at 37 °C. Blastobotrys proliferans has a different branching of the conidiophores, conidiogenous cell size (3–4.5 × 4.5–7 μm), setae with a spathulate apex in older cultures and presence of distinct refraction bodies in the conidiogenous cells.

Colour illustrations. Bees and pot honey in the nest of Melipona scutellaris; chlamydospores, hyaline conidia on hyphae and conidiophores on YM agar for 7 d at 28 °C. Scale bars = 10 μm.
Russula intervenosa
Russula intervenosa

S. Paloi, A.K. Dutta & K. Acharya, sp. nov.

Etymology. ‘Intervenosa’ is the Latin transliteration of ‘intervenose’, referring to the pattern of lamellae.

Classification — Russulaceae, Russulales, Agaricomycetes.

Pileus 26–49 mm diam, convex to broadly convex when young, becoming infundibuliform to appenulate with a central depression in age, surface smooth when young, becoming cracked at maturity, semi moist, dark red (10C8) to brownish red (10D8) at center, pastel red (10A5) to dull red (10B4) towards margin, unchanging with NH₄OH and FeSO₄, pale orange (5A3) to light orange (5A4) with KOH, red (9B8) to brownish red (9C8) with sulfovanillin (SV), red (9A7) with gaucalol; margin translucent striate; context very thin (<1 mm), white (1A1), no colour change when exposed, turns whitish yellow (8A2) to pale yellow (8A3) with FeSO₄, reddish brown (9D8) with SV. Lamellae adnexed, 4–5 mm broad, regular, with intervenose to reticulate like appearance, lamelulae none, dull yellow (3B3), edge even, concolorous, light yellow (4A4) to yellowish orange (4A6) with FeSO₄, pale yellow (3A3) with KOH, reddish brown (9D-E8) with SV, light brown (5D4) to yellowish brown (5E4) with 10% phenol. Stipe central, 8–15 × 4–6 mm, tapered toward the base, smooth, semi moist, greyish red (10C5) to brownish red (10D6), white (1A1) towards extreme base, unchanging on brushing, light brown (7D7) to brown (7E7) with 10% phenol and SV, red (9A6) to brownish red (9C7) with gaucalol; context hollow, white (1A1), unchanging after brushing. Odour and taste mild. Spore print cream. Basidiospores (6.5–)7–7.5–8.0(–9) × (6–)6.5–6.7–7.5–7.7 µm; Q = 1.07–1.12–1.19, subglobose, hyaline, ornamentation amyloid, composed of high (0.6–0.9 µm) and low (0.1–0.4 µm) ridges with irregularly interrupted margin that are aligned or connected to give nearly complete or partial reticulum to reticulate-winged fashion; suprahilar plaque amyloid, up to 2 µm long. Basidia (28–30–34–40) × 10.5–12(–14) µm, 4-spored, clavate to subclavate, thin-walled, oil droplets present when viewed with KOH; sterigmata 3.5–4.5 × 1 µm. Subhymenium pseudoparenchymatous. Lamellar trama composed of sphaerocytes and hyphal cells, sphaerocytes measuring c. 22–39 × 18–29 µm. Hypenial cystidia c. (26–)32–39(–43) × (4.5–)5.5–7.5(–9) µm near gill edge, cylindrical with pointed towards apex, filled with cytoplasmic contents; on gill sides c. 29–34(–39) × 10–12.5(–14.5) µm, appendiculate to fusiform, thin-walled, oil droplets present when viewed with KOH. Pileipellis orthochromatic in cresyl blue, sharply delimiting from the underlying sphaerocytes of the context, distinctly divided into a 43–50 µm deep subpellis composed of loosely arranged, less gelatinized, measuring 2.5–4.5 µm diam, hyaline, thin-walled hyphae and less gelatinized, c. 47–64 µm deep suprapellis composed of interwoven, measuring c. 36–64 × 2.5–4 µm, erect to suberect, thin-walled, hyaline hyphae of subulate to pointed hyphal apex and up to five round cells, measuring 39–47 × 2.5–4.5 µm at base; pileocystidia absent. Stipitpellis up to 42–51 µm thick, composed of loosely arranged subulate hyphae with pointed apex, up to 2.5–4.5 µm broad, often branched, hyaline, thin-walled and caulocystidia measuring 26–32 × 5.5–6.5 µm, subcylinrical to subclavate to subulate with pointed to moniliform apex, filled with cytoplasmic contents. Stipe trama composed of sphaerocytes.

Typus. India, West Bengal, Paschim Midnapur, Lodhasuli forest, ectomycorrhizal with Shorea robusta (Dipterocarpaceae), 13 July 2014, S. Paloi (holotype CAL-1272, IT5 sequence GenBank KT524241, LSU sequence GenBank KU528135, MycoBank MB15953).

Notes — The combination of macro- and micromorphological characters undoubtedly place R. intervenosa in the subgenus Amoenula (Sarnari 1998, Das & Sharma 2005). Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS1-5.8S-ITS2 sequence had highest similarity with R. violeipes (GenBank KF361797; Identities 512/548 (93 %), Gaps = 12/548 (2 %)) and R. mariae (GenBank EU189426; Identities 481/529 (91 %), Gaps = 15/529 (2 %)). However, R. violeipes differs from the newly described species by its more variegated pileus colours, much longer stipe (up to 70 mm) and differently sized basidiospores (6–8 × 6.5–9 µm; Quétel 1898). Russula mariae has a more fleshy pileus with wider cap (up to 5 mm), with flushed pink or purplish surface that does not react with SV and slowly turns blue green with guaiia (Peck 1872, Bills & Miller 1984). (Myco-Bank supplementary data.)

Considering the overall size and ornamentation of the basidiospores and nature of pileipellis, our species is related to R. amoenula and R. amoenicolor. However, R. amoenula, the type species of the subgenus, can be distinguished from the present species in having a pileus coloured shades of purple or violet with velvety cuticle, context that turns violet with phenol, much longer and pruinose stipe (up to 50 mm), dichotomous split of lamellae, presence of a sweetish taste and fragrance like fruit (Quétel 1880, Romagnesi 1967, Sarnari 1998). Russula amoenicolor, originally described from Europe, has much larger (up to 80 mm diam) and velvety pileus coloured purplish brown or purple, and much longer stipe (up to 70 mm; Romagnesi 1967). Among the New Zealand taxa, species with similar shape, colouration of pileus with smaller stipe: R. minitata differs by the presence of white coloured lamellae, larger basidiospores (9.5–11.5 × 8–10 µm), absence of caulocystidia and habitat under Nothofagus sp.; R. pudorina has a white coloured spore print, larger basidiospores (8–10.5 × 7–9 µm), bitter taste and habitat under Leptospermum spp. (McNabb 1973). Within the same subgenus Amoenula, previous described species from the moist deciduous to mixed subtropical forests of India include R. mukteshwarica. But, R. mukteshwarica is more robust (6.5–13 cm) and has a purple coloured pileus with light to brilliant or very greenish yellow centre, white coloured spore print and basidiospores are somewhat larger (7.5–9.5 × 7.5–8 µm; Das et al. 2005).
Crinipellis odorata
**Crinipellis odorata** K.P.D. Latha & Manim., *sp. nov.*

**Etymology.** The name refers to the odoriferous basidiomata of this species.

**Classification —** Marasmiaceae, Agaricales, Agaricomycetes.

*Basidiomata* small to medium-sized, marasmoid, often in dense tufts. *Pileus* 6–31 mm diam, truncate conical or conico-convex with a small central depression when very young, becoming campanulate to broadly campanulate, still with a small central depression; surface dark brown (8F4, 8F5/OAC635) or reddish brown (8F7/OAC636) at the centre and on the squamules and brownish orange (6C5/OAC652) or light brown (6D5/OAC659) elsewhere, not hygrophanous, not striate, appressed- to slightly recurved-squamulose all over; margin initially incurved, becoming decurved to almost reflected with age, finely appendiculate, crenate or somewhat wavy. *Lamellae* adnexed, crowded, yellowish white (4A2/OAC815) when very young, becoming greyish yellow (4B4/OAC806), up to 2 mm wide, with lamelleae of 3 lengths; edge crenate, concolorous with the sides. *Stipe* 39–120 × 2–4 mm, central, terete, or slightly compressed, tapering towards the base, hollow, slightly flexuous towards the base, insinutitious; surface concolorous with the pileus, appressed- to slightly recurved-squamulose all over, densely so towards the apex; base deeply rooted. *Rhizomorphs* absent. *Context* up to 2 mm thick, yellowish brown. *Odour* strong, unpleasant. *Taste* not distinctive. *Basidiospores* 5–8 × 5–7 (6.5 ± 0.77 × 5.9 ± 0.61) µm, Q = 0.86–1.3, Qm = 1.11, subglobose to almost globose, smooth, thin-walled, inamyloid. *Basidia* 23–33 × 6–9 µm, sparse clavate, hyaline, thin-walled, 4-spored; sterigmata up to 4 µm long. *Basidioles* 28–48 × 6–12 µm, abundant, fusoid or clavate, thin-walled, hyaline. *Lamella edge sterile with copious cheilocystidia.* *Cheilocystidia* 22–65 × 7–19 µm, versiform; oblong, clavate, cylindrical, cylindrical with a median constriction, flexuous, nodulose-diverticulate, sometimes capitately, thin- to slightly thick-walled, hyaline or pale yellow. *Pleurocystidia* absent. *Lamellar trama* subregular; *hyphae* 3–12 µm wide, thin-walled, hyaline or pale yellow, inamyloid. *Pileus trama* subregular to interwoven; *hyphae* 6–15 µm wide, thick-walled (up to 2 µm thick), with a pale yellow wall pigment, dextrinoid. *Pileipellis* composed of tufts of fasciculate hairs arising from a hypotrichium; hypotrichial *hyphae* 8–18 µm wide, thick-walled (up to 1.5 µm thick), with pale yellow wall and dense, spiral encrusting pigments; pileal hairs 500–1200 × 5–7.5 µm or more, unbranched, cylindrical or sinusoidal-cylindrical with an obtuse apex, thick-walled (up to 2 µm thick), with a yellowish brown wall pigment, dextrinoid, yellowish brown in KOH. *Stipitipellis* composed of clusters of hairs arising from a hypotrichium with flaing-out cystidiod terminal cells; hypotrichial *hyphae* 3–7 µm wide, thick-walled (up to 1 µm thick), with pale yellow wall and minutely, encrusting pigments; stipitipellis *hyphae* 47.5–452.5 × 7.5–12.5 µm, sinuous-cylindrical, thick-walled (up to 3 µm thick), with a pale brown or yellowish brown wall pigment, dextrinoid, pale yellowish brown in KOH; terminal cells cystidiod 32–95 × 10–16 µm, clavate, cylindrical-clavate or irregular in outline, dextrinoid, thick-walled (up to 2 µm thick), with a pale yellowish brown wall pigment. *Caulocystidia* absent. *Clamp-connections* observed on all hyphae except at the base of basidium.

**Habit, Habitat & Distribution —** In dense caespitose clusters or in small groups, attached to the bark of a living Mytragyna parviflora tree as well as deeply rooted in the nearby soil. Known only from the type locality in Kerala State, India.

**Typus. India,** Kerala State, Wayanad District, Tholpetty, Wayanad Wildlife Sanctuary, 6 July 2013, K.P. Deepna Latha (holotype CAL 1240, ITS sequence GenBank KT952521, MycoBank MB814159).

Notes — Characters such as a brown pileus not reacting with KOH, a long, central stipe, long, thick-walled, dextrinoid hairs on both the pileipellis and the stipitipellis and subglobose basidiospores indicate that the present species belongs to **Crinipellis** sect. **Crinipellis** subsect. Macrosphaerigerae (Singer 1976, 1986). The key to the species of **Crinipellis** by Singer (1953) leads **C. odorata** into **C. macrosphaerigera**, a Brazilian species, as both species have somewhat similar pileus surfaces, adnexed lamellae, subglobose basidiospores, versiform cheilocystidia and association with living trees. However, **C. macrosphaerigera** has smaller basidiomata with a straw-coloured pileus and stipe, distant lamellae, larger basidiospores (12.5–14 × 9.5–11.5 µm), a heterogeneous lamella edge and an indistinct odour. **Crinipellis podocarpis**, a species originally described from Argentina (Singer 1976) and subsequently from Mexico (Bandala et al. 2012) and belonging to sect. **Crinipellis** of subsect. Stipitariniae, seems to be somewhat close to **C. odorata** in having basidiospores of almost similar size and shape. However, **C. podocarpis** differs in all other macro- and microscopic characters. Comparison of the ITS sequence (CAL 1240: 754 bp) generated from **C. odorata** with the nucleotide sequences of taxa available in GenBank suggest that **C. odorata** has a distinct ITS sequence. In a megablast search of the GenBank database using ITS sequence of the species, the closest hit was **C. roccosa** (GenBank KJ698642; Identities = 685/762 (90 %), Gaps = 32/762 (4 %)) followed by **C. zonata** (GenBank FJ167659; Identities = 662/741 (89 %), Gaps = 35/741 (4 %)). **Crinipellis floccosa**, a species recently described from China (Xia et al. 2015), shares a few features such as a reddish brown, squamulose pileus, somewhat similarly-coloured lamellae, similar-sized basidiospores ((5.5–)6–8 × 4–4.5(–5)), somewhat similar-sized cheilocystidia, the absence of pleurocystidia and a similar pileipellis structure with **C. odorata**. **Crinipellis floccosa** is distinguished, however, by its smaller basidiomata, free lamellae with a denticulate margin, a differently-coloured, equal, tomentose-pilose stipe, elliptoid to broadly elliptoid or somewhat amygdaliform basidiospores, scattered cheilocystidia, the hairs of both the pileus and stipe exhibit greenish yellow in KOH and a non-distinctive odour. **Crinipellis zonata**, a species reported from North America (Redhead 1989), Europe ( Antonin & Noordeloos 1997, 2010) and the Republic of Korea (Antonin et al. 2009), has similar looking basidiomata with almost similar colour, crowded lamellae, somewhat similar morphology of cheilocystidia, lamellae devoid of pleurocystidia, similar pileipellis and stipitipellis structure and clamped hyphae. However, **C. zonata** has smaller basidiomata, a tomentose pileus with an inflexed margin, differently attached, pale cream lamellae, a hairy stipe, much narrower (3–4 µm) and cylindrical-ellipsoid basidiospores, smaller pileipellis hairs and an indistinct odour. (MycoBank supplemental data.)
Corynascus citrinus
Corynascus citrinus Giraldo & Crous, sp. nov.

Etymology. From Latin citrinus, citrine or lemon-yellow, referring to the yellow pigment produced in vitro.

Classification — Chaetomiaceae, Sordariales, Sordariomycetes.

Ascomata cleistothecial, submerged or embedded in the aerial mycelium, spherical, brown, 44–83 μm diam, surface of textura epidermoidea, striated. Paraphyses absent. Asci evanescent, subglobose, unitunicate, thin-walled. Ascospores unicellular, broadly fusiform, thick- and smooth-walled, with germ pores at both ends, 9–12 × 6–8 μm, hyaline becoming brown when mature. Conidiophores absent or poorly differentiated. Conidia growing directly on undifferentiated hyphae, lateral, sessile, occasionally on short stalk, globose, 5–7 μm diam, hyaline, thick-walled, tuberculate.

Culture characteristics — Colonies on PDA reaching 41–42 mm diam after 21 d at 25 °C, surface straw at centre and fuscous black at periphery, reverse fuscous black (Rayner 1970), flat, floccose. On OA and MEA attaining 54–55 and 55–56 mm diam, respectively after 21 d at 25 °C, surface straw, flat, granulose. Diffusible pure yellow pigment in all media tested.

Notes — The genus Corynascus (Chaetomiaceae, Sordariales), previously considered as synonym of Myceliophthora (Van den Brink et al. 2012), was recently resurrected by Marin-Felix et al. (2015). Currently, Corynascus contains five species apart from C. citrinus, which are commonly isolated from soil and characterised by their mesophilic habitat, ascomata cleistothecial of textura epidermoidea, ascospores with a germ pore at each end, and a myceliophthora-like asexual morph (Guarro et al. 2012). Corynascus citrinus is phylogenetically closely related to C. sexualis and C. fumimontanus but can be morphologically distinguished from the former species by the presence of the asexual morph in culture, and from the latter species by its smaller ascomata (50–110 μm), ascospores (13–17 × 7–9 μm) and conidia (6–10 μm) (Marin-Felix et al. 2015).

Maximum likelihood (ML) tree based on partial sequences of ITS, tef1 and rpb2 regions from reference and type strains of Corynascus species. The alignment included 1604 bp and was generated with ClustalW under MEGA v. 6.06 (Tamura et al. 2013). Tamura-Nei with Gamma distribution was used as the best nucleotide substitution model. Myceliophthora lutea (Chaetomiaceae, Sordariales) was used as outgroup taxon. The new species is highlighted in bold face. Bootstrap support values above 70 % are shown at the nodes. Ex-type strain. Accession numbers of ITS, tef1 and rpb2 sequences retrieved from GenBank are in parentheses.

Colour illustrations. Thailand, Wang Takhrai waterfall, Mueang Nakorn Nayok district, Nakorn Nayok province (photo: A. Giraldo); colony on PDA after 21 d at 25 °C, ascoma with asci, detail of the peridium wall, immature and mature ascospores, conidia. Scale bars = 10 μm.

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Brunneocarpos banksiae
Brunneocarpos Giraldo & Crous, gen. nov.

Etymology: Brunneus (Latin) = brown, and carpos (Greek) = fruit.

Classification — Mycocaliciaceae, Mycocaliciales, Eurotiomycetes.

Ascomata apothecial, stipitate, growing intermingled among the floral bracts on Banksia cones. Stipe straight or flexuous, mostly branched. Capitulum brown, globose to subglobose. Paraphyses not observed. Asci 8-spored, cylindrical, uniloculate. Ascospores uniseriate, ellipsoidal to slightly fusiform, clavate, 1-celled, brown, smooth-walled. Mycelium consisting of septate, hyaline, smooth- and thin-walled hyphae. Asexual morph producing dictyochlamydospores in chains, subhyaline, thick-walled, lateral or terminal.

Type species. Brunneocarpos banksiae Giraldo & Crous. MycoBank MB816972.

Brunneocarpos banksiae Giraldo & Crous, sp. nov.

Etymology. Name reflects the host genus Banksia, from which the species was isolated.

Ascomata apothecial, stipitate, growing intermingled among the floral bracts on Banksia attenuata cones. Stipe dark brown, shiny, flexuous, mostly branched two or three times at the apex, 1–2 mm long, 50–85 µm wide. Capitulum dark brown, globose to subglobose with a funnel-shaped base, covered by hyaline mycelium when older, 150–285 × 125–206 µm. Paraphyses not observed. Asci 8-spored, cylindrical, uniloculate, 30–34 × 4–5 µm. Ascospores uniseriate, ellipsoidal to slightly fusiform, clavate, 1-celled, brown, thick- and smooth-walled, 4.5–7 × 2–3.5 µm. Mycelium consisting of septate, hyaline, smooth- and thin-walled hyphae, 1.5–2 µm diam. Conidiophores absent or poorly differentiated. Dictyochlamydospores in chains, sessile or with short subconical stalk, subhyaline to pale brown, thick- and smooth-walled, lateral or terminal, 26–60 µm long.

Culture characteristics — Colonies on MEA reaching 3–3.3 cm diam after 2 mo at 25 °C, vinaceous buff (Rayner 1970), depressed at centre, floccose.

Typus. AUSTRALIA, Western Australia, S34°22′19.4″ E118°1′33.6″, on Banksia attenuata (Proteaceae), 23 Sept. 2015, P.W. Crous (holotype CBS H-22633, cultures ex-type CPC 29841 = CBS 141465, ITS sequence GenBank KX228352.1, MycoBank MB816973); CPC 29070, CPC 29072, CPC 29435.

Notes — According to LSU and ITS analyses Brunneocarpos banksiae belongs to Mycocaliciaceae (Mycocaliciales) where four genera are currently accepted; Chaenothecopsis, Phaeocalicum, Mycocalicia and Stenocybe. All produce apothecoid ascomata, usually with a tiny stalk and brown ascospores (Tuovila et al. 2011). These genera harbour resi- niculous species, growing directly on exudate and/or on exu- date-impregnated wood of different hosts, including Acer (Sapin- daceae), Mangifera (Anacardiaceae), Khaya (Meliaceae), Abies (Pinaceae), Picea, Tsuga and Tilia (Malvaceae) (Rikkinen 2003, Tuovila et al. 2011) and known species are lignicolous, algicoli- ous or lichenicolous (Tuovila et al. 2014). So far no species from these genera have been reported growing on Banksia, Species growing in axenic culture produce a phialophora-like (Chaenothecopsis sheffleriae) or coelomycetous asexual morph (Tibell 1991, Tibell & Vinuesa 2005), and in some cases, a hyphomycetous asexual morph with ramoconidia in acropetal chains (C. haematopus) (Tibell & Constantinescu 1991). This morphological character differs from the new taxon proposed here, which produces a chlamydospore-like asexual morph in culture.
Cercophora vinosa A.N. Mill. & J. Fourn., sp. nov.

Etymology. The specific epithet refers to the purple colour in the outermost layer of the ascomatal wall.

Classification — Lasiosphaeriaceae, Sordariales, Sordariomycetes.

Ascomata subglobose to broadly obpyriform with a stout conical to hemispherical neck, 420–670 µm diam × 420–650 µm high, erumpent through a thick, feltly yellowish grey subiculum spreading widely over the substrate, gregarious to loosely clustered, more rarely in contact; underlying wood discoulored greyish brown or unaltered, not stained purple; subiculum encrusted with sand particles, composed of pale brown, septate hyphae 1.5–3.5 µm wide, thin- to moderately thick-walled; neck papillate, broadly conical to rounded, sometimes undifferentiated, 80–170 µm high, ostiolate, black, roughened or obscurely sulcate. Ascomatal wall 34–56 µm thick on sides and at base in longitudinal section, slightly thicker at apex, roughened, dark purple gradually turning blackish, pseudoparenchymatous, leathery, 3-layered: outermost layer 10–15 µm thick, present on upper half of ascomata, fugacious, composed of several rows of thin-walled, hyaline, angular cells containing a purple substance that slightly fadest in 10% KOH and dissolves in chloral-lactophenol; middle layer 20–30 µm thick, composed of independent clusters of subcarbonaceous opaque cells, breaking into small angular plaques upon pressure but lacking a network of hyphae connecting the plaques as in cephaleothecoid walls; inner layer 14–22 µm thick, composed of flattened, thin-walled subhyaline cells. Ascomatal apex periphysate. Centrum hyaline to yellowish. Paraphyses filiform, 4.5–8 µm wide at base and occasionally slightly moniliform, tapering to 2–2.5 µm wide above asci, hyaline, thin-walled, abundant, septate, unbranched, persistent. Asci unitunicate, cylindrical, 320–380 × 19–23 µm, spore-bearing part fusoid-ventricose, apex rounded, long-stipitate, stipe 100–160 µm long, often slightly sinuous, with eight bi- to triseriate ascospores, apical ring double, refractive, 2.7–3 µm wide x 1–1.2 µm high, inamyloid, staining in blue Waterman ink, subapical globule absent. Ascospores cylindric, (54.5–)60.5–73.5(–79.5) × (3–)4–6(–7) µm (66.7 ± 5 µm), straight to slightly sigmoid, geniculate in lower quarter, hyaline, aseptate, densely guttulate; bipolar appendages (27–)35–56 µm long, lath-like, 3–4 µm wide at base, centrally attached on ascospores ends, readily staining in blue Waterman ink and in aqueous nigrosin, sometimes granular at base, persistent; ascospore becoming differentiated into an apical swollen head and a basal tail while inside the ascus; head ellipsoid, 15.5–19 × 8–9 µm, usually 1-septate, remaining hyaline, rarely pigmented; tail 41–50 × 4–5 µm, obscurely 2–4–septate, hyaline, the lower end swelling upon germination; germinating from upper and lower ends, more rarely laterally before being released. Asexual morph: Hyphae largely undifferentiated, 1.5–5 µm wide, thin-walled, hyaline to pale brown. Conidiogenous cells phialidic, commonly produced from pale brown hyphae as single terminal or several lateral phialides, delimited by a basal septum, monophialidic or polyphialidic, cylindrical to obpyriform, 9–18 × 2.5–4 µm at widest part, mostly pale brown, constricted below the colarette, 1–1.5 µm just below the colarette; colarette short, slightly flaring, inconspicuous, same colour as phialide. Conidia subglobose to pyriform, truncate at base, 2.5–4.5 × 1.5–2.5 µm (3.3 × 2.2 µm), hyaline.

Culture characteristics — Colonies (of holotype) slow-growing on all media, covering the PDA plates in 8 wk, 25–30 mm diam after 8 wk on the WA and CMA plates, downy to silky on WA and CMA, subfleeting on PDA, hyaline on WA, greyish yellow (4B3) on CMA, brown (5F8) and becoming greyish red (7B5) at plug on PDA; margin even or wavy, appressed, hyaline on WA and CMA, becoming olive brown (4F8) on PDA; reverse same as the mat.

Typus. France. Ariège, Castelnau-Durban, Artillac stream, down-stream from the marble quarry, c. 410 m elev., on decorticated branch of Salix sp., 8 cm diam, partly submerged, 22 July 2014, J. Fournier, JF 14067 (holotype ILS 79802, cultures ex-type ANM Acc#840-1, -2, -3, -4, -5, deposited in CBS, ITS-LSU sequence GenBank KX171944, beta-tubulin sequence GenBank KX171942, MycoBank MB816935). Other material examined. France; Ariège, Montsegur, Le Lasset stream flowing at the village, 880–890 m elev., on submerged decorticated wood of Populus sp.; soc. Amniculicola lignicola, 16 Nov. 2014, J. Fournier (JF 14156); Illier, Laramade, Vicdessos stream, 630 m elev., on submerged wood of Fraxinus excelsior; 25 Nov. 2014, J. Fournier (JF 14163); Rimont, Paletés, Peyrau brook, c. 400 m elev., on submerged wood of Alnus glutinosa, 4 Dec. 2014, J. Fournier (JF 14170).

Notes — Cercophora vinosa is distinguished by its ascoma that possess a distinct purplish colour in the outermost wall layer, asci with a double ring but lack a subapical globule, long ascospores with lath-like appendages and aquatic habitat. Only two other species of Cercophora are known to have violet-coloured ascomata, C. septentrionalis and C. caerulea. Although these species also possess asci with a double ring but no subapical globule and ascospores with long, lath-like appendages, both have shorter ascospores (38–43 µm and 43–48 µm, respectively) and occur on dung. The ascomata in C. septentrionalis are covered by brown, flexuous hairs, whereas a distinct dark purple to blackish blue subiculum surrounds the ascomata in C. caerulea (Lundqvist 1972). Cercophora vinosa occurs in a well-supported clade with C. solaris in which it shares only a cephalothecoid-like ascomatal wall and lack of a subapical globule (Catania et al. 2011). For phylogenetic tree, see MycoBank.
Uwemyces elaeidis
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**Uwemyces** Hern.-Restr., G.A. Sarria & Crous, *gen. nov.*

*Etymology.* Named for Prof. Uwe Braun, who greatly contributed to our knowledge of dematiaceous hyphomycetous fungi.

*Classification.* — *Mycosphaerellaceae*, *Capnodiales*, *Dothideomycetes*.

*Mycelium* immersed and superficial, hyphae branched, septate, hyaline and brown, smooth-walled. *Conidiophores* fasciculate, simple, dark brown at the base and subhyaline at the apex. *Conidiogenous cells* cylindrical, sympodial, polytretic, with dark scars, terminal and intercalary, brown. *Conidia* straight or curved, cylindrical to obclavate, pale brown to brown, apex subhyaline, verrucose-walled, with a thick, dark brown, truncate scar at the base, septiculate. *Sexual morph* unknown.

Notes — *Uwemyces elaeidis* is related to members of *Mycosphaerellaceae*, and represents a different genus in this family. This species has wide distribution and seems to be restricted to *Elaeis guineensis*, *Arecaceae* (Braun et al. 2014). Unfortunately, it was not possible to propose a formal neotypification, since the geographical origin of the specimen examined was not the same as described in the protologue (Democratic Republic of the Congo, Kodoro).

**Uwemyces elaeidis** (Steyaert) Hern.-Restr., G.A. Sarria & Crous, *comb. nov.*

*Basionym.* *Cercospora elaeidis* Steyaert, Bull. Soc. Roy. Bot. Belgique 80: 35. 1948; as ‘elaeidis’.

≡ *Pseudospiropes elaeidis* (Steyaert) Deighton, Trans. Brit. Mycol. Soc. 85: 4. 1985.

*Mycelium* immersed and superficial, hyphae branched, septate, hyaline and brown, smooth-walled. *Conidiophores* fasciculate, simple, dark brown at the base and subhyaline at the apex, 96.5–188 × 6–9 µm. *Conidiogenous cells* cylindrical, sympodial, with dark brown scars, terminal and intercalary, brown, 28–70 × 5–9 µm. *Conidia* cylindrical to obclavate, straight or curved, pale brown to brown, apex subhyaline, 2–3.5 µm wide, wall verrucose, 82–133 × 6–8.5 µm, 4–8-septate, with a thick, dark brown, truncate scar at the base, 2–3.5 µm wide. *Sexual morph* unknown.

Notes — The generic affinity of this species has been recently discussed by Braun et al. (2014). It was excluded from *Cercospora* and it is not congeneric with *Pseudospiropes* where it was tentatively placed (Steyaert 1948, Deighton 1985). Our molecular result suggests that *Uwemyces elaeidis* is related to members of *Mycosphaerellaceae*, and represents a different genus in this family. This species has wide distribution and seems to be restricted to *Elaeis guineensis*, *Arecaceae* (Braun et al. 2014). Unfortunately, it was not possible to propose a formal neotypification, since the geographical origin of the specimen examined was not the same as described in the protologue (Democratic Republic of the Congo, Kodoro).

### ITS

Based on a megablast search of NCBI’s GenBank database, the closest hits using the ITS sequences are *Pseudocercospora cladistis* (GenBank AB694922; Identities = 463/508 (91 %), Gaps = 22/508 (4 %), GenBank AB694923; Identities = 462/507 (91 %), Gaps = 20/507 (3 %). GenBank AB694921; Identities = 462/507 (91 %), Gaps = 20/507 (3 %)), *Cercospora dolichandreae* (GenBank KJ869140; Identities = 496/546 (91 %), Gaps = 12/546 (2 %)) and *Pseudocercospora ocimicola* (GenBank GU214678; Identities = 497/548 (91 %), Gaps = 10/548 (1 %)).

### LSU

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the LSU sequences are *Mycosphaerella swartii* (GenBank DQ923536; Identities = 828/860 (96 %), Gaps = 8/860 (0 %)), *Mycosphaerella walkeri* (GenBank DQ267574; Identities = 828/860 (96 %), Gaps = 8/860 (0 %)) and *Aceruloseptoria ziziphicola* (GenBank KJ869221; Identities = 796/828 (96 %), Gaps = 8/828 (0 %)).

### rpb2

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the rpb2 sequences are *Pseudocercospora norchiensis* (GenBank JQ739865; Identities = 192/229 (84 %), Gaps = 4/229 (1 %), GenBank KF902320; Identities = 200/239 (84 %), Gaps = 4/239 (1 %), GenBank JX902017; Identities = 200/239 (84 %), Gaps = 4/239 (1 %)) and *Pseudocercospora atromarginalis* (GenBank JX902006; Identities = 205/245 (84 %), Gaps = 4/245 (1 %)).
